Supplemental Figure Legends

Figure S_1 – Northern blot probes.

A list of oligonucleotide sequences used to probe northern blots for mouse tRNA families. Sequences are written 5'-3' and are complementary to the tRNA mature regions.

Figure S_2 – Alignments of the mouse tRNA gene families.

All of the genes in the 35 mouse tRNA families were aligned using ClustalW. Only the mature coding regions and introns (when present) are shown. Mature tRNA sequences are more conserved than the 5' and 3' flanking regions or the introns, although even the mature regions are not as conserved as those in yeast.

Figure S_3 – Set of verified mouse tRNA genes.

446 tRNA genes correspond to the expressed tRNA sequences as confirmed by the microarray analysis. The verified genes are listed with their tRNA gene names, chromosomal location, tRNA gene family, amino acid type, anticodon, presence of an intron, whether the gene is a 'rogue' and the tRNA gene sequence.

Figure S_4 – Set of predicted human tRNA genes.

We sorted the set of predicted tRNA genes using ClustalW and then assigned the genes into families. All of the mouse tRNA gene families had corresponding human families.

Figure S_5 – Northern blot confirmation of predicted tRNA gene families.

We confirmed the expression of tRNA-sized RNAs in RNA samples from four mouse tissues and RNA from actively growing human tissue culture cells (HeLa). The probe sequences are listed in Figure S_1.

Figure S_6 – Predicted structures of the single-copy “orphan” pre-tRNAs that contain introns. There are six intron-containing orphan tRNAs that are detected as expressed by the microarray analysis. However, the intron location of five of seven of the tRNA genes is not consistent with intron locations in yeast, only tF(GAA)O and tP(AGG)P are consistent with yeast. The intron size and insertion location is indicated with an arrow.

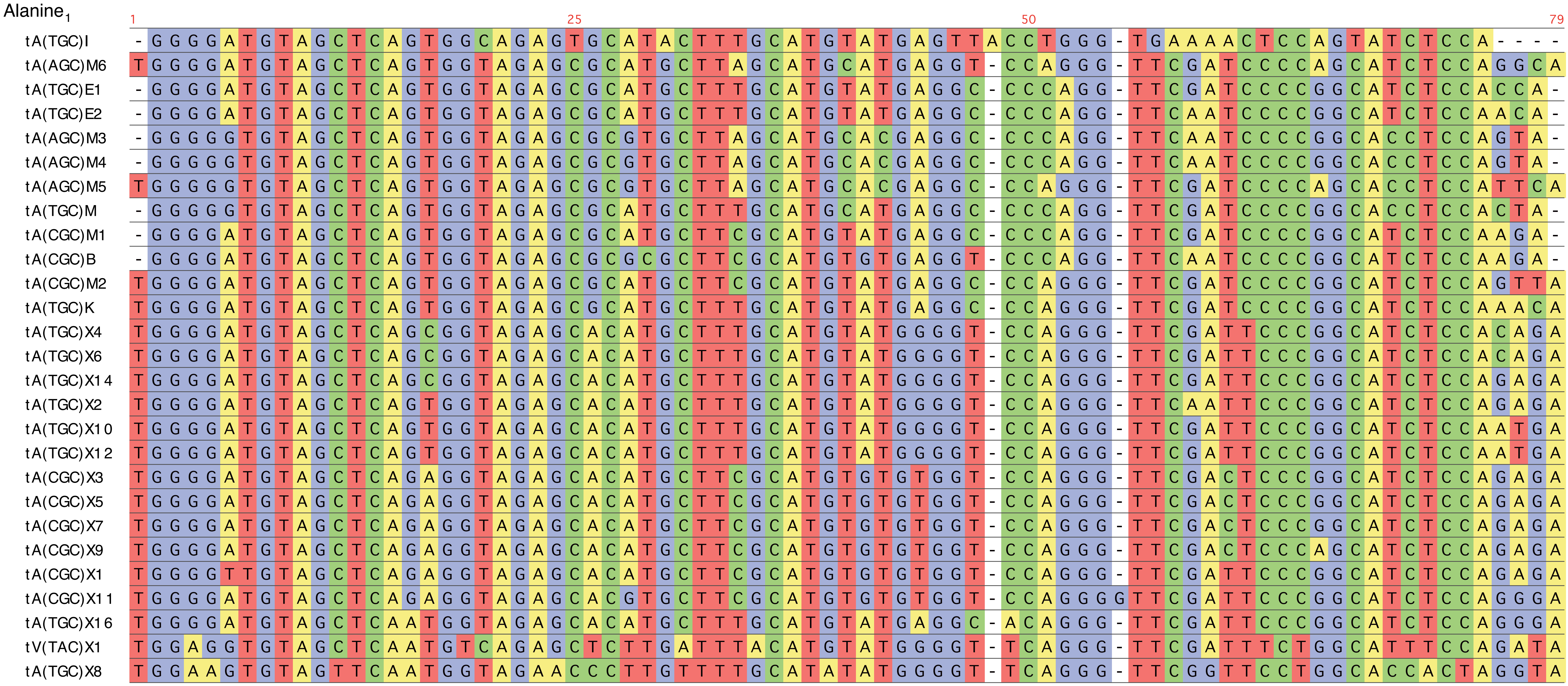
Figure S_7 – Mouse orphan tRNA^{Tyr} gene corresponds to a multi-gene tRNA^{Tyr} family in humans.

An orphan mouse tRNA gene, tY(GTA)B, which exists as a single copy in the mouse genome, corresponds to a probably human tRNA gene with 20 copies. This mouse tRNA gene was detected by only ARAGORN and the 20 human homologues were not detected by tRNAscan-SE. This alignment shows the homology between the mouse gene (shown above) and the 20 human homologues (>90% homology).

Supplemental Figure S1

Mouse tRNA Family	Probe Sequence (5'-3')
Ala1	GCG CTC TAC CAC TGA GCT ACA CC
Ala2	GCT CTA CCA CTG AGC TAA ATC C
Ala3	GCG CTC TAC CAT TTG AGC TAA TCC
Arg1	CGA ACC CTT AAT CTT CTG ATC CG
Arg2	GGA GGC CAA TGC CTT ATC CAT TAG G
Asn	GGC TCG AAC CAC CTA CCT TTC GGT
Asp	GTG ACA GGC GGG GAT ACT CAC C
Cys	CCT GCT GAT CTG TAG TCA AAT GCT C
Gln	CGC TGG ATT CAG AGT CCA GAG TGC
Glu1	GCG CCG AAT CCT AAC CAC TAG ACC A
Glu2	GGC CGC CTG GGT GAA AAC CAG G
Gly1	GTG GGA GGC GAG AAT TCT ACC ACT GAA
Gly2	GAA GGC AGC TAT GCT TAC CAC TAT A
Gly3	CGC AAG AAT GGG AAT CTT GCA TGA T
His	CCT AGG TTG CTG CGG CCA CAA CG
Ile1	CCT TGG CGT TAT TAG CAC CAC GCT C
Ile2	GGT GAG GCT CGA ACT CAC AAC CTC GGC
Leu1	CCG TAG AGA CTG GAG CCT TAA TCC
Leu2	CCT CCA GTG GAG ACT GCG ACC TG
Leu3	CCA ACG CCT TAA CCA CTC AGC CAT CC
Lys1	CCT GAG ATT AAG AGA CTC TTG CTC
Lys2	CAG ATT AAA AGT CTG ATG CTC TAC C
Met1	CTG GGT TAT GGG ACC AGC ACG C
Met2	TGC GCT GCC TAC TAT GCT AAG G
Met3	CGC GCT ACC TAC TGC GCT AAC G
Phe	AGA TCT TCA GTC TAA CGC TCT CC
Pro1	CCT CTC GCA CCC TAA GCG AGA ATC
Pro2	GTG AGA ATC ATA CCC CTA GAC CAA CAA GC
Ser1	GGG ATA CCC CAA TGG ATT TCT AG
Ser2	CCA TCG CCT TAA CCA CTC GGC CAC CTC G
Thr1	GCT GGG ATT CGA ACC CAT GAT CTC CTG
Thr2	CGA GAC CGA CGC CTT ACC ACT TGG
Trp	CTG GAG TCA GAC GTG CTA CCA TTG
Tyr	CAG TCC TCC GCT CTA CCA ACT GAG C
Val1	CGA ACG TGA TAA CCA CTA CAC TAC GG
Val1	CCG GTT TCG AAC CGG TGA CCT TTC GC
Val2	CCT GCA TGT GAG GCG AGC GAT CAC CAC

Supplemental Figure S2



Alanine$_1$

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tA(TGC)E1   -GGGGATGTAGCTCAGTGGTAGAGCGCATGCTTTGCATGTATGAGGC-CCCAGG-TTCGATCCCCGGCATCTCCACCA-
tA(TGC)E2   -GGGGATGTAGCTCAGTGGTAGAGCGCATGCTTTGCATGTATGAGGC-CCCAGG-TTCAATCCCCGGCATCTCCAACA-
tA(AGC)M3   -GGGGGTGTAGCTCAGTGGTAGAGCGCGTGCTTAGCATGCACGAGGC-CCCAGG-TTCAATCCCCGGCACCTCCAGTA-
tA(AGC)M4   -GGGGGTGTAGCTCAGTGGTAGAGCGCGTGCTTAGCATGCACGAGGC-CCCAGG-TTCAATCCCCGGCACCTCCAGTA-
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tA(TGC)M    -GGGGGTGTAGCTCAGTGGTAGAGCGCATGCTTTGCATGCATGAGGC-CCCAGG-TTCGATCCCCGGCACCTCCACTA-
tA(CGC)M1   -GGGGATGTAGCTCAGTGGTAGAGCGCATGCTTCGCATGTATGAGGC-CCCAGG-TTCGATCCCCGGCATCTCCAAGA-
tA(CGC)B    -GGGGATGTAGCTCAGTGGTAGAGCGCGCGCTTCGCATGTGTGAGGT-CCCAGG-TTCAATCCCCGGCATCTCCAAGA-
tA(CGC)M2   TGGGGATGTAGCTCAGTGGTAGAGCGCATGCTTCGCATGTATGAGGC-CCAGGG-TTCGATCCCCGGCATCTCCAGTTA
tA(TGC)K    TGGGGATGTAGCTCAGTGGTAGAGCGCATGCTTTGCATGTATGAGGC-CCAGGG-TTCGATCCCCGGCATCTCCAAACA
tA(TGC)X4   TGGGGATGTAGCTCAGCGGTAGAGCACATGCTTTGCATGTATGGGGT-CCAGGG-TTCGATTCCCGGCATCTCCACAGA
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tA(TGC)X14  TGGGGATGTAGCTCAGCGGTAGAGCACATGCTTTGCATGTATGGGGT-CCAGGG-TTCGATTCCCGGCATCTCCAGAGA
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tA(TGC)X12  TGGGGATGTAGCTCAGTGGTAGAGCACATGCTTTGCATGTATGGGGT-CCAGGG-TTCGATTCCCGGCATCTCCAATGA
tA(CGC)X3   TGGGGATGTAGCTCAGAGGTAGAGCACATGCTTCGCATGTGTGTGGT-CCAGGG-TTCGACTCCCGGCATCTCCAGAGA
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tA(CGC)X7   TGGGGATGTAGCTCAGAGGTAGAGCACATGCTTCGCATGTGTGTGGT-CCAGGG-TTCGACTCCCGGCATCTCCAGAGA
tA(CGC)X9   TGGGGATGTAGCTCAGAGGTAGAGCACATGCTTCGCATGTGTGTGGT-CCAGGG-TTCGACTCCCAGCATCTCCAGAGA
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tV(TAC)X1   TGGAGGTGTAGCTCAATGTCAGAGCTCTTGATTTACATGTATGGGGT-TCAGGG-TTCGATTTCTGGCATTTCCAGATA
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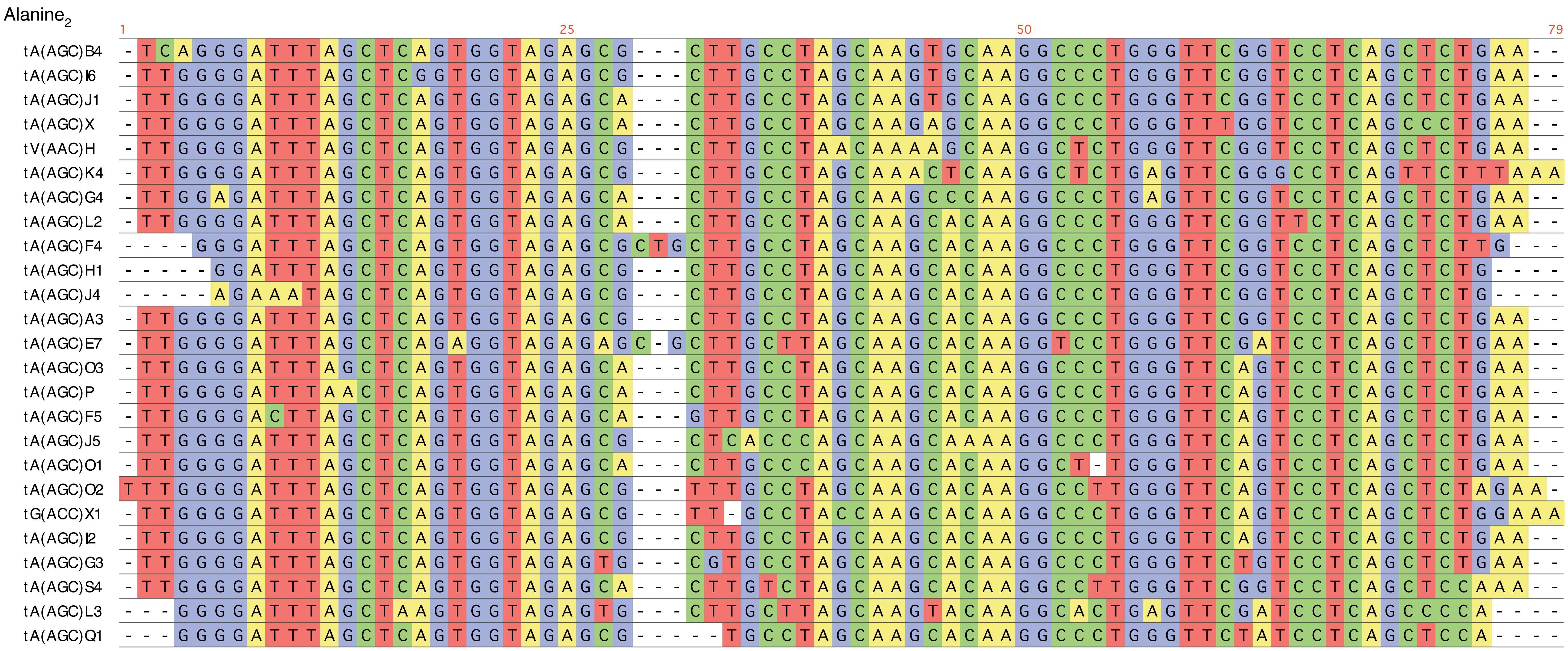

Alanine$_2$

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tA(AGC)J1  -TTGGGGATTTAGCTCAGTGGTAGAGCA---CTTGCCTAGCAAGTGCAAGGCCCTGGGTTCGGTCCTCAGCTCTGAA--
tA(AGC)X   -TTGGGGATTTAGCTCAGTGGTAGAGCA---CTTGCCTAGCAAGAGCAAGGCCCTGGGTTTGGTCCTCAGCCCTGAA--
tV(AAC)H   -TTGGGGATTTAGCTCAGTGGTAGAGCG---CTTGCCTAACAAAAGCAAGGCTCTGGGTTCGGTCCTCAGCTCTGAA--
tA(AGC)K4  -TTGGGGATTTAGCTCAGTGGTAGAGCG---CTTGCCTAGCAAACTCAAGGCTCTGAGTTCGGGCCTCAGTTCTTTAAA
tA(AGC)G4  -TTGGAGATTTAGCTCAGTGGTAGAGCA---CTTGCCTAGCAAGCCCAAGGCCCTGAGTTCGGTCCTCAGCTCTGAA--
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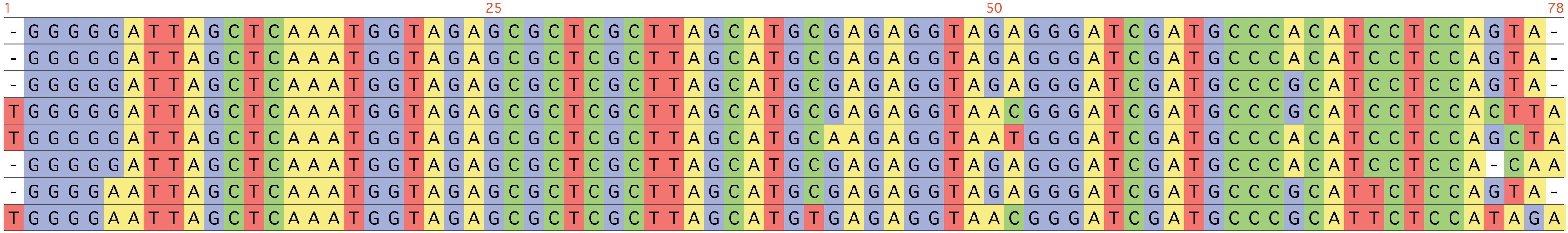
Alanine$_3$



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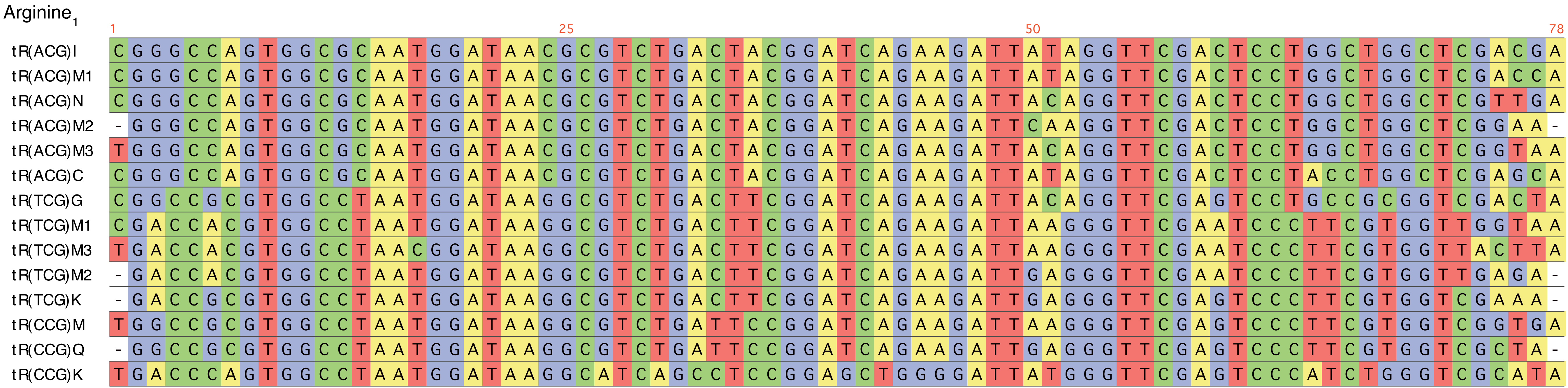

Arginine$_1$

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tR(ACG)N	CGGGCCAGTGGCGCAATGGATAACGCGTCTGACTACGGATCAGAAGATTACAGGTTCGACTCCTGGCTGGCTCGTTGA
tR(ACG)M2	-GGGCCAGTGGCGCAATGGATAACGCGTCTGACTACGGATCAGAAGATTCAAGGTTCGACTCCTGGCTGGCTCGGAA-
tR(ACG)M3	TGGGCCAGTGGCGCAATGGATAACGCGTCTGACTACGGATCAGAAGATTACAGGTTCGACTCCTGGCTGGCTCGGTAA
tR(ACG)C	CGGGCCAGTGGCGCAATGGATAACGCGTCTGACTACGGATCAGAAGATTATAGGTTCGACTCCTACCTGGCTCGAGCA
tR(TCG)G	CGGCCGCGTGGCCTAATGGATAAGGCGTCTGACTTCGGATCAGAAGATTACAGGTTCGAGTCCTGCCGCGGTCGACTA
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tR(TCG)M3	TGACCACGTGGCCTAACGGATAAGGCGTCTGACTTCGGATCAGAAGATTAAGGGTTCGAATCCCTTCGTGGTTACTTA
tR(TCG)M2	-GACCACGTGGCCTAATGGATAAGGCGTCTGACTTCGGATCAGAAGATTGAGGGTTCGAATCCCTTCGTGGTTGAGA-
tR(TCG)K	-GACCGCGTGGCCTAATGGATAAGGCGTCTGACTTCGGATCAGAAGATTGAGGGTTCGAGTCCCTTCGTGGTCGAAA-
tR(CCG)M	TGGCCGCGTGGCCTAATGGATAAGGCGTCTGATTCCGGATCAGAAGATTAAGGGTTCGAGTCCCTTCGTGGTCGGTGA
tR(CCG)Q	-GGCCGCGTGGCCTAATGGATAAGGCGTCTGATTCCGGATCAGAAGATTGAGGGTTCGAGTCCCTTCGTGGTCGCTA-
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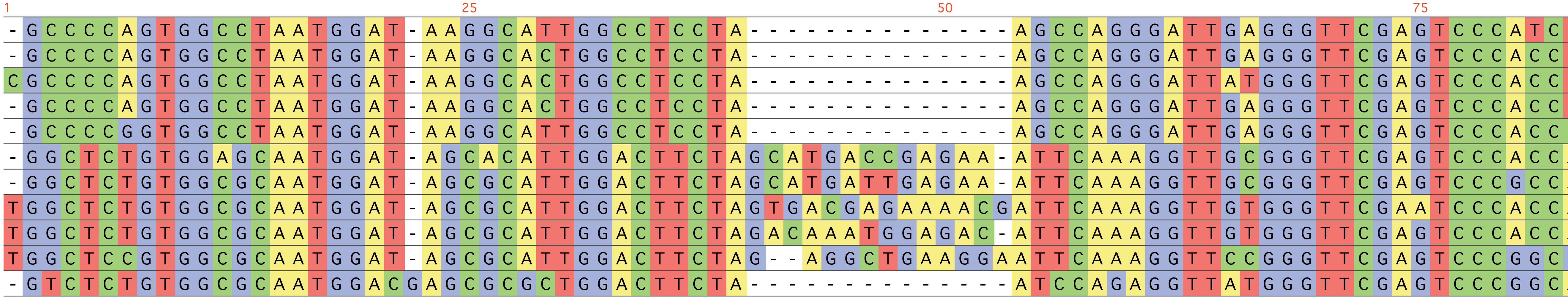
Arginine$_2$



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tR(TCT)C   TGGCTCCGTGGCGCAATGGAT-AGCGCATTGGACTTCTAG--AGGCTGAAGGAATTCAAAGGTTCCGGGTTCGAGTCCCGGC
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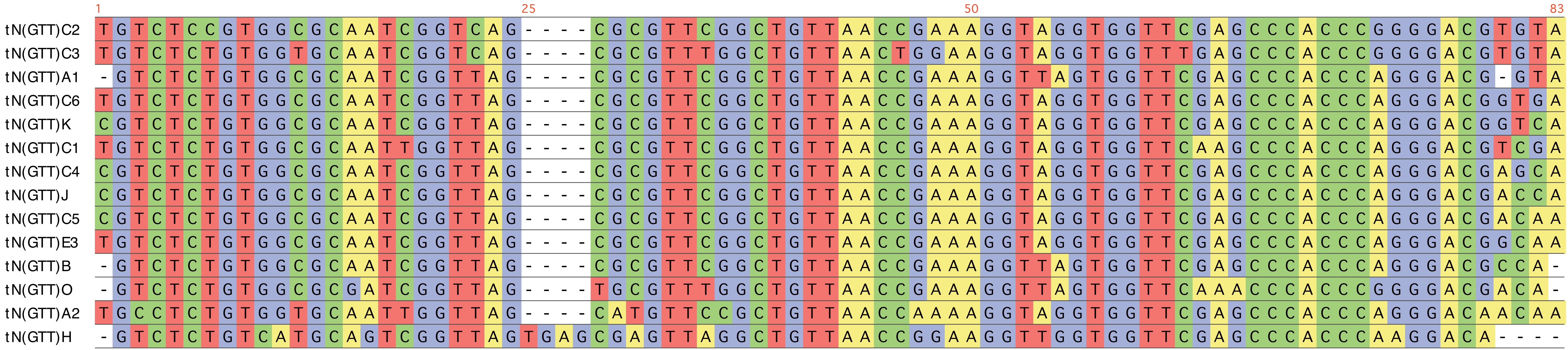
Asparagine



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tN(GTT)C6  TGTCTCTGTGGCGCAATCGGTTAG----CGCGTTCGGCTGTTAACCGAAAGGTAGGTGGTTCGAGCCCACCCAGGGACGGTGA
tN(GTT)K   CGTCTCTGTGGCGCAATCGGTTAG----CGCGTTCGGCTGTTAACCGAAAGGTAGGTGGTTCGAGCCCACCCAGGGACGGTCA
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tN(GTT)J   CGTCTCTGTGGCGCAATCGGTTAG----CGCGTTCGGCTGTTAACCGAAAGGTAGGTGGTTCGAGCCCACCCAGGGACGACCA
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tN(GTT)O   -GTCTCTGTGGCGCGATCGGTTAG----TGCGTTTGGCTGTTAACCGAAAGGTTAGTGGTTCAAACCCACCCGGGGACGACA-
tN(GTT)A2  TGCCTCTGTGGTGCAATTGGTTAG----CATGTTCCGCTGTTAACCAAAAGGTAGGTGGTTCGAGCCCACCCAGGGACAACAA
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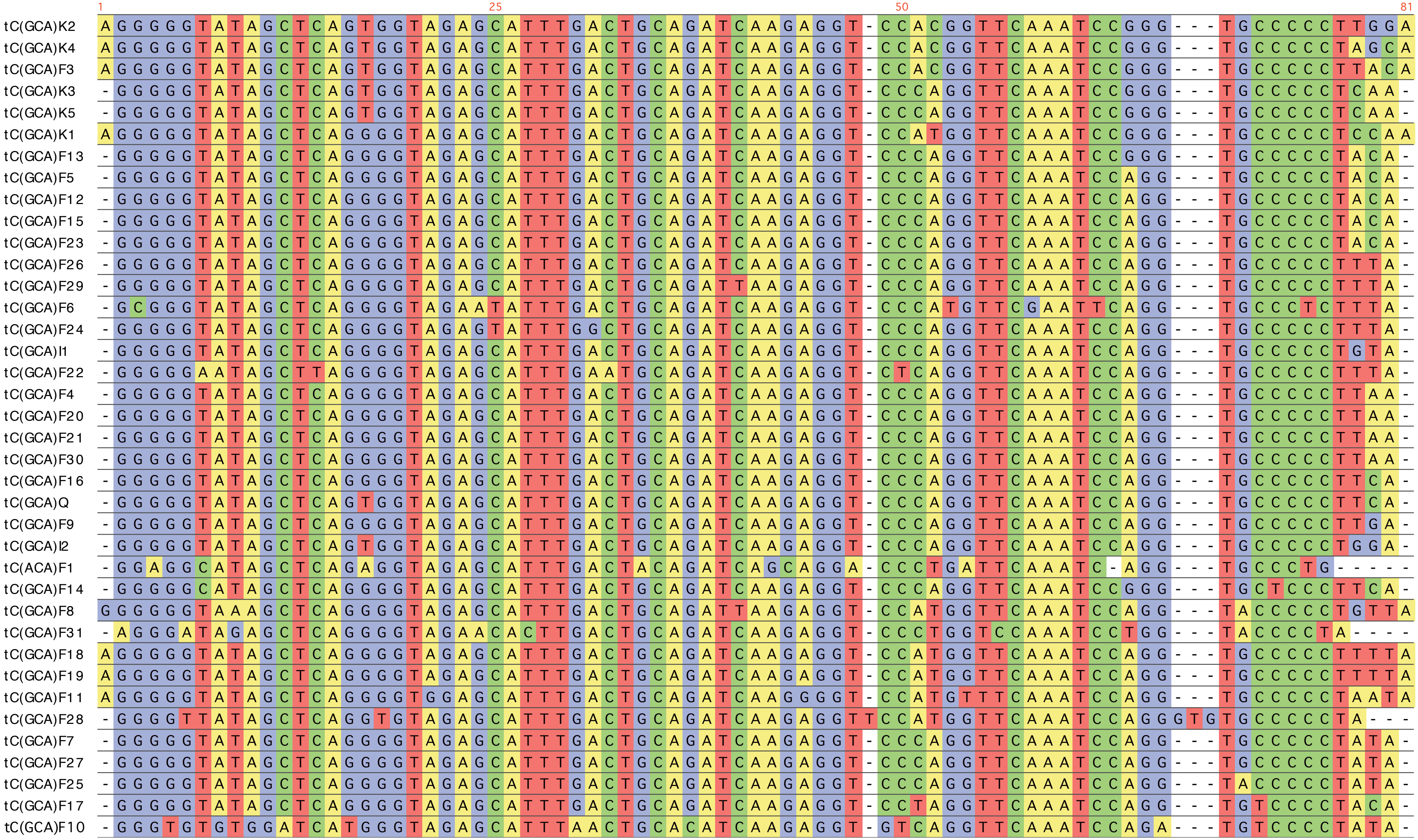
Cysteine



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tC(GCA)F3   AGGGGGTATAGCTCAGTGGTAGAGCATTTGACTGCAGATCAAGAGGT-CCACGGTTCAAATCCGGG---TGCCCCCTTACA
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tC(ACA)F1   -GGAGGCATAGCTCAGAGGTAGAGCATTTGACTACAGATCAGCAGGA-CCCTGATTCAAATC-AGG---TGCCCTG-----
tC(GCA)F14  -GGGGGCATAGCTCAGGGGTAGAGCATTTGACTGCAGATCAAGAGGT-CCCAGGTTCAAATCCGGG---TGCTCCCTTCA-
tC(GCA)F8   GGGGGGTAAAGCTCAGGGGTAGAGCATTTGACTGCAGATTAAGAGGT-CCATGGTTCAAATCCAGG---TACCCCCTGTTA
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tC(GCA)F11  AGGGGGTATAGCTCAGGGGTGGAGCATTTGACTGCAGATCAAGGGGT-CCATGTTTCAAATCCAGG---TGCCCCCTAATA
tC(GCA)F28  -GGGGTTATAGCTCAGGTGTAGAGCATTTGACTGCAGATCAAGAGGTTCCATGGTTCAAATCCAGGGTGTGCCCCCTA---
tC(GCA)F7   -GGGGGTATAGCTCAGGGGTAGAGCATTTGACTGCAGATCAAGAGGT-CCCAGGTTCAAATCCAGG---TGCCCCCTATA-
tC(GCA)F27  -GGGGGTATAGCTCAGGGGTAGAGCATTTGACTGCAGATCAAGAGGT-CCCAGGTTCAAATCCAGG---TGCCCCCTATA-
tC(GCA)F25  -GGGGGTATAGCTCAGGGGTAGAGCATTTGACTGCAGATCAAGAGGT-CCCAGGTTCAAATCCAGG---TACCCCCTATA-
tC(GCA)F17  -GGGGGTATAGCTCAGGGGTAGAGCATTTGACTGCAGATCAAGAGGT-CCTAGGTTCAAATCCAGG---TGTCCCCTACA-
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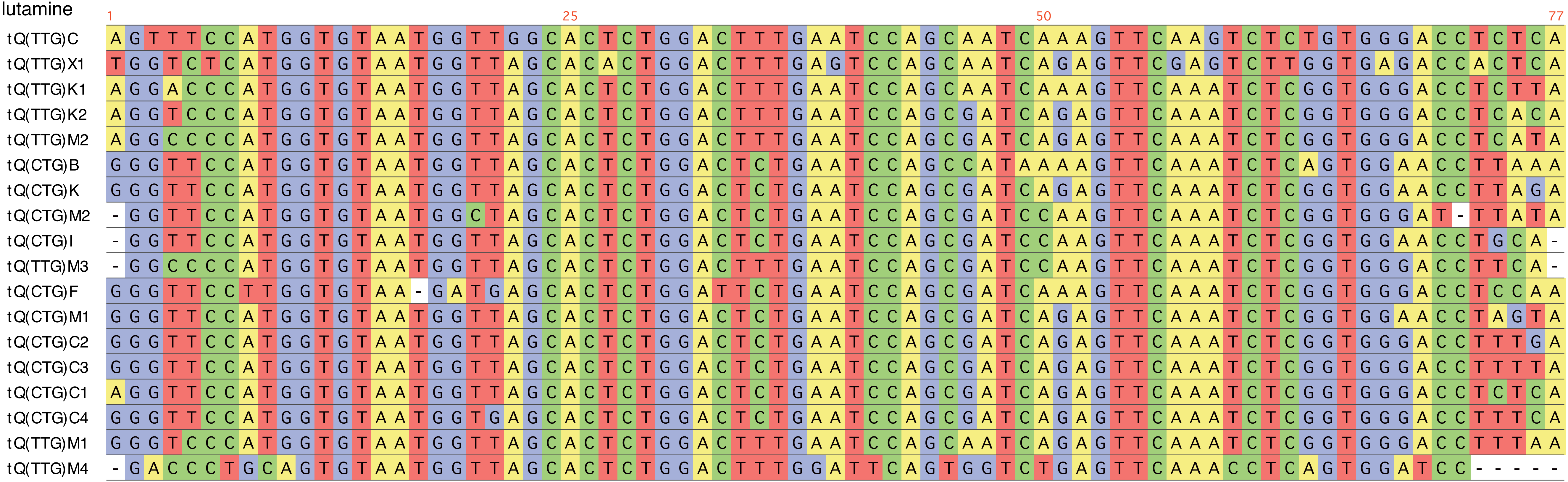
Glutamine



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tQ(TTG)K1   AGGACCCATGGTGTAATGGTTAGCACTCTGGACTTTGAATCCAGCAATCAAAGTTCAAATCTCGGTGGGACCTCTTA
tQ(TTG)K2   AGGTCCCATGGTGTAATGGTTAGCACTCTGGACTTTGAATCCAGCGATCAGAGTTCAAATCTCGGTGGGACCTCACA
tQ(TTG)M2   AGGCCCCATGGTGTAATGGTTAGCACTCTGGACTTTGAATCCAGCGATCAGAGTTCAAATCTCGGTGGGACCTCATA
tQ(CTG)B    GGGTTCCATGGTGTAATGGTTAGCACTCTGGACTCTGAATCCAGCCATAAAAGTTCAAATCTCAGTGGAACCTTAAA
tQ(CTG)K    GGGTTCCATGGTGTAATGGTTAGCACTCTGGACTCTGAATCCAGCGATCAGAGTTCAAATCTCGGTGGAACCTTAGA
tQ(CTG)M2   -GGTTCCATGGTGTAATGGCTAGCACTCTGGACTCTGAATCCAGCGATCCAAGTTCAAATCTCGGTGGGAT-TTATA
tQ(CTG)I    -GGTTCCATGGTGTAATGGTTAGCACTCTGGACTCTGAATCCAGCGATCCAAGTTCAAATCTCGGTGGAACCTGCA-
tQ(TTG)M3   -GGCCCCATGGTGTAATGGTTAGCACTCTGGACTTTGAATCCAGCGATCCAAGTTCAAATCTCGGTGGGACCTTCA-
tQ(CTG)F    GGGTTCCTTGGTGTAA-GATGAGCACTCTGGATTCTGAATCCAGCGATCAAAGTTCAAATCTCGGTGGGACCTCCAA
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tQ(CTG)C2   GGGTTCCATGGTGTAATGGTTAGCACTCTGGACTCTGAATCCAGCGATCAGAGTTCAAATCTCGGTGGGACCTTTGA
tQ(CTG)C3   GGGTTCCATGGTGTAATGGTTAGCACTCTGGACTCTGAATCCAGCGATCAGAGTTCAAATCTCGGTGGGACCTTTTA
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tQ(CTG)C4   GGGTTCCATGGTGTAATGGTGAGCACTCTGGACTCTGAATCCAGCGATCAGAGTTCAAATCTCGGTGGGACCTTTCA
tQ(TTG)M1   GGGTCCCATGGTGTAATGGTTAGCACTCTGGACTTTGAATCCAGCAATCAGAGTTCAAATCTCGGTGGGACCTTTAA
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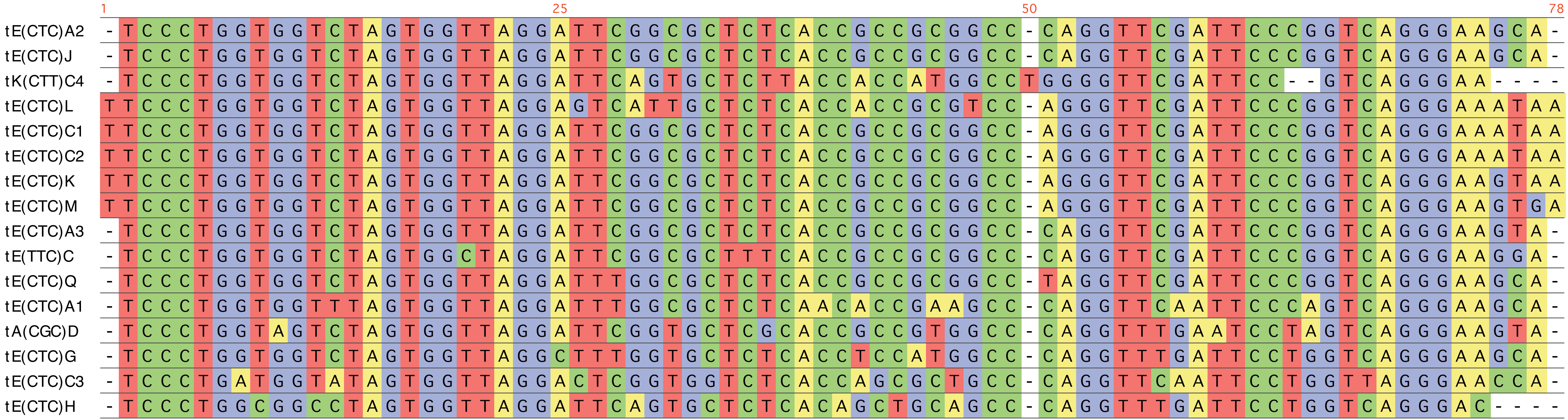
Glutamic Acid$_1$



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tE(CTC)A2	-TCCCTGGTGGTCTAGTGGTTAGGATTCGGCGCTCTCACCGCCGCGGCC-CAGGTTCGATTCCCGGTCAGGGAAGCA-
tE(CTC)J	-TCCCTGGTGGTCTAGTGGTTAGGATTCGGCGCTCTCACCGCCGCGGCC-CAGGTTCGATTCCCGGTCAGGGAAGCA-
tK(CTT)C4	-TCCCTGGTGGTCTAGTGGTTAGGATTCAGTGCTCTTACCACCATGGCCTGGGGTTCGATTCC--GTCAGGGAA----
tE(CTC)L	TTCCCTGGTGGTCTAGTGGTTAGGAGTCATTGCTCTCACCACCGCGTCC-AGGGTTCGATTCCCGGTCAGGGAAATAA
tE(CTC)C1	TTCCCTGGTGGTCTAGTGGTTAGGATTCGGCGCTCTCACCGCCGCGGCC-AGGGTTCGATTCCCGGTCAGGGAAATAA
tE(CTC)C2	TTCCCTGGTGGTCTAGTGGTTAGGATTCGGCGCTCTCACCGCCGCGGCC-AGGGTTCGATTCCCGGTCAGGGAAATAA
tE(CTC)K	TTCCCTGGTGGTCTAGTGGTTAGGATTCGGCGCTCTCACCGCCGCGGCC-AGGGTTCGATTCCCGGTCAGGGAAGTAA
tE(CTC)M	TTCCCTGGTGGTCTAGTGGTTAGGATTCGGCGCTCTCACCGCCGCGGCC-AGGGTTCGATTCCCGGTCAGGGAAGTGA
tE(CTC)A3	-TCCCTGGTGGTCTAGTGGTTAGGATTCGGCGCTCTCACCGCCGCGGCC-CAGGTTCGATTCCCGGTCAGGGAAGTA-
tE(TTC)C	-TCCCTGGTGGTCTAGTGGCTAGGATTCGGCGCTTTCACCGCCGCGGCC-CAGGTTCGATTCCCGGTCAGGGAAGGA-
tE(CTC)Q	-TCCCTGGTGGTCTAGTGGTTAGGATTTGGCGCTCTCACCGCCGCGGCC-TAGGTTCGATTCCCGGTCAGGGAAGCA-
tE(CTC)A1	-TCCCTGGTGGTTTAGTGGTTAGGATTTGGCGCTCTCAACACCGAAGCC-CAGGTTCAATTCCCAGTCAGGGAAGCA-
tA(CGC)D	-TCCCTGGTAGTCTAGTGGTTAGGATTCGGTGCTCGCACCGCCGTGGCC-CAGGTTTGAATCCTAGTCAGGGAAGTA-
tE(CTC)G	-TCCCTGGTGGTCTAGTGGTTAGGCTTTGGTGCTCTCACCTCCATGGCC-CAGGTTTGATTCCTGGTCAGGGAAGCA-
tE(CTC)C3	-TCCCTGATGGTATAGTGGTTAGGACTCGGTGGTCTCACCAGCGCTGCC-CAGGTTCAATTCCTGGTTAGGGAACCA-
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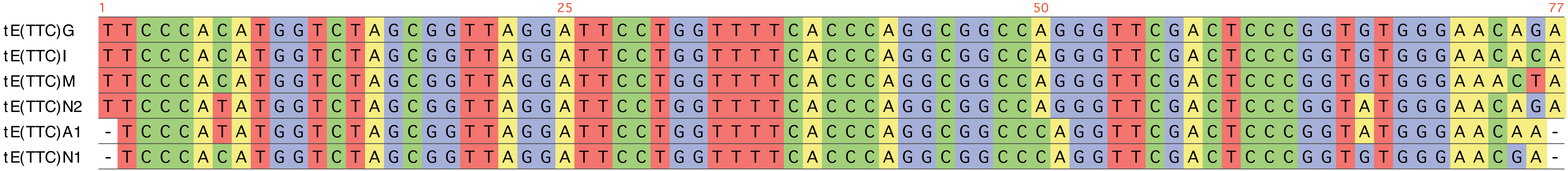
Glutamic Acid$_2$



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tE(TTC)M	TTCCCACATGGTCTAGCGGTTAGGATTCCTGGTTTTCACCCAGGCGGCCAGGGTTCGACTCCCGGTGTGGGAAACTA
tE(TTC)N2	TTCCCATATGGTCTAGCGGTTAGGATTCCTGGTTTTCACCCAGGCGGCCAGGGTTCGACTCCCGGTATGGGAACAGA
tE(TTC)A1	-TCCCATATGGTCTAGCGGTTAGGATTCCTGGTTTTCACCCAGGCGGCCCAGGTTCGACTCCCGGTATGGGAACAA-
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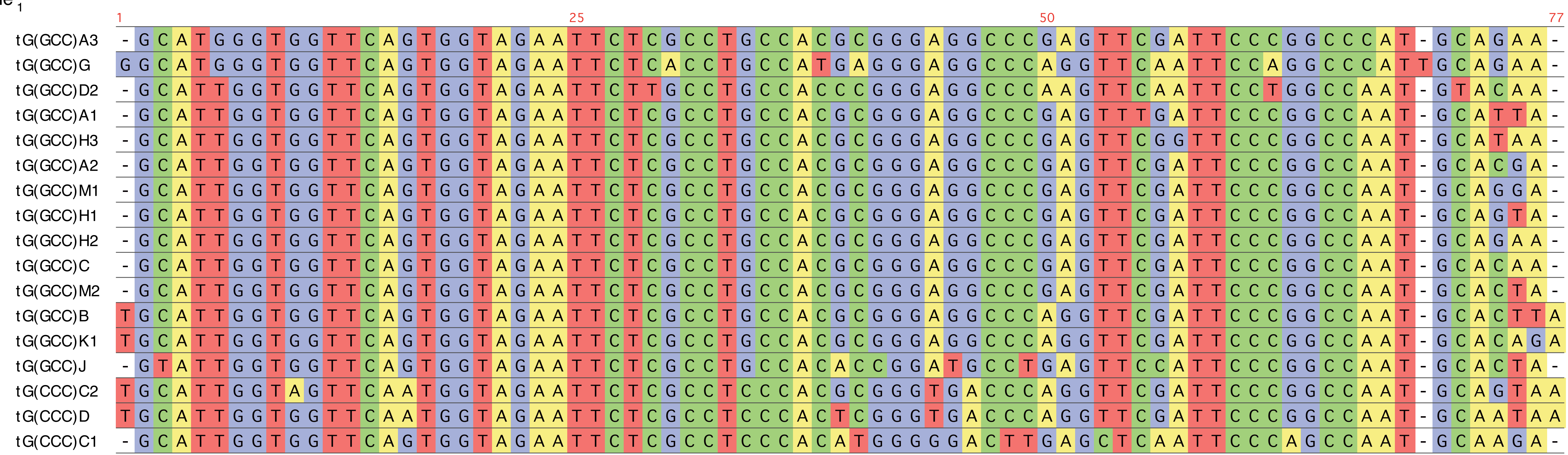
Glycine $_1$



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tG(GCC)D2	-GCATTGGTGGTTCAGTGGTAGAA	TTCTTGCCTGCCACCCGGGAGGCCC	AAGTTCAATTCCTGGCCAAT-GTACAA	-
tG(GCC)A1	-GCATTGGTGGTTCAGTGGTAGAA	TTCTCGCCTGCCACGCGGGAGGCCC	GAGTTTGATTCCCGGCCAAT-GCATTA	-
tG(GCC)H3	-GCATTGGTGGTTCAGTGGTAGAA	TTCTCGCCTGCCACGCGGGAGGCCC	GAGTTCGGTTCCCGGCCAAT-GCATAA	-
tG(GCC)A2	-GCATTGGTGGTTCAGTGGTAGAA	TTCTCGCCTGCCACGCGGGAGGCCC	GAGTTCGATTCCCGGCCAAT-GCACGA	-
tG(GCC)M1	-GCATTGGTGGTTCAGTGGTAGAA	TTCTCGCCTGCCACGCGGGAGGCCC	GAGTTCGATTCCCGGCCAAT-GCAGGA	-
tG(GCC)H1	-GCATTGGTGGTTCAGTGGTAGAA	TTCTCGCCTGCCACGCGGGAGGCCC	GAGTTCGATTCCCGGCCAAT-GCAGTA	-
tG(GCC)H2	-GCATTGGTGGTTCAGTGGTAGAA	TTCTCGCCTGCCACGCGGGAGGCCC	GAGTTCGATTCCCGGCCAAT-GCAGAA	-
tG(GCC)C	-GCATTGGTGGTTCAGTGGTAGAA	TTCTCGCCTGCCACGCGGGAGGCCC	GAGTTCGATTCCCGGCCAAT-GCACAA	-
tG(GCC)M2	-GCATTGGTGGTTCAGTGGTAGAA	TTCTCGCCTGCCACGCGGGAGGCCC	GAGTTCGATTCCCGGCCAAT-GCACTA	-
tG(GCC)B	TGCATTGGTGGTTCAGTGGTAGAA	TTCTCGCCTGCCACGCGGGAGGCCC	AGGTTCGATTCCCGGCCAAT-GCACTT	A
tG(GCC)K1	TGCATTGGTGGTTCAGTGGTAGAA	TTCTCGCCTGCCACGCGGGAGGCCC	AGGTTCGATTCCCGGCCAAT-GCACAG	A
tG(GCC)J	-GTATTGGTGGTTCAGTGGTAGAA	TTCTCGCCTGCCACACCGGATGCCT	GAGTTCCATTCCCGGCCAAT-GCACTA	-
tG(CCC)C2	TGCATTGGTAGTTCAATGGTAGAA	TTCTCGCCTCCCACGCGGGTGACCC	AGGTTCGATTCCCGGCCAAT-GCAGTA	A
tG(CCC)D	TGCATTGGTGGTTCAATGGTAGAA	TTCTCGCCTCCCACTCGGGTGACCC	AGGTTCGATTCCCGGCCAAT-GCAATA	A
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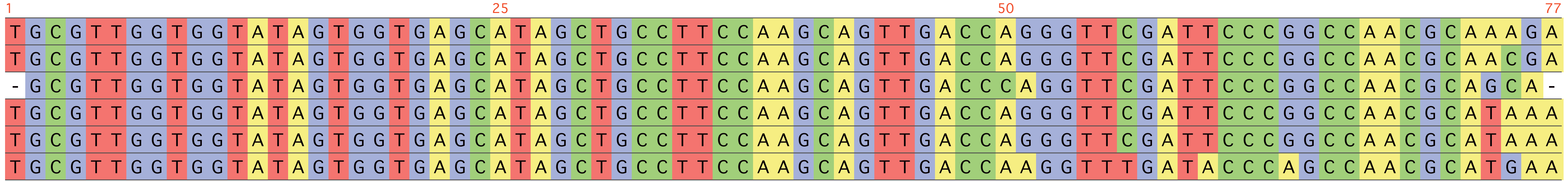
Glycine$_2$



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tG(TCC)A2   -GCGTTGGTGGTATAGTGGTGAGCATAGCTGCCTTCCAAGCAGTTGACCCAGGTTCGATTCCCGGCCAACGCAGCA-
tG(TCC)A3   TGCGTTGGTGGTATAGTGGTGAGCATAGCTGCCTTCCAAGCAGTTGACCAGGGTTCGATTCCCGGCCAACGCATAAA
tG(TCC)C    TGCGTTGGTGGTATAGTGGTGAGCATAGCTGCCTTCCAAGCAGTTGACCAGGGTTCGATTCCCGGCCAACGCATAAA
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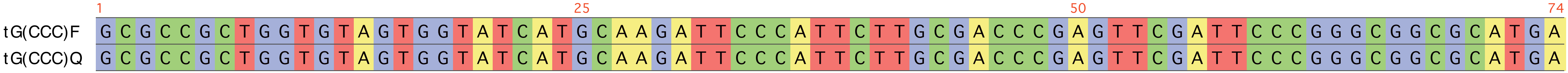
Glycine$_3$



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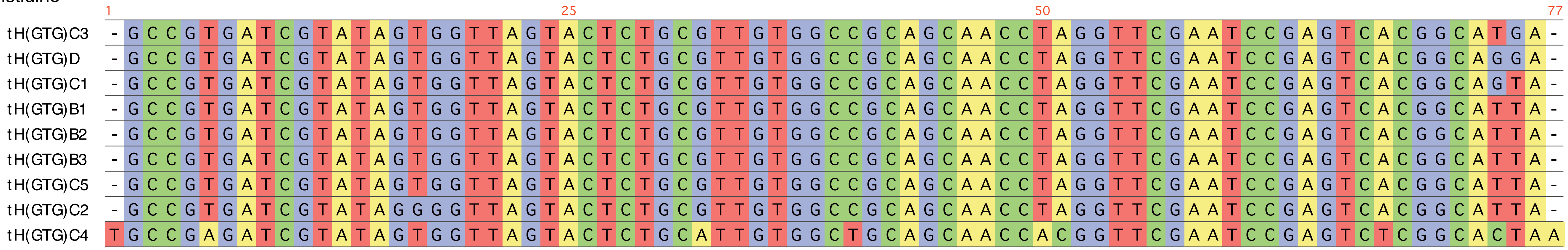
Histidine



tH(GTG)C3	-GCCGTGATCGTATAGTGGTTAGTACTCTGCGTTGTGGCCGCAGCAACCTAGGTTCGAATCCGAGTCACGGCATGA-
tH(GTG)D	-GCCGTGATCGTATAGTGGTTAGTACTCTGCGTTGTGGCCGCAGCAACCTAGGTTCGAATCCGAGTCACGGCAGGA-
tH(GTG)C1	-GCCGTGATCGTATAGTGGTTAGTACTCTGCGTTGTGGCCGCAGCAACCTAGGTTCGAATCCGAGTCACGGCAGTA-
tH(GTG)B1	-GCCGTGATCGTATAGTGGTTAGTACTCTGCGTTGTGGCCGCAGCAACCTAGGTTCGAATCCGAGTCACGGCATTA-
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tH(GTG)B3	-GCCGTGATCGTATAGTGGTTAGTACTCTGCGTTGTGGCCGCAGCAACCTAGGTTCGAATCCGAGTCACGGCATTA-
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tH(GTG)C2	-GCCGTGATCGTATAGGGGTTAGTACTCTGCGTTGTGGCCGCAGCAACCTAGGTTCGAATCCGAGTCACGGCATTA-
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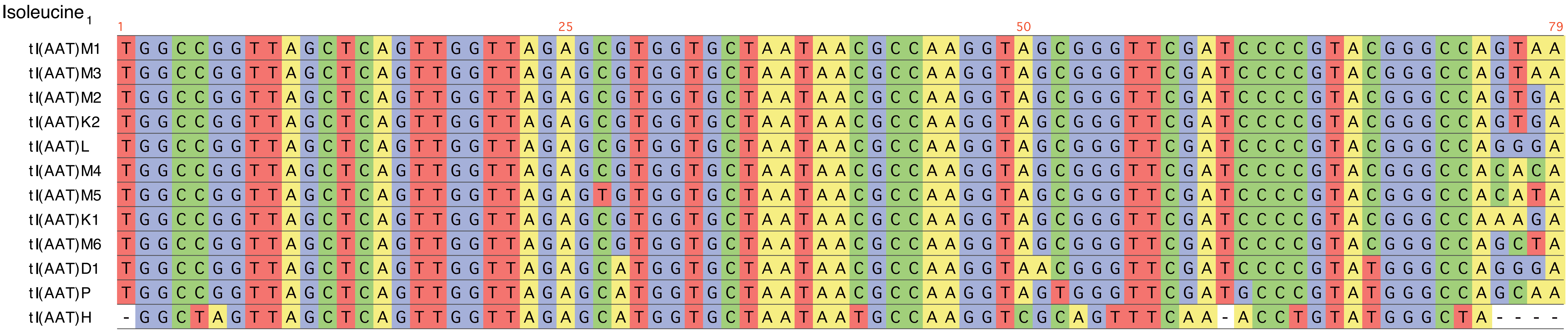
Isoleucine$_1$



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tI(AAT)M2 TGGCCGGTTAGCTCAGTTGGTTAGAGCGTGGTGCTAATAACGCCAAGGTAGCGGGTTCGATCCCCGTACGGGCCAGTGA
tI(AAT)K2 TGGCCGGTTAGCTCAGTTGGTTAGAGCGTGGTGCTAATAACGCCAAGGTAGCGGGTTCGATCCCCGTACGGGCCAGTGA
tI(AAT)L  TGGCCGGTTAGCTCAGTTGGTTAGAGCGTGGTGCTAATAACGCCAAGGTAGCGGGTTCGATCCCCGTACGGGCCAGGGA
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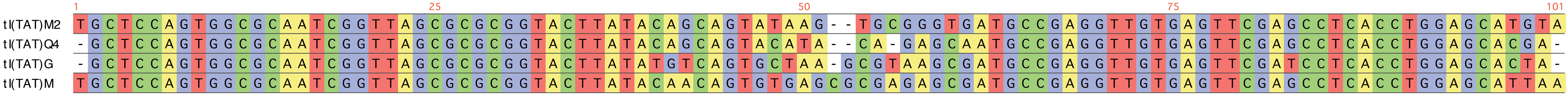
Isoleucine$_2$



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tI(TAT)G  -GCTCCAGTGGCGCAATCGGTTAGCGCGCGGTACTTATATGTCAGTGCTAA-GCGTAAGCGATGCCGAGGTTGTGAGTTCGATCCTCACCTGGAGCACTA-
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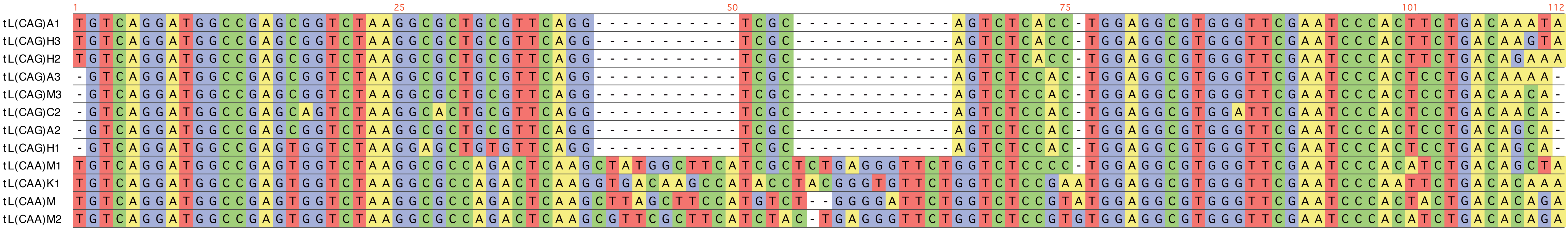
leucine$_1$



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tL(CAG)H2  TGTCAGGATGGCCGAGCGGTCTAAGGCGCTGCGTTCAGG-----------TCGC------------AGTCTCACC-TGGAGGCGTGGGTTCGAATCCCACTTCTGACAGAAA
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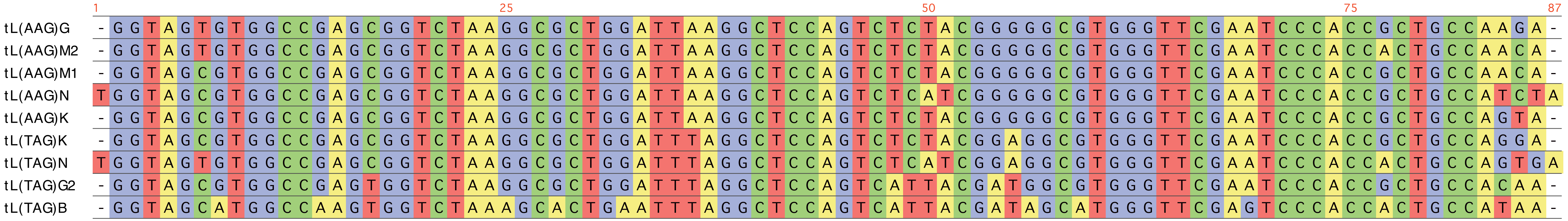
Leucine$_2$



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tL(TAG)G2	-GGTAGCGTGGCCGAGTGGTCTAAGGCGCTGGATTTAGGCTCCAGTCATTACGATGGCGTGGGTTCGAATCCCACCGCTGCCACAA-
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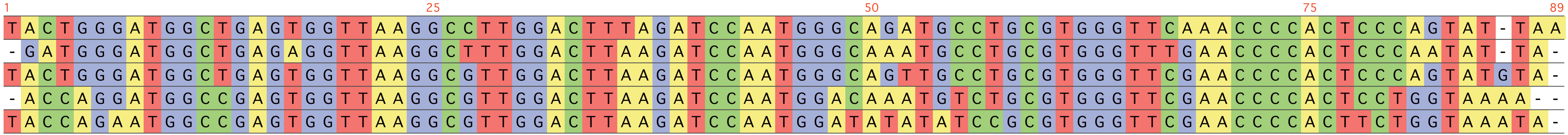
Leucine$_3$



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tL(TAA)M      TACTGGGATGGCTGAGTGGTTAAGGCGTTGGACTTAAGATCCAATGGGCAGTTGCCTGCGTGGGTTCGAACCCCACTCCCAGTATGTA-
tL(TAA)J      -ACCAGGATGGCCGAGTGGTTAAGGCGTTGGACTTAAGATCCAATGGACAAATGTCTGCGTGGGTTCGAACCCCACTCCTGGTAAAA--
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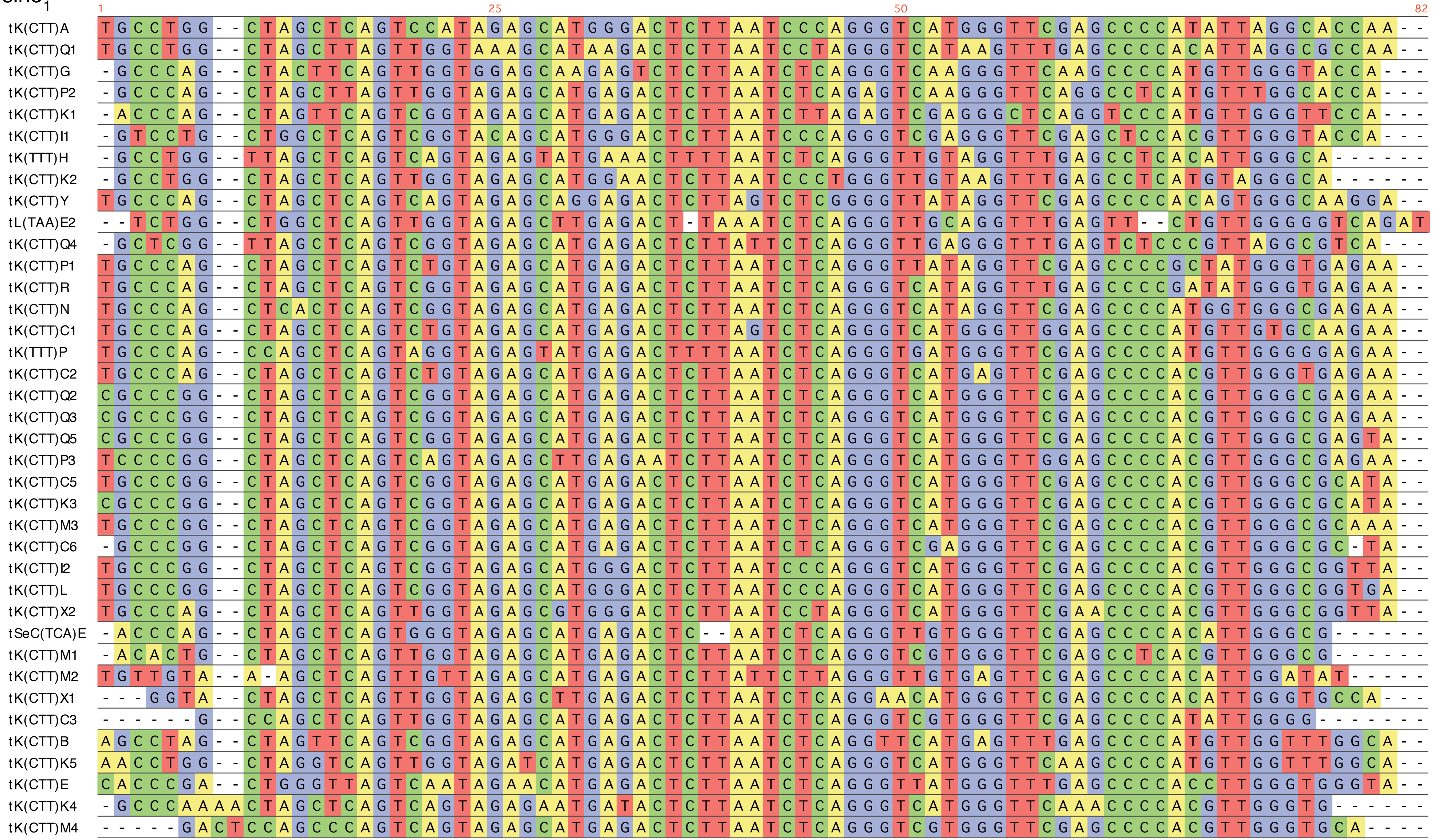
Lysine$_1$



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tSeC(TCA)E   -ACCCAG--CTAGCTCAGTGGGTAGAGCATGAGACTC--AATCTCAGGGTTGTGGGTTCGAGCCCCACATTGGGCG------
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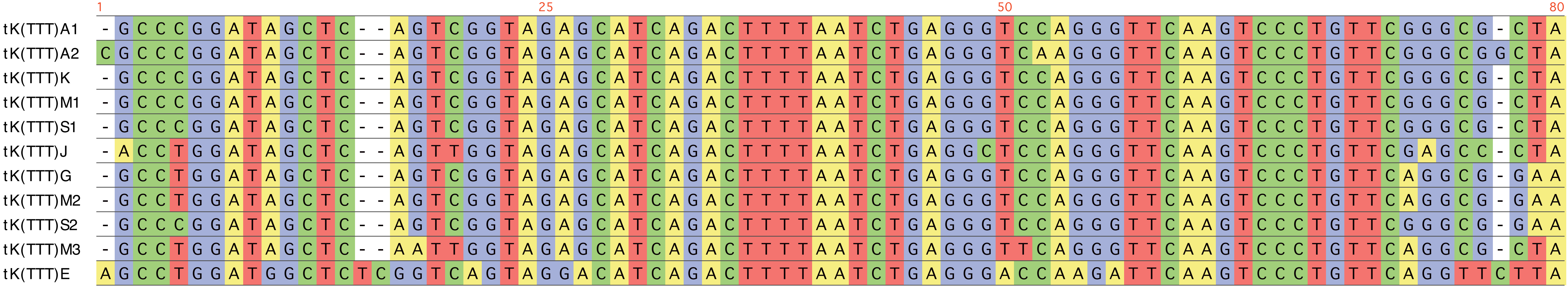
Lysine$_2$



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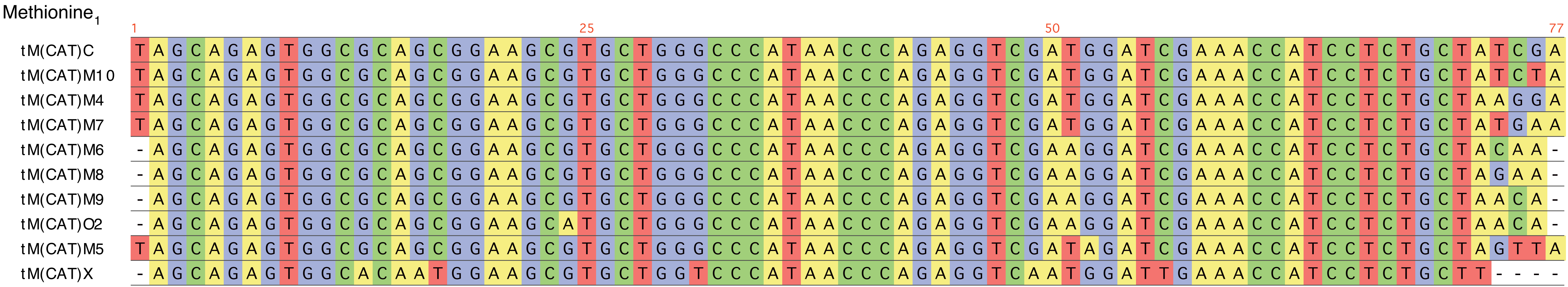

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tM(CAT)M10	T	A	G	C	A	G	A	G	T	G	G	C	G	C	A	G	C	G	G	A	A	G	C	G	T	G	C	T	G	G	G	C	C	C	A	T	A	A	C	C	C	A	G	A	G	G	T	C	G	A	T	G	G	A	T	C	G	A	A	A	C	C	A	T	C	C	T	C	T	G	C	T	A	T	C	T	A
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tM(CAT)O2	-	A	G	C	A	G	A	G	T	G	G	C	G	C	A	G	C	G	G	A	A	G	C	A	T	G	C	T	G	G	G	C	C	C	A	T	A	A	C	C	C	A	G	A	G	G	T	C	G	A	A	G	G	A	T	C	G	A	A	A	C	C	A	T	C	C	T	C	T	G	C	T	A	A	C	A	-
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tM(CAT)X	-	A	G	C	A	G	A	G	T	G	G	C	A	C	A	A	T	G	G	A	A	G	C	G	T	G	C	T	G	G	T	C	C	C	A	T	A	A	C	C	C	A	G	A	G	G	T	C	A	A	T	G	G	A	T	T	G	A	A	A	C	C	A	T	C	C	T	C	T	G	C	T	T	-	-	-	-

Methionine$_2$

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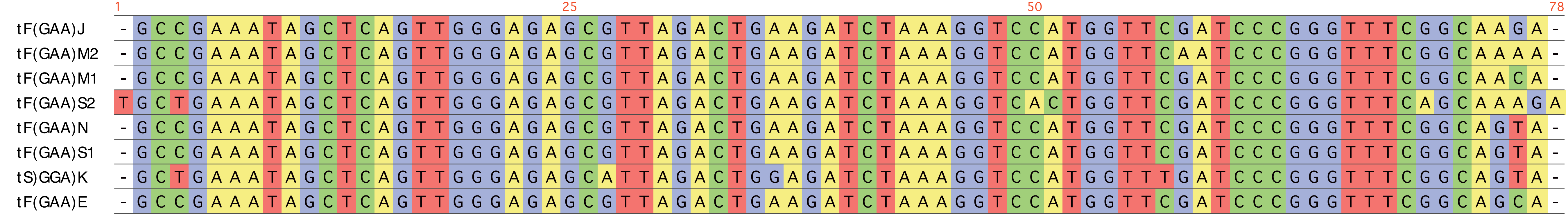
Phenylalanine



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tF(GAA)S2  TGCTGAAATAGCTCAGTTGGGAGAGCGTTAGACTGAAGATCTAAAGGTCACTGGTTCGATCCCGGGTTTCAGCAAAGA
tF(GAA)N   -GCCGAAATAGCTCAGTTGGGAGAGCGTTAGACTGAAGATCTAAAGGTCCATGGTTCGATCCCGGGTTTCGGCAGTA-
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tS)GGA)K   -GCTGAAATAGCTCAGTTGGGAGAGCATTAGACTGGAGATCTAAAGGTCCATGGTTTGATCCCGGGTTTCGGCAGTA-
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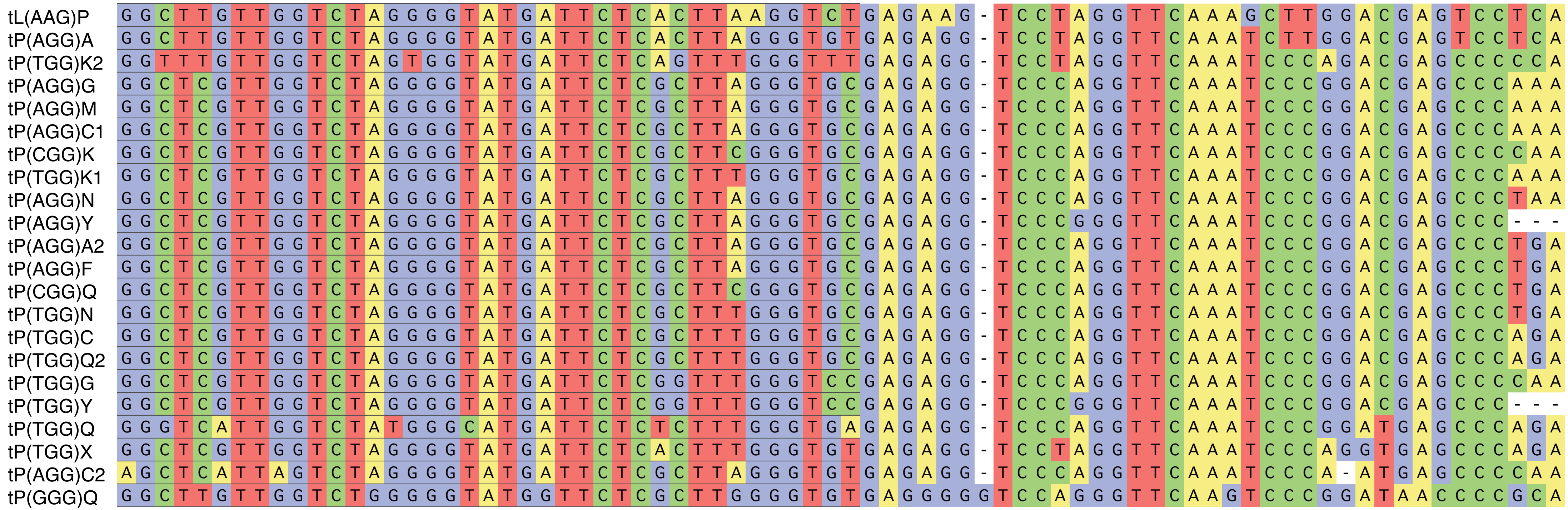
Proline



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tP(AGG)C2	AGCTCATTAGTCTAGGGGTATGATTCTCGCTTAGGGTGTGAGAGG-TCCCAGGTTCAAATCCCA-ATGAGCCCCAA
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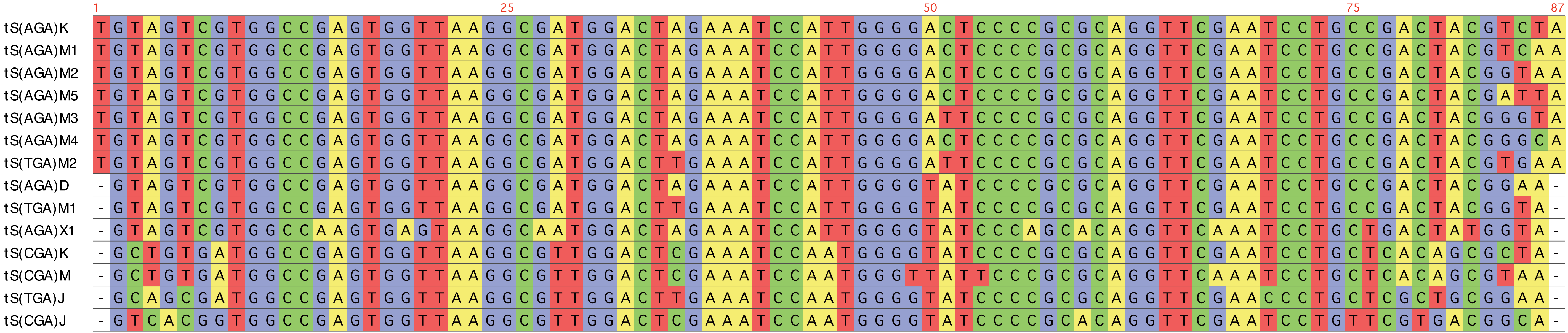
Serine$_1$



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tS(AGA)M2	T	G	T	A	G	T	C	G	T	G	G	C	C	G	A	G	T	G	G	T	T	A	A	G	G	C	G	A	T	G	G	A	C	T	A	G	A	A	A	T	C	C	A	T	T	G	G	G	G	A	C	T	C	C	C	C	G	C	G	C	A	G	G	T	T	C	G	A	A	T	C	C	T	G	C	C	G	A	C	T	A	C	G	G	T	A	A
tS(AGA)M5	T	G	T	A	G	T	C	G	T	G	G	C	C	G	A	G	T	G	G	T	T	A	A	G	G	C	G	A	T	G	G	A	C	T	A	G	A	A	A	T	C	C	A	T	T	G	G	G	G	A	C	T	C	C	C	C	G	C	G	C	A	G	G	T	T	C	G	A	A	T	C	C	T	G	C	C	G	A	C	T	A	C	G	A	T	T	A
tS(AGA)M3	T	G	T	A	G	T	C	G	T	G	G	C	C	G	A	G	T	G	G	T	T	A	A	G	G	C	G	A	T	G	G	A	C	T	A	G	A	A	A	T	C	C	A	T	T	G	G	G	G	A	T	T	C	C	C	C	G	C	G	C	A	G	G	T	T	C	G	A	A	T	C	C	T	G	C	C	G	A	C	T	A	C	G	G	G	T	A
tS(AGA)M4	T	G	T	A	G	T	C	G	T	G	G	C	C	G	A	G	T	G	G	T	T	A	A	G	G	C	G	A	T	G	G	A	C	T	A	G	A	A	A	T	C	C	A	T	T	G	G	G	G	A	C	T	C	C	C	C	G	C	G	C	A	G	G	T	T	C	G	A	A	T	C	C	T	G	C	C	G	A	C	T	A	C	G	G	G	C	A
tS(TGA)M2	T	G	T	A	G	T	C	G	T	G	G	C	C	G	A	G	T	G	G	T	T	A	A	G	G	C	G	A	T	G	G	A	C	T	T	G	A	A	A	T	C	C	A	T	T	G	G	G	G	A	T	T	C	C	C	C	G	C	G	C	A	G	G	T	T	C	G	A	A	T	C	C	T	G	C	C	G	A	C	T	A	C	G	T	G	A	A
tS(AGA)D	-	G	T	A	G	T	C	G	T	G	G	C	C	G	A	G	T	G	G	T	T	A	A	G	G	C	G	A	T	G	G	A	C	T	A	G	A	A	A	T	C	C	A	T	T	G	G	G	G	T	A	T	C	C	C	C	G	C	G	C	A	G	G	T	T	C	G	A	A	T	C	C	T	G	C	C	G	A	C	T	A	C	G	G	A	A	-
tS(TGA)M1	-	G	T	A	G	T	C	G	T	G	G	C	C	G	A	G	T	G	G	T	T	A	A	G	G	C	G	A	T	G	G	A	C	T	T	G	A	A	A	T	C	C	A	T	T	G	G	G	G	T	A	T	C	C	C	C	G	C	G	C	A	G	G	T	T	C	G	A	A	T	C	C	T	G	C	C	G	A	C	T	A	C	G	G	T	A	-
tS(AGA)X1	-	G	T	A	G	T	C	G	T	G	G	C	C	A	A	G	T	G	A	G	T	A	A	G	G	C	A	A	T	G	G	A	C	T	A	G	A	A	A	T	C	C	A	T	T	G	G	G	G	T	A	T	C	C	C	A	G	C	A	C	A	G	G	T	T	C	A	A	A	T	C	C	T	G	C	T	G	A	C	T	A	T	G	G	T	A	-
tS(CGA)K	-	G	C	T	G	T	G	A	T	G	G	C	C	G	A	G	T	G	G	T	T	A	A	G	G	C	G	T	T	G	G	A	C	T	C	G	A	A	A	T	C	C	A	A	T	G	G	G	G	T	A	T	C	C	C	C	G	C	G	C	A	G	G	T	T	C	G	A	A	T	C	C	T	G	C	T	C	A	C	A	G	C	G	C	T	A	-
tS(CGA)M	-	G	C	T	G	T	G	A	T	G	G	C	C	G	A	G	T	G	G	T	T	A	A	G	G	C	G	T	T	G	G	A	C	T	C	G	A	A	A	T	C	C	A	A	T	G	G	G	T	T	A	T	T	C	C	C	G	C	G	C	A	G	G	T	T	C	A	A	A	T	C	C	T	G	C	T	C	A	C	A	G	C	G	T	A	A	-
tS(TGA)J	-	G	C	A	G	C	G	A	T	G	G	C	C	G	A	G	T	G	G	T	T	A	A	G	G	C	G	T	T	G	G	A	C	T	T	G	A	A	A	T	C	C	A	A	T	G	G	G	G	T	A	T	C	C	C	C	G	C	G	C	A	G	G	T	T	C	G	A	A	C	C	C	T	G	C	T	C	G	C	T	G	C	G	G	A	A	-
tS(CGA)J	-	G	T	C	A	C	G	G	T	G	G	C	C	G	A	G	T	G	G	T	T	A	A	G	G	C	G	T	T	G	G	A	C	T	C	G	A	A	A	T	C	C	A	A	T	G	G	G	G	T	A	T	C	C	C	C	G	C	A	C	A	G	G	T	T	C	G	A	A	T	C	C	T	G	T	T	C	G	T	G	A	C	G	G	C	A	-

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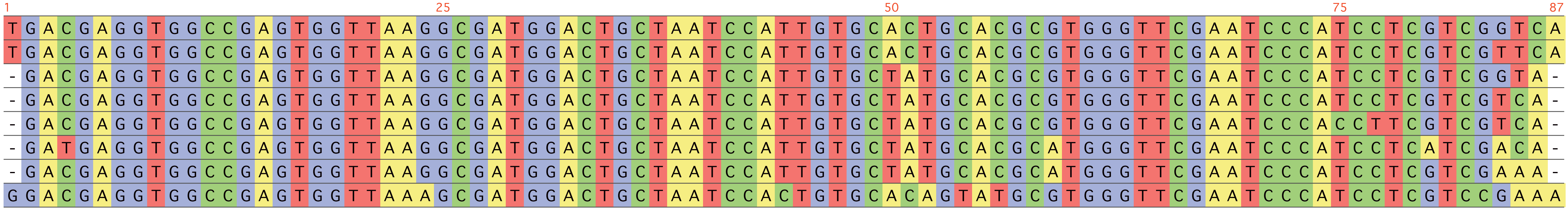

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tS(GCT)M4 TGACGAGGTGGCCGAGTGGTTAAGGCGATGGACTGCTAATCCATTGTGCACTGCACGCGTGGGTTCGAATCCCATCCTCGTCGTTCA
tS(GCT)S  -GACGAGGTGGCCGAGTGGTTAAGGCGATGGACTGCTAATCCATTGTGCTATGCACGCGTGGGTTCGAATCCCATCCTCGTCGGTA-
tS(GCT)K2 -GACGAGGTGGCCGAGTGGTTAAGGCGATGGACTGCTAATCCATTGTGCTATGCACGCGTGGGTTCGAATCCCATCCTCGTCGTCA-
tS(GCT)M2 -GACGAGGTGGCCGAGTGGTTAAGGCGATGGACTGCTAATCCATTGTGCTATGCACGCGTGGGTTCGAATCCCACCTTCGTCGTCA-
tS(GCT)M1 -GATGAGGTGGCCGAGTGGTTAAGGCGATGGACTGCTAATCCATTGTGCTATGCACGCATGGGTTCGAATCCCATCCTCATCGACA-
tS(GCT)B1 -GACGAGGTGGCCGAGTGGTTAAGGCGATGGACTGCTAATCCATTGTGCTATGCACGCATGGGTTCGAATCCCATCCTCGTCGAAA-
tS(GCT)A  GGACGAGGTGGCCGAGTGGTTAAAGCGATGGACTGCTAATCCACTGTGCACAGTATGCGTGGGTTCGAATCCCATCCTCGTCCGAAA
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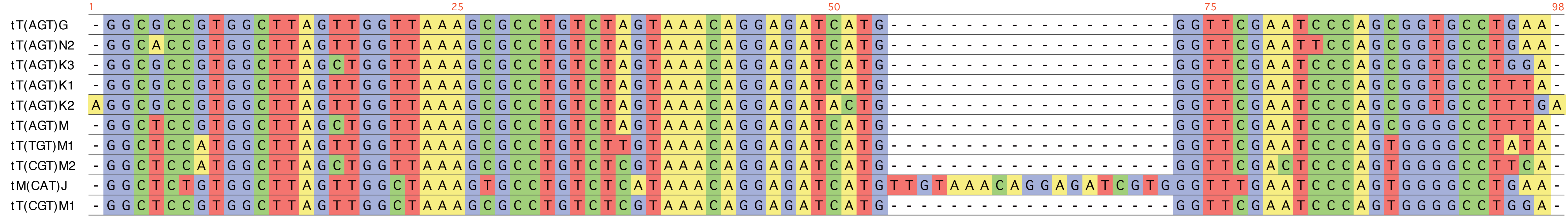
Threonine$_1$



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tT(AGT)G  -GGCGCCGTGGCTTAGTTGGTTAAAGCGCCTGTCTAGTAAACAGGAGATCATG-------------------GGTTCGAATCCCAGCGGTGCCTGAA-
tT(AGT)N2 -GGCACCGTGGCTTAGTTGGTTAAAGCGCCTGTCTAGTAAACAGGAGATCATG-------------------GGTTCGAATTCCAGCGGTGCCTGAA-
tT(AGT)K3 -GGCGCCGTGGCTTAGCTGGTTAAAGCGCCTGTCTAGTAAACAGGAGATCATG-------------------GGTTCGAATCCCAGCGGTGCCTGGA-
tT(AGT)K1 -GGCGCCGTGGCTTAGTTGGTTAAAGCGCCTGTCTAGTAAACAGGAGATCATG-------------------GGTTCGAATCCCAGCGGTGCCTTTA-
tT(AGT)K2 AGGCGCCGTGGCTTAGTTGGTTAAAGCGCCTGTCTAGTAAACAGGAGATACTG-------------------GGTTCGAATCCCAGCGGTGCCTTTGA
tT(AGT)M  -GGCTCCGTGGCTTAGCTGGTTAAAGCGCCTGTCTAGTAAACAGGAGATCATG-------------------GGTTCGAATCCCAGCGGGGCCTTTA-
tT(TGT)M1 -GGCTCCATGGCTTAGTTGGTTAAAGCGCCTGTCTTGTAAACAGGAGATCATG-------------------GGTTCGAATCCCAGTGGGGCCTATA-
tT(CGT)M2 -GGCTCCATGGCTTAGCTGGTTAAAGCGCCTGTCTCGTAAACAGGAGATCATG-------------------GGTTCGACTCCCAGTGGGGCCTTCA-
tM(CAT)J  -GGCTCTGTGGCTTAGTTGGCTAAAGTGCCTGTCTCATAAACAGGAGATCATGTTGTAAACAGGAGATCGTGGGTTTGAATCCCAGTGGGGCCTGAA-
tT(CGT)M1 -GGCTCCGTGGCTTAGTTGGCTAAAGCGCCTGTCTCGTAAACAGGAGATCATG-------------------GGTTCGAATCCCAGTGGGGCCTGGA-
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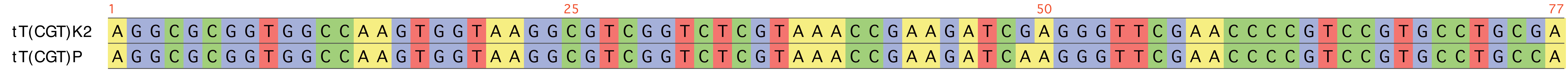
Threonine$_2$



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tT(CGT)K2  AGGCGCGGTGGCCAAGTGGTAAGGCGTCGGTCTCGTAAACCGAAGATCGAGGGTTCGAACCCCGTCCGTGCCTGCGA
tT(CGT)P   AGGCGCGGTGGCCAAGTGGTAAGGCGTCGGTCTCGTAAACCGAAGATCAAGGGTTCGAACCCCGTCCGTGCCTGCCA
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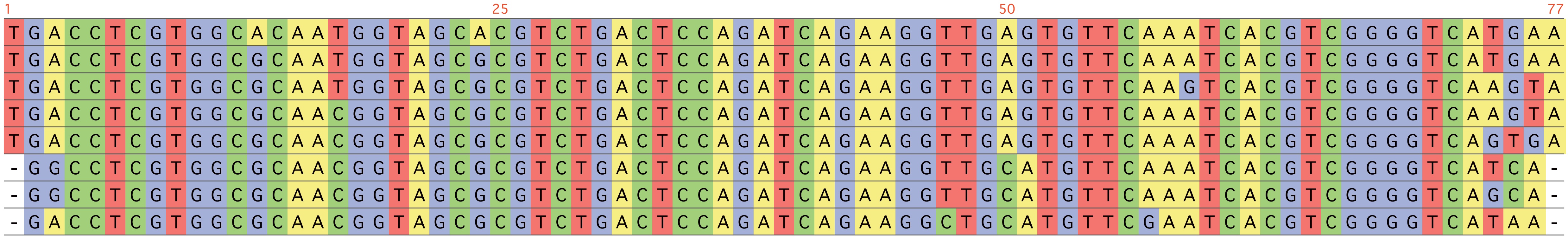
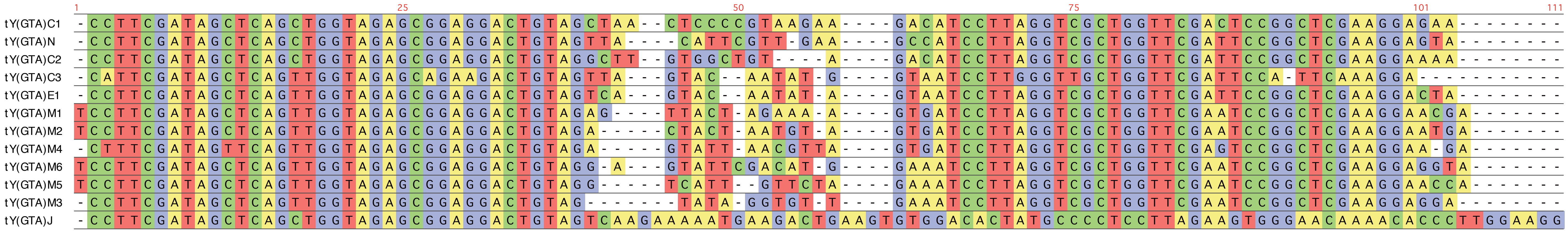
Tryptophan



tW(CCA)J1	TGACCTCGTGGCACAATGGTAGCACGTCTGACTCCAGATCAGAAGGTTGAGTGTTCAAATCACGTCGGGGTCATGAA
tW(CCA)K2	TGACCTCGTGGCGCAATGGTAGCGCGTCTGACTCCAGATCAGAAGGTTGAGTGTTCAAATCACGTCGGGGTCATGAA
tW(CCA)K1	TGACCTCGTGGCGCAATGGTAGCGCGTCTGACTCCAGATCAGAAGGTTGAGTGTTCAAGTCACGTCGGGGTCAAGTA
tW(CCA)M2	TGACCTCGTGGCGCAACGGTAGCGCGTCTGACTCCAGATCAGAAGGTTGAGTGTTCAAATCACGTCGGGGTCAAGTA
tW(CCA)M1	TGACCTCGTGGCGCAACGGTAGCGCGTCTGACTCCAGATCAGAAGGTTGAGTGTTCAAATCACGTCGGGGTCAGTGA
tW(CCA)K3	-GGCCTCGTGGCGCAACGGTAGCGCGTCTGACTCCAGATCAGAAGGTTGCATGTTCAAATCACGTCGGGGTCATCA-
tW(CCA)K4	-GGCCTCGTGGCGCAACGGTAGCGCGTCTGACTCCAGATCAGAAGGTTGCATGTTCAAATCACGTCGGGGTCAGCA-
tW(CCA)J2	-GACCTCGTGGCGCAACGGTAGCGCGTCTGACTCCAGATCAGAAGGCTGCATGTTCGAATCACGTCGGGGTCATAA-

Tyrosine



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            1                       25                       50                       75                        101       111
tY(GTA)C1   -CCTTCGATAGCTCAGCTGGTAGAGCGGAGGACTGTAGCTAA--CTCCCCGTAAGAA----GACATCCTTAGGTCGCTGGTTCGACTCCGGCTCGAAGGAGAA--------
tY(GTA)N    -CCTTCGATAGCTCAGCTGGTAGAGCGGAGGACTGTAGTTA----CATTCGTT-GAA----GCCATCCTTAGGTCGCTGGTTCGATTCCGGCTCGAAGGAGTA--------
tY(GTA)C2   -CCTTCGATAGCTCAGCTGGTAGAGCGGAGGACTGTAGGCTT--GTGGCTGT----A----GACATCCTTAGGTCGCTGGTTCGATTCCGGCTCGAAGGAAAA--------
tY(GTA)C3   -CATTCGATAGCTCAGTTGGTAGAGCAGAAGACTGTAGTTA---GTAC--AATAT-G----GTAATCCTTGGGTTGCTGGTTCGATTCCA-TTCAAAGGA-----------
tY(GTA)E1   -CCTTCGATAGCTCAGTTGGTAGAGCGGAGGACTGTAGTCA---GTAC--AATAT-A----GTAATCCTTAGGTCGCTGGTTCGATTCCGGCTCGAAGGACTA--------
tY(GTA)M1   TCCTTCGATAGCTCAGTTGGTAGAGCGGAGGACTGTAGAG----TTACT-AGAAA-A----GTGATCCTTAGGTCGCTGGTTCGAATCCGGCTCGAAGGAACGA-------
tY(GTA)M2   TCCTTCGATAGCTCAGTTGGTAGAGCGGAGGACTGTAGA-----CTACT-AATGT-A----GTGATCCTTAGGTCGCTGGTTCGAATCCGGCTCGAAGGAATGA-------
tY(GTA)M4   -CTTTCGATAGTTCAGTTGGTAGAGCGGAGGACTGTAGA-----GTATT-AACGTTA----GTGATCCTTAGGTCGCTGGTTCGAGTCCGGCTCGAAGGAA-GA-------
tY(GTA)M6   TCCTTCGATAGCTCAGTTGGTAGAGCGGAGGACTGTAGG-A---GTATTCGACAT-G----GAAATCCTTAGGTCGCTGGTTCGAATCCGGCTCGAAGGAGGTA-------
tY(GTA)M5   TCCTTCGATAGCTCAGTTGGTAGAGCGGAGGACTGTAGG-----TCATT--GTTCTA----GAAATCCTTAGGTCGCTGGTTCGAATCCGGCTCGAAGGAACCA-------
tY(GTA)M3   -CCTTCGATAGCTCAGTTGGTAGAGCGGAGGACTGTAG-------TATA-GGTGT-T----GAAATCCTTAGGTCGCTGGTTCGAATCCGGCTCGAAGGAGGA--------
tY(GTA)J    -CCTTCGATAGCTCAGCTGGTAGAGCGGAGGACTGTAGTCAAGAAAAATGAAGACTGAAGTGTGGACACTATGCCCCTCCTTAGAAGTGGGAACAAAACACCCTTGGAAGG
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Valine$_1$

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          1                       25                       50                            79
tV(CAC)A  -GTTTCCGTAGTGTAGTGGTTATCACGTTCGCCTCACAC-GCGAAAGGTCCACGGTTCGAAACCGGGCGGAAACAGCA-
tV(CAC)M5 -GTTTCCGTAGTGTAGTGGTTATCACGTTCGCCTCACAC-GCGAAAGGTCCACGGTTCGAAACCGGGCGGAAACAGTA-
tV(CAC)C1 TGTTTCTGTAGTGTAGTGGTT-TCACATTTGCCTCACAT-GCAAAAGGTCCACGGTTCTCAACCGGGCAGAAACAACTA
tV(CAC)X7 -GTTTCAGTAGTGTAGTGGTTATCACGTTTGCCTCACGC-ATGAAATGTCCCCGGTTGGAAACCTGG-GGAAACA----
tV(CAC)Q2 -GTTTCCCTAGTGTAGTGGTTATCACGTTCGCCTCACAT-GCAAAAGGTCCATGGTTCGAAACCTGGCGGAAACAGTA-
tV(AAC)C  -GTTTCCGTAGTGTAGTGGTTATCACGTTCGCCTAACAC-GCGAAAGGTCCACGGTTCGAAACCGGGCGGAAACATAA-
tV(AAC)E  -GTTTCCGTAGTGTAGTGGTTATCATGTTTGTCTAACAC-GCGAAAGGTCCACAGTTTGAAACCGGGTGGAAAAAAAA-
tG)ACC)K  -GTTTCCGTAGTGTAGTGGTTAGCGCGTTCGCCTACCAAAGCGAAAGGTCACCGGTTCGAAACCGGGCGGAAACAAAA-
tV(CAC)C3 -GTTTCCGTAGTGTAGTGGTTATCACGTTCGCCTCACAC-GCGAAAGGTCCACGGTTCGAAACCGGGCGGAAACAAGA-
tV(CAC)F  -GTTTCTGTAGTGTAGTGGTTATCACGTTCGCCTCACAC-GCGAAAGGTCCACGGTTCGAAACCGGGCAGAAACAAGA-
tV(AAC)K1 -GTTTCCGTAGTGTAGTGGTTATCACGTTCGCCTAACAC-GCGAAAGGTCCACGGTTCGAAACCGGGCGGAAACAAGA-
tV(CAC)K1 -GTTTCCGTAGTGTAGTGGTTATCACGTTCGCCTCACAC-GCGAAAGGTCCACGGTTCGAAACCGGGCGGAAACAACA-
tV(CAC)M1 TGTTTCCGTAGTGTAGTGGTTATCACGTTCGCCTCACAC-GCGAAAGGTCACCGGTTCGAAACCGGGCGGAAACAATGA
tV(AAC)M1 TGTTTCCGTAGTGTAGTGGTTATCACATTCGCCTAACAC-GCGAAAGGTCACCGGTTCGAAACCGGGCGGAAACACGTA
tV(CAC)M3 -GTTTCCGTAGTGTAGTGGTTATCACGCTCGCCTCACAC-GCGAGAGGTCCACGGTTCGAAACCGGGCGGAAACAGTA-
tV(AAC)M2 TGTTTCCGTAGTGTAGTGGTCATCACGCTCGCCTAACAC-GCGAGAGGTCACCGGTTCGAAACCGGGCGGAAACATTAA
tV(AAC)M4 TGTTTCCGTAGTGTAGTGGTCATCACGCTCGCCTAACAC-GCGAGAGGTCACCGGTTCGAAACCGGGCGGGAACATTTA
tV(AAC)M5 TGTTTCCGTAGTGTAGTGGTCATCACGCTCGCCTAACAC-GCGAGAGGTCACCGGTTCGAAACCGGGCGGAAACATGGA
tV(CAC)M2 TGTTTCCGTAGTGTAGTGGTCATCACGCTCGCCTCACAC-GCGAGAGGTCACCGGTTCGAAACCGGGCGGGAACAACAA
tV(AAC)M3 TGTTTCTGTAGTGTAGTGGTTATCACGCTCGCCTAACAC-GCGAGAGGTCACCGGTTCGAAACCGGGCAGAAACAGTGA
tV(CAC)M4 TGTTTTTGTAGTGTAGCGGTTATCACGCTCGCCTCACAC-GCGAGAGGTCATCGGTTCAAAACCCAGTGGAAACATTTA
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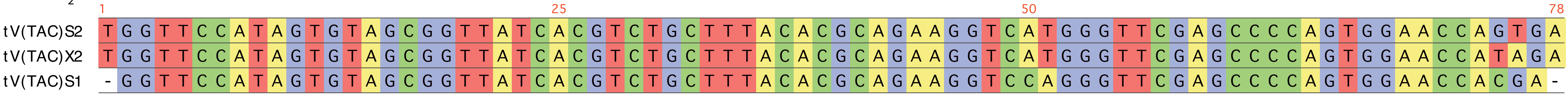
Valine$_2$



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tV(TAC)S2  TGGTTCCATAGTGTAGCGGTTATCACGTCTGCTTTACACGCAGAAGGTCATGGGTTCGAGCCCCAGTGGAACCAGTGA
tV(TAC)X2  TGGTTCCATAGTGTAGCGGTTATCACGTCTGCTTTACACGCAGAAGGTCATGGGTTCGAGCCCCAGTGGAACCATAGA
tV(TAC)S1  -GGTTCCATAGTGTAGCGGTTATCACGTCTGCTTTACACGCAGAAGGTCCAGGGTTCGAGCCCCAGTGGAACCACGA-
```

Supplemental Figure S3

This table lists the predicted mouse tRNA genes that were verified as expressed by microarray or northern blot, along with the gene location and sequence. tRNA genes are named with a lower case t to indicate tRNA, followed by the single character abbreviation for the encoded amino acid. The anticodon is shown parenthetically. The letter following the parenthesis corresponds to the chromosome where the gene is located, and a number follows if there are multiple tRNA genes with the same anticodon on an individual chromosome.

tRNA gene name	**tRNA Family**	**Amino Acid**	**Anti codon**	**Chromosome**	**Sequence Start**	**Sequence End**	**intron**	**Rogue tRNA?**	**tRNA gene sequence (including introns)**
tA(AGC)M3	Ala1	Ala	AGC	13	20602634	20602708			GGGGGTGTAGCTCAGTGGTAGAGCGCGTGCTTAGCATGCACGAGGCCCCAGGTTCAATCCCCGGCACCTCCAGTA
tA(AGC)M4	Ala1	Ala	AGC	13	20614093	20614167			GGGGGTGTAGCTCAGTGGTAGAGCGCGTGCTTAGCATGCACGAGGCCCCAGGTTCAATCCCCGGCACCTCCAGTA
tA(AGC)M5	Ala1	Ala	AGC	13	20622617	20622693			TGGGGGTGTAGCTCAGTGGTAGAGCGCGTGCTTAGCATGCACGAGGCCCAGGGTTCGATCCCCAGCACCTCCATTCA
tA(AGC)M6	Ala1	Ala	AGC	13	20639815	20639891			TGGGGATGTAGCTCAGTGGTAGAGCGCATGCTTAGCATGCATGAGGTCCAGGGTTCGATCCCCAGCATCTCCAGGCA
tA(CGC)B	Ala1	Ala	CGC	2	57135446	57135520			GGGGATGTAGCTCAGTGGTAGAGCGCGCGCTTCGCATGTGTGAGGTCCCAGGTTCAATCCCCGGCATCTCCAAGA
tA(CGC)M1	Ala1	Ala	CGC	13	20634268	20634342			GGGGATGTAGCTCAGTGGTAGAGCGCATGCTTCGCATGTATGAGGCCCCAGGTTCGATCCCCGGCATCTCCAAGA
tA(CGC)M2	Ala1	Ala	CGC	13	22818817	22818893			TGGGGATGTAGCTCAGTGGTAGAGCGCATGCTTCGCATGTATGAGGCCCAGGGTTCGATCCCCGGCATCTCCAGTTA
tA(CGC)X1	Ala1	Ala	CGC	X	126374882	126374958			TGGGGTTGTAGCTCAGAGGTAGAGCACATGCTTCGCATGTGTGTGGTCCAGGGTTCGATTCCCGGCATCTCCAGAGA
tA(CGC)X3	Ala1	Ala	CGC	X	126386524	126386600			TGGGGATGTAGCTCAGAGGTAGAGCACATGCTTCGCATGTGTGTGGTCCAGGGTTCGACTCCCGGCATCTCCAGAGA
tA(CGC)X5	Ala1	Ala	CGC	X	126402680	126402756			TGGGGATGTAGCTCAGAGGTAGAGCACATGCTTCGCATGTGTGTGGTCCAGGGTTCGACTCCCGGCATCTCCAGAGA
tA(CGC)X7	Ala1	Ala	CGC	X	126409029	126409105			TGGGGATGTAGCTCAGAGGTAGAGCACATGCTTCGCATGTGTGTGGTCCAGGGTTCGACTCCCGGCATCTCCAGAGA
tA(CGC)X9	Ala1	Ala	CGC	X	126575023	126575099			TGGGGATGTAGCTCAGAGGTAGAGCACATGCTTCGCATGTGTGTGGTCCAGGGTTCGACTCCCAGCATCTCCAGAGA
tA(CGC)X11	Ala1	Ala	CGC	X	126576924	126577001			TGGGGATGTAGCTCAGAGGTAGAGCACGTGCTTCGCATGTGTGTGGTCCAGGGGTTCGATTCCCGGCATCTCCAGGGA
tV(TAC)X1	Ala1	Val	TAC	X	126337960	126338036		Rogue	TGGAGGTGTAGCTCAATGTCAGAGCTCTTGATTTACATGTATGGGGTTCAGGGTTCGATTTCTGGCATTTCCAGATA
tA(TGC)E1	Ala1	Ala	TGC	5	122945945	122946019			GGGGATGTAGCTCAGTGGTAGAGCGCATGCTTTGCATGTATGAGGCCCCAGGTTCGATCCCCGGCATCTCCACCA
tA(TGC)E2	Ala1	Ala	TGC	5	122951170	122951244			GGGGATGTAGCTCAGTGGTAGAGCGCATGCTTTGCATGTATGAGGCCCCAGGTTCAATCCCCGGCATCTCCAACA
tA(TGC)I	Ala1	Ala	TGC	9	66457904	66457976			GGGGATGTAGCTCAGTGGCAGAGTGCATACTTTGCATGTATGAGTTACCTGGGTGAAAACTCCAGTATCTCCA
tA(TGC)K	Ala1	Ala	TGC	11	48474160	48474236			TGGGGATGTAGCTCAGTGGTAGAGCGCATGCTTTGCATGTATGAGGCCCAGGGTTCGATCCCCGGCATCTCCAAACA
tA(TGC)M	Ala1	Ala	TGC	13	20620993	20621067			GGGGGTGTAGCTCAGTGGTAGAGCGCATGCTTTGCATGCATGAGGCCCCAGGTTCGATCCCCGGCACCTCCACTA
tA(TGC)X2	Ala1	Ala	TGC	X	126364763	126364839			TGGGGATGTAGCTCAGTGGTAGAGCACATGCTTTGCATGTATGGGGTCCAGGGTTCAATTCCCGGCATCTCCAGAGA
tA(TGC)X4	Ala1	Ala	TGC	X	126387908	126387984			TGGGGATGTAGCTCAGCGGTAGAGCACATGCTTTGCATGTATGGGGTCCAGGGTTCGATTCCCGGCATCTCCACAGA
tA(TGC)X6	Ala1	Ala	TGC	X	126404065	126404141			TGGGGATGTAGCTCAGCGGTAGAGCACATGCTTTGCATGTATGGGGTCCAGGGTTCGATTCCCGGCATCTCCACAGA
tA(TGC)X8	Ala1	Ala	TGC	X	126421635	126421711			TGGAAGTGTAGTTCAATGGTAGAACCCTTGTTTTGCATATATGGGGTTCAGGGTTCGGTTCCTGGCACCACTAGGTA
tA(TGC)X10	Ala1	Ala	TGC	X	126437523	126437599			TGGGGATGTAGCTCAGTGGTAGAGCACATGCTTTGCATGTATGGGGTCCAGGGTTCGATTCCCGGCATCTCCAATGA
tA(TGC)X12	Ala1	Ala	TGC	X	126560886	126560962			TGGGGATGTAGCTCAGTGGTAGAGCACATGCTTTGCATGTATGGGGTCCAGGGTTCGATTCCCGGCATCTCCAATGA
tA(TGC)X14	Ala1	Ala	TGC	X	126576407	126576483			TGGGGATGTAGCTCAGCGGTAGAGCACATGCTTTGCATGTATGGGGTCCAGGGTTCGATTCCCGGCATCTCCAGAGA
tA(TGC)X16	Ala1	Ala	TGC	X	126597526	126597602			TGGGGATGTAGCTCAATGGTAGAGCACATGCTTTGCATGTATGAGGCACAGGGTTCGATTCCCGGCATCTCCAGGGA
tV(AAC)H	Ala2	Val	AAC	8	4082112	4082184		Rogue	TTGGGGATTTAGCTCAGTGGTAGAGCGCTTGCCTAACAAAAGCAAGGCTCTGGGTTCGGTCCTCAGCTCTGAA
tG(ACC)X1	Ala2	Gly	ACC	X	21564907	21564980		Rogue	TTGGGGATTTAGCTCAGTGGTAGAGCGTTGCCTACCAAGCACAAGGCCCTGGGTTCAGTCCTCAGCTCTGGAAA
tA(AGC)A3	Ala2	Ala	AGC	1	145819931	145820003			TTGGGGATTTAGCTCAGTGGTAGAGCGCTTGCCTAGCAAGCACAAGGCCCTGGGTTCGGTCCTCAGCTCTGAA
tA(AGC)B4	Ala2	Ala	AGC	2	120194117	120194189			TCAGGGATTTAGCTCAGTGGTAGAGCGCTTGCCTAGCAAGTGCAAGGCCCTGGGTTCGGTCCTCAGCTCTGAA
tA(AGC)E7	Ala2	Ala	AGC	5	91844561	91844635			TTGGGGATTTAGCTCAGAGGTAGAGAGCGCTTGCTTAGCAAGCACAAGGTCCTGGGTTCGATCCTCAGCTCTGAA
tA(AGC)F4	Ala2	Ala	AGC	6	97626627	97626698			GGGATTTAGCTCAGTGGTAGAGCGCTGCTTGCCTAGCAAGCACAAGGCCCTGGGTTCGGTCCTCAGCTCTTG
tA(AGC)F5	Ala2	Ala	AGC	6	116211554	116211626			TTGGGGACTTAGCTCAGTGGTAGAGCAGTTGCCTAGCAAGCACAAGGCCCTGGGTTCAGTCCTCAGCTCTGAA
tA(AGC)G3	Ala2	Ala	AGC	7	32467780	32467852			TTGGGGATTTAGCTCAGTGGTAGAGTGCGTGCCTAGCAAGCACAAGGCCCTGGGTTCTGTCCTCAGCTCTGAA
tA(AGC)G4	Ala2	Ala	AGC	7	45399804	45399876			TTGGAGATTTAGCTCAGTGGTAGAGCACTTGCCTAGCAAGCCCAAGGCCCTGAGTTCGGTCCTCAGCTCTGAA
tA(AGC)H1	Ala2	Ala	AGC	8	32175313	32175379			GGATTTAGCTCAGTGGTAGAGCGCTTGCCTAGCAAGCACAAGGCCCTGGGTTCGGTCCTCAGCTCTG
tA(AGC)I2	Ala2	Ala	AGC	9	55652779	55652851			TTGGGGATTTAGCTCAGTGGTAGAGCGCTTGCCTAGCAAGCACAAGGCCCTGGGTTCAGTCCTCAGCTCTGAA
tA(AGC)I6	Ala2	Ala	AGC	9	95869025	95869097			TTGGGGATTTAGCTCGGTGGTAGAGCGCTTGCCTAGCAAGTGCAAGGCCCTGGGTTCGGTCCTCAGCTCTGAA
tA(AGC)J1	Ala2	Ala	AGC	10	43319775	43319847			TTGGGGATTTAGCTCAGTGGTAGAGCACTTGCCTAGCAAGTGCAAGGCCCTGGGTTCGGTCCTCAGCTCTGAA
tA(AGC)J4	Ala2	Ala	AGC	10	72310320	72310386			AGAAATAGCTCAGTGGTAGAGCGCTTGCCTAGCAAGCACAAGGCCCTGGGTTCGGTCCTCAGCTCTG
tA(AGC)J5	Ala2	Ala	AGC	10	80239235	80239307			TTGGGGATTTAGCTCAGTGGTAGAGCGCTCACCCAGCAAGCAAAAGGCCCTGGGTTCAGTCCTCAGCTCTGAA
tA(AGC)K4	Ala2	Ala	AGC	11	61980219	61980293			TTGGGGATTTAGCTCAGTGGTAGAGCGCTTGCCTAGCAAACTCAAGGCTCTGAGTTCGGGCCTCAGTTCTTTAAA
tA(AGC)L2	Ala2	Ala	AGC	12	21906568	21906640			TTGGGGATTTAGCTCAGTGGTAGAGCACTTGCCTAGCAAGCACAAGGCCCTGGGTTCGGTTCTCAGCTCTGAA
tA(AGC)L3	Ala2	Ala	AGC	12	32067034	32067102			GGGGATTTAGCTAAGTGGTAGAGTGCTTGCTTAGCAAGTACAAGGCACTGAGTTCGATCCTCAGCCCCA
tA(AGC)O1	Ala2	Ala	AGC	15	41259553	41259624			TTGGGGATTTAGCTCAGTGGTAGAGCACTTGCCCAGCAAGCACAAGGCTTGGGTTCAGTCCTCAGCTCTGAA
tA(AGC)O2	Ala2	Ala	AGC	15	47814572	47814646			TTTGGGGATTTAGCTCAGTGGTAGAGCGTTTGCCTAGCAAGCACAAGGCCTTGGGTTCAGTCCTCAGCTCTAGAA
tA(AGC)O3	Ala2	Ala	AGC	15	63206629	63206701			TTGGGGATTTAGCTCAGTGGTAGAGCACTTGCCTAGCAAGCACAAGGCCCTGGGTTCAGTCCTCAGCTCTGAA
tA(AGC)P	Ala2	Ala	AGC	16	25074149	25074221			TTGGGGATTTAACTCAGTGGTAGAGCACTTGCCTAGCAAGCACAAGGCCCTGGGTTCAGTCCTCAGCTCTGAA
tA(AGC)Q1	Ala2	Ala	AGC	17	30416505	30416571			GGGGATTTAGCTCAGTGGTAGAGCGTGCCTAGCAAGCACAAGGCCCTGGGTTCTATCCTCAGCTCCA
tA(AGC)S4	Ala2	Ala	AGC	19	45310870	45310942			TTGGGGATTTAGCTCAGTGGTAGAGCACTTGTCTAGCAAGCACAAGGCCTTGGGTTCGGTCCTCAGCTCCAAA
tA(AGC)X	Ala2	Ala	AGC	X	134259185	134259257			TTGGGGATTTAGCTCAGTGGTAGAGCACTTGCCTAGCAAGAGCAAGGCCCTGGGTTTGGTCCTCAGCCCTGAA
tA(AGC)C1	Ala3	Ala	AGC	3	19303425	19303500			GGGGGATTAGCTCAAATGGTAGAGCGCTCGCTTAGCATGCGAGAGGTAGAGGGATCGATGCCCGCATCCTCCAGTA
tA(AGC)E3	Ala3	Ala	AGC	5	29296699	29296776			TGGGGGATTAGCTCAAATGGTAGAGCGCTCGCTTAGCATGCGAGAGGTAACGGGATCGATGCCCGCATCCTCCACTTA
tA(AGC)M7	Ala3	Ala	AGC	13	22665773	22665848			GGGGGATTAGCTCAAATGGTAGAGCGCTCGCTTAGCATGCGAGAGGTAGAGGGATCGATGCCCACATCCTCCAGTA
tA(AGC)M8	Ala3	Ala	AGC	13	22679185	22679260			GGGGGATTAGCTCAAATGGTAGAGCGCTCGCTTAGCATGCGAGAGGTAGAGGGATCGATGCCCACATCCTCCAGTA
tA(AGC)M9	Ala3	Ala	AGC	13	22780916	22780991			GGGGGATTAGCTCAAATGGTAGAGCGCTCGCTTAGCATGCGAGAGGTAGAGGGATCGATGCCCACATCCTCCACAA
tA(AGC)M10	Ala3	Ala	AGC	13	22793061	22793138			TGGGGGATTAGCTCAAATGGTAGAGCGCTCGCTTAGCATGCAAGAGGTAATGGGATCGATGCCCACATCCTCCAGCTA
tA(AGC)M11	Ala3	Ala	AGC	13	22811536	22811611			GGGGAATTAGCTCAAATGGTAGAGCGCTCGCTTAGCATGCGAGAGGTAGAGGGATCGATGCCCGCATTCTCCAGTA
tA(AGC)S1	Ala3	Ala	AGC	19	3364636	3364713			TGGGGAATTAGCTCAAATGGTAGAGCGCTCGCTTAGCATGTGAGAGGTAACGGGATCGATGCCCGCATTCTCCATAGA
tR(ACG)C	Arg1	Arg	ACG	3	19302385	19302462			CGGGCCAGTGGCGCAATGGATAACGCGTCTGACTACGGATCAGAAGATTATAGGTTCGACTCCTACCTGGCTCGAGCA
tR(ACG)I	Arg1	Arg	ACG	9	123543770	123543847			CGGGCCAGTGGCGCAATGGATAACGCGTCTGACTACGGATCAGAAGATTATAGGTTCGACTCCTGGCTGGCTCGACGA
tR(ACG)M1	Arg1	Arg	ACG	13	21401264	21401341			CGGGCCAGTGGCGCAATGGATAACGCGTCTGACTACGGATCAGAAGATTATAGGTTCGACTCCTGGCTGGCTCGACCA
tR(ACG)M2	Arg1	Arg	ACG	13	22826913	22826988			GGGCCAGTGGCGCAATGGATAACGCGTCTGACTACGGATCAGAAGATTCAAGGTTCGACTCCTGGCTGGCTCGGAA
tR(ACG)M3	Arg1	Arg	ACG	13	22880642	22880719			TGGGCCAGTGGCGCAATGGATAACGCGTCTGACTACGGATCAGAAGATTACAGGTTCGACTCCTGGCTGGCTCGGTAA
tR(ACG)N	Arg1	Arg	ACG	14	46491443	46491520			CGGGCCAGTGGCGCAATGGATAACGCGTCTGACTACGGATCAGAAGATTACAGGTTCGACTCCTGGCTGGCTCGTTGA
tR(CCG)K	Arg1	Arg	CCG	11	106683990	106684067			TGACCCAGTGGCCTAATGGATAAGGCATCAGCCTCCGGAGCTGGGGATTATGGGTTCGAGTCCCATCTGGGTCGCATA
tR(CCG)M	Arg1	Arg	CCG	13	20595502	20595579			TGGCCGCGTGGCCTAATGGATAAGGCGTCTGATTCCGGATCAGAAGATTAAGGGTTCGAGTCCCTTCGTGGTCGGTGA
tR(CCG)Q	Arg1	Arg	CCG	17	22146189	22146264			GGCCGCGTGGCCTAATGGATAAGGCGTCTGATTCCGGATCAGAAGATTGAGGGTTCGAGTCCCTTCGTGGTCGCTA
tR(TCG)G	Arg1	Arg	TCG	7	66546217	66546294			CGGCCGCGTGGCCTAATGGATAAGGCGTCTGACTTCGGATCAGAAGATTACAGGTTCGAGTCCTGCCGCGGTCGACTA
tR(TCG)K	Arg1	Arg	TCG	11	115084908	115084983			GACCGCGTGGCCTAATGGATAAGGCGTCTGACTTCGGATCAGAAGATTGAGGGTTCGAGTCCCTTCGTGGTCGAAA
tR(TCG)M1	Arg1	Arg	TCG	13	20659743	20659820			CGACCACGTGGCCTAATGGATAAGGCGTCTGACTTCGGATCAGAAGATTAAGGGTTCGAATCCCTTCGTGGTTGGTAA
tR(TCG)M2	Arg1	Arg	TCG	13	22884101	22884176			GACCACGTGGCCTAATGGATAAGGCGTCTGACTTCGGATCAGAAGATTGAGGGTTCGAATCCCTTCGTGGTTGAGA
tR(TCG)M3	Arg1	Arg	TCG	13	22906576	22906653			TGACCACGTGGCCTAACGGATAAGGCGTCTGACTTCGGATCAGAAGATTAAGGGTTCGAATCCCTTCGTGGTTACTTA
tR(CCT)F	Arg2	Arg	CCT	6	38462972	38463047			GCCCCAGTGGCCTAATGGATAAGGCATTGGCCTCCTAAGCCAGGGATTGAGGGTTCGAGTCCCATCTGGGGTGGTA
tR(CCT)K1	Arg2	Arg	CCT	11	115084110	115084185			GCCCCAGTGGCCTAATGGATAAGGCACTGGCCTCCTAAGCCAGGGATTGAGGGTTCGAGTCCCACCTGGGGTAAAA
tR(CCT)K2	Arg2	Arg	CCT	11	115084429	115084506			CGCCCCAGTGGCCTAATGGATAAGGCACTGGCCTCCTAAGCCAGGGATTATGGGTTCGAGTCCCACCTGGGGTGGTGA
tR(CCT)Q	Arg2	Arg	CCT	17	22144694	22144769			GCCCCGGTGGCCTAATGGATAAGGCATTGGCCTCCTAAGCCAGGGATTGAGGGTTCGAGTCCCACCCGGGGTAATA
tR(CCT)X2	Arg2	Arg	CCT	X	102704669	102704744			GCCCCAGTGGCCTAATGGATAAGGCACTGGCCTCCTAAGCCAGGGATTGAGGGTTCGAGTCCCACCTGGGGTGGTA
tR(TCT)A	Arg2	Arg	TCT	1	173520466	173520542			GTCTCTGTGGCGCAATGGACGAGCGCGCTGGACTTCTAATCCAGAGGTTATGGGTTCGAGTCCCGGCAGAGATGATA
tR(TCT)C	Arg2	Arg	TCT	3	122675382	122675471	I		TGGCTCCGTGGCGCAATGGATAGCGCATTGGACTTCTAGAGGCTGAAGGAATTCAAAGGTTCCGGGTTCGAGTCCCGGCGGAGTCGGAAA
tR(TCT)I	Arg2	Arg	TCT	9	83459349	83459437	I		GGCTCTGTGGAGCAATGGATAGCACATTGGACTTCTAGCATGACCGAGAAATTCAAAGGTTGCGGGTTCGAGTCCCACCAGAGTTGACA
tR(TCT)K	Arg2	Arg	TCT	11	68736034	68736125	I		TGGCTCTGTGGCGCAATGGATAGCGCATTGGACTTCTAGTGACGAGAAAACGATTCAAAGGTTGTGGGTTCGAATCCCACCAGAGTCGGTTA
tR(TCT)M	Arg2	Arg	TCT	13	21297283	21297371	I		GGCTCTGTGGCGCAATGGATAGCGCATTGGACTTCTAGCATGATTGAGAAATTCAAAGGTTGCGGGTTCGAGTCCCGCCAGAGTCGACA
tR(TCT)S	Arg2	Arg	TCT	19	11261938	11262028	I		TGGCTCTGTGGCGCAATGGATAGCGCATTGGACTTCTAGACAAATGGAGACATTCAAAGGTTGTGGGTTCGAGTCCCACCAGAGTCGCTTA
tN(GTT)A1	Asn	Asn	GTT	1	171111504	171111580			GTCTCTGTGGCGCAATCGGTTAGCGCGTTCGGCTGTTAACCGAAAGGTTAGTGGTTCGAGCCCACCCAGGGACGGTA
tN(GTT)A2	Asn	Asn	GTT	1	188611697	188611775			TGCCTCTGTGGTGCAATTGGTTAGCATGTTCCGCTGTTAACCAAAAGGTAGGTGGTTCGAGCCCACCCAGGGACAACAA
tN(GTT)B	Asn	Asn	GTT	2	18642798	18642874			GTCTCTGTGGCGCAATCGGTTAGCGCGTTCGGCTGTTAACCGAAAGGTTAGTGGTTCGAGCCCACCCAGGGACGCCA
tN(GTT)C1	Asn	Asn	GTT	3	96327800	96327878			TGTCTCTGTGGCGCAATTGGTTAGCGCGTTCGGCTGTTAACCGAAAGGTAGGTGGTTCAAGCCCACCCAGGGACGTCGA
tN(GTT)C2	Asn	Asn	GTT	3	96340339	96340417			TGTCTCCGTGGCGCAATCGGTCAGCGCGTTCGGCTGTTAACCGAAAGGTAGGTGGTTCGAGCCCACCCGGGGACGTGTA
tN(GTT)C3	Asn	Asn	GTT	3	96340792	96340870			TGTCTCTGTGGTGCAATCGGTCAGCGCGTTTGGCTGTTAACTGGAAGGTAGGTGGTTTGAGCCCACCCGGGGACGTGTA
tN(GTT)C4	Asn	Asn	GTT	3	96403400	96403478			CGTCTCTGTGGCGCAATCGGTTAGCGCGTTCGGCTGTTAACCGAAAGGTAGGTGGTTCGAGCCCACCCAGGGACGAGCA
tN(GTT)C5	Asn	Asn	GTT	3	96453176	96453254			CGTCTCTGTGGCGCAATCGGTTAGCGCGTTCGGCTGTTAACCGAAAGGTAGGTGGTTCGAGCCCACCCAGGGACGACAA
tN(GTT)C6	Asn	Asn	GTT	3	96501560	96501638			TGTCTCTGTGGCGCAATCGGTTAGCGCGTTCGGCTGTTAACCGAAAGGTAGGTGGTTCGAGCCCACCCAGGGACGGTGA
tN(GTT)E3	Asn	Asn	GTT	5	146564060	146564138			TGTCTCTGTGGCGCAATCGGTTAGCGCGTTCGGCTGTTAACCGAAAGGTAGGTGGTTCGAGCCCACCCAGGGACGGCAA
tN(GTT)H	Asn	Asn	GTT	8	120076832	120076909			GTCTCTGTCATGCAGTCGGTTAGTGAGCGAGTTAGGCTGTTAACCGGAAGGTTGGTGGTTCGAGCCCACCCAAGGACA
tN(GTT)J	Asn	Asn	GTT	10	80150086	80150164			CGTCTCTGTGGCGCAATCGGTTAGCGCGTTCGGCTGTTAACCGAAAGGTAGGTGGTTCGAGCCCACCCAGGGACGACCA
tN(GTT)K	Asn	Asn	GTT	11	97373568	97373646			CGTCTCTGTGGCGCAATCGGTTAGCGCGTTCGGCTGTTAACCGAAAGGTAGGTGGTTCGAGCCCACCCAGGGACGGTCA
tN(GTT)O	Asn	Asn	GTT	15	16185170	16185246			GTCTCTGTGGCGCGATCGGTTAGTGCGTTTGGCTGTTAACCGAAAGGTTAGTGGTTCAAACCCACCCGGGGACGACA
tD(GTC)A1	Asp	Asp	GTC	1	171114591	171114665			TCCTCGTTAGTATAGTGGTGAGTATCCCCGCCTGTCACGCGGGAGACCGAGGTTCGATTCCCCGACGGGGAGACA
tD(GTC)A2	Asp	Asp	GTC	1	171143364	171143438			TCCTCGTTAGTATAGTGGTGAGTATCCCCGCCTGTCACGCGGGAGACCGAGGTTCGATTCCCCGACGGGGAGAGA
tD(GTC)A3	Asp	Asp	GTC	1	171173626	171173700			TCCTCGTTAGTATAGTGGTGAGTATCCCCGCCTGTCACGCGGGAGACCGAGGTTCGATTCCCCGACGGGGAGATA
tD(GTC)B	Asp	Asp	GTC	2	113884942	113885018			TTCCTCGTTAGTATAGTGGTGAGTATCCCTGCCTGTCACGCAGGACACCAGGGTTCGATTTCCTGACGGGGAGGCAA
tD(GTC)E1	Asp	Asp	GTC	5	98329089	98329163			TCCTCGTTAGTATAGTGGTGAGTATCCCCGCCTGTCACACAGGAGACCGAGGTTCGATTCCCCGATGGGGAGAGA
tD(GTC)E2	Asp	Asp	GTC	5	122947301	122947377			TTCCTCGTTAGTATAGTGGTGAGTATCCCCGCCTGTCACGCGGGAGACCAGGGTTCGATTCCCCGACGGGGAGATTA
tD(GTC)E3	Asp	Asp	GTC	5	122950711	122950785			TCCTCGTTAGTATAGTGGTGAGTATCCCCGCCTGTCACGCGGGAGACCGAGGTTCGATTCCCCGACGGGGAGGCA
tD(GTC)J1	Asp	Asp	GTC	10	90952735	90952811			CTCCTCGTTAGTATAGTGGTTAGTATCCCCGCCTGTCACGCGGGAGACCAGGGTTCAATTCCCCGACGGGGAGGTTA
tD(GTC)J2	Asp	Asp	GTC	10	93224814	93224890			TTCCTCGTTAGTATAGTGGTGAGTATCCCCGCCTGTCACGCGGGAGACCAGGGTTCGATTCCCCGACGGGGAGGTAA
tD(GTC)K1	Asp	Asp	GTC	11	7764570	7764644			TCCTCGTTAGTATAGTGGTGAGTATCCCCGCCTGTCACGCGGGAGACCGAGGTTCGATTCCCCGACGGGGAGATA
tD(GTC)K2	Asp	Asp	GTC	11	68653539	68653615			CTCCTCGTTAGTATAGTGGTGAGTATCCCCGCCTGTCACGCGGGAGACCAGGGTTCGATTCCCCGACGGGGAGAAGA
tD(GTC)M1	Asp	Asp	GTC	13	21291436	21291512			CTCCTCGTTAGTATAGTGGTGAGTATCCCCGCCTGTCACGCGGGAGACCAGGGTTCGATTCCCCGACGGGGAGTCTA
tD(GTC)M2	Asp	Asp	GTC	13	21315617	21315693			TTCCTCGTTAGTATAGTGGTGAGTATCCCCGCCTGTCACGCGGGAGACCAGGGTTCGATTCCCCGACGGGGAGAAGA
tD(GTC)M3	Asp	Asp	GTC	13	21320440	21320514			TCCTCGTTAGTATAGTGGTGAGTATCCCCGCCTGTCACGCGGGAGACCGAGGTTCGATTCCCCGACGGGGAGAGA
tC(ACA)F1	Cys	Cys	ACA	6	48124169	48124238			GGAGGCATAGCTCAGAGGTAGAGCATTTGACTACAGATCAGCAGGACCCTGATTCAAATCAGGTGCCCTG
tC(GCA)F3	Cys	Cys	GCA	6	47887487	47887563			AGGGGGTATAGCTCAGTGGTAGAGCATTTGACTGCAGATCAAGAGGTCCACGGTTCAAATCCGGGTGCCCCCTTACA
tC(GCA)F4	Cys	Cys	GCA	6	48042818	48042892			GGGGGTATAGCTCAGGGGTAGAGCATTTGACTGCAGATCAAGAGGTCCCAGGTTCAAATCCAGGTGCCCCCTTAA
tC(GCA)F5	Cys	Cys	GCA	6	48070603	48070677			GGGGGTATAGCTCAGGGGTAGAGCATTTGACTGCAGATCAAGAGGTCCCAGGTTCAAATCCAGGTGCCCCCTACA
tC(GCA)F6	Cys	Cys	GCA	6	48071598	48071672			GCGGGTATAGCTCAGGGGTAGAATATTTGACTGCAGATCAAGAGGTCCCATGTTCGAATTCAGGTGCCCTCTTTA
tC(GCA)F7	Cys	Cys	GCA	6	48074525	48074599			GGGGGTATAGCTCAGGGGTAGAGCATTTGACTGCAGATCAAGAGGTCCCAGGTTCAAATCCAGGTGCCCCCTATA
tC(GCA)F8	Cys	Cys	GCA	6	48096655	48096731			GGGGGGTAAAGCTCAGGGGTAGAGCATTTGACTGCAGATTAAGAGGTCCATGGTTCAAATCCAGGTACCCCCTGTTA
tC(GCA)F9	Cys	Cys	GCA	6	48107364	48107438			GGGGGTATAGCTCAGGGGTAGAGCATTTGACTGCAGATCAAGAGGTCCCAGGTTCAAATCCAGGTGCCCCCTTGA
tC(GCA)F10	Cys	Cys	GCA	6	48113324	48113398			GGGTGTGTGGATCATGGGTAGAGCATTTAACTGCACATCAAGAGGTGTCAGGTTCAAATCCAGATGTCCCCTATA
tC(GCA)F11	Cys	Cys	GCA	6	48114641	48114717			AGGGGGTATAGCTCAGGGGTGGAGCATTTGACTGCAGATCAAGGGGTCCATGTTTCAAATCCAGGTGCCCCCTAATA
tC(GCA)F12	Cys	Cys	GCA	6	48117022	48117096			GGGGGTATAGCTCAGGGGTAGAGCATTTGACTGCAGATCAAGAGGTCCCAGGTTCAAATCCAGGTGCCCCCTACA
tC(GCA)F13	Cys	Cys	GCA	6	48119409	48119483			GGGGGTATAGCTCAGGGGTAGAGCATTTGACTGCAGATCAAGAGGTCCCAGGTTCAAATCCGGGTGCCCCCTACA
tC(GCA)F14	Cys	Cys	GCA	6	48133976	48134050			GGGGGCATAGCTCAGGGGTAGAGCATTTGACTGCAGATCAAGAGGTCCCAGGTTCAAATCCGGGTGCTCCCTTCA
tC(GCA)F15	Cys	Cys	GCA	6	48160950	48161024			GGGGGTATAGCTCAGGGGTAGAGCATTTGACTGCAGATCAAGAGGTCCCAGGTTCAAATCCAGGTGCCCCCTACA
tC(GCA)F16	Cys	Cys	GCA	6	48168737	48168811			GGGGGTATAGCTCAGGGGTAGAGCATTTGACTGCAGATCAAGAGGTCCCAGGTTCAAATCCAGGTGCCCCCTTCA
tC(GCA)F17	Cys	Cys	GCA	6	48169714	48169788			GGGGGTATAGCTCAGGGGTAGAGCATTTGACTGCAGATCAAGAGGTCCTAGGTTCAAATCCAGGTGTCCCCTACA
tC(GCA)F18	Cys	Cys	GCA	6	48178369	48178445			AGGGGGTATAGCTCAGGGGTAGAGCATTTGACTGCAGATCAAGAGGTCCATGGTTCAAATCCAGGTGCCCCCTTTTA
tC(GCA)F19	Cys	Cys	GCA	6	48186762	48186838			AGGGGGTATAGCTCAGGGGTAGAGCATTTGACTGCAGATCAAGAGGTCCATGGTTCAAATCCAGGTGCCCCCTTTTA
tC(GCA)F20	Cys	Cys	GCA	6	48190235	48190309			GGGGGTATAGCTCAGGGGTAGAGCATTTGACTGCAGATCAAGAGGTCCCAGGTTCAAATCCAGGTGCCCCCTTAA
tC(GCA)F21	Cys	Cys	GCA	6	48191990	48192064			GGGGGTATAGCTCAGGGGTAGAGCATTTGACTGCAGATCAAGAGGTCCCAGGTTCAAATCCAGGTGCCCCCTTAA
tC(GCA)F22	Cys	Cys	GCA	6	48196271	48196345			GGGGGAATAGCTTAGGGGTAGAGCATTTGAATGCAGATCAAGAGGTCTCAGGTTCAAATCCAGGTGCCCCCTTTA
tC(GCA)F23	Cys	Cys	GCA	6	48197250	48197324			GGGGGTATAGCTCAGGGGTAGAGCATTTGACTGCAGATCAAGAGGTCCCAGGTTCAAATCCAGGTGCCCCCTACA
tC(GCA)F24	Cys	Cys	GCA	6	48206355	48206429			GGGGGTATAGCTCAGGGGTAGAGTATTTGGCTGCAGATCAAGAGGTCCCAGGTTCAAATCCAGGTGCCCCCTTTA
tC(GCA)F25	Cys	Cys	GCA	6	48210487	48210561			GGGGGTATAGCTCAGGGGTAGAGCATTTGACTGCAGATCAAGAGGTCCCAGGTTCAAATCCAGGTACCCCCTATA
tC(GCA)F26	Cys	Cys	GCA	6	48214916	48214990			GGGGGTATAGCTCAGGGGTAGAGCATTTGACTGCAGATCAAGAGGTCCCAGGTTCAAATCCAGGTGCCCCCTTTA
tC(GCA)F27	Cys	Cys	GCA	6	48216430	48216504			GGGGGTATAGCTCAGGGGTAGAGCATTTGACTGCAGATCAAGAGGTCCCAGGTTCAAATCCAGGTGCCCCCTATA
tC(GCA)F28	Cys	Cys	GCA	6	48218873	48218949			GGGGTTATAGCTCAGGTGTAGAGCATTTGACTGCAGATCAAGAGGTTCCATGGTTCAAATCCAGGGTGTGCCCCCTA
tC(GCA)F29	Cys	Cys	GCA	6	48219885	48219959			GGGGGTATAGCTCAGGGGTAGAGCATTTGACTGCAGATTAAGAGGTCCCAGGTTCAAATCCAGGTGCCCCCTTTA
tC(GCA)F30	Cys	Cys	GCA	6	48277546	48277620			GGGGGTATAGCTCAGGGGTAGAGCATTTGACTGCAGATCAAGAGGTCCCAGGTTCAAATCCAGGTGCCCCCTTAA
tC(GCA)F31	Cys	Cys	GCA	6	48278462	48278533			AGGGATAGAGCTCAGGGGTAGAACACTTGACTGCAGATCAAGAGGTCCCTGGTCCAAATCCTGGTACCCCTA
tC(GCA)I1	Cys	Cys	GCA	9	104322027	104322101			GGGGGTATAGCTCAGGGGTAGAGCATTTGACTGCAGATCAAGAGGTCCCAGGTTCAAATCCAGGTGCCCCCTGTA
tC(GCA)I2	Cys	Cys	GCA	9	104325963	104326037			GGGGGTATAGCTCAGTGGTAGAGCATTTGACTGCAGATCAAGAGGTCCCAGGTTCAAATCCAGGTGCCCCCTGGA
tC(GCA)K1	Cys	Cys	GCA	11	97440948	97441024			AGGGGGTATAGCTCAGGGGTAGAGCATTTGACTGCAGATCAAGAGGTCCATGGTTCAAATCCGGGTGCCCCCTCCAA
tC(GCA)K2	Cys	Cys	GCA	11	97468194	97468270			AGGGGGTATAGCTCAGTGGTAGAGCATTTGACTGCAGATCAAGAGGTCCACGGTTCAAATCCGGGTGCCCCCTTGGA
tC(GCA)K3	Cys	Cys	GCA	11	97470026	97470100			GGGGGTATAGCTCAGTGGTAGAGCATTTGACTGCAGATCAAGAGGTCCCAGGTTCAAATCCGGGTGCCCCCTCAA
tC(GCA)K4	Cys	Cys	GCA	11	97659365	97659441			AGGGGGTATAGCTCAGTGGTAGAGCATTTGACTGCAGATCAAGAGGTCCACGGTTCAAATCCGGGTGCCCCCTAGCA
tC(GCA)K5	Cys	Cys	GCA	11	97660043	97660117			GGGGGTATAGCTCAGTGGTAGAGCATTTGACTGCAGATCAAGAGGTCCCAGGTTCAAATCCGGGTGCCCCCTCAA
tC(GCA)Q	Cys	Cys	GCA	17	70031560	70031634			GGGGGTATAGCTCAGTGGTAGAGCATTTGACTGCAGATCAAGAGGTCCCAGGTTCAAATCCAGGTGCCCCCTTCA
tQ(CTG)B	Gln	Gln	CTG	2	112100587	112100663			GGGTTCCATGGTGTAATGGTTAGCACTCTGGACTCTGAATCCAGCCATAAAAGTTCAAATCTCAGTGGAACCTTAAA
tQ(CTG)C1	Gln	Gln	CTG	3	96346978	96347054			AGGTTCCATGGTGTAATGGTTAGCACTCTGGACTCTGAATCCAGCGATCAGAGTTCAAATCTCGGTGGGACCTCTCA
tQ(CTG)C2	Gln	Gln	CTG	3	96400238	96400314			GGGTTCCATGGTGTAATGGTTAGCACTCTGGACTCTGAATCCAGCGATCAGAGTTCAAATCTCGGTGGGACCTTTGA
tQ(CTG)C3	Gln	Gln	CTG	3	96483170	96483246			GGGTTCCATGGTGTAATGGTTAGCACTCTGGACTCTGAATCCAGCGATCAGAGTTCAAATCTCGGTGGGACCTTTTA
tQ(CTG)C4	Gln	Gln	CTG	3	97681246	97681322			GGGTTCCATGGTGTAATGGTGAGCACTCTGGACTCTGAATCCAGCGATCAGAGTTCAAATCTCGGTGGGACCTTTCA
tQ(CTG)F	Gln	Gln	CTG	6	90101905	90101980			GGGTTCCTTGGTGTAAGATGAGCACTCTGGATTCTGAATCCAGCGATCAAAGTTCAAATCTCGGTGGGACCTCCAA
tQ(CTG)I	Gln	Gln	CTG	9	64977091	64977165			GGTTCCATGGTGTAATGGTTAGCACTCTGGACTCTGAATCCAGCGATCCAAGTTCAAATCTCGGTGGAACCTGCA
tQ(CTG)K	Gln	Gln	CTG	11	68737159	68737235			GGGTTCCATGGTGTAATGGTTAGCACTCTGGACTCTGAATCCAGCGATCAGAGTTCAAATCTCGGTGGAACCTTAGA
tQ(CTG)M1	Gln	Gln	CTG	13	21314081	21314157			GGGTTCCATGGTGTAATGGTTAGCACTCTGGACTCTGAATCCAGCGATCAGAGTTCAAATCTCGGTGGAACCTAGTA
tQ(CTG)M2	Gln	Gln	CTG	13	21376702	21376776			GGTTCCATGGTGTAATGGCTAGCACTCTGGACTCTGAATCCAGCGATCCAAGTTCAAATCTCGGTGGGATTTATA
tQ(TTG)C	Gln	Gln	TTG	3	96393467	96393543			AGTTTCCATGGTGTAATGGTTGGCACTCTGGACTTTGAATCCAGCAATCAAAGTTCAAGTCTCTGTGGGACCTCTCA
tQ(TTG)K1	Gln	Gln	TTG	11	85863832	85863908			AGGACCCATGGTGTAATGGTTAGCACTCTGGACTTTGAATCCAGCAATCAAAGTTCAAATCTCGGTGGGACCTCTTA
tQ(TTG)K2	Gln	Gln	TTG	11	95530291	95530367			AGGTCCCATGGTGTAATGGTTAGCACTCTGGACTTTGAATCCAGCGATCAGAGTTCAAATCTCGGTGGGACCTCACA
tQ(TTG)M1	Gln	Gln	TTG	13	20648513	20648589			GGGTCCCATGGTGTAATGGTTAGCACTCTGGACTTTGAATCCAGCAATCAGAGTTCAAATCTCGGTGGGACCTTTAA
tQ(TTG)M2	Gln	Gln	TTG	13	22899173	22899249			AGGCCCCATGGTGTAATGGTTAGCACTCTGGACTTTGAATCCAGCGATCAGAGTTCAAATCTCGGTGGGACCTCATA
tQ(TTG)M3	Gln	Gln	TTG	13	22899737	22899811			GGCCCCATGGTGTAATGGTTAGCACTCTGGACTTTGAATCCAGCGATCCAAGTTCAAATCTCGGTGGGACCTTCA
tQ(TTG)M4	Gln	Gln	TTG	13	43115851	43115921			GACCCTGCAGTGTAATGGTTAGCACTCTGGACTTTGGATTCAGTGGTCTGAGTTCAAACCTCAGTGGATCC
tQ(TTG)X1	Gln	Gln	TTG	X	12190883	12190959			TGGTCTCATGGTGTAATGGTTAGCACACTGGACTTTGAGTCCAGCAATCAGAGTTCGAGTCTTGGTGAGACCACTCA
tA(CGC)D	Glu1	Ala	CGC	4	130374246	130374320		Rogue	TCCCTGGTAGTCTAGTGGTTAGGATTCGGTGCTCGCACCGCCGTGGCCCAGGTTTGAATCCTAGTCAGGGAAGTA
tE(CTC)A1	Glu1	Glu	CTC	1	156493583	156493657			TCCCTGGTGGTTTAGTGGTTAGGATTTGGCGCTCTCAACACCGAAGCCCAGGTTCAATTCCCAGTCAGGGAAGCA
tE(CTC)A2	Glu1	Glu	CTC	1	171142159	171142233			TCCCTGGTGGTCTAGTGGTTAGGATTCGGCGCTCTCACCGCCGCGGCCCAGGTTCGATTCCCGGTCAGGGAAGCA
tE(CTC)A3	Glu1	Glu	CTC	1	171174298	171174372			TCCCTGGTGGTCTAGTGGTTAGGATTCGGCGCTCTCACCGCCGCGGCCCAGGTTCGATTCCCGGTCAGGGAAGTA
tE(CTC)C1	Glu1	Glu	CTC	3	96505223	96505299			TTCCCTGGTGGTCTAGTGGTTAGGATTCGGCGCTCTCACCGCCGCGGCCAGGGTTCGATTCCCGGTCAGGGAAATAA
tE(CTC)C2	Glu1	Glu	CTC	3	97158903	97158979			TTCCCTGGTGGTCTAGTGGTTAGGATTCGGCGCTCTCACCGCCGCGGCCAGGGTTCGATTCCCGGTCAGGGAAATAA
tE(CTC)C3	Glu1	Glu	CTC	3	124296998	124297072			TCCCTGATGGTATAGTGGTTAGGACTCGGTGGTCTCACCAGCGCTGCCCAGGTTCAATTCCTGGTTAGGGAACCA
tE(CTC)G	Glu1	Glu	CTC	7	86818335	86818409			TCCCTGGTGGTCTAGTGGTTAGGCTTTGGTGCTCTCACCTCCATGGCCCAGGTTTGATTCCTGGTCAGGGAAGCA
tE(CTC)H	Glu1	Glu	CTC	8	35497246	35497317			TCCCTGGCGGCCTAGTGGTTAGGATTCAGTGCTCTCACAGCTGCAGCCCAGGTTTGATTCCTGGTCAGGGAC
tE(CTC)J	Glu1	Glu	CTC	10	30599981	30600055			TCCCTGGTGGTCTAGTGGTTAGGATTCGGCGCTCTCACCGCCGCGGCCCAGGTTCGATTCCCGGTCAGGGAAGCA
tE(CTC)K	Glu1	Glu	CTC	11	57914700	57914776			TTCCCTGGTGGTCTAGTGGTTAGGATTCGGCGCTCTCACCGCCGCGGCCAGGGTTCGATTCCCGGTCAGGGAAGTAA
tE(CTC)L	Glu1	Glu	CTC	12	37488909	37488985			TTCCCTGGTGGTCTAGTGGTTAGGAGTCATTGCTCTCACCACCGCGTCCAGGGTTCGATTCCCGGTCAGGGAAATAA
tE(CTC)M	Glu1	Glu	CTC	13	20540343	20540419			TTCCCTGGTGGTCTAGTGGTTAGGATTCGGCGCTCTCACCGCCGCGGCCAGGGTTCGATTCCCGGTCAGGGAAGTGA
tE(CTC)Q	Glu1	Glu	CTC	17	54371374	54371448			TCCCTGGTGGTCTAGTGGTTAGGATTTGGCGCTCTCACCGCCGCGGCCTAGGTTCGATTCCCGGTCAGGGAAGCA
tK(CTT)C4	Glu1	Lys	CTT	3	19853717	19853787		Rogue	TCCCTGGTGGTCTAGTGGTTAGGATTCAGTGCTCTTACCACCATGGCCTGGGGTTCGATTCCGTCAGGGAA
tE(TTC)C	Glu1	Glu	TTC	3	96388584	96388658			TCCCTGGTGGTCTAGTGGCTAGGATTCGGCGCTTTCACCGCCGCGGCCCAGGTTCGATTCCCGGTCAGGGAAGGA
tE(TTC)A1	Glu2	Glu	TTC	1	34718273	34718347			TCCCATATGGTCTAGCGGTTAGGATTCCTGGTTTTCACCCAGGCGGCCCAGGTTCGACTCCCGGTATGGGAACAA
tE(TTC)G	Glu2	Glu	TTC	7	46001323	46001399			TTCCCACATGGTCTAGCGGTTAGGATTCCTGGTTTTCACCCAGGCGGCCAGGGTTCGACTCCCGGTGTGGGAACAGA
tE(TTC)I	Glu2	Glu	TTC	9	104330525	104330601			TTCCCACATGGTCTAGCGGTTAGGATTCCTGGTTTTCACCCAGGCGGCCAGGGTTCGACTCCCGGTGTGGGAACACA
tE(TTC)M	Glu2	Glu	TTC	13	22843658	22843734			TTCCCACATGGTCTAGCGGTTAGGATTCCTGGTTTTCACCCAGGCGGCCAGGGTTCGACTCCCGGTGTGGGAAACTA
tE(TTC)N1	Glu2	Glu	TTC	14	67916770	67916844			TCCCACATGGTCTAGCGGTTAGGATTCCTGGTTTTCACCCAGGCGGCCCAGGTTCGACTCCCGGTGTGGGAACGA
tE(TTC)N2	Glu2	Glu	TTC	14	71254905	71254981			TTCCCATATGGTCTAGCGGTTAGGATTCCTGGTTTTCACCCAGGCGGCCAGGGTTCGACTCCCGGTATGGGAACAGA
tG(CCC)C1	Gly1	Gly	CCC	3	96316992	96317065			GCATTGGTGGTTCAGTGGTAGAATTCTCGCCTCCCACATGGGGGACTTGAGCTCAATTCCCAGCCAATGCAAGA
tG(CCC)C2	Gly1	Gly	CCC	3	96425970	96426045			TGCATTGGTAGTTCAATGGTAGAATTCTCGCCTCCCACGCGGGTGACCCAGGTTCGATTCCCGGCCAATGCAGTAA
tG(CCC)D	Gly1	Gly	CCC	4	32461608	32461683			TGCATTGGTGGTTCAATGGTAGAATTCTCGCCTCCCACTCGGGTGACCCAGGTTCGATTCCCGGCCAATGCAATAA
tG(GCC)A1	Gly1	Gly	GCC	1	75276975	75277048			GCATTGGTGGTTCAGTGGTAGAATTCTCGCCTGCCACGCGGGAGGCCCGAGTTTGATTCCCGGCCAATGCATTA
tG(GCC)A2	Gly1	Gly	GCC	1	171122532	171122605			GCATTGGTGGTTCAGTGGTAGAATTCTCGCCTGCCACGCGGGAGGCCCGAGTTCGATTCCCGGCCAATGCACGA
tG(GCC)A3	Gly1	Gly	GCC	1	171144638	171144711			GCATGGGTGGTTCAGTGGTAGAATTCTCGCCTGCCACGCGGGAGGCCCGAGTTCGATTCCCGGCCCATGCAGAA

This table lists
location and se
encoded amino
the gene is loca

tRNA gene name
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tA(AGC)M5
tA(AGC)M6
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tA(CGC)M1
tA(CGC)M2
tA(CGC)X1
tA(CGC)X3
tA(CGC)X5
tA(CGC)X7
tA(CGC)X9
tA(CGC)X11
tV(TAC)X1
tA(TGC)E1
tA(TGC)E2
tA(TGC)I
tA(TGC)K
tA(TGC)M
tA(TGC)X2
tA(TGC)X4
tA(TGC)X6
tA(TGC)X8
tA(TGC)X10
tA(TGC)X12
tA(TGC)X14
tA(TGC)X16
tV(AAC)H
tG(ACC)X1
tA(AGC)A3
tA(AGC)B4
tA(AGC)E7
tA(AGC)F4
tA(AGC)F5
tA(AGC)G3
tA(AGC)G4
tA(AGC)H1
tA(AGC)I2
tA(AGC)I6
tA(AGC)J1
tA(AGC)J4
tA(AGC)J5
tA(AGC)K4
tA(AGC)L2
tA(AGC)L3
tA(AGC)O1
tA(AGC)O2
tA(AGC)O3
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tA(AGC)S4
tA(AGC)X
tA(AGC)C1
tA(AGC)E3
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tA(AGC)M9
tA(AGC)M10
tA(AGC)M11
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tR(ACG)I
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tR(ACG)M2
tR(ACG)M3
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tR(CCG)K
tR(CCG)M
tR(CCG)Q
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tR(TCG)K
tR(TCG)M1
tR(TCG)M2
tR(TCG)M3
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tR(CCT)K1
tR(CCT)K2
tR(CCT)Q
tR(CCT)X2
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tR(TCT)C
tR(TCT)I
tR(TCT)K
tR(TCT)M
tR(TCT)S
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tC(GCA)K4
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tQ(CTG)C1
tQ(CTG)C2
tQ(CTG)C3
tQ(CTG)C4
tQ(CTG)F
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tQ(CTG)K
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tQ(CTG)M2
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tQ(TTG)K1
tQ(TTG)K2
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tQ(TTG)M2
tQ(TTG)M3
tQ(TTG)M4
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tE(CTC)A2
tE(CTC)A3
tE(CTC)C1
tE(CTC)C2
tE(CTC)C3
tE(CTC)G
tE(CTC)H
tE(CTC)J
tE(CTC)K
tE(CTC)L
tE(CTC)M
tE(CTC)Q
tK(CTT)C4
tE(TTC)C
tE(TTC)A1
tE(TTC)G
tE(TTC)I
tE(TTC)M
tE(TTC)N1
tE(TTC)N2
tG(CCC)C1
tG(CCC)C2
tG(CCC)D
tG(GCC)A1
tG(GCC)A2
tG(GCC)A3

This table lists
location and se
encoded aminc
the gene is loca

tRNA gene name
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tA(AGC)M5
tA(AGC)M6
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tA(CGC)M1
tA(CGC)M2
tA(CGC)X1
tA(CGC)X3
tA(CGC)X5
tA(CGC)X7
tA(CGC)X9
tA(CGC)X11
tV(TAC)X1
tA(TGC)E1
tA(TGC)E2
tA(TGC)I
tA(TGC)K
tA(TGC)M
tA(TGC)X2
tA(TGC)X4
tA(TGC)X6
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tA(TGC)X12
tA(TGC)X14
tA(TGC)X16
tV(AAC)H
tG(ACC)X1
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tA(AGC)B4
tA(AGC)E7
tA(AGC)F4
tA(AGC)F5
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tA(AGC)G4
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tA(AGC)I6
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tA(AGC)K4
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tA(AGC)L3
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tQ(CTG)C2
tQ(CTG)C3
tQ(CTG)C4
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tQ(CTG)K
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tQ(CTG)M2
tQ(TTG)C
tQ(TTG)K1
tQ(TTG)K2
tQ(TTG)M1
tQ(TTG)M2
tQ(TTG)M3
tQ(TTG)M4
tQ(TTG)X1
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tE(CTC)A2
tE(CTC)A3
tE(CTC)C1
tE(CTC)C2
tE(CTC)C3
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tE(CTC)H
tE(CTC)J
tE(CTC)K
tE(CTC)L
tE(CTC)M
tE(CTC)Q
tK(CTT)C4
tE(TTC)C
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tE(TTC)G
tE(TTC)I
tE(TTC)M
tE(TTC)N1
tE(TTC)N2
tG(CCC)C1
tG(CCC)C2
tG(CCC)D
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tG(GCC)A2
tG(GCC)A3

This table lists
location and se
encoded amin
the gene is loc

tRNA gene name
tA(AGC)M3
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tA(AGC)M5
tA(AGC)M6
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tA(CGC)M2
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tA(CGC)X3
tA(CGC)X5
tA(CGC)X7
tA(CGC)X9
tA(CGC)X11
tV(TAC)X1
tA(TGC)E1
tA(TGC)E2
tA(TGC)I
tA(TGC)K
tA(TGC)M
tA(TGC)X2
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tA(TGC)X6
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tA(TGC)X10
tA(TGC)X12
tA(TGC)X14
tA(TGC)X16
tV(AAC)H
tG(ACC)X1
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tA(AGC)F5
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tA(AGC)G4
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tA(AGC)I6
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tA(AGC)J4
tA(AGC)J5
tA(AGC)K4
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tA(AGC)L3
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tA(AGC)O2
tA(AGC)O3
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tA(AGC)Q1
tA(AGC)S4
tA(AGC)X
tA(AGC)C1
tA(AGC)E3
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tA(AGC)M8
tA(AGC)M9
tA(AGC)M10
tA(AGC)M11
tA(AGC)S1
tR(ACG)C
tR(ACG)I
tR(ACG)M1
tR(ACG)M2
tR(ACG)M3
tR(ACG)N
tR(CCG)K
tR(CCG)M
tR(CCG)Q
tR(TCG)G
tR(TCG)K
tR(TCG)M1
tR(TCG)M2
tR(TCG)M3
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tR(CCT)K1
tR(CCT)K2
tR(CCT)Q
tR(CCT)X2
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tR(TCT)C
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tR(TCT)K
tR(TCT)M
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tN(GTT)C2
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tN(GTT)O
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tD(GTC)A3
tD(GTC)B
tD(GTC)E1
tD(GTC)E2
tD(GTC)E3
tD(GTC)J1
tD(GTC)J2
tD(GTC)K1
tD(GTC)K2
tD(GTC)M1
tD(GTC)M2
tD(GTC)M3
tC(ACA)F1
tC(GCA)F3
tC(GCA)F4
tC(GCA)F5
tC(GCA)F6
tC(GCA)F7
tC(GCA)F8
tC(GCA)F9
tC(GCA)F10
tC(GCA)F11
tC(GCA)F12
tC(GCA)F13
tC(GCA)F14
tC(GCA)F15
tC(GCA)F16
tC(GCA)F17
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tC(GCA)F28
tC(GCA)F29
tC(GCA)F30
tC(GCA)F31
tC(GCA)I1
tC(GCA)I2
tC(GCA)K1
tC(GCA)K2
tC(GCA)K3
tC(GCA)K4
tC(GCA)K5
tC(GCA)Q
tQ(CTG)B
tQ(CTG)C1
tQ(CTG)C2
tQ(CTG)C3
tQ(CTG)C4
tQ(CTG)F
tQ(CTG)I
tQ(CTG)K
tQ(CTG)M1
tQ(CTG)M2
tQ(TTG)C
tQ(TTG)K1
tQ(TTG)K2
tQ(TTG)M1
tQ(TTG)M2
tQ(TTG)M3
tQ(TTG)M4
tQ(TTG)X1
tA(CGC)D
tE(CTC)A1
tE(CTC)A2
tE(CTC)A3
tE(CTC)C1
tE(CTC)C2
tE(CTC)C3
tE(CTC)G
tE(CTC)H
tE(CTC)J
tE(CTC)K
tE(CTC)L
tE(CTC)M
tE(CTC)Q
tK(CTT)C4
tE(TTC)C
tE(TTC)A1
tE(TTC)G
tE(TTC)I
tE(TTC)M
tE(TTC)N1
tE(TTC)N2
tG(CCC)C1
tG(CCC)C2
tG(CCC)D
tG(GCC)A1
tG(GCC)A2
tG(GCC)A3

tRNA gene name	tRNA Family	Amino Acid	Anticodon	Chromosome	Sequence Start	Sequence End	intron	Rogue tRNA?	tRNA gene sequence (including introns)
tG(GCC)B	Gly1	Gly	GCC	2	57135758	57135833			TGCATTGGTGGTTCAGTGGTAGAATTCTCGCCTGCCACGCGGGAGGCCCAGGTTCGATTCCCGGCCAATGCACTTA
tG(GCC)C	Gly1	Gly	GCC	3	84628966	84629039			GCATTGGTGGTTCAGTGGTAGAATTCTCGCCTGCCACGCGGGAGGCCCGAGTTCGATTCCCGGCCAATGCACAA
tG(GCC)D2	Gly1	Gly	GCC	4	131567923	131567996			GCATTGGTGGTTCAGTGGTAGAATTCTTGCCTGCCACCCGGGAGGCCCAAGTTCAATTCCTGGCCAATGTACAA
tG(GCC)G	Gly1	Gly	GCC	7	15381733	15381808			GGCATGGGTGGTTCAGTGGTAGAATTCTCACCTGCCATGAGGGAGGCCCAGGTTCAATTCCAGGCCCATTGCAGAA
tG(GCC)H1	Gly1	Gly	GCC	8	109954782	109954855			GCATTGGTGGTTCAGTGGTAGAATTCTCGCCTGCCACGCGGGAGGCCCGAGTTCGATTCCCGGCCAATGCAGTA
tG(GCC)H2	Gly1	Gly	GCC	8	109955475	109955548			GCATTGGTGGTTCAGTGGTAGAATTCTCGCCTGCCACGCGGGAGGCCCGAGTTCGATTCCCGGCCAATGCAGAA
tG(GCC)H3	Gly1	Gly	GCC	8	110388966	110389039			GCATTGGTGGTTCAGTGGTAGAATTCTCGCCTGCCACGCGGGAGGCCCGAGTTCGGTTCCCGGCCAATGCATAA
tG(GCC)J	Gly1	Gly	GCC	10	99815477	99815550			GTATTGGTGGTTCAGTGGTAGAATTCTCGCCTGCCACACCGGATGCCTGAGTTCCATTCCCGGCCAATGCACTA
tG(GCC)K1	Gly1	Gly	GCC	11	68731346	68731421			TGCATTGGTGGTTCAGTGGTAGAATTCTCGCCTGCCACGCGGGAGGCCCAGGTTCGATTCCCGGCCAATGCACAGA
tG(GCC)M1	Gly1	Gly	GCC	13	21090704	21090777			GCATTGGTGGTTCAGTGGTAGAATTCTCGCCTGCCACGCGGGAGGCCCGAGTTCGATTCCCGGCCAATGCAGGA
tG(GCC)M2	Gly1	Gly	GCC	13	22897327	22897400			GCATTGGTGGTTCAGTGGTAGAATTCTCGCCTGCCACGCGGGAGGCCCGAGTTCGATTCCCGGCCAATGCACTA
tG(TCC)A1	Gly2	Gly	TCC	1	171115558	171115634			TGCGTTGGTGGTATAGTGGTGAGCATAGCTGCCTTCCAAGCAGTTGACCAGGGTTCGATTCCCGGCCAACGCAAAGA
tG(TCC)A2	Gly2	Gly	TCC	1	171142701	171142775			GCGTTGGTGGTATAGTGGTGAGCATAGCTGCCTTCCAAGCAGTTGACCCAGGTTCGATTCCCGGCCAACGCAGCA
tG(TCC)A3	Gly2	Gly	TCC	1	171174010	171174086			TGCGTTGGTGGTATAGTGGTGAGCATAGCTGCCTTCCAAGCAGTTGACCAGGGTTCGATTCCCGGCCAACGCATAAA
tG(TCC)C	Gly2	Gly	TCC	3	96504785	96504861			TGCGTTGGTGGTATAGTGGTGAGCATAGCTGCCTTCCAAGCAGTTGACCAGGGTTCGATTCCCGGCCAACGCATAAA
tG(TCC)K	Gly2	Gly	TCC	11	68653830	68653906			TGCGTTGGTGGTATAGTGGTGAGCATAGCTGCCTTCCAAGCAGTTGACCAGGGTTCGATTCCCGGCCAACGCAACGA
tG(TCC)X1	Gly2	Gly	TCC	X	33574164	33574240			TGCGTTGGTGGTATAGTGGTGAGCATAGCTGCCTTCCAAGCAGTTGACCAAGGTTTGATACCCAGCCAACGCATGAA
tG(CCC)F	Gly3	Gly	CCC	6	86775971	86776044			GCGCCGCTGGTGTAGTGGTATCATGCAAGATTCCCATTCTTGCGACCCGAGTTCGATTCCCGGGCGGCGCATGA
tG(CCC)Q	Gly3	Gly	CCC	17	24474352	24474425			GCGCCGCTGGTGTAGTGGTATCATGCAAGATTCCCATTCTTGCGACCCGAGTTCGATTCCCGGGCGGCGCATGA
tH(GTG)B1	His	His	GTG	2	122124514	122124588			GCCGTGATCGTATAGTGGTTAGTACTCTGCGTTGTGGCCGCAGCAACCTAGGTTCGAATCCGAGTCACGGCATTA
tH(GTG)B2	His	His	GTG	2	122126383	122126457			GCCGTGATCGTATAGTGGTTAGTACTCTGCGTTGTGGCCGCAGCAACCTAGGTTCGAATCCGAGTCACGGCATTA
tH(GTG)B3	His	His	GTG	2	122126991	122127065			GCCGTGATCGTATAGTGGTTAGTACTCTGCGTTGTGGCCGCAGCAACCTAGGTTCGAATCCGAGTCACGGCATTA
tH(GTG)C1	His	His	GTG	3	96411252	96411326			GCCGTGATCGTATAGTGGTTAGTACTCTGCGTTGTGGCCGCAGCAACCTAGGTTCGAATCCGAGTCACGGCAGTA
tH(GTG)C2	His	His	GTG	3	96437878	96437952			GCCGTGATCGTATAGGGGTTAGTACTCTGCGTTGTGGCCGCAGCAACCTAGGTTCGAATCCGAGTCACGGCATTA
tH(GTG)C3	His	His	GTG	3	96454247	96454321			GCCGTGATCGTATAGTGGTTAGTACTCTGCGTTGTGGCCGCAGCAACCTAGGTTCGAATCCGAGTCACGGCATGA
tH(GTG)C4	His	His	GTG	3	96467748	96467824			TGCCGAGATCGTATAGTGGTTAGTACTCTGCATTGTGGCTGCAGCAACCACGGTTCGAATCCGAGTCTCGGCACTAA
tH(GTG)C5	His	His	GTG	3	96504143	96504217			GCCGTGATCGTATAGTGGTTAGTACTCTGCGTTGTGGCCGCAGCAACCTAGGTTCGAATCCGAGTCACGGCATTA
tH(GTG)D	His	His	GTG	4	80894465	80894539			GCCGTGATCGTATAGTGGTTAGTACTCTGCGTTGTGGCCGCAGCAACCTAGGTTCGAATCCGAGTCACGGCAGGA
tI(AAT)D1	Ile	Ile	AAT	4	28050591	28050669			TGGCCGGTTAGCTCAGTTGGTTAGAGCATGGTGCTAATAACGCCAAGGTAACGGGTTCGATCCCCGTATGGGCCAGGGA
tI(AAT)H	Ile	Ile	AAT	8	46264143	46264215			GGCTAGTTAGCTCAGTTGGTTAGAGCATGGTGCTAATAATGCCAAGGTCGCAGTTTCAAACCTGTATGGGCTA
tI(AAT)K1	Ile	Ile	AAT	11	68649558	68649636			TGGCCGGTTAGCTCAGTTGGTTAGAGCGTGGTGCTAATAACGCCAAGGTAGCGGGTTCGATCCCCGTACGGGCCAAAGA
tI(AAT)K2	Ile	Ile	AAT	11	68674872	68674950			TGGCCGGTTAGCTCAGTTGGTTAGAGCGTGGTGCTAATAACGCCAAGGTAGCGGGTTCGATCCCCGTACGGGCCAGTGA
tI(AAT)L	Ile	Ile	AAT	12	105591749	105591827			TGGCCGGTTAGCTCAGTTGGTTAGAGCGTGGTGCTAATAACGCCAAGGTAGCGGGTTCGATCCCCGTACGGGCCAGGGA
tI(AAT)M1	Ile	Ile	AAT	13	21235440	21235518			TGGCCGGTTAGCTCAGTTGGTTAGAGCGTGGTGCTAATAACGCCAAGGTAGCGGGTTCGATCCCCGTACGGGCCAGTAA
tI(AAT)M2	Ile	Ile	AAT	13	21262153	21262231			TGGCCGGTTAGCTCAGTTGGTTAGAGCGTGGTGCTAATAACGCCAAGGTAGCGGGTTCGATCCCCGTACGGGCCAGTGA
tI(AAT)M3	Ile	Ile	AAT	13	21409346	21409424			TGGCCGGTTAGCTCAGTTGGTTAGAGCGTGGTGCTAATAACGCCAAGGTAGCGGGTTCGATCCCCGTACGGGCCAGTAA
tI(AAT)M4	Ile	Ile	AAT	13	22689172	22689250			TGGCCGGTTAGCTCAGTTGGTTAGAGCGTGGTGCTAATAACGCCAAGGTAGCGGGTTCGATCCCCGTACGGGCCACACA
tI(AAT)M5	Ile	Ile	AAT	13	22777183	22777261			TGGCCGGTTAGCTCAGTTGGTTAGAGTGTGGTGCTAATAACGCCAAGGTAGCGGGTTCGATCCCCGTACGGGCCACATA
tI(AAT)M6	Ile	Ile	AAT	13	22818229	22818307			TGGCCGGTTAGCTCAGTTGGTTAGAGCGTGGTGCTAATAACGCCAAGGTAGCGGGTTCGATCCCCGTACGGGCCAGCTA
tI(AAT)P	Ile	Ile	AAT	16	75787284	75787362			TGGCCGGTTAGCTCAGTTGGTTAGAGCATGGTGCTAATAACGCCAAGGTAGTGGGTTCGATGCCCGTATGGGCCAGCAA
tI(TAT)G	Ile2	Ile	TAT	7	17337157	17337254	I		GCTCCAGTGGCGCAATCGGTTAGCGCGCGGTACTTATATGTCAGTGCTAAGCGTAAGCGATGCCGAGGTTGTGAGTTCGATCCTCACCTGGAGCACTA
tI(TAT)M2	Ile2	Ile	TAT	13	21277058	21277156	I		TGCTCCAGTGGCGCAATCGGTTAGCGCGCGGTACTTATACAGCAGTATAAGTGCGGGTGATGCCGAGGTTGTGAGTTCGAGCCTCACCTGGAGCATGTA
tI(TAT)M	Ile2	Ile	TAT	13	22650541	22650641	I		TGCTCCAGTGGCGCAATCGGTTAGCGCGCGGTACTTATACAACAGTGTGAGCGCGAGAGCGATGCCGAGGTTGTGAGTTCGAGCCTCACCTGGAGCATTAA
tI(TAT)Q4	Ile2	Ile	TAT	17	82434678	82434773	I		GCTCCAGTGGCGCAATCGGTTAGCGCGCGGTACTTATACAGCAGTACATACAGAGCAATGCCGAGGTTGTGAGTTCGAGCCTCACCTGGAGCACGA
tL(CAA)K1	Leu1	Leu	CAA	11	57914997	57915108	I		TGTCAGGATGGCCGAGTGGTCTAAGGCGCCAGACTCAAGGTGACAAGCCATACCTACGGGTGTTCTGGTCTCCGAATGGAGGCGTGGGTTCGAATCCCAATTCTGACACAAA
tL(CAA)M1	Leu1	Leu	CAA	13	20552608	20552718	I		TGTCAGGATGGCCGAGTGGTCTAAGGCGCCAGACTCAAGCTATGGCTTCATCGCTCTGAGGGTTCTGGTCTCCCCTGGAGGCGTGGGTTCGAATCCCACATCTGACAGCTA
tL(CAA)M	Leu1	Leu	CAA	13	20580242	20580351	I		TGTCAGGATGGCCGAGTGGTCTAAGGCGCCAGACTCAAGCTTAGCTTCCATGTCTGGGGATTCTGGTCTCCGTATGGAGGCGTGGGTTCGAATCCCACTACTGACACAGA
tL(CAA)M2	Leu1	Leu	CAA	13	21294961	21295071	I		TGTCAGGATGGCCGAGTGGTCTAAGGCGCCAGACTCAAGCGTTCGCTTCATCTACTGAGGGTTCTGGTCTCCGTGTGGAGGCGTGGGTTCGAATCCCACATCTGACACAGA
tL(CAG)A1	Leu1	Leu	CAG	1	171116178	171116265			TGTCAGGATGGCCGAGCGGTCTAAGGCGCTGCGTTCAGGTCGCAGTCTCACCTGGAGGCGTGGGTTCGAATCCCACTTCTGACAAATA
tL(CAG)A2	Leu1	Leu	CAG	1	171143994	171144079			GTCAGGATGGCCGAGCGGTCTAAGGCGCTGCGTTCAGGTCGCAGTCTCCACTGGAGGCGTGGGTTCGAATCCCACTCCTGACAGCA
tL(CAG)A3	Leu1	Leu	CAG	1	171173090	171173175			GTCAGGATGGCCGAGCGGTCTAAGGCGCTGCGTTCAGGTCGCAGTCTCCACTGGAGGCGTGGGTTCGAATCCCACTCCTGACAAAA
tL(CAG)C2	Leu1	Leu	CAG	3	23926279	23926364			GTCAGGATGGCCGAGCAGTCTAAGGCACTGCGTTCAGGTCGCAGTCTCCACTGGAGGCGTGGATTCGAATCCCACTCCTGACAACA
tL(CAG)H1	Leu1	Leu	CAG	8	37257589	37257674			GTCAGGATGGCCGAGTGGTCTAAGGAGCTGTGTTCAGGTCGCAGTCTCCACTGGAGGCGTGGGTTCGAATCCCACTCCTGACAGCA
tL(CAG)H2	Leu1	Leu	CAG	8	94051476	94051563			TGTCAGGATGGCCGAGCGGTCTAAGGCGCTGCGTTCAGGTCGCAGTCTCACCTGGAGGCGTGGGTTCGAATCCCACTTCTGACAGAAA
tL(CAG)H3	Leu1	Leu	CAG	8	94051846	94051933			TGTCAGGATGGCCGAGCGGTCTAAGGCGCTGCGTTCAGGTCGCAGTCTCACCTGGAGGCGTGGGTTCGAATCCCACTTCTGACAAGTA
tL(CAG)M3	Leu1	Leu	CAG	13	22833553	22833638			GTCAGGATGGCCGAGCGGTCTAAGGCGCTGCGTTCAGGTCGCAGTCTCCACTGGAGGCGTGGGTTCGAATCCCACTCCTGACAACA
tL(AAG)G	Leu2	Leu	AAG	7	108212915	108212999			GGTAGTGTGGCCGAGCGGTCTAAGGCGCTGGATTAAGGCTCCAGTCTCTACGGGGGCGTGGGTTCGAATCCCACCGCTGCCAAGA
tL(AAG)K	Leu2	Leu	AAG	11	48496706	48496790			GGTAGCGTGGCCGAGCGGTCTAAGGCGCTGGATTAAGGCTCCAGTCTCTACGGGGGCGTGGGTTCGAATCCCACCGCTGCCAGTA
tL(AAG)M1	Leu2	Leu	AAG	13	20549598	20549682			GGTAGCGTGGCCGAGCGGTCTAAGGCGCTGGATTAAGGCTCCAGTCTCTACGGGGGCGTGGGTTCGAATCCCACCGCTGCCAACA
tL(AAG)M2	Leu2	Leu	AAG	13	20549768	20549852			GGTAGTGTGGCCGAGCGGTCTAAGGCGCTGGATTAAGGCTCCAGTCTCTACGGGGGCGTGGGTTCGAATCCCACCACTGCCAACA
tL(AAG)N	Leu2	Leu	AAG	14	43757328	43757414			TGGTAGCGTGGCCGAGCGGTCTAAGGCGCTGGATTAAGGCTCCAGTCTCATCGGGGGCGTGGGTTCGAATCCCACCGCTGCCATCTA
tL(TAG)B	Leu2	Leu	TAG	2	37881384	37881468			GGTAGCATGGCCAAGTGGTCTAAAGCACTGAATTTAGGCTCCAGTCATTACGATAGCATGGGTTCGAGTCCCACCACTGCCATAA
tL(TAG)G2	Leu2	Leu	TAG	7	108130874	108130958			GGTAGCGTGGCCGAGTGGTCTAAGGCGCTGGATTTAGGCTCCAGTCATTACGATGGCGTGGGTTCGAATCCCACCGCTGCCACAA
tL(TAG)K	Leu2	Leu	TAG	11	68736797	68736881			GGTAGCGTGGCCGAGCGGTCTAAGGCGCTGGATTTAGGCTCCAGTCTCTACGGAGGCGTGGGTTCGAATCCCACCGCTGCCAGGA
tL(TAG)N	Leu2	Leu	TAG	14	43776273	43776359			TGGTAGTGTGGCCGAGCGGTCTAAGGCGCTGGATTTAGGCTCCAGTCTCATCGGAGGCGTGGGTTCGAATCCCACCACTGCCAGTGA
tL(TAA)J	Leu3	Leu	TAA	10	12633339	12633424			ACCAGGATGGCCGAGTGGTTAAGGCGTTGGACTTAAGATCCAATGGACAAATGTCTGCGTGGGTTCGAACCCCACTCCTGGTAAAA
tL(TAA)M	Leu3	Leu	TAA	13	21228142	21228229			TACTGGGATGGCTGAGTGGTTAAGGCGTTGGACTTAAGATCCAATGGGCAGTTGCCTGCGTGGGTTCGAACCCCACTCCCAGTATGTA
tL(TAA)S	Leu3	Leu	TAA	19	11261436	11261523			TACCAGAATGGCCGAGTGGTTAAGGCGTTGGACTTAAGATCCAATGGATATATATCCGCGTGGGTTCGAACCCCACTTCTGGTAAATA
tL(TAA)X1	Leu3	Leu	TAA	X	151104987	151105072			GATGGGATGGCTGAGAGGTTAAGGCTTTGGACTTAAGATCCAATGGGCAAATGCCTGCGTGGGTTTGAACCCCACTCCCAATATTA
tStop(TTA)M	Leu3	Stop	TTA	13	21175922	21176009		Rogue	TACTGGGATGGCTGAGTGGTTAAGGCCTTGGACTTTAGATCCAATGGGCAGATGCCTGCGTGGGTTCAAACCCCACTCCCAGTATTAA
tK(CTT)A	Lys1	Lys	CTT	1	110913332	110913409			TGCCTGGCTAGCTCAGTCCATAGAGCATGGGACTCTTAATCCCAGGGTCATGGGTTCGAGCCCCATATTAGGCACCAA
tK(CTT)B	Lys1	Lys	CTT	2	86035043	86035120			AGCCTAGCTAGTTCAGTCGGTAGAGCATGAGACTCTTAATCTCAGGTTCATGAGTTTGAGCCCCATGTTGGTTTGGCA
tK(CTT)C1	Lys1	Lys	CTT	3	3126070	3126147			TGCCCAGCTAGCTCAGTCTGTAGAGCATGAGACTCTTAGTCTCAGGGTCATGGGTTGGAGCCCCATGTTGTGCAAGAA
tK(CTT)C2	Lys1	Lys	CTT	3	3151823	3151900			TGCCCAGCTAGCTCAGTCTGTAGAGCATGAGACTCTTAATCTCAGGGTCATGAGTTCGAGCCCCACGTTGGGTGAGAA
tK(CTT)C3	Lys1	Lys	CTT	3	3201314	3201380			GCCAGCTCAGTTGGTAGAGCATGAGACTCTTAATCTCAGGGTCGTGGGTTCGAGCCCCATATTGGGG
tK(CTT)C5	Lys1	Lys	CTT	3	96430140	96430217			TGCCCGGCTAGCTCAGTCGGTAGAGCATGAGACTCTTAATCTCAGGGTCATGGGTTCGAGCCCCACGTTGGGCGCATA
tK(CTT)C6	Lys1	Lys	CTT	3	96503289	96503364			GCCCGGCTAGCTCAGTCGGTAGAGCATGAGACTCTTAATCTCAGGGTCGAGGGTTCGAGCCCCACGTTGGGCGCTA
tK(CTT)E	Lys1	Lys	CTT	5	89343013	89343090			CACCCGACTGGGTTAGTCAATAGAACATGAGACTCTTAATCTCAGGGTTATGGGTTTGAGCCCCACCTTGGGTGGGTA
tK(CTT)G	Lys1	Lys	CTT	7	114653411	114653486			GCCCAGCTACTTCAGTTGGTGGAGCAAGAGTCTCTTAATCTCAGGGTCAAGGGTTCAAGCCCCATGTTGGGTACCA
tK(CTT)I1	Lys1	Lys	CTT	9	14794790	14794865			GTCCTGCTGGCTCAGTCGGTACAGCATGGGACTCTTAATCCCAGGGTCGAGGGTTCGAGCTCCACGTTGGGTACCA
tK(CTT)I2	Lys1	Lys	CTT	9	89954947	89955024			TGCCCGGCTAGCTCAGTCGGTAGAGCATGGGACTCTTAATCCCAGGGTCATGGGTTCGAGCCCCACGTTGGGCGGTTA
tK(CTT)K1	Lys1	Lys	CTT	11	22386936	22387011			ACCCAGCTAGTTCAGTCGGTAGAGCATGAGACTCTTAATCTTAGAGTCGAGGGCTCAGGTCCCATGTTGGGTTCCA
tK(CTT)K2	Lys1	Lys	CTT	11	29296855	29296927			GCCTGGCTAGCTCAGTTGGTAGAGCATGGAACTCTTAATCCCTGGGTTGTAAGTTTGAGCCTCATGTAGGGCA
tK(CTT)K3	Lys1	Lys	CTT	11	48473614	48473691			CGCCCGGCTAGCTCAGTCGGTAGAGCATGAGACTCTTAATCTCAGGGTCATGGGTTCGAGCCCCACGTTGGGCGCATA
tK(CTT)K4	Lys1	Lys	CTT	11	52291514	52291588			GCCCAAAACTAGCTCAGTCAGTAGAGAATGATACTCTTAATCTCAGGGTCATGGGTTCAAACCCCACGTTGGGTG
tK(CTT)K5	Lys1	Lys	CTT	11	73749866	73749943			AACCTGGCTAGGTCAGTTGGTAGATCATGAGACTCTTAATCTCAGGGTCATGGGTTCAAGCCCCATGTTGGTTTGGCA
tK(CTT)L	Lys1	Lys	CTT	12	66236117	66236194			TGCCCGGCTAGCTCAGTCGGTAGAGCATGGGACTCTTAATCCCAGGGTCATGGGTTCGAGCCCCACGTTGGGCGGTGA
tK(CTT)M1	Lys1	Lys	CTT	13	3994182	3994254			ACACTGCTAGCTCAGTTGGTAGAGCATGAGACTCTTAATCTCAGGGTCGTGGGTTCGAGCCTCACGTTGGGCG
tK(CTT)M2	Lys1	Lys	CTT	13	11726878	11726951			TGTTGTAAAGCTCAGTTGTTAGAGCATGAGACTCTTATTCTTAGGGTTGTGAGTTCGAGCCCCACATTGGATAT
tK(CTT)M3	Lys1	Lys	CTT	13	22816463	22816540			TGCCCGGCTAGCTCAGTCGGTAGAGCATGAGACTCTTAATCTCAGGGTCATGGGTTCGAGCCCCACGTTGGGCGCAAA
tK(CTT)M4	Lys1	Lys	CTT	13	69310465	69310537			GACTCCAGCCCAGTCAGTAGAGCATGAGACTCTTAATCTCAGGGTCGTGGGTTCGAGCCCCACGTTGGGTGCA
tK(CTT)N	Lys1	Lys	CTT	14	53538938	53539015			TGCCCAGCTCACTCAGTCGGTAGAGCATGAGACTCTTAATCTCAGGGTCATAGGTTCGAGCCCCATGGTGGGCGAGAA
tK(CTT)P1	Lys1	Lys	CTT	16	3026421	3026498			TGCCCAGCTAGCTCAGTCTGTAGAGCATGAGACTCTTAATCTCAGGGTTATAGGTTCGAGCCCCGCTATGGGTGAGAA
tK(CTT)P2	Lys1	Lys	CTT	16	16630954	16631029			GCCCAGCTAGCTTAGTTGGTAGAGCATGAGACTCTTAATCTCAGAGTCAAGGGTTCAGGCCTCATGTTTGGCACCA
tK(CTT)P3	Lys1	Lys	CTT	16	47201463	47201540			TCCCCGGCTAGCTCAGTCAGTAGAGCTTGAGAATCTTAATCTCAGGGTCATGGGTTGGAGCCCCACGTTGGGCGAGAA
tK(CTT)Q1	Lys1	Lys	CTT	17	7286782	7286859			TGCCTGGCTAGCTTAGTTGGTAAAGCATAAGACTCTTAATCCTAGGGTCATAAGTTTGAGCCCCACATTAGGCGCCAA
tK(CTT)Q2	Lys1	Lys	CTT	17	22129888	22129965			CGCCCGGCTAGCTCAGTCGGTAGAGCATGAGACTCTTAATCTCAGGGTCATGGGTTCGAGCCCCACGTTGGGCGAGAA
tK(CTT)Q3	Lys1	Lys	CTT	17	22131255	22131332			CGCCCGGCTAGCTCAGTCGGTAGAGCATGAGACTCTTAATCTCAGGGTCATGGGTTCGAGCCCCACGTTGGGCGAGAA
tK(CTT)Q4	Lys1	Lys	CTT	17	22137022	22137097			GCTCGGTTAGCTCAGTCGGTAGAGCATGAGACTCTTATTCTCAGGGTTGAGGGTTTGAGTCTCCCGTTAGGCGTCA
tK(CTT)Q5	Lys1	Lys	CTT	17	22143288	22143365			CGCCCGGCTAGCTCAGTCGGTAGAGCATGAGACTCTTAATCTCAGGGTCATGGGTTCGAGCCCCACGTTGGGCGAGTA
tK(CTT)R	Lys1	Lys	CTT	18	3136757	3136834			TGCCCAGCTAGCTCAGTCGGTAGAGCATGAGACTCTTAATCTCAGGGTCATAGGTTTGAGCCCCGATATGGGTGAGAA
tK(CTT)X1	Lys1	Lys	CTT	X	89076047	89076120			GGTACTAGCTCAGTTGGTAGAGCTTGAGACTCTTAATCTCAGGAACATGGGTTCGAGCCCCACATTGGGTGCCA
tK(CTT)X2	Lys1	Lys	CTT	X	126202890	126202967			TGCCCAGCTAGCTCAGTTGGTAGAGCGTGGGACTCTTAATCCTAGGGTCATGGGTTCGAACCCCACGTTGGGCGGTTA
tK(CTT)Y	Lys1	Lys	CTT	Y	47724709	47724786			TGCCCAGCTAGCTCAGTCAGTAGAGCAGGAGACTCTTAGTCTCGGGGTTATAGGTTCGAGCCCCACAGTGGGCAAGGA
tL(TAA)E2	Lys1	Leu	TAA	5	90894680	90894754		Rogue	TCTGGCTGGCTCAGTTGGTAGAGCTTGAGACTTAAATCTCAGGGTTGCAGGTTTGAGTTCTGTTGGGGGTCAGAT
tSeC(TCA)E	Lys1	SeC	TCA	5	5634400	5634470		Rogue	ACCCAGCTAGCTCAGTGGGTAGAGCATGAGACTCAATCTCAGGGTTGTGGGTTCGAGCCCCACATTGGGCG
tK(TTT)H	Lys1	Lys	TTT	8	79077031	79077103			GCCTGGTTAGCTCAGTCAGTAGAGTATGAAACTTTTAATCTCAGGGTTGTAGGTTTGAGCCTCACATTGGGCA
tK(TTT)P	Lys1	Lys	TTT	16	3120615	3120692			TGCCCAGCCAGCTCAGTAGGTAGAGTATGAGACTTTTAATCTCAGGGTGATGGGTTCGAGCCCCATGTTGGGGGAGAA
tK(TTT)A1	Lys2	Lys	TTT	1	132915912	132915987			GCCCGGATAGCTCAGTCGGTAGAGCATCAGACTTTTAATCTGAGGGTCCAGGGTTCAAGTCCCTGTTCGGGCGCTA
tK(TTT)A2	Lys2	Lys	TTT	1	132916273	132916350			CGCCCGGATAGCTCAGTCGGTAGAGCATCAGACTTTTAATCTGAGGGTCAAGGGTTCAAGTCCCTGTTCGGGCGGCTA
tK(TTT)E	Lys2	Lys	TTT	5	30095683	30095762			AGCCTGGATGGCTCTCGGTCAGTAGGACATCAGACTTTTAATCTGAGGGACCAAGATTCAAGTCCCTGTTCAGGTTCTTA
tK(TTT)G	Lys2	Lys	TTT	7	17762839	17762914			GCCTGGATAGCTCAGTCGGTAGAGCATCAGACTTTTAATCTGAGGGTCCAGGGTTCAAGTCCCTGTTCAGGCGGAA
tK(TTT)J	Lys2	Lys	TTT	10	87577726	87577801			ACCTGGATAGCTCAGTTGGTAGAGCATCAGACTTTTAATCTGAGGCTCCAGGGTTCAAGTCCCTGTTCGAGCCCTA
tK(TTT)K	Lys2	Lys	TTT	11	68737729	68737804			GCCCGGATAGCTCAGTCGGTAGAGCATCAGACTTTTAATCTGAGGGTCCAGGGTTCAAGTCCCTGTTCGGGCGCTA
tK(TTT)M1	Lys2	Lys	TTT	13	20547634	20547709			GCCCGGATAGCTCAGTCGGTAGAGCATCAGACTTTTAATCTGAGGGTCCAGGGTTCAAGTCCCTGTTCGGGCGCTA
tK(TTT)M2	Lys2	Lys	TTT	13	21288064	21288139			GCCTGGATAGCTCAGTCGGTAGAGCATCAGACTTTTAATCTGAGGGTCCAGGGTTCAAGTCCCTGTTCAGGCGGAA
tK(TTT)M3	Lys2	Lys	TTT	13	21351912	21351987			GCCTGGATAGCTCAATTGGTAGAGCATCAGACTTTTAATCTGAGGGTTCAGGGTTCAAGTCCCTGTTCAGGCGCTA
tK(TTT)S1	Lys2	Lys	TTT	19	11256393	11256468			GCCCGGATAGCTCAGTCGGTAGAGCATCAGACTTTTAATCTGAGGGTCCAGGGTTCAAGTCCCTGTTCGGGCGCTA
tK(TTT)S2	Lys2	Lys	TTT	19	11260047	11260122			GCCCGGATAGCTCAGTCGGTAGAGCATCAGACTTTTAATCTGAGGGTCCAGGGTTCAAGTCCCTGTTCGGGCGGAA
tM(CAT)C	Met1	Met	CAT	3	90904791	90904867			TAGCAGAGTGGCGCAGCGGAAGCGTGCTGGGCCCATAACCCAGAGGTCGATGGATCGAAACCATCCTCTGCTATCGA
tM(CAT)M4	Met1	Met	CAT	13	21091117	21091193			TAGCAGAGTGGCGCAGCGGAAGCGTGCTGGGCCCATAACCCAGAGGTCGATGGATCGAAACCATCCTCTGCTAAGGA
tM(CAT)M5	Met1	Met	CAT	13	21287234	21287310			TAGCAGAGTGGCGCAGCGGAAGCGTGCTGGGCCCATAACCCAGAGGTCGATAGATCGAAACCATCCTCTGCTAGTTA
tM(CAT)M6	Met1	Met	CAT	13	21311290	21311364			AGCAGAGTGGCGCAGCGGAAGCGTGCTGGGCCCATAACCCAGAGGTCGAAGGATCGAAACCATCCTCTGCTACAA
tM(CAT)M7	Met1	Met	CAT	13	21355155	21355231			TAGCAGAGTGGCGCAGCGGAAGCGTGCTGGGCCCATAACCCAGAGGTCGATGGATCGAAACCATCCTCTGCTATGAA
tM(CAT)M8	Met1	Met	CAT	13	22880204	22880278			AGCAGAGTGGCGCAGCGGAAGCGTGCTGGGCCCATAACCCAGAGGTCGAAGGATCGAAACCATCCTCTGCTAGAA
tM(CAT)M9	Met1	Met	CAT	13	22897816	22897890			AGCAGAGTGGCGCAGCGGAAGCGTGCTGGGCCCATAACCCAGAGGTCGAAGGATCGAAACCATCCTCTGCTAACA
tM(CAT)M10	Met1	Met	CAT	13	22910468	22910544			TAGCAGAGTGGCGCAGCGGAAGCGTGCTGGGCCCATAACCCAGAGGTCGATGGATCGAAACCATCCTCTGCTATCTA
tM(CAT)O2	Met1	Met	CAT	15	69662937	69663011			AGCAGAGTGGCGCAGCGGAAGCATGCTGGGCCCATAACCCAGAGGTCGAAGGATCGAAACCATCCTCTGCTAACA
tM(CAT)X	Met1	Met	CAT	X	117155003	117155074			AGCAGAGTGGCACAATGGAAGCGTGCTGGTCCCATAACCCAGAGGTCAATGGATTGAAACCATCCTCTGCTT
tM(CAT)E	Met2	Met	CAT	5	107162848	107162925			TGCCTCCTTAGCATAGTAGGCAGCGCATCAGTCTCATAATCTGAAGGTCATGAGTTTGAACCTCAGAGGGGTCAACCA
tM(CAT)K	Met2	Met	CAT	11	121635187	121635264			TGCCTCCTTAGTGTAGTAGGCATTGCGTCAGTCTCATAATCTGAAGGTCATGAGTTCAAGCCTCAGAGTGGGCAAACA
tM(CAT)M1	Met2	Met	CAT	13	20547165	20547242			TGCCTCCTTAGCGCAGTAGGCAGCGCGTCAGTCTCATAATCTGAAGGTCATGAGTTCGAACCTCAGAGGGGGCAGTTA
tM(CAT)M2	Met2	Met	CAT	13	20549245	20549322			TGCCTCCTTAGCGCAGTAGGCAGCGCGTCAGTCTCATAATCTGAAGGTCATGAGTTCGAACCTCAGAGGGGGCAACCA
tM(CAT)M3	Met2	Met	CAT	13	20706761	20706838			TGCCTTCTTAGCGCAGTAGGCAGCGCGTCAGTCTCATAATCTGAAGGTCATGAGTTCGAACCTCAGAGAGGGCAGATA
tM(CAT)H	Met3	Met	CAT	8	121054586	121054661			GCCTCGTTAGCGCAGTAGGTAGCGCGTCAGTCTCATAATCTGAAGGTCGAGAGTTCGATCCTCACACGGGGCATCA
tM(CAT)O1	Met3	Met	CAT	15	58172200	58172277			TGCCTCGTTAGCGCAGTAGGTAGCGCGTCAGTCTCATAATCTGAAGGTCATGAGTTCGATCCTCACACGGGGCACAAA
tF(GAA)E	Phe	Phe	GAA	5	122947750	122947825			GCCGAAATAGCTCAGTTGGGAGAGCGTTAGACTGAAGATCTAAAGGTCCATGGTTCGATCCCGGGTTTCGGCAGCA
tF(GAA)J	Phe	Phe	GAA	10	80149889	80149964			GCCGAAATAGCTCAGTTGGGAGAGCGTTAGACTGAAGATCTAAAGGTCCATGGTTCGATCCCGGGTTTCGGCAAGA
tF(GAA)M1	Phe	Phe	GAA	13	20540967	20541042			GCCGAAATAGCTCAGTTGGGAGAGCGTTAGACTGAAGATCTAAAGGTCCATGGTTCGATCCCGGGTTTCGGCAACA
tF(GAA)M2	Phe	Phe	GAA	13	21263006	21263081			GCCGAAATAGCTCAGTTGGGAGAGCGTTAGACTGAAGATCTAAAGGTCCATGGTTCAATCCCGGGTTTCGGCAAAA
tF(GAA)N	Phe	Phe	GAA	14	110410830	110410905			GCCGAAATAGCTCAGTTGGGAGAGCGTTAGACTGAAGATCTAAAGGTCCATGGTTCGATCCCGGGTTTCGGCAGTA
tF(GAA)S1	Phe	Phe	GAA	19	11252590	11252665			GCCGAAATAGCTCAGTTGGGAGAGCGTTAGACTGAAGATCTAAAGGTCCATGGTTCGATCCCGGGTTTCGGCAGTA
tF(GAA)S2	Phe	Phe	GAA	19	11258898	11258975			TGCTGAAATAGCTCAGTTGGGAGAGCGTTAGACTGAAGATCTAAAGGTCACTGGTTCGATCCCGGGTTTCAGCAAAGA
tS(GGA)K	Phe	Ser	GGA	11	100209281	100209356		Rogue	GCTGAAATAGCTCAGTTGGGAGAGCATTAGACTGGAGATCTAAAGGTCCATGGTTTGATCCCGGGTTTCGGCAGTA
tL(AAG)P	Pro	Leu	AAG	16	3121043	3121117		Rogue	GGCTTGTTGGTCTAGGGGTATGATTCTCACTTAAGGTCTGAGAAGTCCTAGGTTCAAAGCTTGGACGAGTCCTCA
tP(AGG)A2	Pro	Pro	AGG	1	165658432	165658506			GGCTCGTTGGTCTAGGGGTATGATTCTCGCTTAGGGTGCGAGAGGTCCCAGGTTCAAATCCCGGACGAGCCCTGA
tP(AGG)A	Pro	Pro	AGG	1	78768123	78768197			GGCTTGTTGGTCTAGGGGTATGATTCTCACTTAGGGTGTGAGAGGTCCTAGGTTCAAATCTTGGACGAGTCCTCA
tP(AGG)C1	Pro	Pro	AGG	3	51424036	51424110			GGCTCGTTGGTCTAGGGGTATGATTCTCGCTTAGGGTGCGAGAGGTCCCAGGTTCAAATCCCGGACGAGCCCAAA
tP(AGG)C2	Pro	Pro	AGG	3	72241677	72241750			AGCTCATTAGTCTAGGGGTATGATTCTCGCTTAGGGTGTGAGAGGTCCCAGGTTCAAATCCCAATGAGCCCCAA
tP(AGG)F	Pro	Pro	AGG	6	29247221	29247295			GGCTCGTTGGTCTAGGGGTATGATTCTCGCTTAGGGTGCGAGAGGTCCCAGGTTCAAATCCCGGACGAGCCCTGA
tP(AGG)G	Pro	Pro	AGG	7	86087070	86087144			GGCTCGTTGGTCTAGGGGTATGATTCTCGCTTAGGGTGCGAGAGGTCCCAGGTTCAAATCCCGGACGAGCCCAAA
tP(AGG)M	Pro	Pro	AGG	13	22817115	22817189			GGCTCGTTGGTCTAGGGGTATGATTCTCGCTTAGGGTGCGAGAGGTCCCAGGTTCAAATCCCGGACGAGCCCAAA
tP(AGG)N	Pro	Pro	AGG	14	43758257	43758331			GGCTCGTTGGTCTAGGGGTATGATTCTCGCTTAGGGTGCGAGAGGTCCCAGGTTCAAATCCCGGACGAGCCCTAA
tP(AGG)Y	Pro	Pro	AGG	Y	35257556	35257627			GGCTCGTTGGTCTAGGGGTATGATTCTCGCTTAGGGTGCGAGAGGTCCCGGGTTCAAATCCCGGACGAGCCC
tP(CGG)K	Pro	Pro	CGG	11	68652941	68653015			GGCTCGTTGGTCTAGGGGTATGATTCTCGCTTCGGGTGCGAGAGGTCCCAGGTTCAAATCCCGGACGAGCCCCAA
tP(CGG)Q	Pro	Pro	CGG	17	22136844	22136918			GGCTCGTTGGTCTAGGGGTATGATTCTCGCTTCGGGTGCGAGAGGTCCCAGGTTCAAATCCCGGACGAGCCCTGA
tP(GGG)Q	Pro	Pro	GGG	17	22133601	22133676			GGCTTGTTGGTCTGGGGGTATGGTTCTCGCTTGGGGTGTGAGGGGGTCCAGGGTTCAAGTCCCGGATAACCCCGCA
tP(TGG)C	Pro	Pro	TGG	3	51422983	51423057			GGCTCGTTGGTCTAGGGGTATGATTCTCGCTTTGGGTGCGAGAGGTCCCAGGTTCAAATCCCGGACGAGCCCAGA
tP(TGG)G	Pro	Pro	TGG	7	86086812	86086886			GGCTCGTTGGTCTAGGGGTATGATTCTCGGTTTGGGTCCGAGAGGTCCCAGGTTCAAATCCCGGACGAGCCCCAA
tP(TGG)K1	Pro	Pro	TGG	11	48496015	48496089			GGCTCGTTGGTCTAGGGGTATGATTCTCGCTTTGGGTGCGAGAGGTCCCAGGTTCAAATCCCGGACGAGCCCAAA
tP(TGG)K2	Pro	Pro	TGG	11	66903687	66903761			GGTTTGTTGGTCTAGTGGTATGATTCTCAGTTTGGGTTTGAGAGGTCCTAGGTTCAAATCCCAGACGAGCCCCCA
tP(TGG)N	Pro	Pro	TGG	14	43784094	43784168			GGCTCGTTGGTCTAGGGGTATGATTCTCGCTTTGGGTGCGAGAGGTCCCAGGTTCAAATCCCGGACGAGCCCTGA
tP(TGG)Q2	Pro	Pro	TGG	17	22142402	22142476			GGCTCGTTGGTCTAGGGGTATGATTCTCGCTTTGGGTGCGAGAGGTCCCAGGTTCAAATCCCGGACGAGCCCAGA
tP(TGG)Q	Pro	Pro	TGG	17	22134692	22134766			GGGTCATTGGTCTATGGGCATGATTCTCTCTTTGGGTGAGAGAGGTCCCAGGTTCAAATCCCGGATGAGCCCAGA
tP(TGG)X	Pro	Pro	TGG	X	13034334	13034408			GGCTCGTTGGTCTAGGGGTATGATTCTCACTTTGGGTGTGAGAGGTCCTAGGTTCAAATCCCAGGTGAGCCCAGA
tP(TGG)Y	Pro	Pro	TGG	Y	35257817	35257888			GGCTCGTTGGTCTAGGGGTATGATTCTCGGTTTGGGTCCGAGAGGTCCCGGGTTCAAATCCCGGACGAGCCC
tS(AGA)D	Ser1	Ser	AGA	4	10800278	10800362			GTAGTCGTGGCCGAGTGGTTAAGGCGATGGACTAGAAATCCATTGGGGTATCCCCGCGCAGGTTCGAATCCTGCCGACTACGGAA
tS(AGA)K	Ser1	Ser	AGA	11	68650032	68650118			TGTAGTCGTGGCCGAGTGGTTAAGGCGATGGACTAGAAATCCATTGGGGACTCCCCGCGCAGGTTCGAATCCTGCCGACTACGTCTA
tS(AGA)M1	Ser1	Ser	AGA	13	21299338	21299424			TGTAGTCGTGGCCGAGTGGTTAAGGCGATGGACTAGAAATCCATTGGGGACTCCCCGCGCAGGTTCGAATCCTGCCGACTACGTCAA
tS(AGA)M2	Ser1	Ser	AGA	13	21307980	21308066			TGTAGTCGTGGCCGAGTGGTTAAGGCGATGGACTAGAAATCCATTGGGGACTCCCCGCGCAGGTTCGAATCCTGCCGACTACGGTAA
tS(AGA)M3	Ser1	Ser	AGA	13	21317214	21317300			TGTAGTCGTGGCCGAGTGGTTAAGGCGATGGACTAGAAATCCATTGGGGATTCCCCGCGCAGGTTCGAATCCTGCCGACTACGGGTA
tS(AGA)M4	Ser1	Ser	AGA	13	21321034	21321120			TGTAGTCGTGGCCGAGTGGTTAAGGCGATGGACTAGAAATCCATTGGGGACTCCCCGCGCAGGTTCGAATCCTGCCGACTACGGGCA
tS(AGA)M5	Ser1	Ser	AGA	13	22881077	22881163			TGTAGTCGTGGCCGAGTGGTTAAGGCGATGGACTAGAAATCCATTGGGGACTCCCCGCGCAGGTTCGAATCCTGCCGACTACGATTA
tS(AGA)X1	Ser1	Ser	AGA	X	157022395	157022479			GTAGTCGTGGCCAAGTGAGTAAGGCAATGGACTAGAAATCCATTGGGGTATCCCAGCACAGGTTCAAATCCTGCTGACTATGGTA
tS(CGA)J	Ser1	Ser	CGA	10	128585227	128585311			GTCACGGTGGCCGAGTGGTTAAGGCGTTGGACTCGAAATCCAATGGGGTATCCCCGCACAGGTTCGAATCCTGTTCGTGACGGCA
tS(CGA)K	Ser1	Ser	CGA	11	68723475	68723559			GCTGTGATGGCCGAGTGGTTAAGGCGTTGGACTCGAAATCCAATGGGGTATCCCCGCGCAGGTTCGAATCCTGCTCACAGCGCTA
tS(CGA)M	Ser1	Ser	CGA	13	21402540	21402624			GCTGTGATGGCCGAGTGGTTAAGGCGTTGGACTCGAAATCCAATGGGTTATTCCCGCGCAGGTTCAAATCCTGCTCACAGCGTAA
tS(TGA)J	Ser1	Ser	TGA	10	63194756	63194840			GCAGCGATGGCCGAGTGGTTAAGGCGTTGGACTTGAAATCCAATGGGGTATCCCCGCGCAGGTTCGAACCCTGCTCGCTGCGGAA
tS(TGA)M1	Ser1	Ser	TGA	13	21305056	21305140			GTAGTCGTGGCCGAGTGGTTAAGGCGATGGACTTGAAATCCATTGGGGTATCCCCGCGCAGGTTCGAATCCTGCCGACTACGGTA
tS(TGA)M2	Ser1	Ser	TGA	13	22898269	22898355			TGTAGTCGTGGCCGAGTGGTTAAGGCGATGGACTTGAAATCCATTGGGGATTCCCCGCGCAGGTTCGAATCCTGCCGACTACGTGAA
tS(GCT)A	Ser2	Ser	GCT	1	182141342	182141428			GGACGAGGTGGCCGAGTGGTTAAAGCGATGGACTGCTAATCCACTGTGCACAGTATGCGTGGGTTCGAATCCCATCCTCGTCCGAAA
tS(GCT)B1	Ser2	Ser	GCT	2	118828323	118828407			GACGAGGTGGCCGAGTGGTTAAGGCGATGGACTGCTAATCCATTGTGCTATGCACGCATGGGTTCGAATCCCATCCTCGTCGAAA
tS(GCT)K2	Ser2	Ser	GCT	11	68675595	68675679			GACGAGGTGGCCGAGTGGTTAAGGCGATGGACTGCTAATCCATTGTGCTATGCACGCGTGGGTTCGAATCCCATCCTCGTCGTCA
tS(GCT)M1	Ser2	Ser	GCT	13	20872890	20872974			GATGAGGTGGCCGAGTGGTTAAGGCGATGGACTGCTAATCCATTGTGCTATGCACGCATGGGTTCGAATCCCATCCTCATCGACA
tS(GCT)M2	Ser2	Ser	GCT	13	21374311	21374395			GACGAGGTGGCCGAGTGGTTAAGGCGATGGACTGCTAATCCATTGTGCTATGCACGCGTGGGTTCGAATCCCACCTTCGTCGTCA
tS(GCT)M3	Ser2	Ser	GCT	13	21430806	21430892			TGACGAGGTGGCCGAGTGGTTAAGGCGATGGACTGCTAATCCATTGTGCACTGCACGCGTGGGTTCGAATCCCATCCTCGTCGGTCA
tS(GCT)M4	Ser2	Ser	GCT	13	22901993	22902079			TGACGAGGTGGCCGAGTGGTTAAGGCGATGGACTGCTAATCCATTGTGCACTGCACGCGTGGGTTCGAATCCCATCCTCGTCGTTCA
tS(GCT)S	Ser2	Ser	GCT	19	4826771	4826855			GACGAGGTGGCCGAGTGGTTAAGGCGATGGACTGCTAATCCATTGTGCTATGCACGCGTGGGTTCGAATCCCATCCTCGTCGGTA
tT(AGT)G	Thr1	Thr	AGT	7	23656861	23656937			GGCGCCGTGGCTTAGTTGGTTAAAGCGCCTGTCTAGTAAACAGGAGATCATGGGTTCGAATCCCAGCGGTGCCTGAA
tT(AGT)K1	Thr1	Thr	AGT	11	68650409	68650485			GGCGCCGTGGCTTAGTTGGTTAAAGCGCCTGTCTAGTAAACAGGAGATCATGGGTTCGAATCCCAGCGGTGCCTTTA
tT(AGT)K2	Thr1	Thr	AGT	11	68675296	68675374			AGGCGCCGTGGCTTAGTTGGTTAAAGCGCCTGTCTAGTAAACAGGAGATACTGGGTTCGAATCCCAGCGGTGCCTTTGA
tT(AGT)K3	Thr1	Thr	AGT	11	68723021	68723097			GGCGCCGTGGCTTAGCTGGTTAAAGCGCCTGTCTAGTAAACAGGAGATCATGGGTTCGAATCCCAGCGGTGCCTGGA
tT(AGT)M	Thr1	Thr	AGT	13	22830746	22830822			GGCTCCGTGGCTTAGCTGGTTAAAGCGCCTGTCTAGTAAACAGGAGATCATGGGTTCGAATCCCAGCGGGGCCTTTA
tT(AGT)N2	Thr1	Thr	AGT	14	50810563	50810639			GGCACCGTGGCTTAGTTGGTTAAAGCGCCTGTCTAGTAAACAGGAGATCATGGGTTCGAATTCCAGCGGTGCCTGAA
tM(CAT)J	Thr1	Met	CAT	10	62958645	62958740		Rogue	GGCTCTGTGGCTTAGTTGGCTAAAGTGCCTGTCTCATAAACAGGAGATCATGTTGTAAACAGGAGATCGTGGGTTTGAATCCCAGTGGGGCCTGAA
tT(CGT)M1	Thr1	Thr	CGT	13	20644628	20644704			GGCTCCGTGGCTTAGTTGGCTAAAGCGCCTGTCTCGTAAACAGGAGATCATGGGTTCGAATCCCAGTGGGGCCTGGA
tT(CGT)M2	Thr1	Thr	CGT	13	20702861	20702937			GGCTCCATGGCTTAGCTGGTTAAAGCGCCTGTCTCGTAAACAGGAGATCATGGGTTCGACTCCCAGTGGGGCCTTCA
tT(TGT)M1	Thr1	Thr	TGT	13	20656004	20656080			GGCTCCATGGCTTAGTTGGTTAAAGCGCCTGTCTTGTAAACAGGAGATCATGGGTTCGAATCCCAGTGGGGCCTATA
tT(CGT)K2	Thr2	Thr	CGT	11	79317205	79317281			AGGCGCGGTGGCCAAGTGGTAAGGCGTCGGTCTCGTAAACCGAAGATCGAGGGTTCGAACCCCGTCCGTGCCTGCGA
tT(CGT)P	Thr2	Thr	CGT	16	13180952	13181028			AGGCGCGGTGGCCAAGTGGTAAGGCGTCGGTCTCGTAAACCGAAGATCAAGGGTTCGAACCCCGTCCGTGCCTGCCA
tW(CCA)J1	Trp	Trp	CCA	10	23539187	23539263			TGACCTCGTGGCACAATGGTAGCACGTCTGACTCCAGATCAGAAGGTTGAGTGTTCAAATCACGTCGGGGTCATGAA
tW(CCA)J2	Trp	Trp	CCA	10	90952051	90952125			GACCTCGTGGCGCAACGGTAGCGCGTCTGACTCCAGATCAGAAGGCTGCATGTTCGAATCACGTCGGGGTCATAA
tW(CCA)K1	Trp	Trp	CCA	11	61020452	61020528			TGACCTCGTGGCGCAATGGTAGCGCGTCTGACTCCAGATCAGAAGGTTGAGTGTTCAAGTCACGTCGGGGTCAAGTA

tRNA gene name
tG(GCC)B
tG(GCC)C
tG(GCC)D2
tG(GCC)G
tG(GCC)H1
tG(GCC)H2
tG(GCC)H3
tG(GCC)J
tG(GCC)K1
tG(GCC)M1
tG(GCC)M2
tG(TCC)A1
tG(TCC)A2
tG(TCC)A3
tG(TCC)C
tG(TCC)K
tG(TCC)X1
tG(CCC)F
tG(CCC)Q
tH(GTG)B1
tH(GTG)B2
tH(GTG)B3
tH(GTG)C1
tH(GTG)C2
tH(GTG)C3
tH(GTG)C4
tH(GTG)C5
tH(GTG)D
tI(AAT)D1
tI(AAT)H
tI(AAT)K1
tI(AAT)K2
tI(AAT)L
tI(AAT)M1
tI(AAT)M2
tI(AAT)M3
tI(AAT)M4
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tI(AAT)M6
tI(AAT)P
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tI(TAT)M2
tI(TAT)M
tI(TAT)Q4
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tL(CAA)M1
tL(CAA)M
tL(CAA)M2
tL(CAG)A1
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tL(CAG)H2
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tL(AAG)G
tL(AAG)K
tL(AAG)M1
tL(AAG)M2
tL(AAG)N
tL(TAG)B
tL(TAG)G2
tL(TAG)K
tL(TAG)N
tL(TAA)J
tL(TAA)M
tL(TAA)S
tL(TAA)X1
tStop(TTA)M
tK(CTT)A
tK(CTT)B
tK(CTT)C1
tK(CTT)C2
tK(CTT)C3
tK(CTT)C5
tK(CTT)C6
tK(CTT)E
tK(CTT)G
tK(CTT)I1
tK(CTT)I2
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tK(CTT)K3
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tK(CTT)L
tK(CTT)M1
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tK(CTT)P1
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tK(CTT)P3
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tK(CTT)Q5
tK(CTT)R
tK(CTT)X1
tK(CTT)X2
tK(CTT)Y
tL(TAA)E2
tSeC(TCA)E
tK(TTT)H
tK(TTT)P
tK(TTT)A1
tK(TTT)A2
tK(TTT)E
tK(TTT)G
tK(TTT)J
tK(TTT)K
tK(TTT)M1
tK(TTT)M2
tK(TTT)M3
tK(TTT)S1
tK(TTT)S2
tM(CAT)C
tM(CAT)M4
tM(CAT)M5
tM(CAT)M6
tM(CAT)M7
tM(CAT)M8
tM(CAT)M9
tM(CAT)M10
tM(CAT)O2
tM(CAT)X
tM(CAT)E
tM(CAT)K
tM(CAT)M1
tM(CAT)M2
tM(CAT)M3
tM(CAT)H
tM(CAT)O1
tF(GAA)E
tF(GAA)J
tF(GAA)M1
tF(GAA)M2
tF(GAA)N
tF(GAA)S1
tF(GAA)S2
tS(GGA)K
tL(AAG)P
tP(AGG)A2
tP(AGG)A
tP(AGG)C1
tP(AGG)C2
tP(AGG)F
tP(AGG)G
tP(AGG)M
tP(AGG)N
tP(AGG)Y
tP(CGG)K
tP(CGG)Q
tP(GGG)Q
tP(TGG)C
tP(TGG)G
tP(TGG)K1
tP(TGG)K2
tP(TGG)N
tP(TGG)Q2
tP(TGG)Q
tP(TGG)X
tP(TGG)Y
tS(AGA)D
tS(AGA)K
tS(AGA)M1
tS(AGA)M2
tS(AGA)M3
tS(AGA)M4
tS(AGA)M5
tS(AGA)X1
tS(CGA)J
tS(CGA)K
tS(CGA)M
tS(TGA)J
tS(TGA)M1
tS(TGA)M2
tS(GCT)A
tS(GCT)B1
tS(GCT)K2
tS(GCT)M1
tS(GCT)M2
tS(GCT)M3
tS(GCT)M4
tS(GCT)S
tT(AGT)G
tT(AGT)K1
tT(AGT)K2
tT(AGT)K3
tT(AGT)M
tT(AGT)N2
tM(CAT)J
tT(CGT)M1
tT(CGT)M2
tT(TGT)M1
tT(CGT)K2
tT(CGT)P
tW(CCA)J1
tW(CCA)J2
tW(CCA)K1

tRNA gene name
tG(GCC)B
tG(GCC)C
tG(GCC)D2
tG(GCC)G
tG(GCC)H1
tG(GCC)H2
tG(GCC)H3
tG(GCC)J
tG(GCC)K1
tG(GCC)M1
tG(GCC)M2
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tG(TCC)A2
tG(TCC)A3
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tG(TCC)K
tG(TCC)X1
tG(CCC)F
tG(CCC)Q
tH(GTG)B1
tH(GTG)B2
tH(GTG)B3
tH(GTG)C1
tH(GTG)C2
tH(GTG)C3
tH(GTG)C4
tH(GTG)C5
tH(GTG)D
tI(AAT)D1
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tT(CGT)P
tW(CCA)J1
tW(CCA)J2
tW(CCA)K1

tRNA gene name
tG(GCC)B
tG(GCC)C
tG(GCC)D2
tG(GCC)G
tG(GCC)H1
tG(GCC)H2
tG(GCC)H3
tG(GCC)J
tG(GCC)K1
tG(GCC)M1
tG(GCC)M2
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tG(TCC)A2
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tG(TCC)K
tG(TCC)X1
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tG(CCC)Q
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tH(GTG)B3
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tT(CGT)P
tW(CCA)J1
tW(CCA)J2
tW(CCA)K1

tRNA gene name	tRNA Family	Amino Acid	Anti codon	Chromo some	Sequence Start	Sequence End	intr on	Rogue tRNA?	tRNA gene sequence (including introns)
tW(CCA)K2	Trp	Trp	CCA	11	62358559	62358635			TGACCTCGTGGCGCAATGGTAGCGCGTCTGACTCCAGATCAGAAGGTTGAGTGTTCAAATCACGTCGGGGTCATGAA
tW(CCA)K3	Trp	Trp	CCA	11	68654382	68654456			GGCCTCGTGGCGCAACGGTAGCGCGTCTGACTCCAGATCAGAAGGTTGCATGTTCAAATCACGTCGGGGTCATCA
tW(CCA)K4	Trp	Trp	CCA	11	68676048	68676122			GGCCTCGTGGCGCAACGGTAGCGCGTCTGACTCCAGATCAGAAGGTTGCATGTTCAAATCACGTCGGGGTCAGCA
tW(CCA)M1	Trp	Trp	CCA	13	22878229	22878305			TGACCTCGTGGCGCAACGGTAGCGCGTCTGACTCCAGATCAGAAGGTTGAGTGTTCAAATCACGTCGGGGTCAGTGA
tW(CCA)M2	Trp	Trp	CCA	13	22886642	22886718			TGACCTCGTGGCGCAACGGTAGCGCGTCTGACTCCAGATCAGAAGGTTGAGTGTTCAAATCACGTCGGGGTCAAGTA
tY(GTA)C1	Tyr	Tyr	GTA	3	19302785	19302880	I		CCTTCGATAGCTCAGCTGGTAGAGCGGAGGACTGTAGCTAACTCCCCGTAAGAAGACATCCTTAGGTCGCTGGTTCGACTCCGGCTCGAAGGAGAA
tY(GTA)C2	Tyr	Tyr	GTA	3	19303212	19303303	I		CCTTCGATAGCTCAGCTGGTAGAGCGGAGGACTGTAGGCTTGTGGCTGTAGACATCCTTAGGTCGCTGGTTCGATTCCGGCTCGAAGGAAAA
tY(GTA)C3	Tyr	Tyr	GTA	3	92212300	92212387	i		CATTCGATAGCTCAGTTGGTAGAGCAGAAGACTGTAGTTAGTACAATATGGTAATCCTTGGGTTGCTGGTTCGATTCCATTCAAAGGA
tY(GTA)E1	Tyr	Tyr	GTA	5	29296268	29296359	I		CCTTCGATAGCTCAGTTGGTAGAGCGGAGGACTGTAGTCAGTACAATATAGTAATCCTTAGGTCGCTGGTTCGATTCCGGCTCGAAGGACTA
tY(GTA)J	Tyr	Tyr	GTA	10	96777476	96777585	i		CCTTCGATAGCTCAGCTGGTAGAGCGGAGGACTGTAGTCAAGAAAAATGAAGACTGAAGTGTGGACACTATGCCCCTCCTTAGAAGTGGGAACAAAACACCCTTGGAAGG
tY(GTA)M1	Tyr	Tyr	GTA	13	22805766	22805859	I		TCCTTCGATAGCTCAGTTGGTAGAGCGGAGGACTGTAGAGTTACTAGAAAAGTGATCCTTAGGTCGCTGGTTCGAATCCGGCTCGAAGGAACGA
tY(GTA)M2	Tyr	Tyr	GTA	13	22806628	22806720	I		TCCTTCGATAGCTCAGTTGGTAGAGCGGAGGACTGTAGACTACTAATGTAGTGATCCTTAGGTCGCTGGTTCGAATCCGGCTCGAAGGAATGA
tY(GTA)M3	Tyr	Tyr	GTA	13	22807216	22807304	I		CCTTCGATAGCTCAGTTGGTAGAGCGGAGGACTGTAGTATAGGTGTTGAAATCCTTAGGTCGCTGGTTCGAATCCGGCTCGAAGGAGGA
tY(GTA)M4	Tyr	Tyr	GTA	13	22808859	22808950	I		CTTTCGATAGTTCAGTTGGTAGAGCGGAGGACTGTAGAGTATTAACGTTAGTGATCCTTAGGTCGCTGGTTCGAGTCCGGCTCGAAGGAAGA
tY(GTA)M5	Tyr	Tyr	GTA	13	22813110	22813202	I		TCCTTCGATAGCTCAGTTGGTAGAGCGGAGGACTGTAGGTCATTGTTCTAGAAATCCTTAGGTCGCTGGTTCGAATCCGGCTCGAAGGAACCA
tY(GTA)M6	Tyr	Tyr	GTA	13	22847199	22847293	I		TCCTTCGATAGCTCAGTTGGTAGAGCGGAGGACTGTAGGAGTATTCGACATGGAAATCCTTAGGTCGCTGGTTCGAATCCGGCTCGAAGGAGGTA
tY(GTA)N	Tyr	Tyr	GTA	14	43782936	43783028	I		CCTTCGATAGCTCAGCTGGTAGAGCGGAGGACTGTAGTTACATTCGTTGAAGCCATCCTTAGGTCGCTGGTTCGATTCCGGCTCGAAGGAGTA
tV(AAC)C	Val1	Val	AAC	3	30365837	30365912			GTTTCCGTAGTGTAGTGGTTATCACGTTCGCCTAACACGCGAAAGGTCCACGGTTCGAAACCGGGCGGAAACATAA
tV(AAC)E	Val1	Val	AAC	5	15480961	15481036			GTTTCCGTAGTGTAGTGGTTATCATGTTTGTCTAACACGCGAAAGGTCCACAGTTTGAAACCGGGTGGAAAAAAAA
tV(AAC)K1	Val1	Val	AAC	11	48496372	48496447			GTTTCCGTAGTGTAGTGGTTATCACGTTCGCCTAACACGCGAAAGGTCCACGGTTCGAAACCGGGCGGAAACAAGA
tV(AAC)M1	Val1	Val	AAC	13	21395911	21395988			TGTTTCCGTAGTGTAGTGGTTATCACATTCGCCTAACACGCGAAAGGTCACCGGTTCGAAACCGGGCGGAAACACGTA
tV(AAC)M2	Val1	Val	AAC	13	22665524	22665601			TGTTTCCGTAGTGTAGTGGTCATCACGCTCGCCTAACACGCGAGAGGTCACCGGTTCGAAACCGGGCGGAAACATTAA
tV(AAC)M3	Val1	Val	AAC	13	22678904	22678981			TGTTTCTGTAGTGTAGTGGTTATCACGCTCGCCTAACACGCGAGAGGTCACCGGTTCGAAACCGGGCAGAAACAGTGA
tV(AAC)M4	Val1	Val	AAC	13	22781193	22781270			TGTTTCCGTAGTGTAGTGGTCATCACGCTCGCCTAACACGCGAGAGGTCACCGGTTCGAAACCGGGCGGGAACATTTA
tV(AAC)M5	Val1	Val	AAC	13	22793368	22793445			TGTTTCCGTAGTGTAGTGGTCATCACGCTCGCCTAACACGCGAGAGGTCACCGGTTCGAAACCGGGCGGAAACATGGA
tG(ACC)K	Val1	Gly	ACC	11	48463463	48463539		Rogue	GTTTCCGTAGTGTAGTGGTTAGCGCGTTCGCCTACCAAAGCGAAAGGTCACCGGTTCGAAACCGGGCGGAAACAAAA
tV(CAC)A	Val1	Val	CAC	1	171182812	171182887			GTTTCCGTAGTGTAGTGGTTATCACGTTCGCCTCACACGCGAAAGGTCCACGGTTCGAAACCGGGCGGAAACAGCA
tV(CAC)C1	Val1	Val	CAC	3	59607018	59607094			TGTTTCTGTAGTGTAGTGGTTTCACATTTGCCTCACATGCAAAAGGTCCACGGTTCTCAACCGGGCAGAAACAACTA
tV(CAC)C3	Val1	Val	CAC	3	96338468	96338543			GTTTCCGTAGTGTAGTGGTTATCACGTTCGCCTCACACGCGAAAGGTCCACGGTTCGAAACCGGGCGGAAACAAGA
tV(CAC)F	Val1	Val	CAC	6	9831301	9831376			GTTTCTGTAGTGTAGTGGTTATCACGTTCGCCTCACACGCGAAAGGTCCACGGTTCGAAACCGGGCAGAAACAAGA
tV(CAC)K1	Val1	Val	CAC	11	48458277	48458352			GTTTCCGTAGTGTAGTGGTTATCACGTTCGCCTCACACGCGAAAGGTCCACGGTTCGAAACCGGGCGGAAACAACA
tV(CAC)M1	Val1	Val	CAC	13	21406671	21406748			TGTTTCCGTAGTGTAGTGGTTATCACGTTCGCCTCACACGCGAAAGGTCACCGGTTCGAAACCGGGCGGAAACAATGA
tV(CAC)M2	Val1	Val	CAC	13	22680245	22680322			TGTTTCCGTAGTGTAGTGGTCATCACGCTCGCCTCACACGCGAGAGGTCACCGGTTCGAAACCGGGCGGGAACAACAA
tV(CAC)M3	Val1	Val	CAC	13	22687753	22687828			GTTTCCGTAGTGTAGTGGTTATCACGCTCGCCTCACACGCGAGAGGTCCACGGTTCGAAACCGGGCGGAAACAGTA
tV(CAC)M4	Val1	Val	CAC	13	22792197	22792274			TGTTTTTGTAGTGTAGCGGTTATCACGCTCGCCTCACACGCGAGAGGTCATCGGTTCAAAACCCAGTGGAAACATTTA
tV(CAC)M5	Val1	Val	CAC	13	22826263	22826338			GTTTCCGTAGTGTAGTGGTTATCACGTTCGCCTCACACGCGAAAGGTCCACGGTTCGAAACCGGGCGGAAACAGTA
tV(CAC)Q2	Val1	Val	CAC	17	57400716	57400791			GTTTCCCTAGTGTAGTGGTTATCACGTTCGCCTCACATGCAAAAGGTCCATGGTTCGAAACCTGGCGGAAACAGTA
tV(CAC)X7	Val1	Val	CAC	X	37314459	37314530			GTTTCAGTAGTGTAGTGGTTATCACGTTTGCCTCACGCATGAAATGTCCCCGGTTGGAAACCTGGGGAAACA
tV(TAC)S1	Val2	Val	TAC	19	11262285	11262360			GGTTCCATAGTGTAGCGGTTATCACGTCTGCTTTACACGCAGAAGGTCCAGGGTTCGAGCCCCAGTGGAACCACGA
tV(TAC)S2	Val2	Val	TAC	19	11262619	11262696			TGGTTCCATAGTGTAGCGGTTATCACGTCTGCTTTACACGCAGAAGGTCATGGGTTCGAGCCCCAGTGGAACCAGTGA
tV(TAC)X2	Val2	Val	TAC	X	150735962	150736039			TGGTTCCATAGTGTAGCGGTTATCACGTCTGCTTTACACGCAGAAGGTCATGGGTTCGAGCCCCAGTGGAACCATAGA
tV(AAC)K2		Val	AAC	11	64344654	64344725			GCTGACCTTAGCTCAGTGGCAGAGCATGGGACTAACACGCACAAAGCTCTGGGTTCTGTTCCCAGTGCAACA
tI(AAT)G		Ile	AAT	7	125033749	125033823			GGGTAGGCGTGGCTTAGTGGCAAAGTAGGTACTTAATATGCACAAGGCCCTGGGTTCAATCTCCAGCAGCACCCA
tG(ACC)E		Gly	ACC	5	91642399	91642465			GGATGTAGCTCTGTGGTAGAACACTTGTCTACCATACACAGGGTTCTGGGTTCGAATCCCAGCACCA
tS(AGA)N		Ser	AGA	14	57933281	57933354			CTGGGGACTTAGCTCAGTGGTAGAGTGTTTACTTAGAAAGGGCAAGACCCTGGGTTCCATCCTCAGCTCCTAGG
tP(AGG)P		Pro	AGG	16	93798387	93798473	I		CAAGGGAGTGGGCAAGGTAGCTCAGTGATTAGGAACACTTGCTTTTCTTACTGAGGACCTGGGTTCAATTCCCAGCACCCATGTAGA
tH(ATG)A		His	ATG	1	171740670	171740747			CGGACCAGTGGTGCAATGGATAACACGTCTGACTATGGATCAGAAGATTATAGGTTCGACTCCTGTCTGGCTCGTTGA
tN(ATT)X		Asn	ATT	X	132925018	132925089			GGTTATATAGCTCAGTGGTAGAGTACGTGTTCATTATGCAGGAGGCCCTAGATTCCATCTCTAGTACAAAAA
tL(CAA)K		Leu	CAA	11	115171001	115171129	I		GTCAGACTAGCTGGCTAAGGGCACAGCTCAGTGGACAGGGTGGTGGGCAATGTGTGGGAGGGACTGGTCTAACAGTGCAGAGTTCTCAAAGCACTGAGCAGCACTGTCCGAGT
tV(CAC)N		Val	CAC	14	39549215	39549298			TCCGGGTGGGGTGTGCAGGGAGCACTTGCGGGTCACAGCCGCAGCAACAAGAAGCCGCGGGGTCTCCTCCCGCACCTGGGAAGA
tG(CCC)I		Gly	CCC	9	57369946	57370021			GGGGATCTAGCCCAGTGGTAGAGCGCACACTCTTCCCATGTGTGAGGTCATGGGTTCAATCCCAGCATCTCCAAGA
tT(CGT)X		Thr	CGT	X	140986759	140986833			GGGGATGTAGCTCAGAGATAGAGTGTGTGCCTCGTATGTGTGAGGTCCCAGGTTCAATCCCCTGCATCTCCAAGA
tF(GAA)O		Phe	GAA	15	3687891	3688442	I		
tA(GGC)H2		Ala	GGC	8	109962872	109962942			GCGTTGGTAGTTTAACGGGAGAATTCTCCACTGGCACGTGGGAGCCCTGGGTTTGATTACCAGCCAGTACA
tA(GGC)O1		Ala	GGC	15	42435453	42435534	I		GGGGATGGAGGAATGGTTCAGTCCTTAAGAGCACTGGCTGCTCTTGCAGAGGACCTGGGTTCAATTCCCAGCACCCCCATGA
tT(GGT)J		Thr	GGT	10	126722048	126722119			TTAGGGATTGAGCCCAGTGGTAGGGCCTTGCCTGGTAAGCACAAGGTCTTAGGTTCAGTTCTCACCTCTGAG
tY(GTA)B		Tyr	GTA	2	22579293	22579362			GGTAAAATGGCTGAGTAAGCATTAGACTGTAAATCTAAACACAGAGGTTAAAATCCTCTTTTTACCAGAA
tV(TAC)G		Val	TAC	7	23020210	23020352	I		GGGGATGTGGCTCAGTGGTAGAACACTTGCCTAGAATCCCCCCCCCCCCAAGTGAGGGATTGGGATGGGGGGGTGGGGCTTAGTTCTAGAGCAATTGTCAACTACGTGCAAGGC
tSec(TCA)G		Sec	TCA	7	10824326	10824415			GCCCGGATGATCCTCAGTGGTCTGGGGTGCAGGCTTCAAACCTGTAGCTATTTAGCGACAGAGTGGTTCAATTCCACCTTTCGGGCGGGA
tS(TGA)X		Ser	TGA	X	126591980	126592051			TGAGACTTAGCTCAGTGGTAGAGCTGGTGTTCTGAAAGCATGTGGTCCCAGGTTCAATTCCTGGGGTCTTTA
tA(TGC)G		Ala	TGC	7	113109603	113109673			GAGATGATAGCTCAGTGGTAGAGGACACACCCTGCACCTGTGAGGTCCTGGGTTCTAGCCGCAGCATCCCC
tT(TGT)E1		Thr	TGT	5	24158456	24158574	I		TTAGGGTTGGCTTACAGGATCTGAGGTTCAGTCCATTACCATCAAGGCGAGAGCATGAGAGTGTCCAGGTAATTGTGGGACTGGAGGAGCTGAGGGTTCAATATCTTCATCCAAAG
tT(TGT)O		Thr	TGT	15	27354831	27354908			GGTGCGGTGGCTGAGCTGGTTAAAGCACCTGTCTTGTTAACAGGGCAGCCTGGGTTTGATTCCCAGAGCCCCCCACCC
tT(TGT)X2		Thr	TGT	X	126614305	126614379			GGGGAGGTAGCTCAATGGTAGAGCACATGCTTTGTGTGTATGAGGCACCAGGTTCTATTCCCGCCTGCTTTTTTA

tRNA gene name	
tW(CCA)K2	
tW(CCA)K3	
tW(CCA)K4	
tW(CCA)M1	
tW(CCA)M2	
tY(GTA)C1	
tY(GTA)C2	
tY(GTA)C3	
tY(GTA)E1	
tY(GTA)J	
tY(GTA)M1	
tY(GTA)M2	
tY(GTA)M3	
tY(GTA)M4	
tY(GTA)M5	
tY(GTA)M6	
tY(GTA)N	
tV(AAC)C	
tV(AAC)E	
tV(AAC)K1	
tV(AAC)M1	
tV(AAC)M2	
tV(AAC)M3	
tV(AAC)M4	
tV(AAC)M5	
tG(ACC)K	
tV(CAC)A	
tV(CAC)C1	
tV(CAC)C3	
tV(CAC)F	
tV(CAC)K1	
tV(CAC)M1	
tV(CAC)M2	
tV(CAC)M3	
tV(CAC)M4	
tV(CAC)M5	
tV(CAC)Q2	
tV(CAC)X7	
tV(TAC)S1	
tV(TAC)S2	
tV(TAC)X2	
tV(AAC)K2	
tI(AAT)G	
tG(ACC)E	
tS(AGA)N	
tP(AGG)P	
tH(ATG)A	
tN(ATT)X	
tL(CAA)K	CAGCGATCTGGTCAGA
tV(CAC)N	
tG(CCC)I	
tT(CGT)X	
tF(GAA)O	GAAAACACACGGTGGGACTCGTGGTTCTAGTGCAAATGTAGCAGAAGATGGCCTAGTCGGTCATCAATGGGAGGAGAGGCCCTTAATACTGTGAAGGTTAAATGCCCCAGTATAGGGGACTGCAAGGGCCAGGAAGAAGGAGTGTGTACTGGCTAGTTTTGTGTCAACTTGA
tA(GGC)H2	
tA(GGC)O1	
tT(GGT)J	
tY(GTA)B	
tV(TAC)G	TCTGGGTTCAATTCTCAGTATGCCCCAAA
tSec(TCA)G	
tS(TGA)X	
tA(TGC)G	
tT(TGT)E1	GTA
tT(TGT)O	
tT(TGT)X2	

tRNA gene name	
tW(CCA)K2	
tW(CCA)K3	
tW(CCA)K4	
tW(CCA)M1	
tW(CCA)M2	
tY(GTA)C1	
tY(GTA)C2	
tY(GTA)C3	
tY(GTA)E1	
tY(GTA)J	
tY(GTA)M1	
tY(GTA)M2	
tY(GTA)M3	
tY(GTA)M4	
tY(GTA)M5	
tY(GTA)M6	
tY(GTA)N	
tV(AAC)C	
tV(AAC)E	
tV(AAC)K1	
tV(AAC)M1	
tV(AAC)M2	
tV(AAC)M3	
tV(AAC)M4	
tV(AAC)M5	
tG(ACC)K	
tV(CAC)A	
tV(CAC)C1	
tV(CAC)C3	
tV(CAC)F	
tV(CAC)K1	
tV(CAC)M1	
tV(CAC)M2	
tV(CAC)M3	
tV(CAC)M4	
tV(CAC)M5	
tV(CAC)Q2	
tV(CAC)X7	
tV(TAC)S1	
tV(TAC)S2	
tV(TAC)X2	
tV(AAC)K2	
tI(AAT)G	
tG(ACC)E	
tS(AGA)N	
tP(AGG)P	
tH(ATG)A	
tN(ATT)X	
tL(CAA)K	
tV(CAC)N	
tG(CCC)I	
tT(CGT)X	
tF(GAA)O	CACAGGTGGAGTAATCACAGAGAAGGAGCTTCAGTTGAGGAAATGCCTCCATGAGATCCAGCATTAAGGCATTTTCTCAATTAGTGATCAAGGGGGAAAGGCCCCTTGTGGGAGGGACCATCTCTGGGCTGGTAGTCTTGGGTTCTATAAGAGAGCAGGCTGAGCAAGCCAG
tA(GGC)H2	
tA(GGC)O1	
tT(GGT)J	
tY(GTA)B	
tV(TAC)G	
tSec(TCA)G	
tS(TGA)X	
tA(TGC)G	
tT(TGT)E1	
tT(TGT)O	
tT(TGT)X2	

tRNA gene name	
tW(CCA)K2	
tW(CCA)K3	
tW(CCA)K4	
tW(CCA)M1	
tW(CCA)M2	
tY(GTA)C1	
tY(GTA)C2	
tY(GTA)C3	
tY(GTA)E1	
tY(GTA)J	
tY(GTA)M1	
tY(GTA)M2	
tY(GTA)M3	
tY(GTA)M4	
tY(GTA)M5	
tY(GTA)M6	
tY(GTA)N	
tV(AAC)C	
tV(AAC)E	
tV(AAC)K1	
tV(AAC)M1	
tV(AAC)M2	
tV(AAC)M3	
tV(AAC)M4	
tV(AAC)M5	
tG(ACC)K	
tV(CAC)A	
tV(CAC)C1	
tV(CAC)C3	
tV(CAC)F	
tV(CAC)K1	
tV(CAC)M1	
tV(CAC)M2	
tV(CAC)M3	
tV(CAC)M4	
tV(CAC)M5	
tV(CAC)Q2	
tV(CAC)X7	
tV(TAC)S1	
tV(TAC)S2	
tV(TAC)X2	
tV(AAC)K2	
tI(AAT)G	
tG(ACC)E	
tS(AGA)N	
tP(AGG)P	
tH(ATG)A	
tN(ATT)X	
tL(CAA)K	
tV(CAC)N	
tG(CCC)I	
tT(CGT)X	
tF(GAA)O	GAGAAGCAAGCCAGTAAAGAACATCCCTCCATGGCCTCTGAATCAGCTCCTGCTTCCTGACCTGCTTGAGTTCTATTCCTGACTTCCTTGATA
tA(GGC)H2	
tA(GGC)O1	
tT(GGT)J	
tY(GTA)B	
tV(TAC)G	
tSec(TCA)G	
tS(TGA)X	
tA(TGC)G	
tT(TGT)E1	
tT(TGT)O	
tT(TGT)X2	

Supplemental Figure S4

This table lists the predicted human tRNA gene families that were verified as expressed by northern blot, along with the gene location and sequence. tRNA genes are named with a lower case t to indicate tRNA, followed by the single character abbreviation for the encoded amino acid. The anticodon is shown parenthetically. The letter following the parenthesis corresponds to the chromosome where the gene is located, and a number follows if there are multiple tRNA genes with the same anticodon on an individual chromosome.

tRNA gene name	**tRNA family**	**Chromosome**	**Sequence Start**	**Sequence End**	**aa type**	**Anticodon**	**Intron**	**tRNA gene sequence (including introns)**
tV(AAC)F5	Hs_Ala1	6	28811256	28811185	Val	AAC		GGGGGTGTAGCTCAGTGGTAGAGCGTATGCTTAACATTCATGAGGCTCTGGGTTCGATCCCCAGCACTTCCA
tA(AGC)F12	Hs_Ala1	6	28682912	28682983	Ala	AGC		GGGGGTGTAGCTCAGTGGTAGAGCGCGTGCTTAGCATGTACGAGGTCCCGGGTTCAATCCCCGGCACCTCCA
tA(AGC)F14	Hs_Ala1	6	28786345	28786416	Ala	AGC		GGGGGTGTAGCTCAGTGGTAGAGCGCGTGCTTAGCATGCACGAGGCCCTGGGTTCAATCCCCAGCACCTCCA
tA(AGC)F15	Hs_Ala1	6	28795460	28795531	Ala	AGC		GGGGGTGTAGCTCAGTGGTAGAGCGCGTGCTTAGCATGCACGAGGCCCCGGGTTCAATCCCTGGCACCTCCA
tA(AGC)F16	Hs_Ala1	6	28871791	28871720	Ala	AGC		GGGGGTATAGCTCAGTGGTAGAGCGCGTGCTTAGCATGCACGAGGTCCTGGGTTCGATCCCCAGTACCTCCA
tA(AGC)F17	Hs_Ala1	6	28887899	28887828	Ala	AGC		GGGGGTATAGCTCAGCGGTAGAGCGCGTGCTTAGCATGCACGAGGTCCTGGGTTCAATCCCCAATACCTCCA
tA(AGC)F18	Hs_Ala1	6	28914271	28914200	Ala	AGC		GGGGGTGTAGCTCAGTGGTAGAGCGCGTGCTTAGCATGCACGAGGCCCCGGGTTCAATCCCCGGCACCTCCA
tA(AGC)F19	Hs_Ala1	6	28939512	28939441	Ala	AGC		GGGGGTGTAGCTCAGTGGTAGAGCGCGTGCTTAGCATGCACGAGGCCCCGGGTTCAATCCCCGGCACCTCCA
tA(CGC)F1	Hs_Ala1	6	26661710	26661781	Ala	CGC		GGGGATGTAGCTCAGTGGTAGAGCGCATGCTTCGCATGTATGAGGTCCCGGGTTCGATCCCCGGCATCTCCA
tA(CGC)F2	Hs_Ala1	6	28749663	28749592	Ala	CGC		GGGGATGTAGCTCAGTGGTAGAGCGCATGCTTCGCATGTATGAGGCCCCGGGTTCGATCCCCGGCATCTCCA
tA(CGC)F3	Hs_Ala1	6	28771759	28771688	Ala	CGC		GGGGGTGTAGATCAGTGGTAGAGCGCATGCTTCGCATGTACGAGGTCCCTGGTTCAATCCCTGGTACCTCCA
tA(CGC)F	Hs_Ala1	6	28805071	28805142	Ala	CGC		GGGGGTGTAGCTCAGTGGTAGAGCGCGTGCTTCGCATGTACGAGGCCCCGGGTTCGACCCCCGGCTCCTCCA
tA(CGC)B	Hs_Ala1	2	157082789	157082860	Ala	CGC		GGGGATGTAGCTCAGTGGTAGAGCGCGCGCTTCGCATGTGTGAGGTCCCGGGTTCAATCCCCGGCATCTCCA
tA(TGC)F1	Hs_Ala1	6	28719201	28719272	Ala	TGC		GGGGATGTAGCTCAGTGGTAGAGCGCATGCTTTGCATGTATGAGGTCCCGGGTTCGATCCCCGGCATCTCCA
tA(TGC)F2	Hs_Ala1	6	28834191	28834120	Ala	TGC		GGGGGTGTAGCTCAGTGGTAGAGCACATGCTTTGCATGTGTGAGGCCCCGGGTTCGATCCCCGGCACCTCCA
tA(TGC)F3	Hs_Ala1	6	28865597	28865526	Ala	TGC		GGGGGTGTAGCTCAGTGGTAGAGCGCATGCTTTGCATGTATGAGGTCCCGGGTTCGATCCCCGGCACCTCCA
tA(TGC)F4	Hs_Ala1	6	28878626	28878556	Ala	TGC		GGGGGTGTAGCTCAGTGGTAGAGCGCATGCTTTGCATGTATGAGGCCTCGGTTCGATCCCCGACACCTCCA
tA(TGC)F5	Hs_Ala1	6	28893062	28892991	Ala	TGC		GGGGGTGTAGCTCAGTGGTAGAGCGCATGCTTTGCATGTATGAGGCCTCGGGTTCGATCCCCGACACCTCCA
tA(TGC)K	Hs_Ala1	11	50190526	50190455	Ala	TGC		GGGGGTGTAGCTCAGTGGTAGAGCGGATGCTTTGCATGTATGAGACTTTGGGTTGGATCCCCAGCACCTCCA
tA(TGC)L1	Hs_Ala1	12	123931252	123931181	Ala	TGC		GGGGATGTAGCTCAGTGGTAGAGCGCATGCTTTGCATGTATGAGGCCCCGGGTTCGATCCCCGGCATCTCCA
tA(TGC)L2	Hs_Ala1	12	123949392	123949463	Ala	TGC		GGGGATGTAGCTCAGTGGTAGAGCGCATGCTTTGCACGTATGAGGCCCCGGGTTCAATCCCCGGCATCTCCA
tA(TGC)E	Hs_Ala1	5	180566474	180566545	Ala	TGC		GGGGATGTAGCTCAGTGGTAGAGCGCATGCTTTGCATGTATGAGGCCCCGGGTTCGATCCCCGGCATCTCCA
tA(AGC)F1	Hs_Ala2	6	26680143	26680071	Ala	AGC		GGGGAATTAGCTCAAATGGTAGAGCGCTCGCTTAGCATGCGAGAGGTAGCGGGATCGATGCCCGCATTCTCCA
tA(AGC)F6	Hs_Ala2	6	26836235	26836307	Ala	AGC		GGGGAATTGGCTCAAGCGGTAGAGCGCTTGCTTAGCATGCAAGAGGTAGCAGGATCGACGCCTGCACTCTCCA
tA(AGC)F7	Hs_Ala2	6	26838716	26838788	Ala	AGC		GGGGAATTAGCTCAGGCGGTAGAGCGCTCGCTTAGCATGCGAGAGGTAGCGGGATCGACGCCCGCATTCTCCA
tA(AGC)F8	Hs_Ala2	6	26859897	26859969	Ala	AGC		GGGGGATTAGCTCAAGCGGTAGGGTGCCTGCTTAGCATGCAAGAGGTAGCAGGATCGACGCCTGCATTCTCCA
tA(AGC)F9	Hs_Ala2	6	26879341	26879269	Ala	AGC		GGGGAATTAGCTCAGGCGGTAGAGCGCTCGCTTAGCATGCGAGAGGTAGCGGGATCGACGCCCGCATTCTCCA
tA(AGC)F10	Hs_Ala2	6	26881822	26881750	Ala	AGC		GGGGAATTGGCTCAAGCGGTAGAGCGCTTGCTTAGCATGCAAGAGGTAGCAGGATCGACGCCTGCACTCTCCA
tA(AGC)B	Hs_Ala2	2	27185733	27185805	Ala	AGC		GGGGGATTAGCTCAAATGGTAGAGCGCTCGCTTAGCATGCGAGAGGTAGCGGGATCGATGCCCGCATCCTCCA
tA(AGC)F20	Hs_Ala2	6	58249908	58249836	Ala	AGC		GGGGAATTAGCTCAAGCGGTAGAGCGCTCCCTTAGCATGCGAGAGGTAGCGGGATCGACGCCCCCATTCTCTA
tA(AGC)F21	Hs_Ala2	6	58250620	58250548	Ala	AGC		GGGGGATTAGCTCAAGCGGTAGAGCGCCTGCTTAGCATGCAAGAGGTAGCAGGATCGATGCCTGCATTCTCCA
tA(AGC)H	Hs_Ala2	8	67188978	67189050	Ala	AGC		GGGGGATTAGCTCAAATGGTAGAGCGCTCGCTTAGCATGCGAGAGGTAGCGGGATCGATGCCCGCATCCTCCA
tA(AGC)N	Hs_Ala2	14	88515195	88515267	Ala	AGC		GGGGAATTAGCTCAAGTGGTAGAGCGCTCGCTTAGCATGCGAGAGGTAGTGGGATCGATGCCCGCATTCTCCA
tA(AGC)F2	Hs_Ala3	6	26781569	26781641	Ala	AGC		GGGGAATTAGCTCAAGTGGTAGAGCGCTTGCTTAGCATGCAAGAGGTAGTGGGATCAATGCCCACATTCTCCA
tA(AGC)F3	Hs_Ala3	6	26790694	26790766	Ala	AGC		GGGGAATTAGCTCAAGTGGTAGAGCGCTTGCTTAGCATGCAAGAGGTAGTGGGATCGATGCCCACATTCTCCA
tA(AGC)F4	Hs_Ala3	6	26795464	26795536	Ala	AGC		GGGGAATTAGCTCAAGTGGTAGAGCGCTTGCTTAGCACGCAAGAGGTAGTGGGATCGATGCCCACATTCTCCA
tA(AGC)F5	Hs_Ala3	6	26813585	26813657	Ala	AGC		GGGGAATTAGCTCAAGCGGTAGAGCGCTTGCTTAGCATGCAAGAGGTAGTGGGATCGATGCCCACATTCTCCA
tA(AGC)F11	Hs_Ala3	6	26904057	26903985	Ala	AGC		GGGGAATTAGCTCAAGTGGTAGAGCGCTTGCTTAGCATGCAAGAGGTAGTGGGATCGATGCCCACATTCTCCA
tA(AGC)F13	Hs_Ala3	6	28734064	28733993	Ala	AGC		GGGGATGTAGCTCAGTGGTAGAGCGCATGCTTAGCATGCATGAGGTCCCGGGTTCGATCCCCAGCATCTCCA
tA(AGC)F22	Hs_Ala3	6	58272659	58272587	Ala	AGC		GGGGAATTAGCTCAAGCGGTAGAGCGCTTGCTTAGCATGCAAGAGGTAGTGGGATCGATGCCCACATTCTCCA
tA(AGC)F23	Hs_Ala3	6	58290710	58290638	Ala	AGC		GGGGAATTAGCTCAAGTGGTAGAGCGCTTGCTTAGCATGCAAGAGGTAGTGGGATCGATGCCCACATTCTCCA
tA(AGC)F24	Hs_Ala3	6	58295475	58295403	Ala	AGC		GGGGAATTAGCGCAAGTGGTAGAGTGCTTGCTTAGCATGCAAGAGGTAGTGGGATCGATGCCCACATTCTCCA

tA(AGC)F25	Hs_Ala3	6	58304654	58304582	Ala	AGC		GGGGAATTAGCCCAAGTGGTAGAGCGCTTGCTTAGCATGCAAGAGGTAGTGGGATCGATGCCCACATTCTCCA
tR(CCG)Q	Hs_Arg1	7_random	1279261	1279333	Arg	CCG		GACCCAGTGGCCTAATGGATAAGGCATCAGCCTCCGGAGCTGGGGATTGTGGGTTCGAGTCCCATCTGGGTCG
tR(CCG)P	Hs_Arg1	16	3140676	3140748	Arg	CCG		GGCCGCGTGGCCTAATGGATAAGGCGTCTGATTCCGGATCAGAAGATTGAGGGTTCGAGTCCCTTCGTGGTCG
tR(CCG)F1	Hs_Arg1	6	28818780	28818708	Arg	CCG		GGCCGCGTGGCCTAATGGATAAGGCGTCTGATTCCGGATCAGAAGATTGAGGGTTCGAGTCCCTTCGTGGTCG
tR(CCG)F2	Hs_Arg1	6	28957144	28957216	Arg	CCG		GGCCGCGTGGCCTAATGGATAAGGCGTCTGATTCCGGATCAGAAGATTGAGGGTTCGAGTCCCTTCGTGGTCG
tR(TCG)F1	Hs_Arg1	6	26407884	26407956	Arg	TCG		GACCACGTGGCCTAATGGATAAGGCGTCTGACTTCGGATCAGAAGATTGAGGGTTCGAATCCCTTCGTGGTTA
tR(TCG)F2	Hs_Arg1	6	26431025	26431097	Arg	TCG		GACCACGTGGCCTAATGGATAAGGCGTCTGACTTCGGATCAGAAGATTGAGGGTTCGAATCCCTCCGTGGTTA
tR(TCG)F3	Hs_Arg1	6	28618942	28618870	Arg	TCG		GACCACGTGGCCTAATGGATAAGGCGTCTGACTTCGGATCAGAAGATTGAGGGTTCGAATCCCTTCGTGGTTG
tR(TCG)Q	Hs_Arg1	17	70542803	70542875	Arg	TCG		GACCGCGTGGCCTAATGGATAAGGCGTCTGACTTCGGATCAGAAGATTGAGGGTTCGAGTCCCTTCGTGGTCG
tR(TCG)O	Hs_Arg1	15	87679308	87679380	Arg	TCG		GGCCGCGTGGCCTAATGGATAAGGCGTCTGACTTCGGATCAGAAGATTGCAGGTTCGAGTCCTGCCGCGGTCG
tR(TCG)I	Hs_Arg1	9	110040358	110040430	Arg	TCG		GGCCGTGTGGCCTAATGGATAAGGCGTCTGACTTCGGATCAAAAGATTGCAGGTTTGAGTTCTGCCACGGTCG
tQ(TTG)D	Hs_Arg1	4	40749743	40749671	Gln	TTG		GACCATGTGGCCTAAGGGAAAAGACATCTCACTTTGGGTCAGAAGATTGAGGGTTCAAGTCCTTTCATGGTCA
tR(ACG)N	Hs_Arg2	14	22468750	22468822	Arg	ACG		GGGCCAGTGGCGCAATGGATAACGCGTCTGACTACGGATCAGAAGATTCCAGGTTCGACTCCTGGCTGGCTCG
tR(ACG)F1	Hs_Arg2	6	26436347	26436419	Arg	ACG		GGGCCAGTGGCGCAATGGATAACGCGTCTGACTACGGATCAGAAGATTCCAGGTTCGACTCCTGGCTGGCTCG
tR(ACG)F2	Hs_Arg2	6	26645705	26645777	Arg	ACG		GGGCCAGTGGCGCAATGGATAACGCGTCTGACTACGGATCAGAAGATTCCAGGTTCGACTCCTGGCTGGCTCG
tR(ACG)F3	Hs_Arg2	6	27289674	27289602	Arg	ACG		GGGCCAGTGGCGCAATGGATAACGCGTCTGACTACGGATCAGAAGATTCTAGGTTCGACTCCTGGCTGGCTCG
tR(ACG)F4	Hs_Arg2	6	27290931	27291003	Arg	ACG		GGGCCAGTGGCGCAATGGATAACGCGTCTGACTACGGATCAGAAGATTCTAGGTTCGACTCCTGGCTGGCTCG
tR(ACG)F5	Hs_Arg2	6	27746395	27746323	Arg	ACG		GGGCCAGTGGCGCAATGGATAACGCGTCTGACTACGGATCAGAAGATTCTAGGTTCGACTCCTGGCTGGCTCG
tR(ACG)C	Hs_Arg2	3	45705567	45705495	Arg	ACG		GGGCCAGTGGCGCAATGGATAACGCGTCTGACTACGGATCAGAAGATTCTAGGTTCGACTCCTGGCTGGCTCG
tR(CCG)Q	Hs_Arg3	17	63446547	63446475	Arg	CCG		GACCCAGTGGCCTAATGGATAAGGCATCAGCCTCCGGAGCTGGGGATTGTGGGTTCGAGTCCCATCTGGGTCG
tR(CCT)P1	Hs_Arg3	16	3142902	3142974	Arg	CCT		GCCCCGGTGGCCTAATGGATAAGGCATTGGCCTCCTAAGCCAGGGATTGTGGGTTCGAGTCCCACCCGGGGTA
tR(CCT)P2	Hs_Arg3	16	3183919	3183991	Arg	CCT		GCCCCAGTGGCCTGATGGATAAGGTACTGGCCTCCTAAGCCAGGGATTGTGGGTTCGAGTTCCACCTGGGGTA
tR(CCT)Q1	Hs_Arg3	17	70541596	70541668	Arg	CCT		GCCCCAGTGGCCTAATGGATAAGGCACTGGCCTCCTAAGCCAGGGATTGTGGGTTCGAGTCCCACCTGGGGTA
tR(CCT)Q2	Hs_Arg3	17	70542193	70542121	Arg	CCT		GCCCCAGTGGCCTAATGGATAAGGCACTGGCCTCCTAAGCCAGGGATTGTGGGTTCGAGTCCCACCTGGGGTG
tR(CCT)G	Hs_Arg3	7	138482701	138482773	Arg	CCT		GCCCCAGTGGCCTAATGGATAAGGCATTGGCCTCCTAAGCCAGGGATTGTGGGTTCGAGTCCCATCTGGGGTG
tR(TCT)Q	Hs_Arg4	17	7964968	7965055	Arg	TCT	Yes	GGCTCTGTGGCGCAATGGATAGCGCATTGGACTTCTAGTGACGAATAGAGCAATTCAAAGGTTGTGGGTTCGAATCCCACCAGAGTCG
tR(TCT)F	Hs_Arg4	6	27637942	27638028	Arg	TCT	Yes	GGCTCTGTGGCGCAATGGATAGCGCATTGGACTTCTAGCCTAAATCAAGAGATTCAAAGGTTGCGGGTTCGAGTCCCTCCAGAGTCG
tR(TCT)K	Hs_Arg4	11	59075343	59075428	Arg	TCT	Yes	GGCTCTGTGGCGCAATGGATAGCGCATTGGACTTCTAGATAGTTAGAGAAATTCAAAGGTTGTGGGTTCGAGTCCCACCAGAGTCG
tR(TCT)A1	Hs_Arg4	1	94025150	94025234	Arg	TCT	Yes	GGCTCCGTGGCGCAATGGATAGCGCATTGGACTTCTAGAGGCTGAAGGCATTCAAAGGTTCCGGGTTCGAGTCCCGGCGGAGTCG
tR(TCT)I	Hs_Arg4	9	128181999	128181909	Arg	TCT	Yes	GGCTCTGTGGCGCAATGGATAGCGCATTGGACTTCTAGCTGAGCCTAGTGTGGTCATTCAAAGGTTGTGGGTTCGAGTCCCACCAGAGTCG
tN(GTT)A	Hs_Asn	1_random	906435	906508	Asn	GTT		GTCTCTGTGGCGCAATCGGCTAGCGCGTTTGGCTGTTAACTAAAAGGTTGGCGGTTCGAACCCACCCAGAGGCG
tN(GTT)S	Hs_Asn	19	1334562	1334635	Asn	GTT		GTCTCTGTGGCGCAATCGGTTAGCGCGTTCGGCTGTTAACCGAAAGGTTGGTGGTTCGAGCCCACCCAGGGACG
tN(GTT)A1	Hs_Asn	1	16592459	16592386	Asn	GTT		GTCTCTGTGGCGCAATCGGTTAGCGCGTTCGGCTGTTAACTGAAAGGTTGGTGGTTCGAGCCCACCCAGGGACG
tN(GTT)A2	Hs_Asn	1	16947264	16947337	Asn	GTT		GTCTCTGTGGTGCAATCGGTTAGCGCGTTCGGCTGTTAACCATAAGGTTGGTGGTTAGAGACCACCCAGGGACG
tN(GTT)A3	Hs_Asn	1	16961478	16961551	Asn	GTT		GTCTCTGTGGCGCAATCGGTTAGCGCGTTCGGCTGTTAACCGAAAGATTGGTGGTTCGAGCCCACCCAGGGACG
tN(GTT)J	Hs_Asn	10	22558517	22558444	Asn	GTT		GTCTCTGTGGCGCAATCGGTTAGCGCGTTCGGCTGTTAACCGAAAGGTTGGTGGTTCGAGCCCACCCAGGGACG
tN(GTT)M	Hs_Asn	13	30146174	30146101	Asn	GTT		GTCTCTGTGGCGCAATCGGTTAGCGCGTTCGGCTGTTAACCGAAAGGTTGGTGGTTCGAGCCCACCCAGGGACG
tN(GTT)Q	Hs_Asn	17	34161633	34161560	Asn	GTT		GTCTCTGTGGCGCAATCGGTTAGCGCGTTCGGCTGTTAACCGAAAGGTTGGTGGTTCGAGCCCACCCAGGGACG
tN(GTT)A4	Hs_Asn	1	141878966	141879039	Asn	GTT		GTCTCTGTGGTGCAATCGGTTAGCGCGTTCCGCTGTTAACCGAAAGCTTGGTGGTTCGAGCCCACCCAGGGATG
tN(GTT)A5	Hs_Asn	1	141886042	141885969	Asn	GTT		GTCTCTGTGGCGCAATCGGTTAGCGCGTTTGACTGTTAACTGAAAGGTTGGTGGTGCAAGCCCATCCAGGGATG
tN(GTT)A6	Hs_Asn	1	142059195	142059268	Asn	GTT		GTCTCTGTGGTGCAATCGGTTAGCGCGTTCCGCTGTTAACCGAAAGCTTGGTGGTTTGAGCCCACCCAGGGATG
tN(GTT)A7	Hs_Asn	1	142066271	142066198	Asn	GTT		GTCTCTGTGGCGCAATCGGTTAGCGCGTTTGACTGTTAACTGAAAGGTTGGTGGTGCAAGCCCATCCAGGGATG
tN(GTT)A8	Hs_Asn	1	143448656	143448583	Asn	GTT		GTCTCTGTGGCGCAATCGGTTAGCGCGTTCGGCTGTTAACTGAAAGGTTAGTGGTTCGAGCCCACCCGGGGACG
tN(GTT)A9	Hs_Asn	1	144745656	144745583	Asn	GTT		GTCTCTGTGGCGCAATCGGTTAGCGCGTTCGGCTGTTAACTGAAAGGTTAGTGGTTCGAGCCCACCCGGGGACG
tN(GTT)A10	Hs_Asn	1	144992449	144992522	Asn	GTT		GTCTCTGTGGCGCAATCGGTTAGCGCGTTTGACTGTTAACTGAAAGGTTGGTGGTGCAAGCCCATCCAGGGATG
tN(GTT)A11	Hs_Asn	1	145115717	145115790	Asn	GTT		GTCTCTGTGGCGTAGTCGGTTAGCGCGTTCGGCTGTTAACCGAAAAGTTGGTGGTTCGAGCCCACCCAGGAACG
tN(GTT)A12	Hs_Asn	1	145377979	145377906	Asn	GTT		GTCTCTGTGGCGCAATCGGTTAGCGCATTCGGCTGTTAACCGAAAGGTTGGTGGTTCGAGCCCACCCAGGGACG
tN(GTT)A13	Hs_Asn	1	145540021	145539948	Asn	GTT		GTCTCTGTGGCGCAATCGGTTAGCGCATTCGGCTGTTAACCGAAAGGTTGGTGGTTCGAGCCCACCCAGGGACG
tN(GTT)A14	Hs_Asn	1	146010235	146010162	Asn	GTT		GTCTCTGTGGCGCAATGGGTTAGCGCGTTCGGCTGTTAACCGAAAGGTTGGTGGTTCGAGCCCATCCAGGGACG

tN(GTT)A15	Hs_Asn	1	146421682	146421755	Asn	GTT	GTCTCTGTGGCGCAATCGGTTAGCGCGTTTGACTGTTAACTGAAAGGTTGGTGGTGCAAGCCCATCCAGGGATG
tN(GTT)A16	Hs_Asn	1	146428763	146428690	Asn	GTT	GTCTCTGTGGTGCAATCGGTTAGCGCGTTCCGCTGTTAACCGAAAGCTTGGTGGTTCGAGCCCACCCAGGGATG
tN(GTT)A17	Hs_Asn	1	146524944	146524871	Asn	GTT	GTCTCTGTGGCGCAATCGGCTAGCGCGTTTGGCTGTTAACTAAAAGGTTGGTGGTTCGAACCCACCCAGAGGCG
tN(GTT)A18	Hs_Asn	1	158211013	158210940	Asn	GTT	GTCTCTGTGGCGCAATCGGTTAGCGCGTTCGGCTGTTAACCGAAAGGTTGGTGGTTCGAGCCCACCCAGGGACG
tN(GTT)A19	Hs_Asn	1	158323086	158323159	Asn	GTT	GTCTCTGTGGCGCAATCGGTTAGCGCGTTCGGCTGTTAACCGAAAGGTTGGTGGTTCGATCCCACCCAGGGACG
tR(TCT)A2	Hs_Asn	1	155924547	155924474	Arg	TCT	GTCTCTGTGGCGCAATGGACGAGCGCGCTGGACTTCTAATCCAGAGGTTCCGGGTTCGAGTCCCGGCAGAGATG
tD(GTC)Q	Hs_Asp	17	8066352	8066281	Asp	GTC	TCCTCGTTAGTATAGTGGTGAGTATCCCCGCCTGTCACGCGGGAGACCGGGGTTCGATTCCCCGACGGGGAG
tD(GTC)F1	Hs_Asp	6	27555432	27555503	Asp	GTC	TCCTCGTTAGTATAGTGGTGAGTATCCCCGCCTGTCACGCGGGAGACCGGGGTTCGATTCCCCGACGGGGAG
tD(GTC)F2	Hs_Asp	6	27579502	27579573	Asp	GTC	TCCTCGTTAGTATAGTGGTGAGTATCCCCGCCTGTCACGCGGGAGACCGGGGTTCGATTCCCCGACGGGGAG
tD(GTC)F3	Hs_Asp	6	27659286	27659215	Asp	GTC	TCCTCGTTAGTATAGTGGTGAGTGTCCCCGTCTGTCACGCGGGAGACCGGGGTTCGATTCCCCGACGGGGAG
tD(GTC)L1	Hs_Asp	12	94932267	94932338	Asp	GTC	TCCTCGTTAGTATAGTGGTGAGTATCCCCGCCTGTCACGCGGGAGACCGGGGTTCGATTCCCCGACGGGGAG
tD(GTC)L2	Hs_Asp	12	97399749	97399820	Asp	GTC	TCCTCGTTAGTATAGTGGTTAGTATCCCCGCCTGTCACGCGGGAGACCGGGGTTCAATTCCCCGACGGGGAG
tD(GTC)L3	Hs_Asp	12	121385804	121385874	Asp	GTC	TCCTTGTTAGTATAGTGGTGAGTGTTTCTGCCTGTCATGTGGAGACTGGAGTTTGAGTCCCCAACAGGGAG
tD(GTC)L4	Hs_Asp	12	123936842	123936771	Asp	GTC	TCCTCGTTAGTATAGTGGTGAGTATCCCCGCCTGTCACGCGGGAGACCGGGGTTCGATTCCCCGACGGGGAG
tD(GTC)L5	Hs_Asp	12	123949144	123949073	Asp	GTC	TCCTCGTTAGTATAGTGGTGAGTATCCCCGCCTGTCACGCGGGAGACCGGGGTTCGATTCCCCGACGGGGAG
tD(GTC)A1	Hs_Asp	1	158223759	158223688	Asp	GTC	TCCTCGTTAGTATAGTGGTGAGTATCCCCGCCTGTCACGCGGGAGACCGGGGTTCGATTCCCCGACGGGGAG
tD(GTC)A2	Hs_Asp	1	158231159	158231088	Asp	GTC	TCCTCGTTAGTATAGTGGTGAGTATCCCCGCCTGTCACGCGGGAGACCGGGGTTCGATTCCCCGACGGGGAG
tD(GTC)A3	Hs_Asp	1	158238540	158238469	Asp	GTC	TCCTCGTTAGTATAGTGGTGAGTATCCCCGCCTGTCACGCGGGAGACCGGGGTTCGATTCCCCGACGGGGAG
tD(GTC)A4	Hs_Asp	1	158245950	158245879	Asp	GTC	TCCTCGTTAGTATAGTGGTGAGTATCCCCGCCTGTCACGCGGGAGACCGGGGTTCGATTCCCCGACGGGGAG
tD(GTC)A5	Hs_Asp	1	158253331	158253260	Asp	GTC	TCCTCGTTAGTATAGTGGTGAGTATCCCCGCCTGTCACGCGGGAGACCGGGGTTCGATTCCCCGACGGGGAG
tD(GTC)C	Hs_Asp	3	185848867	185848797	Asp	GTC	TTCTTGTTAATATAGTGGTGAGTATTCCCACCTGTCATGCGGGAGACGGGGTTCAATTCCCTGATGGGGAG
tS(AGA)G	Hs_Cys	7	148743115	148743186	Ser	AGA	GGGTGTATGGCTCAGGGGTAGAGAATTTGACTAGAGATCAAGAGGTCCCTGGTTCAAATCCAGGTGCCCCCT
tC(GCA)Q1	Hs_Cys	17	34271534	34271463	Cys	GCA	GGGGGTATAGCTCAGGGGTAGAGCATTTGACTGCAGATCAAGAAGTCCCCGGTTCAAATCCGGGTGCCCCCT
tC(GCA)Q2	Hs_Cys	17	34277424	34277495	Cys	GCA	GGGGGTATAGCTCAGTGGTAGAGCATTTGACTGCAGATCAAGAGGTCCCCGGTTCAAATCCGGGTGCCCCCT
tC(GCA)Q3	Hs_Cys	17	34279142	34279071	Cys	GCA	GGGGGTATAGCTCAGTGGTAGAGCATTTGACTGCAGATCAAGAGGTCCCTGGTTCAAATCCGGGTGCCCCCT
tC(GCA)Q4	Hs_Cys	17	34563584	34563513	Cys	GCA	GGGGGTATAGCTCAGTGGTAGAGCATTTGACTGCAGATCAAGAGGTCCCCGGTTCAAATCCGGGTGCCCCCT
tC(GCA)Q	Hs_Cys	17	34564341	34564270	Cys	GCA	GGGGGTATAGCTCAGTGGTAGAGCATTTGACTGCAGATCAAGAGGTCCCCGGTTCAAATCCGGGTGCCCCCT
tC(GCA)N	Hs_Cys	14	72499432	72499503	Cys	GCA	GGGGGTATAGCTCAGGGGTAGAGCATTTGACTGCAGATCAAGAGGTCCCCGGTTCAAATCCGGGTGCCCCCT
tC(GCA)O	Hs_Cys	15	77824052	77824124	Cys	GCA	GGGGGTATAGCTCAGTGGGTAGAGCATTTGACTGCAGATCAAGAGGTCCCCGGTTCAAATCCGGGTGCCCCCT
tC(GCA)A	Hs_Cys	1	93693927	93693855	Cys	GCA	GGGGGTATAGCTCAGGTGGTAGAGCATTTGACTGCAGATCAAGAGGTCCCCGGTTCAAATCCGGGTGCCCCCT
tC(GCA)D	Hs_Cys	4	124787681	124787610	Cys	GCA	GGGGGTATAGCTCAGTGGTAGAGCATTTGACTGCAGATCAAGAGGTCCCCGGTTCAAATCCGGGTGCCCCCT
tC(GCA)C1	Hs_Cys	3	133430713	133430642	Cys	GCA	GGGGGTGTAGCTCAGTGGTAGAGCATTTGACTGCAGATCAAGAGGTCCCTGGTTCAAATCCAGGTGCCCCCT
tC(GCA)C2	Hs_Cys	3	133433411	133433340	Cys	GCA	GGGGGTATAGCTCAGGGGTAGAGCATTTGACTGCAGATCAAGAGGTCCCTGGTTCAAATCCAGGTGCCCCCT
tC(GCA)G1	Hs_Cys	7	148444929	148445000	Cys	GCA	GGGGGCATAGCTCAGTGGTAGAGCATTTGACTGCAGATCAAGAGGTCCCTGGTTCAAATCCAGGTGCCCCCT
tC(GCA)G2	Hs_Cys	7	148465868	148465939	Cys	GCA	GGGGGTATAGCTCAGGGGTAGAGCATTTGACTGCAGATCAAGAGGTCCCTGGTTCAAATCCAGGTGCCCCCT
tC(GCA)G3	Hs_Cys	7	148490485	148490414	Cys	GCA	GGGGGTATAGCTCAGGGGTAGAGCATTTGACTGCAGATCAAGAGGTCCCCAGTTCAAATCTGGGTGCCCCCT
tC(GCA)G4	Hs_Cys	7	148510569	148510498	Cys	GCA	GGGGGTATAGTTCAGGGGTAGAGCATTTGACTGCAGATCAAGAGGTCCCTGGTTCAAATCCAGGTGCCCCCT
tC(GCA)G5	Hs_Cys	7	148512320	148512249	Cys	GCA	GGGGGTATAGCTCAGGGGTAGAGCATTTGACTGCAGATCAAGAGGTCCCTGGTTCAAATCCAGGTGCCCCCC
tC(GCA)G6	Hs_Cys	7	148549948	148549877	Cys	GCA	GGGGGTATAGCTTAGCGGTAGAGCATTTGACTGCAGATCAAGAGGTCCCCGGTTCAAATCCGGGTGCCCCCT
tC(GCA)G7	Hs_Cys	7	148681279	148681350	Cys	GCA	GGGGGTATAGCTCAGGGGTAGAGCACTTGACTGCAGATCAAGAAGTCCTTGGTTCAAATCCAGGTGCCCCCT
tC(GCA)G8	Hs_Cys	7	148691450	148691521	Cys	GCA	GGGCGTATAGCTCAGGGGTAGAGCATTTGACTGCAGATCAAGAGGTCCCCAGTTCAAATCTGGGTGCCCACT
tC(GCA)G9	Hs_Cys	7	148719464	148719535	Cys	GCA	GGGGGTATAGCTCAGGGGTAGAGCATTTGACTGCAGATCAAGAGGTCTCTGGTTCAAATCCAGGTGCCCCCT
tC(GCA)G10	Hs_Cys	7	148723883	148723812	Cys	GCA	GGGGGTATAGCTCAGGGGTAGAGCACTTGACTGCAGATCAAGAGGTCCCTGGTTCAAATCCAGGTGCCCCCCT
tC(GCA)G11	Hs_Cys	7	148730024	148729953	Cys	GCA	GGGGGTATAGCTCACAGGTAGAGCATTTGACTGCAGATCAAGAGGTCCCCGGTTCAAATCCGGTTACTCCCT
tC(GCA)G12	Hs_Cys	7	148732694	148732765	Cys	GCA	GGGCGTATAGCTCAGGGGTAGAGCATTTGACTGCAGATCAAGAGGTCCCCAGTTCAAATCTGGGTGCCCCCT
tC(GCA)G13	Hs_Cys	7	148747875	148747804	Cys	GCA	GGGGGTATAGCTCAGGGGTAGAGCATTTGACTGCAAATCAAGAGGTCCCTGATTCAAATCCAGGTGCCCCCT
tC(GCA)G14	Hs_Cys	7	148770426	148770497	Cys	GCA	GGGGGTATAGCTCAGGGGTAGAGCATTTGACTGCAGATCAAGAGGTCCCTGGTTCAAATCCAGGTGCCCCCT
tC(GCA)G15	Hs_Cys	7	148781765	148781694	Cys	GCA	GGGGGTATAGCTTAGGGGTAGAGCATTTGACTGCAGATCAAAAGGTCCCTGGTTCAAATCCAGGTGCCCCTT
tC(GCA)G16	Hs_Cys	7	148799563	148799634	Cys	GCA	GGGGGTATAGCTCACAGGTAGAGCATTTGACTGCAGATCAAGAGGTCCCCGGTTCAAATCTGGGTGCCCCCT

tC(GCA)G17	Hs_Cys	7	148825991	148825920	Cys	GCA	GGGGATATAGCTCAGGGGTAGAGCATTTGACTGCAGATCAAGAGGTCCCCGGTTCAAATCCGGGTGCCCCCC
tC(GCA)G18	Hs_Cys	7	148842408	148842479	Cys	GCA	GGGGGTATAGCTCAGGGGTAGAGCATTTGACTGCAGATCAAGAGGTCCCTGGTTCAAATCCAGGTGCCCCCT
tQ(CTG)A1	Hs_Gln	1	143432853	143432924	Gln	CTG	GGTTCCATGGTGTAATGGTGAGCACTCTGGACTCTGAATCCAGCGATCCGAGTTCGAGTCTCGGTGGAACCT
tQ(CTG)A2	Hs_Gln	1	144729854	144729925	Gln	CTG	GGTTCCATGGTGTAATGGTGAGCACTCTGGACTCTGAATCCAGCGATCCGAGTTCGAGTCTCGGTGGAACCT
tQ(CTG)A3	Hs_Gln	1	144852365	144852294	Gln	CTG	GGTTCCATGGTGTAATGGTAAGCACTCTGGACTCTGAATCCAGCGATCCGAGTTCGAGTCTCGGTGGAACCT
tQ(CTG)A4	Hs_Gln	1	144915849	144915920	Gln	CTG	GGTTCCATGGTGTAATGGTAAGCACTCTGGACTCTGAATCCAGCCATCTGAGTTCGAGTCTCTGTGGAACCT
tQ(CTG)A5	Hs_Gln	1	145965717	145965788	Gln	CTG	GGTTCCATGGTGTAATGGTAAGCACTCTGGACTCTGAATCCAGCGATCCGAGTTCGAGTCTCGGTGGAACCT
tQ(CTG)Q	Hs_Gln1	17	7963795	7963866	Gln	CTG	GGTTCCATGGTGTAATGGTTAGCACTCTGGACTCTGAATCCAGCGATCCGAGTTCAAATCTCGGTGGAACCT
tQ(CTG)F1	Hs_Gln1	6	18944381	18944452	Gln	CTG	GGTTCCATGGTGTAATGGTTAGCACTCTGGACTCTGAATCCAGCGATCCGAGTTCAAATCTCGGTGGAACCT
tQ(CTG)F2	Hs_Gln1	6	27371191	27371262	Gln	CTG	GGTTCCATGGTGTAATGGTTAGCACTCTGGACTCTGAATCCGGTAATCCGAGTTCAAATCTCGGTGGAACCT
tQ(CTG)F3	Hs_Gln1	6	27595287	27595358	Gln	CTG	GGTTCCATGGTGTAATGGTTAGCACTCTGGACTCTGAATCCAGCGATCCGAGTTCAAATCTCGGTGGAACCT
tQ(CTG)F4	Hs_Gln1	6	27623581	27623510	Gln	CTG	GGTTCCATGGTGTAATGGTTAGCACTCTGGACTCTGAATCCAGCGATCCGAGTTCAAGTCTCGGTGGAACCT
tQ(CTG)F5	Hs_Gln1	6	27867185	27867114	Gln	CTG	GGCCCCATGGTGTAATGGTCAGCACTCTGGACTCTGAATCCAGCGATCCGAGTTCAAATCTCGGTGGGACCC
tQ(CTG)F6	Hs_Gln1	6	29017428	29017357	Gln	CTG	GGTTCCATGGTGTAATGGTTAGCACTCTGGACTCTGAATCCAGCGATCCGAGTTCAAATCTCGGTGGAACCT
tQ(CTG)O	Hs_Gln1	15	63948525	63948454	Gln	CTG	GGTTCCATGGTGTAATGGTTAGCACTCTGGACTCTGAATCCAGCGATCCGAGTTCAAATCTCGGTGGAACCT
tQ(TTG)F1	Hs_Gln1	6	26419474	26419403	Gln	TTG	GGCCCCATGGTGTAATGGTTAGCACTCTGGACTTTGAATCCAGCGATCCGAGTTCAAATCTCGGTGGGACCT
tQ(TTG)F2	Hs_Gln1	6	26420025	26419954	Gln	TTG	GGCCCCATGGTGTAATGGTTAGCACTCTGGACTTTGAATCCAGCGATCCGAGTTCAAATCTCGGTGGGACCT
tQ(TTG)F3	Hs_Gln1	6	27871690	27871619	Gln	TTG	GGCCCCATGGTGTAATGGTTAGCACTCTGGACTTTGAATCCAGCGATCCGAGTTCAAATCTCGGTGGGACCT
tQ(TTG)F4	Hs_Gln1	6	28665135	28665206	Gln	TTG	GGTCCCATGGTGTAATGGTTAGCACTCTGGACTTTGAATCCAGCAATCCGAGTTCGAATCTCGGTGGGACCT
tQ(TTG)Q	Hs_Gln1	17	44624889	44624960	Gln	TTG	GGTCCCATGGTGTAATGGTTAGCACTCTGGACTTTGAATCCAGCGATCCGAGTTCAAATCTCGGTGGGACCT
tQ(TTG)F5	Hs_Gln1	6	145545552	145545623	Gln	TTG	GGTCCCATGGTGTAATGGTTAGCACTCTGGGCTTTGAATCCAGCAATCCGAGTTCGAATCTTGGTGGGACCT
tE(CTC)F1	Hs_Glu	6	29057955	29058026	Glu	CTC	TCCCTGGTGGTCTAGTGGTTAGGATTCGGCGCTCTCACCGCCGCGGCCCGGGTTCGATTCCCGGTCAGGGAA
tE(CTC)F2	Hs_Glu	6	126143157	126143086	Glu	CTC	TCCCTGGTGGTCTAGTGGTTAGGATTCGGCGCTCTCACCGCCGCGGCCCGGGTTCGATTCCCGGTCAGGGAA
tE(CTC)A2	Hs_Glu	1	158230144	158230073	Glu	CTC	TCCCTGGTGGTCTAGTGGTTAGGATTCGGCGCTCTCACCGCCGCGGCCCGGGTTCGATTCCCGGTCAGGGAA
tE(CTC)A3	Hs_Glu	1	158237524	158237453	Glu	CTC	TCCCTGGTGGTCTAGTGGTTAGGATTCGGCGCTCTCACCGCCGCGGCCCGGGTTCGATTCCCGGTCAGGGAA
tE(TTC)A2	Hs_Glu	1	16944384	16944455	Glu	TTC	TCCCTGGTGGTCTAGTGGCTAGGATTCGGCGCTTTCACCGCCGCGGCCCGGGTTCGATTCCCGGCCAGGGAA
tE(TTC)O	Hs_Glu	15	23878545	23878474	Glu	TTC	TCCCACATGGTCTAGCGGTTAGGATTCCTGGTTTTCACCCAGGCGGCCCGGGTTCGACTCCCGGTGTGGGAA
tE(TTC)M1	Hs_Glu	13	40532945	40532874	Glu	TTC	TCCCATATGGTCTAGCGGTTAGGATTCCTGGTTTTCACCCAGGTGGCCCGGGTTCGACTCCCGGTATGGGAA
tE(TTC)M2	Hs_Glu	13	44390133	44390062	Glu	TTC	TCCCACATGGTCTAGCGGTTAGGATTCCTGGTTTTCACCCAGGCGGCCCGGGTTCGACTCCCGGTGTGGGAA
tE(TTC)B	Hs_Glu	2	130811002	130810931	Glu	TTC	TCCCATATGGTCTAGCGGTTAGGATTCCTGGTTTTCACCCAGGTGGCCCGGGTTCGACTCCCGGTATGGGAA
tE(CTC)A1	Hs_Glu1	1	142888348	142888277	Glu	CTC	TCCCTGGTGGTCTAGTGGTTAGGATTCGGCGCTCTCACCGCCGCGGCCCGGGTTCGATTCCCGGTCAGGGAA
tE(CTC)A4	Hs_Glu1	1	158244935	158244864	Glu	CTC	TCCCTGGTGGTCTAGTGGTTAGGATTCGGCGCTCTCACCGCCGCGGCCCGGGTTCGATTCCCGGTCAGGGAA
tE(CTC)A5	Hs_Glu1	1	158252315	158252244	Glu	CTC	TCCCTGGTGGTCTAGTGGTTAGGATTCGGCGCTCTCACCGCCGCGGCCCGGGTTCGATTCCCGGTCAGGGAA
tE(CTC)A6	Hs_Glu1	1	245378198	245378269	Glu	CTC	TCCCTGGTGGTCTAGTGGTTAGGATTCGGCGCTCTCACCGCCGCGGCCCGGGTTCGATTCCCGGTCAGGAAA
tE(TTC)A1	Hs_Glu1	1	16607151	16607080	Glu	TTC	TCCCTGGTGGTCTAGTGGCTAGGATTCGGCGCTTTCACCGCCGCGGCCCGGGTTCGATTCCCGGTCAGGGAA
tE(TTC)A3	Hs_Glu1	1	146477500	146477428	Glu	TTC	TCCCTGGTGGTCTAGTGGCTAGGATTCGGCGCTTTCACCGCCTGCAGCTCGAGTTCGATTCCTGGTCAGGGAA
tE(TTC)A4	Hs_Glu1	1	158205027	158204956	Glu	TTC	TCCCTGGTGGTCTAGTGGCTAGGATTCGGCGCTTTCACCGCCGCGGCCCGGGTTCGATTCCCGGTCAGGGAA
tG(CCC)A1	Hs_Gly1	1	16617810	16617740	Gly	CCC	GCATTGGTGGTTCAGTGGTAGAATTCTCGCCTCCCACGCGGGAGACCCGGGTTCAATTCCCGGCCAATGCA
tG(CCC)A2	Hs_Gly1	1	16750142	16750072	Gly	CCC	GCGTTGGTGGTTTAGTGGTAGAATTCTCGCCTCCCATGCGGGAGACCCGGGTTCAATTCCCGGCCACTGCA
tG(CCC)A3	Hs_Gly1	1	16799086	16799156	Gly	CCC	GCCTTGGTGGTGCAGTGGTAGAATTCTCGCCTCCCACGTGGGAGACCCGGGTTCAATTCCCGGCCAATGCA
tG(CCC)A4	Hs_Gly1	1	16933722	16933792	Gly	CCC	GCATTGGTGGTTCAGTGGTAGAATTCTCGCCTCCCACGCGGGAGACCCGGGTTCAATTCCCGGCCAATGCA
tG(CCC)Q	Hs_Gly1	17	19704767	19704837	Gly	CCC	GCATTGGTGGTTCAATGGTAGAATTCTCGCCTCCCACGCAGGAGACCCAGGTTCGATTCCTGGCCAATGCA
tG(GCC)Q	Hs_Gly1	17	7969789	7969859	Gly	GCC	GCATTGGTGGTTCAGTGGTAGAATTCTCGCCTGCCACGCGGGAGGCCCGGGTTCGATTCCCGGCCAATGCA
tG(GCC)U	Hs_Gly1	21	17749048	17748978	Gly	GCC	GCATGGGTGGTTCAGTGGTAGAATTCTCGCCTGCCACGCGGGAGGCCCGGGTTCGATTCCCGGCCCATGCA
tG(GCC)F	Hs_Gly1	6	27978735	27978665	Gly	GCC	GCATTGGTGGTTCAGTGGTAGAATTCTCGCCTGCCACGCGGGAGGCCCGGGTTCGATTCCCGGCCAATGCA
tG(GCC)P1	Hs_Gly1	16	69369685	69369615	Gly	GCC	GCATTGGTGGTTCAGTGGTAGAATTCTCGCCTGCCACGCGGGAGGCCCGGGTTTGATTCCCGGCCAGTGCA
tG(GCC)P2	Hs_Gly1	16	69370513	69370443	Gly	GCC	GCATTGGTGGTTCAGTGGTAGAATTCTCGCCTGCCACGCGGGAGGCCCGGGTTCGATTCCCGGCCAATGCA
tG(GCC)P3	Hs_Gly1	16	69380098	69380168	Gly	GCC	GCATTGGTGGTTCAGTGGTAGAATTCTCGCCTGCCATGCGGGCGGCCGGGCTTCGATTCCTGGCCAATGCA
tG(GCC)P4	Hs_Gly1	16	69380911	69380981	Gly	GCC	GCATTGGTGGTTCAGTGGTAGAATTCTCGCCTGCCACGCGGGAGGCCCGGGTTCGATTCCCGGCCAATGCA

tG(GCC)B	Hs_Gly1	2	157083237	157083167	Gly	GCC		GCATTGGTGGTTCAGTGGTAGAATTCTCGCCTGCCACGCGGGAGGCCCGGGTTCGATTCCCGGCCAATGCA
tG(GCC)A1	Hs_Gly1	1	158226167	158226237	Gly	GCC		GCATGGGTGGTTCAGTGGTAGAATTCTCGCCTGCCACGCGGGAGGCCCGGGTTCGATTCCCGGCCCATGCA
tG(GCC)A2	Hs_Gly1	1	158233522	158233592	Gly	GCC		GCATGGGTGGTTCAGTGGTAGAATTCTCGCCTGCCACGCGGGAGGCCCGGGTTCGATTCCCGGCCCATGCA
tG(GCC)A3	Hs_Gly1	1	158240953	158241023	Gly	GCC		GCATGGGTGGTTCAGTGGTAGAATTCTCGCCTGCCACGCGGGAGGCCCGGGTTCGATTCCCGGCCCATGCA
tG(GCC)A4	Hs_Gly1	1	158248313	158248383	Gly	GCC		GCATGGGTGGTTCAGTGGTAGAATTCTCGCCTGCCACGCGGGAGGCCCGGGTTCGATTCCCGGCCCATGCA
tG(GCC)A5	Hs_Gly1	1	158263411	158263481	Gly	GCC		GCATAGGTGGTTCAGTGGTAGAATTCTTGCCTGCCACGCAGGAGGCCCAGGTTTGATTCCTGGCCCATGCA
tG(GCC)A6	Hs_Gly1	1	158306762	158306692	Gly	GCC		GCATTGGTGGTTCAGTGGTAGAATTCTCGCCTGCCACGCGGGAGGCCCGGGTTCGATTCCCGGCCAATGCA
tG(TCC)S	Hs_Gly2	19	4675082	4675153	Gly	TCC		GCGTTGGTGGTATAGTGGTTAGCATAGCTGCCTTCCAAGCAGTTGACCCGGGTTCGATTCCCGGCCAACGCA
tG(TCC)Q	Hs_Gly2	17	8065591	8065662	Gly	TCC		GCGTTGGTGGTATAGTGGTAAGCATAGCTGCCTTCCAAGCAGTTGACCCGGGTTCGATTCCCGGCCAACGCA
tG(TCC)A1	Hs_Gly2	1	142886979	142886908	Gly	TCC		GCGTTGGTGGTATAGTGGTGAGCATAGCTGCCTTCCAAGCAGTTGACCCGGGTTCGATTCCCGGCCAACGCA
tG(TCC)A2	Hs_Gly2	1	158223105	158223034	Gly	TCC		GCGTTGGTGGTATAGTGGTGAGCATAGTTGCCTTCCAAGCAGTTGACCCGGGCTCGATTCCCGCCCAACGCA
tG(TCC)A3	Hs_Gly2	1	158230501	158230430	Gly	TCC		GCGTTGGTGGTATAGTGGTGAGCATAGCTGCCTTCCAAGCAGTTGACCCGGGTTCGATTCCCGGCCAACGCA
tG(TCC)A4	Hs_Gly2	1	158237882	158237811	Gly	TCC		GCGTTGGTGGTATAGTGGTGAGCATAGCTGCCTTCCAAGCAGTTGACCCGGGTTCGATTCCCGGCCAACGCA
tG(TCC)A5	Hs_Gly2	1	158245292	158245221	Gly	TCC		GCGTTGGTGGTATAGTGGTGAGCATAGCTGCCTTCCAAGCAGTTGACCCGGGTTCGATTCCCGGCCAACGCA
tG(TCC)A6	Hs_Gly2	1	158252673	158252602	Gly	TCC		GCGTTGGTGGTATAGTGGTGAGCATAGCTGCCTTCCAAGCAGTTGACCCGGGTTCGATTCCCGGCCAACGCA
tG(TCC)A7	Hs_Gly2	1	158313958	158314029	Gly	TCC		GCGTTGGTGGTATAGTGGTGAGCATAGCTGCCTTCCAAGCAGTTGACCCGGGTTCGATTCCCGGCCAACGCA
tG(CCC)P	Hs_Gly3	16	626807	626737	Gly	CCC		GCGCCGCTGGTGTAGTGGTATCATGCAAGATTCCCATTCTTGCGACCCGGGTTCGATTCCCGGGCGGCGCA
tG(CCC)B	Hs_Gly3	2	70387844	70387774	Gly	CCC		GCGCCGCTGGTGTAGTGGTATCATGCAAGATTCCCATTCTTGCGACCCGGGTTCGATTCCCGGGCGGCGCA
tH(GTG)I	Hs_His	9	14424009	14423938	His	GTG		GCCGTGATCGTATAGTGGTTAGTACTCTGCGTTGTGGCCGCAGCAACCTCGGTTCGAATCCGAGTCACGGCA
tH(GTG)F	Hs_His	6	27233885	27233956	His	GTG		GCCGTGATCGTATAGTGGTTAGTACTCTGCGTTGTGGCCGCAGCAACCTCGGTTCGAATCCGAGTCACGGCA
tH(GTG)O1	Hs_His	15	43278167	43278096	His	GTG		GCCGTGATCGTATAGTGGTTAGTACTCTGCGTTGTGGCCGCAGCAACCTCGGTTCGAATCCGAGTCACGGCA
tH(GTG)O2	Hs_His	15	43279974	43279903	His	GTG		GCCGTGATCGTATAGTGGTTAGTACTCTGCGTTGTGGCCGCAGCAACCTCGGTTCGAATCCGAGTCACGGCA
tH(GTG)O3	Hs_His	15	43280641	43280712	His	GTG		GCCGTGATCGTATAGTGGTTAGTACTCTGCGTTGTGGCCGCAGCAACCTCGGTTCGAATCCGAGTCACGGCA
tH(GTG)A1	Hs_His	1	142885996	142885925	His	GTG		GCCGTGATCGTATAGTGGTTAGTACTCTGCGTTGTGGCCGCAGCAACCTCGGTTCGAATCCGAGTCACGGCA
tH(GTG)A2	Hs_His	1	143769589	143769660	His	GTG		GCCGTGATCGTATAGTGGTTAGTACTCTGCGTTGTGGCCGCAGCAACCTCGGTTCGAATCCGAGTCACGGCA
tH(GTG)A3	Hs_His	1	144868383	144868454	His	GTG		GCCGTGATCGTATAGTGGTTAGTACTCTGCGTTGTGGCCGCAGCAACCTCGGTTCGAATCCGAGTCACGGCA
tH(GTG)A4	Hs_His	1	144889828	144889757	His	GTG		GCCGTGATCGTATAGTGGTTAGTACTCTGCGTTGTGGCCGCAGCAACCTCGGTTCGAATCCGAGTCACGGCA
tH(GTG)A5	Hs_His	1	145935491	145935420	His	GTG		GCCATGATCGTATAGTGGTTAGTACTCTGCGCTGTGGCCGCAGCAACCTCGGTTCGAATCCGAGTCACGGCA
tI(AAT)Q1	Hs_Ile1	17	8031636	8031709	Ile	AAT		GGCCGGTTAGCTCAGTTGGTTAGAGCGTGGTGCTAATAACGCCAAGGTCGCGGGTTCGATCCCCGTACGGGCCA
tI(AAT)Q2	Hs_Ile1	17	8071107	8071034	Ile	AAT		GGCCGGTTAGCTCAGTTGGTTAGAGCGTGGTGCTAATAACGCCAAGGTCGCGGGTTCGAACCCCGTACGGGCCA
tI(AAT)F1	Hs_Ile1	6	26662329	26662402	Ile	AAT		GGCCGGTTAGCTCAGTTGGTTAGAGCGTGGTGCTAATAACGCCAAGGTCGCGGGTTCGATCCCCGTACGGGCCA
tI(AAT)F2	Hs_Ile1	6	26829273	26829200	Ile	AAT		GGCCGGTTAGCTCAGTTGGTCAGAGCGTGGTGCTAATAACGCCAAGGTCGCGGGTTCGATCCCCGTACGGGCCA
tI(AAT)F3	Hs_Ile1	6	26853307	26853234	Ile	AAT		GGCCGGTTAGCTCAGTTGGTTAGAGCGTGGTGCTAATAACGCTAAGGTCGCGGGTTCGATCCCCGTACTGGCCA
tI(AAT)F4	Hs_Ile1	6	26888811	26888884	Ile	AAT		GGCCGGTTAGCTCAGTTGGTCAGAGCGTGGTGCTAATAACGCCAAGGTCGCGGGTTCGATCCCCGTACGGGCCA
tI(AAT)F5	Hs_Ile1	6	27253046	27252973	Ile	AAT		GGCCGGTTAGCTCAGTTGGTTAGAGCGTGGTGCTAATAACGCCAAGGTCGCGGGTTCGATCCCCGTACGGGCCA
tI(AAT)F6	Hs_Ile1	6	27313402	27313329	Ile	AAT		GGCCGGTTAGCTCAGTTGGTTAGAGCGTGGTGCTAATAACGCCAAGGTCGCGGGTTCGATCCCCGTACGGGCCA
tI(AAT)F7	Hs_Ile1	6	27349718	27349791	Ile	AAT		GGCTGGTTAGTTCAGTTGGTTAGAGCGTGGTGCTAATAACGCCAAGGTCGTGGGTTCGATCCCCATATCGGCCA
tI(AAT)F8	Hs_Ile1	6	27351042	27350969	Ile	AAT		GGCTGGTTAGCTCAGTTGGTTAGAGCGTGGTGCTAATAACGCCAAGGTCGCGGGTTCGATCCCCGTACTGGCCA
tI(AAT)F9	Hs_Ile1	6	27744341	27744414	Ile	AAT		GGCCGGTTAGCTCAGTCGGCTAGAGCGTGGTGCTAATAACGCCAAGGTCGCGGGTTCGATCCCCGTACGGGCCA
tI(AAT)F10	Hs_Ile1	6	27763946	27764019	Ile	AAT		GGCCGGTTAGCTCAGTTGGTTAGAGCGTGGTGCTAATAACGCCAAGGTCGCGGGTTCGATCCCCGTACTGGCCA
tI(AAT)F11	Hs_Ile1	6	58257213	58257286	Ile	AAT		GGCCGGTTAGCTCAGTTGGTTAGAGCGTGGCGCTAATAACGCCAAGGTCGCGGGTTCGATCCCCGTACGGGCCA
tI(AAT)N	Hs_Ile1	14	101853182	101853255	Ile	AAT		GGCCGGTTAGCTCAGTTGGTTAGAGCGTGGTGCTAATAACGCCAAGGTCGCGGGTTCGATCCCCGTACGGGCCA
tI(GAT)X1	Hs_Ile1	X_random	86496	86423	Ile	GAT		GGCCGGTTAGCTCAGTTGGTAAGAGCGTGGTGCTGATAACACCAAGGTCGCGGGCTCGACTCCCGCACCGGCCA
tI(GAT)X2	Hs_Ile1	X_random	118398	118471	Ile	GAT		GGCCGGTTAGCTCAGTTGGTAAGAGCGTGGTGCTGATAACACCAAGGTCGCGGGCTCGACTCCCGCACCGGCCA
tI(GAT)X3	Hs_Ile1	X_random	399021	398948	Ile	GAT		GGCCGGTTAGCTCAGTTGGTAAGAGCGTGGTGCTGATAACACCAAGGTCGCGGGCTCGACTCCCGCACCGGCCA
tI(GAT)X4	Hs_Ile1	X_random	406943	407016	Ile	GAT		GGCCGGTTAGCTCAGTTGGTAAGAGCGTGGTGCTGATAACACCAAGGTCGCGGGCTCGACTCCCGCACCGGCCA
tI(GAT)X5	Hs_Ile1	X_random	465544	465617	Ile	GAT		GGCCGGTTAGCTCAGTTGGTAAGAGCGTGGTGCTGATAACACCAAGGTCGCGGGCTCGACTCCCGCACCGGCCA
tI(TAT)F1	Hs_Ile2	6	27096104	27096197	Ile	TAT	Yes	GCTCCAGTGGCGCAATCGGTTAGCGCGCGGTACTTATATGGCAGTATGTGTGCGAGTGATGCCGAGGTTGTGAGTTCGAGCCTCACCTGGAGCA
tI(TAT)F2	Hs_Ile2	6	27707179	27707272	Ile	TAT	Yes	GCTCCAGTGGCGCAATCGGTTAGCGCGCGGTACTTATACAACAGTATATGTGCGGGTGATGCCGAGGTTGTGAGTTCGAGCCTCACCTGGAGCA

tI(TAT)F3	Hs_Ile2	6	28613346	28613439	Ile	TAT	Yes	GCTCCAGTGGCGCAATCGGTTAGCGCGCGGTACTTATAAGACAGTGCACCTGTGAGCAATGCCGAGGTTGTGAGTTCAAGCCTCACCTGGAGCA
tI(TAT)B	Hs_Ile2	2	42949327	42949419	Ile	TAT	Yes	GCTCCAGTGGCGCAATCGGTTAGCGCGCGGTACTTATACAGCAGTACATGCAGAGCAATGCCGAGGTTGTGAGTTCGAGCCTCACCTGGAGCA
tI(TAT)S	Hs_Ile2	19	44594740	44594648	Ile	TAT	Yes	GCTCCAGTGGCGCAATCGGTTAGCGCGCGGTACTTATATGACAGTGCGAGCGGAGCAATGCCGAGGTTGTGAGTTCGATCCTCACCTGGAGCA
tL(AAG)N	Hs_Leu1	14	20148131	20148212	Leu	AAG		GGTAGCGTGGCCGAGCGGTCTAAGGCGCTGGATTAAGGCTCCAGTCTCTTCGGGGGCGTGGGTTCGAATCCCACCGCTGCCA
tL(AAG)P	Hs_Leu1	16	22215962	22216043	Leu	AAG		GGTAGCGTGGCCGAGCGGTCTAAGGCGCTGGATTAAGGCTCCAGTCTCTTCGGGGGCGTGGGTTCGAATCCCACCGCTGCCA
tL(AAG)F1	Hs_Leu1	6	28554460	28554379	Leu	AAG		GGTAGCGTGGCCGAGTGGTCTAAGACGCTGGATTAAGGCTCCAGTCTCTTCGGGGGCGTGGGTTTGAATCCCACCGCTGCCA
tL(AAG)F2	Hs_Leu1	6	29019459	29019378	Leu	AAG		GGTAGCGTGGCCGAGCGGTCTAAGGCGCTGGATTAAGGCTCCAGTCTCTTCGGGGGCGTGGGTTCGAATCCCACCGCTGCCA
tL(AAG)F3	Hs_Leu1	6	29064758	29064839	Leu	AAG		GGTAGCGTGGCCGAGCGGTCTAAGGCGCTGGATTAAGGCTCCAGTCTCTTCGGGGGCGTGGGTTCAAATCCCACCGCTGCCA
tL(AAG)E1	Hs_Leu1	5	180457161	180457080	Leu	AAG		GGTAGCGTGGCCGAGCGGTCTAAGGCGCTGGATTAAGGCTCCAGTCTCTTCGGAGGCGTGGGTTCGAATCCCACCGCTGCCA
tL(AAG)E2	Hs_Leu1	5	180461446	180461527	Leu	AAG		GGTAGCGTGGCCGAGCGGTCTAAGGCGCTGGATTAAGGCTCCAGTCTCTTCGGAGGCGTGGGTTCGAATCCCACCGCTGCCA
tL(AAG)E3	Hs_Leu1	5	180533731	180533650	Leu	AAG		GGTAGCGTGGCCGAGCGGTCTAAGGCGCTGGATTAAGGCTCCAGTCTCTTCGGAGGCGTGGGTTCGAATCCCACCGCTGCCA
tL(AAG)E4	Hs_Leu1	5	180547307	180547388	Leu	AAG		GGTAGCGTGGCCGAGCGGTCTAAGGCGCTGGATTAAGGCTCCAGTCTCTTCGGGGGCGTGGGTTCGAATCCCACCGCTGCCA
tL(TAG)Q	Hs_Leu1	17	7964438	7964357	Leu	TAG		GGTAGCGTGGCCGAGCGGTCTAAGGCGCTGGATTTAGGCTCCAGTCTCTTCGGAGGCGTGGGTTCGAATCCCACCGCTGCCA
tL(TAG)N	Hs_Leu1	14	20163369	20163450	Leu	TAG		GGTAGTGTGGCCGAGCGGTCTAAGGCGCTGGATTTAGGCTCCAGTCTCTTCGGGGGCGTGGGTTCGAATCCCACCACTGCCA
tL(TAG)P	Hs_Leu1	16	22114614	22114533	Leu	TAG		GGTAGCGTGGCCGAGTGGTCTAAGGCGCTGGATTTAGGCTCCAGTCATTTCGATGGCGTGGGTTCGAATCCCACCGCTGCCA
tL(CAA)F1	Hs_Leu2	6	27678433	27678327	Leu	CAA	Yes	GTCAGGATGGCCGAGTGGTCTAAGGCGCCAGACTCAAGTTGCTACTTCCCAGGTTTGGGGCTTCTGGTCTCCGCATGGAGGCGTGGGTTCGAATCCCACTTCTGACA
tL(CAA)F2	Hs_Leu2	6	27681503	27681396	Leu	CAA	Yes	GTCAGGATGGCCGAGTGGTCTAAGGCGCCAGACTCAAGCTTACTGCTTCCTGTGTTCGGGTCTTCTGGTCTCCGTATGGAGGCGTGGGTTCGAATCCCACTTCTGACA
tL(CAA)F3	Hs_Leu2	6	28972084	28971979	Leu	CAA	Yes	GTCAGGATGGCCGAGTGGTCTAAGGCGCCAGACTCAAGCTAAGCTTCCTCCGCGGTGGGGATTCTGGTCTCCAATGGAGGCGTGGGTTCGAATCCCACTTCTGACA
tL(CAA)F4	Hs_Leu2	6	29016809	29016913	Leu	CAA	Yes	GTCAGGATGGCCGAGTGGTCTAAGGCGCCAGACTCAAGCTTGGCTTCCTCGTGTTGAGGATTCTGGTCTCCAATGGAGGCGTGGGTTCGAATCCCACTTCTGACA
tL(CAA)A	Hs_Leu2	1	245377805	245377910	Leu	CAA	Yes	GTCAGGATGGCCGAGTGGTCTAAGGCGCCAGACTCAAGGTAAGCACCTTGCCTGCGGGCTTTCTGGTCTCCGGATGGAGGCGTGGGTTCGAATCCCACTTCTGACA
tL(CAG)F	Hs_Leu2	6	26629415	26629497	Leu	CAG		GTCAGGATGGCCGAGCGGTCTAAGGCGCTGCGTTCAGGTCGCAGTCTCCCCTGGAGGCGTGGGTTCGAATCCCACTCCTGACA
tL(CAG)P1	Hs_Leu2	16	55891364	55891446	Leu	CAG		GTCAGGATGGCCGAGCGGTCTAAGGCGCTGCGTTCAGGTCGCAGTCTCCCCTGGAGGCGTGGGTTCGAATCCCACTTCTGACA
tL(CAG)P2	Hs_Leu2	16	55891975	55891893	Leu	CAG		GTCAGGATGGCCGAGCGGTCTAAGGCGCTGCGTTCAGGTCGCAGTCTCCCCTGGAGGCGTGGGTTCGAATCCCACTTCTGACA
tL(CAG)A1	Hs_Leu2	1	158224396	158224478	Leu	CAG		GTCAGGATGGCCGAGCGGTCTAAGGCGCTGCGTTCAGGTCGCAGTCTCCCCTGGAGGCGTGGGTTCGAATCCCACTCCTGACA
tL(CAG)A2	Hs_Leu2	1	158231796	158231878	Leu	CAG		GTCAGGATGGCCGAGCGGTCTAAGGCGCTGCGTTCAGGTCGCAGTCTCCCCTGGAGGCGTGGGTTCGAATCCCACTCCTGACA
tL(CAG)A3	Hs_Leu2	1	158239177	158239259	Leu	CAG		GTCAGGATGGCCGAGCGGTCTAAGGCGCTGCGTTCAGGTCGCAGTCTCCCCTGGAGGCGTGGGTTCGAATCCCACTCCTGACA
tL(CAG)A4	Hs_Leu2	1	158246587	158246669	Leu	CAG		GTCAGGATGGCCGAGCGGTCTAAGGCGCTGCGTTCAGGTCGCAGTCTCCCCTGGAGGCGTGGGTTCGAATCCCACTCCTGACA
tL(CAG)A5	Hs_Leu2	1	158253968	158254050	Leu	CAG		GTCAGGATGGCCGAGCGGTCTAAGGCGCTGCGTTCAGGTCGCAGTCTCCCCTGGAGGCGTGGGTTCGAATCCCACTCCTGACA
tL(CAG)A6	Hs_Leu2	1	158313269	158313187	Leu	CAG		GTCAGGATGGCCGAGCGGTCTAAGGCGCTGCGTTCAGGTCGCAGTCTCCCCTGGAGGCGTGGGTTCGAATCCCACTCCTGACA
tL(TAA)F1	Hs_Leu3	6	27306395	27306313	Leu	TAA		ACCGGGATGGCTGAGTGGTTAAGGCGTTGGACTTAAGATCCAATGGACAGGTGTCCGCGTGGGTTCGAGCCCCACTCCCGGTA
tL(TAA)F2	Hs_Leu3	6	27796959	27796877	Leu	TAA		ACCGGGATGGCCGAGTGGTTAAGGCGTTGGACTTAAGATCCAATGGGCTGGTGCCCGCGTGGGTTCGAACCCCACTCTCGGTA
tL(TAA)K	Hs_Leu3	11	59075804	59075886	Leu	TAA		ACCAGAATGGCCGAGTGGTTAAGGCGTTGGACTTAAGATCCAATGGATTCATATCCGCGTGGGTTCGAACCCCACTTCTGGTA
tL(TAA)F3	Hs_Leu3	6	144579377	144579459	Leu	TAA		ACCAGGATGGCCGAGTGGTTAAGGCGTTGGACTTAAGATCCAATGGACATATGTCCGCGTGGGTTCGAACCCCACTCCTGGTA
tK(CTT)P1	Hs_Lys1	16	3147479	3147407	Lys	CTT		GCCCGGCTAGCTCAGTCGGTAGAGCATGAGACCCTTAATCTCAGGGTCGTGGGTTCGAGCCCCACGTTGGGCG
tK(CTT)P2	Hs_Lys1	16	3165693	3165765	Lys	CTT		GCCCGGCTAGCTCAGTCGGTAGAGCATGAGACTCTTAATCTCAGGGTCGTGGGTTCGAGCCCCACGTTGGGCG
tK(CTT)P3	Hs_Lys1	16	3170628	3170556	Lys	CTT		GCCCGGCTAGCTCAGTCGATAGAGCATGAGACTCTTAATCTCAGGGTCGTGGGTTCGAGCCGCACGTTGGGCG
tK(CTT)P4	Hs_Lys1	16	3181502	3181574	Lys	CTT		GCCCGGCTAGCTCAGTCGGTAGAGCATGGGACTCTTAATCTCAGGGTCGTGGGTTCGAGCCCCACGTTGGGCG
tK(CTT)F	Hs_Lys1	6	26664753	26664825	Lys	CTT		GCCCGGCTAGCTCAGTCGGTAGAGCATGAGACTCTTAATCTCAGGGTCGTGGGTTCGAGCCCCACGTTGGGCG
tK(CTT)R	Hs_Lys1	18	41923341	41923269	Lys	CTT		GACGAGCTAGCTCAGTCGGTAGAGCATGGGACTCTTAATCCCAGGGTCGTGGGTTTGAGCCCCATGTTGGGCA
tK(CTT)A1	Hs_Lys1	1	55135635	55135563	Lys	CTT		GCCCAGCTAGCTCAGTCGGTAGAGCATGAGACTCTTAATCTCAGGGTCATGGGTTTGAGCCCCACGTTTGGTG
tK(CTT)N	Hs_Lys1	14	57776438	57776366	Lys	CTT		GCCCGGCTAGCTCAGTCGGTAGAGCATGGGACTCTTAATCCCAGGGTCGTGGGTTCGAGCCCCACGTTGGGCG
tK(CTT)O	Hs_Lys1	15	76939959	76940031	Lys	CTT		GCCCGGCTAGCTCAGTCGGTAGAGCATGGGACTCTTAATCCCAGGGTCGTGGGTTCGAGCCCCACGTTGGGCG
tK(CTT)A2	Hs_Lys1	1	142884638	142884566	Lys	CTT		GCCCGGCTAGCTCAGTCGGTAGAGCATGAGACTCTTAATCTCAGGGTCGTGGGTTCGAGCCCCACGTTGGGCG
tK(CTT)E1	Hs_Lys1	5	180567361	180567433	Lys	CTT		GCCCGGCTAGCTCAGTCGGTAGAGCATGAGACTCTTAATCTCAGGGTCGTGGGTTCGAGCCCCACGTTGGGCG
tK(CTT)E2	Hs_Lys1	5	180581657	180581585	Lys	CTT		GCCCGGCTAGCTCAGTCGGTAGAGCATGAGACTCTTAATCTCAGGGTCGTGGGTTCGAGCCCCACGTTGGGCG
tK(TTT)A1	Hs_Lys1	1	201207312	201207384	Lys	TTT		GCCCGGATAGCTCAGTCGGTAGAGCATCAGACTTTTAATCTGAGGGTCCAGGGTTCAAGTCCCTGTTCGGGCG
tK(TTT)A2	Hs_Lys1	1	201207887	201207815	Lys	TTT		GCCCGGATAGCTCAGTCGGTAGAGCATCAGACTTTTAATCTGAGGGTCCAGGGTTCAAGTCCCTGTTCGGGCG
tK(TTT)A3	Hs_Lys1	1	202174928	202175000	Lys	TTT		GCCCGGAGAGCTCAGTGGGTAGAGCATCAGACTTTTAATCTGAGGGTCCAGGGTTCAAGTCCTCGTTCGGGCA
tSUP(TTA)Q	Hs_Lys2	17	56218375	56218445	Sup	TTA		GCCCGGATAGTTCAGTTGGTAGAGCATCAGACTTAATCAGAGGGTCCAGGGTTCAAGTCCCTGTTTGGGTG

tK(TTT)G	Hs_Lys2	7_random	626926	627002	Lys	TTT		GCCCACGTAGCTCAATGGTCAGAGCGTGCGGCTTTTAACCGCAAGGAAGGCTGCGAGTTCGACCCTCGCCGTGGGCT
tK(TTT)Q	Hs_Lys2	17	7963198	7963270	Lys	TTT		GCCCGGATAGCTCAGTCGGTAGAGCATCAGACTTTTAATCTGAGGGTCCAGGGTTCAAGTCCCTGTTCGGGCG
tK(TTT)F1	Hs_Lys2	6	27410820	27410748	Lys	TTT		GCCTGGGTAGCTCAGTCGGTAGAGCATCAGACTTTTAATCTGAGGGTCCAGGGTTCAAGTCCCTGTCCAGGCG
tK(TTT)F2	Hs_Lys2	6	27651825	27651897	Lys	TTT		ACCTGGGTAGCTCAGTAGGTAGAACATCAGACTTTTAATCTGAGGGTCTAGGGTTCAAGTCCCTGTCCAGGCG
tK(TTT)F3	Hs_Lys2	6	27667644	27667572	Lys	TTT		GCCTGGATAGCTCAGTCGGTAGAGCATCAGACTTTTAATCTGAGGGTCCAGGGTTCAAGTCCCTGTTCAGGCG
tK(TTT)F4	Hs_Lys2	6	28823500	28823572	Lys	TTT		GCCTGGATAGCTCAGTTGGTAGAACATCAGACTTTTAATCTGACGGTGCAGGGTTCAAGTCCCTGTTCAGGCG
tK(TTT)F5	Hs_Lys2	6	29026785	29026857	Lys	TTT		GCCCGGATAGCTCAGTCGGTAGAGCATCAGACTTTTAATCTGAGGGTCCAGGGTTCAAGTCCCTGTTCGGGCG
tK(TTT)S	Hs_Lys2	19	54729817	54729745	Lys	TTT		ACCTGGGTAGCTTAGTTGGTAGAGCATTGGACTTTTAATTTGAGGGCCCAGGTTTCAAGTCCCTGTTTGGGTG
tK(TTT)K1	Hs_Lys2	11	59080478	59080550	Lys	TTT		GCCCGGATAGCTCAGTCGGTAGAGCATCAGACTTTTAATCTGAGGGTCCGGGGTTCAAGTCCCTGTTCGGGCG
tK(TTT)K2	Hs_Lys2	11	59084456	59084384	Lys	TTT		GCCCGGATAGCTCAGTCGGTAGAGCATCAGACTTTTAATCTGAGGGTCCAGGGTTCAAGTCCCTGTTCGGGCG
tK(TTT)P	Hs_Lys2	16	72069789	72069717	Lys	TTT		GCCTGGATAGCTCAGTTGGTAGAGCATCAGACTTTTAATCTGAGGGTCCAGGGTTCAAGTCCCTGTTCAGGCA
tK(TTT)K3	Hs_Lys2	11	121935865	121935937	Lys	TTT		GCCTGGATAGCTCAGTTGGTAGAGCATCAGACTTTTAATCTGAGGGTCCAGGGTTCAAGTCCCTGTTCAGGCG
tL(CAA)K	Hs_Met1	11	9253366	9253439	Leu	CAA		GCCTCCTTAGTGCAGTAGGTAGCGCATCAGTCTCAAAATCTGAATGGTCCTGAGTTCAAGCCTCAGAGGGGGCA
tM(CAT)F4	Hs_Met1	6	26809691	26809763	Met	CAT		GCCCTCTTAGCGCAGCTGGCAGCGCGTCAGTCTCATAATCTGAAGGTCCTGAGTTCAAGCCTCAGAGAGGGCA
tM(CAT)F5	Hs_Met1	6	26843625	26843553	Met	CAT		GCCCTCTTAGCGCAGCGGGCAGCGCGTCAGTCTCATAATCTGAAGGTCCTGAGTTCGAGCCTCAGAGAGGGCA
tM(CAT)F6	Hs_Met1	6	26866601	26866529	Met	CAT		GCCCTCTTAGCGCAGCGGGCAGCGCGTCAGTCTCATAATCTGAAGGTCCTGAGTTCGAGCCTCAGAGAGGGCA
tM(CAT)F7	Hs_Met1	6	26874423	26874495	Met	CAT		GCCCTCTTAGCGCAGCGGGCAGCGCGTCAGTCTCATAATCTGAAGGTCCTGAGTTCGAGCCTCAGAGAGGGCA
tM(CAT)F12	Hs_Met1	6	29020331	29020403	Met	CAT		GCCTCCTTAGCGCAGTAGGCAGCGCGTCAGTCTCATAATCTGAAGGTCCTGAGTTCGAACCTCAGAGGGGGCA
tM(CAT)F13	Hs_Met1	6	29029093	29029021	Met	CAT		GCCTCCTTAGCGCAGTAGGCAGCGCGTCAGTCTCATAATCTGAAGGTCCTGAGTTCGAACCTCAGAGGGGGCA
tM(CAT)F14	Hs_Met1	6	58276523	58276451	Met	CAT		GCCCTCTTAGTGCAGCTGGCAGCGCGTCAGTTTCATAATCTGAAAGTCCTGAGTTCAAGCCTCAGAGAGGGCA
tM(CAT)P1	Hs_Met1	16	70017897	70017969	Met	CAT		GCCCTCTTAGCGCAGTGGGCAGCGCGTCAGTCTCATAATCTGAAGGTCCTGAGTTCGAGCCTCAGAGAGGGCA
tM(CAT)P2	Hs_Met1	16	85975201	85975129	Met	CAT		GCCTCGTTAGCGCAGTAGGCAGCGCGTCAGTCTCATAATCTGAAGGTCGTGAGTTCGAGCCTCACACGGGGCA
tM(CAT)H	Hs_Met1	8	124238723	124238651	Met	CAT		GCCTCGTTAGCGCAGTAGGTAGCGCGTCAGTCTCATAATCTGAAGGTCGTGAGTTCGATCCTCACACGGGGCA
tM(CAT)F1	Hs_Met2	6	26394733	26394804	Met	CAT		AGCAGAGTGGCGCAGCGGAAGCGTGCTGGGCCCATAACCCAGAGGTCGATGGATCGAAACCATCCTCTGCTA
tM(CAT)F2	Hs_Met2	6	26421402	26421331	Met	CAT		AGCAGAGTGGCGCAGCGGAAGCGTGCTGGGCCCATAACCCAGAGGTCGATGGATCGAAACCATCCTCTGCTA
tM(CAT)F3	Hs_Met2	6	26438579	26438508	Met	CAT		AGCAGAGTGGCGCAGCGGAAGCGTGCTGGGCCCATAACCCAGAGGTCGATGGATCGAAACCATCCTCTGCTA
tM(CAT)F8	Hs_Met2	6	27408814	27408743	Met	CAT		AGCAGAGTGGCGCAGCGGAAGCGTGCTGGGCCCATAACCCAGAGGTCGATGGATCGAAACCATCCTCTGCTA
tM(CAT)F9	Hs_Met2	6	27668650	27668579	Met	CAT		AGCAGAGTGGCGCAGCGGAAGCGTGCTGGGCCCATAACCCAGAGGTCGATGGATCGAAACCATCCTCTGCTA
tM(CAT)F10	Hs_Met2	6	27853643	27853714	Met	CAT		AGCAGAGTGGCGCAGCGGAAGCGTGCTGGGCCCATAACCCAGAGGTCGATGGATCTAAACCATCCTCTGCTA
tM(CAT)F11	Hs_Met2	6	27978321	27978250	Met	CAT		AGCAGAGTGGCGCAGCGGAAGCGTGCTGGGCCCATAACCCAGAGGTCGATGGATCGAAACCATCCTCTGCTA
tM(CAT)Q	Hs_Met2	17	78045957	78045886	Met	CAT		AGCAGAGTGGCGCAGCGGAAGCGTGCTGGGCCCATAACCCAGAGGTCGATGGATCGAAACCATCCTCTGCTA
tM(CAT)A	Hs_Met2	1	150456799	150456870	Met	CAT		AGCAGAGTGGCGCAGCGGAAGCGTGCTGGGCCCATAACCCAGAGGTCGATGGATCGAAACCATCCTCTGCTA
tF(GAA)S	Hs_Phe	19	1334433	1334361	Phe	GAA		GCCGAAATAGCTCAGTTGGGAGAGCGTTAGACTGAAGATCTAAAGGTCCCTGGTTCGATCCCGGGTTTCGGCA
tF(GAA)F1	Hs_Phe	6	28839426	28839353	Phe	GAA		GCTGAAATAGCTCAGTTGGGAGAGCGTTAGACTGAAGATCTTAAAGTTCCCTGGTTCAACCCTGGGTTTCAGCC
tF(GAA)F2	Hs_Phe	6	28840143	28840215	Phe	GAA		GCCAAAATTGCTCAGTTGGGAGAGCGTTAGACTGAAGATCTAAAGGTCCCTGGTTCGATCCCGGGTTTCACCA
tF(GAA)F3	Hs_Phe	6	28866550	28866478	Phe	GAA		GCCGAAATAGCTCAGTTGGGAGAGCGTTAGACTGAAGATCTAAAGGTCCCTGGTTCGATCCCGGGTTTCGGCA
tF(GAA)F4	Hs_Phe	6	28883661	28883589	Phe	GAA		GCCGAGATAGCTCAGTTGGGAGAGCGTTAGACTGAAGATCTAAAGGTCCCTGGTTCAATCCCGGGTTTCGGCA
tF(GAA)F5	Hs_Phe	6	28899145	28899072	Phe	GAA		GCCGAAATAGCTCAGTTGGGAGAGCGTTAGACCGAAGATCTTAAAGGTCCCTGGTTCAATCCCGGGTTTCGGCA
tF(GAA)F6	Hs_Phe	6	29057500	29057428	Phe	GAA		GCCGAAATAGCTCAGTTGGGAGAGCGTTAGACTGAAGATCTAAAGGTCCCTGGTTCGATCCCGGGTTTCGGCA
tF(GAA)K1	Hs_Phe	11	59081618	59081546	Phe	GAA		GCCGAAATAGCTCAGTTGGGAGAGCGTTAGACTGAAGATCTAAAGGTCCCTGGTTCGATCCCGGGTTTCGGCA
tF(GAA)K2	Hs_Phe	11	59090501	59090429	Phe	GAA		GCCGAAATAGCTCAGTTGGGAGAGCGTTAGACTGAAGATCTAAAGGTCCCTGGTTCAATCCCGGGTTTCGGCA
tF(GAA)M	Hs_Phe	13	93999977	93999905	Phe	GAA		GCCGAAATAGCTCAGTTGGGAGAGCGTTAGACTGAAGATCTAAAGGTCCCTGGTTCGATCCCGGGTTTCGGCA
tF(GAA)L	Hs_Phe	12	123937341	123937269	Phe	GAA		GCCGAAATAGCTCAGTTGGGAGAGCGTTAGACTGAAGATCTAAAGGTCCCTGGTTCGATCCCGGGTTTCGGCA
tP(AGG)P1	Hs_Pro	16	3150387	3150481	Pro	AGG	Yes	GGCTCGTTGGTCTAGGGGTGTGGTTCTCGCTTAGGGACCACAGGGACAAGCCCGGGAGACCCAAGAGGTCCCGGGTTCAAATCCCGGACGAGCCC
tP(AGG)P2	Hs_Pro	16	3172707	3172636	Pro	AGG		GGCTCGTTGGTCTAGGGGTATGATTCTCGCTTAGGGTGCGAGAGGTCCCGGGTTCAAATCCCGGACGAGCCC
tP(AGG)P3	Hs_Pro	16	3179635	3179706	Pro	AGG		GGCTCGTTGGTCTAGGGGTATGATTCTCGCTTAGGGTGCGAGAGGTCCCGGGTTCAAATCCCGGACGAGCCC
tP(AGG)P4	Hs_Pro	16	3181990	3182061	Pro	AGG		GGCTCGTTGGTCTAGGGGTATGATTCTCGCTTAGGATGCGAGAGGTCCCGGGTTCAAATCCCGGACGAGCCC
tP(AGG)N1	Hs_Pro	14	20147406	20147335	Pro	AGG		GGCTCGTTGGTCTAGGGGTATGATTCTCGCTTAGGGTGCGAGAGGTCCCGGGTTCAAATCCCGGACGAGCCC
tP(AGG)N2	Hs_Pro	14	20151471	20151400	Pro	AGG		GGCTCGTTGGTCTAGGGGTATGATTCTCGCTTAGGGTGCGAGAGGTCCCGGGTTCAAATCCCGGACGAGCCC

tP(AGG)F	Hs_Pro	6	26663477	26663548	Pro	AGG	GGCTCGTTGGTCTAGGGGTATGATTCTCGCTTAGGGTGCGAGAGGTCCCGGGTTCAAATCCCGGACGAGCCC
tP(AGG)K	Hs_Pro	11	75624205	75624276	Pro	AGG	GGCTCGTTGGTCTAGGGGTATGATTCTCGCTTAGGGTGCGAGAGGTCCCGGGTTCAAATCCCGGACGAGCCC
tP(AGG)G	Hs_Pro	7	128017455	128017526	Pro	AGG	GGCTCGTTGGTCTAGGGGTATGATTCTCGCTTAGGGTGCGAGAGGTCCCGGGTTCAAATCCCGGACGAGCCC
tP(AGG)A	Hs_Pro	1	164416454	164416383	Pro	AGG	GGCTCGTTGGTCTAGGGGTATGATTCTCGCTTAGGGTGCGAGAGGTCCCGGGTTCAAATCCCGGACGAGCCC
tP(CGG)P	Hs_Pro	16	3162050	3162121	Pro	CGG	GGCTCGTTGGTCTAGGGGTATGATTCTCGCTTCGGGTGCGAGAGGTCCCGGGTTCAAATCCCGGACGAGCCC
tP(CGG)Q	Hs_Pro	17	8066947	8066876	Pro	CGG	GGCTCGTTGGTCTAGGGGTATGATTCTCGCTTCGGGTGCGAGAGGTCCCGGGTTCAAATCCCGGACGAGCCC
tP(CGG)F	Hs_Pro	6	27167500	27167571	Pro	CGG	GGCTCGTTGGTCTAGGGGTATGATTCTCGCTTCGGGTGTGAGAGGTCCCGGGTTCAAATCCCGGACGAGCCC
tP(CGG)A	Hs_Pro	1	164415620	164415691	Pro	CGG	GGCTCGTTGGTCTAGGGGTATGATTCTCGCTTCGGGTGCGAGAGGTCCCGGGTTCAAATCCCGGACGAGCCC
tP(TGG)P1	Hs_Pro	16	3148924	3148995	Pro	TGG	GGCTCGTTGGTCTAGGGGTATGATTCTCGCTTTGGGTGCGAGAGGTCCCGGGTTCAAATCCCGGACGAGCCC
tP(TGG)P2	Hs_Pro	16	3174205	3174134	Pro	TGG	GGCTCGTTGGTCTAGGGGTATGATTCTCGCTTTGGGTGCGAGAGGTCCCGGGTTCAAATCCCGGACGAGCCC
tP(TGG)P3	Hs_Pro	16	3178095	3178166	Pro	TGG	GGCTCGTTGGTCTAGGGGTATGATTCTCGCTTTGGGTGCGAGAGGTCCCGGGTTCAAATCCCGGACGAGCCC
tP(TGG)N1	Hs_Pro	14	20171005	20171076	Pro	TGG	GGCTCGTTGGTCTAGTGGTATGATTCTCGCTTTGGGTGCGAGAGGTCCCGGGTTCAAATCCCGGACGAGCCC
tP(TGG)N2	Hs_Pro	14	20222015	20222086	Pro	TGG	GGCTCGTTGGTCTAGGGGTATGATTCTCGCTTTGGGTGCGAGAGGTCCCGGGTTCAAATCCCGGACGAGCCC
tP(TGG)K	Hs_Pro	11	75624588	75624517	Pro	TGG	GGCTCGTTGGTCTAGGGGTATGATTCTCGGTTTGGGTCCGAGAGGTCCCGGGTTCAAATCCCGGACGAGCCC
tP(TGG)E	Hs_Pro	5	180548531	180548460	Pro	TGG	GGCTCGTTGGTCTAGGGGTATGATTCTCGCTTTGGGTGCGAGAGGTCCCGGGTTCAAATCCCGGACGAGCCC
tSeC(TCA)V	Hs_SeC	22	42871438	42871523	SeC(e)	TCA	GCTCGGATGATCCTCAGTGGTCTGGGGTGCAGGCTTCAAACCTGTAGCTGTCTAGTGACAGAGTGGTTCAATTCCACCTTTGTAGG
tSeC(TCA)S	Hs_SeC	19	50673785	50673700	SeC(e)	TCA	GCCCGGATGATCCTCAGTGGTCTGGGGTGCAGGCTTCAAACCTGTAGCTGTCTAGCGACAGAGTGGTTCAATTCCACCTTTCGGGC
tS(AGA)Q	Hs_Ser1	17	8070734	8070653	Ser	AGA	GTAGTCGTGGCCGAGTGGTTAAGGCGATGGACTAGAAATCCATTGGGGTCTCCCCGCGCAGGTTCGAATCCTGCCGACTACG
tS(AGA)F1	Hs_Ser1	6	26435796	26435877	Ser	AGA	GTAGTCGTGGCCGAGTGGTTAAGGCGATGGACTAGAAATCCATTGGGGTCTCCCCGCGCAGGTTCGAATCCTGCCGACTACG
tS(AGA)F2	Hs_Ser1	6	27554570	27554651	Ser	AGA	GTAGTCGTGGCCGAGTGGTTAAGGCGATGGACTAGAAATCCATTGGGGTCTCCCCGCGCAGGTTCGAATCCTGCCGACTACG
tS(AGA)F3	Hs_Ser1	6	27571572	27571653	Ser	AGA	GTAGTCGTGGCCGAGTGGTTAAGGCGATGGACTAGAAATCCATTGGGGTCTCCCCGCGCAGGTTCGAATCCTGCCGACTACG
tS(AGA)F4	Hs_Ser1	6	27578797	27578878	Ser	AGA	GTAGTCGTGGCCGAGTGGTTAAGGCGATGGACTAGAAATCCATTGGGGTCTCCCCGCGCAGGTTCGAATCCTGCCGACTACG
tS(AGA)F5	Hs_Ser1	6	27607966	27608047	Ser	AGA	GTAGTCGTGGCCGAGTGGTTAAGGCGATGGACTAGAAATCCATTGGGGTTTCCCCACGCAGGTTCGAATCCTGCCGACTACG
tS(AGA)F6	Hs_Ser1	6	27617614	27617533	Ser	AGA	GTAGTCGTGGCCGAGTGGTTAAGGCGATGGACTAGAAATCCATTGGGGTTTCCCCGCGCAGGTTCGAATCCTGCCGACTACG
tS(AGA)F7	Hs_Ser1	6	27629252	27629171	Ser	AGA	GTAGTCGTGGCCGAGTGGTTAAGGTGATGGACTAGAAACCCATTGGGGTCTCCCCGCGCAGGTTCGAATCCTGCCGACTACG
tS(AGA)H	Hs_Ser1	8	96351142	96351061	Ser	AGA	GTAGTCGTGGCCGAGTGGTTAAGGCGATGGACTAGAAATCCATTGGGGTCTCCCCGCGCAGGTTCGAATCCTGCCGACTACG
tS(CGA)Q	Hs_Ser1	17	7983005	7982924	Ser	CGA	GCTGTGATGGCCGAGTGGTTAAGGCGTTGGACTCGAAATCCAATGGGGTCTCCCCGCGCAGGTTCGAATCCTGCTCACAGCG
tS(CGA)F1	Hs_Ser1	6	27285607	27285688	Ser	CGA	GCTGTGATGGCCGAGTGGTTAAGGCGTTGGACTCGAAATCCAATGGGGTCTCCCCGCGCAGGTTCAAATCCTGCTCACAGCG
tS(CGA)F2	Hs_Ser1	6	27748289	27748208	Ser	CGA	GCTGTGATGGCCGAGTGGTTAAGGTGTTGGACTCGAAATCCAATGGGGGTTCCCCGCGCAGGTTCAAATCCTGCTCACAGCG
tS(CGA)L	Hs_Ser1	12	54870415	54870496	Ser	CGA	GTCACGGTGGCCGAGTGGTTAAGGCGTTGGACTCGAAATCCAATGGGGTTTCCCCGCACAGGTTCGAATCCTGTTCGTGACG
tS(TGA)F1	Hs_Ser1	6	26420884	26420803	Ser	TGA	GTAGTCGTGGCCGAGTGGTTAAGGCGATGGACTTGAAATCCATTGGGGTCTCCCCGCGCAGGTTCGAATCCTGCCGACTACG
tS(TGA)F2	Hs_Ser1	6	27581667	27581586	Ser	TGA	GTAGTCGTGGCCGAGTGGTTAAGGCGATGGACTTGAAATCCATTGGGGTTTCCCCGCGCAGGTTCGAATCCTGTCGGCTACG
tS(TGA)F3	Hs_Ser1	6	27621447	27621528	Ser	TGA	GTAGTCGTGGCCGAGTGGTTAAGGCGATGGACTTGAAATCCATTGGGGTTTCCCCGCGCAGGTTCGAATCCTGCCGACTACG
tS(TGA)J	Hs_Ser1	10	69194267	69194348	Ser	TGA	GCAGCGATGGCCGAGTGGTTAAGGCGTTGGACTTGAAATCCAATGGGGTCTCCCCGCGCAGGTTCGAACCCTGCTCGCTGCG
tS(GCT)Q	Hs_Ser2	17	8030909	8030990	Ser	GCT	GACGAGGTGGCCGAGTGGTTAAGGCGATGGACTGCTAATCCATTGTGCTCTGCACGCGTGGGTTCGAATCCCATCCTCGTCG
tS(GCT)F1	Hs_Ser2	6	26413780	26413697	Ser	GCT	GGAGAGGCCTGGCCGAGTGGTTAAGGCGATGGACTGCTAATCCATTGTGCTCTGCACGCGTGGGTTCGAATCCCATCCTCGTCG
tS(GCT)F2	Hs_Ser2	6	27173064	27173145	Ser	GCT	GACGAGGTGGCCGAGTGGTTAAGGCGATGGACTGCTAATCCATTGTGCTCTGCACGCGTGGGTTCGAATCCCACCCTCGTCG
tS(GCT)F3	Hs_Ser2	6	27373754	27373835	Ser	GCT	GACGAGGTGGCCGAGTGGTTAAGGCGATGGACTGCTAATCCATTGTGCTCTGCACGCGTGGGTTCGAATCCCACCTTCGTCG
tS(GCT)F4	Hs_Ser2	6	28288794	28288875	Ser	GCT	GACGAGGTGGCCGAGTGGTTAAGGCGATGGACTGCTAATCCATTGTGCTCTGCACACGTGGGTTCGAATCCCATCCTCGTCG
tS(GCT)F5	Hs_Ser2	6	28673177	28673096	Ser	GCT	GACGAGGTGGCCGAGTGGTTAAGGCGATGGACTGCTAATCCATTGTGCTCTGCACGCGTGGGTTCGAATCCCATCCTCGTCG
tS(GCT)O	Hs_Ser2	15	38673396	38673315	Ser	GCT	GACGAGGTGGCCGAGTGGTTAAGGCGATGGACTGCTAATCCATTGTGCTCTGCACGCGTGGGTTCGAATCCCATCCTCGTCG
tS(GCT)K	Hs_Ser2	11	65872167	65872248	Ser	GCT	GACGAGGTGGCCGAGTGGTTAAGGCGATGGACTGCTAATCCATTGTGCTTTGCACGCGTGGGTTCGAATCCCATCCTCGTCG
tL(TAA)D	Hs_Ser2	4	156742657	156742583	Leu	TAA	GTTAAGATGGCAGAGCCTGGTAATTGCATAAAACTTAAAATTTTATAATCAGAGGTTCAACTCCTCTTCTTAACA
tT(AGT)Q1	Hs_Thr1	17	7983568	7983495	Thr	AGT	GGCGCCGTGGCTTAGCTGGTTAAAGCGCCTGTCTAGTAAACAGGAGATCCTGGGTTCGAATCCCAGCGGTGCCT
tT(AGT)Q2	Hs_Thr1	17	8031203	8031276	Thr	AGT	GGCGCCGTGGCTTAGTTGGTTAAAGCGCCTGTCTAGTAAACAGGAGATCCTGGGTTCGAATCCCAGCGGTGCCT
tT(AGT)Q3	Hs_Thr1	17	8070351	8070278	Thr	AGT	GGCGCCGTGGCTTAGTTGGTTAAAGCGCCTGTCTAGTAAACAGGAGATCCTGGGTTCGAATCCCAGCGGTGCCT
tT(AGT)F1	Hs_Thr1	6	26641197	26641124	Thr	AGT	GGCTCCGTGGCTTAGCTGGTTAAAGCGCCTGTCTAGTAAACAGGAGATCCTGGGTTCGAATCCCAGCGGGGCCT
tT(AGT)F2	Hs_Thr1	6	27238029	27238102	Thr	AGT	GGCCCTGTGGCTTAGCTGGTCAAAGCGCCTGTCTAGTAAACAGGAGATCCTGGGTTCGAATCCCAGCGGGGCCT
tT(AGT)F3	Hs_Thr1	6	27760526	27760453	Thr	AGT	GGCTCCGTGGCTTAGCTGGTTAAAGCGCCTGTCTAGTAAACAGGAGATCCTGGGTTCGAATCCCAGCGGGGCCT

tT(AGT)F4	Hs_Thr1	6	27802452	27802525	Thr	AGT		GGCTTCGTGGCTTAGCTGGTTAAAGCGCCTGTCTAGTAAACAGGAGATCCTGGGTTCGAATCCCAGCGAGGCCT
tT(AGT)F5	Hs_Thr1	6	28801774	28801847	Thr	AGT		GGCTCCGTAGCTTAGTTGGTTAAAGCGCCTGTCTAGTAAACAGGAGATCCTGGGTTCGACTCCCAGCGGGGCCT
tT(AGT)S	Hs_Thr1	19	38359803	38359876	Thr	AGT		GGCGCCGTGGCTTAGTTGGTTAAAGCGCCTGTCTAGTAAACAGGAGATCCTGGGTTCGAATCCCAGCGGTGCCT
tT(CGT)P	Hs_Thr1	16	14287251	14287322	Thr	CGT		GGCGCGGTGGCCAAGTGGTAAGGCGTCGGTCTCGTAAACCGAAGATCACGGGTTCGAACCCCGTCCGTGCCT
tT(CGT)Q	Hs_Thr1	17	26901213	26901284	Thr	CGT		GGCGCGGTGGCCAAGTGGTAAGGCGTCGGTCTCGTAAACCGAAGATCGCGGGTTCGAACCCCGTCCGTGCCT
tT(CGT)F2	Hs_Thr1	6	28564822	28564749	Thr	CGT		GGCTCTATGGCTTAGTTGGTTAAAGCGCCTGTCTCGTAAACAGGAGATCCTGGGTTCGACTCCCAGTGGGGCCT
tT(CGT)F3	Hs_Thr1	6	28724036	28723963	Thr	CGT		GGCTCTGTGGCTTAGTTGGCTAAAGCGCCTGTCTCGTAAACAGGAGATCCTGGGTTCGAATCCCAGCGGGGCCT
tT(TGT)F	Hs_Thr1	6	28550381	28550308	Thr	TGT		GGCTCTATGGCTTAGTTGGTTAAAGCGCCTGTCTTGTAAACAGGAGATCCTGGGTTCGAATCCCAGTAGAGCCT
tT(CGT)F1	Hs_Thr2	6	27694114	27694187	Thr	CGT		GGCCCTGTAGCTCAGCGGTTGGAGCGCTGGTCTCGTAAACCTAGGGGTCGTGAGTTCAAATCTCACCAGGGCCT
tT(TGT)A1	Hs_Thr2	1_random	1654722	1654794	Thr	TGT		GGCTCCATAGCTCAGTGGTTAGAGCACTGGTCTTGTAAACCAGGGGTCGCGAGTTCGATCCTCGCTGGGGCCT
tT(TGT)A2	Hs_Thr2	1_random	2030046	2030118	Thr	TGT		GGCTCCATAGCTCAGTGGTTAGAGCACTGGTCTTGTAAACCAGGGGTCGCGAGTTCGATCCTCGCTGGGGCCT
tT(TGT)N1	Hs_Thr2	14	20151861	20151789	Thr	TGT		GGCTCCATAGCTCAGGGGTTAGAGCGCTGGTCTTGTAAACCAGGGGTCGCGAGTTCAATTCTCGCTGGGGCCT
tT(TGT)N2	Hs_Thr2	14	20169231	20169159	Thr	TGT		GGCTCCATAGCTCAGGGGTTAGAGCACTGGTCTTGTAAACCAGGGGTCGCGAGTTCAAATCTCGCTGGGGCCT
tT(TGT)N3	Hs_Thr2	14	20219689	20219761	Thr	TGT		GGCCCTATAGCTCAGGGGTTAGAGCACTGGTCTTGTAAACCAGGGGTCGCGAGTTCAAATCTCGCTGGGGCCT
tT(TGT)E	Hs_Thr2	5	180551364	180551293	Thr	TGT		GGCTCCATAGCTCAGGGGTTAGAGCACTGGTCTTGTAAACCAGGGTCGCGAGTTCAAATCTCGCTGGGGCCT
tT(TGT)A	Hs_Thr2	1	219026742	219026814	Thr	TGT		GGCTCCATAGCTCAGTGGTTAGAGCACTGGTCTTGTAAACCAGGGGTCGCGAGTTCGATCCTCGCTGGGGCCT
tW(CCA)Q1	Hs_Trp	17	8030401	8030472	Trp	CCA		GACCTCGTGGCGCAACGGTAGCGCGTCTGACTCCAGATCAGAAGGTTGCGTGTTCAAATCACGTCGGGGTCA
tW(CCA)Q2	Hs_Trp	17	8064983	8064912	Trp	CCA		GGCCTCGTGGCGCAACGGTAGCGCGTCTGACTCCAGATCAGAAGGTTGCGTGTTCAAATCACGTCGGGGTCA
tW(CCA)Q3	Hs_Trp	17	19352086	19352157	Trp	CCA		GACCTCGTGGCGCAATGGTAGCGCGTCTGACTCCAGATCAGAAGGTTGCGTGTTCAAGTCACGTCGGGGTCA
tW(CCA)F1	Hs_Trp	6	26427380	26427309	Trp	CCA		GACCTCGTGGCGCAACGGTAGCGCGTCTGACTCCAGATCAGAAGGTTGCGTGTTCAAATCACGTCGGGGTCA
tW(CCA)F2	Hs_Trp	6	26439722	26439651	Trp	CCA		GACCTCGTGGCGCAACGGTAGCGCGTCTGACTCCAGATCAGAAGGTTGCGTGTTCAAATCACGTCGGGGTCA
tW(CCA)L	Hs_Trp	12	97400498	97400569	Trp	CCA		GACCTCGTGGCGCAACGGTAGCGCGTCTGACTCCAGATCAGAAGGCTGCGTGTTCGAATCACGTCGGGGTCA
tW(CCA)G	Hs_Trp	7	98711958	98712029	Trp	CCA		GACCTCGTGGCGCAACGGCAGCGCGTCTGACTCCAGATCAGAAGGTTGCGTGTTCAAATCACGTCGGGGTCA
tY(ATA)B	Hs_Tyr	2	218936055	218936147	Tyr	ATA	Yes	CCTTCAATAGTTCAGCTGGTAGAGCAGAGGACTATAGCTACTTCCTCAGTAGGAGACGTCCTTAGGTTGCTGGTTCGATTCCAGCTTGAAGGA
tY(GTA)N1	Hs_Tyr	14	20191191	20191098	Tyr	GTA	Yes	CCTTCGATAGCTCAGCTGGTAGAGCGGAGGACTGTAGCCTGTAGAAACATTTGTGGACATCCTTAGGTCGCTGGTTCGATTCCGGCTCGAAGGA
tY(GTA)N2	Hs_Tyr	14	20195556	20195463	Tyr	GTA	Yes	CCTTCGATAGCTCAGCTGGTAGAGCGGAGGACTGTAGATTGTATAGACATTTGCGGACATCCTTAGGTCGCTGGTTCGATTCCAGCTCGAAGGA
tY(GTA)N3	Hs_Tyr	14	20198050	20197957	Tyr	GTA	Yes	CCTTCGATAGCTCAGCTGGTAGAGCGGAGGACTGTAGACTGCGGAAACGTTTGTGGACATCCTTAGGTCGCTGGTTCAATTCCGGCTCGAAGGA
tY(GTA)N4	Hs_Tyr	14	20201284	20201191	Tyr	GTA	Yes	CCTTCGATAGCTCAGCTGGTAGAGCGGAGGACTGTAGATTGTACAGACATTTGCGGACATCCTTAGGTCGCTGGTTCGATTCCGGCTCGAAGGA
tY(GTA)N5	Hs_Tyr	14	20221272	20221360	Tyr	GTA	Yes	CCTTCGATAGCTCAGCTGGTAGAGCGGAGGACTGTAGTACTTAATGTGTGGTCATCCTTAGGTCGCTGGTTCGATTCCGGCTCGAAGGA
tY(GTA)F1	Hs_Tyr	6	26677065	26677155	Tyr	GTA	Yes	CCTTCGATAGCTCAGTTGGTAGAGCGGAGGACTGTAGTTGGCTGTGTCCTTAGACATCCTTAGGTCGCTGGTTCGAATCCGGCTCGAAGGA
tY(GTA)F2	Hs_Tyr	6	26683777	26683866	Tyr	GTA	Yes	CTTTCGATAGCTCAGTTGGTAGAGCGGAGGACTGTAGGTTCATTAAACTAAGGCATCCTTAGGTCGCTGGTTCGAATCCGGCTCGAAGGA
tY(GTA)F3	Hs_Tyr	6	26685311	26685399	Tyr	GTA	Yes	CCTTCGATAGCTCAGTTGGTAGAGCGGAGGACTGTAGGCTCATTAAGCAAGGTATCCTTAGGTCGCTGGTTCGAATCCGGCTCGGAGGA
tY(GTA)F4	Hs_Tyr	6	26703081	26703169	Tyr	GTA	Yes	CCTTCGATAGCTCAGCTGGTAGAGCGGAGGACTGTAGGGGTTTGAATGTGGTCATCCTTAGGTCGCTGGTTCGAATCCGGCTCGGAGGA
tY(GTA)B	Hs_Tyr	2	27185301	27185389	Tyr	GTA	Yes	CCTTCGATAGCTCAGTTGGTAGAGCGGAGGACTGTAGTGGATAGGGCGTGGCAATCCTTAGGTCGCTGGTTCGATTCCGGCTCGAAGGA
tY(GTA)H1	Hs_Tyr	8	66772173	66772086	Tyr	GTA	Yes	TCTTCAATAGCTCAGCTGGTAGAGCGGAGGACTGTAGGTGCACGCCCGTGGCCATTCTTAGGTGCTGGTTTGATTCCGACTTGGAGAG
tY(GTA)H2	Hs_Tyr	8	67188156	67188248	Tyr	GTA	Yes	CCTTCGATAGCTCAGCTGGTAGAGCGGAGGACTGTAGCTACTTCCTCAGCAGGAGACATCCTTAGGTCGCTGGTTCGATTCCGGCTCGAAGGA
tY(GTA)H3	Hs_Tyr	8	67188777	67188865	Tyr	GTA	Yes	CCTTCGATAGCTCAGCTGGTAGAGCGGAGGACTGTAGGCGCGCGCCCGTGGCCATCCTTAGGTCGCTGGTTCGATTCCGGCTCGAAGGA
tV(AAC)F1	Hs_Val	6	27311267	27311339	Val	AAC		GTTTCCGTAGTGTAGTGGTTATCACGTTTGCCTAACACGCGAAAGGTCCCCGGTTCGAAACCGGGCAGAAACA
tV(AAC)F2	Hs_Val	6	27726758	27726686	Val	AAC		GTTTCCGTAGTGTAGTGGTTATCACGTTCGCCTAACACGCGAAAGGTCCCTGGATCAAAACCAGGCGGAAACA
tV(AAC)F3	Hs_Val	6	27756936	27756864	Val	AAC		GTTTCCGTAGTGTAGTGGTTATCACGTTCGCCTAACACGCGAAAGGTCCGCGGTTCGAAACCGGGCGGAAACA
tV(AAC)F4	Hs_Val	6	27829230	27829158	Val	AAC		GTTTCCGTAGTGTAGTGGTTATCACGTTCGCCTAACACGCGAAAGGTCCCCGGTTCGAAACCGGGCGGAAACA
tV(AAC)C	Hs_Val	3	170972720	170972792	Val	AAC		GTTTCCGTAGTGTAGTGGTTATCACGTTCGCCTAACACGCGAAAGGTCCCCGGTTCGAAACCGGGCGGAAACA
tV(AAC)E1	Hs_Val	5	180523760	180523832	Val	AAC		GTTTCCGTAGTGTAGTGGTTATCACGTTCGCCTAACACGCGAAAGGTCCCCGGTTCGAAACCGGGCGGAAACA
tV(AAC)E2	Hs_Val	5	180529216	180529288	Val	AAC		GTTTCCGTAGTGTAGTGGTTATCACGTTCGCCTAACACGCGAAAGGTCCCCGGTTCGAAACCGGGCGGAAACA
tV(AAC)E3	Hs_Val	5	180548094	180548022	Val	AAC		GTTTCCGTAGTGTAGTGGTCATCACGTTCGCCTAACACGCGAAAGGTCCCCGGTTCGAAACCGGGCGGAAACA
tV(AAC)E4	Hs_Val	5	180577948	180577876	Val	AAC		GTTTCCGTAGTGTAGTGGTTATCACGTTCGCCTAACACGCGAAAGGTCCCCGGTTCGAAACCGGGCGGAAACA
tV(CAC)S	Hs_Val	19	4675719	4675647	Val	CAC		GTTTCCGTAGTGTAGCGGTTATCACATTCGCCTCACACGCGAAAGGTCCCCGGTTCGATCCCGGGCGGAAACA
tV(CAC)A1	Hs_Val	1	16751879	16751807	Val	CAC		GTTTCTGTGGTGTAGTGGTTATCATGTTCGCCTCACACGAGAAAAGTCCCTGATTCGAGACTGGGTGGGAACG
tV(CAC)F1	Hs_Val	6	26646261	26646333	Val	CAC		GTTTCCGTAGTGTAGTGGTTATCACGTTCGCCTCACACGCGAAAGGTCCCCGGTTCGAAACCGGGCGGAAACA

tV(CAC)F2	Hs_Val	6	27226001	27226073	Val	CAC	GTTTCTGTAGTATGGTGGTTATCACGTTAGTCTCACACGTGAAAGGTCCCTGGTTCGAAACCAGGTGGAAACA
tV(CAC)F3	Hs_Val	6	27281918	27281846	Val	CAC	GTTTCCGTAGTGGAGTGGTTATCACGTTCGCCTCACACGCGAAAGGTCCCCGGTTTGAAACCAGGCGGAAACA
tV(CAC)F4	Hs_Val	6	27356100	27356028	Val	CAC	GCTTCTGTAGTGTAGTGGTTATCACGTTCGCCTCACACGCGAAAGGTCCCCGGTTCGAAACCGGGCAGAAGCA
tV(CAC)F5	Hs_Val	6	27804378	27804306	Val	CAC	GTTTCCGTAGTGTAGTGGTTATTATGTTCGCCTCACACGCGAAAAGTCCCCGGTTCGAAATCAGGCGGGAACA
tV(CAC)A3	Hs_Val	1	146078219	146078147	Val	CAC	GTTTCCGTAGTGTAGTGGTTATCACGTTCGCCTCACACGCGAAAGGTCCCCGGTTCGAAACTGGGCGGAAACA
tV(CAC)A4	Hs_Val	1	146497234	146497161	Val	CAC	GTTTCCGTAGTGTAGTGGTTATCACGTTCGCCTCACACGCGTAAAGGTCCCCGGTTCGAAACCGGGCGGAAACA
tV(CAC)A5	Hs_Val	1	158182635	158182563	Val	CAC	GTTTCCGTAGTGTAGTGGTTATCACGTTCGCCTCACACGCGAAAGGTCCCCGGTTCGAAACCGGGCGGAAACA
tV(CAC)E1	Hs_Val	5	180456676	180456748	Val	CAC	GTTTCCGTAGTGTAGTGGTTATCACGTTCGCCTCACACGCGAAAGGTCCCCGGTTCGAAACCGGGCGGAAACA
tV(CAC)E2	Hs_Val	5	180461931	180461859	Val	CAC	GTTTCCGTAGTGTAGTGGTTATCACGTTCGCCTCACACGCGAAAGGTCCCCGGTTCGAAACCGGGCGGAAACA
tV(CAC)E3	Hs_Val	5	180533256	180533328	Val	CAC	GTTTCCGTAGTGTAGTGGTTATCACGTTCGCCTCACACGCGAAAGGTCCCCGGTTCGAAACCGGGCGGAAACA
tV(CAC)E4	Hs_Val	5	180582073	180582001	Val	CAC	GTTTCCGTAGTGTAGTGGTTATCACGTTCGCCTCACACGCGAAAGGTCCCCGGTTCGAAACCGGGCGGAAACA
tV(TAC)J	Hs_Val	10	5935752	5935680	Val	TAC	GGTTCCATAGTGTAGTGGTTATCACATCTGCTTTACACGCAGAAGGTCCTGGGTTCAAGCCCCAGTGGAACCA
tV(TAC)X	Hs_Val	X	18452758	18452686	Val	TAC	GGTTCCATAGTGTAGTGGTTATCACGTCTGCTTTACACGCAGAAGGTCCTGGGTTCGAGCCCCAGTGGAACCA
tV(TAC)F	Hs_Val	6	27366384	27366456	Val	TAC	GTTTCCGTGGTGTAGTGGTTATCACATTCGCCTTACACGCGAAAGGTCCTCGGGTCGAAACCGAGCGGAAACA
tV(TAC)K1	Hs_Val	11	59074750	59074678	Val	TAC	GGTTCCATAGTGTAGTGGTTATCACGTCTGCTTTACACGCAGAAGGTCCTGGGTTCGAGCCCCAGTGGAACCA
tV(TAC)K2	Hs_Val	11	59075108	59075036	Val	TAC	GGTTCCATAGTGTAGCGGTTATCACGTCTGCTTTACACGCAGAAGGTCCTGGGTTCGAGCCCCAGTGGAACCA
tV(CAC)A2		1	146074328	146074258	Val	CAC	GCACTGGTGGTTCAGTGGTAGAATTCTCGCCTCACACGCGGGACACCCGGGTTCAATTCCCGGTCAAGGCA

Figure S_4

Supplemental Figure S5

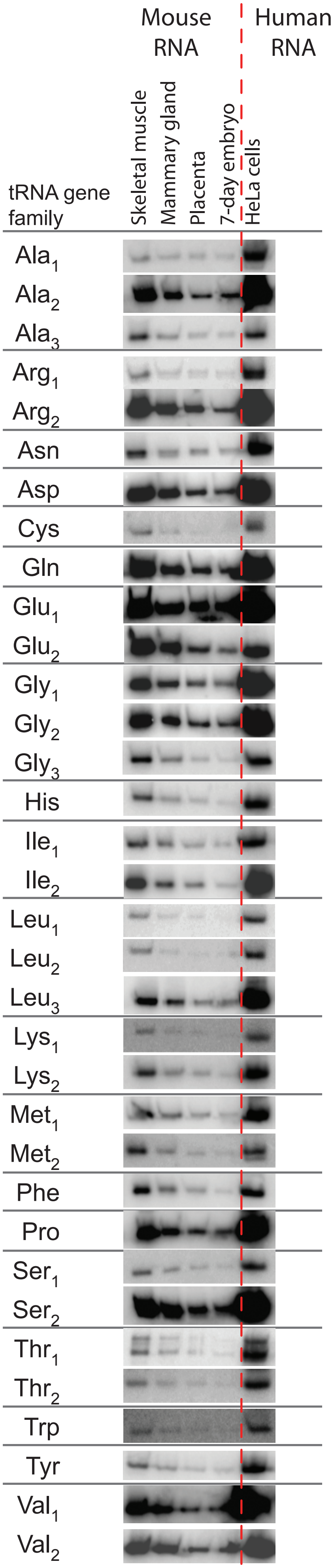
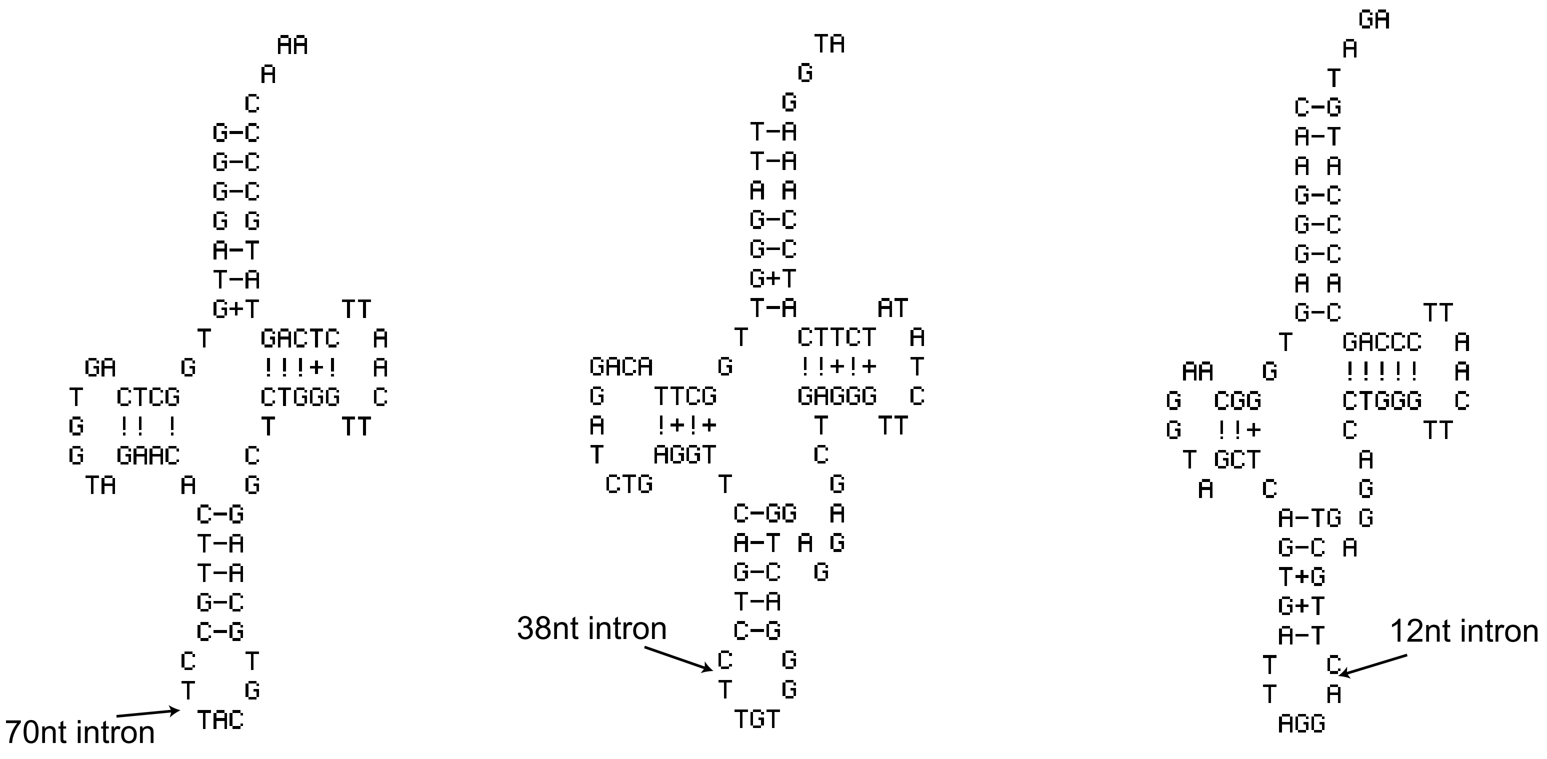
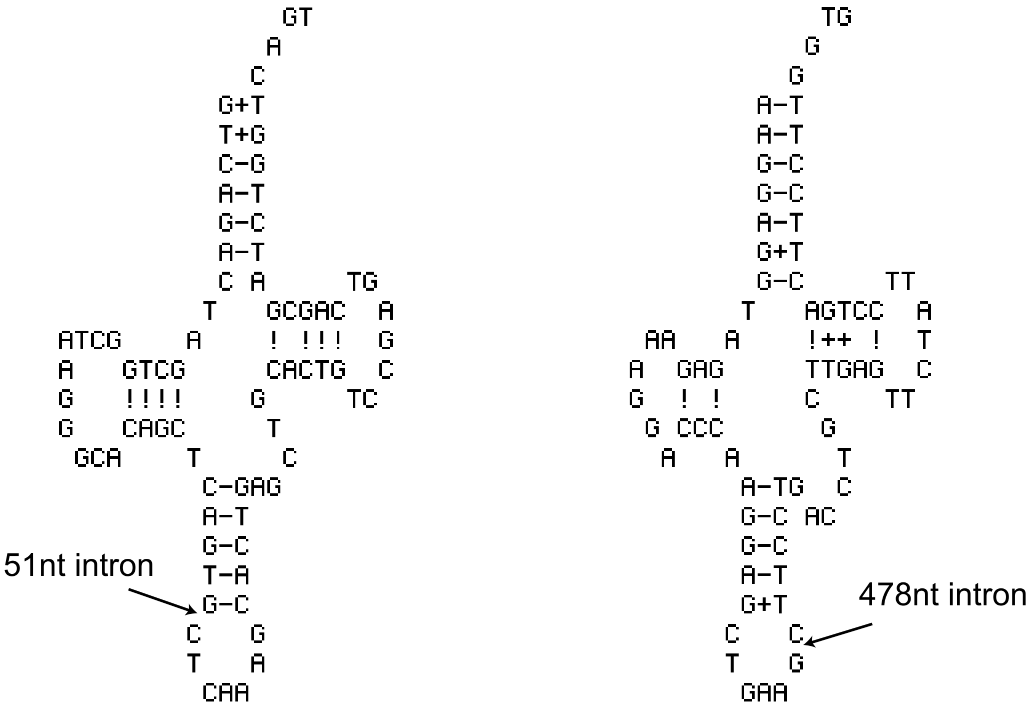


Figure S_6 - Structure of intron-containing orphan tRNAs

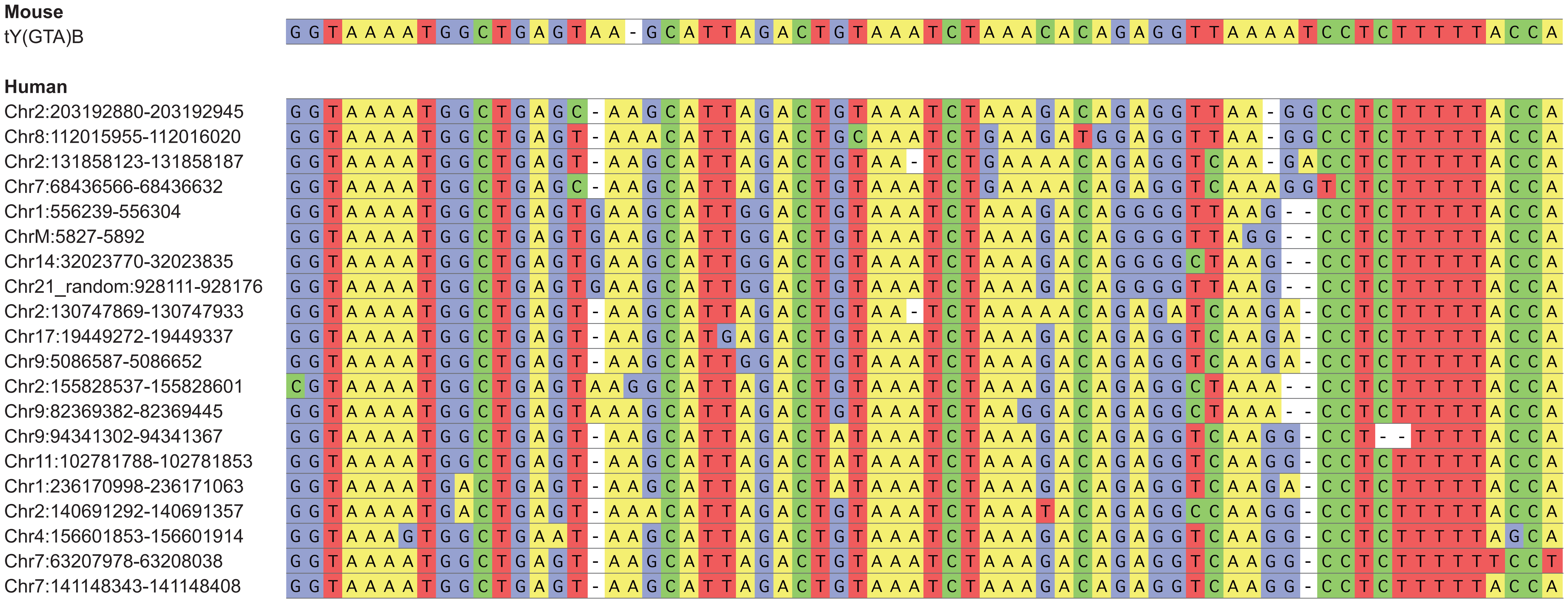


tV(TAC)G tT(TGT)E1 tP(AGG)P



tL(CAA)K tF(GAA)O tA(GGC)O1

Figure S_7



Mouse

tY(GTA)B	GGTAAAATGGCTGAGTAA-GCATTAGACTGTAAATCTAAACACAGAGGTTAAAATCCTCTTTTTACCA

Human

Chr2:203192880-203192945	GGTAAAATGGCTGAGC-AAGCATTAGACTGTAAATCTAAAGACAGAGGTTAA-GGCCTCTTTTTACCA
Chr8:112015955-112016020	GGTAAAATGGCTGAGT-AAACATTAGACTGCAAATCTGAAGATGGAGGTTAA-GGCCTCTTTTTACCA
Chr2:131858123-131858187	GGTAAAATGGCTGAGT-AAGCATTAGACTGTAA-TCTGAAAACAGAGGTCAA-GACCTCTTTTTACCA
Chr7:68436566-68436632	GGTAAAATGGCTGAGC-AAGCATTAGACTGTAAATCTGAAAACAGAGGTCAAAGGTCTCTTTTTACCA
Chr1:556239-556304	GGTAAAATGGCTGAGTGAAGCATTGGACTGTAAATCTAAAGACAGGGGTTAAG--CCTCTTTTTACCA
ChrM:5827-5892	GGTAAAATGGCTGAGTGAAGCATTGGACTGTAAATCTAAAGACAGGGGTTAGG--CCTCTTTTTACCA
Chr14:32023770-32023835	GGTAAAATGGCTGAGTGAAGCATTGGACTGTAAATCTAAAGACAGGGGCTAAG--CCTCTTTTTACCA
Chr21_random:928111-928176	GGTAAAATGGCTGAGTGAAGCATTGGACTGTAAATCTAAAGACAGGGGTTAAG--CCTCTTTTTACCA
Chr2:130747869-130747933	GGTAAAATGGCTGAGT-AAGCATTAGACTGTAA-TCTAAAAACAGAGATCAAGA-CCTCTTTTTACCA
Chr17:19449272-19449337	GGTAAAATGGCTGAGT-AAGCATGAGACTGTAAATCTAAAGACAGAGGTCAAGA-CCTCTTTTTACCA
Chr9:5086587-5086652	GGTAAAATGGCTGAGT-AAGCATTGGACTGTAAATCTAAAGACAGAGGTCAAGA-CCTCTTTTTACCA
Chr2:155828537-155828601	CGTAAAATGGCTGAGTAAGGCATTAGACTGTAAATCTAAAGACAGAGGCTAAA--CCTCTTTTTACCA
Chr9:82369382-82369445	GGTAAAATGGCTGAGTAAAGCATTAGACTGTAAATCTAAGGACAGAGGCTAAA--CCTCTTTTTACCA
Chr9:94341302-94341367	GGTAAAATGGCTGAGT-AAGCATTAGACTATAAATCTAAAGACAGAGGTCAAGG-CCT--TTTTACCA
Chr11:102781788-102781853	GGTAAAATGGCTGAGT-AAGCATTAGACTATAAATCTAAAGACAGAGGTCAAGG-CCTCTTTTTACCA
Chr1:236170998-236171063	GGTAAAATGACTGAGT-AAGCATTAGACTATAAATCTAAAGACAGAGGTCAAGA-CCTCTTTTTACCA
Chr2:140691292-140691357	GGTAAAATGACTGAGT-AAACATTAGACTGTAAATCTAAATACAGAGGCCAAGG-CCTCTTTTTACCA
Chr4:156601853-156601914	GGTAAAGTGGCTGAAT-AAGCATTAGACTGTAAATCTAAAGACAGAGGTCAAGG-CCTCTTTTTAGCA
Chr7:63207978-63208038	GGTAAAATGGCTGAGT-AAGCATTAGACTGTAAATCTAAAGACAGAGGTCAAGG-CCTCTTTTTTCCT
Chr7:141148343-141148408	GGTAAAATGGCTGAGT-AAGCATTAGACTGTAAATCTAAAGACAGAGGTCAAGG-CCTCTTTTTACCA