Supplementary Figure 4.

Gene	Accession	Length	E-Value	Score	Overlap (Shown In Red)
progesterone receptor (PGR)	NM_000926	19	0.002	38.2	5' – TT GCU GUC UGG CCA GUC CAC A – 3' 3' – CGA CAG ACC GGU CAG GUG U TT – 5'
ataxin 2 (ATXN2)	NM_002973	15	0.44	30.2	5' – TT GCU GUC UGG CCA GUC CAC A – 3' 3' – CGA CAG ACC GGU CAG GUG U TT – 5'
unc-13 homolog D	NM_199242	14	1.7	28.2	5' – TT GCU GUC UGG CCA GUC CAC A – 3' 3' – CGA CAG ACC GGU CAG GUG U TT – 5'
family with sequence similarity 83, member G (FAM83G)	NM_001039999	14	1.7	28.2	5' – TT GCU GUC UGG CCA GUC CAC A – 3' 3' – CGA CAG ACC GGU CAG GUG U TT – 5'
apoptotic chromatin condensation inducer 1 (ACIN1),	NM_014977	14	1.7	28.2	5' – TT GCU GUC UGG CCA GUC CAC A – 3' 3' – CGA CAG ACC GGU CAG GUG U TT – 5'
chromosome 8 open reading frame 13 (C8orf13)	NM_053279	14	1.7	28.2	5' – TT GCU GUC UGG CCA GUC CAC A – 3' 3' – CGA CAG ACC GGU CAG GUG U TT – 5'
microtubule associated monoxygenase, calponin and LIM domain containing 1 (MICAL1)	NM_022765	14	1.7	28.2	5' – TT GCU GUC UGG CCA GUC CAC A – 3' 3' – CGA CAG ACC GGU CAG GUG U TT – 5'
arachidonate 5-lipoxygenase (ALOX5)[*]	XM_001127464	13	6.9	26.3	5' – TT GCU GUC UGG CCA GUC CAC A – 3' 3' – CGA CAG ACC GGU CAG GUG U TT – 5'

Supplementary Fig. 4 A) Contiguous sequence similarity results of PR11. NCBI's Homo Sapiens RefSeq RNA database (a comprehensive database of non-redundant RNA transcripts) was searched using the Blastn method (a direct nucleotide comparison) for both strands of the PR11 duplex using a word size setting of 7, a nucleotide mismatch penalty of -3, and an expect value cut off value of 1000. The most significant hit was a 19 base exact match to the progesterone receptor promoter with an expect-value (the number of times the sequence in question is expected to occur just by chance when searching a database of size n, n=39,240 for RefSeq RNA) of 0.002. The next hit was only 15 bases long and had an Expect-value of 0.44. All additional hits were 14 bases or less in length and received Expect-values of 1.7 and above.

Supplementary Figure 4 (cont).

Gene	Accession	Length	MM	E-Value	Overlap (Shown In Red)
progesterone receptor (PGR)	NM_000926	19	0	0.11	5' – GCU GUC UGG CCA GUC CAC A TT – 3' 3' – TT CGA CAG ACC GGU CAG GUG U – 5'
tubulin, alpha 1 (TUBA1)	NM_006000.1	19	2	8.6	5' – GCU GUC UGG CCA GUC CAC A TT – 3' 3' – TT CGA CAG ACC CAG CAG GUG U – 5'
similar to potassium channel tetramerisation domain containing 1 (LOC389768)	XR_017025.1	19	2	8.6	5' – GCU GUC UGG CCA GUC CAC A TT – 3' 3' – TT CGA CAG ACC GGU CAG GUG U – 5'
similar to Aldose reductase (AR) (Aldehyde reductase) (LOC390482)	XR_018461.1	19	3	77	5' – GCU GUC UGG CCA GUC CAC A TT – 3' 3' – TT CGA CAG ACC GGU CAG GUG U – 5'
T-cell lymphoma invasion and metastasis 2 (TIAM2),	NM_012454.3	19	3	77	5' – GCU GUC UGG CCA GUC CAC A TT – 3' 3' – TT CGA CAG ACC GGU CAG GUG U – 5'
receptor-interacting serine-threonine kinase 3 (RIPK3)	NM_006871.3	19	3	77	5' – GCU GUC UGG CCA GUC CAC A TT – 3' 3' – TT CGA CAG ACC GGU CAG GUG U – 5'
SH3 and PX domains 2A (SH3PXD2A)	NM_014631.2	19	3	77	5' – GCU GUC UGG CCA GUC CAC A TT – 3' 3' – TT CGA CAG ACC GGU CAG GUG U – 5'
thioredoxin reductase 1 (TXNRD1)	NM_003330.2	19	3	77	5' – GCU GUC UGG CCA GUC CAC A TT – 3' 3' – TT CGA CAG ACC GGU CAG GUG U – 5'
nuclear mitotic apparatus protein 1 (NUMA1)	NM_006185.2	19	3	77	5' – GCU GUC UGG CCA GUC CAC A TT – 3' 3' – TT CGA CAG ACC GGU CAG GUG U – 5'
GTP binding protein 1 (GTPBP1)	NM_004286.4	19	3	77	5' – GCU GUC UGG CCA GUC CAC A TT – 3' 3' – TT CGA CAG ACC GGU CAG GUG U – 5'
collagen, type VIII, alpha 2 (COL8A2)	NM_005202.1	19	3	77	5' – GCU GUC UGG CCA GUC CAC A TT – 3' 3' – TT CGA CAG ACC GGU CAG GUG U – 5'

Supplementary Fig. 4 B) **Non-contiguous sequence similarity results of PR11.** NCBI's Homo Sapiens RefSeq RNA database (a comprehensive database of non-redundant RNA transcripts) was searched using the Blastn method (a direct nucleotide comparison) for both strands of the PR11 duplex using a word size setting of 7, a nucleotide mismatch penalty of -1, and an expect value cut off value of 1000. The most significant hit was a 19 base exact match to the progesterone receptor promoter with an expect-value (the number of times the sequence in question is expected to occur just by chance when searching a database of size n, n=39,240 for RefSeq RNA) of 0.11. All additional hits contained two or more mismatches and expect values of 8.6 and above.

Supplementary Figure 4 (cont).

Gene	Accession	Length	E-Value	Score	Overlap (Shown In Red)
progesterone receptor (PGR)	NM_000926	19	0.002	38.2	5' – GUU GUU AGA AAG CUG UCU G TT – 3' 3' – TT CAA CAA UCU UUC GAC AGA C – 5'
metastasis associated lung adenocarcinoma transcript 1 (non-coding RNA) (MALAT1)	NR_002819.1	15	1.5	30.2	5' – GUU GUU AGA AAG CUG UCU G TT – 3' 3' – TT CAA CAA UCU UUC GAC AGA C – 5'
inter-alpha (globulin) inhibitor H5 (ITIH5)	NM_030569.3	14	1.5	28.2	5' – GUU GUU AGA AAG CUG UCU G TT – 3' 3' – TT CAA CAA UCU UUC GAC AGA C – 5'
calsequestrin 2 (cardiac muscle) (CASQ2)	NM_001232.1	14	1.7	28.2	5' – GUU GUU AGA AAG CUG UCU G TT – 3' 3' – TT CAA CAA UCU UUC GAC AGA C – 5'
coiled-coil domain containing 100 (CCDC100)	NM_153223.2	13	5.7	26.3	5' – GUU GUU AGA AAG CUG UCU G TT – 3' 3' – TT CAA CAA UCU UUC GAC AGA C – 5'

Supplementary Fig. 4 C) **Contiguous sequence similarity results of PR22.** NCBI's Homo Sapiens RefSeq RNA database (a comprehensive database of non-redundant RNA transcripts) was searched using the Blastn method (a direct nucleotide comparison) for both strands of the PR22 duplex using a word size setting of 7, a nucleotide mismatch penalty of -3, and an expect value cut off value of 1000. The most significant hit was a 19 base exact match to the progesterone receptor promoter with an expect-value (the number of times the sequence in question is expected to occur just by chance when searching a database of size n, n=39,240 for RefSeq RNA) of 0.002. The next hit was only 15 bases long and had an Expect-value of 1.5. All additional hits were 14 bases or less in length and received Expect-values of 1.5 and above.

Supplementary Figure 4 (cont.)

Gene	Accession	Length	MM	E-Value	Overlap (Shown In Red)
progesterone receptor (PGR)	NM_000926.3	19	0	0.11	5' – GUU GUU AGA AAG CUG UCU G TT – 3' 3' – TT CAA CAA UCU UUC GAC AGA C – 5'
transcription factor 12 (HTF4, helix-loop-helix transcription factors 4) (TCF12)	NM_003205.3	19	3	77	5' – GUU GUU AGA AAG CUG UCU G TT – 3' 3' – TT CAA CAA UCU UUC GAC AGA C – 5'
HIV-1 Rev binding protein (HRB)	NM_004504.3	19	3	77	5' – GUU GUU AGA AAG CUG UCU G TT – 3' 3' – TT CAA CAA UCU UUC GAC AGA C – 5'
glycosyltransferase 1 domain containing 1 (GLT1D1)	NM_144669.1	19	3	77	5' – GUU GUU AGA AAG CUG UCU G TT – 3' 3' – TT CAA CAA UCU UUC GAC AGA C – 5'
carboxypeptidase A6 (CPA6)	NM_020361.2	19	3	77	5' – GUU GUU AGA AAG CUG UCU G TT – 3' 3' – TT CAA CAA UCU UUC GAC AGA C – 5'
leucine rich repeat transmembrane neuronal 2 (LRRTM2)	NM_015564.1	19	3	77	5' – GUU GUU AGA AAG CUG UCU G TT – 3' 3' – TT CAA CAA UCU UUC GAC AGA C – 5'
low density lipoprotein-related protein 2 (LRP2)	NM_004525.1	19	3	77	5' – GUU GUU AGA AAG CUG UCU G TT – 3' 3' – TT CAA CAA UCU UUC GAC AGA C – 5'

Supplementary Fig. 4 D) **Non-contiguous sequence similarity results of PR22.** NCBI's Homo Sapiens RefSeq RNA database (a comprehensive database of non-redundant RNA transcripts) was searched using the Blastn method (a direct nucleotide comparison) for both strands of the PR22 duplex using a word size setting of 7, a nucleotide mismatch penalty of -1, and an expect value cut off value of 1000. The most significant hit was a 19 base exact match to the progesterone receptor promoter with an expect-value (the number of times the sequence in question is expected to occur just by chance when searching a database of size n, n=39,240 for RefSeq RNA) of 0.11. All additional hits contained three or more mismatches and expect values of 77 and above.

Gene	Accession	Length	MM
progesterone receptor (PGR)	NM_000926	19	0

Supplementary Fig. 4 E) Common Blast results of PR11 and PR22. NCBI's Homo Sapiens RefSeq RNA database (a comprehensive database of non-redundant RNA transcripts) was searched using the Blastn method (a direct nucleotide comparison) for both strands of the PR11 and PR22 duplexes using a word size setting of 7, a nucleotide mismatch penalty of -1, and an expect value cut off value of 1000. The only common hit was the 19 base exact match to the progesterone receptor promoter.