

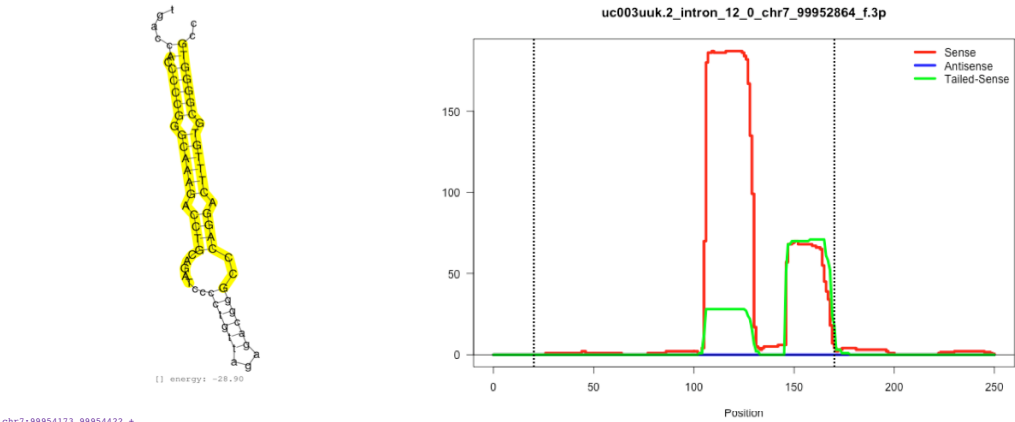
Supplemental Figure S3.

Results of control mirtron annotations run genomewide using intron coordinates shifted 30 nt upstream in human and mouse. The first locus shows the only hit amongst 453,367 "shifted" human intron termini, resident in an intron of *PILRB*. This locus might simply represent an intronic canonical miRNA, but its lack of "lower stem" basepairing may potentially suggest it as an endo-shRNA.

The second locus shows the one of the hits from 358,228 "shifted" intron termini in mouse, resident in *Pdgfra*. The annotated splice site is highly conserved across vertebrates, but curiously the 3' end of the dominant 3p reads end in CAGt, where the terminal nucleotide is untemplated; otherwise CAG terminating reads are the next most-abundant. We speculate that these shifted coordinates fortuitously uncover a cryptic intron that happens to generate a mirtron.

The only other hit from the mouse shifted introns is located in abParts. The annotated splice acceptor is not a canonical signal, terminating in TGG. Curiously, the shifted locus corresponds to a straight hairpin that generates precise miRNA/star reads, for which the 3' end of the 3p species terminate in the vicinity of a CAG sequence. In fact, a spliced EST (CN661462) supporting its precise usage as a functional splice site has been sequenced. We infer that this mirtron was generated by splicing of CN661462, followed by trimming of the 3' terminal nucleotide; note that CAG and CAGt reads were also recorded.

ID: uc003uuk.2_intron_12_0_chr7_99952864_f.3p SPECIES: hg19



chr7:99954173_99954422 +

☒ (3) AGO-IP

☐ (7) BRAIN

☐ (12) CELL_LINE

☐ (2) UICER

☐ (1) URUSA

☐ (89) OTHER

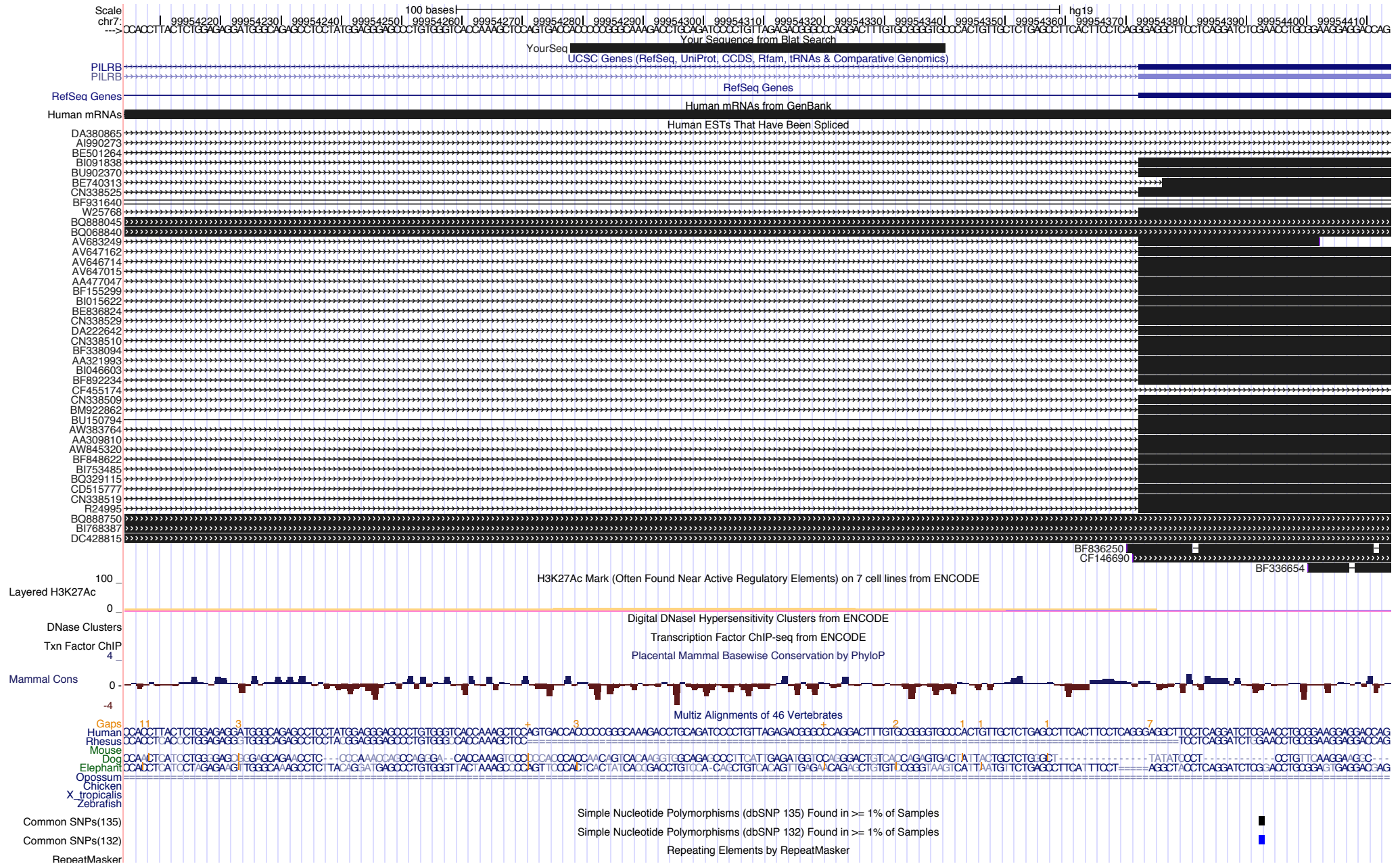
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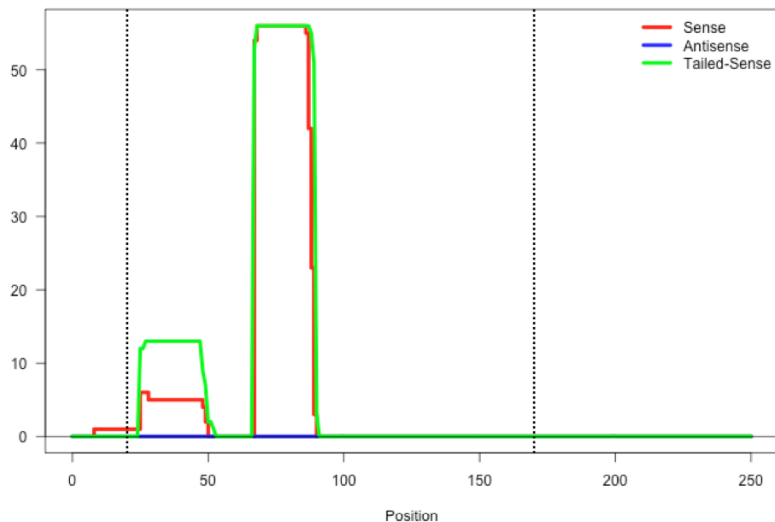
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Sense strand									
Sequence	Size	Perfect hit	Total Norm	Perfect Norm	SRX207113 (ENSEMBL) (Ago1-IP Ago2-IP RNA-Seq)	SRX207114 (ENSEMBL) (Ago1-IP Ago2-IP RNA-Seq)	SRX207115 (ENSEMBL) (Ago1-IP Ago2-IP RNA-Seq)	SRX207116 (ENSEMBL) (Ago1-IP Ago2-IP RNA-Seq)	SRX207117 (ENSEMBL) (Ago1-IP Ago2-IP RNA-Seq)
.....102.....170.....	24	1	63.00	63.00	1.00	0.00	0.00	0.00	0.00
.....ACCCCGGGCAAGACCTGCAAT.....	23	1	22.00	22.00	0.00	0.00	0.00	0.00	0.00
.....CACCCCGGGCAAGACCTGCAAG.....	23	1	19.00	19.00	0.00	0.00	0.00	0.00	0.00
.....ACCCCGGGCAAGACCTGCAAG.....	24	1	17.00	17.00	0.00	0.00	0.00	0.00	0.00
.....CACCCCGGGCAAGACCTGCAAG.....	24	1	15.00	15.00	0.00	0.00	0.00	0.00	0.00
.....CACCCCGGGCAAGACCTGCAAG.....	22	1	15.00	15.00	3.00	0.00	0.00	0.00	0.00
.....GCCCGAGCTTTGTGCGGGTGC.....	23	t	12.00	15.00	0.00	0.00	0.00	0.00	0.00
.....ACCCCGGGCAAGACCTGCAAG.....	22	1	10.00	10.00	3.00	1.00	0.00	0.00	0.00
.....CACCCCGGGCAAGACCTGCAAG.....	22	1	9.00	9.00	0.00	0.00	0.00	0.00	0.00
.....GCCCGAGCTTTGTGCGGG.....	19	1	9.00	9.00	0.00	0.00	0.00	0.00	0.00
.....CACCCCGGGCAAGACCTGCAAG.....	18	1	8.00	8.00	0.00	0.00	0.00	0.00	0.00
.....ACCCCGGGCAAGACCTGCAAG.....	25	1	8.00	8.00	0.00	0.00	0.00	0.00	0.00
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.....GCCCGAGCTTTGTGCGGGT.....	20	t	7.00	9.00	0.00	0.00	0.00	0.00	0.00
.....GCCCGAGCTTTGTGCGGGTGC.....	22	t	7.00	2.00	0.00	0.00	0.00	0.00	0.00
.....GCCCGAGCTTTGTGCGGG.....	20	1	5.00	5.00	0.00	0.00	0.00	0.00	0.00
.....GCCCGAGCTTTGTGCGGGT.....	21	1	5.00	5.00	0.00	0.00	0.00	0.00	0.00
.....GCCCGAGCTTTGTGCGGGTGC.....	25	aa	5.00	7.00	0.00	0.00	0.00	0.00	0.00
.....GCCCGAGCTTTGTGCGGGTGC.....	22	1	4.00	4.00	0.00	0.00	0.00	0.00	0.00
.....ACCCCGGGCAAGACCTGCAAG.....	24	a	4.00	19.00	0.00	0.00	0.00	0.00	0.00
.....ACCCCGGGCAAGACCTGCAAG.....	21	1	4.00	4.00	0.00	0.00	0.00	0.00	0.00
.....CACCCCGGGCAAGACCTGCAAG.....	26	t	3.00	17.00	0.00	0.00	0.00	0.00	0.00
.....GCCCGAGCTTTGTGCGGGTGC.....	22	aaa	3.00	9.00	0.00	0.00	0.00	0.00	0.00
.....CACCCCGGGCAAGACCTGCAAG.....	24	at	3.00	4.00	0.00	0.00	0.00	0.00	0.00
.....GCCCGAGCTTTGTGCGGGTGC.....	25	a	3.00	15.00	0.00	0.00	0.00	0.00	0.00
.....GCCCGAGCTTTGTGCGGGTGC.....	20	a	3.00	9.00	0.00	0.00	0.00	0.00	0.00
.....ACCCCGGGCAAGACCTGCAAG.....	24	1	3.00	3.00	0.00	0.00	0.00	0.00	0.00
.....ACCCCGGGCAAGACCTGCAAG.....	25	t	2.00	63.00	0.00	0.00	0.00	0.00	0.00
.....GCCCGAGCTTTGTGCGGGTGC.....	22	1	2.00	2.00	0.00	0.00	0.00	0.00	0.00
.....GCCCGAGCTTTGTGCGGGTGC.....	25	at	2.00	7.00	0.00	0.00	0.00	0.00	0.00
.....CTGTGTAGAGAGGGCCAG.....	20	1	2.00	2.00	0.00	0.00	0.00	0.00	0.00
.....CACCCCGGGCAAGACCTGCAAG.....	23	1	2.00	2.00	0.00	0.00	0.00	0.00	0.00
.....ACCCCGGGCAAGACCTGCAAG.....	26	1	2.00	2.00	0.00	0.00	0.00	0.00	0.00
.....GCCCGAGCTTTGTGCGGGTGC.....	23	t	2.00	4.00	0.00	0.00	0.00	0.00	0.00
.....GCCCGAGCTTTGTGCGGGTGC.....	23	ggc	2.00	5.00	0.00	0.00	0.00	0.00	0.00
.....GCCCGAGCTTTGTGCGGGTGC.....	23	1	2.00	2.00	0.00	0.00	0.00	0.00	0.00
.....GCCCGAGCTTTGTGCGGGTGC.....	24	a	2.00	7.00	0.00	0.00	0.00	0.00	0.00
.....ACCCCGGGCAAGACCTGCAAG.....	19	1	2.00	2.00	0.00	0.00	0.00	0.00	0.00
.....GCCCGAGCTTTGTGCGGGTGC.....	21	1	2.00	2.00	0.00	0.00	0.00	0.00	0.00
.....ACCCCGGGCAAGACCTGCAAG.....	27	tt	1.00	8.00	0.00	0.00	0.00	0.00	0.00
.....ACCCCGGGCAAGACCTGCGAAG.....	24	cgaa	1.00	1.00	0.00	0.00	0.00	0.00	0.00
.....GCCCGAGCTTTGTGCGGGTGC.....	23	tcat	1.00	1.00	0.00	0.00	0.00	0.00	0.00
.....CACCCCGGGCAAGACCTGCAAG.....	23	a	1.00	9.00	0.00	0.00	0.00	0.00	0.00
.....CACCCCGGGCAAGACCTGCAAG.....	26	1	1.00	1.00	0.00	0.00	0.00	0.00	0.00
.....CTGTGTAGAGAGGGCCAG.....	20	1	1.00	1.00	0.00	0.00	0.00	0.00	0.00
.....GCCCGAGCTTTGTGCGGGTGC.....	30	1	1.00	1.00	0.00	1.00	0.00	0.00	0.00
.....ACCCCGGGCAAGACCTGCAAG.....	27	a	1.00	2.00	0.00	0.00	0.00	0.00	0.00
.....GCCCGAGCTTTGTGCGGG.....	19	1	1.00	1.00	0.00	0.00	0.00	0.00	0.00
.....ACCCCGGGCAAGACCTGCAAG.....	20	1	1.00	1.00	0.00	0.00	0.00	0.00	0.00
.....GCCCGAGCTTTGTGCGGGTGC.....	20	1	1.00	1.00	0.00	0.00	0.00	0.00	0.00
.....CTGTGTAGAGAGGGCCAG.....	20	cg	1.00	0.00	0.00	0.00	0.00	0.00	0.00
.....GCCCGAGCTTTGTGCGGGTGC.....	32	1	1.00	1.00	0.00	0.00	0.00	0.00	0.00
.....GCCCGAGCTTTGTGCGGGTGC.....	21	aga	1.00	8.00	0.00	0.00	0.00	0.00	0.00
.....GCCCGAGCTTTGTGCGGGTGC.....	22	t	1.00	5.00	0.00	0.00	0.00	0.00	0.00
.....CCTGTGGGTCAACAAAGCTCAGAT.....	25	1	1.00	1.00	0.00	0.00	0.00	0.00	0.00
.....CACCCCGGGCAAGACCTGCAAG.....	22	ggct	1.00	0.00	0.00	0.00	0.00	0.00	0.00
.....CACCCCGGGCAAGACCTGCAAG.....	21	t	1.00	0.00	0.00	0.00	0.00	0.00	0.00
.....CACCCCGGGCAAGACCTGCAAG.....	23	t	1.00	10.00	0.00	0.00	0.00	0.00	0.00

[illegible]

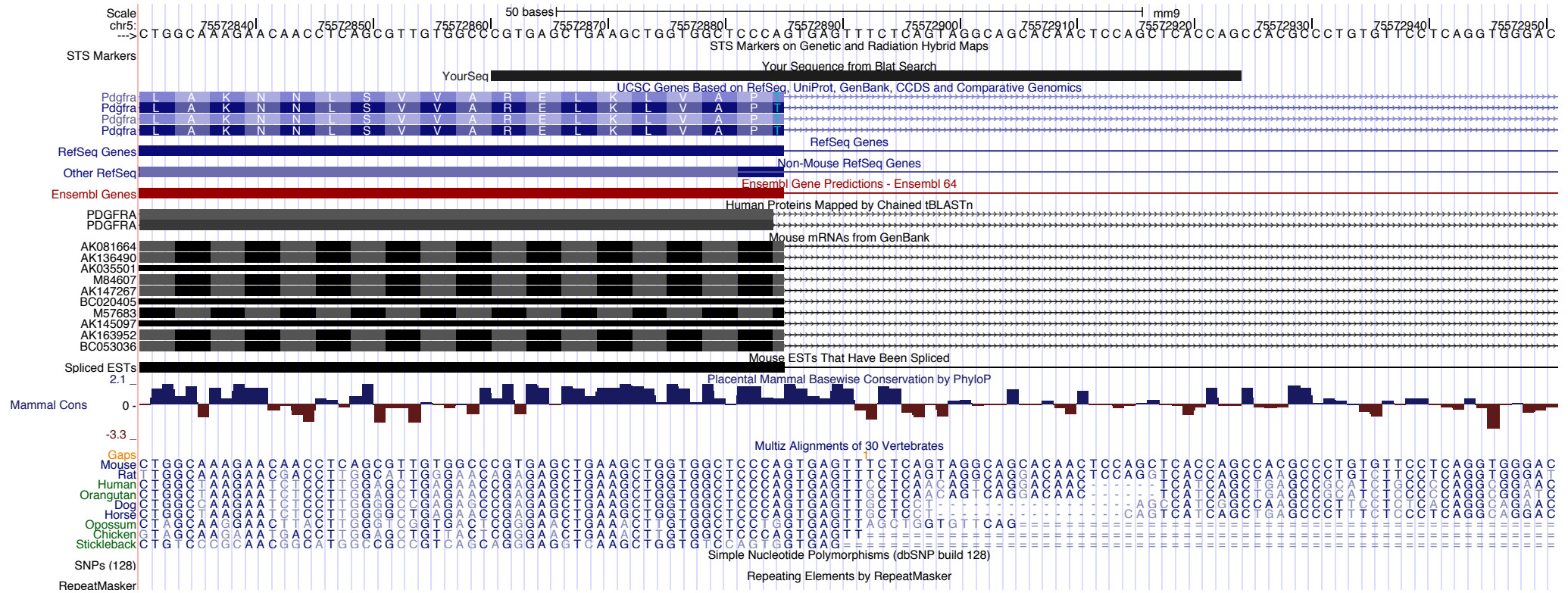


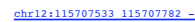
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☐ (5) ☐ (1) ☐ (2) ☐ (1) ☐ (14) ☐ (12) ☐ (1) ☐ (3) ☐ (6)
 BRAIN CELL_LINE CTRL DGCR8(-) EMBRYO OTHER OVARY PIWI-IP TESTES

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Antisense strand

2 of 2

