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Gene name	RSS (i)			Reading Frame (ii)	Coding sequence (iii)	Splice site (iv)
	Nonamer	Spacer	Heptamer			
bTRAJ1	GCTTTCTGT	AATGAAGACAGT	GAGAGTG	2	AGATGGAGGTGTTGGCTCCAGATGCAGTTTGGCAAGGGAACCAGAGTCTCCATCACTCCAG D G G V G S Q M Q F G K G T R V S I T P	GTATG
bTRAJ2	AGTTTCTGT	AATGGTGTCCCC	AGCAGTG	3	TGAATACAGGAGGAGCGATCGGTAAACTCACTTTTGGGAAAGGAACCCAAGTGCATAAATCTG N T G G A I G K L T F G K G T Q V S I I S	GTGAG
bTRAJ3	GGTTATTGC	AAAGACCTTACC	CTCAGTG	2	GAGATTCGGCACTGATAAGTTAACTTCGGAGCAGGGACCAGACTGAGTGTCCATCCAA R F G T D K L N F G A G T R L S V H P	GTGAG
bTRAJ4	GCATCCTC	TAGTGGGTGTCT	TCTGGTG	3	TCTACAATAAGCTGACCTTTGGAACCGGAACCAGGCTGACTGTACACTCAC Y N K L T F G T G T R L T V H S	GTGAG
bTRAJ5	AGTATTTGT	ACTGCATTGTGG	CAGGGTG	3	TGAACACAGGCAGCAGAACAACACTCACTTTTGGGAGTGAACAAGACTCCGAGTGCATCCAA N T G S R T L T F G S G T R L R V H P	GTAAG
bTRAJ6	GGTTTTAGC	AAGGCCTTTCCT	TGCTGTG	2	TGTATCAAGACTAAAGTATGGATTTATTTTGGAAACAGGGACCAAGCTTGTGTTCAACCCAC V S R L K Y G F I F G T G T K L V V H P	GTGAG
bTRAJ7	TGTTTTTGT	AATGCACTTACC	CAGAGTG	2	TGATTATGGGAACAGACTCACTTTTGGAAATGGGACTCGAGTGTGCTGGTCACACCAA D Y G N R L T F G N G T R V L V T P	GTAAG
bTRAJ8-1	CCATTTTGT	ATAGAGTTATGT	CAGAGTG	3	TGAGCAGAGTTATCAGAAATTCGTATTTGGAACCTGGCACCAACTTTTGATCAACCCAA S T G Y Q K F V F G T G T Q L L I N P	GTAAG
bTRAJ9	CCATTTTGT	CACAGCACAAT	CACTGTG	1	GGATATACTGGAGCTTCAAATTTGTTTGGGACAGGAACAAGCTATTTATTGAAACAA G Y T G G F K F V F G T G T K L F I E T	GTAAG
bTRAJ8-2	CCATTTTGT	ACAGAGTTATGT	CAGAGTG	3	TGAACACAGGTTATCAGAACTCACATTTGGAACCTGGCACCAACTTTTAATCAACCCAA N T G Y Q K L T F G T G T Q L L I N P	GTAAG
bTRAJ10	AGTTTATTG	TGAGGCATCAA	CACTGTG	3	GGAATTTGGGAGGAGGAAACAACACTCATCTTTGGGAAAGGCACCCACCTACAAGTGAAGCTGA N W G G G N K L I F G K G T H L Q V K L	GTAAG
bTRAJ11	TATTTTTGT	ATGGGGTGTGC	TACAGTG	3	TGAATTCAGGATACAACACTTACTTTTGGAAAGGCACCTGTGCTTCTTGTCTTTCCAG N S G Y N T L T F G K G T V L L V F P	GTAAA
bTRAJ12	GGTTTTTGA	CTGACTAAGAAA	CACTGTG	3	GGAAGGATGGAGGCTATACATGGACCTTCGGAAGTGGGACTAGACTGTCTGGTCAGGCCTG K D G G Y T W T F G S G T R L L V R P	GTGAG
bTRAJ13	CCATCCTGT	ATAGGCCTGCAT	TGTAGCG	3	TGAATCCTAGGGGTGACCGAAAGGTTGCCTTTGGAACCTGGAACGACACTTCAAGTCAACCCAA N P R G D R K V A F G T G T T L Q V T P	GTAAG
bTRAJ14	AATTATTGT	CAGGCAGCACGG	TGCTGTG	1	ATTTATAACACATTCATCTTTGCGAGTGGGACAAGATTATCAGTAAACCCA I Y N T F I F A S G T R L S V K P	GTAAG
bTRAJ15	GGTATTTGC	AGGACCTTGT	CACTGTG	3	CCTACCAGGGAGGAAATGCATTTGGTCTTTGGGAAAGGAACCAAGTATCAGTGCATCCCA Y Q G G N A L V F G K G T T V S V H P	GTAAG
bTRAJ16	GGTTTTTGT	GGTGAAGTAGAT	CACTGTG	1	GGTTTTCAAGTGGCCAGAAGTTGGTTTTTGGAAAGTGGGACCATGTAAAGGTGAATCTTA G F S S G Q K L V F G S G T M L K V N L	GTAAG
bTRAJ17	GGTTTTTGC	TGGGCCTTGAAT	CACTGTG	3	TGACCACCACTGCAGGGACCTAACCTTTGGAGAAGGAACCAAGGCTGATAGTCAAGCTGA T T T A G T K L T F G E G T R L I V K L	GTGAG
bTRAJ18	GGTCTTGT	AAAGGGGGCCGG	CACTGTG	3	TCAATAGAGGCTCAAGTCTGGGGAGGTTCTACTTTGGAAGAGGAACCCGGCTAAGTGTACAGCCTG N R G S S L G R F Y F G R G T R L T V Q P	GTGAG

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	Nonamer	Spacer	Heptamer			
bTRAJ19	TGATTCTGC	AAAGGACTGCAA	AGGACAG	3	TCTATCAGAGTTTTCGCAAGTTCACCTTTGGAAAAGGATCCAACACAATGACAATCCAA Y Q S F R K F T F G K G S K H N D N P	CTAAG
bTRAJ20	GGTTTGC GT	AGGAAGACGTAG	CACTGTG	1	ACTCTAAATAACTACAAGCTCACCTTTGGATCAGGAACCACAGTAAGTGTGAGAGCAA T L N N Y K L T F G S G T T V T V R A	GTAAG
bTRAJ21	ACTTTTTGT	AATGGTAGTAAA	CATGGTG	1	TATAACACCAACAGATTTTACTTCCGGATCTGGGACAAAACCTCAGAGTAAAGCCAA Y N T N R F Y F G S G T K L R V K P	GTAAG
bTRAJ22	GGTTTTTGT	TGTTGGGCTTAT	CACAGTG	3	CTTCCTCTAGTTCAGGCTGGCAACTGACCTTTGGATCTGGGACCCAACTGACTGTTGTACCTG S S S S G W Q L T F G S G T Q L T V V P	GTAGG
bTRAJ23	TGTTTTTGA	CAGGCTGTATAA	CACTGTG	3	TGAATTATAACCAGGGAGGAAAGCTTATCTTCGGACAGGGAACCGAGTTATCTGTGAAGCCCA N Y N Q G G K L I F G Q G T E L S V K P	GTAAG
bTRAJ24	CCATTTTGT	AGAGGTGTTTGT	CACAGTG	3	TGACAACTGACGGCTGGGGGAAATTGAATTTGGAGCGGGACCCGGTTGTGGTCACCCAG T T D G W G K L N F G A G T R V V V T P	GTAAG
bTRAJ25	GGTTTTTGA	TGCTGAGATAAT	CACTGTG	3	GGGAAGGACAAGGCTTCTCCCTCGTCTTTGGGAAGGGGACAAGGCTGCTTGTCAAGCCGA E G Q G F S L V F G K G T R L L V K P	GTAAG
bTRAJ26	GCTTTTTGT	AAAGCCAGGGG	CACTGTG	3	GGAATAACTATGGCCAGGGTTTGATCTTCAGTGGAGGAACCAGACTGTCTGTGCAGCCCC N N Y G Q G G L I F S G C T R L S V Q P	GTAAG
bTRAJ27	GGTTATTGC	AATAGCACTGAA	CACTGTG	2	TAACACCGGTACAGGCAAAATTAACCTTTGGGACGGGACTCGCTCACTGTGAGCCGA N T G T G K L T F G D G T A L T V K P	GTAAG
bTRAJ28	GGTTTTTGC	AAAGAAAGGAAA	CTCTGTG	3	CCTACTCTGGGACTGGGAGTTACCAACTCACCTTCGGGAAGGGACCAAACTCTTGGTCACACCAA Y S G T G S Y Q L T F G K G T K L L V T P	GTAAG
bTRAJ29	AGTTTTTGT	GATGAAGGCAAT	CACTGTG	3	GGGATTCAGGAAACAGGCAACTTGTCTTTGGAAAAGGCACAAGACTTGCTGTGACTCCAA D S G N R Q L V F G K G T R L A V T P	GTAAG
bTRAJ30	AGTTTTTGT	TGTGGCCCAAT	CACAGTG	2	TGAACAAACCTCTGGCAAAATGTCTTTGGAAGAGGGACTCAGCTTCATGTTCTCCCA E Q T S G K I V F G R G T Q L H V L P	GTAAG
bTRAJ31	GGTTCAGT	AAAAGCAGGAAA	TGCTGTG	1	GGGACTGACAATTCAGAATCTTCTTTGGAAGTGGAAACCCAGGTGGTAAAGCCCA G T D N S R I F F G T G T Q V V V K P	GTAAG
bTRAJ32	GGTTGTTGT	AAGGCACTGAAA	GGCTGTG	3	TGAATTATGGGGTGTGCTGCCAACCACTCATCTTTGGGACTGGCAGCTGCTTTCTGTCAAGCCAA N Y G G A A N Q L I F G T G T L L S V K P	GTACG
bTRAJ33	GGTTTTTGT	TAAGTTTTTGT	CTCTGTG	3	TGGATGGCAACTATCAGTGGATCTGGGGCTCTGGGACCAAACTAATATAAGCCAG D G N Y Q W I W G S G T K L I I K P	GTAAG
bTRAJ34	GGTTTTTGT	AGGCCTTGGTAT	CACTGTG	3	TCTCCAACAGGGACAACACTCATCTTTGGGGCTGGAACCAAGATTACAAGTTTTTCCAA S N R D K L I F G A G T R L Q V F P	GTAAG
bTRAJ35	GGTTTTTGT	AGTGGAGTCAGC	CATGGTG	2	GAACTTTGGGAATGTGCTGCATTTGGGGTCTGGCACTCAAGTGATCGTTATGCCTC N F G N V L H L G S G T Q V I V M P	GTAAG
bTRAJ36	TGTTTTTGT	ACTGGCAGAAA	CACTGTG	1	TTAACCTCTGGAGCAAACAGCTTGTCTTTGGGACAGGAACCAAGCCTCACCATCCTCCCC L T S G A N Q L V F G T G T S L T I L P	GTAAG
bTRAJ37	AGTTTTTGT	AAAGTAGAGCAT	TACAGTG	2	TGACTCAGGAAACACAGGAAGACTCACCTTTGGGCAGGGGACAATGTTACAAGTAAAACCAAG D S G N T G R L T F G Q G T M L Q V K P	GTAGG
bTRAJ38	GGTTTCTGT	AAAGCTTCCAT	GACTGTG	2	TAATACTGGCAACAACCGTAAGCTGATTTGGGGACTGGGGACAAGTCTGGCAGTAAATCCAA N T G N N R K L I W G L G T S L A V N P	GTGAG

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	Nonamer	Spacer	Heptamer			
bTRAJ39	GGTTTTTGC	TGAGCTGAAGAT	CACTGTG	3	TGAATAATAATGCAGGCAACATATTCACATTTGGAGGGGGAACAAGGTTAATGGTCAAACCTC N N N A G N I F T F G G G T R L M V K P	GTGAG
bTRAJ40	GGTTTATGT	AGAGCCACATAG	CACTGTG	3	ACTCAGGAAACTACAAATACGTCTTTGGAGCGGGCACTAGGCTGCAGGTTTAAACAA S G N Y K Y V F G A G T R L Q V L T	GTGAG
bTRAJ41	GGTTTTTGT	TTAGGGAAGGTG	CACTGTG	1	GAACTCAATGCCGGCTACGCGCTCCACTTTGGCCAAGGCACCTCAGTGCTGGTCACACCCG E L N A G Y A L H F G Q G T S V L V T P	GTGAG
bTRAJ42	GGTAATTGT	AAGGTCCCATAT	GACTGTG	3	TGAATGTTGGCAGCGGCAAGGACAGCTCATCTTTGGAAAAGGCATATGGTCTCTGTTAAACCAA N V G S G Q G Q L I F G K G T M V S V K P	GTAAG
bTRAJ43	GGTTTTTGT	TAGAGGGTGTAC	TGCTGTG	3	GCAATAATAACAACAACCTACGCTTTGGAGCAGGGACCAGACTGACGGTAAAACCAA N N N N N L R F G A G T R L T V K P	GTAAG
bTRAJ44	GGTTTCTGT	CATGGAGCATCT	CACAGTG	2	TAACACGGGCACTGGCGGGAAAGTCATATTTGGGACTGGAACGAGACTTCAGGTCACCCTTG N T G S G G K V I F G T G T R L Q V T L	GTAGG
bTRAJ45	GATTTATGT	AAAGGTTAACA	TGGGGTG	3	TGAATACAGGAGGAAGTAACAGACTCATCTTTGGAAAAGGCATCATCCAGCCCC N T G G S N R L I F G K G T Q L I I Q P	GTAAG
bTRAJ46	CGTTTCTGT	AAAGCTGCTGAC	AACAGTG	3	AGAAGAGTGGCAGCGGAGACAGGCTGACTTTGGGACCGGGACGCGTTTAGCAGTGAGGCCAA K S G S G D R L T F G T G T R L A V R P	GTAAG
bTRAJ47	TGTTTTTGT	AGAGGAGTTTGA	TGCTGTG	3	TGAATTCGGAACACACTGATCTTTGGCTCAGGAACCACTTTGACAGTCAAGCCTC N S G N T L I F G S G T T L T V K P	GTGAG
bTRAJ48	GGTTTTTGT	AATGACTTAGAA	CACTGTG	3	TGTCTAACTACCAAGGCACTCAATTAACCTTTGGAACGGAAGTACTCACCATCACAGCCA S N Y Q G S Q L N F G T G T R L T I T A	GTAAG
bTRAJ49	GGTTTTTGT	TGAGCTTCTAT	CACAGTG	2	GAACAGCTACGGCCAGAACTATTTGGGAGAGGGACAAGTTGACAGTCATTCCAA N S Y G Q N Y F G R G T S L T V I P	GTAAG
bTRAJ50	AGTTATTGC	AAAGTGTTTCGAT	GGCTGTG	2	TGACAACCTCTACAAGTTGATGTTTGGGCAAGGGACGAGCTTATCAGTCATTCCAA D N S Y K L M F G Q G T S L S V I P	GTAAG
bTRAJ51	AGTCGTTGT	AAAACCTCCAC	TGCAGGG		AGTAGCACGGCAGCTCTGAGTTAGAAAAAGAAAGAACTTGACTAACCGTGAAGCCAA	GAAGC
bTRAJ52	GGTTCTTGT	AAAGGCTTCCAT	TGCAGTG	3	TAAATACTGGTGGTAGTGCCTATGGAAGCTGATGTTCGGACAAGGAACCCTTTGACTGTCCATCCAA N T G G S A Y G K L M F G Q G T T L T V H P	GTAAG
bTRAJ53	TGTTTTTGT	AAAGCCTCCCT	GACTGTG	3	AGACTAGTGGAACTAGCAGCTATAAACAGACATTTGAAAAGGCCTCTCTAATTGTGAATCCAA T S G T S S Y K Q T F G K G T L L I V N P	GTAAG
bTRAJ54	AGTTTGTGT	AAAGCTCTTTCG	TGGGGTG	1	TGACTCAGAGGTGCAGGCCAGAAGCTGGTATTCGGGCGAGGAACCAGGCTGACCATCAACCCCA * L R G A G Q K L V F G R G T R L T I N P	GTAGG
bTRAJ55	TGATGCTGA	GCAGGGCTCCCT	GTTGGTG		ACAAAAGATAGCAATGTCCCGGTTGGAGAGGAGAAGAGAATAAGTCCAAAAATAAGTGCAA	ATAAG
bTRAJ56	AGTTTTTGT	AGAGTCTCGTGT	CATTGTG	1	TGATACTCCAATAATAAGCTGACATTTGAAAAGGAACAATCCTGAATGTTAGACCAG * Y S N N K L T F G K G T I L N V R P	GTATG
bTRAJ57	GGTATTTGT	AAAGCAGTCTAT	GGGGGTG	3	TAACTCAGGGCGGATCTGAAAGACTCCTCTTTGGAAAAGGGAACGAAACTGACAGTAAACCCAC T Q G G S E R L L F G K G T K L T V N P	GTAAG
bTRAJ58	GGTTTTTGC	AAAGCCTTGAG	CATTGTG	3	TTCAACAAACCAGTGGCTCTAAGATGATATTTGGAAAAGGACTCAGCTCACAGTGCAACTTG Q Q T S G S K M I F G K G T Q L T V Q L	GTAAG

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bTRAJ59	AGTTTATGT	AAAGGTGTCTGC	TCCTGTG	2	GGAAGCAAGGCAATTTACATTTCGGAACCGGGACTCAAGTGAGAGTGAACTTA E A R Q F T F G T G T Q V R V K L	GTAAG
bTRAJ60	ACTTTTGGT	AAAGGGCCCAGG	CACTGTG	3	TAAAGAGCACTGAGAAATTCACCTTTGGGAAAGGGACTCAGTTAATTGTAAGCCTGG K S T E K F T F G K G T Q L I V S L	GTGAG
bTRAJ61	AGTTTTTGT	AAAGGTGTTTAC	TCCTGTG		SGAATGGGGTTAATAGGAAACTGACATTTTGGAAACCAAGACTAGAGGAATCTTGAAACTCA	GTGAG

B

bTRAJ	Stop codon in coding region	Loss of canonical FGxG motif	Defective splice site	RS defect
bTRAJ4				•
bTRAJ13				•
bTRAJ14*		•		
bTRAJ19			•	•
bTRAJ26*		•		
bTRAJ33*		•		
bTRAJ35*		•		
bTRAJ51	•		•	•
bTRAJ55	•		•	
bTRAJ61	•			

* These genes have been classified as non-functional due to loss of the canonical FGxG motif. However, the functionality of these genes may have to be determined empirically; hTRAJ16 is considered functional despite absence of the FGxG motif, whilst mTRAJ44 and 47 are considered non-functional due to absence of the FGxG motif.