

Supplementary Figures and Tables

Supplementary Figure 1 Distribution of the distance between the predicted NRSE sites and their the nearest genes. The distance is measured by the number of nucleotides located between a NRSE site and the transcriptional start site of its corresponding gene. Negative numbers indicate that NRSE sites are located upstream of the genes.

Supplementary Figure 2 A list of identified NRSE target genes that are specifically expressed in brain-related tissues. Each row represents the normalized expression levels of a gene across 61 mouse tissues. Please see the Methods section on how the expression values are normalized and on how the genes are selected.

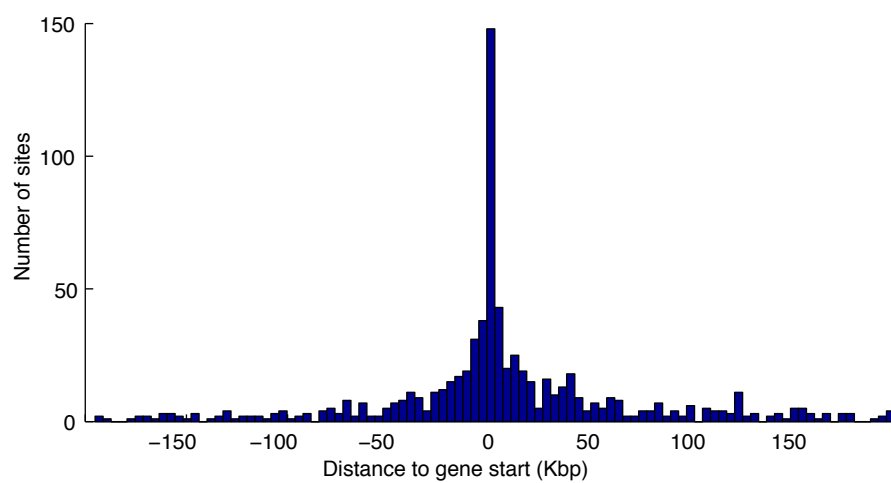
Supplementary Figure 3 Gene expression of the predicted miRNA targets in 61 mouse tissues. (A), (B) and (C) show the expression of predicted targets for miR-124a, miR-132, and miR-9 respectively. Note that only a subset of genes that are specifically expressed in brain-related tissues is shown. The expression for all target genes is provided in the supplementary website. The expression values are normalized such that the mean expression values for each gene across different tissues is zero and standard deviation is 1. Please see the Methods section on the analysis of gene expression data and how the brain-related genes are selected.

Supplementary Figure 4 Conservation and EST evidences support a longer *REST* 3'UTR transcript. Shown are the annotations in this region from the UCSC genome browser. The predicted new 3'UTR is highlighted in yellow. Note that this region is packed with human ESTs, highly conserved even with chicken, and have few transposable elements.

Supplementary Figure 5 Expression of protein-coding genes hosting miRNAs in their introns. The expression for each gene is measured across 61 mouse tissues. The gene *Slit3* is expressed at relative high level in amygdala, but with even much higher expression in fertilized egg. *Slit3* is known to play a key role in the neural development, especially for the development of cranial motoneurons. It is possible that its high expression in fertilized egg might reflect its particular role implicated in neural development.

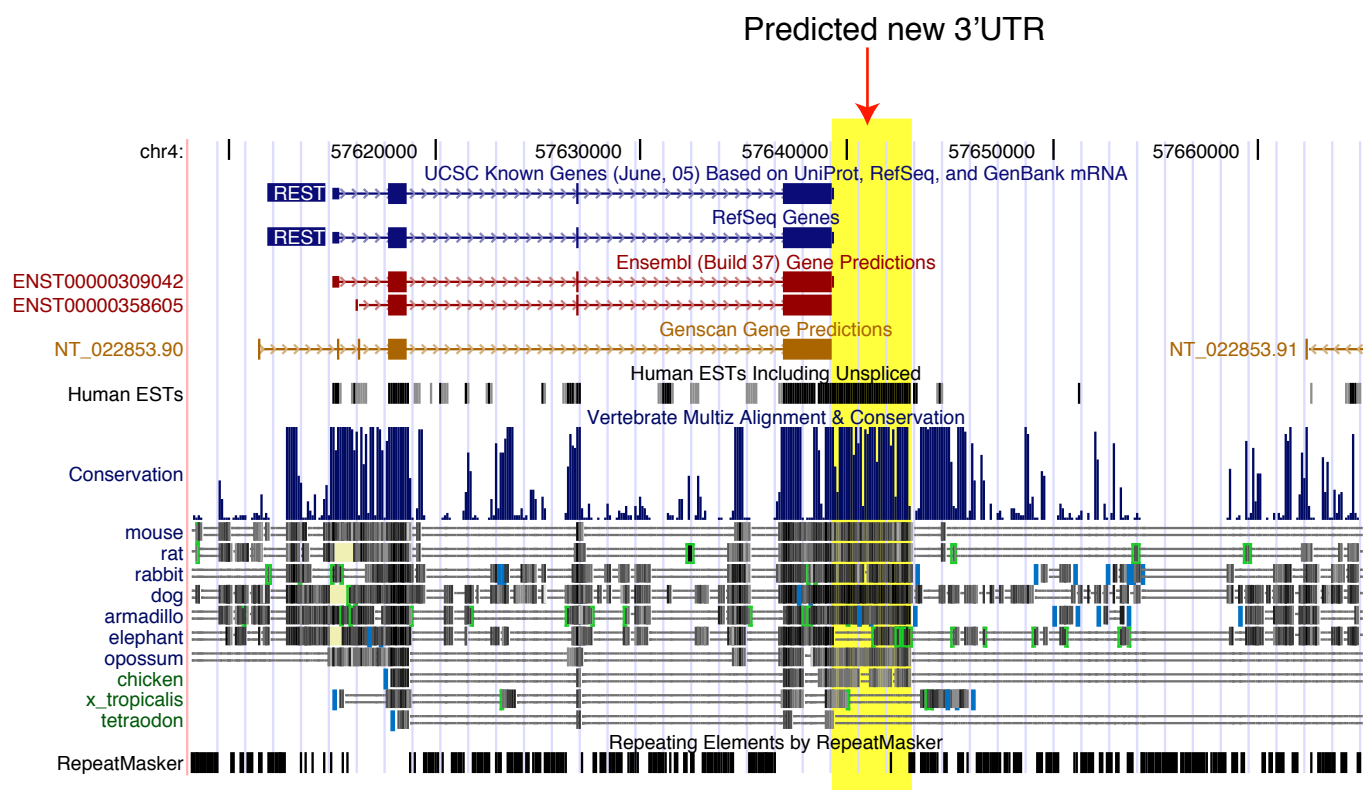
Supplementary Figure 6 Expression of 160 genes across different mouse tissues ordered by log-odds score of their corresponding NRSE sites.

Supplementary Table 1 A list of known NRSE sites and their conservation properties.

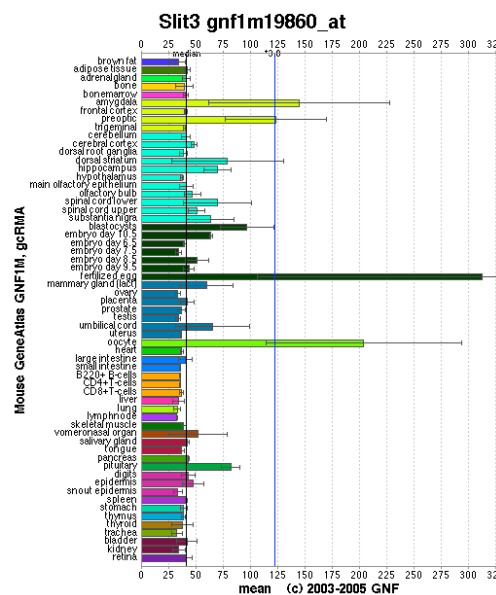
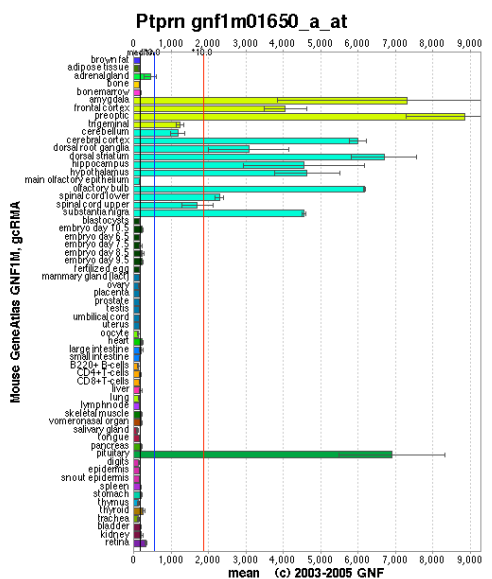
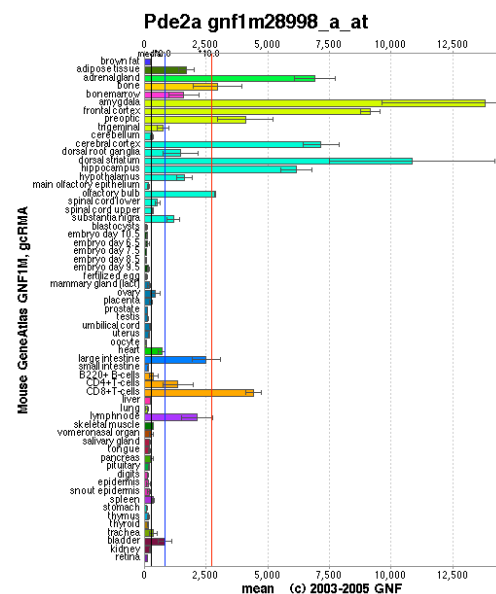
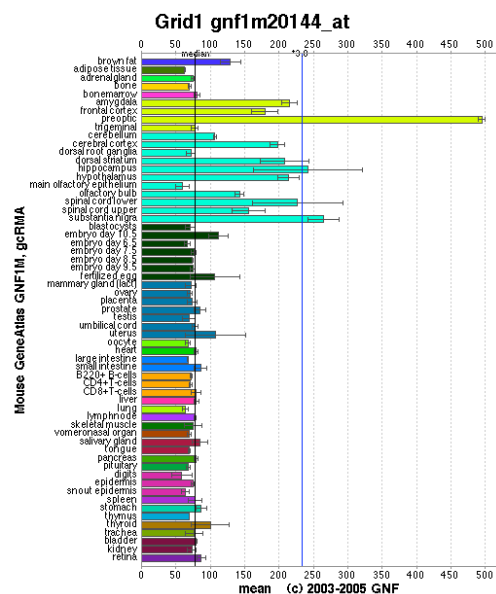
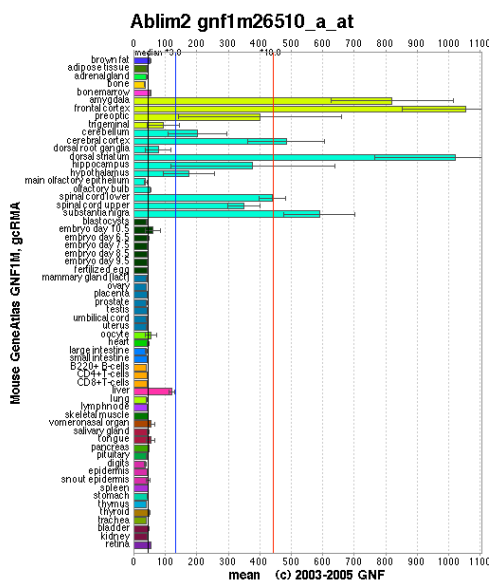


Supplementary Figure 1

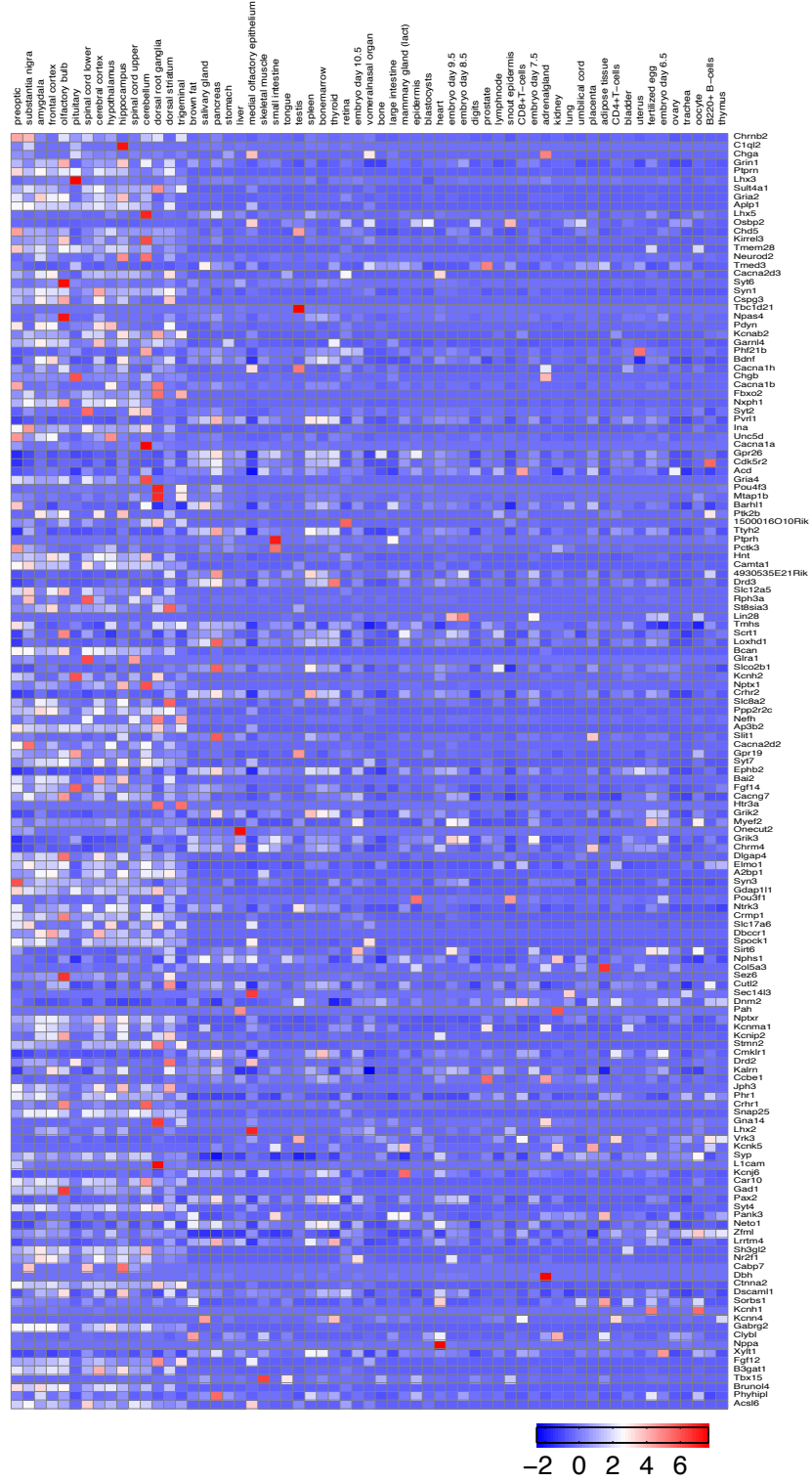




Supplementary Figure 4



Supplementary Figure 5



Supplementary Figure 6

Supplementary Table 1 A list of known RE1/NRSE sites and their conservation properties in human/mouse/rat/dog

Sequence	Mutation in the first 17 bases	Mutation in positions 1 to 8 and 11 to 16	Difference from NRSE consensus	Log-odds score	Genome coordinates and strand
>nrse_chr11_27698819_m BDNF					
TTCAGCACCTTGGACAGAGCC	0	0	0	31.4	hg17.chr11:27698799-27698819,-
TTCAGCACCTTGGACAGAGCC	0	0	0	31.6	mm5.chr2:109567568-109567588,+
TTCAGCACCTTGGACAGAGCC	0	0	0	31.6	rn3.chr3_random:930771-930791,+
TTCAGCACCTTGGACAGAGCC	0	0	0	31.4	canFam1.chr21:50514521-50514541,-
>nrse_chr8_80684341_p STMN2					
TTCAGCACCAAGGAGAGTGCC	0	0	0	27.9	hg17.chr8:80684341-80684361,+
TTCAGCACCAAGGAGAGTGCC	2	1	0	33.8	mm5.chr3:8544331-8544351,+
TTCAGCACCAAGGAGAGTGCC	1	0	0	30.0	rn3.chr2:95279221-95279241,-
TTCAGCACCAAGGAGAGTGCC	0	0	0	27.9	canFam1.chr29:30067518-30067538,+
>nrse_chr2_165920501_p SCN2A2					
CTCAGCACCATGGACAGCGTT	0	0	0	27.4	hg17.chr2:165920501-165920521,+
TTCAGCACCAAGGAGAGTGCC	2	0	0	34.0	mm5.chr2:65558600-65558620,+
TTCAGCACCAAGGAGAGTGCC	3	1	0	30.5	rn3.chr3:47483668-47483688,+
TTCAGCACCAAGGAGAGTGCC	2	0	0	31.1	canFam1.chr36:13584742-13584762,+
>nrse_chrX_152661866_m L1CAM					
GTCAGCACCATGGACAGGGAC	0	0	1	23.9	hg17.chrX:152661846-152661866,-
GTCAGCACCATGGACAGGGAC	1	1	0	26.6	mm5.chrX:65427921-65427941,-
GTCAGCACCATGGACAGGGAC	1	1	0	26.6	rn3.chrX:159876613-159876633,-
gTCAGCACCATGGACAGGGAC	2	1	0	25.9	canFam1.chrX:124778187-124778207,-
>nrse_chrX_152661824_m L1CAM					
TTCAGCACCAAGGAGAGTGCC	0	0	0	27.6	hg17.chrX:152661804-152661824,-
TTCAGCACCAAGGAGAGTGCC	2	1	1	25.0	mm5.chrX:65427891-65427911,-
TTCAGCACCAAGGAGAGTGCC	3	2	2	19.8	rn3.chrX:159876580-159876600,-
TTCAGCACCAAGGAGAGTGCC	2	1	1	26.1	canFam1.chrX:124778158-124778178,-
>nrse_chr20_10148269_p SNAP25					
CTCAGCACCATGGACAGGGAC	0	0	1	21.1	hg17.chr20:10148269-10148289,+
CTCAGCACCATGGACAGGGAC	1	1	0	23.0	mm5.chr2:136463311-136463331,+
CTCAGCACCATGGACAGGGAC	1	1	0	23.0	rn3.chr3:124712985-124713005,+
GTCAGCACCATGGACAGGGAC	2	1	0	25.8	canFam1.chr24:15095171-15095191,-
>nrse_chr20_10148320_p SNAP25					
TTCAGCACCAAGGAGAGTGCC	0	0	0	27.7	hg17.chr20:10148320-10148340,+
TTCAGCACCAAGGAGAGTGCC	1	0	0	31.3	mm5.chr2:136463361-136463381,+
TTCAGCACCAAGGAGAGTGCC	1	0	0	31.3	rn3.chr3:124713035-124713055,+
TTCAGCACCAAGGAGAGTGCC	2	1	0	29.7	canFam1.chr24:15095120-15095140,-
>nrse_chr9_137309549_p GRIN1					
TTCAGCACCAAGGAGAGTGCC	0	0	0	34.5	hg17.chr9:137309549-137309569,+
TTCAGCACCAAGGAGAGTGCC	1	0	0	32.4	mm5.chr2:25279036-25279056,-
TTCAGCACCAAGGAGAGTGCC	1	0	0	30.0	rn3.chr3:3480288-3480308,-
TTCAGCACCAAGGAGAGTGCC	0	0	0	34.5	canFam1.chr9:41044966-41044986,-
>nrse_chr5_151284508_p GLRA1					
TTCAGCACCAAGGAGAGTGCC	0	0	0	29.9	hg17.chr5:151284508-151284528,+
TTCAGCACCAAGGAGAGTGCC	0	0	0	30.2	mm5.chr11:55247677-55247697,+
TTCAGCACCAAGGAGAGTGCC	0	0	0	30.2	rn3.chr10:41035413-41035433,+
TTCAGCACCAAGGAGAGTGCC	0	0	0	29.9	canFam1.chr4:60614365-60614385,-
>nrse_chr1_151353503_p CHRN2					
TTCAGCACCAAGGAGAGTGCC	0	0	0	35.4	hg17.chr1:151353503-151353523,+
TTCAGCACCAAGGAGAGTGCC	0	0	0	33.8	mm5.chr3:90189446-90189466,-
TTCAGCACCAAGGAGAGTGCC	0	0	0	33.8	rn3.chr2:181919553-181919573,-
TTCAGCACCAAGGAGAGTGCC	1	0	0	34.5	canFam1.chr7:45410505-45410525,-
>nrse_chr8_91164252_m CALB1					
AGCAGCACCAAGGAGAGTGCC	0	0	1	25.2	hg17.chr8:91164232-91164252,-
AGCAGCACCAAGGAGAGTGCC	1	0	1	27.6	mm5.chr4:15808391-15808411,+
AGCAGCACCAAGGAGAGTGCC	1	0	1	27.6	rn3.chr5:30455674-30455694,+
CTCAGCACCAAGGAGAGTGCC	2	1	0	28.0	canFam1.chr29:38572206-38572226,-
>nrse_chr1_11840056_m NPPA					
TTCAGCACCAAGGAGAGTGCC	0	0	0	26.6	hg17.chr1:11840036-11840056,-
TTCAGCACCAAGGAGAGTGCC	1	0	0	26.7	mm5.chr4:145887995-145888015,+
TTCAGCACCAAGGAGAGTGCC	1	0	0	28.6	rn3.chr5:165085986-165086006,+
TTCAGCACCAAGGAGAGTGCC	1	0	0	32.1	canFam1.chr2:86623257-86623277,+
>nrse_chr1_6046932_p KCNAB2					
TTCAGCACCAAGGAGAGTGCC	0	0	0	31.8	hg17.chr1:6046932-6046952,+
TTCAGCACCAAGGAGAGTGCC	2	0	0	30.2	mm5.chr4:150310481-150310501,-
TTCAGCACCAAGGAGAGTGCC	2	0	0	30.2	rn3.chr5:169668695-169668715,-

TTCAGCATCTGGGGCAGCACT	3	2	2	16.4	canFam1.chr5:63032964-63032984,+
>nrse_chr2_219652224_m CDK5R2					
CTCAGCACCTCGGACAGTTCC	0	0	0	26.5	hg17.chr2:219652204-219652224,-
CTCAGCACCTCGGACAATTCC	1	1	1	21.8	mm5.chr1:75317485-75317505,-
CTCAGCACCTCGGACAATTCC	1	1	1	21.8	rn3.chr9:74340946-74340966,-
ATCAGCACCTCAGACAGCTCC	2	1	0	23.5	canFam1.chr37:28510580-28510600,-
>nrse_chr2_219653264_m CDK5R2					
TTCAGCACCAACGGACAGCGAA	0	0	0	30.8	hg17.chr2:219653244-219653264,-
TTCAGCACCAACGGACAGCGAA	0	0	0	31.1	mm5.chr1:75318462-75318482,-
TTCAGCACCAACGGACAGCGAA	0	0	0	31.1	rn3.chr9:74341934-74341954,-
ATCAGCACCAACGGACAGCGAA	1	0	0	28.0	canFam1.chr37:28511567-28511587,-
>nrse_chr19_19186936_p CSPG3					
TTCAGCACCAACGGACAGGTCC	0	0	0	32.0	hg17.chr19:19186936-19186956,+
TTCAGCACCAAGGACAGATCG	1	0	0	26.8	mm5.chr8:69152990-69153010,-
TTCAGCACCAAGGACAGGTCC	1	0	0	30.5	rn3.chr16:19788177-19788197,+
TTCAGCACCAACGGATAGGTCC	1	1	1	26.8	canFam1.chr20:46827133-46827153,-
>nrse_chr1_111001541_m KCNA3					
TTCAGCACCAAGGACAGAGAC	0	0	0	30.4	hg17.chr1:111001521-111001541,-
TTCAGCACCATGGACAAGGGT	2	1	1	24.5	mm5.chr3:107342354-107342374,+
TTCAGCACCAAGGACAGGGTG	0	0	0	26.4	rn3.chr2:202353732-202353752,+
TTCAGCACCAAGGACAGAAGC	0	0	0	28.6	canFam1.chr6:42825633-42825653,+
>nrse_chr3_115380519_m DRD3					
TTCAGCACCAAGGACAGAACC	0	0	0	30.2	hg17.chr3:115380499-115380519,-
CTCAGCACCAAGGACAGAGAG	1	0	0	24.1	mm5.chr16:43630422-43630442,+
CTCAGCACCAAGGACAGAGAG	1	0	0	24.1	rn3.chr11:58587125-58587145,-
TTCAGCACCAAGGACAGTGCC	0	0	0	31.2	canFam1.chr33:21483747-21483767,-
>nrse_chr9_136322946_m LHX3					
TTCAGCACCGCGGACAGCGCC	0	0	0	34.5	hg17.chr9:136322926-136322946,-
TTCAGCACCGCGGACAGCGCC	0	0	0	35.1	mm5.chr2:26168294-26168314,-
TTCAGCACCGCGGACAGCGCC	0	0	0	35.1	rn3.chr3:4389191-4389211,-
TTCAGCACCGCGGACAGCGCC	0	0	0	34.5	canFam1.chr9:41786607-41786627,+
>nrse_chr12_112380809_m LHX5					
TTCAGCACCGCGGACAGCTCC	0	0	0	32.7	hg17.chr12:112380789-112380809,-
TTCAGCACCGCGGACAGCTCC	0	0	0	33.2	mm5.chr5:117915809-117915829,+
TTCAGCACCGCGGACAGCTCC	0	0	0	33.2	rn3.chr12:37203815-37203835,-
ATCAGCACCGCGGACAGCTCC	1	0	0	29.9	canFam1.chr26:13956517-13956537,-
>nrse_chr13_101369969_p FGF14					
TTCAGCACCGCGGACAGGGAT	0	0	0	29.2	hg17.chr13:101369969-101369989,+
TTCAGCACCGCGGACAGTGAC	0	0	0	30.8	mm5.chr14:116491551-116491571,+
TTCAGCACCGTGAGACAGTGAC	1	0	0	29.9	rn3.chr15:109316548-109316568,+
TTCAGCACCGAGGACAGGGAT	2	1	1	23.3	canFam1.chr22:54512919-54512939,+
>nrse_chr14_92459621_p CHGA					
TTCAGCACCGCGGACAGCGCC	0	0	0	34.5	hg17.chr14:92459621-92459641,+
TTCAGCACCTCGGACAGCACCC	1	0	0	32.4	mm5.chr12:97233700-97233720,+
TTCAGCACCTCGGACAGCACCC	1	0	0	32.4	rn3.chr6:126825403-126825423,+
TTCAGCACCGCGGACAGCGCC	0	0	0	34.5	canFam1.chr8:4944156-4944176,+
>nrse_chr2_219998566_m PTPRN					
TTCAGCACCGCGGACAGCGCC	0	0	0	34.5	hg17.chr2:219998546-219998566,-
TTCAGAACCATGGACAGCGCC	3	1	0	31.5	mm5.chr1:75709818-75709838,-
TTCAGCACCAACGGACAGCATC	2	1	1	27.3	rn3.chr9:74688760-74688780,-
TTCAGCACCGCGGACAGCGCC	0	0	0	34.5	canFam1.chr37:28832304-28832324,-
>nrse_chr5_161428260_p GABRG2					
TTCAGCACCAAGGACAGCAGT	0	0	0	26.9	hg17.chr5:161428260-161428280,+
TTCAGCACCAAGGACAGCGGT	1	0	0	30.3	mm5.chr11:41639386-41639406,-
TTCAGCACCAAGGACAGCGAT	1	0	0	30.2	rn3.chr10:27126446-27126466,-
TTCAGCACCAAGGACAGCAGT	0	0	0	26.9	canFam1.chr4:52070373-52070393,-
>nrse_chr1_11853814_m NPPB					
ATCAGCACCAACGGACAGCGGC	0	0	0	31.0	hg17.chr1:11853794-11853814,-
ATCAGAACCAACGGACAGCTAC	1	1	0	25.9	mm5.chr4:145871317-145871337,+
ATCAGAACCATGGACAGCTAC	2	1	0	25.1	rn3.chr5:165071977-165071997,+
CTCAGCACCAACGGACAGCGGC	1	0	0	30.8	canFam1.chr2:86610700-86610720,+
>nrse_chr1_207301544_p KCNH1					
ATCAGCACCAAGGACAGCATC	0	0	0	24.8	hg17.chr1:207301544-207301564,+
GTCAGCACCTGGACAGCTCC	2	0	0	28.1	mm5.chr1:192353285-192353305,-
GTCAGTACCTGGACAGCATC	3	1	1	20.5	rn3.chr13:108549570-108549590,-
ATCAGCACCTGGACAGAGTG	1	0	0	22.3	canFam1.chr7:11912396-11912416,+
>nrse_chr1_207288522_p KCNH1					
TTCAGAACCATGGACAGTTCC	0	0	0	27.0	hg17.chr1:207288522-207288542,+
TTCAGGACCATGGACAGTTCT	1	1	1	24.2	mm5.chr1:192367627-192367647,-
TTCAGGACCAACGGACAGTGCC	2	1	1	29.0	rn3.chr13:108557186-108557206,-

TTCAGCACCCCTGGACAGTGCC	2	1	0	30.1	canFam1.chr7:11900079-11900099,+
>nrse_chr15_68055979_m	TLE3				
TTCAGAACCATGGACAGAGGC	0	0	0	27.9	hg17.chr15:68055959-68055979,-
TTCAGAACCATGGACAGAGGC	0	0	0	28.1	mm5.chr9:61707118-61707138,+
TTCAGAACCATGGACAGAGGC	0	0	0	28.1	rn3.chr8:65617619-65617639,+
TTCAGAACCATGGACAGAGGC	0	0	0	27.9	canFam1.chr30:36732582-36732602,-
>nrse_chr22_35364989_m	CACNG2				
TTCAGCACCTTGGAGAGCATC	0	0	0	25.8	hg17.chr22:35364969-35364989,-
TTCAGCACCTTGGAGAGCTCC	0	0	0	28.3	mm5.chr15:78393924-78393944,-
TTCAGCACCTTGGAGAGCACC	0	0	0	28.3	rn3.chr7:116018162-116018182,-
TTCAGCACCAAGGAGAGCACC	2	0	0	28.7	canFam1.chr10:30977690-30977710,+
>nrse_chr10_120345766_p	GPR10				
GTCAGCACCCAGGACAGCTTC	0	0	0	28.1	hg17.chr10:120345766-120345786,+
ATCAGCACCCAGGGCAGCTCC	2	1	1	26.6	mm5.chr19:59860036-59860056,+
ATCAGCACCTCGGGCAGCTCC	3	1	1	25.0	rn3.chr1:267281791-267281811,+
TTCAGCACACGGGACAGCTCC	3	1	1	27.0	canFam1.chr28:31995439-31995459,+
>nrse_chr13_77035503_m	SCEL				
TTCAGCACCGTGGACAGGGTT	0	0	0	27.8	hg17.chr13:77035483-77035503,-
TTCAGCACCATGGACAGGCAC	1	0	0	27.7	mm5.chr14:95781930-95781950,-
TTCAGCACCATGGACAGGCAC	1	0	0	27.7	rn3.chr15:87589807-87589827,-
TTCAGCACCGTGGACAGGGTT	0	0	0	27.8	canFam1.chr22:34020238-34020258,-
>nrse_chr22_37545209_m	NPTXR				
TTCAGCACCCCTGGACAGGGCA	0	0	0	27.9	hg17.chr22:37545189-37545209,-
TTCAGCACCCCTGGACAGAGCA	0	0	0	28.2	mm5.chr15:80119289-80119309,-
TTCAGCACCCAGGACAGGGCG	2	0	0	30.7	rn3.chr7:118063259-118063279,-
TTCAGCACCCCTGGACAGGGCA	0	0	0	27.9	canFam1.chr10:29181384-29181404,+
>nrse_chr7_150118828_m	KCNH2				
TTCAGCACCTTGGACAGAGAC	0	0	0	29.8	hg17.chr7:150118808-150118828,-
TTCAGCACCTCGGACAGAGGC	1	0	0	30.9	mm5.chr5:22755639-22755659,-
TTCAGCACCTTGGACAGAGAC	0	0	0	29.9	rn3.chr4:6186606-6186626,+
TTCAGCACCTTGGACAGAGAC	0	0	0	29.8	canFam1.chr16:16883946-16883966,-
>nrse_chr20_5840350_p	CHGB				
GTCAGCACCCGGGACAGCGCC	0	0	0	31.2	hg17.chr20:5840350-5840370,+
TTCAGCACCCCGGACAGCTCC	2	0	0	32.1	mm5.chr2:132530817-132530837,+
TTCAGAACCTCGGACAGCTCC	3	1	0	28.9	rn3.chr3:120477432-120477452,+
ATCAGCACCCGGGACAGCGCT	1	0	0	29.7	canFam1.chr24:18944570-18944590,-
>nrse_chr22_28199238_m	NEFH				
TTCAGCACCGGGGACAGGGCC	0	0	0	29.6	hg17.chr22:28199218-28199238,-
TTCAGCACCCAGGACAGCAGC	2	0	0	32.4	mm5.chr11:4844186-4844206,+
TTCAGAACCATGGACAGCGCC	3	1	0	31.5	rn3.chr14:85625288-85625308,+
TTCAGCACCAAGGACAGGGCC	2	0	0	32.0	canFam1.chr26:25862535-25862555,-
>nrse_chr15_86510797_m	NTRK3				
TTCAGCACCATGGCCAGAGCC	0	0	0	28.5	hg17.chr15:86510777-86510797,-
TTCAGCACCATGGCCAGGGCT	0	0	0	26.9	mm5.chr7:65560136-65560156,-
TTCAGCACCATGGCCAGGGCT	0	0	0	26.9	rn3.chr1:134296513-134296533,-
TTCAGCACCATGGCCAGAGCC	0	0	0	28.5	canFam1.chr3:54375781-54375801,-
>nrse_chr11_61091418_m	SYT7				
TTCAGCACCTTGGACAGCTCT	0	0	0	29.3	hg17.chr11:61091398-61091418,-
TTCAGTACCAAGGCGAGCACC	4	2	2	22.3	mm5.chr19:9502400-9502420,+
TTCAGTACCAAGGCGAGCACC	4	2	2	24.2	rn3.chr1:213048931-213048951,+
TTCAGCACCAAGGACAGATCC	2	0	0	32.0	canFam1.chr18:65203709-65203729,+

Note:

*Known NRSE consensus: NTYAGMRCCNNRGMSAG

*Mutation: the number of nucleotides different from the human sequence

*Aligned sequences are in the order of human, mouse, rat and dog