Scale chr13:	50 bases mm39 48,689,470  48,689,480  48,689,500  48,689,510  48,689,520  48,689,520  48,689,540  48,689,550  48,689,570  48,689,570  48,689,590  48,689,590
PR	CAGAAAGGAAACGTATGCTGGTATAATAAGGCCCTAAGAAAGGCAGGTGCGTATAGTTAACTCCTTGTGGCAAAATCTCTGCCCCTAAAACTATGCAACCTACTACCTCTTCCTAGGAACCCATTTTATTCTTGCTGGTCTTC CKGNVCWYNKALRKAAGGIVNSLWAKKA KAAGGIVNSLWAKSLP <mark>-</mark> NYATYYLFLG FRKETYAGIIRP <mark>-1</mark> ERQQVVV <mark>-1</mark> LTPCGQNLCPKT <mark>M</mark> QQPTITSS
■ K	AERKR <u>M</u> LV GPKKGSRSYS LLV GK SALKLCNLLPLPRNPFYSCWSS User Supplied Track
User Track	Gap Locations GENCODE VM05
6720427I07Rik	Miletral  Miletral
568094/XM 036158292.1	NCBI RefSeq genes, curated and predicted (NM_*, XM_*, NR_*, XR_*, NP_*, YP_*) - Annotation Release NCBI RefSeq GCF_000001635.27-RS_2024_02 (2024-02-08)
	Mirlet74NR_0298561 NCBI RelfSeq genes, curated subset (NM_", NR_", NP_" or YP_") - Annotation Release NCBI RelfSeq GCF_000001635.27-RS_2024_02 (2024-02-08)
	MirleT/dNR_029566.1  UCSC annotations of RefSeq RNAs (NM_" and NR_")
	Mide/7d/NR, 029556  Genscan Gene Predictions  RefSeq mRNAs mapped to this assembly Mouse mRNAs from GenBank
AK042687	MOUSE MINIVAS TROM GENERAK
KY467470 AK160312	
	CoG Islands (Islands < 300 Bases are Light Green)
Cons 35 Verts 4.28 _	35 vertebrates Basewise Conservation by PhyloP
-4.1 _	AA _AA A # FF T-A*GCCCTAAGAAAGGCAGCAGGT-GTATAGTTA CTCCTTGTG+BCAAAATC.CTGCCC+AAAACTATGCAACC+ACTACCTCCTAGGA-CC+A + 4G FCT+-
Gaps	3 1 Multiz Alignments of 35 Vertebrates 3 2
Rat	LABAAAGGAAACGTATGCTGGTATAATAAGGCCCTAAGAAAGGAGCAGGTCGTATAGTTAACTCCTTGTTGGGCCAAAACTATGCACCTACTACCTCTTCCTAGGAACCCATTTTATTCTTGCTGGTCTTC  CAGCAAGGAAACGTATAGCTGGTATGATAAGGCCCTAAGAAAGGCAGCAGGTCGTATAGTTAACTCCTTGTTGGGCAAAATCTTGCCACAACCTATGCACCCTCTTCCTAGGAACCCCATTTTATTCTTGCTGGTCTC  CAGCAAGGAAAGCTATAGCTGGTATGATAAGGCCCTAAGAAAGGCAGCAGGTCGTATAGTTAACCTCTTGTTGGGCAAAATCTCTGCCCTAAAACCTATGCAACCTCTTCCTAGGAACCCATTTTATTCTTGCTGGTCTC  TAGCAAGGAAAGTTAACCTAGGAATAATAAGGCCCTAAGAAGGCAGCAGGTCGTATAGTTAACCTCTTTGTTGGGCAAAATCTCCTGCCCTAAAACCTATGCAACCTCATCACCCTCTTCCTAGGAACCCATTTTATTCTTGCTGGTCTC  TAGCAAGGAAAACTTAACCTGGGATTAGTAAGGCCCTAAGAAGGAGCAGGTCGTATAGTTAACCTCCTTTGTTGGGCAAAATCCTGCCCTAAAACCTATGCAACCTACTACCTCTTCCTAGGAACCCATTTTTTTCTTGTCAGTCTTC  TAGCAAGGAAACTTAACCTGGGATTAGTAAGGCCCTAAGAAGGAGCAGGTCGTATAGTTAACCTCCTTTGTGGGCAAAATCCTGCCCTAAAACCTATGCAACCTACTACCTCTTCCTAGGAACCCATTTTTTTCTTGCTGGTCTTC  TAGCAAGGAAAACTTAACCTGAACCTAAAACCTATGCAACCTAAAACCTATGCAACCTACTACCTCTTCCTAGGAACCCATTTTTTTCTTGCTGGTCTTC  TAGCAAGGAAAACTTAACAAGCCCATAGAAAGCAGCAGGTCGTATAGTTAACTCCTCTTTGTTGGGCAAAATCCTGCCCTAAAACCTATGCAACCTACTACCTCTTCCTAGGAACCCCATTTTTTTCTTGCTGGTCTTC  TAGCAAGGAAACTTAACAAGCCCATAGAAAGCAGCAGGTCGTATAGTTAACTCCTCTTTTGTGGGCAAAATCCTGCCCTAAAACCTATGCAACCTACTACCTCTTCCTAGGAACCCCATTTTTTTCTTGCTGGTCTTC  TAGCAAGGAAACTTAACAAGCCCATAGAAAAGCAGAAAGCAGAAGGTCGTATAGTTAACTCCTCTTTTGTGGGCAAAATCCTGCCCTAAAACCTATGCAACCTACTACCTCTTCCTAGGAACCCCATTTTTTTT
SINE	Repeating Elements by RepeatMasker
LINE LTR DNA Simple Low Complexity Satellite	
RNA Other	
Unknown	Short Genetic Variants from European Variant Archive Release 4
rs248064564 EVA SNP Release 5	Short Genetic Variants from European Variant Archive Release 5