

	0	5	10	15	20	25	30	35	40	45	50	55	60	65	70	75	80	85	90	95	100	105	110
18331	GGAGTT	CACGACCACCT	GGGGCAACAAGGCAAAAC	-	CCCGTCTCTACT	-	-	AAAAAT	-	ACAAAAAGCTAGCCAGGCGTGGTGGTGTGCATCTGTAACCCCAGCTACTGGGGA													
34336	GGGGTT	CGAGACCAGCTTGGCCAGCATGGTGAAAC	-	CCTGTCTCTACT	-	-	AAAAAT	-	AC-AAAAATTAGCTGGGCGTAATGGCGCACGCCTGTAATCCTAGCTACTCGGGG														
35889	GGAGTT	CAAGACCAGCCTGGCCAACATGGTGAAAC	-	CTCGTCTCTACT	-	-	AACAAT	-	AC-AAAAATTAGCCTGGTGTGGTGGTGGGTGCCTGTAATCCCAGCTACTGGGAA														
40716	GGAGTT	CGAGACCAGCCTGACCAACATGGAGAAAC	-	CACGTCTCTACT	-	-	AAAAAT	-	AC--AAAATTAGCCAGGCGTGGTGGTGCATGCCTATAATCCCAGCTACTCGGGG														
-48429	GGAGTTT	TGAGACCAGCCTGTCCAACATGGTGAAAC	-	TCCGTCTCTACT	-	-	AAAAAT	-	AC-AAAAATTAGCCGGGCATGGTGGCACATGCCTATAATCCCAGCTACTCCGGA														
50769	GGAGTT	CAAGACCAGCCTGGTTAAGATGGTGAAAC	-	CCCATCTCTACT	-	-	AAAAATTAA	-	AAAAATTAGCTGGGTGTGGTGATGGGCACCTGTAATCCAAGCTACTCAGGA														
77269	GGAGTT	CAAGACCAGCCTGACCAACATGATGAAAC	-	CCCATCTCTACT	-	AAAAATAC	-	AA-AAAAATTAGCCAGGTGTGGTTGCGGGGCACCTGTAATCCCAGCTACTCGGGA															
-92928	GGAGTTT	TGAGACCAGCCTGGCCAACATGGCGAAAC	-	CCTGTCTCTACT	-	-	AAAAAT	-	AC-AAAAATTAGCCAGGTGTGATGGTGGGTGCCTACAGTCCCAGCCACTCAAGA														
-105233	GGAATT	CAAGACCAGCTTGGTCAACATGCCGAAAC	-	CCCATCTCTACT	AAAAAAAAAT	-	AC-AAAAATTAGCCAGGCGTGGTGGTGCACACCTGTGGTCCCAGCTACTCGGGA																
-117611	GGAGTT	CAAGACCAGCCTGGTCAACATGGTGAAAC	-	CCCATCTCTACC	-	-	AAAAAT	-	AC-AAAAATTAGCTGGACACGGTGATGCACGCTTGTAATCCCAGCTACTCGGGA														
-121584	GGAGAT	CGAGACCATCTGGGTTAACACGGTGAAAC	-	CCCGTCTCTACT	-	AAAAATAC	-	AA-AAAAATTAGCCAGGCACAGTGGCAGGTGCCTGTAGTCCCAGCTACTCGGGA															
131094	GGAGTT	CAAGACCAGCCTGGCCA	-	CATGGCTAAAC	-	CCCATCTCTACT	-	-	AAAAAT	-	AC-AAAAATTAGTCGGGCATAGTGGTGGGTGCCTGTAATCCCAGCTTCTTGGTA												
160730	AGAGTT	CAAGACCAGCCC	GGGCAACATGGTGAAAC	-	CCTGTGTCTACA	-	-	AAAAAT	-	AC-AAAAATTAGTCGGGTGTGGTGATGTGCATTTGTAGTCCCAGCTACTCGAGA													
-168253	GGAGAT	TGAGACCATCCTGGCTAACAGGGTGAAAC	-	CCCATCTCTACT	-	-	AAAAAT	-	ACAAAAAATTCACCGGGCGCGGTGGCAGGTGCCTGTAGTCCCAGTTACTGGGGA														
-174332	GTAGTT	CAAGACCAGCCTGGGCAACATGGCAAAATGCCCATCTCTAC	-	-	AAAAAAAT	-	AC-AAAAATTAGCCAGGCGTGGTGGCATGTACCTGTAGTCCCAACTACTCAGGA																
-197103	AGAGAT	CGAGACCATCCTGGACAATATGGTGAAAC	-	CC-GTCTCTACT	-	-	AAAAAT	-	AC-AAAAATTAGCTGGGCGTGGTGGTGGTGCACCTGTAGTCCCAGCTACTCGGGC														