Supplementary text

RESULTS

Detecting millions of high-quality SNPs

The total number of bases covered with at least one read ranged from 800 to 904 Mb within populations and varied with depth of coverage. The low rate of false positive SNPs in our data is illustrated by the fact that we only observed 218,662 non-reference alleles when resequencing the partially inbred reference bird in comparison to 3-5 million non-reference alleles when resequencing other populations. Furthermore, a large proportion of these 218,662 SNPs are not false positives but represent regions of the genome that are heterozygous in the reference bird and where only one of the alleles at heterozygous positions was represented in the genome assembly. To estimate the error rate associated with our approach for SNP detection we analyzed SNP data from the Z chromosome since the female reference bird is hemizygous Z/W. We scored 276,936 SNP positions with at least one SOLiD read from the reference bird and observed only the reference base at 267,471 positions (96.6%), only the non-reference base at 8,450 positions (3.0%) and both nucleotides at 1,015 positions (0.4%). We conclude that the majority of cases where we exclusively observed the non-reference nucleotide are due to sequence errors in the reference genome sequence based on the low quality scores for the majority of these positions (Supplementary Fig. 1). The few remaining discrepancies are most likely explained by duplicated sequences not correctly annotated in the assembly leading to false heterozygosity, alignment problems of short SOLiD reads (for instance due to insertions/deletions) and SOLiD sequencing errors. Based on this finding we decided to eliminate all putative SNPs where (i) we only called the non-reference allele, (ii) we had at least one read from the reference bird and (iii) the quality score in the reference sequence was below 50 since most of these will reflect sequence errors. (We only applied this filtering to SNPs located on specific chromosomes but not on unassigned contigs, but not on unassigned contigs, i.e., _random, in the Chicken May 2006 assembly.) We identified 40,058 putative SNPs fulfilling these criteria and after these had been removed, a final number of 7,453,845 confident SNP loci remained.

However, some false positives will occur as a function of sequence coverage. Using the Z chromosome reads from the reference bird, we estimated the per-position single read error rate at 0.64%. Combining this with the distribution of depth of coverage for all lines combined, we can estimate the number of times we would likely see three or more of the same false call at a position. We estimate from this that we would have ~335,000 erroneous SNP calls due to SOLiD errors, or ~4.5% of our SNPs, but all of these will be low frequency SNPs with little impact on our estimates of heterozygosities or search for selected variants. In reality, this is likely to be an overestimate, because most of our SNPs are derived from analysis of sequence from individual lines, where lower coverage would greatly reduce the probability of three identical errors at a site (see Methods for more details).

We carried out a validation test for 384 SNPs using an Illumina Golden Gate assay (Supplementary Table 2). We obtained reliable genotype calls for 318 SNP assays from all tested individuals. Only one of the tested SNPs reflected an error in the SOLiD sequencing data. The error was confirmed experimentally to be caused by a five bp insertion/deletion that was erroneously interpreted as a SNP by the SNP calling algorithm. Nevertheless, 317 out of 318 (99.7%) of the SNPs were validated indicating that the majority of the ~7.4 million SNPs detected in this study are true SNPs.

The major reason for false negatives is that we can only detect SNPs for the part of the genome that is represented in the genome assembly. There are still many regions that are not covered, as this is not a finished assembly. Furthermore, we can only carry out SNP detection in the non-repetitive part of the chicken genome with these short reads. Finally, we are missing some SNPs because they occur in the vicinity of insertions/deletions or as clusters of SNPs that preclude a correct alignment of the short reads. In order to examine this issue we compared the number of SNPs detected for the *yellow skin/BCDO2* haplotype that we previously resequenced using classical Sanger sequencing[1]. We identified a total of 175 SNPs over a 23.8 kb region using Sanger sequencing and 163 of these (93.1%) were also detected using the SOLiD data when we combined data from all domestic lines.

A previous study based on classical Sanger sequencing of a White Leghorn chicken, a broiler chicken and a Silkie domestic chicken, each to about 0.25X coverage, revealed a total of 2.8 million SNPs when comparing these reads to each other and to the reference sequence[2]. We notice that 63% of these are confirmed in our SNP list. The most common explanation for the missing 37% is that they represent rare alleles not detected when sequencing pooled samples in the present study and sites missed in the present study due to various problems with the alignment of short reads. However, a certain fraction will also represent sequencing errors in the previous study since a single read of high quality score was sufficient to call a SNP.

We used the allele frequencies of the 7.45 million SNPs in the 10 populations to construct a genetic distance tree summarizing the genetic relationships between populations (Supplementary Figure 2). This resulted in a star-like tree with no general clustering of the domestic populations. The genetic distance from a White Leghorn line to a broiler line is as long as from a White Leghorn line to a red junglefowl population, a pattern consistent with previous results from partial genome sequencing[2]. The three White Leghorn lines (WL-A, WL-B and OS) showed clustering, as expected, but with long branch-lengths. Similarly, the phenotypically divergent High and Low growth selection lines that originated from a common ancestral population also clustered. The Rhode Island Red population did not show a close genetic relationship to the White Leghorn populations although they are all layers, a result consistent with previous data[3]. These results provide important background information for our attempts to identify loci under selection in the domestic populations.

Identification of selective sweeps

Allele counts at identified SNP positions were used to identify signatures of selection in sliding windows for three pools of sequence data (breed pools): A: all eight domestic lines, B: the two commercial broiler lines (CB-1 and CB-2) and C: three layer populations (WL-A, WL-B and RIR). We analyzed sliding 40 kb windows with a step size of 20 kb, giving a total of 46,906 windows scanned along chicken chromosomes 1–28 represented in the v2.1 draft assembly. With the depth of sequencing used in this study, most SNP positions will not be covered by reads originating from each individual chromosome in the DNA pools. The chance of an individual chromosome being sampled will vary with coverage and the information content will thus differ between SNPs within a window. Had each SNP been assigned the same weight, the resulting allele ratios would be devoid of any sampling information. Taking this into account, we decided to maximize the information contained within each window by assigning weights to SNPs, with these weights being dependent on the number of observed alleles.

We searched for signatures of selection in sliding windows by determining normalized pooled heterozygosity values (H_p) in individual breed pools. H_p values were calculated from window sums of reads representing the most- and least abundant alleles observed at individual SNP positions (Full Methods). The numbers of SNP alleles observed within a window thus dictate the amount of information available to infer H_p. Examination of distributions of SNP content for windows sized 10 kb, 20 kb and 40 kb showed that the fraction of windows where we had identified very few SNPs was much lower for the 40 kb size (Supplementary Figure 4). Spurious fixation signals are more likely to occur when few chromosomes are sampled from a DNA pool, thus speaking in favor of analyzing windows with adequate numbers of polymorphic loci. Of all 40 kb windows where at least one SNP had been identified (n=46,912), all but seven (99.99 %) contained more than 10 SNPs. The ability to detect a selection signature using a 40 kb window size was shown by the strong selection signal observed for a window overlapping a known selective sweep at the *yellow skin/BCDO2* locus (Figs. 2b and c). We concluded that a window size of 40 kb allowed us to screen a very large fraction of the genome, that the false positive rate is likely to be lower for this size than for smaller windows and that the 40 kb size detected a fixation signal at a locus known to have been selected in domestic chicken. In this study the threshold for candidate selective sweeps was set at ZH_p <= -6 as windows below this threshold represented the extreme lower end of the heterozygosity distribution (Fig. 2a). We however believe that loci further down the list merit further examination in follow-up studies. All windows that fell below ZH_p = -4 in any breed pool are listed in Supplementary Table 3.

In Fig. 2c it can be seen that not all windows that reach the -6 threshold in the all domestic comparison fall below the same threshold in layers and commercial broilers. The *TSHR* region approached our significance threshold also for the broiler and layer comparisons with ZH_p scores of 4.7 and 4.9, respectively. Both groups showed complete homozygosity at the *TSHR* locus but failed to reach the -6 threshold because the sweep regions did not cover a full 40 kb window. Furthermore, a larger number of loci were highly fixed in the layer and commercial broiler data pools than in the “all domestic” data pool. Thus, the failure to detect a clear selection signal for instance in commercial broilers, while detecting low heterozygosity both in “all domestic” and layers can be due to the additional three populations (High, Low and OS) sharing a haplotype with the layers. This relates to the definition of an “all domestic” sweep signal, which does not necessarily indicate complete fixation across all domestic lines. The *BCDO2/yellow skin* locus for instance is not completely fixed in all domestic breeds as a few individuals were heterozygous at this locus. One could envision that other loci selected during domestication may also still be segregating, either at low frequencies across certain domestic lines or in individual lines where the trait controlled by the locus is no longer desired.

The size of a selective sweep may depend on factors such as the local recombination rate, whether the selected variant ever reached complete fixation, the number of generations it took before fixation and any population admixture at a time point after the sweep initially occurred. Thus, selective sweeps are likely to vary in size due to several variables, making it difficult to determine an optimal window size in which to search for signatures of selection. We cannot rule out that our approach may have failed to detect sweeps that had been detected using other fixed or variable window sizes. In our scan for selective sweeps we gave SNPs weights that were dependent on read coverage, thereby using information from the full repertoire of sequence reads drawn from DNA pools. Additional information would be gained if DNA pools had been sequenced at higher coverage or optimally if genotypes at polymorphic loci had been ascertained by sequencing large quantities of individual samples. Such studies would make it possible to reduce or eliminate the sampling biases associated with DNA pools and would enable screens for selected loci at a higher resolution.

Detecting deleterious mutations – is less more?

To identify potential stop mutations, we first heavily filtered the Ensembl transcripts (version 50) to identify complete ORFs at least 100 codons long. Within 8,364 transcripts retained after filtering, we identified 118 unique sites where one allele created an in-frame stop codon in at least one transcript. We manually reviewed all sites for validity of the SNP call and the gene model. Four sites were apparently false positives due to multi-base events mistaken for SNPs and did not truly result in a stop. We note that a rate of four false positives in 118 (3%)

is much higher than was seen in our random validation, most likely because of strong selection against the presence of true SNPs altering stop codons.

After review, we retained 35 of the 114 real SNPs as true probable stop codon changes and an additional one as a likely splice mutation. The remainder were true SNPs in erroneous gene annotations. Of the 35 real stop SNPs, 34 created a new stop codon, although 5 of these occurred within 6 codons of the C-terminus and may be real but have no functional effect. One destroyed the annotated stop (*EDEM2*), and it appears the sequenced reference bird contains a null allele, because this stop is 1200 bases short of the alignment of the C terminal end of the human homolog. A complete list of genes containing stop codons along with validation results is provided as Supplementary Table 5. We do not find any cases of variant stops that segregate between wild and domestic chickens or between broilers and layers in a manner suggestive of strong selection, suggesting that gene loss due to stop mutation has not been a significant factor in chicken domestication. However, we note that due to the fragmentary nature of gene annotation in the chicken genome, we can only currently assay ~25-30% of all chicken genes by this method.

Because of the pooled nature of our data, it is difficult to directly infer copy number variation, with the exception of deletions relative to the reference genome that are fixed within one or more populations. The deletion needs to be about 100 bp or larger to be detected with the sequence coverage obtained in this study. We scanned the genome for such regions and identified 1,284 deletions ranging in size from 106 bp to 67 kb; only 16 were larger than 16 kb (Supplementary Table 6; Supplementary Figure 3). We next intersected these deletions with the coding regions of genes from the Ensembl build 50 annotation. This resulted in 27 potential coding deletions. Each of these was manually reviewed, leaving only seven high confidence candidates (Supplementary Table 7); the remainder were mostly discarded as poorly supported or erroneous gene models, although a small number of deletions were false positives. We validated four of these by PCR and used sequencing to determine the exact breakpoints. The predicted positions of deletion breakpoints were very accurate, in most cases within 10 bp. In no case have we designed successful PCR assays which invalidate a deletion, although one of the validated deletions was 30 bp shorter than predicted and completely intronic (not shown in Supplementary Table 7). We also looked for deletions that overlapped highly conserved elements predicted by phastCons (downloaded from genome.ucsc.edu) and identified 143 deletions covering one or more non-exonic conserved elements. Ninety-five of these removed intergenic conserved elements and 48 intronic, with a total of 368 conserved elements deleted. As we have no direct knowledge of the function of any of these elements, we can only hypothesize that some might have phenotypic consequence. However, we did identify two genic deletions, one known and one novel, with associated phenotypes known or expected to be under selection.

It may appear contradictory that the growth-promoting haplotype associated with the *SH3RF2* deletion is still segregating in the Low growth line despite the more than 40 generations of selection for reduced growth (Supplementary Table 7). However, in contrast to the High growth line the Low line has reached a selection plateau where artificial selection for low juvenile growth is counterbalanced by natural selection for sufficient growth to reproduce successfully[4,5]. It is possible that the *SH3RF2* polymorphism contributes to this balancing selection.

Discussion

The present study is a major advance in chicken genomics. We report more than seven million high quality SNPs (about 1 SNP/150 bp throughout the genome), and more than five million of these have not been reported previously. The current genome assembly for chicken can be further improved by taking into account our results since we found ~40,000 single base sequencing errors. The study is also a breakthrough in regard to the utilization of the chicken as a model for biomedical research, we demonstrate how to take advantage of new high-throughput sequencing technologies and the long history of phenotypic selection in domestic animals for high-resolution identification of loci under selection. We sequenced pools of chickens with the specific aim to detect the most common allele in each population at all loci in the non-repetitive part of the genome. The rationale behind this approach is to search for the variants that have been under strong positive selection during domestication. We have come a long way towards this ambitious goal, however missing are some loci due to the incomplete state of the current genome assembly and the difficulty of aligning short reads to highly polymorphic regions. Although we were not able to search for insertions/deletions shorter than 100 bp, this can be achieved by using paired reads, making it possible to use one read to anchor the fragment to the genome and then align the other with an algorithm allowing gaps in the alignment.

A major aim in the current study was to detect selective sweeps characterized by regions of homozygosity flanking one or several mutations favored by selection[6]. The grand challenge in this analysis is to distinguish sweeps from regions of homozygosity due to genetic drift. The expected size of regions of homozygosity has a complex background reflecting population history pre- and post-domestication as well as the local recombination rate that varies extensively in the chicken genome[7]. Our approach to reduce false positives is to search for regions of homozygosity shared by populations selected for similar traits because alleles of major importance in breeding are often widely distributed among populations[1,8]. This approach however fails to detect sweeps when different alleles with similar effects have been selected in different populations. Another reason for failure is if the sweep region is significantly shorter than the 40 kb sliding windows used in the present study. For instance, sweeps shared by all eight populations included in our study must have occurred prior to the split between meat and layer types that occurred during the 1920s, i.e. before modern breeding methods were developed on the basis of the theory of quantitative genetics founded by Fisher, Wright and Haldane. Before then, selection responses were slow, except for simple monogenic traits, and such sweep regions will therefore be small because there has been time to break up linkage between a favoured mutation and flanking markers. Thus, a screen with deeper coverage and including more populations will allow searches with smaller windows, which should be even more powerful to detect sweeps.

Our study has important implications as regards application of genomics to practical animal breeding. The selection response for growth and egg production has been remarkable over the last 50 years and it may be argued that this is the reason why chicken meat and eggs are currently the most important global source of animal protein. We have now identified a number of the loci that have made it possible to transform the red junglefowl to an extremely efficient production animal. Chicken breeding in developed countries relies entirely on a few breeding companies that control breeding stocks of crucial importance for human nutrition. Our study has unraveled some of the “secrets” underlying the genetics of their very successful breeding programs. This information can for instance be exploited during the development of a new chicken line combining high productivity with other favored characteristics such as resistance to infectious disease present in an exotic population with low productivity.

References

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Supplementary Table 1 Summary of SNP detection using whole genome resequencing in chicken

	Layers[a]				Broilers[b]				Red junglefowl[c]		
	WL-A	WL-B	OS	RIR	CB-1	CB-2	High	Low	Pool	Ref	Total
Sequence coverage[d]	3.37x	4.00x	3.61x	3.32x	5.18x	4.01x	5.19x	5.53x	6.95x	3.34x	44.5x
Assembly coverage[e]	79%	82%	79%	77%	85%	80%	85%	85%	87%	78%	92%
Covered SNPs	6,539,295	6,875,201	6,500,459	6,400,010	7,145,974	6,718,745	7,071,082	7,134,252	7,275,293	6,657,279	7,493,903
Non-ref alleles	3,456,950	3,916,180	2,945,059	3,228,116	4,648,735	3,815,522	4,100,466	4,245,408	4,743,832	218,662	7,409,603
Unique alleles	41,851	42,321	41,636	41,679	65,104	39,861	70,326	80,311	186,790	3,697	6,796,027
Heterozygosity[f] ($x10^{-3}$)	2.04	2.70	0.74	1.98	3.88	2.85	1.99	2.17	4.07	0.20	n/a

Sequence coverage, the total number of SNP positions covered with at least one read, the number of detected non-reference alleles and the number of unique alleles are presented.

[a]WL-A=White Leghorn line 13; WL-B=commercial White Leghorn; OS=White Leghorn Obese strain; RIR=Rhode Island Red.

[b]CB-1=Commercial broiler 1; CB-2=Commercial broiler 2; High=High growth selection line; Low=Low growth selection line.

[c]Pool=Pool of red junglefowl birds from two zoo populations; Ref=the red junglefowl female bird used to produce the chicken draft genome sequence

[d]Sequence coverage was computed as the average depth of coverage of bases which had at least one read covering them. Given the level of coverage for most lines, we assume the vast majority of uncovered bases are due to alignability issues and do not reflect lack of coverage in the actual sequence data.

[e]Assembly coverage was calculated as the proportion of bases in the genome assembly covered by at least one read; the total number of bases in May 2006 (v2.1) assembly is 1,100,480,441 but 57,914,081 bp of these are Ns representing gaps in the assembly so the denominator used to calculate the percentage of bases covered was 1,042,566,360 bp.

[f]Heterozygosity was estimated by summing the maximum likelihood estimate of heterozygosity across all sites with at least two reads. Note that all positions at which no SNPs were detected were considered homozygous in all lines for these purposes, making this an underestimate of true heterozygosity.

Supplementary Table 2a Results of SNP validation using Illumina Golden Gate Assays

	Number of SNPs
Total number of SNP assays	384
Failed SNPs assay	54
Excluded SNPs due to missing genotypes among reference samples	9
Erroneous base call in genome assembly	3[a]
Total number of successful SNP assays	318
Erroneous base call in SOLiD data	1[b]
Verified SNPs	317

[a]See Table S2b below

[b]Erroneous SOLiD base call caused by a 6 bp insertion

Supplementary Table 2b Erroneous base calls in the chicken genome assembly (May 2006, galGal3 assembly) detected using SOLiD sequencing and SNP typing of the reference bird

Position	Genome assembly		Correct base call[b]
	Base call	Quality score[a]	
Chr3:86,575,625	A	11.5	G
Chr5:19,326,414	G	18.3	A
Chr13:10,304,357	G	10.7	A

[a]Maximum value 100, these are all low quality scores

[b]Based on SOLiD sequencing and SNP typing

Supplementary Table 3 Genomic regions identified as candidate selective sweeps in: all domestic lines (AD), two commercial broiler lines (CB) and three layer lines (LR). Consecutive 40 kb sliding windows with heterozygosity Z-scores (ZH_P) < -4 were merged. Regions in bold font represent those where the ZH_P of at least one window was < -6.

Coordinates[a]	Line[b]	N win[c]	SNPs[d]	Reads[e]	ZH_P[f]	H_P AD[g]	H_P CB[g]	H_P LR[g]	Genes overlapping region or within 20 kb [h]
chr1:7.94–7.98	CB	1	54	356/22	-4.3	0.35	0.11	0.38	[6] ENSGALG00000006628 Q5ZKU3_CHICK *DMTF1
chr1:9.20–9.36	**AD**	**7**	**223**	**6196/410**	**-8.7**	**0.08**	**0.04**	**0.06**	
chr1:9.20–9.24	LR	1	46	338/10	-5.3	0.1	0.18	0.06	
chr1:9.26–9.36	CB	4	163	1301/45	-5.8	0.08	0.04	0.18	
chr1:18.96–19.00	CB	1	137	930/58	-4.3	0.38	0.11	0.38	
chr1:21.14–21.24	LR	4	290	2441/124	-5.2	0.34	0.31	0.06	
chr1:25.24–25.30	CB	2	551	4128/286	-4.6	0.4	0.1	0.34	[4] ENSGALG00000009029 NP_001007850.1 *TSPAN12 [5] ENSGALG00000021899 KCND2 [6] ENSGALG00000009023 NP_001025904.1
chr1:27.16–27.20	CB	1	84	796/23	-5.5	0.25	0.05	0.44	[5] ENSGALG00000009411 NP_001006229.1 *TFEC
chr1:29.72–29.80	LR	3	399	3343/179	-4.7	0.37	0.27	0.09	
chr1:29.82–29.90	LR	3	489	3612/184	-5.0	0.37	0.35	0.07	[6] ENSGALG00000023479 **AC019102.13, AL079341.19-1, AL133345.11, AL590069.5, AL606469.8-1, Z83846.1
chr1:34.26–34.30	LR	1	150	1131/52	-4.7	0.23	0.17	0.08	
chr1:34.30–34.36	CB	2	272	1711/120	-4.3	0.32	0.11	0.11	
chr1:34.32–34.40	LR	3	287	2083/103	-5.1	0.32	0.11	0.07	[6] ENSGALG00000009764 Q9W7I9_CHICK
chr1:34.46–34.50	CB	1	185	1238/67	-4.6	0.32	0.1	0.18	
chr1:34.62–34.66	LR	1	260	1881/113	-4.2	0.3	0.24	0.11	
chr1:36.18–36.22	CB	1	265	1912/114	-4.4	0.26	0.11	0.32	[5] ENSGALG00000009879 TMBIM4 [5] ENSGALG00000019358 CL031_CHICK

chr1:43.68–43.72	AD	1	38	863/116	-4.6	0.21	0.17	0.22	[1] ENSGALG00000019347 [6] ENSGALG00000011144 ALX1
chr1:44.94–44.98	AD	1	143	3041/391	-4.8	0.2	0.19	0.21	
chr1:57.26–57.36	LR	4	438	3342/156	-5.6	0.28	0.14	0.04	[4] ENSGALG00000012755 IGF1_CHICK
chr1:57.34–57.56	**CB**	**10**	**1578**	**11010/294**	**-6.6**	**0.29**	**0**	**0.14**	**[1] ENSGALG00000012756 CL048_CHICK *C12orf48** **[1] ENSGALG00000012757 *PMCH** **[1] ENSGALG00000012759 NUP37** **[1] ENSGALG00000012760 CCDC53** **[1] ENSGALG00000012761 *AC084398.25-1** **[1] ENSGALG00000019299** **[3] ENSGALG00000012755 IGF1_CHICK** **[6] ENSGALG00000012763 GNPTAB**
chr1:57.68–57.72	CB	1	334	2319/128	-4.5	0.35	0.1	0.28	[4] ENSGALG00000012783 MYBPC1 [6] ENSGALG00000023081
chr1:57.86–57.90	CB	1	317	2313/155	-4.1	0.33	0.12	0.14	[2] ENSGALG00000012791 TBXAS1
chr1:68.08–68.12	LR	1	255	2091/118	-4.3	0.33	0.31	0.1	[4] ENSGALG00000013204 NP_001004385.1 *SOX5
chr1:70.72–70.76	LR	1	425	3389/217	-4.1	0.31	0.33	0.11	[3] ENSGALG00000014178 SCUBE1 [4] ENSGALG00000014167 NP_001012558.1 *TTLL12 [5] ENSGALG00000014166 TSPO
chr1:83.66–83.70	LR	1	372	2970/164	-4.4	0.37	0.36	0.1	[1] ENSGALG00000015016 SLC22A15 **SLC22A5 [6] ENSGALG00000015006 C1orf161 [6] ENSGALG00000015018 CASQ1_CHICK *CASQ2
chr1:85.00–85.04	LR	1	318	3010/97	-5.2	0.32	0.31	0.06	[2] ENSGALG00000015087
chr1:100.16–100.20	AD	1	173	4657/701	-4.0	0.23	0.21	0.24	
chr1:100.22–100.28	AD	2	206	4569/646	-5.4	0.18	0.19	0.22	[5] ENSGALG00000015519 Q90Z41_CHICK
chr1:100.32–100.38	**CB**	**2**	**271**	**1778/55**	**-6.2**	**0.24**	**0.02**	**0.34**	**[2] ENSGALG00000015519 Q90Z41_CHICK**
chr1:104.48–104.52	CB	1	134	3807/188	-4.8	0.16	0.09	0.08	[1] ENSGALG00000025519 [4] ENSGALG00000022847 [5] ENSGALG00000021740 [6] ENSGALG00000021752

chr1:104.48–104.52	LR	1	134	2869/122	-4.8	0.16	0.09	0.08	[1] ENSGALG00000025519 [4] ENSGALG00000022847 [5] ENSGALG00000021740 [6] ENSGALG00000021752
chr1:104.48–104.54	**AD**	**2**	**225**	**13706/1727**	**-6.0**	**0.16**	**0.09**	**0.08**	**[1] ENSGALG00000025519** **[4] ENSGALG00000022847** **[5] ENSGALG00000021740** **[6] ENSGALG00000021752**
chr1:110.72–110.78	CB	2	351	2787/113	-5.5	0.3	0.06	0.28	[6] ENSGALG00000016054 KCNJ6
chr1:119.46–119.50	LR	1	136	1085/70	-4.1	0.41	0.32	0.11	
chr1:127.88–127.92	LR	1	143	1229/67	-4.4	0.36	0.34	0.1	[2] ENSGALG00000016602 ARHGAP6
chr1:130.92–130.96	LR	1	142	944/55	-4.3	0.29	0.25	0.1	[1] ENSGALG00000025476 [2] ENSGALG00000016628 **NLGN4X, NLGN4Y
chr1:131.24–131.32	CB	3	165	1061/50	-5.1	0.24	0.08	0.09	
chr1:131.26–131.30	LR	1	78	577/29	-4.5	0.24	0.08	0.09	
chr1:131.78–131.82	AD	1	122	2706/369	-4.6	0.21	0.18	0.1	
chr1:131.78–131.82	LR	1	122	930/51	-4.4	0.21	0.18	0.1	
chr1:138.04–138.08	LR	1	177	1416/82	-4.3	0.35	0.28	0.1	[3] ENSGALG00000016784 **IL1RL2 [5] ENSGALG00000016783 NP_990816.1 **IL1RL2 [6] ENSGALG00000016785 NP_001019761.1 *IL1RL1
chr1:138.08–138.12	LR	1	189	1658/94	-4.3	0.35	0.32	0.1	[1] ENSGALG00000016785 NP_001019761.1 *IL1RL1 [6] ENSGALG00000016786 IL18R1
chr1:145.86–146.00	CB	6	602	3955/217	-5.1	0.22	0.07	0.03	
chr1:145.86–146.02	LR	7	683	4848/163	-5.8	0.22	0.07	0.03	
chr1:145.90–145.96	AD	2	315	6911/1059	-4.2	0.22	0.07	0.03	
chr1:146.18–146.22	LR	1	132	1103/53	-4.6	0.32	0.17	0.09	
chr1:146.22–146.30	LR	3	214	1531/92	-4.8	0.32	0.2	0.08	[1] ENSGALG00000022760

chr1:152.66–152.70	LR	1	11	53/3	-4.3	0.27	0.23	0.1	[1] ENSGALG00000024438
chr1:152.70–152.82	AD	5	61	1666/229	-5.6	0.18	0.26	0.09	[6] ENSGALG00000024438
chr1:152.74–152.78	LR	1	25	224/11	-4.6	0.22	0.26	0.09	
chr1:152.80–152.84	LR	1	23	211/9	-4.8	0.25	0.32	0.08	
chr1:153.14–153.22	CB	3	113	853/43	-5.8	0.27	0.04	0.39	
chr1:153.36–153.40	AD	1	40	807/112	-4.5	0.21	0.27	0.23	
chr1:154.44–154.48	CB	1	85	690/42	-4.3	0.3	0.11	0.23	[6] ENSGALG00000016904 SLITRK6
chr1:155.18–155.22	CB	1	78	675/33	-4.8	0.26	0.09	0.39	
chr1:155.36–155.40	LR	1	81	597/38	-4.1	0.34	0.43	0.11	
chr1:164.64–164.74	LR	4	159	1275/63	-4.8	0.31	0.21	0.08	
chr1:164.72–164.76	CB	1	17	104/5	-4.8	0.27	0.09	0.35	
chr1:164.78–164.82	LR	1	33	281/17	-4.2	0.33	0.3	0.11	
chr1:164.88–164.94	LR	2	98	706/31	-5.2	0.38	0.33	0.06	
chr1:168.54–168.58	LR	1	137	1105/43	-5.0	0.43	0.36	0.07	
chr1:172.24–172.28	CB	1	362	2419/121	-4.7	0.39	0.09	0.34	[2] ENSGALG00000016984 ZC3H13 [5] ENSGALG00000016985 CPB2
chr1:179.66–179.70	LR	1	344	2863/154	-4.4	0.35	0.34	0.1	[3] ENSGALG00000017084 NP_001012847.1 *UBL3
chr1:182.60–182.64	LR	1	179	1650/80	-4.6	0.37	0.24	0.09	[5] ENSGALG00000017124 NM_204399.1 *FGF9
chr1:195.50–195.80	**AD**	**14**	**705**	**14874/1414**	**-7.7**	**0.11**	**0.06**	**0.02**	**[1] ENSGALG00000022710 Q2AB82_CHICK *TAS2R4**
chr1:195.50–195.56	CB	2	97	542/43	-4.5	0.15	0.1	0.18	
chr1:195.56–195.68	**LR**	**5**	**423**	**2645/117**	**-6.0**	**0.12**	**0.22**	**0.02**	
chr1:195.66–195.76	CB	4	193	1175/68	-5.5	0.11	0.06	0.24	[6] ENSGALG00000022710 Q2AB82_CHICK *TAS2R4

chr2:8.52–8.58	CB	2	579	4025/279	-4.3	0.33	0.11	0.35	[4] ENSGALG00000006461 NP_001026138.1 *UBE3C
chr2:11.70–11.76	CB	2	159	1279/72	-4.6	0.24	0.1	0.3	[1] ENSGALG00000007056 NP_001026140.1 *COPEB
chr2:11.86–11.90	CB	1	86	671/46	-4.1	0.25	0.12	0.33	
chr2:11.88–11.94	AD	2	98	2875/393	-4.9	0.2	0.14	0.28	
chr2:11.96–12.00	AD	1	55	1757/193	-5.6	0.18	0.2	0.19	
chr2:12.04–12.10	AD	2	145	4095/581	-4.9	0.2	0.18	0.22	
chr2:24.60–24.64	LR	1	262	2279/147	-4.1	0.27	0.38	0.11	[1] ENSGALG00000009737 TAC1 [3] ENSGALG00000009748 ASNS_CHICK
chr2:27.14–27.18	CB	1	126	752/44	-4.4	0.39	0.1	0.27	
chr2:28.12–28.20	AD	3	411	9448/1348	-5.0	0.2	0.17	0.17	
chr2:34.98–35.02	CB	1	173	1234/85	-4.1	0.27	0.12	0.19	
chr2:36.38–36.42	CB	1	147	1084/73	-4.1	0.23	0.12	0.3	[4] ENSGALG00000011283 ZNF659 *ZNF385D
chr2:36.84–36.88	CB	1	185	1504/86	-4.5	0.31	0.1	0.35	[4] ENSGALG00000011286 UBE2E1
chr2:36.88–36.92	CB	1	298	2421/166	-4.1	0.36	0.12	0.34	[2] ENSGALG00000011286 UBE2E1
chr2:50.74–50.78	CB	1	52	434/16	-5.2	0.28	0.07	0.24	[6] ENSGALG00000021831
chr2:51.80–51.86	AD	2	145	3452/503	-4.7	0.2	0.15	0.19	[4] ENSGALG00000012354 *RP11-775L16.2 [6] ENSGALG00000012353
chr2:51.88–51.92	AD	1	117	2840/405	-4.3	0.22	0.15	0.22	[3] ENSGALG00000012354 *RP11-775L16.2 [3] ENSGALG00000012360 LANCL2
chr2:51.94–51.98	CB	1	96	656/40	-4.3	0.22	0.11	0.21	[3] ENSGALG00000012363 EGFR_CHICK [6] ENSGALG00000012360 LANCL2
chr2:51.94–52.28	AD	16	851	20331/2516	-5.8	0.17	0.11	0.16	[1] ENSGALG00000012363 EGFR_CHICK [1] ENSGALG00000013107 SEC61G [6] ENSGALG00000012360 LANCL2
chr2:52.04–52.08	CB	1	101	705/46	-4.2	0.17	0.11	0.18	[2] ENSGALG00000012363 EGFR_CHICK

chr2:53.8–53.88	AD	3	204	4557/602	-5.6	0.18	0.12	0.19	[1] ENSGALG00000024970 7SK [2] ENSGALG00000012369 *TPK1
chr2:53.9–54.10	AD	9	621	13129/1669	-5.1	0.19	0.09	0.2	[2] ENSGALG00000012369 *TPK1
chr2:53.92–53.98	CB	2	149	843/49	-4.7	0.19	0.09	0.26	[2] ENSGALG00000012369 *TPK1
chr2:54.10–54.16	CB	2	234	1444/99	-4.2	0.22	0.11	0.2	[4] ENSGALG00000012369 *TPK1
chr2:54.12–54.18	AD	2	222	4664/689	-4.6	0.21	0.11	0.17	[4] ENSGALG00000012369 *TPK1
chr2:54.18–54.26	AD	3	278	6086/845	-5.4	0.18	0.14	0.19	
chr2:54.26–54.32	AD	2	194	3956/594	-4.4	0.22	0.21	0.18	[1] ENSGALG00000019593
chr2:54.32–54.38	AD	2	156	3127/435	-5.2	0.19	0.14	0.22	[6] ENSGALG00000012389 *CNTNAP2
chr2:54.44–54.48	AD	1	135	2825/408	-4.3	0.22	0.17	0.26	
chr2:54.50–54.56	AD	2	156	3202/462	-4.9	0.2	0.2	0.2	[5] ENSGALG00000023008 [6] ENSGALG00000023010 **many2many: AL133414.4, FCAR, GP6, KIR2DL1, KIR2DL2, KIR2DS4, KIR3DL1, KIR3DL3, KIR3DX1, LILRA1, LILRA2, LILRA3, LILRA4, LILRA5, LILRB2, LILRB3, LILRB4, LILRB5, NCR1
chr2:55.98–56.02	LR	1	123	1118/62	-4.4	0.23	0.35	0.1	[3] ENSGALG00000012433 ADCY1 [6] ENSGALG00000012435
chr2:60.64–60.68	CB	1	176	1387/93	-4.1	0.38	0.12	0.28	[2] ENSGALG00000012680 *E2F3 [4] ENSGALG00000012681 NM_001030997.1 *MBOAT1
chr2:61.88–61.94	LR	2	441	3256/201	-4.5	0.38	0.33	0.09	
chr2:62.42–62.46	LR	1	327	3047/185	-4.2	0.36	0.29	0.11	[2] ENSGALG00000012703 DTBP1_CHICK *DTNBP1
chr2:71.72–71.76	AD	1	95	2486/316	-4.9	0.2	0.19	0.24	
chr2:72.62–72.66	CB	1	99	806/45	-4.5	0.35	0.1	0.34	[3] ENSGALG00000012923 CDH9
chr2:74.24–74.28	AD	1	102	2903/390	-4.6	0.21	0.23	0.25	
chr2:74.50–74.54	CB	1	123	802/52	-4.2	0.37	0.11	0.29	

chr2:74.54–74.58	CB	1	103	704/39	-4.5	0.24	0.1	0.19	
chr2:75.26–75.30	CB	1	77	480/32	-4.1	0.35	0.12	0.3	
chr2:84.16–84.56	**AD**	**19**	**261**	**7575/918**	**-7.7**	**0.11**	**0.17**	**0.13**	**[1] ENSGALG00000013114 VSTM2A** **[1] ENSGALG00000022910** **[1] ENSGALG00000022911** **[1] ENSGALG00000022912**
chr2:84.60–84.64	AD	1	22	343/45	-4.7	0.21	0.25	0.17	
chr2:84.66–84.92	**AD**	**12**	**178**	**4636/461**	**-8.5**	**0.08**	**0.05**	**0**	
chr2:84.66–84.72	CB	2	31	171/5	-5.7	0.08	0.05	0.06	
chr2:84.68–84.76	**LR**	**3**	**42**	**267/8**	**-6.5**	**0.08**	**0.05**	**0**	
chr2:84.76–84.90	LR	6	112	977/44	-5.8	0.13	0.17	0.03	
chr2:84.94–85.00	LR	2	129	1082/60	-4.6	0.37	0.38	0.09	
chr2:88.52–88.58	AD	2	305	7529/1029	-5.0	0.2	0.12	0.23	
chr2:88.54–88.58	CB	1	216	1533/107	-4.0	0.2	0.12	0.24	
chr2:88.96–89.14	AD	8	198	5448/688	-5.7	0.17	0.18	0.14	
chr2:91.72–91.76	CB	1	362	2617/153	-4.4	0.29	0.1	0.34	[6] ENSGALG00000013568 NR4A3
chr2:94.28–94.32	AD	1	304	8606/1238	-4.3	0.22	0.11	0.23	[1] ENSGALG00000013704 *AC008021.10-1 [1] ENSGALG00000013708 CYB5_CHICK *CYB5A [5] ENSGALG00000013709 C18orf55
chr2:94.28–94.34	CB	2	484	3669/223	-4.6	0.22	0.1	0.23	[1] ENSGALG00000013704 *AC008021.10-1 [1] ENSGALG00000013708 CYB5_CHICK *CYB5A [3] ENSGALG00000013709 C18orf55 [6] ENSGALG00000013720 FBXO15
chr2:95.34–95.40	CB	2	199	1355/90	-4.7	0.32	0.09	0.35	
chr2:95.84–95.88	LR	1	153	1244/79	-4.1	0.3	0.28	0.11	
chr2:96.42–96.70	**CB**	**13**	**1339**	**10852/170**	**-6.6**	**0.24**	**0.01**	**0.26**	**[1] ENSGALG00000013757 TXNDC10 *TMX3** **[1] ENSGALG00000013762**

									[1] ENSGALG00000019509 CCDC102B
chr2:97.08–97.16	**CB**	**3**	**470**	**3084/151**	**-6.3**	**0.36**	**0.02**	**0.27**	**[5] ENSGALG00000013766 C18orf4**
chr2:97.48–97.56	CB	3	251	1709/94	-5.2	0.21	0.07	0.1	
chr2:97.50–97.54	AD	1	96	2336/313	-4.6	0.21	0.07	0.11	
chr2:97.50–97.56	LR	2	181	1393/85	-4.3	0.21	0.07	0.1	
chr2:98.04–98.10	LR	2	152	1240/62	-4.8	0.31	0.26	0.08	
chr2:98.20–98.26	AD	2	171	3760/479	-5.5	0.18	0.12	0.15	
chr2:98.20–98.24	CB	1	130	800/53	-4.2	0.18	0.12	0.15	
chr2:98.26–98.32	CB	2	244	1783/116	-4.5	0.25	0.1	0.24	
chr2:100.58–100.64	AD	2	284	6500/754	-5.4	0.18	0.05	0.31	[1] ENSGALG00000022875 **many2many: BTN1A1, BTN2A1, BTN2A2, BTN2A3, BTN3A1, BTN3A2, BTN3A3, BTNL2, BTNL3, BTNL8, BTNL9, ERMAP, MOG, RP5-915N17.9, 2 [4] ENSGALG00000013932 **NAPG
chr2:100.58–100.66	CB	3	371	2476/111	-5.6	0.18	0.05	0.31	[1] ENSGALG00000022875 **many2many: BTN1A1, BTN2A1, BTN2A2, BTN2A3, BTN3A1, BTN3A2, BTN3A3, BTNL2, BTNL3, BTNL8, BTNL9, ERMAP, MOG, RP5-915N17.9 [4] ENSGALG00000013932 **NAPG
chr2:119.34–119.38	AD	1	131	3211/423	-4.7	0.21	0.19	0.22	[2] ENSGALG00000014512 *COPS5 [5] ENSGALG00000015520 TRIM55 [6] ENSGALG00000015521 Q703P0_CHICK *CRH [6] ENSGALG00000022814
chr2:122.36–122.40	AD	1	199	4291/553	-4.8	0.2	0.16	0.15	[1] ENSGALG00000022800 [6] ENSGALG00000015633 NP_989711.2 **AP005212.2-3, TERF1
chr2:123.52–123.62	**AD**	**4**	**335**	**7507/928**	**-6.0**	**0.16**	**0.03**	**0.09**	**[3] ENSGALG00000015670 HNF4G**
chr2:123.52–123.72	**CB**	**9**	**602**	**4114/111**	**-6.4**	**0.16**	**0.02**	**0.09**	**[3] ENSGALG00000015670 HNF4G**
chr2:123.54–123.60	LR	2	223	1597/97	-4.6	0.16	0.03	0.09	[5] ENSGALG00000015670 HNF4G

chr2:123.64–123.70	AD	2	138	3280/419	-5.0	0.2	0.02	0.12	
chr2:123.74–123.80	CB	2	128	812/67	-4.2	0.27	0.12	0.2	
chr2:123.80–123.84	CB	1	61	393/25	-4.3	0.35	0.11	0.2	
chr2:124.22–124.26	AD	1	31	781/90	-5.4	0.19	0.09	0.14	[3] ENSGALG00000015673 ZFHX4
chr2:124.22–124.26	CB	1	31	245/12	-4.8	0.19	0.09	0.14	[3] ENSGALG00000015673 ZFHX4
chr2:126.44–126.50	AD	2	454	10161/1449	-5.8	0.17	0.21	0.15	
chr2:126.58–126.70	AD	5	1334	27267/3688	-5.1	0.19	0.16	0.2	
chr2:126.72–126.80	AD	3	805	16556/2465	-4.4	0.22	0.18	0.21	
chr2:127.04–127.12	AD	3	790	15511/2150	-5.8	0.17	0.17	0.17	[1] ENSGALG00000019458 [6] ENSGALG00000015797 RALYL
chr2:132.62–132.66	LR	1	85	706/29	-4.9	0.36	0.3	0.08	[2] ENSGALG00000016015 *STK3 [5] ENSGALG00000017690 *KCNS2
chr2:132.92–132.96	CB	1	28	67/3	-4.9	0.28	0.08	0.35	[4] ENSGALG00000016029 VPS13B
chr2:135.16–135.22	LR	2	154	1124/70	-4.3	0.34	0.31	0.1	[2] ENSGALG00000016074 RIMS2
chr2:137.50–137.58	LR	3	373	3725/148	-5.1	0.26	0.3	0.07	[1] ENSGALG00000016097 TTC35
chr2:146.98–147.02	AD	1	241	5482/774	-4.4	0.22	0.24	0.27	[2] ENSGALG00000016270 EFR3A [5] ENSGALG00000016257 NP_001028816.1 *OC90
chr2:147.06–147.18	AD	5	488	12100/1456	-5.9	0.17	0.13	0.23	[3] ENSGALG00000016246 KCNQ3 [6] ENSGALG00000016257 NP_001028816.1 *OC90
chr2:148.32–148.36	CB	1	337	2348/101	-5.0	0.33	0.08	0.36	[1] ENSGALG00000018290 gga-mir-30d [1] ENSGALG00000018291 gga-mir-30b [5] ENSGALG00000016204 [6] ENSGALG00000016207 ZFAT
chr2:150.22–150.28	LR	2	305	2828/163	-5.3	0.3	0.31	0.06	[2] ENSGALG00000016195 COL22A1
chr2:152.66–152.72	CB	2	264	1888/112	-5.1	0.25	0.08	0.23	

chr2:152.72–152.78	**AD**	**2**	**199**	**5022/389**	**-7.7**	**0.11**	**0.23**	**0.09**	
chr2:152.72–152.76	LR	1	110	829/41	-4.6	0.11	0.23	0.09	
chr2:152.86–152.90	LR	1	137	1109/60	-4.4	0.3	0.27	0.1	[6] ENSGALG00000016161 *TSNARE1
chr2:152.88–153.00	AD	5	330	10185/1278	-5.5	0.18	0.12	0.24	
chr2:152.92–152.96	CB	1	171	1521/104	-4.1	0.2	0.12	0.39	
chr3:1.14–1.22	AD	3	117	3383/466	-4.5	0.21	0.32	0.19	
chr3:1.22–1.26	CB	1	107	1011/65	-4.2	0.28	0.11	0.17	
chr3:1.46–1.52	CB	2	170	1624/59	-5.8	0.3	0.04	0.36	
chr3:13.92–13.96	LR	1	402	3488/192	-4.4	0.35	0.29	0.1	
chr3:14.00–14.04	LR	1	308	2713/118	-4.8	0.31	0.37	0.08	[6] ENSGALG00000009028 BTBD3
chr3:14.48–14.52	LR	1	281	2666/134	-4.5	0.34	0.35	0.09	[4] ENSGALG00000009013 MKKS [4] ENSGALG00000009016 C20orf94
chr3:14.84–14.88	LR	1	315	3027/154	-4.5	0.28	0.15	0.09	[1] ENSGALG00000008918 C20orf103 [3] ENSGALG00000008907 PLCB4 [3] ENSGALG00000008947 PAK7
chr3:15.60–15.68	LR	3	502	4127/260	-4.2	0.35	0.31	0.11	[5] ENSGALG00000008845 HAO1 [6] ENSGALG00000025215
chr3:21.12–21.16	AD	1	203	5043/750	-4.1	0.23	0.15	0.28	[4] ENSGALG00000009645 NP_001007082.1 **many2many: ESR1, ESR2, ESRRA, ESRRB, ESRRG, NR4A2, NR4A3
chr3:21.34–21.40	AD	2	370	8237/1002	-5.6	0.18	0.32	0.1	[2] ENSGALG00000009645 NP_001007082.1 **many2many: ESR1, ESR2, ESRRA, ESRRB, ESRRG, NR4A2, NR4A3
chr3:21.36–21.40	LR	1	227	1677/92	-4.4	0.21	0.34	0.1	[2] ENSGALG00000009645 NP_001007082.1 **many2many: ESR1, ESR2, ESRRA, ESRRB, ESRRG, NR4A2, NR4A3
chr3:22.42–22.46	LR	1	205	1644/84	-4.5	0.34	0.35	0.09	[3] ENSGALG00000009791 PROX1_CHICK
chr3:24.86–24.90	**AD**	**1**	**221**	**4639/429**	**-6.3**	**0.15**	**0.24**	**0.17**	**[2] ENSGALG00000009915 EML4**

chr3:25.24–25.32	CB	3	510	4490/205	-5.7	0.33	0.05	0.34	[3] ENSGALG00000009926 HAAO [6] ENSGALG00000018109
chr3:25.54–25.62	LR	3	418	3357/115	-5.6	0.25	0.32	0.04	
chr3:29.98–30.02	AD	1	231	5678/753	-4.7	0.21	0.26	0.15	[2] ENSGALG00000010055 DAAM2
chr3:33.58–33.62	CB	1	316	1911/75	-5.1	0.35	0.07	0.35	[2] ENSGALG00000010597 CRIM1_CHICK
chr3:33.84–33.92	CB	3	434	3332/184	-5.0	0.27	0.08	0.35	
chr3:36.30–36.36	CB	2	377	2867/178	-4.6	0.29	0.1	0.3	[4] ENSGALG00000010709 AKT3 [6] ENSGALG00000020030
chr3:37.98–38.04	CB	2	225	1712/99	-5.2	0.25	0.07	0.31	[4] ENSGALG00000010778 ACM3_CHICK *CHRM3
chr3:39.30–39.36	CB	2	142	792/36	-5.4	0.33	0.06	0.28	[3] ENSGALG00000010838 ERO1LB [3] ENSGALG00000010843 NP_001026233.1 *GPR137B [6] ENSGALG00000014369 NP_001012405.2 *EDARADD
chr3:39.72–39.80	AD	3	110	2837/415	-5.2	0.19	0.12	0.22	[4] ENSGALG00000014327 XR_027108.1 *ARID4B [6] ENSGALG00000013921 TOMM20 [6] ENSGALG00000014328 RBM34 [6] ENSGALG00000025517
chr3:48.24–48.28	CB	1	110	966/53	-4.6	0.23	0.1	0.39	[2] ENSGALG00000012297 **many2many: AC130364.5-1, GRM1, GRM2, GRM3, GRM4, GRM5, GRM6, GRM7, GRM8,
chr3:48.24–48.32	AD	3	389	10115/1288	-5.3	0.19	0.1	0.29	[2] ENSGALG00000012297 **many2many: AC130364.5-1, GRM1, GRM2, GRM3, GRM4, GRM5, GRM6, GRM7, GRM8
chr3:54.30–54.34	CB	1	450	3449/240	-4.0	0.37	0.12	0.31	[2] ENSGALG00000019976 *ADAT2 [6] ENSGALG00000013773 FUCA2
chr3:54.60–54.66	CB	2	186	1592/86	-5.3	0.22	0.06	0.2	[6] ENSGALG00000013795 HIVEP2
chr3:54.60–54.64	AD	1	102	3105/443	-4.3	0.22	0.06	0.2	
chr3:55.34–55.42	LR	3	290	2243/140	-5.8	0.26	0.31	0.03	
chr3:62.62–62.66	LR	1	48	364/23	-4.1	0.38	0.3	0.11	[3] ENSGALG00000013651 RNF217
chr3:64.04–64.18	LR	6	472	4263/227	-5.4	0.35	0.33	0.05	

chr3:66.02–66.06	LR	1	358	3041/138	-4.7	0.4	0.36	0.08	[3] ENSGALG00000014902 GOPC [3] ENSGALG00000014907 DCBLD1 [6] ENSGALG00000014900
chr3:71.52–71.56	CB	1	230	1836/127	-4.1	0.29	0.12	0.26	[3] ENSGALG00000015410 POPD3_CHICK [3] ENSGALG00000015411 LN28B_CHICK
chr3:71.54–71.58	AD	1	337	7732/1122	-4.2	0.22	0.16	0.3	[3] ENSGALG00000015411 LN28B_CHICK [5] ENSGALG00000015410 POPD3_CHICK
chr3:71.82–71.90	AD	3	138	4106/506	-5.3	0.19	0.38	0.03	[1] ENSGALG00000015417
chr3:71.82–71.90	LR	3	138	1352/52	-5.9	0.19	0.38	0.03	[1] ENSGALG00000015417
chr3:72.46–72.54	AD	3	345	6865/923	-4.9	0.2	0.13	0.15	
chr3:76.44–76.48	AD	1	219	5093/743	-4.2	0.22	0.21	0.26	
chr3:80.38–80.42	LR	1	402	3081/174	-4.3	0.37	0.34	0.1	[2] ENSGALG00000015846 NP_001012969.1 *SNAP91
chr3:80.86–80.90	CB	1	250	2269/142	-4.3	0.26	0.11	0.23	
chr3:82.88–82.92	CB	1	163	1288/61	-4.8	0.24	0.09	0.07	
chr3:82.88–82.94	LR	2	326	2807/159	-5.0	0.24	0.09	0.07	
chr3:86.52–86.56	AD	1	131	2767/412	-4.1	0.23	0.21	0.18	
chr3:86.60–86.74	**AD**	**6**	**454**	**10591/1120**	**-8.2**	**0.09**	**0.03**	**0.08**	
chr3:86.62–86.84	**CB**	**10**	**808**	**5448/193**	**-6.0**	**0.09**	**0.03**	**0.08**	
chr3:86.64–86.68	LR	1	172	1183/55	-4.7	0.09	0.03	0.08	
chr3:86.98–87.02	LR	1	208	1582/96	-4.2	0.32	0.25	0.11	
chr4:7.78–7.82	CB	1	241	1715/99	-4.5	0.32	0.1	0.36	
chr4:8.86–8.90	CB	1	244	1703/117	-4.1	0.37	0.12	0.34	[2] ENSGALG00000007028
chr4:8.90–8.96	CB	2	603	4378/285	-4.6	0.34	0.1	0.3	[4] ENSGALG00000007028
chr4:13.72–13.76	CB	1	397	3146/157	-4.7	0.31	0.09	0.35	[4] ENSGALG00000008074 AMMECR1

chr4:21.42–21.48	LR	2	96	949/38	-5.2	0.27	0.34	0.06	[1] ENSGALG00000009272 [4] ENSGALG00000009268 NP_990320.1 *FGG [4] ENSGALG00000009276 LRAT *LRAT [6] ENSGALG00000009266 FIBA_CHICK *FGA
chr4:24.90–24.98	**LR**	**3**	**366**	**3510/145**	**-6.1**	**0.27**	**0.35**	**0.02**	**[1] ENSGALG00000009554 KLHL2 *KLHL2** **[1] ENSGALG00000009560 ERG25_CHICK *SC4MOL** **[1] ENSGALG00000017930 7SK** **[6] ENSGALG00000009528 TMEM192** **[6] ENSGALG00000009563 CPE *CPE**
chr4:28.02–28.06	AD	1	256	5420/768	-4.4	0.22	0.25	0.14	[5] ENSGALG00000009719 Q9YGR4_CHICK *PCDH10
chr4:29.50–29.56	AD	2	325	6881/904	-5.5	0.18	0.2	0.15	
chr4:29.72–29.76	CB	1	113	863/39	-4.9	0.31	0.08	0.24	[5] ENSGALG00000009732 Q9YGR2_CHICK *PCDH18
chr4:35.26–35.32	LR	2	416	4266/201	-5.3	0.35	0.32	0.05	[1] ENSGALG00000010130 INT10_CHICK *INTS10 [1] ENSGALG00000010136 HGSNAT *HGSNAT [1] ENSGALG00000010138 SG196_CHICK *AC113191.13-1 [1] ENSGALG00000010142 C8orf40 *C8orf40 [1] ENSGALG00000023351 [4] ENSGALG00000010159 NP_001026304.1 *SLC20A2
chr4:40.56–40.62	CB	2	441	3047/192	-5.1	0.26	0.07	0.14	[1] ENSGALG00000010596 TACR3
chr4:40.60–40.64	LR	1	415	2905/104	-5.1	0.28	0.2	0.07	[5] ENSGALG00000010596 TACR3 [6] ENSGALG00000010601 UFSP2_CHICK [6] ENSGALG00000010604 LRP2BP
chr4:40.66–40.72	LR	2	641	5430/271	-5.8	0.35	0.31	0.03	[1] ENSGALG00000010610 SNX25 [3] ENSGALG00000010604 LRP2BP [5] ENSGALG00000010601 UFSP2_CHICK
chr4:43.16–43.20	AD	1	92	2331/324	-4.5	0.21	0.15	0.27	
chr4:49.10–49.16	AD	2	738	16070/2503	-4.6	0.21	0.19	0.14	
chr4:49.98–50.04	**AD**	**2**	**251**	**7330/879**	**-7.3**	**0.12**	**0.09**	**0.19**	
chr4:50.00–50.04	CB	1	111	1060/50	-4.8	0.12	0.09	0.19	

chr4:52.78–52.82	AD	1	186	5141/773	-4.1	0.23	0.33	0.25	[6] ENSGALG00000011680 EPHA5_CHICK
chr4:53.82–53.86	LR	1	249	1957/122	-4.1	0.38	0.32	0.11	
chr4:58.16–58.20	AD	1	224	5040/654	-4.8	0.2	0.36	0.1	[2] ENSGALG00000012036 KCC2D_CHICK
chr4:58.16–58.20	LR	1	224	1572/91	-4.3	0.2	0.36	0.1	[2] ENSGALG00000012036 KCC2D_CHICK
chr4:58.44–58.48	CB	1	343	2355/132	-4.5	0.38	0.1	0.13	[2] ENSGALG00000012044 Q90716_CHICK *ANK2
chr4:58.46–58.56	LR	4	872	6367/208	-5.5	0.15	0.15	0.05	[2] ENSGALG00000012044 Q90716_CHICK *ANK2
chr4:58.5–58.56	**AD**	**2**	**517**	**11660/1207**	**-6.3**	**0.15**	**0.18**	**0.07**	**[2] ENSGALG00000012044 Q90716_CHICK *ANK2**
chr4:64.56–64.60	AD	1	215	5044/690	-4.5	0.21	0.35	0.15	[2] ENSGALG00000020156 [6] ENSGALG00000013590 **AL592183.10-2, CU459211.2-1, FRG1, FRG1B [6] ENSGALG00000013599 NP_001006453.1 *ASAH1
chr4:64.76–64.80	AD	1	195	4666/669	-4.3	0.22	0.36	0.02	[1] ENSGALG00000023067 [4] ENSGALG00000013615 MTUS1 *MTUS1 [6] ENSGALG00000023068
chr4:64.76–64.80	**LR**	**1**	**195**	**1543/18**	**-6.0**	**0.22**	**0.36**	**0.02**	**[1] ENSGALG00000023067 [4] ENSGALG00000013615 MTUS1 *MTUS1 [6] ENSGALG00000023068**
chr4:65.06–65.10	AD	1	299	6680/882	-4.7	0.21	0.32	0.18	[3] ENSGALG00000013661 EFHA2 [6] ENSGALG00000013655 ZDHHC2 [6] ENSGALG00000013663 FGF20
chr4:71.72–71.86	**CB**	**6**	**433**	**3115/83**	**-6.7**	**0.29**	**0**	**0.31**	**[1] ENSGALG00000013521 TBC1D1 [5] ENSGALG00000000486 NP_001026554.1 **PGM2**
chr4:72.40–72.50	CB	4	212	1502/79	-5.3	0.21	0.06	0.27	[3] ENSGALG00000014343 CENTD1 **ARAP3
chr4:72.46–72.50	AD	1	80	1916/262	-4.5	0.21	0.12	0.27	[5] ENSGALG00000014343 CENTD1 **ARAP3
chr4:76.14–76.18	AD	1	83	2256/337	-4.1	0.23	0.2	0.31	[3] ENSGALG00000014391 CCDC149 *CCDC149 [3] ENSGALG00000018557 SOD3
chr4:78.40–78.46	CB	2	178	1325/69	-5.5	0.27	0.05	0.09	

chr4:78.42–78.46	LR	1	111	965/49	-4.5	0.27	0.05	0.09	
chr4:80.32–80.36	AD	1	283	6429/930	-4.3	0.22	0.29	0.26	[1] ENSGALG00000014522 *FAM44A [1] ENSGALG00000014919 [5] ENSGALG00000017391
chr4:80.38–80.42	AD	1	337	7127/1028	-4.3	0.22	0.14	0.31	[4] ENSGALG00000014931 RAB28 *RAB28 [6] ENSGALG00000017391
chr4:80.40–80.46	CB	2	453	2722/169	-4.5	0.24	0.1	0.34	[3] ENSGALG00000014931 RAB28
chr4:80.44–80.48	AD	1	240	5235/763	-4.2	0.22	0.17	0.3	[3] ENSGALG00000014931 RAB28
chr4:80.76–80.84	AD	3	337	8055/1019	-5.8	0.17	0.11	0.18	[1] ENSGALG00000014932
chr4:80.80–80.84	CB	1	148	1107/70	-4.3	0.2	0.11	0.32	[4] ENSGALG00000014932
chr4:84.26–84.32	AD	2	74	1658/246	-4.8	0.2	0.18	0.09	
chr4:84.26–84.30	LR	1	55	417/21	-4.5	0.2	0.21	0.09	
chr4:84.46–84.58	**LR**	**5**	**565**	**5738/42**	**-6.4**	**0.22**	**0.26**	**0.01**	**[5] ENSGALG00000015608 ADRA2C**
chr4:84.46–84.52	AD	2	387	11549/1693	-4.4	0.22	0.26	0.01	
chr4:84.52–84.56	AD	1	106	3250/461	-4.4	0.22	0.32	0.03	
chr5:2.42–2.48	AD	2	133	3238/424	-4.9	0.2	0.23	0.25	[2] ENSGALG00000003777 NELL1 [6] ENSGALG00000025380
chr5:2.98–3.02	AD	1	18	511/71	-4.5	0.21	0.24	0.23	[4] ENSGALG00000003655 GAS2 *GAS2 [6] ENSGALG00000003660 FANCF
chr5:3.40–3.44	AD	1	23	678/102	-4.1	0.23	0.16	0.29	[1] ENSGALG00000013304 SLC5A12 [3] ENSGALG00000013311 TMEM16C *ANO3
chr5:3.52–3.56	AD	1	31	544/70	-4.8	0.2	0.23	0.15	[4] ENSGALG00000013297 BBOX1 *BBOX1 [5] ENSGALG00000023904 *FIBIN [6] ENSGALG00000023903
chr5:3.64–3.70	AD	2	50	1288/212	-4.3	0.22	0.28	0.22	[3] ENSGALG00000012191 LGR4 [4] ENSGALG00000012194 NP_001026239.1 *CCDC34

chr5:3.80–3.84	AD	1	58	1548/215	-4.5	0.21	0.29	0.28	[1] ENSGALG00000012162
chr5:4.16–4.20	LR	1	149	1156/44	-5.0	0.27	0.28	0.07	
chr5:4.22–4.26	LR	1	74	571/31	-4.4	0.24	0.26	0.1	
chr5:4.24–4.28	AD	1	72	1676/236	-4.4	0.22	0.25	0.13	
chr5:12.24–12.28	CB	1	100	677/41	-4.4	0.34	0.11	0.34	[2] ENSGALG00000006074 SOX6
chr5:18.82–18.88	LR	2	195	1396/34	-5.5	0.31	0.34	0.05	[3] ENSGALG00000007566 [6] ENSGALG00000007563 FGF3_CHICK
chr5:19.38–19.48	**LR**	**4**	**216**	**1651/67**	**-6.3**	**0.32**	**0.16**	**0.01**	**[2] ENSGALG00000007719 SHANK2**
chr5:20.22–20.28	LR	2	146	1218/55	-5.4	0.24	0.23	0.05	[1] ENSGALG00000007817 EHF [6] ENSGALG00000020471
chr5:20.54–20.58	LR	1	123	944/44	-4.7	0.41	0.31	0.09	[2] ENSGALG00000007849 Q9W6S4_CHICK *CD44 [6] ENSGALG00000023393
chr5:21.98–22.04	CB	2	174	1257/71	-4.9	0.35	0.08	0.23	
chr5:23.02–23.08	AD	2	284	6133/987	-4.8	0.2	0.14	0.16	
chr5:23.20–23.24	LR	1	135	1105/66	-4.2	0.33	0.3	0.11	
chr5:23.48–23.54	AD	2	150	2997/379	-5.6	0.18	0.17	0.29	[1] ENSGALG00000013428
chr5:24.58–24.68	**AD**	**4**	**175**	**4427/592**	**-6.4**	**0.15**	**0.35**	**0.03**	
chr5:24.58–24.66	LR	3	119	961/23	-5.8	0.15	0.36	0.03	
chr5:32.22–32.28	LR	2	489	3897/156	-5.1	0.38	0.21	0.06	
chr5:34.32–34.38	LR	2	191	1761/70	-5.5	0.32	0.2	0.05	[2] ENSGALG00000020438 ATPBD4
chr5:34.54–34.60	AD	2	301	6572/984	-4.9	0.2	0.14	0.24	[1] ENSGALG00000009838 AQR [5] ENSGALG00000009817 ZNF770 *ZNF770 [6] ENSGALG00000009844 ACTC_CHICK **ACTC1
chr5:34.64–34.70	CB	2	268	1611/57	-5.6	0.29	0.05	0.32	[5] ENSGALG00000009845 NP_989913.1 *GJD2

chr5:34.82–34.88	LR	2	140	1354/62	-4.9	0.3	0.31	0.07	[3] ENSGALG00000009850 NOVA1 *NOVA1 [6] ENSGALG00000009847 STXBP6
chr5:35.10–35.16	LR	2	229	1916/125	-4.2	0.34	0.31	0.11	[2] ENSGALG00000009850 NOVA1
chr5:36.94–37.00	AD	2	341	8546/1078	-5.1	0.19	0.12	0.22	[3] ENSGALG00000009983 NUBPL
chr5:36.96–37.00	CB	1	198	1438/98	-4.1	0.19	0.12	0.3	[5] ENSGALG00000009983 NUBPL
chr5:39.24–39.30	LR	2	368	2692/171	-4.3	0.39	0.34	0.1	[2] ENSGALG00000010117 SLC25A21
chr5:41.24–41.28	LR	1	262	2106/95	-4.7	0.36	0.31	0.08	[6] ENSGALG00000010368 XR_027126.1 *VASH1 [6] ENSGALG00000023101
chr5:41.28–41.32	AD	1	226	5249/739	-4.4	0.22	0.3	0.22	[1] ENSGALG00000010368 XR_027126.1 *VASH1 [1] ENSGALG00000010372 NP_001026376.1 *ANGEL1 [4] ENSGALG00000010378 C14orf166B *C14orf166B
chr5:42.74–42.80	AD	2	182	5616/680	-5.1	0.19	0.22	0.18	[2] ENSGALG00000010518 *NRXN3
chr5:43.02–43.08	LR	2	273	2124/128	-4.4	0.23	0.34	0.1	
chr5:43.20–43.28	**AD**	**3**	**514**	**11388/1148**	**-9.2**	**0.06**	**0.09**	**0.07**	**[1] ENSGALG00000010572 NP_001029022.1 *TSHR** **[3] ENSGALG00000010576 NP_001026378.1 *GTF2A1** **[6] ENSGALG00000010562 *C14orf145**
chr5:43.22–43.26	LR	1	312	2156/85	-4.9	0.06	0.09	0.07	[3] ENSGALG00000010572 NP_001029022.1 *TSHR [5] ENSGALG00000010576 NP_001026378.1 *GTF2A1
chr5:43.22–43.28	CB	2	417	2583/173	-4.7	0.06	0.09	0.07	[3] ENSGALG00000010572 NP_001029022.1 *TSHR [3] ENSGALG00000010576 NP_001026378.1 *GTF2A1
chr5:44.24–44.32	AD	3	252	5418/688	-5.5	0.18	0.12	0.23	
chr5:44.28–44.32	CB	1	143	880/58	-4.2	0.18	0.12	0.26	
chr5:50.06–50.14	AD	3	775	17278/2506	-4.9	0.2	0.18	0.19	
chr6:10.36–10.40	CB	1	107	804/49	-4.3	0.35	0.11	0.3	[1] ENSGALG00000003196 RSFR_CHICK [1] ENSGALG00000024284 KRFJ_CHICK [1] ENSGALG00000024285 KRFJ_CHICK [4] ENSGALG00000003249 CWF19L1 *CWF19L1 [5] ENSGALG00000024287 KRFJ_CHICK [5] ENSGALG00000024288

									[6] ENSGALG00000003289 IKKA_CHICK *CHUK
chr6:17.12–17.16	LR	1	414	3471/179	-4.5	0.34	0.2	0.09	[5] ENSGALG00000005226 MYOZ1 [6] ENSGALG00000005232 USP54
chr6:17.18–17.24	LR	2	630	4962/275	-4.5	0.34	0.22	0.09	[1] ENSGALG00000023957 [3] ENSGALG00000005232 USP54 [4] ENSGALG00000005243 NP_001025511.1 *PPP3CB
chr6:19.40–19.46	LR	2	359	2852/153	-4.7	0.23	0.35	0.08	[2] ENSGALG00000006137 ARHGAP22
chr6:20.38–20.50	CB	5	1044	7153/289	-5.8	0.15	0.04	0.14	[1] ENSGALG00000006352 CH25H *CH25H [1] ENSGALG00000006378 Q5ZLQ2_CHICK *LIPA [1] ENSGALG00000006384 **IFIT1, IFIT1L, IFIT2, IFIT3, IFIT5, [1] ENSGALG00000006421 SLC16A12 *SLC16A12 [1] ENSGALG00000018330 gga-mir-107 [3] ENSGALG00000006431 PANK1 *PANK1
chr6:20.40–20.50	**AD**	**4**	**928**	**21647/2653**	**-6.5**	**0.15**	**0.04**	**0.21**	**[1] ENSGALG00000006352 CH25H *CH25H** **[1] ENSGALG00000006378 Q5ZLQ2_CHICK *LIPA** **[1] ENSGALG00000006384 **IFIT1, IFIT1L, IFIT2, IFIT3, IFIT5 [1] ENSGALG00000006421 SLC16A12 *SLC16A12** **[1] ENSGALG00000018330 gga-mir-107** **[3] ENSGALG00000006431 PANK1 *PANK1**
chr6:21.82–21.86	CB	1	253	1914/132	-4.1	0.32	0.12	0.34	[1] ENSGALG00000020784 [4] ENSGALG00000006763 NP_001012923.1 *EXOC6 [5] ENSGALG00000006778 HHEX_CHICK
chr7:6.72–6.80	CB	3	228	1931/96	-5.6	0.43	0.05	0.4	[1] ENSGALG00000006126 CO6A2_CHICK [1] ENSGALG00000006131 FTCD_CHICK [1] ENSGALG00000018157 [1] ENSGALG00000018158 [1] ENSGALG00000018160 [3] ENSGALG00000005974 CO6A1_CHICK [4] ENSGALG00000018163 [5] ENSGALG00000004363 MCM3AP *MCM3AP [5] ENSGALG00000018165 [5] ENSGALG00000018166 [5] ENSGALG00000018168 [5] ENSGALG00000018170 [6] ENSGALG00000006133 [6] ENSGALG00000018164

									[6] ENSGALG00000018167 [6] ENSGALG00000018169 [6] ENSGALG00000018171 [6] ENSGALG00000025409 [6] ENSGALG00000025432
chr7:6.80–6.84	CB	1	65	486/29	-4.4	0.4	0.11	0.35	[1] ENSGALG00000006133 [1] ENSGALG00000018164 [1] ENSGALG00000018165 [1] ENSGALG00000018166 [1] ENSGALG00000018167 [1] ENSGALG00000018168 [1] ENSGALG00000018169 [1] ENSGALG00000018170 [3] ENSGALG00000004363 MCM3AP *MCM3AP [3] ENSGALG00000018163 [5] ENSGALG00000006126 CO6A2_CHICK [5] ENSGALG00000018157 [5] ENSGALG00000023711 [6] ENSGALG00000006131 FTCD_CHICK [6] ENSGALG00000006141 Q7T1N6_CHICK *POFUT2 [6] ENSGALG00000018158 [6] ENSGALG00000018160 [6] ENSGALG00000023710 [6] ENSGALG00000023715 PRR13
chr7:8.82–8.88	CB	2	46	374/28	-4.5	0.43	0.1	0.37	[1] ENSGALG00000007552 NP_001026419.1 *GLS [3] ENSGALG00000007651 NP_001012932.1 *STAT1
chr7:9.24–9.28	LR	1	199	1734/77	-4.8	0.37	0.36	0.08	[2] ENSGALG00000007729 OBFC2A *OBFC2A [2] ENSGALG00000007759 TMEFF2
chr7:9.32–9.36	LR	1	235	1969/111	-4.3	0.32	0.25	0.1	[3] ENSGALG00000007729 OBFC2A
chr7:10.78–10.84	CB	2	377	3412/201	-4.8	0.33	0.09	0.28	[3] ENSGALG00000007944 HECW2 [4] ENSGALG00000007924 NP_001026420.1
chr7:12.58–12.62	**AD**	**1**	**385**	**9956/993**	**-6.0**	**0.16**	**0.21**	**0.13**	**[3] ENSGALG00000008415 ALS2** **[4] ENSGALG00000008398 MPP4** **[6] ENSGALG00000008381 ALS2CR4**
chr7:23.04–23.08	AD	1	224	5030/726	-4.3	0.22	0.25	0.23	[1] ENSGALG00000011131 TANK

chr7:23.10–23.14	AD	1	239	5894/823	-4.4	0.22	0.24	0.19	
chr7:25.42–25.46	LR	1	334	2725/145	-4.4	0.25	0.23	0.1	[2] ENSGALG00000011541 NP_001006524.1 *BIN1
chr7:25.90–25.94	LR	1	376	2973/162	-4.4	0.35	0.26	0.1	[1] ENSGALG00000025223
chr7:26.76–26.82	LR	2	555	4563/246	-4.9	0.33	0.33	0.08	[1] ENSGALG00000011592 NP_989820.1 *MRAS [3] ENSGALG00000011591
chr7:30.46–30.52	AD	2	524	11542/1498	-5.9	0.17	0.14	0.17	[1] ENSGALG00000012129 CCD93_CHICK *CCDC93 [5] ENSGALG00000012147 DDX18 *DDX18
chr7:30.84–30.88	LR	1	262	2078/109	-4.5	0.26	0.33	0.09	[2] ENSGALG00000012156 DPP10
chr7:38.08–38.18	AD	4	175	4365/580	-5.0	0.2	0.24	0.12	[1] ENSGALG00000012570 TANC1 [3] ENSGALG00000012564 DAPL1 [3] ENSGALG00000012574 WSDU1_CHICK [5] ENSGALG00000012561 NP_001006529.1 *PK4P [5] ENSGALG00000012579 BAZ2B_CHICK [6] ENSGALG00000023103
chr7:38.18–38.22	AD	1	38	950/132	-4.5	0.21	0.17	0.21	[3] ENSGALG00000012579 BAZ2B_CHICK *BAZ2B [4] ENSGALG00000012574 WSDU1_CHICK [5] ENSGALG00000012570 TANC1
chr7:38.24–38.38	**AD**	**6**	**250**	**5846/777**	**-6.7**	**0.14**	**0.15**	**0.09**	**[1] ENSGALG00000012584 MARCH7 *38417** **[1] ENSGALG00000012587 NAT5** **[4] ENSGALG00000012579 BAZ2B_CHICK**
chr7:38.28–38.34	LR	2	117	912/60	-4.6	0.14	0.15	0.09	[4] ENSGALG00000012584 xxxMARCH7 *MARCH7 [6] ENSGALG00000012579 BAZ2B_CHICK [6] ENSGALG00000012587 NAT5
chr8:1.74–1.78	CB	1	311	2132/146	-4.1	0.3	0.12	0.29	
chr8:1.76–1.82	AD	2	398	8613/1233	-4.8	0.2	0.13	0.24	
chr8:8.98–9.04	**AD**	**2**	**565**	**12243/1439**	**-6.3**	**0.15**	**0.27**	**0.09**	
chr8:8.98–9.02	LR	1	354	2464/118	-4.6	0.15	0.27	0.09	
chr8:9.06–9.10	AD	1	508	10627/1471	-4.5	0.21	0.29	0.12	

chr8:9.14–9.20	AD	2	600	12531/1735	-5.6	0.18	0.25	0.12	
chr8:9.2–9.40	**AD**	**9**	**1067**	**23786/2554**	**-7.0**	**0.13**	**0.25**	**0.06**	
chr8:9.22–9.26	LR	1	203	1371/69	-4.5	0.15	0.26	0.09	
chr8:9.28–9.38	LR	4	518	3781/174	-5.3	0.13	0.25	0.06	
chr8:9.44–9.56	AD	5	782	17805/2442	-5.0	0.2	0.25	0.14	
chr8:9.58–9.62	AD	1	206	5618/731	-4.8	0.2	0.22	0.17	
chr8:9.66–9.72	**AD**	**2**	**290**	**6482/694**	**-7.0**	**0.13**	**0.24**	**0.09**	
chr8:9.66–9.70	LR	1	207	1496/77	-4.5	0.13	0.24	0.09	
chr8:12.34–12.4	AD	2	223	4905/811	-4.2	0.22	0.15	0.27	[1] ENSGALG00000005208 [1] ENSGALG00000020884 [1] ENSGALG00000025580 [4] ENSGALG00000005229 DPH5 *DPH5
chr8:12.62–12.66	AD	1	137	3130/406	-4.8	0.2	0.15	0.15	[1] ENSGALG00000005329 HIAT1 [3] ENSGALG00000005302 SAS6_CHICK [3] ENSGALG00000005340 NP_001026445.1 *SLC35A3 [5] ENSGALG00000005284 [5] ENSGALG00000005344 [6] ENSGALG00000005290 CCDC76 *CCDC76
chr8:12.66–12.70	LR	1	176	1536/97	-4.1	0.3	0.21	0.11	[1] ENSGALG00000005344 [4] ENSGALG00000005340 NP_001026445.1 *SLC35A3 [6] ENSGALG00000005329 HIAT1 *HIAT1
chr8:13.28–13.32	AD	1	121	2793/415	-4.1	0.23	0.15	0.29	[2] ENSGALG00000005509 DPYD
chr8:13.78–13.82	CB	1	137	974/57	-4.4	0.23	0.1	0.16	[6] ENSGALG00000021872
chr8:13.84–13.94	AD	4	395	9688/1236	-5.2	0.19	0.13	0.25	
chr8:14.92–14.96	LR	1	334	2579/155	-4.2	0.34	0.32	0.11	[1] ENSGALG00000005977 KIAA1107 [3] ENSGALG00000006004 BTBD8 *BTBD8 [4] ENSGALG00000023490 C1orf146 *C1orf146 [5] ENSGALG00000005959 GLMN *GLMN [5] ENSGALG00000006019 ABHD7 *ABHD7

chr8:19.02–19.10	CB	3	341	2663/133	-5.1	0.3	0.08	0.34	
chr8:19.72–19.78	AD	2	453	10400/1427	-5.1	0.19	0.25	0.24	[1] ENSGALG00000008988 ZZZ3 [5] ENSGALG00000008974 USP33 [5] ENSGALG00000009005 AK5
chr8:25.04–25.10	LR	2	375	3891/87	-5.9	0.3	0.2	0.03	[1] ENSGALG00000010613 **AC055876.16-2, ZFYVE9 [3] ENSGALG00000010619 CC2D1B
chr9:11.00–11.04	CB	1	411	2926/202	-4.1	0.35	0.12	0.32	[3] ENSGALG00000002958 DNER
chr9:12.56–12.60	CB	1	150	1188/71	-4.4	0.14	0.11	0.12	[3] ENSGALG00000006783 PLOD2
chr9:12.56–12.62	**AD**	**2**	**289**	**7714/654**	**-6.9**	**0.14**	**0.11**	**0.12**	**[3] ENSGALG00000006783 PLOD2**
chr9:13.36–13.50	**AD**	**6**	**1096**	**23389/2734**	**-7.0**	**0.13**	**0.16**	**0.07**	**[1] ENSGALG00000024000 AGTR1_CHICK** **[3] ENSGALG00000006811 NP_989585.1 *ZIC2**
chr9:13.44–13.54	LR	4	781	5700/307	-5.1	0.15	0.2	0.07	[1] ENSGALG00000006834 CPB1 *CPB1 [1] ENSGALG00000024000 AGTR1_CHICK [5] ENSGALG00000006843 NCBP2 *NCBP2 [5] ENSGALG00000006855 NP_990538.1 *MFI2
chr9:21.98–22.02	AD	1	197	5557/721	-4.8	0.2	0.36	0.19	[6] ENSGALG00000021785
chr9:24.94–24.98	AD	1	190	3678/496	-4.6	0.21	0.19	0.02	[3] ENSGALG00000010361 MBNL1_CHICK [6] ENSGALG00000010357 P2RY1_CHICK
chr9:24.94–25.00	**LR**	**2**	**293**	**1853/64**	**-6.0**	**0.21**	**0.19**	**0.02**	**[1] ENSGALG00000010361 MBNL1_CHICK** **[5] ENSGALG00000010362 SUCNR1** **[5] ENSGALG00000010364 **AADAC, AADACL2** **[5] ENSGALG00000025203** **[6] ENSGALG00000010357 P2RY1_CHICK**
chr10:10.38–10.42	AD	1	31	680/100	-4.2	0.22	0.27	0.09	[1] ENSGALG00000004752 **LYSMD2 [1] ENSGALG00000018976 **LYSMD2 [3] ENSGALG00000004766 SCG3
chr10:10.38–10.42	LR	1	31	236/12	-4.5	0.22	0.27	0.09	[1] ENSGALG00000004752 **LYSMD2, [1] ENSGALG00000018976 **LYSMD2 [3] ENSGALG00000004766 SCG3 *SCG3,
chr10:10.94–10.98	LR	1	121	1171/68	-4.3	0.33	0.35	0.1	[3] ENSGALG00000021295

chr10:14.52–14.56	AD	1	471	10733/1575	-4.2	0.22	0.3	0.19	[1] ENSGALG00000006579 PLIN [1] ENSGALG00000006579 PLIN [1] ENSGALG00000006611 KIF7 [1] ENSGALG00000006631 C15orf42 [1] ENSGALG00000006631 C15orf42 **C15orf42, [1] ENSGALG00000023394 **C15orf42 [1] ENSGALG00000023394 **C15orf42, [1] ENSGALG00000023395 [1] ENSGALG00000023395 [4] ENSGALG00000006635 RHCG_CHICK [4] ENSGALG00000006635 RHCG_CHICK [5] ENSGALG00000006534 PEX11A [5] ENSGALG00000006534 PEX11A
chr10:19.26–19.30	LR	1	134	1257/62	-4.6	0.3	0.3	0.09	[2] ENSGALG00000007069 ADAMTS17
chr11:0.30–0.34	LR	1	192	1707/87	-4.5	0.28	0.21	0.09	[4] ENSGALG00000000774 NP_001025729.1 [4] ENSGALG00000000860 Q5ZLL4_CHICK *SLC7A6 [5] ENSGALG00000000804 SLC7A6OS [5] ENSGALG00000000874 A0FJX3_CHICK *NDRG4 [6] ENSGALG00000000800 NP_001005831.1 *PRMT7
chr11:1.40–1.44	CB	1	357	2381/158	-4.2	0.29	0.12	0.28	[1] ENSGALG00000017825 SNORA46 [1] ENSGALG00000017826 SNORA50 [4] ENSGALG00000002301 CNOT1 [5] ENSGALG00000002247 SETD6_CHICK [5] ENSGALG00000002313 SLC38A7 [5] ENSGALG00000002321 AATM_CHICK *GOT2 [6] ENSGALG00000021425
chr11:1.52–1.56	LR	1	414	3304/144	-4.8	0.3	0.3	0.08	[2] ENSGALG00000002407 HYDIN
chr11:1.60–1.66	AD	2	519	11102/1396	-5.4	0.18	0.28	0.09	[1] ENSGALG00000018008 [1] ENSGALG00000018009 [3] ENSGALG00000002407 HYDIN [4] ENSGALG00000002458 NP_001025735.1
chr11:1.60–1.66	LR	2	519	3486/236	-4.6	0.18	0.28	0.09	[1] ENSGALG00000018008 [1] ENSGALG00000018009 [3] ENSGALG00000002407 HYDIN [4] ENSGALG00000002458 NP_001025735.1
chr11:2.46–2.50	LR	1	75	712/30	-4.8	0.28	0.33	0.08	[1] ENSGALG00000003258 LRRC50 [1] ENSGALG00000003273 NP_001005837.1 *HSDL1 [1] ENSGALG00000023789

									[4] ENSGALG00000003293 MBTPS1 [5] ENSGALG00000003201 FBXL8 [5] ENSGALG00000003224 HSF4 [5] ENSGALG00000003309 EFCBP2 [6] ENSGALG00000003302 SLC38A8
chr11:2.54–2.64	**AD**	**4**	**153**	**3796/440**	**-6.3**	**0.15**	**0.02**	**0.17**	**[1] ENSGALG00000003323 OSGIN1 *OSGIN1** **[4] ENSGALG00000003309 EFCBP2** **[4] ENSGALG00000021325** **[5] ENSGALG00000003330** **[6] ENSGALG00000021324 XR_027040.1 **many2many: OR14A16, OR14A2, OR14K1, OR5U1**
chr11:2.54–2.64	**CB**	**4**	**153**	**1132/36**	**-6.2**	**0.15**	**0.02**	**0.17**	**[1] ENSGALG00000003323 OSGIN1 *OSGIN1** **[4] ENSGALG00000003309 EFCBP2** **[4] ENSGALG00000021325** **[5] ENSGALG00000003330** **[6] ENSGALG00000021324 XR_027040.1 **many2many: OR14A16, OR14A2, OR14K1, OR5U1**
chr11:3.24–3.34	AD	4	143	3905/473	-5.7	0.17	0.06	0.21	[1] ENSGALG00000003396 NFATC3 [3] ENSGALG00000003374 RB35B_CHICK *RBM35B
chr11:3.24–3.34	CB	4	143	1185/55	-5.3	0.17	0.06	0.21	[1] ENSGALG00000003396 NFATC3 [3] ENSGALG00000003374 RB35B_CHICK *RBM35B
chr11:3.38–3.46	CB	3	123	913/54	-5.2	0.18	0.07	0.26	[1] ENSGALG00000003415 DDX28 [1] ENSGALG00000003425 [1] ENSGALG00000003433 **DPEP2, DPEP3 [4] ENSGALG00000003407 DUS2L [4] ENSGALG00000021316 Q5ZJ80_CHICK *SLC12A4
chr11:3.40–3.54	AD	6	239	6137/819	-5.4	0.18	0.07	0.17	[1] ENSGALG00000003433 **DPEP2, DPEP3 [1] ENSGALG00000021316 Q5ZJ80_CHICK *SLC12A4 [4] ENSGALG00000003425 [5] ENSGALG00000003415 DDX28 [5] ENSGALG00000003560 NP_990047.1 *SLC6A2 [6] ENSGALG00000003407 DUS2L
chr11:3.48–3.52	CB	1	83	627/41	-4.2	0.2	0.12	0.21	[3] ENSGALG00000021316 Q5ZJ80_CHICK *SLC12A4
chr11:3.56–3.60	AD	1	55	1418/184	-4.8	0.2	0.13	0.26	[2] ENSGALG00000003560 NP_990047.1 *SLC6A2
chr11:14.6–14.64	AD	1	78	2189/314	-4.3	0.22	0.21	0.03	

chr11:14.60–14.66	LR	2	121	1051/26	-5.8	0.22	0.16	0.03	
chr12:17.20–17.24	AD	1	43	1184/177	-4.1	0.23	0.16	0.21	[3] ENSGALG00000007819 PDZRN3
chr13:3.68–3.90	LR	10	2002	16204/611	-5.7	0.29	0.3	0.04	[1] ENSGALG00000002080 DOCK2 [1] ENSGALG00000002105 FOXI1 [1] ENSGALG00000021504 *AC008449.6 [3] ENSGALG00000001942 CCDC99 [4] ENSGALG00000021904
chr13:9.16–9.26	CB	4	489	3907/136	-5.9	0.28	0.04	0.27	[1] ENSGALG00000002893 STC2 [6] ENSGALG00000002886 NKX25_CHICK *NKX2-5
chr13:9.66–9.70	AD	1	137	3558/482	-4.6	0.21	0.15	0.17	
chr13:12.88–12.94	AD	2	607	31609/4820	-5.3	0.19	0.14	0.27	[1] ENSGALG00000025189 [4] ENSGALG00000004134 GLRA1 [5] ENSGALG00000004160 NP_001006150.1 *G3BP1
chr13:18.06–18.14	CB	3	553	4182/238	-4.7	0.38	0.09	0.33	[5] ENSGALG00000007404 YIPF5 [6] ENSGALG00000012322 KCTD16
chr14:2.98–3.02	CB	1	376	3347/89	-5.6	0.35	0.05	0.3	[2] ENSGALG00000004224 MAD1L1
chr14:3.54–3.58	LR	1	252	1923/123	-4.1	0.29	0.24	0.11	[4] ENSGALG00000004420 SDK1_CHICK
chr14:8.54–8.58	CB	1	68	587/39	-4.2	0.24	0.12	0.38	[2] ENSGALG00000006829 *AC092375.4-5 [6] ENSGALG00000006780 NP_001006171.1 *ARL6IP1
chr14:9.02–9.10	CB	3	641	4807/220	-5.4	0.35	0.06	0.32	[1] ENSGALG00000007119 NP_001025814.1 *DAGLB [1] ENSGALG00000007130 NM_205017.1 *RAC1 [1] ENSGALG00000007133 *Z83826.13-1 [3] ENSGALG00000007089 ERD22_CHICK *KDELR2 [4] ENSGALG00000007149 PSCD3 *CYTH3 [5] ENSGALG00000007070 OTOA
chr14:10.02–10.06	AD	1	72	2447/330	-4.6	0.21	0.34	0.29	[4] ENSGALG00000007283
chr14:11.36–11.40	LR	1	83	668/43	-4.1	0.35	0.31	0.11	[4] ENSGALG00000007366 A2BP1
chr15:3.04–3.08	LR	1	136	1325/81	-4.2	0.35	0.37	0.11	[2] ENSGALG00000002536 *STX2 [5] ENSGALG00000002557 GPR133

chr18:0–0.04	AD	1	42	1252/161	-4.8	0.2	0.19	0.21	[4] ENSGALG00000000346 NP_001025866.1 **ZNF814
chr19:4.36–4.44	LR	3	680	6767/372	-4.8	0.38	0.36	0.08	[1] ENSGALG00000002140 AP2B1 [1] ENSGALG00000002151 PEX12 [1] ENSGALG00000025021 snoZ30 [3] ENSGALG00000002186 UNC45B [5] ENSGALG00000002081 MMP28 [5] ENSGALG00000020906 GAS2L2 [6] ENSGALG00000002086 RASL10B [6] ENSGALG00000002212 RAD51L3 [6] ENSGALG00000002225 NP_001025882.1 *RFFL
chr19:9.06–9.22	LR	7	170	1819/71	-5.6	0.23	0.42	0.04	[1] ENSGALG00000005668 NP_990203.1 *WSB1 [1] ENSGALG00000005685 KSR1 [1] ENSGALG00000005693 NOS2_CHICK [3] ENSGALG00000005697 [6] ENSGALG00000005660 NF1_CHICK [6] ENSGALG00000005699 NLK
chr20:0.36–0.40	AD	1	59	1540/231	-4.1	0.23	0.19	0.33	[4] ENSGALG00000001046 DLGAP4
chr20:0.42–0.46	AD	1	60	1444/216	-4.1	0.23	0.25	0.26	[1] ENSGALG00000001054 Q5ZMJ3_CHICK *C20orf24 [1] ENSGALG00000024081 TGIF2 [3] ENSGALG00000001046 DLGAP4 [3] ENSGALG00000001050 MLRM_CHICK *MYL9 [4] ENSGALG00000001062 GGTL3 *GGT7
chr20:5.56–5.60	CB	1	315	2242/150	-4.1	0.31	0.12	0.32	[5] ENSGALG00000004498 SLC2A10
chr20:5.58–5.62	CB	1	334	2423/169	-4.0	0.33	0.12	0.33	
chr20:6.84–6.90	CB	2	609	4612/204	-5.2	0.29	0.07	0.24	[1] ENSGALG00000021220 PPP1R3D [1] ENSGALG00000021820 [1] ENSGALG00000024473 [6] ENSGALG00000004880 SYCP2
chr20:6.94–6.98	CB	1	290	1891/115	-4.3	0.32	0.11	0.23	[3] ENSGALG00000023778
chr21:0–0.10	AD	4	91	2025/267	-5.1	0.19	0.28	0.18	[1] ENSGALG00000000420 KLHDC7A [1] ENSGALG00000000426 IGSF21 [5] ENSGALG00000000449 ARHGEF10L
chr21:3.68–3.72	CB	1	324	2222/149	-4.1	0.34	0.12	0.38	[1] ENSGALG00000002797 Q5ZIZ0_CHICK *PGD [3] ENSGALG00000002726 KIF1B [5] ENSGALG00000002820 DFFA

									[6] ENSGALG00000002836 PEX14 [6] ENSGALG00000024481 *APITD1
chr22:0.26–0.32	AD	2	72	1482/232	-4.3	0.22	0.21	0.13	[1] ENSGALG00000000119 GKN2 [1] ENSGALG00000000120 Q70GM8_CHICK *BMP10 [1] ENSGALG00000000132 NP_001026054.1 *ARHGAP25 [5] ENSGALG00000000165 CDS2 [6] ENSGALG00000000098 ANTXR1 [6] ENSGALG00000000114 GKN1
chr22:0.86–0.90	AD	1	25	650/87	-4.6	0.21	0.29	0.17	[2] ENSGALG00000000311 PPP2R2A *DOCK5
chr22:1.06–1.10	AD	1	51	1534/179	-5.3	0.19	0.18	0.22	[4] ENSGALG00000000357 Q5F3G5_CHICK **ADAM28, ADAM7
chr22:2.60–2.68	AD	3	82	2036/278	-5.2	0.19	0.17	0.17	[1] ENSGALG00000003473 SFRP1_CHICK [1] ENSGALG00000003483 GOGA7_CHICK [1] ENSGALG00000003492 NP_990276.1 [1] ENSGALG00000003518 AGPAT6 [1] ENSGALG00000018503 NKX6-3 [1] ENSGALG00000018734 [1] ENSGALG00000024080 [3] ENSGALG00000003594 Q90715_CHICK *ANK1 [6] ENSGALG00000003470 ZMAT4
chr23:5.74–5.78	LR	1	39	263/13	-4.6	0.3	0.28	0.09	[1] ENSGALG00000003816 NT5C1A [1] ENSGALG00000003829 HPCAL4 [1] ENSGALG00000021593 HEYL [4] ENSGALG00000003800 **PABPC4L, PABPC5 [4] ENSGALG00000003838 [5] ENSGALG00000003851 TRIT1 [5] ENSGALG00000024064 **BMP8A, BMP8B [5] ENSGALG00000024065 [6] ENSGALG00000013383 PPIE [6] ENSGALG00000017846 SNORA55 [6] ENSGALG00000017847 [6] ENSGALG00000017848 SNORA55
chr24:6.24–6.30	**AD**	**2**	**446**	**10071/947**	**-8.3**	**0.09**	**0.14**	**0.14**	**[1] ENSGALG00000007846 C11orf34** **[1] ENSGALG00000007848 Q8UVX7_CHICK *PTS** **[1] ENSGALG00000007868 BCDO2** **[1] ENSGALG00000007874 IL18_CHICK** **[3] ENSGALG00000007878 NP_001006321.1 *SDHD** **[5] ENSGALG00000007882 C11orf57** **[5] ENSGALG00000007904 DLAT**

									[6] ENSGALG00000007885 PIH1D2
chr26:0.04–0.12	CB	3	74	541/25	-5.1	0.23	0.08	0.29	[1] ENSGALG00000000890 *SRPK1 [1] ENSGALG00000000897 LHPL5_CHICK *LHFPL5 [1] ENSGALG00000000900 COL_CHICK *CLPS [1] ENSGALG00000000947 NP_001005431.1 *FKBP5 [1] ENSGALG00000006370 NP_989946.1 *TULP1 [4] ENSGALG00000000953 TEAD3_CHICK [4] ENSGALG00000019759 Q5ZLJ0_CHICK *MAPK14 [5] ENSGALG00000000844 SLC26A8 [5] ENSGALG00000019751 [6] ENSGALG00000000954 SMPD2
chr26:0.06–0.10	AD	1	47	1157/174	-4.1	0.23	0.08	0.31	[1] ENSGALG00000000897 LHPL5_CHICK *LHFPL5 [1] ENSGALG00000000900 COL_CHICK *CLPS [1] ENSGALG00000000947 NP_001005431.1 *FKBP5 [3] ENSGALG00000000890 *SRPK1 [4] ENSGALG00000006370 NP_989946.1 *TULP1 [4] ENSGALG00000019759 Q5ZLJ0_CHICK *MAPK14 [6] ENSGALG00000000953 TEAD3_CHICK
chr26:0.12–0.22	CB	4	143	1202/69	-5.0	0.26	0.08	0.39	[1] ENSGALG00000000776 BRPF3 [1] ENSGALG00000000826 MAPK13 [1] ENSGALG00000000844 SLC26A8 [3] ENSGALG00000000753 TBC1D22B [3] ENSGALG00000019759 Q5ZLJ0_CHICK *MAPK14 [5] ENSGALG00000000742 PIM3 *PIM1 [6] ENSGALG00000000890 *SRPK1 [6] ENSGALG00000019781
chr26:4.04–4.08	LR	1	316	2696/173	-4.1	0.34	0.36	0.11	[2] ENSGALG00000002723 ANKS1A
chr27:4.64–4.70	LR	2	25	230/5	-5.9	0.16	0.21	0.03	[1] ENSGALG00000002973 NP_001006332.1 [1] ENSGALG00000002978 CNTD1 [1] ENSGALG00000002979 CCDC56 [1] ENSGALG00000002986 [1] ENSGALG00000003001 VPS25 [1] ENSGALG00000003068 EZH1 [1] ENSGALG00000003123 XR_027137.1 *CNTNAP1 [1] ENSGALG00000024449 RAMP2 [4] ENSGALG00000002937 PSME3_CHICK [5] ENSGALG00000003150 **TUBG1, TUBG2 [6] ENSGALG00000003162 FAM134C [6] ENSGALG00000023786 **PLEKHH3

chr27:4.64–4.82	AD	8	99	2784/334	-6.1	0.16	0.02	0.03	[1] ENSGALG00000002781 NP_989500.1 *BRCA1 [1] ENSGALG00000002804 RND2 [1] ENSGALG00000002818 VAT1 [1] ENSGALG00000002823 [1] ENSGALG00000002832 IFI35 [1] ENSGALG00000002837 RL27_CHICK **AL049830.3-1, RPL27 [1] ENSGALG00000002856 RUNDC1 [1] ENSGALG00000002880 AARSD1 [1] ENSGALG00000002937 PSME3_CHICK **AOC2, AOC3 [1] ENSGALG00000002973 NP_001006332.1 [1] ENSGALG00000002978 CNTD1 [1] ENSGALG00000002979 CCDC56 [1] ENSGALG00000002986 [1] ENSGALG00000003001 VPS25 [4] ENSGALG00000002765 *NBR1 [5] ENSGALG00000002740 XR_027139.1 *MPP2 [5] ENSGALG00000003150 **TUBG1, TUBG2 [6] ENSGALG00000003162 FAM134C [6] ENSGALG00000023786 **PLEKHH3
chr27:4.70–4.82	CB	5	74	643/25	-6.3	0.18	0.02	0.19	[1] ENSGALG00000002781 NP_989500.1 *BRCA1 [1] ENSGALG00000002804 RND2 [1] ENSGALG00000002818 VAT1 [1] ENSGALG00000002823 [1] ENSGALG00000002832 IFI35 [1] ENSGALG00000002837 RL27_CHICK [1] ENSGALG00000002856 RUNDC1 [1] ENSGALG00000002880 AARSD1 [1] ENSGALG00000023752 [1] ENSGALG00000023756 [3] ENSGALG00000002937 PSME3_CHICK **AOC2, AOC3 [4] ENSGALG00000002765 *NBR1 [5] ENSGALG00000002740 XR_027139.1 *MPP2 [5] ENSGALG00000002978 CNTD1 [5] ENSGALG00000002986 [6] ENSGALG00000002973 NP_001006332.1 [6] ENSGALG00000002979 CCDC56
chr28:3.64–3.72	CB	3	733	5185/193	-6.0	0.31	0.03	0.23	[1] ENSGALG00000003579 Q90822_CHICK *INSR [1] ENSGALG00000003703 NP_001026110.1 *USE1 [1] ENSGALG00000024257 [2] ENSGALG00000003771 SIN3B [3] ENSGALG00000003717 MYO9B [4] ENSGALG00000003572 ARHGEF18

chr28:3.90–3.94	CB	1	222	1646/75	-4.9	0.37	0.08	0.32	[1] ENSGALG00000021601 EPS15L1 [5] ENSGALG00000003824 Q5ZIS7_CHICK *CHERP [5] ENSGALG00000003914 CALR3 [5] ENSGALG00000003939 *KLF2 [6] ENSGALG00000021883 C19orf44
chr28:4.20–4.26	LR	2	95	768/42	-4.5	0.33	0.27	0.09	[2] ENSGALG00000004048 NP_990738.1 *PTPRS
chr28:4.34–4.38	LR	1	40	372/21	-4.3	0.33	0.33	0.1	[4] ENSGALG00000004091 Q5ZMG6_CHICK **AP002383.3, KDM4B, KDM4D [5] ENSGALG00000004132 UHRF1 *UHRF1

[a]Coordinates of region in Megabases. [b]Line combination in which the heterozygosity Z-score (ZH_P) < -4. [c]Numbers of consecutive ZH_P < -4 windows that were merged. [d]Numbers of SNPs that were identified in region (for merged windows, the number is that of all windows). [e]Sums of major (nMAJ) and minor alleles (nMIN) observed at all SNPs in the region for the line combination in column 2. [f]The lowest ZH_P observed for a 40 kb window in the region for the line combination in column 2. [g]The lowest pooled heterozygosity (H_P) observed for a 40 kb window in the region for AD, CB and LR. [h]Gene(s) overlapping putative sweep region: [1] = Gene contained within region. [2] = Region contained within gene(s). [3] Region overlaps 5'-end of gene(s). [4] = Region overlaps 3'-end of gene(s). [5] = the 5'-end of gene(s) is within 20 kb of region. [6] = the 3'-end of gene(s) is within 20 kb of region. The ENSEMBL ID of the chicken gene is, if applicable, followed by the chicken gene name and/or gene name of human ortholog(s). *Name of human one2one ortholog. **Names of human one2many orthologs.

Supplementary Table 4 Allele frequencies at eight SNPs located in the *TSHR* selective sweep region for 271 chickens representing 36 different breeds. The *TSHR* missense mutation is located at position 43,250,347 on chromosome 5.

				SNP position on chromosome 5							
Breed	Provider	Origin	n	43,225,301	43,229,857	43,233,207	43,246,714	43,250,347	43,255,533	43,257,377	43,259,196
White Leghorn Line 13 (WL-A)	SLU/P. Jensen	Sweden	11	1	1	1	1	1	1	1	1
White Leghorn Hy-Line (WL-B)	J. Altimiras	USA	7	1	1	1	1	1	1	1	1
Rhode Island Red	Hendrix, Aviandiv	Netherlands	10	1	1	1	1	1	1	1	1
Rhode Island Red (RIR)	Hubbard-ISA, AvianDiv	France	8	1	1	1	1	1	1	1	1
Australorp	AvianDiv	Australia	5	1	1	1	1	1	1	1	1
Järhöns	AvianDiv	Norway	8	1	1	1	1	1	1	1	1
Poltava clay	AvianDiv	Ukraine	8	1	1	1	1	1	1	1	1
Dorking	AvianDiv	United Kingdom	3	0.67	0.67	0.67	0.67	0.67	0.67	0.67	0.67
Broiler Dam Line G	Anak, AvianDiv	Israel	8	0.85	1	1	1	1	1	1	1
Broiler Dam Line B (CB-2)	Hubbard-ISA (41)	France	9	0.67	1	1	1	1	1	1	1
Broiler Sire Line B	Hubbard-ISA (42)	France	10	0.85	1	1	1	1	1	1	1
Broiler Ross 308 (CB-1)	J. Altimiras	USA	9	1	1	1	1	1	1	1	1
Broiler Sire Line E	Cobb, AvianDiv	USA	10	0.75	1	1	1	1	1	1	1
High growth line	Paul Siegel	USA	11	1	1	1	1	1	1	1	1
Low growth line	Paul Siegel	USA	10	1	1	1	1	1	1	1	1
Fayoumi	AvianDiv	Egypt	5	1	1	1	1	1	1	1	1
Bourbonnaise	AvianDiv	France	8	1	1	1	1	1	1	1	1
Cochin	AvianDiv	China	8	1	1	1	1	1	1	1	1
Coucou de Rennes	AvianDiv	France	7	0.79	1	1	1	1	1	1	1
Czech Golden Pencilled	AvianDiv	Czech Republic	5	1	1	1	1	1	1	1	1
Finnish Landrace	AvianDiv	Finland	5	0.7	1	1	1	1	1	1	1
Friesian fowl	AvianDiv	Netherlands	5	1	1	1	1	1	1	1	1

Houdan	AvianDiv	France	5	1	1	1	1	1	1	1	1
Marans	AvianDiv	France	8	0.56	1	1	1	1	1	1	1
Owl-bearded	AvianDiv	Netherlands	8	1	1	1	1	1	1	1	1
Red Villafranquina	AvianDiv	Spain	5	1	1	1	1	1	1	1	1
Transsylvanian Naked Neck	AvianDiv	Hungary	5	1	1	1	1	1	1	1	1
Westfälischer Totleger	AvianDiv	Germany	3	0.67	0.67	0.67	0.67	0.67	0.67	0.67	1
Yurlov crower	Dr Irina Moiseyeva (Russia)	Russia	4	0.63	1	1	1	1	1	1	1
Icelandic	Freyja Imsland	Iceland	12	0.79	0.92	0.92	0.92	0.92	0.92	0.92	1
Silkie	S. Kerje, Prof Chen C-F, Prof Lee Y-P. Taiwan	China	10	0.9	1	1	0.75	0.95	0.95	0.95	1
Hua-Tung	Chih-Feng Chen (Taiwan)	China	3	1	1	1	1	1	1	1	1
Inhibition of Gold	B. Bed'hom, M. Tixier-Boichard	UE GFA, Tours, France	3	1	1	1	1	1	1	1	1
Coucou du Vercors	B. Bed'hom, M. Tixier-Boichard	France	5	1	1	1	1	1	1	1	1
Obese strain (OS)	S. Kerje	USA	18	1	1	1	1	1	1	1	1
SASSO	B. Bed'hom, M. Tixier-Boichard	France	12	1	1	1	1	1	1	1	1
Red junglefowl			51	0.37	0.80	0.88	0.49	0.35	0.40	0.41	0.91

Supplementary Table 5 Putative stop or splice-affecting mutations

Gene	Ensembl ID	Chr	Position	Lines identified	Line tested
Validated					
MLLT4	ENSGALT00000018484	3	44,034,443	LOW	LOW
	ENSGALT00000037676				
CCDC111	ENSGALT00000017306	4	40,887,198	WL-A, RIR, CB-1, LOW, RJF-Pool	WLH-A
	ENSGALT00000038264				
SLC4A3	ENSGALT00000018302	7	23,608,526	WL-A, WL-B, RIR, CB-1, CB-2, HIGH, RJF-Pool	WL-B
RFC4	ENSGALT00000039711	9	17,302,516	WL-A, WL-B, OS, RJF-Pool	WL-B
ATAD5	ENSGALT00000005217	18	6,644,339	All except ref	WL-B
SRCRB4D	ENSGALT00000040256	19	4,186,589	OS, CB-1, CB-2, HIGH, LOW, RJF-Pool	HIGH
EDEM2	ENSGALT00000040368	20	2,539,381	WL-A, WL-B, OS, CB-1, HIGH, LOW, RJF-Pool	WL-B
Invalidated					
PHLDB2	ENSGALT00000024811	1	91,793,278	CB-1, LOW	LOW
CPNE4	ENSGALT00000037634	2	42,028,048	CB-1, HIGH	HIGH
KCNK5	ENSGALT00000016364	3	30,441,829	CB-1, HIGH	HIGH
CHRM3	ENSGALT00000017530	3	377,32,933	WL-B, OS, HIGH, LOW	LOW
KDR	ENSGALT00000022562	4	67,082,538	WL-A, RIR, CB-1, LOW, RJF-Pool	WL-A
CHRM4	ENSGALT00000013620	5	25,799,091	WL-A, OS, CB-1	WL-A
HSP90AA1	ENSGALT00000018521	5	51,984,450	CB-1, CB-2, HIGH, RJF-Pool, RJF-Ref	HIGH
SUPV3L1	ENSGALT00000006679	6	11,934,016	CB-1, CB-2, LOW, RJF-	CB-1

	ENSGALT00000040774			Pool, RJF-Ref	
SEC24C	ENSGALT00000008325	6	17,039,965	HIGH, LOW	HIGH
PITX3	ENSGALT00000009008	6	17,891,186	WL-A, WL-B, CB-1	CB-1
NDUFB8	ENSGALT00000033463	6	18,495,712	WL-A, CB-2	CB-1
ERCC6	ENSGALT00000010107	6	19,830,887	WL-A, LOW	LOW
GPR26	ENSGALT00000015762	6	33,329,823	WL-A, WL-B	WL-B
MYSM1	ENSGALT00000038040	8	27,109,708	RIR, RJF-Pool	RIR
ECT2	ENSGALT00000014916	9	20,792,752	CB-1, HIGH	CB-1
USP10	ENSGALT00000039042	11	18,798,400	CB-1	CB-1
MARVELD3	ENSGALT00000001296	11	21,802,422	CB-1, LOW	CB-1
SLC5A11	ENSGALT00000009548	14	6,599,664	WL-B, CB-1	CB-1
	ENSGALT00000033722				
n/a	ENSGALT00000034183	15	7,184,190	RIR, HIGH, RJF-Pool	HIGH
POLE	ENSGALT00000012422	15	10,293,398	HIGH, LOW, RJF-Pool	LOW
FIGNL2	ENSGALT00000009635	E22[a]	40,859	CB-1, RJF-Pool	CB-1
WDR41	ENSGALT00000006940	Z	22,635,794	RIR, CB-1, LOW	CB-1
TJP2	ENSGALT00000024377	Z	34,320,514	CB-1, RJF-Pool	CB-1
C9orf72	ENSGALT00000002894	Z	67,025,023	WL-B, CB-1	CB-1
<u>Not tested</u>					
MAP4K4	ENSGALT00000036581	1	137,878,053	All except OS	
	ENSGALT00000008104				
	ENSGALT00000027092				
LIMS1	ENSGALT00000027130	1	140,552,011	WL-B	
	ENSGALT00000027132				
DDC	ENSGALT00000022889	2	83,040,752	WL-B, CB-2, RJF-Pool	
	ENSGALT00000021376				
n/a	ENSGALT00000016280	3	28,355,920	All expect ref	

INTS2	ENSGALT00000008456	19	7,424,629	WL-A, OS, CB-1, RJF-Ref
CTSZ	ENSGALT00000012067	20	10,848,216	WL-A, WL-B, HIGH, RJF-Pool

[a] Assembly fragment labelled E22C19W28_E50C23 in the genome build.

Supplementary Table 6 Deletions detected in different chicken populations using whole genome resequencing

Chrom	Start (bp)	End (bp)	Length (bp)	Population(s)[a]	p-value[b]
1	653600	654131	532	OS, RIR, RJF-Pool, WL-A, WL-B, CB-2, High	$2.22x10^{-16}$
1	1454343	1454816	474	RIR	$1.05x10^{-11}$
1	1743267	1745394	2128	OS	$2.84x10^{-53}$
1	1745430	1746915	1486	OS	$1.53x10^{-31}$
1	1748243	1757734	9492	OS	$1.60x10^{-116}$
1	3629508	3631199	1692	WL-A, High, Low	$1.71x10^{-13}$
1	4001375	4001758	384	RIR, WL-A, CB-2	$5.22x10^{-9}$
1	4762433	4763923	1491	WL-A, High	$5.00x10^{-9}$
1	8230472	8230869	398	WL-A, Low	$3.14x10^{-16}$
1	8425688	8426545	858	OS	$9.37x10^{-12}$
1	8426746	8427926	1181	OS	$3.68x10^{-21}$
1	8602486	8602707	222	OS, Low	$9.30x10^{-11}$
1	8830897	8834680	3784	OS, RJF-Pool, WL-B, CB-1, CB-2, Low	$1.28x10^{-9}$
1	9112643	9113225	583	Low	$1.65x10^{-18}$
1	9764704	9765135	432	RIR	$4.11x10^{-11}$
1	9894836	9897604	2769	OS, WL-A	$3.45x10^{-32}$
1	11728838	11729370	533	High, Low	$1.14x10^{-11}$
1	11826625	11826865	241	High, Low	$3.99x10^{-12}$
1	14378163	14378762	600	WL-A	$1.27x10^{-16}$
1	14398123	14398867	745	RJF-Pool, WL-A, WL-B, CB-1, CB-2, High, Low	$1.39x10^{-28}$
1	15129767	15130452	686	OS, RIR, WL-A, High, Low	$8.35x10^{-26}$
1	18127046	18127419	374	High	$2.86x10^{-14}$

1	20226024	20226681	658	OS, Low	7.33×10^{-15}
1	20988010	20988720	711	High	2.99×10^{-28}
1	21512651	21513813	1163	Low	6.97×10^{-51}
1	21683637	21684984	1348	Low	2.66×10^{-10}
1	21685250	21685854	605	RJF-Pool, Low	3.87×10^{-14}
1	22463267	22463476	210	Low	2.66×10^{-10}
1	23026736	23028357	1622	OS, CB-2, Low	5.77×10^{-19}
1	23149637	23150913	1277	OS, WL-A, WL-B, Low	2.39×10^{-25}
1	23957397	23958038	642	High	1.95×10^{-30}
1	24789731	24790526	796	RIR	3.35×10^{-21}
1	25701203	25702014	812	OS	2.53×10^{-15}
1	25773574	25773883	310	RJF-Pool	1.18×10^{-14}
1	25932127	25932625	499	RJF-Pool, CB-2	8.80×10^{-19}
1	27818966	27819276	311	OS, WL-A	9.37×10^{-12}
1	28079704	28080187	484	OS, RIR, High	4.37×10^{-12}
1	28672640	28672877	238	RIR	9.72×10^{-9}
1	29937603	29937931	329	High	6.68×10^{-10}
1	29983997	29986708	2712	WL-A, WL-B, High	6.24×10^{-34}
1	30075704	30075908	205	High	3.27×10^{-11}
1	30829792	30830074	283	OS	7.78×10^{-9}
1	31682708	31683402	695	High	1.43×10^{-22}
1	31857245	31857422	178	OS, RIR, RJF-Pool, WL-A, High, Low	4.82×10^{-11}
1	33078534	33079239	706	OS, WL-A, WL-B, High, Low	6.83×10^{-17}
1	33297718	33298778	1061	OS, WL-B	1.53×10^{-31}
1	33396721	33400825	4105	OS	4.91×10^{-110}
1	33557097	33557298	202	OS, WL-B	1.28×10^{-9}
1	33754139	33754626	488	OS, WL-A, WL-B, CB-1	1.86×10^{-10}
1	34072443	34073115	673	OS	1.64×10^{-20}

1	34380135	34381048	914	OS, RIR, WL-B, CB-1	$1.00x10^{-9}$
1	34499980	34500519	540	OS	$9.37x10^{-12}$
1	35854882	35855484	603	Low	$2.39x10^{-25}$
1	37290498	37291011	514	OS, WL-B	$1.82x10^{-12}$
1	39656825	39657339	515	RJF-Pool, CB-2, High	$2.32x10^{-21}$
1	40312403	40312924	522	OS	$1.06x10^{-13}$
1	40684072	40684453	382	OS	$1.06x10^{-13}$
1	42486482	42486844	363	OS	$2.24x10^{-13}$
1	42521185	42521501	317	OS	$3.92x10^{-10}$
1	42990976	42995570	4595	OS	$6.66x10^{-139}$
1	44948853	44949405	553	OS, RIR, WL-A, CB-1, CB-2, High, Low	$1.63x10^{-19}$
1	44973864	44977179	3316	RIR	$2.04x10^{-65}$
1	47316791	47316971	181	Low	$3.99x10^{-12}$
1	47403229	47403536	308	CB-2, High, Low	$3.26x10^{-11}$
1	47599364	47599732	369	Low	$3.85x10^{-17}$
1	48447028	48447546	519	OS	$1.45x10^{-18}$
1	49808925	49809191	267	OS, RIR, WL-A, WL-B, High, Low	$6.20x10^{-9}$
1	50976747	50977222	476	RIR, WL-B	$1.45x10^{-15}$
1	50977240	50977631	392	RIR, CB-1	$2.88x10^{-15}$
1	52978555	52985131	6577	OS	$5.21x10^{-123}$
1	53525564	53526542	979	OS	$1.86x10^{-10}$
1	53526578	53527156	579	OS	$4.17x10^{-11}$
1	55722265	55723090	826	High	$3.57x10^{-39}$
1	56193503	56193753	251	OS, WL-A, WL-B, CB-1, CB-2, High, Low	$7.60x10^{-10}$
1	56361246	56361566	321	OS	$8.81x10^{-11}$
1	56734232	56734674	443	RIR, RJF-Pool, WL-A, WL-B, CB-2, High, Low	$1.47x10^{-11}$
1	56737133	56737466	334	RIR, CB-2, High, Low	$1.71x10^{-13}$

1	56863047	56863286	240	OS, RJF-Pool, WL-A, WL-B, High	5.18×10^{-10}
1	57978972	57979156	185	WL-A, High, Low	2.17×10^{-9}
1	58559465	58559789	325	OS, RIR, WL-A	2.10×10^{-12}
1	58853779	58854369	591	High	4.37×10^{-12}
1	59003734	59003963	230	Low	9.30×10^{-11}
1	60695339	60700187	4849	OS	9.80×10^{-85}
1	61111953	61112227	275	High	3.27×10^{-11}
1	61173627	61176350	2724	High	2.73×10^{-45}
1	61673990	61674346	357	WL-A, High	4.37×10^{-12}
1	61905495	61905710	216	High	8.94×10^{-11}
1	62391080	62391548	469	WL-A, WL-B	2.48×10^{-10}
1	64298467	64298803	337	WL-B, High	2.90×10^{-9}
1	64298959	64299399	441	OS, WL-A, WL-B, High	3.34×10^{-18}
1	65782307	65782689	383	OS	8.81×10^{-11}
1	66202825	66203320	496	OS, WL-A, WL-B, CB-2	5.89×10^{-15}
1	67474331	67474829	499	OS, RIR, WL-A, High	2.86×10^{-14}
1	67570220	67571808	1589	OS, RIR, WL-A, WL-B, CB-2	2.68×10^{-53}
1	68155954	68156286	333	WL-B	4.82×10^{-11}
1	68635376	68635851	476	Low	1.35×10^{-17}
1	68977070	68977461	392	OS	4.17×10^{-11}
1	69125653	69126153	501	High, Low	7.07×10^{-20}
1	69153768	69154049	282	OS, High, Low	7.60×10^{-10}
1	70008835	70009081	247	CB-2, High	2.14×10^{-13}
1	70009199	70009568	370	High	1.05×10^{-14}
1	71070908	71071173	266	OS, RIR, RJF-Pool, WL-A, WL-B, Low	3.34×10^{-16}
1	71125536	71125896	361	OS, CB-2	2.53×10^{-15}
1	72307113	72307678	566	OS	6.44×10^{-18}

1	72506164	72506668	505	OS, WL-B, High	1.91×10^{-23}
1	73578291	73578798	508	OS	3.92×10^{-10}
1	73629491	73630253	763	OS, WL-A, WL-B, CB-1, CB-2, High	1.72×10^{-15}
1	73631181	73631503	323	Low	1.71×10^{-13}
1	74936630	74937071	442	Low	1.40×10^{-12}
1	75102232	75102784	553	RJF-Pool, WL-B, CB-1, CB-2, High, Low	3.87×10^{-14}
1	75434237	75434745	509	Low	1.30×10^{-22}
1	80895594	80896092	499	OS, RIR, Low	2.87×10^{-17}
1	81073931	81074578	648	OS, RIR, WL-A, Low	1.05×10^{-11}
1	81811637	81813897	2261	RJF-Pool	2.89×10^{-18}
1	82937978	82938483	506	OS, RIR, High	3.69×10^{-9}
1	87328482	87329271	790	High	1.09×10^{-28}
1	88706210	88706890	681	OS, WL-A, CB-2, High	2.44×10^{-10}
1	88933619	88934156	538	OS	6.44×10^{-18}
1	89329473	89329714	242	High	8.94×10^{-11}
1	90057246	90059055	1810	OS, RIR, Low	1.74×10^{-33}
1	91728309	91729859	1551	High, Low	1.19×10^{-63}
1	91928766	91929187	422	Low	4.88×10^{-13}
1	92772252	92772670	419	Low	2.56×10^{-15}
1	93100751	93101603	853	OS, RJF-Pool, WL-A, WL-B	1.39×10^{-28}
1	93204786	93204942	157	Low	9.30×10^{-11}
1	93322043	93322372	330	OS	5.03×10^{-14}
1	93787004	93787809	806	CB-2, Low	2.82×10^{-31}
1	94556654	94561755	5102	RIR	9.72×10^{-9}
1	95022413	95022616	204	RIR, High, Low	1.40×10^{-12}
1	95241450	95241947	498	OS	2.87×10^{-17}
1	96338868	96339386	519	RIR, High	2.86×10^{-14}

1	97757674	97758253	580	OS	$2.38x10^{-14}$
1	98369239	98369658	420	OS, WL-A	$2.76x10^{-9}$
1	98863528	98863883	356	High	$5.00x10^{-9}$
1	99216513	99216939	427	WL-A, WL-B	$4.82x10^{-11}$
1	100207825	100208945	1121	RJF-Pool, WL-B, CB-2	$1.42x10^{-44}$
1	100278831	100279358	528	OS, RIR, WL-A, Low	$3.45x10^{-32}$
1	101447091	101448220	1130	OS	$8.26x10^{-22}$
1	102860166	102860885	720	OS, WL-A	$7.29x10^{-20}$
1	102862423	102863383	961	OS	$4.42x10^{-36}$
1	102932336	102933323	988	OS	$5.67x10^{-28}$
1	103115970	103116816	847	High, Low	$1.43x10^{-38}$
1	103569219	103569556	338	Low	$4.88x10^{-13}$
1	103569889	103570393	505	Low	$8.65x10^{-21}$
1	103799743	103800098	356	WL-B	$1.28x10^{-9}$
1	103800508	103800941	434	WL-B	$2.48x10^{-10}$
1	104454884	104455598	715	WL-A, WL-B, High, Low	$5.58x10^{-9}$
1	104510620	104512834	2215	OS, RIR, CB-2	$1.04x10^{-94}$
1	104708879	104710080	1202	OS, High	$3.99x10^{-29}$
1	104774711	104775235	525	WL-B, High, Low	$4.54x10^{-23}$
1	106103282	106104033	752	WL-A, CB-2	$1.08x10^{-22}$
1	107397506	107397963	458	Low	$2.02x10^{-19}$
1	111059859	111060396	538	OS	$2.70x10^{-16}$
1	112046299	112047773	1475	OS	$6.40x10^{-42}$
1	114624156	114625412	1257	RIR, CB-1, High, Low	$2.02x10^{-19}$
1	115021911	115022657	747	High, Low	$8.65x10^{-21}$
1	115232580	115233212	633	RIR	$1.02x10^{-19}$
1	116269296	116269717	422	RJF-Pool	$1.02x10^{-16}$
1	116475765	116476437	673	OS, RJF-Pool, High, Low	$1.39x10^{-28}$
1	116767946	116768202	257	Low	$5.98x10^{-14}$

1	117060865	117061128	264	OS, High	2.44×10^{-10}
1	117177336	117178734	1399	OS, Low	1.01×10^{-57}
1	118308403	118309399	997	Low	9.86×10^{-32}
1	118382769	118383067	299	OS	1.98×10^{-11}
1	118763090	118763332	243	OS, WL-B	6.57×10^{-9}
1	119711663	119711948	286	High, Low	6.20×10^{-9}
1	120135505	120136600	1096	OS, High, Low	3.45×10^{-32}
1	120883032	120884204	1173	High, Low	1.12×10^{-42}
1	121111107	121111356	250	OS	3.69×10^{-9}
1	122153618	122154077	460	OS	5.03×10^{-14}
1	122472874	122473117	244	Low	6.20×10^{-9}
1	122774125	122774378	254	WL-A	5.58×10^{-9}
1	123330560	123335238	4679	High	1.06×10^{-201}
1	123644130	123644463	334	OS	1.75×10^{-9}
1	123811052	123812258	1207	OS, WL-A	1.27×10^{-40}
1	125996189	125996596	408	WL-A	1.36×10^{-9}
1	127632702	127633138	437	OS, WL-B	1.82×10^{-12}
1	128008895	128011368	2474	High, Low	5.00×10^{-9}
1	129708508	129708809	302	High	2.86×10^{-14}
1	129709058	129710765	1708	High	5.96×10^{-65}
1	129781342	129782033	692	OS, RIR, WL-A, CB-2, Low	1.10×10^{-16}
1	130241317	130242996	1680	OS	3.89×10^{-46}
1	131511883	131512217	335	OS, High	3.27×10^{-11}
1	131888826	131890092	1267	OS	3.46×10^{-20}
1	132670435	132670691	257	WL-B	1.82×10^{-12}
1	133151273	133151754	482	OS, High, Low	3.26×10^{-11}
1	133422208	133423888	1681	WL-A, Low	1.45×10^{-13}
1	133598567	133598860	294	High	3.27×10^{-11}

1	133916795	133917096	302	Low	4.88×10^{-13}
1	135182887	135183977	1091	OS	6.42×10^{-30}
1	135309828	135310720	893	OS, WL-B, High, Low	4.73×10^{-27}
1	135489024	135489815	792	OS	7.76×10^{-21}
1	135492562	135493769	1208	Low	6.57×10^{-30}
1	137087111	137087412	302	OS, High, Low	2.56×10^{-15}
1	137839375	137839766	392	OS, RIR, WL-A, WL-B, CB-1, CB-2, High, Low	6.68×10^{-10}
1	140094162	140095730	1569	OS	2.85×10^{-41}
1	140259746	140260276	531	High	5.11×10^{-16}
1	142298046	142298375	330	OS, RIR, RJF-Pool, WL-A, WL-B, CB-2, Low	4.16×10^{-13}
1	142364167	142364419	253	OS	7.78×10^{-9}
1	142896693	142897125	433	OS	4.44×10^{-12}
1	143088372	143089288	917	High	1.09×10^{-28}
1	143573006	143573849	844	OS, RIR, RJF-Pool, WL-A, WL-B, CB-1	1.70×10^{-9}
1	144862546	144863915	1370	High	3.49×10^{-32}
1	145332926	145334239	1314	OS, WL-A, WL-B, CB-1, CB-2, Low	7.07×10^{-20}
1	145630907	145631607	701	OS	6.44×10^{-18}
1	147491801	147492231	431	OS	1.06×10^{-13}
1	147762742	147763652	911	OS, WL-A, WL-B, Low	1.38×10^{-43}
1	148041799	148042461	663	OS	8.28×10^{-10}
1	149092900	149093356	457	OS	9.37×10^{-12}
1	149672919	149673488	570	OS, High	3.27×10^{-11}
1	149699519	149700887	1369	OS	5.32×10^{-39}
1	149701199	149702224	1026	OS	2.09×10^{-36}
1	149845680	149846029	350	Low	4.71×10^{-18}
1	149976825	149977204	380	OS	4.72×10^{-13}
1	152713711	152716510	2800	OS, RIR, RJF-Pool, WL-	1.93×10^{-53}

				A, WL-B, CB-1	
1	152717372	152719636	2265	OS, RIR, RJF-Pool, WL-A, WL-B, CB-1	$6.57x10^{-23}$
1	153969103	153970016	914	CB-1, CB-2	$1.39x10^{-31}$
1	153970373	153971066	694	CB-1, CB-2	$7.19x10^{-27}$
1	155937261	155938029	769	OS	$9.97x10^{-13}$
1	156255684	156256237	554	WL-B	$1.28x10^{-9}$
1	156588187	156588443	257	OS	$3.92x10^{-10}$
1	156588587	156589317	731	OS	$3.91x10^{-22}$
1	156621292	156622718	1427	OS	$3.69x10^{-9}$
1	157790183	157790599	417	RIR, High, Low	$9.30x10^{-11}$
1	158211451	158211772	322	RIR	$8.14x10^{-11}$
1	158344216	158344662	447	Low	$1.71x10^{-13}$
1	158635733	158635995	263	RIR	$4.91x10^{-9}$
1	160362416	160363085	670	RIR	$6.15x10^{-18}$
1	161949678	161950068	391	WL-B, High, Low	$8.94x10^{-11}$
1	164225250	164227206	1957	OS, WL-A, WL-B	$1.53x10^{-43}$
1	165601977	165603221	1245	CB-2, Low	$3.10x10^{-47}$
1	167093188	167094393	1206	OS	$6.44x10^{-18}$
1	167160070	167160655	586	OS	$1.75x10^{-9}$
1	167352753	167352993	241	Low	$3.99x10^{-12}$
1	170456831	170457677	847	OS	$1.53x10^{-31}$
1	170609735	170610822	1088	OS, RJF-Pool, WL-A, WL-B, CB-2, Low	$3.17x10^{-19}$
1	172191454	172191802	349	High	$3.34x10^{-18}$
1	172260838	172261198	361	High	$9.34x10^{-25}$
1	172419092	172419504	413	OS	$8.28x10^{-10}$
1	172488342	172488538	197	High, Low	$6.68x10^{-10}$
1	172768352	172768667	316	High	$2.14x10^{-13}$
1	172792007	172792838	832	OS, WL-A	$1.64x10^{-20}$

1	173262555	173262905	351	OS, CB-2, Low	3.99×10^{-12}
1	173605661	173605905	245	OS	3.92×10^{-10}
1	174073612	174074475	864	OS, WL-B	4.72×10^{-13}
1	174310096	174310551	456	High	6.83×10^{-17}
1	174804393	174804678	286	OS, RJF-Pool, WL-A, CB-1, CB-2, Low	2.17×10^{-09}
1	174837985	174838182	198	Low	2.66×10^{-10}
1	175326733	175327329	597	Low	3.03×10^{-21}
1	176020590	176021743	1154	Low	1.57×10^{-54}
1	176349811	176350150	340	OS, RIR, RJF-Pool, WL-A, WL-B, CB-1, High, Low	1.58×10^{-10}
1	176378346	176379145	800	OS, RJF-Pool	1.04×10^{-32}
1	176402365	176404007	1643	OS, WL-B	8.73×10^{-47}
1	176484450	176488327	3878	OS	7.60×10^{-105}
1	176567645	176568006	362	OS	5.03×10^{-14}
1	176568042	176570007	1966	OS, High	6.42×10^{-30}
1	176583149	176583800	652	OS	2.70×10^{-16}
1	178462128	178462843	716	OS	3.68×10^{-21}
1	178953368	178953732	365	OS, RIR, RJF-Pool, WL-A, WL-B, CB-2, High, Low	1.10×10^{-15}
1	179311476	179311922	447	High	5.11×10^{-16}
1	179366679	179367432	754	OS, High	1.60×10^{-12}
1	179418759	179419169	411	OS	4.17×10^{-11}
1	179771908	179772161	254	High	1.05×10^{-14}
1	180745419	180746134	716	RIR, High	1.43×10^{-22}
1	180985483	180986420	938	CB-2, High	9.55×10^{-32}
1	182820728	182821418	691	WL-A	9.78×10^{-23}
1	183037036	183037520	485	WL-A, CB-2	1.20×10^{-12}
1	183336571	183336876	306	OS, RIR, WL-A, CB-1,	2.44×10^{-10}

				High, Low	
1	185295407	185295664	258	WL-A, High	5.84×10^{-13}
1	185652021	185652565	545	High	1.40×10^{-15}
1	186653109	186653578	470	WL-A, WL-B, High	1.87×10^{-16}
1	186792942	186794020	1079	High	2.44×10^{-55}
1	187279355	187280255	901	WL-A, WL-B, High	3.99×10^{-29}
1	187419657	187420114	458	High	5.97×10^{-20}
1	187502738	187503266	529	High	1.67×10^{-26}
1	188643036	188644088	1053	OS, WL-A	3.68×10^{-21}
1	188705280	188706282	1003	OS, WL-A, WL-B	2.71×10^{-20}
1	188710745	188711832	1088	OS, WL-A	2.69×10^{-28}
1	188810270	188811211	942	OS, RIR, WL-A, WL-B, CB-1, High, Low	6.34×10^{-35}
1	189886245	189887028	784	RIR, WL-B, CB-1, CB-2, High, Low	2.72×10^{-36}
1	190066244	190066625	382	Low	1.14×10^{-11}
1	190318327	190318710	384	RIR	6.32×10^{-10}
1	190615057	190615514	458	RIR	1.05×10^{-11}
1	191346156	191347438	1283	OS, RIR, Low	8.81×10^{-11}
1	191387979	191389058	1080	Low	1.38×10^{-43}
1	191654572	191655356	785	CB-2, High, Low	3.14×10^{-16}
1	191831445	191831834	390	RIR, CB-2, High, Low	3.99×10^{-12}
1	194909710	194909934	225	OS, High	2.14×10^{-13}
1	197714701	197715781	1081	CB-2, High, Low	7.81×10^{-14}
1	197735769	197738390	2622	CB-2, High	2.28×10^{-9}
1	197738508	197739185	678	CB-2, High, Low	4.37×10^{-12}
1	198941698	198941958	261	OS, RIR, CB-2, High, Low	6.68×10^{-10}
1	199079783	199080850	1068	Low	6.97×10^{-51}
1	199080886	199082267	1382	High, Low	2.72×10^{-36}

1	199288854	199289996	1143	OS	4.72×10^{-13}
1	200332807	200332969	163	Low	6.20×10^{-9}
2	749329	749568	240	Low	3.62×10^{-12}
2	1493501	1494135	635	WL-B, High, Low	5.47×10^{-24}
2	1541232	1541812	581	High, Low	1.01×10^{-18}
2	1710799	1711103	305	High	2.21×10^{-10}
2	1766304	1767011	708	WL-B, High, Low	3.50×10^{-26}
2	3312418	3313378	961	OS, CB-1, High, Low	5.32×10^{-41}
2	3321211	3321522	312	OS	3.92×10^{-11}
2	4218021	4219685	1665	OS	1.02×10^{-27}
2	4500881	4501348	468	RIR	4.06×10^{-14}
2	5206755	5207168	414	OS, RIR, WL-A, WL-B, CB-1, High, Low	1.53×10^{-13}
2	6152454	6152650	197	RJF-Pool, WL-B, High, Low	5.42×10^{-9}
2	6550092	6550595	504	OS, RJF-Pool, High, Low	3.76×10^{-23}
2	6762677	6762883	207	High	1.67×10^{-9}
2	6961491	6962023	533	OS, WL-A, WL-B	1.93×10^{-16}
2	7310234	7310756	523	OS	1.30×10^{-18}
2	7743496	7744074	579	OS, WL-A, WL-B, CB-2, High	4.35×10^{-16}
2	9343422	9343781	360	WL-A	1.22×10^{-9}
2	10611708	10612144	437	WL-A, CB-1	5.01×10^{-11}
2	14341816	14342142	327	RIR, CB-2	2.21×10^{-13}
2	15727963	15728266	304	Low	8.54×10^{-11}
2	17122149	17122652	504	RIR	1.40×10^{-18}
2	18172925	18174362	1438	OS	3.02×10^{-33}
2	18174398	18176970	2573	OS, WL-B	2.00×10^{-79}
2	19108316	19108540	225	OS	3.50×10^{-9}
2	19378807	19379409	603	OS	4.64×10^{-14}

2	20332884	20333783	900	OS, RJF-Pool	$3.32x10^{-31}$
2	20683522	20683858	337	OS	$3.50x10^{-9}$
2	20993252	20993837	586	OS, WL-A, WL-B	$3.73x10^{-12}$
2	21746580	21747326	747	OS, Low	$3.47x10^{-28}$
2	22603933	22604257	325	RIR, CB-1, CB-2, High, Low	$1.17x10^{-17}$
2	23216138	23216582	445	High, Low	$1.72x10^{-19}$
2	24893402	24893811	410	RIR, High	$1.58x10^{-16}$
2	25447612	25448603	992	OS	$4.31x10^{-26}$
2	25703251	25703544	294	OS, Low	$7.03x10^{-10}$
2	25958701	25959027	327	OS	$3.71x10^{-10}$
2	26197315	26198709	1395	OS, WL-B	$3.99x10^{-38}$
2	26308097	26308366	270	OS, RIR	$7.84x10^{-10}$
2	27810373	27813649	3277	OS	$3.37x10^{-35}$
2	28406479	28407049	571	OS, RIR, WL-A, CB-1, CB-2, High, Low	$1.17x10^{-17}$
2	30794449	30795056	608	OS, RIR, CB-1, CB-2, High	$2.96x10^{-29}$
2	31236591	31236965	375	OS	$1.85x10^{-11}$
2	31480666	31481257	592	OS	$4.39x10^{-13}$
2	33079700	33079936	237	Low	$8.54x10^{-11}$
2	33450072	33451235	1164	OS, High	$9.45x10^{-40}$
2	33962017	33962353	337	RIR	$9.76x10^{-12}$
2	34295744	34296125	382	OS, RIR, WL-A, WL-B, CB-1, CB-2, High, Low	$3.34x10^{-17}$
2	35672250	35673178	929	CB-2	$1.94x10^{-35}$
2	36107820	36108270	451	CB-2	$1.50x10^{-15}$
2	36210145	36212783	2639	RIR, RJF-Pool, WL-A	$1.53x10^{-10}$
2	36214256	36219256	5001	RIR, RJF-Pool, WL-A, WL-B, CB-1	$3.58x10^{-13}$
2	36497920	36511728	13809	CB-2	$3.69x10^{-164}$

2	37961384	37963478	2095	OS	$4.07x10^{-65}$
2	37978058	37978502	445	OS, RJF-Pool, Low	$1.04x10^{-15}$
2	38777278	38777855	578	OS, WL-A, WL-B, High, Low	$1.42x10^{-18}$
2	38966534	38966966	433	OS, RJF-Pool, WL-A, WL-B, Low	$1.65x10^{-9}$
2	39788251	39788600	350	OS	$1.96x10^{-12}$
2	40816933	40817368	436	OS, RIR, WL-A, CB-2	$1.73x10^{-10}$
2	41358191	41358422	232	CB-1, Low	$3.62x10^{-10}$
2	41499522	41499930	409	OS, RJF-Pool, WL-A	$9.81x10^{-14}$
2	42288381	42288713	333	OS, RIR, WL-A, High, Low	$1.53x10^{-13}$
2	42404585	42405392	808	RIR, RJF-Pool, WL-A, CB-1, CB-2, High, Low	$1.53x10^{-10}$
2	42879120	42879546	427	OS, RIR, RJF-Pool, High, Low	$1.65x10^{-9}$
2	43068192	43068545	354	OS	$8.77x10^{-12}$
2	43205823	43206261	439	OS	$1.85x10^{-11}$
2	43620217	43620873	657	RIR	$1.32x10^{-15}$
2	43636261	43636878	618	OS	$6.14x10^{-19}$
2	43660868	43661533	666	OS, RIR, CB-1, High, Low	$1.69x10^{-27}$
2	46116684	46116987	304	RIR, High	$1.67x10^{-9}$
2	47972071	47972487	417	WL-A, High, Low	$2.75x10^{-16}$
2	48147000	48147510	511	OS	$1.96x10^{-12}$
2	48652464	48653052	589	OS, WL-A, High	$2.50x10^{-13}$
2	49234763	49235177	415	OS, WL-A, WL-B, CB-1, CB-2, High, Low	$7.89x10^{-16}$
2	49238114	49238494	381	CB-2	$5.36x10^{-17}$
2	49242591	49243100	510	OS, WL-A	$9.81x10^{-14}$
2	49387231	49387946	716	OS	$3.07x10^{-20}$
2	52225245	52225627	383	OS	$1.66x10^{-9}$

2	53826704	53847414	20711	WL-A	$3.64x10^{-177}$
2	54086521	54089591	3071	RIR, CB-2, High	$8.04x10^{-96}$
2	54114310	54115588	1279	WL-A	$7.25x10^{-15}$
2	54117495	54118199	705	RIR, WL-A, CB-1, CB-2, High, Low	$2.45x10^{-10}$
2	54187581	54187925	345	WL-A	$2.96x10^{-10}$
2	54264896	54265296	401	WL-A, WL-B, CB-1, CB-2, Low	$1.26x10^{-12}$
2	54363220	54364884	1665	OS, RIR, WL-A, WL-B, CB-1, CB-2, High, Low	$4.53x10^{-78}$
2	54449453	54450371	919	OS, RIR, WL-A, CB-1, CB-2, High, Low	$2.35x10^{-26}$
2	55239120	55241384	2265	OS, WL-A, WL-B	$9.62x10^{-67}$
2	55248734	55249100	367	High	$1.67x10^{-9}$
2	55468300	55468877	578	OS, WL-A	$1.16x10^{-16}$
2	55469192	55469848	657	OS, WL-A	$2.50x10^{-13}$
2	55491152	55491537	386	WL-A, High	$3.68x10^{-19}$
2	55569777	55570339	563	WL-A	$2.99x10^{-14}$
2	55631668	55632513	846	OS	$2.55x10^{-30}$
2	55925402	55926936	1535	High	$3.97x10^{-48}$
2	56207995	56208532	538	WL-A	$1.23x10^{-13}$
2	56432657	56433283	627	CB-2	$4.18x10^{-14}$
2	56434505	56436069	1565	CB-2	$1.69x10^{-40}$
2	56490681	56491851	1171	OS, RIR, Low	$3.50x10^{-9}$
2	56553181	56553972	792	OS, WL-A, High	$1.27x10^{-26}$
2	57943937	57944481	545	OS, RIR, WL-A, WL-B, High, Low	$9.23x10^{-9}$
2	58336564	58337027	464	OS	$2.07x10^{-13}$
2	58941914	58942372	459	OS, Low	$1.42x10^{-18}$
2	59028626	59029227	602	OS	$1.85x10^{-11}$
2	59029512	59031110	1599	OS	$1.18x10^{-43}$

2	59141931	59142442	512	OS, RIR, RJF-Pool, WL-A, WL-B, CB-1, CB-2, High, Low	$7.12x10^{-21}$
2	59466316	59469321	3006	OS, WL-A, WL-B, Low	$3.88x10^{-61}$
2	59496423	59498006	1584	OS, WL-A, WL-B, Low	$2.53x10^{-48}$
2	60166563	60167942	1380	Low	$2.98x10^{-11}$
2	60168227	60168652	426	Low	$6.50x10^{-15}$
2	60218836	60219764	929	WL-A	$4.35x10^{-24}$
2	60567698	60568252	555	OS, High	$1.78x10^{-20}$
2	60637561	60637963	403	High	$1.67x10^{-9}$
2	60987938	60988332	395	OS	$9.28x10^{-13}$
2	61141585	61141824	240	High	$6.81x10^{-14}$
2	61419136	61419675	540	High	$1.69x10^{-27}$
2	61791956	61792225	270	High	$2.21x10^{-10}$
2	62951058	62951233	176	Low	$2.98x10^{-11}$
2	63683454	63684291	838	OS, RIR, WL-A, WL-B, High, Low	$4.57x10^{-24}$
2	63779113	63779804	692	High	$2.78x10^{-18}$
2	64140517	64140753	237	WL-B, High	$2.21x10^{-10}$
2	65298255	65298714	460	WL-A	$7.18x10^{-11}$
2	65342689	65343084	396	OS, WL-A, WL-B	$1.75x10^{-10}$
2	66539088	66539489	402	High	$1.19x10^{-15}$
2	70872715	70873584	870	High	$1.67x10^{-9}$
2	70890350	70890861	512	High	$4.88x10^{-20}$
2	74397236	74397848	613	OS, CB-2	$9.28x10^{-13}$
2	75187826	75188416	591	WL-B, Low	$7.89x10^{-16}$
2	75256888	75257464	577	Low	$2.45x10^{-10}$
2	75408381	75408889	509	High	$3.28x10^{-15}$
2	75814951	75815587	637	OS, WL-A, CB-2, High	$1.82x10^{-24}$
2	79141363	79142138	776	WL-B	$1.64x10^{-22}$

2	79142174	79143038	865	OS, WL-B	$3.74x10^{-22}$
2	79260972	79263511	2540	WL-B, Low	$5.78x10^{-9}$
2	79996328	79996739	412	OS	$1.66x10^{-9}$
2	82563661	82563987	327	CB-1, CB-2, High	$4.83x10^{-9}$
2	83228571	83229010	440	OS, WL-B, High, Low	$5.14x10^{-13}$
2	83806019	83806332	314	OS, RIR, CB-1	$7.01x10^{-9}$
2	86323715	86324154	440	OS	$3.50x10^{-9}$
2	86648700	86648987	288	WL-B	$6.11x10^{-9}$
2	86684600	86684816	217	OS, High	$4.58x10^{-9}$
2	87099853	87101159	1307	High	$7.72x10^{-36}$
2	87209418	87209912	495	High	$2.78x10^{-18}$
2	87276848	87277708	861	CB-2, High	$4.88x10^{-20}$
2	87683682	87684865	1184	CB-1, High, Low	$1.93x10^{-52}$
2	88150812	88153899	3088	OS, RIR, CB-1, CB-2, High, Low	$4.33x10^{-121}$
2	88205111	88205668	558	OS, Low	$3.09x10^{-22}$
2	89976018	89976528	511	WL-A	$1.74x10^{-11}$
2	91446911	91447165	255	High	$6.81x10^{-14}$
2	94001601	94002409	809	High, Low	$1.26x10^{-39}$
2	94229127	94229677	551	OS	$1.04x10^{-14}$
2	94379778	94380222	445	CB-2, Low	$4.83x10^{-9}$
2	96313969	96314507	539	Low	$4.57x10^{-24}$
2	99123723	99124607	885	OS, WL-A	$7.27x10^{-22}$
2	99371841	99372536	696	OS, RJF-Pool, WL-A, WL-B, CB-1, CB-2, High, Low	$5.24x10^{-25}$
2	100287649	100288472	824	OS	$5.49x10^{-17}$
2	102653800	102654183	384	High	$1.67x10^{-9}$
2	103709113	103709624	512	OS, WL-B	$4.39x10^{-13}$
2	103822906	103823347	442	High	$5.14x10^{-13}$

2	104504818	104505321	504	OS	$1.16x10^{-16}$
2	105010761	105011620	860	OS	$1.96x10^{-12}$
2	105625274	105625623	350	OS	$1.66x10^{-9}$
2	106006173	106006524	352	OS, WL-A, WL-B, High, Low	$1.87x10^{-13}$
2	109094327	109094791	465	OS, WL-B	$1.93x10^{-11}$
2	109634664	109635213	550	OS	$2.19x10^{-14}$
2	110613577	110614178	602	High	$2.96x10^{-29}$
2	110962539	110962757	219	High	$2.93x10^{-11}$
2	111755229	111755721	493	OS	$3.71x10^{-10}$
2	113468709	113469226	518	OS, RIR, RJF-Pool, WL-B, CB-2, High, Low	$8.30x10^{-19}$
2	114078215	114081017	2803	RIR, CB-2, High, Low	$5.35x10^{-14}$
2	114548059	114549638	1580	OS, CB-2, High	$1.29x10^{-44}$
2	115012785	115016886	4102	High	$7.77x10^{-133}$
2	115019230	115020408	1179	High	$6.54x10^{-39}$
2	115265056	115267819	2764	OS, WL-A, WL-B	$4.41x10^{-41}$
2	115454912	115455346	435	OS	$4.64x10^{-14}$
2	116645005	116646894	1890	OS	$1.75x10^{-10}$
2	116960392	116960878	487	WL-A	$4.23x10^{-12}$
2	117315313	117318344	3032	OS, WL-A, WL-B	$2.47x10^{-9}$
2	118596532	118596804	273	Low	$2.45x10^{-10}$
2	119257351	119260389	3039	CB-1, CB-2, Low	$1.17x10^{-12}$
2	119943856	119944180	325	High	$8.04x10^{-11}$
2	119955394	119955866	473	High	$3.68x10^{-19}$
2	123250629	123250964	336	High, Low	$1.87x10^{-13}$
2	124545498	124545963	466	OS	$7.41x10^{-9}$
2	125200902	125201162	261	OS, RIR, CB-2, High, Low	$4.58x10^{-9}$
2	126098901	126099401	501	High, Low	$1.72x10^{-19}$

2	126194962	126195198	237	High, Low	$8.54x10^{-11}$
2	126567722	126568433	712	OS, RIR, RJF-Pool, WL-A, WL-B, CB-1, CB-2, High, Low	$1.60x10^{-25}$
2	126644481	126644856	376	OS, RIR, RJF-Pool, WL-A, WL-B, CB-1, CB-2, High, Low	$4.00x10^{-13}$
2	126685981	126686541	561	High, Low	$6.00x10^{-20}$
2	126769321	126769904	584	OS, WL-B, CB-2, High, Low	$7.89x10^{-16}$
2	127516311	127517013	703	High	$1.08x10^{-29}$
2	128908969	128909313	345	OS	$7.41x10^{-9}$
2	129267856	129268543	688	OS, High	$5.76x10^{-17}$
2	129467271	129467566	296	OS, High	$3.50x10^{-9}$
2	130143590	130144311	722	High	$4.63x10^{-27}$
2	130803271	130803709	439	High	$6.46x10^{-21}$
2	131279570	131279832	263	High	$1.19x10^{-15}$
2	131598162	131598474	313	OS, High	$2.21x10^{-10}$
2	131840429	131841172	744	Low	$8.51x10^{-38}$
2	132387189	132388223	1035	High, Low	$5.78x10^{-9}$
2	132575771	132576319	549	OS, High, Low	$7.64x10^{-18}$
2	132984873	132986246	1374	OS, RIR, RJF-Pool, WL-A, WL-B, CB-1, CB-2, High, Low	$2.64x10^{-34}$
2	133217439	133218353	915	OS, RJF-Pool, WL-B	$8.96x10^{-18}$
2	133665101	133665319	219	WL-A, Low	$5.78x10^{-9}$
2	135411916	135412378	463	OS, Low	$4.06x10^{-18}$
2	136689545	136689967	423	RIR	$9.76x10^{-12}$
2	136861335	136862006	672	OS	$7.84x10^{-10}$
2	137321598	137322046	449	Low	$1.26x10^{-12}$
2	138417514	138417876	363	RIR	$5.96x10^{-10}$
2	139440368	139441624	1257	OS	$4.39x10^{-13}$

2	139604742	139606199	1458	OS, RIR, WL-A, WL-B, CB-2, High, Low	$4.94x10^{-19}$
2	142470074	142477155	7082	Low	$1.26x10^{-12}$
2	142543842	142544425	584	OS, Low	$7.84x10^{-10}$
2	143322227	143322782	556	RIR	$1.25x10^{-12}$
2	143323144	143323457	314	RIR	$2.35x10^{-9}$
2	143323796	143324142	347	RIR	$3.00x10^{-10}$
2	143333268	143333640	373	High	$3.88x10^{-12}$
2	143357337	143358634	1298	OS, WL-A, Low	$6.50x10^{-20}$
2	143932541	143932825	285	RIR	$5.96x10^{-10}$
2	144029828	144031078	1251	High	$3.54x10^{-44}$
2	144062591	144062920	330	High	$2.21x10^{-10}$
2	144323602	144323936	335	OS, High	$2.93x10^{-11}$
2	144422080	144422233	154	Low	$5.78x10^{-9}$
2	144604671	144606692	2022	OS, WL-A, WL-B	$3.25x10^{-61}$
2	144654214	144654829	616	OS	$1.37x10^{-19}$
2	147637537	147638094	558	OS	$4.15x10^{-12}$
2	148049160	148049369	210	High	$3.88x10^{-12}$
2	149510474	149511236	763	OS, WL-A, High	$3.12x10^{-22}$
2	149955530	149957106	1577	OS	$2.50x10^{-43}$
2	150823357	150824131	775	RIR	$7.87x10^{-25}$
2	151408901	151409110	210	OS, High, Low	$4.58x10^{-9}$
2	151522471	151522681	211	CB-2, High, Low	$2.93x10^{-11}$
2	152191429	152191966	538	RIR, WL-A, WL-B	$2.28x10^{-20}$
2	152319652	152320240	589	OS	$4.39x10^{-13}$
2	153989827	153990155	329	OS	$1.85x10^{-11}$
2	154073391	154073992	602	Low	$9.59x10^{-17}$
2	154409292	154409833	542	OS	$3.07x10^{-20}$
2	154593791	154594181	391	Low	$3.62x10^{-12}$

3	446300	447734	1435	OS, RIR, CB-1, CB-2, High, Low	1.02×10^{-27}
3	554602	555044	443	RIR	1.70×10^{-9}
3	675831	676417	587	High	5.79×10^{-15}
3	6102605	6102845	241	OS, RIR, RJF-Pool, WL-A, WL-B, CB-1, CB-2, High, Low	1.66×10^{-13}
3	6505547	6505991	445	High	2.94×10^{-16}
3	6761489	6761727	239	OS, RJF-Pool, WL-A, WL-B, CB-2, High, Low	1.84×10^{-11}
3	7490721	7491315	595	OS	5.81×10^{-19}
3	7585042	7585338	297	Low	4.02×10^{-15}
3	8314264	8314512	249	OS, WL-B, High, Low	7.98×10^{-09}
3	8429375	8429846	472	High	3.22×10^{-10}
3	16268899	16269914	1016	OS	1.95×10^{-39}
3	19219125	19221577	2453	OS, WL-A	5.84×10^{-18}
3	20568111	20568418	308	OS	2.53×10^{-10}
3	20958321	20959002	682	RIR, CB-1, CB-2	1.40×10^{-20}
3	22165668	22166099	432	WL-A	4.02×10^{-13}
3	22833963	22834329	367	OS, RIR, RJF-Pool, WL-A, WL-B, CB-1, CB-2	1.94×10^{-10}
3	23231106	23231482	377	OS, RIR, RJF-Pool, WL-A, WL-B, CB-1, CB-2, Low	4.39×10^{-17}
3	23395920	23396242	323	OS, RIR, WL-A	1.45×10^{-12}
3	24014403	24014868	466	OS, WL-A	8.38×10^{-15}
3	25266875	25267504	630	OS	6.96×10^{-13}
3	25452978	25453431	454	OS	1.45×10^{-12}
3	25495172	25495453	282	CB-2	1.31×10^{-9}
3	26212095	26212490	396	OS	1.33×10^{-11}
3	27400344	27401043	700	RIR, WL-B, CB-2	7.75×10^{-16}
3	27961897	27962285	389	High	3.08×10^{-13}

3	27997527	27998378	852	OS, WL-A	9.23×10^{-24}
3	29499577	29502081	2505	OS, WL-A	7.18×10^{-69}
3	29502121	29502799	679	OS	1.10×10^{-9}
3	31658287	31658521	235	High, Low	1.27×10^{-10}
3	32751592	32751908	317	High, Low	1.60×10^{-11}
3	33064817	33065358	542	OS, RIR, RJF-Pool, WL-A, WL-B, CB-1, High, Low	4.39×10^{-17}
3	34128569	34128859	291	CB-2	9.64×10^{-12}
3	34406333	34407487	1155	OS, CB-2, High	4.19×10^{-39}
3	36017829	36018122	294	WL-A, High, Low	7.13×10^{-13}
3	36595341	36595662	322	OS, RIR, RJF-Pool, WL-A, WL-B, CB-1, CB-2, High, Low	4.02×10^{-15}
3	36962739	36963004	266	OS	2.53×10^{-10}
3	36990199	36990731	533	OS	1.75×10^{-14}
3	37050971	37051938	968	OS, RJF-Pool, WL-A, High	7.87×10^{-38}
3	37203442	37204116	675	WL-A	5.25×10^{-11}
3	37204565	37204869	305	WL-A	8.51×10^{-10}
3	37474108	37475069	962	High	1.42×10^{-20}
3	39473692	39480872	7181	OS	2.30×10^{-9}
3	40375946	40376626	681	RIR	1.23×10^{-15}
3	40494703	40495238	536	Low	3.57×10^{-10}
3	40720333	40724370	4038	OS, CB-2, High, Low	1.64×10^{-11}
3	44181046	44182017	972	OS, RIR, WL-A, WL-B	1.46×10^{-20}
3	45428179	45428994	816	RIR, CB-1, CB-2, High, Low	1.78×10^{-27}
3	46536510	46538381	1872	High	8.96×10^{-51}
3	46695944	46696811	868	High	1.70×10^{-30}
3	46899045	46899520	476	OS	3.33×10^{-13}

3	47241681	47242046	366	OS	$1.10x10^{-9}$
3	48625415	48625991	577	OS, CB-2, High	$1.95x10^{-21}$
3	48950156	48950361	206	OS	$4.81x10^{-9}$
3	49202083	49202327	245	High	$1.19x10^{-10}$
3	49362669	49363201	533	RIR	$1.52x10^{-11}$
3	49363659	49364049	391	RIR	$8.65x10^{-10}$
3	49364515	49366253	1739	RIR	$2.17x10^{-17}$
3	49367434	49368758	1325	RIR	$9.20x10^{-34}$
3	49369476	49369812	337	RIR	$6.52x10^{-9}$
3	49370429	49370712	284	RIR	$4.41x10^{-10}$
3	49371773	49372021	249	RIR	$4.41x10^{-10}$
3	49373490	49374371	882	RIR	$3.67x10^{-26}$
3	49374992	49375641	650	RIR	$1.23x10^{-15}$
3	50071660	50072488	829	OS	$1.47x10^{-28}$
3	53312935	53313422	488	OS	$5.27x10^{-10}$
3	53363781	53364147	367	RIR, WL-A, WL-B, CB-1, High, Low	$4.49x10^{-11}$
3	54192153	54192362	210	WL-B	$4.43x10^{-14}$
3	54276281	54276804	524	OS, RIR, WL-A, CB-1	$1.24x10^{-14}$
3	54280883	54281384	502	OS, CB-1	$1.75x10^{-14}$
3	55645928	55646279	352	OS	$4.81x10^{-9}$
3	56210741	56211357	617	High	$1.30x10^{-26}$
3	57110587	57111058	472	OS, High	$4.03x10^{-17}$
3	57457737	57457944	208	Low	$7.98x10^{-9}$
3	58057522	58058384	863	Low	$4.57x10^{-38}$
3	59049466	59049792	327	OS, WL-A, WL-B, CB-1, High, Low	$2.24x10^{-12}$
3	61299176	61299594	419	OS, WL-A, WL-B, CB-2	$2.69x10^{-18}$
3	62261984	62262698	715	OS, RIR	$5.79x10^{-11}$
3	62983010	62985193	2184	RIR	$7.77x10^{-12}$

3	66929536	66930052	517	WL-A, WL-B	4.15×10^{-21}
3	68265794	68266444	651	WL-A, WL-B	4.15×10^{-21}
3	69609658	69610689	1032	OS, WL-B	2.81×10^{-35}
3	70931376	70931788	413	RJF-Pool, WL-B, CB-2, High, Low	5.39×10^{-13}
3	72195276	72195858	583	OS	1.60×10^{-13}
3	72294328	72294948	621	RIR	5.86×10^{-11}
3	72295186	72296030	845	RIR	2.32×10^{-22}
3	72500067	72501033	967	OS, RIR, RJF-Pool, WL-A, WL-B, CB-1, CB-2, High, Low	1.93×10^{-33}
3	72894063	72894486	424	OS	1.33×10^{-11}
3	72899473	72901181	1709	OS, WL-A, CB-2, High, Low	4.44×10^{-32}
3	72970602	72972198	1597	OS	1.78×10^{-46}
3	72975672	72976616	945	OS	1.76×10^{-22}
3	73291688	73294448	2761	OS, High, Low	9.37×10^{-86}
3	73763732	73764018	287	Low	7.98×10^{-9}
3	73965371	73966455	1085	OS, RIR, WL-A, CB-2, Low	1.63×10^{-47}
3	74277237	74277596	360	High, Low	4.49×10^{-11}
3	75210884	75211521	638	Low	1.43×10^{-24}
3	75605068	75606764	1697	OS	4.48×10^{-48}
3	75850231	75850962	732	OS, Low	4.02×10^{-15}
3	77702149	77703680	1532	OS, RIR, RJF-Pool, WL-A, WL-B, CB-1, High	5.09×10^{-37}
3	78340822	78341105	284	Low	1.27×10^{-10}
3	78649041	78649751	711	OS	2.54×10^{-18}
3	79632606	79633054	449	Low	2.85×10^{-18}
3	80284891	80285497	607	RIR	1.63×10^{-16}
3	80621682	80621877	196	RJF-Pool	2.04×10^{-9}

3	80710850	80711394	545	OS, RIR, RJF-Pool, WL-A, WL-B, CB-1, CB-2, High, Low	$8.51x10^{-27}$
3	82034047	82034965	919	RIR	$8.59x10^{-29}$
3	82381080	82382792	1713	OS	$2.13x10^{-32}$
3	82998347	82998785	439	RIR, CB-1, CB-2, High, Low	$3.57x10^{-10}$
3	83027165	83027747	583	OS	$1.75x10^{-14}$
3	83847346	83849374	2029	OS, WL-A, WL-B, Low	$2.60x10^{-58}$
3	84396670	84396892	223	OS, RIR, WL-B, CB-1, High, Low	$9.42x10^{-9}$
3	85802075	85802415	341	OS	$1.10x10^{-9}$
3	86779401	86780436	1036	OS, RIR, RJF-Pool, WL-A, WL-B, CB-1, CB-2, Low	$1.33x10^{-11}$
3	86782831	86783394	564	WL-B, CB-2, Low	$4.52x10^{-20}$
3	86895232	86895436	205	CB-2, High, Low	$4.42x10^{-11}$
3	88716689	88717037	349	OS	$1.21x10^{-10}$
3	88726219	88726619	401	CB-2, Low	$2.01x10^{-12}$
3	90353444	90353884	441	OS, Low	$8.02x10^{-18}$
3	91184716	91185218	503	RIR, High	$7.93x10^{-16}$
3	91236449	91236941	493	OS, RIR, WL-A, Low	$2.86x10^{-27}$
3	92202515	92203147	633	OS	$1.21x10^{-18}$
3	92483936	92484357	422	OS, RIR, RJF-Pool, WL-A, CB-1, CB-2, High, Low	$4.17x10^{-18}$
3	92739417	92739978	562	OS, High	$5.27x10^{-21}$
3	95532086	95532305	220	High, Low	$3.57x10^{-10}$
3	95688840	95690282	1443	High, Low	$3.22x10^{-32}$
3	95757415	95757909	495	WL-A	$8.06x10^{-13}$
3	97176913	97177814	902	OS	$1.92x10^{-15}$
3	97525481	97525689	209	High	$3.22x10^{-10}$

3	97784784	97785242	459	WL-A, CB-2	$2.00x10^{-13}$
3	98865937	98866717	781	OS	$1.60x10^{-21}$
3	98925869	98926925	1057	OS, WL-A, WL-B, High	$2.94x10^{-16}$
3	99653303	99653880	578	CB-2, High, Low	$3.51x10^{-26}$
3	100582948	100583204	257	RIR, CB-1	$3.56x10^{-9}$
3	100919787	100920182	396	RIR	$2.25x10^{-10}$
3	101106548	101107405	858	OS, WL-A, WL-B, Low	$2.12x10^{-24}$
3	101175843	101176579	737	WL-A, WL-B	$1.74x10^{-15}$
3	101189197	101189980	784	WL-A, WL-B	$7.24x10^{-19}$
3	101881980	101883682	1703	RIR, CB-1	$5.39x10^{-44}$
3	102023420	102023742	323	WL-B	$2.53x10^{-12}$
3	103616408	103616716	309	High	$4.42x10^{-11}$
3	103816481	103816910	430	High	$6.06x10^{-12}$
3	104178022	104178308	287	High	$6.06x10^{-12}$
3	104323870	104324169	300	OS, RIR, WL-A, CB-2, High, Low	$1.27x10^{-10}$
3	104445744	104446131	388	OS, WL-A, WL-B	$1.75x10^{-14}$
3	107034765	107035136	372	OS, WL-B, High, Low	$2.53x10^{-13}$
3	110373064	110373957	894	RIR	$1.87x10^{-26}$
3	110574258	110574801	544	High, Low	$2.68x10^{-22}$
3	110576120	110576900	781	High, Low	$2.44x10^{-28}$
3	110954833	110955424	592	RIR, High, Low	$2.01x10^{-12}$
3	110982886	110984101	1216	RJF-Pool	$3.02x10^{-70}$
3	111233356	111233719	364	OS, RJF-Pool, WL-B	$5.98x10^{-11}$
3	111274704	111275085	382	OS	$2.77x10^{-11}$
3	113086470	113086737	268	WL-A, WL-B, High, Low	$8.98x10^{-14}$
4	3871005	3871291	287	Low	$9.09x10^{-15}$
4	6561464	6562341	878	High	$1.83x10^{-15}$
4	6563184	6563569	386	High	$1.46x10^{-11}$

4	6977083	6977544	462	High	$5.74x10^{-22}$
4	6977934	6978268	335	High	$2.68x10^{-13}$
4	7990392	7991234	843	RIR, Low	$3.47x10^{-25}$
4	8226694	8227561	868	OS, Low	$2.34x10^{-28}$
4	8547708	8548158	451	CB-1, High, Low	$1.74x10^{-17}$
4	12054618	12055214	597	OS, Low	$6.44x10^{-21}$
4	12209488	12209754	267	OS, Low	$8.73x10^{-10}$
4	13297322	13297730	409	Low	$3.98x10^{-16}$
4	14564950	14565434	485	OS	$2.65x10^{-11}$
4	15424202	15424542	341	RIR, High, Low	$9.09x10^{-15}$
4	16105558	16106289	732	OS	$9.18x10^{-25}$
4	16424084	16424454	371	CB-2	$5.93x10^{-09}$
4	16653467	16653985	519	High	$5.31x10^{-25}$
4	16880278	16880801	524	High	$1.07x10^{-10}$
4	17148888	17149240	353	RIR	$4.02x10^{-10}$
4	17284352	17285727	1376	RIR, WL-A, CB-1	$1.95x10^{-32}$
4	19245828	19246998	1171	OS	$5.73x10^{-28}$
4	22900685	22901440	756	Low	$1.52x10^{-26}$
4	23508247	23508737	491	Low	$4.31x10^{-26}$
4	23575547	23576093	547	Low	$1.81x10^{-22}$
4	24281164	24282166	1003	Low	$1.33x10^{-35}$
4	24423248	24423550	303	High, Low	$2.48x10^{-9}$
4	25660897	25661545	649	OS, High	$1.24x10^{-17}$
4	25886241	25886680	440	WL-B	$1.68x10^{-14}$
4	26165465	26165666	202	CB-1, Low	$8.73x10^{-10}$
4	26647782	26648746	965	OS, RIR, RJF-Pool, WL-A, WL-B, Low	$1.13x10^{-15}$
4	29066655	29069641	2987	OS, RJF-Pool, WL-A, High	$5.54x10^{-11}$
4	29796896	29797421	526	OS, RJF-Pool, WL-A,	$1.12x10^{-18}$

				WL-B, Low	
4	29908351	29908630	280	OS, RIR, High	5.80×10^{-9}
4	30559312	30559623	312	OS, RIR	5.08×10^{-10}
4	30848632	30848945	314	OS	1.06×10^{-9}
4	30960831	30961260	430	OS	1.39×10^{-12}
4	31770583	31837267	66685	OS	$< 10^{-308}$
4	34893853	34894131	279	RJF-Pool, WL-B	1.60×10^{-12}
4	35510122	35510516	395	OS	2.22×10^{-9}
4	36574327	36574647	321	OS	5.08×10^{-10}
4	37142358	37143793	1436	OS	9.21×10^{-50}
4	37666081	37667518	1438	OS	1.16×10^{-35}
4	37805404	37805733	330	OS	1.27×10^{-11}
4	38648156	38651990	3835	Low	7.03×10^{-9}
4	39160826	39161314	489	RIR	8.06×10^{-15}
4	40585200	40590847	5648	OS, RJF-Pool, WL-A, WL-B, CB-1, CB-2, High	3.86×10^{-117}
4	40708603	40710422	1820	Low	1.53×10^{-79}
4	41156909	41157227	319	Low	4.74×10^{-12}
4	41613573	41614332	760	Low	3.08×10^{-10}
4	41738110	41738490	381	Low	1.67×10^{-12}
4	44376001	44376643	643	OS	8.64×10^{-16}
4	44909958	44910767	810	OS, RIR, RJF-Pool	6.01×10^{-9}
4	45441653	45442125	473	RJF-Pool, WL-A, WL-B, High, Low	2.08×10^{-13}
4	48077278	48077806	529	OS	8.64×10^{-16}
4	48164452	48165968	1517	OS, RJF-Pool, WL-B	5.87×10^{-10}
4	48528195	48528995	801	OS, WL-A, WL-B, CB-1, CB-2, High, Low	6.92×10^{-33}
4	48834994	48835678	685	OS, RIR, WL-A, WL-B, High, Low	5.57×10^{-32}
4	48947421	48947689	269	RIR, High, Low	1.67×10^{-12}

4	49310267	49310856	590	Low	$1.22x10^{-25}$
4	49969419	49971449	2031	OS, RJF-Pool, WL-A, Low	$3.42x10^{-49}$
4	51372731	51374564	1834	OS, RIR, WL-A, High, Low	$1.05x10^{-58}$
4	52335817	52336350	534	Low	$3.33x10^{-20}$
4	52443548	52443962	415	OS, WL-A, WL-B	$2.21x10^{-12}$
4	53247652	53248191	540	WL-A, WL-B, Low	$2.68x10^{-19}$
4	54087741	54088086	346	Low	$2.48x10^{-9}$
4	54088980	54089162	183	Low	$3.82x10^{-11}$
4	54314221	54314667	447	OS	$2.65x10^{-11}$
4	54570480	54570867	388	OS, WL-A, WL-B, CB-2, High, Low	$1.74x10^{-17}$
4	54600687	54601020	334	WL-A, Low	$5.52x10^{-15}$
4	55159486	55159890	405	CB-2	$5.93x10^{-9}$
4	55513482	55513948	467	OS	$1.23x10^{-19}$
4	55917528	55917942	415	Low	$5.14x10^{-22}$
4	56015149	56017345	2197	OS, RIR, WL-A, Low	$4.35x10^{-79}$
4	56236188	56236671	484	High	$7.89x10^{-10}$
4	56456463	56456761	299	OS, RIR	$2.90x10^{-12}$
4	56625094	56625578	485	OS, WL-B, CB-2, High, Low	$2.16x10^{-18}$
4	56886975	56887962	988	OS	$1.00x10^{-25}$
4	57554957	57555453	497	OS	$3.17x10^{-13}$
4	57779598	57780329	732	High, Low	$2.27x10^{-32}$
4	58155104	58156298	1195	OS, RJF-Pool, WL-A, WL-B, CB-2, High	$6.15x10^{-32}$
4	58156425	58158357	1933	OS, RJF-Pool, WL-A, WL-B, High	$4.85x10^{-41}$
4	59640768	59641391	624	OS	$2.43x10^{-10}$
4	60742324	60742565	242	Low	$2.48x10^{-9}$

4	61170364	61170632	269	CB-2	5.93×10^{-9}
4	61397192	61397419	228	OS	1.06×10^{-9}
4	61710506	61711887	1382	OS	1.13×10^{-18}
4	62127871	62128512	642	OS, WL-B	7.24×10^{-14}
4	62840340	62840929	590	Low	7.93×10^{-24}
4	63131287	63132475	1189	OS	6.26×10^{-29}
4	63142665	63143622	958	OS, RIR, WL-A, WL-B, High, Low	7.93×10^{-24}
4	63586983	63587914	932	OS, RIR, High, Low	3.76×10^{-35}
4	63729525	63729990	466	High, Low	2.58×10^{-14}
4	64237809	64238186	378	RIR	1.04×10^{-10}
4	64272436	64273380	945	OS, RIR, WL-B	6.84×10^{-30}
4	64650575	64651118	544	RIR	1.80×10^{-12}
4	64935458	64935774	317	OS, WL-A	1.06×10^{-9}
4	65982671	65983009	339	High	3.65×10^{-14}
4	65994508	65995871	1364	OS	2.17×10^{-42}
4	66559814	66560401	588	OS	9.45×10^{-17}
4	66629149	66629615	467	OS, WL-B	6.06×10^{-12}
4	66691207	66691491	285	OS, RIR, WL-A, WL-B	1.27×10^{-11}
4	66820568	66821172	605	OS, Low	1.13×10^{-15}
4	67093812	67094629	818	OS, RIR, RJF-Pool, WL-A, CB-1, CB-2, High, Low	3.66×10^{-38}
4	67696115	67696408	294	OS, WL-A	9.72×10^{-9}
4	68450942	68451636	695	RIR, Low	2.68×10^{-19}
4	69298774	69299138	365	OS, RIR, RJF-Pool, WL-B, CB-2	4.92×10^{-13}
4	69754827	69755132	306	RIR, RJF-Pool, WL-B, CB-2, High, Low	1.91×10^{-9}
4	69833855	69835277	1423	High, Low	6.29×10^{-47}
4	69991161	69992049	889	OS, RIR	1.00×10^{-25}

4	71848986	71855897	6912	CB-2, High	$1.46x10^{-11}$
4	73254628	73255461	834	OS	$7.91x10^{-15}$
4	73511752	73512331	580	OS	$2.90x10^{-12}$
4	74154290	74155473	1184	RJF-Pool, CB-1, High, Low	$3.88x10^{-37}$
4	74378999	74380426	1428	RIR, High	$4.95x10^{-15}$
4	74466217	74468647	2431	High	$4.01x10^{-86}$
4	74640561	74643886	3326	High	$9.69x10^{-40}$
4	74843344	74843623	280	High	$7.89x10^{-10}$
4	75516551	75521737	5187	OS	$5.08x10^{-10}$
4	76210768	76219408	8641	RIR, WL-A, WL-B, High	$1.98x10^{-12}$
4	77870493	77871232	740	OS	$4.65x10^{-9}$
4	78340686	78342035	1350	OS	$3.78x10^{-15}$
4	78700304	78701272	969	OS, RIR, RJF-Pool, WL-A, WL-B, CB-1, CB-2, High, Low	$8.16x10^{-12}$
4	79529632	79530840	1209	High	$8.86x10^{-56}$
4	79544596	79544831	236	High	$5.80x10^{-9}$
4	79780354	79780615	262	OS, WL-B	$9.72x10^{-9}$
4	81665762	81666030	269	OS, Low	$7.03x10^{-9}$
4	83309705	83310331	627	OS	$4.52x10^{-17}$
4	83881220	83881462	243	OS, RIR, RJF-Pool, WL-B, CB-1	$6.23x10^{-9}$
4	83939863	83940061	199	OS, High	$1.07x10^{-10}$
4	84028031	84028327	297	High	$9.90x10^{-14}$
4	84117399	84118027	629	OS, RIR, WL-A, CB-1	$3.18x10^{-9}$
4	84394897	84395114	218	High	$5.80x10^{-9}$
4	84767514	84767903	390	OS	$2.43x10^{-10}$
4	85581880	85582136	257	OS, RIR, High, Low	$5.89x10^{-13}$
4	86872918	86873376	459	OS	$2.90x10^{-12}$
4	86964514	86964792	279	High	$3.65x10^{-14}$

4	87390615	87391109	495	OS, High, Low	$1.74x10^{-17}$
4	87469308	87469751	444	RIR, CB-2	$2.60x10^{-9}$
4	88925276	88925673	398	OS	$1.06x10^{-9}$
4	88933421	88933981	561	OS, RIR, WL-A	$3.78x10^{-15}$
4	89601655	89602709	1055	OS	$3.68x10^{-23}$
4	89602745	89649718	46974	OS, WL-A	$1.93x10^{-282}$
4	90337487	90337806	320	OS, RIR, Low	$8.73x10^{-10}$
4	90703708	90704056	349	WL-A	$3.94x10^{-10}$
4	92962722	92963085	364	Low	$1.40x10^{-16}$
4	93025222	93026434	1213	RIR, High, Low	$4.31x10^{-26}$
5	997321	1002305	4985	OS	$6.76x10^{-130}$
5	1074524	1075700	1177	OS, Low	$1.90x10^{-37}$
5	4404302	4404643	342	Low	$2.85x10^{-14}$
5	4404807	4405106	300	Low	$3.57x10^{-15}$
5	4864171	4864718	548	OS, RIR	$2.34x10^{-11}$
5	8395237	8399771	4535	OS, RIR, RJF-Pool, WL-A, WL-B, CB-1	$2.31x10^{-18}$
5	9056800	9057580	781	High	$1.25x10^{-20}$
5	10106871	10107426	556	High	$4.31x10^{-24}$
5	11287554	11288424	871	OS, RIR, WL-A, CB-1, CB-2, High, Low	$2.59x10^{-32}$
5	13474236	13474684	449	OS	$4.56x10^{-10}$
5	14809425	14810265	841	OS	$2.53x10^{-12}$
5	18300668	18301147	480	OS	$1.12x10^{-11}$
5	18349731	18350116	386	OS, CB-1, Low	$4.92x10^{-11}$
5	19988881	19990725	1845	RIR	$2.68x10^{-9}$
5	23589858	23590678	821	OS, RIR, WL-A, CB-1	$4.34x10^{-11}$
5	24616798	24619395	2598	RIR, High	$4.70x10^{-95}$
5	25689079	25689367	289	RIR, High, Low	$9.78x10^{-17}$
5	26376493	26377040	548	WL-A	$2.56x10^{-19}$

5	28177644	28178044	401	OS, High	$3.38x10^{-20}$
5	28930447	28931327	881	High, Low	$4.92x10^{-18}$
5	29237098	29237527	430	WL-A, High	$3.02x10^{-10}$
5	29409177	29411391	2215	OS, RIR, WL-A, High	$6.01x10^{-9}$
5	30040369	30040651	283	OS	$8.85x10^{-9}$
5	30845842	30846268	427	OS	$6.71x10^{-15}$
5	31315460	31315982	523	OS	$2.17x10^{-10}$
5	31881832	31884072	2241	OS, WL-A	$1.09x10^{-49}$
5	31900119	31900916	798	OS, WL-A	$1.84x10^{-27}$
5	36397805	36398252	448	OS	$1.30x10^{-13}$
5	36457036	36458940	1905	OS	$1.49x10^{-53}$
5	36797986	36798417	432	RIR	$4.51x10^{-11}$
5	37480580	37481279	700	OS, RIR	$1.64x10^{-16}$
5	38461895	38462246	352	OS, RIR, RJF-Pool, WL-A, WL-B, CB-1, CB-2, High, Low	$1.46x10^{-11}$
5	39953895	39954102	208	WL-B	$1.22x10^{-10}$
5	43288465	43288753	289	High	$1.12x10^{-10}$
5	43633788	43635126	1339	High, Low	$1.27x10^{-49}$
5	44090916	44091244	329	High	$2.83x10^{-13}$
5	44282539	44282839	301	OS, RIR, WL-A, CB-1, CB-2, High, Low	$4.41x10^{-10}$
5	44645437	44645707	271	High	$2.22x10^{-9}$
5	44698755	44699190	436	RIR, Low	$6.51x10^{-27}$
5	45708536	45709040	505	OS	$4.92x10^{-11}$
5	47090751	47091036	286	High, Low	$4.13x10^{-11}$
5	47421926	47422335	410	RIR, WL-A, CB-1, CB-2	$3.81x10^{-11}$
5	47459150	47459796	647	WL-A	$7.02x10^{-17}$
5	48314472	48314861	390	High, Low	$9.34x10^{-10}$
5	48544808	48545104	297	High	$1.05x10^{-13}$

5	48769314	48769692	379	OS, RIR, WL-A, CB-1	1.24×10^{-12}
5	48807736	48808038	303	RIR	5.29×10^{-9}
5	48870461	48870883	423	High	6.01×10^{-9}
5	50576235	50576681	447	OS, WL-A, High	2.83×10^{-13}
5	50834784	50834994	211	OS, High, Low	2.22×10^{-9}
5	51269803	51270204	402	RIR	6.87×10^{-10}
5	51503522	51504069	548	RIR, WL-A, CB-1, CB-2, High, Low	1.46×10^{-11}
5	55663498	55664404	907	OS, WL-B, High	1.25×10^{-22}
5	56320560	56325468	4909	OS, RIR, RJF-Pool, WL-A, WL-B, CB-1	4.08×10^{-24}
5	56738584	56738904	321	OS, RJF-Pool	3.27×10^{-14}
5	57267701	57268122	422	OS, High, Low	1.82×10^{-12}
5	58618706	58619689	984	High	1.25×10^{-20}
5	59061553	59061814	262	OS, WL-B, High	6.01×10^{-9}
5	59330784	59331174	391	High	2.08×10^{-12}
5	59567414	59568132	719	OS	2.83×10^{-23}
5	59750842	59751516	675	RIR, High, Low	2.46×10^{-18}
5	60346878	60347137	260	OS, WL-A	2.01×10^{-9}
5	60442359	60443595	1237	OS	8.75×10^{-28}
5	61365469	61365840	372	Low	7.47×10^{-9}
5	61483630	61484309	680	OS	4.36×10^{-19}
5	61661241	61661667	427	High, Low	2.85×10^{-14}
5	61847233	61848725	1493	OS, RIR, WL-A, WL-B, High, Low	2.73×10^{-65}
5	61998944	61999328	385	WL-A, WL-B, Low	1.01×10^{-14}
6	3653606	3654128	523	High, Low	1.84×10^{-20}
6	3886310	3886662	353	OS, RIR, RJF-Pool, WL-A, CB-2	3.81×10^{-10}
6	4856974	4857792	819	WL-A	7.43×10^{-27}
6	5409239	5409565	327	OS, WL-A, WL-B, CB-1,	3.81×10^{-10}

				CB-2, High, Low	
6	5481921	5482264	344	OS, High, Low	$1.72x10^{-11}$
6	5491497	5491668	172	OS, RIR, RJF-Pool, CB-1, CB-2, High, Low	$1.26x10^{-10}$
6	5768820	5769104	285	OS, WL-A	$5.70x10^{-11}$
6	5823051	5823333	283	OS, WL-A, WL-B	$1.19x10^{-10}$
6	6218789	6218978	190	OS, WL-A	$2.49x10^{-10}$
6	7024004	7025220	1217	RIR, High, Low	$5.36x10^{-55}$
6	7380502	7381595	1094	OS, RIR, RJF-Pool, WL-A, WL-B, CB-1, CB-2, High, Low	$8.87x10^{-27}$
6	7436105	7436630	526	OS	$2.99x10^{-12}$
6	8171644	8172619	976	WL-A	$5.08x10^{-32}$
6	9229297	9229961	665	Low	$8.31x10^{-22}$
6	10341429	10341948	520	WL-B, Low	$2.33x10^{-21}$
6	10506444	10506716	273	OS, RIR, RJF-Pool, WL-A, WL-B, CB-1, CB-2, High, Low	$1.39x10^{-9}$
6	10552550	10552993	444	OS, CB-2, Low	$2.73x10^{-11}$
6	11280004	11280237	234	RIR	$2.61x10^{-12}$
6	11660054	11661336	1283	OS, RJF-Pool, High, Low	$8.98x10^{-64}$
6	16276258	16276786	529	WL-A	$1.15x10^{-11}$
6	16358494	16358635	142	WL-B	$7.90x10^{-9}$
6	18699727	18700260	534	High, Low	$1.25x10^{-14}$
6	18842572	18843060	489	OS	$2.47x10^{-18}$
6	19177073	19177466	394	OS	$5.21x10^{-10}$
6	22190303	22190903	601	OS	$3.56x10^{-22}$
6	22565850	22567563	1714	OS	$2.64x10^{-51}$
6	23434445	23437762	3318	OS, CB-2	$5.69x10^{-9}$
6	23924176	23924455	280	OS, RIR, WL-B, CB-2, High, Low	$4.54x10^{-11}$

6	24548341	24549621	1281	OS, RIR, RJF-Pool, WL-A	$3.52x10^{-38}$
6	24561107	24561958	852	OS, RIR, WL-A, WL-B, CB-2, High, Low	$1.72x10^{-11}$
6	28265851	28266402	552	OS	$3.59x10^{-14}$
6	29853646	29854029	384	OS, WL-A, WL-B, High, Low	$1.72x10^{-11}$
6	30814251	30814609	359	OS	$6.25x10^{-12}$
6	30992549	30992810	262	Low	$3.81x10^{-10}$
6	32618359	32618778	420	OS, High	$6.48x10^{-9}$
6	36406519	36406833	315	OS, WL-A, High, Low	$2.18x10^{-12}$
6	36434022	36434344	323	OS, CB-1, CB-2, High, Low	$2.68x10^{-12}$
6	36458360	36459373	1014	OS	$2.95x10^{-28}$
6	36618402	36618850	449	OS, High	$1.13x10^{-16}$
6	37136130	37136899	770	OS, WL-A	$3.25x10^{-21}$
7	1381154	1381732	579	RIR, CB-2, Low	$1.13x10^{-17}$
7	1944279	1944618	340	Low	$1.20x10^{-9}$
7	2109697	2110085	389	High	$4.06x10^{-19}$
7	2839751	2839903	153	CB-2	$2.99x10^{-9}$
7	3202598	3203183	586	RJF-Pool, WL-A, High, Low	$1.96x10^{-23}$
7	4687973	4688346	374	OS, RIR, WL-A, WL-B, High	$1.09x10^{-18}$
7	5449942	5450177	236	Low	$1.91x10^{-15}$
7	6890695	6891173	479	OS	$7.84x10^{-12}$
7	6968404	6975285	6882	OS	$5.88x10^{-82}$
7	12780104	12780401	298	High	$3.89x10^{-10}$
7	13510146	13510394	249	Low	$6.84x10^{-16}$
7	14362827	14365781	2955	Low	$2.74x10^{-128}$
7	14665024	14665575	552	RIR, High, Low	$2.06x10^{-14}$
7	14920005	14920334	330	OS, RIR, RJF-Pool, WL-A, WL-B, CB-1, CB-2,	$1.57x10^{-10}$

				High, Low	
7	15648532	15649399	868	OS	$1.52x10^{-17}$
7	15889926	15891296	1371	Low	$5.10x10^{-52}$
7	17556146	17556411	266	OS, High, Low	$4.01x10^{-16}$
7	19351061	19351815	755	OS, WL-B	$3.69x10^{-10}$
7	19867878	19868335	458	OS, WL-B	$1.82x10^{-12}$
7	19884447	19885145	699	OS	$9.78x10^{-14}$
7	20122437	20123037	601	OS, WL-B, CB-2	$1.28x10^{-20}$
7	20701587	20703013	1427	OS, RJF-Pool, WL-B	$2.22x10^{-27}$
7	20739032	20739494	463	OS, WL-B	$3.53x10^{-18}$
7	23174164	23174756	593	OS, WL-A	$2.37x10^{-21}$
7	24335388	24335882	495	OS	$7.84x10^{-12}$
7	25622575	25623032	458	RIR, WL-A	$4.05x10^{-10}$
7	25680825	25682800	1976	OS, WL-A	$7.87x10^{-53}$
7	26122803	26123068	266	OS	$5.62x10^{-9}$
7	28231108	28234722	3615	OS, WL-A, WL-B	$1.94x10^{-39}$
7	28561053	28561402	350	Low	$3.25x10^{-13}$
7	29992728	29993176	449	RIR, RJF-Pool, WL-A, Low	$1.96x10^{-23}$
7	30522999	30523552	554	OS, RJF-Pool, WL-A, WL-B, CB-1, CB-2, High, Low	$1.25x10^{-13}$
7	32983378	32983850	473	OS, RJF-Pool, WL-A	$1.02x10^{-20}$
7	33195674	33195912	239	Low	$1.49x10^{-14}$
7	35853523	35853679	157	OS, RJF-Pool	$5.53x10^{-9}$
7	36069050	36069485	436	Low	$2.37x10^{-20}$
7	38360928	38363649	2722	WL-B, CB-2, High	$5.82x10^{-10}$
7	38370611	38384184	13574	WL-A, WL-B, CB-1, CB-2, Low	$3.69x10^{-10}$
8	1187479	1187803	325	High	$4.70x10^{-19}$
8	2187451	2188279	829	OS, WL-A, Low	$4.35x10^{-28}$

8	2868790	2869396	607	OS	$8.94x10^{-20}$
8	3322177	3322518	342	High	$2.21x10^{-11}$
8	4076405	4077347	943	Low	$2.98x10^{-41}$
8	7447283	7448452	1170	OS	$7.71x10^{-32}$
8	8304682	8305006	325	OS, RJF-Pool	$4.36x10^{-11}$
8	9041882	9042902	1021	OS, RIR, WL-A, WL-B, CB-2, High, Low	$3.04x10^{-37}$
8	9071781	9073142	1362	OS	$1.24x10^{-42}$
8	9344286	9345122	837	OS, RIR, WL-A, WL-B, CB-2, High, Low	$1.88x10^{-18}$
8	9636403	9637139	737	OS, RIR, WL-A, WL-B, CB-2, High, Low	$1.51x10^{-22}$
8	11882561	11883187	627	OS	$3.86x10^{-19}$
8	14644149	14644571	423	OS	$2.23x10^{-14}$
8	14950766	14951813	1048	RIR, WL-A	$6.57x10^{-19}$
8	15578077	15578955	879	High, Low	$3.04x10^{-37}$
8	15603837	15604047	211	RIR, RJF-Pool	$4.74x10^{-10}$
8	16155285	16155958	674	OS	$5.97x10^{-23}$
8	18583354	18583562	209	Low	$1.22x10^{-13}$
8	19179386	19179742	357	RIR	$2.10x10^{-10}$
8	19840299	19840647	349	High	$1.21x10^{-15}$
8	20574445	20574738	294	OS, High, Low	$7.35x10^{-12}$
8	23043847	23044257	411	OS, WL-A	$2.78x10^{-16}$
8	23338807	23339183	377	High	$1.21x10^{-15}$
8	23419012	23420095	1084	High	$2.57x10^{-23}$
8	25406101	25406856	756	OS	$4.80x10^{-21}$
8	26964991	26965245	255	High, Low	$3.46x10^{-9}$
8	27255043	27255351	309	OS, RIR, WL-A, CB-1, CB-2, High, Low	$2.32x10^{-11}$
8	29941111	29941705	595	High	$8.93x10^{-18}$
9	1503402	1506196	2795	High, Low	$8.12x10^{-9}$

9	2797540	2797858	319	WL-B	2.43×10^{-13}
9	2934692	2935007	316	Low	1.70×10^{-14}
9	3537255	3537714	460	OS	1.30×10^{-10}
9	4354177	4354448	272	High, Low	2.18×10^{-11}
9	4663147	4663428	282	OS	6.24×10^{-11}
9	7104686	7105677	992	OS	3.76×10^{-28}
9	7681307	7683416	2110	OS, RIR, WL-B, CB-1, CB-2, High, Low	3.10×10^{-88}
9	7840543	7841629	1087	CB-1, CB-2	1.06×10^{-37}
9	8333532	8334960	1429	OS, RIR, WL-B, CB-2	1.39×10^{-52}
9	8586750	8587203	454	OS	1.44×10^{-11}
9	9551744	9552728	985	OS, High	1.57×10^{-34}
9	13955399	13955515	117	CB-2	1.29×10^{-9}
9	14093960	14094465	506	WL-A, WL-B	1.67×10^{-12}
9	14094653	14094925	273	WL-B	1.74×10^{-9}
9	14841801	14842951	1151	RIR, WL-A, WL-B, CB-1, High, Low	2.27×10^{-43}
9	17346890	17347100	211	WL-B	3.90×10^{-9}
9	18196412	18198338	1927	OS	3.00×10^{-11}
9	19628123	19628874	752	Low	1.73×10^{-30}
9	19680321	19680691	371	OS	1.59×10^{-12}
9	19749190	19753362	4173	OS, WL-A, WL-B	1.02×10^{-118}
9	22579832	22580080	249	WL-A, High	1.19×10^{-12}
9	22611982	22613884	1903	High	2.77×10^{-69}
10	4504176	4504628	453	OS	6.89×10^{-16}
10	4543178	4543780	603	Low	3.92×10^{-23}
10	5222253	5222894	642	OS, RIR, CB-2	4.27×10^{-19}
10	5303824	5305911	2088	RIR, WL-A, WL-B, CB-2, High, Low	3.50×10^{-92}
10	7168357	7168933	577	CB-2, High	7.70×10^{-25}

10	7581723	7582292	570	RIR	7.70×10^{-18}
10	7890791	7891496	706	OS, High	4.22×10^{-30}
10	7988499	7988870	372	OS, RIR, High, Low	1.24×10^{-15}
10	8028002	8029325	1324	OS	7.36×10^{-48}
10	8837106	8837638	533	OS, High, Low	8.71×10^{-11}
10	9498478	9499006	529	OS	6.38×10^{-13}
10	9673755	9674315	561	RIR, Low	2.03×10^{-25}
10	10616860	10617448	589	Low	2.33×10^{-15}
10	10682740	10685988	3249	Low	5.87×10^{-9}
10	10908660	10909554	895	High	3.99×10^{-12}
10	15013570	15014143	574	WL-B	2.38×10^{-13}
10	15419656	15423255	3600	OS, WL-B, CB-2, High	4.89×10^{-148}
10	19762012	19763120	1109	OS, WL-A	9.15×10^{-27}
10	20656154	20656604	451	OS	1.51×10^{-16}
10	20981367	20981777	411	OS, RIR, WL-A, CB-1, CB-2, High, Low	1.29×10^{-10}
11	1145046	1145594	549	High, Low	3.27×10^{-11}
11	5324521	5324812	292	High	7.62×10^{-10}
11	5522136	5523143	1008	OS, WL-A, WL-B	3.83×10^{-30}
11	7848990	7849467	478	RIR	5.33×10^{-15}
11	8539475	8539704	230	Low	1.14×10^{-11}
11	10172435	10173137	703	OS, WL-B	1.28×10^{-22}
11	10535813	10536159	347	High, Low	5.31×10^{-15}
11	12612259	12612971	713	OS, RIR, CB-1, Low	4.83×10^{-24}
11	15232794	15242812	10019	OS, RIR, RJF-Pool, WL-A, WL-B, CB-1, CB-2, High, Low	1.16×10^{-10}
11	20872416	20874127	1712	WL-A	3.79×10^{-9}
11	21123448	21123754	307	OS, WL-B, CB-1	2.52×10^{-10}
12	165035	165350	316	WL-A	3.84×10^{-9}

12	166086	166812	727	WL-A	2.98×10^{-14}
12	1039914	1040330	417	OS, CB-2	1.38×10^{-9}
12	4185526	4185996	471	OS, RIR, WL-A, High, Low	5.51×10^{-16}
12	4396297	4397801	1505	WL-A, WL-B, CB-1, High, Low	2.59×10^{-47}
12	4985212	4985540	329	High	7.25×10^{-14}
12	6857842	6858745	904	OS, WL-A, WL-B, CB-2	3.24×10^{-27}
12	7091878	7092182	305	CB-2, High, Low	3.18×10^{-16}
12	12880258	12880574	317	High	3.33×10^{-9}
12	14213191	14213658	468	WL-A, CB-2, Low	7.00×10^{-19}
12	16881308	16882404	1097	OS, WL-A	8.51×10^{-34}
12	17530966	17531314	349	OS	2.89×10^{-10}
13	511051	512598	1548	High	1.37×10^{-36}
13	526708	530714	4007	OS, RJF-Pool, WL-A, WL-B, CB-1, CB-2, High, Low	4.32×10^{-16}
13	562276	562943	668	WL-A, High	3.13×10^{-11}
13	571669	573155	1487	High	2.95×10^{-13}
13	577485	577971	487	High	6.17×10^{-9}
13	578505	578878	374	High	5.83×10^{-12}
13	705486	705695	210	WL-A	4.55×10^{-9}
13	729034	730876	1843	OS, RJF-Pool, High	1.12×10^{-111}
13	730898	731696	799	OS, RJF-Pool, High	5.39×10^{-69}
13	732170	732369	200	OS, RJF-Pool, High	2.95×10^{-13}
13	732405	732605	201	OS, RJF-Pool, High	8.74×10^{-16}
13	732756	733594	839	OS, RJF-Pool, High	4.11×10^{-63}
13	733830	734661	832	OS, RJF-Pool, High	3.20×10^{-100}
13	734706	734811	106	RJF-Pool	2.48×10^{-9}
13	734848	735884	1037	OS, RJF-Pool, High	6.67×10^{-46}
13	743673	748608	4936	High	3.46×10^{-163}

13	761078	762960	1883	High	$3.42x10^{-58}$
13	764239	764740	502	RIR, WL-A, WL-B	$2.37x10^{-11}$
13	875235	875443	209	Low	$1.43x10^{-11}$
13	2137629	2138046	418	OS	$3.36x10^{-11}$
13	3959189	3959788	600	High	$4.03x10^{-14}$
13	4134025	4134366	342	OS, WL-A	$7.77x10^{-13}$
13	6781006	6781327	322	High	$6.17x10^{-9}$
13	7047571	7048004	434	OS, RIR, CB-1, High	$3.87x10^{-9}$
13	7618819	7619093	275	High	$5.83x10^{-12}$
13	8852791	8853214	424	OS	$1.72x10^{-13}$
13	9124317	9124659	343	OS	$1.58x10^{-11}$
13	10252048	10253929	1882	Low	$2.22x10^{-13}$
13	12330767	12330996	230	High, Low	$1.14x10^{-10}$
13	12715016	12715714	699	OS	$9.98x10^{-19}$
13	13066571	13066818	248	OS, RIR, WL-A, WL-B, CB-1, CB-2, High, Low	$6.29x10^{-13}$
13	16308544	16309165	622	OS, WL-A	$1.10x10^{-9}$
13	18367571	18386536	18966	High	$<10^{-308}$
13	18390273	18390650	378	High	$2.95x10^{-13}$
14	3572818	3573219	402	OS, WL-B	$7.29x10^{-13}$
14	5357291	5357774	484	OS, CB-2	$1.14x10^{-16}$
14	7885515	7886317	803	OS, RIR, WL-B, CB-2, Low	$2.35x10^{-17}$
14	9730082	9730609	528	OS, WL-A	$4.50x10^{-15}$
14	10692552	10694979	2428	OS, RIR	$2.47x10^{-18}$
14	12109288	12112070	2783	CB-2	$4.64x10^{-9}$
14	12161025	12161402	378	High	$4.58x10^{-14}$
14	14449316	14449769	454	OS	$3.87x10^{-12}$
14	14472883	14473192	310	OS	$3.50x10^{-10}$
14	14494717	14496283	1567	OS	$4.09x10^{-28}$

14	14988509	14989219	711	OS	$9.54x10^{-15}$
14	15054559	15056818	2260	OS	$3.91x10^{-57}$
14	15121907	15122440	534	OS, WL-B	$2.47x10^{-18}$
15	1276328	1278055	1728	OS, WL-A	$2.17x10^{-53}$
15	2843789	2844010	222	Low	$4.03x10^{-9}$
15	3034728	3035075	348	Low	$2.01x10^{-14}$
15	3238345	3238805	461	OS, WL-A, High, Low	$5.55x10^{-14}$
15	4035187	4035510	324	Low	$1.46x10^{-9}$
15	4107559	4108635	1077	Low	$8.09x10^{-42}$
15	4192938	4193104	167	High, Low	$4.03x10^{-9}$
15	4208590	4209001	412	High, Low	$7.26x10^{-15}$
15	5079983	5080475	493	OS	$3.26x10^{-14}$
15	9133479	9133760	282	OS	$4.87x10^{-10}$
15	11024249	11024713	465	OS, RIR, RJF-Pool, WL-A, WL-B, CB-1, CB-2, High, Low	$3.10x10^{-25}$
15	12067415	12073766	6352	High	$1.74x10^{-194}$
16	204370	205214	845	WL-A, CB-2, High, Low	$4.81x10^{-12}$
16	212387	214020	1634	RJF-Pool, WL-A, CB-1, CB-2, High, Low	$6.48x10^{-13}$
16	217581	218613	1033	RJF-Pool, WL-A	$7.61x10^{-9}$
16	298289	301277	2989	OS	$9.89x10^{-18}$
16	302330	305035	2706	OS, RJF-Pool, WL-A, Low	$3.57x10^{-11}$
16	327435	329584	2150	OS, RIR, High	$8.56x10^{-10}$
16	329637	330732	1096	OS, WL-A	$1.39x10^{-9}$
16	330780	333125	2346	OS, RIR, WL-A	$1.38x10^{-26}$
16	346480	350577	4098	OS, WL-B, CB-1	$4.61x10^{-12}$
16	352291	353033	743	OS, RIR	$4.80x10^{-23}$
16	354658	355741	1084	OS, RJF-Pool, WL-A, WL-B, CB-1	$7.49x10^{-12}$

17	6276978	6277268	291	Low	$1.29x10^{-16}$
17	9408047	9408604	558	RIR, RJF-Pool, Low	$5.90x10^{-27}$
18	263578	263967	390	OS, RIR, CB-1, CB-2, High, Low	$7.90x10^{-10}$
18	277739	278776	1038	OS, WL-A, WL-B	$2.26x10^{-34}$
18	330113	330440	328	OS	$6.24x10^{-10}$
18	3435612	3435954	343	High, Low	$1.55x10^{-15}$
18	8936412	8936795	384	CB-2	$2.22x10^{-14}$
19	4386586	4386875	290	High	$7.99x10^{-10}$
19	4980713	4981072	360	RIR, CB-2, High, Low	$8.40x10^{-10}$
19	5259907	5260312	406	OS, RIR, RJF-Pool, WL-A, WL-B, CB-1, CB-2, High, Low	$3.73x10^{-16}$
19	5680628	5681169	542	RIR	$2.24x10^{-13}$
19	7811689	7812091	403	RIR, High, Low	$1.48x10^{-14}$
19	8763275	8763702	428	RIR	$1.49x10^{-9}$
20	723932	724545	614	OS	$7.01x10^{-24}$
20	1624854	1625162	309	RIR, High, Low	$3.36x10^{-11}$
20	3546954	3547471	518	OS	$1.84x10^{-12}$
20	3955482	3958272	2791	RIR, CB-2, High, Low	$6.15x10^{-116}$
20	4130964	4131411	448	High	$9.74x10^{-16}$
20	6172578	6172968	391	OS, RIR, RJF-Pool, WL-A, WL-B, CB-1, CB-2, High, Low	$1.85x10^{-13}$
20	6699795	6700163	369	CB-2	$1.57x10^{-16}$
20	6829190	6829705	516	CB-2	$4.50x10^{-14}$
20	7030102	7030497	396	OS	$3.05x10^{-10}$
20	7107865	7108038	174	RIR, RJF-Pool, CB-1, CB-2	$8.16x10^{-13}$
20	7669367	7669620	254	High	$6.70x10^{-10}$
20	8133293	8134365	1073	WL-A, High, Low	$2.02x10^{-37}$

20	9065293	9066991	1699	Low	$7.34x10^{-72}$
20	9620717	9621359	643	RIR, WL-A, WL-B, High, Low	$1.72x10^{-19}$
20	11873428	11874038	611	RIR, High, Low	$3.64x10^{-25}$
21	327532	329274	1743	OS, RIR	$2.59x10^{-21}$
21	1894741	1895599	859	OS, Low	$1.26x10^{-30}$
23	4796066	4796489	424	High	$4.27x10^{-10}$
24	1214178	1214839	662	OS	$1.02x10^{-18}$
26	3775889	3776651	763	RIR	$3.76x10^{-10}$
27	120908	121312	405	WL-A	$9.81x10^{-16}$
27	121692	123117	1426	WL-A	$2.08x10^{-15}$
27	399990	400444	455	OS	$1.40x10^{-13}$
27	451177	451558	382	CB-2, Low	$3.27x10^{-16}$
27	1104866	1105219	354	OS	$1.94x10^{-11}$
27	3435903	3439251	3349	RIR, CB-1, CB-2, High	$2.66x10^{-98}$
28	214781	215285	505	OS, RIR, WL-A, CB-1, High, Low	$9.18x10^{-17}$
28	626958	627311	354	OS, High, Low	$6.97x10^{-12}$
28	3929583	3929908	326	OS, CB-1, CB-2, High, Low	$4.89x10^{-9}$
Z	3341603	3341827	225	High	$1.93x10^{-9}$
Z	3395143	3395470	328	RJF-Pool, CB-1	$4.54x10^{-11}$
Z	3447994	3448381	388	High	$1.93x10^{-9}$
Z	3449793	3451029	1237	High	$4.62x10^{-21}$
Z	4507676	4509644	1969	RJF-Pool, CB-2, High, Low	$3.54x10^{-23}$
Z	5319047	5319377	331	High, Low	$7.32x10^{-13}$
Z	7858179	7858335	157	OS, RIR, WL-B, CB-1, High, Low	$2.68x10^{-13}$
Z	7858918	7859396	479	OS, RIR, RJF-Pool, WL-B, CB-1, High, Low	$1.04x10^{-26}$

Z	7859557	7860162	606	OS, RIR, WL-B, CB-1, High, Low	$4.12x10^{-24}$
Z	7860225	7860886	662	RIR, WL-B, High, Low	$6.29x10^{-13}$
Z	7862361	7862654	294	High, Low	$3.20x10^{-9}$
Z	7862676	7863047	372	OS, RIR, RJF-Pool, WL-B, CB-1, High, Low	$3.18x10^{-22}$
Z	7863237	7863425	189	RIR, RJF-Pool, CB-1, Low	$6.18x10^{-16}$
Z	7863482	7863805	324	OS, RIR, RJF-Pool, WL-B, CB-1, High, Low	$6.19x10^{-20}$
Z	7863905	7864054	150	WL-B, High, Low	$2.98x10^{-15}$
Z	7865018	7865125	108	OS	$2.83x10^{-9}$
Z	7865225	7865382	158	High, Low	$1.33x10^{-10}$
Z	7865628	7866384	757	OS, RIR, RJF-Pool, WL-B, CB-1, High, Low	$7.61x10^{-26}$
Z	7866634	7868131	1498	OS, RIR, WL-B, CB-1	$1.33x10^{-11}$
Z	7869521	7869717	197	OS, RIR, RJF-Pool, WL-B, High, Low	$2.76x10^{-13}$
Z	8128533	8128961	429	High, Low	$1.20x10^{-11}$
Z	9738037	9738607	571	OS, RIR, WL-A	$8.49x10^{-11}$
Z	10892323	10892775	453	OS, RIR, WL-A, CB-2, High, Low	$3.94x10^{-9}$
Z	11206722	11208075	1354	OS, WL-A	$2.23x10^{-27}$
Z	11474087	11475596	1510	OS, RIR, RJF-Pool, WL-B, High, Low	$7.47x10^{-9}$
Z	12186587	12190093	3507	OS, RJF-Pool, WL-A, Low	$1.10x10^{-68}$
Z	12308651	12308925	275	OS, RJF-Pool, WL-A, CB-1, Low	$2.49x10^{-10}$
Z	12988234	12990035	1802	CB-2	$3.13x10^{-28}$
Z	13137891	13138276	386	CB-2, High, Low	$4.84x10^{-11}$
Z	13383308	13384317	1010	OS, WL-A, CB-1, Low	$1.40x10^{-35}$
Z	14015887	14016503	617	OS, CB-1, CB-2, High, Low	$4.48x10^{-14}$

Z	14897011	14897499	489	OS, WL-A, CB-1	$3.34x10^{-17}$
Z	15797620	15798482	863	OS, WL-A	$7.57x10^{-22}$
Z	17301723	17302733	1011	OS, WL-A	$2.39x10^{-21}$
Z	17333469	17334925	1457	OS, WL-A	$9.00x10^{-9}$
Z	17834217	17834920	704	OS, WL-A, WL-B	$8.20x10^{-16}$
Z	18351823	18353828	2006	High	$3.01x10^{-58}$
Z	19140479	19143063	2585	High	$8.34x10^{-23}$
Z	19143217	19144552	1336	High, Low	$1.21x10^{-21}$
Z	19414933	19416176	1244	CB-2	$1.92x10^{-16}$
Z	20715483	20716215	733	OS, WL-A	$2.68x10^{-13}$
Z	24116747	24117315	569	RIR, High	$9.84x10^{-15}$
Z	26471709	26472795	1087	OS, WL-A, WL-B, Low	$2.72x10^{-12}$
Z	27524820	27525275	456	RIR, High, Low	$3.20x10^{-9}$
Z	28646158	28647249	1092	OS, WL-A, CB-2	$8.65x10^{-12}$
Z	29568425	29569561	1137	RIR, Low	$1.33x10^{-25}$
Z	29806806	29807763	958	Low	$1.43x10^{-22}$
Z	30079291	30080127	837	Low	$9.47x10^{-21}$
Z	30221013	30224873	3861	OS, WL-A, CB-2, High	$1.53x10^{-28}$
Z	30225843	30234997	9155	RIR	$3.22x10^{-50}$
Z	33926168	33927277	1110	High, Low	$9.47x10^{-21}$
Z	37386707	37387281	575	OS, WL-A, WL-B, Low	$4.14x10^{-17}$
Z	38442029	38443664	1636	High, Low	$1.85x10^{-30}$
Z	38497963	38498476	514	High, Low	$7.32x10^{-13}$
Z	38504863	38505228	366	RIR	$4.59x10^{-10}$
Z	40814497	40814976	480	OS	$8.20x10^{-16}$
Z	40837874	40838156	283	RIR, CB-1, CB-2, High	$5.05x10^{-10}$
Z	40988304	40988691	388	OS	$9.00x10^{-9}$
Z	42403089	42403904	816	OS, RIR, RJF-Pool, WL-A, WL-B, CB-1	$3.10x10^{-13}$

Z	42988007	42998728	10722	OS, WL-A, WL-B	$8.37x10^{-102}$
Z	43109389	43114151	4763	OS, WL-A, WL-B	$9.06x10^{-96}$
Z	44264289	44264477	189	RIR	$1.35x10^{-9}$
Z	44741091	44742398	1308	OS, WL-A, WL-B, CB-1	$1.93x10^{-38}$
Z	44875179	44875951	773	OS, WL-B, CB-1, CB-2	$5.92x10^{-16}$
Z	45088768	45092418	3651	OS	$3.12x10^{-89}$
Z	45159435	45159703	269	High	$7.34x10^{-9}$
Z	45728350	45729088	739	OS	$2.61x10^{-15}$
Z	46820316	46821518	1203	OS	$2.72x10^{-12}$
Z	46822173	46822730	558	OS	$2.83x10^{-9}$
Z	46933765	46935147	1383	OS, RIR, RJF-Pool, WL-A, WL-B, CB-1	$2.13x10^{-12}$
Z	46948520	46953932	5413	OS, RIR, RJF-Pool, WL-A, WL-B, CB-1	$2.41x10^{-21}$
Z	46953968	46957963	3996	OS, RIR, RJF-Pool, WL-A, WL-B, CB-1, High	$2.07x10^{-32}$
Z	47528013	47529805	1793	High	$1.33x10^{-10}$
Z	47532874	47533972	1099	CB-2, High, Low	$1.23x10^{-28}$
Z	48490105	48491230	1126	OS, RIR, Low	$1.33x10^{-25}$
Z	48734958	48737243	2286	OS, RIR, WL-A, WL-B	$6.72x10^{-31}$
Z	49295059	49295858	800	Low	$4.14x10^{-17}$
Z	49571266	49571810	545	OS, RIR, WL-A	$8.42x10^{-14}$
Z	51755128	51756451	1324	RIR, High, Low	$7.50x10^{-30}$
Z	52855008	52855424	417	OS	$2.79x10^{-10}$
Z	55166932	55167335	404	WL-A	$2.81x10^{-11}$
Z	59453608	59454272	665	OS, RIR, WL-A	$2.79x10^{-10}$
Z	60137437	60139109	1673	RIR	$1.53x10^{-31}$
Z	63308896	63309573	678	WL-A	$3.73x10^{-14}$
Z	63309969	63310376	408	WL-A	$7.04x10^{-9}$
Z	63313797	63315265	1469	OS, WL-A, WL-B	$6.46x10^{-34}$

Z	63985647	63986801	1155	CB-2	$1.63x10^{-17}$
Z	65607320	65607696	377	Low	$4.84x10^{-11}$
Z	65630837	65631926	1090	WL-B, Low	$3.20x10^{-9}$
Z	65818271	65819195	925	OS, WL-A, WL-B, Low	$2.00x10^{-27}$
Z	66370688	66372893	2206	OS, RIR, WL-A, WL-B, CB-1, High, Low	$3.12x10^{-10}$
Z	66396623	66399023	2401	OS, WL-A, CB-1	$2.64x10^{-14}$
Z	66587961	66588599	639	OS, RIR, RJF-Pool, WL-A, WL-B, CB-1, CB-2, High, Low	$1.86x10^{-18}$
Z	67839781	67840066	286	OS, RIR	$1.57x10^{-10}$
Z	69224436	69225106	671	RIR, High, Low	$5.79x10^{-22}$
Z	69356670	69357745	1076	OS, RJF-Pool, WL-A, WL-B, CB-2, High	$5.39x10^{-17}$
Z	70000275	70001959	1685	RIR, High, Low	$5.08x10^{-45}$
Z	70001995	70002342	348	High, Low	$3.20x10^{-9}$
Z	71122079	71123193	1115	High, Low	$9.74x10^{-19}$
Z	72214236	72214881	646	RIR	$1.15x10^{-15}$
Z	72336610	72337191	582	OS, RJF-Pool, WL-A, WL-B, CB-1, CB-2, High, Low	$5.04x10^{-14}$
Z	74527530	74528391	862	RIR	$7.25x10^{-13}$
Z	74551874	74552425	552	OS, RIR, WL-A, Low	$2.75x10^{-11}$

[a]Any line which had a deletion within this region is listed. In some cases, some lines may be heterozygous for the deletion. Because of the merging and bridging code, in some cases, the deletion may not be fully fixed within any of the lines.

[b]P-values were computed as the binomial probability of seeing N reads in the reference strain over a region with 0 reads in the deletion line, assuming random distribution of N reads between reference and deletion lines according to the chromosome-wide ratio of read counts. For deletions which were merged or bridged from multiple events, the lowest p-value for any included event was taken as the p-value for the merged or bridged event.

Supplementary Table 7 Detection of deletions affecting coding sequences in chicken

Gene[a]	Chr	Range (bp)	Size (bp)	Fixed line(s)	Segregating line(s)	Deleted region[b]
ENSGALG-00000019015	1	1,742,902-1,763,907	21,006	OS		Entire gene
CRYBG3/MINA	1	94,556,654-94,561,755	5,102	RI		*CRYBG3*: Ex 21-22 (of 23); *MINA*: 3' UTR only
*ENSGALG-00000021810**	4	89,601,727-89,649,715	47,989	OS	WL-A	Exon 2 (of 5)
*SLC5A9**	8	23,338,821-23,339,187	367	High	Low	Part of exon 1 (of 13)
CIRH1A	11	20,872,416-0,874,127	1,712	WL-A		Exon 1 (of 6)
*SH3RF2**	13	18,367,575-18,386,535	18,961	High	Low, CB-1	Exon 2-11 (of 11)
*GHR**	Z	12,988,256-12,990,035	1,780	CB-2		Part of exon 9 (of 9)

[a]Deletions associated with genes marked with an asterisk (*) have been experimentally validated

[b]Predicted on the basis of the Ensembl gene model

Supplementary Table 8 Allele frequency of deletion alleles within re-sequence pools and across breed in a chicken diversity panel.

		Deletion[1]							
		SH3RF2		*SLC5A9*		*ENS21280*		*GHR*	
	Origin	*n**	q	*n**	q	*n**	q	*n**	q
Pool									
Broiler Ross 308 (CB-1)	USA	10	0.15	10	0.15	10	0.00	10	0.00
Broiler Dam Line B (CB-2)	France	10	0.00	10	0.05	10	0.00	10	1.00
High growth line (High)	USA	11	1.00	11	1.00	11	0.00	11	0.00
Low growth line (Low)	USA	11	0.18	11	0.68	11	0.00	11	0.00
Obese Strain (OS)	USA	10	0.00	10	0.00	10	1.00	10	0.00
Rhode Island Red (RIR)	France	8	0.00	8	0.00	8	0.00	8	0.00
Red junglefowl pool (RJF-pool)	Sweden/ Denmark	8	0.00	8	0.00	8	0.13	8	0.00
White Leghorn Line 13 (WL-A)	Sweden	11	0.00	11	0.00	11	0.91	11	0.00
White Leghorn (WL-B)	USA	8	0.00	8	0.00	8	0.06	8	0.00
Diversity panel									
Black Minorca	Japan	2	0.00	2	0.00	2	1.00	2	0.00
Bourbonnaise	France	7	0.00	8	0.00	7	0.00	8	0.00
Broiler Dam Line F	Israel	10	0.00	10	0.15	10	0.35	10	0.00
Broiler Sire Line B	France	10	0.00	10	0.00	10	0.15	10	0.00
Broiler Sire Line E	USA	10	0.00	10	0.00	10	0.50	10	0.00
Brown Leghorn	Sweden	2	0.00	2	0.00	2	0.25	2	0.00
Brown Line	Sweden	2	0.75	2	0.00	2	0.50	2	0.00
Cochin	China	8	0.00	6	0.00	8	0.00	8	0.00
Coucou de Rennes	France	8	0.00	8	0.00	8	0.13	8	0.00
Fayoumi	Egypt	5	0.00	5	0.00	5	0.00	5	0.00
Hua-Tung	China	3	0.00	3	0.00	3	0.00	3	0.00

Icelandic Landrace	Iceland	11	0.00	12	0.00	12	0.17	28	0.00
Järhöns	Norway	8	0.00	8	0.00	8	0.63	8	0.00
Marans	France	7	0.00	8	0.00	8	0.00	8	0.00
Owl-bearded	Netherlands	8	0.00	8	0.00	6	0.17	8	0.00
Poltava clay	Ukraine	8	0.13	8	0.00	7	0.36	8	0.00
Red junglefowl Ebeltoft [2]	Denmark	2	0.00	2	0.00	2	0.75	1	0.00
Red junglefowl Frösö [2]	Sweden	2	0.00	2	0.00	2	0.00	2	0.00
Red junglefowl Götala[2]	Sweden	2	0.00	2	0.00	2	1.00	2	0.00
Red junglefowl Copenhagen[2]	Denmark	2	0.00	2	0.00	2	0.00	2	0.00
Rhode Island Red	Netherlands	10	0.00	10	0.00	10	0.00	10	0.00
Silkie	China	2	0.00	2	0.00	2	0.00	2	0.00
Smyth Line	Sweden	2	1.00	2	0.00	2	0.00	2	0.00
Yurlov crower	Russia	4	0.25	4	0.00	4	0.00	4	0.00

[1]Deletion allele status is reported as the proportion of the deleted allele observed in the pool or diversity set

*Number of samples tested

[2]Red junglefowls listed by location

Supplementary Table 9 Primer and probe sets used for loss-of-function mutation validation and deletion genotyping.

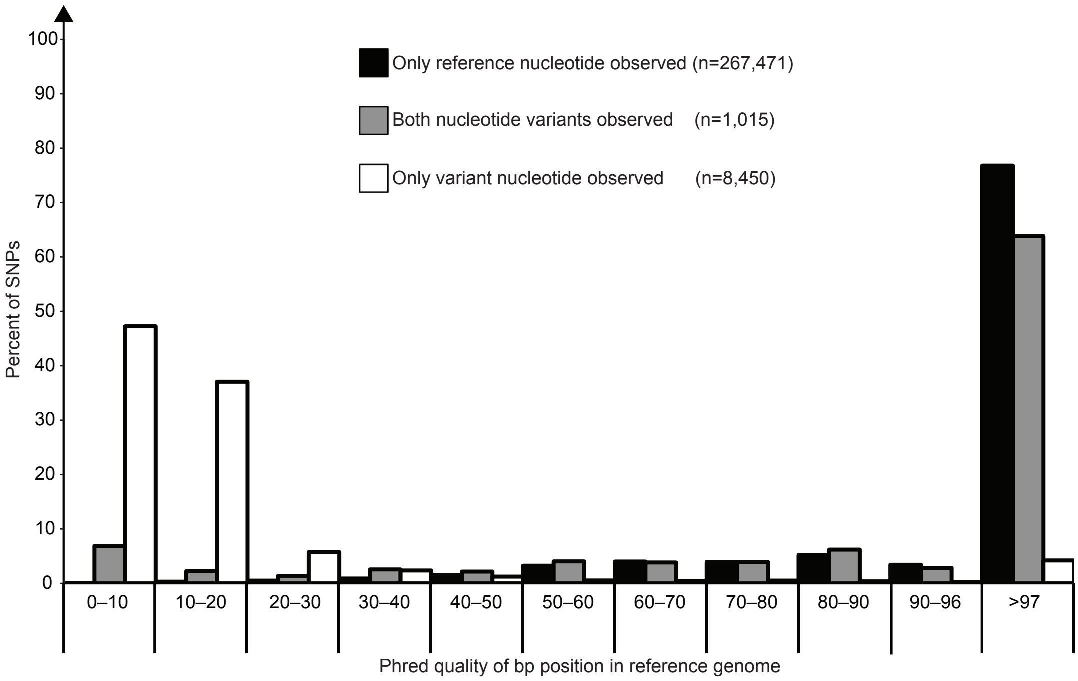
Primer name	Chr	Strand	Start	Stop	Sequence
Stop codon validation primers					
ATAD5_su1	18	+	6644085	6644104	TTGGTTTTCCTGAACCTTGC
ATAD5_sd1	18	-	6644617	6644636	CAAGCAAGCTGTGGAGGTTT
C9orf72_sd1	Z	-	67025294	67025314	CAGTGGAATCTCGGGTGTAGA
C9orf72_su1	Z	+	67024760	67024780	TCCACGCATACTCTGTGAAGA
CCDC111_sd1	4	-	40887469	40887490	TGACCTTAGAATGGGTCTCTGG
CCDC111_su1	4	+	40886930	40886949	CTGGTGCTTGACATGGAATG
CHRM3_sd1	3	-	37733193	37733213	TGTTGAGTCTTGCTTGTGCAG
CHRM3_su1	3	+	37732638	37732657	TCTGCCGTTGCAGTTCATAG
CHRM4_sd1	5	-	25799361	25799380	CCCTCTTGGGGGAGTTATTG
CHRM4_su1	5	+	25798830	25798849	CGACCTCATCATCGGAGTCT
CPNE4_sd1	2	-	42028317	42028336	AAGGGAAGCTGGTCTCACCT
CPNE4_su1	2	+	42027748	42027770	TCGGTTTCCTATCAAAATGACTG
ECT2_sd1	9	-	20792970	20792991	TTCAGAGGCAAGAATTGCTTTA
ECT2_su1	9	+	20792492	20792512	TGATTCACAAAGCAAAGGAGA
EDEM2_sd1	20	-	2539651	2539670	CATACAGCAGTTGGCACACA
EDEM2_su1	20	+	2539096	2539115	GCAGATGCAGGAGGGTAAGT
ERCC6_sd1	6	-	19831151	19831170	CACAGTTCCCAAGTGCTTCA
ERCC6_su1	6	+	19830592	19830611	CCTAATGGCAAATTCCTCCA
GPR26_sd1	6	-	33330069	33330088	TCACGTCAATCCGCTTACAG
GPR26_su1	6	+	33329585	33329604	CGGGATTGTTCATCCTCAAC
HSP90AA1_sd1	5	-	51984657	51984676	GACAAAGGACCAGGTGGCTA
HSP90AA1_su1	5	+	51984161	51984181	TTTGTTGCCATGTATCCCATT
KCNK5_sd1	3	-	30442074	30442095	GCTGGTTTACAAACATGGTTCC
KCNK5_su1	3	+	30441531	30441554	TCAGGGTAATAACTGAGATGCAAA
KDR_sd1	4	-	67082814	67082836	GACTGCAAGATGCTTCTGTATCC

KDR_su1	4	+	67082268	67082287	GGCTGGTTGGGGCATATAAA
MLLT4_sd1	3	-	44034697	44034720	CGGGTAAACCTGAAAGTAACTTGA
MLLT4_su1	3	+	44034148	44034167	AGCTCAGAAACAGGGAGCAA
MYSM1_sd1	8	-	27109960	27109979	GTCGTGGTCTCTGCCTCTTC
MYSM1_su1	8	+	27109476	27109495	TTATCCATGGGGACACTGCT
NDUFB8_sd1	6	-	18495970	18495992	TCCTGACCAGGAGCTTAAGATAA
NDUFB8_su1	6	+	18495464	18495483	GCTGCGTGCATCTAGACTTG
PHLDB2_sd1	1	-	91793558	91793577	TCATGCCATCGAACAGATTG
PHLDB2_su1	1	+	91793025	91793045	GGCATACTTGAAGTCGGATGA
PITX3_sd1	6	-	17891374	17891393	GCTGGATAAACAGGCCAAGA
PITX3_su1	6	+	17890887	17890906	GAGTTGCACGTGTCCCTGTA
POLE_sd1	15	-	10293657	10293676	ATGAGCAGAGCCATCCTGGT
POLE_su1	15	+	10293118	10293137	CCACTGACACCAGAGCAGAA
RFC4_sd1	9	-	17302767	17302786	AAGTGTTGGCCTCCTTCAGA
RFC4_su1	9	+	17302221	17302241	GGTGAGCAGCTACCTCACTTC
SCL4A3_sd1	7	-	23608751	23608770	TGGCTCTTGCTTTCAAGGTT
SCL4A3_su1	7	+	23608252	23608271	GGTCTTCAACTGTGCTGTGC
SEC24C_sd1	6	-	17040197	17040216	TCTCCCACAGCTGCTGAAAT
SEC24C_su1	6	+	17039808	17039828	TTGGTGGTTGTTTTCCCTAAA
SLC5A11_sd1	14	-	6599939	6599958	GATGTCCTGTGTGCCAGGTA
SLC5A11_su1	14	+	6599380	6599399	CCCTTTGTGCAGGGCTATAC
SUPV3L1_sd1	6	-	11934280	11934302	AAATCTGAATGTGAGTGGGATCA
SUPV3L1_su1	6	+	11933737	11933756	GCTGCAAGTTCCCTTGCTTA
USP10_sd1	11	-	18798652	18798672	TGTTAAGATTGTGTGGCAGCA
USP10_su1	11	+	18798123	18798144	GAGGATCTTGATACTGCGAGGT
WDR41_sd1	Z	-	22636066	22636085	GCTCCTTCACCATCCTTTTT
WDR41_su1	Z	+	22635495	22635517	TGTTTTTCAAACAGAAAATGCTC

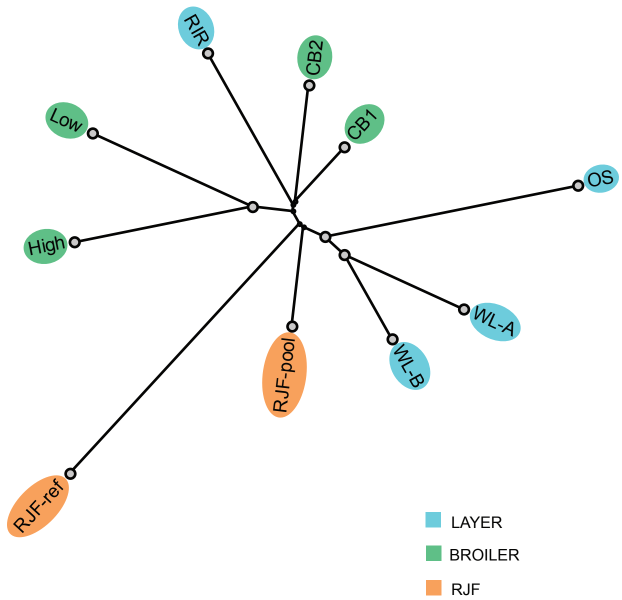
Deletion validation primers

SH3RF2-del-u1	13	+	18367330	18367352	CTTTACCTCTCCTCTGCTCTCCT
SH3RF2-del-d1	13	-	18386617	18386640	TGTTTTCAAACCTTTGTTTCTCTG
SLC5A9_del_u1	8	+	23338531	23338550	AACTCCTTTGCTGCTGGCTA
SLC5A9_del_d1	8	-	23339373	23339392	AGGCTTGGAAAGAAGCCATT
ENS21810_del_u1	4	+	89601476	89601497	TCAGGTGACATTTTAACCACCA
ENS21810_del_d1	4	-	89601813	89601835	TTTACAGGAATTTCCAAACATGG
GHR-del-u1	Z	+	12988000	12988019	TTCACCATGGACAATGCCTA
GHR-del-d1	Z	-	12990172	12990191	TCGGGACAGATCAAAGACAA
Deletion multiplex primers					
SH3RF2_m1	13	+	18367301	18367320	TGCTTCGGGCTGAGCCTTCT
SH3RF2_m2	13	-	18367587	18367606	TAGCGCCCAAGCTGTGTCCT
SH3RF2_m3	13	-	18386658	18386677	CTGTCGGGCACGTGAGTGAA
SLC5A9-m1	8	+	23338720	23338739	GTGCACCAAAGTCCAGTGTG
SLC5A9-m2	8	-	23338930	23338949	AATCAAATGCTGTCCCAAGC
SLC5A9-m3	8	-	23339259	23339281	AGACCTCCATAAAGCAACATGAA
ENS21810-m1	4	+	89601622	89601641	GGTTCCTTGCCTGGAAGAAT
ENS21810-m2	4	-	89601882	89601904	TGTCTCAGGAACGCATTAAGTTT
ENS21810-m3	4	-	89649771	89649792	TGTTAGTGATGCTGCTGCTACC
GHR-m1	Z	+	12988153	12988172	CTTGGAGCTTCAATGGCAGA
GHR-m2	Z	-	12988324	12988346	AAGAATTGCTACGGCATGATTTT
GHR-m3	Z	-	12990169	12990192	GTCGGGACAGATCAAAGACAATAC
SH3RF2 expression primers					
chSH3RF2E1.196.F	13	+	18362724	18362743	AACCTGCTGCTCATCCGTCT
chSH3RF2E1.266.R	13	-	18362778	18362794	TGCATGGAGCCAAAGCG
chSH3RF2E25.249.F	13	+	18373419	18373438	CGACTGCCTGTCATTCCACA
chSH3RF2E25.309.R	13	-	18374975	18374995	GTTGCCATCGACTCTGCTGAT

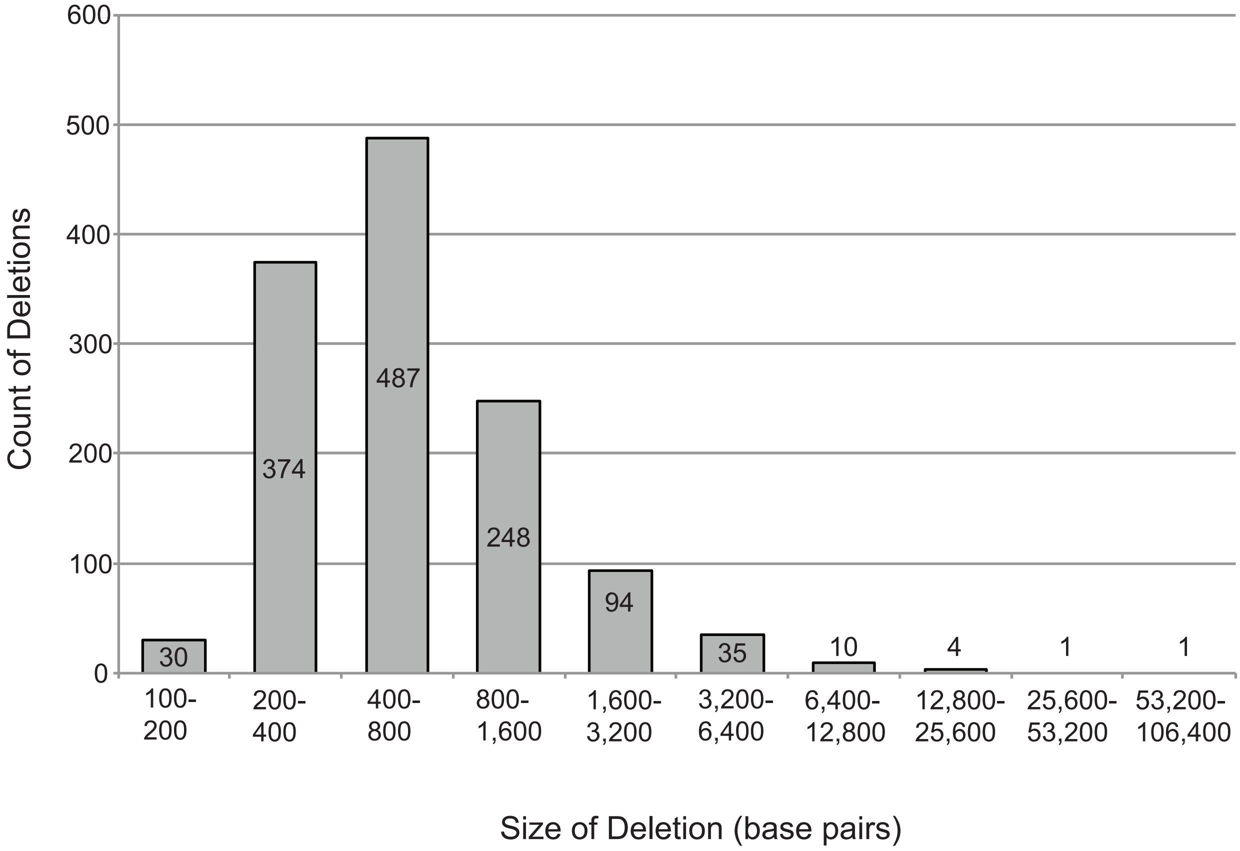
Supplementary figures



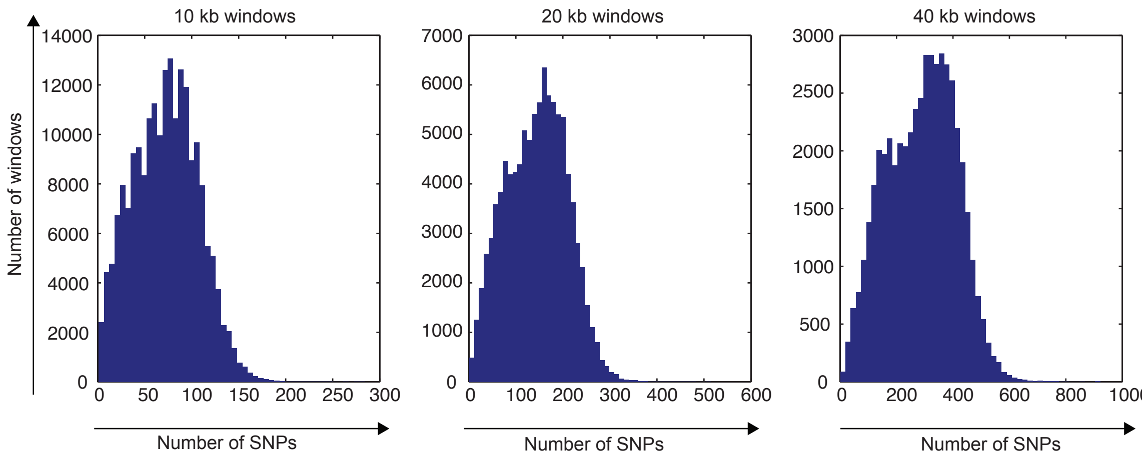
Supplementary Fig. 1
Histogram showing percentage of variant sites on chromosome Z when resequencing the single red junglefowl female used to establish the chicken reference genome sequence. The number of SNP sites in each category (reference only, both nucleotides or non-reference only) are plotted according to the base quality of the assembled base. Sites where only non-reference alleles were observed are highly biased towards low assembly quality, suggesting that these are mostly reference genome errors rather than errors in the SOLiD SNP calling. The small number of sites showing both alleles have more evenly distributed quality scores (the majority of the bases in the assembly have very high quality) and likely result from duplications which are not represented in the reference, rather than single base errors.



Supplementary Fig. 2
Phylogenetic tree based on FST at SNP sites from resequencing. Note that the long branches to OS and the single RJF reference bird represent the reduced heterozygosity in these lines due to inbreeding. Reduced heterozygosity is associated with long branches because FST values increase as a function of the inbreeding coefficient, a larger proportion of the genetic diversity is then distributed between populations.



Supplementary Fig. 3
Distribution of the size of deletions detected in chicken using whole genome resequencing.



Supplementary Fig. 4   SNP coverage depending on size of sliding window
Distributions of SNP numbers observed in 10 kb-, 20 kb- and 40 kb sliding windows along chicken chromosomes 1–28. Only a small fraction of 40 kb windows contain very low numbers of SNPs, whereas the corresponding fractions are increasingly higher for 20 kb and 10 kb sizes.