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SUPPLEMENTARY TEXT

1. Additional notes on genome sequencing and assembly

DM Illumina library construction and sequencing:

Libraries with an insert size of 200 and 500 bp were prepared following the manufacturer's instructions (Illumina, San Diego, CA). For construction of 2, 5, and 10 kb insert-size libraries, several steps of DNA circularization, digestion of linear DNA, fragmentation of circularized DNA, and purification of biotinylated DNA were performed before adapter ligation. After library preparation and quality control of DNA samples, template DNA fragments were hybridized to the surface of flow cells on an Illumina Genome Analyzer II sequencer (GA2), amplified to form clusters, and sequenced following the standard Illumina protocol.

DM 454 pyrosequencing library construction and whole genome shotgun sequencing:

The DM DNA shotgun and paired-end (~8 and ~20 kb span) tag libraries were prepared using the GS FLX Titanium Library Preparation kit and protocols as recommended by the manufacturer (Roche Applied Science, Mannheim, Germany). The DM DNA was fragmented by hydrodynamic shearing to generate 8 and 20 kb span paired-end tag libraries by following the manufacter's procedures (Roche Applied Science, Mannheim, Germany). Quantitated DNA fragments, flanked with proper amplification and sequencing adaptors, from the single-stranded DNA shotgun and paired-end libraries were immobilized onto microspheres (beads) and the entire bead-bound library was then emulsified with the amplification reagents (GS FLX Titanium LV emPCR kit). After the emPCR step, the DNA-carrying beads were cleaned and enriched before loading into the wells of a PicoTiterPlate device (GS FLX Titanium PicoTiterPlate Kit 70 × 75) so that the wells contain no more than a single DNA bead. The loaded PTP device was then inserted into the Genome Sequencer FLX Instrument, and sequencing reagents were sequentially flowed over the plate. The sequencing was done using the GS FLX Titanium Sequencing Kit and the Genome Sequencer FLX Instrument strictly following the recommendations of the manufacturer (Roche Applied Science, Mannheim, Germany). The raw output comprising a set of digital images (PIF files) was processed to obtain the sequence of the DNA library fragments/reads and then subjected to further downstream analysis.

DM BAC and fosmid library construction and end sequencing:

A BAC library (LuSpBAC, 100,224 clones, average insert size > 100 kb) was constructed in the pSMART-BAC vector from sheared DM nuclear DNA (Lucigen, Middleton, WI). Three separate fosmid libraries (POTATO-F-01-40KB, POTATO-F-02-40KB, POTATO-F-03-40KB) were constructed from sheared DM nuclear DNA in the pCC1FOS™ Vector (Epicentre, Madison, WI). Templates for Sanger end sequencing were prepared using a high throughput alkaline lysis method, sequenced on ABI 3730xl sequencers using standard high throughput sequencing methods. Sequences were processed with Paracel Trace Tuner (http://sourceforge.net/projects/tracetuner), trimmed to remove vector, low-quality, and *E. coli* sequences using Lucy[1].

RH BAC-by-BAC sequencing:

The majority of the BACs were assigned to the corresponding chromosomal location on the basis of Amplified Fragment Length Polymorphism markers from the ultra-high density genetic map, with additional anchor points coming from simple sequence repeat (SSR) mapping, fluorescent *in situ* hybridizations (FISH), or tomato sequences[2,3].

Consensus base calling errors in the BAC sequences were corrected using custom Python and C scripts using a similar approach described previously[4]. Briefly, 31-mers were extracted from the RH whole-genome Illumina GA2 paired-end data and 31-mers with a frequency lower than three were discarded. These 31-mers were subsequently aligned to the BAC sequences, after which erroneous base-calls in the BAC sequences were detected as positions that were covered by less than ten distinct, overlapping 31-mers. Errors were corrected by changing the nucleotide at that position through substitution, insertion or deletion, such that valid 31-mer coverage was maximized. In total, 17,114 base-calling errors were repaired, corresponding to one corrected error every 12 kb (Supplementary Table 30). Approximately 45% of these involved deletions at contig edges, which is likely the result of incorrect base calls due to low sequence coverage in these regions.

Additional notes on the DM genome assembly:

The de Bruijn graph method was used to represent all possible sequences assembled by Illumina reads, with a K-mer as a node and the K-1 bases overlap between two K-mers as an edge. To reduce sequencing errors and eliminate branches, tips, and low coverage, K-mers in the graph were excluded. The de Bruijn graph was then converted to a contiging graph by turning a series of linearly connected K-mers to a pre-contig node. Bubbles detected using Dijkstra's algorithm were then merged into a single path given that sequences of branches were sufficiently similar. Following this approach, repeat regions were assembled into consensus sequences.

Paired reads were further used to link contigs to a scaffolding graph. Edges in this graph were connections between contigs and the branch lengths indicated the gap sizes estimated from the insert size of paired-end reads. Subsequently, we used sub-graph linearization to turn interleaving contigs into a linear structure and the repeat masking method to mask the complicated connections of repeat contigs. By this method, contigs in any "non-linear sub-graph" were assumed to be compatible. Paired-end information was then used step by step with increasing insert sizes of 200 and 500 bp, and 2, 5 and 10 kb and the initial Illumina contigs and scaffolds were constructed. To fill gaps inside scaffolds, the majority of which were composed of repeats masked during the scaffold construction, we used the paired-end information to retrieve read pairs that had one read well-aligned on the contigs and another read located in the gap region, and then conducted a local assembly for the collected reads.

The following terms are used to describe the WGS assembly of DM. A contig is a contiguous genomic sequence in which the order of bases is known to a high confidence level and therefore will not contain Ns. A scaffold is a portion of the genome sequence reconstructed from end-sequenced whole genome shotgun clones or fragments and are composed of contigs with associated gaps. A superscaffold is constructed from two or more scaffolds that are connected using 100 'Ns'. Joining of scaffolds into superscaffolds is supported by BAC and/or fosmid pair end sequences. The nomenclature for scaffolds and superscaffolds is PGSC0003DMS######### and PGSC0003DMB#########, in which PGSC is the short name of potato genome sequencing consortium, 3 represents the third version of the genome assembly, DM is the genotype that was sequenced, and S and B represent scaffolds and superscaffolds, respectively. "#########' is the unique identifier for the scaffold or superscaffold. PGSC0003DMC######### is the identifier for a contig.

2. Additional genome assembly quality assessments

DM fosmid and BAC end sequence comparisons:

Paired-end sequences of BACs (DM and RH) and DM fosmids were used to assess the quality of the v3.0 assembly. End sequences mapping on the scaffolds and super-scaffolds with incorrect orientation (plus-plus and minus-minus) or direction (ends looking outwards rather than inwards) were considered an indicator of potential mis-assembly (Supplementary Table 3). The overall estimated mis-assemblies are less than 0.12% for scaffolds and 0.23% for super-scaffolds using 60 and 300 kb maximal insert sizes for the fosmid and BACs, respectively. This is expected, since generation of both scaffolds and superscaffolds is an error prone process. The data actually indicate that each of the two processes has a very low error rate (below 0.15%). RH BACs gave a significantly higher estimation of mis-assembly (0.24% and 0.37% for scaffolds and superscaffolds, respectively) when mapped on the DM assembly, most likely attributable to rearrangements between the RH and DM genomes.

DM BAC vs WGS comparisons:

To evaluate the quality of the assembled genome, DM BACs from euchromatic regions as well as randomly selected regions were sequenced using Sanger shotgun sequencing methods[5]. Five DM BACs from chromosome 3 and four DM BACs from chromosome 4 were identified by BLAST-based comparison of the entire DM BAC-end-sequence database against finished tomato BAC sequences (for chromosome 4-derived BACs) or DM scaffolds previously identified as being derived from chromosome 3 (by BLAST-based comparisons with chromosome 3-specific BACs from RH089-039-16). Two further BACs were chosen at random from the DM BAC library to yield a total of 11 BACs that were sequenced to a minimum six-fold coverage using standard Sanger methods. Subclone libraries with insert sizes of 2-3 kb were used and both ends of subclones were sequenced. BACs were assembled to a minimum standard of HTGS Phase II using standard assembly methods. A minimum phred threshold score of 20 was used for inclusion of sequences in the primary assembly. The eleven BACs were submitted to Genbank/EMBL nucleotide sequence databases under the accession numbers: AC243865 – AC243869, FR823285 – FR823289, and FR823512.

Graphical alignments between sequenced BACs and their equivalent scaffold regions (including inserted N-gaps) were prepared in the GenomeComp program[6]. To highlight small sequence differences not visible on the BLAST-based comparison, BAC and scaffold sequences were aligned using the ClustalW2 and FSA programs[7,8] and the positions of all sequence differences rendered graphically using a PERL script. These outputs were manually merged with the GenomeComp output to produce composite figures (Supplementary Fig. 2a). Coverage plots for the DM scaffolds were created from the alignment of Illumina read pairs from the DM 5 kb insert library to the DM scaffold sequences using Bowtie[9]. Based on all observed insert sizes, an upper and lower boundary for the library insert size was determined. With these boundaries it was possible to assess if each read pair aligns at the expected distance, within the boundaries. The accurately aligning read-pairs were assembled into a pseudo-coverage plot (green, Supplementary Fig. 2b). All read-pairs aligning at a greater distance than the expected range were assembled into the red pseudo coverage plot.

Concatenated Phase 2 BAC contig sequences and the equivalent scaffold sequences were compressed by removing all gaps and unresolved ('N') nucleotides. Compressed BAC and scaffold sequences were aligned using the ClustalW2 program. Alignment lengths and sequence differences were calculated by the *infoalign* and and *diffseq* programs of the EMBOSS software suite with the *wordsize=6* and *globaldifferences=N* parameters. Matching regions of the sequence alignments greater than the word-size were considered to calculate values for single nucleotide differences, mismatches and In/Dels presented in Supplementary Table 2 (the value for the latter was adjusted to remove differences associated with artificial contig joins in Phase 2 BACs).

Nine of the BACs were aligned to seven individual superscaffolds and one BAC to two (contiguous) superscaffolds (Supplementary Fig. 2a). In a total alignment length of 1054916 bp, 1031292 bp of superscaffold sequence and 1010040bp of BAC sequence was represented. Alignments showed length differences for equivalent BAC/scaffold regions in all cases. In three cases, the differences were relatively minor (BAC sequences were between 23 and 623 nucleotides longer). In the remaining cases the scaffold exceeded the equivalent BAC region. The majority of the differences (which were under 7 kb) were attributable to the overestimation of gaps inserted into the superscaffold sequences (represented by runs of ‘N’s in the sequence) during the assembly of the NGS reads. This was supported by mapping read-pairs from the Illumina 5 kb paired-end library back to the DM scaffold sequence (Supplementary Fig. 2b). In a single instance, the superscaffold sequence exceeded the equivalent BAC sequence by 30kb. Contrary to what was observed in all of the other comparisons, almost all of the length difference in this comparison was represented by superscaffold sequence that appeared in regions between the contig breaks in the Phase 2 BAC, implying that the BAC sequence was incomplete in this case.

Taking these factors into account, the comparisons suggest relatively few gross misassembly events in the superscaffolds. One exception was the comparison involving BAC FR823287, where a stretch of misplaced sequence prevented the joining of the two contiguous superscaffolds to which the BAC spans.

At a local alignment level, only relatively minor differences were apparent between the BAC and scaffold sequences (Supplementary Table 2). These differences comprised largely SNP and small In/Del differences, of which 428 and 222, respectively, were observed in a total sequence alignment length of 1,054,916 bp. Other minor sequence differences such as longer mismatches and differences in the length of mononucleotide repeats were also observed at a very low rate between the sequences (summarised in Supplementary Table 2). Since the DM clone is homozygous, all of the differences are attributable to sequencing or minor assembly errors in one or both sets of sequences. The eleventh DM BAC (which was chosen at random from the DM BAC library) did not exhibit extensive synteny to any single superscaffold, suggesting it represents a region not covered by the Illumina assembly.

3. Genome comparison of DM and RH

Comparison of DM and RH assemblies:

Superscaffolds of DM and RH were aligned using megablast with a minimum sequence identity of 90% to identify potential collinear segments. Repetitive matches between a single RH superscaffold and multiple DM superscaffolds, and matches spanning less than 20 kb, were discarded using custom Python scripts. The resulting groups of potentially collinear superscaffolds were subjected to a more accurate alignment using Blastz[10] with the "--gfextend --chain --gapped" parameters. These alignments were filtered for a minimum match length of 1000 bp and a minimum sequence identity of 90%, and repetitive matches were discarded using custom Python scripts. Sequence polymorphism and InDel frequencies were derived from the lastz alignments using custom python scripts. To avoid overestimation of small InDels due to sequencing errors, InDels of 1 and 2 bp were not considered if the distance between them was less than 30 bp or the identity of 10 bp of flanking sequence on each side was smaller than 95%. The same methodology was applied to investigate the sequence diversity between the corresponding linkage-specific superscaffolds of RH.

K-mer analysis of the genome sequence of RH and DM:

A set of scripts was used to produce and process K-mer data:

− By sliding a K base-pair long window over each read, extracting basic K-mers. K-mers without degenerate nucleotides (e.g., Ns) are retained, normalized (reverse-complementing K-mers with a G or T in the middle position) and counted, producing a K-mer-count table.

− K-mer-count table subsets are produced by applying minimum and maximum count thresholds to a K-mer count table.

− K-mer-count table intersections are produced by comparing two K-mer-count tables, producing four separate K-mer-count tables: 1) with K-mers unique to the first input file, 2) with K-mers unique to the second input file, 3) with common K-mers and corresponding counts from the first input file, and 4) with common K-mers and corresponding counts from the second input file.

−K-mer-count tables are converted into K-mer volume histograms (as shown in Fig. 3b, Supplementary Fig. 9) by computing, for each K-mer frequency, the volume of K-mers in the dataset occurring at that frequency.

Choice of a useful value for K depends on sequencing error rates and uniqueness of K-mers in the underlying genome. In our case we chose K=31. K-mer-count tables denoted 'DM_all' and

'RH_all' (Fig. 3b) were produced from the complete DM Illumina dataset and the complete RH Illumina paired-end dataset respectively. Sub-selecting (thresholds 10 and infinite) K-mer-counts from 'DM_all' yielded table 'DM_proper'. The second output file of the intersection of 'DM_proper' with 'RH_all' yields 'RH_specific' (Supplementary Fig. 12). The complete set of Illumina RNA-sequences yielded K-mer-count table 'RNA_all', which, intersected with 'RH_all', yields 'RH_WGS_counts_of_exome' (fourth output file, Supplementary Table 12).

Because the large volume of erroneous K-mers and putative multi-copy and repetitive K-mers would adversely affect a straightforward automatic fit, overlapping normal distributions were simply fitted manually, with an emphasis on the central part of the bi-modal distribution. The homozygous peak is expected to be located at twice the frequency of the heterozygous peak, with an estimated peak-width of twice the width of the heterozygous peak, leaving 4 parameters to be estimated: one peak position and standard deviation and two peak heights. The volume under the fitted homozygous peak divided by the combined volume under hetero- and homozygous fitted peaks yields a K-mer homozygosity estimate, which can be converted into a nucleotide identity estimate by taking the K-th power root (assuming random distribution of differences).

4. Genome annotation

Repetitive sequences:

Long terminal repeats (LTRs) are the most predominant class of TEs in potato, representing 29.4% of the genome, similar to *Arabidopsis thaliana* (28.5%)[11] but much greater than rice (14.7%)[12], cucumber (10.4%)[13] and grape (11.6%)[14]. The peak divergence rate of TEs, as measured by the percentage of substitutions in well-aligned regions between annotated repeats in potato and consensus sequences in Repbase[15], was approximately 32% indicating that most of the identified repeats are relatively ancient (Supplementary Fig. 13).

Gene prediction:

Solanum species used in EST alignments: *Capsicum annuum*, *Petunia* x *hybrida*, *Solanum tuberosum*, *Nicotiana benthamiana*, *Nicotiana langsdorffii* x *Nicotiana sanderae*, *Nicotiana sylvestris*, *Nicotiana tabacum*, *Solanum lycopersicum*, *Solanum chacoense*, *Solanum pennellii*, and *Solanum habrochaites;* 163a, corresponding to GenBank Release 163 (27 December 2007). Metrics of the final gene models indicate longer untranslated regions than that of *A. thaliana* (Supplementary Table 31) most likely attributable to the use of deep RNA-seq transcriptome data. Functional annotation of the final gene set was comparable to other angiosperms (Supplementary Table 32).

5. Chloroplast and mitochondrial genomes

Organelle genomes were assembled from the sequence traces. All reads were searched for chloroplast and mitochondrial sequences using Bowtie[9] with *Solanum* and *Nicotiana* query sequences derived from GenBank (DQ386163; DQ231562; Z00044;AM087200; BA000042; FJ374974) and unpublished mitochondrial sequences from potato cv. Spunta small insert libraries. Traces were assembled using CAP3[16] (http://seq.cs.iastate.edu/) and Celera WGA Assembler[17] (http://sourceforge.net/apps/mediawiki/wgs-assembler/). The chloroplast genome was 155,251 and 155,483 bp for DM and RH, respectively. Overall nucleotide similarity was 99.84%, including a 241 bp deletion (present in DM and not in RH), previously reported to be restricted to *S. tuberosum*[18]. Annotation of the DM chloroplast genome was performed using Dual Organellar GenoMe Annotator[19] (DOGMA; http://dogma.ccbb.utexas.edu/). The chloroplast genome codes for 106 genes: 73 proteins, 29 tRNAs and 4 rRNAs.

The dynamic structure of plant mitochondria represented by a family of recombinant circles of different sizes prevented the assembly of sequences in a single molecule. All data retrieved were assembled in 71 and 135 scaffolds for DM and RH, spanning 441,953 and 471,559 bp, respectively. Overall similarity of homologous regions was 98.32%. The consensus mitochondrial genome codes for 137 genes (112 proteins, 23 tRNAs and 2 rRNAs) for DM and 150 genes (125 proteins, 23 tRNAs and 2 rRNAs) for RH, with a high degree of duplication. Mitochondrial gene loss and transfer to nuclear DNA during evolution was previously reported[20,21]. In this respect, 36 genes presented in the published tobacco genome[21] (BA000042) were absent from both DM and RH. However, the high number of genes lost suggests a quantum evolutionary change of the mitochondrial genome in the Solanaceae.

Accession numbers for the DM and RH organellar genomes are JF772170- JF772173.

6. Transcriptome sequencing

DM transcriptome:

Vegetative and reproductive tissues (leaves, stolons, petioles, tubers, whole mature flowers, sepals, petals, stamens, carpels, berries) were taken from greenhouse-grown plants for RNA isolation (Supplementary Table 4). To induce biotic stress, we performed three separate detached leaf assays using *Phytophthora infestans* (Pi isolate US8: Pi02-007) and two chemical inducers, acibenzolar-S-methyl (BTH) and DL-β-amino-n-butyric acid (BABA). A mock inoculation with sterile water was conducted in parallel. For each detached leaf test, six fully developed leaves were collected immediately before treatments and placed on top of a plastic mesh in a 29.3 l plastic box containing six layers of wet absorbent paper towels. For *P. infestans* inoculations, sporangia were harvested from 11-13 days old cultures grown on Rye A Agar[22]. Sporangial suspensions of approximately 30,000 sporangia/ml were used for spray inoculations (0.5-0.7 ml). Inoculated leaves were incubated in the dark at room temperature for 8-10 h and then maintained in light at room temperature for seven days. For chemical treatments, BABA (2 mg/ml) and BTH (100 /ml) were dissolved in water and sprayed onto the leaves. Inoculated leaves were incubated in light at room temperature for seven days. Tissue samples from inoculated and mock inoculated leaves were collected at 24, 36, and 72h after inoculation and stored at –80°C prior to RNA isolation.

For abiotic stress treatments and isolation of shoot and roots from *in vitro* grown plants, DM plants were grown *in vitro* at 22°C day/18°C night with a 16 h photoperiod in three separate media (A, B, C) (Supplementary Table 4). Medium A (4.3 g/l MS salts, 3% sucrose, 0.17 g/l sodium phosphate, 2.5 mg/l thiamine, 0.1 g/l myo-inositol) was used for control and heat treatment (35°C 24 hr). Medium B (half-strength MS salts with 1.5% sucrose) was used for *in vitro* root and shoot tissues, salt (150 mM NaCl), and mannitol (260 µM) treatment. Medium C (half-strength MS salts and vitamins supplemented with 1.5% sucrose) was used for control, abscisic acid (ABA; 50 µM), indole-3-acetic acid (IAA; 10 µM), giberellic acid (GA3; 50 µM), and 6 benzylaminopurine (BAP; 10 µM) treatment. All abiotic stress was for 24 h and roots and shoots were harvested together. Callus was generated from DM leaves and stems on Step I medium (4.4 g/l MS salts, 30 g/l sucrose, 0.9 mg/l thiamine, 0.8 mg/l zeatin riboside, and 2 mg/l 2,4-D; 16 h light/8 h dark at room temperature) with explants transferred to fresh media once a week.

Total RNA was isolated using a phenol method. Samples were treated with DNAse in the presence of RNAse inhibitor prior to cDNA synthesis. All samples were separated on an Agilent Bioanalyzer 2100 to check for RNA integrity. cDNA was constructed using the Illumina RNA-Seq kit (mRNA-Seq Sample Prep Kit P/N 1004814) and was sequenced on Illumina GA2 sequencers using 36 bp single reads with a subset sequenced using the paired end read module (76/76 and 105/85 bp).

RH transcriptome:

RH tubers were planted in soil-filled pots in the greenhouse. After plant emergence and several weeks of growth, non-tuberizing stolons were harvested (RH Stolon). Around one week after the first swellings were observed, small tubers were collected with a maximum size of 1cm (RH Young tuber). Around the same time, anthesis occurred and both open flowers and developing flower buds were harvested (RH flower).

Around the 12th leaf stage (4 weeks after first visible swelling) various tissues were harvested, including leaves (fully expanded), shoot apex, petioles, stem, tubers (RH Mature Tuber) and roots, and immediately frozen in liquid nitrogen. Stamens were collected at the same time from fully opened flowers. All tissue samples were collected from at least five different plants. For the water-stressed leaf tissue sample, a subset of plants was denied water for 2 days after which wilting leaves were harvested (2nd – 4th fully expanded leaf). For the tuber cross section, plants were left to senescence. Tubers were then collected, and peel, cortex and pith tissues were sampled and immediately frozen in liquid nitrogen. Sprouts of previously harvested RH tubers were harvested after storage at RT in the dark for 3–4 months. RH *in vitro* plants were grown on standard MS medium on 2% sucrose with 16 h of light at 24°C for 2 weeks, after which the whole explant, including roots, was harvested.

A total of 16 tissues was collected (Supplementary Table 4) and RNA was isolated using the RNeasy kit (Qiagen), except for the tuber and root tissues, which were isolated using the hot-phenol method. The latter samples were than purified using the RNAeasy columns. For all samples, on-column DNAseI treatment was performed and the quality and integrity of the obtained RNA was checked using the ND-100 spectrophotometer (Nanodrop Technologies) and agarose gel-electrophoresis. cDNA libraries were constructed and sequenced as described for the DM samples without the paired end read module.

Gene expression visualization:

Complete linkage hierarchical clustering, using uncentred Pearson's correlation as distance measure was performed on both transcripts and samples using the clustering software Cluster 3.0[23]. For visualization purposes, FPKM values were normalized to the total expression of each transcript. A subset of the gene expression data set was selected, omitting samples from whole plant or stressed tissue, and genes with a FPKM value less than 5 were subjected to hierarchical clustering.

7. The karyotype of DM potato

Meiotic pachytene chromosomes were prepared from the flower buds of the DM clone. Individual pachytene chromosomes were identified by fluorescence *in situ* hybridization (FISH) using chromosome-specific BAC clones[2,24]. Chromosome 1 and 10 represent the longest and the shortest pachytene chromosomes, respectively (Supplementary Table 6). The karyotype of DM is generally similar to the RH clone described previously[2]. All potato chromosomes are metacentric or submetacentric, except chromosome 2, the only nucleolus organizer chromosome in the potato genome, which is acrocentric and has a very small short arm (Fig. 1, Supplementary Fig. 5).

Most of the cytologically distinct heterochromatin, which is represented by brightly stained regions by 4',6-diamidino-2-phenylindole (DAPI), is confined to the pericentromeric region of each chromosome (Supplementary Fig. 5). The transition between the heterochromatic and the euchromatic regions was often not sharp and thus difficult to locate on some chromosomes. The heterochromatic domains of chromosome 9 account for ~43% of the chromosomal length, representing the most heterochromatic chromosome in the potato genome. Distinct heterochromatic knobs were associated with the distal ends of most chromosomes. Some heterochromatic knobs or domains observed on the DM chromosomes were not reported in RH, such as a distinct subtelomeric knob on the long arm of chromosome 10 (Supplementary Fig. 5). Thus, the DM and RH clones are polymorphic at the cytological level.

8. Carotenoid analyses

Carotenoids are nutritionally important compounds. To measure carotenoid levels, peeled potato tuber tissues from greenhouse grown plants were ground to a powder in liquid nitrogen and pigments extracted in methanol: chloroform as described[25]. Separation and quantification of carotenoids was performed using reverse phase HPLC using an Ascentis 2.7 μM particle 100 x 3 mm column (Supelco, Park Bellefonte, PA) and a gradient system of solvent A, acetonitrile-water (70:30 v/v) and solvent B, acetonitrile-isopropanol (50:50 v/v). The column was equilibrated with 15% buffer B and separations performed with the following gradients: 0–3.5 min, 15 to 44% B; 3.5-6 min, 44 to 81.4% B; 6-10 min 81.4 to 95% B. 95% buffer B was maintained for an additional 1 min at which time the column was re-equilibrated with 15% buffer B. Carotenoids were detected by absorbance using a Shimadzu SPD-M20A Diode Array Detector and quantified at 450 nm relative to a 5 point curve of purified standards. Racemic tocol (Matreya Pleasant Gap, PA, USA) was used as an internal standard to correct for recovery during extraction and was detected by fluorescence at 290 nm excitation and 325 nm emission using a Shimadzu FLX-10AXL fluorometer. Carotenoid levels, as well as the mRNA of several genes in the enzymatic pathway, differed between DM and RH, consistent with the visual pigmentation differences in the tuber flesh (Supplementary Fig. 14, Table 33).

In particular, DM tubers show higher expression than RH of the non-heme beta-carotene hydroxylases *Chy2* and *Chy3* (Supplementary Fig. 14, Table 33); the chromosomal position of these genes corresponds to that of the *yellow* locus, underpinning tuber carotenoid content[26,27] (Supplementary Table 34). Several duplications are observed in carotenoid genes, some more ancient (the *LCYb*-*CYCb* duplication is found in potato, tomato and grape), others more recent (the *PSY1*-*PSY2* and *CHY1*-*CHY2* duplications are found in potato and tomato) (Supplementary Fig. 15). Interestingly, orthologous genes in potato and tomato show a similar pattern of tissue-specific expression: for instance, *PSY1*, *CYCb* and *CHY2* are highly expressed in the flowers of both species (data not shown).

9. Kunitz protein invertase analysis methods

In order to identify the Kunitz-type proteinase inhibitor genes in the potato, tomato and *Populus* genomes, we performed a Blast search[28] of the protein sequence (NCBI accession number: AAC49602.1) to the potato, tomato and *Populus* protein sets (potato protein set, tomato protein set: BGI v2.10, *Populus* protein set: JGI v2.0) (Expect Value < 1e-5 and coverage >80%). Following multiple alignment using ClustalW[8], Neighbor-Joining trees[29] were constructed using the p-distance model and 650 bootstrap replications with the MEGA 4.0[30] software package. Expression pattern heatmaps were drawn using Cluster 3.0[23] with expression levels of each gene in 12 DM and 16 RH transcriptome libraries.

10. SP gene analysis methods

To elucidate the dynamic changes of SP gene family in potato and tomato genome, we downloaded the protein sequences of SP genes from NCBI[31] (Accession: SP-U84140, SP2G-AY186734, SP3D-AY186735, SP5G-AY186736, SP6A-AY186737, and SP9D-AY186738). In order to identify all potential SP homologues, we performed an extensive homologue-based search against the proteomes of potato and tomato with the SP sequences using similarity $\geq$80% and coverage $\geq$ 80%. To clarify the extent of synteny erosion for each tomato-potato SP orthologous pair, we plotted the corresponding homologous region plus 100 kb flanking for each SP gene. As seen from Supplementary Fig. 7, while preserved in many cases, slight changes of the number of duplicates occurred in the corresponding orthologous potato-tomato regions, resulting from tandem duplication, transposon activity, and gene gain or loss. In total, 3 duplicates in potato correspond to 2 in tomato in chromosome 1, for chromosome 3: 2 vs. 2, chromosome 5: 2 vs. 2, chromosome 6: 1 vs. 1, chromosome 9: 1 vs. 1, chromosome 11: 2 vs. 1, respectively. Additionally, for SP2G, located on tomato chromosome 2, no homologous counterpart in the potato genome was detected. The potato gene set was obtained from PGSC annotation version 3.2, and the reconstruction of the pseudochromosomes are based on the AGP file version 2.0 and confirmed with v3.4 of the annotation. Tomato genes were based on BGI annotation of tomato genome assembly version 2.1.

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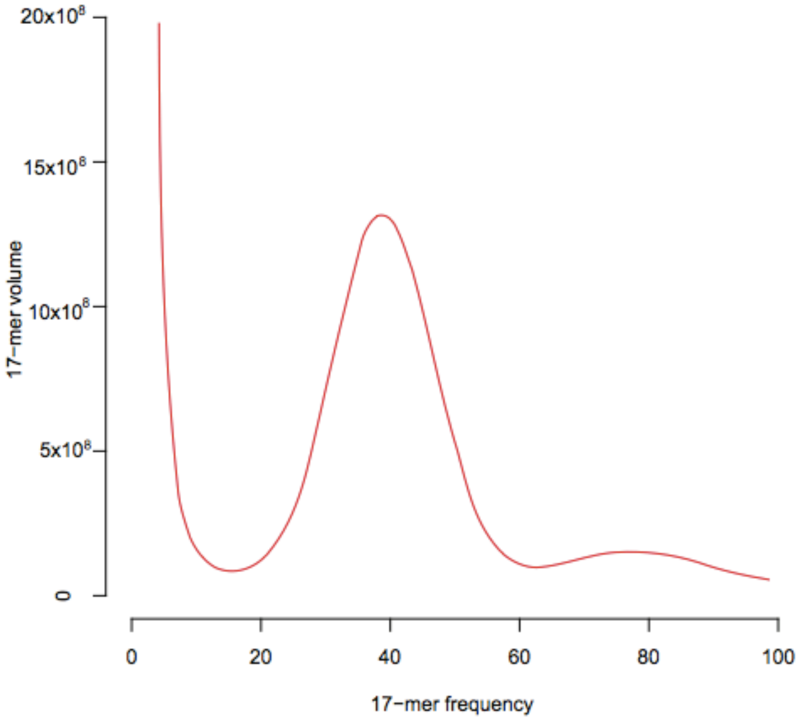
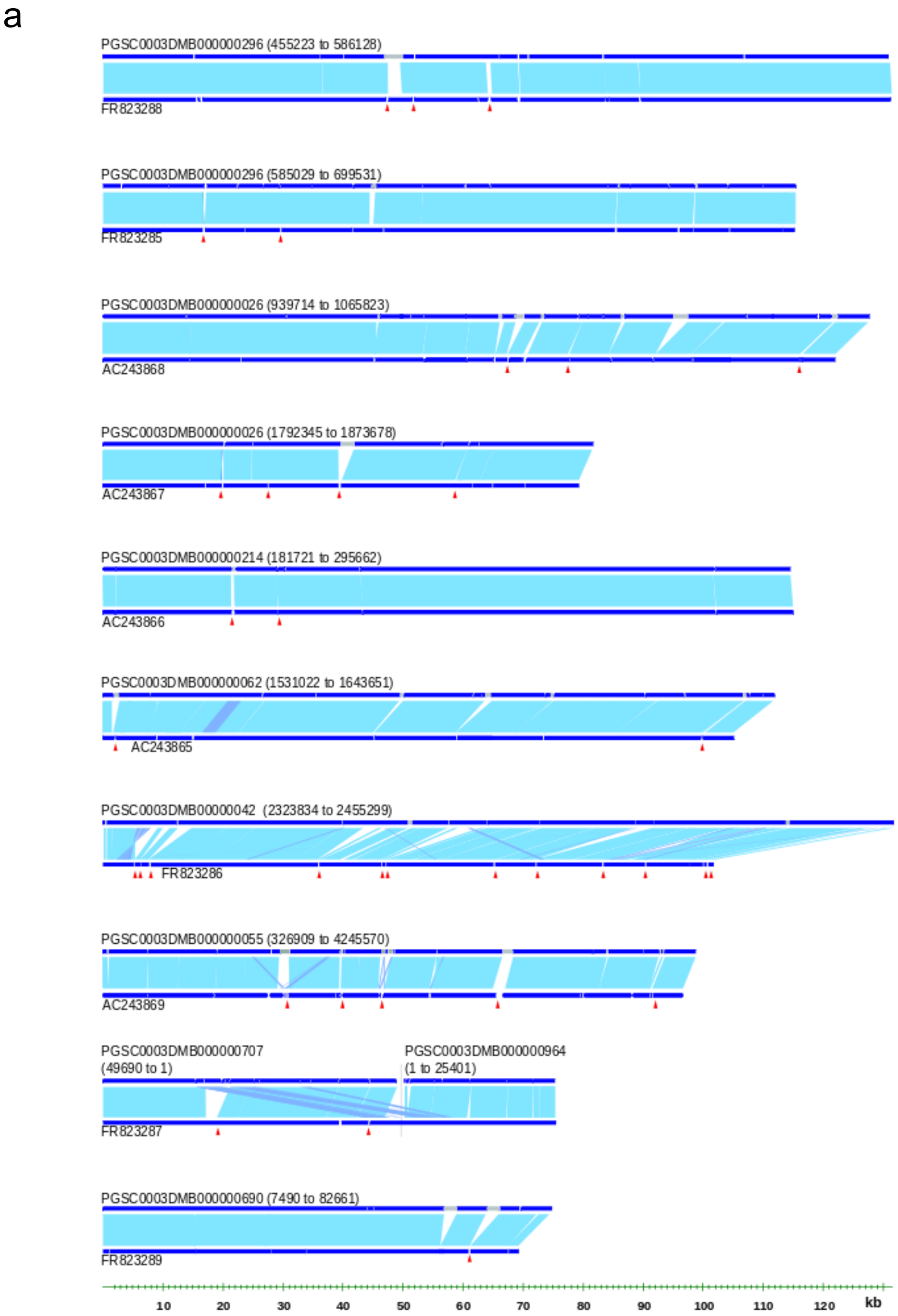
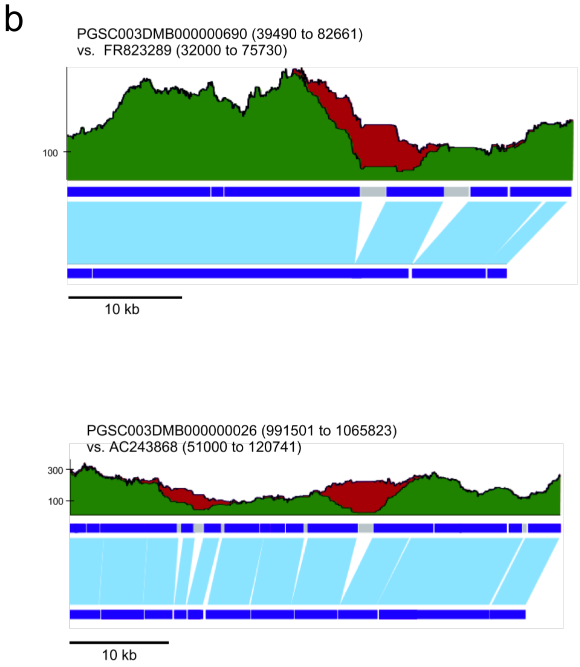


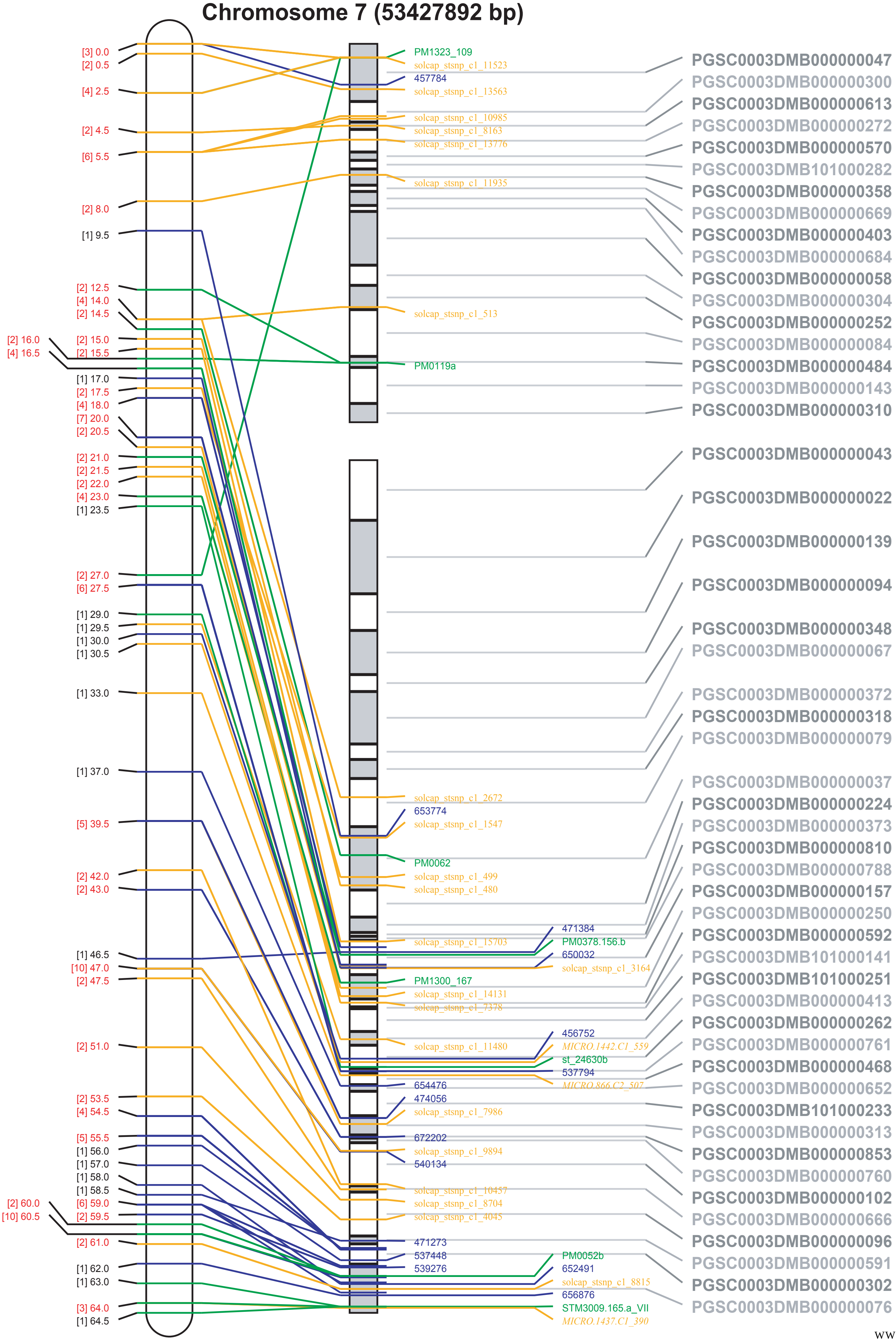
Supplementary Figure 1. Illumina 17-mer volume histograms of DM. The volume of K-mers is plotted against the frequency at which they occur. The left-hand, truncated, peak at low frequency and high volume represents K-mers containing essentially random sequencing errors, while the right-hand distribution represents proper (putatively error-free) data. The total K-mer number is 33,761,617,031, and the volume peak is 40. The genome size can be estimated as (total K-mer number)/(the volume peak), which is 844.0 Mb.



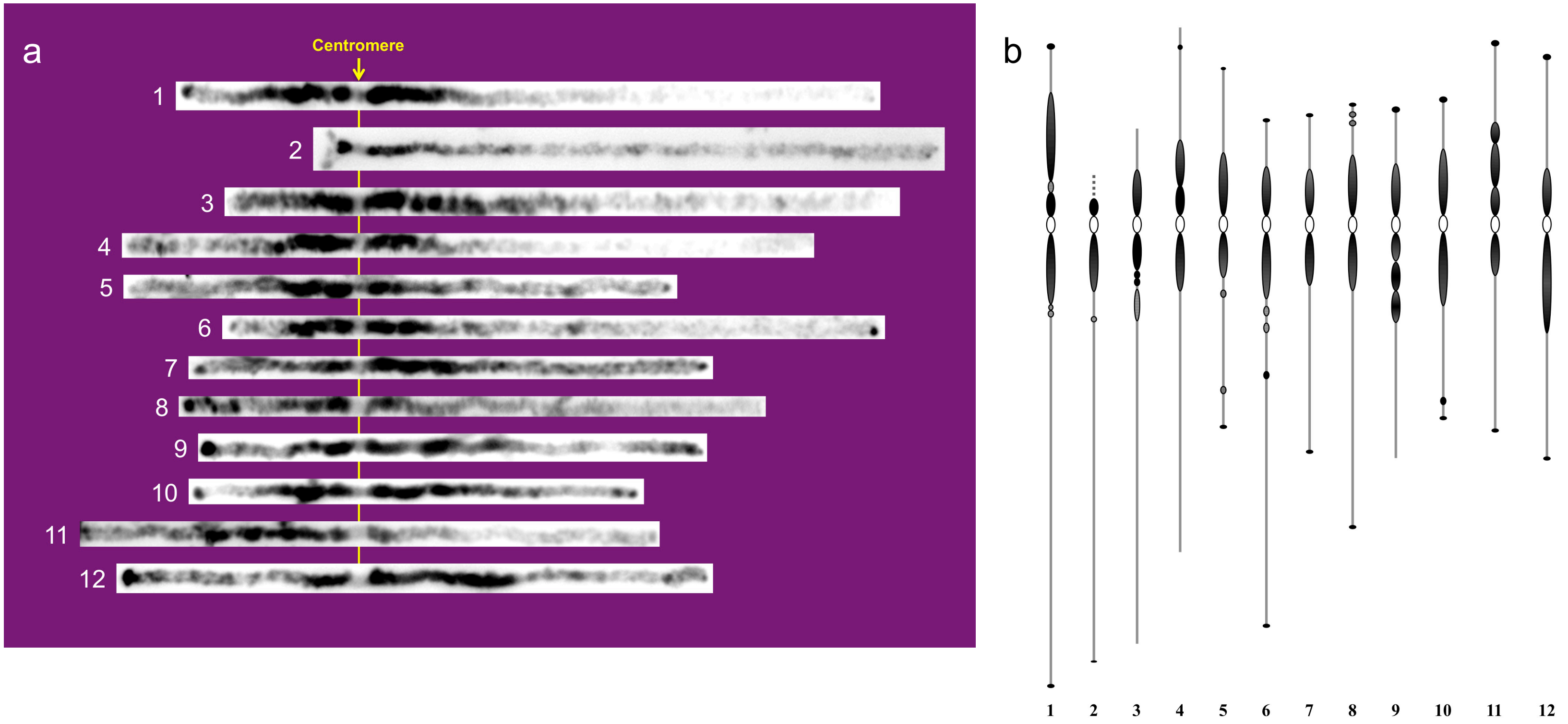


Supplementary Figure 2. a, Nucleotide alignments of ten sequenced BACs from DM to their equivalent superscaffold regions in the Illumina assembly. Dark blue tracks represent superscaffolds (top) and BACs (bottom) respectively. Light blue shading between the superscaffold and BAC tracks represents areas of 100% nucleotide identity, with rearrangements indicated by shading. Grey regions on the superscaffold tracks indicate large N runs in the sequence. White gaps on the superscaffold and BAC tracks indicate the position of all nucleotide differences. All BACs were assembled to HTGS Phase 2, and contig ends are indicated by red triangles. **b,** A portion of the alignment of two DM BAC sequences with their corresponding Illumina scaffolds. Several large N-runs inserted into the sequence to indicate a gap in the superscaffold are visible. BAC assemblies suggest that the gap size is generally overestimated. The upper coverage plots show read pairs from the 5kb Illumina paired-end library mapped back to the scaffold sequence. Green areas represent read pairs aligning in the expected range according to library size, red regions represent read pairs aligning at a greater distance than the expected range. Regions in with a large proportion of the latter category (red) are frequently observed to correspond to N-run regions representing gaps and thus supporting the overestimation of gap size.

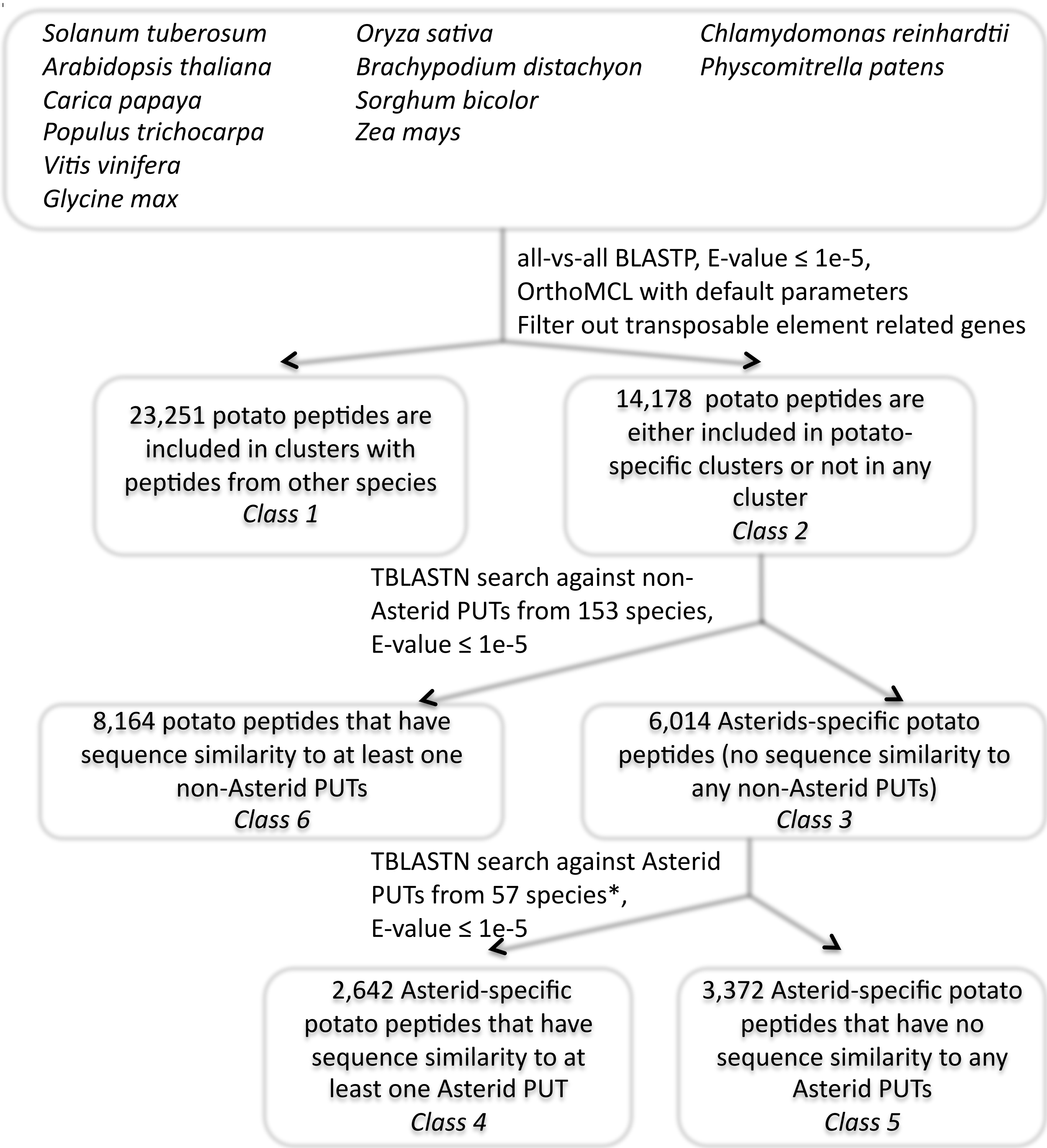
Chromosome 7 (53427892 bp)



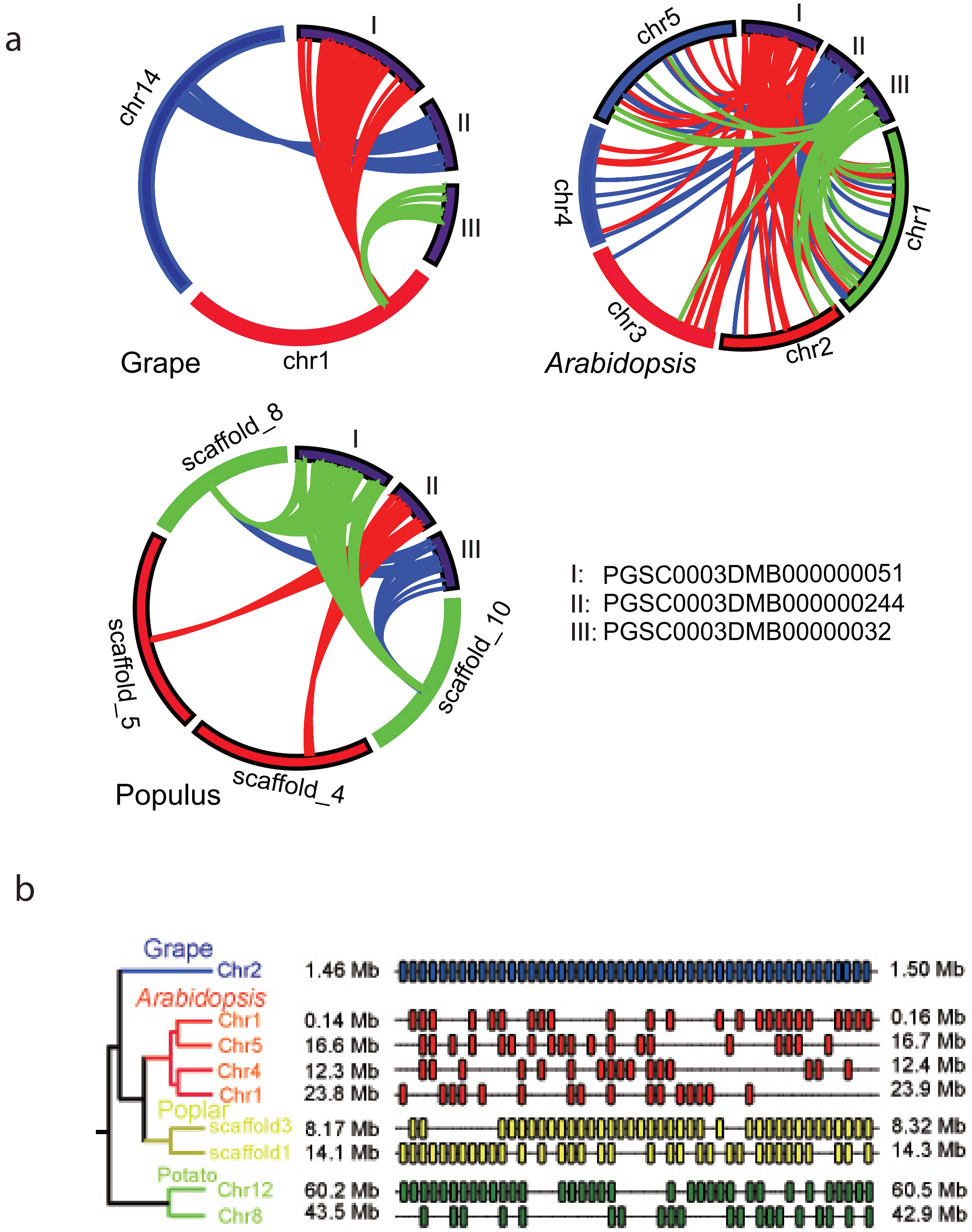
Supplementary Figure 3. Comparison of genetic and physical maps of potato chromosome 7 drawn on 180 individuals of the DM/DI//DI progeny and the DM line, respectively. Genetic loci are binned to 0.5 cM and those with multiple marker occupancy are shown in red. All markers are indicated but only one label is shown for each marker type in a bin of ~150kb. Where more than one marker is present in a sequence bin, the number of markers is indicated in parentheses. DArT markers are shown in blue, SSRs in green, and SNPs in orange. This figure was prepared using the DMap software (DMA Martin, manuscript in preparation).



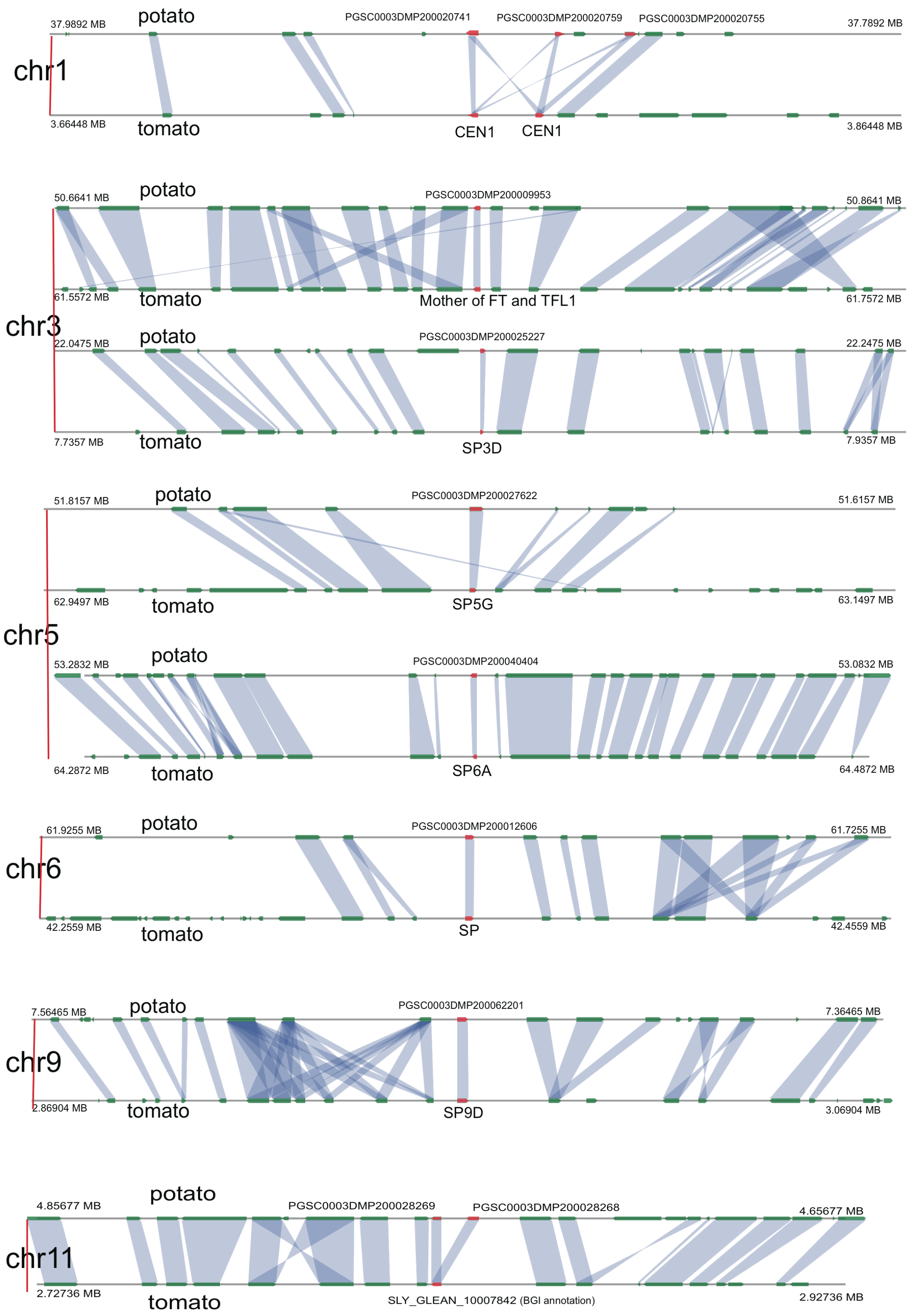
Supplementary Figure 4. a, Pachytene karyotype of the DM potato. Chromosomes were stained with DAPI and the vertical line is aligned with the centromeres of the chromosomes. **b,** Ideogram of the distribution of heterochromatin on pachytene chromosomes of DM potato. The heterochromatic regions are represented by solid/shaded thickenings based on the staining pattern of DAPI. Shaded thickenings indicate regions that were less stained by DAPI than the regions marked by solid thickenings. Hatched thickenings indicate regions that were not consistently observed in every cell and were sometimes separated into multiple smaller regions on early pachytene chromosomes. Open circles represent the centromeres.



Supplementary Figure 5. Identification of lineage specific genes. Potato proteins not clustering with 11 sequenced plant species were filtered for transposable elements and searched against a suite of transcriptome datasets (See Table S32).



Supplementary Figure 6. Colinear blocks between potato and three rosid genomes (Grape, Arabidopsis and Populus). a, Colinearity between three paralogous potato genomics regions (I, II, III) and their putative orthologs in rosids genomes. **b,** Two syntenic blocks in potato correspond to one block in grape, two in poplar and four in Arabidopsis


chr1
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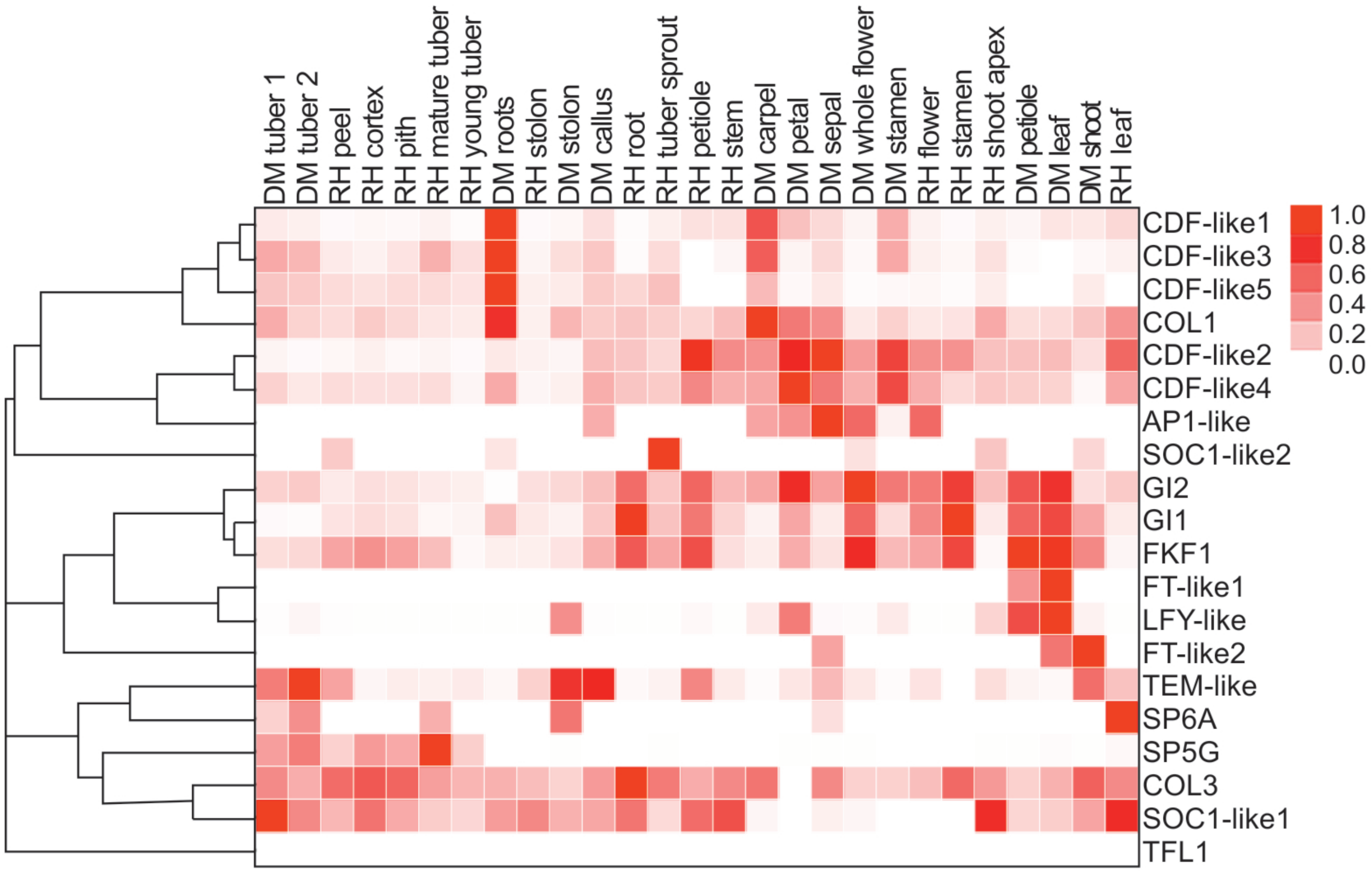
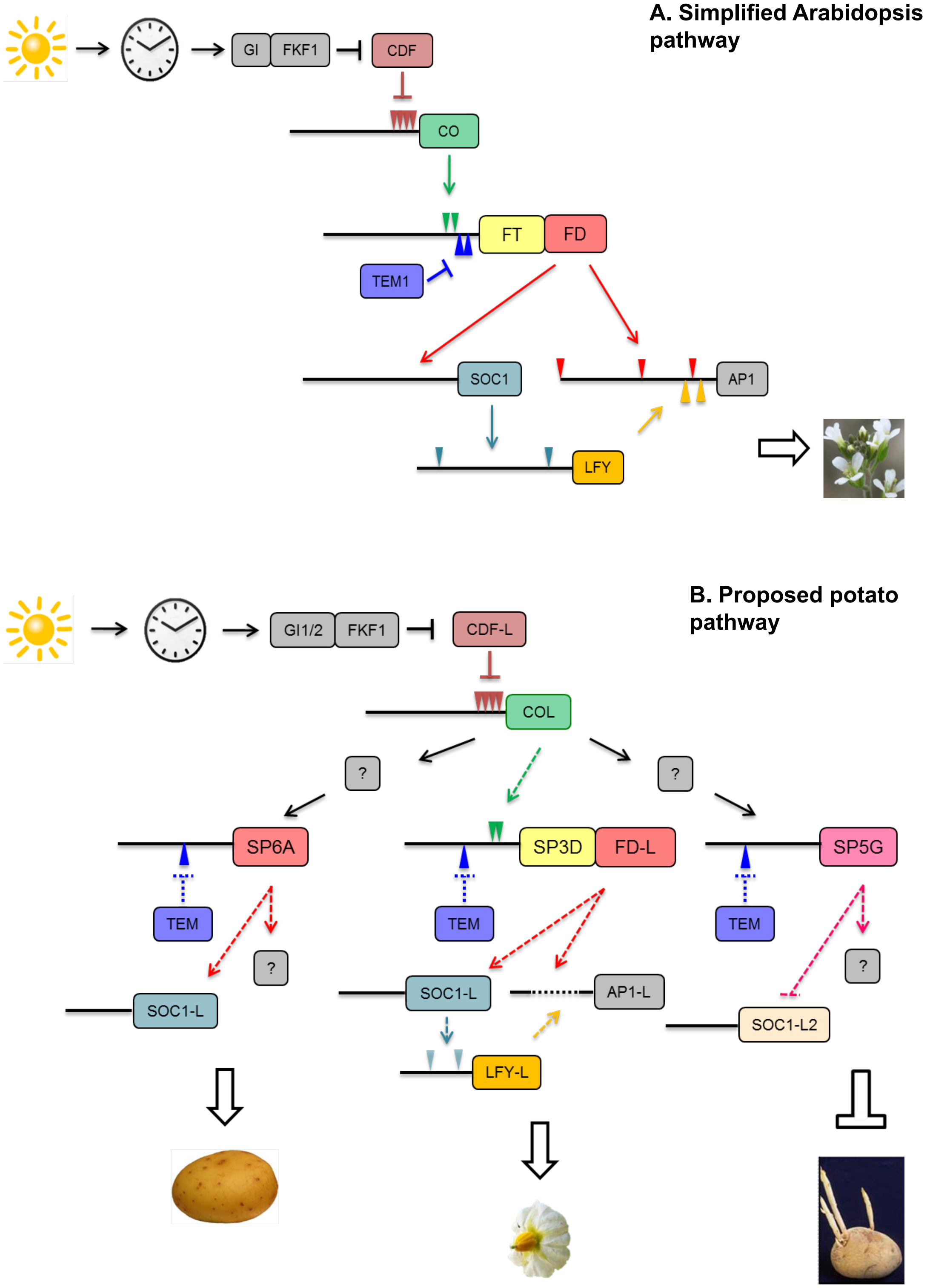
potato
PGSC0003DMP200020741
PGSC0003DMP200020759
PGSC0003DMP200020755
37.7892 MB
3.66448 MB
tomato
CEN1
CEN1
3.86448 MB
chr3
50.6641 MB
potato
PGSC0003DMP200009953
50.8641 MB
61.5572 MB
tomato
Mother of FT and TFL1
61.7572 MB
22.0475 MB
potato
PGSC0003DMP200025227
22.2475 MB
7.7357 MB
tomato
SP3D
7.9357 MB
chr5
51.8157 MB
potato
PGSC0003DMP200027622
51.6157 MB
62.9497 MB
tomato
SP5G
63.1497 MB
53.2832 MB
potato
PGSC0003DMP200040404
53.0832 MB
64.2872 MB
tomato
SP6A
64.4872 MB
chr6
61.9255 MB
potato
PGSC0003DMP200012606
61.7255 MB
42.2559 MB
tomato
SP
42.4559 MB
chr9
7.56465 MB
potato
PGSC0003DMP200062201
7.36465 MB
2.86904 MB
tomato
SP9D
3.06904 MB
chr11
4.85677 MB
potato
PGSC0003DMP200028269
PGSC0003DMP200028268
4.65677 MB
2.72736 MB
tomato
SLY_GLEAN_10007842 (BGI annotation)
2.92736 MB

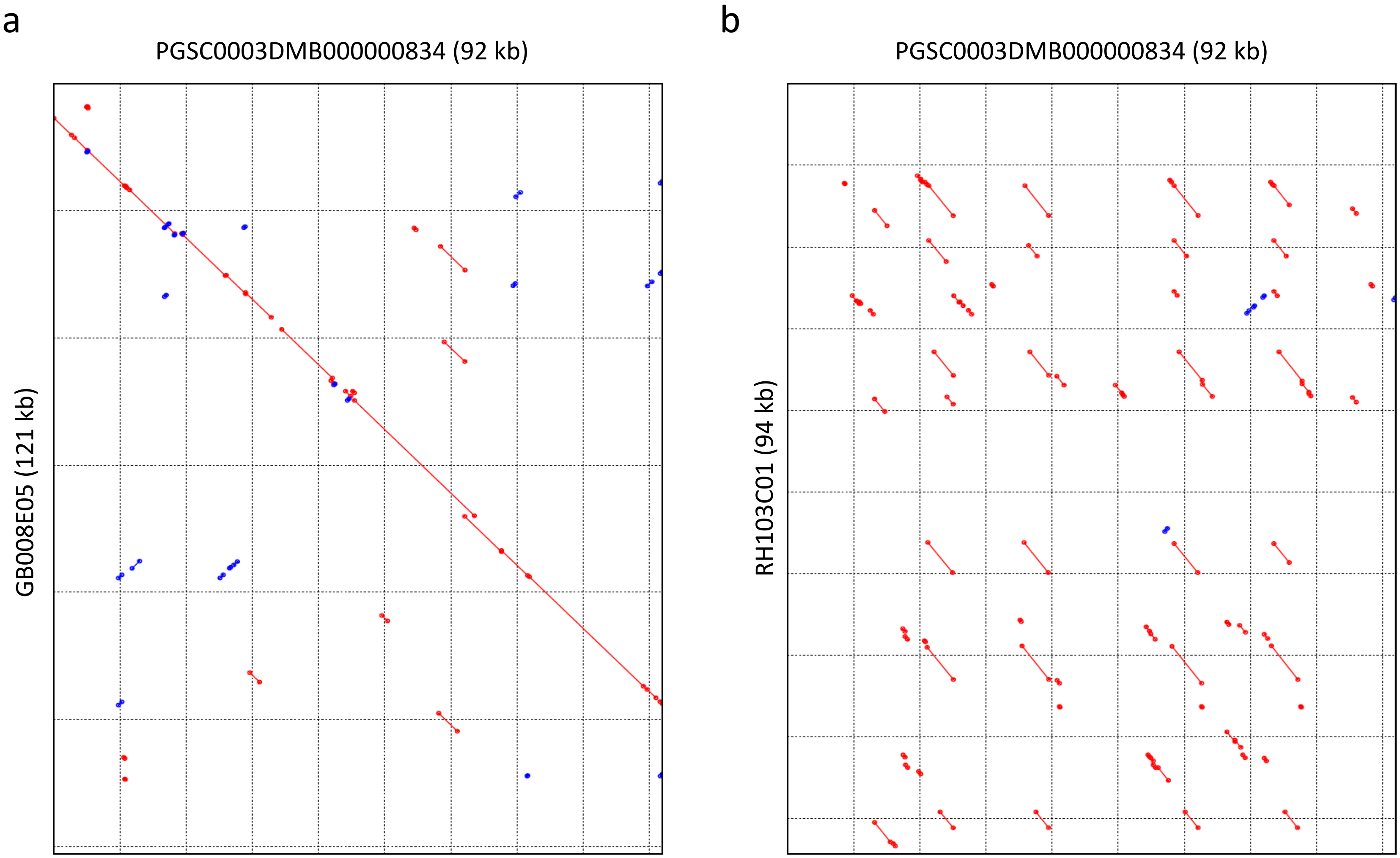
Supplementary Figure 7. SP/FT gene family distribution in potato and tomato. Homologous relationships between potato and tomato chromosomes for the SP/FT genes (red) and other protein coding genes (green) are linked by light blue blocks.



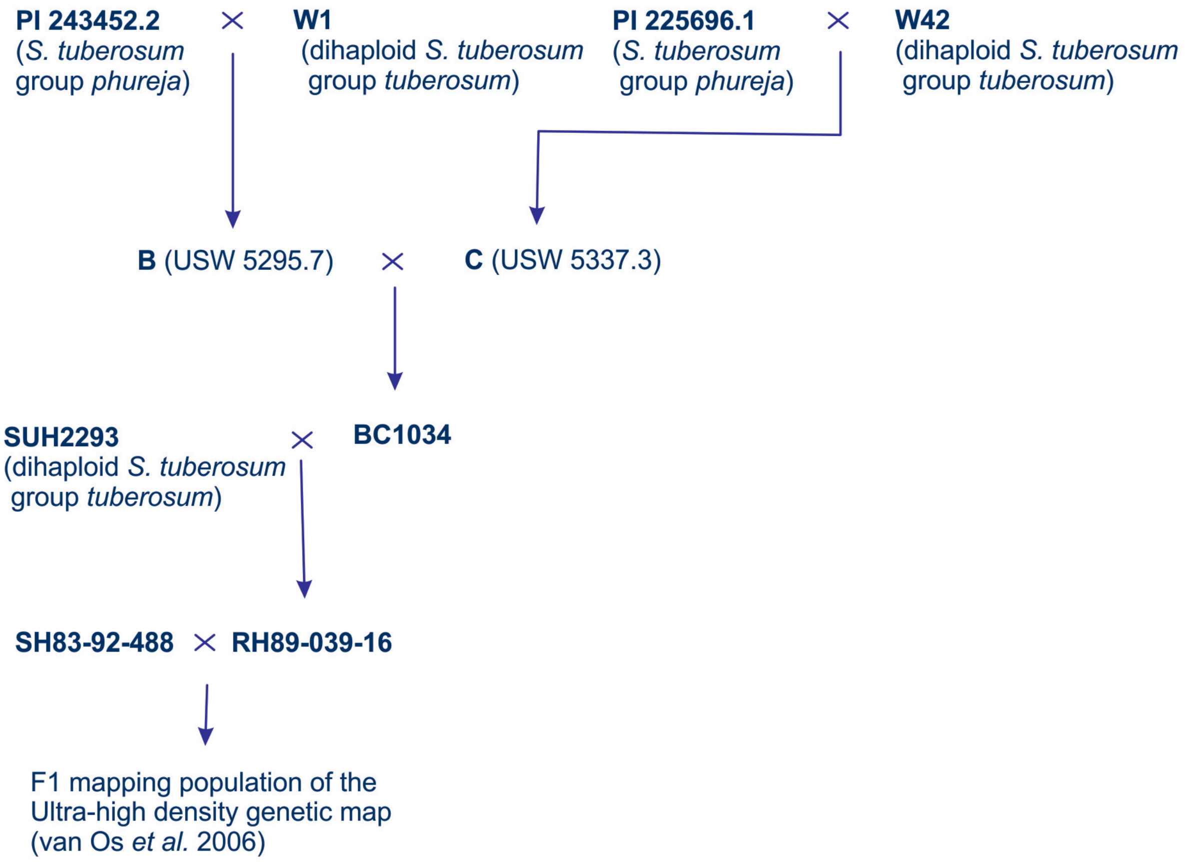
Supplementary Figure 8. Expression of selected genes involved in control of tuber formation. A dendrogram of the gene expression clustering is shown on the left and the clustering of tissues is as in Fig. 3. Abbreviation of genes is as follows: CDF-like1: Cycling DOF-like; COL: Constans-like; AP1-like: Apetala 1-like; SOC1 like: Suppressor of Constans 1 like; GI1-2: Gigantea 1-2; FKF1: Flavin-binding, Kelch Repeat, F-box 1; FT-like: Flowering locus T-like; LFY-like; Leafy-like; TEM-like; Tempranillo-like; SP6A: Self-pruning 6A (FT-homologue controlling tuber formation): SP5G: Self-pruning 5G (FT-homologue possibly controlling sprouting); TFL1: Terminal Flower 1.



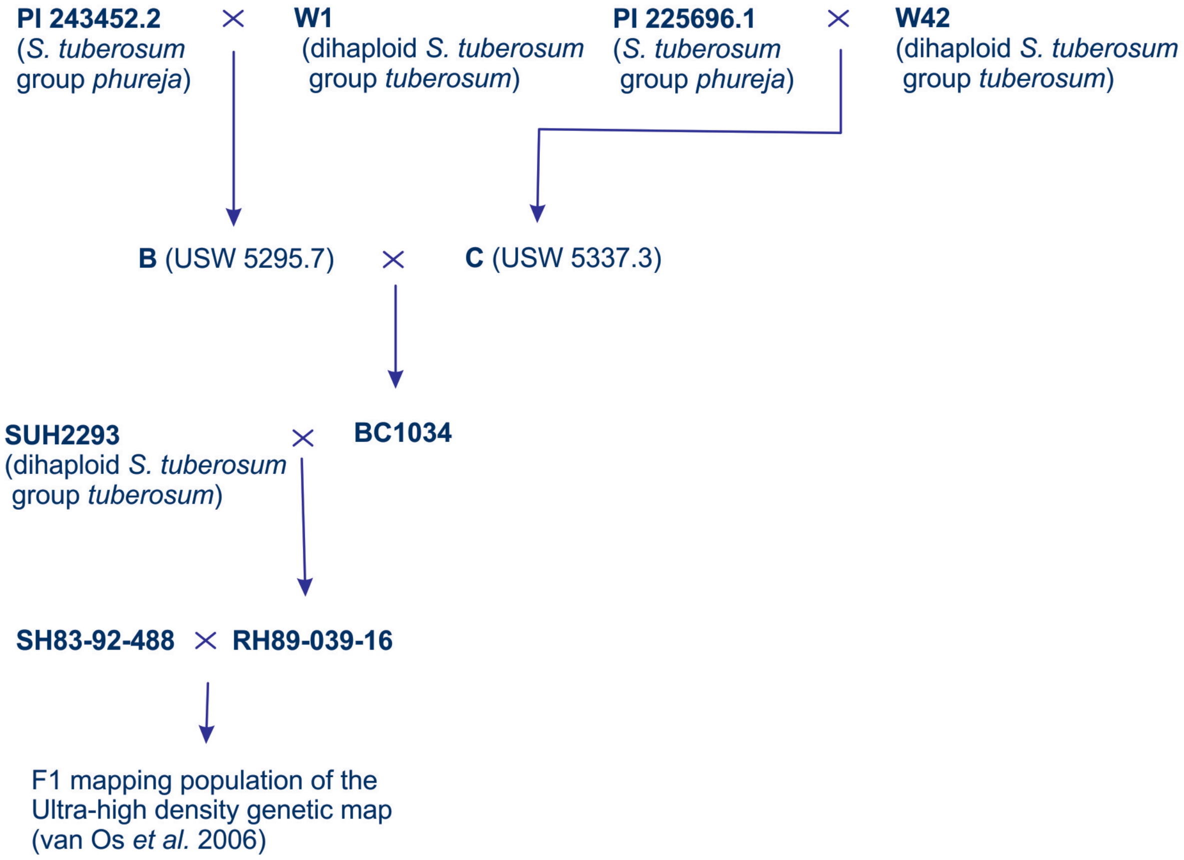
Supplementary Figure 9. Proposed roles of FT homologues in potato. A, Simplified Arabidopsis pathway, redrawn according to Michaels (ref. 57 in Supplemental Text). B, Proposed potato pathway. SP3D regulates flowering time, SP6A regulates tuber initiation and SP5G represses sprouting. A functional homolog of FD-L exists in potato (S. Prat, personal communication).



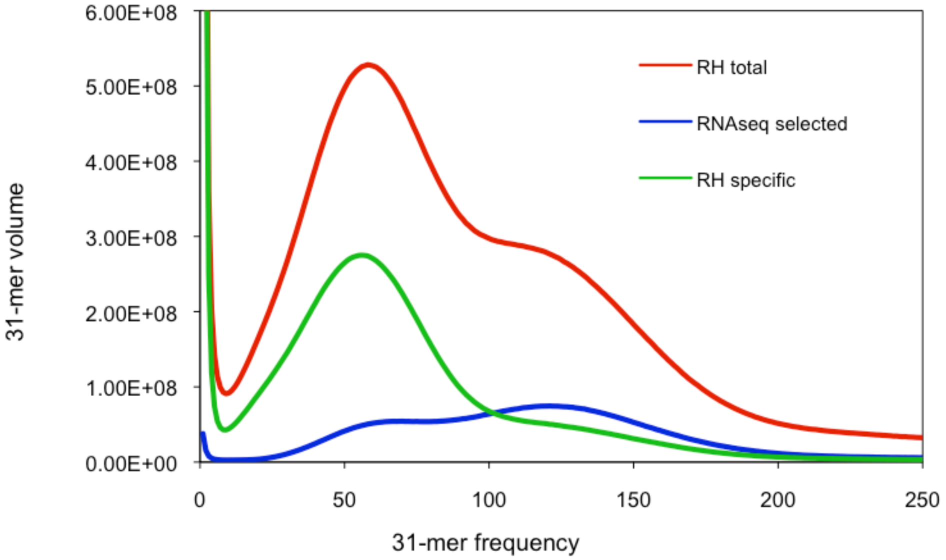
Supplementary Figure 10: Sequence alignment plots showing allelic diversity in the R1 disease resistance gene cluster on chromosome 5. **a,** BAC GB008E05 from the {0} haplotype of genotype RH is colinear with DM superscaffold PGSC0003DMB000000834. **b,** BAC RH103C01 from the corresponding {1} haplotype in genotype RH is not colinear with DM superscaffold PGSC0003DMB000000834.



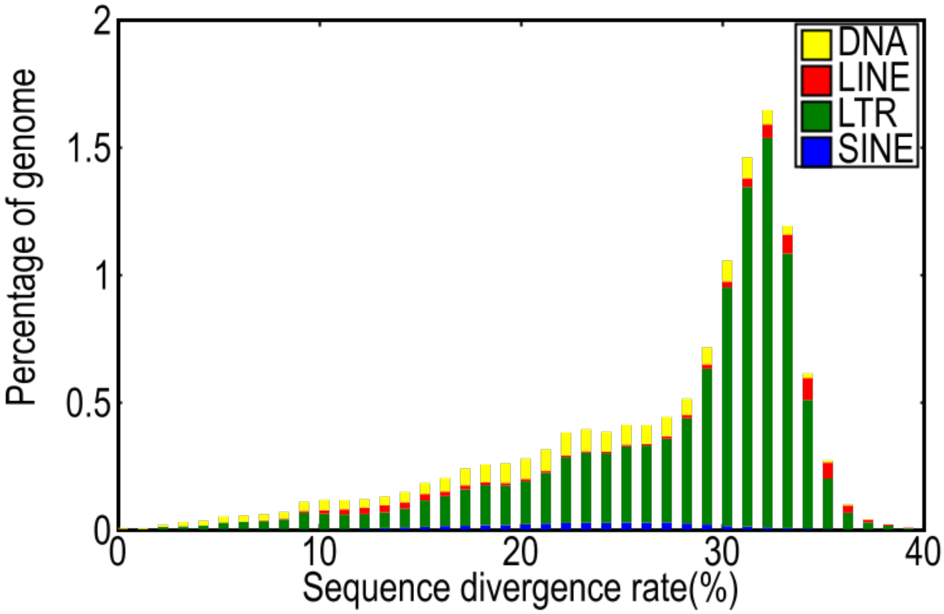
Supplementary Figure 11. Pedigree of RH89-039-16



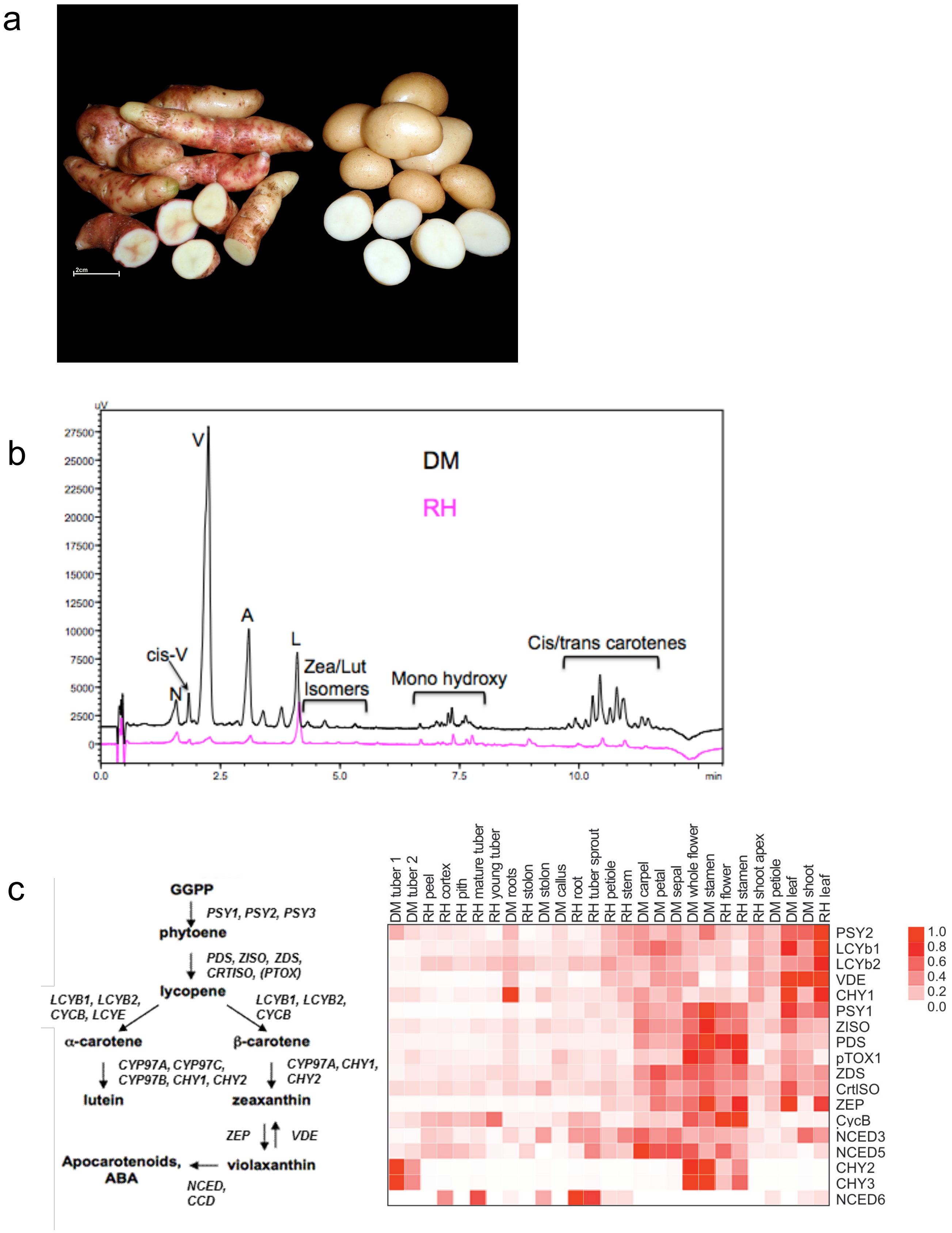
Supplementary Figure 11. Pedigree of RH89-039-16



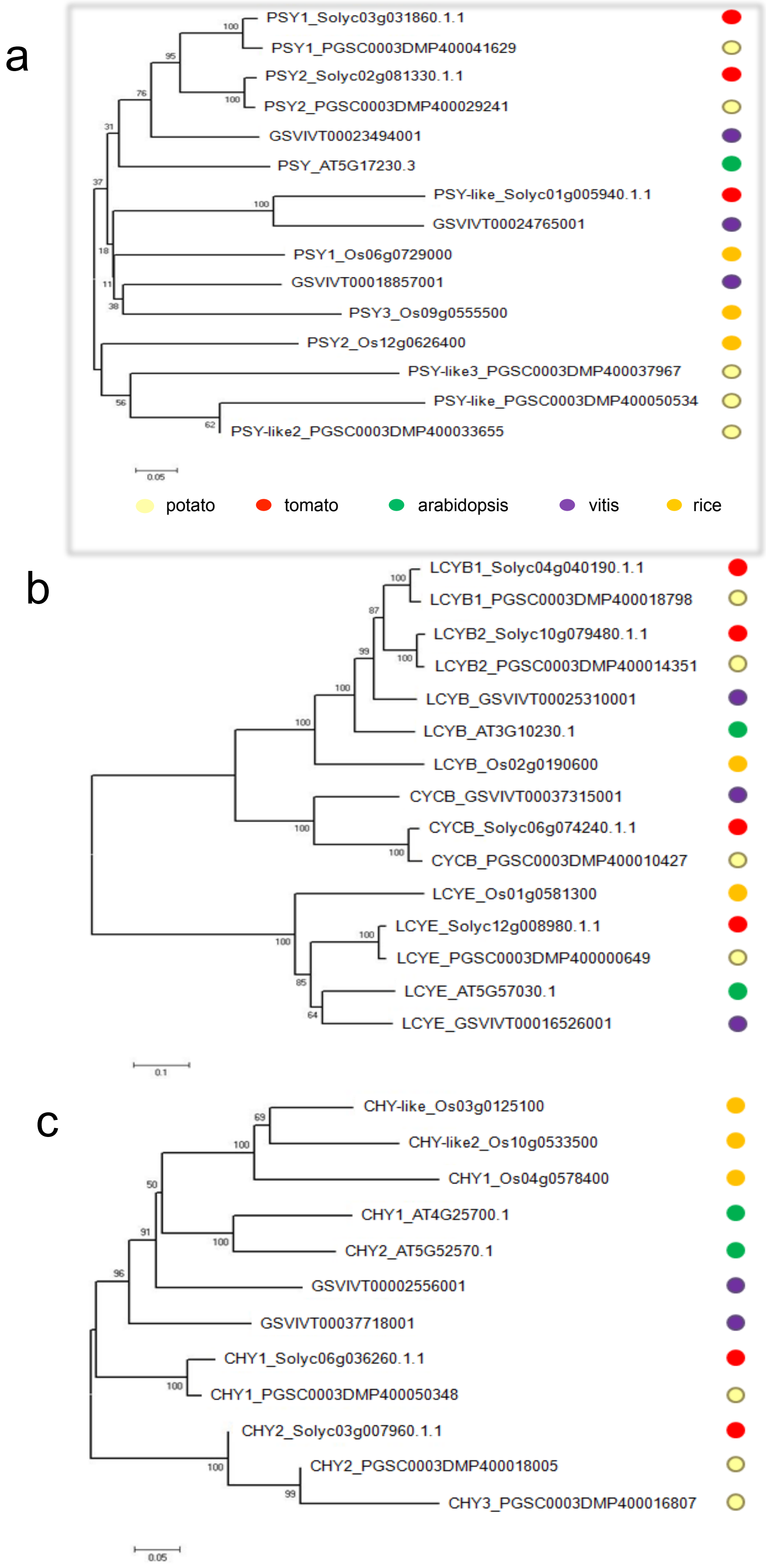
Supplementary Figure 12. Illumina K-mer (with K=31) volume graphs of the fraction of K-mers unique to RH (green), the RH K-mers selected by the RNASeq data (blue) compared to the total K-mers (red). In these figures, the volume of K-mers in the respective Illumina datasets (Y axis) is plotted against the frequency at which they occur (X axis). The left-hand, truncated, peak at low frequency yet high volume represents K-mers containing essentially random sequencing errors, while the right-hand distribution represents proper (putatively error free) data. The distribution exhibits clear bi-modality caused by heterozygosity. Homozygous K-mers on the right-hand side of the distribution occur at twice the frequency of heterozygous K-mers on the left-hand side. The green graph was obtained by removing all DM K-mers from the RH data, thus resulting in a histogram for K-mers unique to RH. The relatively lower right-hand shoulder in this graph illustrates that sequences differing between DM and RH also have a predisposition to differ between alleles of RH. The blue graph was obtained by using the RNA-seq data to select K-mers from the WGS dataset. The large shift in relative heights of the peaks underlying the bimodal distribution (towards more homozygosity) illustrates that exonic sequences exhibit a much higher level of conservation between alleles in RH.



Supplementary Figure 13. Distribution of divergence rate for different types of transposable elements generated from alignments of potato transposable elements identified via RepeatMasker against entries in the Repbase library. Divergence rate is shown on the x-axis and the frequency of occurrence in the genome shown on the y-axis. DNA: DNA elements; LINE: Long interspersed nuclear elements; LTR: Long Terminal Repeat transposable element; SINE: Short interspersed nuclear elements.


a
2cm
b
uV
27500
25000
22500
20000
17500
15000
12500
10000
7500
5000
2500
0
0.0
2.5
5.0
7.5
10.0
min
DM
RH
V
A
L
cis-V
N
Zea/Lut Isomers
Mono hydroxy
Cis/trans carotenes
c
GGPP
PSY1, PSY2, PSY3
phytoene
PDS, ZISO, ZDS, CRTISO, (PTOX)
lycopene
LCYB1, LCYB2, CYCB, LCYE
LCYB1, LCYB2, CYCB
α-carotene
β-carotene
CYP97A, CYP97C, CYP97B, CHY1, CHY2
CYP97A, CHY1, CHY2
lutein
zeaxanthin
ZEP
VDE
Apocarotenoids, ABA
violaxanthin
NCED, CCD
DM tuber 1
DM tuber 2
RH peel
RH cortex
RH pith
RH mature tuber
RH young tuber
DM roots
RH stolon
DM stolon
DM callus
RH root
RH tuber sprout
RH petiole
RH stem
DM carpel
DM petal
DM sepal
DM whole flower
DM stamen
RH flower
RH stamen
RH shoot apex
DM petiole
DM leaf
DM shoot
RH leaf
PSY2
LCYb1
LCYb2
VDE
CHY1
PSY1
ZISO
PDS
pTOX1
ZDS
CrtISO
ZEP
CycB
NCED3
NCED5
CHY2
CHY3
NCED6
1.0
0.8
0.6
0.4
0.2
0.0

Supplementary Figure 14 a, Photograph of tubers from DM (left) and RH (right). **b,** HPLC analysis of tuber carotenoids. Pigments were extracted, separated and identified by spectral characteristics and co-migration with purified standards. The trace shown is at 450nm using equal amounts of tissue from the two lines. N, neoxanthin; cis-V and V, cis- and trans-violaxanthin, respectively; A, antheraxanthin; L, lutein; Zea/Lut isomers, various cis isomers of lutein and zeaxanthin; Mono hydroxy, a complex mixture of alpha, beta and delta-carotene isomers that migrate in a region containing cyclized carotenes with a single hydroxyl group; Cis/trans carotenes, complex mixture of various cyclized isomers (e.g., alpha, beta, delta) carotenes and uncyclized (e.g., zeta-carotene, neurosporene, phytofluene) carotenes. **c,** A simplified carotenoid biosynthesis pathway is shown to the left. Tissue specific expression of genes participating in carotenoid biosynthesis shown as a heat-map on the right. Level of expression is indicated by shades of red, where white indicates no expression. (PSY=phytoene synthases; PDS= phytoene desaturase; ZDS= zeta-carotene desaturase; ZISO= 9,15,9'-tri-cis-zeta-carotene isomerase; CrtISO=7,9,7',9'-tetra-cis-lycopene isomerase; LCYb, CYCb=lycopene beta-cyclases; LCYe=lycopene epsilon-cyclase; CYP=P450 hydroxylases; CHY=non-heme hydroxylases; ZEP=zeaxanthin epoxidase; VDE=violaxanthin deepoxidase; pTOX=alternative oxidase; NCED, CCD=carotenoid cleavage enzymes.



Supplementary Figure 15. ClustalW dendrograms of **a**, Phytoene Synthases, **b**, Lycopene Cyclases and **c**, Non-heme hydroxylases, respectively, from different sequenced plant genomes.

Supplementary Table 1. Statistics of repetitive elements in the DM genome assembly and DM BAC/Fosmid end sequences.

DM Genome Assembly

	Repbase TEs		TE proteins		De novo		Combined TEs	
Type	Length (Bp)	% in genome	Length (Bp)	% in genome	Length (Bp)	% in genome	Length (Bp)	% in genome
DNA	12,361,720	1.70	2,136,101	0.29	23,710,499	3.26	28,651,825	3.94
LINE	4,672,437	0.64	2,625,786	0.36	13,009,895	1.79	16,363,155	2.25
SINE	2,891,285	0.40	0	0.00	3,388,813	0.47	4,688,731	0.64
LTR	70,578,204	9.70	5,005,519	0.69	207,479,333	28.52	214,148,094	29.44
Other	9,447	0.00	0	0.00	0	0.00	9,447	0.00
Unknown	96,781	0.01	2,670	0.00	202,301,562	27.81	202,374,962	27.82
Total	89,972,826	12.37	5,183,930	0.71	444,197,765	61.06	452,451,253	62.20

DM BAC/Fosmid end sequences

	Repbase TEs		TE proteins		De novo		Combined TEs	
Type	Length (Bp)	% in genome	Length (Bp)	% in genome	Length (Bp)	% in genome	Length (Bp)	% in genome
DNA	1,729,250	1.34	859,167	0.66	3,176,051	2.45	4,507,300	3.48
LINE	1,034,624	0.80	1,123,126	0.87	2,532,620	1.96	3,830,366	2.96
SINE	335,073	0.26	0	0.00	529,547	0.41	667,484	0.52
LTR	13,762,345	10.63	13,440,745	10.39	35,941,033	27.77	49,701,663	38.40
Other	816	0.00	0	0.00	0	0.00	816	0.00
Unknown	12,625	0.01	0	0.00	40,618,757	31.38	40,627,225	31.39
Total	16,783,357	12.97	15,422,760	11.92	80,883,474	62.50	96,860,821	74.84

Supplementary Table 2. Summary of the differences between the BAC sequences and their equivalent scaffold sequences

BAC Accession No.	BAC Length, bp[1]	Superscaffold ID/ Co-ordinates	Equivalent scaff. Length	Nr. of Ns in the equiv. Scaffold length	Alignment length, bp[2]	Covered by BACs, bp[3]	Covered by scaffolds, bp[3]	Indel (>2)[4]	Mismatch (>2)[5]	Single nucleotide changes A>T, A>C, etc.[6]	Mononucleotide Stretch[7]
FR823288	131,182	PGSC0003DMB000000296 455223 to 586128	130,906	2,779	131,440	131,178	128,127	6	3	19	11
FR823285	114,526	PGSC0003DMB000000296 585029 to 699531	114,503	993	115,004	114,517	113,510	16	22	47	15
AC243868	120,741	PGSC0003DMB000000026 939714 to 1065823	126,110	6,322	121,251	120,641	119,788	17	8	45	29
AC243867	79,125	PGSC0003DMB000000026 1792345 to 1873678	81,334	2,665	79,407	78,917	78,669	11	0	14	5
AC243866	114,565	PGSC0003DMB000000214 181721 to 295662	113,942	407	114,634	114,464	113,535	7	7	17	6
AC243865	105,923	PGSC0003DMB000000062 1531022 to 1643651	112,630	3,452	109,966	105,923	109,178	8	7	27	6
FR823286	101,818	PGSC0003DMB000000042 2323834 to 2455299	131,466	1,333	131,908	101,818	130,133	24	12	31	37
AC243869	95,552	PGSC0003DMB000000055 326909 to 424557	97,649	5,804	97,217	95,452	91,845	42	3	45	16
FR823287	77,214	PGSC0003DMB000000707 1 to 49690 PGSC0003DMB000000964 1 to 25401	79,295	4,304	82,023	77,214	74,991	43	59	178	47
FR823289	69,953	PGSC0003DMB000000690 7490 to 82661	75,172	3,656	72,066	69,916	71,516	22	2	5	17
Total	**1,010,599**	**-**	**1,063,007**	**31,715**	**1,054,916**	**1,010,040**	**1,031,292**	**196**	**123**	**428**	**189**

[1] BAC length as calculated from the final BAC assembly

[2] Alignment length calculated from ClustalW2 alignment of compressed (unresolved nucleotides excluded) BAC and superscaffold sequences.

[3] Unresolved nucleotides (including inserted N-runs) for the scaffold and BAC sequences respectively were subtracted from the alignment length to calculate the coverage values presented in subsequent two columns.

[4] Insertions and Deletions of greater than 2 nucleotides between the two sequences in the alignment. Adjusted for gaps between contigs in PhaseII BACs

[5] Runs of mismatches of 2 or more nucleotides between the sequences in the aligning segments

[6] Discrete single nucleotide differences only. Includes differences due to single nucleotide gaps and ambiguous bases in one sequence relative to the other

[7] Mononucleotide runs of greater than 2 nucleotides which differ by at least one nucleotide between the sequences. Excludes N runs.

*Figures based on comparison of the BAC to a composite sequence derived from the equivalent regions of two independant superscaffolds.

Supplementary Table 3. Mapping of BAC and fosmid paired end sequences of the genome assembly

On Scaffolds	DM BACs		DM fosmids		RH BACs	
No. matepairs:	62,975	100.00%	26,956	100.00%	64,267	100.00%
on different scaffolds	7,762	12.33%	2,137	7.93%	5,576	8.68%
on same scaffold	20,531	32.60%	12,174	45.16%	7,656	11.91%
incorrect orientation	33	0.05%	9	0.03%	53	0.08%
incorrect direction	33	0.05%	19	0.07%	97	0.15%
too far*	0	0.00%	3	0.01%	2	0.00%
Potential misassemblies	66	0.10%	31	0.12%	152	0.24%

On Superscaffolds	DM BACs		DM fosmids		RH BACs	
No. matepairs:	62,975	100.00%	26,956	100.00%	64,267	100.00%
on different superscaffolds	3,193	5.07%	813	3.02%	2,091	3.25%
on same superscaffold	25,040	39.76%	13,479	50.00%	11,065	17.22%
incorrect orientation	63	0.10%	10	0.04%	125	0.19%
incorrect direction	56	0.09%	39	0.14%	102	0.16%
too far*	7	0.01%	14	0.05%	13	0.02%
Potential misassemblies	126	0.20%	63	0.23%	240	0.37%

*Cutoff used were: >300 Kb for BACs and >60 Kb for fosmids.

Ends were cleaned from duplicates and mapped on the assembly using Blastn. Stringent parameters (minimum end length 300bp, identity > 98%, end coverage > 95%, and only one hit/end) were used to obtain unambiguous mapping.

Supplementary Table 4. List of tissues, genotypes, and read lengths for whole transcriptome sequencing.

Genotype	Tissue Name	Tissue Description	Single Reads	Paired Reads	Total Reads: Single Reads	Paired Reads	Total Reads: Paired Reads
DM1-3 516 R44	ABA	Whole plants, treated with 50 uM ABA, 24 hr	36 bp		16,941,649		
DM1-3 516 R44	BABA	Detached leaves, elicitor (BABA) pooled at 24 h, 48 hr, 72 hr	36 bp		33,733,539		
DM1-3 516 R44	BAP	Whole plants, treated with 10 uM BAP, 24 hr	36 bp		25,112,442		
DM1-3 516 R44	BTH	Detached leaves, elicitor (BTH) pooled at 24 h, 48 hr, 72 hr	36 bp		28,564,425		
DM1-3 516 R44	Callus	Callus (10 and 11 week old) generated from leaves and stems	36 bp	105/85 bp	15,852,698	105/85 bp	25,128,520
DM1-3 516 R44	Carpels	Carpels	36 bp		20,723,777		
DM1-3 516 R44	Control	Detached leaves, control for biotic stress pooled at 24 h, 48 hr, 72 hr	36 bp		27,792,294		

DM1-3 516 R44	Control	Whole plants, Control for salt and mannitol treatment	36 bp		22,044,484		
DM1-3 516 R44	Control	Whole plants, Control for IAA, GA3, BAP, and ABA treatment	36 bp		18,874,010		
DM1-3 516 R44	Control	Whole plants, Control for 35 C treatment	36 bp	105/85 bp	17,560,056	105/85 bp	39,071,562
DM1-3 516 R44	Fruit mesocarp and endocarp	DM x A132-238, 4 week mesocarp and endocarp	36bp		37,090,514		
DM1-3 516 R44	GA3	Whole plants, treated with 50 uM GA3, 24 hr	36 bp		19,756,489		
DM1-3 516 R44	Heat	Whole plants, heat treated (35 C), 24 hr, dark	36 bp		29,974,942		
DM1-3 516 R44	IAA	Whole plants, treated with 10 uM IAA, 24 hr	36 bp		20,070,861		
DM1-3 516 R44	Immature whole fruit	DM x P055-14, 2.5 week immature whole fruit	36bp		38,285,431		

DM1-3 516 R44	Leaves	No treatment	36 bp		26,157,013		
DM1-3 516 R44	Mannitol	Whole plants, treated with 260 uM Mannitol, 24 hr	36 bp		17,540,271		
DM1-3 516 R44	Mature whole fruit	DM x S701-2, 6.5 week whole fruit	36bp		39,225,431		
DM1-3 516 R44	*P. infestans*	Detached leaves, pathogen challenge pooled at 24 h, 48 hr, 72 hr	36 bp		46,120,230		
DM1-3 516 R44	Petals	Petals	36 bp		29,066,497		
DM1-3 516 R44	Petioles	Petioles	36 bp	76 bp	22,225,870	76 bp	49,114,314
DM1-3 516 R44	Roots	Roots	36 bp	76 bp	20,044,161	76 bp	91,723,550
DM1-3 516 R44	Salt	Whole plants, treated with 150 mM NaCl, 24 hr	36 bp		20,536,983		

DM1-3 516 R44	Sepals	Sepals	36 bp		16,291,966		
DM1-3 516 R44	Shoots	Shoots	36 bp		25,824,317		
DM1-3 516 R44	Stamens	Stamens	36 bp		20,037,385		
DM1-3 516 R44	Stolons	Some stolons were above ground and were green	36 bp	76 bp	15,957,004	76 bp	24,982,942
DM1-3 516 R44	Tubers, Sample 1	Whole tubers, Harvested 5-5-09	36 bp		16,004,340		
DM1-3 516 R44	Tubers, Sample 2	Whole tubers, Harvested 6-1-09	36 bp	105/85 bp	20,025,196	105/85 bp	41,459,674
DM1-3 516 R44	Whole Mature Flowers	Whole mature flowers	36 bp	76 bp	26,317,607	76 bp	47,829,268
DM1-3 516 R44	Wounding, Primary	Wounded bottom two leaflets, 24 hr post wounding	36 bp		25,329,361		

DM1-3 516 R44	Wounding, secondary	Non-wounded leaflets, 24 hr post wounding	36 bp	105/85 bp	17,019,337	105/85 bp	37,446,274
RH89-039-16	Flower	Whole flower buds pre- and post-anthesis	36 bp		6,133,946		
RH89-039-16	Leaf	1st and 2nd fully expanded leaf	36 bp		6,694,818		
RH89-039-16	Mature Tuber	Large tuber with average size range between 2.5 and 3.5 cm (tuber filling stage)	36 bp		6,291,767		
RH89-039-16	Petiole	Petiole of 1st, 2nd and 3rd fully expanded leaf	36 bp		6,548,759		
RH89-039-16	Root	Collected Root tissue from soil grown plants	36 bp		12,209,179		
RH89-039-16	Shoot apex	Top part of the shoot with apical meristem and young leafs	36 bp		6,634,548		
RH89-039-16	Stamen	Intact stamens collected from fully developed open flowers	36 bp		12,083,841		

RH89-039-16	Stem	Internodes from the main shoot, young and older internodes	36 bp	6,276,156
RH89-039-16	Stolon	Non-tuberizing stolon tips (2 - 6 cm in length)	36 bp	6,345,392
RH89-039-16	Tuber cortex	Section of fully matured tubers between vascular tissues and epidermis	36 bp	11,286,464
RH89-039-16	Tuber peel	Outer cell layers (2-4mm) of fully matured tuber including phellem, epidermis and additional cell layers	36 bp	9,626,503
RH89-039-16	Tuber pith	Central pith of fully matured tubers was collected	36 bp	12,187,256
RH89-039-16	Tuber sprout	Tubers were stored at RT in the dark until significant sprouting was observed (3-4 months)	36 bp	11,393,776
RH89-039-16	Water stressed leaf	Soil grown plants were denied water for a period of 2 days afterw hich samples were collected from 2nd to 4th wilting leaf	36 bp	12,281,440
RH89-039-16	Whole *in vitro* plant	Plants were grown in MS20 medium, 4 week old plantlets including roots were harvested	36 bp	8,315,792

RH89-039-16	Young Tuber	Small developing tuber with size of around 1cm	36 bp	6,066,010

Supplementary Table 5.Classification of Prediction at the Transcript and Gene Level

	Number	Percentage
Transcripts with:		
Protein Support[a]	45,790	81.50%
EST &/or RNA-Seq Support[b,c]	38,250	68.04%
Protein & EST &/or RNA-Seq Support	34,637	61.61%
Protein OR EST &/or RNA-Seq Support	49,403	87.88%
Protein Support Only	11,153	19.84%
EST &/or RNA-Seq Support Only	3,613	6.43%
Ab initio	6,815	12.12%
	56,218	
Genes with:		
Protein Support	29,901	76.61%
EST &/or RNA-Seq Support	23,617	60.51%
Protein & EST &/or RNA-Seq Support	21,036	53.90%
Protein OR EST &/or RNA-Seq Support	32,403	83.02%
Protein Support Only	11,153	28.57%
EST &/or RNA-Seq Support Only	3,086	7.91%
Ab initio	3,765	9.65%

[a] Protein support criterion : identity >=30%, e value < 1 e-20 for the protein whose length are greater than 150. While for other proteins, the condition Identity>=(5+480x(match_lengthx(-0.32x(1+exp(match_length/1000) based on the reference (Rost, B. (1999). "Twilight zone of protein sequence alignments." Protein Engineering 12(2): 85-94.)

[b] EST filtering criterion : identity >=95%, EST coverage >=90%

[c] RNA-seq support criterion is based on the Cufflinks prediction

Supplementary Table 6. Absolute length, arm ratio and percentage of heterochromatin of individual pachytene chromosome of DM1-3

Chr.	Absolute length (μm)	Short arm (μm)	Long arm (μm)	Arm ratio (L/S)	Centromere index	Het. total (%)	Het. SA %	Het. LA %	n
1	68.2 ± 9.9	17.6 ± 2.7	50.6 ± 7.4	2.9 ± 0.2	25.9 ± 1.3	27.6 ± 0.9	53.1 ± 4.5	18.7 ± 2.2	5
2	48.0 ± 2.6	2.1 ± 0.1	45.9 ± 2.3	23.7 ± 5.7	4.3 ± 1.1	25.7 ± 3.8	100 ± 0.0	22.4 ± 3.3	6
3	56.7 ± 15.0	9.2 ± 1.2	47.4 ± 14.2	5.1 ± 1.1	16.8 ± 2.8	25.7 ± 4.9	49.5 ± 6.1	21.0 ± 4.8	7
4	55.1 ± 5.7	19.6 ± 1.7	35.5 ± 4.2	1.8 ± 0.1	35.7 ± 1.6	23.6 ± 3.6	33.3 ± 3.7	18.3 ± 4.5	5
5	37.4 ± 4.7	16.6 ± 2.1	20.8 ± 2.9	1.2 ± 0.1	44.5 ± 1.9	38.1 ± 4.4	42.4 ± 5.3	34.6 ± 5.0	5
6	53.3 ± 8.4	10.5 ± 1.9	42.8 ± 6.9	4.1 ± 0.5	19.8 ± 2.0	26.3 ± 3.3	52.5 ± 6.4	20.0 ± 4.1	7
7	34.3 ± 5.9	10.5 ± 2.6	23.7 ± 3.5	2.3 ± 0.3	30.5 ± 3.0	34.0 ± 3.5	44.5 ± 7.3	29.7 ± 3.8	8
8	43.7 ± 2.6	12.1 ± 1.0	31.6 ± 2.2	2.6 ± 0.2	27.8 ± 1.9	31.7 ± 2.6	50.0 ± 2.3	24.7 ± 3.0	7
9	36.3 ± 1.6	11.4 ± 0.5	24.9 ± 1.5	2.2 ± 0.1	31.5 ± 1.5	43.2 ± 2.8	46.2 ± 5.4	41.8 ± 2.5	5
10	31.6 ± 2.8	11.8 ± 1.0	19.8 ± 1.9	1.7 ± 0.1	37.3 ± 1.2	40.6 ± 3.7	48.1 ± 2.2	36.2 ± 5.7	6
11	40.6 ± 6.3	19.4 ± 3.2	21.2 ± 3.2	1.1 ± 0.1	47.8 ± 1.6	29.7 ± 5.6	39.7 ± 8.7	20.5 ± 4.2	5
12	42.3 ± 6.4	17.1 ± 2.8	25.2 ± 3.8	1.5 ± 0.1	40.4 ± 1.8	41.0 ± 4.0	27.4 ± 7.2	50.2 ± 4.4	6

Het. SA (LA) %: Heterochromatin of the short (long) arm (μm)/ Length of the short (long) arm (μm).

Supplementary Table 7. Top 50 Pfam domains in non-Asterid and Asterid-specific gene sets.

A. Top 50 Pfam domains in non-Asterid-specific potato genes.

Pfam	Function	Counts
PF01535	Pentatricopeptide repeat	4135
PF00560	Leucine-rich repeat	2446
PF00069	Serine/threonine-protein kinase-like domain	870
PF00400	WD40 repeat, subgroup	788
PF00067	Cytochrome P450	514
PF00931	NB-ARC	454
PF00249	Myb, DNA-binding	373
PF00076	RNA recognition motif, RNP-1	363
PF07714	Serine-threonine/tyrosine-protein kinase	348
PF00646	F-box domain, cyclin-like	318
PF00097	Zinc finger, C3HC4 RING-type	296
PF00201	UDP-glucuronosyl/UDP-glucosyltransferase	275
PF08263	Leucine-rich repeat-containing N-terminal domain, type 2	273
PF00847	Pathogenesis-related transcriptional factor/ERF, DNA-binding	233
PF00036	EF-hand	218
PF03171	Oxoglutarate/iron-dependent oxygenase	191
PF00023	Ankyrin repeat	174
PF00153	Mitochondrial substrate/solute carrier	165
PF00005	ABC transporter-like	162
PF02458	Transferase	160
PF00319	Transcription factor, MADS-box	149
PF00168	C2 calcium-dependent membrane targeting	143
PF02519	Auxin responsive SAUR protein	140
PF01554	Multi antimicrobial extrusion protein MatE	134
PF00141	Haem peroxidase, plant/fungal/bacterial	128
PF00010	Helix-loop-helix DNA-binding domain	127
PF00004	ATPase, AAA-type, core	115
PF02362	Transcriptional factor B3	110
PF02365	No apical meristem (NAM) protein	107
PF00106	Short-chain dehydrogenase/reductase SDR	104
PF00226	Heat shock protein DnaJ, N-terminal	102
PF04043	Pectinesterase inhibitor	102
PF00083	General substrate transporter	100
PF00046	Homeobox	99
PF00657	Lipase, GDSL	98
PF03106	DNA-binding WRKY	98
PF00514	Armadillo	96
PF00082	Peptidase S8/S53, subtilisin/kexin/sedolisin	95

PF00515	Tetratricopeptide TPR-1	92
PF00234	lant lipid transfer protein/seed storage/trypsin-alpha amylase inhibit	90
PF00098	Zinc finger, CCHC-type	89
PF00642	Zinc finger, CCCH-type	87
PF01453	Curculin-like (mannose-binding) lectin	87
PF00561	Alpha/beta hydrolase fold-1	86
PF00190	Cupin 1	85
PF00240	Ubiquitin	85
PF00854	Oligopeptide transporter	85
PF01715	tRNA isopentenyltransferase	85
PF07734	F-box associated domain, type 1	84
PF00481	Protein phosphatase 2C, N-terminal	82

B. Top 50 Pfam domains in Asterid-specific potato genes.

Pfam	Function	Counts
PF02902	Peptidase C48, SUMO/Sentrin/Ubl1	30
PF03226	Yippee-like protein	6
PF10536	Aminotransferase-like, plant mobile domain	6
PF02365	No apical meristem (NAM) protein	5
PF03058	Systemic acquired resistance protein SAR	4
PF00031	Proteinase inhibitor I25, cystatin	3
PF00098	Zinc finger, CCHC-type	3
PF01585	D111/G-patch	3
PF05938	Plant self-incompatibility S1	3
PF00168	C2 calcium-dependent membrane targeting	2
PF06839	Zinc finger, GRF-type	2
PF07145	Ataxin-2, C-terminal	2
PF07333	S locus-related glycoprotein 1 binding pollen coat	2
PF07714	Serine-threonine/tyrosine-protein kinase	2
PF08387	FBD	2
PF09331	Domain of unknown function DUF1985	2
PF12061	Late blight resistance protein R1	2
PF00249	Myb, DNA-binding	1
PF00407	Bet v I allergen	1
PF00560	Leucine-rich repeat	1
PF00646	F-box domain, cyclin-like	1
PF00931	NB-ARC	1
PF02362	Transcriptional factor B3	1
PF02458	Transferase	1
PF02671	Paired amphipathic helix	1
PF02797	Chalcone/stilbene synthase, C-terminal	1
PF02977	Proteinase inhibitor I37, carboxypeptidase A	1

PF03195	Lateral organ boundaries, LOB	1
PF04043	Pectinesterase inhibitor	1
PF04770	ZF-HD homeobox protein, Cys/His-rich dimerisation domain	1
PF05498	Rapid ALkalinization Factor	1
PF07172	Glycine rich protein	1
PF07734	F-box associated domain, type 1	1
PF08263	Leucine-rich repeat-containing N-terminal domain, type 2	1
PF08646	Replication factor A, C-terminal	1
PF09668	Peptidase aspartic, eukaryotic predicted	1

Supplementary Table 8. Statistics on syntenic blocks within Arabidopsis, grape and potato.

Species	No. of syntenic blocks		No.of gene pairs per block		No. of genes involved	
	10Kb	20Kb	10Kb	20Kb	10Kb	20Kb
Arabidopsis	6,315	4,613	19.9	40.3	15,272	20,075
Grape	457	1,617	7.7	10	3,674	8,354
Potato	284	1,811	11.6	16.8	3,286	10,046

Note: Syntenic blocks within each species were detected by Mcscan software. At least five genes are required to call synteny. The intergenic sizes of 10kb and 20kb were used, respectively. The intergenic size is defined as the distance from the stop codon of the former gene to the start codon of the latter one.

Supplementary Table 9. RH sequence data of BACs, organized per chromosome. All BACs not assigned to any chromosome were combined into a virtual chromosome 0.

	Chromosome													
	1	2	3	4	5	6	7	8	9	10	11	12	0	Total
Number of sequences	3,390	174	430	767	5,810	2,111	313	167	1,366	374	600	752	974	17,228
Total sequence length	39,416,252	2,150,289	6,033,695	10,306,172	69,044,492	22,536,121	7,994,542	1,598,666	13,583,059	3,986,047	8,118,603	6,598,057	11,810,820	203,176,815
Minimum sequence length	35	507	286	198	112	84	364	528	29	199	3	32	33	3
Maximum sequence length	155,460	79,841	120,722	107,847	134,177	112,064	175,778	149,534	133,864	76,465	151,103	146,171	122,038	175,778
Average sequence length	11,627	12,358	14,032	13,437	11,884	10,676	25,542	9,573	9,944	10,658	13,531	8,774	12,126	11,793
Median sequence length	6,382	6,691	6,960	8,519	6,884	5,103	9,781	4,698	4,299	5,968	5,052	1,718	6,285	6,128
N50 sequence length	23,393	27,542	29,007	23,411	21,303	22,057	69,670	18,160	21,987	21,596	37,414	33,061	25,332	23,896
A content	32.08	32.46	32.84	32.64	32.27	32.41	32.41	32.23	32.54	31.13	32.70	32.66	31.62	32.28
C content	18.05	17.60	17.29	17.28	17.80	17.56	17.39	17.52	17.30	18.75	17.26	17.41	18.56	17.75
G content	17.90	17.50	17.17	17.35	17.71	17.60	17.49	17.58	17.52	18.64	17.29	17.33	18.40	17.70
T content	31.97	32.43	32.67	32.74	32.21	32.41	32.71	32.68	32.64	31.49	32.75	32.21	31.34	32.24
N content	0.00	0.00	0.03	0.00	0.01	0.01	0.00	0.00	0.00	0.00	0.00	0.39	0.08	0.02

Supplementary Table 10. RH sequence data of the superscaffolds generated from the BACs, organized per chromosome. All superscaffolds consisting of BACs not assigned to any chromosome were combined into a virtual chromosome 0.

	Chromosome													
	1	2	3	4	5	6	7	8	9	10	11	12	0	Total
Number of sequences	464	55	92	117	1,016	508	94	38	442	109	151	387	295	3,768
Total sequence length	35,194,823	2,146,765	6,200,479	8,603,066	55,297,855	21,254,289	7,680,957	1,634,212	12,222,574	3,627,202	7,617,599	5,495,571	11,098,484	178,073,876
Minimum sequence length	35	567	286	198	296	84	366	955	29	199	3	32	33	3
Maximum sequence length	642,579	358,478	294,220	690,852	643,428	448,350	502,327	262,308	367,793	198,610	292,582	312,227	435,238	690,852
Average sequence length	75,851	39,032	67,397	73,530	54,427	41,839	81,712	43,006	27,653	33,277	50,448	14,200	37,622	47,260
Median sequence length	28,259	5,336	37,150	30,589	13,181	5,452	58,981	22,820	1,762	9,278	14,948	1,252	11,671	9,229
N50 sequence length	174,853	123,371	140,403	150,765	167,097	133,651	147,381	99,089	126,089	111,174	133,018	124,670	115,411	143,991
A content	30.78	31.42	31.66	31.65	31.07	31.12	31.94	29.96	31.56	30.14	31.59	31.55	30.74	31.13
C content	17.26	17.07	16.67	16.66	17.16	16.90	17.16	16.35	16.77	17.75	16.62	17.00	17.68	17.09
G content	17.25	16.86	16.71	16.83	17.06	16.83	17.27	16.41	16.85	17.39	16.61	16.81	17.60	17.05
T content	30.81	31.28	31.75	31.77	31.02	31.24	32.39	30.52	31.48	30.00	31.71	31.35	30.56	31.15
N content	3.90	3.37	3.20	3.09	3.69	3.90	1.23	6.76	3.34	4.73	3.47	3.30	3.42	3.59

Supplementary Table 11. GenBank accession numbers for BAC sequences from potato genotype RH (RH89-039-16).

Accession	Name	Base pairs	Sequence fragments	Chromosome
AC239955	RH001C14	107357	9	6
AC238959	RH001D10	90328	3	3
AC233343	RH001E23	127212	7	5
AC237902	RH001F12	99557	8	6
AC239956	RH001G02	95331	8	5
AC237903	RH001H07	93791	7	5
AC240287	RH001H20	123428	2	7
AC243013	RH001H21	134210	2	11
AC231993	RH001K16	121667	12	1
AC237904	RH001O10	111436	9	5
AC237905	RH002E09	110689	3	9
AC235607	RH002F20	136570	8	9
AC239957	RH002G12	110462	10	7
AC237824	RH002G20	103598	11	0
AC239958	RH002J19	113338	5	0
AC231994	RH002L01	116918	6	5
AC231995	RH002P11	178622	22	1
AC237906	RH003B10	123432	3	11
AC237907	RH003D20	155461	1	1
AC239286	RH003G17	51750	3	9
AC237908	RH003H09	118677	17	5
AC233344	RH003K20	120034	9	1
AC237909	RH004C10	93274	15	5
AC243014	RH004D16			
AC215216	RH004E03	132944	9	6
AC233345	RH004H06	118815	3	5
AC237910	RH004H24	96288	9	5
AC237911	RH004I22	105641	12	6
AC237912	RH004I24	133586	3	5
AC211296	RH004J06	134505	20	4
AC233346	RH004M02	116168	2	5
AC237913	RH004P07	178639	32	5
AC237914	RH005A19	114736	6	12
JF317597	RH005A22	99250	51	12
AC237915	RH005E12	107184	12	5
AC237916	RH005E20	141622	15	1
AC237597	RH005F20	131891	13	3
AC235608	RH005G04	120514	9	9

AC237917	RH005G22	126439	15	5
AC237918	RH005I02	109211	8	5
AC225326	RH005J09	34186	1	6
AC237919	RH005L02	108246	11	5
AC237825	RH005N07	139171	2	0
AC239959	RH005P10	135109	19	0
AC233347	RH006A03	99644	6	5
AC237920	RH006D03	108890	3	5
AC233348	RH006D17	114596	9	1
JF317598	RH006G03	110609	4	12
AC216947	RH006L15	109684	12	6
AC237921	RH006M08	109537	14	5
AC237922	RH007C01	154277	32	1
AC240288	RH007D20	130424	10	7
AC233602	RH007E14	105341	8	4
AC237923	RH007L17	159185	11	5
AC239960	RH007L22	185706	31	4
AC237924	RH007N06	106766	13	5
AC217826	RH008A10	125608	9	6
AC233349	RH008K06	100620	14	5
AC237925	RH008O03	126125	12	5
AC237926	RH008O14	32870	2	5
AC237927	RH008P12	125692	3	11
AC233350	RH009A20	79426	9	5
AC237928	RH009B21	99155	10	5
AC239287	RH009D23	168763	32	9
AC239962	RH009I12	101077	14	0
AC235609	RH009K01	110307	19	9
AC237929	RH009N08	109728	8	5
AC233351	RH009O06	114995	10	1
AC239963	RH009O14	117751	11	5
AC235610	RH010D12	124726	12	9
AC239288	RH010G14	234743	44	9
AC239964	RH010H08	143491	10	0
AC235611	RH010H21	7452	5	9
AC237930	RH010L20	120122	5	6
AC233694	RH010N18	111661	17	6
AC233352	RH010P11	126730	7	5
AC239965	RH010P17	113999	4	11
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AC217100	RH063L11	128753	9	6
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AC239309	RH065C11	120264	20	9
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AC238124	RH079O07	126721	5	4
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AC238143	RH085B09	130297	5	5
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AC238144	RH085C18	115006	6	5
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AC238154	RH086N05	142614	9	6
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AC238165	RH091F11	120905	4	5
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AC239318	RH091N18	111365	30	9
AC232867	RH091O16	144839	8	6
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AC217721	RH092C10	144204	4	1
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AC238170	RH093D09	177387	14	5
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AC238208	RH104O02	109695	9	5
AC232083	RH105A22	136895	11	1
AC237856	RH105B16	124232	10	5
AC237857	RH105D06	140971	5	0
AC238209	RH105E10	150457	27	5
AC233480	RH105J02	129074	6	1
AC239953	RH105L18	162495	19	3
AC238210	RH105N06	211329	19	5
AC240008	RH105N09	67044	11	11
AC233482	RH105N22	98760	8	5
AC233483	RH105O24	248025	19	2
AC231849	RH105P10	186682	30	6
AC240009	RH106C02	155047	24	0
AC238211	RH106C12	147384	5	6

AC237858	RH106F19	104076	2	0
AC233484	RH106G12	191562	11	1
AC243388	RH106G13	149845	8	5
AC232084	RH106H24	96230	6	1
AC217726	RH106J13	170217	8	1
AC238212	RH106O04	112694	14	5
AC238213	RH109J16	183309	19	5
AC238214	RH111D07	115145	8	5
AC238215	RH115J03	109210	7	5
AC238216	RH115L20	117829	12	5
AC238217	RH116P21	188843	14	5
AC243389	RH118N04	122238	14	5
AC238218	RH119N02	147212	12	5
AC237859	RH120B09	53184	3	0
AC243035	RH120F08	157001	2	11
AC233485	RH120L06	99016	4	1
JF317615	RH120P23	115714	11	12
AC217727	RH121C15	112581	4	1
AC232085	RH121C16	16183	1	5
AC231670	RH121D01	112395	1	11
AC233486	RH121D18	128611	9	1
AC237666	RH121F22	132044	3	3
AC240316	RH121H04	112113	4	7
AC238219	RH121H11	124539	10	5
AC233487	RH121J02	114087	2	5
AC238220	RH121L12	131147	12	5
AC237860	RH122C15	121070	6	0
AC240010	RH122G20	110965	27	9
JF317616	RH122I19	117095	15	12
AC239321	RH122I22	139257	11	9
AC217828	RH122J04	123265	10	6
AC243036	RH122L11	14283	1	11
AC235645	RH122M23	111602	11	9
AC232810	RH122N23	157213	15	6
AC238221	RH123D21	103877	6	6
AC233488	RH123G21	112128	5	1
AC234539	RH123H06	141772	8	1
AC243037	RH123I06			
AC240317	RH123I15	169262	7	4
AC233489	RH123J06	139205	8	5
AC238222	RH123P09	69173	72	6
AC239322	RH124C01	112342	9	9
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AC233490	RH124H11	155178	3	1
AC240011	RH124N10	115537	7	0
AC233491	RH124O16	129517	5	1
AC217646	RH125A20	126107	9	6
AC238223	RH125C20	130992	21	5
AC233492	RH125C24	117182	8	1
AC239178	RH125E03	121800	6	3
AC240012	RH125E08	112587	19	0
AC240318	RH125G05	113702	7	7
AC238224	RH125G09	116894	19	5
AC232086	RH125H16	125710	2	1
AC238225	RH125I04	115508	12	5
AC234707	RH125I21	130517	20	6
AC240013	RH125J07	136617	13	0
AC238226	RH125M03	100943	16	5
AC240014	RH125M10	131579	6	11
AC240319	RH126B22	153442	6	7
JF317590	RH126B24	92652	12	12
AC233493	RH126D06	187374	17	1
AC233494	RH126H02	107063	1	5
AC238227	RH126I21	121278	18	6
HQ896309	RH126J23	77110	1	0
AC240122	RH126O17	113648	11	5
AC236589	RH126P10	131948	8	3
AC234708	RH127B20	108720	4	6
AC234540	RH127E04	116744	7	5
AC238228	RH127F09	128541	10	5
AC238229	RH127I11	113616	3	5
AC243390	RH127J02	159385	18	8
AC216951	RH127J15	127575	4	6
AC232087	RH127K11	158801	11	5
AC237861	RH127M01	114619	3	0
AC238967	RH127M02	170059	11	3
AC238230	RH128A06	108270	18	5
AC234709	RH128E11	136255	10	6
AC240015	RH128F11	115521	9	11
AC238231	RH128F20	47967	2	5
AC209525	RH128G04	55865	12	1
AC235646	RH128G19	162858	25	9
AC243038	RH128H14	29576	1	11
AC238232	RH128H15	130824	9	5
AC232088	RH128L19	142844	8	1
AC238233	RH128L23	100401	15	5

AC240320	RH128M24	124797	1	7
AC237667	RH128N23	110413	10	3
AC243039	RH129024			
AC240016	RH129B02	154459	13	8
AC240017	RH129G22	118739	6	10
AC239323	RH129L15	89758	34	9
AC243391	RH129M17	40156	5	1
AC233495	RH130E21	90031	12	5
AC233496	RH130G14	144858	7	1
AC232089	RH130I12	108580	9	5
AC232318	RH130I13	60790	1	11
AC234541	RH130I21	125818	4	1
AC238234	RH130J23	101666	17	1
AC233497	RH130L03	106774	2	5
AC237862	RH130M06	42126	1	0
AC237863	RH130M21	114214	6	0
AC238235	RH130O22	120500	6	5
AC213724	RH130P10	144534	12	6
AC240018	RH130P11	114002	6	10
AC238236	RH131F18	126713	10	5
AC238237	RH131J02	99867	11	5
AC243392	RH131O15	109176	20	5
AC238238	RH131P02	129196	13	5
AC238239	RH132B19	111235	13	5
AC233498	RH132C18	123107	10	5
AC233499	RH132D05	113427	13	5
AC233500	RH132E14	129475	12	1
AC238240	RH132J19	151495	9	5
AC236590	RH132M21	125317	6	3
AC238241	RH132O23	134166	9	5
AC238242	RH132P09	117597	7	5
AC238243	RH132P23	123378	10	5
AC240019	RH133D07	124763	5	10
AC238244	RH133F12	41229	5	5
AC236626	RH133G12	155945	30	5
AC240321	RH133H05	127171	2	7
AC238245	RH133I18	108706	7	5
AC238246	RH133N20	123430	4	5
AC235647	RH134A22	129193	20	9
AC238247	RH134E14	147837	11	5
AC234697	RH134F01	115623	5	6
AC232090	RH134G07	127567	3	5
AC238248	RH134G11	170374	7	5

AC236591	RH134I23	133358	9	3
AC240322	RH134L03	128341	7	7
AC236746	RH134M14	128790	4	4
AC233501	RH134N13	130707	3	1
AC236627	RH134P05	154819	6	1
AC233628	RH135G07	102676	7	4
AC235648	RH135I22	121709	2	9
AC237864	RH135L11	110147	3	0
AC237865	RH135M18	148586	6	0
AC238249	RH135N06	125738	5	5
AC238250	RH136E22	108118	4	5
AC233502	RH136G24	141561	13	1
AC234542	RH136H10	110875	6	1
AC240020	RH136H12	117436	7	0
AC238251	RH136H24	120208	3	5
AC233629	RH136J13	157089	18	4
AC234690	RH136K02	121609	11	6
AC238252	RH136K19	111906	5	5
AC238253	RH136O01	115575	3	5
AC233503	RH137J18	116657	8	1
AC236846	RH137K05	109491	10	6
AC237866	RH137K16	50554	3	0
AC233504	RH137L15	110496	2	5
AC238254	RH138C23	109709	4	5
AC232091	RH138F06	132958	20	1
JF317618	RH138F16	143697	2	12
AC240356	RH138I21	115369	5	unknown
AC238255	RH138K13	60896	3	5
AC240123	RH138M23	103532	14	4
AC238256	RH138N05	116871	8	5
AC239324	RH138P01	146975	11	9
AC240021	RH139C15	94472	16	0
AC213863	RH139E21	100286	13	6
AC240022	RH139G21	97193	20	11
AC239325	RH139I09	136967	13	9
AC240023	RH140F06	148677	10	9
AC235649	RH140N04	119760	18	9
AC233505	RH140O18	132299	8	1
AC238257	RH140O20	124246	5	1
AC232092	RH141A04	42339	2	0
AC233506	RH141C04	157767	10	5
AC240024	RH141E03	67479	11	11
AC240323	RH141J16	49784	1	7

AC233507	RH141L09	121354	3	1
AC237869	RH141L24	154076	19	5
AC238258	RH141P08	124351	5	5
AC237870	RH141P18	122053	1	0
AC240025	RH142A12	129211	7	7
AC233508	RH142B11	134783	2	1
AC238259	RH142B16	116618	7	5
AC235650	RH142C19	112654	13	9
AC240026	RH142H10	48990	24	10
AC236747	RH142I08	160103	8	4
AC232093	RH142J23	137258	3	1
AC240027	RH142K09	58772	17	4
AC238260	RH142L01	109862	7	5
AC233509	RH142M15	115114	3	5
AC231973	RH143A24	128145	12	6
AC233510	RH143C20	109345	6	5
AC232094	RH143D14	123864	4	0
AC240324	RH143L23	131436	4	7
AC238261	RH143M21	101642	3	4
AC233511	RH144D22	150523	11	1
AC238262	RH144F10	111116	6	5
AC238263	RH144F22	125635	6	5
AC240028	RH144F23	67146	7	0
AC238264	RH144G18	130041	5	5
AC237668	RH144I14	111698	4	3
AC238265	RH144I18	134804	19	5
AC234543	RH144I22	121796	11	1
AC238266	RH144J06	122846	10	1
AC243042	RH144O01	50076	1	11
AC236629	RH144O02	153514	15	5
AC238267	RH144O03	139457	17	5
AC240029	RH144P01	125795	7	11
AC232095	RH145A24	177462	17	1
AC240124	RH145B06	92215	3	9
AC232096	RH145B23	97125	26	1
AC217647	RH145D12	23917	3	unknown
AC240030	RH145E19	124429	21	0
AC218123	RH145G10	126206	10	6
AC238268	RH145H03	139567	9	4
AC239326	RH145H21	141031	8	9
AC239327	RH145K07	65996	3	9
AC233512	RH145L13	119162	4	1
AC233513	RH145M01	129980	3	1

AC240325	RH146A02	128766	4	7
AC243043	RH146E08			
AC233514	RH146F20	111833	7	1
JF317619	RH146H02	107907	11	12
AC240031	RH147C10	118848	11	0
AC238269	RH147D22	120528	6	5
AC238270	RH147E16	113145	7	5
AC234544	RH147F16	123148	8	1
AC240125	RH147G23	124402	17	1
AC243393	RH147I01	158168	16	12
AC238271	RH147J19	112134	3	3
AC233630	RH147K10	146706	9	4
AC216952	RH147M20	119959	8	6
AC238272	RH147M21	132633	16	5
AC238273	RH148B08	130236	11	3
AC233515	RH148B12	132098	6	2
AC239954	RH148D02	125322	4	11
AC239328	RH148E07	135531	12	9
AC232097	RH148K09	145288	9	1
AC238274	RH148L18	64268	4	6
AC236630	RH148O06	109051	19	1
AC237873	RH148O20	76225	1	0
AC232098	RH149A16	143176	21	1
AC238275	RH149C08	111376	13	5
AC233516	RH149C23	112767	5	1
AC236631	RH149D09	95784	8	1
AC232099	RH149F06	120617	13	5
AC240326	RH149F10	127995	3	4
AC237874	RH149G10	108837	6	0
AC238276	RH149H18	126777	10	5
AC235651	RH149J19	135531	8	9
AC232100	RH149K08	146720	6	5
AC233517	RH149K17	71623	2	1
AC232101	RH149L10	116280	4	0
AC243394	RH149L23	122572	4	5
AC238277	RH149N09	114425	1	5
AC235652	RH149P12	117414	4	9
AC238278	RH150D03	111185	7	5
AC232102	RH150D18	42511	1	0
AC240327	RH150F15	112382	9	7
AC238279	RH150G07	119380	9	5
AC238280	RH150G14	181388	18	5
AC240032	RH150H11	112825	10	0

AC231524	RH150K08	109230	10	6
AC240033	RH150L02	141580	6	0
AC232878	RH150M13	165649	18	6
AC232103	RH150M21	47603	3	0
AC238281	RH150O10	118989	5	5
AC238282	RH151B14	84888	23	1
AC238283	RH151C01	111931	6	6
AC238284	RH151F02	130695	2	5
AC240034	RH151J09	134225	10	0
AC240035	RH151K12	101295	5	0
AC235969	RH151K19	121044	10	6
AC234546	RH151M01	112928	9	1
AC234591	RH151M22	133521	15	5
AC236632	RH151P03	114710	9	5
AC243044	RH152E20			
AC233518	RH152G01	123093	7	1
AC232105	RH152G12	52346	2	0
AC238285	RH152M02	109860	13	1
AC238974	RH152M21	108736	1	0
AC238286	RH153A03	122198	24	1
AC235970	RH153A08	126689	10	6
AC238287	RH153B22	130431	10	5
AC235653	RH153C21	118789	2	9
AC238288	RH153F16	106063	2	5
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AC238291	RH153N17	107470	7	12
AC235654	RH154D19	145972	14	9
AC243395	RH154G05	122011	14	5
AC240036	RH154I16	103130	7	0
AC240037	RH154J09	109560	5	9
AC238292	RH155M20	130611	6	11
AC238293	RH156F04	110014	6	6
AC232106	RH156I19	119226	17	1
AC240038	RH156J02	81128	20	11
AC232107	RH156M09	123903	7	1
AC243396	RH156N08	133931	9	1
AC233631	RH157C17	128689	6	4
AC238294	RH157C24	110364	10	1
AC240039	RH157I11	40190	9	0
AC240040	RH157M15	94656	3	0
AC238295	RH158C09	131879	19	5
AC233519	RH158F19	129776	7	5

AC238296	RH158G03	113364	6	5
AC234547	RH158H10	110406	10	1
AC238297	RH158J20	127796	13	5
AC238298	RH158K01	101464	41	1
AC238299	RH158K09	59416	23	6
AC217728	RH158N18	152248	7	1
JF317620	RH158O09	87252	25	12
AC233632	RH159A24	145425	12	4
AC236633	RH159C21	128394	12	1
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AC240328	RH159J14	114575	1	7
AC234548	RH159L02	121642	6	1
AC238301	RH159L13	104500	4	5
AC238302	RH159M14	155360	4	5
AC238303	RH159N19	110491	5	5
AC236714	RH159O01	132236	10	3
AC238304	RH159P03	56898	20	6
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AC238305	RH160A07	82531	5	1
AC217729	RH160B23	146900	6	1
AC204500	RH160C14	137278	4	6
AC240329	RH160E03	128080	4	7
AC237669	RH160E15	120723	1	0
AC235655	RH160F08	115853	28	9
AC233520	RH160F18	110508	6	5
AC240041	RH160G21	104759	9	7
AC240042	RH160J08	111146	3	0
AC231548	RH160K03	119705	4	6
AC243397	RH160L13	30199	2	5
AC238306	RH160N05	107029	4	12
AC243398	RH160O21	112031	3	5
AC236847	RH161M15	130871	8	6
AC217817	RH161N18	114620	11	6
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AC238307	RH162D01	114237	11	4
AC238308	RH162D10	123931	6	5
AC238309	RH162D21	112043	6	5
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AC238310	RH162G20	53880	13	5
AC238311	RH162H12	121444	20	5
AC234549	RH162L11	122555	9	1
AC238312	RH162L15	160294	10	5

AC236748	RH162M08	164840	9	4
AC243046	RH162O21			
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AC232108	RH163B17	112903	7	1
AC238314	RH163C24	129104	5	12
AC216953	RH163H01	103198	9	6
AC240331	RH163I17	136901	6	4
AC240043	RH163J17	109117	12	7
AC217730	RH163K01	106002	4	1
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AC243399	RH164A15	114323	11	5
AC232709	RH164L12	104512	11	6
AC238317	RH164L24	122297	6	5
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AC236848	RH164O16	105990	8	6
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AC235656	RH165G14	127637	9	9
AC233522	RH165H04	126580	7	5
AC232109	RH165I16	50682	8	0
AC239329	RH165J16	110660	6	9
AC232110	RH165K04	44696	2	0
AC238321	RH165M06	114723	5	5
AC240126	RH165O03	115222	15	5
AC238322	RH166C13	109207	15	5
AC240127	RH166D06	135815	25	5
AC238323	RH166F01	121106	2	5
AC243400	RH166F13	130291	12	5
AC238324	RH166G03	110982	12	1
AC236634	RH166G13	122905	11	5
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AC243047	RH166M24			
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AC238325	RH167B02	113727	9	5
AC234551	RH167C13	111643	9	1
AC238326	RH167C18	104155	11	5
AC238327	RH167D14	114692	15	5
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AC238329	RH167G22	133079	29	5

AC238330	RH167I06	108157	8	5
AC240332	RH167I20	110882	6	7
AC238331	RH167J04	129864	14	6
AC238332	RH167J15	130481	15	1
AC232111	RH167J23	120284	1	5
AC238333	RH167M08	115248	2	5
AC233523	RH167N12	133687	10	1
AC232112	RH167N13	117897	6	1
AC234552	RH167O11	104396	10	5
AC243401	RH167O20	108862	6	5
AC238334	RH167O23	114162	14	5
AC240333	RH168B10	191915	3	7
AC237875	RH168B16	39951	1	0
AC232811	RH168D09	114221	10	6
AC239330	RH168F09	107795	6	9
AC243402	RH168G10	153165	12	5
AC233634	RH168I03	112175	6	4
AC233524	RH168I06	121813	8	5
AC240334	RH168N10	128428	8	7
AC232113	RH169C15	119926	5	1
AC238335	RH169D20	15285	2	5
AC238336	RH169F21	160146	19	6
AC238337	RH169I18	114456	3	5
AC238338	RH169K01	137150	9	5
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AC232389	RH169M08	125787	6	6
AC238339	RH170A06	100095	12	5
AC234553	RH170A10	130471	18	1
AC240047	RH170E13	113498	16	0
AC234554	RH170G14	99200	8	5
AC233525	RH170I10	141710	12	5
AC233526	RH170J20	130173	5	1
AC243049	RH170L21			
AC240335	RH170M01	139517	3	7
AC238340	RH170N15	103665	22	11
AC238341	RH170N19	92697	3	5
AC238342	RH170O21	26477	1	5
AC238343	RH171B14	108082	9	0
AC233527	RH171E23	116278	6	5
AC243403	RH171H17	149452	25	5
AC234555	RH171I01	108288	6	5
AC239331	RH171I16	118230	4	9
AC232114	RH171N08	112720	11	5

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AC216954	RH171N20	121085	2	6
AC237101	RH171P07	105998	13	3
AC237876	RH171P20	56479	6	0
AC234592	RH172A11	132202	10	5
AC243404	RH172A21	122071	12	5
AC238344	RH172C14	113663	5	6
AC238345	RH172D24	110794	16	5
AC234593	RH172E15	139641	24	5
AC238346	RH172G10	103003	10	5
AC240048	RH172G12	66117	31	9
AC232115	RH172J22	198263	17	1
AC236635	RH172L21	106756	5	1
AC238347	RH172N06	130619	3	5
AC235971	RH173B21	111037	6	6
AC238348	RH173E05	127710	6	5
AC238349	RH173E21	21117	2	5
AC234556	RH173F13	88193	26	0
AC233635	RH173G11	116738	5	4
AC238350	RH173H12	66528	7	12
AC233528	RH173I04	130153	14	1
AC238351	RH173N10	116875	5	5
AC232116	RH174E07	104902	8	0
AC240049	RH174G13	109324	5	8
AC238352	RH174H15	107949	5	0
AC240337	RH174J15	107491	2	7
AC237877	RH174K15	31065	1	0
AC216955	RH174L03	165803	13	6
AC237878	RH175B04	116224	12	0
AC237879	RH175D24	149315	22	5
AC240050	RH175H08	126235	9	0
AC217732	RH175L13	116343	5	1
AC235657	RH176B23	111569	6	9
AC237880	RH176O03	78176	2	0
AC237881	RH176P20	107336	13	0
AC237882	RH176P24	111048	6	0
AC238353	RH177A02	107364	9	5
AC233529	RH177F15	105068	10	5
AC234557	RH177G23	51443	5	0
AC237883	RH177I17	111017	7	0
AC238354	RH177J01	108475	14	5
AC217039	RH177L07	128278	12	6
AC237884	RH177L23	140308	11	0

AC237885	RH177M24	54253	6	0
AC240338	RH178C19	160127	5	7
AC238355	RH178I23	127264	8	1
AC238356	RH178O02	117011	3	5
AC233530	RH179B16	97964	8	1
AC238357	RH179C19	100445	6	4
AC236749	RH179G04	122943	9	4
AC240339	RH179H03	176194	6	7
AC234784	RH179H13	230818	63	6
AC217733	RH179H19	134851	3	1
AC231671	RH179O17	153913	3	11
AC240051	RH180C13	109486	14	10
AC233636	RH180E04	147623	12	4
AC233531	RH180G18	118531	4	1
AC240128	RH180I09	121934	52	1
AC237886	RH180K14	107640	4	0
AC233532	RH181C08	109583	11	1
AC238358	RH181C12	144928	5	5
AC237887	RH181D06	37042	1	0
AC238359	RH181E11	129389	13	1
AC238360	RH181E24	137732	6	5
AC240052	RH181H24	127983	11	5
AC238361	RH181J07	105886	5	5
AC234559	RH181N01	137968	13	1
AC243050	RH182G13			
AC233637	RH182K13	126730	8	4
AC238362	RH182N11	115260	3	5
AC240340	RH182P02	124685	6	7
AC235658	RH183G07	103827	12	9
AC234594	RH183K03	129183	12	1
AC237888	RH183L22	31025	1	0
AC237889	RH183M06	40280	2	5
AC240053	RH184A02	145593	15	0
JF317622	RH184C22	97959	11	12
AC238363	RH184D14	106002	8	5
AC239333	RH184G10	119006	8	9
AC240341	RH184I18	151632	3	7
AC240054	RH184K12	71258	16	1
AC240129	RH184K24	150930	16	10
AC238364	RH184L04	106794	16	5
AC243405	RH184M23	72672	3	1
AC238365	RH184N07	118276	3	5
AC238366	RH185B09	115295	3	0

AC233533	RH185B10	112612	9	1
AC238367	RH185C17	120768	8	12
AC240055	RH185F02	116582	6	11
AC236849	RH185G09	159361	23	6
AC233534	RH185H09	121350	12	5
AC238368	RH185I12	123206	4	1
AC238369	RH185L11	127206	15	5
AC238370	RH185O05	98444	13	5
AC238371	RH185P10	114613	11	5
AC240056	RH186A15	167905	14	11
AC233535	RH186C12	122327	9	5
AC240057	RH186C17	102618	1	9
AC237084	RH186D16	127517	12	3
AC240058	RH186E11	116598	7	10
AC236750	RH186E19	136556	5	4
AC238372	RH186H09	115307	8	6
AC237890	RH186I21	142401	4	0
AC239334	RH186K05	89141	6	9
AC240342	RH186K23	131661	2	7
AC235972	RH186L05	102160	11	6
AC231672	RH186L12	124595	1	11
AC237891	RH186O03	143069	8	0
AC238373	RH187A20	127429	4	5
AC236637	RH187B23	107068	7	1
AC238374	RH187I08	117557	7	2
AC243051	RH187J22			
AC238375	RH188A15	98645	12	5
AC237892	RH188B03	134279	10	0
AC238376	RH188B06	122032	7	5
AC236638	RH188C09	141707	13	1
AC237893	RH188F23	108072	8	0
AC236639	RH188J06	112167	7	1
AC217734	RH188J09	100373	9	1
AC234595	RH188M09	128679	22	1
AC238377	RH188M18	126710	21	5
AC214037	RH188N15	149623	12	6
AC239335	RH188O21	130066	13	9
AC238378	RH189F04	110197	3	5
AC234560	RH189H09	141379	11	1
AC238379	RH189J11	121332	8	5
AC238969	RH189K17	126080	8	3
AC239336	RH190A17	101734	5	9
AC238380	RH190C13	104211	7	5

AC235659	RH190E04	132833	15	9
AC239337	RH190G21	111567	9	9
AC240059	RH190I20	107191	1	7
AC238381	RH190J05	116490	6	5
AC238382	RH191A05	126422	9	5
AC237894	RH191B13	142527	14	0
AC238383	RH191B23	137833	4	5
AC240060	RH191E08	120385	4	0
AC238384	RH191G07	122344	9	5
AC233638	RH191G20	37232	2	4
AC237895	RH191I22	147670	14	5
AC237896	RH191J01	112221	6	0
AC233639	RH191L17	110000	8	4
AC238385	RH191M06	122692	8	5
AC239778	RH191M23	95764	1	0
AC239338	RH191O06	117627	1	9
AC239339	RH192C09	107014	3	9
AC238386	RH192G12	133181	4	12
AC238387	RH192P22	117817	10	12
AC231673	RH193D01	116204	1	11
AC238388	RH193J02	85853	8	5
AC237897	RH193K01	158987	11	0
AC236640	RH193L05	140321	27	0
AC238389	RH193M15	132152	10	5
AC236641	RH193O04	128152	21	5
AC238390	RH193O24	156653	8	5
AC238391	RH194A18	143682	11	5
AC234596	RH194J03	132986	17	1
AC236642	RH194L01	135411	23	1
AC209520	RH194M18	136309	5	6
AC235973	RH194N01	184228	18	6
AC238392	RH194O19	144468	12	5
AC234561	RH195B06	147845	21	1
AC240130	RH195B16	130881	11	12
AC240061	RH195B21	191856	17	10
AC232117	RH195E14	163873	14	1
AC238393	RH195G24	130559	4	5
AC235974	RH195H05	133527	27	6
AC232118	RH195I04	201680	19	1
AC238394	RH195I08	132809	19	1
AC240062	RH195I15	173634	12	7
AC231674	RH195J04	142640	1	11
AC240063	RH195J15	121077	8	9

AC236643	RH195K14	137014	12	5
AC232808	RH195K24	168530	26	6
AC235975	RH195M17	140207	9	6
AC237898	RH195O01	114057	6	0
AC238395	RH196B14	154111	11	1
AC238396	RH196D19	135747	5	0
AC238397	RH196E02	144542	13	5
AC238398	RH196E12	144350	4	5
AC238399	RH196F10	141308	6	5
AC232710	RH196G04	162095	17	6
AC236644	RH196H13	160662	25	5
AC235660	RH196J08	174813	7	9
AC240064	RH196L18	143829	15	0
AC238400	RH197C19	131909	8	1
JF317596	RH197G21	195361	16	6
AC236645	RH197J01	149794	13	5
AC234597	RH197J09	141841	19	1
AC217735	RH197K20	171955	13	1
AC219015	RH197N21	163447	15	6
AC236646	RH197P05	125069	8	1
AC217145	RH198A04	140443	19	6
AC233580	RH198A12	158592	28	6
AC235976	RH198B20	171039	33	6
AC238401	RH198D19	151160	15	1
AC235661	RH198G15	152276	8	9
HQ896311	RH198H19	136416	1	0
AC233536	RH198J18	132077	11	1
AC238402	RH198K10	142851	12	5
AC238403	RH198L17	160415	7	5
AC237900	RH198L23	167586	27	0
AC233537	RH199A09	148294	12	5
AC243406	RH199B23	82054	45	5
AC232119	RH199E21	128935	16	5
AC233538	RH199E23	155407	14	5
AC240065	RH199H05	135304	5	9
AC238404	RH199H21	136024	7	1
AC238405	RH199J10	30401	2	5
AC232813	RH199K09	155610	30	6
AC232120	RH199K20	166439	14	1
AC238406	RH199M03	55959	4	5
AC236647	RH199N09	148700	21	1
AC236648	RH199O13	130236	18	1
AC240131	RH199P24	107911	9	1

AC235695	RH200E03	159297	13	6
AC240066	RH200E19	175455	20	10
AC240067	RH200E20	153701	8	7
AC235977	RH200F13	151368	12	6
AC238407	RH200I12	153845	12	5
AC217103	RH200K19	158032	8	6
AC240343	RH200P15	149532	1	8
AC238408	RH201A02	145943	17	5
AC238409	RH201A13	139664	5	5
AC217802	RH201A18	165830	14	6
AC234563	RH201B24	164170	21	5
AC238410	RH201C20	143573	13	5
AC236850	RH201D07	189967	25	6
AC232121	RH201F12	77584	75	1
AC236851	RH201G10	149520	20	6
AC236649	RH201G17	129815	16	1
AC238411	RH201H03	186966	20	5
AC236650	RH201H08	163545	13	1
HQ896310	RH201H22	211591	1	0
AC233640	RH201K05	160147	24	4
AC240068	RH201L15	133022	7	0
AC243052	RH201N04			
AC236651	RH201O06	140568	18	5
AC234828	RH201O11	142476	11	6
AC243053	RH202F21			
AC240069	RH202G21	162348	22	11
AC238412	RH202H24	139301	9	5
AC236652	RH202I20	155254	23	5
AC240070	RH202J02	139611	18	7
AC236653	RH202M11	134796	13	1
AC240071	RH202M15	132590	42	11
AC238413	RH202N02	143683	13	5
AC232122	RH203D07	134457	13	5
AC238414	RH203D20	143836	13	5
AC209526	RH203E21	193156	11	1
AC232123	RH203H13	153330	13	5
AC238415	RH203I22	143770	6	5
AC243407	RH203J04	194944	9	5
AC232124	RH203J16	141241	13	1
AC232125	RH203K07	165517	19	5
AC233539	RH203L23	123824	37	5
AC238416	RH203M15	158911	7	5
AC238417	RH204A02	143129	10	5

AC235978	RH204A17	165818	17	6
AC240072	RH204B22	93818	40	8
AC238418	RH204E05	128122	14	5
AC236654	RH204E19	153736	7	1
AC218090	RH204G08	131164	16	6
AC232126	RH204G09	141532	12	5
AC240073	RH204G21	155680	23	11
AC232127	RH204H15	130262	12	5
AC237901	RH204H17	89134	9	0
AC239340	RH204J10	96418	18	9
AC217736	RH204M15	166966	17	1

Supplementary Table 12. Kmer counts in RH Illumina datasets.

	RH total	RNAseq selected	RH specific	DM total
1	8541574293	37796962	3982281929	4355472029
2	975874984	15743270	815671370	536312390
3	359191824	8105544	249143043	188088036
4	203224196	5201664	119277676	105387412
5	142444400	3847845	73731445	70356700
6	113764548	3153966	54454746	56176644
7	99464057	2814819	46026820	46921483
8	92873176	2672568	42908864	41920712
9	90853182	2637621	42706359	38369430
10	91941670	2640510	44342840	36577500
11	95165114	2673979	47153733	36084840
12	99825096	2690928	50574000	37123248
13	105780311	2731859	54653404	39850135
14	112826994	2775206	59203046	44435650
15	120467310	2831970	63967245	51290970
16	128376368	2907360	68671936	60781408
17	136758149	3051687	73727079	72999020
18	145459854	3231342	78958566	88131186
19	154625648	3472383	84218336	106344615
20	163499540	3758360	89224940	127709540
21	172769499	4126311	94409427	152154135
22	182061066	4583898	99702900	179350908
23	191589931	5117845	104870961	209402810
24	201209808	5727720	110118288	241746504
25	211517700	6383775	115715250	275990950
26	221532896	7085728	121247048	312208650
27	232061247	7923690	127038483	349761159
28	243058788	8829828	132901104	388332364
29	254030169	9737446	138777383	426835224
30	265370820	10834680	144694950	465898350
31	277340880	11971735	151000659	503826787
32	289604128	13172160	157677984	540273056
33	301994187	14439942	164335644	575049717
34	314592582	15721566	170902428	606665706
35	327247655	17106705	177820930	634617165
36	340464996	18668304	184821768	658183176
37	353433953	20074017	191706324	675689930
38	366221238	21644002	198343774	688367948
39	379515942	23248485	205398882	694583214
40	391912240	24831760	211911320	694997520
41	404979140	26614125	218845618	688774539

42	416858652	28236894	225131172	676647006
43	428715891	29877131	231429010	659636082
44	440382228	31613340	237157536	637498796
45	451515150	33305625	242704485	610676640
46	461391684	34982770	247889998	580824796
47	471374468	36598853	252846370	548683640
48	480674688	38200272	257321040	514400928
49	489104084	39855081	261365461	479282181
50	496878700	41248750	264858250	443659200
51	503920749	42592395	268213794	408463437
52	510335280	43999592	270740080	374206560
53	515037093	45371604	272560662	341825726
54	519378858	46531854	273751488	310701798
55	522721265	47607010	274717795	281739150
56	525706328	48609512	274977528	254785104
57	526825920	49462776	274660770	230131572
58	528227808	50467192	274017056	207998962
59	527510681	51126155	272229658	187645665
60	526491780	51783300	270034920	169540320
61	524972649	52314149	267397160	153744278
62	522069388	52847746	264111878	139568262
63	518921991	53145162	260557605	127194543
64	514874752	53667776	256311744	116539456
65	510000790	53822535	251764500	107267680
66	504691638	54030504	246891282	99109560
67	498968028	54146184	241800186	92280909
68	492257304	54061972	236138636	86518576
69	485430456	54203088	230050209	81728430
70	478178120	54294800	223914950	77465430
71	469670254	54032704	217256308	73982355
72	461795976	54096696	210528792	71059896
73	453305691	53910792	203930537	69002447
74	444566322	53856090	196789088	66929892
75	436513050	54024525	189992100	65336175
76	427779680	53769696	183009368	64086544
77	418999042	53758166	175729323	63096033
78	410100834	53744340	168593256	62141352
79	401762321	53745280	161761190	61163064
80	393859200	53806240	154917680	60577520
81	385750755	54015093	148434282	59904360
82	377845176	53983634	141782100	59189814
83	370327989	54377284	135588883	58592937
84	363154008	54568248	129501036	57921024

85	356097810	54848035	123842110	57157655
86	349422128	55229802	118000084	56560394
87	343413708	55554633	112600533	55768305
88	337450960	56039016	107491384	54814144
89	331734328	56442376	102545355	53866805
90	326865510	56973780	98168580	52899120
91	322543585	57605275	93941666	51787736
92	317717676	57890540	89884644	50847848
93	314485824	58663191	86324646	49726914
94	310937148	59263616	82996454	48629490
95	307478995	59947090	79628145	47410225
96	305006592	60629568	76806912	46032672
97	302555901	61473556	74138555	44863276
98	300948396	62523314	71567636	43678502
99	299068605	63092304	69520671	42360912
100	297285700	63816200	67481500	41247400
101	295645483	64646262	65785340	40062761
102	294544074	65428308	64316916	38992356
103	293295590	66179457	62841124	37768246
104	292850376	67057536	61668984	36643880
105	291751950	67788735	60375735	35564445
106	290802308	68457026	59455718	34528016
107	290399284	69092682	58547618	33565151
108	289791972	69823188	57507084	32744628
109	289086094	70466756	56718477	31799551
110	288117280	70816240	55975370	31004490
111	287711556	71717433	55284438	30311991
112	286981744	72342256	54587568	29562960
113	285881299	72584194	54003717	28861217
114	285122550	72932640	53571564	28264134
115	284346930	73418760	53094925	27712010
116	283201820	73814976	52519812	27241672
117	282107709	74028591	52124436	26678106
118	281115766	74312860	51681404	26286742
119	279952498	74357388	51361233	25964491
120	278309640	74398560	50929080	25663080
121	276535941	74566492	50168173	25247860
122	274832938	74323498	50002432	24969862
123	272924700	74268384	49237146	24605535
124	271315348	74205444	48864184	24345416
125	268934750	73827750	48276625	24191125
126	266171976	73571778	47574954	23908752
127	264227945	73474707	47074455	23615269

128	261662592	73000448	46513024	23454080
129	259248333	72770319	46144977	23157435
130	256199060	72025980	45513780	22965800
131	253495218	71643376	44853221	22688545
132	250402548	70970988	44375496	22500588
133	247406201	70648669	43662969	22323119
134	244188870	69600806	43017886	22028126
135	240416235	68684760	42351795	21983130
136	237049088	67994968	41607432	21545120
137	233745427	67130000	40902994	21481600
138	230135424	66241242	40185324	21202182
139	226338426	65189054	39517283	21020136
140	222904780	64383620	38827740	20667220
141	218924355	63179421	38075358	20584308
142	215228832	62163908	37462582	20357972
143	211438370	61136790	36572250	19997406
144	207462960	60045408	35822160	19875888
145	203410495	58882035	35141040	19527295
146	199442570	57711902	34314526	19375222
147	195361236	56558103	33626544	19195113
148	191093160	55355996	32779336	18921208
149	187277206	54177890	31919525	18620977
150	182907750	52790850	31078800	18371250
151	178798194	51675522	30447489	18106410
152	174828424	50470080	29695176	17862584
153	171029673	49312665	29013390	17531505
154	166808642	47897696	28278404	17409546
155	162844240	46780705	27501650	17085805
156	159194100	45744972	26758992	17018352
157	155129345	44551576	26163265	16684233
158	150774976	43170814	25413352	16477188
159	147181848	42225471	24595392	16261248
160	143107680	41007680	24113760	16172160
161	139504246	39865049	23245985	15934814
162	135565002	38633274	22587174	15796296
163	132123399	37615673	21838903	15494128
164	128395764	36445884	21273260	15361388
165	125148045	35543970	20534415	15177030
166	121547192	34402504	19885638	15131232
167	117786770	33109253	19183791	14976727
168	114639336	32183760	18583152	14729904
169	111138456	31066763	17968418	14580982
170	108231350	30129610	17459340	14577500

171	105231861	29235528	16809813	14370327
172	102604536	28378968	16313856	14267744
173	99584682	27468940	15711168	14142750
174	96621678	26547876	15251796	13983510
175	93946475	25731300	14706825	13874175
176	91257232	24735216	14196336	13764960
177	88672221	24048813	13704402	13653426
178	86220886	23165988	13163100	13450926
179	83929162	22436755	12845756	13459189
180	81447660	21646980	12387420	13412700
181	79458819	21046318	11939303	13180963
182	77238434	20322666	11636716	13091806
183	75345309	19736001	11201064	12978177
184	73314432	18958256	10812208	12837128
185	71384470	18398065	10317635	12713200
186	69608826	17688786	10113750	12726678
187	67904562	17226253	9767945	12589214
188	66241424	16632548	9482344	12513844
189	64576386	16100343	9221877	12513501
190	63129780	15679370	8959070	12264310
191	61769591	15151266	8714757	12243864
192	60073536	14570112	8369088	12017856
193	59008399	14228539	8064119	11995915
194	57722566	13772642	7875818	11960876
195	56460105	13342485	7599735	11843325
196	55335112	12924240	7471520	11713156
197	54278425	12507136	7270876	11594435
198	53450694	12225510	7044444	11507166
199	52220784	11856022	6835451	11421406
200	51345800	11484200	6680200	11346800
201	50579841	11159520	6635010	11156304
202	49717048	10878912	6391280	11151410
203	48958322	10618524	6287519	11062485
204	48307200	10365648	6069612	10850556
205	47416910	10018350	5973495	10828920
206	46891162	9769756	5833508	10763294
207	46356822	9655308	5735556	10650150
208	45618768	9360208	5673200	10538320
209	44957781	9117834	5442151	10472781
210	44510970	8999130	5389440	10472490
211	43879771	8818323	5333447	10341532
212	43538864	8729100	5291520	10264828
213	43331868	8573889	5208276	10162443

214	42706482	8375960	5078434	10118990
215	42230515	8177525	5067765	10053830
216	41756472	8039736	4965624	9928656
217	41394920	7919632	4934580	9933826
218	40975716	7816826	4763736	9711246
219	40719108	7745592	4724925	9671040
220	40358780	7611780	4668180	9718060
221	40011829	7513116	4650503	9571952
222	39726456	7414356	4564320	9596394
223	39309994	7310163	4530468	9321623
224	38984960	7116928	4482912	9376640
225	38666700	7062525	4405500	9302175
226	38515372	6986790	4350500	9307358
227	38232248	6973440	4313908	9151732
228	37910700	6918204	4201812	9047952
229	37663401	6846413	4201005	9072980
230	37391100	6798340	4106650	8960340
231	37113615	6754209	4114803	8882412
232	36731168	6647728	3993184	8874464
233	36542089	6616501	3919526	8917143
234	36155808	6388668	3929562	8732178
235	36092475	6409860	3899825	8648235
236	35738660	6289400	3822492	8661436
237	35508525	6310599	3784416	8623956
238	35198534	6218702	3709468	8571332
239	34963071	6150665	3688487	8511029
240	34458480	6105840	3655200	8414160
241	34505175	6164539	3631388	8393548
242	34034154	6090656	3529812	8389414
243	33751728	6007203	3462507	8274150
244	33820352	6033144	3535072	8231828
245	33365080	5924835	3445190	8152375
246	33186138	5976816	3402672	8166708
247	33038473	5965050	3389087	8158163
248	32702024	5907360	3315760	8027016
249	32617506	5809668	3384906	8022531
250	32381000	5855500	3306000	7934000

Supplementary Table 13. Genes with premature stops

Premature Stop Code	Category	Gene in DM	Transcript in DM	Chromosome	RNA-seq Support in DM	RNA-seq support in RH	Functional annotation
1	Heterozygous PS in RH, shared by DM	PGSC0003DMG400000113	PGSC0003DMT400000335	chr09	NO	NO	
2	Heterozygous PS in RH, shared by DM	PGSC0003DMG400000339	PGSC0003DMT400000899	chr07	NO	NO	
3	Heterozygous PS in RH, shared by DM	PGSC0003DMG400000341	PGSC0003DMT400000908	chr01	yes	NO	
4	Heterozygous PS in RH, shared by DM	PGSC0003DMG400000348	PGSC0003DMT400000930	chr03	yes	yes	
5	Heterozygous PS in RH, shared by DM	PGSC0003DMG400000387	PGSC0003DMT400001035	chr09	yes	yes	GO:0004672; protein kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
6	Heterozygous PS in RH, shared by DM	PGSC0003DMG400000408	PGSC0003DMT400001076	chr01	NO	NO	
7	Heterozygous PS in RH, shared by DM	PGSC0003DMG400000421	PGSC0003DMT400001109	chr12	NO	NO	
8	Heterozygous PS in RH, shared by DM	PGSC0003DMG400000491	PGSC0003DMT400001292	chr11	yes	NO	GO:0004553; hydrolase activity, hydrolyzing O-glycosyl compounds; Molecular Function GO:0005975; carbohydrate metabolic process; Biological Process
9	Heterozygous PS in RH, shared by DM	PGSC0003DMG402000515	PGSC0003DMT400001383	chr01	yes	NO	

10	Heterozygous PS in RH, shared by DM	PGSC0003DMG400000690	PGSC0003DMT400001836	chr04	yes	yes	
11	Heterozygous PS in RH, shared by DM	PGSC0003DMG400000711	PGSC0003DMT400001888	chr06	NO	NO	
12	Heterozygous PS in RH, shared by DM	PGSC0003DMG400000724	PGSC0003DMT400001912	chr01	NO	NO	
13	Heterozygous PS in RH, shared by DM	PGSC0003DMG400000728	PGSC0003DMT400001921	chr09	NO	NO	
14	Heterozygous PS in RH, shared by DM	PGSC0003DMG400000729	PGSC0003DMT400001923	chr01	yes	NO	
15	Heterozygous PS in RH, shared by DM	PGSC0003DMG400000830	PGSC0003DMT400002168	chr09	NO	NO	GO:0003676; nucleic acid binding; Molecular Function
16	Heterozygous PS in RH, shared by DM	PGSC0003DMG400001052	PGSC0003DMT400002726	chr12	yes	NO	GO:0016747; transferase activity, transferring acyl groups other than amino-acyl groups; Molecular Function
17	Heterozygous PS in RH, shared by DM	PGSC0003DMG400001191	PGSC0003DMT400003013	chr04	NO	NO	
18	Heterozygous PS in RH, shared by DM	PGSC0003DMG400001257	PGSC0003DMT400003176	chr06	yes	yes	GO:0004497; monooxygenase activity; Molecular Function GO:0005506; iron ion binding; Molecular Function GO:0009055; electron carrier activity; Molecular Function GO:0020037; heme binding; Molecular Function
19	Heterozygous PS in RH, shared by DM	PGSC0003DMG400001290	PGSC0003DMT400003257				
20	Heterozygous PS in RH, shared by DM	PGSC0003DMG400001294	PGSC0003DMT400003264	chr03	yes	NO	

21	Heterozygous PS in RH, shared by DM	PGSC0003DMG400001386	PGSC0003DMT400003515	chr01	yes	NO	
22	Heterozygous PS in RH, shared by DM	PGSC0003DMG400001432	PGSC0003DMT400003632	chr11	yes	yes	
23	Heterozygous PS in RH, shared by DM	PGSC0003DMG400001458	PGSC0003DMT400003697	chr06	yes	NO	GO:0045454; cell redox homeostasis; Biological Process
24	Heterozygous PS in RH, shared by DM	PGSC0003DMG400001475	PGSC0003DMT400003744	chr07	yes	NO	GO:0003677; DNA binding; Molecular Function
25	Heterozygous PS in RH, shared by DM	PGSC0003DMG400001503	PGSC0003DMT400003795	chr04	NO	NO	GO:0005515; protein binding; Molecular Function
26	Heterozygous PS in RH, shared by DM	PGSC0003DMG400001606	PGSC0003DMT400004068	chr12	yes	NO	GO:0005524; ATP binding; Molecular Function GO:0006915; apoptosis; Biological Process
27	Heterozygous PS in RH, shared by DM	PGSC0003DMG400001711	PGSC0003DMT400004314	chr04	NO	NO	
28	Heterozygous PS in RH, shared by DM	PGSC0003DMG400001781	PGSC0003DMT400004466	chr10	NO	NO	
29	Heterozygous PS in RH, shared by DM	PGSC0003DMG400001887	PGSC0003DMT400004767	-	yes	NO	
30	Heterozygous PS in RH, shared by DM	PGSC0003DMG400001890	PGSC0003DMT400004770	-	yes	NO	
31	Heterozygous PS in RH, shared by DM	PGSC0003DMG400001900	PGSC0003DMT400004785	chr05	yes	yes	
32	Heterozygous PS in RH, shared by DM	PGSC0003DMG400001967	PGSC0003DMT400004973	chr09	yes	NO	

33	Heterozygous PS in RH, shared by DM	PGSC0003DMG400002067	PGSC0003DMT400005246	-	NO	NO	
34	Heterozygous PS in RH, shared by DM	PGSC0003DMG400002154	PGSC0003DMT400005513	chr12	NO	NO	GO:0003676; nucleic acid binding; Molecular Function GO:0008270; zinc ion binding; Molecular Function
35	Heterozygous PS in RH, shared by DM	PGSC0003DMG400002387	PGSC0003DMT400006135	chr06	yes	NO	
36	Heterozygous PS in RH, shared by DM	PGSC0003DMG400002491	PGSC0003DMT400006372	chr07	yes	NO	
37	Heterozygous PS in RH, shared by DM	PGSC0003DMG400002547	PGSC0003DMT400006532	chr08	NO	NO	
38	Heterozygous PS in RH, shared by DM	PGSC0003DMG401002553	PGSC0003DMT400006564	chr09	yes	yes	GO:0016021; integral to membrane; Cellular Component
39	Heterozygous PS in RH, shared by DM	PGSC0003DMG400002585	PGSC0003DMT400006642	chr06	NO	NO	
40	Heterozygous PS in RH, shared by DM	PGSC0003DMG400002608	PGSC0003DMT400006709	chr05	NO	NO	
41	Heterozygous PS in RH, shared by DM	PGSC0003DMG400002612	PGSC0003DMT400006726	chr11	NO	NO	
42	Heterozygous PS in RH, shared by DM	PGSC0003DMG400002641	PGSC0003DMT400006812	chr08	NO	NO	
43	Heterozygous PS in RH, shared by DM	PGSC0003DMG400002650	PGSC0003DMT400006827	chr12	NO	NO	
44	Heterozygous PS in RH, shared by DM	PGSC0003DMG400002808	PGSC0003DMT400007294	chr05	yes	NO	

45	Heterozygous PS in RH, shared by DM	PGSC0003DMG400002818	PGSC0003DMT400007319	chr03	NO	NO	
46	Heterozygous PS in RH, shared by DM	PGSC0003DMG400002833	PGSC0003DMT400007370	chr06	yes	yes	GO:0005524; ATP binding; Molecular Function GO:0006915; apoptosis; Biological Process
47	Heterozygous PS in RH, shared by DM	PGSC0003DMG401002888	PGSC0003DMT400007484	chr01	yes	NO	
48	Heterozygous PS in RH, shared by DM	PGSC0003DMG400003109	PGSC0003DMT400008044	chr09	NO	NO	
49	Heterozygous PS in RH, shared by DM	PGSC0003DMG400003485	PGSC0003DMT400008946	chr08	NO	NO	
50	Heterozygous PS in RH, shared by DM	PGSC0003DMG400003588	PGSC0003DMT400009242	chr06	NO	NO	
51	Heterozygous PS in RH, shared by DM	PGSC0003DMG400003596	PGSC0003DMT400009269	chr10	NO	NO	
52	Heterozygous PS in RH, shared by DM	PGSC0003DMG400003621	PGSC0003DMT400009319	chr02	yes	NO	GO:0005634; nucleus; Cellular Component
53	Heterozygous PS in RH, shared by DM	PGSC0003DMG400003810	PGSC0003DMT400009741	chr07	yes	yes	
54	Heterozygous PS in RH, shared by DM	PGSC0003DMG400003817	PGSC0003DMT400009752	chr10	NO	NO	
55	Heterozygous PS in RH, shared by DM	PGSC0003DMG401004079	PGSC0003DMT400010443	chr06	yes	yes	
56	Heterozygous PS in RH, shared by DM	PGSC0003DMG400004182	PGSC0003DMT400010721	chr07	NO	NO	

57	Heterozygous PS in RH, shared by DM	PGSC0003DMG400004235	PGSC0003DMT400010827	chr02	yes	NO	
58	Heterozygous PS in RH, shared by DM	PGSC0003DMG401004281	PGSC0003DMT400010931	chr01	NO	NO	
59	Heterozygous PS in RH, shared by DM	PGSC0003DMG402004406	PGSC0003DMT400011248	chr07	yes	NO	GO:0008152; metabolic process; Biological Process
60	Heterozygous PS in RH, shared by DM	PGSC0003DMG400004408	PGSC0003DMT400011255	chr02	yes	NO	GO:0016491; oxidoreductase activity; Molecular Function
61	Heterozygous PS in RH, shared by DM	PGSC0003DMG400004492	PGSC0003DMT400011446	chr10	NO	NO	
62	Heterozygous PS in RH, shared by DM	PGSC0003DMG400004582	PGSC0003DMT400011660	chr03	yes	NO	
63	Heterozygous PS in RH, shared by DM	PGSC0003DMG400004723	PGSC0003DMT400012041	chr05	yes	NO	
64	Heterozygous PS in RH, shared by DM	PGSC0003DMG402004751	PGSC0003DMT400012103	chr05	yes	NO	
65	Heterozygous PS in RH, shared by DM	PGSC0003DMG400004792	PGSC0003DMT400012219	chr05	NO	NO	
66	Heterozygous PS in RH, shared by DM	PGSC0003DMG400004842	PGSC0003DMT400012359	chr09	yes	yes	
67	Heterozygous PS in RH, shared by DM	PGSC0003DMG400004843	PGSC0003DMT400012361	chr01	yes	yes	
68	Heterozygous PS in RH, shared by DM	PGSC0003DMG402004862	PGSC0003DMT400012418	chr10	yes	NO	

69	Heterozygous PS in RH, shared by DM	PGSC0003DMG401004870	PGSC0003DMT400012446	chr03	yes	NO	
70	Heterozygous PS in RH, shared by DM	PGSC0003DMG400004956	PGSC0003DMT400012718	chr01	NO	NO	
71	Heterozygous PS in RH, shared by DM	PGSC0003DMG400005056	PGSC0003DMT400012976	chr12	NO	NO	
72	Heterozygous PS in RH, shared by DM	PGSC0003DMG400005108	PGSC0003DMT400013090	chr04	yes	NO	
73	Heterozygous PS in RH, shared by DM	PGSC0003DMG400005121	PGSC0003DMT400013107	chr04	yes	NO	
74	Heterozygous PS in RH, shared by DM	PGSC0003DMG400005128	PGSC0003DMT400013130	chr03	yes	NO	GO:0016021; integral to membrane; Cellular Component
75	Heterozygous PS in RH, shared by DM	PGSC0003DMG402005139	PGSC0003DMT400013159				
76	Heterozygous PS in RH, shared by DM	PGSC0003DMG400005141	PGSC0003DMT400013164	chr05	yes	yes	GO:0005525; GTP binding; Molecular Function
77	Heterozygous PS in RH, shared by DM	PGSC0003DMG400005149	PGSC0003DMT400013180	-	NO	NO	
78	Heterozygous PS in RH, shared by DM	PGSC0003DMG400005186	PGSC0003DMT400013292	chr04	yes	NO	
79	Heterozygous PS in RH, shared by DM	PGSC0003DMG400005267	PGSC0003DMT400013497	chr08	NO	NO	
80	Heterozygous PS in RH, shared by DM	PGSC0003DMG400005295	PGSC0003DMT400013560	-	NO	NO	

81	Heterozygous PS in RH, shared by DM	PGSC0003DMG400005393	PGSC0003DMT400013773	chr03	NO	NO	
82	Heterozygous PS in RH, shared by DM	PGSC0003DMG400005529	PGSC0003DMT400014098	chr09	yes	NO	GO:0004553; hydrolase activity, hydrolyzing O-glycosyl compounds; Molecular Function GO:0005975; carbohydrate metabolic process; Biological Process
83	Heterozygous PS in RH, shared by DM	PGSC0003DMG400005742	PGSC0003DMT400014732	chr04	NO	NO	
84	Heterozygous PS in RH, shared by DM	PGSC0003DMG400005830	PGSC0003DMT400014940	chr08	NO	NO	
85	Heterozygous PS in RH, shared by DM	PGSC0003DMG400005875	PGSC0003DMT400015046				
86	Heterozygous PS in RH, shared by DM	PGSC0003DMG400005997	PGSC0003DMT400015373	chr07	yes	NO	GO:0047800; cysteamine dioxygenase activity; Molecular Function GO:0055114; oxidation reduction; Biological Process
87	Heterozygous PS in RH, shared by DM	PGSC0003DMG400006059	PGSC0003DMT400015519	chr12	NO	NO	
88	Heterozygous PS in RH, shared by DM	PGSC0003DMG401006099	PGSC0003DMT400015627	chr10	yes	NO	
89	Heterozygous PS in RH, shared by DM	PGSC0003DMG401006284	PGSC0003DMT400016072	chr04	NO	NO	
90	Heterozygous PS in RH, shared by DM	PGSC0003DMG400006416	PGSC0003DMT400016423	chr05	yes	NO	
91	Heterozygous PS in RH, shared by DM	PGSC0003DMG400006758	PGSC0003DMT400017373	chr04	yes	yes	

92	Heterozygous PS in RH, shared by DM	PGSC0003DMG400006769	PGSC0003DMT400017408	chr09	NO	NO	
93	Heterozygous PS in RH, shared by DM	PGSC0003DMG400006845	PGSC0003DMT400017642	chr01	yes	NO	
94	Heterozygous PS in RH, shared by DM	PGSC0003DMG400006891	PGSC0003DMT400017745	chr07	NO	NO	
95	Heterozygous PS in RH, shared by DM	PGSC0003DMG400007073	PGSC0003DMT400018218	chr06	NO	NO	GO:0006633; fatty acid biosynthetic process; Biological Process GO:0008415; acyltransferase activity; Molecular Function GO:0016020; membrane; Cellular Component GO:0016747; transferase activity, transferring acyl groups other than amino-acyl groups; Molecular Function
96	Heterozygous PS in RH, shared by DM	PGSC0003DMG400007112	PGSC0003DMT400018308	chr03	yes	yes	
97	Heterozygous PS in RH, shared by DM	PGSC0003DMG400007405	PGSC0003DMT400019126	chr07	NO	NO	
98	Heterozygous PS in RH, shared by DM	PGSC0003DMG400007523	PGSC0003DMT400019465	-	yes	NO	GO:0000287; magnesium ion binding; Molecular Function GO:0008152; metabolic process; Biological Process GO:0016829; lyase activity; Molecular Function
99	Heterozygous PS in RH, shared by DM	PGSC0003DMG400007526	PGSC0003DMT400019468	chr06	yes	NO	
100	Heterozygous PS in RH, shared by DM	PGSC0003DMG400007590	PGSC0003DMT400019639	chr07	NO	NO	
101	Heterozygous PS in RH, shared by DM	PGSC0003DMG402007686	PGSC0003DMT400019870	chr04	yes	NO	

102	Heterozygous PS in RH, shared by DM	PGSC0003DMG400007825	PGSC0003DMT400020238	chr07	NO	NO	
103	Heterozygous PS in RH, shared by DM	PGSC0003DMG400007848	PGSC0003DMT400020297	chr06	NO	NO	
104	Heterozygous PS in RH, shared by DM	PGSC0003DMG400007876	PGSC0003DMT400020367	chr10	NO	NO	
105	Heterozygous PS in RH, shared by DM	PGSC0003DMG400007925	PGSC0003DMT400020492	chr07	yes	NO	GO:0003676; nucleic acid binding; Molecular Function
106	Heterozygous PS in RH, shared by DM	PGSC0003DMG400007994	PGSC0003DMT400020635				
107	Heterozygous PS in RH, shared by DM	PGSC0003DMG400008176	PGSC0003DMT400021111	chr01	NO	NO	
108	Heterozygous PS in RH, shared by DM	PGSC0003DMG400008323	PGSC0003DMT400021449	chr11	NO	NO	
109	Heterozygous PS in RH, shared by DM	PGSC0003DMG400008507	PGSC0003DMT400021933	chr06	NO	NO	
110	Heterozygous PS in RH, shared by DM	PGSC0003DMG400008582	PGSC0003DMT400022121	chr01	yes	NO	
111	Heterozygous PS in RH, shared by DM	PGSC0003DMG400008618	PGSC0003DMT400022205	chr01	NO	NO	GO:0003676; nucleic acid binding; Molecular Function GO:0008270; zinc ion binding; Molecular Function
112	Heterozygous PS in RH, shared by DM	PGSC0003DMG400008701	PGSC0003DMT400022450	chr11	NO	NO	
113	Heterozygous PS in RH, shared by DM	PGSC0003DMG400008842	PGSC0003DMT400022793	chr03	yes	NO	GO:0008270; zinc ion binding; Molecular Function

114	Heterozygous PS in RH, shared by DM	PGSC0003DMG400008907	PGSC0003DMT400023009	chr03	NO	NO	
115	Heterozygous PS in RH, shared by DM	PGSC0003DMG401008915	PGSC0003DMT400023035	-	NO	NO	
116	Heterozygous PS in RH, shared by DM	PGSC0003DMG400008942	PGSC0003DMT400023090	chr08	yes	NO	
117	Heterozygous PS in RH, shared by DM	PGSC0003DMG400009066	PGSC0003DMT400023412	chr08	yes	yes	
118	Heterozygous PS in RH, shared by DM	PGSC0003DMG400009146	PGSC0003DMT400023625	chr07	yes	yes	GO:0003723; RNA binding; Molecular Function GO:0003964; RNA-directed DNA polymerase activity; Molecular Function GO:0006278; RNA-dependent DNA replication; Biological Process
119	Heterozygous PS in RH, shared by DM	PGSC0003DMG402009171	PGSC0003DMT400023711	chr02	NO	NO	
120	Heterozygous PS in RH, shared by DM	PGSC0003DMG400009217	PGSC0003DMT400023822	chr07	NO	NO	GO:0004252; serine-type endopeptidase activity; Molecular Function GO:0006508; proteolysis; Biological Process
121	Heterozygous PS in RH, shared by DM	PGSC0003DMG400009342	PGSC0003DMT400024168	chr03	yes	NO	GO:0005506; iron ion binding; Molecular Function GO:0016226; iron-sulfur cluster assembly; Biological Process GO:0051536; iron-sulfur cluster binding; Molecular Function

122	Heterozygous PS in RH, shared by DM	PGSC0003DMG401009603	PGSC0003DMT400024843	chr02	yes	NO	GO:0003824; catalytic activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006754; ATP biosynthetic process; Biological Process GO:0006812; cation transport; Biological Process GO:0008152; metabolic process; Biological Process GO:0015662; ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism; Molecular Function GO:0016020; membrane; Cellular Component GO:0016820; hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances; Molecular Function
123	Heterozygous PS in RH, shared by DM	PGSC0003DMG400009631	PGSC0003DMT400024924	chr04	yes	NO	GO:0006629; lipid metabolic process; Biological Process GO:0016788; hydrolase activity, acting on ester bonds; Molecular Function
124	Heterozygous PS in RH, shared by DM	PGSC0003DMG400009634	PGSC0003DMT400024931	chr11	yes	yes	GO:0008152; metabolic process; Biological Process GO:0016491; oxidoreductase activity; Molecular Function
125	Heterozygous PS in RH, shared by DM	PGSC0003DMG400009685	PGSC0003DMT400025083	chr06	yes	NO	
126	Heterozygous PS in RH, shared by DM	PGSC0003DMG400009703	PGSC0003DMT400025113	chr08	yes	NO	GO:0004672; protein kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
127	Heterozygous PS in RH, shared by DM	PGSC0003DMG400009715	PGSC0003DMT400025139	chr04	NO	NO	
128	Heterozygous PS in RH, shared by DM	PGSC0003DMG400009852	PGSC0003DMT400025511	chr01	yes	NO	

129	Heterozygous PS in RH, shared by DM	PGSC0003DMG400009901	PGSC0003DMT400025634	chr06	yes	yes	
130	Heterozygous PS in RH, shared by DM	PGSC0003DMG400009908	PGSC0003DMT400025655	chr12	NO	NO	
131	Heterozygous PS in RH, shared by DM	PGSC0003DMG400009966	PGSC0003DMT400025807	chr10	yes	NO	GO:0003824; catalytic activity; Molecular Function
132	Heterozygous PS in RH, shared by DM	PGSC0003DMG400010041	PGSC0003DMT400026022	chr12	yes	NO	GO:0042318; penicillin biosynthetic process; Biological Process
133	Heterozygous PS in RH, shared by DM	PGSC0003DMG400010042	PGSC0003DMT400026026	chr05	NO	NO	
134	Heterozygous PS in RH, shared by DM	PGSC0003DMG400010086	PGSC0003DMT400026172	chr09	yes	NO	
135	Heterozygous PS in RH, shared by DM	PGSC0003DMG400010159	PGSC0003DMT400026319	chr04	yes	NO	
136	Heterozygous PS in RH, shared by DM	PGSC0003DMG400010299	PGSC0003DMT400026654	chr09	NO	NO	
137	Heterozygous PS in RH, shared by DM	PGSC0003DMG400010321	PGSC0003DMT400026708	chr09	yes	yes	
138	Heterozygous PS in RH, shared by DM	PGSC0003DMG401010456	PGSC0003DMT400027098	chr06	NO	NO	
139	Heterozygous PS in RH, shared by DM	PGSC0003DMG400010493	PGSC0003DMT400027205	chr02	yes	NO	
140	Heterozygous PS in RH, shared by DM	PGSC0003DMG400010801	PGSC0003DMT400028010	chr10	yes	NO	

141	Heterozygous PS in RH, shared by DM	PGSC0003DMG400010892	PGSC0003DMT400028257	chr07	yes	NO	GO:0006897; endocytosis; Biological Process GO:0016020; membrane; Cellular Component
142	Heterozygous PS in RH, shared by DM	PGSC0003DMG400010895	PGSC0003DMT400028264	-	yes	yes	GO:0005515; protein binding; Molecular Function
143	Heterozygous PS in RH, shared by DM	PGSC0003DMG403010943	PGSC0003DMT400028400	chr06	NO	NO	GO:0005507; copper ion binding; Molecular Function GO:0008131; amine oxidase activity; Molecular Function GO:0009308; amine metabolic process; Biological Process GO:0048038; quinone binding; Molecular Function GO:0055114; oxidation reduction; Biological Process
144	Heterozygous PS in RH, shared by DM	PGSC0003DMG400011057	PGSC0003DMT400028724	chr11	yes	yes	
145	Heterozygous PS in RH, shared by DM	PGSC0003DMG400011065	PGSC0003DMT400028752	chr12	yes	NO	GO:0006855; multidrug transport; Biological Process GO:0015238; drug transporter activity; Molecular Function GO:0015297; antiporter activity; Molecular Function GO:0016020; membrane; Cellular Component GO:0055085; transmembrane transport; Biological Process
146	Heterozygous PS in RH, shared by DM	PGSC0003DMG402011400	PGSC0003DMT400029658	chr04	NO	NO	GO:0016021; integral to membrane; Cellular Component
147	Heterozygous PS in RH, shared by DM	PGSC0003DMG400011472	PGSC0003DMT400029849	chr07	yes	NO	
148	Heterozygous PS in RH, shared by DM	PGSC0003DMG400011477	PGSC0003DMT400029866	chr08	yes	NO	
149	Heterozygous PS in RH, shared by DM	PGSC0003DMG400011503	PGSC0003DMT400029964	chr05	yes	NO	GO:0016787; hydrolase activity; Molecular Function

150	Heterozygous PS in RH, shared by DM	PGSC0003DMG400011508	PGSC0003DMT400029984	chr03	yes	NO	
151	Heterozygous PS in RH, shared by DM	PGSC0003DMG400011513	PGSC0003DMT400029999	chr08	yes	NO	
152	Heterozygous PS in RH, shared by DM	PGSC0003DMG401011522	PGSC0003DMT400030027	chr10	yes	NO	GO:0000166; nucleotide binding; Molecular Function GO:0003676; nucleic acid binding; Molecular Function GO:0004812; aminoacyl-tRNA ligase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0005737; cytoplasm; Cellular Component GO:0006412; translation; Biological Process GO:0006418; tRNA aminoacylation for protein translation; Biological Process
153	Heterozygous PS in RH, shared by DM	PGSC0003DMG400011670	PGSC0003DMT400030473	chr11	NO	NO	GO:0008152; metabolic process; Biological Process GO:0016758; transferase activity, transferring hexosyl groups; Molecular Function
154	Heterozygous PS in RH, shared by DM	PGSC0003DMG402011681	PGSC0003DMT400030500	chr06	yes	yes	
155	Heterozygous PS in RH, shared by DM	PGSC0003DMG400011835	PGSC0003DMT400030892	chr09	NO	NO	GO:0016491; oxidoreductase activity; Molecular Function
156	Heterozygous PS in RH, shared by DM	PGSC0003DMG400011890	PGSC0003DMT400031035	chr10	NO	NO	GO:0005618; cell wall; Cellular Component GO:0030599; pectinesterase activity; Molecular Function GO:0042545; cell wall modification; Biological Process
157	Heterozygous PS in RH, shared by DM	PGSC0003DMG400011977	PGSC0003DMT400031252	chr11	NO	NO	

158	Heterozygous PS in RH, shared by DM	PGSC0003DMG400012028	PGSC0003DMT400031379	chr07	yes	NO	GO:0004252; serine-type endopeptidase activity; Molecular Function GO:0006508; proteolysis; Biological Process
159	Heterozygous PS in RH, shared by DM	PGSC0003DMG400012042	PGSC0003DMT400031413	chr03	yes	NO	
160	Heterozygous PS in RH, shared by DM	PGSC0003DMG400012138	PGSC0003DMT400031653	chr04	NO	NO	
161	Heterozygous PS in RH, shared by DM	PGSC0003DMG400012166	PGSC0003DMT400031711	chr09	yes	yes	GO:0005515; protein binding; Molecular Function GO:0006886; intracellular protein transport; Biological Process GO:0016192; vesicle-mediated transport; Biological Process GO:0030117; membrane coat; Cellular Component
162	Heterozygous PS in RH, shared by DM	PGSC0003DMG400012284	PGSC0003DMT400032020	-	NO	NO	
163	Heterozygous PS in RH, shared by DM	PGSC0003DMG400012371	PGSC0003DMT400032198	chr07	yes	NO	
164	Heterozygous PS in RH, shared by DM	PGSC0003DMG400012425	PGSC0003DMT400032346	chr06	NO	NO	
165	Heterozygous PS in RH, shared by DM	PGSC0003DMG401012477	PGSC0003DMT400032484	chr06	yes	NO	GO:0003677; DNA binding; Molecular Function GO:0003700; transcription factor activity; Molecular Function GO:0006352; transcription initiation; Biological Process GO:0006355; regulation of transcription, DNA-dependent; Biological Process GO:0016987; sigma factor activity; Molecular Function
166	Heterozygous PS in RH, shared by DM	PGSC0003DMG400012543	PGSC0003DMT400032652	chr03	yes	NO	GO:0004866; endopeptidase inhibitor activity; Molecular Function

167	Heterozygous PS in RH, shared by DM	PGSC0003DMG400012595	PGSC0003DMT400032799	chr04	yes	NO	
168	Heterozygous PS in RH, shared by DM	PGSC0003DMG400012599	PGSC0003DMT400032806	-	yes	yes	
169	Heterozygous PS in RH, shared by DM	PGSC0003DMG400012789	PGSC0003DMT400033300	chr10	yes	yes	GO:0004197; cysteine-type endopeptidase activity; Molecular Function GO:0006508; proteolysis; Biological Process
170	Heterozygous PS in RH, shared by DM	PGSC0003DMG400012860	PGSC0003DMT400033477				
171	Heterozygous PS in RH, shared by DM	PGSC0003DMG402012874	PGSC0003DMT400033514	chr11	yes	NO	
172	Heterozygous PS in RH, shared by DM	PGSC0003DMG400012880	PGSC0003DMT400033530	chr12	yes	yes	
173	Heterozygous PS in RH, shared by DM	PGSC0003DMG400012900	PGSC0003DMT400033588	chr05	NO	NO	
174	Heterozygous PS in RH, shared by DM	PGSC0003DMG400013016	PGSC0003DMT400033876	chr04	yes	NO	GO:0003700; transcription factor activity; Molecular Function GO:0005634; nucleus; Cellular Component GO:0006355; regulation of transcription, DNA-dependent; Biological Process GO:0043565; sequence-specific DNA binding; Molecular Function GO:0046983; protein dimerization activity; Molecular Function
175	Heterozygous PS in RH, shared by DM	PGSC0003DMG400013091	PGSC0003DMT400034063	chr08	NO	NO	
176	Heterozygous PS in RH, shared by DM	PGSC0003DMG400013095	PGSC0003DMT400034080	chr05	yes	yes	GO:0031072; heat shock protein binding; Molecular Function

177	Heterozygous PS in RH, shared by DM	PGSC0003DMG401013193	PGSC0003DMT400034309	chr07	NO	NO	GO:0016747; transferase activity, transferring acyl groups other than amino-acyl groups; Molecular Function
178	Heterozygous PS in RH, shared by DM	PGSC0003DMG402013193	PGSC0003DMT400034311				
179	Heterozygous PS in RH, shared by DM	PGSC0003DMG400013232	PGSC0003DMT400034411	-	NO	NO	GO:0008565; protein transporter activity; Molecular Function GO:0015031; protein transport; Biological Process GO:0016021; integral to membrane; Cellular Component
180	Heterozygous PS in RH, shared by DM	PGSC0003DMG400013236	PGSC0003DMT400034422	chr11	yes	NO	GO:0006520; cellular amino acid metabolic process; Biological Process
181	Heterozygous PS in RH, shared by DM	PGSC0003DMG400013290	PGSC0003DMT400034577	chr02	yes	yes	
182	Heterozygous PS in RH, shared by DM	PGSC0003DMG400013351	PGSC0003DMT400034750	chr01	yes	NO	GO:0006364; rRNA processing; Biological Process GO:0032040; small-subunit processome; Cellular Component
183	Heterozygous PS in RH, shared by DM	PGSC0003DMG400013507	PGSC0003DMT400035135	chr09	yes	NO	GO:0016491; oxidoreductase activity; Molecular Function
184	Heterozygous PS in RH, shared by DM	PGSC0003DMG401013522	PGSC0003DMT400035183	chr04	NO	NO	
185	Heterozygous PS in RH, shared by DM	PGSC0003DMG400013568	PGSC0003DMT400035313	chr06	yes	NO	
186	Heterozygous PS in RH, shared by DM	PGSC0003DMG400013647	PGSC0003DMT400035505	chr06	yes	NO	
187	Heterozygous PS in RH, shared by DM	PGSC0003DMG400013649	PGSC0003DMT400035511	chr04	NO	NO	GO:0005524; ATP binding; Molecular Function GO:0006915; apoptosis; Biological Process
188	Heterozygous PS in RH, shared by DM	PGSC0003DMG400013662	PGSC0003DMT400035535	chr10	yes	NO	

189	Heterozygous PS in RH, shared by DM	PGSC0003DMG400013680	PGSC0003DMT400035576	-	NO	NO	
190	Heterozygous PS in RH, shared by DM	PGSC0003DMG400013693	PGSC0003DMT400035605	chr12	yes	NO	GO:0004672; protein kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
191	Heterozygous PS in RH, shared by DM	PGSC0003DMG400013938	PGSC0003DMT400036212	chr04	NO	NO	
192	Heterozygous PS in RH, shared by DM	PGSC0003DMG400014047	PGSC0003DMT400036467	chr09	yes	NO	GO:0004871; signal transducer activity; Molecular Function GO:0009416; response to light stimulus; Biological Process
193	Heterozygous PS in RH, shared by DM	PGSC0003DMG401014048	PGSC0003DMT400036468	chr05	yes	yes	
194	Heterozygous PS in RH, shared by DM	PGSC0003DMG401014186	PGSC0003DMT400036786	chr01	NO	NO	
195	Heterozygous PS in RH, shared by DM	PGSC0003DMG400014399	PGSC0003DMT400037315	chr02	yes	yes	GO:0004672; protein kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process GO:0016998; cell wall macromolecule catabolic process; Biological Process
196	Heterozygous PS in RH, shared by DM	PGSC0003DMG401014450	PGSC0003DMT400037441	chr11	yes	NO	GO:0005524; ATP binding; Molecular Function GO:0016020; membrane; Cellular Component GO:0016887; ATPase activity; Molecular Function
197	Heterozygous PS in RH, shared by DM	PGSC0003DMG400014482	PGSC0003DMT400037547	chr06	yes	NO	GO:0005524; ATP binding; Molecular Function GO:0006915; apoptosis; Biological Process
198	Heterozygous PS in RH, shared by DM	PGSC0003DMG400014711	PGSC0003DMT400038147	chr04	NO	NO	

199	Heterozygous PS in RH, shared by DM	PGSC0003DMG400014717	PGSC0003DMT400038163	chr03	yes	NO	
200	Heterozygous PS in RH, shared by DM	PGSC0003DMG400014873	PGSC0003DMT400038532	chr05	yes	NO	GO:0005524; ATP binding; Molecular Function GO:0006915; apoptosis; Biological Process
201	Heterozygous PS in RH, shared by DM	PGSC0003DMG400014977	PGSC0003DMT400038753	chr09	NO	NO	
202	Heterozygous PS in RH, shared by DM	PGSC0003DMG400015053	PGSC0003DMT400038923	chr03	NO	NO	GO:0005515; protein binding; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0044267; cellular protein metabolic process; Biological Process
203	Heterozygous PS in RH, shared by DM	PGSC0003DMG400015215	PGSC0003DMT400039341	chr05	yes	NO	GO:0005524; ATP binding; Molecular Function GO:0006915; apoptosis; Biological Process
204	Heterozygous PS in RH, shared by DM	PGSC0003DMG400015231	PGSC0003DMT400039387	chr02	yes	NO	GO:0003676; nucleic acid binding; Molecular Function
205	Heterozygous PS in RH, shared by DM	PGSC0003DMG400015281	PGSC0003DMT400039522	chr12	NO	NO	
206	Heterozygous PS in RH, shared by DM	PGSC0003DMG400015443	PGSC0003DMT400039923	chr03	NO	NO	
207	Heterozygous PS in RH, shared by DM	PGSC0003DMG400015491	PGSC0003DMT400040046	chr04	NO	NO	GO:0003677; DNA binding; Molecular Function GO:0005634; nucleus; Cellular Component
208	Heterozygous PS in RH, shared by DM	PGSC0003DMG400015499	PGSC0003DMT400040065	chr11	yes	NO	
209	Heterozygous PS in RH, shared by DM	PGSC0003DMG400015793	PGSC0003DMT400040848	chr05	yes	NO	
210	Heterozygous PS in RH, shared by DM	PGSC0003DMG400015854	PGSC0003DMT400040979	chr04	NO	NO	

211	Heterozygous PS in RH, shared by DM	PGSC0003DMG402015879	PGSC0003DMT400041052	chr03	yes	NO	
212	Heterozygous PS in RH, shared by DM	PGSC0003DMG400015969	PGSC0003DMT400041251	chr01	yes	NO	GO:0003924; GTPase activity; Molecular Function GO:0005525; GTP binding; Molecular Function
213	Heterozygous PS in RH, shared by DM	PGSC0003DMG400015970	PGSC0003DMT400041253	chr10	yes	NO	GO:0003924; GTPase activity; Molecular Function GO:0005525; GTP binding; Molecular Function
214	Heterozygous PS in RH, shared by DM	PGSC0003DMG400016015	PGSC0003DMT400041350	chr09	yes	NO	
215	Heterozygous PS in RH, shared by DM	PGSC0003DMG400016029	PGSC0003DMT400041376	chr01	yes	NO	
216	Heterozygous PS in RH, shared by DM	PGSC0003DMG401016070	PGSC0003DMT400041460	chr06	NO	NO	GO:0004672; protein kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
217	Heterozygous PS in RH, shared by DM	PGSC0003DMG400016091	PGSC0003DMT400041513	chr01	yes	NO	GO:0005524; ATP binding; Molecular Function GO:0016301; kinase activity; Molecular Function GO:0016310; phosphorylation; Biological Process
218	Heterozygous PS in RH, shared by DM	PGSC0003DMG400016132	PGSC0003DMT400041615	-	NO	NO	GO:0003723; RNA binding; Molecular Function GO:0003964; RNA-directed DNA polymerase activity; Molecular Function GO:0006278; RNA-dependent DNA replication; Biological Process
219	Heterozygous PS in RH, shared by DM	PGSC0003DMG400016357	PGSC0003DMT400042158	chr08	yes	NO	
220	Heterozygous PS in RH, shared by DM	PGSC0003DMG400016439	PGSC0003DMT400042395	chr05	yes	NO	

221	Heterozygous PS in RH, shared by DM	PGSC0003DMG400016497	PGSC0003DMT400042531	chr03	yes	yes	GO:0004190; aspartic-type endopeptidase activity; Molecular Function GO:0016021; integral to membrane; Cellular Component
222	Heterozygous PS in RH, shared by DM	PGSC0003DMG400016501	PGSC0003DMT400042540	chr10	yes	yes	
223	Heterozygous PS in RH, shared by DM	PGSC0003DMG400016522	PGSC0003DMT400042604	chr11	NO	NO	
224	Heterozygous PS in RH, shared by DM	PGSC0003DMG402016626	PGSC0003DMT400042871	chr05	NO	NO	
225	Heterozygous PS in RH, shared by DM	PGSC0003DMG400016644	PGSC0003DMT400042928	-	yes	NO	
226	Heterozygous PS in RH, shared by DM	PGSC0003DMG400016681	PGSC0003DMT400043011	chr09	yes	NO	GO:0005618; cell wall; Cellular Component GO:0030599; pectinesterase activity; Molecular Function GO:0042545; cell wall modification; Biological Process
227	Heterozygous PS in RH, shared by DM	PGSC0003DMG400016754	PGSC0003DMT400043177	chr03	yes	NO	
228	Heterozygous PS in RH, shared by DM	PGSC0003DMG400016795	PGSC0003DMT400043258	chr03	NO	NO	GO:0006508; proteolysis; Biological Process GO:0008234; cysteine-type peptidase activity; Molecular Function
229	Heterozygous PS in RH, shared by DM	PGSC0003DMG400016849	PGSC0003DMT400043405	chr03	NO	NO	
230	Heterozygous PS in RH, shared by DM	PGSC0003DMG400016861	PGSC0003DMT400043434	chr08	NO	NO	GO:0004672; protein kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
231	Heterozygous PS in RH, shared by DM	PGSC0003DMG400016886	PGSC0003DMT400043490	chr07	NO	NO	

232	Heterozygous PS in RH, shared by DM	PGSC0003DMG400016931	PGSC0003DMT400043601	chr06	yes	NO	
233	Heterozygous PS in RH, shared by DM	PGSC0003DMG400016968	PGSC0003DMT400043689	chr04	NO	NO	
234	Heterozygous PS in RH, shared by DM	PGSC0003DMG403016981	PGSC0003DMT400043733	chr04	NO	NO	GO:0005215; transporter activity; Molecular Function GO:0006810; transport; Biological Process GO:0016021; integral to membrane; Cellular Component GO:0055085; transmembrane transport; Biological Process
235	Heterozygous PS in RH, shared by DM	PGSC0003DMG400017061	PGSC0003DMT400043961	chr07	yes	NO	GO:0003723; RNA binding; Molecular Function GO:0003964; RNA-directed DNA polymerase activity; Molecular Function GO:0006278; RNA-dependent DNA replication; Biological Process
236	Heterozygous PS in RH, shared by DM	PGSC0003DMG400017069	PGSC0003DMT400043981	chr08	yes	yes	GO:0006629; lipid metabolic process; Biological Process GO:0016788; hydrolase activity, acting on ester bonds; Molecular Function
237	Heterozygous PS in RH, shared by DM	PGSC0003DMG400017087	PGSC0003DMT400044032	chr01	yes	yes	GO:0005215; transporter activity; Molecular Function GO:0006814; sodium ion transport; Biological Process GO:0016020; membrane; Cellular Component GO:0055085; transmembrane transport; Biological Process
238	Heterozygous PS in RH, shared by DM	PGSC0003DMG400017163	PGSC0003DMT400044207	-	yes	NO	
239	Heterozygous PS in RH, shared by DM	PGSC0003DMG400017235	PGSC0003DMT400044390	chr12	NO	NO	
240	Heterozygous PS in RH, shared by DM	PGSC0003DMG400017447	PGSC0003DMT400044985	-	NO	NO	

241	Heterozygous PS in RH, shared by DM	PGSC0003DMG400017560	PGSC0003DMT400045267	chr11	NO	NO	
242	Heterozygous PS in RH, shared by DM	PGSC0003DMG400017605	PGSC0003DMT400045367	chr11	yes	yes	
243	Heterozygous PS in RH, shared by DM	PGSC0003DMG400017620	PGSC0003DMT400045412	chr09	yes	yes	
244	Heterozygous PS in RH, shared by DM	PGSC0003DMG400017777	PGSC0003DMT400045835				
245	Heterozygous PS in RH, shared by DM	PGSC0003DMG400017789	PGSC0003DMT400045859	chr06	yes	yes	
246	Heterozygous PS in RH, shared by DM	PGSC0003DMG400018061	PGSC0003DMT400046529	chr06	yes	yes	GO:0005737; cytoplasm; Cellular Component GO:0005975; carbohydrate metabolic process; Biological Process GO:0016614; oxidoreductase activity, acting on CH-OH group of donors; Molecular Function GO:0016616; oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor; Molecular Function GO:0046168; glycerol-3-phosphate catabolic process; Biological Process GO:0051287; NAD or NADH binding; Molecular Function GO:0055114; oxidation reduction; Biological Process
247	Heterozygous PS in RH, shared by DM	PGSC0003DMG400018102	PGSC0003DMT400046621	-	NO	NO	
248	Heterozygous PS in RH, shared by DM	PGSC0003DMG400018195	PGSC0003DMT400046853	chr02	yes	NO	GO:0008152; metabolic process; Biological Process GO:0016758; transferase activity, transferring hexosyl groups; Molecular Function

249	Heterozygous PS in RH, shared by DM	PGSC0003DMG400018261	PGSC0003DMT400047018	chr11	yes	NO	
250	Heterozygous PS in RH, shared by DM	PGSC0003DMG400018269	PGSC0003DMT400047047	chr11	yes	NO	GO:0010181; FMN binding; Molecular Function GO:0016491; oxidoreductase activity; Molecular Function
251	Heterozygous PS in RH, shared by DM	PGSC0003DMG400018322	PGSC0003DMT400047206	chr03	yes	yes	GO:0016616; oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor; Molecular Function GO:0051287; NAD or NADH binding; Molecular Function
252	Heterozygous PS in RH, shared by DM	PGSC0003DMG400018337	PGSC0003DMT400047231	chr01	NO	NO	
253	Heterozygous PS in RH, shared by DM	PGSC0003DMG401018347	PGSC0003DMT400047256	chr10	NO	NO	
254	Heterozygous PS in RH, shared by DM	PGSC0003DMG400018369	PGSC0003DMT400047299	chr12	NO	NO	
255	Heterozygous PS in RH, shared by DM	PGSC0003DMG400018411	PGSC0003DMT400047378	chr12	yes	yes	
256	Heterozygous PS in RH, shared by DM	PGSC0003DMG400018489	PGSC0003DMT400047576	chr12	yes	yes	
257	Heterozygous PS in RH, shared by DM	PGSC0003DMG400018491	PGSC0003DMT400047580	chr01	yes	NO	GO:0005524; ATP binding; Molecular Function GO:0006915; apoptosis; Biological Process
258	Heterozygous PS in RH, shared by DM	PGSC0003DMG400018499	PGSC0003DMT400047599	chr10	NO	NO	GO:0006812; cation transport; Biological Process GO:0015299; solute:hydrogen antiporter activity; Molecular Function GO:0016021; integral to membrane; Cellular Component GO:0055085; transmembrane transport; Biological Process

259	Heterozygous PS in RH, shared by DM	PGSC0003DMG400018513	PGSC0003DMT400047633	chr12	NO	NO	GO:0003677; DNA binding; Molecular Function GO:0045449; regulation of transcription; Biological Process
260	Heterozygous PS in RH, shared by DM	PGSC0003DMG400018591	PGSC0003DMT400047836	chr01	yes	NO	GO:0006621; protein retention in ER lumen; Biological Process GO:0016021; integral to membrane; Cellular Component GO:0046923; ER retention sequence binding; Molecular Function
261	Heterozygous PS in RH, shared by DM	PGSC0003DMG400018623	PGSC0003DMT400047919	-	yes	NO	
262	Heterozygous PS in RH, shared by DM	PGSC0003DMG402018643	PGSC0003DMT400047980	chr02	yes	yes	
263	Heterozygous PS in RH, shared by DM	PGSC0003DMG402018748	PGSC0003DMT400048258	chr11	yes	yes	
264	Heterozygous PS in RH, shared by DM	PGSC0003DMG400018755	PGSC0003DMT400048272	chr09	NO	NO	
265	Heterozygous PS in RH, shared by DM	PGSC0003DMG400018778	PGSC0003DMT400048328	chr09	yes	yes	
266	Heterozygous PS in RH, shared by DM	PGSC0003DMG401018864	PGSC0003DMT400048561	-	NO	NO	
267	Heterozygous PS in RH, shared by DM	PGSC0003DMG400018866	PGSC0003DMT400048565	chr06	NO	NO	
268	Heterozygous PS in RH, shared by DM	PGSC0003DMG400018885	PGSC0003DMT400048610	chr12	NO	NO	
269	Heterozygous PS in RH, shared by DM	PGSC0003DMG400019145	PGSC0003DMT400049243	chr06	yes	yes	
270	Heterozygous PS in RH, shared by DM	PGSC0003DMG400019210	PGSC0003DMT400049445	chr10	yes	NO	

271	Heterozygous PS in RH, shared by DM	PGSC0003DMG402019226	PGSC0003DMT400049482	-	NO	NO	
272	Heterozygous PS in RH, shared by DM	PGSC0003DMG400019237	PGSC0003DMT400049507	chr10	yes	NO	GO:0005524; ATP binding; Molecular Function GO:0006810; transport; Biological Process GO:0016021; integral to membrane; Cellular Component GO:0016887; ATPase activity; Molecular Function GO:0042626; ATPase activity, coupled to transmembrane movement of substances; Molecular Function GO:0055085; transmembrane transport; Biological Process
273	Heterozygous PS in RH, shared by DM	PGSC0003DMG400019324	PGSC0003DMT400049738	chr02	NO	NO	
274	Heterozygous PS in RH, shared by DM	PGSC0003DMG400019370	PGSC0003DMT400049853	chr09	NO	NO	
275	Heterozygous PS in RH, shared by DM	PGSC0003DMG400019544	PGSC0003DMT400050302	chr12	yes	NO	
276	Heterozygous PS in RH, shared by DM	PGSC0003DMG400019580	PGSC0003DMT400050373	chr06	yes	NO	
277	Heterozygous PS in RH, shared by DM	PGSC0003DMG400019655	PGSC0003DMT400050574	chr08	yes	NO	
278	Heterozygous PS in RH, shared by DM	PGSC0003DMG400020074	PGSC0003DMT400051692	chr11	NO	NO	
279	Heterozygous PS in RH, shared by DM	PGSC0003DMG401020229	PGSC0003DMT400052119	chr03	yes	NO	

280	Heterozygous PS in RH, shared by DM	PGSC0003DMG403020229	PGSC0003DMT400052131	chr07	yes	NO	GO:0005622; intracellular; Cellular Component GO:0006464; protein modification process; Biological Process GO:0016881; acid-amino acid ligase activity; Molecular Function
281	Heterozygous PS in RH, shared by DM	PGSC0003DMG400020234	PGSC0003DMT400052151	chr07	yes	NO	
282	Heterozygous PS in RH, shared by DM	PGSC0003DMG400020249	PGSC0003DMT400052209	chr06	yes	NO	GO:0004190; aspartic-type endopeptidase activity; Molecular Function GO:0006508; proteolysis; Biological Process
283	Heterozygous PS in RH, shared by DM	PGSC0003DMG400020316	PGSC0003DMT400052337	chr02	yes	NO	
284	Heterozygous PS in RH, shared by DM	PGSC0003DMG400020365	PGSC0003DMT400052472	chr01	yes	NO	
285	Heterozygous PS in RH, shared by DM	PGSC0003DMG400020383	PGSC0003DMT400052535	chr10	yes	yes	
286	Heterozygous PS in RH, shared by DM	PGSC0003DMG400020428	PGSC0003DMT400052626	chr03	NO	NO	
287	Heterozygous PS in RH, shared by DM	PGSC0003DMG400020435	PGSC0003DMT400052645	chr10	yes	NO	GO:0005622; intracellular; Cellular Component GO:0008270; zinc ion binding; Molecular Function
288	Heterozygous PS in RH, shared by DM	PGSC0003DMG400020491	PGSC0003DMT400052800	chr08	yes	yes	GO:0005524; ATP binding; Molecular Function GO:0016020; membrane; Cellular Component GO:0016887; ATPase activity; Molecular Function
289	Heterozygous PS in RH, shared by DM	PGSC0003DMG400020523	PGSC0003DMT400052899	chr02	NO	NO	
290	Heterozygous PS in RH, shared by DM	PGSC0003DMG400020671	PGSC0003DMT400053258	chr02	yes	yes	

291	Heterozygous PS in RH, shared by DM	PGSC0003DMG400020793	PGSC0003DMT400053597	chr10	NO	NO	
292	Heterozygous PS in RH, shared by DM	PGSC0003DMG400020851	PGSC0003DMT400053754	chr09	NO	NO	
293	Heterozygous PS in RH, shared by DM	PGSC0003DMG400020878	PGSC0003DMT400053823	chr04	yes	yes	
294	Heterozygous PS in RH, shared by DM	PGSC0003DMG400020989	PGSC0003DMT400054119	chr05	NO	NO	
295	Heterozygous PS in RH, shared by DM	PGSC0003DMG400021144	PGSC0003DMT400054480	chr10	NO	NO	
296	Heterozygous PS in RH, shared by DM	PGSC0003DMG400021200	PGSC0003DMT400054625	chr07	NO	NO	
297	Heterozygous PS in RH, shared by DM	PGSC0003DMG400021203	PGSC0003DMT400054636	chr11	yes	NO	
298	Heterozygous PS in RH, shared by DM	PGSC0003DMG400021409	PGSC0003DMT400055162	chr04	yes	NO	GO:0016020; membrane; Cellular Component
299	Heterozygous PS in RH, shared by DM	PGSC0003DMG400021472	PGSC0003DMT400055319	chr11	yes	yes	
300	Heterozygous PS in RH, shared by DM	PGSC0003DMG400021595	PGSC0003DMT400055608	chr08	NO	NO	
301	Heterozygous PS in RH, shared by DM	PGSC0003DMG400021644	PGSC0003DMT400055739	chr02	NO	NO	
302	Heterozygous PS in RH, shared by DM	PGSC0003DMG400021658	PGSC0003DMT400055769	chr12	NO	NO	

303	Heterozygous PS in RH, shared by DM	PGSC0003DMG400021668	PGSC0003DMT400055790	-	NO	NO	
304	Heterozygous PS in RH, shared by DM	PGSC0003DMG400021795	PGSC0003DMT400056108	chr10	yes	yes	
305	Heterozygous PS in RH, shared by DM	PGSC0003DMG400021849	PGSC0003DMT400056238				
306	Heterozygous PS in RH, shared by DM	PGSC0003DMG400021871	PGSC0003DMT400056296	chr04	NO	NO	GO:0006629; lipid metabolic process; Biological Process GO:0016788; hydrolase activity, acting on ester bonds; Molecular Function
307	Heterozygous PS in RH, shared by DM	PGSC0003DMG400022033	PGSC0003DMT400056658	-	NO	NO	
308	Heterozygous PS in RH, shared by DM	PGSC0003DMG400022113	PGSC0003DMT400056847	chr03	yes	yes	
309	Heterozygous PS in RH, shared by DM	PGSC0003DMG401022253	PGSC0003DMT400057292	chr09	yes	yes	GO:0003677; DNA binding; Molecular Function GO:0008270; zinc ion binding; Molecular Function GO:0045449; regulation of transcription; Biological Process
310	Heterozygous PS in RH, shared by DM	PGSC0003DMG400022258	PGSC0003DMT400057320	chr06	yes	yes	
311	Heterozygous PS in RH, shared by DM	PGSC0003DMG400022294	PGSC0003DMT400057418	chr08	yes	yes	
312	Heterozygous PS in RH, shared by DM	PGSC0003DMG400022422	PGSC0003DMT400057758	-	NO	NO	
313	Heterozygous PS in RH, shared by DM	PGSC0003DMG400022438	PGSC0003DMT400057795	chr03	yes	NO	

314	Heterozygous PS in RH, shared by DM	PGSC0003DMG400022512	PGSC0003DMT400057990	chr05	yes	NO	
315	Heterozygous PS in RH, shared by DM	PGSC0003DMG400022517	PGSC0003DMT400057997	chr06	yes	NO	GO:0000276; mitochondrial proton-transporting ATP synthase complex, coupling factor F(o); Cellular Component GO:0015078; hydrogen ion transmembrane transporter activity; Molecular Function GO:0015986; ATP synthesis coupled proton transport; Biological Process
316	Heterozygous PS in RH, shared by DM	PGSC0003DMG400022532	PGSC0003DMT400058039	chr06	yes	NO	GO:0003676; nucleic acid binding; Molecular Function
317	Heterozygous PS in RH, shared by DM	PGSC0003DMG400022558	PGSC0003DMT400058116	-	yes	yes	
318	Heterozygous PS in RH, shared by DM	PGSC0003DMG400022609	PGSC0003DMT400058225	-	yes	NO	GO:0008270; zinc ion binding; Molecular Function
319	Heterozygous PS in RH, shared by DM	PGSC0003DMG400022753	PGSC0003DMT400058574	chr01	yes	NO	
320	Heterozygous PS in RH, shared by DM	PGSC0003DMG400022787	PGSC0003DMT400058657	chr04	NO	NO	
321	Heterozygous PS in RH, shared by DM	PGSC0003DMG400022790	PGSC0003DMT400058668	chr09	yes	NO	GO:0004553; hydrolase activity, hydrolyzing O-glycosyl compounds; Molecular Function GO:0005975; carbohydrate metabolic process; Biological Process
322	Heterozygous PS in RH, shared by DM	PGSC0003DMG400022891	PGSC0003DMT400058923	chr09	NO	NO	GO:0004497; monooxygenase activity; Molecular Function GO:0005506; iron ion binding; Molecular Function GO:0009055; electron carrier activity; Molecular Function GO:0020037; heme binding; Molecular Function

323	Heterozygous PS in RH, shared by DM	PGSC0003DMG401023052	PGSC0003DMT400059327	chr11	yes	NO	GO:0003677; DNA binding; Molecular Function GO:0045449; regulation of transcription; Biological Process
324	Heterozygous PS in RH, shared by DM	PGSC0003DMG400023053	PGSC0003DMT400059330	chr04	yes	yes	GO:0003677; DNA binding; Molecular Function GO:0005634; nucleus; Cellular Component
325	Heterozygous PS in RH, shared by DM	PGSC0003DMG400023385	PGSC0003DMT400060114	chr08	NO	NO	GO:0003824; catalytic activity; Molecular Function GO:0005992; trehalose biosynthetic process; Biological Process
326	Heterozygous PS in RH, shared by DM	PGSC0003DMG401023433	PGSC0003DMT400060236	chr05	yes	yes	GO:0005524; ATP binding; Molecular Function GO:0006915; apoptosis; Biological Process
327	Heterozygous PS in RH, shared by DM	PGSC0003DMG400023537	PGSC0003DMT400060513	chr09	yes	NO	GO:0004568; chitinase activity; Molecular Function GO:0006032; chitin catabolic process; Biological Process GO:0016998; cell wall macromolecule catabolic process; Biological Process
328	Heterozygous PS in RH, shared by DM	PGSC0003DMG400023663	PGSC0003DMT400060833	chr05	NO	NO	
329	Heterozygous PS in RH, shared by DM	PGSC0003DMG400023750	PGSC0003DMT400061035	chr09	yes	yes	
330	Heterozygous PS in RH, shared by DM	PGSC0003DMG400023800	PGSC0003DMT400061161	chr04	yes	yes	
331	Heterozygous PS in RH, shared by DM	PGSC0003DMG400023819	PGSC0003DMT400061190				
332	Heterozygous PS in RH, shared by DM	PGSC0003DMG400023914	PGSC0003DMT400061444	chr11	NO	NO	
333	Heterozygous PS in RH, shared by DM	PGSC0003DMG400023957	PGSC0003DMT400061553	chr04	NO	NO	

334	Heterozygous PS in RH, shared by DM	PGSC0003DMG400024117	PGSC0003DMT400061965	chr01	NO	NO	
335	Heterozygous PS in RH, shared by DM	PGSC0003DMG400024209	PGSC0003DMT400062205	chr01	yes	yes	GO:0006886; intracellular protein transport; Biological Process GO:0008565; protein transporter activity; Molecular Function
336	Heterozygous PS in RH, shared by DM	PGSC0003DMG400024277	PGSC0003DMT400062379	chr08	yes	yes	GO:0015671; oxygen transport; Biological Process GO:0019825; oxygen binding; Molecular Function
337	Heterozygous PS in RH, shared by DM	PGSC0003DMG400024356	PGSC0003DMT400062593	chr03	yes	NO	GO:0004867; serine-type endopeptidase inhibitor activity; Molecular Function
338	Heterozygous PS in RH, shared by DM	PGSC0003DMG402024473	PGSC0003DMT400062874	-	NO	NO	
339	Heterozygous PS in RH, shared by DM	PGSC0003DMG400024474	PGSC0003DMT400062877	chr01	yes	NO	
340	Heterozygous PS in RH, shared by DM	PGSC0003DMG400024608	PGSC0003DMT400063270	chr10	NO	NO	
341	Heterozygous PS in RH, shared by DM	PGSC0003DMG400024655	PGSC0003DMT400063385	chr08	NO	NO	
342	Heterozygous PS in RH, shared by DM	PGSC0003DMG402024817	PGSC0003DMT400063848	chr06	yes	NO	GO:0004640; phosphoribosylanthranilate isomerase activity; Molecular Function GO:0006568; tryptophan metabolic process; Biological Process
343	Heterozygous PS in RH, shared by DM	PGSC0003DMG400024823	PGSC0003DMT400063864	-	yes	yes	GO:0004672; protein kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
344	Heterozygous PS in RH, shared by DM	PGSC0003DMG400024989	PGSC0003DMT400064322	chr03	yes	NO	GO:0005622; intracellular; Cellular Component GO:0008270; zinc ion binding; Molecular Function

345	Heterozygous PS in RH, shared by DM	PGSC0003DMG400025054	PGSC0003DMT400064478	chr01	yes	NO	GO:0000160; two-component signal transduction system (phosphorelay); Biological Process GO:0004871; signal transducer activity; Molecular Function
346	Heterozygous PS in RH, shared by DM	PGSC0003DMG400025122	PGSC0003DMT400064673	chr02	yes	yes	GO:0016021; integral to membrane; Cellular Component GO:0055085; transmembrane transport; Biological Process
347	Heterozygous PS in RH, shared by DM	PGSC0003DMG400025175	PGSC0003DMT400064824	chr06	NO	NO	
348	Heterozygous PS in RH, shared by DM	PGSC0003DMG400025227	PGSC0003DMT400064957	chr10	NO	NO	
349	Heterozygous PS in RH, shared by DM	PGSC0003DMG400025283	PGSC0003DMT400065069	chr02	yes	NO	
350	Heterozygous PS in RH, shared by DM	PGSC0003DMG400025331	PGSC0003DMT400065176	chr06	yes	NO	
351	Heterozygous PS in RH, shared by DM	PGSC0003DMG400025373	PGSC0003DMT400065273	chr12	NO	NO	GO:0004857; enzyme inhibitor activity; Molecular Function GO:0030599; pectinesterase activity; Molecular Function
352	Heterozygous PS in RH, shared by DM	PGSC0003DMG400025379	PGSC0003DMT400065290	chr07	yes	yes	
353	Heterozygous PS in RH, shared by DM	PGSC0003DMG401025391	PGSC0003DMT400065314	chr10	yes	NO	
354	Heterozygous PS in RH, shared by DM	PGSC0003DMG400025448	PGSC0003DMT400065440	chr11	NO	NO	GO:0005622; intracellular; Cellular Component GO:0006464; protein modification process; Biological Process GO:0016881; acid-amino acid ligase activity; Molecular Function
355	Heterozygous PS in RH, shared by DM	PGSC0003DMG400025487	PGSC0003DMT400065512	-	NO	NO	

356	Heterozygous PS in RH, shared by DM	PGSC0003DMG400025489	PGSC0003DMT400065515	-	NO	NO	
357	Heterozygous PS in RH, shared by DM	PGSC0003DMG400025491	PGSC0003DMT400065517	chr04	NO	NO	
358	Heterozygous PS in RH, shared by DM	PGSC0003DMG400025586	PGSC0003DMT400065742	chr03	yes	NO	
359	Heterozygous PS in RH, shared by DM	PGSC0003DMG400025721	PGSC0003DMT400066070	chr08	yes	NO	GO:0004252; serine-type endopeptidase activity; Molecular Function GO:0006508; proteolysis; Biological Process GO:0042802; identical protein binding; Molecular Function GO:0043086; negative regulation of catalytic activity; Biological Process
360	Heterozygous PS in RH, shared by DM	PGSC0003DMG400025795	PGSC0003DMT400066337	chr06	yes	NO	
361	Heterozygous PS in RH, shared by DM	PGSC0003DMG400026188	PGSC0003DMT400067356	chr12	NO	NO	
362	Heterozygous PS in RH, shared by DM	PGSC0003DMG400026305	PGSC0003DMT400067641	chr10	yes	NO	
363	Heterozygous PS in RH, shared by DM	PGSC0003DMG400026313	PGSC0003DMT400067663	chr08	NO	NO	
364	Heterozygous PS in RH, shared by DM	PGSC0003DMG402026387	PGSC0003DMT400067846	chr07	NO	NO	GO:0003676; nucleic acid binding; Molecular Function
365	Heterozygous PS in RH, shared by DM	PGSC0003DMG402026407	PGSC0003DMT400067900	chr04	NO	NO	GO:0003676; nucleic acid binding; Molecular Function GO:0008270; zinc ion binding; Molecular Function
366	Heterozygous PS in RH, shared by DM	PGSC0003DMG400026426	PGSC0003DMT400067940	chr11	NO	NO	

367	Heterozygous PS in RH, shared by DM	PGSC0003DMG400026499	PGSC0003DMT400068128	chr05	yes	NO	
368	Heterozygous PS in RH, shared by DM	PGSC0003DMG401026514	PGSC0003DMT400068174	-	yes	NO	GO:0004221; ubiquitin thiolesterase activity; Molecular Function GO:0006511; ubiquitin-dependent protein catabolic process; Biological Process
369	Heterozygous PS in RH, shared by DM	PGSC0003DMG402026514	PGSC0003DMT400068172	chr01	yes	NO	
370	Heterozygous PS in RH, shared by DM	PGSC0003DMG401026519	PGSC0003DMT400068189	chr04	NO	NO	
371	Heterozygous PS in RH, shared by DM	PGSC0003DMG400026736	PGSC0003DMT400068752	chr10	yes	NO	
372	Heterozygous PS in RH, shared by DM	PGSC0003DMG400026782	PGSC0003DMT400068861	chr04	NO	NO	
373	Heterozygous PS in RH, shared by DM	PGSC0003DMG400026819	PGSC0003DMT400068951	chr08	yes	NO	
374	Heterozygous PS in RH, shared by DM	PGSC0003DMG400026829	PGSC0003DMT400068977	chr06	yes	yes	GO:0005515; protein binding; Molecular Function
375	Heterozygous PS in RH, shared by DM	PGSC0003DMG400026864	PGSC0003DMT400069062	chr07	yes	yes	
376	Heterozygous PS in RH, shared by DM	PGSC0003DMG400026899	PGSC0003DMT400069145	chr09	yes	yes	
377	Heterozygous PS in RH, shared by DM	PGSC0003DMG400026908	PGSC0003DMT400069175	chr08	yes	NO	
378	Heterozygous PS in RH, shared by DM	PGSC0003DMG401026931	PGSC0003DMT400069232	chr01	yes	NO	

379	Heterozygous PS in RH, shared by DM	PGSC0003DMG400027022	PGSC0003DMT400069507	chr10	yes	NO	GO:0004672; protein kinase activity; Molecular Function GO:0005515; protein binding; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
380	Heterozygous PS in RH, shared by DM	PGSC0003DMG400027149	PGSC0003DMT400069822	chr07	NO	NO	
381	Heterozygous PS in RH, shared by DM	PGSC0003DMG400027183	PGSC0003DMT400069901	chr11	NO	NO	
382	Heterozygous PS in RH, shared by DM	PGSC0003DMG400027384	PGSC0003DMT400070437	chr07	NO	NO	
383	Heterozygous PS in RH, shared by DM	PGSC0003DMG400027464	PGSC0003DMT400070649	-	yes	NO	GO:0004553; hydrolase activity, hydrolyzing O-glycosyl compounds; Molecular Function GO:0005618; cell wall; Cellular Component GO:0005975; carbohydrate metabolic process; Biological Process GO:0006073; cellular glucan metabolic process; Biological Process GO:0016762; xyloglucan:xyloglucosyl transferase activity; Molecular Function GO:0048046; apoplast; Cellular Component
384	Heterozygous PS in RH, shared by DM	PGSC0003DMG400027465	PGSC0003DMT400070650	chr11	yes	NO	GO:0004672; protein kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
385	Heterozygous PS in RH, shared by DM	PGSC0003DMG402027687	PGSC0003DMT400071195	chr04	NO	NO	
386	Heterozygous PS in RH, shared by DM	PGSC0003DMG400027783	PGSC0003DMT400071406	chr03	yes	NO	

387	Heterozygous PS in RH, shared by DM	PGSC0003DMG400027809	PGSC0003DMT400071473	chr05	yes	yes	GO:0005634; nucleus; Cellular Component
388	Heterozygous PS in RH, shared by DM	PGSC0003DMG400028054	PGSC0003DMT400072105	chr11	yes	NO	
389	Heterozygous PS in RH, shared by DM	PGSC0003DMG400028165	PGSC0003DMT400072375	chr01	yes	NO	
390	Heterozygous PS in RH, shared by DM	PGSC0003DMG400028221	PGSC0003DMT400072533				
391	Heterozygous PS in RH, shared by DM	PGSC0003DMG400028271	PGSC0003DMT400072655	chr11	yes	NO	GO:0004497; monooxygenase activity; Molecular Function GO:0005506; iron ion binding; Molecular Function GO:0009055; electron carrier activity; Molecular Function GO:0020037; heme binding; Molecular Function
392	Heterozygous PS in RH, shared by DM	PGSC0003DMG400028311	PGSC0003DMT400072750	chr10	yes	yes	GO:0005643; nuclear pore; Cellular Component GO:0016973; poly(A)+ mRNA export from nucleus; Biological Process
393	Heterozygous PS in RH, shared by DM	PGSC0003DMG400028343	PGSC0003DMT400072858	chr02	NO	NO	GO:0000151; ubiquitin ligase complex; Cellular Component GO:0004672; protein kinase activity; Molecular Function GO:0004842; ubiquitin-protein ligase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process GO:0016567; protein ubiquitination; Biological Process
394	Heterozygous PS in RH, shared by DM	PGSC0003DMG400028366	PGSC0003DMT400072910	chr01	yes	NO	

395	Heterozygous PS in RH, shared by DM	PGSC0003DMG400028373	PGSC0003DMT400072928	chr11	yes	NO	GO:0004497; monooxygenase activity; Molecular Function GO:0005506; iron ion binding; Molecular Function GO:0009055; electron carrier activity; Molecular Function GO:0020037; heme binding; Molecular Function
396	Heterozygous PS in RH, shared by DM	PGSC0003DMG400028405	PGSC0003DMT400073019	chr06	NO	NO	
397	Heterozygous PS in RH, shared by DM	PGSC0003DMG400028473	PGSC0003DMT400073277	chr04	yes	NO	
398	Heterozygous PS in RH, shared by DM	PGSC0003DMG400028493	PGSC0003DMT400073320	chr02	yes	NO	
399	Heterozygous PS in RH, shared by DM	PGSC0003DMG400028706	PGSC0003DMT400073876	-	yes	yes	
400	Heterozygous PS in RH, shared by DM	PGSC0003DMG400028825	PGSC0003DMT400074161	chr08	NO	NO	
401	Heterozygous PS in RH, shared by DM	PGSC0003DMG400028833	PGSC0003DMT400074187	chr02	yes	NO	
402	Heterozygous PS in RH, shared by DM	PGSC0003DMG400028846	PGSC0003DMT400074230	chr02	NO	NO	
403	Heterozygous PS in RH, shared by DM	PGSC0003DMG400028898	PGSC0003DMT400074348	-	NO	NO	
404	Heterozygous PS in RH, shared by DM	PGSC0003DMG400028958	PGSC0003DMT400074506	chr04	NO	NO	
405	Heterozygous PS in RH, shared by DM	PGSC0003DMG400029178	PGSC0003DMT400075018	chr06	NO	NO	

406	Heterozygous PS in RH, shared by DM	PGSC0003DMG400029192	PGSC0003DMT400075052	chr07	yes	NO	
407	Heterozygous PS in RH, shared by DM	PGSC0003DMG400029193	PGSC0003DMT400075055	chr06	NO	NO	
408	Heterozygous PS in RH, shared by DM	PGSC0003DMG400029301	PGSC0003DMT400075342	chr05	NO	NO	
409	Heterozygous PS in RH, shared by DM	PGSC0003DMG400029342	PGSC0003DMT400075431	chr08	yes	NO	
410	Heterozygous PS in RH, shared by DM	PGSC0003DMG400029360	PGSC0003DMT400075504	chr12	yes	NO	
411	Heterozygous PS in RH, shared by DM	PGSC0003DMG400029382	PGSC0003DMT400075558	chr06	NO	NO	GO:0005622; intracellular; Cellular Component GO:0006464; protein modification process; Biological Process GO:0016881; acid-amino acid ligase activity; Molecular Function
412	Heterozygous PS in RH, shared by DM	PGSC0003DMG400029495	PGSC0003DMT400075862	-	yes	yes	GO:0005515; protein binding; Molecular Function
413	Heterozygous PS in RH, shared by DM	PGSC0003DMG400029584	PGSC0003DMT400076080	chr01	yes	NO	GO:0004857; enzyme inhibitor activity; Molecular Function GO:0030599; pectinesterase activity; Molecular Function
414	Heterozygous PS in RH, shared by DM	PGSC0003DMG400029819	PGSC0003DMT400076675	-	yes	NO	
415	Heterozygous PS in RH, shared by DM	PGSC0003DMG400030041	PGSC0003DMT400077234	chr05	yes	NO	GO:0004672; protein kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
416	Heterozygous PS in RH, shared by DM	PGSC0003DMG400030092	PGSC0003DMT400077364	chr01	yes	NO	

417	Heterozygous PS in RH, shared by DM	PGSC0003DMG400030219	PGSC0003DMT400077668	chr08	yes	NO	
418	Heterozygous PS in RH, shared by DM	PGSC0003DMG400030267	PGSC0003DMT400077806	chr06	yes	yes	
419	Heterozygous PS in RH, shared by DM	PGSC0003DMG400030314	PGSC0003DMT400077944	chr01	yes	NO	
420	Heterozygous PS in RH, shared by DM	PGSC0003DMG400030335	PGSC0003DMT400077996	chr08	NO	NO	GO:0006355; regulation of transcription, DNA-dependent; Biological Process
421	Heterozygous PS in RH, shared by DM	PGSC0003DMG400030367	PGSC0003DMT400078071	chr10	NO	NO	
422	Heterozygous PS in RH, shared by DM	PGSC0003DMG400030371	PGSC0003DMT400078084	chr08	NO	NO	
423	Heterozygous PS in RH, shared by DM	PGSC0003DMG400030411	PGSC0003DMT400078175	chr08	yes	NO	GO:0005515; protein binding; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006915; apoptosis; Biological Process
424	Heterozygous PS in RH, shared by DM	PGSC0003DMG400030413	PGSC0003DMT400078178	chr05	yes	yes	GO:0004672; protein kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
425	Heterozygous PS in RH, shared by DM	PGSC0003DMG400030465	PGSC0003DMT400078274	chr07	yes	NO	
426	Heterozygous PS in RH, shared by DM	PGSC0003DMG400030508	PGSC0003DMT400078357	chr09	yes	yes	GO:0004553; hydrolase activity, hydrolyzing O-glycosyl compounds; Molecular Function GO:0005975; carbohydrate metabolic process; Biological Process

427	Heterozygous PS in RH, shared by DM	PGSC0003DMG400030542	PGSC0003DMT400078463	chr04	yes	NO	GO:0004497; monooxygenase activity; Molecular Function GO:0005506; iron ion binding; Molecular Function GO:0009055; electron carrier activity; Molecular Function GO:0020037; heme binding; Molecular Function
428	Heterozygous PS in RH, shared by DM	PGSC0003DMG400030558	PGSC0003DMT400078502	chr06	yes	NO	
429	Heterozygous PS in RH, shared by DM	PGSC0003DMG400030622	PGSC0003DMT400078698	chr11	yes	yes	GO:0004553; hydrolase activity, hydrolyzing O-glycosyl compounds; Molecular Function GO:0005618; cell wall; Cellular Component GO:0005975; carbohydrate metabolic process; Biological Process GO:0006073; cellular glucan metabolic process; Biological Process GO:0016762; xyloglucan:xyloglucosyl transferase activity; Molecular Function GO:0048046; apoplast; Cellular Component
430	Heterozygous PS in RH, shared by DM	PGSC0003DMG400030745	PGSC0003DMT400079001	chr12	yes	NO	
431	Heterozygous PS in RH, shared by DM	PGSC0003DMG400030794	PGSC0003DMT400079121	-	yes	yes	
432	Heterozygous PS in RH, shared by DM	PGSC0003DMG400030801	PGSC0003DMT400079138	chr12	NO	NO	
433	Heterozygous PS in RH, shared by DM	PGSC0003DMG400030855	PGSC0003DMT400079272	chr04	yes	yes	
434	Heterozygous PS in RH, shared by DM	PGSC0003DMG400030904	PGSC0003DMT400079392	chr02	yes	NO	

435	Heterozygous PS in RH, shared by DM	PGSC0003DMG402030921	PGSC0003DMT400079432	chr09	yes	NO	
436	Heterozygous PS in RH, shared by DM	PGSC0003DMG400030968	PGSC0003DMT400079535	chr09	yes	yes	
437	Heterozygous PS in RH, shared by DM	PGSC0003DMG400031039	PGSC0003DMT400079690	chr05	NO	NO	
438	Heterozygous PS in RH, shared by DM	PGSC0003DMG400031087	PGSC0003DMT400079832	-	yes	NO	
439	Heterozygous PS in RH, shared by DM	PGSC0003DMG401031089	PGSC0003DMT400079836	chr09	yes	NO	GO:0004672; protein kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
440	Heterozygous PS in RH, shared by DM	PGSC0003DMG400031095	PGSC0003DMT400079843	-	yes	yes	GO:0004888; transmembrane receptor activity; Molecular Function GO:0005515; protein binding; Molecular Function GO:0007165; signal transduction; Biological Process GO:0031224; intrinsic to membrane; Cellular Component GO:0045087; innate immune response; Biological Process
441	Heterozygous PS in RH, shared by DM	PGSC0003DMG400031153	PGSC0003DMT400080005	-	NO	NO	
442	Heterozygous PS in RH, shared by DM	PGSC0003DMG400031184	PGSC0003DMT400080083	-	yes	NO	GO:0004221; ubiquitin thiolesterase activity; Molecular Function GO:0006511; ubiquitin-dependent protein catabolic process; Biological Process
443	Heterozygous PS in RH, shared by DM	PGSC0003DMG400031190	PGSC0003DMT400080102	chr05	yes	NO	GO:0004672; protein kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process

444	Heterozygous PS in RH, shared by DM	PGSC0003DMG400031214	PGSC0003DMT400080182	chr02	yes	NO	GO:0003676; nucleic acid binding; Molecular Function
445	Heterozygous PS in RH, shared by DM	PGSC0003DMG402031251	PGSC0003DMT400080283	chr02	NO	NO	
446	Heterozygous PS in RH, shared by DM	PGSC0003DMG400031320	PGSC0003DMT400080445	-	NO	NO	
447	Heterozygous PS in RH, shared by DM	PGSC0003DMG400031333	PGSC0003DMT400080479	chr03	NO	NO	
448	Heterozygous PS in RH, shared by DM	PGSC0003DMG400031437	PGSC0003DMT400080723	chr07	yes	yes	
449	Heterozygous PS in RH, shared by DM	PGSC0003DMG400031491	PGSC0003DMT400080864	chr07	NO	NO	
450	Heterozygous PS in RH, shared by DM	PGSC0003DMG400031746	PGSC0003DMT400081216	chr10	yes	NO	
451	Heterozygous PS in RH, shared by DM	PGSC0003DMG400031896	PGSC0003DMT400081515	chr12	yes	NO	GO:0009772; photosynthetic electron transport in photosystem II; Biological Process GO:0019684; photosynthesis, light reaction; Biological Process GO:0030077; plasma membrane light-harvesting complex; Cellular Component GO:0045156; electron transporter, transferring electrons within the cyclic electron transport pathway of photosynthesis activity; Molecular Function
452	Heterozygous PS in RH, shared by DM	PGSC0003DMG401032161	PGSC0003DMT400081926				
453	Heterozygous PS in RH, shared by DM	PGSC0003DMG400032554	PGSC0003DMT400082469	chr06	NO	NO	GO:0005525; GTP binding; Molecular Function

454	Heterozygous PS in RH, shared by DM	PGSC0003DMG400032573	PGSC0003DMT400082496	chr10	NO	NO	
455	Heterozygous PS in RH, shared by DM	PGSC0003DMG400032773	PGSC0003DMT400082703	chr02	yes	NO	
456	Heterozygous PS in RH, shared by DM	PGSC0003DMG400032817	PGSC0003DMT400082789	chr01	yes	NO	
457	Heterozygous PS in RH, shared by DM	PGSC0003DMG400033056	PGSC0003DMT400083108	chr08	yes	NO	
458	Heterozygous PS in RH, shared by DM	PGSC0003DMG400033567	PGSC0003DMT400083733	chr04	yes	NO	GO:0005215; transporter activity; Molecular Function GO:0006810; transport; Biological Process GO:0016020; membrane; Cellular Component GO:0055085; transmembrane transport; Biological Process
459	Heterozygous PS in RH, shared by DM	PGSC0003DMG401034311	PGSC0003DMT400084735	chr06	NO	NO	
460	Heterozygous PS in RH, shared by DM	PGSC0003DMG400034328	PGSC0003DMT400084757	chr12	yes	yes	
461	Heterozygous PS in RH, shared by DM	PGSC0003DMG400034440	PGSC0003DMT400084869	chr08	yes	yes	GO:0004252; serine-type endopeptidase activity; Molecular Function GO:0006508; proteolysis; Biological Process GO:0042802; identical protein binding; Molecular Function GO:0043086; negative regulation of catalytic activity; Biological Process
462	Heterozygous PS in RH, shared by DM	PGSC0003DMG400034479	PGSC0003DMT400084908	chr11	yes	yes	

463	Heterozygous PS in RH, shared by DM	PGSC0003DMG400034550	PGSC0003DMT400084979	chr03	NO	NO	GO:0000166; nucleotide binding; Molecular Function GO:0004813; alanine-tRNA ligase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0005737; cytoplasm; Cellular Component GO:0006412; translation; Biological Process GO:0006419; alanyl-tRNA aminoacylation; Biological Process
464	Heterozygous PS in RH, shared by DM	PGSC0003DMG400034551	PGSC0003DMT400084980	chr09	yes	NO	
465	Heterozygous PS in RH, shared by DM	PGSC0003DMG400034552	PGSC0003DMT400084981	chr06	NO	NO	GO:0004497; monooxygenase activity; Molecular Function GO:0005506; iron ion binding; Molecular Function GO:0009055; electron carrier activity; Molecular Function GO:0020037; heme binding; Molecular Function
466	Heterozygous PS in RH, shared by DM	PGSC0003DMG400034599	PGSC0003DMT400085028	chr11	yes	NO	
467	Heterozygous PS in RH, shared by DM	PGSC0003DMG400034600	PGSC0003DMT400085029	chr09	NO	NO	
468	Heterozygous PS in RH, shared by DM	PGSC0003DMG400034646	PGSC0003DMT400085075	chr11	yes	NO	
469	Heterozygous PS in RH, shared by DM	PGSC0003DMG400034693	PGSC0003DMT400085122	chr06	NO	NO	GO:0004497; monooxygenase activity; Molecular Function GO:0005506; iron ion binding; Molecular Function GO:0009055; electron carrier activity; Molecular Function GO:0020037; heme binding; Molecular Function
470	Heterozygous PS in RH, shared by DM	PGSC0003DMG400034716	PGSC0003DMT400085145	chr04	NO	NO	

471	Heterozygous PS in RH, shared by DM	PGSC0003DMG400034729	PGSC0003DMT400085158	-	NO	NO	GO:0009058; biosynthetic process; Biological Process GO:0016769; transferase activity, transferring nitrogenous groups; Molecular Function GO:0030170; pyridoxal phosphate binding; Molecular Function
472	Heterozygous PS in RH, shared by DM	PGSC0003DMG400034956	PGSC0003DMT400085385	chr09	NO	NO	GO:0005097; Rab GTPase activator activity; Molecular Function GO:0005622; intracellular; Cellular Component GO:0032313; regulation of Rab GTPase activity; Biological Process
473	Heterozygous PS in RH, shared by DM	PGSC0003DMG400035099	PGSC0003DMT400085528	chr12	NO	NO	
474	Heterozygous PS in RH, shared by DM	PGSC0003DMG400035120	PGSC0003DMT400085549	chr03	yes	NO	GO:0003735; structural constituent of ribosome; Molecular Function GO:0005622; intracellular; Cellular Component GO:0005840; ribosome; Cellular Component GO:0006412; translation; Biological Process
475	Heterozygous PS in RH, shared by DM	PGSC0003DMG400035390	PGSC0003DMT400085819	chr12	NO	NO	
476	Heterozygous PS in RH, shared by DM	PGSC0003DMG400035433	PGSC0003DMT400085862	chr07	yes	NO	GO:0003723; RNA binding; Molecular Function GO:0033897; ribonuclease T2 activity; Molecular Function
477	Heterozygous PS in RH, shared by DM	PGSC0003DMG400035452	PGSC0003DMT400085881	chr08	NO	NO	
478	Heterozygous PS in RH, shared by DM	PGSC0003DMG400035508	PGSC0003DMT400085937	chr07	yes	NO	
479	Heterozygous PS in RH, shared by DM	PGSC0003DMG400035534	PGSC0003DMT400085963	chr10	yes	yes	

480	Heterozygous PS in RH, shared by DM	PGSC0003DMG400035552	PGSC0003DMT400085981	chr12	yes	yes	GO:0003723; RNA binding; Molecular Function GO:0003964; RNA-directed DNA polymerase activity; Molecular Function GO:0006278; RNA-dependent DNA replication; Biological Process
481	Heterozygous PS in RH, shared by DM	PGSC0003DMG400035668	PGSC0003DMT400086097	-	NO	NO	
482	Heterozygous PS in RH, shared by DM	PGSC0003DMG400035669	PGSC0003DMT400086098	chr12	NO	NO	
483	Heterozygous PS in RH, shared by DM	PGSC0003DMG400035682	PGSC0003DMT400086111	chr07	yes	NO	GO:0000148; 1,3-beta-glucan synthase complex; Cellular Component GO:0003843; 1,3-beta-glucan synthase activity; Molecular Function GO:0006075; 1,3-beta-glucan biosynthetic process; Biological Process GO:0016020; membrane; Cellular Component
484	Heterozygous PS in RH, shared by DM	PGSC0003DMG400035713	PGSC0003DMT400086142	chr01	yes	yes	GO:0004713; protein tyrosine kinase activity; Molecular Function GO:0005515; protein binding; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
485	Heterozygous PS in RH, shared by DM	PGSC0003DMG400035714	PGSC0003DMT400086143	chr11	yes	NO	
486	Heterozygous PS in RH, shared by DM	PGSC0003DMG400035810	PGSC0003DMT400086239	chr08	NO	NO	GO:0003676; nucleic acid binding; Molecular Function GO:0008270; zinc ion binding; Molecular Function
487	Heterozygous PS in RH, shared by DM	PGSC0003DMG400036064	PGSC0003DMT400086493				
488	Heterozygous PS in RH, shared by DM	PGSC0003DMG400036133	PGSC0003DMT400086562	chr06	yes	yes	

489	Heterozygous PS in RH, shared by DM	PGSC0003DMG400036165	PGSC0003DMT400086594	chr01	yes	NO	
490	Heterozygous PS in RH, shared by DM	PGSC0003DMG400036305	PGSC0003DMT400086734	chr08	NO	NO	
491	Heterozygous PS in RH, shared by DM	PGSC0003DMG400036369	PGSC0003DMT400086798	chr12	yes	NO	GO:0005515; protein binding; Molecular Function
492	Heterozygous PS in RH, shared by DM	PGSC0003DMG400036554	PGSC0003DMT400086983	chr01	yes	NO	GO:0005515; protein binding; Molecular Function
493	Heterozygous PS in RH, shared by DM	PGSC0003DMG400036575	PGSC0003DMT400087004	chr12	yes	NO	
494	Heterozygous PS in RH, shared by DM	PGSC0003DMG400036743	PGSC0003DMT400087172	chr11	yes	NO	
495	Heterozygous PS in RH, shared by DM	PGSC0003DMG400036747	PGSC0003DMT400087176	chr01	yes	NO	GO:0003677; DNA binding; Molecular Function GO:0046983; protein dimerization activity; Molecular Function
496	Heterozygous PS in RH, shared by DM	PGSC0003DMG400037031	PGSC0003DMT400087460	chr02	NO	NO	
497	Heterozygous PS in RH, shared by DM	PGSC0003DMG400037103	PGSC0003DMT400087532	chr10	yes	yes	GO:0005634; nucleus; Cellular Component
498	Heterozygous PS in RH, shared by DM	PGSC0003DMG400037161	PGSC0003DMT400087590				
499	Heterozygous PS in RH, shared by DM	PGSC0003DMG400037398	PGSC0003DMT400087827	chr06	yes	NO	
500	Heterozygous PS in RH, shared by DM	PGSC0003DMG400037517	PGSC0003DMT400087946	chr10	NO	NO	GO:0005634; nucleus; Cellular Component GO:0006355; regulation of transcription, DNA-dependent; Biological Process

501	Heterozygous PS in RH, shared by DM	PGSC0003DMG400037571	PGSC0003DMT400088000	chr03	yes	yes	
502	Heterozygous PS in RH, shared by DM	PGSC0003DMG400037583	PGSC0003DMT400088012	chr02	NO	NO	
503	Heterozygous PS in RH, shared by DM	PGSC0003DMG400037616	PGSC0003DMT400088045	chr12	yes	NO	
504	Heterozygous PS in RH, shared by DM	PGSC0003DMG400037735	PGSC0003DMT400088164	chr03	yes	NO	GO:0016787; hydrolase activity; Molecular Function
505	Heterozygous PS in RH, shared by DM	PGSC0003DMG400037910	PGSC0003DMT400088339	-	NO	NO	
506	Heterozygous PS in RH, shared by DM	PGSC0003DMG400038095	PGSC0003DMT400088524	chr05	NO	NO	
507	Heterozygous PS in RH, shared by DM	PGSC0003DMG400038218	PGSC0003DMT400088647	chr07	NO	NO	
508	Heterozygous PS in RH, shared by DM	PGSC0003DMG400038416	PGSC0003DMT400088845	chr11	yes	NO	
509	Heterozygous PS in RH, shared by DM	PGSC0003DMG400038427	PGSC0003DMT400088856	chr04	NO	NO	
510	Heterozygous PS in RH, shared by DM	PGSC0003DMG400038523	PGSC0003DMT400088952	chr05	yes	NO	
511	Heterozygous PS in RH, shared by DM	PGSC0003DMG400038582	PGSC0003DMT400089011	chr06	yes	NO	GO:0004672; protein kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
512	Heterozygous PS in RH, shared by DM	PGSC0003DMG400038650	PGSC0003DMT400089079	chr12	yes	NO	

513	Heterozygous PS in RH, shared by DM	PGSC0003DMG400038651	PGSC0003DMT400089080	chr06	NO	NO	
514	Heterozygous PS in RH, shared by DM	PGSC0003DMG400038758	PGSC0003DMT400089187	chr01	yes	NO	GO:0016747; transferase activity, transferring acyl groups other than amino-acyl groups; Molecular Function
515	Heterozygous PS in RH, shared by DM	PGSC0003DMG400038842	PGSC0003DMT400089271				
516	Heterozygous PS in RH, shared by DM	PGSC0003DMG400038843	PGSC0003DMT400089272				
517	Heterozygous PS in RH, shared by DM	PGSC0003DMG400039007	PGSC0003DMT400089436	chr12	yes	NO	
518	Heterozygous PS in RH, shared by DM	PGSC0003DMG400039067	PGSC0003DMT400089496	chr01	NO	NO	GO:0004177; aminopeptidase activity; Molecular Function GO:0005622; intracellular; Cellular Component GO:0006508; proteolysis; Biological Process
519	Heterozygous PS in RH, shared by DM	PGSC0003DMG400039155	PGSC0003DMT400089584	chr05	NO	NO	
520	Heterozygous PS in RH, shared by DM	PGSC0003DMG400039340	PGSC0003DMT400089769				
521	Heterozygous PS in RH, shared by DM	PGSC0003DMG400039347	PGSC0003DMT400089776	chr06	yes	yes	GO:0008270; zinc ion binding; Molecular Function
522	Heterozygous PS in RH, shared by DM	PGSC0003DMG400039355	PGSC0003DMT400089784	chr01	yes	NO	
523	Heterozygous PS in RH, shared by DM	PGSC0003DMG400039361	PGSC0003DMT400089790	chr05	NO	NO	
524	Heterozygous PS in RH, shared by DM	PGSC0003DMG400039446	PGSC0003DMT400089875	chr10	yes	yes	

525	Heterozygous PS in RH, shared by DM	PGSC0003DMG400039474	PGSC0003DMT400089903	chr04	NO	NO	
526	Heterozygous PS in RH, shared by DM	PGSC0003DMG400039525	PGSC0003DMT400089954	chr06	yes	yes	
527	Heterozygous PS in RH, shared by DM	PGSC0003DMG400039542	PGSC0003DMT400089971	-	yes	NO	GO:0004672; protein kinase activity; Molecular Function GO:0005515; protein binding; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
528	Heterozygous PS in RH, shared by DM	PGSC0003DMG400039590	PGSC0003DMT400090019	chr05	NO	NO	
529	Heterozygous PS in RH, shared by DM	PGSC0003DMG400040029	PGSC0003DMT400090458	chr02	yes	NO	GO:0003677; DNA binding; Molecular Function GO:0005634; nucleus; Cellular Component
530	Heterozygous PS in RH, shared by DM	PGSC0003DMG400040069	PGSC0003DMT400090498	chr09	NO	NO	
531	Heterozygous PS in RH, shared by DM	PGSC0003DMG400040071	PGSC0003DMT400090500	chr08	NO	NO	GO:0004190; aspartic-type endopeptidase activity; Molecular Function GO:0006508; proteolysis; Biological Process
532	Heterozygous PS in RH, shared by DM	PGSC0003DMG400040207	PGSC0003DMT400090636	chr11	NO	NO	
533	Heterozygous PS in RH, shared by DM	PGSC0003DMG400040234	PGSC0003DMT400090663	-	NO	NO	
534	Heterozygous PS in RH, shared by DM	PGSC0003DMG400040271	PGSC0003DMT400090700	chr06	yes	yes	
535	Heterozygous PS in RH, shared by DM	PGSC0003DMG400040327	PGSC0003DMT400090756	chr11	NO	NO	

536	Heterozygous PS in RH, shared by DM	PGSC0003DMG400040427	PGSC0003DMT400090856	chr10	NO	NO	GO:0003824; catalytic activity; Molecular Function GO:0004356; glutamate-ammonia ligase activity; Molecular Function GO:0006807; nitrogen compound metabolic process; Biological Process GO:0008152; metabolic process; Biological Process
537	Heterozygous PS in RH, shared by DM	PGSC0003DMG400040439	PGSC0003DMT400090868	-	yes	NO	
538	Heterozygous PS in RH, shared by DM	PGSC0003DMG400040510	PGSC0003DMT400090939	chr01	yes	yes	GO:0003677; DNA binding; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006260; DNA replication; Biological Process
539	Heterozygous PS in RH, shared by DM	PGSC0003DMG400040593	PGSC0003DMT400091022	chr06	NO	NO	GO:0005622; intracellular; Cellular Component GO:0007165; signal transduction; Biological Process
540	Heterozygous PS in RH, shared by DM	PGSC0003DMG400040614	PGSC0003DMT400091043	chr06	yes	NO	
541	Heterozygous PS in RH, shared by DM	PGSC0003DMG400040684	PGSC0003DMT400091113	chr01	yes	NO	
542	Heterozygous PS in RH, shared by DM	PGSC0003DMG400040707	PGSC0003DMT400091136	chr12	yes	NO	GO:0005515; protein binding; Molecular Function
543	Heterozygous PS in RH, shared by DM	PGSC0003DMG400040891	PGSC0003DMT400091320	chr12	NO	NO	
544	Heterozygous PS in RH, shared by DM	PGSC0003DMG400040977	PGSC0003DMT400091406				
545	Heterozygous PS in RH, shared by DM	PGSC0003DMG400041099	PGSC0003DMT400091528	-	yes	NO	
546	Heterozygous PS in RH, shared by DM	PGSC0003DMG400041123	PGSC0003DMT400091552	chr11	yes	NO	

547	Heterozygous PS in RH, shared by DM	PGSC0003DMG400041312	PGSC0003DMT400091741	chr03	NO	NO	GO:0006508; proteolysis; Biological Process GO:0008234; cysteine-type peptidase activity; Molecular Function
548	Heterozygous PS in RH, shared by DM	PGSC0003DMG400041319	PGSC0003DMT400091748	chr06	NO	NO	
549	Heterozygous PS in RH, shared by DM	PGSC0003DMG400041327	PGSC0003DMT400091756	chr04	NO	NO	
550	Heterozygous PS in RH, shared by DM	PGSC0003DMG400041334	PGSC0003DMT400091763	chr09	NO	NO	
551	Heterozygous PS in RH, shared by DM	PGSC0003DMG400041484	PGSC0003DMT400091913	chr06	yes	NO	GO:0003743; translation initiation factor activity; Molecular Function GO:0006413; translational initiation; Biological Process
552	Heterozygous PS in RH, shared by DM	PGSC0003DMG400041510	PGSC0003DMT400091939	chr07	NO	NO	
553	Heterozygous PS in RH, shared by DM	PGSC0003DMG400041521	PGSC0003DMT400091950	-	NO	NO	
554	Heterozygous PS in RH, shared by DM	PGSC0003DMG400041620	PGSC0003DMT400092049	chr01	yes	NO	GO:0004672; protein kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
555	Heterozygous PS in RH, shared by DM	PGSC0003DMG400041685	PGSC0003DMT400092114	chr04	NO	NO	
556	Heterozygous PS in RH, shared by DM	PGSC0003DMG400041690	PGSC0003DMT400092119	chr05	yes	NO	
557	Heterozygous PS in RH, shared by DM	PGSC0003DMG400041698	PGSC0003DMT400092127	chr04	yes	NO	GO:0043234; protein complex; Cellular Component GO:0051258; protein polymerization; Biological Process

558	Heterozygous PS in RH, shared by DM	PGSC0003DMG400041790	PGSC0003DMT400092219	chr01	yes	NO	GO:0005215; transporter activity; Molecular Function GO:0006810; transport; Biological Process GO:0016021; integral to membrane; Cellular Component GO:0055085; transmembrane transport; Biological Process
559	Heterozygous PS in RH, shared by DM	PGSC0003DMG400041868	PGSC0003DMT400092297	chr03	NO	NO	GO:0000287; magnesium ion binding; Molecular Function GO:0008152; metabolic process; Biological Process GO:0016829; lyase activity; Molecular Function
560	Heterozygous PS in RH, shared by DM	PGSC0003DMG400041913	PGSC0003DMT400092342	chr09	NO	NO	
561	Heterozygous PS in RH, shared by DM	PGSC0003DMG400042114	PGSC0003DMT400092543	chr01	yes	yes	GO:0016491; oxidoreductase activity; Molecular Function
562	Heterozygous PS in RH, shared by DM	PGSC0003DMG400042168	PGSC0003DMT400092597	chr10	NO	NO	
563	Heterozygous PS in RH, shared by DM	PGSC0003DMG400042224	PGSC0003DMT400092653	chr06	yes	NO	
564	Heterozygous PS in RH, shared by DM	PGSC0003DMG400042228	PGSC0003DMT400092657	chr03	yes	yes	GO:0004143; diacylglycerol kinase activity; Molecular Function GO:0007205; activation of protein kinase C activity by G-protein coupled receptor protein signaling pathway; Biological Process
565	Heterozygous PS in RH, shared by DM	PGSC0003DMG400042232	PGSC0003DMT400092661	chr07	NO	NO	
566	Heterozygous PS in RH, shared by DM	PGSC0003DMG400042286	PGSC0003DMT400092715	chr03	yes	yes	

567	Heterozygous PS in RH, shared by DM	PGSC0003DMG400042351	PGSC0003DMT400092780	chr09	NO	NO	
568	Heterozygous PS in RH, shared by DM	PGSC0003DMG400042402	PGSC0003DMT400092831	chr10	NO	NO	
569	Heterozygous PS in RH, shared by DM	PGSC0003DMG400042441	PGSC0003DMT400092870	chr03	yes	yes	GO:0004252; serine-type endopeptidase activity; Molecular Function GO:0006508; proteolysis; Biological Process GO:0042802; identical protein binding; Molecular Function GO:0043086; negative regulation of catalytic activity; Biological Process
570	Heterozygous PS in RH, shared by DM	PGSC0003DMG400042468	PGSC0003DMT400092897	chr09	yes	NO	GO:0003824; catalytic activity; Molecular Function GO:0006631; fatty acid metabolic process; Biological Process GO:0008152; metabolic process; Biological Process GO:0016491; oxidoreductase activity; Molecular Function
571	Heterozygous PS in RH, shared by DM	PGSC0003DMG400042476	PGSC0003DMT400092905	chr07	NO	NO	GO:0005515; protein binding; Molecular Function
572	Heterozygous PS in RH, shared by DM	PGSC0003DMG400042480	PGSC0003DMT400092909	chr02	NO	NO	
573	Heterozygous PS in RH, shared by DM	PGSC0003DMG400042484	PGSC0003DMT400092913	chr06	yes	yes	
574	Heterozygous PS in RH, shared by DM	PGSC0003DMG400042520	PGSC0003DMT400092949	chr05	NO	NO	
575	Heterozygous PS in RH, shared by DM	PGSC0003DMG400042536	PGSC0003DMT400092965	-	yes	NO	GO:0003723; RNA binding; Molecular Function GO:0003964; RNA-directed DNA polymerase activity; Molecular Function GO:0006278; RNA-dependent DNA replication; Biological Process

576	Heterozygous PS in RH, shared by DM	PGSC0003DMG400042633	PGSC0003DMT400093062	chr04	yes	NO	GO:0005515; protein binding; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0044267; cellular protein metabolic process; Biological Process
577	Heterozygous PS in RH, shared by DM	PGSC0003DMG400042661	PGSC0003DMT400093090	chr01	yes	NO	
578	Heterozygous PS in RH, shared by DM	PGSC0003DMG400042762	PGSC0003DMT400093191	-	yes	yes	GO:0016747; transferase activity, transferring acyl groups other than amino-acyl groups; Molecular Function GO:0008146; sulfotransferase activity; Molecular Function
579	Heterozygous PS in RH, shared by DM	PGSC0003DMG400042819	PGSC0003DMT400093248	chr05	yes	NO	
580	Heterozygous PS in RH, shared by DM	PGSC0003DMG400042877	PGSC0003DMT400093306	chr03	NO	NO	
581	Heterozygous PS in RH, shared by DM	PGSC0003DMG400042892	PGSC0003DMT400093321	chr05	yes	NO	
582	Heterozygous PS in RH, shared by DM	PGSC0003DMG400042894	PGSC0003DMT400093323	chr10	NO	NO	
583	Heterozygous PS in RH, shared by DM	PGSC0003DMG400042975	PGSC0003DMT400093404	chr11	NO	NO	
584	Heterozygous PS in RH, shared by DM	PGSC0003DMG400042981	PGSC0003DMT400093410	chr09	NO	NO	
585	Heterozygous PS in RH, shared by DM	PGSC0003DMG400043090	PGSC0003DMT400093519	chr06	yes	yes	GO:0008270; zinc ion binding; Molecular Function GO:0016491; oxidoreductase activity; Molecular Function GO:0055114; oxidation reduction; Biological Process
586	Heterozygous PS in RH, shared by DM	PGSC0003DMG400043110	PGSC0003DMT400093539	chr01	yes	NO	

587	Heterozygous PS in RH, shared by DM	PGSC0003DMG400043294	PGSC0003DMT400093723	chr12	NO	NO	GO:0004672; protein kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
588	Heterozygous PS in RH, shared by DM	PGSC0003DMG400043378	PGSC0003DMT400093807	chr03	yes	yes	
589	Heterozygous PS in RH, shared by DM	PGSC0003DMG400043408	PGSC0003DMT400093837	chr04	yes	NO	GO:0004672; protein kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process GO:0007165; signal transduction; Biological Process
590	Heterozygous PS in RH, shared by DM	PGSC0003DMG400043481	PGSC0003DMT400093910	chr08	yes	yes	
591	Heterozygous PS in RH, shared by DM	PGSC0003DMG400043606	PGSC0003DMT400094035	chr11	NO	NO	
592	Heterozygous PS in RH, shared by DM	PGSC0003DMG400043689	PGSC0003DMT400094118	chr11	yes	NO	
593	Heterozygous PS in RH, shared by DM	PGSC0003DMG400043749	PGSC0003DMT400094178	-	NO	NO	
594	Heterozygous PS in RH, shared by DM	PGSC0003DMG400043752	PGSC0003DMT400094181	chr09	yes	yes	GO:0004672; protein kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
595	Heterozygous PS in RH, shared by DM	PGSC0003DMG400043868	PGSC0003DMT400094297	chr04	yes	yes	
596	Heterozygous PS in RH, shared by DM	PGSC0003DMG400043890	PGSC0003DMT400094319	chr01	yes	NO	

597	Heterozygous PS in RH, shared by DM	PGSC0003DMG400043955	PGSC0003DMT400094384	chr04	yes	NO	GO:0004497; monooxygenase activity; Molecular Function GO:0005506; iron ion binding; Molecular Function GO:0009055; electron carrier activity; Molecular Function GO:0020037; heme binding; Molecular Function
598	Heterozygous PS in RH, shared by DM	PGSC0003DMG400044045	PGSC0003DMT400094474	-	yes	NO	GO:0005515; protein binding; Molecular Function
599	Heterozygous PS in RH, shared by DM	PGSC0003DMG400044048	PGSC0003DMT400094477	chr02	NO	NO	
600	Heterozygous PS in RH, shared by DM	PGSC0003DMG400044137	PGSC0003DMT400094566	chr12	NO	NO	
601	Heterozygous PS in RH, shared by DM	PGSC0003DMG400044146	PGSC0003DMT400094575	chr02	yes	NO	
602	Heterozygous PS in RH, shared by DM	PGSC0003DMG400044187	PGSC0003DMT400094616	chr06	yes	yes	
603	Heterozygous PS in RH, shared by DM	PGSC0003DMG400044188	PGSC0003DMT400094617	-	NO	NO	
604	Heterozygous PS in RH, shared by DM	PGSC0003DMG400044203	PGSC0003DMT400094632	chr01	NO	NO	
605	Heterozygous PS in RH, shared by DM	PGSC0003DMG400044323	PGSC0003DMT400094752	chr02	yes	yes	GO:0004672; protein kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
606	Heterozygous PS in RH, shared by DM	PGSC0003DMG400044412	PGSC0003DMT400094841	chr04	yes	NO	GO:0004672; protein kinase activity; Molecular Function GO:0005515; protein binding; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process

607	Heterozygous PS in RH, shared by DM	PGSC0003DMG400044438	PGSC0003DMT400094867	chr07	NO	NO	
608	Heterozygous PS in RH, shared by DM	PGSC0003DMG400044481	PGSC0003DMT400094910	-	NO	NO	
609	Heterozygous PS in RH, shared by DM	PGSC0003DMG400044484	PGSC0003DMT400094913	chr09	yes	NO	
610	Heterozygous PS in RH, shared by DM	PGSC0003DMG400044747	PGSC0003DMT400095176	chr04	yes	yes	
611	Heterozygous PS in RH, shared by DM	PGSC0003DMG400044843	PGSC0003DMT400095272	chr01	yes	yes	
612	Heterozygous PS in RH, shared by DM	PGSC0003DMG400044863	PGSC0003DMT400095292	chr04	yes	NO	GO:0005215; transporter activity; Molecular Function GO:0006857; oligopeptide transport; Biological Process GO:0016020; membrane; Cellular Component
613	Heterozygous PS in RH, shared by DM	PGSC0003DMG400044871	PGSC0003DMT400095300	-	NO	NO	
614	Heterozygous PS in RH, shared by DM	PGSC0003DMG400044939	PGSC0003DMT400095368	chr01	yes	NO	
615	Heterozygous PS in RH, shared by DM	PGSC0003DMG400045119	PGSC0003DMT400095548	chr09	NO	NO	
616	Heterozygous PS in RH, shared by DM	PGSC0003DMG400045166	PGSC0003DMT400095595	chr02	yes	NO	GO:0004672; protein kinase activity; Molecular Function GO:0005515; protein binding; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
617	Heterozygous PS in RH, shared by DM	PGSC0003DMG400045185	PGSC0003DMT400095614	-	yes	yes	

618	Heterozygous PS in RH, shared by DM	PGSC0003DMG400045186	PGSC0003DMT400095615	chr01	yes	NO	
619	Heterozygous PS in RH, shared by DM	PGSC0003DMG400045217	PGSC0003DMT400095646	chr01	NO	NO	
620	Heterozygous PS in RH, shared by DM	PGSC0003DMG400045226	PGSC0003DMT400095655	chr05	yes	yes	
621	Heterozygous PS in RH, shared by DM	PGSC0003DMG400045246	PGSC0003DMT400095675	-	NO	NO	
622	Heterozygous PS in RH, shared by DM	PGSC0003DMG400045267	PGSC0003DMT400095696	chr12	yes	NO	
623	Heterozygous PS in RH, shared by DM	PGSC0003DMG400045394	PGSC0003DMT400095823	chr07	yes	NO	GO:0004672; protein kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0005529; sugar binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
624	Heterozygous PS in RH, shared by DM	PGSC0003DMG400045804	PGSC0003DMT400096233	chr06	yes	yes	
625	Heterozygous PS in RH, shared by DM	PGSC0003DMG400045810	PGSC0003DMT400096239	chr02	yes	NO	GO:0005515; protein binding; Molecular Function
626	Heterozygous PS in RH, shared by DM	PGSC0003DMG400045968	PGSC0003DMT400096397	chr02	yes	NO	
627	Heterozygous PS in RH, shared by DM	PGSC0003DMG400046018	PGSC0003DMT400096447				
628	Heterozygous PS in RH, shared by DM	PGSC0003DMG400046080	PGSC0003DMT400096509	chr02	yes	yes	

629	Heterozygous PS in RH, shared by DM	PGSC0003DMG400046151	PGSC0003DMT400096580	chr04	yes	NO	
630	Heterozygous PS in RH, shared by DM	PGSC0003DMG400046172	PGSC0003DMT400096601	chr11	NO	NO	
631	Heterozygous PS in RH, shared by DM	PGSC0003DMG400046297	PGSC0003DMT400096726	chr03	NO	NO	
632	Heterozygous PS in RH, shared by DM	PGSC0003DMG400046427	PGSC0003DMT400096856	chr03	yes	NO	
633	Heterozygous PS in RH, shared by DM	PGSC0003DMG400046437	PGSC0003DMT400096866	-	NO	NO	
634	Heterozygous PS in RH, shared by DM	PGSC0003DMG400046464	PGSC0003DMT400096893	chr12	NO	NO	
635	Heterozygous PS in RH, shared by DM	PGSC0003DMG400046470	PGSC0003DMT400096899				
636	Heterozygous PS in RH, shared by DM	PGSC0003DMG400046512	PGSC0003DMT400096941	chr05	yes	NO	GO:0004713; protein tyrosine kinase activity; Molecular Function GO:0005515; protein binding; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
637	Heterozygous PS in RH, shared by DM	PGSC0003DMG400046549	PGSC0003DMT400096978	chr10	yes	NO	
638	Heterozygous PS in RH, shared by DM	PGSC0003DMG400046621	PGSC0003DMT400097050	chr08	NO	NO	GO:0004497; monooxygenase activity; Molecular Function GO:0005506; iron ion binding; Molecular Function GO:0009055; electron carrier activity; Molecular Function GO:0020037; heme binding; Molecular Function

639	Heterozygous PS in RH, shared by DM	PGSC0003DMG400046625	PGSC0003DMT400097054	chr07	yes	NO	
640	Heterozygous PS in RH, shared by DM	PGSC0003DMG400046780	PGSC0003DMT400097209	chr12	NO	NO	
641	Heterozygous PS in RH, shared by DM	PGSC0003DMG400046791	PGSC0003DMT400097220	chr04	NO	NO	
642	Heterozygous PS in RH, shared by DM	PGSC0003DMG400046847	PGSC0003DMT400097276	chr11	NO	NO	
643	Heterozygous PS in RH, shared by DM	PGSC0003DMG400046877	PGSC0003DMT400097306	chr04	NO	NO	GO:0003723; RNA binding; Molecular Function GO:0003964; RNA-directed DNA polymerase activity; Molecular Function GO:0006278; RNA-dependent DNA replication; Biological Process
644	Heterozygous PS in RH, shared by DM	PGSC0003DMG400046907	PGSC0003DMT400097336	-	yes	NO	GO:0005515; protein binding; Molecular Function
645	Heterozygous PS in RH, shared by DM	PGSC0003DMG400047005	PGSC0003DMT400097434	chr03	yes	NO	GO:0016491; oxidoreductase activity; Molecular Function
646	Heterozygous PS in RH, shared by DM	PGSC0003DMG400047036	PGSC0003DMT400097465	chr09	yes	yes	GO:0016884; carbon-nitrogen ligase activity, with glutamine as amido-N-donor; Molecular Function
647	Heterozygous PS in RH, shared by DM	PGSC0003DMG400047079	PGSC0003DMT400097508	chr08	yes	NO	
648	Heterozygous PS in RH, shared by DM	PGSC0003DMG400047103	PGSC0003DMT400097532	-	yes	NO	GO:0003677; DNA binding; Molecular Function GO:0005634; nucleus; Cellular Component GO:0006511; ubiquitin-dependent protein catabolic process; Biological Process GO:0007275; multicellular organismal development; Biological Process

649	Heterozygous PS in RH, shared by DM	PGSC0003DMG400047112	PGSC0003DMT400097541	chr09	NO	NO	GO:0003700; transcription factor activity; Molecular Function GO:0005667; transcription factor complex; Cellular Component GO:0006355; regulation of transcription, DNA-dependent; Biological Process
650	Heterozygous PS in RH, shared by DM	PGSC0003DMG400047184	PGSC0003DMT400097613	chr12	NO	NO	
651	Heterozygous PS in RH, shared by DM	PGSC0003DMG400047275	PGSC0003DMT400097704	-	NO	NO	
652	Heterozygous PS in RH, shared by DM	PGSC0003DMG400047346	PGSC0003DMT400097775	chr01	yes	NO	GO:0004553; hydrolase activity, hydrolyzing O-glycosyl compounds; Molecular Function GO:0005975; carbohydrate metabolic process; Biological Process
653	PS in DM only	PGSC0003DMG400000214	PGSC0003DMT400000605	chr09	yes	NO	
654	PS in DM only	PGSC0003DMG401000479	PGSC0003DMT400001251	chr05	NO	NO	GO:0008152; metabolic process; Biological Process GO:0016491; oxidoreductase activity; Molecular Function GO:0055114; oxidation reduction; Biological Process
655	PS in DM only	PGSC0003DMG400000483	PGSC0003DMT400001270	chr08	NO	NO	
656	PS in DM only	PGSC0003DMG400000637	PGSC0003DMT400001705	-	NO	NO	
657	PS in DM only	PGSC0003DMG400000682	PGSC0003DMT400001821	chr12	yes	NO	
658	PS in DM only	PGSC0003DMG400000815	PGSC0003DMT400002131	chr03	yes	yes	
659	PS in DM only	PGSC0003DMG400000905	PGSC0003DMT400002367	chr06	yes	NO	GO:0003735; structural constituent of ribosome; Molecular Function GO:0005622; intracellular; Cellular Component GO:0005840; ribosome; Cellular Component GO:0006412; translation; Biological Process

660	PS in DM only	PGSC0003DMG400000971	PGSC0003DMT400002545	chr03	yes	NO	GO:0005524; ATP binding; Molecular Function GO:0006810; transport; Biological Process GO:0016021; integral to membrane; Cellular Component GO:0016887; ATPase activity; Molecular Function GO:0042626; ATPase activity, coupled to transmembrane movement of substances; Molecular Function GO:0055085; transmembrane transport; Biological Process
661	PS in DM only	PGSC0003DMG400001286	PGSC0003DMT400003249	chr10	yes	NO	GO:0004672; protein kinase activity; Molecular Function GO:0005515; protein binding; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
662	PS in DM only	PGSC0003DMG400002019	PGSC0003DMT400005106	chr12	NO	NO	
663	PS in DM only	PGSC0003DMG400002693	PGSC0003DMT400006951	chr01	yes	NO	GO:0016020; membrane; Cellular Component
664	PS in DM only	PGSC0003DMG400002730	PGSC0003DMT400007068				
665	PS in DM only	PGSC0003DMG400002740	PGSC0003DMT400007079	chr07	yes	NO	
666	PS in DM only	PGSC0003DMG400003097	PGSC0003DMT400008016	chr12	yes	NO	
667	PS in DM only	PGSC0003DMG400003158	PGSC0003DMT400008191	chr07	yes	yes	
668	PS in DM only	PGSC0003DMG400003198	PGSC0003DMT400008300	chr10	yes	NO	GO:0004672; protein kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process

669	PS in DM only	PGSC0003DMG400003332	PGSC0003DMT400008607	chr10	NO	NO	GO:0005215; transporter activity; Molecular Function GO:0006810; transport; Biological Process GO:0016021; integral to membrane; Cellular Component GO:0055085; transmembrane transport; Biological Process
670	PS in DM only	PGSC0003DMG400003405	PGSC0003DMT400008765	chr10	NO	NO	
671	PS in DM only	PGSC0003DMG401003479	PGSC0003DMT400008933	-	NO	NO	
672	PS in DM only	PGSC0003DMG400003587	PGSC0003DMT400009240	-	NO	NO	
673	PS in DM only	PGSC0003DMG400003813	PGSC0003DMT400009745	chr12	yes	NO	GO:0004553; hydrolase activity, hydrolyzing O-glycosyl compounds; Molecular Function GO:0005975; carbohydrate metabolic process; Biological Process
674	PS in DM only	PGSC0003DMG400003836	PGSC0003DMT400009801	chr04	NO	NO	
675	PS in DM only	PGSC0003DMG402004079	PGSC0003DMT400010448	-	NO	NO	
676	PS in DM only	PGSC0003DMG400004447	PGSC0003DMT400011355	chr05	NO	NO	
677	PS in DM only	PGSC0003DMG400004669	PGSC0003DMT400011895	chr09	yes	yes	GO:0003676; nucleic acid binding; Molecular Function GO:0008168; methyltransferase activity; Molecular Function GO:0032259; methylation; Biological Process

678	PS in DM only	PGSC0003DMG400004714	PGSC0003DMT400012008	chr01	yes	NO	GO:0004506; squalene monooxygenase activity; Molecular Function GO:0008033; tRNA processing; Biological Process GO:0016021; integral to membrane; Cellular Component GO:0016491; oxidoreductase activity; Molecular Function GO:0050660; FAD binding; Molecular Function GO:0055114; oxidation reduction; Biological Process
679	PS in DM only	PGSC0003DMG400004930	PGSC0003DMT400012612	-	yes	NO	GO:0003676; nucleic acid binding; Molecular Function
680	PS in DM only	PGSC0003DMG400005236	PGSC0003DMT400013426	chr11	yes	NO	GO:0005524; ATP binding; Molecular Function GO:0006139; nucleobase, nucleoside, nucleotide and nucleic acid metabolic process; Biological Process GO:0019205; nucleobase, nucleoside, nucleotide kinase activity; Molecular Function
681	PS in DM only	PGSC0003DMG400005262	PGSC0003DMT400013490	chr04	NO	NO	
682	PS in DM only	PGSC0003DMG400005347	PGSC0003DMT400013679	chr12	NO	NO	
683	PS in DM only	PGSC0003DMG400005480	PGSC0003DMT400013979	chr04	yes	NO	
684	PS in DM only	PGSC0003DMG400005566	PGSC0003DMT400014199	-	yes	NO	
685	PS in DM only	PGSC0003DMG403005658	PGSC0003DMT400014423	chr01	yes	NO	
686	PS in DM only	PGSC0003DMG400005689	PGSC0003DMT400014530	chr02	yes	NO	GO:0016702; oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen; Molecular Function GO:0046872; metal ion binding; Molecular Function GO:0055114; oxidation reduction; Biological Process

687	PS in DM only	PGSC0003DMG400006292	PGSC0003DMT400016096	chr07	yes	NO	GO:0004497; monooxygenase activity; Molecular Function GO:0005506; iron ion binding; Molecular Function GO:0009055; electron carrier activity; Molecular Function GO:0020037; heme binding; Molecular Function
688	PS in DM only	PGSC0003DMG400006297	PGSC0003DMT400016107	chr03	yes	NO	
689	PS in DM only	PGSC0003DMG400006318	PGSC0003DMT400016166	chr07	NO	NO	
690	PS in DM only	PGSC0003DMG400006556	PGSC0003DMT400016766	chr06	yes	NO	
691	PS in DM only	PGSC0003DMG400006760	PGSC0003DMT400017381	chr02	yes	NO	GO:0006508; proteolysis; Biological Process GO:0008234; cysteine-type peptidase activity; Molecular Function GO:0010181; FMN binding; Molecular Function
692	PS in DM only	PGSC0003DMG400006804	PGSC0003DMT400017547	chr06	yes	yes	
693	PS in DM only	PGSC0003DMG400007341	PGSC0003DMT400018933	chr07	NO	NO	
694	PS in DM only	PGSC0003DMG400007687	PGSC0003DMT400019872	chr05	NO	NO	
695	PS in DM only	PGSC0003DMG400008914	PGSC0003DMT400023033	chr04	yes	yes	GO:0005622; intracellular; Cellular Component GO:0008270; zinc ion binding; Molecular Function GO:0016758; transferase activity, transferring hexosyl groups; Molecular Function GO:0031227; intrinsic to endoplasmic reticulum membrane; Cellular Component
696	PS in DM only	PGSC0003DMG402008955	PGSC0003DMT400023129	chr05	NO	NO	
697	PS in DM only	PGSC0003DMG400009059	PGSC0003DMT400023388	chr03	NO	NO	
698	PS in DM only	PGSC0003DMG400009156	PGSC0003DMT400023666	chr01	NO	NO	
699	PS in DM only	PGSC0003DMG400009294	PGSC0003DMT400024024	-	yes	NO	
700	PS in DM only	PGSC0003DMG402009322	PGSC0003DMT400024106	chr10	NO	NO	

701	PS in DM only	PGSC0003DMG400009747	PGSC0003DMT400025228	chr10	yes	NO	
702	PS in DM only	PGSC0003DMG400010043	PGSC0003DMT400026030	-	NO	NO	
703	PS in DM only	PGSC0003DMG400010336	PGSC0003DMT400026752	chr05	yes	NO	GO:0005524; ATP binding; Molecular Function
704	PS in DM only	PGSC0003DMG400010546	PGSC0003DMT400027345	chr06	yes	yes	
705	PS in DM only	PGSC0003DMG400010559	PGSC0003DMT400027382	chr07	yes	NO	GO:0004497; monooxygenase activity; Molecular Function GO:0005506; iron ion binding; Molecular Function GO:0009055; electron carrier activity; Molecular Function GO:0020037; heme binding; Molecular Function
706	PS in DM only	PGSC0003DMG400010604	PGSC0003DMT400027512	chr06	yes	NO	
707	PS in DM only	PGSC0003DMG400010648	PGSC0003DMT400027611	chr05	yes	NO	
708	PS in DM only	PGSC0003DMG400010720	PGSC0003DMT400027841	chr07	NO	NO	
709	PS in DM only	PGSC0003DMG400010741	PGSC0003DMT400027905	chr01	yes	NO	
710	PS in DM only	PGSC0003DMG400010813	PGSC0003DMT400028038	chr08	yes	yes	
711	PS in DM only	PGSC0003DMG400010946	PGSC0003DMT400028423	chr11	NO	NO	
712	PS in DM only	PGSC0003DMG400011035	PGSC0003DMT400028660	chr01	yes	yes	
713	PS in DM only	PGSC0003DMG400011236	PGSC0003DMT400029207	chr07	NO	NO	
714	PS in DM only	PGSC0003DMG400011623	PGSC0003DMT400030375	chr04	NO	NO	
715	PS in DM only	PGSC0003DMG400012208	PGSC0003DMT400031822	chr08	yes	NO	
716	PS in DM only	PGSC0003DMG400012424	PGSC0003DMT400032345	chr04	yes	yes	
717	PS in DM only	PGSC0003DMG400012721	PGSC0003DMT400033129	chr01	NO	NO	

718	PS in DM only	PGSC0003DMG400012863	PGSC0003DMT400033485	chr05	yes	NO	
719	PS in DM only	PGSC0003DMG400013428	PGSC0003DMT400034931	chr06	yes	NO	GO:0004601; peroxidase activity; Molecular Function GO:0005506; iron ion binding; Molecular Function GO:0009055; electron carrier activity; Molecular Function GO:0016021; integral to membrane; Cellular Component GO:0016491; oxidoreductase activity; Molecular Function GO:0050660; FAD binding; Molecular Function GO:0050664; oxidoreductase activity, acting on NADH or NADPH, with oxygen as acceptor; Molecular Function GO:0055114; oxidation reduction; Biological Process
720	PS in DM only	PGSC0003DMG400013498	PGSC0003DMT400035105	chr07	NO	NO	
721	PS in DM only	PGSC0003DMG400013516	PGSC0003DMT400035162	chr07	yes	NO	GO:0005215; transporter activity; Molecular Function GO:0006857; oligopeptide transport; Biological Process GO:0016020; membrane; Cellular Component
722	PS in DM only	PGSC0003DMG400013899	PGSC0003DMT400036088	chr02	NO	NO	
723	PS in DM only	PGSC0003DMG400014132	PGSC0003DMT400036640	chr01	yes	yes	GO:0006508; proteolysis; Biological Process GO:0008237; metallopeptidase activity; Molecular Function
724	PS in DM only	PGSC0003DMG400014137	PGSC0003DMT400036646	-	NO	NO	
725	PS in DM only	PGSC0003DMG402014139	PGSC0003DMT400036657	chr02	yes	NO	
726	PS in DM only	PGSC0003DMG400014153	PGSC0003DMT400036697	chr03	yes	NO	GO:0004497; monooxygenase activity; Molecular Function GO:0005506; iron ion binding; Molecular Function GO:0009055; electron carrier activity; Molecular Function GO:0020037; heme binding; Molecular Function

727	PS in DM only	PGSC0003DMG400014231	PGSC0003DMT400036919	chr09	yes	NO	
728	PS in DM only	PGSC0003DMG400014314	PGSC0003DMT400037130	chr10	yes	yes	
729	PS in DM only	PGSC0003DMG400014382	PGSC0003DMT400037280	-	NO	NO	
730	PS in DM only	PGSC0003DMG400014492	PGSC0003DMT400037569	chr12	NO	NO	
731	PS in DM only	PGSC0003DMG400014562	PGSC0003DMT400037748	chr03	yes	NO	GO:0004672; protein kinase activity; Molecular Function GO:0005488; binding; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
732	PS in DM only	PGSC0003DMG400014693	PGSC0003DMT400038105	chr08	yes	yes	
733	PS in DM only	PGSC0003DMG400015646	PGSC0003DMT400040413	-	yes	yes	GO:0004888; transmembrane receptor activity; Molecular Function GO:0007165; signal transduction; Biological Process GO:0031224; intrinsic to membrane; Cellular Component GO:0045087; innate immune response; Biological Process
734	PS in DM only	PGSC0003DMG402015717	PGSC0003DMT400040654	-	NO	NO	
735	PS in DM only	PGSC0003DMG400015784	PGSC0003DMT400040816	chr10	NO	NO	
736	PS in DM only	PGSC0003DMG400015801	PGSC0003DMT400040868	chr07	NO	NO	
737	PS in DM only	PGSC0003DMG400016372	PGSC0003DMT400042194	-	yes	NO	
738	PS in DM only	PGSC0003DMG400016524	PGSC0003DMT400042609	chr05	yes	NO	GO:0003700; transcription factor activity; Molecular Function GO:0043565; sequence-specific DNA binding; Molecular Function GO:0045449; regulation of transcription; Biological Process

739	PS in DM only	PGSC0003DMG400016827	PGSC0003DMT400043339	chr01	NO	NO	
740	PS in DM only	PGSC0003DMG400016844	PGSC0003DMT400043395	chr10	NO	NO	GO:0008152; metabolic process; Biological Process GO:0016491; oxidoreductase activity; Molecular Function
741	PS in DM only	PGSC0003DMG401016929	PGSC0003DMT400043597	chr12	yes	yes	
742	PS in DM only	PGSC0003DMG400017272	PGSC0003DMT400044497	chr11	yes	yes	
743	PS in DM only	PGSC0003DMG400017528	PGSC0003DMT400045191	chr11	NO	NO	GO:0003824; catalytic activity; Molecular Function GO:0009252; peptidoglycan biosynthetic process; Biological Process GO:0009274; peptidoglycan-based cell wall; Cellular Component
744	PS in DM only	PGSC0003DMG400017628	PGSC0003DMT400045443	chr09	yes	NO	GO:0015205; nucleobase transmembrane transporter activity; Molecular Function GO:0015931; nucleobase, nucleoside, nucleotide and nucleic acid transport; Biological Process GO:0016020; membrane; Cellular Component GO:0055085; transmembrane transport; Biological Process
745	PS in DM only	PGSC0003DMG400017785	PGSC0003DMT400045850	chr06	NO	NO	
746	PS in DM only	PGSC0003DMG400017883	PGSC0003DMT400046080	-	yes	NO	GO:0005515; protein binding; Molecular Function
747	PS in DM only	PGSC0003DMG400017916	PGSC0003DMT400046156	chr08	yes	NO	
748	PS in DM only	PGSC0003DMG400018527	PGSC0003DMT400047665	chr11	NO	NO	
749	PS in DM only	PGSC0003DMG400018565	PGSC0003DMT400047760	chr01	NO	NO	GO:0045735; nutrient reservoir activity; Molecular Function
750	PS in DM only	PGSC0003DMG401018603	PGSC0003DMT400047866	chr12	NO	NO	
751	PS in DM only	PGSC0003DMG400018820	PGSC0003DMT400048455	chr04	yes	yes	

752	PS in DM only	PGSC0003DMG400019113	PGSC0003DMT400049172	chr12	NO	NO	GO:0016747; transferase activity, transferring acyl groups other than amino-acyl groups; Molecular Function
753	PS in DM only	PGSC0003DMG400019578	PGSC0003DMT400050367	chr01	yes	NO	GO:0004888; transmembrane receptor activity; Molecular Function GO:0005515; protein binding; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006915; apoptosis; Biological Process GO:0007165; signal transduction; Biological Process GO:0031224; intrinsic to membrane; Cellular Component GO:0045087; innate immune response; Biological Process
754	PS in DM only	PGSC0003DMG400019800	PGSC0003DMT400050984	-	NO	NO	
755	PS in DM only	PGSC0003DMG400019943	PGSC0003DMT400051347	chr08	yes	NO	
756	PS in DM only	PGSC0003DMG400019953	PGSC0003DMT400051368	chr10	NO	NO	
757	PS in DM only	PGSC0003DMG400020045	PGSC0003DMT400051614	chr03	NO	NO	
758	PS in DM only	PGSC0003DMG403020339	PGSC0003DMT400052398	chr08	yes	NO	
759	PS in DM only	PGSC0003DMG400020833	PGSC0003DMT400053696	chr03	NO	NO	
760	PS in DM only	PGSC0003DMG400021000	PGSC0003DMT400054146	chr06	NO	NO	
761	PS in DM only	PGSC0003DMG400021135	PGSC0003DMT400054453	chr05	yes	NO	GO:0008152; metabolic process; Biological Process GO:0016758; transferase activity, transferring hexosyl groups; Molecular Function
762	PS in DM only	PGSC0003DMG400021238	PGSC0003DMT400054695	-	NO	NO	
763	PS in DM only	PGSC0003DMG400021244	PGSC0003DMT400054721	chr01	yes	NO	

764	PS in DM only	PGSC0003DMG400021314	PGSC0003DMT400054929	-	yes	NO	GO:0008152; metabolic process; Biological Process GO:0016758; transferase activity, transferring hexosyl groups; Molecular Function
765	PS in DM only	PGSC0003DMG400021343	PGSC0003DMT400054994	chr04	yes	yes	
766	PS in DM only	PGSC0003DMG401021412	PGSC0003DMT400055168	chr09	yes	NO	
767	PS in DM only	PGSC0003DMG400021433	PGSC0003DMT400055216	chr05	yes	NO	GO:0005622; intracellular; Cellular Component GO:0006464; protein modification process; Biological Process GO:0016881; acid-amino acid ligase activity; Molecular Function
768	PS in DM only	PGSC0003DMG402021491	PGSC0003DMT400055358	chr02	NO	NO	GO:0004806; triacylglycerol lipase activity; Molecular Function GO:0006629; lipid metabolic process; Biological Process
769	PS in DM only	PGSC0003DMG400021541	PGSC0003DMT400055477	chr06	NO	NO	
770	PS in DM only	PGSC0003DMG400021560	PGSC0003DMT400055522	chr12	NO	NO	
771	PS in DM only	PGSC0003DMG400021688	PGSC0003DMT400055839	chr08	yes	NO	
772	PS in DM only	PGSC0003DMG400021863	PGSC0003DMT400056268	-	yes	NO	GO:0004672; protein kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
773	PS in DM only	PGSC0003DMG400022141	PGSC0003DMT400056940	chr01	yes	NO	
774	PS in DM only	PGSC0003DMG400022217	PGSC0003DMT400057197	chr08	yes	yes	
775	PS in DM only	PGSC0003DMG400022221	PGSC0003DMT400057204	chr12	NO	NO	
776	PS in DM only	PGSC0003DMG400022359	PGSC0003DMT400057581	-	yes	NO	
777	PS in DM only	PGSC0003DMG402022539	PGSC0003DMT400058058	chr06	NO	NO	

778	PS in DM only	PGSC0003DMG400022562	PGSC0003DMT400058126	chr04	NO	NO	
779	PS in DM only	PGSC0003DMG400022574	PGSC0003DMT400058159	-	NO	NO	
780	PS in DM only	PGSC0003DMG400022730	PGSC0003DMT400058520	chr08	yes	yes	
781	PS in DM only	PGSC0003DMG400022750	PGSC0003DMT400058564	chr01	yes	yes	GO:0005515; protein binding; Molecular Function
782	PS in DM only	PGSC0003DMG400022977	PGSC0003DMT400059155	chr09	yes	NO	GO:0008146; sulfotransferase activity; Molecular Function
783	PS in DM only	PGSC0003DMG400023210	PGSC0003DMT400059701	chr05	NO	NO	
784	PS in DM only	PGSC0003DMG400023556	PGSC0003DMT400060553	chr03	NO	NO	
785	PS in DM only	PGSC0003DMG400023712	PGSC0003DMT400060959	chr02	yes	NO	
786	PS in DM only	PGSC0003DMG400023736	PGSC0003DMT400061007	-	yes	NO	GO:0004888; transmembrane receptor activity; Molecular Function GO:0007165; signal transduction; Biological Process GO:0031224; intrinsic to membrane; Cellular Component GO:0045087; innate immune response; Biological Process
787	PS in DM only	PGSC0003DMG400023766	PGSC0003DMT400061082	-	NO	NO	
788	PS in DM only	PGSC0003DMG400024021	PGSC0003DMT400061719	chr08	NO	NO	
789	PS in DM only	PGSC0003DMG400024036	PGSC0003DMT400061760	chr05	yes	NO	
790	PS in DM only	PGSC0003DMG400024037	PGSC0003DMT400061767	chr02	yes	NO	

791	PS in DM only	PGSC0003DMG400024061	PGSC0003DMT400061842	chr09	NO	NO	GO:0003700; transcription factor activity; Molecular Function GO:0005634; nucleus; Cellular Component GO:0006355; regulation of transcription, DNA-dependent; Biological Process GO:0043565; sequence-specific DNA binding; Molecular Function
792	PS in DM only	PGSC0003DMG400024075	PGSC0003DMT400061875	chr01	NO	NO	
793	PS in DM only	PGSC0003DMG402024077	PGSC0003DMT400061881	chr09	NO	NO	
794	PS in DM only	PGSC0003DMG400024273	PGSC0003DMT400062366	chr11	NO	NO	GO:0005524; ATP binding; Molecular Function GO:0006810; transport; Biological Process GO:0016021; integral to membrane; Cellular Component GO:0016887; ATPase activity; Molecular Function GO:0042626; ATPase activity, coupled to transmembrane movement of substances; Molecular Function GO:0055085; transmembrane transport; Biological Process
795	PS in DM only	PGSC0003DMG400024646	PGSC0003DMT400063357	chr05	NO	NO	
796	PS in DM only	PGSC0003DMG400024682	PGSC0003DMT400063430	chr05	yes	yes	GO:0005086; ARF guanyl-nucleotide exchange factor activity; Molecular Function GO:0005622; intracellular; Cellular Component GO:0032012; regulation of ARF protein signal transduction; Biological Process
797	PS in DM only	PGSC0003DMG400024835	PGSC0003DMT400063898	chr12	yes	NO	
798	PS in DM only	PGSC0003DMG400024880	PGSC0003DMT400064010	chr07	NO	NO	
799	PS in DM only	PGSC0003DMG400024952	PGSC0003DMT400064226	chr05	yes	NO	
800	PS in DM only	PGSC0003DMG400024994	PGSC0003DMT400064329	chr09	NO	NO	GO:0003676; nucleic acid binding; Molecular Function

801	PS in DM only	PGSC0003DMG400025100	PGSC0003DMT400064590	chr07	yes	NO	
802	PS in DM only	PGSC0003DMG400025113	PGSC0003DMT400064635	chr12	yes	NO	
803	PS in DM only	PGSC0003DMG400025267	PGSC0003DMT400065035	chr04	NO	NO	
804	PS in DM only	PGSC0003DMG400025584	PGSC0003DMT400065736	chr09	NO	NO	
805	PS in DM only	PGSC0003DMG402025828	PGSC0003DMT400066424	chr11	NO	NO	
806	PS in DM only	PGSC0003DMG400025864	PGSC0003DMT400066550	chr05	yes	NO	GO:0005524; ATP binding; Molecular Function GO:0006915; apoptosis; Biological Process
807	PS in DM only	PGSC0003DMG401025908	PGSC0003DMT400066676				
808	PS in DM only	PGSC0003DMG400025940	PGSC0003DMT400066745	chr04	yes	NO	
809	PS in DM only	PGSC0003DMG400026167	PGSC0003DMT400067292	chr01	yes	NO	GO:0016747; transferase activity, transferring acyl groups other than amino-acyl groups; Molecular Function
810	PS in DM only	PGSC0003DMG400026243	PGSC0003DMT400067496	chr08	NO	NO	GO:0004252; serine-type endopeptidase activity; Molecular Function GO:0006508; proteolysis; Biological Process GO:0042802; identical protein binding; Molecular Function GO:0043086; negative regulation of catalytic activity; Biological Process
811	PS in DM only	PGSC0003DMG400026475	PGSC0003DMT400068074	chr12	yes	yes	
812	PS in DM only	PGSC0003DMG400026491	PGSC0003DMT400068109	chr05	yes	NO	GO:0008152; metabolic process; Biological Process GO:0016758; transferase activity, transferring hexosyl groups; Molecular Function
813	PS in DM only	PGSC0003DMG400026711	PGSC0003DMT400068698	chr03	NO	NO	
814	PS in DM only	PGSC0003DMG400026990	PGSC0003DMT400069420	chr06	NO	NO	

815	PS in DM only	PGSC0003DMG400027075	PGSC0003DMT400069641				
816	PS in DM only	PGSC0003DMG401027084	PGSC0003DMT400069666	-	yes	NO	
817	PS in DM only	PGSC0003DMG400027162	PGSC0003DMT400069848	chr01	yes	NO	
818	PS in DM only	PGSC0003DMG401027210	PGSC0003DMT400069970	chr06	NO	NO	
819	PS in DM only	PGSC0003DMG400027339	PGSC0003DMT400070314	chr07	yes	NO	GO:0004497; monooxygenase activity; Molecular Function GO:0005506; iron ion binding; Molecular Function GO:0009055; electron carrier activity; Molecular Function GO:0020037; heme binding; Molecular Function
820	PS in DM only	PGSC0003DMG400027572	PGSC0003DMT400070909	chr09	yes	NO	GO:0016491; oxidoreductase activity; Molecular Function
821	PS in DM only	PGSC0003DMG400027862	PGSC0003DMT400071626	-	NO	NO	GO:0003700; transcription factor activity; Molecular Function GO:0043565; sequence-specific DNA binding; Molecular Function GO:0045449; regulation of transcription; Biological Process
822	PS in DM only	PGSC0003DMG400027962	PGSC0003DMT400071865	chr10	NO	NO	
823	PS in DM only	PGSC0003DMG400028194	PGSC0003DMT400072467	chr07	yes	NO	
824	PS in DM only	PGSC0003DMG400028401	PGSC0003DMT400073015	chr02	NO	NO	
825	PS in DM only	PGSC0003DMG402028496	PGSC0003DMT400073327	chr06	yes	NO	
826	PS in DM only	PGSC0003DMG403028522	PGSC0003DMT400073404	chr01	NO	NO	GO:0016747; transferase activity, transferring acyl groups other than amino-acyl groups; Molecular Function
827	PS in DM only	PGSC0003DMG401028731	PGSC0003DMT400073934	chr09	NO	NO	
828	PS in DM only	PGSC0003DMG400028742	PGSC0003DMT400073963	-	yes	yes	

829	PS in DM only	PGSC0003DMG400029229	PGSC0003DMT400075135	chr03	yes	NO	GO:0003924; GTPase activity; Molecular Function GO:0005525; GTP binding; Molecular Function
830	PS in DM only	PGSC0003DMG400029276	PGSC0003DMT400075273	-	yes	yes	
831	PS in DM only	PGSC0003DMG400029297	PGSC0003DMT400075333	-	NO	NO	
832	PS in DM only	PGSC0003DMG400029350	PGSC0003DMT400075463	chr05	NO	NO	
833	PS in DM only	PGSC0003DMG400029376	PGSC0003DMT400075540	chr08	yes	NO	
834	PS in DM only	PGSC0003DMG400029574	PGSC0003DMT400076052	chr08	NO	NO	
835	PS in DM only	PGSC0003DMG400029606	PGSC0003DMT400076145	chr09	yes	yes	
836	PS in DM only	PGSC0003DMG400029872	PGSC0003DMT400076803	chr10	yes	NO	GO:0005215; transporter activity; Molecular Function GO:0006857; oligopeptide transport; Biological Process GO:0016020; membrane; Cellular Component
837	PS in DM only	PGSC0003DMG400029922	PGSC0003DMT400076933	chr06	yes	yes	
838	PS in DM only	PGSC0003DMG400030079	PGSC0003DMT400077337	chr02	NO	NO	GO:0005634; nucleus; Cellular Component GO:0006334; nucleosome assembly; Biological Process
839	PS in DM only	PGSC0003DMG400030441	PGSC0003DMT400078227	chr11	yes	NO	
840	PS in DM only	PGSC0003DMG400030985	PGSC0003DMT400079573	chr04	yes	NO	
841	PS in DM only	PGSC0003DMG400031236	PGSC0003DMT400080247	chr02	NO	NO	GO:0004298; threonine-type endopeptidase activity; Molecular Function GO:0005839; proteasome core complex; Cellular Component GO:0051603; proteolysis involved in cellular protein catabolic process; Biological Process

842	PS in DM only	PGSC0003DMG400032496	PGSC0003DMT400082356	chr07	yes	NO	GO:0003824; catalytic activity; Molecular Function GO:0008152; metabolic process; Biological Process
843	PS in DM only	PGSC0003DMG400033645	PGSC0003DMT400083893	chr12	yes	NO	GO:0003677; DNA binding; Molecular Function GO:0004518; nuclease activity; Molecular Function GO:0006289; nucleotide-excision repair; Biological Process
844	PS in DM only	PGSC0003DMG400033673	PGSC0003DMT400083948	chr03	NO	NO	GO:0003700; transcription factor activity; Molecular Function GO:0005634; nucleus; Cellular Component GO:0006355; regulation of transcription, DNA-dependent; Biological Process GO:0043565; sequence-specific DNA binding; Molecular Function
845	PS in DM only	PGSC0003DMG400033681	PGSC0003DMT400083956	chr04	NO	NO	
846	PS in DM only	PGSC0003DMG400034493	PGSC0003DMT400084922	chr02	yes	NO	GO:0003677; DNA binding; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006260; DNA replication; Biological Process
847	PS in DM only	PGSC0003DMG400034577	PGSC0003DMT400085006	chr10	NO	NO	
848	PS in DM only	PGSC0003DMG400034851	PGSC0003DMT400085280	chr06	NO	NO	GO:0004497; monooxygenase activity; Molecular Function GO:0005506; iron ion binding; Molecular Function GO:0009055; electron carrier activity; Molecular Function GO:0020037; heme binding; Molecular Function
849	PS in DM only	PGSC0003DMG400035004	PGSC0003DMT400085433	chr01	yes	NO	GO:0005515; protein binding; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006915; apoptosis; Biological Process
850	PS in DM only	PGSC0003DMG400035355	PGSC0003DMT400085784	chr10	NO	NO	

851	PS in DM only	PGSC0003DMG400035363	PGSC0003DMT400085792	chr06	yes	NO	GO:0004221; ubiquitin thiolesterase activity; Molecular Function GO:0006511; ubiquitin-dependent protein catabolic process; Biological Process
852	PS in DM only	PGSC0003DMG400035379	PGSC0003DMT400085808	chr01	yes	NO	
853	PS in DM only	PGSC0003DMG400035398	PGSC0003DMT400085827	chr06	NO	NO	GO:0006621; protein retention in ER lumen; Biological Process GO:0016021; integral to membrane; Cellular Component GO:0046923; ER retention sequence binding; Molecular Function
854	PS in DM only	PGSC0003DMG400035449	PGSC0003DMT400085878	chr05	NO	NO	
855	PS in DM only	PGSC0003DMG400035451	PGSC0003DMT400085880	chr07	NO	NO	
856	PS in DM only	PGSC0003DMG400035809	PGSC0003DMT400086238	chr01	yes	NO	
857	PS in DM only	PGSC0003DMG400035813	PGSC0003DMT400086242	chr11	NO	NO	
858	PS in DM only	PGSC0003DMG400035869	PGSC0003DMT400086298	chr03	yes	NO	GO:0005634; nucleus; Cellular Component GO:0008270; zinc ion binding; Molecular Function GO:0016568; chromatin modification; Biological Process GO:0018024; histone-lysine N-methyltransferase activity; Molecular Function
859	PS in DM only	PGSC0003DMG400035909	PGSC0003DMT400086338	chr01	yes	NO	
860	PS in DM only	PGSC0003DMG400036076	PGSC0003DMT400086505	chr04	NO	NO	GO:0005215; transporter activity; Molecular Function GO:0006810; transport; Biological Process GO:0016021; integral to membrane; Cellular Component GO:0055085; transmembrane transport; Biological Process
861	PS in DM only	PGSC0003DMG400036137	PGSC0003DMT400086566	chr06	NO	NO	

862	PS in DM only	PGSC0003DMG400036207	PGSC0003DMT400086636	chr09	yes	NO	GO:0016491; oxidoreductase activity; Molecular Function
863	PS in DM only	PGSC0003DMG400036462	PGSC0003DMT400086891	chr10	yes	NO	
864	PS in DM only	PGSC0003DMG400036768	PGSC0003DMT400087197	chr12	NO	NO	
865	PS in DM only	PGSC0003DMG400036842	PGSC0003DMT400087271	chr03	yes	NO	GO:0030528; transcription regulator activity; Molecular Function GO:0045449; regulation of transcription; Biological Process
866	PS in DM only	PGSC0003DMG400036909	PGSC0003DMT400087338	chr12	yes	yes	GO:0005515; protein binding; Molecular Function
867	PS in DM only	PGSC0003DMG400036982	PGSC0003DMT400087411	chr04	yes	NO	GO:0005737; cytoplasm; Cellular Component
868	PS in DM only	PGSC0003DMG400037147	PGSC0003DMT400087576	chr05	yes	NO	
869	PS in DM only	PGSC0003DMG400037445	PGSC0003DMT400087874	chr12	yes	NO	GO:0003824; catalytic activity; Molecular Function GO:0008152; metabolic process; Biological Process
870	PS in DM only	PGSC0003DMG400037447	PGSC0003DMT400087876	chr01	NO	NO	
871	PS in DM only	PGSC0003DMG400037498	PGSC0003DMT400087927	chr06	yes	NO	
872	PS in DM only	PGSC0003DMG400037782	PGSC0003DMT400088211	-	NO	NO	
873	PS in DM only	PGSC0003DMG400037906	PGSC0003DMT400088335	chr06	NO	NO	
874	PS in DM only	PGSC0003DMG400038026	PGSC0003DMT400088455	chr09	NO	NO	GO:0003700; transcription factor activity; Molecular Function GO:0005634; nucleus; Cellular Component GO:0006355; regulation of transcription, DNA-dependent; Biological Process GO:0043565; sequence-specific DNA binding; Molecular Function
875	PS in DM only	PGSC0003DMG400038159	PGSC0003DMT400088588	chr07	NO	NO	

876	PS in DM only	PGSC0003DMG400038223	PGSC0003DMT400088652	-	yes	NO	
877	PS in DM only	PGSC0003DMG400038271	PGSC0003DMT400088700	chr12	NO	NO	GO:0003700; transcription factor activity; Molecular Function GO:0006355; regulation of transcription, DNA-dependent; Biological Process
878	PS in DM only	PGSC0003DMG400038282	PGSC0003DMT400088711	chr12	yes	yes	GO:0016747; transferase activity, transferring acyl groups other than amino-acyl groups; Molecular Function
879	PS in DM only	PGSC0003DMG400038429	PGSC0003DMT400088858	chr01	NO	NO	
880	PS in DM only	PGSC0003DMG400038452	PGSC0003DMT400088881	chr12	NO	NO	
881	PS in DM only	PGSC0003DMG400038993	PGSC0003DMT400089422	chr01	NO	NO	
882	PS in DM only	PGSC0003DMG400039002	PGSC0003DMT400089431	chr02	yes	NO	GO:0000228; nuclear chromosome; Cellular Component
883	PS in DM only	PGSC0003DMG400039028	PGSC0003DMT400089457	chr10	NO	NO	
884	PS in DM only	PGSC0003DMG400039182	PGSC0003DMT400089611	chr03	NO	NO	
885	PS in DM only	PGSC0003DMG400039327	PGSC0003DMT400089756	chr01	yes	NO	
886	PS in DM only	PGSC0003DMG400039637	PGSC0003DMT400090066	chr02	yes	NO	
887	PS in DM only	PGSC0003DMG400039701	PGSC0003DMT400090130	chr04	NO	NO	
888	PS in DM only	PGSC0003DMG400039739	PGSC0003DMT400090168	chr10	yes	NO	
889	PS in DM only	PGSC0003DMG400040017	PGSC0003DMT400090446	chr09	NO	NO	
890	PS in DM only	PGSC0003DMG400040099	PGSC0003DMT400090528	chr02	yes	yes	
891	PS in DM only	PGSC0003DMG400040214	PGSC0003DMT400090643	chr05	yes	NO	
892	PS in DM only	PGSC0003DMG400040326	PGSC0003DMT400090755	-	NO	NO	GO:0003824; catalytic activity; Molecular Function GO:0008152; metabolic process; Biological Process

893	PS in DM only	PGSC0003DMG400040381	PGSC0003DMT400090810	chr11	NO	NO	
894	PS in DM only	PGSC0003DMG400040440	PGSC0003DMT400090869	chr10	NO	NO	
895	PS in DM only	PGSC0003DMG400040694	PGSC0003DMT400091123	chr04	yes	yes	
896	PS in DM only	PGSC0003DMG400040959	PGSC0003DMT400091388	chr10	yes	NO	
897	PS in DM only	PGSC0003DMG400041112	PGSC0003DMT400091541	chr07	yes	NO	
898	PS in DM only	PGSC0003DMG400041212	PGSC0003DMT400091641	chr10	NO	NO	
899	PS in DM only	PGSC0003DMG400041399	PGSC0003DMT400091828	chr05	yes	NO	
900	PS in DM only	PGSC0003DMG400041617	PGSC0003DMT400092046				
901	PS in DM only	PGSC0003DMG400041862	PGSC0003DMT400092291	chr08	NO	NO	
902	PS in DM only	PGSC0003DMG400041954	PGSC0003DMT400092383	chr11	NO	NO	
903	PS in DM only	PGSC0003DMG400042106	PGSC0003DMT400092535	chr10	NO	NO	
904	PS in DM only	PGSC0003DMG400042118	PGSC0003DMT400092547	chr10	NO	NO	
905	PS in DM only	PGSC0003DMG400042161	PGSC0003DMT400092590	chr10	yes	NO	
906	PS in DM only	PGSC0003DMG400042259	PGSC0003DMT400092688	chr03	yes	NO	
907	PS in DM only	PGSC0003DMG400042310	PGSC0003DMT400092739	chr03	yes	NO	GO:0004672; protein kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
908	PS in DM only	PGSC0003DMG400042672	PGSC0003DMT400093101	chr07	yes	yes	
909	PS in DM only	PGSC0003DMG400042781	PGSC0003DMT400093210	chr12	yes	NO	GO:0005515; protein binding; Molecular Function

910	PS in DM only	PGSC0003DMG400042926	PGSC0003DMT400093355	chr04	yes	NO	
911	PS in DM only	PGSC0003DMG400043167	PGSC0003DMT400093596	chr09	NO	NO	
912	PS in DM only	PGSC0003DMG400043388	PGSC0003DMT400093817	chr06	NO	NO	
913	PS in DM only	PGSC0003DMG400043392	PGSC0003DMT400093821	chr03	yes	NO	
914	PS in DM only	PGSC0003DMG400043626	PGSC0003DMT400094055	chr02	yes	yes	
915	PS in DM only	PGSC0003DMG400043948	PGSC0003DMT400094377	chr11	NO	NO	
916	PS in DM only	PGSC0003DMG400044174	PGSC0003DMT400094603	-	NO	NO	
917	PS in DM only	PGSC0003DMG400044211	PGSC0003DMT400094640	chr03	yes	NO	
918	PS in DM only	PGSC0003DMG400044216	PGSC0003DMT400094645	chr06	NO	NO	GO:0003824; catalytic activity; Molecular Function
919	PS in DM only	PGSC0003DMG400044616	PGSC0003DMT400095045	chr07	yes	yes	
920	PS in DM only	PGSC0003DMG400044699	PGSC0003DMT400095128	chr05	yes	yes	GO:0031072; heat shock protein binding; Molecular Function
921	PS in DM only	PGSC0003DMG400044900	PGSC0003DMT400095329	chr10	NO	NO	GO:0006511; ubiquitin-dependent protein catabolic process; Biological Process GO:0031461; cullin-RING ubiquitin ligase complex; Cellular Component GO:0031625; ubiquitin protein ligase binding; Molecular Function
922	PS in DM only	PGSC0003DMG400045171	PGSC0003DMT400095600	-	yes	NO	
923	PS in DM only	PGSC0003DMG400045216	PGSC0003DMT400095645	chr07	yes	NO	
924	PS in DM only	PGSC0003DMG400045259	PGSC0003DMT400095688	chr12	NO	NO	
925	PS in DM only	PGSC0003DMG400045261	PGSC0003DMT400095690	chr06	yes	yes	

926	PS in DM only	PGSC0003DMG400045499	PGSC0003DMT400095928	chr03	NO	NO	
927	PS in DM only	PGSC0003DMG400045522	PGSC0003DMT400095951	chr06	NO	NO	GO:0006621; protein retention in ER lumen; Biological Process GO:0016021; integral to membrane; Cellular Component GO:0046923; ER retention sequence binding; Molecular Function
928	PS in DM only	PGSC0003DMG400045640	PGSC0003DMT400096069	chr07	NO	NO	
929	PS in DM only	PGSC0003DMG400045723	PGSC0003DMT400096152	chr06	yes	NO	
930	PS in DM only	PGSC0003DMG400045817	PGSC0003DMT400096246	chr01	NO	NO	GO:0005543; phospholipid binding; Molecular Function
931	PS in DM only	PGSC0003DMG400045819	PGSC0003DMT400096248	chr11	NO	NO	
932	PS in DM only	PGSC0003DMG400046073	PGSC0003DMT400096502	chr06	yes	NO	GO:0004497; monooxygenase activity; Molecular Function GO:0005506; iron ion binding; Molecular Function GO:0009055; electron carrier activity; Molecular Function GO:0020037; heme binding; Molecular Function
933	PS in DM only	PGSC0003DMG400046096	PGSC0003DMT400096525	chr10	NO	NO	
934	PS in DM only	PGSC0003DMG400046189	PGSC0003DMT400096618	-	yes	NO	
935	PS in DM only	PGSC0003DMG400046374	PGSC0003DMT400096803	chr03	NO	NO	
936	PS in DM only	PGSC0003DMG400046515	PGSC0003DMT400096944	chr06	NO	NO	
937	PS in DM only	PGSC0003DMG400046659	PGSC0003DMT400097088	chr04	yes	NO	GO:0003824; catalytic activity; Molecular Function GO:0008152; metabolic process; Biological Process
938	PS in DM only	PGSC0003DMG400046996	PGSC0003DMT400097425	chr03	NO	NO	
939	PS in DM only	PGSC0003DMG400047035	PGSC0003DMT400097464	chr12	NO	NO	

940	PS in DM only	PGSC0003DMG400047299	PGSC0003DMT400097728	chr10	yes	NO	GO:0004252; serine-type endopeptidase activity; Molecular Function GO:0006508; proteolysis; Biological Process
941	Heterozygous PS in RH, not shared by DM	PGSC0003DMG402000020	PGSC0003DMT400000067	chr01	yes	NO	
942	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400000043	PGSC0003DMT400000146	chr08	NO	NO	
943	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401000100	PGSC0003DMT400000296	chr06	yes	NO	
944	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400000118	PGSC0003DMT400000345	chr06	NO	NO	
945	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400000136	PGSC0003DMT400000383	chr09	yes	NO	GO:0008270; zinc ion binding; Molecular Function GO:0016491; oxidoreductase activity; Molecular Function GO:0055114; oxidation reduction; Biological Process
946	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400000149	PGSC0003DMT400000436	chr09	yes	yes	
947	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400000239	PGSC0003DMT400000674	chr09	yes	NO	GO:0016747; transferase activity, transferring acyl groups other than amino-acyl groups; Molecular Function
948	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400000280	PGSC0003DMT400000761	chr06	yes	NO	
949	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400000286	PGSC0003DMT400000776	chr01	NO	NO	
950	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400000295	PGSC0003DMT400000795	chr04	yes	NO	

951	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400000296	PGSC0003DMT400000798	chr07	yes	NO	
952	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401000299	PGSC0003DMT400000806	chr07	yes	yes	
953	Heterozygous PS in RH, not shared by DM	PGSC0003DMG402000299	PGSC0003DMT400000808	chr12	yes	yes	GO:0003723; RNA binding; Molecular Function
954	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400000339	PGSC0003DMT400000899	chr03	yes	NO	GO:0003676; nucleic acid binding; Molecular Function
955	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400000341	PGSC0003DMT400000908	-	yes	yes	GO:0003676; nucleic acid binding; Molecular Function
956	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400000348	PGSC0003DMT400000930	chr12	NO	NO	
957	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400000355	PGSC0003DMT400000946	chr03	yes	NO	
958	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400000370	PGSC0003DMT400000995	chr03	yes	NO	
959	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400000408	PGSC0003DMT400001076	chr05	yes	yes	
960	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400000421	PGSC0003DMT400001109	chr07	NO	NO	
961	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400000468	PGSC0003DMT400001238	-	NO	NO	
962	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400000505	PGSC0003DMT400001350	chr12	yes	NO	

963	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400000509	PGSC0003DMT400001369	chr11	yes	NO	
964	Heterozygous PS in RH, not shared by DM	PGSC0003DMG402000515	PGSC0003DMT400001383	chr06	yes	NO	GO:0005529; sugar binding; Molecular Function GO:0006486; protein amino acid glycosylation; Biological Process GO:0008378; galactosyltransferase activity; Molecular Function GO:0016020; membrane; Cellular Component
965	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400000516	PGSC0003DMT400001389	chr09	yes	NO	GO:0004672; protein kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
966	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400000534	PGSC0003DMT400001446	chr05	yes	yes	
967	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400000565	PGSC0003DMT400001522	chr06	yes	NO	
968	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401000594	PGSC0003DMT400001596	chr05	yes	NO	GO:0005215; transporter activity; Molecular Function GO:0006857; oligopeptide transport; Biological Process GO:0016020; membrane; Cellular Component
969	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400000632	PGSC0003DMT400001691	chr03	yes	NO	GO:0005215; transporter activity; Molecular Function GO:0006857; oligopeptide transport; Biological Process GO:0016020; membrane; Cellular Component
970	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400000655	PGSC0003DMT400001750	chr01	yes	yes	
971	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400000710	PGSC0003DMT400001885	chr09	NO	NO	

972	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400000719	PGSC0003DMT400001903	chr10	NO	NO	GO:0006629; lipid metabolic process; Biological Process GO:0016788; hydrolase activity, acting on ester bonds; Molecular Function
973	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400000724	PGSC0003DMT400001912	chr02	yes	NO	GO:0009059; macromolecule biosynthetic process; Biological Process GO:0030176; integral to endoplasmic reticulum membrane; Cellular Component
974	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400000728	PGSC0003DMT400001921	chr01	NO	NO	GO:0003677; DNA binding; Molecular Function GO:0005634; nucleus; Cellular Component GO:0006352; transcription initiation; Biological Process GO:0016570; histone modification; Biological Process
975	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400000729	PGSC0003DMT400001923	chr10	yes	NO	
976	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400000784	PGSC0003DMT400002055	chr08	yes	NO	GO:0005515; protein binding; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006915; apoptosis; Biological Process
977	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400000830	PGSC0003DMT400002168	chr02	yes	NO	GO:0008168; methyltransferase activity; Molecular Function
978	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400000836	PGSC0003DMT400002184	chr04	yes	yes	GO:0004721; phosphoprotein phosphatase activity; Molecular Function
979	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400000867	PGSC0003DMT400002268	chr02	NO	NO	
980	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400000869	PGSC0003DMT400002273	chr06	yes	yes	GO:0004672; protein kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process

981	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400000879	PGSC0003DMT400002293	-	NO	NO	
982	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400001016	PGSC0003DMT400002647	chr04	yes	NO	
983	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400001052	PGSC0003DMT400002726	chr06	NO	NO	
984	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400001093	PGSC0003DMT400002809	-	yes	NO	GO:0004497; monooxygenase activity; Molecular Function GO:0005506; iron ion binding; Molecular Function GO:0009055; electron carrier activity; Molecular Function GO:0020037; heme binding; Molecular Function
985	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400001117	PGSC0003DMT400002866	chr07	yes	yes	GO:0005529; sugar binding; Molecular Function
986	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400001143	PGSC0003DMT400002920	chr08	yes	NO	GO:0003995; acyl-CoA dehydrogenase activity; Molecular Function GO:0003997; acyl-CoA oxidase activity; Molecular Function GO:0005777; peroxisome; Cellular Component GO:0006635; fatty acid beta-oxidation; Biological Process GO:0055114; oxidation reduction; Biological Process
987	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400001191	PGSC0003DMT400003013	chr02	yes	NO	
988	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400001211	PGSC0003DMT400003054	chr06	yes	NO	GO:0003723; RNA binding; Molecular Function
989	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400001259	PGSC0003DMT400003185	chr06	yes	NO	
990	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400001294	PGSC0003DMT400003264	chr02	yes	NO	

991	Heterozygous PS in RH, not shared by DM	PGSC0003DMG403001309	PGSC0003DMT400003302	chr06	NO	NO	
992	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400001386	PGSC0003DMT400003515	chr01	NO	NO	
993	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400001413	PGSC0003DMT400003573	chr01	yes	NO	GO:0004888; transmembrane receptor activity; Molecular Function GO:0005515; protein binding; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006915; apoptosis; Biological Process GO:0007165; signal transduction; Biological Process GO:0031224; intrinsic to membrane; Cellular Component GO:0045087; innate immune response; Biological Process
994	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400001425	PGSC0003DMT400003602	chr12	yes	NO	
995	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400001432	PGSC0003DMT400003632	chr12	yes	NO	
996	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400001458	PGSC0003DMT400003697	chr03	NO	NO	
997	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400001492	PGSC0003DMT400003765	chr07	NO	NO	
998	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400001503	PGSC0003DMT400003795	chr09	NO	NO	
999	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400001529	PGSC0003DMT400003878	chr08	NO	NO	
1000	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400001546	PGSC0003DMT400003919	chr01	NO	NO	

1001	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400001682	PGSC0003DMT400004228	chr04	yes	NO	
1002	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400001711	PGSC0003DMT400004314	chr01	yes	NO	GO:0004252; serine-type endopeptidase activity; Molecular Function GO:0006508; proteolysis; Biological Process GO:0042802; identical protein binding; Molecular Function GO:0043086; negative regulation of catalytic activity; Biological Process
1003	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400001730	PGSC0003DMT400004359	chr07	yes	NO	
1004	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400001751	PGSC0003DMT400004396	chr07	yes	NO	
1005	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400001752	PGSC0003DMT400004399	chr11	yes	NO	GO:0004252; serine-type endopeptidase activity; Molecular Function GO:0006508; proteolysis; Biological Process
1006	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400001781	PGSC0003DMT400004466	chr05	NO	NO	
1007	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400001863	PGSC0003DMT400004712	-	NO	NO	
1008	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400001866	PGSC0003DMT400004720	chr09	NO	NO	
1009	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400001890	PGSC0003DMT400004770	chr05	yes	NO	GO:0005515; protein binding; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006915; apoptosis; Biological Process

1010	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400001900	PGSC0003DMT400004785	chr03	yes	NO	GO:0004497; monooxygenase activity; Molecular Function GO:0005506; iron ion binding; Molecular Function GO:0009055; electron carrier activity; Molecular Function GO:0020037; heme binding; Molecular Function
1011	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400001967	PGSC0003DMT400004973	chr01	NO	NO	
1012	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400001996	PGSC0003DMT400005052	chr10	yes	NO	
1013	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400002019	PGSC0003DMT400005106	chr05	yes	NO	GO:0000156; two-component response regulator activity; Molecular Function GO:0000160; two-component signal transduction system (phosphorelay); Biological Process GO:0006355; regulation of transcription, DNA-dependent; Biological Process
1014	Heterozygous PS in RH, not shared by DM	PGSC0003DMG402002024	PGSC0003DMT400005127	chr09	NO	NO	
1015	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400002030	PGSC0003DMT400005137	-	NO	NO	
1016	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400002054	PGSC0003DMT400005207	chr12	NO	NO	
1017	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400002067	PGSC0003DMT400005246	chr05	yes	yes	
1018	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400002082	PGSC0003DMT400005337	chr09	NO	NO	
1019	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400002129	PGSC0003DMT400005455	chr09	yes	NO	

1020	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400002136	PGSC0003DMT400005473	chr01	yes	NO	
1021	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400002154	PGSC0003DMT400005513	chr12	yes	yes	
1022	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400002228	PGSC0003DMT400005682	chr07	yes	NO	
1023	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400002338	PGSC0003DMT400006012	chr12	yes	NO	GO:0000287; magnesium ion binding; Molecular Function GO:0008152; metabolic process; Biological Process GO:0016829; lyase activity; Molecular Function
1024	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400002381	PGSC0003DMT400006124	chr06	yes	yes	GO:0004869; cysteine-type endopeptidase inhibitor activity; Molecular Function
1025	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400002382	PGSC0003DMT400006125	chr03	yes	NO	
1026	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400002387	PGSC0003DMT400006135	chr08	NO	NO	
1027	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400002415	PGSC0003DMT400006209	-	NO	NO	
1028	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400002423	PGSC0003DMT400006222	chr03	NO	NO	
1029	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400002470	PGSC0003DMT400006323	chr01	yes	NO	
1030	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400002491	PGSC0003DMT400006372	chr05	yes	NO	
1031	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400002544	PGSC0003DMT400006523	chr06	yes	NO	

1032	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400002547	PGSC0003DMT400006532	chr01	yes	NO	GO:0005622; intracellular; Cellular Component
1033	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400002580	PGSC0003DMT400006632	chr08	yes	yes	
1034	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400002581	PGSC0003DMT400006633	chr05	yes	yes	
1035	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400002590	PGSC0003DMT400006654	chr09	yes	NO	GO:0016021; integral to membrane; Cellular Component GO:0016758; transferase activity, transferring hexosyl groups; Molecular Function
1036	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400002608	PGSC0003DMT400006709	chr05	yes	NO	GO:0016209; antioxidant activity; Molecular Function GO:0016491; oxidoreductase activity; Molecular Function GO:0045454; cell redox homeostasis; Biological Process
1037	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400002646	PGSC0003DMT400006823	chr08	yes	NO	GO:0005515; protein binding; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006915; apoptosis; Biological Process
1038	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400002678	PGSC0003DMT400006901	chr08	yes	NO	
1039	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401002721	PGSC0003DMT400007046	chr10	NO	NO	
1040	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400002750	PGSC0003DMT400007105	chr06	yes	NO	
1041	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400002818	PGSC0003DMT400007319	chr09	NO	NO	
1042	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400002833	PGSC0003DMT400007370	chr12	yes	NO	

1043	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400002920	PGSC0003DMT400007570	chr03	yes	NO	GO:0005515; protein binding; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006915; apoptosis; Biological Process
1044	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400003072	PGSC0003DMT400007944	chr04	NO	NO	
1045	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400003090	PGSC0003DMT400007990	chr05	yes	yes	
1046	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400003109	PGSC0003DMT400008044	chr09	yes	NO	
1047	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400003117	PGSC0003DMT400008083	chr08	yes	yes	GO:0003700; transcription factor activity; Molecular Function GO:0006355; regulation of transcription, DNA-dependent; Biological Process GO:0008270; zinc ion binding; Molecular Function GO:0043565; sequence-specific DNA binding; Molecular Function
1048	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400003236	PGSC0003DMT400008383	chr09	yes	NO	
1049	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400003257	PGSC0003DMT400008432	chr11	yes	NO	GO:0008152; metabolic process; Biological Process
1050	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400003269	PGSC0003DMT400008457	chr01	NO	NO	

1051	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400003340	PGSC0003DMT400008622	chr02	yes	yes	GO:0003824; catalytic activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006754; ATP biosynthetic process; Biological Process GO:0008152; metabolic process; Biological Process GO:0016020; membrane; Cellular Component GO:0016820; hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances; Molecular Function
1052	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400003377	PGSC0003DMT400008704	chr09	NO	NO	
1053	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400003380	PGSC0003DMT400008721	chr05	NO	NO	
1054	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400003446	PGSC0003DMT400008875	-	yes	NO	GO:0004497; monooxygenase activity; Molecular Function GO:0005506; iron ion binding; Molecular Function GO:0009055; electron carrier activity; Molecular Function GO:0020037; heme binding; Molecular Function
1055	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400003485	PGSC0003DMT400008946	chr07	NO	NO	
1056	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401003570	PGSC0003DMT400009199	chr12	yes	yes	
1057	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400003588	PGSC0003DMT400009242	chr01	NO	NO	
1058	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400003596	PGSC0003DMT400009269	chr07	yes	NO	
1059	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400003621	PGSC0003DMT400009319	chr10	NO	NO	

1060	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400003623	PGSC0003DMT400009324	chr05	yes	NO	
1061	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401003636	PGSC0003DMT400009351	chr07	yes	yes	
1062	Heterozygous PS in RH, not shared by DM	PGSC0003DMG402003636	PGSC0003DMT400009355	chr10	yes	NO	
1063	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400003724	PGSC0003DMT400009548	-	NO	NO	
1064	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400003739	PGSC0003DMT400009587	chr01	yes	NO	
1065	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400003760	PGSC0003DMT400009634	chr03	yes	NO	GO:0004571; mannosyl-oligosaccharide 1,2-alpha-mannosidase activity; Molecular Function GO:0005509; calcium ion binding; Molecular Function GO:0016020; membrane; Cellular Component
1066	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400003781	PGSC0003DMT400009686	chr04	NO	NO	
1067	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400003810	PGSC0003DMT400009741	chr12	NO	NO	
1068	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400003817	PGSC0003DMT400009752	chr05	NO	NO	
1069	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400003829	PGSC0003DMT400009781	chr04	yes	yes	GO:0005524; ATP binding; Molecular Function GO:0006915; apoptosis; Biological Process
1070	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400003853	PGSC0003DMT400009835	-	NO	NO	

1071	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400003885	PGSC0003DMT400009913	chr02	yes	NO	
1072	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400003906	PGSC0003DMT400009982	chr07	NO	NO	
1073	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400003912	PGSC0003DMT400009990	-	NO	NO	
1074	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400003919	PGSC0003DMT400010002	chr11	yes	yes	
1075	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400003932	PGSC0003DMT400010033	chr05	yes	yes	GO:0004871; signal transducer activity; Molecular Function GO:0009416; response to light stimulus; Biological Process
1076	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400003942	PGSC0003DMT400010069	-	yes	yes	
1077	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400003950	PGSC0003DMT400010087	chr06	NO	NO	
1078	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401003979	PGSC0003DMT400010155	chr04	yes	NO	GO:0004497; monooxygenase activity; Molecular Function GO:0005506; iron ion binding; Molecular Function GO:0009055; electron carrier activity; Molecular Function GO:0020037; heme binding; Molecular Function
1079	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400004014	PGSC0003DMT400010265	chr11	NO	NO	
1080	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400004039	PGSC0003DMT400010344	chr02	yes	NO	
1081	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400004046	PGSC0003DMT400010363	chr05	NO	NO	

1082	Heterozygous PS in RH, not shared by DM	PGSC0003DMG402004125	PGSC0003DMT400010556	chr03	yes	NO	
1083	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400004182	PGSC0003DMT400010721	chr08	yes	NO	GO:0004672; protein kinase activity; Molecular Function GO:0005515; protein binding; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
1084	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400004204	PGSC0003DMT400010758	chr04	NO	NO	
1085	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400004205	PGSC0003DMT400010761	chr08	NO	NO	GO:0000184; nuclear-transcribed mRNA catabolic process, nonsense-mediated decay; Biological Process GO:0003677; DNA binding; Molecular Function GO:0004386; helicase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0005737; cytoplasm; Cellular Component GO:0008270; zinc ion binding; Molecular Function
1086	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400004211	PGSC0003DMT400010772	chr09	yes	NO	
1087	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400004235	PGSC0003DMT400010827	chr10	NO	NO	
1088	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401004281	PGSC0003DMT400010931	chr07	NO	NO	
1089	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400004296	PGSC0003DMT400010970	chr01	NO	NO	
1090	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400004309	PGSC0003DMT400011000	chr02	NO	NO	

1091	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400004361	PGSC0003DMT400011145	chr09	yes	NO	
1092	Heterozygous PS in RH, not shared by DM	PGSC0003DMG402004406	PGSC0003DMT400011248	chr01	NO	NO	
1093	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400004408	PGSC0003DMT400011255	chr10	NO	NO	
1094	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400004446	PGSC0003DMT400011353	chr11	NO	NO	GO:0003700; transcription factor activity; Molecular Function GO:0005634; nucleus; Cellular Component GO:0006355; regulation of transcription, DNA-dependent; Biological Process GO:0043565; sequence-specific DNA binding; Molecular Function
1095	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400004448	PGSC0003DMT400011357	chr03	yes	NO	
1096	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400004492	PGSC0003DMT400011446	chr07	yes	NO	GO:0004672; protein kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
1097	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400004494	PGSC0003DMT400011451	chr12	yes	NO	GO:0003735; structural constituent of ribosome; Molecular Function GO:0005622; intracellular; Cellular Component GO:0005840; ribosome; Cellular Component GO:0006412; translation; Biological Process
1098	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400004511	PGSC0003DMT400011487	chr09	NO	NO	
1099	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400004534	PGSC0003DMT400011524	chr06	NO	NO	

1100	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400004548	PGSC0003DMT400011563	chr01	yes	NO	GO:0006629; lipid metabolic process; Biological Process GO:0016788; hydrolase activity, acting on ester bonds; Molecular Function
1101	Heterozygous PS in RH, not shared by DM	PGSC0003DMG402004603	PGSC0003DMT400011733	chr01	yes	NO	
1102	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400004641	PGSC0003DMT400011815	-	yes	NO	GO:0005515; protein binding; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006915; apoptosis; Biological Process
1103	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400004723	PGSC0003DMT400012041	chr05	yes	yes	
1104	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400004725	PGSC0003DMT400012045	chr10	NO	NO	
1105	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400004737	PGSC0003DMT400012075	chr04	NO	NO	
1106	Heterozygous PS in RH, not shared by DM	PGSC0003DMG402004755	PGSC0003DMT400012120	chr03	yes	NO	
1107	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400004776	PGSC0003DMT400012185	chr05	yes	NO	GO:0004594; pantothenate kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0015937; coenzyme A biosynthetic process; Biological Process
1108	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400004792	PGSC0003DMT400012219	chr04	yes	NO	
1109	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400004811	PGSC0003DMT400012260	chr03	NO	NO	GO:0006820; anion transport; Biological Process GO:0015380; anion exchanger activity; Molecular Function GO:0016021; integral to membrane; Cellular Component

1110	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401004813	PGSC0003DMT400012263	chr07	NO	NO	
1111	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400004842	PGSC0003DMT400012359	chr01	yes	NO	
1112	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400004843	PGSC0003DMT400012361	chr02	yes	NO	GO:0004497; monooxygenase activity; Molecular Function GO:0005506; iron ion binding; Molecular Function GO:0009055; electron carrier activity; Molecular Function GO:0020037; heme binding; Molecular Function
1113	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401004850	PGSC0003DMT400012375	chr11	yes	NO	
1114	Heterozygous PS in RH, not shared by DM	PGSC0003DMG402004858	PGSC0003DMT400012405	chr08	yes	NO	
1115	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400004859	PGSC0003DMT400012409	chr07	NO	NO	
1116	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401004870	PGSC0003DMT400012446	chr04	NO	NO	
1117	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400004873	PGSC0003DMT400012479	chr12	yes	NO	GO:0005524; ATP binding; Molecular Function GO:0006915; apoptosis; Biological Process
1118	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400004879	PGSC0003DMT400012496	chr01	NO	NO	

1119	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400004962	PGSC0003DMT400012732	chr10	NO	NO	GO:0004497; monooxygenase activity; Molecular Function GO:0004499; flavin-containing monooxygenase activity; Molecular Function GO:0050660; FAD binding; Molecular Function GO:0050661; NADP or NADPH binding; Molecular Function GO:0055114; oxidation reduction; Biological Process
1120	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400004984	PGSC0003DMT400012791	chr12	NO	NO	
1121	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400005020	PGSC0003DMT400012897	chr01	yes	NO	
1122	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400005021	PGSC0003DMT400012898	chr01	yes	yes	GO:0005524; ATP binding; Molecular Function GO:0016020; membrane; Cellular Component GO:0016887; ATPase activity; Molecular Function GO:0004190; aspartic-type endopeptidase activity; Molecular Function GO:0006508; proteolysis; Biological Process
1123	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400005033	PGSC0003DMT400012912	chr01	NO	NO	
1124	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400005037	PGSC0003DMT400012926	chr05	NO	NO	
1125	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400005090	PGSC0003DMT400013050	chr02	yes	NO	
1126	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400005094	PGSC0003DMT400013059	chr11	yes	yes	
1127	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400005105	PGSC0003DMT400013082	chr11	yes	NO	
1128	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400005108	PGSC0003DMT400013090	chr08	NO	NO	

1129	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400005121	PGSC0003DMT400013107	chr01	yes	NO	
1130	Heterozygous PS in RH, not shared by DM	PGSC0003DMG402005139	PGSC0003DMT400013159	chr02	NO	NO	GO:0005215; transporter activity; Molecular Function GO:0006810; transport; Biological Process GO:0016021; integral to membrane; Cellular Component GO:0055085; transmembrane transport; Biological Process
1131	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400005174	PGSC0003DMT400013242	chr10	NO	NO	
1132	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400005177	PGSC0003DMT400013249	-	NO	NO	
1133	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400005178	PGSC0003DMT400013254	chr08	NO	NO	
1134	Heterozygous PS in RH, not shared by DM	PGSC0003DMG402005180	PGSC0003DMT400013266	chr08	yes	NO	
1135	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400005186	PGSC0003DMT400013292	chr04	yes	NO	GO:0003700; transcription factor activity; Molecular Function GO:0043565; sequence-specific DNA binding; Molecular Function GO:0045449; regulation of transcription; Biological Process
1136	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400005200	PGSC0003DMT400013327	chr02	yes	NO	GO:0016491; oxidoreductase activity; Molecular Function GO:0055114; oxidation reduction; Biological Process
1137	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400005213	PGSC0003DMT400013370	chr01	yes	yes	GO:0030528; transcription regulator activity; Molecular Function GO:0045449; regulation of transcription; Biological Process
1138	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400005267	PGSC0003DMT400013497	chr11	NO	NO	

1139	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400005298	PGSC0003DMT400013565	chr01	yes	NO	
1140	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400005335	PGSC0003DMT400013650	chr06	yes	NO	GO:0004888; transmembrane receptor activity; Molecular Function GO:0007165; signal transduction; Biological Process GO:0031224; intrinsic to membrane; Cellular Component GO:0045087; innate immune response; Biological Process
1141	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400005359	PGSC0003DMT400013704	chr09	NO	NO	
1142	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400005369	PGSC0003DMT400013725	chr01	NO	NO	
1143	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400005385	PGSC0003DMT400013757	chr02	NO	NO	
1144	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400005410	PGSC0003DMT400013831	chr03	NO	NO	
1145	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400005441	PGSC0003DMT400013902	chr06	yes	yes	
1146	Heterozygous PS in RH, not shared by DM	PGSC0003DMG402005482	PGSC0003DMT400013987	chr09	NO	NO	
1147	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400005498	PGSC0003DMT400014020	chr07	yes	NO	GO:0004672; protein kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process

1148	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400005529	PGSC0003DMT400014098	chr08	yes	NO	GO:0006855; multidrug transport; Biological Process GO:0015238; drug transporter activity; Molecular Function GO:0015297; antiporter activity; Molecular Function GO:0016020; membrane; Cellular Component GO:0055085; transmembrane transport; Biological Process
1149	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400005597	PGSC0003DMT400014271	chr12	NO	NO	
1150	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400005610	PGSC0003DMT400014301	chr04	NO	NO	
1151	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400005660	PGSC0003DMT400014425	chr03	NO	NO	
1152	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400005673	PGSC0003DMT400014472	-	NO	NO	GO:0003676; nucleic acid binding; Molecular Function
1153	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400005676	PGSC0003DMT400014488	chr05	NO	NO	GO:0008152; metabolic process; Biological Process GO:0016787; hydrolase activity; Molecular Function
1154	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400005695	PGSC0003DMT400014548	chr06	yes	NO	
1155	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400005758	PGSC0003DMT400014772	chr10	yes	NO	GO:0004497; monooxygenase activity; Molecular Function GO:0005506; iron ion binding; Molecular Function GO:0009055; electron carrier activity; Molecular Function GO:0020037; heme binding; Molecular Function
1156	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400005799	PGSC0003DMT400014846	chr04	yes	yes	
1157	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400005820	PGSC0003DMT400014918	chr04	NO	NO	

1158	Heterozygous PS in RH, not shared by DM	PGSC0003DMG404005966	PGSC0003DMT400015295	chr12	yes	NO	GO:0008152; metabolic process; Biological Process GO:0016491; oxidoreductase activity; Molecular Function
1159	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400005967	PGSC0003DMT400015301	chr09	NO	NO	GO:0016787; hydrolase activity; Molecular Function
1160	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400006058	PGSC0003DMT400015517	chr11	NO	NO	
1161	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400006077	PGSC0003DMT400015568	chr09	yes	NO	GO:0005515; protein binding; Molecular Function
1162	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400006113	PGSC0003DMT400015664	-	NO	NO	
1163	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400006119	PGSC0003DMT400015670	chr09	yes	NO	
1164	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400006210	PGSC0003DMT400015887	chr11	yes	NO	GO:0008152; metabolic process; Biological Process GO:0016758; transferase activity, transferring hexosyl groups; Molecular Function
1165	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400006239	PGSC0003DMT400015945	chr08	yes	NO	
1166	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400006247	PGSC0003DMT400015969	chr06	yes	NO	
1167	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400006248	PGSC0003DMT400015974	chr05	NO	NO	
1168	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401006258	PGSC0003DMT400015998	chr11	yes	NO	GO:0004672; protein kinase activity; Molecular Function GO:0005515; protein binding; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process

1169	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400006268	PGSC0003DMT400016034	chr12	NO	NO	
1170	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400006269	PGSC0003DMT400016035	chr01	NO	NO	
1171	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400006278	PGSC0003DMT400016058	chr12	yes	NO	GO:0055085; transmembrane transport; Biological Process
1172	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401006284	PGSC0003DMT400016072	chr12	NO	NO	
1173	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400006292	PGSC0003DMT400016096	chr09	yes	NO	GO:0016757; transferase activity, transferring glycosyl groups; Molecular Function
1174	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400006294	PGSC0003DMT400016102	chr05	yes	NO	
1175	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400006296	PGSC0003DMT400016105	chr12	yes	NO	
1176	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400006297	PGSC0003DMT400016107	chr05	NO	NO	
1177	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400006304	PGSC0003DMT400016127	chr08	NO	NO	
1178	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400006344	PGSC0003DMT400016233	chr10	yes	NO	GO:0016021; integral to membrane; Cellular Component
1179	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400006399	PGSC0003DMT400016369	chr02	yes	NO	GO:0004871; signal transducer activity; Molecular Function GO:0005515; protein binding; Molecular Function GO:0009416; response to light stimulus; Biological Process
1180	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400006416	PGSC0003DMT400016423	chr09	NO	NO	

1181	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400006488	PGSC0003DMT400016599	chr12	NO	NO	
1182	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400006527	PGSC0003DMT400016697	chr01	NO	NO	
1183	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400006528	PGSC0003DMT400016703	chr10	yes	NO	
1184	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400006594	PGSC0003DMT400016849	chr05	yes	yes	
1185	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400006605	PGSC0003DMT400016886	chr10	yes	NO	
1186	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400006635	PGSC0003DMT400016981	chr12	NO	NO	
1187	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400006644	PGSC0003DMT400017006	chr06	NO	NO	
1188	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400006661	PGSC0003DMT400017057	chr05	yes	yes	
1189	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400006672	PGSC0003DMT400017087	chr06	yes	yes	
1190	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400006698	PGSC0003DMT400017163	chr01	yes	NO	GO:0008152; metabolic process; Biological Process GO:0016758; transferase activity, transferring hexosyl groups; Molecular Function
1191	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400006705	PGSC0003DMT400017187	chr12	NO	NO	
1192	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400006733	PGSC0003DMT400017277	chr04	NO	NO	

1193	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400006759	PGSC0003DMT400017379	chr12	yes	yes	
1194	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400006762	PGSC0003DMT400017386	chr12	yes	NO	GO:0016747; transferase activity, transferring acyl groups other than amino-acyl groups; Molecular Function
1195	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400006765	PGSC0003DMT400017392	chr07	yes	NO	GO:0004497; monooxygenase activity; Molecular Function GO:0005506; iron ion binding; Molecular Function GO:0009055; electron carrier activity; Molecular Function GO:0020037; heme binding; Molecular Function
1196	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400006769	PGSC0003DMT400017408	chr06	yes	NO	GO:0009055; electron carrier activity; Molecular Function GO:0015035; protein disulfide oxidoreductase activity; Molecular Function GO:0045454; cell redox homeostasis; Biological Process
1197	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400006784	PGSC0003DMT400017459	-	NO	NO	
1198	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400006785	PGSC0003DMT400017461	chr11	NO	NO	GO:0016747; transferase activity, transferring acyl groups other than amino-acyl groups; Molecular Function
1199	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400006815	PGSC0003DMT400017572	chr01	NO	NO	GO:0003824; catalytic activity; Molecular Function GO:0008152; metabolic process; Biological Process
1200	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401006826	PGSC0003DMT400017592	chr04	yes	NO	
1201	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400006835	PGSC0003DMT400017624	-	NO	NO	
1202	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400006851	PGSC0003DMT400017657	chr01	yes	NO	GO:0003677; DNA binding; Molecular Function GO:0005634; nucleus; Cellular Component GO:0006352; transcription initiation; Biological Process GO:0016570; histone modification; Biological Process

1203	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400006877	PGSC0003DMT400017726	-	yes	yes	GO:0008483; transaminase activity; Molecular Function GO:0030170; pyridoxal phosphate binding; Molecular Function
1204	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400007005	PGSC0003DMT400018033	chr03	yes	NO	GO:0016491; oxidoreductase activity; Molecular Function GO:0055114; oxidation reduction; Biological Process
1205	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400007073	PGSC0003DMT400018218	chr05	yes	NO	
1206	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400007076	PGSC0003DMT400018230	chr10	yes	NO	GO:0004672; protein kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
1207	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400007109	PGSC0003DMT400018304	chr07	yes	yes	
1208	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400007112	PGSC0003DMT400018308	chr12	NO	NO	
1209	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400007115	PGSC0003DMT400018321	chr09	yes	NO	GO:0004672; protein kinase activity; Molecular Function GO:0005515; protein binding; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
1210	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400007150	PGSC0003DMT400018425	chr04	yes	NO	
1211	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400007157	PGSC0003DMT400018447	chr03	NO	NO	
1212	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400007218	PGSC0003DMT400018602	-	NO	NO	

1213	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400007239	PGSC0003DMT400018688	chr11	NO	NO	
1214	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400007250	PGSC0003DMT400018717	-	yes	NO	
1215	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400007251	PGSC0003DMT400018718	chr12	NO	NO	GO:0005249; voltage-gated potassium channel activity; Molecular Function GO:0006813; potassium ion transport; Biological Process GO:0008076; voltage-gated potassium channel complex; Cellular Component GO:0016020; membrane; Cellular Component
1216	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400007270	PGSC0003DMT400018758	chr10	yes	yes	GO:0006904; vesicle docking during exocytosis; Biological Process GO:0016192; vesicle-mediated transport; Biological Process
1217	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400007271	PGSC0003DMT400018760	chr04	yes	NO	
1218	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400007310	PGSC0003DMT400018854	chr08	yes	NO	
1219	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400007351	PGSC0003DMT400018961	chr12	yes	NO	
1220	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400007412	PGSC0003DMT400019156	chr04	NO	NO	
1221	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400007445	PGSC0003DMT400019250	chr02	yes	NO	GO:0004672; protein kinase activity; Molecular Function GO:0005515; protein binding; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
1222	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400007504	PGSC0003DMT400019412	chr07	NO	NO	

1223	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400007523	PGSC0003DMT400019465	chr02	NO	NO	
1224	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400007526	PGSC0003DMT400019468	chr06	yes	NO	
1225	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400007566	PGSC0003DMT400019562	chr12	yes	NO	GO:0005507; copper ion binding; Molecular Function GO:0016491; oxidoreductase activity; Molecular Function GO:0055114; oxidation reduction; Biological Process
1226	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400007590	PGSC0003DMT400019639	chr09	yes	NO	GO:0005576; extracellular region; Cellular Component GO:0008083; growth factor activity; Molecular Function GO:0008283; cell proliferation; Biological Process
1227	Heterozygous PS in RH, not shared by DM	PGSC0003DMG402007604	PGSC0003DMT400019672	chr12	NO	NO	
1228	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400007622	PGSC0003DMT400019727	chr01	yes	yes	
1229	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400007639	PGSC0003DMT400019769	chr03	NO	NO	
1230	Heterozygous PS in RH, not shared by DM	PGSC0003DMG402007748	PGSC0003DMT400020029	chr04	yes	NO	GO:0004497; monooxygenase activity; Molecular Function GO:0005506; iron ion binding; Molecular Function GO:0009055; electron carrier activity; Molecular Function GO:0020037; heme binding; Molecular Function
1231	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400007769	PGSC0003DMT400020068	chr06	yes	NO	

1232	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400007770	PGSC0003DMT400020072	chr03	yes	NO	GO:0004616; phosphogluconate dehydrogenase (decarboxylating) activity; Molecular Function GO:0006098; pentose-phosphate shunt; Biological Process GO:0055114; oxidation reduction; Biological Process
1233	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400007848	PGSC0003DMT400020297	chr12	NO	NO	
1234	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400007908	PGSC0003DMT400020466	chr07	NO	NO	
1235	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400007994	PGSC0003DMT400020635	chr12	NO	NO	
1236	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400007995	PGSC0003DMT400020637	chr04	NO	NO	
1237	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400008030	PGSC0003DMT400020749	chr04	NO	NO	
1238	Heterozygous PS in RH, not shared by DM	PGSC0003DMG402008054	PGSC0003DMT400020808	chr03	NO	NO	
1239	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400008148	PGSC0003DMT400021053	chr05	yes	NO	
1240	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400008176	PGSC0003DMT400021111	chr07	yes	yes	
1241	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400008267	PGSC0003DMT400021318	chr07	yes	NO	
1242	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400008306	PGSC0003DMT400021403	chr07	yes	NO	GO:0004672; protein kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process

1243	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400008308	PGSC0003DMT400021420	-	yes	NO	GO:0008152; metabolic process; Biological Process GO:0016758; transferase activity, transferring hexosyl groups; Molecular Function
1244	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400008323	PGSC0003DMT400021449	chr05	NO	NO	
1245	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400008384	PGSC0003DMT400021612	chr01	NO	NO	
1246	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400008394	PGSC0003DMT400021634	chr12	NO	NO	
1247	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400008403	PGSC0003DMT400021662	chr04	yes	NO	GO:0005524; ATP binding; Molecular Function GO:0006915; apoptosis; Biological Process
1248	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400008408	PGSC0003DMT400021673	chr03	yes	yes	
1249	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400008410	PGSC0003DMT400021675	chr06	NO	NO	GO:0005525; GTP binding; Molecular Function
1250	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400008411	PGSC0003DMT400021679	chr12	NO	NO	
1251	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400008431	PGSC0003DMT400021726	chr04	NO	NO	
1252	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400008432	PGSC0003DMT400021731	chr09	yes	yes	
1253	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400008462	PGSC0003DMT400021802	chr05	yes	NO	

1254	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401008474	PGSC0003DMT400021832	chr01	yes	NO	GO:0003700; transcription factor activity; Molecular Function GO:0005667; transcription factor complex; Cellular Component GO:0006355; regulation of transcription, DNA-dependent; Biological Process
1255	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400008519	PGSC0003DMT400021970	chr02	yes	NO	
1256	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400008524	PGSC0003DMT400021985	chr06	yes	yes	
1257	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400008527	PGSC0003DMT400021991	chr12	yes	NO	GO:0003746; translation elongation factor activity; Molecular Function GO:0005622; intracellular; Cellular Component GO:0006414; translational elongation; Biological Process
1258	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400008591	PGSC0003DMT400022143	chr03	yes	NO	GO:0047800; cysteamine dioxygenase activity; Molecular Function GO:0055114; oxidation reduction; Biological Process
1259	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400008597	PGSC0003DMT400022163				
1260	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400008606	PGSC0003DMT400022182	chr05	yes	NO	GO:0004672; protein kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
1261	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400008614	PGSC0003DMT400022195	chr09	yes	yes	GO:0016021; integral to membrane; Cellular Component
1262	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400008628	PGSC0003DMT400022247	chr03	yes	NO	
1263	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400008633	PGSC0003DMT400022255	chr11	yes	NO	

1264	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400008688	PGSC0003DMT400022405	chr01	yes	yes	
1265	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400008733	PGSC0003DMT400022527	chr12	NO	NO	
1266	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400008750	PGSC0003DMT400022570	chr04	NO	NO	GO:0004811; tRNA isopentenyltransferase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0008033; tRNA processing; Biological Process
1267	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400008806	PGSC0003DMT400022705	chr05	yes	NO	
1268	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400008845	PGSC0003DMT400022798	chr08	yes	NO	GO:0004252; serine-type endopeptidase activity; Molecular Function GO:0006508; proteolysis; Biological Process GO:0042802; identical protein binding; Molecular Function GO:0043086; negative regulation of catalytic activity; Biological Process
1269	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401008856	PGSC0003DMT400022843	chr09	yes	NO	
1270	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400008887	PGSC0003DMT400022937	chr12	NO	NO	
1271	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400008905	PGSC0003DMT400023000	chr12	yes	NO	GO:0005524; ATP binding; Molecular Function GO:0006915; apoptosis; Biological Process GO:0008168; methyltransferase activity; Molecular Function
1272	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400008907	PGSC0003DMT400023009	chr08	yes	NO	GO:0004713; protein tyrosine kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process

1273	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400008911	PGSC0003DMT400023024	chr11	NO	NO	
1274	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400008939	PGSC0003DMT400023083	chr10	NO	NO	
1275	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400008942	PGSC0003DMT400023090	chr12	yes	NO	
1276	Heterozygous PS in RH, not shared by DM	PGSC0003DMG402008946	PGSC0003DMT400023099	chr06	NO	NO	
1277	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400009024	PGSC0003DMT400023297	chr07	NO	NO	GO:0004497; monooxygenase activity; Molecular Function GO:0005506; iron ion binding; Molecular Function GO:0009055; electron carrier activity; Molecular Function GO:0020037; heme binding; Molecular Function
1278	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400009066	PGSC0003DMT400023412	chr12	NO	NO	GO:0000156; two-component response regulator activity; Molecular Function GO:0000160; two-component signal transduction system (phosphorelay); Biological Process GO:0006355; regulation of transcription, DNA-dependent; Biological Process
1279	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400009146	PGSC0003DMT400023625	chr03	yes	NO	
1280	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400009149	PGSC0003DMT400023639	chr02	NO	NO	
1281	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400009160	PGSC0003DMT400023680	chr10	yes	NO	
1282	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400009235	PGSC0003DMT400023883	chr11	yes	NO	

1283	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400009241	PGSC0003DMT400023901	chr06	NO	NO	
1284	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401009270	PGSC0003DMT400023968	chr11	NO	NO	
1285	Heterozygous PS in RH, not shared by DM	PGSC0003DMG402009270	PGSC0003DMT400023971	chr04	yes	yes	
1286	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400009284	PGSC0003DMT400024004	chr04	NO	NO	
1287	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401009306	PGSC0003DMT400024061	-	NO	NO	GO:0004672; protein kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
1288	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401009323	PGSC0003DMT400024108	chr05	yes	NO	
1289	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400009339	PGSC0003DMT400024161	chr11	yes	NO	GO:0004888; transmembrane receptor activity; Molecular Function GO:0005515; protein binding; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006915; apoptosis; Biological Process GO:0007165; signal transduction; Biological Process GO:0031224; intrinsic to membrane; Cellular Component GO:0045087; innate immune response; Biological Process
1290	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400009351	PGSC0003DMT400024197	-	NO	NO	
1291	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400009352	PGSC0003DMT400024201	chr08	yes	NO	

1292	Heterozygous PS in RH, not shared by DM	PGSC0003DMG402009389	PGSC0003DMT400024292	chr09	NO	NO	
1293	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400009462	PGSC0003DMT400024475	chr06	yes	NO	
1294	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400009532	PGSC0003DMT400024635	chr12	NO	NO	
1295	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400009556	PGSC0003DMT400024713	chr02	NO	NO	GO:0005622; intracellular; Cellular Component GO:0008270; zinc ion binding; Molecular Function
1296	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400009574	PGSC0003DMT400024766	chr12	NO	NO	
1297	Heterozygous PS in RH, not shared by DM	PGSC0003DMG403009595	PGSC0003DMT400024816	chr07	yes	yes	
1298	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400009614	PGSC0003DMT400024866	chr08	yes	NO	
1299	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400009623	PGSC0003DMT400024897	chr10	yes	NO	GO:0003677; DNA binding; Molecular Function GO:0003899; DNA-directed RNA polymerase activity; Molecular Function GO:0006350; transcription; Biological Process
1300	Heterozygous PS in RH, not shared by DM	PGSC0003DMG402009628	PGSC0003DMT400024909	chr10	yes	yes	
1301	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400009703	PGSC0003DMT400025113	chr12	NO	NO	GO:0005515; protein binding; Molecular Function
1302	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400009715	PGSC0003DMT400025139	chr04	yes	NO	GO:0005515; protein binding; Molecular Function
1303	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400009721	PGSC0003DMT400025155	chr11	yes	NO	

1304	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400009730	PGSC0003DMT400025178	chr12	NO	NO	
1305	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401009756	PGSC0003DMT400025253	chr01	yes	NO	GO:0005622; intracellular; Cellular Component
1306	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400009785	PGSC0003DMT400025346	chr01	yes	NO	GO:0016747; transferase activity, transferring acyl groups other than amino-acyl groups; Molecular Function
1307	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400009810	PGSC0003DMT400025411	-	yes	NO	
1308	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400009848	PGSC0003DMT400025502	chr07	yes	NO	
1309	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400009851	PGSC0003DMT400025510	chr07	yes	yes	
1310	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400009853	PGSC0003DMT400025512	chr09	NO	NO	
1311	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400009883	PGSC0003DMT400025581	chr12	NO	NO	
1312	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400009899	PGSC0003DMT400025631				
1313	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400009901	PGSC0003DMT400025634	chr12	yes	NO	
1314	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400009913	PGSC0003DMT400025673	chr07	yes	NO	
1315	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400009944	PGSC0003DMT400025759	-	NO	NO	

1316	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400010041	PGSC0003DMT400026022	-	yes	yes	GO:0004672; protein kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
1317	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400010043	PGSC0003DMT400026030	chr12	NO	NO	
1318	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400010055	PGSC0003DMT400026062	chr05	yes	NO	
1319	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400010082	PGSC0003DMT400026154	chr05	yes	NO	
1320	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400010086	PGSC0003DMT400026172	chr12	yes	NO	
1321	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400010094	PGSC0003DMT400026194	chr03	NO	NO	
1322	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400010096	PGSC0003DMT400026200	chr03	yes	yes	
1323	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400010137	PGSC0003DMT400026272	chr11	yes	NO	GO:0005524; ATP binding; Molecular Function GO:0016020; membrane; Cellular Component GO:0016887; ATPase activity; Molecular Function
1324	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400010150	PGSC0003DMT400026296	chr05	NO	NO	
1325	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400010159	PGSC0003DMT400026319	chr02	NO	NO	GO:0003676; nucleic acid binding; Molecular Function GO:0004386; helicase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0008026; ATP-dependent helicase activity; Molecular Function

1326	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400010161	PGSC0003DMT400026324	chr09	yes	NO	GO:0031072; heat shock protein binding; Molecular Function
1327	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400010180	PGSC0003DMT400026391	chr06	yes	yes	
1328	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400010212	PGSC0003DMT400026457	chr07	yes	NO	
1329	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400010219	PGSC0003DMT400026480	chr09	NO	NO	
1330	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400010253	PGSC0003DMT400026556	chr07	NO	NO	
1331	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400010293	PGSC0003DMT400026643	chr10	yes	NO	GO:0019867; outer membrane; Cellular Component
1332	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400010299	PGSC0003DMT400026654	chr04	NO	NO	
1333	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400010322	PGSC0003DMT400026710	chr02	yes	NO	GO:0000175; 3'-5'-exoribonuclease activity; Molecular Function GO:0003723; RNA binding; Molecular Function GO:0006396; RNA processing; Biological Process
1334	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400010336	PGSC0003DMT400026752	chr04	yes	NO	GO:0005524; ATP binding; Molecular Function GO:0006915; apoptosis; Biological Process
1335	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400010353	PGSC0003DMT400026828	chr02	yes	NO	GO:0003993; acid phosphatase activity; Molecular Function
1336	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400010372	PGSC0003DMT400026882	chr12	yes	NO	

1337	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400010387	PGSC0003DMT400026935	chr06	NO	NO	GO:0003700; transcription factor activity; Molecular Function GO:0006355; regulation of transcription, DNA-dependent; Biological Process GO:0043565; sequence-specific DNA binding; Molecular Function GO:0046983; protein dimerization activity; Molecular Function
1338	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400010461	PGSC0003DMT400027122	chr10	yes	yes	
1339	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400010467	PGSC0003DMT400027134	chr02	NO	NO	
1340	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400010493	PGSC0003DMT400027205	chr04	NO	NO	
1341	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400010548	PGSC0003DMT400027351	chr10	yes	yes	
1342	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400010611	PGSC0003DMT400027525	chr07	yes	NO	GO:0004672; protein kinase activity; Molecular Function GO:0005515; protein binding; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
1343	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400010612	PGSC0003DMT400027529	chr09	NO	NO	
1344	Heterozygous PS in RH, not shared by DM	PGSC0003DMG402010614	PGSC0003DMT400027538	chr06	yes	NO	GO:0004553; hydrolase activity, hydrolyzing O-glycosyl compounds; Molecular Function GO:0005529; sugar binding; Molecular Function GO:0005975; carbohydrate metabolic process; Biological Process
1345	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400010678	PGSC0003DMT400027709	chr06	NO	NO	

1346	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400010688	PGSC0003DMT400027760	chr11	yes	yes	
1347	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400010700	PGSC0003DMT400027792	chr12	yes	NO	GO:0004650; polygalacturonase activity; Molecular Function GO:0005975; carbohydrate metabolic process; Biological Process
1348	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400010703	PGSC0003DMT400027805	chr07	yes	NO	
1349	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400010717	PGSC0003DMT400027835	chr02	yes	NO	GO:0004806; triacylglycerol lipase activity; Molecular Function GO:0006629; lipid metabolic process; Biological Process
1350	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400010801	PGSC0003DMT400028010	chr08	yes	NO	GO:0004672; protein kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0005529; sugar binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
1351	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400010857	PGSC0003DMT400028148	chr05	yes	yes	
1352	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400010891	PGSC0003DMT400028253	chr12	yes	NO	
1353	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400010892	PGSC0003DMT400028257	chr01	NO	NO	
1354	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401010896	PGSC0003DMT400028272	chr04	NO	NO	
1355	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400010901	PGSC0003DMT400028291	-	yes	NO	

1356	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400010912	PGSC0003DMT400028306	chr11	yes	yes	GO:0004497; monooxygenase activity; Molecular Function GO:0005506; iron ion binding; Molecular Function GO:0009055; electron carrier activity; Molecular Function GO:0020037; heme binding; Molecular Function
1357	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400010939	PGSC0003DMT400028382	chr06	yes	NO	GO:0005524; ATP binding; Molecular Function GO:0006915; apoptosis; Biological Process
1358	Heterozygous PS in RH, not shared by DM	PGSC0003DMG403010943	PGSC0003DMT400028400	chr06	NO	NO	
1359	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400010977	PGSC0003DMT400028508	chr03	NO	NO	GO:0005789; endoplasmic reticulum membrane; Cellular Component GO:0006506; GPI anchor biosynthetic process; Biological Process GO:0016021; integral to membrane; Cellular Component
1360	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401010991	PGSC0003DMT400028537	chr08	NO	NO	
1361	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400011011	PGSC0003DMT400028617	chr03	yes	NO	
1362	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400011065	PGSC0003DMT400028752	chr07	yes	NO	GO:0004672; protein kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0005529; sugar binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
1363	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400011080	PGSC0003DMT400028782	chr04	yes	yes	
1364	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400011085	PGSC0003DMT400028797	chr06	yes	NO	

1365	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400011129	PGSC0003DMT400028912	chr10	NO	NO	
1366	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400011142	PGSC0003DMT400028944	chr03	yes	NO	GO:0008565; protein transporter activity; Molecular Function GO:0015031; protein transport; Biological Process
1367	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400011219	PGSC0003DMT400029173	-	NO	NO	
1368	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400011277	PGSC0003DMT400029351	chr10	yes	NO	GO:0016020; membrane; Cellular Component
1369	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401011400	PGSC0003DMT400029652	chr10	NO	NO	GO:0003700; transcription factor activity; Molecular Function GO:0005634; nucleus; Cellular Component GO:0006355; regulation of transcription, DNA-dependent; Biological Process GO:0043565; sequence-specific DNA binding; Molecular Function
1370	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400011445	PGSC0003DMT400029782	chr12	NO	NO	GO:0016757; transferase activity, transferring glycosyl groups; Molecular Function
1371	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400011472	PGSC0003DMT400029849	chr12	NO	NO	GO:0003700; transcription factor activity; Molecular Function GO:0006355; regulation of transcription, DNA-dependent; Biological Process
1372	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400011477	PGSC0003DMT400029866	chr07	yes	yes	GO:0004553; hydrolase activity, hydrolyzing O-glycosyl compounds; Molecular Function GO:0005975; carbohydrate metabolic process; Biological Process
1373	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400011518	PGSC0003DMT400030012	chr12	NO	NO	
1374	Heterozygous PS in RH, not shared by DM	PGSC0003DMG402011540	PGSC0003DMT400030118	chr07	yes	NO	

1375	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400011542	PGSC0003DMT400030126	chr04	yes	yes	GO:0004497; monooxygenase activity; Molecular Function GO:0005506; iron ion binding; Molecular Function GO:0009055; electron carrier activity; Molecular Function GO:0020037; heme binding; Molecular Function
1376	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401011559	PGSC0003DMT400030207	-	yes	yes	
1377	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400011562	PGSC0003DMT400030219	chr11	yes	yes	GO:0003723; RNA binding; Molecular Function GO:0004540; ribonuclease activity; Molecular Function
1378	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400011612	PGSC0003DMT400030342	chr09	NO	NO	
1379	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400011616	PGSC0003DMT400030358	chr03	yes	NO	
1380	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400011629	PGSC0003DMT400030383	chr05	yes	NO	GO:0008152; metabolic process; Biological Process GO:0016758; transferase activity, transferring hexosyl groups; Molecular Function
1381	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400011633	PGSC0003DMT400030388	chr06	NO	NO	
1382	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400011670	PGSC0003DMT400030473	chr12	yes	NO	
1383	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400011678	PGSC0003DMT400030484	-	yes	NO	GO:0016765; transferase activity, transferring alkyl or aryl (other than methyl) groups; Molecular Function
1384	Heterozygous PS in RH, not shared by DM	PGSC0003DMG403011681	PGSC0003DMT400030502	chr01	yes	NO	
1385	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400011683	PGSC0003DMT400030505	chr10	yes	NO	

1386	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400011691	PGSC0003DMT400030530	chr12	yes	NO	GO:0016020; membrane; Cellular Component
1387	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400011723	PGSC0003DMT400030611	chr08	yes	yes	
1388	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400011729	PGSC0003DMT400030624	chr11	yes	NO	
1389	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400011764	PGSC0003DMT400030707	chr02	yes	NO	
1390	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400011786	PGSC0003DMT400030769	chr02	yes	yes	GO:0003700; transcription factor activity; Molecular Function GO:0006355; regulation of transcription, DNA-dependent; Biological Process GO:0043565; sequence-specific DNA binding; Molecular Function
1391	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400011793	PGSC0003DMT400030787	chr06	NO	NO	
1392	Heterozygous PS in RH, not shared by DM	PGSC0003DMG402011794	PGSC0003DMT400030789	chr10	yes	NO	GO:0006457; protein folding; Biological Process
1393	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400011829	PGSC0003DMT400030871	chr08	yes	NO	
1394	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400011892	PGSC0003DMT400031047	chr06	yes	yes	
1395	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400011907	PGSC0003DMT400031082	chr11	NO	NO	
1396	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400011977	PGSC0003DMT400031252	chr04	NO	NO	

1397	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400011978	PGSC0003DMT400031254	chr11	yes	NO	GO:0004888; transmembrane receptor activity; Molecular Function GO:0007165; signal transduction; Biological Process GO:0031224; intrinsic to membrane; Cellular Component GO:0045087; innate immune response; Biological Process
1398	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400012042	PGSC0003DMT400031413	chr04	yes	NO	GO:0004553; hydrolase activity, hydrolyzing O-glycosyl compounds; Molecular Function GO:0005975; carbohydrate metabolic process; Biological Process
1399	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400012053	PGSC0003DMT400031434	chr11	yes	NO	GO:0004888; transmembrane receptor activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006915; apoptosis; Biological Process GO:0007165; signal transduction; Biological Process GO:0031224; intrinsic to membrane; Cellular Component GO:0045087; innate immune response; Biological Process
1400	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400012068	PGSC0003DMT400031469	chr02	yes	yes	
1401	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400012083	PGSC0003DMT400031515	chr12	NO	NO	GO:0003676; nucleic acid binding; Molecular Function GO:0008270; zinc ion binding; Molecular Function
1402	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400012134	PGSC0003DMT400031636	chr04	yes	yes	
1403	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400012166	PGSC0003DMT400031711	chr10	NO	NO	GO:0005525; GTP binding; Molecular Function
1404	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400012208	PGSC0003DMT400031822	chr09	yes	NO	GO:0004672; protein kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process

1405	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400012213	PGSC0003DMT400031836	chr09	NO	NO	
1406	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401012256	PGSC0003DMT400031941	chr06	NO	NO	
1407	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400012265	PGSC0003DMT400031974	-	yes	NO	GO:0045735; nutrient reservoir activity; Molecular Function
1408	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400012277	PGSC0003DMT400032002	chr09	NO	NO	
1409	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400012284	PGSC0003DMT400032020	chr12	NO	NO	
1410	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400012288	PGSC0003DMT400032028	chr10	NO	NO	GO:0004601; peroxidase activity; Molecular Function GO:0006979; response to oxidative stress; Biological Process GO:0020037; heme binding; Molecular Function GO:0055114; oxidation reduction; Biological Process
1411	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400012311	PGSC0003DMT400032077	chr07	yes	yes	
1412	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400012320	PGSC0003DMT400032094	chr02	yes	NO	
1413	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401012324	PGSC0003DMT400032102	chr04	NO	NO	GO:0003700; transcription factor activity; Molecular Function GO:0006355; regulation of transcription, DNA-dependent; Biological Process GO:0043565; sequence-specific DNA binding; Molecular Function GO:0046983; protein dimerization activity; Molecular Function
1414	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400012326	PGSC0003DMT400032107	chr01	NO	NO	

1415	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400012408	PGSC0003DMT400032307	chr11	NO	NO	
1416	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400012417	PGSC0003DMT400032327	chr06	NO	NO	GO:0016747; transferase activity, transferring acyl groups other than amino-acyl groups; Molecular Function
1417	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400012466	PGSC0003DMT400032442	chr09	yes	yes	
1418	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400012470	PGSC0003DMT400032453	chr12	yes	NO	GO:0005524; ATP binding; Molecular Function
1419	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400012471	PGSC0003DMT400032454	chr03	NO	NO	GO:0008152; metabolic process; Biological Process GO:0016491; oxidoreductase activity; Molecular Function
1420	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401012477	PGSC0003DMT400032484	chr09	yes	NO	
1421	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400012488	PGSC0003DMT400032512	-	yes	NO	
1422	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400012489	PGSC0003DMT400032514	chr09	NO	NO	
1423	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400012514	PGSC0003DMT400032577	chr07	yes	yes	GO:0005515; protein binding; Molecular Function
1424	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400012539	PGSC0003DMT400032641	chr05	yes	NO	GO:0004672; protein kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
1425	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400012540	PGSC0003DMT400032643	chr12	yes	NO	

1426	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400012541	PGSC0003DMT400032646	chr03	yes	NO	GO:0016491; oxidoreductase activity; Molecular Function
1427	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400012543	PGSC0003DMT400032652	chr12	yes	NO	
1428	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400012599	PGSC0003DMT400032806	chr07	NO	NO	
1429	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400012605	PGSC0003DMT400032823	chr09	NO	NO	
1430	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400012634	PGSC0003DMT400032889	chr01	yes	yes	
1431	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400012689	PGSC0003DMT400033049	chr11	yes	NO	
1432	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400012757	PGSC0003DMT400033221	chr05	yes	NO	
1433	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400012762	PGSC0003DMT400033232	chr04	yes	yes	
1434	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400012780	PGSC0003DMT400033273	chr07	yes	yes	GO:0009538; photosystem I reaction center; Cellular Component GO:0015979; photosynthesis; Biological Process
1435	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400012789	PGSC0003DMT400033300	chr11	NO	NO	
1436	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400012793	PGSC0003DMT400033309	chr08	NO	NO	GO:0008060; ARF GTPase activator activity; Molecular Function GO:0008270; zinc ion binding; Molecular Function GO:0032312; regulation of ARF GTPase activity; Biological Process

1437	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400012799	PGSC0003DMT400033322	chr01	NO	NO	
1438	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400012860	PGSC0003DMT400033477	chr10	NO	NO	GO:0003824; catalytic activity; Molecular Function GO:0004794; L-threonine ammonia-lyase activity; Molecular Function GO:0008152; metabolic process; Biological Process GO:0009097; isoleucine biosynthetic process; Biological Process GO:0030170; pyridoxal phosphate binding; Molecular Function
1439	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400012917	PGSC0003DMT400033632	chr01	yes	NO	GO:0004185; serine-type carboxypeptidase activity; Molecular Function GO:0006508; proteolysis; Biological Process
1440	Heterozygous PS in RH, not shared by DM	PGSC0003DMG403012981	PGSC0003DMT400033790	chr07	yes	NO	
1441	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400012993	PGSC0003DMT400033818	chr07	yes	yes	GO:0016491; oxidoreductase activity; Molecular Function GO:0050660; FAD binding; Molecular Function
1442	Heterozygous PS in RH, not shared by DM	PGSC0003DMG402013075	PGSC0003DMT400034013	-	NO	NO	
1443	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400013091	PGSC0003DMT400034063	chr09	yes	yes	GO:0004713; protein tyrosine kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
1444	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400013164	PGSC0003DMT400034241	chr01	NO	NO	
1445	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400013171	PGSC0003DMT400034262	chr11	yes	NO	

1446	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401013193	PGSC0003DMT400034309	chr12	yes	NO	GO:0004888; transmembrane receptor activity; Molecular Function GO:0005515; protein binding; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006915; apoptosis; Biological Process GO:0007165; signal transduction; Biological Process GO:0031224; intrinsic to membrane; Cellular Component GO:0045087; innate immune response; Biological Process
1447	Heterozygous PS in RH, not shared by DM	PGSC0003DMG402013193	PGSC0003DMT400034311	chr10	yes	yes	
1448	Heterozygous PS in RH, not shared by DM	PGSC0003DMG402013284	PGSC0003DMT400034560	chr06	NO	NO	
1449	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400013286	PGSC0003DMT400034564	-	yes	NO	
1450	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400013355	PGSC0003DMT400034759	chr07	yes	yes	GO:0008152; metabolic process; Biological Process GO:0016758; transferase activity, transferring hexosyl groups; Molecular Function
1451	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400013376	PGSC0003DMT400034800	-	yes	NO	
1452	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400013378	PGSC0003DMT400034805	chr10	yes	NO	
1453	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400013424	PGSC0003DMT400034923	chr09	NO	NO	
1454	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400013435	PGSC0003DMT400034955	chr12	NO	NO	

1455	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400013462	PGSC0003DMT400035008	chr12	yes	yes	GO:0008152; metabolic process; Biological Process GO:0016758; transferase activity, transferring hexosyl groups; Molecular Function
1456	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400013490	PGSC0003DMT400035090	chr09	NO	NO	
1457	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400013495	PGSC0003DMT400035099	chr11	NO	NO	
1458	Heterozygous PS in RH, not shared by DM	PGSC0003DMG402013517	PGSC0003DMT400035167	chr04	NO	NO	
1459	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400013520	PGSC0003DMT400035180	chr12	yes	yes	GO:0016740; transferase activity; Molecular Function
1460	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401013522	PGSC0003DMT400035183	chr11	yes	NO	
1461	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400013567	PGSC0003DMT400035311	chr08	yes	NO	
1462	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400013568	PGSC0003DMT400035313	chr10	yes	NO	GO:0019787; small conjugating protein ligase activity; Molecular Function GO:0043687; post-translational protein modification; Biological Process GO:0051246; regulation of protein metabolic process; Biological Process
1463	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400013573	PGSC0003DMT400035325	chr10	yes	NO	
1464	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400013586	PGSC0003DMT400035352	chr10	NO	NO	
1465	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400013608	PGSC0003DMT400035406	chr05	yes	NO	

1466	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400013646	PGSC0003DMT400035502	chr01	NO	NO	
1467	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400013647	PGSC0003DMT400035505	chr12	yes	NO	GO:0004185; serine-type carboxypeptidase activity; Molecular Function GO:0006508; proteolysis; Biological Process
1468	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400013673	PGSC0003DMT400035558	chr04	yes	NO	GO:0005215; transporter activity; Molecular Function GO:0006857; oligopeptide transport; Biological Process GO:0016020; membrane; Cellular Component
1469	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400013693	PGSC0003DMT400035605	chr12	yes	NO	
1470	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400013702	PGSC0003DMT400035624	chr06	yes	NO	
1471	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400013713	PGSC0003DMT400035647	chr04	NO	NO	
1472	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400013726	PGSC0003DMT400035679	chr12	NO	NO	
1473	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401013731	PGSC0003DMT400035699	chr09	NO	NO	
1474	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400013732	PGSC0003DMT400035702	chr06	yes	yes	
1475	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400013816	PGSC0003DMT400035884	chr01	yes	NO	
1476	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400013887	PGSC0003DMT400036055	chr12	NO	NO	

1477	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400013898	PGSC0003DMT400036087	chr10	NO	NO	
1478	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400013904	PGSC0003DMT400036104	chr03	yes	NO	
1479	Heterozygous PS in RH, not shared by DM	PGSC0003DMG402013921	PGSC0003DMT400036154	chr08	yes	NO	GO:0003700; transcription factor activity; Molecular Function GO:0005634; nucleus; Cellular Component GO:0006355; regulation of transcription, DNA-dependent; Biological Process GO:0043565; sequence-specific DNA binding; Molecular Function GO:0046983; protein dimerization activity; Molecular Function
1480	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400013929	PGSC0003DMT400036189	chr04	NO	NO	
1481	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400013933	PGSC0003DMT400036200	chr08	yes	NO	
1482	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400013973	PGSC0003DMT400036326	chr01	yes	NO	GO:0004497; monooxygenase activity; Molecular Function GO:0005506; iron ion binding; Molecular Function GO:0009055; electron carrier activity; Molecular Function GO:0020037; heme binding; Molecular Function
1483	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400014014	PGSC0003DMT400036401	chr02	yes	yes	GO:0005524; ATP binding; Molecular Function GO:0006915; apoptosis; Biological Process
1484	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400014023	PGSC0003DMT400036417	chr04	yes	yes	GO:0008171; O-methyltransferase activity; Molecular Function

1485	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400014094	PGSC0003DMT400036566	chr05	yes	NO	GO:0003700; transcription factor activity; Molecular Function GO:0043565; sequence-specific DNA binding; Molecular Function GO:0045449; regulation of transcription; Biological Process
1486	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401014186	PGSC0003DMT400036786	chr05	yes	NO	
1487	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400014236	PGSC0003DMT400036927	chr06	NO	NO	
1488	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400014258	PGSC0003DMT400036991	chr03	yes	NO	GO:0005634; nucleus; Cellular Component GO:0008270; zinc ion binding; Molecular Function GO:0016568; chromatin modification; Biological Process GO:0018024; histone-lysine N-methyltransferase activity; Molecular Function
1489	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400014286	PGSC0003DMT400037068	chr02	NO	NO	
1490	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400014300	PGSC0003DMT400037101	chr10	NO	NO	
1491	Heterozygous PS in RH, not shared by DM	PGSC0003DMG402014350	PGSC0003DMT400037214	chr05	NO	NO	
1492	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400014509	PGSC0003DMT400037627	chr07	NO	NO	
1493	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400014528	PGSC0003DMT400037667	chr04	NO	NO	
1494	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400014535	PGSC0003DMT400037682	chr06	NO	NO	

1495	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400014711	PGSC0003DMT400038147	chr01	yes	NO	
1496	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400014756	PGSC0003DMT400038242	chr09	NO	NO	
1497	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400014776	PGSC0003DMT400038291	chr02	yes	NO	GO:0015986; ATP synthesis coupled proton transport; Biological Process GO:0015992; proton transport; Biological Process GO:0016469; proton-transporting two-sector ATPase complex; Cellular Component GO:0016820; hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances; Molecular Function GO:0033178; proton-transporting two-sector ATPase complex, catalytic domain; Cellular Component GO:0046034; ATP metabolic process; Biological Process GO:0046933; hydrogen ion transporting ATP synthase activity, rotational mechanism; Molecular Function GO:0046961; proton-transporting ATPase activity, rotational mechanism; Molecular Function
1498	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400014782	PGSC0003DMT400038307	chr11	yes	NO	GO:0016020; membrane; Cellular Component
1499	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401014852	PGSC0003DMT400038482	chr12	yes	yes	
1500	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400014873	PGSC0003DMT400038532	chr06	NO	NO	
1501	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400014962	PGSC0003DMT400038714	chr09	NO	NO	GO:0016491; oxidoreductase activity; Molecular Function

1502	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400015002	PGSC0003DMT400038820	chr12	yes	NO	
1503	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400015004	PGSC0003DMT400038827	-	yes	yes	
1504	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400015053	PGSC0003DMT400038923	chr07	yes	NO	
1505	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400015070	PGSC0003DMT400038948	chr06	NO	NO	
1506	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400015079	PGSC0003DMT400038995	-	NO	NO	
1507	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400015087	PGSC0003DMT400039029	chr04	yes	NO	
1508	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400015094	PGSC0003DMT400039042	chr08	yes	NO	
1509	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400015128	PGSC0003DMT400039125	chr03	yes	NO	
1510	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400015231	PGSC0003DMT400039387	chr03	yes	yes	
1511	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400015281	PGSC0003DMT400039522	chr01	yes	yes	GO:0004497; monooxygenase activity; Molecular Function GO:0005506; iron ion binding; Molecular Function GO:0009055; electron carrier activity; Molecular Function GO:0020037; heme binding; Molecular Function

1512	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400015283	PGSC0003DMT400039527	chr07	yes	NO	GO:0004888; transmembrane receptor activity; Molecular Function GO:0005515; protein binding; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006915; apoptosis; Biological Process GO:0007165; signal transduction; Biological Process GO:0031224; intrinsic to membrane; Cellular Component GO:0045087; innate immune response; Biological Process
1513	Heterozygous PS in RH, not shared by DM	PGSC0003DMG402015329	PGSC0003DMT400039638	-	yes	yes	
1514	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400015468	PGSC0003DMT400039994				
1515	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400015491	PGSC0003DMT400040046	chr11	yes	NO	
1516	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400015503	PGSC0003DMT400040075	chr06	NO	NO	GO:0003993; acid phosphatase activity; Molecular Function
1517	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400015642	PGSC0003DMT400040393	chr08	yes	NO	
1518	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400015653	PGSC0003DMT400040433	chr12	NO	NO	
1519	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400015660	PGSC0003DMT400040449	chr08	yes	NO	GO:0005524; ATP binding; Molecular Function GO:0006915; apoptosis; Biological Process
1520	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400015668	PGSC0003DMT400040462	chr05	NO	NO	
1521	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401015669	PGSC0003DMT400040463	chr06	yes	yes	GO:0005524; ATP binding; Molecular Function

1522	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400015675	PGSC0003DMT400040488	chr08	yes	NO	
1523	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400015705	PGSC0003DMT400040616	chr05	NO	NO	GO:0003700; transcription factor activity; Molecular Function GO:0006355; regulation of transcription, DNA-dependent; Biological Process GO:0043565; sequence-specific DNA binding; Molecular Function
1524	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400015793	PGSC0003DMT400040848	chr03	yes	yes	GO:0003723; RNA binding; Molecular Function
1525	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400015824	PGSC0003DMT400040909	chr03	NO	NO	
1526	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400015831	PGSC0003DMT400040927	chr06	yes	NO	
1527	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400015835	PGSC0003DMT400040940	chr04	yes	yes	
1528	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400015841	PGSC0003DMT400040947	chr06	yes	NO	GO:0003676; nucleic acid binding; Molecular Function GO:0004386; helicase activity; Molecular Function GO:0005524; ATP binding; Molecular Function
1529	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400015852	PGSC0003DMT400040974	chr03	yes	yes	GO:0005515; protein binding; Molecular Function
1530	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400015857	PGSC0003DMT400040993	chr05	yes	yes	GO:0004650; polygalacturonase activity; Molecular Function GO:0005975; carbohydrate metabolic process; Biological Process
1531	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401015867	PGSC0003DMT400041014	chr07	NO	NO	

1532	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400015872	PGSC0003DMT400041023	chr04	yes	NO	
1533	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401015879	PGSC0003DMT400041049	chr03	yes	NO	GO:0004871; signal transducer activity; Molecular Function GO:0009416; response to light stimulus; Biological Process
1534	Heterozygous PS in RH, not shared by DM	PGSC0003DMG402015879	PGSC0003DMT400041052	chr02	yes	NO	
1535	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400015917	PGSC0003DMT400041120	chr01	yes	yes	GO:0003676; nucleic acid binding; Molecular Function GO:0008270; zinc ion binding; Molecular Function
1536	Heterozygous PS in RH, not shared by DM	PGSC0003DMG402015935	PGSC0003DMT400041184	chr11	NO	NO	
1537	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400015955	PGSC0003DMT400041222	chr07	yes	yes	GO:0004672; protein kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0005529; sugar binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process GO:0048544; recognition of pollen; Biological Process
1538	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400015991	PGSC0003DMT400041310	chr02	yes	NO	
1539	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400016008	PGSC0003DMT400041333	chr01	NO	NO	
1540	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400016015	PGSC0003DMT400041350	chr04	yes	yes	
1541	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400016031	PGSC0003DMT400041379	chr04	yes	yes	

1542	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400016035	PGSC0003DMT400041383	chr10	yes	NO	GO:0008152; metabolic process; Biological Process GO:0016787; hydrolase activity; Molecular Function
1543	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401016070	PGSC0003DMT400041460	chr07	NO	NO	
1544	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400016123	PGSC0003DMT400041595	chr03	yes	NO	
1545	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400016125	PGSC0003DMT400041600	chr05	yes	NO	GO:0003700; transcription factor activity; Molecular Function GO:0043565; sequence-specific DNA binding; Molecular Function GO:0045449; regulation of transcription; Biological Process
1546	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400016132	PGSC0003DMT400041615	chr11	yes	NO	GO:0000151; ubiquitin ligase complex; Cellular Component GO:0004842; ubiquitin-protein ligase activity; Molecular Function GO:0016567; protein ubiquitination; Biological Process
1547	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401016141	PGSC0003DMT400041634	chr06	yes	NO	
1548	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400016156	PGSC0003DMT400041670	chr04	yes	yes	
1549	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400016207	PGSC0003DMT400041783	chr12	yes	NO	GO:0003700; transcription factor activity; Molecular Function GO:0006355; regulation of transcription, DNA-dependent; Biological Process GO:0008270; zinc ion binding; Molecular Function GO:0043565; sequence-specific DNA binding; Molecular Function
1550	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400016263	PGSC0003DMT400041926	chr01	NO	NO	GO:0005515; protein binding; Molecular Function

1551	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400016276	PGSC0003DMT400041960				
1552	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400016287	PGSC0003DMT400041989	chr01	NO	NO	
1553	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400016352	PGSC0003DMT400042153	chr03	NO	NO	
1554	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400016392	PGSC0003DMT400042232	chr11	yes	yes	
1555	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401016399	PGSC0003DMT400042251	chr03	yes	NO	GO:0006457; protein folding; Biological Process GO:0031072; heat shock protein binding; Molecular Function GO:0051082; unfolded protein binding; Molecular Function
1556	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400016410	PGSC0003DMT400042324	chr02	yes	NO	
1557	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400016418	PGSC0003DMT400042347	chr02	NO	NO	GO:0016747; transferase activity, transferring acyl groups other than amino-acyl groups; Molecular Function
1558	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400016447	PGSC0003DMT400042415	-	yes	NO	
1559	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400016462	PGSC0003DMT400042454	chr05	yes	yes	GO:0004857; enzyme inhibitor activity; Molecular Function GO:0005618; cell wall; Cellular Component GO:0030599; pectinesterase activity; Molecular Function GO:0042545; cell wall modification; Biological Process
1560	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400016494	PGSC0003DMT400042523	chr12	NO	NO	
1561	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400016497	PGSC0003DMT400042531	chr08	yes	NO	

1562	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400016580	PGSC0003DMT400042719	chr10	NO	NO	
1563	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400016581	PGSC0003DMT400042721	-	yes	yes	
1564	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400016616	PGSC0003DMT400042825	chr09	yes	NO	
1565	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401016617	PGSC0003DMT400042826	chr01	yes	NO	
1566	Heterozygous PS in RH, not shared by DM	PGSC0003DMG402016626	PGSC0003DMT400042871	chr04	yes	NO	GO:0004867; serine-type endopeptidase inhibitor activity; Molecular Function
1567	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400016635	PGSC0003DMT400042903	-	NO	NO	
1568	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400016644	PGSC0003DMT400042928	-	yes	NO	
1569	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400016653	PGSC0003DMT400042949	chr01	yes	NO	GO:0003824; catalytic activity; Molecular Function GO:0008152; metabolic process; Biological Process
1570	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400016741	PGSC0003DMT400043143	chr07	NO	NO	
1571	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400016742	PGSC0003DMT400043146	chr05	yes	yes	GO:0004970; ionotropic glutamate receptor activity; Molecular Function GO:0005234; extracellular-glutamate-gated ion channel activity; Molecular Function GO:0016020; membrane; Cellular Component
1572	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400016751	PGSC0003DMT400043168				

1573	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400016754	PGSC0003DMT400043177	chr11	NO	NO	
1574	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400016808	PGSC0003DMT400043301	-	NO	NO	
1575	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400016822	PGSC0003DMT400043326	chr10	yes	NO	GO:0004765; shikimate kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function
1576	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400016830	PGSC0003DMT400043345	chr05	yes	NO	GO:0004252; serine-type endopeptidase activity; Molecular Function GO:0006508; proteolysis; Biological Process GO:0042802; identical protein binding; Molecular Function GO:0043086; negative regulation of catalytic activity; Biological Process
1577	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400016861	PGSC0003DMT400043434	chr11	NO	NO	
1578	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400016886	PGSC0003DMT400043490	chr10	yes	NO	GO:0003747; translation release factor activity; Molecular Function GO:0005737; cytoplasm; Cellular Component GO:0006415; translational termination; Biological Process GO:0016149; translation release factor activity, codon specific; Molecular Function
1579	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400016900	PGSC0003DMT400043528	chr05	yes	NO	GO:0005215; transporter activity; Molecular Function GO:0006857; oligopeptide transport; Biological Process GO:0016020; membrane; Cellular Component
1580	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401016926	PGSC0003DMT400043585	-	yes	NO	
1581	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400016931	PGSC0003DMT400043601	chr12	yes	NO	

1582	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400016968	PGSC0003DMT400043689	chr01	yes	NO	
1583	Heterozygous PS in RH, not shared by DM	PGSC0003DMG402016979	PGSC0003DMT400043719	chr04	yes	NO	GO:0008152; metabolic process; Biological Process GO:0016758; transferase activity, transferring hexosyl groups; Molecular Function
1584	Heterozygous PS in RH, not shared by DM	PGSC0003DMG403016979	PGSC0003DMT400043725	-	NO	NO	
1585	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401016981	PGSC0003DMT400043731	chr06	NO	NO	
1586	Heterozygous PS in RH, not shared by DM	PGSC0003DMG403016981	PGSC0003DMT400043733	chr07	yes	NO	GO:0004672; protein kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
1587	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400016983	PGSC0003DMT400043751	chr02	NO	NO	
1588	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400017017	PGSC0003DMT400043844	chr09	yes	NO	GO:0004713; protein tyrosine kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
1589	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400017033	PGSC0003DMT400043891	chr07	yes	NO	GO:0004672; protein kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
1590	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401017076	PGSC0003DMT400043995	chr06	yes	NO	

1591	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401017077	PGSC0003DMT400044015	chr05	yes	NO	GO:0004672; protein kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
1592	Heterozygous PS in RH, not shared by DM	PGSC0003DMG402017077	PGSC0003DMT400044014	chr01	NO	NO	GO:0000151; ubiquitin ligase complex; Cellular Component GO:0004842; ubiquitin-protein ligase activity; Molecular Function GO:0016567; protein ubiquitination; Biological Process
1593	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400017111	PGSC0003DMT400044099	chr02	NO	NO	
1594	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400017124	PGSC0003DMT400044122	chr04	yes	NO	
1595	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400017136	PGSC0003DMT400044145	chr11	yes	NO	GO:0005515; protein binding; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006915; apoptosis; Biological Process
1596	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400017235	PGSC0003DMT400044390	chr03	NO	NO	
1597	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400017243	PGSC0003DMT400044425	chr10	NO	NO	
1598	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400017247	PGSC0003DMT400044441	chr04	yes	yes	
1599	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400017300	PGSC0003DMT400044564	chr12	yes	NO	GO:0004672; protein kinase activity; Molecular Function GO:0005515; protein binding; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process

1600	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400017315	PGSC0003DMT400044608	chr02	yes	NO	GO:0005789; endoplasmic reticulum membrane; Cellular Component GO:0006506; GPI anchor biosynthetic process; Biological Process GO:0016740; transferase activity; Molecular Function
1601	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400017317	PGSC0003DMT400044611	chr11	yes	NO	GO:0003824; catalytic activity; Molecular Function GO:0009451; RNA modification; Biological Process GO:0051536; iron-sulfur cluster binding; Molecular Function GO:0051539; 4 iron, 4 sulfur cluster binding; Molecular Function
1602	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400017318	PGSC0003DMT400044620	-	yes	NO	
1603	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400017321	PGSC0003DMT400044650	chr02	NO	NO	
1604	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400017322	PGSC0003DMT400044652	chr06	NO	NO	
1605	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400017327	PGSC0003DMT400044668	chr07	yes	NO	GO:0005515; protein binding; Molecular Function GO:0005789; endoplasmic reticulum membrane; Cellular Component GO:0006467; protein thiol-disulfide exchange; Biological Process GO:0009055; electron carrier activity; Molecular Function GO:0016671; oxidoreductase activity, acting on sulfur group of donors, disulfide as acceptor; Molecular Function GO:0050660; FAD binding; Molecular Function GO:0055114; oxidation reduction; Biological Process
1606	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400017358	PGSC0003DMT400044735	chr09	yes	NO	

1607	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400017432	PGSC0003DMT400044938	chr10	NO	NO	
1608	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400017444	PGSC0003DMT400044981	chr12	yes	NO	GO:0004888; transmembrane receptor activity; Molecular Function GO:0007165; signal transduction; Biological Process GO:0031224; intrinsic to membrane; Cellular Component GO:0045087; innate immune response; Biological Process
1609	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400017456	PGSC0003DMT400045009	chr09	yes	NO	
1610	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401017464	PGSC0003DMT400045039	-	yes	NO	
1611	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400017466	PGSC0003DMT400045052	chr07	yes	NO	
1612	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400017527	PGSC0003DMT400045189	chr12	yes	NO	GO:0005524; ATP binding; Molecular Function GO:0005975; carbohydrate metabolic process; Biological Process GO:0016773; phosphotransferase activity, alcohol group as acceptor; Molecular Function
1613	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400017569	PGSC0003DMT400045299	chr02	yes	NO	GO:0004713; protein tyrosine kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0005529; sugar binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process GO:0048544; recognition of pollen; Biological Process

1614	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400017592	PGSC0003DMT400045336	chr01	yes	yes	GO:0004252; serine-type endopeptidase activity; Molecular Function GO:0006508; proteolysis; Biological Process GO:0042802; identical protein binding; Molecular Function GO:0043086; negative regulation of catalytic activity; Biological Process
1615	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400017600	PGSC0003DMT400045355	chr02	yes	NO	
1616	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400017620	PGSC0003DMT400045412	chr04	yes	NO	GO:0004672; protein kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
1617	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400017667	PGSC0003DMT400045556	chr10	yes	yes	
1618	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400017680	PGSC0003DMT400045580	chr06	NO	NO	
1619	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400017681	PGSC0003DMT400045587	chr03	NO	NO	
1620	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400017687	PGSC0003DMT400045600	chr08	yes	NO	
1621	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400017697	PGSC0003DMT400045630	chr04	NO	NO	
1622	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400017707	PGSC0003DMT400045647	chr06	NO	NO	GO:0005375; copper ion transmembrane transporter activity; Molecular Function GO:0006825; copper ion transport; Biological Process GO:0016021; integral to membrane; Cellular Component
1623	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400017734	PGSC0003DMT400045733	chr02	NO	NO	

1624	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400017739	PGSC0003DMT400045745	chr12	NO	NO	
1625	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400017749	PGSC0003DMT400045769	chr09	NO	NO	
1626	Heterozygous PS in RH, not shared by DM	PGSC0003DMG402017754	PGSC0003DMT400045787	chr08	NO	NO	
1627	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400017777	PGSC0003DMT400045835	chr10	yes	NO	
1628	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400017792	PGSC0003DMT400045865	chr01	yes	NO	
1629	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400017844	PGSC0003DMT400045993	chr10	yes	NO	GO:0005524; ATP binding; Molecular Function GO:0006810; transport; Biological Process GO:0016021; integral to membrane; Cellular Component GO:0016887; ATPase activity; Molecular Function GO:0042626; ATPase activity, coupled to transmembrane movement of substances; Molecular Function GO:0055085; transmembrane transport; Biological Process
1630	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400017845	PGSC0003DMT400045998	chr02	yes	yes	GO:0003824; catalytic activity; Molecular Function GO:0044237; cellular metabolic process; Biological Process GO:0050662; coenzyme binding; Molecular Function
1631	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400017850	PGSC0003DMT400046008	chr10	NO	NO	GO:0003676; nucleic acid binding; Molecular Function GO:0004523; ribonuclease H activity; Molecular Function
1632	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400017926	PGSC0003DMT400046189	chr01	yes	yes	

1633	Heterozygous PS in RH, not shared by DM	PGSC0003DMG402017944	PGSC0003DMT400046228	chr07	NO	NO	GO:0016021; integral to membrane; Cellular Component
1634	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400017946	PGSC0003DMT400046233	chr03	yes	yes	GO:0005634; nucleus; Cellular Component GO:0045449; regulation of transcription; Biological Process
1635	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400017971	PGSC0003DMT400046298	chr09	yes	NO	
1636	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400017992	PGSC0003DMT400046356	chr08	yes	NO	
1637	Heterozygous PS in RH, not shared by DM	PGSC0003DMG402018005	PGSC0003DMT400046387	chr02	yes	NO	
1638	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401018040	PGSC0003DMT400046470	chr06	NO	NO	
1639	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400018050	PGSC0003DMT400046505	chr08	NO	NO	
1640	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400018055	PGSC0003DMT400046517	-	yes	NO	
1641	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400018061	PGSC0003DMT400046529	chr08	yes	NO	
1642	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400018132	PGSC0003DMT400046701	chr12	NO	NO	GO:0003824; catalytic activity; Molecular Function GO:0008152; metabolic process; Biological Process
1643	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400018197	PGSC0003DMT400046857	chr08	NO	NO	
1644	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400018236	PGSC0003DMT400046953	chr06	yes	yes	

1645	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400018253	PGSC0003DMT400046993	chr10	yes	yes	
1646	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400018256	PGSC0003DMT400047001	chr11	yes	yes	GO:0008270; zinc ion binding; Molecular Function GO:0016491; oxidoreductase activity; Molecular Function GO:0055114; oxidation reduction; Biological Process
1647	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400018261	PGSC0003DMT400047018	chr09	yes	yes	GO:0005215; transporter activity; Molecular Function GO:0006810; transport; Biological Process GO:0016020; membrane; Cellular Component
1648	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400018269	PGSC0003DMT400047047	chr08	NO	NO	GO:0008060; ARF GTPase activator activity; Molecular Function GO:0008270; zinc ion binding; Molecular Function GO:0032312; regulation of ARF GTPase activity; Biological Process
1649	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400018281	PGSC0003DMT400047082	chr10	yes	yes	
1650	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400018337	PGSC0003DMT400047231	chr04	yes	NO	
1651	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400018367	PGSC0003DMT400047295	chr01	yes	NO	GO:0016884; carbon-nitrogen ligase activity, with glutamine as amido-N-donor; Molecular Function
1652	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400018473	PGSC0003DMT400047533	chr12	NO	NO	
1653	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400018477	PGSC0003DMT400047541	chr05	yes	NO	GO:0005524; ATP binding; Molecular Function GO:0006915; apoptosis; Biological Process
1654	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400018491	PGSC0003DMT400047580	chr06	yes	NO	GO:0016491; oxidoreductase activity; Molecular Function

1655	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400018513	PGSC0003DMT400047633	-	NO	NO	
1656	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400018527	PGSC0003DMT400047665	chr09	yes	NO	
1657	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400018550	PGSC0003DMT400047726	chr03	yes	NO	GO:0004553; hydrolase activity, hydrolyzing O-glycosyl compounds; Molecular Function GO:0005529; sugar binding; Molecular Function GO:0005975; carbohydrate metabolic process; Biological Process
1658	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400018598	PGSC0003DMT400047847	-	NO	NO	GO:0004672; protein kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
1659	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401018599	PGSC0003DMT400047855	chr05	yes	NO	
1660	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400018612	PGSC0003DMT400047882	chr04	yes	NO	
1661	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400018619	PGSC0003DMT400047907	chr04	yes	yes	GO:0003824; catalytic activity; Molecular Function GO:0006464; protein modification process; Biological Process
1662	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400018629	PGSC0003DMT400047926	-	yes	NO	GO:0004497; monooxygenase activity; Molecular Function GO:0005506; iron ion binding; Molecular Function GO:0009055; electron carrier activity; Molecular Function GO:0020037; heme binding; Molecular Function
1663	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401018705	PGSC0003DMT400048139	chr12	NO	NO	

1664	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400018727	PGSC0003DMT400048208	chr12	yes	NO	
1665	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400018731	PGSC0003DMT400048219	chr10	NO	NO	
1666	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400018733	PGSC0003DMT400048223	chr08	yes	NO	GO:0003913; DNA photolyase activity; Molecular Function GO:0006281; DNA repair; Biological Process
1667	Heterozygous PS in RH, not shared by DM	PGSC0003DMG402018748	PGSC0003DMT400048258	chr09	yes	yes	
1668	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400018756	PGSC0003DMT400048275	chr08	yes	NO	
1669	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400018779	PGSC0003DMT400048331	-	NO	NO	
1670	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400018780	PGSC0003DMT400048335	chr02	NO	NO	
1671	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400018866	PGSC0003DMT400048565	chr12	NO	NO	
1672	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400018888	PGSC0003DMT400048615	chr02	NO	NO	
1673	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400019019	PGSC0003DMT400048945	chr04	NO	NO	
1674	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400019084	PGSC0003DMT400049098	chr12	NO	NO	

1675	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400019141	PGSC0003DMT400049234	chr08	NO	NO	GO:0004497; monooxygenase activity; Molecular Function GO:0005506; iron ion binding; Molecular Function GO:0009055; electron carrier activity; Molecular Function GO:0020037; heme binding; Molecular Function
1676	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400019145	PGSC0003DMT400049243	chr11	NO	NO	
1677	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400019146	PGSC0003DMT400049246	-	yes	NO	GO:0016021; integral to membrane; Cellular Component
1678	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400019158	PGSC0003DMT400049292	chr07	yes	yes	
1679	Heterozygous PS in RH, not shared by DM	PGSC0003DMG402019176	PGSC0003DMT400049361	chr10	yes	NO	
1680	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400019210	PGSC0003DMT400049445	chr03	NO	NO	
1681	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400019221	PGSC0003DMT400049465	chr01	yes	yes	GO:0005515; protein binding; Molecular Function
1682	Heterozygous PS in RH, not shared by DM	PGSC0003DMG402019226	PGSC0003DMT400049482	chr09	NO	NO	
1683	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400019234	PGSC0003DMT400049496	chr09	NO	NO	GO:0008219; cell death; Biological Process GO:0016021; integral to membrane; Cellular Component
1684	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400019237	PGSC0003DMT400049507	chr04	NO	NO	
1685	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400019312	PGSC0003DMT400049701	chr11	NO	NO	

1686	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400019367	PGSC0003DMT400049845	chr09	yes	NO	GO:0004497; monooxygenase activity; Molecular Function GO:0005506; iron ion binding; Molecular Function GO:0009055; electron carrier activity; Molecular Function GO:0020037; heme binding; Molecular Function
1687	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400019372	PGSC0003DMT400049859	chr10	yes	NO	
1688	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400019373	PGSC0003DMT400049861	chr04	yes	yes	
1689	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400019381	PGSC0003DMT400049877	chr09	NO	NO	
1690	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400019544	PGSC0003DMT400050302	chr12	yes	NO	GO:0005515; protein binding; Molecular Function
1691	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400019553	PGSC0003DMT400050321	chr06	NO	NO	
1692	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400019580	PGSC0003DMT400050373	-	NO	NO	
1693	Heterozygous PS in RH, not shared by DM	PGSC0003DMG402019589	PGSC0003DMT400050399	chr10	NO	NO	GO:0003676; nucleic acid binding; Molecular Function GO:0003723; RNA binding; Molecular Function
1694	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401019602	PGSC0003DMT400050432	chr03	NO	NO	GO:0005524; ATP binding; Molecular Function
1695	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401019640	PGSC0003DMT400050540	chr03	yes	NO	
1696	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400019644	PGSC0003DMT400050551	chr10	NO	NO	

1697	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400019657	PGSC0003DMT400050580	chr11	NO	NO	
1698	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401019682	PGSC0003DMT400050678	chr04	NO	NO	GO:0003700; transcription factor activity; Molecular Function GO:0043565; sequence-specific DNA binding; Molecular Function GO:0045449; regulation of transcription; Biological Process
1699	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400019711	PGSC0003DMT400050750	-	yes	yes	
1700	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401019736	PGSC0003DMT400050813	chr09	yes	NO	GO:0000287; magnesium ion binding; Molecular Function GO:0008152; metabolic process; Biological Process GO:0016829; lyase activity; Molecular Function
1701	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400019844	PGSC0003DMT400051098	chr04	NO	NO	
1702	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400019912	PGSC0003DMT400051268	-	NO	NO	
1703	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400019997	PGSC0003DMT400051479	chr03	NO	NO	
1704	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400020023	PGSC0003DMT400051546	-	NO	NO	
1705	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400020050	PGSC0003DMT400051632	chr12	NO	NO	

1706	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400020074	PGSC0003DMT400051692	chr03	NO	NO	GO:0005215; transporter activity; Molecular Function GO:0006810; transport; Biological Process GO:0016021; integral to membrane; Cellular Component GO:0055085; transmembrane transport; Biological Process
1707	Heterozygous PS in RH, not shared by DM	PGSC0003DMG402020085	PGSC0003DMT400051740	chr03	NO	NO	
1708	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401020115	PGSC0003DMT400051829	chr04	yes	yes	
1709	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400020220	PGSC0003DMT400052092	chr04	yes	NO	GO:0004672; protein kinase activity; Molecular Function GO:0005515; protein binding; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
1710	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401020221	PGSC0003DMT400052097	chr12	NO	NO	
1711	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401020229	PGSC0003DMT400052119	chr04	yes	NO	GO:0005515; protein binding; Molecular Function
1712	Heterozygous PS in RH, not shared by DM	PGSC0003DMG403020229	PGSC0003DMT400052131	chr10	NO	NO	
1713	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400020359	PGSC0003DMT400052453	chr08	yes	yes	GO:0008152; metabolic process; Biological Process GO:0008415; acyltransferase activity; Molecular Function
1714	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400020360	PGSC0003DMT400052458	chr02	yes	NO	
1715	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400020365	PGSC0003DMT400052472	chr03	yes	yes	GO:0046907; intracellular transport; Biological Process

1716	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400020372	PGSC0003DMT400052492	chr01	NO	NO	
1717	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400020391	PGSC0003DMT400052553	chr01	yes	NO	GO:0004672; protein kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
1718	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400020418	PGSC0003DMT400052600	-	yes	NO	
1719	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400020424	PGSC0003DMT400052613	chr08	yes	NO	GO:0008152; metabolic process; Biological Process GO:0016491; oxidoreductase activity; Molecular Function
1720	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400020426	PGSC0003DMT400052621	chr04	NO	NO	
1721	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400020428	PGSC0003DMT400052626	chr06	NO	NO	GO:0005778; peroxisomal membrane; Cellular Component GO:0007031; peroxisome organization; Biological Process
1722	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400020435	PGSC0003DMT400052645	chr01	NO	NO	
1723	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401020444	PGSC0003DMT400052663	-	yes	yes	
1724	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400020467	PGSC0003DMT400052739	chr06	yes	NO	GO:0006629; lipid metabolic process; Biological Process GO:0016788; hydrolase activity, acting on ester bonds; Molecular Function
1725	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400020578	PGSC0003DMT400053021	chr04	yes	NO	GO:0004807; triose-phosphate isomerase activity; Molecular Function GO:0008152; metabolic process; Biological Process

1726	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401020596	PGSC0003DMT400053095	chr03	yes	NO	GO:0005634; nucleus; Cellular Component GO:0008270; zinc ion binding; Molecular Function GO:0030528; transcription regulator activity; Molecular Function GO:0045449; regulation of transcription; Biological Process
1727	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400020646	PGSC0003DMT400053192	chr05	NO	NO	
1728	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400020671	PGSC0003DMT400053258	chr04	NO	NO	
1729	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400020680	PGSC0003DMT400053285	-	NO	NO	
1730	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400020690	PGSC0003DMT400053311	chr05	yes	NO	GO:0005524; ATP binding; Molecular Function GO:0006915; apoptosis; Biological Process
1731	Heterozygous PS in RH, not shared by DM	PGSC0003DMG402020702	PGSC0003DMT400053351	chr04	yes	NO	GO:0005515; protein binding; Molecular Function
1732	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400020759	PGSC0003DMT400053517	chr12	NO	NO	
1733	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400020791	PGSC0003DMT400053593	chr06	yes	NO	
1734	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400020851	PGSC0003DMT400053754	chr10	NO	NO	
1735	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400020880	PGSC0003DMT400053830	chr11	NO	NO	
1736	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400020917	PGSC0003DMT400053916	chr03	yes	NO	

1737	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400020925	PGSC0003DMT400053934	chr08	NO	NO	GO:0003676; nucleic acid binding; Molecular Function
1738	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400020956	PGSC0003DMT400054011	chr04	NO	NO	GO:0006508; proteolysis; Biological Process GO:0008234; cysteine-type peptidase activity; Molecular Function
1739	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400020968	PGSC0003DMT400054066	chr01	yes	yes	GO:0003676; nucleic acid binding; Molecular Function
1740	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400020989	PGSC0003DMT400054119	-	NO	NO	
1741	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401021049	PGSC0003DMT400054259	chr04	NO	NO	
1742	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400021072	PGSC0003DMT400054304	-	yes	NO	GO:0008415; acyltransferase activity; Molecular Function GO:0009058; biosynthetic process; Biological Process
1743	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400021074	PGSC0003DMT400054308	chr06	yes	NO	
1744	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400021087	PGSC0003DMT400054334	chr10	yes	NO	GO:0004175; endopeptidase activity; Molecular Function GO:0004298; threonine-type endopeptidase activity; Molecular Function GO:0005839; proteasome core complex; Cellular Component GO:0006511; ubiquitin-dependent protein catabolic process; Biological Process GO:0051603; proteolysis involved in cellular protein catabolic process; Biological Process
1745	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400021118	PGSC0003DMT400054405	chr01	yes	NO	GO:0004497; monooxygenase activity; Molecular Function GO:0005506; iron ion binding; Molecular Function GO:0009055; electron carrier activity; Molecular Function GO:0020037; heme binding; Molecular Function

1746	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400021144	PGSC0003DMT400054480	chr04	NO	NO	
1747	Heterozygous PS in RH, not shared by DM	PGSC0003DMG402021183	PGSC0003DMT400054593	chr07	yes	NO	
1748	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400021194	PGSC0003DMT400054613	chr12	NO	NO	
1749	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400021203	PGSC0003DMT400054636	chr12	NO	NO	GO:0042256; mature ribosome assembly; Biological Process GO:0043022; ribosome binding; Molecular Function
1750	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400021212	PGSC0003DMT400054667	chr09	NO	NO	
1751	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400021241	PGSC0003DMT400054712	chr06	yes	NO	GO:0005634; nucleus; Cellular Component
1752	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400021262	PGSC0003DMT400054786	-	yes	NO	GO:0004672; protein kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
1753	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400021339	PGSC0003DMT400054985	chr02	yes	NO	
1754	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400021355	PGSC0003DMT400055044	chr12	yes	NO	
1755	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400021405	PGSC0003DMT400055155	chr02	NO	NO	
1756	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400021472	PGSC0003DMT400055319	chr09	NO	NO	

1757	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401021491	PGSC0003DMT400055353	chr02	yes	yes	GO:0008270; zinc ion binding; Molecular Function
1758	Heterozygous PS in RH, not shared by DM	PGSC0003DMG402021491	PGSC0003DMT400055358	chr06	yes	yes	
1759	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400021502	PGSC0003DMT400055381	chr12	NO	NO	GO:0008152; metabolic process; Biological Process GO:0016758; transferase activity, transferring hexosyl groups; Molecular Function
1760	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400021637	PGSC0003DMT400055726	chr06	yes	NO	
1761	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400021644	PGSC0003DMT400055739	chr09	yes	NO	
1762	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400021733	PGSC0003DMT400055953	chr12	NO	NO	
1763	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400021743	PGSC0003DMT400055971	-	NO	NO	
1764	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400021779	PGSC0003DMT400056053	chr12	NO	NO	
1765	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400021800	PGSC0003DMT400056118	chr11	yes	NO	
1766	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400021827	PGSC0003DMT400056178	chr12	yes	yes	GO:0006470; protein amino acid dephosphorylation; Biological Process GO:0008138; protein tyrosine/serine/threonine phosphatase activity; Molecular Function

1767	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400021848	PGSC0003DMT400056235	chr03	yes	yes	GO:0004871; signal transducer activity; Molecular Function GO:0007186; G-protein coupled receptor protein signaling pathway; Biological Process GO:0019001; guanyl nucleotide binding; Molecular Function
1768	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400021861	PGSC0003DMT400056265	chr01	NO	NO	
1769	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401021870	PGSC0003DMT400056290	chr05	yes	yes	GO:0005215; transporter activity; Molecular Function GO:0006857; oligopeptide transport; Biological Process GO:0016020; membrane; Cellular Component
1770	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400021878	PGSC0003DMT400056317	chr11	yes	NO	
1771	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400021952	PGSC0003DMT400056494	-	yes	NO	
1772	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400021985	PGSC0003DMT400056551	-	yes	NO	GO:0005985; sucrose metabolic process; Biological Process
1773	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400022004	PGSC0003DMT400056602	chr06	yes	NO	GO:0003993; acid phosphatase activity; Molecular Function
1774	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400022096	PGSC0003DMT400056814	chr11	yes	NO	GO:0019904; protein domain specific binding; Molecular Function
1775	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400022113	PGSC0003DMT400056847	chr09	NO	NO	
1776	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400022185	PGSC0003DMT400057108	chr12	yes	yes	
1777	Heterozygous PS in RH, not shared by DM	PGSC0003DMG402022215	PGSC0003DMT400057191	chr09	yes	yes	

1778	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400022223	PGSC0003DMT400057210	chr10	yes	yes	
1779	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400022417	PGSC0003DMT400057740	chr10	NO	NO	
1780	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400022422	PGSC0003DMT400057758	-	yes	NO	GO:0055085; transmembrane transport; Biological Process
1781	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400022438	PGSC0003DMT400057795	chr07	yes	NO	
1782	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400022453	PGSC0003DMT400057824	-	NO	NO	
1783	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400022512	PGSC0003DMT400057990	chr07	NO	NO	
1784	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400022532	PGSC0003DMT400058039	chr06	NO	NO	
1785	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400022592	PGSC0003DMT400058190	chr08	NO	NO	
1786	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400022699	PGSC0003DMT400058450	chr07	yes	yes	GO:0004672; protein kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
1787	Heterozygous PS in RH, not shared by DM	PGSC0003DMG402022702	PGSC0003DMT400058458	chr08	NO	NO	
1788	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400022703	PGSC0003DMT400058461	chr06	yes	yes	
1789	Heterozygous PS in RH, not shared by DM	PGSC0003DMG402022708	PGSC0003DMT400058473	chr03	NO	NO	

1790	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400022712	PGSC0003DMT400058484	chr04	NO	NO	
1791	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400022740	PGSC0003DMT400058538	chr08	yes	NO	GO:0003824; catalytic activity; Molecular Function GO:0008152; metabolic process; Biological Process GO:0030170; pyridoxal phosphate binding; Molecular Function
1792	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400022753	PGSC0003DMT400058574	chr07	yes	NO	
1793	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400022865	PGSC0003DMT400058851				
1794	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400022956	PGSC0003DMT400059103	chr07	yes	yes	
1795	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400022977	PGSC0003DMT400059155	chr04	NO	NO	
1796	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400023022	PGSC0003DMT400059259	-	yes	NO	
1797	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400023040	PGSC0003DMT400059297	chr08	yes	NO	
1798	Heterozygous PS in RH, not shared by DM	PGSC0003DMG402023109	PGSC0003DMT400059483	chr12	NO	NO	
1799	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400023203	PGSC0003DMT400059686	chr09	yes	NO	GO:0005524; ATP binding; Molecular Function GO:0006915; apoptosis; Biological Process
1800	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400023213	PGSC0003DMT400059708	chr12	NO	NO	

1801	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400023349	PGSC0003DMT400060008	chr06	yes	NO	GO:0004185; serine-type carboxypeptidase activity; Molecular Function GO:0006508; proteolysis; Biological Process
1802	Heterozygous PS in RH, not shared by DM	PGSC0003DMG402023369	PGSC0003DMT400060080	chr11	NO	NO	
1803	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400023377	PGSC0003DMT400060099	chr12	yes	NO	
1804	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400023537	PGSC0003DMT400060513	chr04	NO	NO	
1805	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400023577	PGSC0003DMT400060615	chr11	yes	yes	GO:0004672; protein kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
1806	Heterozygous PS in RH, not shared by DM	PGSC0003DMG402023595	PGSC0003DMT400060663	chr04	yes	NO	
1807	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400023629	PGSC0003DMT400060748	chr03	yes	NO	GO:0045454; cell redox homeostasis; Biological Process
1808	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400023641	PGSC0003DMT400060788				
1809	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400023681	PGSC0003DMT400060876	chr12	yes	NO	
1810	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400023682	PGSC0003DMT400060882	chr06	yes	NO	GO:0005524; ATP binding; Molecular Function GO:0006915; apoptosis; Biological Process
1811	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400023702	PGSC0003DMT400060938	chr09	NO	NO	

1812	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400023800	PGSC0003DMT400061161	chr06	yes	NO	
1813	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400023819	PGSC0003DMT400061190	-	NO	NO	
1814	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401023866	PGSC0003DMT400061316	chr07	yes	yes	
1815	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400023914	PGSC0003DMT400061444	chr04	yes	NO	
1816	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401023991	PGSC0003DMT400061630	chr04	yes	yes	
1817	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400024021	PGSC0003DMT400061719	chr12	NO	NO	
1818	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400024030	PGSC0003DMT400061738	chr05	yes	yes	
1819	Heterozygous PS in RH, not shared by DM	PGSC0003DMG402024077	PGSC0003DMT400061881	chr10	yes	yes	GO:0003735; structural constituent of ribosome; Molecular Function GO:0005622; intracellular; Cellular Component GO:0005840; ribosome; Cellular Component GO:0006412; translation; Biological Process
1820	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400024080	PGSC0003DMT400061888	chr04	NO	NO	
1821	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401024096	PGSC0003DMT400061916	chr12	yes	NO	GO:0003824; catalytic activity; Molecular Function GO:0008152; metabolic process; Biological Process
1822	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400024125	PGSC0003DMT400061991	chr04	yes	NO	

1823	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400024127	PGSC0003DMT400061998	chr10	yes	NO	
1824	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400024207	PGSC0003DMT400062197	chr12	NO	NO	
1825	Heterozygous PS in RH, not shared by DM	PGSC0003DMG402024222	PGSC0003DMT400062256	chr11	NO	NO	
1826	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400024279	PGSC0003DMT400062383	chr05	yes	NO	
1827	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400024295	PGSC0003DMT400062427	chr01	yes	NO	GO:0005737; cytoplasm; Cellular Component GO:0005975; carbohydrate metabolic process; Biological Process GO:0016614; oxidoreductase activity, acting on CH-OH group of donors; Molecular Function GO:0016616; oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor; Molecular Function GO:0046168; glycerol-3-phosphate catabolic process; Biological Process GO:0051287; NAD or NADH binding; Molecular Function GO:0055114; oxidation reduction; Biological Process
1828	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400024353	PGSC0003DMT400062588	chr08	yes	NO	GO:0003824; catalytic activity; Molecular Function GO:0044237; cellular metabolic process; Biological Process GO:0050662; coenzyme binding; Molecular Function
1829	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400024385	PGSC0003DMT400062659	chr11	NO	NO	

1830	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400024438	PGSC0003DMT400062785	chr09	yes	NO	GO:0004478; methionine adenosyltransferase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006730; one-carbon metabolic process; Biological Process
1831	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400024453	PGSC0003DMT400062819	chr11	NO	NO	
1832	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400024457	PGSC0003DMT400062828	chr09	NO	NO	
1833	Heterozygous PS in RH, not shared by DM	PGSC0003DMG402024473	PGSC0003DMT400062874	chr05	NO	NO	GO:0008146; sulfotransferase activity; Molecular Function
1834	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400024474	PGSC0003DMT400062877	chr11	NO	NO	
1835	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400024518	PGSC0003DMT400063011	chr07	yes	yes	
1836	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400024609	PGSC0003DMT400063273	chr10	yes	NO	GO:0006508; proteolysis; Biological Process GO:0008234; cysteine-type peptidase activity; Molecular Function
1837	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400024657	PGSC0003DMT400063388	chr04	yes	NO	
1838	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400024690	PGSC0003DMT400063452	chr05	NO	NO	
1839	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400024713	PGSC0003DMT400063561	chr01	yes	NO	GO:0004553; hydrolase activity, hydrolyzing O-glycosyl compounds; Molecular Function GO:0005975; carbohydrate metabolic process; Biological Process
1840	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400024807	PGSC0003DMT400063816	chr10	NO	NO	

1841	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400024809	PGSC0003DMT400063818	-	yes	NO	
1842	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400024814	PGSC0003DMT400063833	chr12	yes	NO	
1843	Heterozygous PS in RH, not shared by DM	PGSC0003DMG402024817	PGSC0003DMT400063848	chr07	yes	NO	
1844	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400024823	PGSC0003DMT400063864	chr03	NO	NO	
1845	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400024827	PGSC0003DMT400063870	chr04	yes	NO	
1846	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400024829	PGSC0003DMT400063876	chr04	yes	NO	GO:0016787; hydrolase activity; Molecular Function
1847	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400024881	PGSC0003DMT400064014	chr04	yes	NO	
1848	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400024883	PGSC0003DMT400064020	chr06	NO	NO	GO:0003676; nucleic acid binding; Molecular Function GO:0008270; zinc ion binding; Molecular Function
1849	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400024891	PGSC0003DMT400064041	chr05	NO	NO	
1850	Heterozygous PS in RH, not shared by DM	PGSC0003DMG403024894	PGSC0003DMT400064050	-	NO	NO	
1851	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400024906	PGSC0003DMT400064096	chr07	NO	NO	
1852	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400024908	PGSC0003DMT400064100	chr06	NO	NO	

1853	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400024922	PGSC0003DMT400064148	chr11	NO	NO	
1854	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400024951	PGSC0003DMT400064225	chr04	NO	NO	GO:0003676; nucleic acid binding; Molecular Function GO:0005622; intracellular; Cellular Component GO:0008270; zinc ion binding; Molecular Function
1855	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400024987	PGSC0003DMT400064314	chr07	NO	NO	
1856	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400024989	PGSC0003DMT400064322	-	NO	NO	GO:0005618; cell wall; Cellular Component GO:0030599; pectinesterase activity; Molecular Function GO:0042545; cell wall modification; Biological Process
1857	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400024993	PGSC0003DMT400064326	chr01	NO	NO	
1858	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400024995	PGSC0003DMT400064337	-	yes	NO	GO:0004497; monooxygenase activity; Molecular Function GO:0055114; oxidation reduction; Biological Process
1859	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400025108	PGSC0003DMT400064620	chr06	yes	NO	GO:0000175; 3'-5'-exoribonuclease activity; Molecular Function GO:0003723; RNA binding; Molecular Function GO:0006396; RNA processing; Biological Process
1860	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400025122	PGSC0003DMT400064673	chr12	NO	NO	
1861	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400025124	PGSC0003DMT400064681	chr12	yes	yes	

1862	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400025148	PGSC0003DMT400064740	chr02	yes	NO	GO:0004672; protein kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0005529; sugar binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process GO:0048544; recognition of pollen; Biological Process
1863	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400025175	PGSC0003DMT400064824	chr11	yes	NO	
1864	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400025182	PGSC0003DMT400064854	chr04	yes	yes	GO:0005524; ATP binding; Molecular Function GO:0006915; apoptosis; Biological Process
1865	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400025195	PGSC0003DMT400064882	-	NO	NO	
1866	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400025276	PGSC0003DMT400065051	chr10	yes	NO	GO:0003700; transcription factor activity; Molecular Function GO:0005634; nucleus; Cellular Component GO:0006355; regulation of transcription, DNA-dependent; Biological Process
1867	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400025283	PGSC0003DMT400065069	chr04	yes	yes	
1868	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400025373	PGSC0003DMT400065273	chr05	yes	NO	
1869	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400025383	PGSC0003DMT400065295	chr04	NO	NO	
1870	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400025384	PGSC0003DMT400065297	chr05	NO	NO	
1871	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400025454	PGSC0003DMT400065446	chr08	NO	NO	

1872	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400025487	PGSC0003DMT400065512	chr08	NO	NO	
1873	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400025489	PGSC0003DMT400065515	chr05	yes	NO	GO:0004615; phosphomannomutase activity; Molecular Function GO:0005737; cytoplasm; Cellular Component GO:0019307; mannose biosynthetic process; Biological Process
1874	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400025504	PGSC0003DMT400065555	-	NO	NO	
1875	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400025540	PGSC0003DMT400065650	chr10	yes	yes	GO:0005524; ATP binding; Molecular Function GO:0006915; apoptosis; Biological Process
1876	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400025553	PGSC0003DMT400065687	chr08	yes	NO	GO:0008654; phospholipid biosynthetic process; Biological Process GO:0016020; membrane; Cellular Component GO:0016780; phosphotransferase activity, for other substituted phosphate groups; Molecular Function
1877	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400025582	PGSC0003DMT400065732	chr09	NO	NO	
1878	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400025599	PGSC0003DMT400065769	chr05	yes	NO	
1879	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400025611	PGSC0003DMT400065792	chr10	yes	yes	GO:0005524; ATP binding; Molecular Function GO:0006915; apoptosis; Biological Process
1880	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400025613	PGSC0003DMT400065801	chr04	yes	NO	
1881	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400025635	PGSC0003DMT400065855	chr06	yes	NO	

1882	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400025652	PGSC0003DMT400065899	chr09	NO	NO	
1883	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400025686	PGSC0003DMT400065984	chr12	NO	NO	
1884	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400025695	PGSC0003DMT400066004	-	yes	NO	
1885	Heterozygous PS in RH, not shared by DM	PGSC0003DMG403025788	PGSC0003DMT400066304	chr01	NO	NO	
1886	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400025795	PGSC0003DMT400066337	-	NO	NO	
1887	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400025800	PGSC0003DMT400066349	chr08	yes	NO	
1888	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400025827	PGSC0003DMT400066414	chr10	yes	yes	GO:0005515; protein binding; Molecular Function
1889	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401025828	PGSC0003DMT400066419	chr09	NO	NO	
1890	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400025878	PGSC0003DMT400066576	chr03	yes	yes	GO:0004672; protein kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0005529; sugar binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
1891	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401025898	PGSC0003DMT400066626	chr01	yes	NO	GO:0004601; peroxidase activity; Molecular Function GO:0006979; response to oxidative stress; Biological Process GO:0020037; heme binding; Molecular Function GO:0055114; oxidation reduction; Biological Process

1892	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400025951	PGSC0003DMT400066756	chr06	NO	NO	GO:0009058; biosynthetic process; Biological Process GO:0016769; transferase activity, transferring nitrogenous groups; Molecular Function GO:0030170; pyridoxal phosphate binding; Molecular Function
1893	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400026089	PGSC0003DMT400067114	chr01	yes	NO	
1894	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400026188	PGSC0003DMT400067356	chr03	yes	NO	
1895	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400026251	PGSC0003DMT400067513	chr07	NO	NO	GO:0016787; hydrolase activity; Molecular Function
1896	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400026271	PGSC0003DMT400067568	chr01	yes	NO	
1897	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400026305	PGSC0003DMT400067641	chr01	yes	yes	
1898	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401026387	PGSC0003DMT400067845	chr07	yes	NO	GO:0003777; microtubule motor activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0007018; microtubule-based movement; Biological Process
1899	Heterozygous PS in RH, not shared by DM	PGSC0003DMG402026387	PGSC0003DMT400067846	chr07	yes	NO	
1900	Heterozygous PS in RH, not shared by DM	PGSC0003DMG402026407	PGSC0003DMT400067900	chr09	NO	NO	

1901	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400026410	PGSC0003DMT400067908	chr05	NO	NO	GO:0016020; membrane; Cellular Component GO:0030001; metal ion transport; Biological Process GO:0046873; metal ion transmembrane transporter activity; Molecular Function GO:0055085; transmembrane transport; Biological Process
1902	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400026459	PGSC0003DMT400068033	chr05	NO	NO	
1903	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400026506	PGSC0003DMT400068155	chr08	yes	NO	GO:0008080; N-acetyltransferase activity; Molecular Function GO:0008152; metabolic process; Biological Process
1904	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401026514	PGSC0003DMT400068174	chr02	yes	NO	GO:0016998; cell wall macromolecule catabolic process; Biological Process GO:0033903; endo-1,3(4)-beta-glucanase activity; Molecular Function
1905	Heterozygous PS in RH, not shared by DM	PGSC0003DMG402026514	PGSC0003DMT400068172	chr01	yes	NO	
1906	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401026519	PGSC0003DMT400068189	chr08	yes	NO	
1907	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400026520	PGSC0003DMT400068212	chr08	NO	NO	
1908	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400026547	PGSC0003DMT400068290	chr07	yes	NO	GO:0003676; nucleic acid binding; Molecular Function GO:0008270; zinc ion binding; Molecular Function
1909	Heterozygous PS in RH, not shared by DM	PGSC0003DMG402026624	PGSC0003DMT400068473	chr08	yes	NO	
1910	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400026640	PGSC0003DMT400068503	chr03	yes	yes	

1911	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401026661	PGSC0003DMT400068536	chr03	yes	NO	
1912	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400026666	PGSC0003DMT400068569	chr06	yes	NO	
1913	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400026690	PGSC0003DMT400068637	chr09	yes	yes	GO:0004713; protein tyrosine kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
1914	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400026698	PGSC0003DMT400068662	chr03	yes	yes	GO:0004601; peroxidase activity; Molecular Function GO:0006979; response to oxidative stress; Biological Process GO:0020037; heme binding; Molecular Function GO:0055114; oxidation reduction; Biological Process
1915	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400026749	PGSC0003DMT400068787	chr06	yes	NO	GO:0006812; cation transport; Biological Process GO:0008324; cation transmembrane transporter activity; Molecular Function GO:0016020; membrane; Cellular Component GO:0055085; transmembrane transport; Biological Process
1916	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400026760	PGSC0003DMT400068804	chr04	yes	NO	GO:0003735; structural constituent of ribosome; Molecular Function GO:0005507; copper ion binding; Molecular Function GO:0005622; intracellular; Cellular Component GO:0005840; ribosome; Cellular Component GO:0006412; translation; Biological Process GO:0016491; oxidoreductase activity; Molecular Function GO:0055114; oxidation reduction; Biological Process
1917	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400026829	PGSC0003DMT400068977	chr05	yes	yes	

1918	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400026860	PGSC0003DMT400069046	chr03	NO	NO	GO:0008270; zinc ion binding; Molecular Function
1919	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400026863	PGSC0003DMT400069059	chr08	NO	NO	GO:0000151; ubiquitin ligase complex; Cellular Component GO:0004842; ubiquitin-protein ligase activity; Molecular Function GO:0005634; nucleus; Cellular Component GO:0008270; zinc ion binding; Molecular Function GO:0016567; protein ubiquitination; Biological Process
1920	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400026864	PGSC0003DMT400069062	chr04	yes	yes	
1921	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400026867	PGSC0003DMT400069067	chr06	NO	NO	
1922	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400026869	PGSC0003DMT400069076	chr02	yes	NO	
1923	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400026879	PGSC0003DMT400069104	chr01	yes	yes	GO:0005622; intracellular; Cellular Component GO:0008270; zinc ion binding; Molecular Function
1924	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400026913	PGSC0003DMT400069189	chr06	NO	NO	GO:0004866; endopeptidase inhibitor activity; Molecular Function
1925	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400026927	PGSC0003DMT400069225	chr04	yes	NO	GO:0030528; transcription regulator activity; Molecular Function GO:0045449; regulation of transcription; Biological Process
1926	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400026955	PGSC0003DMT400069293	chr04	yes	NO	
1927	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400026966	PGSC0003DMT400069321	chr10	yes	NO	GO:0008152; metabolic process; Biological Process GO:0016491; oxidoreductase activity; Molecular Function

1928	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401027016	PGSC0003DMT400069493	chr10	yes	yes	
1929	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400027038	PGSC0003DMT400069555	chr04	yes	NO	
1930	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400027057	PGSC0003DMT400069593	chr03	yes	NO	GO:0008270; zinc ion binding; Molecular Function
1931	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400027149	PGSC0003DMT400069822	chr01	NO	NO	
1932	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400027183	PGSC0003DMT400069901	chr01	yes	yes	
1933	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400027246	PGSC0003DMT400070067	chr08	yes	NO	
1934	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400027289	PGSC0003DMT400070214	chr12	NO	NO	
1935	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400027306	PGSC0003DMT400070235	chr02	yes	NO	GO:0004345; glucose-6-phosphate dehydrogenase activity; Molecular Function GO:0006006; glucose metabolic process; Biological Process GO:0055114; oxidation reduction; Biological Process
1936	Heterozygous PS in RH, not shared by DM	PGSC0003DMG403027324	PGSC0003DMT400070283	-	yes	NO	
1937	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400027336	PGSC0003DMT400070308	chr03	yes	NO	

1938	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400027343	PGSC0003DMT400070323	chr04	yes	NO	GO:0004497; monooxygenase activity; Molecular Function GO:0005506; iron ion binding; Molecular Function GO:0009055; electron carrier activity; Molecular Function GO:0020037; heme binding; Molecular Function
1939	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400027377	PGSC0003DMT400070419	chr11	NO	NO	
1940	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400027384	PGSC0003DMT400070437				
1941	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400027401	PGSC0003DMT400070475	chr04	NO	NO	
1942	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400027436	PGSC0003DMT400070587	chr06	yes	yes	
1943	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400027447	PGSC0003DMT400070609	chr12	NO	NO	
1944	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400027464	PGSC0003DMT400070649	chr05	NO	NO	
1945	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401027501	PGSC0003DMT400070728	-	yes	NO	
1946	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400027520	PGSC0003DMT400070780	chr01	NO	NO	
1947	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400027539	PGSC0003DMT400070823	chr02	yes	NO	
1948	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400027540	PGSC0003DMT400070825	chr01	yes	yes	GO:0005524; ATP binding; Molecular Function GO:0006915; apoptosis; Biological Process

1949	Heterozygous PS in RH, not shared by DM	PGSC0003DMG402027687	PGSC0003DMT400071195	chr12	yes	yes	GO:0003700; transcription factor activity; Molecular Function GO:0006355; regulation of transcription, DNA-dependent; Biological Process GO:0043565; sequence-specific DNA binding; Molecular Function
1950	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400027710	PGSC0003DMT400071263	chr02	NO	NO	
1951	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400027758	PGSC0003DMT400071348	chr03	NO	NO	
1952	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400027789	PGSC0003DMT400071421	chr10	yes	yes	GO:0004871; signal transducer activity; Molecular Function GO:0005515; protein binding; Molecular Function GO:0009416; response to light stimulus; Biological Process
1953	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400027867	PGSC0003DMT400071638	chr08	NO	NO	GO:0004672; protein kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
1954	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400027950	PGSC0003DMT400071840	chr08	yes	NO	GO:0003676; nucleic acid binding; Molecular Function GO:0005622; intracellular; Cellular Component
1955	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400027956	PGSC0003DMT400071854	chr10	NO	NO	
1956	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400027966	PGSC0003DMT400071871	chr09	yes	NO	GO:0016491; oxidoreductase activity; Molecular Function
1957	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400027971	PGSC0003DMT400071897	-	NO	NO	
1958	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400028072	PGSC0003DMT400072141	chr11	NO	NO	GO:0005524; ATP binding; Molecular Function

1959	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400028085	PGSC0003DMT400072173	chr02	yes	yes	GO:0008152; metabolic process; Biological Process GO:0016597; amino acid binding; Molecular Function
1960	Heterozygous PS in RH, not shared by DM	PGSC0003DMG402028118	PGSC0003DMT400072255	chr08	yes	yes	
1961	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401028133	PGSC0003DMT400072292	-	NO	NO	
1962	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400028156	PGSC0003DMT400072349	chr10	NO	NO	
1963	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400028221	PGSC0003DMT400072533	chr06	NO	NO	GO:0005515; protein binding; Molecular Function
1964	Heterozygous PS in RH, not shared by DM	PGSC0003DMG402028232	PGSC0003DMT400072559	chr01	yes	NO	
1965	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400028241	PGSC0003DMT400072574	chr10	NO	NO	
1966	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400028251	PGSC0003DMT400072601	chr02	yes	NO	
1967	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400028267	PGSC0003DMT400072644	-	yes	NO	
1968	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400028271	PGSC0003DMT400072655	chr12	NO	NO	
1969	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400028295	PGSC0003DMT400072713	chr04	NO	NO	

1970	Heterozygous PS in RH, not shared by DM	PGSC0003DMG403028300	PGSC0003DMT400072720	-	yes	NO	GO:0005215; transporter activity; Molecular Function GO:0006810; transport; Biological Process GO:0016020; membrane; Cellular Component GO:0055085; transmembrane transport; Biological Process
1971	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400028316	PGSC0003DMT400072765	chr01	NO	NO	
1972	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401028328	PGSC0003DMT400072809	chr04	NO	NO	
1973	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400028338	PGSC0003DMT400072841	-	NO	NO	
1974	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400028339	PGSC0003DMT400072845	chr04	NO	NO	
1975	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400028349	PGSC0003DMT400072874	chr07	yes	NO	
1976	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400028350	PGSC0003DMT400072875	chr09	NO	NO	
1977	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400028366	PGSC0003DMT400072910	chr12	NO	NO	
1978	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401028370	PGSC0003DMT400072923	chr06	yes	NO	
1979	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400028373	PGSC0003DMT400072928	chr01	yes	NO	

1980	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401028385	PGSC0003DMT400072977	chr09	yes	NO	GO:0003700; transcription factor activity; Molecular Function GO:0043565; sequence-specific DNA binding; Molecular Function GO:0045449; regulation of transcription; Biological Process
1981	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400028405	PGSC0003DMT400073019	chr06	yes	NO	GO:0009058; biosynthetic process; Biological Process
1982	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400028448	PGSC0003DMT400073150	chr07	yes	NO	GO:0003677; DNA binding; Molecular Function GO:0005634; nucleus; Cellular Component
1983	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400028474	PGSC0003DMT400073281	chr06	NO	NO	GO:0008152; metabolic process; Biological Process GO:0016758; transferase activity, transferring hexosyl groups; Molecular Function
1984	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400028493	PGSC0003DMT400073320	chr10	NO	NO	GO:0004672; protein kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
1985	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400028505	PGSC0003DMT400073342	chr12	NO	NO	
1986	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401028565	PGSC0003DMT400073530	chr05	yes	NO	
1987	Heterozygous PS in RH, not shared by DM	PGSC0003DMG402028577	PGSC0003DMT400073573	chr10	NO	NO	
1988	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400028653	PGSC0003DMT400073754	-	yes	NO	
1989	Heterozygous PS in RH, not shared by DM	PGSC0003DMG402028683	PGSC0003DMT400073827	chr05	yes	NO	

1990	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400028706	PGSC0003DMT400073876	chr01	yes	NO	
1991	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401028714	PGSC0003DMT400073897	chr01	yes	NO	GO:0004672; protein kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
1992	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400028732	PGSC0003DMT400073939	chr06	yes	yes	
1993	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400028768	PGSC0003DMT400074009	chr01	yes	NO	
1994	Heterozygous PS in RH, not shared by DM	PGSC0003DMG402028796	PGSC0003DMT400074096	chr01	yes	NO	GO:0005975; carbohydrate metabolic process; Biological Process GO:0042578; phosphoric ester hydrolase activity; Molecular Function
1995	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400028804	PGSC0003DMT400074108	chr04	yes	NO	GO:0004497; monooxygenase activity; Molecular Function GO:0005506; iron ion binding; Molecular Function GO:0009055; electron carrier activity; Molecular Function GO:0020037; heme binding; Molecular Function
1996	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400028808	PGSC0003DMT400074117	chr08	yes	NO	GO:0016787; hydrolase activity; Molecular Function
1997	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400028825	PGSC0003DMT400074161	chr11	NO	NO	
1998	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401028829	PGSC0003DMT400074177	chr10	yes	yes	
1999	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400028833	PGSC0003DMT400074187	-	NO	NO	

2000	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400028846	PGSC0003DMT400074230	chr05	NO	NO	
2001	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400028873	PGSC0003DMT400074290	chr11	yes	yes	
2002	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400028893	PGSC0003DMT400074333	chr11	NO	NO	
2003	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400028912	PGSC0003DMT400074393	chr07	NO	NO	
2004	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400029069	PGSC0003DMT400074755	chr11	NO	NO	
2005	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400029141	PGSC0003DMT400074927	chr09	NO	NO	
2006	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400029160	PGSC0003DMT400074970	chr12	NO	NO	
2007	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400029192	PGSC0003DMT400075052	chr06	yes	NO	GO:0008152; metabolic process; Biological Process GO:0008168; methyltransferase activity; Molecular Function
2008	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400029193	PGSC0003DMT400075055	chr04	NO	NO	
2009	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401029202	PGSC0003DMT400075073	chr09	yes	NO	
2010	Heterozygous PS in RH, not shared by DM	PGSC0003DMG402029202	PGSC0003DMT400075074	chr02	yes	NO	
2011	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400029218	PGSC0003DMT400075117	chr11	yes	NO	

2012	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400029220	PGSC0003DMT400075120	-	NO	NO	
2013	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400029229	PGSC0003DMT400075135	chr08	yes	NO	GO:0003676; nucleic acid binding; Molecular Function GO:0003950; NAD+ ADP-ribosyltransferase activity; Molecular Function GO:0006471; protein amino acid ADP-ribosylation; Biological Process
2014	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400029282	PGSC0003DMT400075285	-	NO	NO	
2015	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400029301	PGSC0003DMT400075342	chr11	yes	yes	
2016	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400029342	PGSC0003DMT400075431	chr08	yes	NO	
2017	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401029345	PGSC0003DMT400075441	chr12	yes	NO	GO:0005737; cytoplasm; Cellular Component GO:0006364; rRNA processing; Biological Process GO:0008168; methyltransferase activity; Molecular Function
2018	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400029360	PGSC0003DMT400075504	chr06	yes	NO	GO:0006807; nitrogen compound metabolic process; Biological Process GO:0016810; hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds; Molecular Function
2019	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400029382	PGSC0003DMT400075558	chr12	NO	NO	
2020	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400029415	PGSC0003DMT400075625	chr05	NO	NO	
2021	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400029504	PGSC0003DMT400075881	-	yes	yes	

2022	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400029592	PGSC0003DMT400076100	chr04	yes	NO	GO:0006950; response to stress; Biological Process
2023	Heterozygous PS in RH, not shared by DM	PGSC0003DMG403029595	PGSC0003DMT400076108	chr11	yes	yes	
2024	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400029623	PGSC0003DMT400076187				
2025	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400029638	PGSC0003DMT400076240	chr09	yes	NO	GO:0004553; hydrolase activity, hydrolyzing O-glycosyl compounds; Molecular Function GO:0005975; carbohydrate metabolic process; Biological Process
2026	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400029644	PGSC0003DMT400076250	chr01	yes	NO	GO:0008168; methyltransferase activity; Molecular Function
2027	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400029712	PGSC0003DMT400076407	chr06	NO	NO	
2028	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400029748	PGSC0003DMT400076507	chr11	yes	NO	GO:0031072; heat shock protein binding; Molecular Function
2029	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400029846	PGSC0003DMT400076743	chr11	yes	NO	
2030	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401029918	PGSC0003DMT400076918	chr11	yes	NO	
2031	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400029936	PGSC0003DMT400076960	chr12	NO	NO	

2032	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400029952	PGSC0003DMT400077008	chr03	yes	yes	GO:0000166; nucleotide binding; Molecular Function GO:0003676; nucleic acid binding; Molecular Function GO:0004812; aminoacyl-tRNA ligase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0005737; cytoplasm; Cellular Component GO:0006412; translation; Biological Process GO:0006418; tRNA aminoacylation for protein translation; Biological Process
2033	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400029986	PGSC0003DMT400077096	chr09	NO	NO	
2034	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400029988	PGSC0003DMT400077099	chr10	yes	NO	GO:0004497; monooxygenase activity; Molecular Function GO:0005506; iron ion binding; Molecular Function GO:0009055; electron carrier activity; Molecular Function GO:0020037; heme binding; Molecular Function
2035	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400029989	PGSC0003DMT400077106	chr09	yes	yes	GO:0003677; DNA binding; Molecular Function GO:0005634; nucleus; Cellular Component GO:0006355; regulation of transcription, DNA-dependent; Biological Process GO:0009725; response to hormone stimulus; Biological Process GO:0045449; regulation of transcription; Biological Process
2036	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400029994	PGSC0003DMT400077126	chr03	yes	NO	
2037	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400030038	PGSC0003DMT400077231	chr06	yes	NO	
2038	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400030041	PGSC0003DMT400077234	chr11	yes	NO	

2039	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400030049	PGSC0003DMT400077252	chr05	NO	NO	GO:0003700; transcription factor activity; Molecular Function GO:0005634; nucleus; Cellular Component GO:0006355; regulation of transcription, DNA-dependent; Biological Process GO:0043565; sequence-specific DNA binding; Molecular Function
2040	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400030050	PGSC0003DMT400077254	chr10	yes	yes	GO:0006855; multidrug transport; Biological Process GO:0015238; drug transporter activity; Molecular Function GO:0015297; antiporter activity; Molecular Function GO:0016020; membrane; Cellular Component GO:0055085; transmembrane transport; Biological Process
2041	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401030070	PGSC0003DMT400077302	chr09	yes	NO	
2042	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400030071	PGSC0003DMT400077313	chr01	yes	NO	GO:0003676; nucleic acid binding; Molecular Function
2043	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400030072	PGSC0003DMT400077321	chr01	NO	NO	
2044	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400030073	PGSC0003DMT400077322	chr12	yes	NO	
2045	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400030087	PGSC0003DMT400077354	chr03	NO	NO	GO:0008061; chitin binding; Molecular Function
2046	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400030098	PGSC0003DMT400077375	chr11	yes	NO	
2047	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400030103	PGSC0003DMT400077390	chr02	yes	NO	

2048	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400030167	PGSC0003DMT400077570	chr07	yes	NO	
2049	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400030174	PGSC0003DMT400077583	chr06	yes	NO	GO:0008152; metabolic process; Biological Process GO:0016491; oxidoreductase activity; Molecular Function
2050	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400030216	PGSC0003DMT400077655	-	yes	NO	GO:0005737; cytoplasm; Cellular Component GO:0016788; hydrolase activity, acting on ester bonds; Molecular Function GO:0019478; D-amino acid catabolic process; Biological Process
2051	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401030227	PGSC0003DMT400077696	-	yes	yes	
2052	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400030280	PGSC0003DMT400077840	chr07	NO	NO	
2053	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400030282	PGSC0003DMT400077845	chr01	yes	yes	
2054	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400030290	PGSC0003DMT400077862	chr08	NO	NO	
2055	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400030291	PGSC0003DMT400077864	chr08	yes	yes	GO:0005515; protein binding; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006915; apoptosis; Biological Process
2056	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400030335	PGSC0003DMT400077996	chr02	yes	yes	
2057	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400030336	PGSC0003DMT400078001	chr04	yes	NO	GO:0009058; biosynthetic process; Biological Process GO:0016769; transferase activity, transferring nitrogenous groups; Molecular Function GO:0030170; pyridoxal phosphate binding; Molecular Function

2058	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400030434	PGSC0003DMT400078213	chr08	NO	NO	GO:0004497; monooxygenase activity; Molecular Function GO:0005506; iron ion binding; Molecular Function GO:0009055; electron carrier activity; Molecular Function GO:0020037; heme binding; Molecular Function
2059	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400030465	PGSC0003DMT400078274	chr05	yes	NO	GO:0005506; iron ion binding; Molecular Function GO:0009055; electron carrier activity; Molecular Function GO:0016021; integral to membrane; Cellular Component GO:0016491; oxidoreductase activity; Molecular Function GO:0050660; FAD binding; Molecular Function
2060	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400030471	PGSC0003DMT400078293	chr12	yes	yes	
2061	Heterozygous PS in RH, not shared by DM	PGSC0003DMG402030499	PGSC0003DMT400078339	chr08	yes	NO	
2062	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400030510	PGSC0003DMT400078360	chr05	yes	NO	GO:0005507; copper ion binding; Molecular Function GO:0016491; oxidoreductase activity; Molecular Function GO:0055114; oxidation reduction; Biological Process
2063	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401030515	PGSC0003DMT400078371	chr06	yes	NO	GO:0005524; ATP binding; Molecular Function GO:0006810; transport; Biological Process GO:0016021; integral to membrane; Cellular Component GO:0016887; ATPase activity; Molecular Function GO:0042626; ATPase activity, coupled to transmembrane movement of substances; Molecular Function GO:0055085; transmembrane transport; Biological Process
2064	Heterozygous PS in RH, not shared by DM	PGSC0003DMG402030517	PGSC0003DMT400078381	chr12	NO	NO	

2065	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400030522	PGSC0003DMT400078400	chr02	yes	NO	
2066	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400030533	PGSC0003DMT400078441	chr01	yes	NO	
2067	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400030538	PGSC0003DMT400078455	chr02	yes	yes	GO:0004672; protein kinase activity; Molecular Function GO:0005515; protein binding; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
2068	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400030542	PGSC0003DMT400078463	chr07	NO	NO	
2069	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400030551	PGSC0003DMT400078485	chr07	NO	NO	
2070	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400030594	PGSC0003DMT400078610	chr09	yes	NO	
2071	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400030618	PGSC0003DMT400078678	chr10	yes	NO	GO:0005643; nuclear pore; Cellular Component GO:0006810; transport; Biological Process
2072	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400030636	PGSC0003DMT400078748	chr04	yes	NO	
2073	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400030740	PGSC0003DMT400078996	chr06	yes	yes	GO:0005524; ATP binding; Molecular Function
2074	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400030745	PGSC0003DMT400079001	chr08	yes	NO	GO:0003824; catalytic activity; Molecular Function GO:0006631; fatty acid metabolic process; Biological Process GO:0008152; metabolic process; Biological Process GO:0016491; oxidoreductase activity; Molecular Function

2075	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400030803	PGSC0003DMT400079144	chr04	yes	NO	GO:0009507; chloroplast; Cellular Component GO:0046422; violaxanthin de-epoxidase activity; Molecular Function GO:0055114; oxidation reduction; Biological Process
2076	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400030806	PGSC0003DMT400079154	chr06	NO	NO	
2077	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401030822	PGSC0003DMT400079197	chr08	yes	yes	
2078	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400030823	PGSC0003DMT400079201	chr04	yes	NO	
2079	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401030883	PGSC0003DMT400079342	chr04	NO	NO	GO:0009055; electron carrier activity; Molecular Function GO:0015035; protein disulfide oxidoreductase activity; Molecular Function GO:0045454; cell redox homeostasis; Biological Process
2080	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400030906	PGSC0003DMT400079395	chr03	yes	NO	
2081	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400030918	PGSC0003DMT400079424	chr07	yes	yes	GO:0008152; metabolic process; Biological Process GO:0016491; oxidoreductase activity; Molecular Function
2082	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400031000	PGSC0003DMT400079611	chr03	yes	yes	
2083	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400031005	PGSC0003DMT400079617	chr04	yes	NO	
2084	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401031036	PGSC0003DMT400079684	-	yes	NO	

2085	Heterozygous PS in RH, not shared by DM	PGSC0003DMG402031036	PGSC0003DMT400079683	chr11	NO	NO	GO:0004553; hydrolase activity, hydrolyzing O-glycosyl compounds; Molecular Function GO:0005975; carbohydrate metabolic process; Biological Process
2086	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400031039	PGSC0003DMT400079690	-	NO	NO	
2087	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400031087	PGSC0003DMT400079832	chr04	NO	NO	
2088	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401031089	PGSC0003DMT400079836	chr07	yes	NO	
2089	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400031091	PGSC0003DMT400079839	-	NO	NO	
2090	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400031137	PGSC0003DMT400079969	chr02	yes	NO	
2091	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400031153	PGSC0003DMT400080005	chr09	NO	NO	
2092	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400031173	PGSC0003DMT400080060	chr07	NO	NO	GO:0003676; nucleic acid binding; Molecular Function GO:0008270; zinc ion binding; Molecular Function
2093	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400031184	PGSC0003DMT400080083	chr08	yes	yes	
2094	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400031185	PGSC0003DMT400080085	chr09	NO	NO	
2095	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400031208	PGSC0003DMT400080173	chr12	NO	NO	
2096	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401031260	PGSC0003DMT400080293	chr05	yes	yes	

2097	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400031271	PGSC0003DMT400080327	chr07	yes	NO	GO:0016787; hydrolase activity; Molecular Function
2098	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400031292	PGSC0003DMT400080369	chr02	NO	NO	
2099	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400031301	PGSC0003DMT400080384	-	NO	NO	
2100	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400031304	PGSC0003DMT400080391	chr10	NO	NO	
2101	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400031306	PGSC0003DMT400080398	chr12	yes	NO	
2102	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400031307	PGSC0003DMT400080403	chr03	yes	NO	GO:0004222; metalloendopeptidase activity; Molecular Function GO:0006508; proteolysis; Biological Process GO:0016020; membrane; Cellular Component
2103	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400031313	PGSC0003DMT400080416	chr07	NO	NO	
2104	Heterozygous PS in RH, not shared by DM	PGSC0003DMG402031319	PGSC0003DMT400080442	chr11	yes	NO	GO:0005524; ATP binding; Molecular Function GO:0006915; apoptosis; Biological Process
2105	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400031428	PGSC0003DMT400080700	chr01	NO	NO	
2106	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400031477	PGSC0003DMT400080822	chr05	yes	NO	GO:0005524; ATP binding; Molecular Function GO:0006915; apoptosis; Biological Process
2107	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400031491	PGSC0003DMT400080864	chr05	yes	NO	GO:0005215; transporter activity; Molecular Function GO:0006857; oligopeptide transport; Biological Process GO:0016020; membrane; Cellular Component

2108	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400031525	PGSC0003DMT400080940	chr06	yes	NO	
2109	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400031799	PGSC0003DMT400081334	chr05	yes	NO	GO:0005524; ATP binding; Molecular Function GO:0006915; apoptosis; Biological Process
2110	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400031834	PGSC0003DMT400081430	chr01	NO	NO	GO:0004221; ubiquitin thiolesterase activity; Molecular Function GO:0005622; intracellular; Cellular Component GO:0006511; ubiquitin-dependent protein catabolic process; Biological Process
2111	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401031907	PGSC0003DMT400081529	chr07	NO	NO	GO:0003676; nucleic acid binding; Molecular Function GO:0003677; DNA binding; Molecular Function GO:0004386; helicase activity; Molecular Function GO:0005524; ATP binding; Molecular Function
2112	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400031908	PGSC0003DMT400081531	chr12	NO	NO	
2113	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400032101	PGSC0003DMT400081746	chr10	yes	NO	GO:0004190; aspartic-type endopeptidase activity; Molecular Function GO:0006508; proteolysis; Biological Process
2114	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400032132	PGSC0003DMT400081835	chr05	NO	NO	
2115	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400032151	PGSC0003DMT400081902	chr01	NO	NO	GO:0003700; transcription factor activity; Molecular Function GO:0005634; nucleus; Cellular Component GO:0006355; regulation of transcription, DNA-dependent; Biological Process GO:0043565; sequence-specific DNA binding; Molecular Function

2116	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400032269	PGSC0003DMT400082118	chr11	yes	yes	GO:0003824; catalytic activity; Molecular Function GO:0044237; cellular metabolic process; Biological Process GO:0050662; coenzyme binding; Molecular Function
2117	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400032496	PGSC0003DMT400082356	chr05	yes	NO	GO:0004672; protein kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
2118	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400032509	PGSC0003DMT400082384	chr10	yes	yes	
2119	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400032554	PGSC0003DMT400082469	chr09	NO	NO	
2120	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400032773	PGSC0003DMT400082703	-	yes	NO	
2121	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400032781	PGSC0003DMT400082722	chr09	NO	NO	
2122	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400032795	PGSC0003DMT400082754	chr12	NO	NO	
2123	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400033031	PGSC0003DMT400083037	chr11	yes	yes	
2124	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400033145	PGSC0003DMT400083259	chr05	NO	NO	GO:0003700; transcription factor activity; Molecular Function GO:0006355; regulation of transcription, DNA-dependent; Biological Process GO:0043565; sequence-specific DNA binding; Molecular Function GO:0046983; protein dimerization activity; Molecular Function

2125	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400033332	PGSC0003DMT400083467	chr04	yes	yes	GO:0005507; copper ion binding; Molecular Function GO:0009055; electron carrier activity; Molecular Function
2126	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400033357	PGSC0003DMT400083502	chr12	yes	NO	
2127	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400033567	PGSC0003DMT400083733	chr04	yes	NO	
2128	Heterozygous PS in RH, not shared by DM	PGSC0003DMG401033568	PGSC0003DMT400083734	chr05	NO	NO	
2129	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400033583	PGSC0003DMT400083785	chr01	yes	NO	
2130	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400033664	PGSC0003DMT400083937	chr12	yes	yes	GO:0004190; aspartic-type endopeptidase activity; Molecular Function GO:0016021; integral to membrane; Cellular Component
2131	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400033681	PGSC0003DMT400083956	chr10	yes	NO	GO:0004672; protein kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
2132	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400033873	PGSC0003DMT400084199	-	NO	NO	
2133	Heterozygous PS in RH, not shared by DM	PGSC0003DMG402033880	PGSC0003DMT400084215	chr01	yes	NO	
2134	Heterozygous PS in RH, not shared by DM	PGSC0003DMG402033888	PGSC0003DMT400084232	-	NO	NO	
2135	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400033913	PGSC0003DMT400084286	chr09	NO	NO	

2136	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400033933	PGSC0003DMT400084315	chr01	yes	NO	GO:0005515; protein binding; Molecular Function
2137	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400034106	PGSC0003DMT400084511	chr10	yes	yes	
2138	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400034328	PGSC0003DMT400084757	chr03	yes	yes	
2139	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400034368	PGSC0003DMT400084797	chr04	yes	NO	GO:0004222; metalloendopeptidase activity; Molecular Function GO:0006508; proteolysis; Biological Process GO:0008270; zinc ion binding; Molecular Function
2140	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400034436	PGSC0003DMT400084865	chr07	NO	NO	
2141	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400034442	PGSC0003DMT400084871	chr03	NO	NO	
2142	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400034453	PGSC0003DMT400084882	chr04	NO	NO	
2143	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400034467	PGSC0003DMT400084896	chr08	yes	yes	GO:0005524; ATP binding; Molecular Function GO:0006915; apoptosis; Biological Process
2144	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400034493	PGSC0003DMT400084922	chr07	yes	NO	GO:0004497; monooxygenase activity; Molecular Function GO:0005506; iron ion binding; Molecular Function GO:0009055; electron carrier activity; Molecular Function GO:0020037; heme binding; Molecular Function
2145	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400034532	PGSC0003DMT400084961	chr06	NO	NO	
2146	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400034537	PGSC0003DMT400084966	chr10	NO	NO	

2147	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400034550	PGSC0003DMT400084979				
2148	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400034551	PGSC0003DMT400084980	chr10	yes	yes	
2149	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400034576	PGSC0003DMT400085005	chr06	yes	NO	GO:0005622; intracellular; Cellular Component GO:0008270; zinc ion binding; Molecular Function
2150	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400034597	PGSC0003DMT400085026	chr12	NO	NO	
2151	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400034599	PGSC0003DMT400085028	chr01	yes	NO	
2152	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400034645	PGSC0003DMT400085074	chr03	NO	NO	GO:0008152; metabolic process; Biological Process GO:0016491; oxidoreductase activity; Molecular Function
2153	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400034646	PGSC0003DMT400085075	-	yes	NO	
2154	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400034677	PGSC0003DMT400085106	chr06	NO	NO	
2155	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400034683	PGSC0003DMT400085112	chr01	yes	NO	
2156	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400034699	PGSC0003DMT400085128	chr03	yes	NO	

2157	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400034702	PGSC0003DMT400085131	chr04	yes	yes	GO:0004672; protein kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0005529; sugar binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process GO:0048544; recognition of pollen; Biological Process
2158	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400034710	PGSC0003DMT400085139	chr03	yes	NO	
2159	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400034716	PGSC0003DMT400085145	chr06	yes	NO	GO:0004221; ubiquitin thiolesterase activity; Molecular Function GO:0005622; intracellular; Cellular Component GO:0006511; ubiquitin-dependent protein catabolic process; Biological Process
2160	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400034786	PGSC0003DMT400085215	chr08	NO	NO	
2161	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400034798	PGSC0003DMT400085227	chr07	NO	NO	GO:0004721; phosphoprotein phosphatase activity; Molecular Function
2162	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400034801	PGSC0003DMT400085230	chr03	NO	NO	
2163	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400034829	PGSC0003DMT400085258	chr12	NO	NO	
2164	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400034869	PGSC0003DMT400085298	chr05	NO	NO	
2165	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400034906	PGSC0003DMT400085335	chr06	NO	NO	

2166	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400034953	PGSC0003DMT400085382	chr02	yes	NO	GO:0005215; transporter activity; Molecular Function GO:0006810; transport; Biological Process GO:0016021; integral to membrane; Cellular Component GO:0055085; transmembrane transport; Biological Process
2167	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400034954	PGSC0003DMT400085383	chr02	yes	NO	GO:0005681; spliceosomal complex; Cellular Component GO:0007067; mitosis; Biological Process
2168	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400034957	PGSC0003DMT400085386	chr10	NO	NO	
2169	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400034982	PGSC0003DMT400085411	chr06	yes	NO	
2170	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400034997	PGSC0003DMT400085426	-	NO	NO	
2171	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400035022	PGSC0003DMT400085451	chr05	NO	NO	
2172	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400035026	PGSC0003DMT400085455	chr05	yes	yes	
2173	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400035051	PGSC0003DMT400085480	chr01	yes	NO	GO:0005215; transporter activity; Molecular Function GO:0006810; transport; Biological Process GO:0016021; integral to membrane; Cellular Component GO:0055085; transmembrane transport; Biological Process
2174	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400035066	PGSC0003DMT400085495	chr12	yes	yes	GO:0005515; protein binding; Molecular Function
2175	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400035092	PGSC0003DMT400085521	-	NO	NO	

2176	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400035124	PGSC0003DMT400085553	chr03	NO	NO	GO:0009058; biosynthetic process; Biological Process GO:0016769; transferase activity, transferring nitrogenous groups; Molecular Function GO:0030170; pyridoxal phosphate binding; Molecular Function
2177	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400035168	PGSC0003DMT400085597	chr01	NO	NO	
2178	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400035180	PGSC0003DMT400085609	chr02	yes	yes	GO:0006505; GPI anchor metabolic process; Biological Process GO:0006886; intracellular protein transport; Biological Process GO:0016788; hydrolase activity, acting on ester bonds; Molecular Function GO:0031227; intrinsic to endoplasmic reticulum membrane; Cellular Component
2179	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400035237	PGSC0003DMT400085666	chr12	NO	NO	
2180	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400035238	PGSC0003DMT400085667	chr03	yes	yes	
2181	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400035245	PGSC0003DMT400085674	chr06	yes	NO	GO:0004672; protein kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
2182	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400035273	PGSC0003DMT400085702	chr06	NO	NO	
2183	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400035293	PGSC0003DMT400085722	-	NO	NO	GO:0003723; RNA binding; Molecular Function GO:0033897; ribonuclease T2 activity; Molecular Function
2184	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400035324	PGSC0003DMT400085753	chr02	yes	NO	

2185	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400035358	PGSC0003DMT400085787	chr09	NO	NO	
2186	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400035362	PGSC0003DMT400085791	chr01	yes	NO	GO:0003824; catalytic activity; Molecular Function GO:0008152; metabolic process; Biological Process
2187	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400035364	PGSC0003DMT400085793	chr10	yes	yes	
2188	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400035426	PGSC0003DMT400085855	chr06	yes	NO	GO:0016491; oxidoreductase activity; Molecular Function
2189	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400035432	PGSC0003DMT400085861	chr03	yes	NO	GO:0016491; oxidoreductase activity; Molecular Function GO:0055114; oxidation reduction; Biological Process
2190	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400035455	PGSC0003DMT400085884	chr12	NO	NO	GO:0003735; structural constituent of ribosome; Molecular Function GO:0005622; intracellular; Cellular Component GO:0005840; ribosome; Cellular Component GO:0006412; translation; Biological Process
2191	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400035461	PGSC0003DMT400085890	chr10	NO	NO	
2192	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400035475	PGSC0003DMT400085904	chr01	yes	yes	GO:0003723; RNA binding; Molecular Function GO:0003746; translation elongation factor activity; Molecular Function GO:0006452; translational frameshifting; Biological Process GO:0043022; ribosome binding; Molecular Function GO:0045901; positive regulation of translational elongation; Biological Process GO:0045905; positive regulation of translational termination; Biological Process

2193	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400035479	PGSC0003DMT400085908	chr08	yes	yes	
2194	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400035483	PGSC0003DMT400085912	chr03	yes	NO	
2195	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400035529	PGSC0003DMT400085958	chr10	NO	NO	
2196	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400035534	PGSC0003DMT400085963	chr04	yes	NO	GO:0006855; multidrug transport; Biological Process GO:0015238; drug transporter activity; Molecular Function GO:0015297; antiporter activity; Molecular Function GO:0016020; membrane; Cellular Component GO:0055085; transmembrane transport; Biological Process
2197	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400035552	PGSC0003DMT400085981	chr06	yes	yes	
2198	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400035553	PGSC0003DMT400085982	chr07	yes	NO	GO:0003824; catalytic activity; Molecular Function GO:0008152; metabolic process; Biological Process
2199	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400035594	PGSC0003DMT400086023	chr06	yes	NO	
2200	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400035609	PGSC0003DMT400086038	chr12	yes	NO	GO:0005515; protein binding; Molecular Function
2201	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400035629	PGSC0003DMT400086058	chr11	yes	NO	
2202	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400035671	PGSC0003DMT400086100				
2203	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400035678	PGSC0003DMT400086107	chr05	yes	NO	

2204	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400035704	PGSC0003DMT400086133	chr05	NO	NO	
2205	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400035713	PGSC0003DMT400086142	chr08	yes	yes	
2206	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400035723	PGSC0003DMT400086152	chr05	yes	NO	GO:0005669; transcription factor TFIID complex; Cellular Component GO:0006367; transcription initiation from RNA polymerase II promoter; Biological Process GO:0016251; general RNA polymerase II transcription factor activity; Molecular Function
2207	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400035757	PGSC0003DMT400086186	chr05	NO	NO	
2208	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400035763	PGSC0003DMT400086192	-	yes	yes	GO:0005198; structural molecule activity; Molecular Function
2209	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400035782	PGSC0003DMT400086211	chr10	yes	yes	
2210	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400035801	PGSC0003DMT400086230	chr03	yes	yes	GO:0003723; RNA binding; Molecular Function GO:0003964; RNA-directed DNA polymerase activity; Molecular Function GO:0006278; RNA-dependent DNA replication; Biological Process GO:0008380; RNA splicing; Biological Process
2211	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400035810	PGSC0003DMT400086239	-	yes	NO	
2212	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400035851	PGSC0003DMT400086280	chr02	yes	NO	
2213	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400035919	PGSC0003DMT400086348	chr07	yes	NO	

2214	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400035997	PGSC0003DMT400086426	-	yes	NO	
2215	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400036076	PGSC0003DMT400086505	chr08	yes	NO	
2216	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400036089	PGSC0003DMT400086518	chr06	NO	NO	
2217	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400036107	PGSC0003DMT400086536	chr09	NO	NO	
2218	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400036165	PGSC0003DMT400086594	chr10	NO	NO	
2219	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400036178	PGSC0003DMT400086607	chr10	yes	NO	GO:0003995; acyl-CoA dehydrogenase activity; Molecular Function GO:0003997; acyl-CoA oxidase activity; Molecular Function GO:0005777; peroxisome; Cellular Component GO:0006635; fatty acid beta-oxidation; Biological Process GO:0016627; oxidoreductase activity, acting on the CH-CH group of donors; Molecular Function GO:0055114; oxidation reduction; Biological Process
2220	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400036236	PGSC0003DMT400086665	-	yes	NO	
2221	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400036257	PGSC0003DMT400086686	chr05	yes	NO	GO:0016491; oxidoreductase activity; Molecular Function
2222	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400036315	PGSC0003DMT400086744	chr05	yes	NO	
2223	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400036369	PGSC0003DMT400086798	chr09	yes	NO	

2224	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400036448	PGSC0003DMT400086877	chr04	yes	NO	GO:0004672; protein kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
2225	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400036567	PGSC0003DMT400086996	chr07	yes	NO	
2226	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400036575	PGSC0003DMT400087004	chr02	yes	NO	
2227	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400036598	PGSC0003DMT400087027	chr06	NO	NO	
2228	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400036600	PGSC0003DMT400087029	chr04	NO	NO	
2229	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400036615	PGSC0003DMT400087044	chr08	NO	NO	
2230	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400036621	PGSC0003DMT400087050	chr06	yes	NO	
2231	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400036686	PGSC0003DMT400087115	chr06	yes	NO	
2232	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400036690	PGSC0003DMT400087119	chr07	yes	yes	
2233	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400036700	PGSC0003DMT400087129	chr01	yes	NO	GO:0008152; metabolic process; Biological Process GO:0016491; oxidoreductase activity; Molecular Function
2234	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400036707	PGSC0003DMT400087136	chr11	NO	NO	

2235	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400036709	PGSC0003DMT400087138	chr04	yes	NO	
2236	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400036712	PGSC0003DMT400087141	-	NO	NO	
2237	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400036743	PGSC0003DMT400087172	chr01	NO	NO	
2238	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400036854	PGSC0003DMT400087283	chr04	NO	NO	GO:0004672; protein kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
2239	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400036859	PGSC0003DMT400087288	-	yes	NO	GO:0004497; monooxygenase activity; Molecular Function GO:0005506; iron ion binding; Molecular Function GO:0009055; electron carrier activity; Molecular Function GO:0020037; heme binding; Molecular Function
2240	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400036860	PGSC0003DMT400087289	-	NO	NO	
2241	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400036884	PGSC0003DMT400087313	chr01	yes	NO	GO:0004672; protein kinase activity; Molecular Function GO:0005515; protein binding; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
2242	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400036920	PGSC0003DMT400087349	chr08	yes	NO	
2243	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400036950	PGSC0003DMT400087379	chr10	NO	NO	
2244	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400036976	PGSC0003DMT400087405	chr04	yes	yes	

2245	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400036994	PGSC0003DMT400087423	chr11	NO	NO	
2246	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400037026	PGSC0003DMT400087455	-	NO	NO	
2247	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400037031	PGSC0003DMT400087460	chr05	NO	NO	
2248	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400037033	PGSC0003DMT400087462	chr12	yes	NO	GO:0000166; nucleotide binding; Molecular Function GO:0004814; arginine-tRNA ligase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0005737; cytoplasm; Cellular Component GO:0006412; translation; Biological Process GO:0006420; arginyl-tRNA aminoacylation; Biological Process
2249	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400037040	PGSC0003DMT400087469	chr06	yes	NO	GO:0012511; monolayer-surrounded lipid storage body; Cellular Component GO:0016021; integral to membrane; Cellular Component
2250	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400037098	PGSC0003DMT400087527	chr01	yes	NO	GO:0009055; electron carrier activity; Molecular Function GO:0016491; oxidoreductase activity; Molecular Function
2251	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400037112	PGSC0003DMT400087541	chr10	yes	NO	
2252	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400037143	PGSC0003DMT400087572	-	NO	NO	
2253	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400037147	PGSC0003DMT400087576	chr03	NO	NO	

2254	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400037192	PGSC0003DMT400087621	chr08	yes	NO	GO:0004553; hydrolase activity, hydrolyzing O-glycosyl compounds; Molecular Function GO:0005576; extracellular region; Cellular Component GO:0005975; carbohydrate metabolic process; Biological Process GO:0030246; carbohydrate binding; Molecular Function
2255	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400037213	PGSC0003DMT400087642	-	NO	NO	
2256	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400037266	PGSC0003DMT400087695	chr05	yes	NO	
2257	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400037274	PGSC0003DMT400087703	chr10	NO	NO	GO:0006457; protein folding; Biological Process
2258	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400037288	PGSC0003DMT400087717	chr05	yes	yes	
2259	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400037342	PGSC0003DMT400087771	chr08	yes	NO	GO:0003824; catalytic activity; Molecular Function GO:0008152; metabolic process; Biological Process GO:0030170; pyridoxal phosphate binding; Molecular Function
2260	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400037352	PGSC0003DMT400087781	chr02	yes	yes	
2261	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400037431	PGSC0003DMT400087860	chr09	NO	NO	
2262	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400037447	PGSC0003DMT400087876	chr11	yes	NO	
2263	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400037456	PGSC0003DMT400087885	chr01	yes	NO	

2264	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400037533	PGSC0003DMT400087962	chr06	NO	NO	
2265	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400037539	PGSC0003DMT400087968	chr09	NO	NO	
2266	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400037558	PGSC0003DMT400087987	chr12	NO	NO	
2267	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400037586	PGSC0003DMT400088015	chr08	yes	NO	
2268	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400037590	PGSC0003DMT400088019	chr06	NO	NO	
2269	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400037616	PGSC0003DMT400088045	chr02	yes	NO	
2270	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400037628	PGSC0003DMT400088057	chr12	yes	NO	GO:0006855; multidrug transport; Biological Process GO:0015238; drug transporter activity; Molecular Function GO:0015297; antiporter activity; Molecular Function GO:0016020; membrane; Cellular Component GO:0055085; transmembrane transport; Biological Process
2271	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400037700	PGSC0003DMT400088129	chr02	NO	NO	
2272	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400037701	PGSC0003DMT400088130	chr09	NO	NO	
2273	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400037729	PGSC0003DMT400088158	chr03	yes	NO	
2274	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400037774	PGSC0003DMT400088203	chr11	NO	NO	

2275	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400037798	PGSC0003DMT400088227	chr11	yes	yes	GO:0004888; transmembrane receptor activity; Molecular Function GO:0005515; protein binding; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006915; apoptosis; Biological Process GO:0007165; signal transduction; Biological Process GO:0031224; intrinsic to membrane; Cellular Component GO:0045087; innate immune response; Biological Process
2276	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400037832	PGSC0003DMT400088261	-	NO	NO	GO:0005524; ATP binding; Molecular Function GO:0006915; apoptosis; Biological Process
2277	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400037875	PGSC0003DMT400088304	chr03	NO	NO	
2278	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400037895	PGSC0003DMT400088324	chr06	NO	NO	
2279	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400037923	PGSC0003DMT400088352	chr06	yes	NO	
2280	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400037943	PGSC0003DMT400088372	chr05	yes	yes	
2281	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400037974	PGSC0003DMT400088403	chr07	NO	NO	GO:0003677; DNA binding; Molecular Function GO:0006355; regulation of transcription, DNA-dependent; Biological Process
2282	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400037979	PGSC0003DMT400088408	-	yes	yes	

2283	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400037991	PGSC0003DMT400088420	chr01	yes	NO	GO:0009055; electron carrier activity; Molecular Function GO:0016491; oxidoreductase activity; Molecular Function GO:0046872; metal ion binding; Molecular Function GO:0051536; iron-sulfur cluster binding; Molecular Function GO:0055114; oxidation reduction; Biological Process
2284	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400038044	PGSC0003DMT400088473	chr05	yes	yes	
2285	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400038052	PGSC0003DMT400088481	chr06	yes	NO	
2286	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400038095	PGSC0003DMT400088524	chr08	yes	yes	GO:0005524; ATP binding; Molecular Function GO:0005634; nucleus; Cellular Component GO:0016818; hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides; Molecular Function GO:0045449; regulation of transcription; Biological Process
2287	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400038177	PGSC0003DMT400088606	chr02	yes	NO	
2288	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400038181	PGSC0003DMT400088610	chr04	NO	NO	
2289	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400038205	PGSC0003DMT400088634	chr08	yes	yes	
2290	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400038206	PGSC0003DMT400088635	chr01	yes	yes	GO:0003723; RNA binding; Molecular Function
2291	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400038255	PGSC0003DMT400088684	chr11	yes	NO	

2292	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400038280	PGSC0003DMT400088709	-	NO	NO	
2293	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400038281	PGSC0003DMT400088710	chr11	yes	NO	
2294	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400038339	PGSC0003DMT400088768	chr09	yes	NO	GO:0004497; monooxygenase activity; Molecular Function GO:0005506; iron ion binding; Molecular Function GO:0009055; electron carrier activity; Molecular Function GO:0020037; heme binding; Molecular Function
2295	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400038355	PGSC0003DMT400088784	chr09	yes	NO	
2296	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400038359	PGSC0003DMT400088788	-	yes	yes	GO:0003676; nucleic acid binding; Molecular Function GO:0003677; DNA binding; Molecular Function GO:0004386; helicase activity; Molecular Function GO:0005524; ATP binding; Molecular Function
2297	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400038383	PGSC0003DMT400088812	chr03	yes	NO	
2298	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400038403	PGSC0003DMT400088832	chr03	yes	yes	GO:0008152; metabolic process; Biological Process GO:0016491; oxidoreductase activity; Molecular Function
2299	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400038416	PGSC0003DMT400088845	chr10	yes	NO	GO:0003735; structural constituent of ribosome; Molecular Function GO:0005622; intracellular; Cellular Component GO:0005840; ribosome; Cellular Component GO:0006412; translation; Biological Process
2300	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400038426	PGSC0003DMT400088855	chr01	yes	NO	GO:0004185; serine-type carboxypeptidase activity; Molecular Function GO:0006508; proteolysis; Biological Process

2301	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400038427	PGSC0003DMT400088856	chr10	yes	yes	
2302	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400038438	PGSC0003DMT400088867	chr10	NO	NO	
2303	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400038459	PGSC0003DMT400088888	chr10	NO	NO	
2304	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400038520	PGSC0003DMT400088949	chr11	NO	NO	
2305	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400038523	PGSC0003DMT400088952	chr04	yes	NO	GO:0008152; metabolic process; Biological Process GO:0016758; transferase activity, transferring hexosyl groups; Molecular Function
2306	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400038540	PGSC0003DMT400088969	chr01	NO	NO	
2307	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400038554	PGSC0003DMT400088983	chr10	yes	yes	
2308	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400038560	PGSC0003DMT400088989	chr08	yes	NO	
2309	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400038567	PGSC0003DMT400088996	chr02	NO	NO	
2310	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400038588	PGSC0003DMT400089017	chr02	yes	NO	
2311	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400038596	PGSC0003DMT400089025	-	NO	NO	
2312	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400038609	PGSC0003DMT400089038	chr11	yes	NO	

2313	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400038622	PGSC0003DMT400089051	chr12	NO	NO	
2314	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400038639	PGSC0003DMT400089068	chr07	yes	NO	
2315	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400038641	PGSC0003DMT400089070	chr11	NO	NO	GO:0004553; hydrolase activity, hydrolyzing O-glycosyl compounds; Molecular Function GO:0005975; carbohydrate metabolic process; Biological Process
2316	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400038646	PGSC0003DMT400089075	chr02	NO	NO	
2317	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400038648	PGSC0003DMT400089077	chr05	yes	NO	GO:0045735; nutrient reservoir activity; Molecular Function
2318	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400038650	PGSC0003DMT400089079	chr01	yes	yes	GO:0005506; iron ion binding; Molecular Function GO:0005783; endoplasmic reticulum; Cellular Component GO:0006633; fatty acid biosynthetic process; Biological Process GO:0016491; oxidoreductase activity; Molecular Function GO:0055114; oxidation reduction; Biological Process
2319	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400038656	PGSC0003DMT400089085	chr12	yes	NO	GO:0005524; ATP binding; Molecular Function GO:0006810; transport; Biological Process GO:0016021; integral to membrane; Cellular Component GO:0016887; ATPase activity; Molecular Function GO:0042626; ATPase activity, coupled to transmembrane movement of substances; Molecular Function GO:0055085; transmembrane transport; Biological Process
2320	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400038695	PGSC0003DMT400089124	chr03	NO	NO	

2321	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400038696	PGSC0003DMT400089125	chr08	NO	NO	GO:0004497; monooxygenase activity; Molecular Function GO:0005506; iron ion binding; Molecular Function GO:0006629; lipid metabolic process; Biological Process GO:0009055; electron carrier activity; Molecular Function GO:0020037; heme binding; Molecular Function
2322	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400038706	PGSC0003DMT400089135	chr07	NO	NO	
2323	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400038769	PGSC0003DMT400089198	chr09	NO	NO	
2324	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400038773	PGSC0003DMT400089202	chr01	yes	NO	
2325	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400038814	PGSC0003DMT400089243				
2326	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400038841	PGSC0003DMT400089270	chr10	yes	yes	
2327	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400038863	PGSC0003DMT400089292	chr01	yes	yes	GO:0004672; protein kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
2328	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400038872	PGSC0003DMT400089301	chr10	NO	NO	
2329	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400038894	PGSC0003DMT400089323	chr06	NO	NO	
2330	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400038991	PGSC0003DMT400089420	chr12	yes	NO	

2331	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400039002	PGSC0003DMT400089431	chr10	NO	NO	
2332	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400039004	PGSC0003DMT400089433	-	yes	yes	GO:0016765; transferase activity, transferring alkyl or aryl (other than methyl) groups; Molecular Function
2333	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400039007	PGSC0003DMT400089436	chr04	NO	NO	
2334	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400039017	PGSC0003DMT400089446	chr01	yes	NO	
2335	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400039019	PGSC0003DMT400089448	chr06	NO	NO	
2336	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400039048	PGSC0003DMT400089477	chr04	yes	NO	
2337	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400039073	PGSC0003DMT400089502	chr03	NO	NO	
2338	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400039096	PGSC0003DMT400089525	chr12	NO	NO	
2339	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400039163	PGSC0003DMT400089592	chr09	yes	NO	GO:0004672; protein kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
2340	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400039165	PGSC0003DMT400089594	chr06	yes	yes	GO:0004652; polynucleotide adenylyltransferase activity; Molecular Function GO:0006350; transcription; Biological Process GO:0016779; nucleotidyltransferase activity; Molecular Function
2341	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400039182	PGSC0003DMT400089611	chr06	yes	yes	

2342	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400039204	PGSC0003DMT400089633	-	yes	NO	GO:0005198; structural molecule activity; Molecular Function
2343	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400039207	PGSC0003DMT400089636				
2344	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400039248	PGSC0003DMT400089677	chr06	NO	NO	
2345	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400039256	PGSC0003DMT400089685	chr02	NO	NO	
2346	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400039265	PGSC0003DMT400089694	chr07	yes	yes	
2347	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400039272	PGSC0003DMT400089701	chr02	yes	NO	GO:0005524; ATP binding; Molecular Function GO:0006915; apoptosis; Biological Process
2348	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400039305	PGSC0003DMT400089734	chr04	yes	NO	GO:0001522; pseudouridine synthesis; Biological Process GO:0003723; RNA binding; Molecular Function GO:0009451; RNA modification; Biological Process GO:0009982; pseudouridine synthase activity; Molecular Function
2349	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400039328	PGSC0003DMT400089757	chr10	yes	NO	GO:0005515; protein binding; Molecular Function
2350	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400039347	PGSC0003DMT400089776	chr01	NO	NO	
2351	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400039360	PGSC0003DMT400089789	chr05	yes	yes	

2352	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400039361	PGSC0003DMT400089790	chr02	NO	NO	GO:0003735; structural constituent of ribosome; Molecular Function GO:0005622; intracellular; Cellular Component GO:0005840; ribosome; Cellular Component GO:0006412; translation; Biological Process
2353	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400039474	PGSC0003DMT400089903	chr11	NO	NO	
2354	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400039475	PGSC0003DMT400089904	chr10	NO	NO	
2355	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400039476	PGSC0003DMT400089905	chr10	yes	yes	
2356	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400039524	PGSC0003DMT400089953	chr07	yes	NO	GO:0004497; monooxygenase activity; Molecular Function GO:0005506; iron ion binding; Molecular Function GO:0009055; electron carrier activity; Molecular Function GO:0020037; heme binding; Molecular Function
2357	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400039537	PGSC0003DMT400089966	chr09	yes	yes	
2358	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400039542	PGSC0003DMT400089971	chr02	yes	NO	
2359	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400039597	PGSC0003DMT400090026	chr05	yes	NO	
2360	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400039637	PGSC0003DMT400090066	chr12	NO	NO	
2361	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400039647	PGSC0003DMT400090076	chr10	NO	NO	

2362	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400039707	PGSC0003DMT400090136	chr04	yes	NO	
2363	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400039728	PGSC0003DMT400090157	chr12	NO	NO	
2364	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400039732	PGSC0003DMT400090161	chr11	NO	NO	GO:0005515; protein binding; Molecular Function
2365	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400039759	PGSC0003DMT400090188	chr05	yes	yes	GO:0004650; polygalacturonase activity; Molecular Function GO:0005975; carbohydrate metabolic process; Biological Process
2366	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400039761	PGSC0003DMT400090190	chr11	yes	NO	
2367	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400039806	PGSC0003DMT400090235	chr08	yes	yes	GO:0003924; GTPase activity; Molecular Function GO:0005525; GTP binding; Molecular Function
2368	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400039811	PGSC0003DMT400090240	chr12	NO	NO	
2369	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400039842	PGSC0003DMT400090271	chr11	NO	NO	
2370	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400039843	PGSC0003DMT400090272	chr10	NO	NO	GO:0005524; ATP binding; Molecular Function GO:0006810; transport; Biological Process GO:0016021; integral to membrane; Cellular Component GO:0016887; ATPase activity; Molecular Function GO:0042626; ATPase activity, coupled to transmembrane movement of substances; Molecular Function GO:0055085; transmembrane transport; Biological Process
2371	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400039845	PGSC0003DMT400090274	chr10	NO	NO	

2372	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400039874	PGSC0003DMT400090303	chr02	yes	yes	
2373	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400039878	PGSC0003DMT400090307	chr09	yes	NO	GO:0005515; protein binding; Molecular Function
2374	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400039917	PGSC0003DMT400090346	chr05	yes	yes	
2375	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400039921	PGSC0003DMT400090350	chr08	yes	yes	
2376	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400039982	PGSC0003DMT400090411	chr07	yes	yes	
2377	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400039985	PGSC0003DMT400090414	chr05	yes	NO	GO:0004252; serine-type endopeptidase activity; Molecular Function GO:0006508; proteolysis; Biological Process
2378	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400040003	PGSC0003DMT400090432				
2379	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400040009	PGSC0003DMT400090438	chr06	NO	NO	
2380	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400040029	PGSC0003DMT400090458	chr07	yes	yes	GO:0005507; copper ion binding; Molecular Function GO:0016491; oxidoreductase activity; Molecular Function GO:0055114; oxidation reduction; Biological Process
2381	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400040071	PGSC0003DMT400090500	chr02	NO	NO	
2382	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400040094	PGSC0003DMT400090523	chr11	NO	NO	

2383	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400040102	PGSC0003DMT400090531	chr03	yes	yes	GO:0003677; DNA binding; Molecular Function GO:0003700; transcription factor activity; Molecular Function GO:0006352; transcription initiation; Biological Process GO:0006355; regulation of transcription, DNA-dependent; Biological Process GO:0016987; sigma factor activity; Molecular Function
2384	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400040109	PGSC0003DMT400090538	chr08	yes	yes	GO:0005737; cytoplasm; Cellular Component GO:0008119; thiopurine S-methyltransferase activity; Molecular Function GO:0008152; metabolic process; Biological Process
2385	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400040121	PGSC0003DMT400090550	chr05	yes	NO	
2386	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400040141	PGSC0003DMT400090570	chr06	yes	NO	GO:0004497; monooxygenase activity; Molecular Function GO:0005506; iron ion binding; Molecular Function GO:0009055; electron carrier activity; Molecular Function GO:0020037; heme binding; Molecular Function
2387	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400040149	PGSC0003DMT400090578	chr01	NO	NO	GO:0005524; ATP binding; Molecular Function GO:0006915; apoptosis; Biological Process
2388	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400040152	PGSC0003DMT400090581	chr12	NO	NO	
2389	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400040177	PGSC0003DMT400090606	chr11	yes	NO	GO:0016021; integral to membrane; Cellular Component
2390	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400040207	PGSC0003DMT400090636	chr07	NO	NO	
2391	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400040271	PGSC0003DMT400090700	chr03	yes	NO	

2392	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400040283	PGSC0003DMT400090712	chr11	yes	NO	
2393	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400040293	PGSC0003DMT400090722	chr03	yes	yes	GO:0005524; ATP binding; Molecular Function
2394	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400040297	PGSC0003DMT400090726	chr05	NO	NO	
2395	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400040313	PGSC0003DMT400090742	chr02	yes	yes	
2396	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400040320	PGSC0003DMT400090749	chr06	yes	yes	GO:0005515; protein binding; Molecular Function GO:0006915; apoptosis; Biological Process
2397	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400040327	PGSC0003DMT400090756	chr06	NO	NO	
2398	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400040353	PGSC0003DMT400090782	chr07	NO	NO	GO:0016791; phosphatase activity; Molecular Function
2399	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400040407	PGSC0003DMT400090836	chr11	yes	NO	GO:0004672; protein kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
2400	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400040427	PGSC0003DMT400090856	chr12	yes	NO	
2401	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400040439	PGSC0003DMT400090868	-	NO	NO	
2402	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400040448	PGSC0003DMT400090877	chr06	NO	NO	
2403	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400040494	PGSC0003DMT400090923	-	NO	NO	

2404	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400040499	PGSC0003DMT400090928	chr04	NO	NO	
2405	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400040546	PGSC0003DMT400090975	-	yes	NO	GO:0004672; protein kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006355; regulation of transcription, DNA-dependent; Biological Process GO:0006468; protein amino acid phosphorylation; Biological Process
2406	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400040597	PGSC0003DMT400091026	chr10	yes	yes	
2407	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400040684	PGSC0003DMT400091113	chr10	NO	NO	
2408	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400040723	PGSC0003DMT400091152	chr04	NO	NO	
2409	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400040754	PGSC0003DMT400091183	chr12	NO	NO	
2410	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400040763	PGSC0003DMT400091192	chr12	yes	NO	GO:0005515; protein binding; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006915; apoptosis; Biological Process
2411	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400040768	PGSC0003DMT400091197	-	yes	yes	GO:0004601; peroxidase activity; Molecular Function GO:0006979; response to oxidative stress; Biological Process GO:0020037; heme binding; Molecular Function GO:0055114; oxidation reduction; Biological Process
2412	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400040770	PGSC0003DMT400091199	chr01	yes	NO	

2413	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400040815	PGSC0003DMT400091244	chr03	yes	yes	GO:0009055; electron carrier activity; Molecular Function GO:0016491; oxidoreductase activity; Molecular Function
2414	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400040947	PGSC0003DMT400091376	chr05	yes	yes	
2415	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400040948	PGSC0003DMT400091377	-	yes	NO	
2416	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400040961	PGSC0003DMT400091390	chr04	NO	NO	
2417	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400041006	PGSC0003DMT400091435	chr07	yes	NO	
2418	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400041016	PGSC0003DMT400091445	chr11	yes	NO	
2419	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400041023	PGSC0003DMT400091452	chr05	NO	NO	
2420	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400041052	PGSC0003DMT400091481	chr12	yes	NO	
2421	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400041053	PGSC0003DMT400091482	chr02	NO	NO	
2422	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400041099	PGSC0003DMT400091528	chr12	NO	NO	
2423	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400041123	PGSC0003DMT400091552	chr10	yes	NO	

2424	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400041131	PGSC0003DMT400091560	chr03	yes	NO	GO:0004672; protein kinase activity; Molecular Function GO:0005515; protein binding; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
2425	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400041140	PGSC0003DMT400091569	chr01	yes	NO	
2426	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400041147	PGSC0003DMT400091576	chr12	NO	NO	
2427	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400041172	PGSC0003DMT400091601	chr08	yes	NO	GO:0003700; transcription factor activity; Molecular Function GO:0006355; regulation of transcription, DNA-dependent; Biological Process
2428	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400041182	PGSC0003DMT400091611	chr09	NO	NO	
2429	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400041187	PGSC0003DMT400091616	chr05	yes	yes	GO:0008146; sulfotransferase activity; Molecular Function
2430	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400041198	PGSC0003DMT400091627	chr09	yes	yes	GO:0005515; protein binding; Molecular Function
2431	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400041202	PGSC0003DMT400091631	chr11	yes	NO	GO:0005524; ATP binding; Molecular Function GO:0006810; transport; Biological Process GO:0016021; integral to membrane; Cellular Component GO:0016887; ATPase activity; Molecular Function GO:0042626; ATPase activity, coupled to transmembrane movement of substances; Molecular Function GO:0055085; transmembrane transport; Biological Process

2432	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400041267	PGSC0003DMT400091696	chr10	yes	NO	GO:0004497; monooxygenase activity; Molecular Function GO:0005506; iron ion binding; Molecular Function GO:0009055; electron carrier activity; Molecular Function GO:0020037; heme binding; Molecular Function
2433	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400041281	PGSC0003DMT400091710	chr04	NO	NO	
2434	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400041297	PGSC0003DMT400091726	chr11	yes	NO	GO:0005515; protein binding; Molecular Function
2435	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400041312	PGSC0003DMT400091741	chr11	NO	NO	
2436	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400041329	PGSC0003DMT400091758	chr08	NO	NO	GO:0004252; serine-type endopeptidase activity; Molecular Function GO:0006508; proteolysis; Biological Process
2437	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400041330	PGSC0003DMT400091759	chr06	yes	NO	GO:0000151; ubiquitin ligase complex; Cellular Component GO:0004672; protein kinase activity; Molecular Function GO:0004842; ubiquitin-protein ligase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process GO:0016567; protein ubiquitination; Biological Process
2438	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400041356	PGSC0003DMT400091785	chr11	yes	NO	
2439	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400041444	PGSC0003DMT400091873	chr01	NO	NO	
2440	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400041455	PGSC0003DMT400091884	chr06	NO	NO	

2441	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400041620	PGSC0003DMT400092049	chr08	NO	NO	
2442	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400041631	PGSC0003DMT400092060	chr09	NO	NO	
2443	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400041636	PGSC0003DMT400092065	chr01	yes	NO	GO:0005515; protein binding; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006915; apoptosis; Biological Process
2444	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400041644	PGSC0003DMT400092073	chr12	yes	NO	
2445	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400041674	PGSC0003DMT400092103	chr02	yes	NO	GO:0004601; peroxidase activity; Molecular Function GO:0006979; response to oxidative stress; Biological Process GO:0020037; heme binding; Molecular Function GO:0055114; oxidation reduction; Biological Process
2446	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400041679	PGSC0003DMT400092108	chr12	yes	NO	
2447	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400041685	PGSC0003DMT400092114	chr03	yes	yes	GO:0006486; protein amino acid glycosylation; Biological Process GO:0008378; galactosyltransferase activity; Molecular Function GO:0016020; membrane; Cellular Component
2448	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400041698	PGSC0003DMT400092127	chr01	yes	NO	
2449	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400041710	PGSC0003DMT400092139	chr01	yes	yes	

2450	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400041730	PGSC0003DMT400092159	-	yes	NO	GO:0003824; catalytic activity; Molecular Function GO:0004086; carbamoyl-phosphate synthase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006807; nitrogen compound metabolic process; Biological Process GO:0008152; metabolic process; Biological Process
2451	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400041737	PGSC0003DMT400092166	chr01	NO	NO	
2452	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400041788	PGSC0003DMT400092217	chr12	yes	NO	
2453	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400041790	PGSC0003DMT400092219	chr05	NO	NO	GO:0004672; protein kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
2454	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400041804	PGSC0003DMT400092233	chr01	yes	NO	GO:0005515; protein binding; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006915; apoptosis; Biological Process
2455	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400041837	PGSC0003DMT400092266	chr04	NO	NO	
2456	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400041853	PGSC0003DMT400092282	chr02	yes	NO	
2457	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400042055	PGSC0003DMT400092484	chr05	yes	NO	GO:0003676; nucleic acid binding; Molecular Function GO:0004523; ribonuclease H activity; Molecular Function
2458	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400042060	PGSC0003DMT400092489	chr04	yes	NO	GO:0015031; protein transport; Biological Process

2459	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400042065	PGSC0003DMT400092494	chr07	NO	NO	
2460	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400042114	PGSC0003DMT400092543	chr01	yes	NO	
2461	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400042130	PGSC0003DMT400092559	chr10	NO	NO	GO:0003924; GTPase activity; Molecular Function GO:0005525; GTP binding; Molecular Function
2462	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400042143	PGSC0003DMT400092572	chr04	NO	NO	
2463	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400042170	PGSC0003DMT400092599	chr04	yes	NO	GO:0005515; protein binding; Molecular Function
2464	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400042192	PGSC0003DMT400092621	chr06	yes	yes	GO:0004970; ionotropic glutamate receptor activity; Molecular Function GO:0005234; extracellular-glutamate-gated ion channel activity; Molecular Function GO:0016020; membrane; Cellular Component
2465	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400042205	PGSC0003DMT400092634	chr07	yes	NO	
2466	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400042223	PGSC0003DMT400092652	chr05	NO	NO	
2467	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400042224	PGSC0003DMT400092653	chr01	yes	NO	
2468	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400042283	PGSC0003DMT400092712	chr12	NO	NO	
2469	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400042286	PGSC0003DMT400092715	chr06	yes	NO	

2470	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400042379	PGSC0003DMT400092808	chr11	NO	NO	GO:0003700; transcription factor activity; Molecular Function GO:0006355; regulation of transcription, DNA-dependent; Biological Process
2471	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400042402	PGSC0003DMT400092831	chr04	yes	NO	
2472	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400042405	PGSC0003DMT400092834	chr07	yes	yes	GO:0006071; glycerol metabolic process; Biological Process GO:0008889; glycerophosphodiester phosphodiesterase activity; Molecular Function
2473	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400042422	PGSC0003DMT400092851	chr09	NO	NO	
2474	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400042425	PGSC0003DMT400092854	chr06	NO	NO	
2475	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400042434	PGSC0003DMT400092863	chr02	yes	NO	
2476	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400042439	PGSC0003DMT400092868	chr06	NO	NO	
2477	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400042480	PGSC0003DMT400092909	chr06	yes	NO	
2478	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400042484	PGSC0003DMT400092913	chr06	yes	NO	GO:0045454; cell redox homeostasis; Biological Process
2479	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400042520	PGSC0003DMT400092949	chr07	yes	NO	

2480	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400042529	PGSC0003DMT400092958	chr06	yes	NO	GO:0004427; inorganic diphosphatase activity; Molecular Function GO:0009678; hydrogen-translocating pyrophosphatase activity; Molecular Function GO:0015992; proton transport; Biological Process GO:0016020; membrane; Cellular Component
2481	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400042545	PGSC0003DMT400092974	chr03	yes	yes	
2482	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400042551	PGSC0003DMT400092980	chr10	NO	NO	
2483	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400042570	PGSC0003DMT400092999	chr01	NO	NO	
2484	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400042588	PGSC0003DMT400093017	chr06	NO	NO	
2485	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400042589	PGSC0003DMT400093018	chr10	NO	NO	
2486	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400042602	PGSC0003DMT400093031	chr11	NO	NO	GO:0010181; FMN binding; Molecular Function GO:0016491; oxidoreductase activity; Molecular Function
2487	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400042630	PGSC0003DMT400093059	chr12	yes	NO	
2488	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400042633	PGSC0003DMT400093062				
2489	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400042643	PGSC0003DMT400093072	chr10	yes	NO	
2490	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400042645	PGSC0003DMT400093074	chr05	yes	NO	

2491	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400042646	PGSC0003DMT400093075	-	yes	yes	
2492	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400042664	PGSC0003DMT400093093	chr12	NO	NO	
2493	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400042754	PGSC0003DMT400093183	chr12	yes	NO	
2494	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400042781	PGSC0003DMT400093210				
2495	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400042855	PGSC0003DMT400093284	chr09	yes	NO	
2496	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400042870	PGSC0003DMT400093299	chr01	NO	NO	
2497	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400042882	PGSC0003DMT400093311	chr09	yes	NO	
2498	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400042890	PGSC0003DMT400093319	chr08	yes	NO	
2499	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400042897	PGSC0003DMT400093326	chr12	NO	NO	
2500	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400042921	PGSC0003DMT400093350	-	yes	yes	GO:0005524; ATP binding; Molecular Function GO:0006915; apoptosis; Biological Process
2501	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400042927	PGSC0003DMT400093356				
2502	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400042943	PGSC0003DMT400093372	chr09	yes	NO	

2503	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400042955	PGSC0003DMT400093384				
2504	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400042985	PGSC0003DMT400093414	chr01	yes	NO	GO:0031072; heat shock protein binding; Molecular Function
2505	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400042997	PGSC0003DMT400093426	chr04	yes	yes	GO:0004672; protein kinase activity; Molecular Function GO:0005515; protein binding; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
2506	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400043009	PGSC0003DMT400093438	chr10	NO	NO	
2507	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400043013	PGSC0003DMT400093442	-	NO	NO	
2508	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400043032	PGSC0003DMT400093461	-	yes	NO	GO:0005515; protein binding; Molecular Function GO:0016070; RNA metabolic process; Biological Process
2509	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400043178	PGSC0003DMT400093607	chr03	yes	NO	GO:0004672; protein kinase activity; Molecular Function GO:0005515; protein binding; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
2510	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400043182	PGSC0003DMT400093611	chr05	yes	NO	
2511	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400043204	PGSC0003DMT400093633	chr04	yes	NO	
2512	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400043226	PGSC0003DMT400093655	chr10	yes	NO	GO:0004713; protein tyrosine kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process

2513	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400043228	PGSC0003DMT400093657	chr07	NO	NO	
2514	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400043254	PGSC0003DMT400093683	chr11	yes	NO	GO:0045735; nutrient reservoir activity; Molecular Function
2515	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400043262	PGSC0003DMT400093691	chr04	yes	NO	
2516	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400043346	PGSC0003DMT400093775	chr04	yes	NO	
2517	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400043370	PGSC0003DMT400093799	-	NO	NO	
2518	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400043420	PGSC0003DMT400093849	chr03	yes	yes	
2519	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400043438	PGSC0003DMT400093867	chr03	yes	NO	GO:0016747; transferase activity, transferring acyl groups other than amino-acyl groups; Molecular Function
2520	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400043456	PGSC0003DMT400093885	chr06	NO	NO	
2521	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400043461	PGSC0003DMT400093890	-	NO	NO	
2522	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400043521	PGSC0003DMT400093950	chr01	yes	NO	
2523	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400043525	PGSC0003DMT400093954	chr12	yes	NO	

2524	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400043542	PGSC0003DMT400093971	-	yes	NO	GO:0003735; structural constituent of ribosome; Molecular Function GO:0005622; intracellular; Cellular Component GO:0005840; ribosome; Cellular Component GO:0006412; translation; Biological Process
2525	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400043550	PGSC0003DMT400093979	chr02	NO	NO	GO:0004888; transmembrane receptor activity; Molecular Function GO:0007165; signal transduction; Biological Process GO:0031224; intrinsic to membrane; Cellular Component GO:0045087; innate immune response; Biological Process
2526	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400043553	PGSC0003DMT400093982	chr02	NO	NO	GO:0030528; transcription regulator activity; Molecular Function GO:0045449; regulation of transcription; Biological Process
2527	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400043564	PGSC0003DMT400093993	chr01	yes	yes	
2528	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400043566	PGSC0003DMT400093995	chr06	yes	NO	GO:0003824; catalytic activity; Molecular Function GO:0044237; cellular metabolic process; Biological Process GO:0050662; coenzyme binding; Molecular Function
2529	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400043592	PGSC0003DMT400094021	chr01	NO	NO	
2530	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400043600	PGSC0003DMT400094029	chr12	yes	NO	
2531	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400043603	PGSC0003DMT400094032	chr04	yes	NO	GO:0004672; protein kinase activity; Molecular Function GO:0005515; protein binding; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process

2532	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400043626	PGSC0003DMT400094055	chr12	yes	yes	
2533	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400043628	PGSC0003DMT400094057	chr02	yes	yes	
2534	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400043629	PGSC0003DMT400094058	chr06	NO	NO	
2535	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400043638	PGSC0003DMT400094067	chr06	yes	NO	
2536	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400043680	PGSC0003DMT400094109	chr06	yes	NO	
2537	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400043704	PGSC0003DMT400094133	chr06	yes	NO	
2538	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400043705	PGSC0003DMT400094134	chr06	NO	NO	
2539	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400043714	PGSC0003DMT400094143	chr12	NO	NO	GO:0009058; biosynthetic process; Biological Process GO:0016740; transferase activity; Molecular Function
2540	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400043739	PGSC0003DMT400094168	chr07	yes	NO	
2541	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400043748	PGSC0003DMT400094177	chr09	yes	NO	
2542	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400043773	PGSC0003DMT400094202	chr04	yes	yes	
2543	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400043792	PGSC0003DMT400094221	chr04	NO	NO	

2544	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400043811	PGSC0003DMT400094240	chr08	yes	NO	GO:0008237; metallopeptidase activity; Molecular Function GO:0008270; zinc ion binding; Molecular Function
2545	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400043828	PGSC0003DMT400094257	chr04	yes	NO	
2546	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400043868	PGSC0003DMT400094297	chr02	NO	NO	GO:0000148; 1,3-beta-glucan synthase complex; Cellular Component GO:0003843; 1,3-beta-glucan synthase activity; Molecular Function GO:0006075; 1,3-beta-glucan biosynthetic process; Biological Process GO:0016020; membrane; Cellular Component
2547	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400043911	PGSC0003DMT400094340	chr08	yes	yes	GO:0008152; metabolic process; Biological Process GO:0016616; oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor; Molecular Function GO:0048037; cofactor binding; Molecular Function GO:0051287; NAD or NADH binding; Molecular Function
2548	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400043912	PGSC0003DMT400094341	chr09	NO	NO	
2549	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400043928	PGSC0003DMT400094357	chr08	NO	NO	
2550	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400044005	PGSC0003DMT400094434	chr06	yes	NO	
2551	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400044045	PGSC0003DMT400094474	chr01	yes	NO	
2552	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400044049	PGSC0003DMT400094478	-	NO	NO	

2553	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400044115	PGSC0003DMT400094544	chr01	yes	NO	GO:0004672; protein kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
2554	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400044146	PGSC0003DMT400094575	-	NO	NO	
2555	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400044159	PGSC0003DMT400094588	chr09	NO	NO	GO:0008168; methyltransferase activity; Molecular Function
2556	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400044193	PGSC0003DMT400094622	chr10	yes	NO	
2557	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400044203	PGSC0003DMT400094632	chr04	yes	NO	GO:0004497; monooxygenase activity; Molecular Function GO:0005506; iron ion binding; Molecular Function GO:0009055; electron carrier activity; Molecular Function GO:0020037; heme binding; Molecular Function
2558	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400044266	PGSC0003DMT400094695	chr10	yes	NO	GO:0008152; metabolic process; Biological Process GO:0008415; acyltransferase activity; Molecular Function
2559	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400044270	PGSC0003DMT400094699	chr04	NO	NO	
2560	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400044288	PGSC0003DMT400094717	chr01	NO	NO	
2561	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400044318	PGSC0003DMT400094747	chr03	yes	NO	GO:0005515; protein binding; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0019538; protein metabolic process; Biological Process
2562	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400044342	PGSC0003DMT400094771	chr02	NO	NO	

2563	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400044375	PGSC0003DMT400094804	chr06	yes	NO	
2564	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400044383	PGSC0003DMT400094812	chr12	yes	NO	
2565	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400044458	PGSC0003DMT400094887	chr02	yes	NO	
2566	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400044484	PGSC0003DMT400094913	chr11	yes	NO	
2567	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400044485	PGSC0003DMT400094914	-	NO	NO	
2568	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400044560	PGSC0003DMT400094989	chr09	yes	NO	GO:0000287; magnesium ion binding; Molecular Function GO:0008152; metabolic process; Biological Process GO:0016829; lyase activity; Molecular Function
2569	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400044584	PGSC0003DMT400095013	-	yes	NO	GO:0015031; protein transport; Biological Process
2570	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400044650	PGSC0003DMT400095079	-	NO	NO	GO:0004806; triacylglycerol lipase activity; Molecular Function GO:0006629; lipid metabolic process; Biological Process
2571	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400044679	PGSC0003DMT400095108	chr09	yes	NO	GO:0004672; protein kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
2572	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400044688	PGSC0003DMT400095117	chr04	yes	NO	
2573	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400044692	PGSC0003DMT400095121	chr07	yes	NO	GO:0003677; DNA binding; Molecular Function GO:0015074; DNA integration; Biological Process

2574	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400044698	PGSC0003DMT400095127	chr03	NO	NO	
2575	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400044702	PGSC0003DMT400095131	chr08	yes	yes	
2576	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400044708	PGSC0003DMT400095137	chr10	NO	NO	GO:0005525; GTP binding; Molecular Function
2577	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400044715	PGSC0003DMT400095144	chr12	yes	NO	GO:0005515; protein binding; Molecular Function
2578	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400044732	PGSC0003DMT400095161	chr03	yes	NO	GO:0008152; metabolic process; Biological Process GO:0008168; methyltransferase activity; Molecular Function
2579	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400044791	PGSC0003DMT400095220	chr02	NO	NO	
2580	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400044804	PGSC0003DMT400095233	chr09	NO	NO	
2581	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400044834	PGSC0003DMT400095263	chr04	NO	NO	
2582	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400044835	PGSC0003DMT400095264	chr10	NO	NO	
2583	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400044843	PGSC0003DMT400095272	chr07	yes	yes	
2584	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400044853	PGSC0003DMT400095282	-	NO	NO	
2585	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400044862	PGSC0003DMT400095291	-	yes	NO	

2586	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400044885	PGSC0003DMT400095314	chr09	NO	NO	GO:0003700; transcription factor activity; Molecular Function GO:0005634; nucleus; Cellular Component GO:0006355; regulation of transcription, DNA-dependent; Biological Process GO:0043565; sequence-specific DNA binding; Molecular Function
2587	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400044933	PGSC0003DMT400095362	chr04	yes	NO	
2588	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400044939	PGSC0003DMT400095368	chr07	yes	yes	GO:0004672; protein kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
2589	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400044954	PGSC0003DMT400095383	chr06	NO	NO	
2590	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400044965	PGSC0003DMT400095394	chr10	yes	NO	
2591	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400045035	PGSC0003DMT400095464	chr01	yes	NO	
2592	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400045053	PGSC0003DMT400095482	chr10	yes	yes	
2593	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400045071	PGSC0003DMT400095500	-	NO	NO	
2594	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400045082	PGSC0003DMT400095511	chr04	yes	yes	GO:0003723; RNA binding; Molecular Function GO:0003964; RNA-directed DNA polymerase activity; Molecular Function GO:0006278; RNA-dependent DNA replication; Biological Process

2595	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400045095	PGSC0003DMT400095524	chr04	yes	yes	
2596	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400045125	PGSC0003DMT400095554	chr02	NO	NO	
2597	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400045131	PGSC0003DMT400095560	-	NO	NO	
2598	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400045164	PGSC0003DMT400095593	chr07	yes	yes	GO:0004751; ribose-5-phosphate isomerase activity; Molecular Function GO:0009052; pentose-phosphate shunt, non-oxidative branch; Biological Process
2599	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400045176	PGSC0003DMT400095605				
2600	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400045252	PGSC0003DMT400095681	chr01	NO	NO	
2601	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400045258	PGSC0003DMT400095687	chr01	yes	NO	
2602	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400045260	PGSC0003DMT400095689	chr02	yes	NO	
2603	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400045271	PGSC0003DMT400095700	chr11	yes	NO	GO:0016311; dephosphorylation; Biological Process GO:0016791; phosphatase activity; Molecular Function
2604	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400045288	PGSC0003DMT400095717	chr07	yes	NO	
2605	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400045330	PGSC0003DMT400095759	chr12	NO	NO	

2606	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400045335	PGSC0003DMT400095764	chr10	yes	NO	GO:0004332; fructose-bisphosphate aldolase activity; Molecular Function GO:0005515; protein binding; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006096; glycolysis; Biological Process GO:0006915; apoptosis; Biological Process
2607	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400045356	PGSC0003DMT400095785	chr05	NO	NO	
2608	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400045398	PGSC0003DMT400095827	chr08	NO	NO	GO:0004190; aspartic-type endopeptidase activity; Molecular Function GO:0006508; proteolysis; Biological Process
2609	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400045416	PGSC0003DMT400095845				
2610	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400045427	PGSC0003DMT400095856	chr10	NO	NO	
2611	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400045434	PGSC0003DMT400095863	chr04	yes	NO	
2612	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400045449	PGSC0003DMT400095878	-	NO	NO	
2613	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400045453	PGSC0003DMT400095882	chr04	NO	NO	GO:0003735; structural constituent of ribosome; Molecular Function GO:0005622; intracellular; Cellular Component GO:0005840; ribosome; Cellular Component GO:0006412; translation; Biological Process GO:0016491; oxidoreductase activity; Molecular Function GO:0055114; oxidation reduction; Biological Process

2614	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400045511	PGSC0003DMT400095940	chr12	yes	yes	GO:0004553; hydrolase activity, hydrolyzing O-glycosyl compounds; Molecular Function GO:0005975; carbohydrate metabolic process; Biological Process
2615	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400045583	PGSC0003DMT400096012	chr03	yes	NO	GO:0008152; metabolic process; Biological Process GO:0016758; transferase activity, transferring hexosyl groups; Molecular Function
2616	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400045598	PGSC0003DMT400096027	-	NO	NO	
2617	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400045690	PGSC0003DMT400096119	chr10	yes	NO	
2618	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400045706	PGSC0003DMT400096135	-	yes	NO	
2619	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400045726	PGSC0003DMT400096155	chr04	NO	NO	
2620	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400045738	PGSC0003DMT400096167	chr09	yes	NO	GO:0008152; metabolic process; Biological Process GO:0016491; oxidoreductase activity; Molecular Function GO:0055114; oxidation reduction; Biological Process
2621	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400045754	PGSC0003DMT400096183	chr07	yes	NO	GO:0005507; copper ion binding; Molecular Function GO:0009055; electron carrier activity; Molecular Function
2622	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400045777	PGSC0003DMT400096206	chr10	yes	NO	
2623	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400045783	PGSC0003DMT400096212	chr01	NO	NO	

2624	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400045803	PGSC0003DMT400096232	chr09	NO	NO	
2625	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400045804	PGSC0003DMT400096233	chr02	yes	NO	GO:0005506; iron ion binding; Molecular Function GO:0009055; electron carrier activity; Molecular Function GO:0020037; heme binding; Molecular Function
2626	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400045810	PGSC0003DMT400096239	chr04	yes	NO	
2627	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400045819	PGSC0003DMT400096248	chr03	yes	NO	GO:0005515; protein binding; Molecular Function
2628	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400045827	PGSC0003DMT400096256	chr12	NO	NO	
2629	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400045828	PGSC0003DMT400096257	chr08	NO	NO	
2630	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400045833	PGSC0003DMT400096262	chr02	yes	yes	GO:0016429; tRNA (adenine-N1-)-methyltransferase activity; Molecular Function GO:0030488; tRNA methylation; Biological Process
2631	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400045844	PGSC0003DMT400096273	chr01	yes	NO	
2632	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400045918	PGSC0003DMT400096347	chr12	NO	NO	
2633	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400045943	PGSC0003DMT400096372	chr10	yes	NO	
2634	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400045962	PGSC0003DMT400096391	chr09	NO	NO	GO:0006284; base-excision repair; Biological Process

2635	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400045968	PGSC0003DMT400096397	chr01	yes	NO	
2636	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400045982	PGSC0003DMT400096411	chr04	yes	NO	GO:0016020; membrane; Cellular Component
2637	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400045989	PGSC0003DMT400096418	chr06	yes	NO	GO:0003700; transcription factor activity; Molecular Function GO:0006355; regulation of transcription, DNA-dependent; Biological Process
2638	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400045992	PGSC0003DMT400096421	-	yes	yes	
2639	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400046009	PGSC0003DMT400096438	chr07	yes	NO	
2640	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400046033	PGSC0003DMT400096462	-	yes	NO	
2641	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400046064	PGSC0003DMT400096493	chr06	NO	NO	
2642	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400046084	PGSC0003DMT400096513	-	NO	NO	
2643	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400046102	PGSC0003DMT400096531	chr04	NO	NO	
2644	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400046162	PGSC0003DMT400096591	chr02	yes	NO	
2645	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400046178	PGSC0003DMT400096607	chr03	NO	NO	GO:0005634; nucleus; Cellular Component GO:0008270; zinc ion binding; Molecular Function GO:0016568; chromatin modification; Biological Process GO:0018024; histone-lysine N-methyltransferase activity; Molecular Function

2646	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400046180	PGSC0003DMT400096609	chr05	yes	NO	
2647	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400046201	PGSC0003DMT400096630	chr03	yes	NO	
2648	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400046243	PGSC0003DMT400096672	chr08	yes	NO	
2649	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400046265	PGSC0003DMT400096694	chr10	yes	yes	GO:0000103; sulfate assimilation; Biological Process GO:0005524; ATP binding; Molecular Function GO:0016301; kinase activity; Molecular Function GO:0016772; transferase activity, transferring phosphorus-containing groups; Molecular Function
2650	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400046266	PGSC0003DMT400096695	chr01	NO	NO	GO:0045735; nutrient reservoir activity; Molecular Function
2651	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400046297	PGSC0003DMT400096726	chr07	yes	NO	GO:0019787; small conjugating protein ligase activity; Molecular Function GO:0043687; post-translational protein modification; Biological Process GO:0051246; regulation of protein metabolic process; Biological Process
2652	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400046305	PGSC0003DMT400096734	chr11	NO	NO	
2653	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400046306	PGSC0003DMT400096735	chr02	NO	NO	GO:0003676; nucleic acid binding; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0008026; ATP-dependent helicase activity; Molecular Function
2654	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400046312	PGSC0003DMT400096741	chr10	yes	NO	GO:0003676; nucleic acid binding; Molecular Function

2655	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400046357	PGSC0003DMT400096786	-	NO	NO	
2656	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400046375	PGSC0003DMT400096804	chr08	NO	NO	GO:0004190; aspartic-type endopeptidase activity; Molecular Function GO:0006508; proteolysis; Biological Process
2657	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400046382	PGSC0003DMT400096811	chr07	NO	NO	
2658	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400046415	PGSC0003DMT400096844	chr09	yes	NO	
2659	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400046419	PGSC0003DMT400096848	chr09	yes	NO	GO:0004497; monooxygenase activity; Molecular Function GO:0005506; iron ion binding; Molecular Function GO:0009055; electron carrier activity; Molecular Function GO:0020037; heme binding; Molecular Function
2660	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400046427	PGSC0003DMT400096856	chr12	NO	NO	GO:0000287; magnesium ion binding; Molecular Function GO:0008152; metabolic process; Biological Process GO:0016829; lyase activity; Molecular Function
2661	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400046437	PGSC0003DMT400096866	chr01	yes	NO	
2662	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400046445	PGSC0003DMT400096874	chr06	yes	yes	
2663	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400046512	PGSC0003DMT400096941	chr11	yes	NO	
2664	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400046549	PGSC0003DMT400096978	chr05	yes	yes	

2665	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400046578	PGSC0003DMT400097007	chr07	yes	NO	
2666	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400046594	PGSC0003DMT400097023	chr02	yes	yes	
2667	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400046621	PGSC0003DMT400097050	chr12	NO	NO	GO:0016491; oxidoreductase activity; Molecular Function
2668	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400046647	PGSC0003DMT400097076	chr12	yes	yes	
2669	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400046659	PGSC0003DMT400097088	chr06	NO	NO	
2670	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400046722	PGSC0003DMT400097151	chr11	yes	NO	GO:0004888; transmembrane receptor activity; Molecular Function GO:0005515; protein binding; Molecular Function GO:0007165; signal transduction; Biological Process GO:0031224; intrinsic to membrane; Cellular Component GO:0045087; innate immune response; Biological Process
2671	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400046727	PGSC0003DMT400097156	chr03	NO	NO	
2672	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400046744	PGSC0003DMT400097173	-	NO	NO	
2673	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400046780	PGSC0003DMT400097209	chr03	yes	NO	GO:0003735; structural constituent of ribosome; Molecular Function GO:0005622; intracellular; Cellular Component GO:0005840; ribosome; Cellular Component GO:0006412; translation; Biological Process
2674	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400046789	PGSC0003DMT400097218	chr12	yes	yes	GO:0005524; ATP binding; Molecular Function GO:0006915; apoptosis; Biological Process

2675	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400046796	PGSC0003DMT400097225	chr04	yes	NO	GO:0004867; serine-type endopeptidase inhibitor activity; Molecular Function
2676	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400046800	PGSC0003DMT400097229	chr11	NO	NO	
2677	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400046845	PGSC0003DMT400097274	chr12	yes	yes	
2678	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400046847	PGSC0003DMT400097276	chr05	yes	yes	
2679	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400046848	PGSC0003DMT400097277	chr10	NO	NO	GO:0016702; oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen; Molecular Function GO:0046872; metal ion binding; Molecular Function GO:0055114; oxidation reduction; Biological Process
2680	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400046882	PGSC0003DMT400097311	chr03	yes	NO	GO:0003700; transcription factor activity; Molecular Function GO:0043565; sequence-specific DNA binding; Molecular Function GO:0045449; regulation of transcription; Biological Process
2681	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400046903	PGSC0003DMT400097332	chr01	yes	yes	
2682	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400046916	PGSC0003DMT400097345	chr01	yes	yes	
2683	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400046938	PGSC0003DMT400097367	chr04	yes	yes	GO:0016787; hydrolase activity; Molecular Function

2684	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400046977	PGSC0003DMT400097406	chr02	yes	NO	GO:0000155; two-component sensor activity; Molecular Function GO:0004872; receptor activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006355; regulation of transcription, DNA-dependent; Biological Process GO:0007165; signal transduction; Biological Process GO:0007600; sensory perception; Biological Process GO:0008020; G-protein coupled photoreceptor activity; Molecular Function GO:0016020; membrane; Cellular Component GO:0018298; protein-chromophore linkage; Biological Process GO:0045449; regulation of transcription; Biological Process
2685	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400046995	PGSC0003DMT400097424	chr04	yes	NO	GO:0008152; metabolic process; Biological Process GO:0016758; transferase activity, transferring hexosyl groups; Molecular Function
2686	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400047004	PGSC0003DMT400097433	chr05	yes	NO	
2687	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400047005	PGSC0003DMT400097434	chr06	NO	NO	
2688	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400047037	PGSC0003DMT400097466	chr03	yes	NO	
2689	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400047075	PGSC0003DMT400097504	-	yes	NO	
2690	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400047078	PGSC0003DMT400097507	chr08	yes	yes	

2691	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400047088	PGSC0003DMT400097517	chr04	yes	NO	
2692	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400047103	PGSC0003DMT400097532	chr03	yes	NO	
2693	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400047120	PGSC0003DMT400097549	chr04	yes	NO	
2694	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400047153	PGSC0003DMT400097582	-	yes	yes	
2695	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400047170	PGSC0003DMT400097599	chr10	yes	NO	
2696	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400047244	PGSC0003DMT400097673	chr05	yes	yes	
2697	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400047266	PGSC0003DMT400097695	chr12	NO	NO	GO:0003700; transcription factor activity; Molecular Function GO:0043565; sequence-specific DNA binding; Molecular Function GO:0045449; regulation of transcription; Biological Process
2698	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400047275	PGSC0003DMT400097704	chr04	NO	NO	
2699	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400047304	PGSC0003DMT400097733	chr10	yes	NO	
2700	Heterozygous PS in RH, not shared by DM	PGSC0003DMG400047351	PGSC0003DMT400097780	chr05	yes	NO	GO:0003676; nucleic acid binding; Molecular Function GO:0004523; ribonuclease H activity; Molecular Function
2701	Homozygous PS in RH	PGSC0003DMG401000097	PGSC0003DMT400000290	chr05	yes	NO	

2702	Homozygous PS in RH	PGSC0003DMG400000098	PGSC0003DMT400000293	chr05	NO	NO	GO:0006629; lipid metabolic process; Biological Process GO:0016788; hydrolase activity, acting on ester bonds; Molecular Function
2703	Homozygous PS in RH	PGSC0003DMG400000252	PGSC0003DMT400000701	chr12	yes	NO	GO:0003735; structural constituent of ribosome; Molecular Function GO:0005622; intracellular; Cellular Component GO:0005840; ribosome; Cellular Component GO:0006412; translation; Biological Process
2704	Homozygous PS in RH	PGSC0003DMG400000255	PGSC0003DMT400000704	chr04	NO	NO	
2705	Homozygous PS in RH	PGSC0003DMG400000358	PGSC0003DMT400000956	chr02	yes	NO	GO:0003700; transcription factor activity; Molecular Function GO:0043565; sequence-specific DNA binding; Molecular Function GO:0045449; regulation of transcription; Biological Process
2706	Homozygous PS in RH	PGSC0003DMG400000483	PGSC0003DMT400001270	chr02	yes	NO	GO:0045735; nutrient reservoir activity; Molecular Function
2707	Homozygous PS in RH	PGSC0003DMG400000578	PGSC0003DMT400001565	chr07	NO	NO	
2708	Homozygous PS in RH	PGSC0003DMG403000585	PGSC0003DMT400001582	chr02	NO	NO	
2709	Homozygous PS in RH	PGSC0003DMG400000595	PGSC0003DMT400001611	chr06	NO	NO	
2710	Homozygous PS in RH	PGSC0003DMG400000599	PGSC0003DMT400001617	chr10	yes	yes	
2711	Homozygous PS in RH	PGSC0003DMG400000637	PGSC0003DMT400001705	chr07	NO	NO	GO:0003677; DNA binding; Molecular Function GO:0005634; nucleus; Cellular Component
2712	Homozygous PS in RH	PGSC0003DMG400000682	PGSC0003DMT400001821	chr08	yes	yes	GO:0004421; hydroxymethylglutaryl-CoA synthase activity; Molecular Function GO:0008299; isoprenoid biosynthetic process; Biological Process
2713	Homozygous PS in RH	PGSC0003DMG400000799	PGSC0003DMT400002100	chr04	NO	NO	

2714	Homozygous PS in RH	PGSC0003DMG400000806	PGSC0003DMT400002115	chr05	yes	NO	GO:0003924; GTPase activity; Molecular Function GO:0005525; GTP binding; Molecular Function
2715	Homozygous PS in RH	PGSC0003DMG400000885	PGSC0003DMT400002312	chr12	NO	NO	
2716	Homozygous PS in RH	PGSC0003DMG402000911	PGSC0003DMT400002377	chr11	yes	NO	
2717	Homozygous PS in RH	PGSC0003DMG402000914	PGSC0003DMT400002382	chr07	NO	NO	
2718	Homozygous PS in RH	PGSC0003DMG400001155	PGSC0003DMT400002955	-	NO	NO	GO:0008152; metabolic process; Biological Process GO:0016758; transferase activity, transferring hexosyl groups; Molecular Function
2719	Homozygous PS in RH	PGSC0003DMG400001242	PGSC0003DMT400003131	chr06	NO	NO	
2720	Homozygous PS in RH	PGSC0003DMG400001597	PGSC0003DMT400004045	-	yes	yes	
2721	Homozygous PS in RH	PGSC0003DMG400001637	PGSC0003DMT400004139	chr10	yes	NO	GO:0005515; protein binding; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006915; apoptosis; Biological Process
2722	Homozygous PS in RH	PGSC0003DMG400001867	PGSC0003DMT400004722	chr04	NO	NO	
2723	Homozygous PS in RH	PGSC0003DMG402001968	PGSC0003DMT400004975	chr12	NO	NO	
2724	Homozygous PS in RH	PGSC0003DMG400001970	PGSC0003DMT400004986	chr10	yes	NO	GO:0008168; methyltransferase activity; Molecular Function GO:0008171; O-methyltransferase activity; Molecular Function GO:0046983; protein dimerization activity; Molecular Function
2725	Homozygous PS in RH	PGSC0003DMG400002203	PGSC0003DMT400005615	chr04	yes	NO	GO:0004672; protein kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
2726	Homozygous PS in RH	PGSC0003DMG400002213	PGSC0003DMT400005645	chr07	yes	NO	

2727	Homozygous PS in RH	PGSC0003DMG400002401	PGSC0003DMT400006174	-	NO	NO	
2728	Homozygous PS in RH	PGSC0003DMG401002538	PGSC0003DMT400006502	chr11	yes	NO	GO:0004497; monooxygenase activity; Molecular Function GO:0005506; iron ion binding; Molecular Function GO:0009055; electron carrier activity; Molecular Function GO:0020037; heme binding; Molecular Function
2729	Homozygous PS in RH	PGSC0003DMG400002541	PGSC0003DMT400006512	-	yes	NO	
2730	Homozygous PS in RH	PGSC0003DMG400002560	PGSC0003DMT400006581	chr02	yes	yes	
2731	Homozygous PS in RH	PGSC0003DMG400002682	PGSC0003DMT400006915	chr10	yes	NO	GO:0004672; protein kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
2732	Homozygous PS in RH	PGSC0003DMG400002740	PGSC0003DMT400007079	chr02	yes	yes	GO:0003676; nucleic acid binding; Molecular Function GO:0008270; zinc ion binding; Molecular Function
2733	Homozygous PS in RH	PGSC0003DMG400002924	PGSC0003DMT400007575	chr04	yes	yes	
2734	Homozygous PS in RH	PGSC0003DMG400002984	PGSC0003DMT400007723	chr08	NO	NO	
2735	Homozygous PS in RH	PGSC0003DMG400003097	PGSC0003DMT400008016	chr05	NO	NO	
2736	Homozygous PS in RH	PGSC0003DMG400003119	PGSC0003DMT400008091	chr01	yes	yes	GO:0003677; DNA binding; Molecular Function GO:0005634; nucleus; Cellular Component
2737	Homozygous PS in RH	PGSC0003DMG400003134	PGSC0003DMT400008126	chr08	yes	NO	
2738	Homozygous PS in RH	PGSC0003DMG400003158	PGSC0003DMT400008191	chr10	NO	NO	
2739	Homozygous PS in RH	PGSC0003DMG402003185	PGSC0003DMT400008258	chr12	NO	NO	
2740	Homozygous PS in RH	PGSC0003DMG400003351	PGSC0003DMT400008648	chr05	NO	NO	

2741	Homozygous PS in RH	PGSC0003DMG400003374	PGSC0003DMT400008698	-	NO	NO	
2742	Homozygous PS in RH	PGSC0003DMG400003421	PGSC0003DMT400008810	chr06	NO	NO	
2743	Homozygous PS in RH	PGSC0003DMG400003587	PGSC0003DMT400009240	chr07	NO	NO	
2744	Homozygous PS in RH	PGSC0003DMG400003593	PGSC0003DMT400009258	chr10	NO	NO	
2745	Homozygous PS in RH	PGSC0003DMG400003814	PGSC0003DMT400009748	chr05	yes	NO	GO:0008146; sulfotransferase activity; Molecular Function
2746	Homozygous PS in RH	PGSC0003DMG400003836	PGSC0003DMT400009801	chr04	yes	NO	
2747	Homozygous PS in RH	PGSC0003DMG400003879	PGSC0003DMT400009897	chr06	yes	yes	
2748	Homozygous PS in RH	PGSC0003DMG400003903	PGSC0003DMT400009973	chr09	NO	NO	
2749	Homozygous PS in RH	PGSC0003DMG400003946	PGSC0003DMT400010077	chr05	yes	yes	GO:0005515; protein binding; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0044267; cellular protein metabolic process; Biological Process
2750	Homozygous PS in RH	PGSC0003DMG402003998	PGSC0003DMT400010206	chr10	NO	NO	
2751	Homozygous PS in RH	PGSC0003DMG400004134	PGSC0003DMT400010582	chr02	yes	NO	
2752	Homozygous PS in RH	PGSC0003DMG400004271	PGSC0003DMT400010905	chr09	yes	yes	
2753	Homozygous PS in RH	PGSC0003DMG400004307	PGSC0003DMT400010994	chr01	NO	NO	
2754	Homozygous PS in RH	PGSC0003DMG400004360	PGSC0003DMT400011144	chr11	yes	NO	
2755	Homozygous PS in RH	PGSC0003DMG400004711	PGSC0003DMT400012003	chr08	NO	NO	
2756	Homozygous PS in RH	PGSC0003DMG400004714	PGSC0003DMT400012008	-	yes	yes	GO:0003824; catalytic activity; Molecular Function GO:0008152; metabolic process; Biological Process
2757	Homozygous PS in RH	PGSC0003DMG400004721	PGSC0003DMT400012031	chr03	yes	NO	GO:0003723; RNA binding; Molecular Function

2758	Homozygous PS in RH	PGSC0003DMG400004780	PGSC0003DMT400012203	chr12	yes	yes	
2759	Homozygous PS in RH	PGSC0003DMG400004814	PGSC0003DMT400012266	-	NO	NO	
2760	Homozygous PS in RH	PGSC0003DMG400004828	PGSC0003DMT400012322	chr06	yes	NO	GO:0016491; oxidoreductase activity; Molecular Function
2761	Homozygous PS in RH	PGSC0003DMG400004829	PGSC0003DMT400012323	chr06	NO	NO	
2762	Homozygous PS in RH	PGSC0003DMG400004915	PGSC0003DMT400012574	chr03	NO	NO	
2763	Homozygous PS in RH	PGSC0003DMG400004961	PGSC0003DMT400012730	chr06	yes	yes	GO:0005515; protein binding; Molecular Function
2764	Homozygous PS in RH	PGSC0003DMG400004966	PGSC0003DMT400012744	chr03	NO	NO	GO:0004867; serine-type endopeptidase inhibitor activity; Molecular Function
2765	Homozygous PS in RH	PGSC0003DMG400005010	PGSC0003DMT400012867	chr04	NO	NO	
2766	Homozygous PS in RH	PGSC0003DMG400005046	PGSC0003DMT400012949	chr07	yes	NO	GO:0006812; cation transport; Biological Process GO:0008324; cation transmembrane transporter activity; Molecular Function GO:0016020; membrane; Cellular Component GO:0055085; transmembrane transport; Biological Process
2767	Homozygous PS in RH	PGSC0003DMG400005076	PGSC0003DMT400013028	chr06	yes	yes	GO:0005524; ATP binding; Molecular Function GO:0006915; apoptosis; Biological Process
2768	Homozygous PS in RH	PGSC0003DMG400005207	PGSC0003DMT400013354	chr03	yes	yes	GO:0031072; heat shock protein binding; Molecular Function
2769	Homozygous PS in RH	PGSC0003DMG400005351	PGSC0003DMT400013687	chr06	NO	NO	GO:0005743; mitochondrial inner membrane; Cellular Component GO:0008565; protein transporter activity; Molecular Function GO:0015031; protein transport; Biological Process
2770	Homozygous PS in RH	PGSC0003DMG400005566	PGSC0003DMT400014199	chr01	yes	NO	
2771	Homozygous PS in RH	PGSC0003DMG400005613	PGSC0003DMT400014305	chr09	NO	NO	

2772	Homozygous PS in RH	PGSC0003DMG400005666	PGSC0003DMT400014442	chr09	NO	NO	
2773	Homozygous PS in RH	PGSC0003DMG400005722	PGSC0003DMT400014646	chr11	NO	NO	GO:0005524; ATP binding; Molecular Function GO:0006810; transport; Biological Process GO:0016021; integral to membrane; Cellular Component GO:0016887; ATPase activity; Molecular Function GO:0042626; ATPase activity, coupled to transmembrane movement of substances; Molecular Function GO:0055085; transmembrane transport; Biological Process
2774	Homozygous PS in RH	PGSC0003DMG400005749	PGSC0003DMT400014749	chr09	yes	NO	
2775	Homozygous PS in RH	PGSC0003DMG400005901	PGSC0003DMT400015093	chr12	NO	NO	
2776	Homozygous PS in RH	PGSC0003DMG400005920	PGSC0003DMT400015160	chr10	yes	NO	
2777	Homozygous PS in RH	PGSC0003DMG400006044	PGSC0003DMT400015480	chr12	NO	NO	
2778	Homozygous PS in RH	PGSC0003DMG400006048	PGSC0003DMT400015484	chr07	yes	yes	
2779	Homozygous PS in RH	PGSC0003DMG402006174	PGSC0003DMT400015796	-	NO	NO	
2780	Homozygous PS in RH	PGSC0003DMG400006318	PGSC0003DMT400016166	chr10	NO	NO	
2781	Homozygous PS in RH	PGSC0003DMG400006384	PGSC0003DMT400016336	chr09	yes	NO	
2782	Homozygous PS in RH	PGSC0003DMG400006556	PGSC0003DMT400016766	chr07	yes	yes	
2783	Homozygous PS in RH	PGSC0003DMG401006819	PGSC0003DMT400017577	chr02	yes	NO	GO:0016021; integral to membrane; Cellular Component
2784	Homozygous PS in RH	PGSC0003DMG400006838	PGSC0003DMT400017631	chr06	NO	NO	
2785	Homozygous PS in RH	PGSC0003DMG400006972	PGSC0003DMT400017957	chr09	NO	NO	
2786	Homozygous PS in RH	PGSC0003DMG401007052	PGSC0003DMT400018165	chr09	NO	NO	

2787	Homozygous PS in RH	PGSC0003DMG400007205	PGSC0003DMT400018569	chr06	yes	NO	
2788	Homozygous PS in RH	PGSC0003DMG400007217	PGSC0003DMT400018596	chr05	yes	NO	GO:0006508; proteolysis; Biological Process GO:0008234; cysteine-type peptidase activity; Molecular Function
2789	Homozygous PS in RH	PGSC0003DMG400007219	PGSC0003DMT400018608	chr06	NO	NO	
2790	Homozygous PS in RH	PGSC0003DMG400007301	PGSC0003DMT400018832	chr01	yes	yes	
2791	Homozygous PS in RH	PGSC0003DMG400007340	PGSC0003DMT400018927	-	NO	NO	
2792	Homozygous PS in RH	PGSC0003DMG400007341	PGSC0003DMT400018933	chr02	yes	yes	GO:0008152; metabolic process; Biological Process GO:0016787; hydrolase activity; Molecular Function
2793	Homozygous PS in RH	PGSC0003DMG401007356	PGSC0003DMT400018985	chr10	yes	NO	
2794	Homozygous PS in RH	PGSC0003DMG400007485	PGSC0003DMT400019352	chr10	NO	NO	
2795	Homozygous PS in RH	PGSC0003DMG400007505	PGSC0003DMT400019413	chr01	NO	NO	
2796	Homozygous PS in RH	PGSC0003DMG401007615	PGSC0003DMT400019715	-	yes	NO	GO:0005515; protein binding; Molecular Function
2797	Homozygous PS in RH	PGSC0003DMG400007687	PGSC0003DMT400019872	-	yes	NO	
2798	Homozygous PS in RH	PGSC0003DMG402007845	PGSC0003DMT400020293	chr10	NO	NO	GO:0004672; protein kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
2799	Homozygous PS in RH	PGSC0003DMG401007901	PGSC0003DMT400020450	chr07	NO	NO	
2800	Homozygous PS in RH	PGSC0003DMG400007946	PGSC0003DMT400020516	chr05	yes	yes	GO:0004672; protein kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process GO:0007165; signal transduction; Biological Process

2801	Homozygous PS in RH	PGSC0003DMG400008142	PGSC0003DMT400021030	-	NO	NO	GO:0004190; aspartic-type endopeptidase activity; Molecular Function GO:0006508; proteolysis; Biological Process
2802	Homozygous PS in RH	PGSC0003DMG400008189	PGSC0003DMT400021145	chr01	yes	NO	
2803	Homozygous PS in RH	PGSC0003DMG400008191	PGSC0003DMT400021155	chr12	yes	NO	
2804	Homozygous PS in RH	PGSC0003DMG401008350	PGSC0003DMT400021529	-	yes	NO	
2805	Homozygous PS in RH	PGSC0003DMG400008396	PGSC0003DMT400021640	chr10	NO	NO	
2806	Homozygous PS in RH	PGSC0003DMG400008425	PGSC0003DMT400021711	chr08	yes	NO	
2807	Homozygous PS in RH	PGSC0003DMG400008507	PGSC0003DMT400021933	chr01	NO	NO	
2808	Homozygous PS in RH	PGSC0003DMG400008611	PGSC0003DMT400022191	chr02	yes	NO	
2809	Homozygous PS in RH	PGSC0003DMG400008914	PGSC0003DMT400023033	-	NO	NO	
2810	Homozygous PS in RH	PGSC0003DMG400008981	PGSC0003DMT400023188	chr11	yes	NO	GO:0005524; ATP binding; Molecular Function GO:0006915; apoptosis; Biological Process
2811	Homozygous PS in RH	PGSC0003DMG400009006	PGSC0003DMT400023253	chr11	yes	yes	
2812	Homozygous PS in RH	PGSC0003DMG400009035	PGSC0003DMT400023324	chr04	NO	NO	
2813	Homozygous PS in RH	PGSC0003DMG400009059	PGSC0003DMT400023388	chr12	yes	NO	
2814	Homozygous PS in RH	PGSC0003DMG400009195	PGSC0003DMT400023774	chr01	NO	NO	
2815	Homozygous PS in RH	PGSC0003DMG400009239	PGSC0003DMT400023895	chr12	NO	NO	
2816	Homozygous PS in RH	PGSC0003DMG400009253	PGSC0003DMT400023930	chr12	NO	NO	
2817	Homozygous PS in RH	PGSC0003DMG402009322	PGSC0003DMT400024106	-	yes	NO	

2818	Homozygous PS in RH	PGSC0003DMG402009323	PGSC0003DMT400024109	chr03	NO	NO	
2819	Homozygous PS in RH	PGSC0003DMG400009404	PGSC0003DMT400024325	chr06	NO	NO	
2820	Homozygous PS in RH	PGSC0003DMG400009707	PGSC0003DMT400025123	chr08	yes	NO	
2821	Homozygous PS in RH	PGSC0003DMG400009747	PGSC0003DMT400025228	chr09	yes	NO	
2822	Homozygous PS in RH	PGSC0003DMG402009879	PGSC0003DMT400025569	chr10	yes	NO	GO:0030528; transcription regulator activity; Molecular Function GO:0045449; regulation of transcription; Biological Process
2823	Homozygous PS in RH	PGSC0003DMG400009880	PGSC0003DMT400025571	chr12	yes	NO	GO:0004650; polygalacturonase activity; Molecular Function GO:0005975; carbohydrate metabolic process; Biological Process
2824	Homozygous PS in RH	PGSC0003DMG400010031	PGSC0003DMT400025989	chr10	yes	NO	
2825	Homozygous PS in RH	PGSC0003DMG400010084	PGSC0003DMT400026168	chr09	yes	NO	
2826	Homozygous PS in RH	PGSC0003DMG400010228	PGSC0003DMT400026499	chr03	NO	NO	
2827	Homozygous PS in RH	PGSC0003DMG400010386	PGSC0003DMT400026930	chr09	NO	NO	
2828	Homozygous PS in RH	PGSC0003DMG400010442	PGSC0003DMT400027073	chr03	yes	NO	
2829	Homozygous PS in RH	PGSC0003DMG400010559	PGSC0003DMT400027382	chr06	NO	NO	
2830	Homozygous PS in RH	PGSC0003DMG400010604	PGSC0003DMT400027512	chr06	NO	NO	
2831	Homozygous PS in RH	PGSC0003DMG400010672	PGSC0003DMT400027685	chr03	NO	NO	
2832	Homozygous PS in RH	PGSC0003DMG400010683	PGSC0003DMT400027724	chr05	NO	NO	
2833	Homozygous PS in RH	PGSC0003DMG400010774	PGSC0003DMT400027962	chr08	yes	yes	GO:0005524; ATP binding; Molecular Function GO:0006915; apoptosis; Biological Process

2834	Homozygous PS in RH	PGSC0003DMG400010813	PGSC0003DMT400028038	chr12	NO	NO	GO:0008060; ARF GTPase activator activity; Molecular Function GO:0008270; zinc ion binding; Molecular Function GO:0032312; regulation of ARF GTPase activity; Biological Process
2835	Homozygous PS in RH	PGSC0003DMG402010918	PGSC0003DMT400028324	chr09	yes	NO	
2836	Homozygous PS in RH	PGSC0003DMG402011001	PGSC0003DMT400028574	chr09	yes	NO	GO:0016491; oxidoreductase activity; Molecular Function
2837	Homozygous PS in RH	PGSC0003DMG400011035	PGSC0003DMT400028660	-	NO	NO	
2838	Homozygous PS in RH	PGSC0003DMG400011116	PGSC0003DMT400028886	chr03	yes	NO	GO:0005524; ATP binding; Molecular Function GO:0006915; apoptosis; Biological Process
2839	Homozygous PS in RH	PGSC0003DMG400011236	PGSC0003DMT400029207	chr12	yes	NO	
2840	Homozygous PS in RH	PGSC0003DMG400011359	PGSC0003DMT400029528	chr05	NO	NO	
2841	Homozygous PS in RH	PGSC0003DMG400011661	PGSC0003DMT400030446	chr09	NO	NO	
2842	Homozygous PS in RH	PGSC0003DMG400011788	PGSC0003DMT400030773	chr08	NO	NO	
2843	Homozygous PS in RH	PGSC0003DMG400011885	PGSC0003DMT400031020	chr06	yes	yes	
2844	Homozygous PS in RH	PGSC0003DMG400012041	PGSC0003DMT400031411	chr05	NO	NO	
2845	Homozygous PS in RH	PGSC0003DMG400012045	PGSC0003DMT400031418	chr01	NO	NO	
2846	Homozygous PS in RH	PGSC0003DMG400012073	PGSC0003DMT400031487	chr10	yes	yes	
2847	Homozygous PS in RH	PGSC0003DMG400012181	PGSC0003DMT400031751	-	yes	NO	
2848	Homozygous PS in RH	PGSC0003DMG400012424	PGSC0003DMT400032345	chr01	yes	NO	

2849	Homozygous PS in RH	PGSC0003DMG400012563	PGSC0003DMT400032716	chr03	yes	yes	GO:0004672; protein kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
2850	Homozygous PS in RH	PGSC0003DMG400012616	PGSC0003DMT400032846	chr09	yes	yes	GO:0003677; DNA binding; Molecular Function GO:0003916; DNA topoisomerase activity; Molecular Function GO:0005694; chromosome; Cellular Component GO:0006265; DNA topological change; Biological Process
2851	Homozygous PS in RH	PGSC0003DMG400012645	PGSC0003DMT400032922	chr11	yes	NO	
2852	Homozygous PS in RH	PGSC0003DMG400012661	PGSC0003DMT400032968	chr12	NO	NO	
2853	Homozygous PS in RH	PGSC0003DMG400012702	PGSC0003DMT400033080	-	NO	NO	
2854	Homozygous PS in RH	PGSC0003DMG400012705	PGSC0003DMT400033085	chr12	NO	NO	
2855	Homozygous PS in RH	PGSC0003DMG400012721	PGSC0003DMT400033129	-	NO	NO	
2856	Homozygous PS in RH	PGSC0003DMG400012749	PGSC0003DMT400033202	chr10	NO	NO	
2857	Homozygous PS in RH	PGSC0003DMG400012831	PGSC0003DMT400033396	chr05	yes	NO	
2858	Homozygous PS in RH	PGSC0003DMG400012857	PGSC0003DMT400033471	chr02	NO	NO	
2859	Homozygous PS in RH	PGSC0003DMG400012876	PGSC0003DMT400033518	chr03	yes	yes	
2860	Homozygous PS in RH	PGSC0003DMG400013079	PGSC0003DMT400034025	chr06	NO	NO	
2861	Homozygous PS in RH	PGSC0003DMG400013181	PGSC0003DMT400034284	chr01	yes	NO	GO:0004356; glutamate-ammonia ligase activity; Molecular Function GO:0006807; nitrogen compound metabolic process; Biological Process
2862	Homozygous PS in RH	PGSC0003DMG400013222	PGSC0003DMT400034384	chr07	NO	NO	

2863	Homozygous PS in RH	PGSC0003DMG401013254	PGSC0003DMT400034481	chr04	NO	NO	
2864	Homozygous PS in RH	PGSC0003DMG400013294	PGSC0003DMT400034588	chr09	NO	NO	GO:0006508; proteolysis; Biological Process GO:0008234; cysteine-type peptidase activity; Molecular Function
2865	Homozygous PS in RH	PGSC0003DMG402013295	PGSC0003DMT400034593	chr06	yes	yes	GO:0004672; protein kinase activity; Molecular Function GO:0005515; protein binding; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
2866	Homozygous PS in RH	PGSC0003DMG400013320	PGSC0003DMT400034659	chr08	NO	NO	GO:0005198; structural molecule activity; Molecular Function
2867	Homozygous PS in RH	PGSC0003DMG400013407	PGSC0003DMT400034883	chr05	yes	yes	GO:0005524; ATP binding; Molecular Function GO:0006915; apoptosis; Biological Process
2868	Homozygous PS in RH	PGSC0003DMG400013498	PGSC0003DMT400035105	chr07	yes	yes	GO:0006855; multidrug transport; Biological Process GO:0015238; drug transporter activity; Molecular Function GO:0015297; antiporter activity; Molecular Function GO:0016020; membrane; Cellular Component GO:0055085; transmembrane transport; Biological Process
2869	Homozygous PS in RH	PGSC0003DMG400013511	PGSC0003DMT400035152	chr02	yes	NO	
2870	Homozygous PS in RH	PGSC0003DMG400013518	PGSC0003DMT400035172	chr04	yes	NO	GO:0004672; protein kinase activity; Molecular Function GO:0005515; protein binding; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
2871	Homozygous PS in RH	PGSC0003DMG402013630	PGSC0003DMT400035459	chr01	yes	NO	
2872	Homozygous PS in RH	PGSC0003DMG400013736	PGSC0003DMT400035714	chr02	NO	NO	
2873	Homozygous PS in RH	PGSC0003DMG400013889	PGSC0003DMT400036058	chr01	yes	NO	

2874	Homozygous PS in RH	PGSC0003DMG401013919	PGSC0003DMT400036145	chr01	NO	NO	GO:0004672; protein kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0005529; sugar binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process GO:0048544; recognition of pollen; Biological Process
2875	Homozygous PS in RH	PGSC0003DMG400014125	PGSC0003DMT400036630	chr02	NO	NO	
2876	Homozygous PS in RH	PGSC0003DMG400014130	PGSC0003DMT400036638	chr04	yes	NO	GO:0005515; protein binding; Molecular Function
2877	Homozygous PS in RH	PGSC0003DMG401014139	PGSC0003DMT400036656	chr04	NO	NO	
2878	Homozygous PS in RH	PGSC0003DMG400014152	PGSC0003DMT400036695	chr12	yes	NO	GO:0016021; integral to membrane; Cellular Component GO:0016758; transferase activity, transferring hexosyl groups; Molecular Function
2879	Homozygous PS in RH	PGSC0003DMG400014382	PGSC0003DMT400037280	chr09	yes	yes	
2880	Homozygous PS in RH	PGSC0003DMG400014424	PGSC0003DMT400037390	chr12	yes	NO	GO:0005524; ATP binding; Molecular Function GO:0006915; apoptosis; Biological Process
2881	Homozygous PS in RH	PGSC0003DMG400014492	PGSC0003DMT400037569	-	yes	NO	
2882	Homozygous PS in RH	PGSC0003DMG400014585	PGSC0003DMT400037804	chr06	yes	NO	
2883	Homozygous PS in RH	PGSC0003DMG400014600	PGSC0003DMT400037843	chr12	NO	NO	GO:0005779; integral to peroxisomal membrane; Cellular Component GO:0007031; peroxisome organization; Biological Process
2884	Homozygous PS in RH	PGSC0003DMG400014616	PGSC0003DMT400037885	chr11	yes	NO	
2885	Homozygous PS in RH	PGSC0003DMG400014678	PGSC0003DMT400038068				
2886	Homozygous PS in RH	PGSC0003DMG400014766	PGSC0003DMT400038273	chr05	yes	NO	

2887	Homozygous PS in RH	PGSC0003DMG400014862	PGSC0003DMT400038500	-	NO	NO	
2888	Homozygous PS in RH	PGSC0003DMG400014888	PGSC0003DMT400038548	-	yes	NO	GO:0004568; chitinase activity; Molecular Function GO:0006032; chitin catabolic process; Biological Process GO:0008061; chitin binding; Molecular Function GO:0016998; cell wall macromolecule catabolic process; Biological Process
2889	Homozygous PS in RH	PGSC0003DMG400014982	PGSC0003DMT400038769	-	NO	NO	
2890	Homozygous PS in RH	PGSC0003DMG400015020	PGSC0003DMT400038863	chr08	yes	yes	GO:0003676; nucleic acid binding; Molecular Function GO:0008270; zinc ion binding; Molecular Function
2891	Homozygous PS in RH	PGSC0003DMG400015073	PGSC0003DMT400038971	chr06	yes	NO	GO:0016021; integral to membrane; Cellular Component
2892	Homozygous PS in RH	PGSC0003DMG400015156	PGSC0003DMT400039197	chr06	yes	yes	GO:0003677; DNA binding; Molecular Function
2893	Homozygous PS in RH	PGSC0003DMG400015328	PGSC0003DMT400039630	chr01	NO	NO	
2894	Homozygous PS in RH	PGSC0003DMG400015340	PGSC0003DMT400039662	chr04	yes	yes	
2895	Homozygous PS in RH	PGSC0003DMG400015366	PGSC0003DMT400039764	chr09	yes	NO	
2896	Homozygous PS in RH	PGSC0003DMG400015594	PGSC0003DMT400040284	chr08	NO	NO	GO:0005515; protein binding; Molecular Function
2897	Homozygous PS in RH	PGSC0003DMG400015801	PGSC0003DMT400040868	chr07	yes	NO	
2898	Homozygous PS in RH	PGSC0003DMG400015821	PGSC0003DMT400040902	chr10	yes	NO	GO:0006855; multidrug transport; Biological Process GO:0015238; drug transporter activity; Molecular Function GO:0015297; antiporter activity; Molecular Function GO:0016020; membrane; Cellular Component GO:0055085; transmembrane transport; Biological Process
2899	Homozygous PS in RH	PGSC0003DMG402015867	PGSC0003DMT400041013	chr06	yes	yes	

2900	Homozygous PS in RH	PGSC0003DMG400016061	PGSC0003DMT400041441	chr10	NO	NO	
2901	Homozygous PS in RH	PGSC0003DMG400016238	PGSC0003DMT400041847	-	yes	NO	GO:0008152; metabolic process; Biological Process GO:0016758; transferase activity, transferring hexosyl groups; Molecular Function
2902	Homozygous PS in RH	PGSC0003DMG400016372	PGSC0003DMT400042194				
2903	Homozygous PS in RH	PGSC0003DMG400016524	PGSC0003DMT400042609				
2904	Homozygous PS in RH	PGSC0003DMG400016690	PGSC0003DMT400043037				
2905	Homozygous PS in RH	PGSC0003DMG400016734	PGSC0003DMT400043126				
2906	Homozygous PS in RH	PGSC0003DMG400016849	PGSC0003DMT400043405				
2907	Homozygous PS in RH	PGSC0003DMG401016929	PGSC0003DMT400043597				
2908	Homozygous PS in RH	PGSC0003DMG400017106	PGSC0003DMT400044088				
2909	Homozygous PS in RH	PGSC0003DMG400017125	PGSC0003DMT400044123				
2910	Homozygous PS in RH	PGSC0003DMG400017237	PGSC0003DMT400044397				
2911	Homozygous PS in RH	PGSC0003DMG400017332	PGSC0003DMT400044679				
2912	Homozygous PS in RH	PGSC0003DMG400017454	PGSC0003DMT400045006				
2913	Homozygous PS in RH	PGSC0003DMG400017458	PGSC0003DMT400045026				
2914	Homozygous PS in RH	PGSC0003DMG400017502	PGSC0003DMT400045124				
2915	Homozygous PS in RH	PGSC0003DMG400017637	PGSC0003DMT400045466				
2916	Homozygous PS in RH	PGSC0003DMG400017712	PGSC0003DMT400045656				
2917	Homozygous PS in RH	PGSC0003DMG400017801	PGSC0003DMT400045890				

2918	Homozygous PS in RH	PGSC0003DMG400017990	PGSC0003DMT400046351
2919	Homozygous PS in RH	PGSC0003DMG400018163	PGSC0003DMT400046778
2920	Homozygous PS in RH	PGSC0003DMG400018420	PGSC0003DMT400047396
2921	Homozygous PS in RH	PGSC0003DMG401018597	PGSC0003DMT400047844
2922	Homozygous PS in RH	PGSC0003DMG400018631	PGSC0003DMT400047936
2923	Homozygous PS in RH	PGSC0003DMG400018665	PGSC0003DMT400048037
2924	Homozygous PS in RH	PGSC0003DMG402018705	PGSC0003DMT400048142
2925	Homozygous PS in RH	PGSC0003DMG400018820	PGSC0003DMT400048455
2926	Homozygous PS in RH	PGSC0003DMG400018924	PGSC0003DMT400048703
2927	Homozygous PS in RH	PGSC0003DMG400019170	PGSC0003DMT400049324
2928	Homozygous PS in RH	PGSC0003DMG400019171	PGSC0003DMT400049334
2929	Homozygous PS in RH	PGSC0003DMG400019384	PGSC0003DMT400049882
2930	Homozygous PS in RH	PGSC0003DMG400019513	PGSC0003DMT400050239
2931	Homozygous PS in RH	PGSC0003DMG400019517	PGSC0003DMT400050249
2932	Homozygous PS in RH	PGSC0003DMG400019519	PGSC0003DMT400050253
2933	Homozygous PS in RH	PGSC0003DMG400019525	PGSC0003DMT400050265
2934	Homozygous PS in RH	PGSC0003DMG400019578	PGSC0003DMT400050367
2935	Homozygous PS in RH	PGSC0003DMG400019818	PGSC0003DMT400051038
2936	Homozygous PS in RH	PGSC0003DMG402019826	PGSC0003DMT400051061

2937	Homozygous PS in RH	PGSC0003DMG400019943	PGSC0003DMT400051347
2938	Homozygous PS in RH	PGSC0003DMG400020063	PGSC0003DMT400051665
2939	Homozygous PS in RH	PGSC0003DMG402020091	PGSC0003DMT400051759
2940	Homozygous PS in RH	PGSC0003DMG400020118	PGSC0003DMT400051838
2941	Homozygous PS in RH	PGSC0003DMG400020168	PGSC0003DMT400051962
2942	Homozygous PS in RH	PGSC0003DMG400020261	PGSC0003DMT400052233
2943	Homozygous PS in RH	PGSC0003DMG403020339	PGSC0003DMT400052398
2944	Homozygous PS in RH	PGSC0003DMG400020375	PGSC0003DMT400052499
2945	Homozygous PS in RH	PGSC0003DMG400020665	PGSC0003DMT400053242
2946	Homozygous PS in RH	PGSC0003DMG400020720	PGSC0003DMT400053412
2947	Homozygous PS in RH	PGSC0003DMG400020804	PGSC0003DMT400053627
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3229	Homozygous PS in RH	PGSC0003DMG400042265	PGSC0003DMT400092694
3230	Homozygous PS in RH	PGSC0003DMG400042311	PGSC0003DMT400092740
3231	Homozygous PS in RH	PGSC0003DMG400042330	PGSC0003DMT400092759
3232	Homozygous PS in RH	PGSC0003DMG400042471	PGSC0003DMT400092900
3233	Homozygous PS in RH	PGSC0003DMG400042476	PGSC0003DMT400092905
3234	Homozygous PS in RH	PGSC0003DMG400042485	PGSC0003DMT400092914
3235	Homozygous PS in RH	PGSC0003DMG400042505	PGSC0003DMT400092934
3236	Homozygous PS in RH	PGSC0003DMG400042586	PGSC0003DMT400093015
3237	Homozygous PS in RH	PGSC0003DMG400042613	PGSC0003DMT400093042
3238	Homozygous PS in RH	PGSC0003DMG400042663	PGSC0003DMT400093092
3239	Homozygous PS in RH	PGSC0003DMG400042672	PGSC0003DMT400093101
3240	Homozygous PS in RH	PGSC0003DMG400042899	PGSC0003DMT400093328

3241	Homozygous PS in RH	PGSC0003DMG400043072	PGSC0003DMT400093501
3242	Homozygous PS in RH	PGSC0003DMG400043218	PGSC0003DMT400093647
3243	Homozygous PS in RH	PGSC0003DMG400043275	PGSC0003DMT400093704
3244	Homozygous PS in RH	PGSC0003DMG400043396	PGSC0003DMT400093825
3245	Homozygous PS in RH	PGSC0003DMG400043411	PGSC0003DMT400093840
3246	Homozygous PS in RH	PGSC0003DMG400043452	PGSC0003DMT400093881
3247	Homozygous PS in RH	PGSC0003DMG400043634	PGSC0003DMT400094063
3248	Homozygous PS in RH	PGSC0003DMG400043793	PGSC0003DMT400094222
3249	Homozygous PS in RH	PGSC0003DMG400043806	PGSC0003DMT400094235
3250	Homozygous PS in RH	PGSC0003DMG400043810	PGSC0003DMT400094239
3251	Homozygous PS in RH	PGSC0003DMG400043821	PGSC0003DMT400094250
3252	Homozygous PS in RH	PGSC0003DMG400043905	PGSC0003DMT400094334
3253	Homozygous PS in RH	PGSC0003DMG400043933	PGSC0003DMT400094362
3254	Homozygous PS in RH	PGSC0003DMG400043951	PGSC0003DMT400094380
3255	Homozygous PS in RH	PGSC0003DMG400044006	PGSC0003DMT400094435
3256	Homozygous PS in RH	PGSC0003DMG400044145	PGSC0003DMT400094574
3257	Homozygous PS in RH	PGSC0003DMG400044155	PGSC0003DMT400094584
3258	Homozygous PS in RH	PGSC0003DMG400044174	PGSC0003DMT400094603
3259	Homozygous PS in RH	PGSC0003DMG400044211	PGSC0003DMT400094640

3260	Homozygous PS in RH	PGSC0003DMG400044238	PGSC0003DMT400094667
3261	Homozygous PS in RH	PGSC0003DMG400044253	PGSC0003DMT400094682
3262	Homozygous PS in RH	PGSC0003DMG400044394	PGSC0003DMT400094823
3263	Homozygous PS in RH	PGSC0003DMG400044529	PGSC0003DMT400094958
3264	Homozygous PS in RH	PGSC0003DMG400044571	PGSC0003DMT400095000
3265	Homozygous PS in RH	PGSC0003DMG400044719	PGSC0003DMT400095148
3266	Homozygous PS in RH	PGSC0003DMG400044872	PGSC0003DMT400095301
3267	Homozygous PS in RH	PGSC0003DMG400044908	PGSC0003DMT400095337
3268	Homozygous PS in RH	PGSC0003DMG400044923	PGSC0003DMT400095352
3269	Homozygous PS in RH	PGSC0003DMG400044936	PGSC0003DMT400095365
3270	Homozygous PS in RH	PGSC0003DMG400045171	PGSC0003DMT400095600
3271	Homozygous PS in RH	PGSC0003DMG400045244	PGSC0003DMT400095673
3272	Homozygous PS in RH	PGSC0003DMG400045269	PGSC0003DMT400095698
3273	Homozygous PS in RH	PGSC0003DMG400045334	PGSC0003DMT400095763
3274	Homozygous PS in RH	PGSC0003DMG400045407	PGSC0003DMT400095836
3275	Homozygous PS in RH	PGSC0003DMG400045424	PGSC0003DMT400095853
3276	Homozygous PS in RH	PGSC0003DMG400045486	PGSC0003DMT400095915
3277	Homozygous PS in RH	PGSC0003DMG400045498	PGSC0003DMT400095927
3278	Homozygous PS in RH	PGSC0003DMG400045723	PGSC0003DMT400096152

3279	Homozygous PS in RH	PGSC0003DMG400045724	PGSC0003DMT400096153
3280	Homozygous PS in RH	PGSC0003DMG400045789	PGSC0003DMT400096218
3281	Homozygous PS in RH	PGSC0003DMG400045817	PGSC0003DMT400096246
3282	Homozygous PS in RH	PGSC0003DMG400045889	PGSC0003DMT400096318
3283	Homozygous PS in RH	PGSC0003DMG400045954	PGSC0003DMT400096383
3284	Homozygous PS in RH	PGSC0003DMG400046012	PGSC0003DMT400096441
3285	Homozygous PS in RH	PGSC0003DMG400046073	PGSC0003DMT400096502
3286	Homozygous PS in RH	PGSC0003DMG400046159	PGSC0003DMT400096588
3287	Homozygous PS in RH	PGSC0003DMG400046176	PGSC0003DMT400096605
3288	Homozygous PS in RH	PGSC0003DMG400046225	PGSC0003DMT400096654
3289	Homozygous PS in RH	PGSC0003DMG400046274	PGSC0003DMT400096703
3290	Homozygous PS in RH	PGSC0003DMG400046291	PGSC0003DMT400096720
3291	Homozygous PS in RH	PGSC0003DMG400046601	PGSC0003DMT400097030
3292	Homozygous PS in RH	PGSC0003DMG400046623	PGSC0003DMT400097052
3293	Homozygous PS in RH	PGSC0003DMG400046641	PGSC0003DMT400097070
3294	Homozygous PS in RH	PGSC0003DMG400046688	PGSC0003DMT400097117
3295	Homozygous PS in RH	PGSC0003DMG400046702	PGSC0003DMT400097131
3296	Homozygous PS in RH	PGSC0003DMG400046798	PGSC0003DMT400097227
3297	Homozygous PS in RH	PGSC0003DMG400046862	PGSC0003DMT400097291

3298	Homozygous PS in RH	PGSC0003DMG400046868	PGSC0003DMT400097297
3299	Homozygous PS in RH	PGSC0003DMG400046876	PGSC0003DMT400097305
3300	Homozygous PS in RH	PGSC0003DMG400046942	PGSC0003DMT400097371
3301	Homozygous PS in RH	PGSC0003DMG400046951	PGSC0003DMT400097380
3302	Homozygous PS in RH	PGSC0003DMG400046972	PGSC0003DMT400097401
3303	Homozygous PS in RH	PGSC0003DMG400046996	PGSC0003DMT400097425
3304	Homozygous PS in RH	PGSC0003DMG400047036	PGSC0003DMT400097465
3305	Homozygous PS in RH	PGSC0003DMG400047052	PGSC0003DMT400097481
3306	Homozygous PS in RH	PGSC0003DMG400047128	PGSC0003DMT400097557

Supplementary Table 14. Genes with frameshifts.

FS Code	Category	Gene in DM	Transcript in DM	Chromosome	RNA-seq support in DM	RNA-seq support in RH	Functional annotation
1	Heterozygous FS in RH	PGSC0003DMG402009270	PGSC0003DMT400023971	chr11	yes	yes	
2	Homozygous FS in RH	PGSC0003DMG400010174	PGSC0003DMT400026375	chr03	yes	yes	GO:0016021; integral to membrane; Cellular Component
3	Homozygous FS in RH	PGSC0003DMG400015790	PGSC0003DMT400040840	chr03	yes	yes	GO:0004713; protein tyrosine kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
4	Homozygous FS in RH	PGSC0003DMG400015511	PGSC0003DMT400040097	chr02	yes	yes	GO:0003824; catalytic activity; Molecular Function GO:0016020; membrane; Cellular Component
5	Homozygous FS in RH	PGSC0003DMG400022832	PGSC0003DMT400058772	chr10	yes	yes	
6	Heterozygous FS in RH	PGSC0003DMG400041247	PGSC0003DMT400091676	chr01	NO	NO	
7	Homozygous FS in RH	PGSC0003DMG400015501	PGSC0003DMT400040071	chr02	yes	yes	
8	Homozygous FS in RH	PGSC0003DMG400010150	PGSC0003DMT400026296	chr03	yes	yes	
9	Homozygous FS in RH	PGSC0003DMG400009277	PGSC0003DMT400023983	chr11	yes	yes	
10	Heterozygous FS in RH	PGSC0003DMG400015786	PGSC0003DMT400040825	chr03	yes	yes	
11	Heterozygous FS in RH	PGSC0003DMG400008761	PGSC0003DMT400022600	chr01	yes	yes	
12	Homozygous FS in RH	PGSC0003DMG400041225	PGSC0003DMT400091654	chr12	yes	yes	
13	Homozygous FS in RH	PGSC0003DMG400010122	PGSC0003DMT400026242	chr03	yes	yes	
14	Heterozygous FS in RH	PGSC0003DMG400010151	PGSC0003DMT400026299	chr03	yes	yes	
15	Homozygous FS in RH	PGSC0003DMG400010176	PGSC0003DMT400026381	chr03	yes	yes	
16	Homozygous FS in RH	PGSC0003DMG400015495	PGSC0003DMT400040055	chr02	yes	yes	GO:0006950; response to stress; Biological Process GO:0009415; response to water; Biological Process
17	Homozygous FS in RH	PGSC0003DMG401015792	PGSC0003DMT400040845	chr03	yes	yes	
18	Homozygous FS in RH	PGSC0003DMG400008786	PGSC0003DMT400022662	chr11	yes	yes	
19	Homozygous FS in RH	PGSC0003DMG400025629	PGSC0003DMT400065842	chr03	yes	yes	
20	Homozygous FS in RH	PGSC0003DMG400015490	PGSC0003DMT400040043	chr02	yes	yes	GO:0016757; transferase activity, transferring glycosyl groups; Molecular Function
21	Homozygous FS in RH	PGSC0003DMG400010167	PGSC0003DMT400026356	chr03	yes	yes	
22	Heterozygous FS in RH	PGSC0003DMG402017902	PGSC0003DMT400046121	chr01	yes	yes	GO:0006820; anion transport; Biological Process GO:0015380; anion exchanger activity; Molecular Function GO:0016021; integral to membrane; Cellular Component

23	Heterozygous FS in RH	PGSC0003DMG400013928	PGSC0003DMT400036188	chr11	yes	yes	GO:0004672; protein kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
24	Homozygous FS in RH	PGSC0003DMG400010386	PGSC0003DMT400026930	chr02	yes	yes	GO:0016491; oxidoreductase activity; Molecular Function GO:0055114; oxidation reduction; Biological Process
25	Homozygous FS in RH	PGSC0003DMG400023281	PGSC0003DMT400059853	chr11	yes	yes	
26	Homozygous FS in RH	PGSC0003DMG401026624	PGSC0003DMT400068472	chr10	yes	yes	
27	Homozygous FS in RH	PGSC0003DMG400015502	PGSC0003DMT400040074	chr02	yes	yes	GO:0003700; transcription factor activity; Molecular Function GO:0006355; regulation of transcription, DNA-dependent; Biological Process GO:0008270; zinc ion binding; Molecular Function GO:0043565; sequence-specific DNA binding; Molecular Function
28	Heterozygous FS in RH	PGSC0003DMG400026623	PGSC0003DMT400068470	chr10	yes	yes	
29	Homozygous FS in RH	PGSC0003DMG400009278	PGSC0003DMT400023985	chr11	yes	yes	GO:0005524; ATP binding; Molecular Function GO:0006139; nucleobase, nucleoside, nucleotide and nucleic acid metabolic process; Biological Process GO:0016773; phosphotransferase activity, alcohol group as acceptor; Molecular Function
30	Heterozygous FS in RH	PGSC0003DMG400015800	PGSC0003DMT400040866	chr03	yes	yes	GO:0006511; ubiquitin-dependent protein catabolic process; Biological Process
31	Homozygous FS in RH	PGSC0003DMG401033888	PGSC0003DMT400084231	chr01	yes	yes	GO:0006950; response to stress; Biological Process
32	Homozygous FS in RH	PGSC0003DMG400013068	PGSC0003DMT400033993	chr01	yes	yes	GO:0005524; ATP binding; Molecular Function
33	Homozygous FS in RH	PGSC0003DMG400022836	PGSC0003DMT400058778	chr10	yes	yes	GO:0003677; DNA binding; Molecular Function
34	Homozygous FS in RH	PGSC0003DMG400015505	PGSC0003DMT400040083	chr02	yes	yes	GO:0016747; transferase activity, transferring acyl groups other than amino-acyl groups; Molecular Function
35	Homozygous FS in RH	PGSC0003DMG400009257	PGSC0003DMT400023939	chr11	yes	yes	
36	Heterozygous FS in RH	PGSC0003DMG400030273	PGSC0003DMT400077828	chr05	yes	yes	
37	Homozygous FS in RH	PGSC0003DMG402026624	PGSC0003DMT400068473	chr10	yes	yes	GO:0006629; lipid metabolic process; Biological Process GO:0016788; hydrolase activity, acting on ester bonds; Molecular Function

38	Heterozygous FS in RH	PGSC0003DMG400019376	PGSC0003DMT400049870	chr12	yes	yes	
39	Homozygous FS in RH	PGSC0003DMG400010168	PGSC0003DMT400026358	chr03	yes	yes	GO:0005524; ATP binding; Molecular Function GO:0009058; biosynthetic process; Biological Process GO:0016874; ligase activity; Molecular Function
40	Heterozygous FS in RH	PGSC0003DMG400022816	PGSC0003DMT400058733	chr10	yes	yes	
41	Heterozygous FS in RH	PGSC0003DMG400024185	PGSC0003DMT400062149	chr02	yes	yes	
42	Homozygous FS in RH	PGSC0003DMG400010163	PGSC0003DMT400026334	chr03	yes	yes	GO:0000151; ubiquitin ligase complex; Cellular Component GO:0004842; ubiquitin-protein ligase activity; Molecular Function GO:0005634; nucleus; Cellular Component GO:0008270; zinc ion binding; Molecular Function GO:0016567; protein ubiquitination; Biological Process
43	Heterozygous FS in RH	PGSC0003DMG400017904	PGSC0003DMT400046123	chr01	yes	yes	
44	Homozygous FS in RH	PGSC0003DMG400010186	PGSC0003DMT400026409	chr03	yes	yes	
45	Homozygous FS in RH	PGSC0003DMG400022830	PGSC0003DMT400058762	chr10	yes	yes	
46	Heterozygous FS in RH	PGSC0003DMG400015794	PGSC0003DMT400040852	chr03	yes	yes	GO:0016765; transferase activity, transferring alkyl or aryl (other than methyl) groups; Molecular Function
47	Heterozygous FS in RH	PGSC0003DMG400015793	PGSC0003DMT400040848	chr03	yes	yes	GO:0008152; metabolic process; Biological Process GO:0016491; oxidoreductase activity; Molecular Function
48	Heterozygous FS in RH	PGSC0003DMG400015513	PGSC0003DMT400040100	chr02	yes	yes	
49	Heterozygous FS in RH	PGSC0003DMG400010118	PGSC0003DMT400026232	chr03	yes	yes	
50	Heterozygous FS in RH	PGSC0003DMG400010407	PGSC0003DMT400026983	chr02	yes	yes	
51	Homozygous FS in RH	PGSC0003DMG400010169	PGSC0003DMT400026363	chr03	yes	yes	GO:0005506; iron ion binding; Molecular Function GO:0005783; endoplasmic reticulum; Cellular Component GO:0006633; fatty acid biosynthetic process; Biological Process GO:0016491; oxidoreductase activity; Molecular Function GO:0055114; oxidation reduction; Biological Process
52	Heterozygous FS in RH	PGSC0003DMG400010390	PGSC0003DMT400026945	chr02	yes	yes	
53	Heterozygous FS in RH	PGSC0003DMG400018832	PGSC0003DMT400048482	chr05	yes	yes	GO:0006886; intracellular protein transport; Biological Process GO:0016020; membrane; Cellular Component

54	Heterozygous FS in RH	PGSC0003DMG400015484	PGSC0003DMT400040028	chr02	yes	yes	GO:0005507; copper ion binding; Molecular Function GO:0016491; oxidoreductase activity; Molecular Function GO:0055114; oxidation reduction; Biological Process
55	Heterozygous FS in RH	PGSC0003DMG400009256	PGSC0003DMT400023934	chr11	yes	yes	GO:0003747; translation release factor activity; Molecular Function GO:0006415; translational termination; Biological Process
56	Homozygous FS in RH	PGSC0003DMG400020758	PGSC0003DMT400053512	chr05	yes	yes	GO:0008080; N-acetyltransferase activity; Molecular Function GO:0008152; metabolic process; Biological Process
57	Homozygous FS in RH	PGSC0003DMG400009276	PGSC0003DMT400023981	chr11	yes	yes	
58	Heterozygous FS in RH	PGSC0003DMG400039256	PGSC0003DMT400089685	chr11	yes	yes	
59	Homozygous FS in RH	PGSC0003DMG400010175	PGSC0003DMT400026377	chr03	yes	yes	
60	Homozygous FS in RH	PGSC0003DMG400010406	PGSC0003DMT400026981	chr02	yes	yes	
61	Homozygous FS in RH	PGSC0003DMG400022829	PGSC0003DMT400058761	chr10	yes	yes	
62	Homozygous FS in RH	PGSC0003DMG400010387	PGSC0003DMT400026935	chr02	yes	yes	
63	Heterozygous FS in RH	PGSC0003DMG400000949	PGSC0003DMT400002491	chr09	yes	yes	GO:0004221; ubiquitin thiolesterase activity; Molecular Function GO:0005622; intracellular; Cellular Component GO:0006511; ubiquitin-dependent protein catabolic process; Biological Process
64	Homozygous FS in RH	PGSC0003DMG400013088	PGSC0003DMT400034053	chr01	yes	yes	
65	Homozygous FS in RH	PGSC0003DMG400015802	PGSC0003DMT400040869	chr03	yes	yes	GO:0004672; protein kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
66	Homozygous FS in RH	PGSC0003DMG400015788	PGSC0003DMT400040832	chr03	yes	yes	
67	Heterozygous FS in RH	PGSC0003DMG400024181	PGSC0003DMT400062136	chr02	yes	yes	GO:0006633; fatty acid biosynthetic process; Biological Process GO:0008610; lipid biosynthetic process; Biological Process GO:0016020; membrane; Cellular Component GO:0016747; transferase activity, transferring acyl groups other than amino-acyl groups; Molecular Function

68	Heterozygous FS in RH	PGSC0003DMG400015476	PGSC0003DMT400040010	chr02	yes	yes	GO:0004713; protein tyrosine kinase activity; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0006468; protein amino acid phosphorylation; Biological Process
69	Homozygous FS in RH	PGSC0003DMG400026627	PGSC0003DMT400068480	chr10	yes	yes	GO:0015979; photosynthesis; Biological Process GO:0015995; chlorophyll biosynthetic process; Biological Process GO:0016851; magnesium chelatase activity; Molecular Function
70	Heterozygous FS in RH	PGSC0003DMG400043518	PGSC0003DMT400093947	chr11	yes	yes	
71	Heterozygous FS in RH	PGSC0003DMG400022833	PGSC0003DMT400058773	chr10	yes	yes	GO:0003924; GTPase activity; Molecular Function GO:0005525; GTP binding; Molecular Function GO:0006955; immune response; Biological Process
72	Homozygous FS in RH	PGSC0003DMG400022839	PGSC0003DMT400058784	chr10	yes	yes	
73	Homozygous FS in RH	PGSC0003DMG400022819	PGSC0003DMT400058741	chr10	yes	yes	
74	Heterozygous FS in RH	PGSC0003DMG401017902	PGSC0003DMT400046119	chr01	yes	yes	
75	Homozygous FS in RH	PGSC0003DMG400015507	PGSC0003DMT400040088	chr02	yes	yes	
76	Homozygous FS in RH	PGSC0003DMG400015491	PGSC0003DMT400040046	chr02	yes	yes	
77	Heterozygous FS in RH	PGSC0003DMG400026621	PGSC0003DMT400068458	chr10	yes	yes	
78	Homozygous FS in RH	PGSC0003DMG400015492	PGSC0003DMT400040051	chr02	yes	yes	GO:0005524; ATP binding; Molecular Function
79	Homozygous FS in RH	PGSC0003DMG400020757	PGSC0003DMT400053511	chr05	yes	yes	
80	Homozygous FS in RH	PGSC0003DMG402009259	PGSC0003DMT400023943	chr11	yes	yes	

Supplementary Table 15. RH specific genes

Code	RNA-seq support in RH	Functional annotation	Sequence
1	yes	GO:0003676; nucleic acid binding; Molecular Function;	ATGAGCCAGACGCTTGTGTCCGAGTATAAACAACTTAACATGGGGCATGAATGGAAGGACATTATAAACATTCTAGATTGCAAGTTTTTTGTAAAAAAGAGCATATGGGTTAAGTGGAACAGACCTGAGGTTCTATGTGTCAAGATAAATTCTGATGGAAGTTGTTTGGAGGGGCAATGTGGTGGAGGCGGAGTCATAAGGGACAATGATGGTAAGTTTATTTTTGGGTACTCTCTCAAGTTGGGAAAGGGGACTAGCACCTGGGCAGAAGTTGTGGCGCTTGGGTTTGGAATAAAATGGTGTTTAGAGAATGGTTTCCTCTCTTTTACTGCAGAAAGTGACTCCAAAGTTCTTGTGGATAGTGTCAACAATTGTCACTCAACTCCTTGGAGAATTATGGATGATGTTAATGAAATTATTAGACTTAAGGAGCTTGCAGGTTTTAATATGGTGCACTGTTTTTGTCACGCCCCAAATTCAAGGAGCGCAACTGGCTCCTAA
2	yes		ATGACCACCAAATCGCCCGGTCAACCTCTCACTGGGGTTGATTTAGATCTGAAGGAAAGAGAACCAACTTCTAGGCTTGATTTTTTAGCTGCTGTAAGACCATCAAGGGAAGCTAATGCGATGGCGTTGAAACCTATTGTGTATTTTCATGGTGAACCAAGAATAGTATGGGAGGAGGAAGAGGGTGAACGGATGATCGTGAAGGAGAACTTAGAGTATGCAGTGATAGGAAAAATTTCCTATGGTTGGCCTGAGATTCAAGATTTGAGAAAATTAATTCCAAAGCAATGCAAGTTGAAAGGTGAATGCAACATAGGATTGTTAAGCAATAAGCATATTCTGATAAGGGCATTGTTCTTGGAGGACTACGTGAATCTATTATCAAAGCCGACCTTTTACATATTGCATCGTGGGTGGACATATCCAATGCGAACGTTGAAGTGGGAGCCAATGTTCGATCCGGAGGAGGAAACATCAACGGCCATGGCATTGATTTCTTTTCCATCCCTGCCTCCAAATTTCTTTGTGAAGGAGGCAGTTTTTTCATTAGCAGCTGCAGTTGGAAAGCCTTTACAGGTTGATCTAGCAACAAGGAATCAGACTCGACCTAGTTATGCACGGGTGAAGGTGGATGTGGGTTTATTACGTGAATTTCCAAAAAAAATAAACGTAGGGATGCGAAAGCAATCAGGGGAGATTACAGAGAAATGGATTACAATAAGATATGATCATGTTCCAAAATATTGCAAGAACTGTAAGATTCAGGGTCATGATGAGGAGCAATGTTATGTGTTACATACGAATTTATATCCCAAGGAAAAAGAAGGGAAGAAAGAAGAGATGGAAACAGGGGAGATTCATGGGAAGGGGAGGGTCCAGAGGGAGGGGGGTGGAAAACCAGAACAGATATGGCATAAGAAAAATATTCAACATGAGAAAGAGGGAATTACGACTAGCAATAAGTTTGGGGCGCTGAAAGATCAAGATGAATGTGGGGAGACACAAGGTGGACAAAAGGAAAGGGGGGAGGAGGTAGAGATGAAAAAATGGGTTGAGGAAGTGCTCCAAAAAACAAGCAGAATAGATAAGGGGAGTAGTTTGAAAAATACAGTGGAGGATATAAACATGGTAGATGAAGAGGAGACGGTAGGGAGTGAAAACTTCAAGAATAGTGGAAACATTGAGGTAAGCGGGAAACAAAAATGCAGTGAACAGGATGCCAGAAGTAGTAATATGGAGAATACATGTTTGGAGATGGTGGAATTTCATGAGGTGCAGGATAACGATGAGGTTTTGCCTGAGAATCAAAGGAGGGAGAATCAGATTCAGGGGGATAAGTTTCCTGATTTGCTAGAGCTGACATCGTAG

3	yes	ATGACTAACACCTCTCAAGTCTCCCTTCGTCCAAGCAAGAGACTGGAAAACCCCTCGTTCTCTTTCTCTCCTGTTGAGATTTCGGACTCTTCTATGGATGATCTCCCTGCTTCCTCTGCCTCTAACAAAAAATCCTCCCCTTCTGGACATGCACGCAAGAAGCACAAAGCAGATTCCGTGGATTTCAAACCAGAAGACCTGCAATTGTTCTGGAGCTCAGTGGAGAAGGCCAAGTTCATGGCTTTCAAAGACAGAACTTCGGCTCCTGGACGAGTAATTTGCCTCAATCAACTGGAAGGCTCTCATTGCCCTGTGAGTATGTATTTCAATTTCCAGAAACTGCATCTTTTCTTCTTGCTCTGTGAAAATGAAGTGTTTGAGGAACCCGTTAAAATGTTCTATGCAAATCTTCGCGTCTCTAAGGACAATGGTGAATTAGAAACCCTTGTGTTGGGGTATCGCATTGTGCTCAGTCAAGATCTCCTTGAAAAGGTTTTTGGAACTAAGTTCTCTGGAAGAATCTCCTTTTTTAGCGGAAACTGGCCTGATGATTTCGAAGTTACTCTCGAAGAGGCCAAACGAGCCATTGCTGAGAAAGGTTCGAATCTCTCTGATTTTGGACCCTCTACTATCTGTTTTGAACATAGAATCCTGGGTCACATCGTTGCTACTACTCTGCTTCCCCGCAAAAGCTCTCTTAGCTCCCTCACTATTCGAGATGTTTTTGTTGTGTATTGTCTGATAAGGAAAATCAAGATTAATTGGGCTGAATGGTTTCTCGGTTACATGGAGGAAAGCTCTCAAGACTCCAGCGGGTCTGCTAGTCTACCTTATGGGATGGTGATCTCTCGCATCCTTAAGGTTGTTGGGGTAGATCTGTCTGAATACACTGCAAACAAGATCTCTGCTACCTATGATCTCACAACCTTCGCCAGCATGGGATATACTCTTGCAAATGGAAGGTGGACAAAGAAAGCTCTCTTCAAGCCTAAGGTGGGATTTTCAGACGAAGAAAAGGCTACTGCAACCTCTGAAATAGACATCCTAAAGGTGAGTGTAGCAGAATTAATGAAAGAAGCCATGGAGATCAAACACACGTTAGCTGCAGTGGTTGATGGCATACAGAAGGTGCAAGATTCCCTGTCCAGCATTTCTACTCTATCTGAAGGCACAAGTTCAGCTTCAACTGAACCACCTGCGCAGTGA
4	NO	ATGAAGGATGAAGAGGATTGGACGGTGACATTCAACTATTTTGGTTTAAGACTGTTGGTCTTAGAGCGTGTGATCGTGGGATGGGGAAGTGGTTTGGTTGCTATTGTAACTTGTGGGATAGATAGGTTGGAAATCATTGTCGGTTGTAAAGTAAGGGGATTGTGTGGTGAAGAGTGTGTAAGATTGAGGGCAAGAGGTTTTGCAATGGTGAAGAAGGATATTGTTGTGGTGTTGAAACCAGAGGAATTGATGGCTGAATTTGAATTGGCAAGAAAGATTGAGAATTACCTGACCGATGGAGGCACAGTGGTCTACAGAGGAGAGCAAGAGTGA
5	NO	ATGACTAACAAGAAGAATTCAATAGACGTGGGCAGAGCATCAACATATTACACTAGTGTTTCAGCAGGTGGTTGGGCTAGAAGGCCTCCGTTGGGCATAAACCTGGAGTTCCAAGGCATCCTTCATCATTTAAAGAGTCTGGGGGCAGCCCCAGCTTTGACAACGTCTTTGGCTACCTTAATTCCTCAATATTCAGTGTTAGGAGGTGTGAGGTCTTACGAGGAAAAGGCTAGGCATATCCCCACATTGTTCCCTTCAAATCAGGAGTTAAGTCAGAGATTCATCGGAGGGTTGGCTTCACAACTCTGGTTGGTGTGCCTTGAGAGTTACAAAGATAGCGGTAAGGGACCTCGTCACCAGTACAATGGTGACAACATTCCATTTCAAGAGGTAGATAGGGTAGATAACTGTATTGTTCACGTTGGGCTTCACGCTATAGAGGTTTCTATGATTATGGAGGGCTTGAAGAATGATCTAGAGAGTGCCCCAAGAGGGAGTTTCTTTTCCAGGCATTGCAGATATCTGATACTCCCCATGGTAGGGCGGTCGTACTTGGTTGTACATGTGAAGAGCTTGGTTGAGGTTGAGAATGATCCGTTCTATACTTATTGGCCTAAGGCCAAGGCTCTAGGTATTCCTTATTTGGATGTGATTTCATGGCCTTACCCTTTTGTTCTCATTTTTGTGTGA
6	NO	ATGAAGGATATGCCTATCAATGTGGGAGTGGGGTTGATGTCTTTCATGTGGAAGGCTAGAGTGCACATAGGTAGACGGTCTGAGATTGGGGACTTGACCACAAGCTTTTACGGAAAAGAAGGGGTTCCCGAGGAGAGTGTAGATTACATAGAACCCCTGTTCACCACACCTCTAGATGTCACGAAAATGAAGGGGCCTAAAAATGCTCATAGACCCACCCTCACAATAGCAGAGAACAACAAGAAAGATGATTTGAATATGACCCACATGTATAGGCTTGAAATGTTTTTCCACAAAAATGGGTGCCAGGCTTCCACTCTGGAGCAGCTGAGTGACAACAACAGAAGGTACCCTCTCAACTAG

7	yes	ATGGAGACTGAAATTGCAGCACTAATTGAGAATGAAACCTGGGAAGTAGTAGAATTACCAAAAGGAAGGAAAGCTTTACCATCCAAATGGGTGTATAAGATCAAGCACAACTCTGATGGAAGTATAGAAAGGCTAAAAGCACGATTGGTGATTAGAGGAGACATTCAAAAGGAAGGGATTGACTTTAATGAGACCTTTTCACCGGTTGTCAAAATGACAACTATCAGGTGCTTGTTGATTATAGCAGTGAAAAAAGGTTGGGAAATTTCACAAATGGATGTGAATAATGCATTTTTACATGGAGAACTTGATGAGGAGATTTTCATGAAGCTTCCAAATGGAATGCAATCAGTCAATCCGCAACATGTATGCAGGCTCAAAAAGTCCTTGTATGGACTTAGACAAGCTTCAAGACAATGGTACTCAAAATTGGCAGAAGCTTTGAATTCAAAAGGGTTTTCTTCATCACTGAATGATTATTCACTTTTCTTCAAAATATCAGGTTCTCATATTTGTATCGTCGCAGTGTATGTTGATGATATTATTCTAACAGGAAACAACAGAGCCGAGATACAACATCTAAAGGAATTCTTGAATTCACAATTCAAGATTAAGGATTTGGGTGATCTACACTATTTTTTAGGTCTTGAAATCGTAAGAGAACCAACAGGTATGATTGTAAGCCAAAGAAAGTTTACTCTAGAACTTTTGAATGAGTTCAATTGTGATCATTTACCTCTTGTGACTTCTCCACTCGATCCTTCTTCCAAACTGGATTTCTCCACTGGTGAGTTGCTCACTGATCCAACTTCATATCGGAGGCTGCTTGGTAAGCTCAACTATCTCACTCACACTAGACCAGATCTCTCATTTGTTGTACATCATCTCAGTCAGTACATGCAGCAACCAAGAGGTCCTCACTTTGCAGCCGCATTAAGAGTATTGCGGTATCTTCGTTCAAATCCAAGCCAAGGGTTATTCATATCTGCTGATCCTTCATTCAAATTACTAGCTTTCTGCGATGCGGATTGGGGGTCTTGCCCCAATTCTCGTAAATCCATCAGTGGATTCTTCATTAGTCTCGGAGGCTCACCAATCTCATGGAAATCGAAGAAATAA
8	yes	ATGGATTTTTATTCATCTAATGAGAAGTATACCGAAGCTTGCAAAGTGTTCGATGAAATGTCTCATAGAGATACAATAGCTTGGAATGTGTTGATTTCTGTATACATGCGTAACCGACGAACTCGGGATGTTTTGGGTGTATTTGATATGATGCAGAGCTCGTATGATTGCCAACCTGACAATGTTACTTGTTTGATGTTACTTCAGGCTTGTGCAAATTTGAATGCATTGGCATTTGGTGAGAGAGTTCATAGATATTGTGAAGAACATGGTTTTGACAAGGCAATGAATAACTGTAATGCACTTATAACTATGTACTCTCGGTGTGGTTGCCTCGAAAAGGCTTTTGAGGTGTTTAAGGGAATGACCGAGAAAGATGTGGTGTCTTGGACTGCCATGATATCGGGATTGGCTAGCAATGGTTATGGCAGAGATGCAATTGAGGCATTTCGGGAGATGCAAAGTGCAGGTGTTTCCCCTGATGATCAGACTTTCACTGGGGTTCTTTCTGCTTGCAGTCACTCTGGACTACTTGATGAGGGTAGGATGTTTTTCAATAGTATGAGCAAAGAGTTTGGGATTTCACCAAACATTCATCATTATGGGTGTGTGGTTGATCTAATGGGTCGTGCTGGTATGGTTGATGAAGCTTACAACCTTATAAATTCGATGAAGGTCAAACCAGATGCAACAATATGGAGGACTCTACTAGGAGCTTGTAGGATTCATCACCAAGCTGACCTAGGAGAACAAGTCATTGAGCGTTTGATAGAACTTAAAGCACAAGAAGCCGGAGACTATGTACTACTGTTGAATATTTATTCATCGCTTGGTGATTGGGGTAAGGTAATGAACGTGAGAAAAATGATGAAAGACAGGGGAATCCAAACCAACCCTGCTTGTAGTACTATTGAGTTCAGAGGAAAAATACATCAATTCGTTGCAAATGACTTTTCGCACCCAAGAAAGACAGAAATTTACGAGATGTTGGATGAGATCAATCAGCAACTGAGGATAGCAGGATACGTTGCTGAGACAGTGGCAGAGTTGCACAATGTGGGTACAGAAGAGAAGCAGATTGCATTATCTTATCACAGTGAGAAATTGGCTATAGCTTTTGCGGTTCTATCAACTCCACCTGGCACGTCAATTAGAGTTGCAAAAGACCTCCGGATTTGTGTTGACTGCCATAACTTTGCCAAGATATTGTCAGCAGTCTATAGTCGGGAAGTTGTTATTAGAGATCGGAACCGCTTCCATCATTTCAGAGAAGGTCGATGCTCGTGCAATGACTATTGGTAA
9	NO	ATGCATACATGGCTAGGGAATCAAATCGCAATCCACATTCCCTCACACTCATACTGCCTTGGCAAAGTTTTAAAATTTGGTCAACTCAGGCATCTTGGAACATTCAAGGTAGATAGTGATCTAAAAAAAAGCCTCAATGCAGTGATCCCAAGTGGCTGGGGTTCATTGGTCCCTCTGGACCTCTCCCAACCATTTTACCATAGAACTGCCATGTCTCTAAGCCTGAATTGTGCTAATTCAACAGACTTTGTAGGTGAAGGAGGACTTAAGGCAGGGAGCTCTCAAACCCTTGAACTCCTTGTCCATTTAGAAGGAATAGGAGGAGCTGAAGGTGCTGGTGGAGGTCATGTGAGTCCTCGGGACTCCTGA

10	NO		ATGGTAAAATTTCACCCGGATGCAATAAATGATCCCTTAGGTACACCACAAAACAGGGCTAAGATGTTCACACTTCGAATGAAGCATGACCTTGCCGCTCTAATGGGTTGGTTGACACCCCTCATTTTAGATGTTACTCTTATGTGGATGGTTGATGGAGTGAAGATCAAGAAGAAAGATATCAATATTAGCACCTGGTACTGGTTTATGTTCATCATTAGCAACATCATGACATCTTAG
11	NO	GO:0003676; nucleic acid binding; Molecular Function;GO:0008270; zinc ion binding; Molecular Function;	ATGTCACCAGATCAGATTACTGATGAGAATAACAATGAGCATACAACTCATTTCACTGTGATTAATACACCACCTGTTAGTGTAGGTAATCCTGCTAACTCTCCTTCTCTTGATCCTTGTCATCCATACTATTTAAACCCTTATGATAATCTTGGAGTTAATCTAATCAACATTACGTTTGATGGATCCAATTATGGCAATTGGAGGAGAGGAGTTCTTATCTCTCTTTCAGCCAAGAAGAAACTGGGGACATCAGTGAGAGTGATTTATTCACAAACTGCTGTAGAACTCTGGGATGAACTTGAAACTAGATATGGTCAAGCAGATAGTACCAAACTCTTCCAGCTGCAAAGAGAAATCAACAACATCAGCCAAGGGGCAAGTGATATAGCAGGTTGTGAATGCAAATGTGGGGCTAAAGTTCACAACATTAGGATGAATGAAAATAAAAAATTAATTCAATTTCTTATGGGTCTGAATGAAGGATATTCTACTGTGAGAGCTAACATTTTGATGATGAAACCATTCCCCACTATTGCACAAGCATATTCCGTAATTTTGCATCAGGAAAGTCAAAGAGAGGTACACTCTAACTCTGCTTCTACTACAGAATCTTCTACTTTTCTAAACACTGGTGGACAAAGATGGGCACCACAGAGGTATTCAGGGACACAAAAATCAGGAAACCCACATGTCTATGGAGAGAACAATGATGATCAATATTGTAGGTACTGCAAGAAAACTGGGCATCTCATGGTAGATTGTCACAGGTTGATTGGATACCATGCACATTACAAGATTAATAAGCAAAAGAAAAAGGGTCCACAACAGGCAAATATAGCAAATGCTGCCATAACAGCTCAAACTCGGGTGAATGAAATTTCAGCAAATACTCTTTCTACTCTCGTTGCAGGTCAAGGATTCTCTAGAGAACAGTGTAACCAATTGATTCATATGTTTCAAACTGTGCATGGAAGTTCTGAGGCTTCTAATTCCGGGGACAATTCTAAGGCTAATCCATTTGGTATTCATCATGCTTGTTTAGTTCTTAGCTCTTTTCTTTCCAAAGTTACTAATTCACCCTGGATACTTGACAGTGGTGCAACCCAATATTTGACCTATAACAAATCTCTTTTACACAATCTCACAACTCTTCATTTTCCTATTTATGTCAATTTGGCCAACTCTCAACAGGTGGAAGCATTTTCTATGGGAAGTCTGGAACCTTCAATAAGGAAGGTACCAATTATTGGTGATGCTGCTGGAGGACTCTATGTGCTGAAGGATGATACTTCTACTGTGGAATCCAGTCCAACCACATCTTTTGTTCCTGTTTCTAGTTTTGTCAAAAATAAAGTTGAGTCTAGTTCTTTAGGATCTATTTCTTCTTTTTTTTAG
12	yes	GO:0003676; nucleic acid binding; Molecular Function;GO:0003677; DNA binding; Molecular Function;GO:0015074; DNA integration; Biological Process;	ATGAGCACTGCTTACTATCCTCAGACGGATGGCCAATCTGAGGTTCTCAATAAATGTGTTGAACAATATTTGCGTTGTTATGTGGCAGATTCGCCAACTGACTGGGTCAACATGCTTCCTTGGGCAGAGTATTGGTATAATACTTATTTCCAAACCTCGGCTGATGTGTCTCCTTTTCAGGCTTTGTATGGTCGTGCCCCACCAACTCTAGCTCGTTATGTTATTGATGGAAGCTCCCATGAACTGGTAGAGCAGTTTTTCCTTCATCGCGATGAGGTTTTGCAGTCGCTCAAAGCAAACTTGTTGCGAGCTCAAGGTCGTATGAAGAAATTTGCTGATAAAAAAATGCACATGTGTCACTTTGGACGTTGGTGATTCGGCGTATGTCAAATTACAGCCTTACAAACAACATTCCTTGTGTTTACATAAACATCACAAGTTGGATAGGAAGTATTTTGGACCTTTCAAAGTGTTACGACGCATCGATTCTGTGGCTTACAAATTAGAGTTACCAGCGGCTACTTCTATTCATCCTGTCTTTCACGATTCGTTGCTAAAAAAATGTGTCGATCTACCTGAACAACAAATCACTCCATTAAATATCAGTGACACATCTATTGTTGCTTTTGAAACGAACCTTGTGGACAAGGTTCCATTTGGGGTAGGGGTAATGTTATGA

13	NO	ATGCCAAACTTACCACAACACTATGCTCATCAGATAGAAGACACCAAACAATTACTGCATACACATTTCAACTTAAGAGAACTGGAATATTTCTTGGGAATTGAGTTTCTCAGGTCCAGTCAAGGGATAGTGATGAATCAACGGAAGTATGCTCTAGAGTTGATCTCAGAAGTGGGACTAGCTACTGGAAAGACAATACTCACACCACTAGAAAGCAATATGATATTGACTAGTGTGGAATATGATGAAGGGGTTGCCACCTATGATGAATTATTTGAAGATGTTGGGAAGTATCAAAGGCTGATAAGTAAGTTGTTATACCTTACAAATTCCAGGCCAAACATAGTCTTTGTAGTGCGGTCCTTGAGTCAGCTTATGCAGAAACCAAAGGTGTCACATTGGGATGCAGTGTTGAGGGTGATAAGGTATAGAACCACGTAA
14	NO	ATGAATTTCAAGAACTTGACCATTAAGTTTGCCTACAATAACAAGAAACACTTATTGTATGGGAGAACACCTAGAATAGAGACTATACATGCCAAGTCTTTAGATAAAATAGACAAGGGAGATGCACAGTTATTCATGATCAGAATTGTGAATCCAAAAGATACCAATAGTGAGGCTATGTTGCACAATGTGGAGTCTAAACCTGCATTTGTGAATCTAATTCAGGAGTTGTTTGCTGATCCAAAAGGATTACCACCTCAAAGGGACCAATTTGACTACAAAATTTCCTTGACAAATAGTAGTAATCCTGTCAACATGAGATCTTATAGGGATATCATTGATGTAGGAGATGTGAGATCAAGGGATGGTGCAGCCTAG
15	yes	ATGCACCTCCGCTATGGAGCTGCTAGATGCCGGTCAACCAATGCTTATCACTCAGCCCAAGGACCCCACACTAAGGGTCCGATGACGGTGAAGGATGATGGAGTACAGAAACCCTCTTACAGAGAGGCATTTGCTGGAGCCCTAAATATGGATAAGGCACAATCTTCGGCTCCAGTGATAGCAAAACATACGACTCATAATGTTAAGCCGGCAGTCATTTTTAATGCTTCTGATTATTACGGAGTAATAACGGATGAATGTAAATTAACTTTGGTTGGCAAATTCACGATGGGGAGGCCAAAAATTGAGACCATTAGATCGAAATTCTTGGAGCAAACTCCTCTAAAAGGTAAAGTTCGAATAGGTGCCTATGACTATCGCCATGTATTTATAGATTTCACTAATGAACTGGATTTTAATGCTGTTTATTTCAAAAGATTCATGGATATTGCTGGATCTCTTATGCACATGTTCAAGTGGTCTCCAGACTTCGACCCCAACGAAGAGACCTCTTTAGCTCCTATCTGGGTACTATTACCGGAATTGAAATTTCATTTATTCAAATGGGACTACCTTAAGCAAATACTGGCAGCAGTTGGTACCCCTTTGAAGGAAGATTTGGCAACTATAGGTAAATCTAGACCTCATTTGGCTAAGGTAAGGGTAGAAGTTGATTTGTTGAAACCTTTACTGGACTCCATTTGGGTTGGATTAGAAGGAGATGGAGCTGGTAGAAAGGGATATGATCAAAAACTTGAATATGAAGGGGTACCTGCATTTTGTAGATCTTGCAAGATGCAAGGACACGATTTGGACAAATGTAAAGTGGAAGCAAGGAGAAGAGAACAACAAGAGGCAGAAAAAGAAAGAAAAACAAAGAACTTCAGAGCAATAATACTATAG
16	NO	ATGCTCAAAGTGGAGGAAGAGCTTTGGAGAACCAAATCCAGAATGAGTAGGTTGAGTGAGGGAGATGCTAACACCAAATTCTTTCATACTTCCACTATCAATAGAAAAAGAAGAAACAAAATTTGTAGCCTCAAAGATGATTTTGGCAACCTCCTCATCAACCATGAGGACATTGCTAAACACATCCACTCCTACGACATTGTTGGTAATAAAACCTCTAACTTCTTCATAGAGGTCTTCTCCACCAACATGATGCTTGATCACATGAACTCCACCCTACTTTGCCTCATTCCCAAGTATCTTAATGCTTCCAACATCTGGAATTTTAGGCCCATCGGGCTCTGTAACACTGGCTACAAGCTGGTGACAAAAATTATTGTCAACAAGATCAAACATTTGCTCTCCTCCATCATTGGGCCAACCAGGACAGCTTCGTCTCTAATAAGAGTTGTCGACAATGATGTTATTGTCTAA

17	yes		ATGGGGTTTGGGGATAGATGGATAAAGTGGACCAAGTTTTGTATCACAGCAGTAGAGTATTCAGTGATTGCTAACCAAGGGCCTGTGGGATTCTTCTCCCCACAGAAAGGGATCAGACAGGGTGATTCACTTTCACCATTTCTATTTAATTTAGCCATGGAAGGTCGTAAAATGCCTGAAAAGGCTAGGCAAATGGGCTGGATCGAGGGTTTCAAGTGTCGGCTCAAAGAGTGGGATCACAGGCCCCATGTGCCTGACCTAGAAGAGCTATCTAGTATTATGGGATGCACTATTGGTTCACTTCCTACAACCTATTTAGGTCTTTCATTGGGGGCGAAATTCAAGAACTGTGAAATTTGGAATGGAATCATAGAGAGGTTTGAGAAGAGACTTGCATCATGGCAGATTCAATACCTGCCCACGGGTGGCAAGTTAACCCTCATCAACAGTGTTCTAGATAGCATGCCCACATATTTCATGTTCCTATTTCCCATCTCTAAAAAGGTGGAGACTGGAGCATGA
18	NO		ATGCCTGTGGAGCACTCTCGTCTAGAGTCTCTTCTGGGGAAGCGTCAAGAAGGGCACGAATACCCGGCAAAAGGATCGCTGGAGGCGATTGGGAAGGCTCAATTTGGGCATCAATGCCCTTCTCAGAAGTCAAAGAGATGGGGGAATCAGAAGTGA
19	yes	GO:0003676; nucleic acid binding; Molecular Function;GO:0003677; DNA binding; Molecular Function;GO:0015074; DNA integration; Biological Process;	ATGGCGATTGAAGGAGAACCATCGGAAGCTACTGGAGCTAATGTTCATAGATATGGCCTTGCTGCTAATCCTAGATCTATGTTTGATTCCTTCGATCCGCTGTTTTTACAAAATTCTGATATTCCTGGTGTAAATCTAGCTCACTGCGTACTCACAGGAATGGAAAATTATACTATCTGGAGTAAATCAATGCGTATTGCCCTGTTAGGGAAGAATAAAATTGGCTTCGTGGATGGAACTTGCCGGAAGGATATGTATGAAGGTCTAATGGCACAACAATGGGAACGAGTGAATGCAGTAGTGCTATCCTGGATCATTAATGCAGTCTCAAAGGATCTCGTAAATGGAATAGTGTATTCTTCGAATGCTCATAAAGTTTGGGCAGATCTTCAGGAGCGATTTGATAAAGTGAATGCCACGAAAATTTATCATGTTCATCGAGGAATTGCAACACTCACCCAAGGTACATCTTCTATTTCAGTCTATTTTTCCAAGTTGAGGGAGCTTTGGGAAGAGTATGAATCTCTAGTAGCACTTCCTTCGTGTTCATGTGATAAGTCACGAGATTTTATCTCCAATCTGGAACAACAAAAGCTTATGCAGTTTCTAGGTGGTTTAAATGAAACATATAATCAATCAAGAAGCCAAATATTGATGATGCCTAGCATACCTTCTGTAAACCAAGCTTATTCCCTTATTATTCATGAAGAGAGTCAAAGAGCACATTTGAGTGCAATTGCACAGACTTCTCATCTCAGACCACACTATGAAGAAGGTGAATCCTCTGCATTAGCTGCTACTGTCATGAAATCTACTCCTTACTCCAAAGGAAAATCAGTAATGGCATCCCACTATGAGGATGGTGGATATAGAGATTCTGGAACCTCGGGTGGCTATAGAGATTCTGGAAACTCAAGTGGATATAGAGGTACAAATGGTCAAGGTACAAATGGTTACAGGTCTGGTGGATACAGGGCGCATAATGCTAATCTGAGTAATCACTCTGGTGATTTTGAGCAACAACAAGGTTTAGGATTCACAACAGAACAGTTTCAGAAACTTCTCAATTTGATTGATAAGCAAGATTTCCCTGAGAATGTGGCTAACATGGCAGTTTCATCCTTGGACTTAATGTCATCTAGTTCTCTACTTCCACCTTCTCCTCAAAATCAAGTTCACTTACCAAATGGTGCTATGGCTCAGATTACTCATAAAGGAACTTGTCGATTAGCCAAAGATCAGTTCCTTACAGATGATCTTTACACTGGCAAGGTGATGGGAATTGGTAAAGTCAAAAATGGACTATACATTCTCTCAACCAATTCACCATTATCTTCCACAACATCAAATCTGAAAAATGCTTCTGTTTGTTTTTCCACTCAATCTGCCTCTATCAAGAGTTCTATATGGCATCAAATGCTTGGCCATGCTCCATTTCTAGTCATTCTTTTCAATTGGTGCACATGGATGTATGGGGTCCTTATAAGCATAACACATACAATGGAAATAAATACTTTCTTACTCTTGTGGATGATTTCAGTCGAATGA
20	NO		ATGCCTTTGAAGGATGATCACAAGGTCCATATAGAGGTAGTCATCATCATCACTTGCATACTTCAGAACGATTATGGTCATGCAAATAAAGAGGAACTCTTAGCAACAAGATTTTTCATGCCTTTCCCTATTCTTATTAGCAAGTTGTGTGCTCTAGAGGAGATACCATATTTTGAGTTGGACAAAGTTTGCCCTGCTATTGGGGTAATTGATATTGAGAGGAAGCAGGATGTTGAGGCTCCTATAAACAAAAAGAAAAGAACGCAAAATATGGGAGTGTTTATAATTCCCCTGCTCAGGATGTAAGTTAG

21	yes	ATGGAACCTGAATTCTCCGATGATACTCAATTTCCATCAAATTTAGTGCAAGATTCAATCTTGACAATTCCTGTTCTGCCACCAGAACTGATCACTGAAATTGTCTTGAAGCTTCCAGCTATTGAAATGGATTTTTCCATTGAAAATGACATTCATGGGCTCTATGCTATGGGTTCTTGCAATGGATTGGTTTATCTTGCCCGTTCTTGTGAAGGATATTCCCTTTTGTGGAATCCTTCAACTAGAAAGCACAAGGATTTGCCTCTTTTTAGACAGAGATCGGAAAAACACAAATGTGTTGCATATGGTTTTGGATATGATGAACTCCATGATGATTATAAGATAGTGCTTATTTCTTAA
22	NO	ATGAAGGAGAATAACAAAAGTAGGGAAGAACCACCTTCTGAAGAAGTTTCACACATGCAGCAGTGCGAGACGACACAAACTACTGAAAATAAATCGCAGAATCTGAATCAGACTGAGAAGGATGGAACAGACATACAAGTACAACAGATTTTTGAGGCAGAACCAGTGGCAATTCAGAACTCAGCAGATCTTGAAACAGTTGAAACAGAGGCATCAAGCTGGGTGAATTCCCACATTCTAGATTCAAGCAATACTTATGGAGTAGCTTTTGAGGGTTTCAAATCTAAAACTTTGTCTCTCCTCGTGAGAATTGACGAGAGAAAAGTTGCACTGGACAACAAGGAGATGAGGAAAGCAAATGTGACACCTTAG
23	NO	ATGTATAAACTGTTCCCTGGTAGTTTTTCTCACTGTGATAATTCTGGTTTTCCTCCTACTTCCCCTATTTTCTCTGAATCTTCCTCTCCAATCTATCCTTCTGCTTCCTCTCTTCCTGTTGCAGATTCATCACCTCAATCTCCTACACCTTTCAGTTCATCTACTATGTCTATCCCTTCTTCAAGCACTAGTCCTTCTACTTCTGATGCACCTATACCTTTCCCACAGGATGAAGTATTGCCACTAGCAGCAGAAGTGTCTCCACGCAGGTCACAAAGACAACATGTGAAACCTAGGTATTTGTCAGATTATATTTGTGCACTAGCTTTCTCTGTGATCTCGCTTAATCCTCTTATTCATCCATATTATCAGTCGTCTTTTTATGCTTTAACTCCTTCTAATCAGACAACTATTAGTTCCATTTGTCAAATTACTGAACATACTTCTTATCGACAAGCATTGATGAATCCTGGTTGGAAAGCTGCAATGGAGTCAGAATTACAAGCCTTGAACTCCAATCACACTTGGGACCTGGTCAAATTGCCTGCAAATAAGAAACCTTTAGCTTGTAAGTAG
24	NO	ATGAGCCTAATAGTATGGAACTGTAGAGGCGCCAATGGACTCGAATTCAGAAGGAACTTTAGGGCCCTCGTTGATTGGCACAAGTCTCCTTTAGTTGCACTTCTTGAAACCAAGATGCAACATCATCAAATCTTGCTTGATAACTTCCCTTTCAACAAAATGATTGAAGTTCCTGCTATGGGGAACTCGGGTGGCATTGTTGTCCTATGGGATGATAACCTTCTGGAACTCGATGAAATCGCCACCATTGGTCAGGAAATTCATGCCATGATCAAGACCAACCTTAGCATCCATGACCCCGTTGCCATGATCAGAAACAAAGATAGTGCCAACTGGCTATATGATCTCGACAATATCAATGCTAACGTCTTCAATGTTGAATGGGGGGCAGCCTTCCCATTCTTCCTTTGGAACATTTGGCTAAATAGAAATAATAATCTTTATCGGAATACGCGAAGCGAAATCTCCATGTCTCTCCCTATATCCAGAACCCTGGAGTTCATACATTTAGGTCAAGGAGACTTGAGCACTTCGCCCAAAACCATCAGTAAACCCCCCTATGGTAGTTGGACCCCCCCTACTAGTCGCTTTAAGCTTAACATAGATGGTTCCTTTAATGCGAATACATGA

25	yes	ATGCTCTCCCTCGAGTTTTCTCTTCCAGAAGAATTTCGAGAATTCAAACTCTCCTGCGAAGTCTGCAGCGAAAAACTCCTTCCTGCTTATTGGGTTTATCATTGTGGTCCTTGCAGATACTTTGTACACGTCAAATGCGCCGGGAAAAAGAGAATGGCAGCTGATGATAACATCGAGGCCTTTCCTAAGTTGAACTTGGCCCTGCTGCCAGAGGCTAATGAAACTGTGCAACTTATAGTAAGGTTTCTTAATCAAAACGGCATTTTAGAAAATCTAATGCCATTGCAGATTGACAATTTTCAACACAAGATGCATTCGTTAGTTCTTTCAAATAACACAAACAAGGATAAATTAGTCTGTGATGGCTGTGTTGGGCCTATTGTTGACCGGCGGTATTATAGTTGTCAACAGTGCAGTTACTTTCTACATATAACTTGCTCTCAGTTACCGGGTGATCTGGAGCTGTATCATCCATTTCACCCGGAACATCCACTTTACATAAGGCATCCAGAGTATTGCTGTTTCTTCCGGCAATGCAGTCATTGTAAATTAGACACTAACGGTTGGTGGTTTGAATGCACAGAGAGAGATTGTGTCTTCCGCCTTGATATGAAGTGTGCTTTTATACCTAAAGCTATTGCTCATAGATCACATAGGCACCCCCTTTGTCGAATTTCAGTTTCCAATGTTGATTGCAGTGCTTGTGGCAGACGCCTCTCTGGTTCGTCATACGGTTGTAAAGCCTGTGGTTTCTACCTAGGAAATGATTGTGCTCTATTGCCGGCAACTACCACCCACAAATGGGATGAACACCCACTTACCCTCATTTTCCCCCCTTTCACTGACCATCCAGATGAATTCTTGTGTGAGATCTGTGAAACATTTGCACATCCCAAGTATTGGCTCTATCATTGTAGGGAATGTGATCAATCTTTTCATCCACATTGCATCCCTCGACATGGTATGTCTCGCAATATCAAGTTTGGTAGCACCATCCAAATTGCTGAGCACTCACTAAAATTAGTCGAAAAAGGTGAATTTAAGTCCCAGTGTGGTGTATGTCGAAATCATTTGTATGAGACAGAAGCCCTGCTCTGCACAGCTTGTAATTTGCATATTTGCCGCAAATGTATTTGTGTCAATCTGAAAAAGGACGATACAGCAATTATATCGCCTTGCAGTAAAACTCTTGGGGATTCTTAA
26	yes	ATGATGAAATTGGCTTTGCTGTTTCGTGAATTACCCGAGAAATTGTCAATTGTGCCTAATTTAATATCCTATAACGTCGCGATGAAGCCGTTGTGCAAGGCTGGTTCTGTGTATTCTGCTGTGCTTTTGATGGATGAGATTGAAAAGCATGGGATTAAGCCGGATATTGTGACTTGTAATACATTGTTAAAAGCACTTTGTGATAGTAAAAGGTTTTCTGAGGCTGAAAACTTGTGGATTATGATGGAAAAGAGAAATATTCTTCCTGAAAACTGA
27	NO	ATGGGGGGACTGCTTGTTTATCCCCATGAATATGAAGACTTTGCTTGTTGTGTTAATTCATGTGAGTTGTATGACCTTAATTTCTCTAGGAATCCTTTTACTTGGTGGTATGGAAGGATGAATGGAGACTGTATCTTCAAAAGACTAGACAAGGTTGTGGCTAATAATTTATTTCAGGATATCTTTGGAAGTACTGATTTACAACATTTGGCTAGAACGGGTTCAAACCATGCCCCACTATTTCAAACTTGTAGGATTAGCAATCTGACAATAGCTAAGCCTTTTAGGTTTTTGAAGTTTTGGATTGAAAGGGAGGATTTCAAGGAGGTTGTTCAACAAAGTTGGGTGGCAGACAACTCTGTTGATTTTTTTTTACAGTTGAAGCAAAAGCGAAAGAGCACAAAGTTGGCTTTAGCCAAATGGAGTAAAGAAAAGTTTGGTGATATTTTCAAGCAGTTAATTATTAGAGAAGAAATTGTGAAAATCAAGGAAGATCTATTTCAAGAAGAACCTTCTCCTATTAATAGAGCAGTATTAAATCAGGCCCATACAAAATTATAA
28	NO	ATGAGGTGGTTTAAAGACGGAGACAGAAACACAAAGTTCTTCCATGCATATGTGAAAGGGATAAGGAGGAAGTTAAACATTACAGAAATTAGAATGAGGCAGGGGGACATTATAACATCTCCACAGAACATTGGGGAGGAAGCTGTCAACGTCTTCAAAGAGCAGTTCCAGGAAACACATGAAATTACAGATTTTTCAATGCTCCAGTGTATTCCAAATCTTGTCACAGACGAACAGAATCATGAAATTGAGAGGATGCCGACAAAAGAAAAAGTAAAACATGTGGTTTTTAACTTATGGAGATAG

29	NO	ATGGTGTGTTTTGAGTGTTTCTTGTACGAGCACATTCGTAAAGTTTGTGGGCACGTTCCAGGCTTGGATTGTGTCTATTATCGGGGAACAACACCCTTGCATAGGGTAGGACCTCCTGACGAATCAACTTTGTGGCTCTCTGCATGGATTGGCATCGCTCGGAGGTTCTTTAGAAGGGAAAAGTGTCGCAGTTATAGTTTGTTTGTGGTTTTCCGCCTAGAGCATCTTCTGACTGCTTTTACTCTTGTGAGCTCGATGTGCCATACGGGGCAGCCTGTTAATTTAGGTCCGAGCTACAAACTATCTTTTTCTTATACATTGTTGATAAACTCGATGTATCACCCCGGACAACTCGTTGATATACATATTTGGGTTATTGTTAAGCTTGACGTGCCATCGCGGGCGGCCCGTAGATACATCTATCTTAATCTTTTTCATTCGATAAGTTTGAGGTATCATTCCAGTTGGCTCGATGTCCCTTCCGAGCTTCTATTCTCGCTTACTTGGTGTTTTATATTGTATCATAATGAGAATTGA
30	NO	ATGGAATGGTTCAAAGAAGGAGAAAGAAACACTAAGTTCTTTCACACCATAATAAAAGGGAGACGAAGCAGAATGAGGATAAACAGAGTACAAACTGAGCAAGGGGAATGGTTAGAAGAACAAGAGGCGATTGCGGAGACAGCAATAGACTTTTACATAAGACAGTTCACAAAGCAAACATATAGTGAAGATTTTGAGATGCTAAATGAACTGCCTATTGTGATAAATGATGACAAAAATAAAGAATTACAAAGATTGCCATCAATAGAAGAAGTCAGAAGCGCGGTTATGGGGTTGAATAAGAACAGTGCAGGAGGTCCAGATGGTATGACTGGAGCTTTTTTTCAACAGACGTGGGAGATAGTAGGAAATGATATTCATAACATGGTGAAGGCCTTCTTTTGTGGTGCTGAATTGCCAAGATATATCACACACACTAACTTAGTCCTTCTGCCTAAGAAGAGTGTGATAAATATTTTTTCAGATTTAAGGCCTATTTCTTTGAGTAACTTCATGAACAAGGTTTTTTCACGAATTATTCATAAGAGAATCAAATCAGTGCTGCCATTGATTATATCACCTGAATAA
31	NO	ATGTTGGATACGAGTGGGAAATTCACTGTAAAATCAGCTTGGAACTATATCAGACATAAAGAAGTTCCGAATAGAGTTTACAAATGGATATGGACTAAAGGGGTCCCTTTCGAAATGACCTTTTCGATGTGGAGGCTATGGAAATTCAAGATCCCAGTAGATGATAGATTGAGAAGGTGGGGAATTGAGGGGCCATCGAGGTGTTGGTGTTGTGAACAGCCTGATCAGGAGACATTGGCCCATGTCTTTCTCAAATCAGATTTTGCTAATAGGACTTGGTCCTATTTCTATTCTTTTGCAGGTTTTAACATAACAAGATTACCATTGAGAGAGGTGATAATGTTGTGGTGGGGAGAAAGTAGCAAACAAAGCTTGAAGCCTTATTATAGAGCACTTCCTAGCTTTATAATATGGGAACTACGGAAGAGGAGGAATAAGAGGAAGCACGAAGGAAAGAATACATCATTACAAAGAATCATTCATAATGTTACTAAAAGTATGTACATGTTGATAAAAGTGAGAAGGCCAAGGATGAAAGTAGCAGGCAGATGGCCAGATATGCTAAAACAACTGGAGACAACAGGCTCACAGATGAAGATAACCAAGGTAAGTTGGGATTACCCCCCTGAGGGATGGGTAAAATACAACACAGATGGCGCGTCTAGGGGGAGTAAGTTCATATGGATATTGTTTAAGGGATGA

32	yes	GO:0003676; nucleic acid binding; Molecular Function;GO:0003677; DNA binding; Molecular Function;GO:0015074; DNA integration; Biological Process;	ATGCCAGACCCTCTTCTTGATTCTTCTATGACTGATGAAATGTTGGCTGAGGAGCTTCAAAACCTTGAGGTCATGCATTCGTCCAGTATTTCTTACCACGCTATGGCCGGGGGTGACACTGTTTCTGCTCTCCATTTTACTAGTTATATTCAGGGCCCATCGGTGCATGTCATGCTCGATAACGGCAGCACACACAACTTTATTCAAACTCGTGTGGCTAATTTCCTTCACCTGACCGTAGAGACCATTGCTCCGTTCTCAGTTATGGTCGGCAGTGGGCAACGTCTACCATGTAATGGAATTGTCCGACAAGTTTCATTAATGATTCAAGGGTGTCTTCTCACTATGGACTTCTTTGTCCTACCGATGCATGGTTCAGATATTGCCTTAGAGGTTTCTTGGCTAGCTACTTTAGGTCGTGTTGTTACTGATTATGGTCAGCGGATATTTGAATTTGAGTTAAATGGGCAAAAATTCAATTGGAGAGGTGAGTCATCTATTAATATCCAACCGGTCCAGCTTCAATGTTTACGACACTTATGTGCTACTGATGTTATTGCCACCTACTATCATTTGCAATTAATTGGGGCTACACCTTCAAAATCTCCTGAGACTACTCCTCTTGCGATATCTGCTTTATTGGACTCCTTCGAGGACGTTTTTACTAAATCGCAGGGACTTCCGCCTACCCATCTTCAAGACCATGCTATTTATTTGGCTCCAGCCACAGGGCATGTTAATACCCTTATTGCTCAGGCTGCCTTCGAGAATCTTAAGAGTTGTCTCAGTTCTACACCAGTATTAGCTTTGCTTGACTTCAGTCAATCGTTTCAGGTTGAAATTGATGCATCTGGGAAGGGCATTGGGGAGGTTCTCTCTCAAAAAGGACATCTAATTGCTTATTTCAGCCAAAAGTTATGTCCTAGGATGCAACAAGCTTCTACTTATGTGCGCGAAATGTTGGCTATTACTGAAGATGTTAGCAAATGGCGTCAATATCTATTGGGTAGATGGTTTATCATCATTACTGACCAGCAGGCTCTTAAGAATCTCACCAATCAAGGACTTCGTGATAATCCTGCAGCATATCCCGGTTATTTGTATCGAAGAAGGCTCTTGTTCTTTAAAGGGCGCTTGGTACTACCTGCTGATTCATCACCTCACCTCCACCTTCTCAATGAGTTCCACTCATCACCTGTTGGGGGTCATTCAAGCATTGCTCGTACCTTTCATCGTTTATCTTCCAATTTTTATTGGAAAAATATATGTCATGACGTCAAGGTGTTCACATCCTCTTGTCAGATTTGCCAGCAAATGAAGGACCACCATCATCATCCTGCGGGCCTTTTACAGCCTCTCCCAATTCCCGAGCAGGTATTCGAGGAGATCACAATGGATTTTGTGACTTGCATGCCCCCGTCTCGCGGTAAAATGACTATCATGACTGTAGTCGATAGATTGTCCAAATATGGCCACTTCGTACCACTACCTGCCACTTTCACGGCTTTAACTGTTGCTGAAGCTTTTGTGGCCCATATTCTCAAACTTCACGATCCTTCAAAGTCCATTGTCACTGATCGTGATCCTCGTTTCCTACATGTGTTCTGA
33	NO		ATGTGTGGTATGGGAGAAACTGGTGAGTCGGAAATCCCTCAAACTAAAGTCTTGGCCTCTGCGGCTGTAGAACTCTTTCCTACTTGTCCTTCTCAAAATGAAGTTGCCACGTCCTTACCTACTCTTGTACGCTCTCCCTCTCCAAGTAAATCTCAAGATGCCTCAAATAACTCAGAGGCACCGTTTGTCGTCAAACCTCCTACAAATGCCAATCTATCTGACGTAGATGTCACTTCACAATTAGGCCCCATATCCTCCACCATGTCTGAACGAGTGTTTAATGGAAATCTACTAGTAAGGAAAGAGACTGAATCCAACATTTTTGCAGCCAGTGATGAATGGGTTGTTTAG
34	NO	GO:0003676; nucleic acid binding; Molecular Function;	ATGGGGTATCTGATTTTTGCTTATTCCTTGAGGTTAGGTCAAGGCTCTAGTAATTGGGCAGAGGCCAAGGCACTATTGTTTGGTGTGAACTGGTGCATTGACAATGGTTATGATATAATCCTTACAGAAAGTAACTCTAAGCTTTTGGTTGAATGTGTTAATGATCTCAACCAAACTCCTTGGAGAATTCTTAAAGAAGTATCTAACTTGAAAGTCCAGATGGAAAATATAGGTTTCATTCTCCAACACTGTTATAGAGAGGCAAACAAAGTAGCCGACAATCTAGTTTCTTTAAGTTTTGTAGAACCTCACAATCAGACATATGAAGCCTTTGTTGACCTGCCCGCCGAAGCAAGAGGCCTTATGACTATGGACAGATAG

35	NO	ATGGAACATGCAGACATCTGGGAAGTGGTGTCTTTCCCCAGGAAAAGGAACGATGCAGCGCGAAAAGAAAATGCAGGCGCATCCAAAGATTCAGTAGGACAACAACAAAGGCAGGTAAGGGCTTATAACCTTTACGCAGGGCCCACAACTCTAAATACTAAGGCCAACACCACAGCTGTAAAAAGCACAAATAATGTTAAACATCAGCTTTTTACAACCATCAATGAAGAGAGACAAAATCCCAAGAGGGATAATGGTCTCTCAGTCAGTAATCACGCGGATCTAAATCCCAAAGGAAACCTTGGGTCCCAGGGTTTAATGCCTAACCACCCTCTTACCTTCCCTAATGCTCTGACGATCCAAATCACCGCCGCAGCTCAGGCTAAGGAGATGTGCATCTTGGAGACACTCTTCTTCAAGGAGTTCGAGGAGCCCATCAGCACGACAATGTTAGCTTACTGCCTACAGGAGATGAAAATATGCACTTTGAACCTGAGGAACAAGAAGGAACTCAGTCCTGCAGCAGTGGTACTAAACCCCATTGGAATACCCAAGCAGAGATTTCGAGCGGAGAAAGAGAAAGGGAAGGGCTTGCAGGAGAAAGCAACACCACTCGTCTTAATGATGAACTATATCATATAG
36	NO	ATGGCTCAAAGCCCACACCTCATCTATTTCCACCAAAGTACCTCCGACCTCCAACTAGCACAGTTACCGAGTAATCCTGCTCACCAAGATATCAGTGTTCTTCTTGGAGTTTGTATCACCTCCGGCCAGCACACAGATTCAGAACAGGAGAAGTGCTACAAGAAGGGAAGGGAAGAAGACTTGTGTTGGGTACCTAGAAGTGCTGATGCTACTCTTCCTTTGCAACTACCAGATTTGCAAATCAAGCAGTTTTTGGTTTTTTAG
37	NO	ATGGCATCAGAGAACTTAGTTCAACCTTCCATCCCTCATTTTGATGGTCATTATGACCATTGGTGTATGTTGATGGAAAACTTTTTGAAATCAAAGAAATACTGGCAAGTAGTTTCAGAAGGTATACAACAATTGGAAGCTGGTGCAACAGAAGCGCGGAAGGTAGAGATAGAAGCAGTGAAATTGAAAGATCTAAAAGCAAAAAACTATTTGTTTCAGGCTATAGATCGTTCAATCTTGGAGACAATTCTTTGCAAAGACACCTCCAAGCACATATGGGATTCAATGAGAAGGAAATATCAAGGATATGCCAAGACTAAAAGACAACAACTTCAGGCACTTCACACTGAATTTGAGACATTGAAAATGAAGTCTGGAGAATCAATTACAGATTACTTCTCAAGTCTCAAGAGTAATGACCATTGTCAGCAAGATGAGGCTACACGGTGA
38	NO	ATGTTGTCTTTGAAGATACGGATATTGAGAGAAGATCTTATCAATGCGTCAAGAGAACCAGATATGAGTGTGATTGAGTCTGAGGACATTGTAACGGTAGTCACCAAAAGAAGAAAAGAGGTAGAAGGAAAGATTGAACTGCTCGAAGATGGGACTATTGATACAAGGGTGCAAGAGGTAGAGATTCATTTGAGTGAGGATACTCTGAGCATCATCCTGGATGTTTCGTGCAAAGGGATTAGGTCAATAGATAGATGTGCGCCATTGGATGAGTATATTCAAAAGGTAGACAAATTTGAAGGTCTTAAGTGTTCTGGGGTTCCCAAGAAATATCTGAAAGGAGATCACCAACTGTACTTTGAATTTGTCAACAAAGTATTGCTACCTTGCACTGAGAAAAGAATAGTTGCATCATTAGCAGACCTTTTTTCTTATGGAAATCTTGACAAATATGATGCCATTAACCTTCCCGGTATCATGTTGGAACAAATGCACAGGATCATAATAGTCAAGGATAGAAAACCTGGAATGACTTATGGGTACTTGCTGAACAAAGTGTTCTACCATTTCAACGTGCCTGTTGGAAAATGA

39	NO	ATGGTGTGGAGAAGAAACAAGTATAAAAGGGATAAATCAGGGCGAATTGAAGGGGAAATTGAGTACAAAGATGAAAACGCTTTTGAGGCACTAAGAGAAGAGAAAGAACGGGACAAAGACGATAGTAATGAAGAAAGGGCTTTAACAGAAAGTACAAAGGAATGGGTTAAAAAAACATTTGAAAGTAAAAATAAAGGAGAGGCAGAGAACAAGAAAGAAACAGGCAAGGGCGCAAATGAAAATGACGCCAATAGAAAAGAAGAGGTGAATAAGGAAAGCAAACAGATCCAAAGCCCAAACAAAGAGAAGATAGAAAAGCAAGAGGAAAACAACAAAAAAAGGGGTAATAGAGTGGTTCAAGTAGAACAGAACGAAGGGACAATTATAGTATATGGCATGGACAACGAAGAAGTATTACCACTAGCTATCCATAACGGGTATGAAGGCAGCATGGAGAATCACGAAGGTAGTATGGATAAGGTGGATATGCACCATAAAATCAGCAAAGTGGCTATAGAAGGAGATTTATCACCTACACAGGTTGAGAAGATGAAGGACAAGGTGGCCAAAAAGAAGAATCAAGGGGAAAAGGATAATGTTGGGGCGCAAGCATCATCTAGGCAATCCAAGAGAACAATTATAAAAAATTCTAAGAGGTTGGGGATGCAACATGTTGTGGTCAATAATAATGGGAAGATATGGATCTTCATTGATGAAGTCATGGAGTATGAGGTAATTAGGGATGAAGACCAAATGTTAACTGTAAGGGTGAGAAATAGAGAAATGAGCATTGAGGTAATGATCTCAATGGTCTATGCCAAATGCACGCAAGGAGAGAGACTTCAGCTATGGGAGTCATTGTACGAATTGGCTATGACAAGTAACACACCTTGGTTAGTAGGAGGAGATTTTAATGTTATTAGTAATTCCGAAGAGAAATTAGGGGGCAGAGCAGTCACAGAGGCAGAGGTAAGGGACTTTAATCACTGCCTGAATGTGTGTAATTTGGAGGATCGAGGATTCAAGGGGAGTAAATACACTTGGTGGAATGGCAGAACTGATGAGGACTGCATATTCAAACGACTGGATAGAGTATTGAGTAATGACTTACTCCAGGAAGTATTTCCAGTTCTAGAAGTAGAACACTTAGTGAGGAGTGGATATGATCATGCTCTTTTGGCTATTAATTTTGACACGAAAAAAGAAGAAGTGATTAAACCATTTCGCTTCTTGAACTTTTGGGTGATGGAAGATTCTTTTTTGGAAGTGATTCAAAACAATTGGAATGCGGATTTTGAAGGTGACCCTTTTAGTTTATTCCATCATAAACTAAAAAAAGTCAAAAAGGCGTTAACCCAGTGGAGTAAAATGACTTTCGGAAATATTTTCCAAGAAATTGCCACATTAGAGGAAGTTATTAAGGTTCACGAAGCACAGTTTGAGTTGATCCCCTCTGCCAGCAATAGAGCAAGGCTACATAAAGCTCAAGCGGATTTGAAGACACAACTTAACAGAGAAGAAGATTTCTGGAGGCAAAAAGCAGGTATGGATTGGTTCAATGAAGGAGAAAGAAACACTAAATTTTTTCATACTATTGTAAAAGGTAGAAGGAGGAGACTAAGGGTGAACAAGATTCAAAATAAGGAAGGGGAGTGGATAGAGCAGCAAGGGCAGATTGCAGATGCAGCAGTGGAGTTTTACAAGAAGCAATTCACTAAACAAAATACCAGTGAAGAGTTTGGAATGTTAGATGAACTACCAGTGGTAATTACTAGTGACATGAATGACAAACTACAAGAAATGCCATCGCTAAAGGAAGTCAGGGAAGCAGTCATGGGCTTAAATAAGAACAGTGCGGGTGGTCCAGATGGGATGACAGAGGCTTTCTATCAAACCGCATGGGATATAATCGGAGAGGATATTCACATGATGGTTAAAGCCTTCATATGTGGAGCTGAACTACCGAGGTATATCACACACACAAACTTAGTTCTTTTACCTAAGAAGGGTGGAATGGTTGTTTCTGACAAAGGTGCTAAGAAGAATAGGATTCAGAGATAG
40	NO	ATGATTTATCAGATGAATAGCCTTCCCGGATCGTTAGATGTTAGAGTTGCACGGGTTCAGACATATATGCCCATGATCATTGATAGAGCTACTGAGAAATCCTTCGCTACATTGCGTGACAAGGTGAGTAGGTGTGAAGGATTGGTTGAGAGCAATGATGTGAGGTTTTACCACCTCTCTGCTAAACTTGAGGCCTAA

41	yes	ATGCAGCAGGTCATGAATACAGATCAAAGGAATTGTGATAGTAACAATGAGCCAATACCTGAAGTAGCAGTAGAGGGAAATAATGGTAATGTAGAAGGGCTCTTGGGAGATATGGCTGAGGCTCAACAGGGTCACATGTGCAGGGGTAAAGTTGACAAAATGGGTGATACATGTAGAAAGGAACCACATGAATATGATGATGAAGAGTTGAAGAACCAAGTTGAGATGAAAGATACATCGACAACACATGGTAGAGAAGAGAATGAAGATAGTCAATCACTCGCTATAATACCTGCAGCTGCACAAAAATCTGAGATGGAACTGATACTGATGAGCGAGTTGGCAAGTGCTGAATACCATGAACCTTTACAAATAACTGGTGTATCAGATGGTGAAGTAACAAAGAACATTCAAGACCACCAGGAGCCGCTGGAGTTAGAAAATAACAAAGCTGAATCAACATTAGCATCTGTTATTGCTGGAAAATCTGCTCCAATGGACAGGCTATATGAATTGATTTCACATAAATGCCTGAACAAGGACCCTGCAATCATAGCAAAAGAAGTCATACTATCAGAAAAGAGTATAGGTGTAGAGGATAATGAAGAAGAAAAAAATGACACAAATATGCACAACATCTGTAAAGAGGCTGGGCTATCACCAAAGGTGTACTCAAGAGGGAGAAAAGGCAAGGGCAAAGGAGAGACAAGTATTGCAGTGCCTACAGGAGTTCAGACTAGGAGGGGAATTTGGGTGTTTGTTAATAACCATATTCAAGTGGGGGTGGTGGAAGACTCTGACCAACAGTTGACTCTACATCTCACATTAGAAGATGGTAATCAGATCTTAGCTACTGTGGTCTATGCTAAATGCTCTAGCATTGAAAGATTAAGCCTTTGGGAAGAGCTTTCCTCAATAAGTCAGAATCTTACAATGCCTTGGATGGTAGGTGGTGATTTCAATGTGATCCTAGGGGATGAAGAAAAGATTGGTGGTCTACCTGTTTATCCACAGGAATATGAGGATTTTGCCTGGTGTCTTAATTCATGTGATTTATCAGATGTTTATTTCTCTGGAAATCCTTTTACTTGGTGGAATGGTAGAGTAGATGAAGAATGTATTTTCAAGAGATTAGATAGGGTTGTGATTAACCAACTATTTCGTGAATTGTATGGTAATTCTGGACTACAACACTTAGCTAGAACAGGATCTGATCATGCCCCTTTACTCCTTACTTGTGGGGTGGGCAATATTCCTATTGCTAAGCCTTTCAAATTTCTGAAGTTTTGGACTGAAAGTGAAGACTTCAAAGAGATAGTTCAACAGAATTGGATAGCTGATAAGTCTGATAATTCTGTAAACATTTTCATTCAATTGAAGCAGAAACAGAAAAGAACCAAGGCGGCATGTCTAAATGGAGTAGAGATAAGTTTGGTGATATTTTTAAGCAGCTAA
42	NO	ATGGAAGACTATCTTCATCTTTTATCCATTGTTGCTTTTTACGTAAAGGCGAAAGAAAGTTATTGGCAGATGCGAACTCTTAAATGGGAGCCTTGGTTTGAACCAGAAGTAGAAACAACTATTGGAGTGGCTTGGATATCTTTTCCAGATTTACCTACAAATTTCTTTGCAAAGGAGGCGCTTTTCTCAGTAGCCAGTGCGATTGGAAAACCCCTAACAGTGGATATGGCTACAAAGAATCAGACGAGACCTAGTTGTGCGAAGGTCAAAATTGAGGTGGATCTCACTGCAAAGCTTCCCCAAAGAGTGAGAATAAATGAGGAAGATGACAATACAGGGGAGATCAGATACAGGTGGATTAAGGTACAATATGATCATATGCCAAAATACTGTAAGGATTGTTGCCTTCAAAGGCATGATGAACAAAACTGTTGGACGCTACACCCTGAACTATATGAGGCAAACAGTGAAGAAGATAAAAAATTAGAGGAGGAAACAAAATCAATACCAATTATGGGAACAACGGCTGATCAAAGAAGAATGGCAAGTGGCAAAGTAGTGGGGAACAAACAAAATCAACAAGAATGGATGGTACGAAGAAGAAATAAATACAGGAGAGATAAGTATGGCCATATTGAAGGGGAAATAGATTACTACCATGAAAATGCTTTTGAAGCTCTAAGGGAGGAGAAGGAGCACGAAGCTGGTACTGAACAAACGACTAAAGAATGGTTGAACAGTCAATTTGGCAAAGGGAAAGAGAAAGTAGATTCAGAGAAGGAGAAACAACAAGAGGTTGCGGATGCAAGTACAATGCCGAATCAAAGCACGAGATCATTCAAAAAGAACAAGGGAAGGAAGGGTCATCACAATGCACACAAGAAGAGACTTGTAGAGAATCAAAGGATGAGAATGGTAAAAAGAATGAAGGTGCAATGGTGGTATATGGGATGA

43	NO	ATGAATCTGCAAGGCAACAAAGTAGCAGAACAACAACTGGTGATGCGACCTATTGGATACAATGAAGGTGTACCAAGAATCACATGGACGGAGGAGAAGGTTCAACAGATGAATGTAGTTGAGGAGTTACAATTAGCTGTCATAGGAAAGTTTTCCTATGGATGGCCAGAGCTGAATAAATTAAGGACCCTAATTCCTAAACAATGCAAAGTGAAAGGAGACTGCAAAATAGGATTGTTGAGAAACAGATACATCTTGATACGTTTCAATCTAATGAAGGATTACGTAAACATATTGTCGAAAAGCGTCCATTACATAACAACAAAAGATGGTATAGCATATCAAATGAGAACTTTCATTTACGATACTACTTTTACGTCGGAGAAGGAAACAACACAAGTTATGGCCTGGATTTCGTTTCCAGATCTGCTTCCCACTTTCTTTGCGTAA
44	yes	ATGCCTGACACACCACCTCCTTTCTCTGTTACTCCTGGCGTTGCAGCTCAAGTCAGAGGACAAGAGCCTATTGATCACTCTCACCCTTTTTACCTTCATCCCTTAGATTCACCATGTATGCAACTGGTGAGTTTTGTTTTCAATGGCAAAGGATATGGGGGATGGAGAAGAGGAATCCTAATAACCTTGTCTGCTAAAAACAAGGTAGGGTTTATTGATGGCTCCATTTCCCCCCTTCATACTTCTCCAGAACTGCTCAAAGTTTGGACTCGATGCAATGATATGGTGATCTCTTGGATCTTAAATTCTCTTTCAAAAGACATTGCTGAGAGTGTCCTCTACTCAAGCACTGCTAGAGAGATCTGGAAGGACCTTGAAGAGAGGTTTGGACAAAGTAATGGACCTCAACTGTATCAGCTGCAAAAACAAATTAATGAATCAGTGCAAGGAAATCTTGATGTAGCTGGTTATTATACAAAGCTTAAGCGTCTCTGGGATGAGTTAGACAATTTAGACATGGCACAACATTATAATTGTGCATGTGTTTGTGGTGTCAAGTCTCAACAAGATAATAGGCTCATTCAGTTCCTTATGGGTTTGAATGATGCCTACTCTGGTGCACGCAACAACCTGCTCATGTCATCCCCTTTGCCTTTTGTTAATCATGCCTATTCCTTGCTTATTAGGGATGAGAAGCAAAGGGAGGTTCAAAGTTTTCACCAAACTGCAGAATCCTCTTTCTTTGCTGCAAGGAAACATCAAGGTCCTCAGAAATACAACTATGGAGGGAATAGTATTTTGGAAGCAAAGAAGACCAATTTGCTTTGCACTTACTGTAAGAAAACTAATCATGTTATAGCGGATTGTCACAGGTTAATAGGATATCCGGCAGATTTTAAGTTTACTAAGATTAAGAAGATTTTTCTTGGTGCTAAGAGTAATGCTGTGATTACACCAGACGTAGGCACTTTGCAGTCTCTTGCTCTTGGAGACAGACCCATCACTCGAGATCAGTACCATAACCTCTGTCAGATGTACCAGACTGGACAAAAATTGCCTCAAGTTGATTAA
45	yes	ATGACGTCGATAAAGTCCCTAGCACGTGAGCAGTTAATAGGGTTACCGCCCTTTTTCAGAATTTGAAGACCGCTATTTCTGTTCTTGTTTGTCTCATTAGCTCTATTGCCTCTTCTACTTCCTCTGAGTTTGAAGTAAGACGGGGATTGGGGGGTTGGGGAGAGGAGGGGGCAGTACCTAGGATGGAGATGCCACATCGTTCTGGCTCTAGTTCGAGCTCCTCAATGACCCTACCTGAACTATCACTGGGAAAGGAACACCCTAGTAGTACATGTGAATGGGCTTGTAGAGTAGATCTATCATCGGGTTTATCGAAGGGGATGGAAAAAAAGGGGTGTCCTCCTACTGCACCTCTCAAGGGTGGAGTAGGGGAGTCTCCCACGATGGGATGTGGAAGAAGGGAAGATGTGGAAATGGGTAGCTGGCTTGAGGTTGAAGTACTGACGACAACCAAACTTGGTTGTTGTAGGATTTCATTGCCATGTGCATCCCCTCCGAGACTACTTGGGCAATGA
46	NO	ATGCCTAGTAGTGAGCCATCTCTGAGTGTGCAGTCGAGTGAGGTAACTGATAGATTTGTTGATGATGCTAGTGAGAATGATGAGAGGGTCGATGATGATTTGGCCAATGAGACTTATAAGGATGAGCTCAGGAGAGAGGAGGATGAGAAAAGCACTGATCCCCCGGATGATGTCACTCCTCCTAAGACTCCTGATGAGAGCACTCTACACGCATAG
47	NO	ATGGCTCAGAAAATACTTCAATGTAGGTATTACTGGCCCATGATTCATAGAGATGCTCACGACTTGGTGAAGAGGCATGATAAATGCCAACGACAAGGGGCTATCTCAAAGTGTCATAAGATGTCCATGAATCCAATACTCGAAGTGGAACTCTATGATGTTTGGGGCATTGATATCATGGGGCCCTTTATCATTTCATACAGACAACAGTATATATTTTTAGCAGTTAACTATGTGTCGAAGTGGGTGGAACCAGATAATGAAGCAAAGAGTGTTGTAGGGTTTTTGAAGAAGAACATTATCTCTAGGTTTGGCACAACAAGATCAATCATTAGTTCTCTAGGCTACGAAAATAGAATTGACTCAACACAAAAACTTGATGATGCACTTTGGGGTTACCGTACAACTTTTAAGACACCAATATGA

48	NO	ATGGCTCCCAAAACTGCTGCGCACAGGATTAACAGAATTAGAGAAAAAGCTGGTTTCATGGAAAAAAAAATTCCTTTCACCTACTTGGGTAGCCTCATTTATATTGGAATGAAGAAGATCTTCTACTTTGACGGCATGGTCGCTAAAGTGATGAAAAGACTTAACGGTTGGCAAGGAAGGATTCTATCTTTTGGGGGCAAGATCACCTTGATTAAACATGTCTTGCAGTCTCTCCCTACGTACATATTGACAGCTATATGCCCTCCCAAAGGAACTTTGACCCTTCTGGAGAAACACTTTGCAAATTTCTTTTGGGGGCTACTGGTGTTAAGGCTAAATGTCACTGGAGTGCATGGGACAAGCTATGCTTATAAAAAGTAA
49	yes	ATGTTTCTCACGGTGGACCTTCCTGCCCCCCGTGACCCACCTCCGCTACATCTGCAACACCCTCACTCACAGATGGTCACTAACCCCAACCTTCAAATTCATTTCCCACCACTACCAGATCCCAAATACTCTGGCAATTCTGGACTAGTGAGGCAGAACCAAAAACAAGCCTGTACAAATGTTGAAATGGGCAAGCAGATCCCCATCAATCCTGGGCTAGCTGCTCAAAGGAACAAAGGTATGGCCCATACTTCCTACGCAAATGCCACTGTTAACAGAACAGTAAGACAAAATCGAATTCGACTAGAGACGAGAGGATATGAAATCCAGGATGGAAAACCATTAGTGGTTTTCACGAAAGAAGAAAACGATCTTCTCGCTCAAACCTGCAAATGGACTATAATATGTAATATCTCACATATCCGACCTTCAATTGACATTATTCGAAAAGAATTTGCCAAAATGATTTCTAGCAAAGGCAATGTTAAAATCGGAGCGTACGATATGCACCATGTTTTCATTGATTTTGACAATGTCGATGACCACCTCAACGTCTACTCGAAAAACTTCCTCACTTTTGGGGAAACTCATATAATGAAAATCCTCAGATGGACACCCAACTTTAAACTAGAAGCTGAAACCACCTTGGCTCCGGTATGGATCAACCTTCCCGACCTTCCATGGCACTTTTATGAATGGGATGCGATTCAACGAATATGTAAACCTATAGGAACCCCATTGATCATGGATAAAGCCACCAGCTCGAAAACAAGACCGGCAACCGGCAAAGTCAGAATTGAAATAGATCTAACAAGACCCCTTGTGTATGAAGTTCTTGTTGAAATACGAAATGAGGAAGGCAAGATGGAAGTCATTACTCAAAAGGTGGAATATGAGACCATTCCGGCATTCTGCTCCCACTGCAAAGCTCAAGGCCACAGAGATGAAAAGTGCAGGAAACTTCACCCAGAGTTAAGACAAGAGCCTGGAAAAAACACCAATGATGTTGGACAAAGCAAAAATGTAATGGACAACCAATTTACTGATGGAAAGAAAGCTCCAAAGACCAACAAAGAGAAAAATGAGGGTAACAATAAGAATCATATGTCTGCAAACCCACCTCAACAAGATAATGATCCCGGACTTAACCAACAAGAGGATGGGTGGCAAACAGTCGAAAGAAGGAAAGGAAGAACAACAAACAATGAGAAACATCAAGGAAACAATGTTATGCCACAAAGAGTTTGGAAAAATGCACAGGAGACAAAAGGAAGAAGAGTTCTACCACAGGAGAAACAGAATAGTGGAAACTTCTCTCAACTTACTAATGTGTTGGATAAAATGGAGATTACTGAAGATACTACTGCCTCAACCTCCCAAAGAGAGGAAGAATATCACCCAATTCCAACAAGGGTACACAACAAAACCACCATCGATAATATGGACAAGAAAAAACATAAAACCAAGATCCTCAAAGCTCAAAGCAAGATAAGAAGAAACAAACATCAGAAGGAAACTAACTATCCAGACATAAAGCTTCAGGATCAGGATCCAGAGAATCTTTTGATTCGAGTGGAGGGTGAAAATCTCAACAAAACCAATAAAAAGGGTAGGAAATTTGCTAAGAAAATTTCCATACCCCCTGAAGTAACCTTTGTCGCAGAAGAGAGCAGAAACAGGAACAACGACAAGCAGGATATAGGTATCAAACCGTTATTTGGATTGGACCCTATACTATCTGGAATGAACACAAGAAAGAAAGTGAGAGAGATGGAACTGGAGGAAATCAAAAGGAAAAATACAATCTTTGAGCCCGTGGGAGTCAATTGA
50	yes	ATGACCCACTTATACCCGAAAAGTAAGCTAACAGCCCTATGGAAAACAAACGAGAAAATCTTACTAATCGACCTAGGACATGACTACTTCACGGTAAAATTCCTTAAGGAAGAAAACATGAACATGGCCCTCCATGGGGGTCCTTGGTTCATCAATGGTTTCTTCCTATCCATAAGGCGATGTCAACCAAACTTCGTGGCATCAAGTGCAAAGGAAACTATCACTGCAATCTGGTTGAGATTACGGGAACTCCCTACCCAATACTATGATCATAAGAGATTATATATGAAGGGGACGGTATCCTGTGCGTGGAGTGTGGATGTGTGGGCCACACCTACTTGA

51	yes	GO:0003676; nucleic acid binding; Molecular Function;GO:0003677; DNA binding; Molecular Function;GO:0015074; DNA integration; Biological Process;	GTCAAGTGGATAATAGATACAGGGGCAACAAATCATATGGTTGCCAGTTTAGATCTGTTGTCAGATATAAATGAGGACCTTGCCAGTGGGATTTTGAAGGGGATTGGTAAGGAGACTGATGGTTTGTACCTACTTGCTTCACTGCCACATACTGGAACACATAATGGAACCTGTTTCACTGATACATCTGTGACAAAAGCCAACATTGCAGAGCAGAAAAGAGATGATATACTGATGTGGCATAAGAGATTAGCTCATACCTCTAGTTTTTCTATGAAAAATTTGTTTGGTTATAGTCTTGATGAATGTAGGTCAGTCTTAGCTGATTGTGAGAAAACTTGTGTCTACACTCCTCAACAAAATGGAGTAGCTGAAAGAAAGCATAGACATTTGCTTGAATTGGCTAGGGCATTGAGGTTTCAGGGTTGCATTCCATTGAAGTTTTGGGGTCACTGCATTTTACATGCTACATATGTGATTAACAGATTGCCATCTACAGTTCTTAAAGGGAAATCTCCTTATGAACTGTTCTTTGGTAGAAAGCCATCATTTGATCATATCCGGACTCTTGGGTGTCTTTGTTATGCTAGTATATTGCCTCGAGTGGACAAATTTGCCCCTAGAGCAGTTCCCTCGGTCTTCATGGGTTATTCCAGTCTTACCAAGGGGTACATCTTGTTTGACTTAGCCAAGAAAACCTTTTTTATCAATAGAGATGTGATTTTCAAAGAACATATCTTCCCATTTCACAGTGTTACTGCACCTGTTACTTCTGTTGCTCAGTTCCCTGGTTCCTTCGATTATGATCTTTTTGAACCAATTACTCCTGTGGATATCCATATAGACCTGCCTGTTCCTAGCCCAATTGATACTGAATCTGATTCTCCTGCCTTAGATCATCATTCTCCTTCTATGGACCCTGTTCCTATGCCCATTCCTTCTTCTGAAGTTTCTCATTCTGATCCTTGTTCATCCACAACTCACTTACCTGTTCCCCTGAGAAGATCACAAAGGGTGTCTAAGGAGCCTCTTTGGCATGTTGACTATATCACCAAGAAATCTTCTGCTCATGCTTCGTATCCATCAGTGCTTACCTCTCTTATGAGGCACTCTCTCCTTCTCACCAAGCTTATCTTGGAACCTAAGTCCTATAAGAAAGCTGTTCAAGATAGTAGATGGATAGAGGCTATGAATTCTGAATTGCAGGCCCTTCAAGATAATCGTACATGGAAGTTGGTGCAACTTCCTCCTGGCAAGACTGCCATTGGGTGTCGATGGGTCTATAAGGTGAAGTTAAAGGCTACTGGTGAGGTTGAAAGGTTTAAGGCAAGGTTGGTCGCCAAGAGGTATAACCAACAGGAAGGTCTTGACTACCATGAAACCTTTTCCCCTATTGTTAAAATTGTCACTATTCGAGTTGTTTTGTCTCTGGCTGCTCAACATAATTGA
52	yes		ATGCTTGAGAGTTCATTTGAGAACTTCAGGTGGTGCTTTATTGGCATCTACGGGCCACATACTAACCCAGAAAGAGAGGAGATGTGGGATGAACTAGCACGGATAAGGGGATTATGGGAGAATCGGTGGGTCATTGGGGGTGACTTTAATATGTGCAGATCTGAAAGTGAAAGACTCAATTGCACAATGAGATCAAGTGCAATGGCAACATTCTTAGATACTATTAGAGACCTAGACATCATTGATTTCCCTCAACAGGGAGGCCAATTTACTTGGTCTAGAGGAGATAATAACCAACAAGCATCAAGAATTGACAGATTCCTCATTTCACCAGAATGGACCGACTCTTTCAAGGCAATGAGACAGATAGCAATGCCCAAAGTGATCTCAAAACATAGACCCATTTTGTTGGAAAATGGCGACTGGGTCTGGGATGCCACTCCATCTTACTTTAAATTTGAAAATATGTGGCTGGCGGTAGAAGACTCTTTCTAG
53	NO		ATGAGTATCCACAGGAGTCTTCACACTGCCTTAGCCATGCATGAACTATTCAACATGCAAAAGTGTGACTGGATGACTGGCCAATCGGGCAAATATAGTGCCATCGTGGTTCGAGAGTTTTATGACTTGTATGCAACAACGGTGAAGAATGGCTTACATCTGACTGCCAAAGAGCTTGCCCAGCCTTCACTTCTTACCACTTTGGGTGTTGATGCTGAGTGGGTTCGTGATTTCTCAGCCTTTATCAAGAAGGCTTACCTAATTGTTGCAAAGTTTTGGTGGTCCATTGTCCGTGCTAAACTATCTCCTATTATGGTAGACAATCAGTTGTCATTGGACCAGGATGTGATGGCGGCATGCATGATGGCTGGGTGTGAGATTGACTTCGCCTGCATCCTGATTGCTCAGATCCACGAGAGGGCAGACACTTTTCGTGTGGCTGGGAAGGGTACACACACTGAGGCCGGTATGGATAAGGGTGCTGAGGAGCGCAACAGAAAGGGAGAGCGGCGTGCAATTGAGAGGGATTAG

54	yes	ATGAACAAAAAGTTCAACAAGAAAGAAGTTTGGGACATCTTCAGCAACAGTGATGCCAGAGACGTACACCATAGGAAGCCTGTTTACCATAAGGATGAGTTCTTTGACTGTCTTTCTTATGGTCTACCAGAGCATGAATCCATAGTGATGCCCTCTGAACAAATGAGAATAGACAACGAGACCTTTGGAGTAGAGATCCCAATAGTCCATCTGGATCATGAGAACGGACTACACTCGTCTAGGACATCTCAAGCCTCGACCTCGACCTCGACCTCACTTGGTGGCAGAGGACATGTCAATGTGCGTGGTCCTGTAAAACAGGTGTGGAGGCGTGTCTCAAAATGA
55	NO	ATGGAATGGTGTTCTGGTGCTGATCAACTGTCTAAGATGATTTACGTAGCAATCATACGGATGCTCTTTGGAGGAACTTTCTGTGGCATGGCAACAAGGAGAAAAAAAGTTACCATTAAGTCAAATCAAATGGAAAATCTTAGTATTGGCCAAGAAACATTTAAAGGTTTGGGTATCAGGAATCTGCGACAAAAGTCTTCTAATGAAATCGCTTTGGAGACTGCCTAA
56	NO	GCAGAGTGTAGGAGCATGATATCTGTAGTTGCTGAGATTACTTGGCTAGTGGGCTTTTTTAATAAGTTGGTAATGCACATTCAGTTACATGTTACTATATTGAGTAATAGTAAGTTATCTGTTCAGTTAACAACCAATTCACTTTTTCATGAAAGGATCAAGCATATAAAGATAGATTGCCACTTCATCAGGGACAAGATCAAGGCAGGGCTGGTTGAAATTATCTATGGTCATACTCAGGAACACGTTACAGATTCGCTAACTAAAGGTTTGGGTCACACTCAACACTTGCATCTTATAGGCAAGCTTGGTGTGCTCAACATCTTGCACCATTCAACTTGA
57	yes	ATGACGACAATTGCGTGGATATCTTTTCCAGCATTGCCGCCAAGGTTTTTTGGAAGAGAGGCAGTCTTTTCGTTGGCAGCATCAGTGGGAAAGCCACTACATCTACACATGGCGACAAGAAATCAAACAAGGTCAAGTTGTGCGAGGGTGAAGGTCGAAGTGGATTTATTGGGGGAACTTCCCAAATGCATAAACATAGGCTTGAAGAAGAAGAATGGAGAAATTGCTGAAAAATGGATAAGGATCAAGTATGACTATGTGCCAAAGTATTGCAAGACGTGCATGATACAAGGACACAATGAGGAGGAATATTATGTGGAACATCCTGAGTTATACCCTAAGGCAGAGACATCTGACATAGTGGGGGAAAAGCGCAAGAAGGAGGAAGGAAAGGCTAAGGAGGTTGTCCAAAACAAAGAGGAAGAGGGTAAGGCGCAACAAAACACCATCAAAATTGTTGACAATAGAAAGAATAAAGATGATTTCCAGATACATAAAAACATGAGAGGTGAGTGGCGAGGTAATCACCAAGGGATAAAGAATCAAGAGATGAGATGTAATAAGGTGGGTGTTATATCACACAATCAGTTTGAAGCACTAGGAGTGGAAAACAGGGCACACACTAATGCAACAGATAAAATACAAGTCCCTCATGCATCAAAAGAAGGGGTGGAGGAAACATTAGGAAAAGGCTTGCCAAAGATCGATGGGGATAAGATATCAGATTTGGGGAGCAAAGGCGAAGGCGATATGAACAACTCAAATGGGAGCAGCACTTAA
58	NO	ATGGATATGAGGTGGCTACGAGATTCACTAGTGGACGAAGAGTACCGGCGTAAGGTATGTCGTCCCACTACCGAGGGCATTACCAGTGCTTATTTTCCTACTAGGGCACAAAGGTTGTTGTCAATAGGAGTTCGGAGGATTCATTCATCAAGACTTTTACAGAGGCAACAAGAAGGGCTTGTTCCTTCCTGGTTGGTGTCCGCACTTTGTAGACAAGTTGGGGTACCAAAGGATGATACATACCAAACACCAAATATTGACGCCCTATTCAACCCACTGCTGGTGAGGAAGTTACCCGCTCTAGAGTGGAAGAAGAGGAGAGTAGATGAAGTTGGGAGCAACCGTGTCGCAGCAGGTTTAGGCAATGAGGAGGATGAAAATGTTGATGATAATGTCCCTCTTTCCCAGTCCCAACACCCTATTTTTGGCGACTACGTGTAG
59	yes	ATGGACCTTGCAACTGATCACAAAACAAGACCTAGTATGACAAAGGTGAGGGTGGAGGTCGATCTCACGAAGCCTAAATTAACCTCTATTTTTGTGGGATTAGAAGATGATTCTTGTCCATTGAAAGGATACTATATGGTAGATCTAGGCAATAATATGGAAAAAACCAATATCAATGAGGAAAAATATGATACTATCAAAGGCAACAATGAAGCAACCGCTAGCTCTGATAAAGTGCGCAGCAACGAAGACGATCAACAAGTGAGTAAGAATATTGAACAGCATGGTTGGTATTACAAGGAATCATCTTGTGATTGA

60	NO	ATGACCAAAAATGTGAATGTATTGCAAGGTATTACCCTGCTGGAGCTGGGTAACAGCTCAAAGGAGAACACGCTAATGGGATCTCTGATGGGAACACTAGTGGGAAGAAATAAAGCTTTGGGGAACACCCAACCAGGAAAGCAAAGCTCCGAGAAGACATCTTGGGCAGATATAGTAGAGGAAGAAGATGATCAGCTTAATGAGGGAGACAAAAGTAAGTCGGTACGTACATGGAGTAACATTGTGGGAAGGGTAAAACCAATAGAGGGGTTTTATTTGAGTATTGAGGAACAACCAAAGGGAAATATAAAAATCACTCTAGAAGATATACAAGAAGAGGTTGATTATTGGGGAACAGTAGTGATTTGCTATGTATTGGGGTCAATCCCACCGCATTCGGTAATGGAGGGCTATTTTAAGCGGATATGGAAAACCCTACAAATTGACAAAATAGCACAGGTCAATAGAGGAGTATTCTTGGTACGGTTTTGCAATGAAATGAACAGAGGGAAAGTGGTTGAGGAGGGTGTGTAA
61	yes	ATGATCCTAAATGATGAAGGGCAAAAGGCAATTACTAGTTTTTCTGTTGGACTACTTGGAACTGGACCAACTACTTCATCACAAGATGAAGCTACACCTTTGTATTCAAAACCAGGAAAACTGCTACAAATTAGTGGGGTATCCATCAAGCTTCAACAAAAAAAGGGAAATACTGATGGTGGAAAAAGAGGAGCATATCAAGGAGCATATCATGTTCAAGCTGAGCAGAATCCTATTGTCAGTCAGGGACAAGAAAGTCAGGTTATAGCCAATGTGACTGGCCTCTATCAGAAACAAGAGTATGATCCAAGGTGTCAGATGGCTGGAGGAATGAAAGTGCAGCCTGGAGCGTGTGTGTTCTCTAAAGAACAATATGAACAAATACTCCAGATGCTGGAAAAAACCAACTATGCTTCAACAAGTGCTAATGTGGCAGGATCTCTAAGCAATGCAGGTAAAACCAGTGAGACAGACACTGGAGCAACAAACCACGTGGTATCTGATGTTCACATGTTAGATAAGACCTCAGTTACTGCTAATGTCAATCCTAAGAAGGATCTCTCAAGTGGGAAGGTGAAGCAGATAGGTAGACTGGAGGATGGGCTCTATCTACTTAATCTAAAATATGGACACTCTACTCATGAAGTCAAGTTAGCTGTTAACAATACTCAGTCAACAGATAGTGAATCAGATATAAATCTGTGGCATAGGAGGGATGTGGTATTTAAAGAAAATGAATTTCCTTCTATGATTAAAACAGTAGATCCACCACTATTTCAAAAGTTGGATCCTGTATCTCAAAGCTTAGTTAATTCTGATCCTCTTGATAATCATGTGTGCATTAATTCTGATATATGTCTTGATAGTGTTTATTCTAATCTTAAAGTTGATCATAGTGATGAAGGTACATGTAGTAATGATCATTCACAAACCATGACTCAGGAGGGTCAACAACCTGTAGCCCAGCCTAGTGTTCCTATAAGAAGATCAAATAGAGACGAGCAACCACCTATATGGCCAAAGGATTTCACATCAATAACCCAATATCATTAG
62	yes	ATGTCAGATCCTCCAAGAATGGCATTTTCGGAGGATCCGAGCAACATAGCTTTCGAAGCACACTTATTCAAAGAAGCGTCACTTCACCCAGACAAACAAGGTCGGTTGGCTAAATATGCCACTCTGCCTGTGTGGCGAGTGCTGTATGGCTATTAA
63	NO	ATGAAAGGGAAACAAACTTTGGTGGAGGCAACTCCATCGAAGAATCCCAACAGTGTGAACTTGGAAATGACTCTGGCTCTAGGAGGAAAACCAACACCAAACAAGGAATTATCAATGAAGATCTTACTTTGGAACTGTAGGGGTGAACACAGTGCTGATTTTAAGAGGAACCTGCGAGCTTTGATCGATTTGAATTACCCAACTATCTTGGCTCTTACGGAGACAAAAATGGAAGATCATGACAACCTATTGCAAGCATTGGAATATACTGATGTCATACAAGTCACTGCTTTAGGATACTCTGGAGGAATTGCACTCTTTTGGAAAAGCTCAGAAATTACAATTGAGCCTTTCGTCCTAACTGACCAGGAAATTCACTTAACTATCGAGCACTTCTTGTGGCTCCTCCTCCTCAATAAGCTTCCTACTTCCTCCAACCTTTTTAATAGGAAAATCACCACTAACAAAAATTGTGGTACTTGCCCAGACCTAGAGGAAACACCTAACCACATTTTCATGACTTGCCCGGTTGCCAGGAAAATTTGGAACCATTACGGCATAACTCTTAGCAACCATGATCTTCACAGCACCATAAAGCTCCTTTGCTGCTCTAAATCACATGCTACCATCTACAACAATCTTAGAGTGCCTATGGCCATTCTACTATGGCCATTCTAA

64	NO	ATGATAGGGGAGGAAGAACTAGAGGTGAAACAATTCATCGTGAGTGGGGAATGGGACAGGCAGAGGTTAAGCAACCTAATTTCGGAGGAGATGACTGACTTTATTGTAGAGACTATACGAACAATTATTGAAGAAGGGGCATTGGATATTCCTTGGTGGATGGGAAGTAAAAGTGGGAAATTCACTGTGAAGTTTGCTTTTGAGTGCGTAAGGAGGAAAAAGGAGAAGGTCTGGTGGTGGAGTTACATTTGGAGCAAAGGAGTTCCTTTTAAAATCAACTTCTTGCTTTGGAGAAGTTGGAAAGGTAAAGTAGCTACATATGATACGCTCAAAAAGATGAGGATCACTGTAGTGTCCAGATGCTACTGTTGTGATGCACATGAGGAGGAGACAATGAATCACCTTTTTCTAATAGCCCCCATAGCCCAAAAGCTATGGAGAAAGTTTGCTTCTTGTGCAGGAATCAAAATGGAGGGCGGATTACAACAGGATATCACAGAATGGTGGGAAGCAGCTACCAAGCCCAAGTTAAAAGCTATATTTCAGGCTATCCCTTCTATTTTGATGTGGGAACTCTGGAAACGAAGGAATTCCAGAAGATATGGAAGTGAAGTGAAGTATGAGACATTACTTCAACAATGTCAAGAAGCAGTATTCAAGCTAGTCAAGACACTATACCCTTGGATCATGTTTCAAAAAAGTTGGGAGAATCTAGTAGAAGTGCTAAAAGAGTATAAACCCAAGCTACATTACCAAGCTATAACTTGGGTGAAACCATAA
65	NO	ATGGAAGATGAAGAACAAGCATTTCCTAATGAAGATGAACTTCATGTTGCTTCTGCTCTTCTCCTTTTATCAAATACACATTCTCCATCACCCAAAGTGAAGAGCATATCTGAGATTTCACAGATGGCGGCATTGAGTTATACGTCTTCGGTATCGGATTCGACGTCAAAATCGACTGATTCTTCAATTGTAACAGCTGATGATGATGATACACATTCTCCATCTCCTAAAATGAAGATCATATCTGAGATTTCACAGATAGCTGCATTGAGTTACACGACGTCGGTATCGGATTCGAAATCCAAATCGACTGATTCTTCAACTGTAACAGTTGATGATGATGATACACATTCTGCATCTCCAATAGTGAAGAGCATTTCTGAGACTTCACAAATAGCTGCATTGAGTTATGCGACGTCCGTATCGGATTCGAAGTCCAAATCGACTGATTCTTCAACTATAACAGCTGATGATTACGACGATGAGGATGCTGATTATGATGATGATGCCTCGTTTGCTGAGGCTAAAGCAAATGCTCGTCGGATTAAGATGATTCGGATGATTCGTGTCATTAATAAGCTCAAGGCGGTGCGAAGGAGACGATCTAAGAGCTTATGCATTTCCGATTGCCTGAAAATCAGCTCCGGCAAGCCTAAACCGGCGTTTTTTCTGGCTACCTCTTGCACATCAGCTTCGTCGTGTGTGTCCATTGGCTCTACTGCCGCTGGCGACATCTCAAGCGGCGGAAGCTGTGAGGCTAATAGAGTAGTACCAAAGGAAAGAGAGTGTGTTCCGAGGAAGATGAAGTTAGGATTCGTCAGCTTCTTGGTGATAGCCCTGATACCAGCAAAGCCTTGA

66	yes	GO:0003677; DNA binding; Molecular Function;GO:0003899; DNA-directed RNA polymerase activity; Molecular Function;GO:0005666; DNA-directed RNA polymerase III complex; Cellular Component;GO:0006383; transcription from RNA polymerase III promoter; Biological Process;	ATGATTTGGCCTTGGAAAAATCCTCATGGGGTAGATCTTGGTGATATTGTACCTCCAGATAAATATGATGAAAACACCATCAATTGTGCTGCAGAACTTGGTTTGTTGGAGAAAAATGACAAACCACAGATGATTATGTTTCAATTGCCACATCATTTGCTTAAACAACAGAAGGACGACAATGTCACTGCTTCCAGTTCTGAAATTCCCGCAAATGCAAAAGGGAAAGGGAAAGAGAAAGCTTTGGATGATGATCAGGAAGAGGCTAGCGGACGCAGGTGCAAGCTGTTGGTTTACAAAAGTGGAAATGTTAAAATGAAGATCGGAGATGATATATGGGATGTTTCCCCCGGTGTCAATCGCAGATTTTGTCAAGATGTTGTTGCAATCAATACAAGCGACAAGTACTGTGCTCGCTTAGGTAAAGTTGACAAAAACGCTGTTGTGAGTCTTGACTTGGATTTCTTTTGA
67	yes		ATGACGATGGAGGAGCCAGGATTGCCGGAAGAAGCGTCCGTGGATAAACAGTCCAGTACCGGAAAGTCCATTACGCCTTCGTCGATGATGGCAGATAATGCCGCAACTTCAATTGCCAATCTCCGCAAACTCTCCTACTCCCTCTTAGCCTTGCAATGCTGCTTCACTGAGTTAAACCACCATATCAATTCCATTTGGTCCATAATTCACTCTGTGATACCCGGACTTGCGACTAATATCAGTACTCTTTTACCGCCAGCCGCGGTGTCCCCCGCCCCAACCCCAGCCACAGAACCATTCCCAAAGCCAGACACTAACCCAGCCACAGAACCACTCTCAATGCCAGAACCATCTTGGGAATTGTCTTTCGAAATTCAACTGTGCCTCATAAATTGTGAGGAGGGAGTACTTCATCATGCTTGGGACACACTAAGAGCTCCCACCCTTTTCATTTATCCAACCCGAAACGACAATTTTTATTTTATTTTATTTGGTAACACCGAGTAA
68	yes		ATGTTAGAATTGGTCATTCCTAATAATCTTCTATACAAGCAAAATACTAATGCTACTGGATTTTCATCAGCAGTGGCAACTTGGTATGGAGATCCCACTGGAGCTGGAAGTGGGGGAGCTTGTGGACTAGAAGATGATGTAACAAAAGCACCATACAACGCGATGATAACTGCGGGAAATCAAGTTTTATTCAAACATGGTTTAGGATGTGGTGCATGTTATCAGGTATTATGTAATCAAAATGAAGAATGTTCACAAAATCCAATAACAGTAACTCTTACAGATGAGTGTCCAGGAACATGTAATGATGATCCAATTCATTTTGATTTAAGTGGAAATGCCTTTGGAGCTATGTCAAAATTTGGCCAAGCTGACCAATTACGTAATCTTGGAAGAATTGATATTTATTATAAAAGGTGA

69	NO	ATGTTATGTGATTCACCCGGAATTGTATCCCAAAAAGAGAAGGTAGAGGAGGACCAAACCAAAGAAAAAGGAAAAGGGGAGAAGGCGAAGAAACAACAAATAGACAAGGAGAACATGAAGAAGGACGAACATCTAAAAGATACGGAAATAAAGCAATTTAGGGAAATACAGTACAGAAATGGTAGAGGAGGAAGAGGCAATGGTAGAGGTAGACCGGAAAAGGTTTGGAATAAAAAACAAAACCAATTAGTAAGCGAGGGGGTGAGTACAGACAACAAGTTTGATGCTCTGGAAAATCAGGATGAAAATGAAGAAACTGGGCAACTAAAGGGGATAACATCAACAAAGAAATGGGTTGAGGAAAAATTCAAGATAAAGAGAAGGATACAGAAGGGAGTGGGGTGA
70	NO	ATGCAACCTATTGAGGCTCAAGAGTTATGGAAGGAAATTGCAGAGTTTGTGGATGTCAATGACATAGTGAAATCATTTAGCAGTGGGAGGAAATCATGGGCAGATAAAGTGGAGGAGATGGTAGATGTGCCAGCAAAGAAGAGCTCAATATGGGGCAATGTTGGCATTGGCAAGATAGTGAATGTTGGATTCAAGCTAAAGTATGTTGCTCCATCTAGCATAGAGGATAGGAAGGCACTATGGTCTACTCTAAAAGCAATACACAGATCAAACAGGAAGCCATGGCTATTAATGGAAGATTTTAATTCTACACTTCATGCTGAGGATAGGATAGGTGGAAATCATATCTCTTTGACAGATGGGGTGGATTTTACAGAGTGTGTAGATGAGTGTGGATTGATTGAACTTCCTTGA
71	NO	ATGGAGAAATTAAGAAGTTTGGAAGCTATTCAGAAACTTAGAACTTTAAAATATGATGATGACCAGTTGATCAAGGACAATTTAACAATGAGTAAGAAGAAGTGGCAAAGAATGAAGATCCATTGGAGACAGAGATCTAGAATCCAATGTATTAACAACGGGGATAAGAAGACGAAGTTCTTCAAAAAAAAAAAATGGCTACAACTCACAAAAGGATTAA
72	yes	ATGGAAGAAACTGAAAATGTGGAAGATACTGAAGTATCAGAAACTGCTACTCAATGCCGGTCGACTCTGTCTCTAAACTCAGAGATCGAAGATGCTGAAGCAGAAACTACTAAACGCAAGCCGACGCAAGTGATCGGAGAAACTACTAAACGTAGGCGGACGCCGTTGAATCCGGAGTGCGGCGAAGATGCGGAAGCATCAGAGACTTCTAAACTTTTGTCAAAGCCAGTGGATGGAGATGCTTCTAAGCCAGTGGATAGAGATGCCTACGGCAAGATACCACTGGCATTTGCCTCTCCGGAAATATACCAAGCTGTGGCAGAATCTGCACCGCCAGATGTTCGAGCAAAATCCGAAAAAGAAATAGCCGCTTATGTGAATAAAATAATCATGCGATATGCTCCTAGTCAGAAAGAGATGGAACTGCGAGAATACAGGGACAAAATCATATCAGACTATCCGCGGTTACACGAGAAACTATATGCTATTCATCCTACAGAAATTTTTGTCCCTTCCTTTATCAAGGCAATCAATGAGAAAACAGAGGATAGTATCAAGAATATCATTTCTAAGCCCTTTCCGGGTATTTTAACCTTCGAAATCTTTCAACCAGAGTATTGTGAGATGTTGGTGGCTGAGGTAAACCATTTTCAAACCTGGATCCACAAAGCAGACATCCGAACTGAGCATCGGAACAATATGAACAACATGACGTATCTTGATGATTTAGGAATGGGATGTATGCTTCAAAATCTCATGGACAGTTTTATAAGTCCAATTTCCAAAGTTTTTTTCACTCAGGTTGGGGGATCTACCCTTGATGAACATGAGTGCGTTGTTGAGTGTCATACCGATGGCGAAAATGAATTAGCTGTTCAAGTTGATGACGCGGAACTTACCTTAAATGTGTGCTTGGGTCAGCGATTCTCTGGGGGAGAATTGTGCTTCCAGGGTGTATATTGTGAGAAACATGTGGACACTCCGACACGACCTGAGATGATCCCAAGAAAGCTTACTGTAAAGATTGCTACCAAAGAAGAGTGA

73	yes		ATGGAGCTCCTGTCGAACTACATTAATCATCAAGTCGACATCCTCCGATGGGAGCCTATCTCCCTGTCAGCTAACAGCCCTCAATTCTCGCATCTATTCTTTGCAGATGACTTGACTTTAATTTCTCGGGTGACCCAAAAGTCAATCAATACCATGTATGAATGTATGTCTGCTTTTTGTGAACTGTCTGGACAAAAAATAAATGTTGCTAAGTCCAAATCCATTTTCTCTCCATGCTGTGATAACGTCTCTAGGAACCTTGTGCAAGACTGCTTTCGTATTACTCCGTCTTCTGATTTCGGTAAATATCTTGGCTTCCCCATCCTTAACCGTAATCCTAGAGCTGCTGACTTTCATTACATCCTTGACAACATGAGGAAAAAACTTTCCAGTTGGAAGGTGAACTTTCTGACCACTGCAGGACGCATCACTCTTGCTAAATCTACCCTTAATGCCATTCCGGCCTACGCTATGCAATACTTCCAACTTCCTATGAAGATTTGTAACACTATTGATAAAATTCAACGCGATTTTCTTTGGGGTTCCACAACCCACTACATTGCTTGGGAGAAAGTGACCTCCCCGAAAGATTGTGGAGGCCTAGGCTTACAAAAAGCAGACACCAAGAACAAAGCTCTCCTGACCGGTCTTGCTTGGTGCCTCATTACGAACCAATCTTCACTTTGGGCCAAAACCTTAATCATGAAGTATAAATCTCGAACTACTGCCCCTTCCCATTCCTTTATATGGAAAAACATTCTCCTTGGGAGTAATATTTGCTCGAAAGCAATTGCCTGGACTCCGACTAGAGGGCATGCAGATTATTAA
74	yes		ATGCCGTCACCGATGTTTCCTGATCAACCACCAGTCAATTTCCTGTCGTCACCTGTAATTCCTGATCAACCGCCAGAAATATTTCTTCCATCACCGTTAGTTCCCGATCAAGCACCGCCAGTTGCAGTAATTCCGCCATTTGAGTTTCCGCCTCAGCCGGACTCGCCACCATTCGCCTAA
75	NO		ATGGAATTAAAGGTTGAATCGAAGCTGTGGGAGATGAGGCATCTTGAAGTGGAGTTGGCAAAAGAGCGTGCTGCTCGGTTGGAAGCAGAACAAAATTCAGAAGCAGCTCTAATGAACTTGAAAGATATGAGTTTAAAAAAATGGGGAATATTTATGTGTCTTATTTTATGA
76	NO		ATGCCTATACCTCCTCCCCCTTTTCCTAAAAAATTAGTCAAGAAAATCGAGGAAGATCAATATCACAATTTCATCTCGATGCTGAAGCAACTCTCAATTAACGTCCCTTTAATTAAAGTTCTAGAACAAATGTCAGGCTATGCAAAGTTCATGAAGGATCTAGTGACGAAGAAGTGGGCCGCTAGTTTTGAAGGAGATGATAAGTTGCAACATTATAGTGCCATAACCACCATATCGTTCGTGCTGAAGAAGGAGGATCCTTGA
77	NO	GO:0003676; nucleic acid binding; Molecular Function;GO:0008270; zinc ion binding; Molecular Function;	ATGACACACTCTGCTGTTTGGATTCGTCTTCCACAACTACCAACGAAATTTTATGATGGTTCGCTGGTACAAAAGATAGGAGGGGCAATAGGTAAATTGTTAAAAGTCGATGCATGTACGAGTGCCACACTCAAGGGTAGATATGCTCGCCTATGTGTGGAGGTTCCAATGGACGTCCCTGTTATCAACAAAATTCAAATTGGGTCCCATACGCAGACAATAACATATGAAGGAGAAGGTTTATTATGCAAAACATGTGGGCGCCTAGGTCACCTGCAAGCAAATTGTCAGTACATTCCGGTATCCAAGACAGATGCTGGCAATAGCGATAGCTCCTCCAGCATACATGAACCATCACTGAATACCAACCATGACTGGAAGACGATATCTTTTATGAAGAAAGGGAAACCCATGGTCTCACAGAAAGATCATAGTGTACGCACAGAGCAACAAAGTACACGCACAGAGTGGCCCTTACCGGAAAAGAACTCATGTATCAATGTCAAAATATTTTCAGCGGAACCTGTAAGTTGCCCAACACGCTCTGGTGGTGGCGACGCAACCTCTGCATCAACTTCACCAAGCACAATCTTAGATAGAACTTGGACTGAAAGACCAGGCGGTCTTTTTTACGATAGATATAAACGGGGTGAATACAATGATAATCCTCCGAAACCCCAGCTTCCTAGCTCAGCTGGTCACAGAAGGTATGAAGCTGGCGATGGACAACTATGTGAACCATCTCTAGATGGAAAACATGTTGAATCCTCTCGCCCCAGCTGTGGCACCAACCCTCTATCACAACATGCAACCACTCTGGAACTTACCACACTACTTCAATACGCCATTGAGCTTGAACCCTCTAGCCCAACTACTATTCTTCACTCCCCAAGAGGTCTTAGATGGCAACCCACTTTTCTTTCCATGGGTTCCAATACCTCTTCAGGGACACGCAACTCAAAATCCCTCTCCAATGCCAATGGACAGTCACCAGCCGCCAATATGGCAGACTGGGAACGAAGTGCAAGAGGAAGCTCCGAAGGGTTCCTTCTCTGA

78	yes	ATGATTGGAAATCCACTTAAAGTAGATAGAGCAACAACTCAAAAGGAAAGGCTGACATATGCAAGAGTGCTGATAGAGGTACCCCTAAACAAAGAGTATCCAACAGAGATAATGTTTGAGAATGAAGTAGGGAGGATAATCAATCAAAGAGTGGAGTATGAATGGAAACCGGTACTATGTGGCAAGTGTAAAAACTTTGGGCATGATATAAGTAATTGTAGAAGACACATAAGAGATGAACAACAAGGGAAGATAGTTGGGACTGAGGGAAATAAGGAAAATGAAAGGAATAATGAGAAGGAAATTCAGAATGTGCAAGAGAAGGTCAAAGGAATAGGAAGGAAGAGGGGAAATGGAAGAGAAGGAATTATGTGGGAACAACATAAAAGAGTTTGTATTGAAACTACTAATTCTTTTAGTGCATTGGAGAAGGAAGAACAAGGAGGTCAGACCATTTTTTAA
79	NO	ATGACAGTTGGATCGAGACTAAATAAGGATGTTCATGAATCCTTGGTTATGTATGCTGGAAGAGGTAATCAATTCATGGGAAAACCACATGATTCTGTGATATATCCTGGAAATGAAAGAGGTGTTTACAGTTTTATGGGGGATAATTCTCAGATGACTAATTCAATGATATACCCTGGTAATGGAAGAGGTACTCACTATGATCCAATGGCATTTTACACTGGACGAGGTGGATATTTAAGTGGTGGAAATAGCAACTACAATAACTACAAGTTAAATAAGAACTGA
80	yes	ATGAAACCACGAGATATGGGATTCGCTCTTACTGTTAAGACGTCTGAAACTCTTCTTTCTTTACTACTTTCCGCATCGGGGCTGATAAGACGAATGCATGAGGATCAAGATGGGGATGTCGTCCCCTCCTCAGTACGAAGAAGAGAGGGTACTTGTAAGGATTGCGTGAATCCAGACAGTCTCACATTGAAAGCCCGTGTAAAGGAATCATTACAGTAA
81	yes	ATGACTAACTTCATTACTACTTTTGCCACCCTTCCTGATCAAGCTTCATCAATCCTCACATATCCTATTCAATCCTCCCTATCTTATGATTTCTTACAGCCCTCTTACAAATCCTCTCTTGCAGCTTTCACCTCTGTGTTTGAACCTAAGACATTTCAGGAGGCTTCTACTGATCCTCTATGGATTGAAGCCATGCAATCAGAGATCAATGCCCTTCAAGACAATAACACATGGGAATTAGTTTCATTGCCTCCACGGAAGGTTCCAATTGGTTGCAAGTGGGTTTTCAAAATCAAATACCATGCTAATGGTGAGGTGGAGAGGTATAAGGCTAGGTTGGTGACAAAAGGTTATAATCAACTTGAGGGACTGGACTACCACGAGACTTTCTCCCATGTGGTAAAGATTGTCACTGTTAGGACTGTCATATCTATAGCTGCTTCTGCTGGTAGTTCTATTGAGCAAATGGATGTCCACAATGCTTTCTTGTAG
82	yes	ATGTATGTGGTGGGAGAACCACCGACTATCGCTGCAGTGGAGAGATACATTGCTACCCAGGTAAACACAGTCAGTAAGCCCAAGGTGTACTACCATAACGACGGTTATTTCCTGGTACAATTTAATAGCATGGATGATAGGAATGAGCTCTTATATTCAGGTCCTCATATGATGCATACTAAACCAATCATTGTTACACCATGGTCTGCGGATTTTGATTTTAATAAGGAAATACTACAGATTGTGCATGTTTGGGTAAAATATCCAAACCTACCTCTGAATTGCTGGAGTGGGGATTCGCTTAGCAGGATAAGCAGTGGTTTGGGGATTTCACTATATGCAGATGAATGCACCTCAAAAGTTGATAGAATCTCTTATGCACGAGTACTCATTGAAATGGATGTGGCTAGGGAGTTACCTAAGAAAATTAAGGTGGAGGATCCGAATGGAAGAACCTTTTAG
83	NO	ATGAGGCGCATCCAGGAACTCCACATGGAGTTTATCTTTGCTCAGCCCGCTGAGTGCAACTTGCATGTGGTTAAGGAGTTTTATGCCAATTGGGCGATGGAGTTGAGGTCGCACTTTGTGAATGTGCAGGGAGTGAATGTGACCCTCACTCAAGCTCTATTGAATGACATATTGGGAAATGTAGCTCACATTGACCCGTTGGTGCTGATGGGATTAAGCATACGACCTCCGTACCGAGCCATTCAACACACGCTTTGTGGACCTCAGTCAATGGTTCAGTGGACCAAACACAGCTCGAAGAGGTGTAACCAATCTCTTCCTTCTGCACACATGACTAGAGAGGCTCAGTATGTATGGGCTGGAAATGCTGAGACACTAGAATGGATATCGGCCTTCCGTTCAGGAGCAGTTGGGGCAAGTTGA

84	yes		ATGGGGTCTGTTGCAGCATCTCTTCCTGATGTCAACAGAATAACTCTGCACAAAGGCTCTCAACTAAACTATGAACAAAAACTGATGATATGTCAGGAGGTTACAGATAAGAAAATTTATGATGGATTATGGGCTATTGGAGAGGATAAAGCTACGAGGGTTGATGGATTTAATGCATGCTTCAATAAGAAAGCTTGGCCTCACATTAAGGAGGAGTTACTAGAAGCAGTAAAGGATTTTTTCAACACGGGACATATTTATAAAGCTATCAATTGTACGTCTATTACTTTGATTCCGAAAGTTCCAAATCTACCGGTATTAAGGAATTTAGACCAATTCTTGTGGAACACATTTTTGATATGGCTGCAGAAACATCACTTCACAGCAGGCACCTGGGATCAATATGTGGATTGGGCTATCTGTAATGCTAAAGGGAAATCCCAAGCAGCAGCAATTTTCAAGTTGATCTATGCCGAGGTGATGTATAATGTTTGGAGAGAAAGGAACTGTAAAGTCTTTGAGAAACAGATCAAGCAAATTGAAGTTCTTGCCAAAGAGGTGGATTTTTTCTGTACTGCTAAAGGAATTTTCTTTTTTGGCTACTAG
85	NO		ATGCATGAGGTTTGTCACCAAGATCAAATCGATGAACTCGGGGAAAGTATCGATGAAGTGGATTATAGTGGAGATTCATTGGATGTGGTATTATTGAATTATGATGAAGAAGAGATTAGTGACTATGATGAGGTGGTTGATTCTCATGTCGATGTGGGGTCCTTCACATCAAATCCAAAGAAGCTAGACATTGTTTTTTTAAATCATGAAGTGCCTCCAGCCAAGCAATCCATAATTGTACTCCCAAAATTAGAGTTGAAATGGCTTCTTCCAAATCTTTGA
86	NO		ATGGAATGTAGAATCTTACATCCAAAACTGAAAGAGAAGAAGTTGACAGAAAACTTGGCAGAAGAGTCCTATGATGCAGATGCCGATAGTAAAACTCTCATTCAAAGGAGTTTCATCAATGGGAGGGTGGTATTCACCAAATGGACTGTGACTAATAGAAGGTTCAATGCTGATAAAGGAAAACTAATGGATGAGCCACAATCTAAGGTCACTTCTGAGAACCTTTTTGATGTGTTACAAGATGAGGAAGATTCAACTAAGGAGAAGATACAAGAGGCTGAGCATGGGAGATGA
87	NO	GO:0003723; RNA binding; Molecular Function;GO:0003964; RNA-directed DNA polymerase activity; Molecular Function;GO:0006278; RNA-dependent DNA replication; Biological Process;	ATGATGCCATGGAATGGAATCGAAACAACATTTGGTAACATATTCCATAAAAAGAAAAAAATATTGAGACGGTTAGAAGAGATCCAAATGTCCAAAAATTACAGCCATAGCCCTTTCCTAGCAAATTTGGAAAATGACCTTATCAAGGAATATAACTACATTTTACGTATCGAAGAGGACTTCTGGCAACTAAAATCAAGAGTTAACTGGCTAAATGAAGGGGATGCTAACACTAAATTCTTCCATACAACCACCCTCACTAGAAGAAGAAGGAAAAAAATTATAGCCTTACAATCAGACCAAGGTGAATGGACTTATAATCATGCCGAGATTATAAACTCTACCTATGATTTCTTCAAAAATCTATTTACCACCAATAAGTTGTTCTCTTATAGGACCACCCAACCACCTCAAACCCCCTGTAACCCCATAGATCTCTCCAGCTTAGACGATATTCCCACTGAAAAAGAAATATTAGGTGTGGTCCAATCTTTCCAGCCCTTCAAGGCACCTGGACCTGACGGACTTCACTCCTTCTTTTACCAAAGGTATAATGAAACCCACATCTTCTTAATACCAAAAATAAAAAATGCTAATAAGTTGAAGGAATTTCGACCTATAAACCTTTGTAACACAGCATACAAGATAATTACCAAAATTATTTCACAAAGGCTTAGTCCCATCATGGTAAAACTAATTGGGCCTTGCTAG
88	yes		ATGAGAATTGGACTCCAACACTGTTCCTCTCTTGAAATTTCGTTCCTCCGAGAATCTTTTAGAGGTAAGAGAAAAAATAGAAAATTCCCAACGCCATGTATTGTCATATTGTCAGCCGCGGAGAGCCGGATGTTTGACATGATATTAAGATTTCTTGAGTACTCTTACTCATTTGATTCTATGTGA

89	yes	ATGGACCGCATTTCGTATGCTTGTATATGTGTTGAAGTAGATGTATCGCAACCTCTAGTTGAAGCCATTGAGATGATTACGCCTACTTGCAATTTCCATCAGCCTATTGAGTATGACTGGAAACCCAAATTTTGTGGACATTGTCTTCGATTTGGCCATCAAACAGATGAGTGTAGATCTGGACAGGACAACCCCCCAGAAGAGGAATTTAAGGAGGGTCAAAAGAGGAAGAAAAGGAATAGAAGAAGAAGGAAACATGTGCAACAAGGCTGGAAAGTAAAGGAACCTTCCAAAGAAGCAGTAAAAGATGATATGCAAAAAGTAACTACTGTGAATCCAGTGCAGAGTGTGGTGGGACAACCTAAGCAAGTTGAACCTAGTACTTCCAGGGTGGGAACAAATTACCTAGCATCAGGGGTGTCTGATCACTCCCCGGTGCTATTACACTGCACACCAGGTGTGATTTCTAGGCCAAAGCCCTTCAAGTTATTCAAAATTGTCCTGGAGCATCCTAAATTTGTTGATATTGTCGCTGATACATGGGCACAAAGGTATAATGGCACAAGGATGTATCAACTGCAAAGAAAAGTCAAAGCACTGAAGGTTAACCTAAAGGACCTCAACACTTATCTAGTATCCTGA
90	NO	ATGGAGAACCAGGTAGCCATGATCATTATCCAACACCCGATACTCCTTGCTCAGATAGTGTCGGATGGGATGCGTGCGGCAATAAAGACTTTCAACACTCATGTTTGGATGTCGCATGCTCTCTCACTCTCAATGAGCTACCAGTTTCTGGTGATGCTATTCTTCCATGTCTTAACATGGGAAGCCCCTATCCCACCACCCCTTAGCCTTCTCCCACGCTCTGAACCTCCAGGAAATAGACCCCATCTTTCACCACTGGATGATGCAAGGACCACACCAGAATGCTGCCCCACTATCTCCGATATCGACATTGCCGGAATCAATGGGCAACACAGTTGCTCCATGGGTCCCCGTCCCATCAACTGCATCACATGTACCTCCTTTGAACCCACCACCACTTTGTCCAATGATTACCAGTACCCGAGAGATAGAAGAAACATTAGAGTTAATGAGAGAAACTCGAATGGAGATTTCGGTTCTAAAAGAAATAAGACTAATGATATACAAAGAGAGATTCGACAAAAATACATCATTAGTTATCCGCAGAACCTCTTACAAAGTTCGATAGATATCAAAGCACCTTTCAATCCGGAAGTAGGGAAATATGTGCTAATCATGAACCTACAATGA
91	NO	ATGGGGTATGTACTTATTGACACTACTTGGCTTAAAAAGGACTCTGTGAAGGTCAGGATAGAATCCATCAAACCCGCAAGGATCTCTGTTGACTCTGCTGCTATTTGGATGAAGGACTCGAATGAGATTAAGGCACGTTTAACTGCTCTTGAAGAAGAAATCAGCACTGATGTTGGCAAATTACACTTAGCGATGACCAATCTGAAGCAGGATGGTATCTCTACTGTGCATAAACTGATCAAGCAGGTTGACTCTCTCAAGTCTGGAGTCAGCTCTTCCAACACAGACCTTGTTGTGATTGTTCAGAATTCATACTCATCCTTTTCCAAGAATGTTGAGCGCTCTTACAATACCTTCTGCAGGAATGTGCTCAACACTCTCAATTATTTTCTTGGTGATCGCTGA
92	yes	ATGCCCTGCCCAGGGTGTTCATGTGCTGAGTCTAAGAAGTTTCAAGAGCATTGTGAGTATCAACGACTTCTAGAGTTTCTAATGGGGTTGAATGAGACCTATGTTGCAGCCAGAGGTCAGATCCTTATGCAAACTCCAACTCCAAATCTAAATAAGGCCTTCTCCTTCATCATGGATCATGAGAGTCAAAGGAACTTGGCACACATCGGTAGTGATGGTTCTTTACCAAGGATTGTGGAAAGCTCTGCTTTACTGAGCCAGAAAGGAGTAAGTGGACCTCGTCTGAGTGGTCACATCAACCAGGAGAATGTGGTTAAAGGCTATCCAGTTGGCTGGAGATCCAAAAGAAAAACTGGAGGCTTAAATTCCTATGCTAATAATGCTGAAGTTACTCAAAGTGCAGGTTCTCAAAACACTGGAGAGAGTACTGGAGCTAATGTCCCTTCATCACCTACAGCTTTCTTCACACAAGATCAATACCAACAAATTTTGCATTTGCTGACAAAAGGAAGTGACATTGGTGGAGATCCGTCAACCAGTGGAGAGTAG

93	yes		ATGAAGAAACTGATCAGTGAAGAATTAGCTAAAAGACCAAACACAGGACAGAATGTGCCTAGCGTTGTGGCCCGTCTGATGGGACTGGATTCATTATCTGTAGATGAGGAGAGGTTGAGCGAGGTTTCCTCGAGACAAACAGTTTTTGATTCCTTTGACAGACGGAGTAGTAATAGCCTGAAGTTCAACGAACTTAAACCCCGAGAACATCCACAGGAAGAGGAACTACAAAAGTTTAAGAAAGAGTTTGAAGCATACCAAGCAGCAAGGTCCAAGGAATGCTCAAAGTTTGTTGAACTTAGCACCAACACGGTTCTCTACGCGAACTCAACAAGAAAGATGGTTACTGAGAGATCTATAGATCTTAAAGGACTTGCTGCAACAGAAAATATACACGAAAGAGGTATTTCGAAGGTTCAGAAAGATAAAAATGAATTTCTTGCAGCTGCACGAAATAAGACTATTCGTGCATTGAACGTTAAGTCGGGTTCTGCTCCTGCAAAGATTGTAATTTTGAGGCCTGTTTCCGACAGGACGGGGAAAAATGAAGAATCATGGGCTAATTCTCCTAGAATATCCGAAGACGGGAGTAGCATGGAAGAATTTCTTCAGGAGGTTAAGGAAAGACTAAAATTTGAATTGCAAGAGAAGAGTTACCAAAAAATCATTGAGAAGCCATCAGATGCAAAGATAATAGCTCAATGTATTGCAAAACAGGCGCGAGAGAGTGTTACTAGGGACGTTGGACCGACTCACCACCGATCAGAATCAATGCAGTCTTATAGAAGTGAAATCCAACACGACGAGGCTAGCTCACCTGAATTCAGTAATAGAGATACAAGAAGAATTTTGACAGAAAGGTTGAGGAATGTCCTGAGGGACGAATCATCTCATGATATGGACAAACATGGTCGTGTAAGCTCCAGATCAGTAACACAGAATAGGGAAAAGAGCAAAGCTGAAGAAATCAGATATGCTTCGAATGAAGTGTGCCACGGGGACGATATGAAAGATGAATCAGACAGGCAGTGCAGATATTCCAGGCAGGAGCTAGGTAATGATGTTATGCTAGACCAAAAACTATTTCACAGGAACCTGGTTAGATCTTTATCAGCTCCCGTATCACGATCATCATTTGGAAAACTTCTCCTGGAAGATCAAGATATGTTAACGGGGGCTCATATTAGGAGAAAGCACGAAGCTATCGAGGAGGTCACAGTGAACGTTAAGAAATGGCGAAAAGAGAAATTCAATCTTAAGGAAAAAGTTTCCAGCTTTAAGTATAGTTTTATACTTAAAGGAAAGCTCTTTGGTAGAAAATTTCAATCTTTGGAGGAATCACATGGAAACAAACAAATGCACATGAAAGATCTTCAGAGCACACACACTGTTGCATCCAAATTTTATGTGAGACAAGTAAGAAGCTTCAACTGTCCTCTTTCTTTTCGACTATTGAAAATTTTGAGATAA
94	NO		ATGTTTGCAAGTTTTCAGGCAAGCCCCAAAGAATCACATATGAAGGCAGCAAAGCGCATCTTGGGATATCTAAAGGAAACACTTGACCTAGTCTTGTACTACCCTACTGAAGATTCCTTTGATCTGGTTGGATATGCCGATGCAGACTATAGAGGGTACCTGGTCGATAGAAACAGCACTTCAGGATGGCTCACTTTCTGGGGTCATCACTAA
95	NO	GO:0003676; nucleic acid binding; Molecular Function;GO:0004523; ribonuclease H activity; Molecular Function;	ATGTATGCAGAGGCGAAAAGTTTGGGACTAACCACGAACATGGTAGCAGAAGTCACAGCTATTCTACAGGCACTCAGATATTGTAGAAGAAAGAAGATCAATAATGTTCTTGTAGAAATAGACTCATTGGGTATAGTAAAAATGATAAGAAGGGAATGGAGGATTCCATGGCAACAAACACAAAACATAAAGGAAATACAAGAGATATCGCAAGAGATAGATGCACAAATCACACATATATTCAGGGAAGCAAATCAATTAGCAGATAAATTAGCTAATGAGGCGTGTCAGTGCAATGGAAGCATACGGCTAAACAATTTTCAACAACTTTCAGTAGATTGTAGAAGAATTCTTAACTCAGATAAAGCACAAATTTCAACATGGAGGATAAGAACAAAGAAGATAGGACAGAATATGCATTAA

96	NO		ATGGTGTGGGTTCATGAATTCTACGAGGCCTATGCCAAGACACTCCTCAAGAAAAGAAAAGTCATGATTTGCAGACCTTTGGAGGAAATTAAAGTCTGGGGTAAAATGGTAAAGTTTGACCGGACGTCTATTAATGACATATTGGGCATGGAAGGGAATAACGCAGATATGTACAAGCTTCGCATAAAGCATAAGCTTGATGATTTGAAAGGGTGGTTGGTTTCGCTTGTGAGTCATGGAGGGTTGTTGACCTCTTATAGGGAGAGACTTGATAACCTTACCACTCGGGTTGAGGAGCAAGAGAGAGTAAGGGTGATTCTGCTTAGTTGGGAGAGCAGGCCGATGAGGATTATTTGGACGATGATCAGATCTGTGCATTGGCGCTACCAGAGCTACAAGGTATAGAGAAGTTGATTCAGCATCCTACATTGTGGAGATCTCATTTGTTGACCTTTGAGATTCGCACTAATGGGCGTGTCATTCAGTTTCAACTCATCCTTCTCCCGATGTGCTCGACATTGATACCTCTAATTGATACTACACTCCTGATTCCTCCTCTAGATGTGTTGGGTACTAATTATCGAGTTGTTTCTACTCCCACCGAGCAACAGGGCTAG
97	NO	GO:0006508; proteolysis; Biological Process;GO:0008234; cysteine-type peptidase activity; Molecular Function;	ATGAATTTTTTGTATCCAGTTGAAGATTATGGAGTGGCCATTTCCGTTGCCGCAGAGCAGTCCTTCAAGGGCAATAGATGCATGACGCCAGTGTCTCATCAATTTGGCATTAGTTCGTGTGTGCCATTTGTCGTCTGTGACGCCGTTAGTGCAGTATCTGCACTGGAAGTTCCTGGTCATTTACCGTGGAAAGCAATTCCACTCTCTAAGCAGGAGTTAGTGGATTGCGTTCCAGTTGACAGAAAGGGGGTTCATTTTGAACGTGTTTATAAATACGTAATACAAAGGGGTTTACATTCAGAATTCAACTATCCTTATAGGGCTCAGTATGGACTTCCTTGTCTGTGTTTTCCGTTACTGGAAAAGCACAAAGTCGGTATTTTGGGTTATGAACCGCTCTTGAGCGATGCAGCAGTCATAGATGCTTTAGATAATGCTCCTGTGACCGCAACAATTTGTGTTTATGAAAGTTTTTTAAACCGTGGTCGTACTATCGATGTTTATACCAATTTGGAAGGTGAACAACCAAGGTTGAATGAATTTGGGTGTGCATTTACACATGCCGTACTAATTATTGGTCATGGCACATACAAGGATGAAAAGTATTATATCATAAAAAATTCAATGGGGATTGAATGGGGTCTTAACGGCTATACACGTGTTTCACCACGTATGCTATTCCATTTTATTTGTCCGAGAGGTATTGAAATGTTGTAG
98	yes		ATGTCCTCGGAAAAAGGAATTATTGAGTACCTTGAAGTTTTCTTACACAATCGGCTATATCTCTTGTGGGAACTATCTCCAGTTCTAGCAGCATTTGCAATTCCTTCATGGTATGAGATTCATATCCCGTTGTCTGTTGAGATTTCTCACAGTGAAGTGATCAATCCTTTTACACCAGTCAGCTTACAGACTTTATATTTTTCGGAGTTTATCGATGAATAG
99	NO		ATGACTATTGCTATAATATCTGATGATCGGCAGGAGCAGGACAAAGGGTTGGAATTACTGGAACCTCTTCAGGTTGCTACTGCTTTAGAAGAAAGTCATCCACCTGCACAAATACAATACAACCAAAAACATTTGGAGGATGGAAGTAGAGAATCAGAATGTGCTATAATACATGTGGGAGTTAAAAAATCAGTGCCAATGGGGACCTTGCATGCTTTAGTGTAG
100	NO		ATGGCACAATTGCACCTTTCACCCCTTAGTCCTCTAGAATCAGCCTCTAACAATGAAGTATCCAATAGCTCGGAGGCTCAGTTTGAGCCCACTATCGAACCACATTCACCCCAAGAGCGTAGATCTCAGATAGATAAAGTAGTTGAGCAGCATGATGCCACTCCTTCCCAGTCTGAAGAGGAGGGAGATGGCTCAGAGATTGAAAATGTGTCTGGACATGAATCCAATGTCTCTAGAAATAATGTAGTTGGGACTGGGGTGTCGGGTAACCAGATAGTTGATCGTCCCACCGATGCCACTAAATACACATCTGCCACCTTGATCAAAAACCTTGCAAATCCATTATATAGAACAAGAAAAGAGATAGATCCTACTAAGGAGAACTCACCAGCTGATGCAAGTTCTAACACCACTCCAACTACTAATGCCTAG
101	NO		ATGGATGGCCTCTATGCTAGCTCTGAGTTCCTCAGAGCGTTGGATGTATTGCATAATGTGGCTGGGGATGCTGCTAAGGGAGGATTTTACTAG

102	yes	ATGGGAGAAGAAAACAAGGTAACTCTACATGGAATGTGGCTTAGCCCTTATGTGAAGAGAGTTGAACTGGCTCTCAAGGTCAAAGGCATACCTTTTGAGTATATAGAAGAAGATTTAAGCAACAAAAGTCCATTGATCCTCAAATACAACCCAATTCATAAGAAAGTCCCTATACTTGTTCACAATGGAAAGCCAGTAAACGAGTCATTTGTCATCGTTGAATACATAGACGAAACATGGAAGAATGGACCTCAACTCTTGCCAGAAGATCCTTATGAAAGATCCAAAGTCCGGTTCTGGGCTGCTTATATTCAACAGGTGATGGAGTGCATGCTTAATATATTCACTGCAGAAGACCAAAAAAAGGCATGTAAGGAATTTCATCAGAAATTTAGCGTGCTTGAAGATGGATTGAAGACTTTTTTTCCCAGGGGCAATCCTAAAATTGAAAACAGAAACATAGGGCTCGTAGACATTTGGATCGTCGTAGCATTTGGCATGTGCAAAGCACAGGAAGAAGCATTTGGAGTGAACTTTCTGGATCCAGAAAAGGCTCCCCTGATTCTCTCATGGGTTAATAGTCTACTCGAATTGCCCCTGCTTAAAGAAACTGTTCCTAATCATGACAAGACGGTATCATTTCTTCGAGTTTTGAAAGAAAGAAGTACTAATGGTCAAGCTCACTGA
103	yes	ATGCTGGAGCAAGAGACACAAGAGGCGCAGGATCAAAGGAAAGGAGAAGCAGATGAAAACGAAAATCATGAAGGGCTGGAAAATAAAGAGGCAATGGAAGCAACGCCGGGGATACATGGATGTGACAATATGGAAAATAGGAATAAGAAACACACTAGAACAAAGCAAACTACTGCAATAGATTTGAACAGCAGCTCAAAAGGCGAGAATACATCTGAAGGCAGAAGAAGTGGATATAATTATGAACATCAGAAAGAAGGGATATCAGCAGAAAACAGTGAGGAGGTCGTATCAACAATGAAAAACAAGGGCAATAGGCTGGATGGAACAACCAATGTCAGTGCATCACGCATCGTGCTAGAGGCAAGATCAGAACCAGAAGAGGAAGATCACTATTCCAAAGGAATGAATGAGGAAGGAGTAGAATTAACATTACTGGGGGAAGATGAATAG
104	NO	ATGGGAGAGAAGGCTATAGAAAGACATGATAACATCAGTACCAACAACCCTTTTGATGTGCTTAATCAAAAGGAGCATGATGAAGCAACCAACATGGTCAAAAAATCCATACACAATAAGGAACAAAGAGGAAGGCTGGTAGTAGGGGTCAACTTAGAAGTAGATAGCTCATCACAAGGAACAATAAATTCTCACATCAACGTACCAAACATTGAGGTCGCACAACATAATGTTCATAGCATTGCAAGGCATATTTTTATGAGAGATAGTAAACAAGGTAATGTTAAAGAAGGTGAAATAACTGAAGATGGAAAAAGCAGGTGGTAG

105	yes	ATGATTAGAGCTTACGGAATGAGTGATTCACCGGGATATGGTTTTATGTTGTATCAAGAAATGCTAAGGTCAGGTGTGTCACCGAATTCTCTAACATCTTCATTCGTTACAAATTGTTGTATAAAGAGTGGGTCTTTATTTGGTGGGCTACAGATTCATGCTCGAATTTTGAGAGATGGGCATCAATCTGATGGACGACTGCTGACCACATTGATGGATTTTTATTCATCTAATGAGAAGTATACCGAAGCTTGCAAAGTGTTCGATGAAATGTCTCATAGAGATACAATAGCTTGGAATGTGTTGATTTCTGTATACATGCGTAACCGACGAACTCGGGATGTTTTGGGTGTATTTGATATGATGCAGAGCTCGTATGATTGCCAACCTGACAATGTTACTTGTTTGATGTTACTTCAGGCTTGTGCAAATTTGAATGCATTGGCATTTGGTGAGAGAGTTCATAGATATTGTGAAGAACATGGTTTTGACAAGGCAATGAATAACTGTAATGCACTTATAACTATGTACTCTCGGTGTGGTTGCCTCGAAAAGGCTTTTGAGGTGTTTAAGGGAATGACCGAGAAAGATGTGGTGTCTTGGACTGCCATGATATCGGGATTGGCTAGCAATGGTTATGGCAGAGATGCAATTGAGGCATTTCGGGAGATGCAAAGTGCAGGTGTTTCCCCTGATGATCAGACTTTCACTGGGGTTCTTTCTGCTTGCAGTCACTCTGGACTACTTGATGAGGGTAGGATGTTTTTCAATAGTATGAGCAAAGAGTTTGGGATTTCACCAAACATTCATCATTATGGGTGTGTGGTTGATCTAATGGGTCGTGCTGGTATGGTTGATGAAGCTTACAACCTTATAAATTCGATGAAGGTCAAACCAGATGCAACAATATGGAGGACTCTACTAGGAGCTTGTAGGATTCATCACCAAGCTGACCTAGGAGAACAAGTCATTGAGCGTTTGATAGAACTTAAAGCACAAGAAGCCGGAGACTATGTACTACTGTTGAATATTTATTCATCGCTTGGTGATTGGGGTAAGGTAATGAACGTGAGAAAAATGATGAAAGACAGGGGAATCCAAACCAACCCTGCTTGTAGTACTATTGAGTTCAGAGGAAAAATACATCAATTCGTTGCAAATGACTTTTCGCACCCAAGAAAGACAGAAATTTACGAGATGTTGGATGAGATCAATCAGCAACTGAGGATAGCAGGATACGTTGCTGAGACAGTGGCAGAGTTGCACAATGTGGGTACAGAAGAGAAGCAGATTGCATTATCTTATCACAGTGAGAAATTGGCTATAGCTTTTGCGGTTCTATCAACTCCACCTGGCACGTCAATTAGAGTTGCAAAAGACCTCCGGATTTGTGTTGACTGCCATAACTTTGCCAAGATATTGTCAGCAGTCTATAGTCGGGAAGTTGTTATTAGAGATCGGAACCGCTTCCATCATTTCAGAGAAGGTCGATGCTCGTGCAATGACTATTGGTAA
106	yes	ATGAGAACTTTTGTGAGCAGGGATGTCATCTTCCATGAAGATATATTTTCTTTTCAGGCTCCAACAGGTGTGCATCCTGTTTCTACACTACCAGATTACTCCTTATTCACCAAGAAATCATCAGAAGGCATGGTTGTGATTCTAATATATATGGATGATCTCCTTATTACTAGAACTAGCCTTGCCTTAGTTCAAAATACATGGACCATGCTTCAGGGAGCCTTCAAGATTAAGGACTTAGGTGAACTTAAGTTTTTTCTTGGTATTGTTATGCACCAACGCAAATATACCTTGGACCTTATCTCAGATATGAGACTTTCTGGTTCTCAATCTTTTGGGGCACCTGTTGAATTGAATCAGAAACTCACAACTACTGAATTTCACCATCATACAGGGTCTACTGTTGATGAGTCATTAGATGATCCAGGTAGCTATCAAAGACTTGTAGGGAGATTGCTTTATTTGACAAACACAATGCCTGATATGTCTTTTGCGGTGCAAAGTATTAGTCAATTCATGCACAATCCCAAAACTTCTCACATGAATGCAGCTATCAGGGTGGTCAGATATGTGAAGCACTGTCCAGGCTTAGGCATTTTTTTGTCAGCTGCTAGTGCTCCAAAATTGGAGGCATTTTGCGATGCAGATTGGGGTTCTTTCCCCAATACTAGAAGATCTATTACAGGTTACATGGTGAATTTTAGAGAATCTCTGATCTCGTGGAAGTCGAAGAAACATTCTACCATTTCCAGGAGCTCAATTGAGGTTGAGTATCAAAGCCTAGCCTCCACTGTTGCTGAGTTACTTCGCTGA

107	yes	GO:0005524; ATP binding; Molecular Function;GO:0006915; apoptosis; Biological Process;	ATGCCTGGTCTTGGCAAAACAACTCTCGCAAATAAGGTTTTCAAGAGTAGTACTGTTGGATATACATTTGACAATCGCATTTGGGTATATGTCTCTCAATCGTACACCCGAAGAGACCTATTTCTTAACATCATCAACCAATTCACCAGAAACACTGAACAATATCGATATGTAACTGAGGAGGCTCTAGCTGAAGTTATACGCGAACATTTGTTGCCAGGAAAGTATCTGATTGTATTGGATGATGTGTGGACATGGGAACCTTTGGATGATGTCAAAATTGCTTTACCAAACAAGATGAGAGGTAGTAAAGTCTTGTTTACCACTCGAGATGACAAGTTGGGTAAATTTTGTTGCAATGAACCTCATCATTTAAAATTCCTAACAGACAACGAATGCTGGGAGCTACTACAGAAGAAGGTTTTCCACAAGGATAAATGTCCCGCGGATTTGGAAGAACTCGGGGAGCGCATAGCTAAGAAATGTATGGGGCTTCCCCTTGCAGCTTTGGTGATTGCGGGAGCCCTAACCGGGAGAAGCAAGACAAAAAGTGAGTGGGAAATAGTGCATCAATATGTGAGTGAACACATTATTAGTAGTGATATTATGATGACCAAGAAATTGGTGCAGATGAGTTGTGATAGTTTGTCTGTCAACTTGAAAGCTTGCTTCTTATATTGTGGTGCTTTTCCTAAAGGTTCCGAGATCCCTGCTTGGAAGATAGTCCGGTTGTGGATCGCGGAAGGGTTCATTCGAGAAACAATGCAATCAACCGTTGAAATTGTAGCAGAGGGATACTTGAATGAACTTGTCAGCAAGAGCTTACTGATGGTAGCACAAAGGACATCCAATGGCCAAATAAAAACATTCCGCGTGCATGACATGTTACATGAGTTCTGTACGCTCGAAGCAAGTGAGGAAAATCTTTTCAAAGAAATAAAACTAGGTGTCGAGCAATCTTTCCCTAGAAACCAGGTATTAGCCACATTTCGCCGCCTTAGCATTGATTCTTCTGTTCAAGAATTCATTTCTACCAACCCTTATGGTGACAGCATTCGTTCATTCCTCTGTTTCTCCTCTCGGAACATTGTGATGTCCCCATATGAGTTAGAGACAATCCCGAAATCCTTTCCACTACTCAGGGTTCTTGACATTGAGTCCATATTATTTGAGTTAGAGACAATCCCAAAATCCCCATTGCAGAAGCAGTTTTTTCAGCTATATCATTTGAGATACCTTGCTATATCGAGTGACTCGTTAAAGATCCTTCCTAAATTCATGGAGGACCTGTGGAATCTACAAACCCTCATAATTTCGACTCAACAAGAGACATTGAACATAGAAGCAGACATATGTAACATGCCACAACTAAGGCATCTTCACACAAATGCCTCTGCTAAATTGTGTCCCCCTGTCCTAAAAACAAGAAATCATACTTTACAAACTCTTTCTATAATAGAACCTGAAACCTTCACAGAGAATGTGTTGTTTGCAAGGTGTGAAAATCTGAAGAAGTTGGGTATTCGTGGGGATATGGCCAAGTTGGTTGGGCTATTCGAGTTAGAATACCTCGAAAAATTGAAGCTAATGAATTTAGCAAGTGGGGGGTTGCATCTTCGTTCAGAAAATCTATTCCCTCGGAGGTTAAAGCAGTTAACTTTATCAGGTACCTGGTTTGACTGGAATGAGATACGCAGAGTAGTTGGCTATTTGGAGCTCCTCGAAGTGTTCAAGGTGAAAGAGAATGCATTTACGGGGCATTATTGGGAGTTGAACGATTACGTGTTTCCTTGTCTTAAGGTATTATGGATTGAAAGGTCAGAACTAGTTTATTGGAAGGCTTCTGATGAGAATTTTCCGAGCTTAGAGAGGCTTATCCTTCGTAATTTAAATAAGCTTGGGGAAATCCCTATAAACTTTGCCAACATAAGGCACCTGAAAATGATGGAACTGGTGAATACAACCAAATCAACGGTTAAATCTGCCCAGAATATAGAATCCCGCAGTGTATGCACTGGATTCAAGCTAACCATTTTTCCTCCCGATACAATCTCTGATTGCAACTAA
108	NO		ATGGGGTTCGGAGAAAGATTCATCGACATGACTTGGAGGATCATGGCTAATAATTGGTACTCTATAATTGTCAATGGAGCTAGACATGAGTTATTTCATTCCACTAGAGGGCTCAAGCAAGGAGATCCACTTTCACCTGCCCTTTTTTATTTTAGATACAAAGGTTCTTTCAAGGATGATGAACAGGTTGTACTTAAATCCTCATTATCATGGATTTTATATGGAAATGAGATGACCTCAAGTCAACCACCTTAG
109	NO		ATGATTCATTTCATGGAAACCACGAGTTGTGCGGCCAACAACTCAATGTGGTGTGCCATACCACGACATTTTTTCATCCATCAGGGATGCTCTTTTGTTCTGCCTTTTCCGTCACTGTTTGCCACTGCTCATCTGATTCTTCAGACCTTTCATTTTGATTCTACAGCATGGTTGTTTCCATGA

110	yes		ATGCTCATTGACGTTTTTGGTGTAACACATCTTGTATATCCTCTCATGGAGGAAGTTGCAATCCAGGGGAAAGAAAGAAACCAGAGCTTGGAGTTTGGTTCCGCGGAGATTTCGGTTCGAGTGACTCGATCGGTGCAACGTACTCGGGATGGAGTACTTGCTAAATCTACCAAGAAAATTCGTCCAGTGAAAAGAAGTTCCAAGGCACAAGTAGAAAATTATGAGATTGATGTTAACTCTGAAATACATAAGGCTAGGGTATTGTCATTTGGGAAAAGAAGTGTGATTCGAGGTCGGGTTGTTACTGGGTTTGGGGGTGGTGTCATGAGTGAACTACTAGTCCTGTTAGAAGCCCAAGGGTGGACTGCCTTATTCCTTTAA
111	NO		ATGCCAAGAATTCCCTTAAACTCTCAGAGGAGAAGAGCAAACTCGAGGCGCTCTCCTCGACGATCGATCCCCGTGAACTCCCCTGCCCTTCCCCACTCAATTCAACATGAACCATCAACAACCAGCTATATTCCAAACCATACCAATAACAATGGGGGGTCATACCTTTTATGCAACCCAAGCACGAGAACTAAACCAACACCCCCACTCTTGGTTGGAACTGAGCCTCCAAGGCCAAGCTTTATCATTCAGTGCGGAAGTGGAAGGGAGGAATGTGGTCGTACTAGTGCAGAACCCGACTTTCCTAGCCCAAGTAGTATTGGAGGGTATGAGGCTTGCAATAGAGACCTACAACAACCATTTATGGTTGTCGACGGTCCTACAACCCCTTCTGAACCTTCCTTTCCCCCAAATTCCTTTTTACCATCACTCGACCTGGGAAATACCTCTCCTTAA
112	NO		ATGTTCATCCAAGAACCTATGGTTAATGCGAGGAAGATTGATAGATTCAAAAGAATCCTTGAGTATCAACATTGTGCCCACAATATTTCCAATAAGATATGGATCTTTTGGAATAATGATCATCAGATAGACATCCTGAAAGACAAAGATCAACATATGCTCCTTCATATATCCAAAGTCCAACCTATAATATCTTTTCACATTAGTGTTGTGTATGCTAAATGTGATGAGGAATTAAGGAGAGAATTATGGGATGACCTTAGAGACATTGCTAACAATGTTAATGGACTATGGGGAGTGATTGGAGACTTCAATGTCATTACAAAAGCTGAAGAAAAAACAGGTGGAAGACCCTATAAAGCTGAAGAAAGTATTGACTTCCTTTCCTGCTTAACTGATTACAATCTTCAAGATGGTGGTTATTTGGGATCTAGATTTACGTGGAGTGACAATAGGGATCCTCCCAATACCATCTGGAAAAGATTGGATAGACTAGCCTACAATGATCAATGGTTTGATGTCTTTGGAGGCACTACTGTTACTCATCTTTCAAGGACCTGTTCTGATCATGCCCCTCTCCTGATCAATTGTGATACCAACAACTCTAACCACATCAAGTACTTCAAATTTCTTAATGTTTGGACTGAGCATGAAGAGTACTTACCTATTGTCCAAAAAGCTTGGGATGAAGCCCAAATTGGCAACCCCCTTTTTCTGCCTTCACCAAAAAATTAA
113	yes	GO:0003676; nucleic acid binding; Molecular Function;	ATGGTTCTGCAAATCTCTCTCGTCGACCTGAAGAAGGAAAACAGGAGAAGAGGAAAGGAACTCAAGTACAACGAATCAAGGTGGATCTACGATCCATACAATGTCTACGTCGATGAACATCGTATCCTCACTGTTGTCACCGGCAACTACAAGACCGTCGCCAAATGGATCAAGGAGGTTCAGAATACGGCTCCCAATAGCAAACATGGTTTTATTTTCGTCACAATCTGTGTCGAGCGCGATCCCGATATGAGTGGGAACCACTGGGAGATTAAAGATGGCGAGGACTATCCCTACGACCTCCTTCAGGTTTGCACAGGCTCTCACTGCTTACTCTACCGCCTTCCTTTCCCTAAGTACGACGATGATCCTATTCCCAAGGCTATGAAAGACTTCTTCGCTGATCCTAGGGTTATGGTTATTGGAATGAAAATGCGTCGTATTATGAACAGGCTTGATGCTGACTTTGATATCAAGTTTGCTAACCCTGTGGACATCAATATTTTAGCTGAGCTAGGTTTGCAGAGGCATGATTTGGATCTACGCCATTATGACCTTAATCGTCTATCCATGACTGTTATGGGAAAATACTGGGACGTGATCAGGCCTGAAAAGCCGATAGCGTGGTTCCCCAAGGAGGCACGTTGGTGGAGAGATCCTATGAATCCCGAGAAGATAAAATATGCTACCGTGGATCCCTATCTGTGTTTTATGGTTAGTTCTAAAATTCTGGATGGGATGGATGATACGTGGTACCCTGAAGATTTTGAGGATTTCCTGGATAAGAAAAAGAAGAAGAAAAGCAAGAGCAAGAATAAGCGGAAGAAGAAATTCTGA

114	yes		ATGGACGTGGTTAAATTTAATGTTACTATGGTGTATGGGTATAATGATCAAGCTATGAGGATGACTGTGTGGAATGAAATAATTGGAATCAAGAATAACATATGTGGACCTTGGGCAGTAATGAGGGATTTTAATTGTGTGCTGAATATTAATGAAAGGATAGGGAGGCCTGTCAAAATGGCAGAAATAAGAGACTTTAGGAATTGCGTTGATGAATGTGAGATACATGATCTTAAGTCATCAGGATCTTTTTTCACTTGGAATAATAAGCAGAAAGGGGAAGATAGGGTATGGAGTAAGATTGATAGGGTATTGGTGAATGTGGAATGGCTTACACAAATGCCAGCATCAGAAGTTCCTTAA
115	yes	GO:0003723; RNA binding; Molecular Function;GO:0003964; RNA-directed DNA polymerase activity; Molecular Function;GO:0006278; RNA-dependent DNA replication; Biological Process;	GTAACAGAGATCGTTGTGAATCGCATTAAGCCTCTCATCCCCAACATCATAGGCCCAAGCCAAGCAAGCTTTCTTTCCAATAGGAGGGCCTCTGACAATGCAATCATTGTACATAAGGACATTTCCTATTTTGGGAAAATGAAGGAAAAGAGCCCTAACATGATTCTCAAAATTGATCTTGAAAAGGCTTTTGATAGACTTGAATGGTCCTATATAAAGGAAACCATGGCCTACATCCATATTCTCCCTAAGCTCTTCCAGCTCATCATGTCCTTTGTTTCCATTAGTTCCATAGAAGTTCTCATAAATGGAAGGAAAACTAAATTCTTCCAACCATCAAGAGGAATTAGACAAGGAGATCCAATGTCCCCCTATCTCTTCATAATGTGCATGGAAAAGTTGTCCTGGGAAATTGATGCTGCATTCATTGTAAAATAG

116	yes	GO:0003676; nucleic acid binding; Molecular Function;GO:0003677; DNA binding; Molecular Function;GO:0015074; DNA integration; Biological Process;	ATGCCTAACGTAGTTAATACTACTAGTACCGCTGGCACTCACTCGAATGCAAACACTGATAATGCTTTTGGTTTTTTTCCCTTCACTCTTGACCCATCGCACCCTTTCTATATCCATCCTTCTGATAATCCTGGTAGTCAACTAGTGGCAGTACCCTTCTCTGGTTGTAGTTTTGTTCTTTGGCGAAGTAGCATGCTCACTTCTCTGTCTGCCAAGAACAAATTAGGGGTGTTAGATGGTCGATATCCCCAACCTACACCAGATTCTCCCTATTATTCTTATTGGGAGAGGTGCAATGACATGATTAAGGCCTGGATAACCAACTCTGTTTCTAGAGAGGTAGCCACTAGCGTCATGTGTCTTCGAACTACTAGAGAGGTATGGTTGGATATCAATGAGTGTTTTGGTCGGTCCAATGGTTCCAAATATATCCAAATCCAAAGGGACATTAGTTCCACAATTCAGGGCTCATTTGACATAGCTACATATTTTACAAAATTGCGAACTCTTTGGGATGAACTCAATTCTTCTTATGTTGGACCTGATTGTACCTGTGGGGCTTTGGTCAAGTTCATAAAGGATCAGAGACTATTTCAATTTCTCAACGGACTGAATGATTCTTACTCTACTGTCAAAAGCAACATTCTCATGATGAGACCTCTTCCACCGATAACCTCATTTTTTGCTCCATCCTCTTCATCTTCTGTATCCAATAGTGGCAGATCATACAATCAAAAGGTGAATTTTGATCCCAAAAGGAATATCAACTCCTTGTTCTGTAGGTATTGCAAAAGGCCAGGACACAGTGTTGAAAAGTGTTACAAACTCCATGGTTTTCCTCCAGACTTCAAATTCACCAAGAATAAAAGGTCAGCATCTTGTGTTCAAGCAGAGGCTCAGTTGAGTTCTGGTGTTCAGTTGAGCTCTGGCTCTCCCTCTACTTCTCTTAATCCATCTTCTGAGCCTACACCTCATGGATTTAGCAAAGATCAATATGAGCATTTGATGACAATGTTTCAGCTGGCCCAAATTTCCTCTGGATCACCATCTGATGCTTCTCTCCCAGACAATACTACTTATGCACACTTTGCAGGGGGCCCTTCACAGAAGAGGCCTCTGGATATTGGTAAAGCCATTGGGAAGCTCTACTATCTACATTCAGATGCTGATTTGTTTCCCTCCAGCCCTTCTGCTTCTCCATCTACTTCAGTATCATCTGTCCTTCATGATTCTAACATTTGGGGACCCTACAACACCAAAACCTATAATGGGTTCAAATATTTTTTAACTCTAGTGAATGACTACTCTAGAGCCACTTGGACTCATCTACTCTCTTGCAAAGGCAATGCTCTTTCAGTTCTTAAAGCTTTCGCTTCCATGGTAAAAGTTCATTTTCATTCCTCAATTCAAACATTTAGATCTGATAATGCTTATGAGTTGGGATGTAGTTCTGAAGCTATTGTTTTCTTCACTAGCCAAAGGATACTTCATCAAACCACCATTCCTTACACTCCTAAACAAAATGGAGTTGTAGAAAGAAAACACAAACATCTTTTAGAGGTTTCTAGGGCTCTACTTTTTCAATCTAATCTTCCCGTCACATATTGGGGTGAGTGTGTCCTCACTGCCACCTATTTGATCAACCGGATTCCTTCTGTTATACTCAATAACCTTTCTCCTTATGAAAAACTACATGGCAGCCCTCCTACCTATTCTCACTTAAGATCTTTTGGTTGTTTATGTTTTGCCACTTCTCCCAAATCAGGGAAAGATAAATTCCAATTTAGAGCCATTTCATCAGTATTCTTAGGTTATCCCAATGGAAAAAAGGGATACAAATTACTGAATTTGATAACCAACTCTGTTTTCTTTTCTAGAGATGTTATGTTTCATGAAAATATTTTTCCTTATAAATCTGATTCTCCTTCCCTATTTCCTTCGGTTCCTACTCCTGACTTTGTGGATATTTCACTTCCTCCTGTGCCTTCTTTTGTTAGTCCTCAAATTCTTGGATCCTCTTGTGGTTCCCCTTCACCTCCTGGTCCATCTTCTTCTTCTATTCCCCAGACTCCTATCCCTTCTAGACAATCTACTAGACACAATAAGCCTCCTTCCTACCTTACTGATTATATTTGCTCATCCGTCCTACCCCACCCAGCTCCCAATTTACATACTATTCCTTGCAAATGGGTGTACAAAATTAAACGGAAAGCTGATGGTTCCATCGAGAGATATAAAGCCCGTTTGGTTATTAGAGGTGACACACAAATAGAAGGTATTGATTTTCATGAGACTTTCTCTCCGGTTGTCAAACTCACTACCATTAAGTGCCTTCTTACTCTTGCTGTTAAAAGGAACTGGACTGTTTTTCAACTCGATGTTAACAACGCCTTCCTTCATGATGATCTCCATGAAGAAGTATATATAAAGGTTCCTCCTGGCCTTACCATTTCTCCTGCTTCTTCTTCTCCTCCTCTAGTTTGCAAACTCAAGAAGTCTCTTTATGGCCTTCGGCAGGCTTCTCGGCAATGGTTCTCTAAATTGTCTGAAGCTTTGCTGTCCCGAGGTTATATTTCTAGTAAAAATGACTACAGCCCTTTCAC

117	NO	GO:0003676; nucleic acid binding; Molecular Function;GO:0003677; DNA binding; Molecular Function;GO:0003723; RNA binding; Molecular Function;GO:0003964; RNA-directed DNA polymerase activity; Molecular Function;GO:0006278; RNA-dependent DNA replication; Biological Process;GO:0015074; DNA integration; Biological Process;	ATGGTTAAATTATTTTATCTGGGCTCCGTCAGGATATTAAGACAAATGTATTGGTCCATAAGCCCACATCTCTTGATGAGGCCATCTCGTTGACCCAAACCCATAAGCAACGCCTTCAGTTAGAGAGAGGGCACATGACTCCAACCCTTGCTAAGACCCAGCCCTTGCTTCCAACACCACAATCCAGATCAATTGTTCCTGCACGAAATAACCTCAATGCTTTGTCACGCATTCCAGTCAAGCGGCTCTCGCCGACGGAGATGCAACAACGTCGAGAAAAAGGGTTGTGTTATTATTGCGATGAGAAATATACAACAAATCAGAGGTGCAAAACTCTTCCCCAAATACTCTTTCTTGAAGATGATCCAGACGCCCTTTTGTCTGCAACAGAGCAACTCACCTTTGATGAAATGCTAGCAGAGGAGTTACATGCCTTAGAAATGCAGGCTTACTTTACAATATCTTATCATGCTTTGTCTGGTGGTCACTCCCCAACTATTCTGCGTTTCAAGGGGCATGTTCGCGGGTCACCTATTGTCATATTGGTGGACGGCGGCAGTACCCATATTTTTATTCAACCTCGGATGGATGTACTAATTTCAATTCAAGGGGCAGACCTCTTGATGGATTTGTACGTTTTGGCCTTTCATGGAGCGGATGTTATTTTCAGGGTTTCATGGTTGGCCACCTTAGGTCCGGTGCTTACTGACTATTCCACCTGTCACATGGAATTTTATTTGGATGGCAAGCAAGTTAAGTGGGTGGGTAATCCTCCTGATGAATTGCAACCAGCTCAGTTACAAATGTTACGTCGTTACCACACCACTGATGTCGTGGTGGCATGTTTTTATCTATTCATGGTGCACGATGATGCCACAATTACCGATGTTATACCCCTAAACTTAGAAGTCTTGTTGGAATCGTATTCTAGGGTTTTCAACAAACCTCAAGGGGTTCCACCTGCTCGAGACACTAATCATGCCATACATCTCCAACCACATGTCGACCCTGTTAAAAAGAAAGATGGTTCTTGGCGTTTTTGTGTTGATTACAGGGCCTTGAACGCCATCACTGTACGAGACAGATTTACAATACCTTCTATTGATGAACTCTTTGATGAGTTGCATGGTGCTCAATTTTTTTCTAAGCTGGACTTATTAGCAGGTTATCATCAGATTCGAGTTCGTCCAACCGACATTCCCAAAACTGCCTTTCGAACTCATGATGGCCACTACGAGTTCTTAGTCATGCCATTTGGATTGTCGAATGCTCCATCCACTTTCCAAGCTACCATGAATGACATTTTTAGGCAATACCTTCGTAAGTTTGTCCTTGTGTTCTTTGACGATATTCTGATTTATAGTTCTACATGGACCTTACATTTGGAGCGTTTGGAGTTGGTGCTAAAATTGCTCAAACATCACCAGTTGGTTGCTAAGCGTAACAAATGCCATTTTGGGCAGAGTAAGGTTGATTATCTTGGCCACGTCATTACATCAACCAGACTTGCAGTAGATCCATTTAAGATTGATGCCATCCAACAATGGGCCACTCCAAAGTCAATTAAGGAGGTTCGTAGTTTTTTAGGCCTCGCGGGCTACTATCGGTGTTTCATCAGACAATTTGCTACTATTGCTAGTCCCATTTCTGACTTGTTGAAAAATGATAGTTTTCAATGGACAAACCAGGCACAACAGGCTTTTGAGGAGCTAAAATGTCGTCTTAGTTCCACACCTATCTTGGCATTGCCTAATTTCTATGAGGATTTTCACCTGGAGACAGATGTCTCAGGTGTGGGAATTGGAGCAATCCTCTCACAAAGAAAACATCCAGTTGCTTTTTATAGCCAAAAGTTATGCCCTAGGATGCAAAAAGCCTCAACATATCACAAAGAGATGTATGTCATCACACAAGTAATGGCAAAGTGGAGGCAATATTTGTTAGGGCGCAGATTCACTATCTTTACTGACCAGCAATCCCTCAAGAACCTCACAAACCAAGTGATTCAAACTCTAGAACAACAAAAATGGCCGGGGAAGCAGAATAAGGCTGCAGATGCTTTGTCCAGACCCCCAGATGGAGGCGGTCGTTTGGTACTACCACGGGACTCGCCCTTGAAGCAGTTTCTACTTCAAAAGTTCCACGATTCGAAAATAGGGGGGCATGCTGGGGTTGCTCGCACTTTTCATAGATTGTCTTCTAATTTCTCTTTGCCAGCAATGCGCAACGATGTTGGTTTATATTGCTTCATGCCAGACTTACAGCGCTTCAAGGATCGTAATCGATTACCCGCAGGCCTCTTACAACCAATGCTGATCCCATATATGGTTTTTGAGGAAATTGCTATGGATTTCATTACTTGCTTACCTAGTTCAAAGGGGAAGACGACAATCATGACAGTGGTGGATAGGTTGTCCAAATACAGTCATTTTATTCCTCTTCCATCTACTTTCTCCGCCCATATTGTGGCACAAGCTTTTGTCATTCATATCATCAAATTACATGGTCCTTCTCGAACAATTATAACAGATCGTGACCCTCGTTTCTTGCATACTTTTTGGCAAGAGATCAATCGCTTGCA
118	yes		ATGGATGCCATACAAGATTGGAAAAGTCAGAAATTATCACATCACGAGTACACAAGAGGGAATAAGAAAGGGTCGTCTGAGATGGTTAACCATGTCCAACATAAGCATCCAAATGGACTGGTCCTTCAGTGTGACAATATGATGATTGAAACTGTTGAAAAGAGACTGCGTAGACTTAGAATCACATGGAGAGAAATTTCCTTAAAGGACCTATAA

119	yes	ATGCATGTTGAAACAAAGAAAGAACTGAAGTTTGAGAAAGTGAATGAAAAATTTGCTTTTGAGCCATCAGAAAGAACTATTGACAACATGGAAGAATGTCCACTTCAGAAATATCTCTTGGGTTCTTCAGTTGAGTCGCAAGAGATCATAGAGTCTGAGGAAATGCTAAAGCAACAAAAAGGATTACTAGAAGAGTTGACGTTTAAGAAGAAAAACAAAGATAAGAAGAAGAAAAAAGATGCAGGTCATTTCATGAAAAAGATATTGCAGAACCTCCAGCCCAAATCAAAGAGCTCAAATGTCACTGCATCTGTTTCAAGCAAGAAGAAACTCCCTCAGGTCACTACTTAA
120	yes	ATGAGGACCCTTAAATGGGATCCATGGTTAGAACCTGATGTAGAAACAACGATAGGAGTGGCATGGATATCTTTCCCGGATCTACCACCGAATTTCTTTGCGAAGGAGGCAATTTTTTCAATAGCTGCAGCAGTGGGTAAGCCACTAACCGTAGACATGGCAACAAGAAATCAGATAAGACCAAGTTGCGCCAAGGTTAAAATAGAGGTGGATTTGACGGCCAAGTTACCACAAACGGTTAGAAATACAGAGGAAGACGATATCACAGGGGCTATTAAATACAAATGGATTAAGGTGCAATATGACTATATGCCTAAATATTGCAAAGAATGCTGCTTACAAGGACATGATGAGCAAACCTATTGGTCATTGCATCCTGAATTATATGAAACAAAGATTGAAGAAGAGAGGAAGAAGGAGGAGATAAAAGATATAAAAACTATTGGAGGAACGAAAGGGGAACAAAGTAGGATGCTGGCAAGTGGGAGAGTGGTAGGGCCAAAACAAAATAGACAAGAATGGATGGTTAAGGGAAGAAATAAATACAAGCGTGATAAAAATGGGCGAATTGAAGGGGAAAACGATTTGCAAGATGAAAATCCATTTGAGGCATTGGGAAGAGTAGAGGAGAATGAGGAGGGAGTGGTGGAAAACAAAGAAGAAAGATTGAGCACAAAAGATTGGACCAATGGCGAAGATAACAGAGGGGAGGTGGCGAAGAATCAAGAGGGAACACCACAAGTGCATAAAGTGGGATCAACGGAAGAGCAAGAGAACAAGGAGGATGACTTGAAATATGGCCTAGTATTGTTCGAGCCAAACAAGGAGGAATTTTTGCCACTAGCAATTCATAATGACAACCATGAAGGAGCAAGTGATATAGAAAAGGCAAATATGGACAAGGCAGACCTAATCAAAAATATTGAAAAGGCAGCAATTGAAGGAGACTTGTCTCCGAAACAGATTAACAAATTAAAAGGTGCTCACATGAAATCAAGGAAACAAGGGGAAGGAGAAATTATAGTTGCCCAAGCATCGTCAAGGTCTAAGAGAACGATCATAAAAAATTCTAAGTATCAATGA
121	yes	ATGAGAATGGTTTCTGCAAGCAAAAAACAAAGAGAAGAGGAGGAGATGGATTTCTCTGATGCAATGGTGGTCATGTACGCAGATGCAGAACCAATTCCAATTCAGATTGATAGCAGCTCTCAAGAGGGAGATATAGAAGCTAATGCCACCAAATGGATCCAAGAAAACATGATCAGTTTGAGCCTGCACTTCGGGATGGATCTCAAAGGATGCAAAAAGGAAGCATATGCTCTGTTGATGAATCTGGATCAGAGAACAAGAAAGGACAAGAAGACAGTGGAGGGTCAAAGGATCAATAATTAA
122	NO	ATGGGATATCCAAATGATGGAATGGACACAAACAAAGGCAGTACTGCAGTGAACAATGTGACTGGTGGTGAAAGCTCTTATCCAAAGATAGGATGTGTGGAAGAAAAGTCGACTAATGAGCTTGGAGGAAAAGGAGTTTCACTTAACGAGGAATAA

123	yes	ATGACCACTGTGAGATGTCTCTTGTCTGTTGTTGTTAAGAGGGGCTGGAAGGTTTACCAATTGGATGTAAATAACGCTTTTTTGTACGGAGATCTACACGAGGAGGTATATATGCAATACCCTCCTGGTCTTGAGTTGCCTATTTCATCTGTTGTGTGTCGCCTGCATAAGTCTTTGTACGGGTTGAAGCAAGCTTCTCGTCAATGGTACTCGAGACTTTCTTCAGCTCTTGCCACACATGGTTTTGTTTCCTCTCTCAACGATTATTCACTCTTCTTTAAAGTCTCTGGTCAGCTCATCACCATCATTGCCGTGTATGTTGATGATATCCTGCTTAGTGGTAATGATACATTAGAAATCAATAGGGAAAAAGAGGGACTTGTCGTTACCCAACGTAAATTTGCTCTTGAGCTTATGCAAGAGTTCAATTGTCTGGATTGTCGTGTTGTGTCTACTCCTTTGGATCCCAATTTGAAACTTTCTGCTACTTCTGGTTCTCCTTTGCCAGATACTTTGGTATATCGACGACTTCTTGGAAAGTTGAATTTTTTGACCAACACTCGGCCAGATCTTTCCTATGCCGTGCAGACTTTAAGTCAATATATGCACTCTTCACACACCGGGCATCTTGAAGCTACATTACATACCCTTCGTTACTTGGCTAGAGATCCGGGATTAGGTCTTCTCATGAGTTCTTCTGCCTTTTTCCATATTCTTGCCTTTTGCGATGCAGATTGGGCGTCTTGTGTTGACACTCGTCGATCCGTAAGTGGTTTCTTCCTTAGCCTGGGGGGTTGTCCTGTTTCATGGAAATATAAAAAACAACTTGTTTTGGCATTGTCTTCAGCTGAGGCAGAATACCGCTCTATACGTCGTCTTGTCGCTGAAATCACTTGGATTGTTCGCCTTCTTCATGACCTTAGTGCTCCACTTTCATTGCCTATTCCTCTTCATTGTGACAACTAG
124	NO	ATGGTCAAGAAGGAAGGTGGTGATATGACAGAGATAAAGGGTATGCTGCAGCATATACTGGGAAAATGGAAATTTGGAACAGAAATACAAGGAGCACTACCAGCAGACACTGATGTGAATCCAAAAGATATAGGTCCAAAGCAGATGATGGTTATGAGTATTCATCACGGAAGGGATCTAGACGCAGAACAAGAAAAGGCTCAGACAATGAAAGAAGAGGTGCAACCTGCTCAACTACCATTTGAATTAGATGAGTCTGAGAATCTGACCGATGTGATAGAAGAAACGCCTGAGATAGAAAATCGTCAAGTCAGGGACAAGAAAAGGCCTCTGACACCCTTTCAACAGATCAGATTGGCTATGTATAAGAAGAATGATCAGTATAAGAAGTTCATGGAAATGTTGAAACAAATCCAGTTGAACATTCATTGA
125	yes	ATGGACTTGAGTCTGTCGGAGACGGTTATATTCAAGAATGAGAAAGGAGCACTGATTAGACAATATGATTGGAAACCAATCTTATGCAAACATTGTCGTAAATATGGTCACTCTGAGGAAACTTGTAGAAAGAAACAAAATGGTACAAAAGTCCCTATTGTACAGGATCAAACCAGTGTCCAATTTCAGCATGTGAAAAAATATCAGCAATTAAAGAAAACCAAGGTTGGTGACAAGGCAACTTCTCCAGTTAAGGCACAATCTGGACAAAACATGGAATCTGGATGGGTGTCTCCACAGAGGAAGAGTAAAAGTCAGCAGGTGAACGCTCAGCAGGTCGAGAGCTCAAACTCATTTTAG
126	NO	ATGGTTGAAAAGGTTATTAGTAGAATTACTGGATGGCAATCCAAACTTCTCTCAATTGGTGGGAAAGTTGTTCTAATCAAGCATGTCCTCCTTGCACTCCATATTCATCTCCTAGCAGCGATTCATCCTCCAAAAGGTGTTTTAAAACACTTAGAAAGGGTGGTAGCTAGATTTTTCTGGAGTGGTAATGATGAAAAGAAAAAGTTTCATTGGGCCTCTTGGGATGATTTATTCAGACCTTATGACGAAGGTGGTGCCCAGTTTAGAAAACTTCAAGACATATGTGATGCTTTCACAACAAAGCAATGGTGGAATCTTAGAACGAGTCAGTCATTATGGAAGAAATTCCTTATGGCTAAATACTGCCAAAGAGTGCACCCTTTGGTCAAGAAGTGGTACTCAGGTAATGTTACTTTCTGGTATGACAATTGGAGTTCTTTTGGATCTCTTATTGACTTCCTGCCTGATGGAGCAAAACCTGGTTATCACAAAGTCAAAGACATGTTTGTGGATGGACAATGTGATTTGATGGGCTGGGATAGACTTCTCCCTGAAGAAATTTCCTACAATATTTGCAATATGAAGATGGAATTCAACCCGAATGAATTGGACAAGCCTATATGGACTGATGATAGTAAAGGTGTCTTCAAAGTATCTTCTGCTTGGAAGTTACTAAGAAGTACTCACCAAAGTTCTTGGATTGATACTATGACCTGGAATAAAGTCATTCCCTTTAAAATGTCTTTTATTGTTTGGAGAGCTTTAAGGGATAAAATTCCTACTGATCTAAGGATTATGATATCACCATTTGGGGCCAATTGTATAGCATAA

127	NO	ATGATTAAGATTATTGAGCGAGCGATTAAGGCAGCAATGTGCCTATTTAGGGCTGAGGTTGTGTTGCATAAGGCCACTCTAGCCTCATATGAGGAAAGGTTGGATAACCTCATTGCTAAAGTGGCGCCTAGAGAGCAGGGTGAGGATAGCTCTACTGGTTTAACTGAGTTGAGTGTAGAGGTTGCTACACTTAGAGCTAATGTGGACCAGATGAGGTCCAGTAATATCTCCATGCTTTGA
128	NO	ATGGTAATCGGAGGAAATACGTCCACAGGTAACTCTAACACTGGGAAGGCAGGGGAAATACATAGTGCAGGTATGAACGTAGGCGAACTGTGGCCGGAGTTGAAAGGGAATAAAACCCCTCTTCTGACCAGTACGCCACAAGGCCCATCTGGGTCAAAATCAATGGAACAGGAAATGCAAGGAGACTATGATAAAACTGGTGTAGCATCCATCTGCAAAGCATCGACGGATTTATGTCCAGAATCGGTAGGAAAGGGGGAAGAACTTGAGCAGAAAAAATGGGTAAATCTGTTTCAAGGGAATTGA
129	NO	ATGCCCCAAATCAGGCATGAGTTTAGGGAACAAAATAGGACGGCCGACTTGTTAGCAAGGAATGGGAGAATGCTGAAAGAGTTTCTTTTTGAAGAATGGCTAGTTCCCCCAGTGTTTGTTCTTGAAAGTCTAGAAGCAGACAAGGGAGGAACTTCTTTTGCTAGTAATTCAACTATCGTCTGTAATACTAATGGGCACCTAAGCCCAATACTTAACTTTGTTTGTAACGCTTCAAGCAATGTGGCTGATCCTGATGTATTGATGCATGTTAACTAA
130	yes	ATGGTTGGGGGTGCTTCCAAAGGAGGCTTTAGTAAAGACAGTTCTGCCACTCATATTCAGAAATTTGGATTTCCAGCCAGCAAGTCTGTTGTTCATGCTATCTATGATGAATCAGAAATCACCATTTACAAGTCTCCTATGGAAGATGAGAAACCCAAGGTATTCCCTGAAAAAGGTACTAGTATGAATGTTAAGGATATTGGGCAGAAGAGACGAAGCTGTCCTGGTTGGCCCAATGATGGAGGAGAGCAAATGTTTGATCTTGTTGACAATAATTTTTGTCACCAGCTTGTAGCCAGTGTTACAGAGCCCGATGGGCCTAAAATTCCAGATGTTGGAAGCATTAAGATACTTGGGAATGAGGCAAAGTAG
131	yes	ATGGTGGATGGAATTATGAAGAAAGTGCCCAAAGATGTGATTGTTGCTATAATTTTGAAATTTCCAATGAAATCTCTTGTGCGATTCAAATGCATCTCCCAAAATTGCAAGGCTATCATACAATCATCCACTTTTATCAACCAGCATCACAACCGCTTAACAACTGCTACAGATGAATTAATACTCTTCAAAAGGTCCATCAAACAAGACACCAATCAATATAAAACTATCTTGTCTTTTCTTTCAAGTGATGATTGTAATCAGTTCAACCCCATTTTTCCAGATCTAGATGCGACTTACCTAAACTCTAATTATAGTAGTGATTATGATCAACTCATGGGTCCTTGCCATGGTTTGATTGCATTGATGAATTTCTCTAGCACCATATTAGTTAATCCGTCTACACAAAATTATAGGCTTCTCCCACCTAGCCCTTTTAATTGTCCACGAGGATTCTATCGATCCATTGAAAGTGTTGGGTTTGGCTTCGACTCCATTGCAAAAGATTACAAGATTGTTACAATTTTACATGTTTATTTTGAAGGTCCTAGTGGATATCCTGAAGAGATAACGAAAAAGGTTGAGGTTTATGAATTGGAAAATGATTGTTGGAGAGAACTGGATCGTGTGAATCAACAGTTGCCCAGCTTGTTTTGGTTGCCATGTTCTCAAATTTATTTCAGGGGATCTTGTCATTGGATTGCAATCCCAGAGGTAGACCCACTGGTAATTCTTTCTTTTGACATGAGCAAAGAGATTTTTCAAACTATGAAAATGCCCCAGACTTGTTATTTCATTGGTGGGCCAACTTATAGTCTAGTCATCTTAAACGAGTTTTTAACATTGATTTGTTACCGCTATCAACAGCCCGCAATTGACCAAACAAAAGATTTGATTGACATTTGGATAATGAATGATTATGGTGTATGTGAATCTTGGAGTAAGGAATACACAGTTGCAGGTCTTCCTATTGAATCCCCATTATCAATTTGGAATGATTACTTATTGCTGTTTCAAAGTAAAAGTGGAAGTTTGATGTCATATAATCTCAACTCTAATGAAGTCAAGGAATTAAATTTACACGGTTTTCCTGGCACTTTGAGAGTTATAGTTTACAAGGAAAGCTTGATTTCCATTCCAAGAGGAAGCGAGGTTAGTACACAGGTTGAAAAGTTCTAG

132	NO		ATGCTTTTGAGGGACAGACATGAGCAGACATCATTGCCATTCCCGGTCTTAATCACACAGATATGTGAGAAGGCTGGAGTTCCCCTTCAGAGGAAGACTGATGTGTGGGTAATCCCGGCCTCCTCCAATGACATTCAGTGGATTGAGACTGACTATTTACAGAACAATGTGGCCCGAAAGAAGCCTCCACCATCAGACACTATGCATGTGGTTGATCATGCTACTTTAGCTCCTGAGGCCACTCCATCTGCTTCTACTGTGAAGTCATTAGATGTGAGGGCGGCAAGGGTTGAGGCTGACTTACCTAAGCTGTTAGAGAGGTCCATTGAGAAGGTTGTATCTCCTTTGAGAGATAAGTTGACCCGGTGTGAGGCGTCAATCATGCCACATGGTGTGAGGTTGGATAACCTCATTGTTATACTAAAGGCTTGA
133	yes	GO:0003723; RNA binding; Molecular Function;GO:0003964; RNA-directed DNA polymerase activity; Molecular Function;GO:0006278; RNA-dependent DNA replication; Biological Process;	ATGCAGAAAGCTTATGACTCTTCGGAACGACATTTCCTTGAGGAGGTGCTAGCTGGTATGCAGGTCCCTAATAAGTTCATATCAAGGATTATGAGTTATGTTAAGACAGTATCCTACTATATCATGATTAATGGATGCCCTTGTCCACATATTCAGGCTGAGGGAGGGGTGAGGCAAGGGGTCCCTCTATCGCCCTACTTGTTTGTCCTTGATATAGACTACCTCACCAGGATTTTAAGAACTCTGAGGTCCAAAACTACTTTTTAA
134	NO		ATGGTTTTCACTGAAGGACAGTATGACCCGATAATGCAACACTTCAACAAAGGCAACACTCACTCCACTCTATCTAGATCCCACTCAACTGATACTGCAGGTATTATCAATAGTGATGTAATAAGTGATTCAGTAGGATCCAGATGGATAGTCGACACAGGGGCAACTAATCATATAATATCCACTTCTAAATTGCTTTCTGAGGTTCAGAACTTGTCTCATAATGAATCCAAAAGGGTTCACCTGCCTAATGGACAACAAATTCCTATTGCTCTCATTGGGAAGTCTAAACTGGCACACGGAGGACCTTCACATGGGGAGGCTCCAGTTGCAGAATCTGAGTTATCTCCATCATCTCCTACTCAGGATCCTTCAGTTTCCTTTCAGATACTCTCTCAGGATCCACCTATTGTTGTTCCTTGCCTTGAGGTCCCTGAGGTACCACATAGGAGGTCTACTAGACCACCTAAGCCTCCAGGTTGTTACATGACTTTGAACATAGTAGGGAACCTGCTTCCTATGAGGAGGCTATGCAGAGCCCTCACTAGATTCAAGCTATGGATCAGGAGCTGCATGCTTTGCATGATAACCATACTTGAGCCTTGTTCTGCCTCCGGGTAA

135	NO	GO:0003676; nucleic acid binding; Molecular Function;GO:0003677; DNA binding; Molecular Function;GO:0015074; DNA integration; Biological Process;	ATGTCGAAGAAAAGAGGTGAATCGTCCAATTTTGCGGAACAGGAGGAGGAAGAGATATCACTATTACTGGTAACAAAGGAGGAGATTACCAAAAATCAGTGGTACTTAGACACGGGATGCAACAATCATATGACTGGTGTCAAGGAAGCTTTATCAACCTTGGATGAAACTTTTAGAGTCAAAGTGAGGTTTGGAGACGACTCAAAACTTCCAGCAATGGGGAAAGGTCAGGTTACAGTACAAACGAAAGGAAATAGAATACATACAATTTCTAATGTACCTTATGTGCCACGCTTGAAGACTAATTTGCTCGGGCAGTTACAAGAAGAAGGTTATGAGTTGAATATAAAGAATGAAAAGTGCAAAATTCAAGAGGCTAAGCTTGGATTAGTGACACAGGACTTAAAATCCTTCAACAAAAGAACATGGTCACTGGCCTTTCAAAGTTTTAGAAACCTTACAGCTTTTGTGAAGATTGTGTCATCGAAAAGCAACACAGAGAATCTTTTCCCAAAGGTAGAACTCAAAGAGCAAATCAGAAAGAAAACGGTAGCCTACACTCCACAACAAAAGGGAGTGAGCGAGAGGAAGAACCGAGCAATCATGAATATGGTAAGGAGCATGTTGGTTAGAAGCAAAATACCAAAGAAGTTTTGGCCTGAAGCGACAAACTGGAGTATACATATTTTAAACAGGAGTTCAACTTTTGTTGTGCGAGATATAACACCAGAAGAAGCCGGGAATGGGAGAAGACCTGATATTATTGTTAGCAGGGATGTGATTTTCTCTGAAGAAGAGTTTTGGCAGTGGGATGAAGGAGGAGTTAAGAAACATACACCAACATTTTTTGGTGATGAAGAACACATCAACAGTCAGCATGATCCAGAGCAGATGCAAGAGGTTGAATCTTCACATCAAAAATGTGAACTAGTTAGCTTTGATAAAGCAGTCCAGCAACCAAAATGGCAGAAAGCAATGGAAGAGGAAATATCTTCCATTGAGAAGAAAAACACCTGGGAACTTACGACATTACTAGAAGGTCAAAAGAGCGTTGGTGTAAAATGA
136	yes	GO:0005524; ATP binding; Molecular Function;GO:0006915; apoptosis; Biological Process;	ATGCTTGAAATCGTACACAACATTAAAGCTCTGTTTCATGATGCTGCCGTTAACCTTAGAGAAATCAGCGAGATTGATCATGTTGATGGCGTTACCAATCAATTGCAAGTCATCATTCAGAAGACTAAGTTGGAAATCAGATGTAAATACTTATTTCCAAAAGTCAACAAGGATGGTATTGTTGTTACCCCCAAATTTGTAATCGATTTCATTGATACTGTTGTATTGAATCTGGGTGATTTATTGAAGGTTTATTGTTCTAGCTCACTACTTTTTGTTCGTGGACCTAACAAAGAGATGAGGGATGTTTTCAAGGAGTTCAAGTTATTGAGAAATTTTGTATGCTTTGTTACGGACAGATTCATAGAACTGAAAAGCCAACCTATCAATTTCTTCATTCATGTTTTAGAGGTGACCAGTCACGCTGCAATGGTTGCCTGGTTGTATCTCCCAAGCAATGACAACGAAAATCAGGAAACGAATGGTTTTCTTTCTAATCATCTGAACATGAAGATTAAGCCCATTGACCCAAGCATCCGCAAGATCTATATTGATTTGCTGCAAGATCTACGATCAGAATGGCGTCCGATTATTCCAATTAATCATGTAGCTGATTATGTAGCTGGCTTTGTGGAGACTCTCCAACACAACTTGAAGGCACTATCGGTTAGTAATCCCAATACTCATCAAATAGCAGACCTTCAGGAGATGCTCAACGTCTTAATTGCTAATCTGTCCATACAAGATATTGAATTTCACCTTAAAGATATCGACACTGTGATGATTGATTCCGGAATACTCGTTTACTCGTTGTGTGAAGATGTGGTGTTAGGGAGAGTGACTATTGATTTACCAGTTATGATTGAGCATATCAAGATATTGATCTACCACATCATCCGGAAAGAGTTCCAATCTAATTTGCCAAGGATTCATGGAATAGGCTATCTTGATTTTGTCTTAAGTAATTTGAAGGAGTTTCAAAACCGTTATCCAGATTCACTTGCTTTTATGAAGACTCCACTTCAAAAAATTCAAGCAAAACTGGAGAGCGTGCAACCTTTTCTGAGGTTTGTTGCAGAACAACAATACATTATTCACGACAAACTTCAGAATAGTGTGGCTCTACTGATTGGCAAAGCATATGAGGTAGAATATATCGTTGATGCTTGTGTGAGCAAAAGAGTTCCGGACTGGTGTCTCATGCTTTGGCTCTTGGACATTAACGCTGAGGTTGCAGAGATGCAACAAAAGAAACTGTTTAAGGTTGACTTAGTGTCACCTTATACCATTGATACTGATACTTCCAGTAAGTCGTCAGAACTGAAAAAAATGTCAGGGATCAAAGAAAAAATTATAGGTTTTAAAGATGAGATCGAAACATTAGTACACCGGCTAACACGACGATCCAAAGGGGTGGACATTATCTTCATTGTTGGTATGCCTGGAGCAGGAAAGACAACTTTGGCCAACAAACTCTATTCTTGTGATTCAGTTGTCTCTCACTTTGATATTCGTGCATATTGTCATGTGTCTCCAGTATATTCGAAGAGGCGCCTATTATTGTCTCTTCTGGCGACGCTACATGTTTCTATTGATGAGACCTCTAAGACTCGTAAATTAGAACATTCCCTTTACAAAATTTTACAATCCGGGAGATATCTTATCCTCCTTGATGACGTATGGGATCGCAAGTTAGTGAACGCTATCACCTTCGCTTGTTGA

137	yes	ATGAGTAACCTGGTGCTTGGGCCTACACGGGGATTACATATTATCATCTTTTGTTTTTTGGAAAAGTTTGAAGATTGGACCTACTATAGAGAGATCAAGCTCAACAGGCCAAAGAGTGGGCTTGGATCTGAGAAGCTTGGAGAAAAGTTTGCGGCTCAATGGGCTGAATTGAGAGAGAAGAAACACAGAGAAGCTCGGTGGGATGAGTTGAGAGAAAAGCACATGTTCTTGGGTTTTATGCGTGGATTGATTTTTTATATTTTTTTTTATTGTCTCTTTTCTTGGAGAAGATTGGAGTGGACCTGCTTGAAAGAGAGAAGTGATCAAGCTCAACAGGCTGAAGATTGGGCTTGA
138	yes	ATGGACAAACTATCTTCTAAAGGAACAATGTTTAGTAAAGAAGAAGGTAGGAGTATCCGCGGCGATGAGATATTTCCTGATGAACATCTCATCACAATTCATGCAATCAGTGAAAATGAGAGAGAATGGCTAAATTCATTGGAGAAGAGCAGAGATTACCTTGACTCATTGCAGAATCCAAAAATTCAAAAGGTCCCAAAAATGCATCGCGATATTGAATCAAACTTAAGGTGTTATGAGCCTCTTGTGGTTTCTATCGGTCCATTTCACCATGGAAAACCAGAACTTCAATCTATGGAGAAGTACAAGAAGCTACTTGCAATTCAGTTAACTGATGATAAAGTATTTAAAGACCCCTCCTTATCATGGCTTTCGACAAATTCAGTGTCTCTTGATGAGCTTTACAGTAAGGTCAAGGACATTATGCCTGTTGTCAAGGAGTGTTATGCTGAGGAATCGATCAAAGATTACAACGATGAGGAGTTTGCACAGATGATGTTCCTGGATGGATGTTTCATCTTTCAATACCTTCACTGCATTGTGACCAGTAATTATAAAGAGCTGAAAATGAAGAGCCATGATATAGCTTTCATTCGTCGTGATCTGTTCTTACTTGAAAATCAGTTACCATTTGAAGTCCTGGATGTGTTAATGAGATGTAAGCTCAAGGACAATGTAGGAATGAAGATGATAACAACGTTCATCTCGAGTGCACATACAAATCCTTCTCAACGTAAAGGATTCATTCAAAGTATCAAGGATTTCTTTGTTGAATTCTTTAGTGATCTACATCCTGAAAGCTGTACTGAAAAAGCTATGAACTTTCTTAGCAAGATTTGTGGAGGAGAATGTCCTGCCCTTAGCAAAGAAGAAAGCACGAAAAAAACATGGCTTCCGGCTCATCTCCTTGAGCTATTAAAAACAAATCTCATAAACACAACGGATTTCACAAAAGGTGGATGCTATCTAAGGGGTGAGTGGTGCTCGTATCGTTCAGCTATGGAGCTACGTAGAGCAGGAATCCGTTTCAGGCCTGGAAAGAGTCGTCGTCTTTCAGACATGATTCAACCAAGTCACACTTTTTAA
139	NO	ATGTCAAGAAATCCTGTTGATTGTAGCTCCTCCAACTATGACATTGATAACTCTCTTTGGGGAATTCGGCCATGGATAGTCGCTGCTAGAACAGTTCTTTGGAAAAACCTACTTCCCCTTGTTGTCTCAAGAACTCTCGAAGATAACCCTAGTTTAGTAGGTGAGATACCACTAGTTGCACTCCTCGACAGGTTTTGGTCTTGA
140	NO	CCCATTTGGATTAGGCTGGTAGGGCTGGACATCAAATGTTGGGGAAAGAATGCACCTACGAAGATAGCAGAATTAGTGGGAAACCCTCTTAAGGCAGACACAACAACAACAAATATGGTGAGGCTAACATATGCTAGAGTGTTAGTGGAGATGCCGCTGAATAAGGAATACCCAAATGGGACAATGTTTAAGAATGAGATTGGGAAAATAATAGGGCAAAAGGTGGAGTATGAATGGAAACCAGTTTGGTCCACTAAATGTAAGAACTATGGGCATAAGCTAAAGGATTGTTGGAGACAACACAAAGATGCAGATGCATCTAGCAAGAAAGGTAATAAAGAGGGTAAGCAACAAAGGGGCAAGAAAATTCAAGAGGAAGCACAAGTAGACAAATCTAAAAATGGACAGGGTAAGGGAGGAAACATTTAA
141	yes	ATGAGTAGTACTAGGGGCATAATGAAGAAGCAGATACTGGAAGACTTCTTGAAAGAACTTGATGTGTTTGAAGAGAAGAAAATTGAGACAAAGGGGACAAAGTTCCATAAAGCAAAAGATTGGAAAAGGACATTGGGATGTAAGTTTTATGAGGAAAGGCACAATGCTAGTAATAGCAGTGGTGAAGGAATGGATTTGTTATGGGAAAAGTACGAAATCGACTCTATAAAGAAAGAAAATAGAGATAATAAAAAGAATAAGAAGATGAAGAAAAAAGAAGAGGTGAAGAGCTATGTAAAAGTAGAACAGATAAATGAGCACATTGATCAGTTGTGTTGCTTGCAGGCACTAAAGTTGTCAGCTAGGAAAATGAATTTGGGGATTGGAAGGTCTAATTTTGTGAGGATTTCGAAGGCAATTAAAGGGCTTAAATGGATACACCATGTGAGCAAGAATAACAAGAAGGTTCATTGTGGAGATTGA

142	NO	ATGGTGTTGTCTTGGTTGCTGAACTCTCTATCCAAGGAGATATCTGGAAGTGTCATATATTCGAAGACTGCACGGGACCTCTGGGCAGATCTGGAGGCACGTTTTGGCCAAACAAATGGGGCTGAACTCTATCACCTACAAAAGGAGCTAAGCGACTTAGTTCAAGGATCAAGTGACATAGCAGGATATTTCACCAAATTCAAAAGACTGTGTGATGAATTGGAGACTCTAAATGCTGATGTTAACTGTGGATGCACTTGCTCTTGTGGAGCTGTTAGAGGAAACATTCTGATGCTAGCACCTCTTCCTAGTGTTAGTCATGCTTATTCTCTATTAATTCAAGATGAGAAACAAAGGAGGTATATGTTAACAATCAATATCCAGGAGACTCCTCTTCTTTTTTAGCTGCTAAATCTCAGAGCAAGTATTCAGGAAACTCTTATTCTTATCCAACAGCTAGTTATCCGAATAACACATCAAAATTTGAAAACTATGACTGCAAAGAAAAAGCAAAATCTGTTAATCACCTAAGGAGAAACAGTTTTGCTTGCTCTCATTGTAAGAAGATTGGACACTCTATTGATCAGTGTTACAGGATTGTGGGGTTTCCCCCTGACTTCAAATTCACAAAACCAAAGAGGCAACAAGGTGGTGCACAAAGTCATGCAGCATTGGCAGACGGAATTTCTGGACAGTCTATGGATGATGGACATGGTGTTGGGACTCAACATCTCTCACAGGAGCAGTTCACACAGCTTATCCAACTCCTGAATCATGTTAAGGAGAACAAATCAACAAACACACCAATATCAGAGGCCACTGCTAATTCTGTTGCTTATGCTGGTATAACTGACCCTTTTCATCATTGCATTTCCTGCATTCATAATAGGACTGCTTGTTTGACTCACATTAAATCCAACTCCTGGATCTTAGATTCAGGAGCCTCGGAGCATATGGCTTTTGACATCACAATTTTTTCTAATCTTACACCTTTGTGTATGCCTTTAACTGTGAATTTGCCAAACTCACAACAGGTAAAGGATATTGTGGAACTTCCAATTGATCACAAAGCATTACCTTGTAAATGGGTCTACAAGGTAAAGCATAATTCTGATGGTGGAAATGAAAGACTCAAAGACCGATTGGTTATAAGAGGGGATACACAACGTGCAGAGATTGATTTTCATAAAACATTTTCTCCGGTGGTAAAGATGACTACCATTCGTTGCTTATTTACTGTGGCTGTCAAGAATGATTGGAGAGTTTATCAACTAGACGTAAATAATGCTTTTTTACATGGAACCTTACAAGAGGAAGTATATATGAAGTTTCCACCTGGTATGGAACCTCCTCACCCCAAACTGGTCTGTCGTCTAAAGAAATCACTTTATGGGCTGCGACAGGCATCCCGACAGTGGTATGCCAGATTGACTGTTGCTCTTAATTTCAAAGGATATACATCTTCACTCAACGATTATTATCTCTTTTATAAAAAGGTAGGGACTTCTGTTTCTATCGTCGCAGTCTACGTCGATGACATATTGTTAACTGGGAATGATCCCACGGACCTACATACCCTTAAACAATTTCTTGATCATGAATTCAAAATTAAAGATCTCGGGGAGGTTCACTATTTCTTGGGAATGGAAGTCCTTCAAGAGTCTCAAGGACTGATTTTGAGCCAACGGAAGTTTACTTCTGATTTGCTTGCTGAATTTGATACTCCTGAGTCTCCATCTGTTTCTTCTCCTCTTGATCCGTCCCAAAAACTTCGAGCAGATGAAGGGGAGCTTCTTGCTGATCCTAGTGTATATCGACGTCTCATGGTAAAATTGAACTTTCTTACCCATACTCGTCCAGATCTCTCTTTCCCAGTGCAACATCTCAGCCAATATATGCAAAATCCTCGTTTGCCTTGCTTTTTGTGA
143	NO	ATGTCATCCTCAGCACCAACTCCTGACTTGCGCAGATCTCAAAGGGATCACAACCAGCCTAAGTATCTTTCAGATTACTTTTGTCATAATGCATTTTCAGTCATGTCTCCTAATCCCCCTGTTTATCCTTTTTATTCTTCTTCTTTCTCTGCTTTAACTACCTCCAATCACCAATTGGTTACTTCCGTTTGTCAAATTCAAGAACCTGCTTCTTTTTTTCAAGCCGCAATGCATCCTGGTTGGCAGTCTGCTATGGATACTGAGTTTAAAGCATTTGATTCCAACAAAACTTGGGACATCGTACCTCTATCCCCTGGAAAAATTGCATTGCCCTGCAAATGGGTATACAAAGTTAAGCATAAGTCAGATGGTACACTTGAAAGATTAAAGGCACGTTTGGTTATAAGAGGTGATGTTCAACGTGAGGGCGTTGATTATACGGAAACTTTTTCTCCAGTTGTAAAAATGACTACTATCCGTTGTTTATTGGCCATTGCTATCAAGAAGGGTTGGAAATTGTATCAGTTGGATGTTAATAATGCATTTCTTCATGGGGACTTGGATGAAGAAGTATACATGCGTTTGCCTCCTGGTCTTTTTGCTTTATCTCTATCTCATGTTTGTCGGCTTCGTAAATCTTTGTATGGCCTTAAACAAGCCTCTCATCAATAG

144	yes		ATGCCATGTTCAGCATGCAAGCTGCTTCGTAGGCGTTGCACTAAAGATTGCATTTTCTTGCCTCATTTTCCACCTGCTGAACCACATAAATTTATTGTTGTTCATCGTATTTTTGGTGCTAGCAACATCACCAAAATGTTACAAGAGATACCAATGGATAATAGAGAAGATGCAGTAATCAGCATGGTTTATGAAGCTACAGCAAGACTCAGAGATCCAGTTTATGGCAGTGTAGGCATTATTTCTGCCCTCCAGAAACACATATTTCACTTGCAATCCGAGTTAAACAAAGCTTCAGCTGAAGCAATGTCTCTCAGAACACAATTATCCAATGCTTCAACATCCTTACCCTCATCGTTACTGGAAGTTTCTCCATTCACTCCCGAGAACCACGAGTTTCACCATTCCCAGAAGTCGAGCCAGCAAAATGCATATTCTAATAATGACTTGCAGCTTCTACTTCCAGAAGCAGCAGACTATTGTTTCCAAGAAACTGATCAAGTTCTTCCACTGCCTTACTAG
145	NO		ATGTGGTGTGGGCACCCATCCTTCCAACCTCTTGTCCAACTTTGTTTTGACAACCAAGATACCCTCAATGGGGTCATAAACCTCTTCCCAAAAGAGGCCACCACTTGGAATGCCTCTACCTTTGGGAACATTTTCAGAAATATTAGAAAGATTCTGGCAAGACTAGATGGGATCCAGAGATTCCCCAGCTACCACAATAGCACCTTCCTTCAGGAATTAGAGTCTAGTCTCCTCAAAGACTATGACCAACTCTTAGCTACTGAAAAAGAATTCTGGAAAACCAAGTCTAGGATAAATTGTCTTAGTGATGGTGATGTAAATACCAGCTTCTTCCACACTTCCACAATCAATAGAAGGAGAAGAAATTACATTACCTCCATAAAGGATGATTCTGGAAACCTAATAGAGGACCAAAACCAACTCATGAATCATATTTTCAGCTTTTTCAAAACCCTCTACACCACTAACCACCACCACTCCAGCAGAAATAAACCCAATGCTGGGGACCAGGAGCACTTCATCTCTAAAGAAGTGTCCAACAACATGGACTCCCCCTTAGAGATAGTGAGATCATCAATGCCCTCAAGTCCTTCCATCCCCTCAAAGCTCCAGGCCCTGATGATCTGCACCACATGTTCTACCAAAAGTACTGGAACATTGTTGGTAGCAAGACCACAACTTTCTGCAAAATGGCCTTTGATCAGTCCCACATGCCTGACCAAAATAACACCACCCTCTTGTGCATCATCCCAATATGCCCTAACTCTCATACTCTCAAAAGCTACAGGCCCATTAACATGTGCAATACCAATTACAAACTTGTCACAAAAATCATTGTGA
146	NO	GO:0003723; RNA binding; Molecular Function;GO:0003964; RNA-directed DNA polymerase activity; Molecular Function;GO:0006278; RNA-dependent DNA replication; Biological Process;	ATGGGAAGAATTCCAAATGAAGCTGAGGTTAAAGAAGTGGTATTTGGATTGAATGGTGATAGTACAAGTGGGCCTGATGATTTCTCAGGAATGTTCTTTCAAGCAAGTTGGGAGATAATAAGGAAAGACATCACAACAATGGTACAATATTTTTTTTGTGGGCAACAACTCCCAAGATACATAACACACACTAATGTGGTACTACTACCCAAAAAAGAGAAGGTATCTTCATTCACAGATCTAAGACCAGTGAGTCTATGCACTTTTGCCAATAAAATTATTTCAAAAGTGGTACATGGGAGAATAGCAAGATTGCTTCCAAATATTATTTCACAAAACCAATCTAGATTTTTAAAAGGGAGAAGTATTACGAAAAATTTACTATTGGCTCAGGAAATAATTAGGGAAATTAATTTGAGAAGAAAGTATCACAATGTGGTGGTAAAGTTAGATATGGCAAAAGCTTGTGATAGGGTATCCTGGGTCTTCCTTATAAAGGTAATGAGAAGATTTGGATTCTCAGAATTCATCATGGATATAGTTTGGAGGTTGATTTCCAATAATTGGTACTCAATTTTGGTGAATGGGAGGGCTTTTGATTTTTTTCAATCTACAAGGGGATTAAAATAA

147	NO	ATGACAATAGTAGCCTACTGCCCACAGGAGATGAAAAGAAAAGGAAGGGATTGCAGGAGCAAGCAGGGATTGCAGGAGCAAGCAACATCACTCAACTTAATGATGGACTTTATCATATGGAACGCGAGGGGAGTGAATAATGCGAGCTTTAGGCGACAGTGTGGAGCAATAGTGAACATTCACAAGCCCGCATTGCTCGTTCTACAGGAAACAAAAATGACTAAGCACCAAAGCCTCACAGAAGAGCTCAAGTTTGACTCTCAAATCCAATCTACTGCTAATGGCCTTTCCGGAGGGATAGTGATAATGTGGAATGAAGACACCCTGAAGCTTGAGAACCTGTCAATAACCCCCCAAGGAATCCATGTCACCATCAAGGTGGAGACTTCATTGAAGTCCTACATGCCAATGATAAATTAG
148	yes	ATGAAAGTGGAAATTCTTTCATGGAATGTAAGGGGCTTAAATTGGGAGAGTAGGAGGGAGCTTGTGAGGATGCTGCTGAAGCAATGGGGGGCTGATAGACTAATTTTGGGAGGGGGAATTGTATTTGAATGGGAACCAAAGCTTAACTGGAAGAGTCTCTGGGTTAATGATGGTTTCAGCTGGTTAGTCACTGCAGTATACGCAGATTGCAATAGAGGGAGTAGGAGTGCTCTGGCAGGAACTTCTTGA
149	NO	ATGAAGATTACCCCAACCTCATCTAGTGGCATCCAGTTGATCAAGGCAGATTACTTGAGGGATGACACGATAAGGAGAAAGTTGCAACCGACTGACAACACTATGGTAGTTGATGCGACTACCTTGGAGCCTAACATTGTGCATCAGACTGCTACAATGGATCTTTCTGGTATTGGAACTTCTTCAACTGCTACATCTGTTGTACATCCCTCTATATCCCAGCCCCCACTTACACATACCTTAATTCGTTGGATGGATGGCCTTGTCCAATCAGAGGACATTAGAGCTTCTCATCTTGAGAAAAAGTGCACATATATGATTGATACAACCATTGAGGAAGCTCTTGTCACTTTGTGGCCGAGATGGAATATCACCATTCCCTATTTTTTTATTTTGGATGCTCTGAACACTGATGCCCAAGTTGATGTTGTGGTCATTGAGCAACAATGCTAG
150	NO	ATGGTGGCACGGGAAATAAGAGGTCAAGTAGCTGAACTCCATCTAGGAGGGCTGGCAAGCAAGCAGTGGAGCACCACAAAGAAGAGTGGTTTAAGTGTCCAAAGGAGGCCAAGTATCTCGGTGATGAATATGTCAATGAGGTGGGATAGGAGCAAAGACACCGGTAGACATGCCACTCTCCATTATGCTAATCTAAACCAAGTTGAGAGGGTGTGGTTTAAGATTGTGAGCACTATTATATTGCCCTGTAAGTACACCTCTGAGGTTACTAGGGACTTGGTTGTCCTAGTATACATGTTAATGAAGGGTATGCCAATAAATGTGGGGACTGTGCTGAGATGA
151	yes	ATTAAGGGAACAAAGCAGTCAAAGAAGAAGAAGAATTTTGACAGACGCCAAAATTTCCCCAACCCAAAGAAAGCTACGGCTAGACTTCTTAAGCAGGAAAAGAAAGAGGAGTGGCAATGGATTGCAGAAGAGAGAAAAGCTCATGAACAACCCATACTACAGTTCATTCAAGGTTATGATGAACCAGATTCTCCCATACTAGCGTTCATTCAAGGAGGTGATGAAGTGGAATATGGTGAAGACCTGGAGTATGAAAGCGAGGACTATCACTCTGAGGTGGAAGAGCCACTTAACAATATTGCAGTATAA
152	NO	ATGGCTAATACTTCACACTCCCAAGCAGTTGATGCGGCGGCTCCGATCGGCACCCCGCTCGTCCCCTTCATGCGGCATAAACCGGCTTCGGTTGAGATGCCTCGTTTCCATGGTGATAATCCCGAGAGTTGGGTCTTTCAGGCAGAAAGGTATTTCGATTTTTATAATATTTCTGAGGATCATAAACTATCTCTCGCTTCATGCTATTTGGATGGCGAGGCTCGTGAATGGTATCGTTGGTTATTCCGGAACAAGCAATTGAGTGATTGGACTTATTTTGCTTTGAAAGTGACAAGTAGATTTCTTAAGCGTACCTTGCTTCCTGCGGAGGTACGTTTGTCCAAACTCCAGCAGACTTCCACCGTCGTCGATTTTCAGACTGGGTTTGAGTCTATTGCTAATGAGACTAATGATGTCCCTGAGTCGTGGTTGGTTTCGGTGTTCACTTCTGGCCTCCGAGCAGATATTCAAACTGCAGTTCTGGTCCATAAACCCAAAACATTAGATGAGGCTTTTGAATTAGCCCATACTCATGAACAACGCCTCTTGTTTGAGCGGGGTGGGCCTTTTAAACCAGCCTTCACAAATTCCCTTCCTCTATTGCCAAACCCTAATTTTCATCCACATAATGTTATCCGCAATCGCCTTCCAATTAAACGCCTCTCCCTGGTGGAGATCCAGCAACGCCGTGAAGAAGGGTTATGCTTCTGTTGTGATGAAAAGTACTCTACTTGTCATAAATGTAAAGCTCCACCACAATTGTTGTTGCTTGAATACGAAACATAG

153	yes	GO:0003723; RNA binding; Molecular Function;GO:0003964; RNA-directed DNA polymerase activity; Molecular Function;GO:0006278; RNA-dependent DNA replication; Biological Process;	ATGGATGAAGATGGTGAATGGATTGAAGGAAATGACGGGATTGCAGAGGCAGCAGTGAGACATTTTGAAAATGCTTTCAGACAGGAAACTCATATCTCCAACCTGGATGCTTTAAACCATATTGGAAGAATGGTGACTGAAGCGGATAACAAAAGGCTTACCGCCATCCCCACTATGCAAGAAATTAGGGACAGTGTCTTCTCAATTGACAATGAAAGTGCACCTGGTCTGGATGGGTTGAATGGTTGCTTTTACCAAGCTACATGGAGTATTATAAGCAATGATCTTTCTAGAGCTACTGAGGCTTTCTTCAATGGAGCTAAGCTTCCAAAGTTTTTACTCACACTTGTTTGGTAATGATTCCTAAAATAGAGAACCCTCATAAGTTCTCTGACCTTAGACCAATCAGTCTGTGTAATGTCTCCACCAAAATCATCTCCAAGATCATCAATTCTAGACTAGCTGGTAGTTTGCCTATGATCATTTCTCAAAGCGAGTCAGGATTCATCAAGGGAAGGTCTATCTCAGAGAATATAATGCTAGCTCAGGAGATTATTAACGATATCAAGAAGCCTACTAGAGGTGGGAACATTGTTATAAAGTTAGACATGACAAAAGTTTACGACAGAGTATCGTGGGAGTACTTGTGCTTAATTTTGAAAAAGTTTGGCTTCTCAGATTGGTGGGTTCACATTACCAACAACTACATTCCAACAATTGGTACTCAGTCATACTGA
154	yes		ATGGAAGATAGGGAAATAAACAGTCAAAGGAACATGGACATGGAGAATGTTGAGGTATCAAGTTCTTCAGTAGAGCATTATAAAATGCATGGAGATAAGCAAGACGAAGAGAGGCAAGAAACTCATTCAGATGAAGTACCCGCTGGTTCTACAGATTTGAATAGTACAAGACTAGAGAAACATGGAGAGATTAAGGGGGTTGATTGTGCAACAGTTTTAAATCCTGATGAAGATCAGATTTACAATGCTGCAAATATCTCTCCAAGGGCGATGGCGGTTGTTAAGTCAGCAAGAAAGGGCAAGAAACGGGATGATGGAGAACCACCTCAAACTCTTAGAGTTCAACCAAGAAAACAGGTTATATCCCAATAA
155	yes		ATGGCTTGGATTTCACTCCCGAATCTAAAACCCACGTTTTTTGTTAAGGAATCATTATTCTCATTAGCCAAGGCAGTGGGAAAACCTATTCATCTTGACACGGCTACCATAAATAAGACAACACCTAGTTGTGCTAGTATAAATGTACAGGTAGATTTATGTGCTGAGTTGCCATCATATGTTGAAATGGAGATTGTTAATGAGGAAACTAAGAAATCGTGGGTGGAGAAAGTGAAGGTTCAGTATGATATGCTACCCAAATACTGTGGAAATTGCAAGCTACAGGGACATAATGCTTCTGAGTGTAGAGTCTTGCCTCTAGAATTGCAGCAAGTGTACAAGGAGAATAGGGATAAAGAACTAGAAAGGGGAGACGATAAGGAGGAAGGAGAGTTAGAAGACACAGCAACAAGGGGCAGAGGAGATCGAACAAATTTGCCTAGACAAAATTGGAATCCAACAAGGAGAAGATTTATCAAGGAACCAAACAAAATACAAACACAAGTGTCATTTACACTGGAGAAAAATCTTTGTACTAGTAACTCCTTTGACTTACTGGCAGTTGAAGATGAAAGGAACGGGAATATGGACGATAATTCTAACAATATTACATCAGTGGTTAACACTGGGGGAGGGAATAAGGAGATAACAACAAAGGACTGGGTATCCAAGTCTTTTCTTCATCCTCAAGGTGAAGGTAGGACGTATGGTGTAAAGACAAGTCATGCAAAACAACAGCAAGAGGAAGAGATTGCAAAGACAGAACATTAG

156	yes	ATGGTTAAGCCTGACAAATTTTCTCCTAGAGCTGAAGTATGTGTCTTAATGGTATATTCTGCAAATCAAAAGGGTTATTTTCTGGACAGCATGTCCCAAAAGAAGTTTATAGTGAACAGGGATGTTGTGTTTAGAGAAGATGTATTTCCTTTTCACCAGAAGACTAATGCACAACAGCATATGCAGCCAGTGTTCACAGAAGGTGTTTCTCATAATGTTGCTCTTGTGCCTGAAGACAATGAGGACATGCATGTTATTAGAGAGGACACAATCATGGCAGATAACTTGACAAGACAAGATGGAAATCCTTGTGAGGAGAGTGACAATACAGATGCAGTCAATGAAGATATCAATGATACTGATACTACTGAAAGGGTTGATAATGCTCTTGAAAGGACAGAGGTCATAAGTGACATTGCAGCACAAGAAGCTCAAGGACCTAGACACTCTTCTAGGACCTCTCATCCTCCCATATGGATGAAAGATTATGTCACTCATGGATCTAAATCACATCCTTATTCCCAAAGCAATTATGTTTCCTATAGTGGAGTAGCTCCTCAATATAGAGCTTATTTGCCCAAGTTTTCTACAGAAGTTGAGCCCAGAAACTATGAAGAAGCAGTAAAGGATACAAGATGGGTGAATGCTATGCAACAGGAGATTCAGGCCTTGGAGGAAAATGGAACCTGGGAGCTTGTCACCTTGCCAGCAGGGAAGACAACTATAGGGTGCAAATGGGTATTCAAAATCAAGTATAAAGCTGATGGTGTAATTGACAGGTTTAAGGCCAGGTTAGTTGCAAAAGGTTACAGCCAAACTGATCGAGGGGATTGA
157	NO	ATGACTAATCAATTTGCAGCTCTAGCAGAACACGAAGAAGAAAATATTGATGAAAGTAAGGGTAAAGCTCTCACAGATAATAACAATGGGGAGAAGATAATCGAGGAGTCAACAAAGAGTTGGGTGAAAGACACTTTCAGTCACACCAAGGATCAAGAGGAAGACAAGAGTGGATTACAAACAGGGAGGACAGGAACACTTGAAAAAGAAAATGCACCCACATCACAGACAGATGGAAAGGAAAATAAAGAAGTGGAGGATGAAGGTATCTCGAACAAGGAGAATGTTTCAAGACAAGAGATGGGAGACTCAAGTCCATCACAAAGTAATAATAAGGAGAGAACACCTAATACGAATCCTGGCAAAGAACATGAAATCCCAGACCTTGAAGAACTAACAGAGGTAGAAAAAGAAGTAAGGAGAGAAAATGAGGAAGATGAAGATCTTGAAGAAAACATGAATAGTGCAGCAAGGAATGAGGATTATCACCCAGGCAGATAG
158	NO	ATGATTTCCTTAGGTTGTACTTTGATTATTGGAAGGAGGCGGGTTGCTGACTTCTGTGGGATTTTCAACAAGGCAATTAACACAATAAGAGGGTGGTATATTAAATTTATATCTATGGGAGGAAGAGCTACCCTCATTAGACATTTGCTTCTTGTTATTCCTATTCATATCTTGGCGGCAGCCAGCCATCCCAAAGGTACAATTGATCAGATAGAAAAGAAGGTGGACAAGAATATATATTGGAAGGTTGGGAAAGAGGAAGTGGCCTTTTGGCATGATAACTGGTCCTACCTTGGTCCTCTATCCTCGTGGGATCATGTGAACACTGCCCATGATTTGACTAAATCGAATGAAGTTCTGACGAGTGGTACTAGCTTGGAGGTGGGAGAACCTGAGCATCCAACCTTCGGGTGA
159	NO	ATGGTAGAAATAGCTGATCTTGGAGCCATTGCAAAGGATAGAGATGAATGTGGTGGTGATGTGGGACATGATGAGTTTGGTGAGCTTGGGGGGGGAGGGAGTTTACCATTCCAGTCCATCGAAGTGGGAGGTGTACTCTTGGACTATGATGACACTGTTAGAGGCCCTCCTCTTAGAGAGAAAGCTAGCTTGGATGGGTCCAATGATAGTAAGGAGGTAGGGCTTAGTTATATTGGCAATGATATTGGTAACAATTTTGTAACCAATATTACACAGGACAATAGGCCTAAAGTTCTTCAATGTAGTAGCATTCTGACATTTAAGGATTAG
160	yes	ATGGATGTAGGCCATGGTTTCCTTTATATAGGACCATTCAAGTCTATCAAAAGCCTTTTCAAGATCAATTTTGAGAATCATGTTAGGGCTCTTTTCCTTCATTTTCCCAAAATAGGAAATGTCCTTATGTACAATGATTGCATTGTCAGAGGCCCTCCTATTGGAAAGAAAGCTTGCTTGGCTTGGGCCTATGATGTTGGGGATGAGAGGCTTAATGCGATTCACAACGATCTCTGTTACCTATTTGTAACAGGTATAGAGGATTGCACAAAAGCTTCCTTGGCAAAACATGTGATGGAGGCTATCTGGTCTTGGAGCTTTGAACGGCTTGAAGAACTTGAGAGCAGTGGTGATCTATGTGTCCCTATGGGGGCATCCAGCCTTTAG

161	NO	ATGGGAGTGACAGAAGCCCTAGATTTAATTGGGATGTTATCAGACTCACTTCTCGTCAAAATTCTCTCCCTTTTGCCGGCACAAATTGCTTTGACAACAACTATTCTCTCTAAGTGGTGGCACTATGTCTTGCCTTATGTTGATAGCTTCAATTTTACTCGTAAAATTTTTCTGAAAATAAAAGACTTTGTATTCTTTGTAGAGTATGTAAATATAGTTCATTCCTTTTGTTCCAAAATAAAAAGACTTAGAGATCACTGCAGTCACTTGTATCCATACAAATCACATGTTAGTCGATGGCTTAGTTTTGCTATTGAAAAAAATGTGTAA
162	yes	ATGGTGTCTGAAAATGCGCAAACATCTACCAGCAGTGGAATTCAGGTGACACAAACAGTTGATCTTAATCATCCCCTGCATTTACATACATCTTATTTGAGTGGTGTTTCCTTGATTTCTCTTCAATTGACTGGAACAGAGAATTACTCTATTTGGAGTAGATTTATGCGCATAGCTTTGTTAAGAAGAAACAAGCTAGGGTTCATAGATGGTACATGTAAGAAAGAGAAATTTGGAGAAGAATTATGGGCTCAATGGGGGAGGGCTAATGATGTAGTGTTATCGTGGTTGATGAAAGTTGTGTCTAATAGTCTGTTAAGTGGTATTGTTTATGCATCTAATGCATATGTTGTGTGGGAAGAATTGAAAGAAAGATTTGATAAGGTCAATGGTGCAAGAACTTTCAATCTCCACAAAGAAATTACGTCTTTAACTCAGGGAACTTCATCTGTTTCGACCTATTTTACCAAGCTTAAAGGGTTATGGAATGAGCTTAAATCTCTTGTCCCTACTCTTGGGTGTGAGTGTGAAAAATCCAGGGATTTCTTGATTTATCTGTAA
163	NO	ATGGCTAAGGAGTTGTCGAAGCTCCGTTCCGCTTTCGATAACCAACACAAACTGATGCAGGAGGTCTTCTCTCAGGTGGCCTCAATTGGTTCACAGTTGAAAAGTTCCGGCACGAAAACCTCTCGTTCAAAATCAACCGATGTTGCTCTGACGGCAAACCCTCATGGTGGTGTGCCCATCGCACTCTGGCACAAACCGGCGTCGGTGGAGTTGAGTCGGTTCTCCGGGGACTAG
164	yes	ATGGTTGTCATTCATCCTTATTTCTACAGGATGGATGATCTGCAGGAGCAGAGGACCAAACTTTCTCATGACGTGATGATAGACATCTTGAAGCGACTGCCGGCAACATCCCTGATAAGATTCAAGTGTGTATCTAAAGATTGGTACTCTTTGATAAACAGCCCTGATTTTATCTCTATCCATTACAATTATGATTCTCTCTCAAATCACTTCATATTTTTTAAGCGCTACCTCAGGATTGAGGAAAGTACGGACTCCATTTATTATAATGGTACAAATATGCTATCCTTTCATTCAAATGATGAATCTTTCAAATTCATAGCGCCAAATATAGAGTACTCGGATAATTATGTAGGTGTTAACATTGCAGGTCCCTGCAATGGCATAATCTGCATTTCTAGCTACAGAAGTATTCTTTTATATAATCCAACCTTAAGAGAATTTTGGGAACTTCCGCCTAGTATTCTACCTCCTCCCCCATACATATCTACTGATTCTAAAAAGCTTAGCTATCATATGACCATGAACATGGGAATCGGGTTTGATTCTAACACTAATGATTATAAGATTGTTAGAATCCTAAATTCCAGTTATGAACATGAATGTGATGAGTTTGATAATTATAACAAGTATGTTAGTACGGTAGAGGTCTATCGTTTAAGTACAAATTGTTGGAGGAAAATTGAGGATCTAGAATGCATAGTAGATTCCTTTCATTTTTCTCACGTACTGTTTAACGGAGCTTTTCATTGGGTTGGATATACGGAGTCAGATGATTATTGCATCGTTTCTTTCGACTTCAGCACCGAGTCATTCAAACAAATACCCTCTCCTGAGGGCTTATTTAGTGACGGAAGAAAGAGTCCTAATCCTTTCGTCTTGAAGCAAACTCTAACTCTGATTTGTTTTACAGAGATTCACTATCCTCCAGAGGAGGTATTTCACCAATCAATTGATATATGGGTGATGAAAATATATGGTGTGAGGAATTCCTGGATTAAGGAATTTACTGTTGGACCATTGCTTATAAAAGCACCTTTGTCAGTTTGGATGAATGACACGGAACTAATGATGGAAAGTTACAATGGAAAACTGGTCTCTTGTAATCTCCTTTTGCAAGAAACTAAGGACCTTGATATGTATGGTGTTCCCCAGACATTGGAAGCTATTGTTTGCAAAGAGAGCTTGGTTTCCATCAAGAAAGAGAGAGAGAGAAATAGTCCTGATCTAACACCACTGTCATACATGGCATATTGA
165	yes	ATGTGGAAAACGGGATATGGTGGGACACAAGTCTGGGAGAAGATGCTTCAAGCAAGGGATCAGGTGGAGCATCAAATTTGGTGGCAAACGAAAAATGGCACAGCCAGTTTATGGCATGATAATTGGATAGGAATAGGAGATTTATACACAATTTGTGGGCAAAGATATGAATGGGATACTAATCAACAACTTATCCAAGAAGCGGTAAGACATGGAGAGTGGGATGTATAG

166	yes		ATGAGGAGTCGCCACACTTTGATTGAAAAGATGTTGAGTTCTCTAGATAATTTGAAGGGGTGGCATGCCCTATTATTGACAGATGTTACGCCCCCGTGGATTAAAAAGGGAGTGATTATTAAAAAGAAGGGCTTCAACATAGTTGAGAGGGCATCTAAAACTAGGGGCGATCATTGGGCCGATGATAACCTTGAGGGCAAGCAAAATCAAACTTCATTGCCTTTTCTTGGGTTGATCACTTCTTTGTGTCGTAAAGTAGAGGCCAAGTACTCTACGGATAAGGACAATCGAAATAAGAAGGCGCCAGTTGACGTTTGTCCCGTGGTTGAAATAGAGTCTCTACGGGCTGATCTTGTAGGCCCCGCTCCGACTGTTGAAGCTTTAGAGCGCAAGAAGGCCGAGAGTAGTTCAGATGAGTTGATTGCCTTAAAGGCTAATGTTATTAGGTTGAGAAAGGACGTGGATGAGCTGAACTCCACCGATATATATATGTTGTGGAGAGATGTTACCATCCCCGAGGGTCCTGTGACTGAGATTCCTCCGGCCATTGTGACTAGTAGTGTTGGGCGTACAATTGTTGTTGAGCATGCAGTTGATGATGACAACTCCAAGACTTTCGAGAGTAATGTTGAGGACTTAGATGTGACTGACATATAG
167	NO	GO:0003723; RNA binding; Molecular Function;GO:0003964; RNA-directed DNA polymerase activity; Molecular Function;GO:0006278; RNA-dependent DNA replication; Biological Process;	ATGACAAGCCTGAGAGCTGAGATACAACAGTTAGCCAATATAGAAGAGATTTCATGGAGGCAAAAATCTAGGTGCCTCTGGCTCAAGGAAGGGGATAGGAACACCAAATACTTTCAGAAGATTGCTAATTCTAATAGAAAATCCAATTGCATAGACAGATTTCTGGTAGACAATGTGGTCATTAAAGATAATGAGACAATTAAAAAGAAGACACTAGAGTTCTTTGAAGGAGTGTACATTGAACAAGAAGAGTGGAGGCCTACAATCATGTTTGAAGGAATTGTCTCCATCACAGCGGAGAAAAGCAGTAACTTAGAAGCAATTTTTGGAGAGAAGGAAGTACTAGCAACCATTAAATCAAGTGCCCCTGACAAAGCCCCCGGGCGTACTGATTTTACTATGGCTTTCTTCAAGAGCTCTTGGGAGTTTATCAAGATAGATCTATTAGCAGTTATGCAACACTACCATCAACATTGCTGGATAGTTAAGTCTTGTAATGTTTCATTCATACCACTTATTCCTAAGAAAAATGGGGCAAGCGAACTTAGGGATTACAGACCTATTAGTTTGATTGGAAGCATGTACAAGATCATTGCAAAAGTCCTCGCAAATAGATTGAAGACAGTTATGGGGAAACTAGTCTCAAACCAACAAAATGCCTTTATCAAATGGAGACAAATCATTGATGCCTTACTCAAGAGTGTGATATATCATGTTAATGGGGTGCAGAACATTGAGAAGCTGGCAGACATATTGAGTTGTAGAAATGGAATTTTCCCAATCACTTACTTAGGCCTTCTATTGAGGGCTAAATACAAGCGGAAAGCATCTGGAGTGGAATGA
168	yes		ATGCCAGCACAACAAGCCCTGGCTATGGACCCACTATTCTCATATTACTCTCATTTAGGCTTATCAACAGTGGAACAACGAGATACAAGAAAGAGGTCATTCAAATTCTACAACTTTTTAGGAAAACATCCAGATTTCACGAGTAAGGTACAAGCAAGCTGGCAGACACAAGGTGGAGGTATGAAAGCGGTATGGAAAAATTTGAAGCTAGTGAGGAGAGAATTGCAGAATTTAAACCATAAGGAATTTATGGGTGTCTCTAATAAAGTCCAGCTTAGAAGAGAACTCATAGATAAAGAAAGCAACATGAGGGTTGTTCCAGTACCTCAAAGCATTCTTGATGAAAAGAAAGCACTGAGAATAGAGTTGGACATATGGAGTTTGATTGAAGAGGGCATATATAAACAAAAATTCAGAATACAATGGCTCAAGCTAGCTGATGCTAACACTACCTATTTCTTTACTAGTATAAAAGGAAGGAAGTCCCATAATCAGATCATTATGCTAACCAAAGAGCATGGCACTCTCATTAGAGAACCATCATTAATCACCAAGGAAGATGTGGAATTTTACAAAAAGTTACTAGGACAAACCACCGCTCATATGCCAGTTACACAACCAGAAGTGCTTAAAGTTGGACCTGTCCTTATAAGATCACAATAA

169	yes	ATGAATGCAAGACAAGCTCAAACTCTGCGTGTATTCGATTGCCTTACGCCCAACACCATTTTAAGCCTCATTTCAAGATCATCATCGCTCTCCCAAACGCAGCAAGTTCATGCTCATATTCTCAAAACTGGCCATTCCAATGATACCCATTTCACCAACAAGCTCCTTTCCCTCTACGCCAACTTCAACTGCTTTGCTAATGCAGAATCTCTTCTTCACTCGCTTCCCAACCCCAATAGCTTCTCTTTCAAATCTCTCATTCACGCTTCTTCAAAATCTAATCTTTTTAGTTACACCCTTGTTTTATTTTCTCGGTTACTATCAGCGTATATTTTACCTGATGTACATGTACTTCCTAGTGCTATTAAAGCGTGTGCTGGGTTATCGGCGTCGGAAGTTGGGAAACAAGTTCATGGGTATGGTTTAACAACTGGGTTGGCGTTGGATTCTTTTGTTGAAGCTTCTTTAGTTCATATGTATGTGAAATGTGATCAGTTGAAATGTGCACGTAAGGTGTTTGATAAAATGCGTGAGCCGGATGTGGTGTCGTGGAGTGCTTTAACTGGTGGTTATGCGAAGAAAGGGGATGTTGTTAATGCTAAAATGGTGTTTGATGAAGGTGGGAAATTGGGTATTGAGCCGAATCTTGTTTCGTGGAATGGGATGATTGCGGGGTTTAATCAGAGTGGATGTTATTCGGAGGCAGTTTTGATGTTTCAGAGGATGAATTCGGACGGGTTTAGGAGTGATGGGACGAGTATATCGAGTGTTCTTCCTGCAATTAGTGATTTGGAGGATCTCAAGATGGGTGTTCAAGTTCATAGTCATGTGATTAAAATGGGTTTTGAGTCTGATAACTGTATTATCAGCGCGTTAATTGATATGTATGGGAAGTGTAGGTGTACTTCGGAGATGTCACGAGTGTTTGAAGGGGCGGAGGAAATAGATTTGGGTGGTTTTAATGCTTTGGTTGCTGGGCTATCGCGGAATGGCTTTTAA
170	NO	ATGAATCCATCAATACCAAAAGTGGCGCCTAAACCAGTTGTTATGCTACATGGAGAACCTAACATTACGTGGAAATCATCGGAAGTCAGATCGCTAATCTTTCAAGAAAATTTGCAATATGCTATCATAGGCAAGTTTTCGTATGGCAAACCCGCCATAAAGGAATTGAGGAGAACTATACCAGGCCAATATGGAATAAAGAGTGCATGCACCATAGGGGTTCTAAACACAAGGCATGTGTTGATAAGACTGACGACGATGGAAGATTATGTGAATCTTCTATCTACGTCAGCTTTTTATGTTAAGGCCAAGGAGTGTTATTGGCATATGAGAACCCTTAAATGGGATCCATGGTTTGAAACGGATGTGGAAACAACGATTGTAGCAACATGGATATCATTCCCAAATCTACCACCAATTTTTTTTGCAAATGAGGCAATCTTTACAATAGCTAATGCAGTAGGTAAACCGTTGACGGTGGATATGGCGACATAA
171	NO	ATGATTGAAACCCCTAATCCACCATATGAAAGAAGAATTAGAAGCAGAAAAGGCATTCAAAAAGAAGACAGGTCAAGTGTAAATCAGCAGGATCCTAAGGTTCAAGATAAACACCTAAAAATCCCTACTGACACTGGAAATAACAGCAAACGTGGAGAAGTTGAGGTTTCTAAGGACAACGTCACTATGGATGTGGTGGAAAATATGGACCCAGGGAATAAGAGGATAAAGGAAATGAAAACTCAGAGGGACATGGAAACTGAAACTACTAAGGAGCCTATAGTGGATTCAGATAGGAAAGCAACCACGTCAAAGACCACAAACATAACGATGGACAACCAAATGAAGGATGAGTATAAGCACTATGAATCGATGTCAGAGAAGGAGATAAAAGAACAACAATTTCATGATGTTCAGGATCCTAACCAAGACACAGATGCCAACACAGAGTTGGGAAATAACATGAAAAGAACATTGTCGATACGTCCAAAATACAAGAACAATCTCTGA
172	NO	ATGAGAGATGATGAGTTCACTAGCATCCTAGAAGCAAAGGAATTGGAAATCACTCGACTTAGGTCGTGCTTCAAAAGGAAAGATCTGAGGAACCTAGTCCTAGTGCTGATGTATAGGGTGAAATGGACAAATTTCGAGCACAAAATGTCGAATGCCTCGTTGAATGAGGAAGTTAAGTCTTTTACCAAGCAATTATTGCAGGCTCATCCTAAGGCAATAAACCAGATGAATATTCTCATGCAGTCTTTTCCAACAAGCCCTCCATCCTAA

173	yes		ATGGACTGTACTCTGGTGAACAGTGATGATCAACAAATAACTTGTGACATTAGTCATGTAATGTCTCCCCATCATGTTAGGATAACTTTTGTTTATGCAAAATGCAAAGATACCCTCAGAAGACCCCTTTACGATAAAATTCTTCATCAAGACAATACTACTTGGCCCTGGTGCACAGTAGGAGATTTTAATGTTATTACTAATCTAGAAGAGAAGCTTGGTGGTGTCCCCTACAACATGAAAACGAGCTTTGAATTCATAAGCATCATTGAAGCTTGTGGGCAAATGGATTTAGGTTTTAATGGTCAGAAATATACTTGGTCCAACCAAAGAGGTATTAATTTCAAGATTTGGAAAGGACTTGACAGAGCTATGGTTAATAATAAATGGTTAAAGGTCATGCCTTATACCACCATTACTCACTTGCCATCTATGGGGTCTGATCACTCTCCTCTTCTCATGGAATTAATGGAAAAGCAAAACAACCACATCAGGTACTTCAAGTTCCTCAACTGCTGGACAGAACAAAATTCTTTCCTGGACACTATCAAAGAATGTTGGAACAAGAAAATAAAAGGTGATCCTATGTGGAGTTTCCATAAAAAATGA
174	NO	GO:0003723; RNA binding; Molecular Function;GO:0003964; RNA-directed DNA polymerase activity; Molecular Function;GO:0004190; aspartic-type endopeptidase activity; Molecular Function;GO:0006278; RNA-dependent DNA replication; Biological Process;GO:0006508; proteolysis; Biological Process;	ATGGCCGAAGGTACTCATTGGAAGGTCACTTATGACAAGCTAGCTCGACATGATGAACTGTTGACAGATCTGTTGACCTCACAACAGGAGGTACGAAATACACAATTGGGAATTCAAGGCACGCTAGAGTTGATTTTAGAAAGGCTGGGAACATTGGAAAGGGCTCCTGCTGGCCAGAACAATGGAGGAGGACTTTTGCCTACTCCAAACCAAGACAAGAGGAACAGACCTCAACAGGCTATGGTCTTACCTCCTAAATGGGAGCTGCCTAATTTCGAGGGGCATGAACCTAAGGTAGCTATTGAGAAAGCTCGGATGAAAGATATGGCCATTGAGGCTGCAGAAAGGAGAAACAAAGGGGCTACCAGATCTAACCCATCATTAGCACCTGTGGTAGCTAACAAGGCGCCTGTTGTTCCAATTACCAGGAACACCTCTTACAGACTCACTCCTGAGGTCTACGAGTATAGGAAGTCCAATCACCTATGTTTTCGGTGTGGAGAGAAGTATGGACCGGGGCACATTTGTAAGAAGAGGCAGCTGAATTGCCTCATGGGAGTAGTAGAGAGTGAAGTGGAGCTAGATCATTCAGTGGTAGAAGAAGAAAACTCGGAGATAATGATTGAAGGAGTACTAGAACAGGAGATACAACAAGTTGTATGTCTAAATGCCTTAACAGGACACAATAAAGGGGAGAATACAATTTTGGTTGGGGGTACTGTTAAGAAACGACAATTGGCTATATTGATAGATTCAGGCAGTACTCATAGCTTTATTGATGAGCAAACGGTCATAGCGACTGGTTATAATCCAAGTCATTGCCCACCAGTTAGGGTGACAGTGGCAGATGGAAATTATGTCATGTGTACTTCTCAGTGCAAGGGTTTTTTGTGGAAAATGCAAGGTCGATCCTTCCTAGAGGACCTACTAATCATTCATTTGGGTGGTTGCGCCTTGGTGTTAGGGAACGACTGGATGAAGAGACACAATCTTACAAAGTTTGATCACGAAAAGAAATGTGTCACTATAGGCAGGAAGGGAAACAAGTTGGTTTTACCTGGTTTAGCGGATGAGGGCAGGTTAAGCATGATGTCTAGTGGAGCTATGAGCAAAATGTTGAAGAAAGGGCAAGCTCTCGTTGCTCACCTCTTTATGATGAGTCTGGTGACAGCAAATGAAGAAGTGGAAATTGACATTGGGATCCAGGAGGTGCTAGAGAAGTACCCTGAAGTGTTTGCGGAACCAAAATCTCTACCACCTGCTAGAGCTTTTGACCACTCCATACCACTCAAGCCTGGGGCTATGCCACTTAGTTTGAGGCCATACCGATACAACTATCATCAGAAGAATGAGCTGGAGAGACAGGTAAAGGAAATGCTCACTAGTAGGGTAATACAACCAAGCCAATCTCCTTTCTCTTCACCTGCCTTGCTAGTAAAGAAGAAGGATGGGACATGGAGGTTTTGCGTTGACTATAGAGGCCTCAATAATATCACCATTAAAGACAAGTACCCCATTCCTATTGTGAATGATTTGTTAGATGAATTACATGGCGCTTCATTCTTTTCTAAAGTGGATCTTAGGGCAGGTTACCACCAAATTCGAATGAAGGTAGATGATGTTTACAAAACTGCTTTTCGAACCCACATAGGACACTATGAGTTCAAAGTGATGCCTTTTGGACTCACCAATGCACCAGCAACCTTTCAAGCATTGATGAATCAGGTTTTTCAAACCTTTCTTAGGAAGTTTGTTCTAGTTTTCTTTGACGACATACTTATATACAACATGACAAAGGTGGATCACATACAACATCTGAAAGTAGTGTTTGAGACTCTGAAGTCACACTCATTATTTGCTAAGAGGTCTAAATGTTCCTTTGGGCAACCTCAAGTGGAGTATCTAGGGCATATCATCAATAAGGAAGAAGTAGCTACAGATCCTCAAAAGATCAAGGCTATGGTAGATTGGCCTAGACCTAAAACACTCAGGGCTCTCAGGGGGCTTCTAGGTCTAACTGGCTATTACGGGAAATATGTTGAGAACTATGGTACCATGTATAGGCCACTAACAGATTTATTAAAGAAGGAGGCTTTCAAATGGAATCCTGAAGCTGAAATCGCTTTTGACTTAAATCTGCAATGA

175	NO	ATGGAATCACAAACAATCGACAAAGATGAAAATGATAAGGAAGAGAGAAACAGTTCAGGGGCGAAGTATAGTAGGGAAGATGATGAAGATGGGAGAATAAAAGAGATCGTCAGAAATGCATCCGAAGAGATAGATGAACATAAAGAGATTCCGGACCTTCAGGAACTTACAAGAGAAGAGCAACAAGCCAGAAAAGAGGGTGAAAAGGATGAGGAGATAGATGACAACATCGATAAAGTGGCAAGGGAAGGAGATTTATCTCCAAGACAGATTTCTAACTTGAAAAGTGGAGTGAAGAAAGGCAAAACAACTCAACCTTCACTTCCTTTACAAGACAAAACAAGGATCAGGAAGGCATTATTCTGGAATATTAGGTCTGTCAAATCTCAAAAGTCTTTTGAGAGAGTGATGGAACTTAATAGAAGACACCAATACAGTTACATAGCTCTCATGGAACCTTTTCAAGGACCATATGAGTTAGAACTTTACAAAATAAAATTGGGTACAACAAAGGCTTATAGTAATTGCTCAGATAAGATTTGGGTTTTCTTAGAGGAAGATTGGGATGGAGAAGTGATTAAAGACTGTACACAACAAATAACCATGAGGTTAAGAAGAGACAAACTGCAAGTTTTAATCATAGCTGTTTATGGAAGATGTGATGCGATGGAAATGATGGAACTTTGGGAGGAATTTGAGGACATTGCAGAAACAAATCAGTCTCTTTGGATGGTGGGTGGAGATTTCAATGTTATTACAAAGGAGGAAGAAAAACAAGGCGGATTGGTATTTACTCAGGCAGAGGCAATTCATTTCAATCAATGTATTAACAATTGTGCATTGATAGAGATGAAGTATATGGGAAGCAAATTCACCTGGTGGAATGGTAGTATAGAAGATGATTGCATATTTAAACGGTTGGATAGAGTTATGTGCAATCAAGAGCTGCTGGACACTTTTCCTAGTAGTGAAATTCATCACTTGGTGAGACGAGGCTCAGATCATGCTCCGTTACATGTCGTTTGCAATTCGGAGGAGGAAATTAATATAAAGCCGTTCAAATTTCTTAATTTTTGGAGTAAACATCCTAATTTTACGAAAGTAGTTGAGGATAATTGGAAGATAGATTTTATGGGCAGTCCGTTTGTGGAGTTTCAGGTAAAGATGAAAAAGGTTAAAGGGGCATTAGCTAAATGGAGCAAGGAAACTTTTGGGAACATATTCCAACAGATTGCCACTTTAGAAGACGCAATCAGAGTAAAGGAAATTCAATTAGAACTAAATCCCTCAGCAGAAAATAGAGCAACATTAAATAAAGGGGAAGTAGAACTGAAGAAATATTTGTATTTAGAAGGCGAATTCTGGAAACAGAAGGTTGGAATGAGGTGGTTTAAGGATGGCGATAGGAAGTCAAAGGAAGAAGAAGGAGATTACAGATTACAGAAATTCAAACAGATCAAGGGGACTGGATTACCTCTACAGATAATATAG
176	NO	ATGGAACCATTTCAAGATAGACAAGGGCTAGAAGATTATCGAAGAAGGTTAGAGATGCAACATGCTGTTGCAAACTCTAACGGGAAGATATGGGCGTTTATGGATGAGGTAATGGAGTATGAAATAGTGAGAGATGAGGATCAAATGTTAACCCTTAAGTTGCATAATCAAAGTGCTGGAGTGGATGTGATGGTCTCTCTAGTGTATGCTAAGTGCACACGGATTGATAGACTAATCCTGTGGGAGTCTATGTCTGATTTAGCAAGTACAATAAATTTACCATGGATGGTTGGAGGGGACTTCAATGTGATATGTAATGAGGAGGAGAAATTAGGAGGTAGACCTGTTACGGAGGCAGAGGTAAGGGACTTTAACTATTGTATAAATGTATGCAATTTGGAGGATAGGGGCTTTAAAGGTAGCAAATACACTTGGTGGAATGGTAGATTGGAAGAGGAATGCATCTTCAAAAGACTAGACAGGGTACTGGGGGATGAAAAGCTGCAAGATGATTTTTCCGATATTAGAAGTGGAGCATATGGTAAGAAGTGGATCGGATCATACTCCTTTATCGATCACTTTCAAAACCAATACAGAGGAGGTGATTAG
177	yes	ATGAAATTCAGCACAAACAATAGAGCATGCCTTATTACAGCAGTCTATGCACGCTGCAATGCTTTGGAGAGGTTGGAATTGTGGGAACAAATTGAGGACATTGTTCAAGGGACTCTCTTACCTTGGGTGGTTGGCGGAGATTTCAATGCAATTCTCAATGAAGAAGAAAAGTTGGGGTCTTGA

178	NO		ATGAGAAAAAAGGACAGAAGAAATTGTTCACCTTTTGAATCAAGTAGTAAACTTCCTTCTCTAGATGTTCCAGAATATACGCAGTGTTGGTGTGCTAATTACACTCATAAGATTGGAGCTGATGCAAATTTGATAGAAAATAGTCGATGTGATTTGCCTGAGGATATTGCAAATGATCTACATCATCATAAAACTCCAAAAGTGCGGTTGATGACGACAATGAAATCAGATACAATTGTTGCACCTATGGATAAGAGTATCAAGATTTCTCAGAAAAAGAGGAATATGTTTCAAGAAAATGGTCGCAGGTTTGGGATGAATAACATAGATGGTAAATCAGCAAAAAGATCGAAGGCATGTAATCAAAATAAAAAAGTTATGAGGAGTTCTATGAAAAATGTAGTTACTAATTCATGTACAGGAGATAATGGATTTGATGGAGAGAAATTTTGTCTGCAGAGTGGTAGAGAAAGTGTCAATATTAAGCATACAAGTAAAAAGGACTCTGGAGTAAGCAGAAGGAAACATAATCAACAGGCTCAAGTTGTGACTGGATGCTCTCTTCAAATTCTCTTGGAAGGAAAAAACAGTGATCTTGACACTAGTGGATCTGGTGCTAATGTTTTCATTCAATCGTCACATGCTTCTCTAAGTATTGAAAAAGTTCAATGTCATTTGAGGAATAATAATAAATCATTTCATACAAAAAAGCACTCTGATTTGAATAACTTGCTTGAAGATACACATGCCTCTTCTCATAAGAATGCCATTTCTCAACCAGAAAATGAGGAAACATCTCTCCCTGAAAACGAGATAAACCTTAATGAAGTTCAAAATCATTCAAATGTAGCAATACCACAAAGCAATCAACAACCTATGAAGCCGATGGAAACAGGACAATCAACTTATGTACCAACAATGGGTAATTTACAACTTTTCGACAGTATAATTTACAAAATAATTGCAATCATGAAAATCGTAAACGTGGACAAGATTCCCTTGGATCACCTCAAAAAGGAAAGACTATAA
179	yes		ATGTCAAGAGCCTTGAACTCGTTATTGAAGAAGAAGGAGTTCAAAATGTTTAGAATGTCAAGAGGTAGTCCAAAGATTAATCATCTGGCATTTGCAGATGATGTGATCATACTATGCAAAGCAGAACTTGGAACTATGAAACTTATTACGGGAGTATTGGAACAATATGAGAATATGTCAGGGGAGAAGATCAATAAAGAGAAAAATGGGGGAAAGGAAGACACTGGACAAGATGGGCAAACTTATGTCTACCAGTTGAAGAAGGAGGATTGGGTTTCCGAATGCTACATGATGTATCTATGGCACTATTCTGTAAACTGTGGTGGAACTTTAGGACTCAAGAGTCTATGTGAAGTGAATTCATGA
180	yes	GO:0003676; nucleic acid binding; Molecular Function;GO:0003677; DNA binding; Molecular Function;GO:0015074; DNA integration; Biological Process;	ATGGCCCCTTTTATGAGGAAGGCACAAGCTTTTGGTGATGTTAGAGAAGGTCTATATCTTTTGCAACAGGACAATCCCCAGTCTAATAAGGGCACTAAGTCTAGTGCAATGTATGTTAATGATATTCCTAGTGTAAAACTTTGGAATTGTAGACTGGGACATCTTCCTTTTTCAGTAACAAAAACCTTCAGTTTCATTGATTTCCCTTCAAATTCTGAATATGTTTGTGATGTGTGTCCTCAAGCTAAGCAGACTAGACTCTCCTTTGGTATTAGCACTATCAAATGTAAAGTAATTTTTGATGTGATACATATTGATACATGGGATCCATACAAGACTCATACTCACAATGGTTACAAGTTACAAGTATTTCCTTACTATGTAGATGATTTTAGTAGAGGTACTTGGACATTTGTTTTGACTACTAAAATCAATGCTTTCTCTGTTCTTATAGCTTTTCTGTCTATGGTGGAAAGGGTCAAAAGAAATAGATCAGATAATGCATTTAAACTGGGAAAAGGAAGTCAGGAAGCAGCTTTCTTACAAGCAGAAGGTATCATCTACCAAACATCATGTGTTGTTACCCCTCAACAAAATGGAATTGTTGAGAGGAACCATAGACATTTGCTGGAGATTGCAAGAGGTTTTATGTTTCATTCCAAAGTTCCTATCATCAATTGGGGCGACTGCATTTTAACTGCCACACATCTGATCAATTTGATTCCTTCCAAGGCTCTAAAGGCTCAACATAGGGGAAAGTTTGACCATAGAGCTACAGCTTGTGTGTTTCTTGGATATCCACAAAATCAAAAAGGTTACAAGATTTTGGACTGA

181	yes	ATGAACTATGTAGGTATTCCTAAGAAACTTTTAAATGGGGATTATCAATTACTATTTGAGTTAGTCAACAAAGTGCTCCTTCCAAGATATGAGAAAAGAATAGTTGATTCTGCGGCTACTATGTTTCTGATGGAGGCACTTAGCAAGTTCGATCTCTTGAATCTTCCAGTCTTTATTTTAGAACACGTGCACAAGATAGTAGTAAAGCAAAAGGGAAAACTTGGGATGGCGTATCGCTACTTCCTCACCAAACTATTCAAACATTTGGAGATTTCTCTTAGAGCAGGTACTGTAGGAACAATGAAGCAACCCTTCTCCATGTACACTCTGGTTGAGTGTGAGTGTATGGAAGGCCGACCAGGGCAACTGAGCAAAAAGTCTCAATTGGTAGTTGAGAAGAGACAATTAAAGCATGAGCTAGAGGAGATGACTGCCCTGGTGACCAAAGAGAATGCAGAGATAGCCTTACTAAAGGCGCAGTTGGCAAAGGAACAAACAGAGGCATCTGGTTCAGCCGAAGTCACAAAATTGAGGGCTAAGTCTGAATCTCTATTGGCCCAAAATGCTGAACTTACAGAAAAGTTGATCAAAGCACATGATGCTGCCAATGATCATCTTACTCTTGTCATCCAATCCCTTACTCAAAAGCCTCCCTTCTCCTAG
182	yes	ATGAGAACCTTAAAATGGGATCCAATGTTTAATCCAGAGGAGGAGACGTCAACATCGATCGCATGGATATCATTCCCAGCGCTTCCTCCAAACTTTTTTGGGAAGGAAGCAGTTTTCTCACTAGCTGCAGCAGTTGGAAAGCCCCTACAAGTGGACATGGCGACAAAAAACCAAACAAGGCTGAGTTGTGCGCGAGTTAAGGTAGAGGTGGATTTATTGAAGGAATTTCCCAAGCGTATCAAAATTGGGATGAGGAAACAGAATGAAGAGGTAGCAGAGAAGTGGATTAAAATCAAATATGACTATGTTCCAAAGTACTGTCAAACTTGTATGATTCAGGGGCACAATGCATAA
183	NO	ATGTTGTATATAGACCAATTTGATGCTATGAACCATAATCAAGTACGAGCATTGCATTGCATTCATCATATGAGCACTCAGATGAAGCGAGATGTTACTAATGGAACAACATGGAAATGGGCTGAGAATTATGCACCTCCAGATGAGCATGCCGATGGTCCACCAATAAATCTTCCTGCAGGTGGTGGTGGTGTTCGTGCTCGAGGTTGTACTCACATGTCGTAA

184	yes	GO:0005524; ATP binding; Molecular Function;GO:0006915; apoptosis; Biological Process;	ATGGCCAGAGAATCTTGCATTGATGTGAGAAGAACCATCAGTTGCTGTGTGGAGACAGGACATTTAGACAATTCAACCAAGGATCAATTGGAATATGCTAGTAGTCAACTAGTTCCTTTACTTCGGTTTCTACGTGTTCTGGAGAAGGATAACTTTGAGAATGTGATATCTAAAAATCTTAGGCCCCTATTCAGAGAAGCTGACCATGGCTTTTCTGAGATACATTCTCACATGAAGGATCAAGGCCTGACGAGTGATACTAGCAGAATGATTTCAGAGGCGTTAAAAATAATTGAACTCGGAAACATTGCTGAGCAAATCAAAGCTTCAAAGCCATTCATACCATCTATCCCAATCACTGTGGATATGGTGAAGCACACAGTAGCGTGCCTTGATGGTGCTTTTCAACTGGCAAACATCGTAAATGTTGATCCAATTCCACAGGAAAAGCTGGAAAACTTGGAAAATCTAGGATGCTTTCTCATGGTTACTGCAAAGTGGTGCATTGAACATGAGAAAATGAAGGATCTCTTCAACATCGCTGAGGACGTAGCTTATACTGCCACCTGCACAGCTATCCCATTTCATACGAGTGCTAAGAAATCTCAACATCGGGAATGCTTTCTTAAGTTTTCAGAATTGCTGGAAAGGATAAACCCTATTATTAAGCCTGAGTTTAGGCACCTTTATATCAGTGTCTTGAAAGCATCATATTCATCCAGATCAAAAATTTCAATGACAGGTGATAGTCTTCGGTATCTATCCGATGATGTGCTTGTGACATGGAAGTTTACTCATTTTGTCAGAAACAATCTGGAAACGCTACGACGTCATAAAGCCATCTTAACTCATGTTGCCTTTTCTAGTCGATTTCAATGGCTCCTTCTTGGACAACATAAGCTTTGTCAATTTCTCTCTCACTTGAAAGACAAAAAGATTCAGTATGAAGAATTACTTTCTTTTTTACTATCTTATATGGAACCTCTAGCCATTGAGGCAGCAAGTGAAATCTACTCCTTGTATGATGTGGATTTGGAGAAAAATATTGAAATAGACAGTATGCTTCTTCCCTTGCGGATGAAGTTTAATCATTTCAAATTAGAGAAAATTCTTTTTGAGAAACTATCAAAAACCATGATAGATCTTCCGTATCTACTGACATTCTTTAGAACTTTTCTCATGGATACATTGGAGCAGTGCAAAGATCAAGCTCAGCTAACTGATGTTTTGACCCTAATTCAATCTGCGACTACTGTAACAAGGGAACTTGTCGATTCTCTTTCTGGACAATTGTTATGGGAAACTAATCTCGTGCAGCATCACTTGCATATAAAGTATAAATTTTATAGGACAGCAATTAGACAGATATGTCCCGTCTTTTCATCATCAACACCAGAGCATCCTACAATAAATCTTCTGAACTTTCTTCCTGTTAACTTTGAGGACATTGATTTATATTTAACCATTCTGAGATTCCCAGCAACATCATCCCTCCCTAATAACCTGGATTTTAACGAGTATTTCATGGGGTTGCAGGGATATATTCTCGAAAAGCTACTACTCAACGATGAAGGCAATCTAAAACTTACTAATACAGATATGGTCAAAAGGCTACACAACGGGTTGTTGGTCCTGGTAACATTTCTTCTTGATCCCACTACTGAGTACATCGAATACAAGAACCAAAATGATCTCTCGACAGAAATTGGAACCATAGTACTTGAGGCCGAAGCTGCTATCCGTTTATCTAACGAGGATGGTTTTGATAGCAGCAAAAGTATGAAGCTCAATCTTGTGCTTCAGCATTTGACTATTGCTTTCAGTCTAATCAAGTCCGAGGGAAACTTCATGGATCTACTAAAGCACAAATACACTTTGGAAAGTCAAATTCAGGATCTGATAGAAAATGCTCACGAAGAGCTTATGTTCTTTAGAGCCTTTCTTATAGATCTTCTTAGGCAACAAAAAGAGCTTCAGAAATTGGATGATCTCATAAAGCATGCTGAAGTTGCTGCCCGCAAGGCAGCATTAATTAGCCGTTGTAGCTATGGAAGTTTCATGGATGGAAGCAGCTCCGGGAAAATATCTGATTTCCTGGAGGAGATCGAGTCTGTCAAGGTAGTGGTCAGAGAAATATGCTTTGAAATTCTTGATGCTTCACCTTGCAATATGGCATTAATAGATGTTGAAGGCCTTATCAACTTTTTATTAGACCTCCTGGACAGAATGCTTGACTGTGATGTTGTTTCAGTCTCTTGTTTGAAGAACGGAATCCCAGTAATCAAAGAGAGACTAGTGTACTGGGGATCTTTTCTTGCAGATATTGTACAGTACCGCAACATGCATCAAGAACTCCAACACCTTGTCAAACGTGTTCAGGATGTTGCTAATGGTACAAGGTACGTCTTTAACTTCTCTTTCAAGGGCTATGTACCTGCTTGGTTTAACATGCTATGTCTCTCCGATGTCAAGCAATTGCTCAAGTATGTCGAGGAAGAGATCAAAATGATTTGTTTTGAAGTTCCCGATTTGTCAAGTTATACCTTCCCCAAGACAAATGGATTAGGATTTATTGAAATTTTTT

185	NO		ATGGCTAGACCAAAAGTTTCAGGAAAGGGTCCACTGCCCCGAAAAAGAGAAAAATGGGAGGTTATTGTTGCGAAGGCTGCACCTCCTGGACCTTCAAGGCCTCGACCTACTCAAACAAGTACTCGTGGAAATGGAAAACAACAAGCGGAGCCCAGATCAAGCAGTTCTAGTTATGACAGCATGGGAGTATATTCCACCTACCTCACCACATCTAGTTCAGAGAGTGAGAATGATGCAGGTTCTAAGACTCCCATTTGTCATTCAGTGCCAGCAAACGACCATACACTGAAAGGAAGACGTGCTGAGTTTCACTCCGAAGAACTTCATTATCCAGCACGCCTTCTGGCTCATCCAACACCTCCAGCAGAGGCAGAAGAATAG
186	NO		ATGATGCAGCAGGTTCCAAAACTTCAAAAAGGTAGAGCTAGAATTCATTCTAGTGGGAAAGTAGTTGGTGACCCGGGCCGCTGGAATGTTGTTAAAGATAAAATGTGCATTGGCAGTAGTAATGAGCAACCCTTACCTACTTTGACAAACAAATTTCAAGATTTAGCAAACGAGGAATACATGCAGCATGAACAACACAAAGGTGATGAAGATGATAGGGATATAGAGAGAAATGAGAAGCAGAAACAAAATCTAATTGATGAGACAAAAATGGCTCTTGTGGTAGTAGATCAAGCAGCTACATCAGACCCCAAAAAAAAAATTCAACCTGCACAACAACATGCAGTAGAGATCGATACTGATGATTCCAAGGAGGAAAAATCCACAAATTTATCAATTTTCAAAGAGGAGAAAATTTTTAAAGATGCAGATCTCTCTCCTAGGGTGATGAAAGTAGTAAAGACTACTAGAAATGGCAAGAAACAAGGTGTCTCTGCTGATGATAATGCAGTTTTAGGAGTAATTCCAGTTTTCAGGTTAAATGGAGACAGCGGTTATGGTCCTGATGGGTTGTCGGGTAGATTTTTTCAAGAATGTCTGGATATAGTAAGGTCTGACATTATCAGAAAGGTAAAAGACTTCTTTGCTGGTAACACTCTCCCAAAATCCATTGCTCACACCAATTTAGTTCTCATACCGGAAAAGAGAATGTTGAAACTTTCTCCAATATGA
187	NO		ATGTCTGGAACTCACAGAGCGGGAAAAGAGGTTGCGTCTAGAGGTCGTAAGAGGGTGAGGACTGGAACCACCATCCCTCAGGCACATGCAATCCCAGGAGGTCACACCCGCCGCTATGGTAGCAAGGCAGTTACCCTTGAGGGCAAAAAGTTGTACAAAACACACAGCGAAGTAATTTATTTTTCGGATGTGGTGATTGAAGATGTGCACCTGGAGAGGGATTTCCCTCAAATCATACATCACCTTCAAGAGTTCAATTTGGGATTCATCTTCCAAGATCCTATGGAGTTCAATGTGAGTGTGGTTCGGGAATTCTACCCAAACAGACCCCCCGATGCTCAGTCTCATTTTGTTATAGTGCGTGACGTGGAGGTTCCCCTCACACCCTTGGCCATAAATAAATTATTCGGTATTATGGAGGATCCTTCGGCCGTTCTAACTTGGTTAAACATCAGCATATCAACAAATTTGCCATACCTTGTGTGGAGTACAAACCACCGCTAA
188	yes	GO:0003676; nucleic acid binding; Molecular Function;GO:0004523; ribonuclease H activity; Molecular Function;	ATGGGAATTCAGAGAGCAATTCCAGCCATGATAATGTGGGCTCTGTGGAAGAGGAGGAATACATTCAAGCATGGAGGAAGTTGGAGTTTTAATCAGATGAAGGAACACATAAGCATACAGATACATCAATTGATTCAAGTTAAATACCCTTGGATAAAAAGAATTCCTAGAGATTGGGAAAATATAATCAGGGAGGAAACAGGGAATCTGATATATGCACAAGGAGATGATATTGGTATAGGAACTAATATGGAAGAAGAAATCATTGCAATGTTGGAGGCACTAAGATACTGTAAAAGTGTTGGATTAGAGGACATTTGGCTGGAGTCTGACTCACTCAGTCTTGTTAAATATCTAACAAACTCTTGGAAAGTTCCAGGGAATAGAATAGAGCAGGTGGAAGAATGTAGAAGCTTAATGGTGATCACAAAAGCAAAGATTCAGCATACATTGAGGGAGGGGAACAAATTAGCAGATTCCATAGCAAACACAGTAATAGGATCAGAGGGAGTGGTTCATTTCGACACATTCTCAAATCTACCTACTAAAGGAAAGTGCATTATCAATTCGGACAAGGCGCAAATACCGACATTGAGAATCCGAACCAGGCCAATCAAGAATCAGTTAACACAGCATATAGAGGGATAG
189	NO		ATGTCGAATCCAATATATAGGGTAAGCGCGGGTCCAAAAGCACCATTGGCTATTGTGCCAAATCTACCAGCCGAGTCAGCACCAAATGAGGATGGAGATAGAGATACCACAGATGGTACAACCCAAGAAATCTTGGGAGTTAGGCCTACAGCAGTACCTGACTTTTTATCCGTAGGTACAGTTGTCACGATGCCCATGGAATTCTAG

190	NO	ATGCAACATTTGCAACTTATATACCAATTGAACAACTTCGTCAACTACTCACTACAACAAATGCTGGGCATCCAAGGGGCAGACCTTCCCAACGAGAACACAACGGTGAGCGAAGAGGACGACCATATGGAGGATCAGGTGGTACCACAAATGTACACGAGGGGGCCATCACCGCCTATACACCATGCAACGACCATAGAAATGAGAGAAGATGCACTAAACATCCCAGAGCTACACTTGCAAACTCTCTACTTGAGGAACTACTTGACAATAGACATGCAACAAAACATAGAAAGGAAAATCATGATCAAAGTTCCCAAAGAATTTCCAAAAAAATCTCTAAACATACGATGCTAA
191	yes	ATGAATGAACCAACAACAAAGAACTCAATCTGGGGTAATTTTGACATAGGCAAGGTGGTCAATGCTGGATTTAAACTGGAGTATGTTGCTCCAACAAATCAAGGGCAGAATGAGGTTATTCAAGCTGGAATCTACCACTTCTATAGTAAGCCATTCATAGTAAAGGCTTGGCATGCTGATATGGATTTTTCACTAGAAGAACTGCACACAGTGCCTATTTGGATCAAGCTTCCTGGTCTGGACTTTAAGTATTGGAGTCCCAAAGGATTGAGTAAGCTAGGAAGTTTAATTGGGAAACCTCTAATGGTGGATCAAAATACTGAGAGGAAAATTGGATTGAATTTTGCTAGACTTATGGTGGAGGTCGACATGAATGCTGCACTTCCAGATATAATTAATTTTAGGAATGAAAATGGGCAATTGATAGAACAAAAAGTGACATATGAACAAAAAGTTTCATTAATTTCATGGGACAGAGTATGTTTTCCAAAAGTGTAG
192	NO	ATGTCCTTATCTTTAAATGTGCTCATGCAGAATAAAGATTTTAAAAGGTTTGAGATGCCAAGAGGGAGCCTAAAGATCAATCATATGTCATTTGCGGATGTTATGATCATAATGTGCAAAGTGGAGGTTGGTACGATGAAAATGACCAACGACACTTTAAGGAAGTACGAGAAGATATCAGCGTAG
193	NO	ATGTATCATTCAAGGTTGAAGGAACTATGGGACGAATATGATATGATTGTACCAGTGCCGAGTTGTGGTTGTGATAAATCGAAGGATTATGTGGAACATCTTCAGGAGCAGTTGCAATTTCTAGCTTGTTTGAATTATTCCTATGATCACACCAAAAGGCAGATACTACTTAAAATTGTTGCTCCTTCAGTGAATCATGCATACGCGATGATAATTGAGGTAGAAAGTGATCAATCCATAGGTACTAATTCTACAAATCAGAATCAGTCAGATCCTTTAGTAATGAGCTTTGGTAGGGGAAGAGGCCATGCTTATCAGGGAACCACTGATAGAGGACAACCCTATCAAGGTACTGTTGGGAGAGGATAA
194	yes	ATGAATGCTCCTCTTACTGATCCTAGTGTGTATAAGAGGCTTGTTGGCAAACTCAATTTTTTACAACACACTCGTCCAGACATTGCCTTTTCAGTTCAACACCTAAGTCAGTTTCTACAAAAACCCCAAGTGCCCCATATGATGGTTGCTCTCCATGTGCTCCGCTACCTTTTGAATGCTCCTGCTCAGGGTATTTTGCTCACCAACACACCTGACATGTCTCTTGTTGCTTTTTCTGATTCTGACTGGGATTCATGTGCTATTACTCGCAAATCTGTTACGGCTGAATATCGGGCTCTTAGAAAGGTTGTTGCTGAGGTCTCTTGGTTGATCAGATTGCTTGGTGACCTAGGTTTATCCATTTCTGCTCCTGTTCCCATTTTTTGTGATAGCCAGGCTGCTTTTCATATTGCTAAGAACCCCATATTTCATGAGCGCACCAAACACATTGAAGTTGATTGCCACTATGTTCGTGATTGTCTTAATTCGGATTTGATCTCATTGCATTTTGTACGCAGCTCTGCCCAGCTTGCTGATATTATGACCAAGACCCTTGCTGGTCTGCTTCATCGTGGAATTTTATGCAAGCTTGGAGTGTTGTCCCCCTCCAGCTTGAGGGGGGGTGTTAACCGAGACTCCACCGACTAA
195	NO	ATGGTTCCACCATTGGTCTTCAGAATGCCCGTCAATTTTAATGGAGGTATGACAATGTGGATGCTATCAATAAGCTTTGCTCCTCCGATACAGGAGACACTTGTTATGACGATTGCAAAAATTCATAAAAAAGGAGTTGAGCAACAGAAGAATGGGTTGAATTCCGGCTGA

196	yes	GO:0005515; protein binding; Molecular Function;	ATGGCACCAGCATCTTTCCGTACTAAATATGCTTCAAAATTGGAACAGTTATATAGTAAGTTAAAATCTGAAGGTAAGAAAAGGATCATCCTCACTGGGAAAGACGTCGAAATCGAGGACTTAACATGGATTGCAAAAAAGTCAAGTGGTCGTGCTATTGTAGAAGGAATATTTGATTTCACAATATTGTGGGAACTGTCCTTTCCAAATGGTGATATTGATGAAAGACTAGCTTGTAACTTGTCATGTTTATCTCCTCTCGATGAGTGGGAGCTTGAAAATAACAAGAAGGATATAATAAAGGAGGAAAAAGAGACGAGGAAGGAAAAGTTATTGGAGGATCAGATGATAAAAATACTTGAAAGCAAGAAGGTTGTCTTGATATTTGTTGATGGAGCAGGTGAAATGGATGAGCTGAGCATGAATAAGGTGTCTCGTCGCATAAAAGGATTAAAAGCTAATCATGTACAAGAAATTCTTGTTACCACAGCACATGACAATGCTGAAAACCAAGGTCTTGAGGGAGTTATCAAAGTGGAACATAATAAGGACCAAATCAATGGCAATGAGTCACTTTCTTCATGTTGTGAACTTATTGGAAAGACAATCCATACAACTCCAGGGTTACAGTCTAAGTTGCTGCTGGAAAGCATCTTAATTGACTTATGTTGCCGCGAAAACAAGTTCCCTTTTAAGAGTGGAAGGGCACATTACAGTGAGTTGATCACTTATTGGATACTGGAAGGCTTTCTTGGTCCTTTCAATTGTTTTGAGAATGCTTATGAAAAGGGACACCGTGTTCTTATGGCGCTTGCTCATCATGGCTTCATTGAAAAGCTAGCTGCAGGGTATGTTAGGAAAAATAGGAAACCGTTGTTTTTGAGTGCTTGTGATCGTTGTAGAATGGAGGAGACTGTCCGTCTAGGTCTGGCGAATGTTTTTGAAGGTGATCTTGGACGAATCGCACAAGCAGATGGGATCATAAGAACACTTGGTAAGGTTGTAAAAGAGAAAAAAGCATCAACATTGTTGATTGATAGGAACTTTCTCAATGGGGAAGTCTTAGTTGATCTCTTTCAAACCATGGAGGAGATAGAAGCTCTTGCAATCTTCAACCCAACATCCAAACCCGAGCCATTATCCTTGGAGATGCAGAATCTTAGGCTTCTTGTTCTTAGAGGTTGTAATTTTTTAGGGGGCATTGAGAATCTCTTGGAACTAAGACCAACTAAAGCTGACAACATTTCATTCCAGAAACTTACTGTTCTTGAAATATCTGGTCCTAGCCCTTCGTTAACAATCCCTGACAATCTTTTTAAACATATGCCTCATATTCAAAGTCTTAATTTATCATCTCTTCAAGTTTCTTCACTTCCCTCATCCCTTTGTCATCTCACTGAACTAGTTTGGCTCATTCTGAGAGACTGCTCCAGCCTAAAGGAAATAGGAAGTTTAAAAAGCATGACAAGACTTCAGGTTCTCGATCTTTCTGGTTCTACATCTCTAGAGAAGTTCCTTGACAAGAGCTTTGCAATAAATAAGGAGCTTCGAATGCTTAATCTTTCAAACACCAAAATAAAATTGTTACCTTTGATCAAAGACTTGAGAAATCTCACTTATCTCTTGTTACGTGATTGTAAATCACTAAGAAGGTTACGCATGCTTGGTTCACTAAGCAGCCTGCAAATTCTTGACTTGTCAGGTGCCACAAATTTTGTTGAATTTCATGATCAATCCCTAGAACAACTTGGTTATCTCGAAGAAATAAATGTTTCACAAACTCAAATTGAGAAGCTTCCTTCAGATATCTGCAACATACGTCGTCTTTCTTTGAGAGGGTGCTCCATGTTCAAAGGATTTCCACACTTTAAAAACCCCGATGCCCTTCAATTTCTTGACCTTTCAGCCACAAACCTCATTAGTGTGCCATCCATTTCCAATCTTAGTAATCTTAGAGAACTGCTTCTTTCATGCTGCTGCTCCTTGGTGAAATTGGGAGACTTAAGTTCATTAAAAGATTTGCTGGTGCTTGATCTTTCAGGTTGTAAGGCTCTAACTAGATTGGCGGATAACTCATTTGAAAACATGCATTGCCTTCAAAATCTGAACCTCTCTGAGACAAGCATTGAGTATCTGCCATCCCTGTCACATTTGAGTAACCTCCGTTGCCTTTTTCTACAGAAGTGCACTAAATTGAAAAGATTTCCATCACTTGAATCCCTAACAAACCTGGAGGAGCTAAATCTTGCTGGTCTCAAGTGCCTAGGAGAAGTTGATTTCTTGAAGAATATGGTGAATCTTCACCTTCTTGATATTTCTGAAACTGGGGTAACACATTTGCCATCCTTATCAAACCTCAAAAAGCTTAAGCATCTTTCTCTAAGAGGTTGTCAGCAGCTTCCGAATCTGGAAGGAGTCACAACACTTGAAGTTCTGGATATTTCTGGTTCTCGCATTGTAGACTTGCCCTCCTTCGAGGATTTTCACAATCTTCGTCGCCTTATCCTCAGAGATTGCCCAAACATAAAAGAGTTCAAGGATCTGGAGATATCTGAAGTCTTGAAGGCGCCGA

197	yes		ATGATCATCACTCAACGCAAATACACTTTGGAGCTTTTATCAGAATACGATTGTTCTCATCTCCCTCTTGCGTCATCTCCTCTTGACCCTACACAGAAATTAGGGGCTGATATAGGATATTTATTAATAGATCCTACTTACTATCGAGGGCTCGTAGCTTTTTGCGATGCTGATTGGGGTTCTTGCATTGACTCTCGAAGATCTGTTAGTGGATTTGTTACTACCCTTGGTGGTTCTCCAATTTCTTGGAGATCAAAGAAACAAACCTCTATTTCCATCTCTTCAACAGAAGATGAGTATCGATCTATGCGTCGGGTCATTGCTAAATTAACCTGGCTTAATCACTTTCTTGTTGATTTGGGTTCTTCGTCGGACCTTCCAATTCCGGTTCATTCAGATAGCTAA
198	NO	GO:0005525; GTP binding; Molecular Function;	ATGATTGTGGTCTTTACTGGAGGAGATGAGCTTGAAGAAAATGATGTGATTTTGGATGATTACTTGGACCACTGCCCTGTGCCTTTAAAGGAAACTCTTGAAAAATGTGGCAATAGACTTGTACTTTTCGACAATAAGACTGAGGATCCAGTGAAGAAAGATGAACAATTGTGA
199	NO		ATGCCAAAGGGCGAAAGTATTGAGGGCCCAGATCCAGTGGAATCTGTACTTCGGGCTATTGGGAGGCTCAAGAAGGTGGCGAACCGATTTCGTAGAGAACATGCCATTGGGGCAAAGGGACCAATATGGCATGTCATTGCGATTTTCATTCAATCTCACAGTACTAGGCTTAATCCTAATATCCTCAGGGATAGTCACGGAGAAGCTTTCCCAATTCCTACCTTCATGACTCCAGAAATTCCTCAATTTCAGAATGCGTTCATTACAGTTCAACGGCCCTTGGATAAGAGATCTGAGAGATGGAGCATGTGGAATCCATTTATGTGTCCATACGTCGATGATTTACCCGTACCCACTGTCCAAGCTAG
200	NO		ATGTCATATGCAGCCACTTTACAACCTACGATGACAACTCGCGCTCATGTACCAATAAAACCCTTGTCTCTTCTGCATGGGGAACCAAGGGTTATTTGGGAGGAAGAAGAGGTATCTCAGATGATTGTTAATGAAGATTTGGAATATGCAGTTGTTGGGAAATTCTCCTATGGATGGCCAGACATACATGAATTAAGGAAAATTATTTCGAAACAGTGTGAATTAAAAGGAGACGTCAATATTGGTCTATTGTGTAATCGATACGTACTCATAAGGGCCTCAAGGATGGAGGATTATGTGAATCTGCTCTCTAAACCTATATTCTACATTGCCCATAGAAATTGGTATTATCCAATGAGGACATTTAAATGGGATCCTTTCTTTGATCCATTGGAGGAAACGTCGATCGCAGTTGCATGGATCTCACTGCCAGCACTGCCTCCCAATTTATTTGGAAAAGAAACGATCTTTTCTATTGCTGCTGCAGTGGGTAAACCTTTACAAGTGGATACGGCTACTAGCAACAAGACTAGGCCTAGCTGTGCTAGAGTCAAGGTGGAAGTTGATCTAATGGGTGAATTCCCAAAGCGGGTTAATGTTGGTATTAAAAAGAAGTTTGGGGAAATAGCTGCTAAGTGGGTCACCATAAGGTATGATTATCTGCCCAAGTACTGCAAAAATTGTAAATTGCAGGGTCATAATGAGAATGAGTGCTTTGTTTTGCATCCTGAACTATACCCTAAAGAGGAAGACGTGAGTGAAAAGGAAGCCACTGCAAAAGAAGAGATGAAGAAAGATAGGGGCCAGGTGAATGATGAAAAAGGGGTAGAGGACACAGGGAAAGGGAAGGAAAAATGGCATCAGGAGAATAAAACAAAGAACGAAAATAGAAGAGGGTATCAAAACAAAGGGGGATTGACTCAGAGATGGAATCATAAGGAGAAAGCGAATGAGGAAACTAATGTTATTATAGGCAACAAATTTGATGCATTAACCGAAGAAAAAGGGAAAGATGAATCAAAGCAACAACAAAATGAAAGGGATACAACATCAATGAATAGTGCAGGGAAAGAAGTAATGAGTAAAGGGCCTGGTAAAACAAAGAAATGGGTAGAAGAGATTTTTGGGGCACAGAGAGAAGAGGGGGAATTGCCTGTCAAAAGCAACAAAATAGAGGGAGCCACAACAGAAAGAGAAGACTCTGTAAAAGAGTCTACGCAGAAAAATGACAAAACAAGGGAGGCAAGTATAAAGATAATTAGCAAGGATACTGATACACAAGACAAAAATAATGTGGAGGAAGTCAAAGGGAAGAAAGAAGTGAGCAGCAAAGATGATAAATCAGAACAAATAAATGTGGAAGAGAAGCCATCAGACCCTCCAAATGCAGATCACACTAACTTGGAGGGAGAGGGATCATCTATAAATAAGACAGACGAGAGTACCAATGAAGAACGAGAACTAGTTTCTTTGAGGCAAATGCAAGAAGAACCTGATAAAACATTTGAAAGCAGGGATGAAGAAGAGGATGAGAACATCATGGAGAATATTGTTGAAGTGTCAAAAGATGGTGACCTTTCACCAAGGCATATCAAGGAATTGAGAACGGGAATGAAGATCAATAAACTTGAAGGTAAAGTTAGAAGTACAAGAAGTAGTTCGGCAAGACCGCCTTTGTCTAAATGA

201	NO	ATGGCTGAAATACATGCTAAGTTTGTCTTTAAAAAGACTGAACTTAAGCAGATTTTGCCTTCACTAACGCGGATACCTTGCTTGCAAATGCGGAGCGAGTTCTGCAAACGTGGAAGTATTGGAAGCCACCCCTTCACGAATACGGAATCCTCCCTACGAATGCGAAGGCAAGAGGGTCAACCCTACGAGAACGCCTTGAGGCATATGCAAACGCGGAGGTTTAAGATTTTGAGCTCTCTGAACGCGATCAAAGATCTGCGTTCGCAAAGAAAGAACCAGTGTTGCACCAACAACAACTCAAGGCAAGGAATTTCTCCGTTGGGAGTCCAAAACTCGTTCGAAGACCTGTCAACGCAAACCATATATGCTACTTGGATTAAGATGACATTCAAGACGTAA
202	yes	ATGCCGGACGAGACTCATGCTAGGAAGCTTACCCTCTCAGTAGGGTCTCACAATACCCCAAACTCTAAAGTTGATCAGAGGACAACGGCGGAAGTAGTGCGGGGCAACAACAAATTTAAAATGCAGCTTCCACAAGAACTCTATATTGAAAAGCCTGATGGAACTTTGATCACTCAAGCGATAAAGTATGAGTGGACACCACAGTTTTGTCATACCTGTATGAAGATGGAAAATAAGGAAGGTGAATGTAAGCATGGCAAGCCAGCTCCACCAGTTATACATCTAGCAAGGAGAAGAAGACCTCCTCCACCTGTATGGCAAGCTAGGCCTGCTAAGCACCAAGAGCACCCGGCAAAGGGGAAGGAAAAGGAGGACAATAATAAGGAGAATGTCAATGAAGAGAAATCCACTCCTTTCCAAATAGTCAATCCAAAGCTAGGGTATGGGGATATTGAGGCTGATTTTGTAGACCCAGGACGTTCTGATCATACACCTATTGTAGTGAATACATGCACTGTTCAGATTCAGGTTAAAAGGCCATTTAGACCGTTAAATGTGGTGATGAAGCACCATAGCTTTAAGGACCTTGTGATCTCTACTTGGAATCAACAGGTGAATGGATATGAGATGTTTATTATATGTACCAAGCTACAGAAAATAGCCCACCAGGCTCAACACATTCAAAGAGAGTACTCCTCTGTTAATACAAGAAAAATGACCTTTAGCGAGAGGAAATTTGGTTGTGAAAAGTCCAAATTCGGTCGCTAA
203	NO	ATGAACGTTAGCGACAATAATCCCAAAAAAACATATGCTCCTGAAGTTCAAGAAGAAAATATCGTTCCAAAAAATAGTAAGGTTATTGGAACATGCAAGAATTCACAAGTCATCGAGGACGTTACACCATATTTATTTACATCAGATGATATTCAAGCTCCCGAGGAAAAAGATGTTTCCAATAAAGGTAGGTAA
204	NO	ATGAACAAAGTTCAGAGAGACTTCATCTGGGGGACAACAGATGAGAAGAGGAAACTGCATCTCCTTAATTGGGACACCATAACTAACAGGAAAATCATGGGAGGCCTAGGTATTCAGAAAAGTGAGATAAAAAATAGGGTTATTCTCTCAAGCCTAGTATGGAGGGTAGCCCAGAACCCAAATAGACTTTGGAGCAAGGTTTTAACGAGTAAATATTGTAAATCAAATACGAGCTCCAACTCAATAATTGTCTCCAGAACATGGAAAAATATCCAAAATGGCTGGATAGACATAACCAAGGCAACCAAGTGGATAGTGCATAAAGGAAACAAAGTGAATTTCTTGAGTGACAACTGGCTCCCGCACCATGACACTCTGCGCAGCGTCATCCAAGGCTCAATGGCCTATGGAGAAGAAAACATAGAGGTCTCTAAAATCTACCATCAAGGGAATTGGGACTTCGATAAGATCTCCTTTGAACTACCTGGAAATATCAAGACCATAATCAAGAGCTATCTCTTCCCACAAGAAAGCACTAAGGAGGACAAGTTGGTCTGGGGACTGAAAAGTAATGGACTATTCTCAACTAGCTCGGCGTACAATCATATCAAAGAGGAAACCTCCAAGCACTTTCGCAAGCCCAATGAGAAGTTGAAATGGATCTGGAATGCAAACGCACCAAATAGAATCAAGACTTTCCTATGGCTCTTGTACCATCGTAGGCTCCCCACAAACCATTCCCTCCAGCAAAAAGAAATAAATGTTAATCCAAAATGTCACTACTGTGATTACCCAAGGAAAGACTCTAACTACATCTTCTTTTATTGCCAAAAATCACTCAATTTATGGAACTCAATCCAAGCGAGAAGTAGCAATCAAGGATCACCAATCACTGACATCATAAATGAGACTAACTGGATTGATGAATGGAACAAGCTGAGAGGGAAACAGTTCAACCAATGGTTAGATTGGAATACTCTTATACCTTTCTGCCTATGGAATATTTGGATCACCGGGAATAACAATACTTTTAATGACCAAAAGAATTCCATTAGTAGCCATCAAACCATTTCACAGATCAACGAGTACAGTTTACTCATTGGCAAGCAAGGCAATACAAAGGCAAGAAAGACAACCATGATAGTCAAAGAGGAACCTCCTAACCCAGGATCATACAAGTTGAATGTGGATGCCTCTGTGAAACACATCCCTGGCCCATGGGGTATATGA

205	yes	GO:0005524; ATP binding; Molecular Function;GO:0006915; apoptosis; Biological Process;	ATGCATGTTAACTCCGAAGTTCATGCTTACCAAATGATGCCATTGAGTTTATATGATAGTTGGAAGTTACTTCACAAGAAGTTATTTGGTGTAGAACAAAGTTGTCCTGCAGAATTGGAGGAAATAGGTAGGGAAATAGTTGGAAAATGCCAAGGACTGCCGCTAGCTATATTGGTGGTTGCAGGGCATCTCTCCAAAGTTCCCATGACAAAAGTAACCTGGGAAATAGTAGCTAAAAATGTTAATAGAGTTGTTACAAGTGATCCGGAAGGACGCATAGGATTACTTGCTATGGGTTACCAGTACTTGCCTATTCACCTAAAACCCTGCTTCCTCCATATCGGAACATTTCCCGAGGGTAATGAGATTGATGCTTGGACATTGATCAGATTGTGGGTTGCTGAGGGATTCCTAAAGAGTGACAAGTTGAGAAGTCCTGAAGAAGTGGCTGAGGAATGTTTGGAGGATCTTGTCAGTAGAAATTTAGTAATGGTTACAAGGAAGAAGGTGGATGGTCAGATCAAAAGTTGCAGTATGCACGAACTGTTACGGGATTTGAGTGTGAGAGAAGCTGAAAAGGAAAAGCTTTTGAATGTGATTACAAATAATGAAGTTCCTAATTTTTCAGCAGCAAATGAACAGAGTGCTCCGAACTTTAGTTTGCATACCTCTATTTCCTTGGAAAAGTTTATGAAGTCCTCACAAGTTGTACGTTCCTTGTACCTCTTCAAGGAACCAACAGGAAAAACTTCGGAATTCAAAGCTTTGAGAGTGTTGACCATTCCTAAGTCTTCCTTTATCTTTCGCCATCACATGACATTAGGTTCAGCTATCCTGAGATACCTTGAAGTTACTAGTGACAATGATTTAACGGAATTACTCGGATATATGCACAACCTTCAAGCCTTTATATTTTACACCCGTAAAATATTAAAGGTTCTACCTTTGCCCAGAGAATTCTGGAATCTTAAGCAGTTGAGGCATCTCCATGTTATGCATAACATTCATTTACCCAATCCTCAAGGCAATAACTCGTCTGATGTTGATATGCATCATCTACAGGAGCTTTCCAATCTCTGTGTTGCTAGTTGTACAAAGGAGGTACTATCTCGCCTTACGAATCTGAAGAAATTGAGGATCAATGATTTCAGAAGATACATCAAAGACAACGAGATAGAAACATCTTGGAGCTTACTCAATCTTGTCTGCTTAAATAAACTTGAATCCCTTTACCTATGTTTCAAGATGTGCTCACTGTCGTCACCCCTGGCAAATTGTTGTTGTTTCCCAACATCTCTTAAGAGGTTGACCATGTTTGATGGTCACCTTCCCTGGGAAGACTTGGCAACTATTGCGAAGTTGCCCAATCTCGAAGTGCTCAAACTCAGGAACAATTCATTCTATGGTGACATGTGGAAACTAAATGATGATGTTCAGTTCAAGCAGCTAAAGTTCCTGCTACTTCATAACGTGTACATAAAACGGTGGGAGGCTTGCAGTGATAACTTTCCAAATCTTCGCCTCCTAGTGTTACAGCTGATGTGTCACCTGGATAGAATCCCTCTGGAGTTTGCGGATATATGCACCTTGGAGTCAATTGAGTTATATTTCTCCTTGAATCTCTTGAAATCAGCAAGAGAAATTGAAGAGGAAGTTAATTCAGTGGCGGGATACGATTTCCTTCATGTTGGCATCTACGATGATTATTATGAATTGGTTAAAAAACGCGGTGGAAAGGCTTTTGCTTCCTTCAAGCAGGGTGAAAAAATTAGCCCATAA
206	yes		ATGAACAAGACTCAACCAAGTTATGCAAGGGTGAAGGTTCAATTGGATCTACTAGTGGACAAACCTGAATTTGTTCAAATGCAGATAGGAAATAACAACAATCAGGAGAACAAACTTGGTAAAGTTAAAATCCAATATGACTCACTCCCATCATATGGCAAGAGATGTAGAATTCAGGGTCATAAAGAGAAGGAACGCATGATACTTCATCCAGAACTATAA
207	yes		ATGAAAGTAAGAGATCAAAACAAGAAGCATGTTGGTACTTCTAAAGATCAGGAGATCACCGACAACAACATAGAAGTCGTACAACAGGAGAATCTGAACAAAAAGGGGACTAAGAAGGCTAAGGCAAGTATGAATCGAGCGACAACAAATAGCTTCTTGAAACAGATAATGTGGGCTAAGCAAAGATTGAAACAAACACCTGATGAGAAAAGTAAAACAGGCACAAGGAAAGACAACAAAAAGGAAAATAAGCAAAAAAAAAGATCTGAATCTTGTAACTGCAAAAGAGACGGGATATCAAAACAAAGGGAACATGACTACTTCAACAAAAGAGAATATTAATCAGAAGAGTCATAGCAACAATAACCAACACCAGCAGGAAGATCAAATTAGCAAGGCTGGATGTAATATTGATAGAGGGGGAAATGAAGTCACGTCTCCACTGACAGTTGACCCCAATAACTGGGTTGTGGAACGAGGTCCAGCGGATGGTATTAAGCATCCAAATGAGCAGATTGATAATCCAGATCAGAGCATCAACAATACTTTCAACAAAGAAGAGGAAGCAGACTCTTCATATGAGGAGGAAGAAAACAAAGAAGATTGGTCAAACTCATCTGATGAGGAAGTGGCAGAAAGTCTGATTGAAACTTTTGCTCCCAGAAGGCAAAAAGAAGTAGATCATGTTACAAAAGAAACTTCTACGATGATAAGTCAACAAGGTTTATCTCCTAGGGCTAATAAGTACAAACAGAAGAAGGTAAAGGGAGGTCAATCTAGACTTCCTAATAACTAG

208	NO	ATGATAGGGAATCCACTGAAAGCAGATAGGGCAACAACACAGAAGGATAGGCTGTCGTTTACAAGAGTCTTGATAGAAATACCTCTTAATAAGGAATATCCGAAAACAATAATGTTTGAGAATGAAATGGGGAAGATAGTGTACCAGGAGGTTGAGTATGAATGGAAACCAATATTGTGCACGAAATGTAAAAGTTTTGGGCATGATATCAGTGAATGTCGAAGACAATTAAAGAAGAATGAGCAGAATCATAAAGAAGAACCAGTGAGGAATGGAGAAGGTAAGGAGAGAGCAGATAAGGCTGAGGAATTAGAAGGTGATACAAAATCAGTAAGGATCCCAAGTAGAATAAAGATAAAAAGGGGGAAAACTAAAACAGAGGTGACTGAGACGAATAACACATTCAGTGTCATGGGAATGGAAGGGCAAGGAAGCATGGAGACAAACAAAGGGACTAGTGAGATAGGGATTAAGAGAGCCAAAGAAGCAAGAGCGGCTCTTAATCTGTGTAGGGGGTGGTCATTTACAACTAATTTAGCAGCTCACAATAGAGGGATATGGATTTTGTGGAAGCTAGAGGTCTATAATGTTGATGTGAAGGTGGTAACAGGGCAAATAATTCACAGCAAAGTGGAGCATAGAGGAACAAGAAGGGAGAAATTTGGCGACATTGAGAGGAAAGCTGAAGAGGCGAAGGAGGAACTAAGGCAGTGTCAGTTGAAGTTGAGAAGGAATCCAACAAATAACAGCCTGATTGACCATGAATTGGAGATAACAAAAAAATATGGGAAATTTAAGGAGGCTAGAGATCAGTTCTTGAAACAAAAGACAAAGATTCAGTGGATACAAGAAGGTGACCAGAATACGAAGTTCTATCACAACTACATAAAGGCAAGAAGGAATACAAATAGAGTATTTGCAATAAAAGATAAATATGATGAACGACAGGAAAGGATGGAAGGAATCAGTAAAGCTTTTTTAGCGTATTACAAAGAGTTGATAGGGCAGTCAAATATGAAGAGGAAGCATGTATGCAGGGAGATACTCATGAATGGACCAATGGTGAACGAGGAACAATGTACACAGCTAAAAGCAATGTTCACAGAAAATTATGTGAAAGAAGCAATTTGGAGCATAGATGGGAACAAATCTCCAGGACCAGATGGCTATGTAAGTCAATTTTTTAAGGACAATTGGGAGATAGTAGTCAAAGATGTGGTGAAAGGAGTGATGGAGTTCTTTAGGACAAAGAAGATACTTACGGGGATGAACAATACCACAATAACTTTGATACCAAAAGGAAGTCATGCTGACACAGGAGGGGACTATTAA
209	yes	ATGAGAATCTTGTTTGCTATTCAGACACAAGGATGCCAGCAAGTGGCAGATGAAGCTGAAAGGGAGTACAAAAAGATGTCTGAGCGAATCACTGAAGGCAGGGAGGCAATGAAGGGTTCATATTCGACGTTCATGGCAGAACTTCAAGCTAGTGGTGCTCGCTTGTGCAAACAAGCCATTCCTGAGCTGTCACAATCCGTCGAGAAAGCAATAGATACTCTCAAGAACCGTTATGGGATCCATTAA
210	NO	ATGGATTTCAAGCATTGTGCATATCTTATGATTGATGCCACGACTAGATATGAGACAATGTGTTTTATGGATGGTTCATCTGGATACAATCAAATTTGTATTGCACCAAACAATGAAGAACTTACTGCATTTCGTACTCCTAAAGGAATATATTGCTACAATGTAATGTCATTCGGTTTAAAAAATGTTGGAGTTAAATCAAGAAAAAAGGATGACCATTTCAAAGATTTGAGAATGGTGTTTGAACGACTTCGAATATACCATCTCAAAATGAACCCTTTAAAACGTGCCTTTGGGGTTACTTCAGGGAAGTTTCTTGGTTTAATTGTTCGACATCGAGGGATCGAAATTGACCAAGACAAAATAGATGTTATTTTGAAGATGCCCGCGCCTAAAAATATTCATGAGTTGAAAAGCTTGCAGGGAAAATTGGCATACCTTAGAAGGTTTATCTCTAATCAAGATGCCAACCATTCAGTCATCTTATGA

211	NO	ATGAATAGGCTAAAGAGGATGCTTAGCAAGTGGAGCAAGGAATCATATGGAGACATCTTTCAAAAAGTATCCACACTTGAAGATGTGATTAAGGTAAAGGAAGTGCAGTTGGAAGTACATTGTTCAGATGAAAACATGAGAGACTTAAACAAGGCAGAAGAGGAGTTGCAGAAATTTTATCAACTGGAGGAGGATTTTTGGAAACAAAAATCAGGTATGAAATGGTTTAATGATGGCGACAGGAACACGAAATTCTTTCATTCATATGTGAAAGGCAGAAGGAGGAGGCTGCTTATAAATGAAATAGAGGATGAAAATAGAGCTATACTGAGGGAGGATAAAAGCATAGGTGAGGAAGCTGTGAAAGTCTTTGAGGATCAATTTGCAGCTGGAGCAGTTAGTGACGATCAGGCCATGCTAAATTGCATCCCACACATAATTACAGAAGAACAAAAAGAGAAGATGGATAGAACTCCGGAGGAAGAGGAAGTGAGGGATGCTATTTTTTCATTAAACAGTGAAAGCGCTAGTGGCCTAGATGGTTTTTCGGGCAAATTCTTCCAAGCTTGTTGGGAGATCATAAAGGAGGACATTGTAAAATTAGTGATTGCTTTGTTTTGTGGATGGGAACTACCAAGATATGTAATCATACAAATCTGGTTCTCATTCCAAAGAAGGAAAAAGTCACTAGTTTTAAGGACTTGA
212	NO	ATGGGCATCGGCTCCACCCATCTCACCTCCCCTGGATCTGAGAGTGAGGAAGTTGTGGGGTCCAAGACTCCAGTGCACACACCGGCAACAGAGGGAAAGTTGCTAAAGCGAAGGCGCTCAGTACTACGTTCTAAAGAAGTTCATGATCCATTAGCCCAACTTCTAGCACCTCTAGCACCTCCAACTGCAAAGGCATCTAAAGTGCCCCCAGCCCCAGCACAACCTCCTAGATCAATGAATCGACTGAAAGATACTTTCTTACAAACTATTCTGGAGGAGAAGTGGTTGTCCACGGATTGTGTGGTGGATATATATGCAATTTTGTGGGAGAGCCTGCATTTCCATCTACTCCAATAG
213	NO	ATGTTACTAGATAGAAGTTATGACGTGTTCTACTTTGGGGTGAGGCTTAATAATCTTAGGACTAAGATGAGATCTTCCATGAGGATGGAAAATCCTTATTATCATATGGCTGAAAAGAGCGATGACGATTCTCAAGGCTTGGACCTTTCTTTATGTGATGAGACGAGCCAATTCGTGTTCACTGTTGAATGGTTTGAAGCCGACCTAAGCCATGAAATCATCCCTTCTACACACGAAACTGAGGTGACATTAGATAGGGATTTGTTGATTTCTGCTAGAATGGATGGCATGGGGGTTGATGTTTGGAGATTGACTATTCACTTGATTTCTGTGTTGGCTAACGGGAGAGCCAAGAATAATGAGAATAAGCCGGCCAAAGATATCCATCCTTTGAGGAAAGGGAAGTTGGGAGAGAGAAGCTTGATTCAGTATAGAAATGCTACCTTGAGACATTCTTCCTCCAATATCCGCAAGGTTAGGGAGATGATGTCGAGCATTCCTTCTGGATCATCTAAAGCCACCACTGCAGAGGGTGTTCCTCAACCTACTATTCCTTCTATAGCTGTTGCACAAAGAGTGATGTACGACAGGCTTATGCACTTTAGTCAGAGGCAAGGAAGGATAAGAGTAGATGTGAATGACGTTCTGATAGCATTAGTGGATGAAGATAAAGTTCCTGAGCTAGATGATGGGAATTCTTAA
214	yes	ATGTTGCCAGTATATCAAGAGGAGAGTGAGCTGCTAGAGAATGTATTTGAGGAAGAAGAGGTACACGTAATTCGGTCATGTGCACCAAACAAAGCACCTAGCCTTGATGGACTTACTATGGCATTCTTTCCGAAGTCATGGGACTTCATTAAACCAGAGGTAATGGGAGCCATCAACCATTTCCACCAGCAGTGTTACATGGTCAAATCTTGCAATGTCTTCTCCATTGCACTGATTCCCAAAAGGAAGGGGGTTGTTGAGCTTTGA
215	NO	ATGGTAATTTTCATGATTCAGTTGGCACTTGGAGGTTTCGAGAGTTTCTCTACAGGAATCCTCTTGTTTTATAGGTCAAAGGTTGAGGAAGACCATCTAAACATCATTGATGAGTTTAGGGAAGCAAAGGGTGAGGAGTTCATGAGTATCAAACAGGAAGAAACGAGTGTGAAAGAGTATAGCCTCAAGTTCATTCAGCTATCTCGATATGCTCTCGGAGTGGTGTCGACCATGAGGGAAAGGATGAAGATTTTGTGTCAAGAATGGAAAGATGTGTATCTAAGGAGTGTGCTGCAACCATGCTTCACATGCAAGGATATGGATATCTCCAAACTTATGGTTTATGCCCAACAGGTTAAGGTAGAAAAGTTGTGTTGGATTGAGAAAGATTTTGATGATTGA

216	NO	ATGGGGCCAGAACTTGATACTAATAATGGAATTATTTTAGGTCTATTAAAAGAACTCTAGAAGATGTCTCATTGTTATGGCTTCTAAAAGACCACGATCATCCAGAGGTCCGACGTAGTGCACCAAAAGAGGGATCTAAAAAGAGAGGACTAGTTGATGAATCCAATGATAGTTCTAATAGTGACAACAATGTAGTCTCATCTGAAACTCTAGGAGATGATGATATTGAGGATGATGTGGTTCAAGAAAACTTGGAGGATGGGTATTCTATTGAAAACATCAAAGATAGTCTTGATGCTCGTACACGTAGGATAGTCAACTTTACTCTAAGAAATGTAATAAGGGAAAGGTTAATGATTGGGTTTGGAGGGCGGCTGAAATGGATGAATTACTGGTAA
217	yes	ATGGATCGTCCCCTGCAGGACTATGAAATAACTCAAGCTCTTTTCTCCTTCAAACCGTTCAAAGCTCCAGGGCCTGATGGCATACACCCACATTTTTTTCAATCCCAATGGAAAGTAGTGGGTAATTCTGTCATCGAAAGCTGCCAGCAAATTTTTAAGACCCTTCTCTGCCTCATACCTAAGTTCCCTAATGCTAACCATCTGAAGAACTATAGGCCTATTGGTCTATGTAATACCATCTATAAAATCATTGCGAACCGCCTTAAGCCCCACCTCAATAATCTTATCAGTCCCTGCCAAACTAGCTTTCAGAAGGGGAGAAGAGCTTGCCATAATGCCATCCTTATTCAGGAACTTATGACGCCTTAA
218	NO	ATGGAGAAAATGCAAAGTCAACAAAGTGATGATAACAATCAATCAATTGATGCATTTGCAGCAGTCATGAGACATGAACATCTAGGGTGCTTGATATTGTATGGACGAGGAGTTACAAAAACTACTTTGAAAAGGAAAGCACATTCTGAACCCTATTTAAGTGCTAATGATGAGATGATGCAAAAACAAATGGAGGAATTGGAAGATGCATCAGAGGATGGCGGAAAAATTAGAAGAATAAAAGTAACCATACACCGAGAAGTTACATATGATATCCTTGGACGACTTAATCATATGTATCATGAACTTCAATTTGAATGA
219	NO	ATGTTGGATGGAAAAGCTTTGTTTGCTAATGCTCTAGACGCAAAACACCCTATGGAATTGGAACATGCAGGGATGAGAGAAGACATCACTCGCGGAAGACCCTTACCCCTAACTCCAATCAATCATAATGCCTACCATGCGTTGATCGAAGCCACATATTCTAATGATTGCCAACAGAAAAAGCTTGCACAATCTCTACCCAATATTCTCTTGGTCGCTGGAGAAAAAGAAATTAAAGGCGTAACCAGTAACATAGACAATTTGTGCAAATGGGTTGAGGTAGTAGAAGAAGTTATCACAACTTTGAAAACAAACATGAATGACTTAAAGGGGAAAGCTCTAGTAGAAAACTGTGAAATGGATAAGTTGGTTGAAGTAAGTAGGGCATCGAGAAACACCTTTGGACCCATAGATGCTTTGATGCGGAGCATGAGAATTGTTGAAGAAGGAGGATGA
220	NO	ATGGATAGAACTGGTGCTGACACAAGACATGATGAGTCTAGTGAGGTTAGGGGGAAAGTTGAAAAAGATGAGGGAGTCTCTAATGAAGGACCACTCCAGCTTGTCAAAGGCTTTCTCAAGGTCTATTTTGAGGATCATATTGGCCTTTTTGCCTTTCATTTTGTTAAAGTGGCTTGTAGGTGGTGTTCAAAAACCAATGGGTCTGAAGTTCCTGATGCTGGTGGCATTGGAGATCTTAGGAATGAGGCAGAGGAGAGTGTTCATATGTTGAGGCATCCTGCTTGTCGAGAAGACTTCCTTGCAGAATGCACTAGCTTTTGGACCAACAATTCCCCAGAACTTTTGGTAGAAAAGCGGGTGAAACCATCAGGTCCAGGGGCTTTGGTAGCCTTGAAGGATTGGAGGGCTTGGGTGGTAGGAGGTTTGGTTGGTTATGAAGAGATTGATGAAATAGGAGAGAATGTGGCCGGTGATTTGACTCTGGTTGTGCAGAATGTTGCCAGAGTCATCCTGGAGATTGTTTATCCTATTTCTCCTCCTTATGTTGATGGTGGAGGTATGGAAGAAACTGATGTTGGCATCCCCATGGGACAACTAGTAAATTCTAGATTTGGTTCTCCAGAATTCAGCCTCCAACTTGAGAAGATTGTCATACTCTTTGAAGAGGTCGGACTCTAA
221	NO	ATGAGGTCATACCTGGGTAGAGGAAGTCCCGATGTCCGGAACCACTTAAGGAGAGCTCTCCCTCACATTGCCATTGTCCATGGGGATTATTACTTCCCTCTAAGGAGAGAGCTTGCCCCCGCATGCTCATCTCCAACCATGAGTGTCAAGTCTGGTTTGGGTTTGGGAAGTGAGTCGTATAGAACGTCTGACCTCCCAGGGTTATTGGTAGGGTGGGAAGAGTTACAAAAGGTCTTGGGGAGTCTTGTTGTGGACAGTGGCTTGGGAGTTTTTGGTTCTCTTATGGTTTGTTCTTCTGGGAAGAAATGGGAATTCTTGTCTTTTTTAGGGGCTCTATTAAGTCGATATAAATGGAGTTAA

222	yes	ATGAGAGCTTTAATATGGAATATTAGATCGGTAAACACTCAAAAGGCGTTTACTCGACTTATTAATTTGCACAAAAGATACCAATTCTACTTTGTGGGTTTGATGGAGCCGTTTGAAGATAGACATGAAATAGAGGAGTTTAGAAGAAGATTGGGGATGCAACAGGCAGTAGCCAATGCGAATGGGAAGATATGGGCATTTATTGATGAGGTCCTGGAGTATGAAATCATAAGGGATGATGATCAAATGCTAACTGTAATTGTGAAGAATCAATGGATGGGAAGTGAGGTTATGATTTCTTTAGTATATGCTAAATGCACACAAAGAGAAAGATTGCAACTATGGGAGTCGATGTATGATCTGGCAAACACGACTAATCTCCCATGGGTGATAGGTGGTGATTTTAATGTGATTAGTAATGAGGAAGAGAAACTGGGTGGTAGGCCAGTAACTGAGGCGGAGATTAGGGACTTTAATCATTGGATTAATGTGTGCAATTTGGAGGATAAAGGTTTTAAGGGCAGCAAATACACATGGTGGAATGGCAGAACAGAAAAAGATTGCATATTCAAGAGACTAGACAGGGTCTTATGTAATGAACAATTGCAAAATATATTTCCAGTAATGGAAATAGAACATTTGGTGCGAAATGGGTCTGATCATACACCATTATTGATTGTGTTAAAATCAAGTAATGAGAATGTGATTAAGCCTTTCAAATTCTTGAACTTTTGA
223	NO	ATGCAAAAGGGGAGACCTGTTGCTTTTCTTAGCAAAGTGTTAGCCCCTAAGCATAGAGGCAGATCCATCTATGAGAAAGAATATATGACTTTACTTAATGCAGTTGATAAATGGAGGCATTACCTCCAGTTCAAACATTTTGTGGTCAAAACTGACCAACATAGTTTGAAGTATTTGCTCGAACAAAAGGTGACCTCTACTATCCAACAAAAAGGTTTAACCAAGATGCTGGGACTTGACTATGAAGTGCGATACAAGAGAGGAGCAGAAAATAGAGTTGTCGATGCTTTGTCCAGGAAATAG
224	yes	ATGAGGACACTAGGTTGTTTATGCTATGCTACTGATCGTAATCCTCATGACAAATTTTCTCGAAGAGCAATACCTGCTGTTTTCATGGGCTACTCTCCTATTCAGAAAGGTTACAGACTATATAATCTTCAAACTCATGTTTTCTTTGTTAGCCGTGATGTTCATTTCAGAGAACATATTTTCCCTTTTAAGAGTTCTTCTATCTCTAGTTCTGATGCTTCCTCACCCTCTATATCAAATGAACTTCCATCTTATCTCCTTGATTCAGATAGTCCAACATTTTTTCACTCTGCGATCCCTTCCAGTTCAGCTCCTGCTCTTGTTCCTGCTGACATTCCATCACCATCTTCTACTACTCTTGATCCTTCCAACCCATCTCCTACATCTTCTTCTTTATCTCCAGTTCCACTTCCTGCTCAATCACCTGTGCCCACCAGGAAAACCTCTAGAGCTACCAAACCTCCGATCTGGCTGTCTGATTATGTTCAATCACATCCACATCACAAATCACACTCTCATTCCATCAATCATGTTGTCAACTATTCTCACCTTTCTCCTAGTTATCAAGTTTATCTTTCAAAATTTTCTACAACGACTGAACCTCACTCCTACTCTGAAGCCATCTTAGATGACAGATGGGTCCAGGCTATGAAACAAGAAATTGATGCCCTTGAGGAAAACAAAACTTGGGAAATAGTTGATCTACCAGCTGGAAAACTTCCAATAGGCTGTAAGTGGGTATATAAAATCAAATACCATGTTGATGGTTCTATAGAAAGGTTTAAGGCTCGACTGGTGGCCAAGGGTTATACTCAAAAGGAAGGTGTGGACTTTCATGACACTTTCTCTCCTGTTGCAAAGATGGACACAGTTAGATGTGTTCTTGCTTTGGCTGCAATGCATGACTGGCCTGTGTTTCAAATGGATGTCTTTAATGCCTTTCTTCAAGGTGATCTGCATGAGGAGGTTTTTATGGTACTGCCTCAGGGTTTTGGCAGTAAGGGGGAGTCAACACAGGTATGCAGATTAAAGAAGTCTTTGTATGGACTTAAACAAGCATCTAGGCAGTGGAATATAAAGCTTACTACTGCATTGATTGATTCTGGTTTCCATCAAAGCAAACATGATTATTCTTTGTTTACTAAAAGAGTGAAGGAGAAGTTTGTGATGATACTCATATATGTGGATGATTTACTGATCACCGGAAATGATTTGACACTGATCAAGGATTCACAGGCAAGTCTACAACAAACCTTTAAAATCAAGGACCTAGGTGAGTTAAGGTACTTCTTGGGAATAGAGTTCTTGAGATCTAGCAAGGGGATATTGATGACACAGAGAAAGTATATACTAGAATTGATTTCAGAATGGGGTTTAGCAGGAGCAAAACCTGCTATAACACCACTGGAACAACACATGAAGTTCACTACATCTGAGTATGACAAACAGCTGAAAAGGGCAGAAGATGATCCACAATTGGTGGATAAAAATGCTTATAAAAAACTGGTAGGAAAACTACTGTATCTAGCAATGACCAGGCCAGATATTTCCTATGCAGTGCAAACCTTGAGTCAATTCATGCATGACCCAAAGTAG

225	NO	ATGAAGTTGAATTATGTAGCTCATACTGTTCGAAATGGAGATACAATAGTAGAGCTGTGCAAAGACGAAGTAGAGCTCGAGACTGTGAGATGGAAACACGCTTTAATTCTCTATGTGGTGGGGGCTGACCCAACTATTGCTGCAGTAGAACGATATATTTCGGCACAATGGAACTACATAGCAAAACCCAAGGTATTTTACCATAATGATGGCTACTTCCTTGTGCGTTTTAATAGTTTTAAGGATAGGGGTGAATTGCTATATTCAGGGCCTCACATGCTCGGAAACAAGCCAATAATAGTGAAGACTTGGTCGCCGGAGTTTGATCTCAGCAAAGAGATTATGAAAACCATTCCAATATGGGTTAAGTTCCCGAACCTTCCTTTGAATTGCTGGGGAATGCAGTCATTAAGCAGACTTAGTAGTTGGTTGAGTATTCCATTGTACGCTGATGAATGCACAACACAGATTGACAGAGTCTCTTATGCTAAAGTTCTAGTTAAGATGGACATCAGTCAAAAGATGCCAACGGAGGTTAAGGTGGAAGATCTCAATGGGAGAGAATTCACTCAAAAGGTAGTATACGAATGGGTGCCGGCTTATTGTTCAAAGTGTCTGATAATTGGACACAAGTGTCAGCCAAAAGGGGACACACTGAAGCCTAAAGACAAGTTCGTCAAGCCAAGAACAGAGTGGCAACAAAAGATGGTGGAGCCTCGAGGTGAACAAAGTAATGACCCTGAGGAACAAAGGGCTGAGGTGGTAAGGCCAATGACTGTAGAACAGCATGAAGGAAAAGGTGTAGCTAATACAACACAAAAAGAAGGAGAACATGTACTAGTTCATGAGAGTGAGGAGAATTGGGAGGAAGCTAGAGGAAAATCGACAACAAAAGGGAAAAGACAATACATGGGTAAGGCTATAATTCCCACAGCAAATGAGTTTGACATATTTCATAACCATGATACTAGACATATAGCTGGTATGGGAAAAGGGGGAGGAGGATCAAAGGAGGTGGGGAAAGGCAACAATTTTGTCTATCCTAAATGA
226	yes	ATGAGGCATGTTTTCATCGACTTTGATAATATTGAAGACCACCTCGATGTCGCTTCAAGAAGCTATATGCCACTCGGAGGAGACATCATTATGAAAATTGAAAAGTGGAGTACGAACTTCAAACCTGAATCCAACGACACCACTGCCCCTATCTGGATTACCCTTCCAAATCTGCCATGGCATTACTACGAGTGGGATGCAATTTGCCGTATTGTTGAACCAATAGGAATCCCGCTAGTGTTGGACAAAGCTACTGTTTCAAAAACAAGACCAACTACGGCAAAACTGAGAGTAGAAATCGACCTTGCAAAACCAATTCTAAGAGAAATTACAGTTGAAATAAGAGACAAAAATGGCTTCTTTGTGCAAAAGGTAGAATATGATACTCTACCAGCCTTTTGTTGCCATTGTAAAATGCAAGGCCACAACGATAAAAACTGCAGAATTCTTCATCCCGAATTAAGAGAGGAACAAAGAGGAGCGGGGGATAACCAATCTATGAAGGCAGACCCCTCATCCAGTGGCAGGACAGAGTTGGCAAAGAACCTCAAAAAGGATACACTGCCAAGAAATGAAAAGGGGCATAAAATTGGACAGCAACAGTCACAAGCTATTACTCTCACTAAGTCAGTAGACACACAACTTGATTCATATTCAGAAACATCCACAGGTGCTGGTGGATGGAAAACTGTTACAAGAAAGAAGGGAAATGTAGCTAATCCACAAGTCAATAAAACAAAGAACGGAAAATGCAATAGTGTTGGTATGATGATGGCTGAAAAAAACAATACACATACTTGTAGCTCCATAGGTACTCAAAATGCAGTGGTAGTAACTCACAACACTACAGAAGTGGAAAATATGGAGATATCACTCTTGAATGCTCCCAGCATATGCAACAACTCAACACCCAGGTGA
227	yes	ATGGATGTATCCATTCTCCCTGATCAATGGAGACGGCGTGAACATGCTATGACACCAACAAACTTTGGCATATCATTTACAACTCTACTATTAAACCGGCTAGAGACATTTCTGGGGTATAAAACTTCCATCCCAAACCTTGAGGGCAAGGTTCATATCAGGGATGAACTGATGTATGTTATGAACCCAACCAAGATGGAGGATAGTTTCAGAAAAGTTACAAACTATTTGTGGGACCTGAGTTAG
228	NO	ATGATAGCAGACAGAAGGAGGTTATGGGAGCAATTAGTGAATATACACAGCAACAAACAGACACCTTGGCTGGATATGGGAGACTATAATACCTTCCATAGAGGAGAAGATAGATTGGTGGGAACCCCTGTCCAAGAGGTAGAGATAAGAGACTTTGCTGATTTTTTGAGGGACACAAGTATGACAATACAAAAGCACAAAGGTCGTGATTATACTTGGATAAATGGACACACATATAGTAGAATTGATTGGGATCTAGTAAACACCAAATGGATGCTGGATAAGCCAAACTTGGAGGTGCAGATTCTTGATCCGGGCTGTTCTGATCATTCCCCACTAAGTATTAACTTTGGCCAACTGGATGAGATGAGACCTAGGCCGTTTAAATTCCTAAATCATCTAGCAAAGCATGTATAG

229	NO	GO:0003723; RNA binding; Molecular Function;GO:0003964; RNA-directed DNA polymerase activity; Molecular Function;GO:0004190; aspartic-type endopeptidase activity; Molecular Function;GO:0006278; RNA-dependent DNA replication; Biological Process;GO:0006508; proteolysis; Biological Process;	ATGGTATCAGAGCCTCCTGGTGCCTCGACGCTTCCCGGAATGTCATCACCTCCGGAGCTTCAGAGCTTGCAAGACGATATCCGTATGGTGCGAAGCCAACTCTCTGTTTTCGTGGGTGATGTGGGCAAACGTTTCGAAACCCTCGAGTTAAATCACTCACAATTTCAAGTTCAGCTGGGTGAGATTTGTGAGACGAACAAGAAACTCGAATTTATCATTTCGAATATGGGATTGCAGAACACTCCTAGCTCTCCCATGACCACCCCAACTGATTTGACTCCACAGGCGACACCAGGAGGAGGTCAGGGAACCCAGTTCCGTTTGGAAACTGGCCAGACTTCGAATAGCACAGTTCCGATGGTAACTTCCTCTTCTCATATGGTAGGTTCTCAATCTCCATTCACTCCATCTGTTTTTGAAGTAGGTAGGGGATTCACTTTTCCCCCAGCACCTCTCTTCTCGAGCCCTCCTTTGTTTCGGAACCCCCTTTATTCTTCTGCTCCCCCGTTACTCCCCACTCCAATCATACATACTCCAGAATCTGCCTCTCCTCACAGATCTTTCAAACCTAAAATTAATTTTCCAGAATTTGATGGCACTAATCCTCGGAGCTGGTTAAGGAAATGTGAAAAGTTTTTTGAACTATACAATATAGGTGAACAGGAGAAGCTTAGTTATGCATCCGTCCACCTTGGTGAAAGGGTGGATATCTGGTTTGATAGCTTTTTAGTCAACCAGAGGGGAAGGTTGACATGGCCAAGGTTCTGCACTGAAGTTTGCAGAAGATTCGGAAATATTAGGCCCCAAGACATTGTTGATGAATTCAACAAACTCATACAAATGGGGTCTGTGGATCAATACCAGGACAAGTTTGAAGAACTTACTAGCTATATGACTATAATTAACCCTTTGTTGAATGAAACTCACTTTGTAGCAAGTTTCATTAGTGGTCTTAGACCAGAATTGAAGCCCTTGGTAAAACTGGCTAATCCCACAACTGTGCTGGATGCTTATGAGGTCGCTAAGTTGTATGAAGAGTCATTCAGGGCACTTATTCCGTTAGTACCCAACCCAAGGCCATTAGCCATTACCTATCCCAGAAACCCACAACCAAATGCCATGAGACCTCCGATTGTTCCTCCAAATCAGTCACCATTGAGGATAACTTACCATAATCAAAGACCACAAGTTAGGGCTCCATTCAAGCCAAACATGTTGCCACCTAACTTGGAAGCATTGAGGGAACAAGGTCTTTGTTATAAGTGTAAAGAGAAGTATTTTCCTGGTCATCAGTGCAAGCAGAAGGGGTTACATGCTATTGATGGGGTTGAAGTTGAAGGAGAAGTGGAGCAACCTGAGGAGTTTTTGGATGTACCTGATACTCTAGAGGAAGAAGAGGCAATTCCAGCTGAAGTATCTTTAAACGCACTGTTGGGACTGAGTACCTCTAGTGGAATTGTGTCTACCATTAAGATTGTAGGCTATGCTAGAAAGTTGCCAATGACAATCTTAATTGACAGTGGCTCTACTCACTCTTTTGTTGACCCTCACATTGTTAAACTACTGAGAGTGCCCGTACAACCAATGCAGAGACCTCTGCGAGTCACAGTGGCCAATGGGCAGCTAATGAGTTGCCAACTGGAAAGTCCATCATTTGGATGGAAGATGCAGAGTGAACAGTTTAATTTCAATATGAGATTAATGAAAGTAGGAGGTTGTGACATGATATTGGGAATGGACTGGATAGACATGGTTGCCCCTGTAATTTTGCACACCAGGCCACACAGCCTAAGTTTTATGACTGATGGAAAAATGGTCACATTGTACGGGGAGACAGAGGATTCTGAAGTAACCACAATGGATACTGAAGCACTTAAAAGGATGCTCCAGTGTGGGACTTGTGAAATTATAGCGGAATTATCTATGGTGAGTGTTGGATTAGCTATCAAGGACGAACGTGAAGTACATCCAGAAATCACTAAGCTGCTAACAGTTCATAAAGATGTGTTCCAAGAGCCTAAAGAATTACCACCCAAAAGAGATTGTGATCATGTGATCAATTTTGTACCAGGAGCTCAGCCTTTCAACCTCCGACCCTATAGATATTCTTTTGACCAAAAGAATGCTATTGAAGCTATCATTAATGACATGCTCAAGGCCGAAACAGTAGTGAAGAGTCAGTCTTCTTTTGCATCACCAGCTCTACTGGTGAAAAAGAAAGACTCCACTTGGAGACTTTGTGTGGACTACAGGAGATTGAACAGCCTTACTGTTAAGAACAAGTACCCAATCCCTATGATTGATGACTTGTTAGACGAGCTGTTTGGGGCAACTATATTTTCCAAAGTGGATTTAAGGGCTGGGTACCATCAGGTTAGAATGAAGACGGGTGAGGAATTCAAAACAGCATTCAGAACACATCATGGGCTATGGGAGTTCAGGGTTATGCCTTTCGGGCTTACCAATGCACCAGCAACATTTCAGTCTCTGATGAACTCTGTGTTCCAGGATCAACTGAGGAAATTTATACTAGTGTTCTTTGACGATATACTAGTATATAGC

230	NO	ATGGTAGCACTTTTGGAAACCAGGATGACCAGTCATGTTGGACTTAAGGACGAATTTGGATTTGATGACTTCTTTGAGGTCCCTGTGGTGGGTAGATCTGGGGGTTTGGTCTTGCTTTGGAACACTGCTTGGGTTACTGTTACTCGTCTTAGGCATTCTGATCAAGAGATACATGCAATGATTCAGGAGAAATGGGATGGTAATTCCACTAACCGTTCTAGGAGCTCCCGTTTCTGGTCATGTGTGAATCACTGTAACTTAATTGGCCTAGGGTTTAAAGGAAGCCATTACACTTGGTATAATCATATGAATCATAATAAAGGCCTGATTTTAGAGCGACTAGATAGATGTTTTGCTAATGAAAAATGGCTAGCTTATTACCCCAACGCGATAGTCACTCACCTCCCTAAAACCCATTCGGACCATCATCCTCTCCTTGTCACTTTAAGTCTTCGTGCTAATACCCGCACTTCTAGATCCTTTAGACTAGAGAGTAACTGGTTACAACATCCTAAATTTAGAAATATTGTTAATAGTAGTTGGTTGAATAGGGACCTCGTTACCGCTACTGACCATTTTAAGGGCATACTCACTTACAGGAGCAAGAATACCTTTGGTGATATATTCAAAAGGAAAAATAGGTTGCTCGCTAGATTAGATGGTATTCAAAAATCTATGTCCTATCCCTACAGTATCTTCCTCCATCAGTTAGAGCAGGATCTTATTAAGGAATACAATAATATACTCCAAGCCGAGGAAGATTACTAG
231	yes	ATGGGAAATGAGTCCTATTATAAATCTAAAACGGTCTTATGGGGTAGAACTATTCATCCAGAAATTAGGGAGACTCCGGCTGTCAAAAGATTACTGGTCTTGTTTGCGGCTCAGGGGTGGGTAAATGTGTTCTTAAATACTGATGAAATGGTCTATGATAATGAGGTGATTGAGTTCTACACTAACTTGATTGTGTTGGACAATACTGTGGTTTCTTCGTTTGTTCATAGTGTGGACTTAGTCTTTGACAAGGTTAAACTAGGAGAAATCTTTCATATTCCTTGTATTGGGTTGGATGAGTATAACTGGTCGAAGGAGGAAAATTGTATGTTAACTTCAAAATTCTCACAGGGCAGGGTTACTGTTCGTCCTAGGAAGGTATTAAAAGGGGAGATGTCGTTGTTTCACAAGTTGGTGTTTGAGGTGGTACATAAGGGGATACTACCACGGGGTGAGCGACGTCATGAAGCTAGCTTTAGGGATATGGGCATTGGTCATGCCTTAGAAAACATGGACCCAATTGACTGGCCCTCTCTTATGATCAAACATATGGCCAGAGTTGTGGATCCTAAAAGACCTCACCAGTTAGCCTATGGAAATTTGTTGATCACTGTGTTTAAGGAGTTTGGGGTACCCCTTAAGGAAGGTAGGCTTTTGAACAAGAATGACATTTCACCAGGTCGACTCTCGCTGAATGTTCCTGTTGTCCCTCCTCGTGTTGCTGGGAATGTTGCTACTCTTCTCAATGAACTCCGTGTGGCTAAAGATCAGAATGAGGAGTTAAGGGGTGAAATTCTCACTCTTCAGGCGAACTTAGCTGATTCTCAGGGGGAAGTTTCACGGTTGAAAGATCAACTAATCCAGCAACAAATTGCCAATAATGTTCGTATGGATCACATGATGCAAGTCCTTGCTTTGTCTTCCACCCATCCTCATCCCTCTTCCCCAGCTCACTAA

232	yes	GO:0004672; protein kinase activity; Molecular Function;GO:0004713; protein tyrosine kinase activity; Molecular Function;GO:0005524; ATP binding; Molecular Function;GO:0006468; protein amino acid phosphorylation; Biological Process;	ATGATGAATTCCACTCACATTGCAGTCAAGATTTTTGAATTCGAGGAATTAGCAGCTGCAACAAGCAATTTTCATGAGGATTGTCTTCTTGGAGAGAGTGATTACGGAAGAGTTTACAAAGGACAGATCGATTCTAATCAGGTTGTTGCTATCCAGAAAGTGGATCATGATAGAATAAGGAATTTTCTTGTTGAACTTTATTCCGCTCCTGATAAGAAGCAACTTGATTGGAACACTAGGATGAAAATTGCTTCCGAAGCAGCAAAAGGATTAGAGTATTTACATGACAAACAACAGCCAACTGTAATACACCGCGGTATAAACTGCTCTAACATTTTGCTTGGGGAGGGATATCAAGCTAAGCTATCTGGCTTTGGCTTCGCAAAACTGGGGCCTCCAGATGGAAGGAAAGATATCGGAAATTCAAAAGATGGAGAAGAGTCCAATCTTATTGCTTGGGCAAGACCATCGATCAAAGACGACAAATTTTCAGAAATGGCAGATCCAGCACTTCAAGGCCATTATCCTGCAACAGGCTTGAAGCAAGCACGTGTGTCCAAAAGCAACCTCACGGGCGTCCTACCATGGCAGAGGTAG
233	yes		ATGAAACCATCCCTGCCTACTGCTTTCACTGCAAAATCCAAGGACACCAAGATAAGAAAGAAATGCATAAAGCTTCACCCTGAGTTAAGAGGCATAGGCCCCACTAAAGGAAGCTTATTTAACAATCAGAAGAAACAACAACTTACTCCAAGGACAGGAAATGGTATCACTACTATCAACACCGAAAGTGTAGCAACTCATCAGGACAATTCCAGTGATATTAAGGTGCCTGAAAATGTCGAAGGATGGCAAACAGTTACGAAGAGGAAAGGAAAAAACAAGGATGTCCCTACCAAATCAGAAATCGTGATTTGCCCGGGCTCTAATACTAAGGAGAATATGAATGCTTCAAGAGGATCTACTAGTCAAGCTCACTCCACAAAACAAGAAAAGAACCAAATCAACACTACTCACAAAATAGGAACTTCAGAGGACAATATGGATATCACCATCTCAAAAATCCCATCAAGACAACACCAACCTACTCAACAACCTAACCCCCACAACCTCAGATCGTACACAAGAAAAGACAAAATGAAACCCCCCAAAAAGAGCCCTCATCTGAAGAATGTTCAGAAGAACATGAGGAAAGTGACACATAAAAAGGAATCTGTATTCGCAGATGCTCAAGATCAGAATCAAGTTTTGAACTCTAAACTGGTCCATAATTATTCAGCCAACTTTTGTCCTCCTTTGTTTGGCCTGAACCACAAGTTATTATCAGGGAAAACAGGCAGAAAGAATGAAAATAAGGATCATCTGACTTTGAATTCTGTACTAAATCCACTCCAACCTATTGGATTAGTTACCGAGTCCCTCAGTAACAAAGACATATGGGAGGACACCTCTTACAAAGACTGTGTGGAAGACTTGAGTTTAGATATAATGATTGAAGATCCTGGACATTCCCTATCTGATGATGAACTCATTAGAGGTCAAAAGTCTATTCTTCCTAAGATAAAGACTGTGGGTAAGGACTCTCAAGTGCAGCAAAACGTTGCTTATTACAACAACCTATCTCCGAGTGGTAACTTTGATTCCAATTATTTTGTAGTGGATCAAAGCAAATCTCCAAATTCAAATGGATCTAATCTAGACCCGATTTTCCATGATTAA

234	NO	ATGCTTGAATTCTCCAGTTGGATAGAGGAGCTAGAACTTAAAGATCCAACTTCGATGGGTAGGAGTTACACTTGTTTTAGGGGGATTAATCACCAAAGTGCTGCTAAGTTGGACAGTTTTTTGTATTCTATGGAATGGGAGGAGAACTTCAAAAGTATCAGACTGAGAATTCTTCCAAGAGTAGCTTCTGATCAATGTCCTATAATTCTTGAATGTGAACACAGCGAACAGAGACAACCTTATTTCAAATTCGAAAATTGGTGGCTCAAGGTGGAGGGATTTAAGGATATGGTACAGGACTGGTGA
235	yes	ATGAATGGTGACTTGGTGTATGCTGCAACTAAGGGGATTGAGGAAGGAACTAACATCATTGCTAAGGCAAGGCAAAAAAGGAAGGGATACAATGGTGGATTGTCCAGTGAAGAAAAAAGACTTCTTAATATGATAAGACACAAACTTCAAACTTGGCTATACGAAGACATCAAAGAGCAGCACAAACCAATGCAAATCACAATCATGGAGCAAATAGTCAAAGTAGAAGTTGATTGA
236	NO	ATGTTCACTTGGTGGAATGGCATAGCAGAGAAGGAGTGTATATTCAAGAGACTGGACAGAATCCTGAGGATTGCAACATTGGAGGACTTGATCAAGGTAAAAGAAGTGCAGCTAGAAACCCAACCAACCCCAACTAATAGATGTGAGCTGAGTAAGGCGGAAGCAGAGTTAAGGAAGTACCCAGTAATTGAGGATGAGTATTGGAGACAAAAAGCTGGTATGAAAAGGTTTAAGGAAGAGGATAGTAATACAAAGTTCTTCCACTCTTATGTAAGAGGAAGAAGGAAGAAATTGCACCTATCTTGGATTAAAGATATCAGAAGAAATAAAGTAATTACTAATGAACAAATGAGAGAAGCAACTATTGAATACTTTCAAGATCAATTTTCAGAGGAGAACAAAAACCTAGACTTTGATATGCTTCAAATAATTCTGAATCTAATCAGTGATGCACAGAATGCAAAGATCATCAAGCTTCCAAGCATAAAAAAATGGAAGAAGTAG
237	yes	ATGCTCTCCAACCTTTCTGAACCTATCAGTTTCAATCAAGCTTGGGAACATCCAGAATGGAGAAAGGCTATGGAGGAAGAGGTTAAAGCTTTACAGGTCAATCACACTTGGGATGTGGTTTGCTTACCTTTGGGAAAGAAACCATTGCCGTGTAAATTGATCTACAAGGTGAAACATAAATCAGATGGAAGTGTGGAGAGACTAAAGGCTAGACTTCTGGTGAGGGGGGACATTCAAAGGGAAAGGATTGACTACACCGAGACTTTTTCTCCTGAGGAAGAAGTCTACATGAAGTTTCCTGCAGTTTTTACTCCTCCTAAACCTAATCAAGTTTGTCTATTGAGGAAATCACTATATGGGTTGAAGCAGACATCTAGGCAATGGTATGCTAGGCTTGCAGGTGCACTACAATTCAAAGGGTATTCCAATTCCCTGAATGATTACTCCCTATTTTTCAAGAAAACAGGAAGTGCAATTTCAATCATCACCGTGTATGTGGATGATATATTATTGACAGGAGATGATGCTTCTGAGATAGCTGACATCACAAGTTTTCTCAACGCAGAGTTCAAGGCAGAATGGGCGTCATGTAAAGATACAAGGAGATCAGTTCAGTCCTAG
238	yes	ATGCTGATTGAAGCCATTAAGAACAAGGGGAAGAAGGCTGAGCTGATATCTTATTCGAAGAATCCTCTTTCACATGATAATAATAATAGCACAAGTAGAAACTCCAATCACAATCACTTTGACAATAAAGAAGAGGCTGCAGCTTGCCATACTAAGGACTATAAGGGCAAAGCTAAAGTTGGTGATGACAACATGAAAAGAAATGAACATTGTTGGAATAGTAGTGATGATCATGAGACTTGTGATGATCAGTACTGTGAAGATTATCATGTGTCACCAAAGAATAAAAAGTGTGAAGATTTTGTGTCAACCAAAAACAAGCAAAAATATCATACAGCTGAAGCTTATGTGGCCCCTCAAGGAGTTGATCCAAACATCTGCAGGGATCGCTACTGCAAAATACATAGAAGAGGTGGAGGCATGCGAGATTATGTTACTCAAGAAGAAAGACAGAAAAAGTATGCTATGTTTATGCAAATGGGAGGTCACCCTGCTGGATTTTTCAATGGAGAAGCTGCAACTTACATGCCAATTCCTCCATATCAATATGGGCATTATGGTCCGGACCTGGATTATGGGTTTTATCCGCCCGCCCAGCCCATGTCAGGGTTAAATGACTTCACTCGTTATTTTGGTGACCAAGATTCTCGCACTTGCACCATTATGTAA

239	yes	GO:0005524; ATP binding; Molecular Function;GO:0006915; apoptosis; Biological Process;	ATGGCATACACCTCTGTTAACTATTCCGTGAATCATCTGATCCGCCTTCTGAGCTCTCGGGGCCTGATCTTTTCAAAAGAAGGCCAGATCCCCATGCTTAAACTGGAGCTCATCTTCCTGAGAACTTTTCTCTGGTGGACTGCAAAACGCTGTACGGAGAATCAGAATTTGGAACTACTCTTACGGCAAATCGAAGTTGTGGTGCGAAATGCAATTAGTCATATCAAAGCCAGAGATTCGGATGAGTGGTCTCTTCAAGTATTGCATCACACACGACTTCTCAAGCCAGAGATTGAGAAGACTTACATCAAAATTGTTAAGTCTTCTCCTCCTATGCCCGACACACGGGTGGTGGTAGAGTTCATGAACAATCTGATTGACAATCTGAAGAATCTGCTTTGCTATCCGGACTCTTCCACTTTTTCCCCAGAGGAAGAACTCAGACAACTTGTAACTAAGCTAAGGTTCTTGAGAAATCTTCTTAGCTTTGTAGCTACACGTTGCACCGACCATGAGAAGCTGAAACATCTCTCCAATTATGCTGAAGCTATAGCTATAGAAGCAGCATGTCTTCCTTTCATGTGTTCATTTGACCAAAAAGATGGAAACAGTACAAGTTCCATTAAGGACAAGCTCACGGAAATGACACGGAAAATTAATCCTATCACTCCAGACATCAGAAGGATTTACGTGGAAGTCCTCGAAGCACTGAGTCCATTAACAACAGAGACTGACATTTCAGATCCAGACTTGGCATCCTTCATAGATACTCTCCAAGATTGTCTAACAGAGCTAAAACACAATCAGCCGCCTTGGATTCGTTCGTTGAAGGTTAACTTTGAAGCCCTCCACCATGAACTCGCCTTCCTCAGCTCTTTCGCTAAGGACCCTCCGGAGCAATTCATTGAGAGTTACAAGTCGGATGATCCTAAAGTTGATCCAATTCAACTTCTCTTGGGAGAGATGAGAGACTGGAGCGCTTCTAGCGCACATCTGTTCAAGCACTATACAGAACATTTGACATTGAAAGGTCAGTTCACCCGTATTCAAGATCTGGCTGTTAAGGTGGGATGTACCATCTTTTTCTTCTTTAATTTCAACGAAATGGAAGAGCACAAGCTTGCGGAAGAAGAAGCTACACTTGTTGATTTAATCGAAAAGATCAAGCACCTTAAGTCGGAGATCGGAGTTCCCATGTTGACATTGCCTGAGGTGAATATCATAAGGACAGATGACCTGGGTTTTATCAGAAATTTGATAGAGCTGATTAACCAGCAGGCAGGTCCACTCGACTGCCTGAAGCGTCGTGTACAGGGAATTGCTGACGAGCTGGAATTCCTAAGTTCTTTTCTCAAAAAATGTGGAGAGAGGCGCCATGAGCACGAGAAACTGAGGAATCTTGCAGGCCAAATAATGACTGTTGCATACAGAGCTGAATATGTCATTGACTCGTTATTGGTAAGAGATGGTACTCTATTCTACCATTCATTTTGTATTGTTGATGTCGTTGGAGAGATGAAGAGAATCAGAAGGGAGGTCATGGTGTTTGACGAAAAGATGAGCAATGTCATTGAGCCCAAGGTCCTTAATTCGACAATGCCCTCCAGAGACATGGTAAGTGTTGCTATGTCAGAGGAACTAGTGGGCTTAGAGGATGAAAAGGAGAGATTAAGAGATCAACTGATAAATGGATCTCATGCGTTAAGTGCTATACCAATTCTTGGTATTTGTGGACTGGGAAAGACAACTCTTGCCATGAGTCTCTACCACGATGAGCTTGTTGTCAGACACTTTGATATTCGTGCAGCCGTTTCTGTTTCCCATGTATATGACACTGAAAAATTGGTACTTGCAGTGTTGCACAATATCAATGGATATCCTGACACATCTAATGGAGGGGATGGTGATCTGTTGAAAGTCAAAAAAATGATATATTTGTCTTTGAAAGGAAAGAGGTTCTTGATCTTAATAGATGATCTGCGGGATACTGAAGCATACGTTGATTTGGGAAACCTGTTTCCAAACGATTTTACTGGAAGTAGAATTCTCCTCACCACTCGATCATATCAAATAGCTTCATGTGCTGCGCATAGTACTAAAATACATAATCTTCGATTTCTTACAGAAGAAGAGAGTTGGAAATTACTTAAAAAGAAGATATTTCACCAACAATTTTGTCTTCCAGAACTGGAGGAAGCAGGAAAGCGCATGGTCAAACAATGTCACGGGATACCTGCCATGATAGTTTGGATGGCGGATATTGTTGCAAGAACAAGGACAGAAGCCGATTGGATACAAGTTGGGGAATGTAACCAAATTGATGAATATCTTTTCAGCATTAATGAAAAAGAATACAGTGTCATACCAGATCATCTCCGTCCATGCTTCCTTTATTTTGGAGCATTTCCGTTGGAGGAAGAAATTCCAGTATCCAAATTGATCAAGTTGTGGGCTGCAGAAGGTTTCATTCAACAAACTGAAGCAGAGAGCTCTGAGGCTGTCGCAATGGATTACCTAAGGTATCTTGTTGAACGAGGTTTTGTAATGGCCTGCAAACGAAGCT

240	yes	GO:0003676; nucleic acid binding; Molecular Function;GO:0003677; DNA binding; Molecular Function;GO:0015074; DNA integration; Biological Process;	ATGAAAAGTGATGTGTTTCCCATATTAAAGTCTTTCTTTGCTTTAGTTCAAAATCAGTTTAATAAGCATGTGAGGAAGATAAGAACTGACAATGGTACAGAATTCTTTAATTCTGAATGTGGTACTTTGTTTAAAACACTTGGCATTGTACATGAAAGTAGTTGTCCACATAATCCACAGCTGAATGGAGTAGTGGAAAGAAAACATAGGCATATTCTTGAAGTAGCAAGGGCATTGAGGTTTCAAGGTGCTATCCCTATCAGATTTTGGGGAGAATGTGTGTTAGCTACTGTTTATTTGATTAACAGGTTGCCAACTGAGGTGTTAAAAGGGAAATCTCCTTATGAGCAGTTCAAGCAAAGCTTGACCACCTCAGAACAATAG
241	yes		ATGCCATTTTATCAATCTTTTGTTGAGCATGGACGTTCCGAGGACTTGTATGAAACCCATCCGAATGAAGTTGCTGGGCAGGTTGGACGCCATGCTGTTCTGGTCATTGGATTCGGTACTAGGTATGTTGATGGCGTTCGTAGGGGGACTTCTTTATTGTGA
242	yes		ATGAAAGATCTTGGAGAGTTGAAGTTCTTTTTGGGTATAGAATTCTCTAGGTCACACAAAGGCATCCCAATTAATCAGAGAAAATATGCTTTGGAATTGATAGAAGAGCTGGGGTTAAGTGATTCAAAATCAGCTTGGACACCTTTAGAGATCAATCAAAAGTTCACAACAAAGGAACTTGATGAACTCACAACAACTAAGGATGATGATCTTTTAGAAGATAAGGAAAAATACCAAAAATTGATTGGAAAGCTTTTGTACTTGACACTAACTATGCGGGATATTGCATTTGTTGTTTAG
243	yes		ATGTCTGAGCGACTATTTGATGGAGATCTCCCGGCAGAAAAGGAGATGAAGTCGAATATCTTATACGTAGGGGATGAATGGGTCGTGCAAAGCTTGACTGACATGAACGAAGATATCCAAACATCATTTTCTGAAGTGGGGTACAAATCACTAGATCTAGTTGAACACACCATGGTACATGTGCTTGATCACACTCTAGAGACTCGATTACACCTGGATAATGTTCAAGATGACTTGGTGGAAGATGAGGATAATGTTTCTCTAGTGTGGAAAAGGAAGGGCAGGCGGGGAGTGAATGAACAAGAACCTACTCCAACTGAAATAATTGCTCAGCCCTCTTTGGTATCCAAGGATTCACAACAACAACAGGGTCTGAGAAGTGGGTTCCTGAGGAAATCTCAATGTCAGACAAAGGAAAAAGGAAAATGA
244	NO		ATGGTTGCAGCTGCTAGAGTGATCAAGTATGTGAAACAGTCACCTGGACTTGGTGTATTCATGTCAGCCTCTGCATCTCCTCTTCTTACAGCATACTGTGATGCAGACAAGGCTGCGTGTGTCAACACAAGACGATCAGTCACCAGATACTTACTTAAGCTTGGTGATTCCATCATTTCCTGGAAATCCAAGAAGCAGCAAACCATTTCTACAAGTTCAACTGAGGCTGAATACATGAGTCTCGCTTCCATAGTGGCCGAGGTTGTTTGGCTTACAGGTTTACTGGCAGAGTTAGGTATAAACTCTGATGGACCAGTTGCTCTGCTTTGTGACAGTAAATATGCTATTCAGATTGCCACTAACCCAGTATTTCATGAACATACAAAACACAAAGATATAGACTGTCATTTTATACGAGAAAAAATGCAGCTTGGTTTGGTGAAATTGTTGCATATTTCTACTAACGAACAACAGGTTGATATATTGACAAAAGGTCTTGGCGTGGCTTAG

245	NO	ATGAGGGATCTTGAAAATAAACATAGATCGGACAGAGCTTTCACTGTTGGCGAATGGGTTTATCTAAAATTTCAGCCTTACACACAAGTTTCTGTAGTTTTTATGCCCTTCAATATGCTTGCAGCCAAATATTTTGGGCCTTACCCTATTGATGCTAAGATTGGTGTTGTGGCCTATATGCTCTTACTACCAGCGGATATGCTAATTCATCCTGCATTCCATGTGTCTCAGCTTAATAGGTGTCATGAGTTACCATTGGTGACTACACACACTCTAGTGTTTCACTTATCCAGTCCTTATTGTCCTTCTCCTGAGACTATGTTGGACAGGAGATTAGTAAAGAGGGGTAACAAAGTTGTTGAATAG
246	NO	ATGGGGGTGATCAATGACTACCCGACCATATGGGACACCATCATGTTGAATAGATTTGAGCATTTCATAAGAACTCGACCCCTTATGTTTAAGCTTGGGTTCGTGAGTTCTGCATGGCCTATGCAAAGTCCTTGCCCCAAAAAGGAAGGGATTTATTTGGAAACCCTTGGAAGAGGTCGAAATAGGGTAAAGATTGAAAAGAAGGACATCAACATCGTTGCTCAGATTTGGTTCGGGTTTATCAGTAGCAACCTCATGCCATCCAAGAACGAGTGTATCCTTTTTCACCTAAAGGACGTATTGGTTGGAAACATTATTGACCGGAAGGACATCCATGTTGGTGCCATCATAGAAGAGGAGATACTCATGAGATCAGATGCTAGGGCCTCTAGGCTTGAGAGGGAGATGCCCAAATATATGGAGAGGTTGATTGAAGCCGCCATATGCCCTGTTAAGGTTCTCTTGCCCAAGTTGCCTAAGGTTGTGCCTCCTATTAAGATGAGAGTTGATGCACCTGGTGGGGTAGCTAAGAAGCCACCTGATGTTCATGATAAGGCTGATGATGATGTAGTTGAGGAGCTGATGAGGCTGAATTTTGGAGAGAGGATGAGCAGTGATACCCGAGATGATTCCATCCTCTCCAAGCCTGGGGTTCAGAGTTCTTCACATGCATAG

Supplementary Table 16. DM specific genes

Code	DM Gene	Transcript in DM	Chromosome	RNA-seq support in DM	Functional annotation
1	PGSC0003DMG400006617	PGSC0003DMT400016927	chr01	NO	
2	PGSC0003DMG400008518	PGSC0003DMT400021967	chr07	NO	GO:0016884; carbon-nitrogen ligase activity, with glutamine as amido-N-donor; Molecular Function
3	PGSC0003DMG400002666	PGSC0003DMT400006867	chr09	yes	
4	PGSC0003DMG400020031	PGSC0003DMT400051570	-	NO	
5	PGSC0003DMG400043280	PGSC0003DMT400093709	chr04	NO	
6	PGSC0003DMG400007077	PGSC0003DMT400018233	chr07	NO	
7	PGSC0003DMG400001404	PGSC0003DMT400003553	chr02	NO	GO:0008152; metabolic process; Biological Process GO:0008415; acyltransferase activity; Molecular Function
8	PGSC0003DMG400007550	PGSC0003DMT400019527	chr09	yes	
9	PGSC0003DMG400029541	PGSC0003DMT400075948	chr08	yes	
10	PGSC0003DMG400036156	PGSC0003DMT400086585	-	NO	
11	PGSC0003DMG400034450	PGSC0003DMT400084879	-	NO	
12	PGSC0003DMG400010729	PGSC0003DMT400027856	chr11	yes	
13	PGSC0003DMG400042139	PGSC0003DMT400092568	-	NO	
14	PGSC0003DMG400038266	PGSC0003DMT400088695	-	NO	
15	PGSC0003DMG400036460	PGSC0003DMT400086889	chr03	NO	
16	PGSC0003DMG401000497	PGSC0003DMT400001304	chr02	NO	
17	PGSC0003DMG400040508	PGSC0003DMT400090937	chr05	NO	
18	PGSC0003DMG400047221	PGSC0003DMT400097650	-	NO	
19	PGSC0003DMG400042878	PGSC0003DMT400093307	chr08	NO	

20	PGSC0003DMG400038794	PGSC0003DMT400089223	-	NO	
21	PGSC0003DMG400009674	PGSC0003DMT400025045	chr06	NO	
22	PGSC0003DMG400028523	PGSC0003DMT400073428	chr06	NO	GO:0008152; metabolic process; Biological Process GO:0008415; acyltransferase activity; Molecular Function
23	PGSC0003DMG400017450	PGSC0003DMT400044992	chr10	NO	
24	PGSC0003DMG400032524	PGSC0003DMT400082405	-	yes	
25	PGSC0003DMG400038980	PGSC0003DMT400089409	chr10	NO	
26	PGSC0003DMG400038106	PGSC0003DMT400088535	-	NO	
27	PGSC0003DMG400024431	PGSC0003DMT400062770	-	NO	
28	PGSC0003DMG400033868	PGSC0003DMT400084187	-	yes	
29	PGSC0003DMG400045276	PGSC0003DMT400095705	chr08	NO	

Supplementary Table 17. Genes annotated in DM in Figure 3d.

DM Gene Code	Gene in DM	Functional annotation	RNA-seq support in DM	Premature Stop (PS)
A	PGSC0003DMG400030563		yes	
B	PGSC0003DMG400030516		yes	
C1	PGSC0003DMG402030515	GO:0006855; multidrug transport; Biological Process GO:0015238; drug transporter activity; Molecular Function GO:0015297; antiporter activity; Molecular Function GO:0016020; membrane; Cellular Component GO:0055085; transmembrane transport; Biological Process	yes	
C2	PGSC0003DMG401030515		yes	
D	PGSC0003DMG400030562		NO	PS in RH
E	PGSC0003DMG400030514	GO:0005634; nucleus; Cellular Component GO:0006333; chromatin assembly or disassembly; Biological Process	yes	
F	PGSC0003DMG400030561	GO:0005515; protein binding; Molecular Function	yes	
G	PGSC0003DMG400042076		NO	

H	PGSC0003DMG400030560	GO:0015986; ATP synthesis coupled proton transport; Biological Process GO:0015992; proton transport; Biological Process GO:0016469; proton-transporting two-sector ATPase complex; Cellular Component GO:0016820; hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances; Molecular Function GO:0033178; proton-transporting two-sector ATPase complex, catalytic domain; Cellular Component GO:0046034; ATP metabolic process; Biological Process GO:0046933; hydrogen ion transporting ATP synthase activity, rotational mechanism; Molecular Function GO:0046961; proton-transporting ATPase activity, rotational mechanism; Molecular Function	yes	
I	PGSC0003DMG400030559	GO:0009055; electron carrier activity; Molecular Function GO:0016491; oxidoreductase activity; Molecular Function GO:0055114; oxidation reduction; Biological Process	yes	
J	PGSC0003DMG400030513		yes	
K	PGSC0003DMG400030558		yes	
L	PGSC0003DMG400035916		yes	
M	PGSC0003DMG400030511		yes	PS in RH
N	PGSC0003DMG400030557		yes	

O	PGSC0003DMG400030556		yes	
P	PGSC0003DMG400030510		yes	PS in RH
Q	PGSC0003DMG400010740	GO:0016021; integral to membrane; Cellular Component GO:0051205; protein insertion into membrane; Biological Process	yes	
R	PGSC0003DMG400010739		yes	
S	PGSC0003DMG400010771		yes	
T	PGSC0003DMG400010776	GO:0005515; protein binding; Molecular Function GO:0005524; ATP binding; Molecular Function GO:0044267; cellular protein metabolic process; Biological Process	yes	PS in DM
U	PGSC0003DMG400010777		yes	
V	PGSC0003DMG400010778	GO:0003676; nucleic acid binding; Molecular Function	yes	PS in RH
W	PGSC0003DMG400010779	GO:0008202; steroid metabolic process; Biological Process	yes	

Supplementary Table 18. RH specific genes in Figure 3d.

Code	Function annotation	RNA-seq support in RH	Sequence
1	Actin related protein ; K05692 actin beta/gamma	NO	ATGATAATGGACCCTGCTACCTCTCGCCCTGCTCTAGTCATTGATAATGGAACTGGGTATACTAAATTGGGTTTTGCTGGAAATGTTGAACCAAGTTTTATTTTACCGACGGTGGTTGCTGTTAATGAGTCGTTTCTGAATCAGACTCGAGCTACGACTAAGAACAGCAATTGGCTAGCGCAGCATAGTGCAGGGGTTATGGCGGATCTGGATTTTTTTATTGGGGAAGAGGCATTGACTAGATCTAAATCTAGTAATACTTATAATCTTAGTTATCCTATTAAACATGGTCAAGTTGATAATTGGGATGCTATAGAGCGTTTTTGGCAGCAATGTATATTTAATTATCTTCGTTGTGACCCTGAGGATCACTATTTTTTATTGACTGAAAGCCCCATGACTGCACCAGAAAGTCGAGAATATACCGGTGAGATTATGTTTGAGACTTTCAATATACCGGGGCTTTATATTGCTGTGCAGCCGGTGCTTGCTTTGGCGGCTGGATATACAACATCTAAG
2		yes	ATGGGAAAAGGGGAGGGAAATTTGGAATCATGGAAGGATGGTGTATTGCACTCAACAGATATGGCACAAGCACCAAGTGGGCATGCAAGCACGCTTGTGCTGGCGGGAAACAGGACGAGGAGGCCAGACTTTCTTTCTGGTTTCCACAAATACAGAGGTGGATGGGATATTGCCAATAAACACTACTGGACATCTGTTGGTTTTACAGGAGTTGCTGGTATCATACTCGCTCTGCTGTGGTTCATTTCTTTTGGATTGGCTCTTGTAGTGCATTATTGCTGCGGATGGAAGATCAATATTAGAGATGGAGAACGACATTTTTCAGAGAGAATTTGCCTGATCGTGCTTATCATCTTGACATGTGCTGCAGCTATCGGTTGCATTCTTCTTTCTGTTGGACAAGATGATTTTCACGGTGAAGCATTGGACACTCTAAAATATGTTGTAAACCAGTCAGATTACACTGAACAGACATTGAGAAATGTAACACAATATCTGTTACTCGCAAAAACTGTAAATGTGGCCCAGATTTTCCTCCCTTCAGACGTAAAAGATGATATTGATCGCCTAAATGGAGACCTAACTTCTGCAGCAGATAACCTCAAGGAGAAAACAAATGAAAACTCAGGAAAGATACGAAAAGTCTTCAATGCTGTGCGGTCAGCTTTGATCACTGTTGCTGTCGTTATGCTTCTCATATCCATTCTGGGTCTTTGCCTCTCTATCCTTGGCCATCAACACACAATTCACATATTTATCATTAGCGGATGGTTGCTGGTGGCATTTACATTTGTTCTCTATGGAGTTTTTGTCATCATTAACAATGCAATTTCAGACACTTGCATGGCAATGGGAGAGTGGGTGGACAATCCTCATGCTGAAAGTGCTCTTAGCAACATCCTTCCATGTGTTGACCCGAGAACTACAAACCAAACCCTATTCAAGAGCAAACAAGTCACTGTTGATCTCGTAAATATTGTCAACGGATTTATAGACACATATGCAAATTCCAATCCATCTAATCATCTCAATTCAAATTACTATAACCAGTCAGGACCCGTTATGCCACGTCTCTGCTATCCATATGACTCCCAATTGCAAGATCTGCCATGCCCGACTGATCAAGTGTCTATGGCAAATTCTTCAACGGTTTGGCAGAATTATACTTGCAGTATATCTGAGGCCGGAATGTGTACTAGCATCGGTAGGCTGACACCCGACATGTACGAACAGCTAGTGGCAACGGTCAACATAAGCTACGCTCTTGAACATTATGCACCGCCACTGCTTAATCTCCAGAACTGCAATTTTGTCCGCGATACATTCAAGAACATCACGGCCAATCACTGCCCTCCATTGGAACACCATCTCCGAGTCGTTAATGCAGGGCTAGCCGTCATCTCAGTTGGAGTCATGCTAAGCCTTGCGTTGTGGATAGTATATGCAAACCGCCCCCAAAGGGAGGAAGTGTTTGCGAAGCTCTCTTCGCGTATAAAAAGCAGCTGCAATGGTAAGAATGTTAGCTGCAGCAATAGCAACATTGATTTGTCATCAAGAGGCACAACTCCAAAAATTGGAGTGTAG
3		yes	ATGCACATTGCTCGGAATCCGGTTTTCCATGAGAGAACGAAACACGTAGAGCTTGACTGTCACTTTGTTCGACAACAATATCTCTCTGGCCTCATTTCTCTCTCTTTTGTTCCCTCCAAAGATCAACCAGCCGACATTCTCACAAAGCCTTTGTCCGCGCCTTCTCACCATCATCTTCTTCGCAAGATGGGTATCACTTTGCTCCCCTCCATCTTGAGGGGGGATGTTAAAAATACACAGACCTTGAACTCACATTCATCAATGGTGAAGCCATTTTCAGAGAGAAAGAAGAGTTGTTCAGACAATGAGACAAAAGGCACTTTGAAGAATGCAAAGTGTTTTAAGCCTTGTAATAGTCAGCAGCAACGTGACATAGATCAGGCCCTTAATACTGATTTAGTCAAAGAAAAGATTTGTGCCGTCCACATCAGTGACTTCAGGAAGTTTCCTTACAAAGCACGTGACAAGCACAAGCTTGGCATAGACAAGGAA

4		yes	GTGTCACGCAACGAGTCTACACCCTGGGCGGGACCGGCACTCGGAGACCATCACTGGCCCCAAGCGAACCCTTGGCCTGGCGTTCTTAACTCAGCGAAAACCTCAACAAGAATAACTCAAAGCAATGCAGTATTTCAAAACAACTTAACTTATAAAAATATGGCCCTAAGGCAAACCGAATCCCAAAATAGGATATTTACATATATAAGAGACTCAAAACTAACTGATTGTCTGTCTGTCTATGAAGCCTCTAAATTTCTGAGATGGATGTTGGGACAGACCCCGCAACATCCTAATAAGACAAAGCTAAGAACGCAAAACAATTGAGTCCTCCAGAATGCAAGGAGGCTCACCACTGACTCTGGAGTGCTCAGCTGGATCAACGACGTTCAGGCTGCTGATCTGGGATACCTGAATCTGCATCATGAAACGATGCAGGCCAACTGGCATCAGTACATGGAATGTACGAGTATGCAAGCTGGAAAACTAAGCAACAAC
5	estExt_fgenesh4_pg.C_LG_X0521; . ; K10251 beta-keto reductase [EC:1.1.1.-]	yes	TATATCGATCAGTTTTCAAGATGTTTATACGTTGAATACAAACAACATGGTATAGATGTACCATTATATGTTAAAACAAAGATGACTTCAAGAGTTGCAAGCATAGAGAAATCATCATTGTTTAGTCCAACACCAGAGAAGTATGCAAAAGCAGGAGTAGCACAAATAGGATATGGTTGGAGAAGCATGCCTTATTGGCCACATTCAATTCAATGGTGGTTTGCTTCTTTATTGCCTCAACCTCTTCTTGATGCATGGCGCCTCTCCATTGGCCTTAATAGGAGGATTAAAACT
6		yes	ATGGTGAAACGACGTCGCGAAGAAATTGATTCCGATGGAGCAACGGAAACGGAAAATACGACCTCATACAAAACGGTTTTCATAGATACCAACCTTGATACCCACTTGGCTGTAATTGTCTCCGATTCCGATACTATCTCCGATCTTAAAAAAAAGCTCGTGTTTGAACACTTAAGGTGTTTTCCTGAAATGAGTGAGTTGAAGATTTCTTCTGTGAAGGTGAAACGAAAACGACATTACTATCATCTGCCTGACACTATGCTTGTTAGAGGTGTTTTTGAGGGTAGCAAGAAGGAATGGTTCCTTTCTGTTGATGCTTCTAGATTTCAATGCCTTGAAAATGACCAAGGGTTACTTTGCATAGCGTATCCGCAAATTGAAGCTGAAAATCTTCTCCCATGTGATTCATTCAATGCAATGGATAAGCAGAAGGTTTTTGATACTAGTGAATCTTACCCAGCTAATGGGAACTTGGCATCTAGCTCCATCGTGAAACACAAGGAAGTTGCCAAGGTCATAGGTGAACTCAAGAGTGTGAAGCGCGCAGGTAATTCTCAAGAACTTTCTCCCAGATCTGGTCATGTGGCTAAGAAGCGTAAAATAAAGCACAAAGAAGACAGAGTCAACCACCCGGTAACAGGTACCAGCGCTTCAAATCATGGCATAGATAATGGTTTTGAATTTAAAATTGTTGGAAATGATACTACTTTGACAAATTCTAATGAAGGAGAGCGGGAAAATATAAACATGAAACTGGTAGATGTCAATGCTGAACCCTTAATAAACCAACGTTCTGATCCCAGTAAGGTGTCAAAATTGGGAATGAAGAAAAGCAGGAAGGGTAGGGCAAGTGCTGAAATCCTTGGTGTGCAGGATGAGCTCTGTGGAGATAGGAACAATGATGCACTTGGTGAAACATCACACTCTGGGACTCTTGCAAATAAAGTTAAAATTTTGGGTAGCAAGGAAAGCAGTGGAGCTTCCACCGAGTTCAATCATAGGGATAGCTTGAAGATCGCAATTCCAGAGAACTCCACAGCAGGTAAACCAATAAAGGCAGCTTTAGCAGAAGAAACATTAGGGGACCAATCTGTGAGAACAGATACAACCCATAATAAGAGGAAGAAGAAAATTAAGAAGGGGAAGGACTCATCCACGTGCCATGATGAGGTTGCCTGCATGGCTCTGGGTTCCAATGATAAATTTGTGGGAACTAGGGGATTAGAGCAAAAGGAAGGAGTTGAAATGAAGATCTTTGACAAGTTGACTGATGTTGACTCTACTATTCATGCTACTCAATCTAGACTGAAAGAAACATCTTTTGTTAAAGATCATGCGTCAAACAAAGAGTGTCCAGCACCAGTCAGCAAGGGTATTTGTGAAATGAATTTAGTTGGCCAACCTATTCTTGAATCCAATGTCTCTGGAGACGATGAACTTGGAATTGATGTTGCTAACACAACTGGAGAACAGGAGCTGATACCGAACTGTGATTTTGAAATGCCCATGAGTGAAAAGTTGAGTGATCCAAGTACCAGGGGTCCAGTGCCTTCCTACCAGTTGGGAGAATTACAAGGAGCAGCAGAAAATAGCTTTGGGAGGAAGAGAAGCAGGGCCAAGAAGTCAACTTCTCATCAGGAGTTAGATATGAAAAATATTGTTGGGGCTTCTCAAAATGCTTATGCATCTGACCAAGATATAGTCCGTAATGATGGTTCAAGTGATGCAACAACAAAGGTTGGTAGTATGCCAAAAACTGATGTGGATCATATAAATGAAATAGGGATCGAAGGCAAGTTGTCAGTTACTCAAGGTGCTGAGACATCCCCTCTTTTAGATAACAATGAACCAACTGGGGATACTAAAGAACAAGTTCTCTCAGCAA

7	yes	ATGAAAGAAATTAGTGTTTCATCATCATCGATAATAATATCGAAATACATATTTTTCATCGTCCTCATAACAATACCAATCCTCCTTTTTCTCTCTCATCGGAACTCATCTTCTTCCGCTTTCATCTCCACCACAACAACTTCAAATTCCGATTCTGATCTCAAAATTCGTCCCGGATATTCCACCTACGATTCCTACATTAAGAAACAGCTAAACAAAACACTCAATCCAAAACTCAGAAAAATCTGGACGACTCGTGATTGGGATAGAAAAATTGAAGTTTTCTCAAAATTCTTCGGAGAACTTAGAAATGGAAATTTACTCTCAGATTCATCGAAGGTACTCTGTATTGGTGCTCGTATGGGTCAGGAAGTGGAAGCACTGAAACGAGTCGGAGTTTCGGATTCCGTCGGAATGGACCTTGTACCGTATCCGCCATTGGTGGTTAAAGGAGATTTTCATAATCAGCCGTTCGACGATGAGATTTTTGATCTGGAATTCTCCAATGTGTTCGATCACGCGCTTTTCCCGGAGAAATTTGTATCGGAGATCGAACGGACATTGAAGACCGGCGGGGTTTGTGTGTTACACGTGTCGTTATCTAAACGAGCGGATAAGTATTCGGCGAATGATTTGTTTAGTGTTGAACCGTTGAAGAAACTGTTTAAGCGGTCTGAGTTGGTTCATACTCGAACCGTTGATGGGTTCGGTTTAGATACGGAAGTTGTTTTCAGAAAAAAACCGA

Supplementary Table 19 is too large to place in this combined PDF file. It is provided as two XLS files as separate datasets.

Supplementary Table 20. Disease resistance proteins in potato.

Predicted Domains	*Solanum phureja*		*Populus trichocarpa*		*Oryza sativa*		*Arabidopsis thaliana*	
	#	%	#	%	#	%	#	%
TIR NBS	14	3.43	13	3.23	-	-	21	10.14
TIR NBS LRR	35	8.58	78	19.40	-	-	83	40.10
CC NBS	22	5.39	19	4.73	7	1.31	4	1.93
CC NBS LRR	60	14.70	119	29.60	159	29.72	51	24.64
NBS LRR	172	42.16	80	19.90	40	7.48	6	2.90
NBS	105	25.74	49	12.19	45	8.41	1	0.48
Other	NA*	NA*	44	10.95	284	53.08	41	19.81
Total	408		402		535		207	

	Solanum phureja	*Populus trichocarpa*	*Oryza sativa*	*Arabidopsis thaliana*
Total # of predicted genes	39031	45550	37544	25498
Genome Size	~ 800Mb	485 Mb	389Mb	125 Mb
Source	PGSC (2010)	Kohler et al. (2008) G. A. Tuskan, et al. (2006)	IRGSP (2005) G. A. Tuskan, et al. (2006)	Meyers et al. (2003)

Supplementary Table 21. Sequencing statistics for each Illumina DM DNA library

Library ID	Insert Size (bp)	Read length(bp)	Total bases (Gbp)
TUBhswDAADBAAPE	200	40,45	4.53
TUBhswDAADCFBPE	206	40,39,45	0.64
TUBhswDAADCBAPE	220	40,39,41	9.9
TUBhswDAADCCAPE	230	37	6.12
TUBhwfDAADEBAPE	356	42	5.31
TUBhwfDAADEAAPE	400	42	5.22
TUBhswDAADGHAPE	470	40	0.9
TUBhswDAADGHBPE	478	42,73,61	8.6
TUBhswDAADHGBPE	481	39	0.52
TUBhwfDAADIAAPE	509	67	4.45
TUBhswDAADHDAPE	519	40	0.6
TUBhswDAADIJBPE	545	40	3.17
TUBhswDAADIJAPE	549	39,66	3.92
TUBhswDAADIEAPE	553	38	0.33
TUBhwfDABDOBAPE	800	69	6.68
TUBhwfDABDOAAPE	811	70	9.67
TUBhswDAADWBAPE	2180	42	2.6
TUBhswDAADWAAPE	2320	41	2.57
TUBhwfDAADWAAPE	2340	43	2.63
TUBhswDADLAAPE	4540	45	0.79
TUBhswDADLCCPE	5060	45	1.21
TUBhwfDAADLBBPE	6570	43	1.98
TUBhswDADLBBPE	8170	45	1.35
TUBhswDBDLAAPE	8890	45	1.41
TUBhwfDAADLAAPE	9600	43	2.88
TUBhswDCDLAAPE	9770	43	1.3

Supplementary Table 22. Production of Illumina reads from the DM potato genome

Sequencing Data	Insert Size	Total Length (Gb)	Sequence Depth (X)	Read Length (bp)
Solexa Reads	200-356 bp	26.5	36.45	40,45
	400 -811bp	44.06	60.61	38,39,40,42,67
	2-4kb	8.59	11.82	41,42,43,45
	5-6 Kb	3.19	4.39	45,43
	8-10 Kb	6.94	9.55	45,43
Total	--	89.28	122.81	--

Supplementary Table 23. Statistics of number and length for each assembly level

Step	Paired-end insert size	Sequence coverage	Physical coverage (X)	N50 (bp)	N90 (bp)	Total length (bp)
Initial contig				697	125	461,978,406
Scaffold 1	205~330 bp	35X	90.36	8,659	1,203	561,466,364
Scaffold 2	420~562 bp	51.86X	192.77	16,454	2,822	601,449,361
Scaffold 3	729~811bp	61.21X	241.43	22,424	6,346	620,452,457
Scaffold 4	Add 2 kb	72.3X	399.78	67,456	14,569	640,198,017
Scaffold 5	Add 5~6 kb	76.7X	603.75	173,731	37,830	665,731,592
Scaffold 6	Add 8~10 kb	79.2X	1,484	389,563	95,432	727,233,046
Final contig	All	79.2X	1,484	31,429	6,858	682,695,621
Fosmid end & BAC end & 454 PE	8K~150 kb	(fosmid end: 90407; BAC end: 71375; 454 PE:1018623)	14	1,318,511	253,760	727,424,546

Supplementary Table 24. DM scaffold N50 (N90) size.

	Contig Size	Contig Number	Scaffold Size	Scaffold Number	Super scaffold (DM data)	Super scaffold (DM data) number	Super scaffold (DM and RH data)	Super scaffold (DM and RH data) number
N90	6,858	23,392	92,035	1,935	253,760	622	349,019	443
N80	13,084	16,371	168,472	1,366	510,824	423	759,501	301
N70	18,866	12,046	240,175	1,003	784,705	307	1,104,492	222
N60	24,812	8,893	307,947	735	1,068,563	228	1,476,584	165
N50	31,429	6,446	386,629	524	1,318,511	167	1,782,249	121
Total Size	682,695,621	-	727,233,046	-	727,424,546	-	727,451,546	-
Total Number(>100bp)	111,187		66,301		64,386		64,116	
Total Number(>2Kb)	34,457		4,208		2,309		2,043	

Supplementary Table 25. RH whole-genome Illumina data per insert size.

Library type	Insert size	Read length	Total reads	Total bp
Single-end	500 bp	75	107,492,068	8,061,905,100
Paired-end	200 bp	75	174,979,788	13,123,484,100
Paired-end	200 bp	125	326,814,010	40,851,751,250
Paired-end	300 bp	100	82,324,780	8,232,478,000
Paired-end	500 bp	75	528,763,314	39,657,248,550
Paired-end	500 bp	125	200,147,478	25,018,434,750
Matepair	2 kb	35	72,401,032	2,534,036,120
Matepair	5 kb	35	167,488,622	5,862,101,770
Matepair	10 kb	35	41,822,754	1,463,796,390
Total			1,702,233,846	144,805,236,030

Supplementary Table 26. RH whole-genome 454 data

Library type	Insert size	Average read length	Total reads	Total bp
Matepair	20 kb	259	686,844	178,053,005
Matepair	20 kb	255	653,410	166,359,937
Matepair	20 kb	310	765,621	237,055,547
Matepair	20 kb	293	643,577	188,612,498
Total			2,105,875	581,468,489

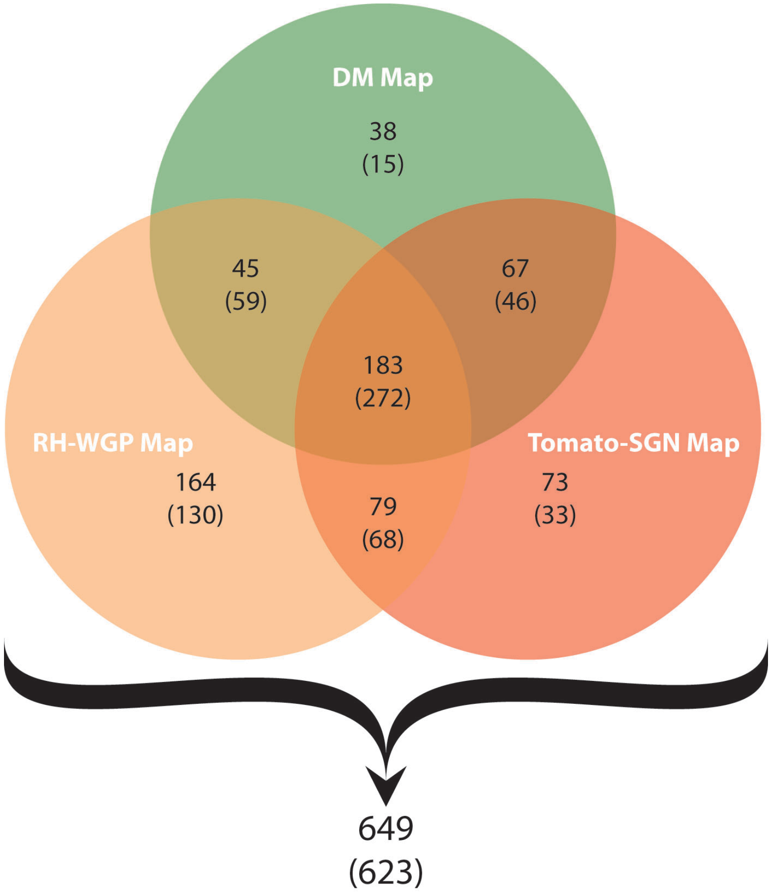
Supplementary Table 27. (A) Anchoring statistics by chromosome for the three different physical maps, de novo (DM) and *in silico* (RH and Tomato).

A.

Chromosome No.	**DM Map**			**RH-WGP Map**			**Tomato-SGN Map**		
	Superscaffold count	Total length (Mb)	Number of markers	Superscaffold count	Total length (Mb)	Number of markers	Superscaffold count	Total length (Mb)	Number of markers
1	39	45	162	69	80	208	43	41	271
2	35	43	175	35	43	120	33	40	233
3	19	24	108	28	27	73	41	45	194
4	34	47	138	51	57	168	40	39	174
5	20	27	74	33	45	137	25	30	112
6	29	34	108	44	46	119	34	34	133
7	26	24	89	35	39	122	32	31	136
8	32	32	152	24	23	57	40	32	129
9	27	28	109	34	33	91	40	39	136
10	31	38	106	34	44	102	26	32	110
11	20	26	113	36	38	110	22	26	116
12	22	26	72	47	52	164	26	28	109
Total	**334**	**394**	**1406**	**470**	**527**	**1471**	**402**	**417**	**1853**

In each map, the number and length (in Mb) of superscaffolds is given for each chromosome along with the number of markers.

B) Combination of the three physical maps.



The number of mapped superscaffolds is given in the appropriate intersection of the three different maps and the length/size (in Mb) of chromosome/genome assembly anchored by these superscaffolds is shown in parenthesis. The total number of mapped superscaffolds is 649 which together anchors 623 Mb of the assembled potato genome.

Supplementary Table 28. The source of proteomes of 11 plant species for OrthoMCL.

Species	URL
Arabidopsis thaliana	ftp://ftp.arabidopsis.org/home/tair/Genes/TAIR9_genome_release/TAIR9_sequences/TAIR9_pep_20090619
Brachypodium distachyon	ftp://ftp.jgi-psf.org/pub/JGI_data/phytozome/v5.0/Bdistachyon/annot/Bradi_1.0.pep.fa.gz
Carica papaya	ftp://asgpb.mhpcc.hawaii.edu/papaya/annotation/
Chlamydomonas reinhardtii	ftp://ftp.jgi-psf.org/pub/JGI_data/phytozome/v6.0/Creinhardtii/annotation/Creinhardtii_153_peptide.fa.gz
Glycine max	ftp://ftp.jgi-psf.org/pub/JGI_data/phytozome/v5.0/Gmax/annotation/Glyma1_highConfidence.pep.fa.gz
*Oryza sativa**	ftp://ftp.plantbiology.msu.edu/pub/data/Eukaryotic_Projects/o_sativa/annotation_dbs/pseudomolecules/version_6.1/all.dir/all.pep
Physcomitrella patens	ftp://ftp.jgi-psf.org/pub/JGI_data/phytozome/v6.0/Ppatens/annotation/Ppatens_152_peptide.fa.gz
Populus trichocarpa	ftp://ftp.jgi-psf.org/pub/JGI_data/phytozome/v6.0/Ptrichocarpa/annotation/Ptrichocarpa_156_peptide.fa.gz
Sorghum bicolor	ftp://ftp.jgi-psf.org/pub/JGI_data/Sorghum_bicolor/v1.0/Sorbi1_GeneModels_Sbi1_4_aa.fasta.gz
Vitis vinifera	ftp://ftp.jgi-psf.org/pub/JGI_data/phytozome/v6.0/Vvinifera/annotation/Vvinifera_145_peptide.fa.gz
Zea mays	http://ftp.maizesequence.org/current/filtered-set/ZmB73_4a.53_filtered_translations.fasta.gz

*: pseudogenes and TE-related genes are excluded

Supplementary Table 29. List of transcript assemblies used to define Asterid specific genes.

A. List of non-Asterid Species

non-Asterid Species Name	Number of PUTs	PUT version
Adiantum capillus-veneris	16,944	171a
Agrostis stolonifera	9,039	173a
Allium cepa	12,990	161a
Amborella trichopoda	15,772	165a
Aquilegia formosa x Aquilegia pubescens	19,615	157a
Arabidopsis thaliana	543,450	169a
Arachis duranensis	18,183	179a
Arachis hypogaea	30,391	171a
Arachis ipaensis	19,201	179a
Aristolochia fimbriata	7,967	165a
Avena barbata	21,360	173a
Avena sativa	13,499	173a
Beta vulgaris	18,009	157a
Brachypodium distachyon	30,991	175a
Brassica napus	145,002	173a
Brassica oleracea	12,843	163a
Brassica oleracea var. alboglabra	13,513	159a
Brassica rapa	44,998	171a
Bruguiera gymnorhiza	13,332	175a
Cajanus cajan	18,151	177a
Cannabis sativa	2,671	177a
Carica papaya	42,169	167a
Cenchrus ciliaris	12,364	165a
Ceratopteris richardii	4,234	157a
Chlamydomonas reinhardtii	50,380	163a
Cicer arietinum	14,386	175a
Citrus aurantium	11,427	167a
Citrus clementina	39,468	171a
Citrus limonia	9,857	173a
Citrus reticulata	46,876	167a
Citrus sinensis	105,294	167a
Citrus trifoliata	35,130	173a
Citrus unshiu	10,489	169a
Cryptomeria japonica	24,299	167a
Cucumis melo subsp. melo	13,692	163a
Cucumis sativus	5,799	175a
Curcuma longa	6,627	157a
Cyamopsis tetragonoloba	7,618	157a
Cycas rumphii	10,901	163a

Cynodon dactylon	12,782	169a
Elaeis guineensis	20,874	171a
Elymus wawawaiensis/Elymus lanceolatus n	8,782	169a
Eragrostis curvula	10,948	165a
Eschscholzia californica	7,546	177a
Eucalyptus globulus	7,106	179a
Eucalyptus gunnii	8,171	165a
Euphorbia esula	27,994	157a
Fagus sylvatica	8,700	179a
Festuca arundinacea	32,650	175a
Festuca pratensis	36,007	173a
Fragaria vesca	11,527	163a
Fragaria x ananassa	9,391	177a
Ginkgo biloba	10,210	169a
Glycine max	259,849	169a
Glycine soja	11,332	157a
Glycyrrhiza uralensis	12,020	173a
Gnetum gnemon	6,193	163a
Gossypium arboreum	24,597	157a
Gossypium barbadense	1,175	179a
Gossypium hirsutum	98,420	165a
Gossypium raimondii	27,355	157a
Hevea brasiliensis	4,896	179a
Hordeum vulgare	134,482	169a
Humulus lupulus	9,789	168a
Jatropha curcas	13,775	179a
Juglans hindsii x Juglans regia	7,753	159a
Leymus cinereus x Leymus triticoides	13,567	163a
Limnanthes alba	4,359	165a
Linum usitatissimum	11,026	177a
Liriodendron tulipifera	14,232	165a
Lolium perenne	10,937	179a
Lotus japonicus	56,525	177a
Malus x domestica	89,158	173a
Manihot esculenta	30,401	165a
Marchantia polymorpha	10,959	157a
Medicago sativa	6,104	163a
Medicago truncatula	65,628	169a
Mesembryanthemum crystallinum	11,317	157a
Mesostigma viride	7,371	157a
Musa ABB Group	5,167	169a
Musa acuminata	4,510	175a
Nuphar advena	13,789	165a

Oryza sativa	44,644	163a
Oryza sativa Indica Group	92,900	171a
Oryza sativa Japonica Group	146,642	163a
Ostreococcus lucimarinus CCE9901	13,940	161a
Panicum virgatum	101,077	169a
Papaver somniferum	16,486	167a
Paullinia cupana var. sorbilis	10,672	167a
Persea americana	10,928	165a
Phaseolus angustissimus	3,499	165a
Phaseolus coccineus	221,911	179a
Phaseolus vulgaris	21,361	165a
Phyllostachys edulis	10,954	175a
Physcomitrella patens	60,395	169a
Picea abies	8,715	175a
Picea engelmannii x Picea glauca	13,880	157a
Picea glauca	48,619	175a
Picea sitchensis	31,054	175a
Pinus banksiana	13,040	177a
Pinus contorta	13,570	175a
Pinus pinaster	15,648	177a
Pinus taeda	72,829	157a
Populus deltoides	8,186	163a
Populus euphratica	9,117	163a
Populus nigra	32,718	163a
Populus tremula	19,633	163a
Populus tremula x Populus alba	15,946	169a
Populus tremula x Populus tremuloides	35,128	157a
Populus tremuloides	5,730	157a
Populus trichocarpa	29,682	157a
Populus trichocarpa x Populus deltoides	23,686	157a
Populus trichocarpa x Populus nigra	9,740	157a
Populus x canadensis	4,940	157a
Prosopis juliflora	1,125	179a
Prunus armeniaca	5,637	157a
Prunus persica	28,475	171a
Pseudoroegneria spicata	10,168	169a
Pseudotsuga menziesii var. menziesii	9,857	161a
Quercus petraea	23,740	177a
Quercus robur	26,509	177a
Raphanus raphanistrum subsp. landra	17,564	165a
Raphanus raphanistrum subsp. maritimus	17,333	165a
Raphanus raphanistrum subsp. raphanistru	33,369	165a
Raphanus sativus	32,502	165a

Raphanus sativus var. oleiformis	19,390	173a
Ricinus communis	12,382	163a
Saccharum hybrid cultivar	48,295	177a
Saccharum hybrid cultivar SP70-1143	18,963	177a
Saccharum hybrid cultivar SP80-3280	81,835	177a
Saccharum officinarum	131,381	157a
Saruma henryi	6,754	157a
Secale cereale	5,977	157a
Selaginella moellendorffii	20,542	165a
Sorghum bicolor	44,954	157a
Sorghum propinquum	9,061	157a
Syntrichia ruralis	7,087	169a
Tamarix hispida	8,616	157a
Thellungiella halophila	16,783	169a
Theobroma cacao	57,035	169a
Trifolium pratense	12,746	157a
Triticum aestivum	301,765	163b
Triticum monococcum	6,987	157a
Triticum turgidum subsp. durum	8,460	169a
Tropaeolum majus	4,696	169a
Vigna unguiculata	34,736	167a
Vitis shuttleworthii	5,905	157a
Vitis vinifera	64,796	169a
Volvox carteri f. nagariensis	20,687	165a
Welwitschia mirabilis	6,606	157a
Zamia vazquezii	7,657	165a
Zea mays	181,717	171a
Zingiber officinale	16,495	157a

B. List of Asterid species

Asterid Species Name	Number_of_PUTs	PUTs version
Actinidia chinensis	18,734	167a
Actinidia deliciosa	24,981	167a
Actinidia eriantha	5,282	167a
Antirrhinum majus	13,801	157a
Artemisia annua	28,799	177a
Barnadesia spinosa	21,811	169a
Capsicum annuum	32,336	171a
Carthamus tinctorius	22,428	159a
Catharanthus roseus	9,675	165a
Centaurea maculosa	28,506	161a
Centaurea solstitialis	26,496	169a

Cichorium endivia	21,603	159a
Cichorium intybus	32,617	171a
Coffea arabica	10,013	175a
Coffea canephora	20,168	157a
Cynara cardunculus var. scolymus	20,915	179a
Gerbera hybrid cultivar	9,660	171a
Guizotia abyssinica	20,579	169a
Helianthus annuus	61,175	169a
Helianthus argophyllus	20,511	157a
Helianthus ciliaris	16,353	159a
Helianthus exilis	21,776	157a
Helianthus paradoxus	20,645	159a
Helianthus petiolaris	14,885	157a
Helianthus tuberosus	25,708	159a
Ipomoea batatas	12,464	169a
Ipomoea nil	22,946	157a
Lactuca perennis	12,747	157a
Lactuca saligna	12,186	157a
Lactuca sativa	29,977	157a
Lactuca serriola	22,957	157a
Lactuca virosa	12,839	157a
Mimulus guttatus	39,577	173a
Mimulus guttatus var. nasutus	9,469	175a
Mimulus lewisii	9,950	175a
Nicotiana benthamiana	25,297	173a
Nicotiana langsdorffii x Nicotiana sanderae	6,791	157a
Nicotiana sylvestris	7,612	163a
Nicotiana tabacum	131,942	173a
Ocimum basilicum	8,926	157a
Panax quinquefolius	3,803	177a
Parthenium argentatum	8,547	177a
Petunia axillaris subsp. axillaris	19,609	173a
Petunia x hybrida	9,884	159a
Salvia miltiorrhiza	5,624	157a
Solanum chacoense	7,110	163a
Solanum habrochaites	12,011	175a
Solanum lycopersicum	56,845	171a
Solanum melongena	25,443	175a
Solanum pennellii	5,008	175a
Solanum torvum	9,182	175a
Striga hermonthica	23,747	177a
Taraxacum kok-saghyz	6,995	177a
Taraxacum officinale	18,333	157a

Triphysaria pusilla	25,947	162b
Triphysaria versicolor	15,255	162b
Zinnia violacea	17,011	171a

Supplementary Table 30. Corrections made to RH BAC sequences using whole-genome Illumina data.

Substitution	Number of changes
A > T substitution	1,223
C > G substitution	322
A > C substitution	505
A > G substitution	1,108
C > A substitution	734
G > A substitution	910
N substitution	230
A / T insertion	3,854
C / G insertion	569
A/T deletion	4,789
C/G deletion	2,763
N deletion	107
total deletions	7,659
total insertions	4,423
total substitutions	5,032
total	17,114

Supplementary Table 31. Metrics of potato gene models

	Transcript Number	Total Transcript Length (bp)	Ave Transcript Length (bp)	Ave Exon Length (bp)	Ave Intron Length (bp)	Ave CDS Length (bp)	Ave 5'UTR Length (bp)[d]	Ave 3'UTR Length (bp)[e]
Potato	56,218	79,572,067	1,415	356	592	905	298	467
Arabidopsis[b]	33,200	50,088,890	1,508	265	164	1,212	149	237
Rice[c]	50,692	78,281,992	1,544	312	414	1,081	254	464

[a] For potato, only protein coding nuclear transcripts were used.

[b] For Arabidopsis (TAIR9), all protein coding transcripts were included except for TE and pseudogenes.

[c] For rice, all protein coding transcripts (MSU Release 6.3) were included except for TE, pseudogenes, organellar insertion, and small genes.

[d] 5'UTR (avg) = Total length of 5'UTR/number of transcripts with 5'UTR

[e] 3'UTR (avg) = Total length of 3'UTR/number of transcripts with 3'UTR

Supplementary Table 32. Comparison of predicted plant proteomes

A.Pfam domains, Gene Ontologies (GO), KEGG, and InterPro assignments to plant proteomes.

	Total Proteins	Pfam Domain	GO	KEGG	Interpro
Potato	56,218	32,442	20,961	23,817	32,442
Arabidopsis	33,200	25,272	17,890	16,501	26,280
Grapevine	26,346	17,751	13,368	13,715	18,584
Soybean	46,384	36,637	26,551	25,788	38,266
Poplar	45,554	30,777	23,116	21,686	32,381
Cucumber	26,820	17,355	12,649	11,864	18,099
Rice	40,337	24,662	18,113	17,653	25,900

B. Total Pfam domains and proteins with multiple Pfam domains across plant genomes.

	Total Proteins	Total Pfam Domain	No. Proteins with >= 1 Pfam domain
Potato	56,218	55,572	32,442
Arabidopsis	33,200	45,883	25,272
Cucumber	26,820	31,072	17,355
Poplar	45,554	53,579	30,777
Soybean	46,384	67,463	36,637
Grapevine	26,346	34,112	17,751
Rice	40,337	41,756	24,662

Supplementary Table 33. Levels of individual carotenoids in DM and RH tuber tissues (mgm/gram fresh weight).

	Neoxanthin	Vioxanthin	Anthera-xanthin	Lutein	Zeaxanthin	Zea/Lut isomers	Mono hydroxy	Cis/Trans Carotenes	Total Carotenoids
DM	0.55 +/-0.05	11.51 +/-0.93	2.63 +/-0.45	1.49 +/-0.15	0.29 +/-0.07	0.26 +/-0.02	2.42 +/-0.29	3.05 +/-0.24	22.19 +/-1.57
RH	0.16 +/-0.02	0.18 +/-0.03	0.10 +/-0.01	0.60 +/-0.01	0.02 +/-0.00	nd	0.50 +/-0.05	0.24 +/-0.04	1.80 +/-0.10

Data are averages and standard deviation of 5 independent extractions and HPLC analyses (refer to Figure S9 for a representative HPLC trace of each variety). Zea/Lut isomers are the sum of various cis isomers of lutein and zeaxanthin; Mono hydroxy is the sum of a complex mixture of alpha, beta and delta-carotene isomers that migrate in a region containing cyclized carotenes with a single hydroxyl group; Cis/trans carotenes, are a complex mixture of various cyclized isomers (e.g., alpha, beta, delta) carotenes and uncyclized (e.g., zeta-carotene, neurosporene, phytofluene) carotenes. nd, not detected.

Supplementary Table 34. List of Carotenoid biosynthetic genes and their genetic position.

Best Transcript	Description	DM super-scaffold ID	DM scaffold ID	Chr	Chr position supported by following maps
PGSC0003DMT400074346	CHY1	PGSC0003DMB000000315	PGSC0003DMS000000935	6	DM, wgp, tom
PGSC0003DMT400026363	CHY2	PGSC0003DMB000000159	PGSC0003DMS000000374	3	wgp,tom
PGSC0003DMT400024575	CHY3	PGSC0003DMB000000400	PGSC0003DMS000000023	3	tom
PGSC0003DMT400072543	CrtISO	PGSC0003DMB000000008	PGSC0003DMS000001421	10	DM, wgp
PGSC0003DMT400015066	CycB	PGSC0003DMB000000345	PGSC0003DMS000002348	6	DM, wgp, tom
PGSC0003DMT400027593	LCYb1	PGSC0003DMB000000480	PGSC0003DMS000000051	4	tom
PGSC0003DMT400021074	LCYb2	PGSC0003DMB000000129	PGSC0003DMS000003447	10	DM, wgp, tom
PGSC0003DMT400071048	NCED3	PGSC0003DMB000000096	PGSC0003DMS000002396	7	DM, wgp, tom
PGSC0003DMT400039054	NCED5	PGSC0003DMB000000232	PGSC0003DMS000000052	1	RH
PGSC0003DMT400049305	NCED6	PGSC0003DMB000000106	PGSC0003DMS000000777	10	DM, wgp, tom
PGSC0003DMT400023667	PDS	PGSC0003DMB000000040	PGSC0003DMS000001764	3	DM, wgp, tom
PGSC0003DMT400061846	PSY1	PGSC0003DMB000000039	PGSC0003DMS000001131	3	DM, wgp, tom
PGSC0003DMT400043104	PSY2	PGSC0003DMB000000099	PGSC0003DMS000002349	2	DM, wgp, tom
PGSC0003DMT400034708	pTOX1	PGSC0003DMB000000148	PGSC0003DMS000000825	11	DM, wgp
PGSC0003DMT400027760	VDE	PGSC0003DMB000000018	PGSC0003DMS000002115	4	DM, wgp, tom
PGSC0003DMT400057865	ZDS	PGSC0003DMB000000092	PGSC0003DMS000001954	1	DM, wgp, tom
PGSC0003DMT400010287	ZEP	PGSC0003DMB000000012	PGSC0003DMS000002087	2	DM, wgp, tom
PGSC0003DMT400011667	ZISO	PGSC0003DMB000000114	PGSC0003DMS000000879	12	DM, wgp, tom