

	10	20	30	40	50	60
51_Pabe	ATGCTGACT	CCGCTCGGAAAG	TTCTCAACT	TGCAAAGTTT	GCTGTCCGGCT	GTCTGGGGTCTGGGA
89_Hsap	ATGCTGACT	CCGCTCGGAAAG	TTCTCAACT	TGCAAAGTTT	GCTGTCCGGCT	GCCTAGGGTCTGGGA
93_Ggor	ATGCTGACT	CCGCTCGGAAAG	TTCTCAACT	TGCAAAGTTT	GCTGTCCGGCT	GTCTAGGGTCTGGGA
14_Mmur	ATGCTGACT	CGGCGCCG	CAGGTCCG	CCGCGAAGG	CCCCGCAGCTG	-----
67_Ogar	-----	-----	-----	-----	-----	-----
38_Nleu	ATGCTGACT	CGGCTCGGAAAG	TTCTCAACT	TGCAAAGTTT	GCCGTCCGGCT	GCCTAGGGTCTGGGA
27_Cjac	-----	-----	-----	-----	-----	-----
98_Mmul	-----	-----	-----	-----	-----	-----
41_Ptro	ATGCTGACT	CCGCTCGGAAAG	TTCTCAACT	TGCAAAGTTT	GCTGTCCGGCT	GCCTAGGGTCTGGGA
93_Tsyr	ATGCTGACT	CCGCTGCCAAG	TTCGCAGCT	GCCAAGTTGGCA	-----	-----GA



Subst



Indel

	70	80	90	100	110	120	130
51_Pabe	AGCTCGGGCA	CCCTCCCGCT	CCGGGGCT	CCCTGCTCCCA	CTCCAGCCCCC	---CCGTCACGGCT	
89_Hsap	AGCTCGGGCA	CCCTCCCTCT	CCGGGGCT	CCCTGCTCCCA	CCCCCTCCGG	CCCCCCCCA	CCGTGCGGCT
93_Ggor	AGCTCGGGCA	CCCTCCCTCT	CCGGGGCT	CCCTGCTCGCA	CCCCCTCCGG	CCCCCCCC	---CCGTGCGGCT
14_Mmur	-----	CCCCCCCCG	CTCCGCGCG	GTCCCCCGG	CCCCCGCTCC	GCGGTCCCCCG	GGC---
67_Ogar	-----	-----	-----	-----	-----	-----	-----
38_Nleu	AGCTCGGGCA	CCCTCCCGCT	CCGGGGCT	TTCTGCTTCCA	CCCCCTTGG	CCCCCA	---CCGTGCGACT
27_Cjac	-----	-----	-----	-----	-----	-----	-----
98_Mmul	-----	-----	-----	-----	-----	-----	-----
41_Ptro	AGCTCGGGCA	CCCTCCCTCT	CCGGGGCT	CCCTGCTCCCA	CCCCCTCCGG	CCCCCCCCA	CCGTGCGGCT
93_Tsyr	GGGCGGGTCT	CTTCCGCCGGGG	CTTCTTGC	GCTCGGCAC	-----	-----	CCATCGCGCT



Subst



Indel

	140	150	160	170	180	190
51_Pabe	CCTCCAGGCTGGGCCTGTGGCCGCGGTACTTTTAAATTTTCCCCCAGCTCAGAAAATTGCTGTTTC					
89_Hsap	CCTCCAGGCTGGGCCTGTGGCCGCGGTGCTTTTAAATTTTCCCCCAGCTCAGAAATCTTGCTGCTC					
93_Ggor	CCTCCAGGCTGGGCCTGTGGCCGCGGTGCTTTTAAATCTTCCCCCAGCTCAGAAATCTTGCTGCTC					
14_Mmur	-----GGCCTGTGGCCGCGAGCCGCCGATCTGCCCCGGCTCAGAAATCCTGCCGCC					
67_Ogar	-----					
38_Nleu	CCTACAGGCTGGGCCTGTGGCCGCGGTGCTTTTAAATCTTCCCCCAGCTCAGAAAATTGCTGCTC					
27_Cjac	-----					
98_Mmul	-----					
41_Ptro	CCTCCAGGCTGGGCCTGTGGCCGCGGTGCTTTTAAATTTTCCCCCAGCTCAGAAATCTTGCTGCTC					
93_Tsyr	CCTCCGGGCCCCGGCCCGTGGCTGCAGAACTTTCTGATCTTCCCCCAGCACCGAAAATCGCTGCTC					



Subst



Indel

	200	210	220	230	240	250	260
51_Pabe	GGCCCGCAGGAGAGC---AACTCAACGGGAACGATGTGGAAGGTGTCAGCCCTGCTCTTCGTTTT						
89_Hsap	GGCCCCCAGGAGAGCAACAACCTCAACGGGAACGATGTGGAAGGTGTCAGCTCTGCTCTTCGTTTT						
93_Ggor	GGCCCCCAGGAGAGCAACAACCTCAACAGGAACGATGTGGAAGGTGTCAGCTCTGCTCTTCGTTTT						
14_Mmur	GGCCCCCGGGAGAGC---AAGTCGGCCGCCAGGATGTGGAAGGTGCCAGTTCTGCTCTTCGTTTT						
67_Ogar	-----						
38_Nleu	GGCCCCCAGGAGAGC---AACTCAACGGGAACGATGTGGAAGGTGTCAGCTCTGCTCTTCGTTTT						
27_Cjac	-----ATGTGGAAGGTGTCAGCTCTACTCTTCGTTTT						
98_Mmul	-----ATGTGGAAGGTGTCAGCTCTGCTCTTCGTTTT						
41_Ptro	GGCCCCCAGGAGAGCAACAACCTCAACGGGAACGATGTGGAAGGTGTCAGCTCTGCTCTTCGTTTT						
93_Tsyr	GGCCCCCAGGAGATC-----AGTCGCCGGGAATGTGGAAGGCGCCGGTTCTGCTCTGGGTCTT						



Subst



Indel

	270	280	290	300	310	320
51_Pabe	GGGAAGCGCATCGCTCTGGGTTCTGGCA	---	GAAGGAGCCAGCACAGGCCAGCCAGAAGATGACA			
89_Hsap	GGGAAGCGCGTCGCTCTGGGTCCCTGGCA	---	GAAGGAGCCAGCACAGGCCAGCCAGAAGATGACA			
93_Ggor	GGGAAGCGCGTCGCTCTGGGTCCCTGGCA	---	GAAGGAGCCAGCACAGGCCAGCCAGAAGATGACA			
14_Mmur	GGGAAGCGCATCGCTCTGGGTCCCGGCA	---	GCAGGAGCCAGCACGAACCCGGCCAGAAGATGACA			
67_Ogar	-----	TGGCTCAATCTGTGTTCTTCAGCAGTCACATATAGGCCAGAAGATGACA				
38_Nleu	GGGAAGCGCATCGCTCTGGGTCCCTGGCA	---	GAAGGAGGTAAGACCCAGCCGAACAGAGACTTGCT			
27_Cjac	GGGAGCGCGTCGCTCTGGGTCCCTGGCA	---	GAAGGAGCCAGCACGGGCCAGCCAGAAGATGACA			
98_Mmul	GGGAAGCGCATCGCTCTGGGTCCCTGGCA	---	GAAGGAGCCAGCACGGGCCAGCCAGAAGATGACA			
41_Ptro	GGGAAGCGCTTCGTATGGGTCCCTGGCA	---	GAAGGAGCCAGCACAGGCCAGCCAGAAGATGACA			
93_Tsyr	GGGAAGCGCATCGGTCTGGGTCCCTGGCA	---	CAGGCAGCTAACACCTTGGGGCCAGAAGATGACC			



Subst



Indel

	330	340	350	360	370	380	390
51_Pabe	TTGAGACTACAGGTACGGAAGGCGGTGTTGCCATGCCAGGTGCCGAAGATGATGTGGTGACCCCG						
89_Hsap	CTGAGACTACAGGTTTGGAAGGCGGCGTTGCCATGCCAGGTGCCGAAGATGATGTGGTGACTCCA						
93_Ggor	CTGAGACTACAGGTTTGGAAGGCGGCGTTGCCATGCCAGGTGCCGAAGATGATGTGGTGACTCCA						
14_Mmur	TTGAGACTCCAGGTGTAGAAAGAAGATGTGACAAACCCAGGTATAGAAGAT---	GTGACAAACCCCA					
67_Ogar	TCATGACTCCAGGAACAAAAGATGGCCTTGGGACCCAT-----	GTAGAAGACGTCCTCAACCCCA					
38_Nleu	TGGAATGCCCCGGGCCTGGAATAATGGAGTCCCTCTCATTTGGCCCCCTCTTCTTCATTG-----	CCC					
27_Cjac	TGAGACTCCAGGTACAGAAGGCAGCATTGTGATGCCAGGTGCCGAAGATGATGTGCTGACCCCA						
98_Mmul	TTGAGACTACAGGTATGGAAGGCGGCGTTGCGATGCCAGGTGCCGAAGATGATGTGGTGACTCCA						
41_Ptro	CTGAGACTACAGGTTTGGAAGGCGGCGTTGCCATGCCAGGTGCCGAAGATGATGTGGTGACTCCA						
93_Tsyr	TTGTGACTCCAGGTGGGCAAGAGAGCACCTTGCCCCAAGGTGCAGAAGATGATTTGGTGACCCCA						



Subst



Indel

	400	410	420	430	440	450
51_Pabe	GGAGCCAGCGAAGACCGCTATAAGTCT	---	GGCTTGACAACTCTGGTAGCAACAAGTGTCAACAG			
89_Hsap	GGAACCCAGCGAAGACCGCTATAAGTCT	---	GGCTTGACAACTCTGGTGGCAACAAGTGTCAACAG			
93_Ggor	GGAACCCAGCGAAGACCGCTATAAGTCT	---	GGCTTGACAACTCTGGTGGCAACAAGTGTCAACAG			
14_Mmur	GGAGCCACTGAAGAGCCCTCTAAGCCTGCT	GGCCCGACAA	CCCCGATGGCAACGAGTGC	AAAAGAG		
67_Ogar	GCAGCTAGTGAAGAGCTCTCAAAGTCT	---	GGCTTCACAA	CCCTGGTGACAA	CAGGTGCCATGAG	
38_Nleu	AGTTCAGCTGCAGAAACCCCTCAAAGTG	---	TTGCCCTCAA	CTTTGGGAGGGGGTACTGTGCAGAC		
27_Cjac	GGAGCTGGTGAAGACCTCTCTACGGCT	---	GGCTTGACAACTCTGGTGGCAACGAGTGTCAAGAG			
98_Mmul	GGAACCCAGCGAAGACCGCTATAAGTCT	---	GGCTTGACAACTCCGGTAGCAACAAGTGTCAACAG			
41_Ptro	GGAACCCAGCGAAGACCGCTATAAGTCT	---	GGCTTGACAACTCTGGTGGCAACAAGTGTCAACAG			
93_Tsyr	GGAGCCCATGAAGAGTTCTACAATTCTCCT	GGCATGACAACTCTGGTGGCAACAAGCACCAAGAG				



Subst



Indel

	460	470	480	490	500	510	520
51_Pabe	TGTAACAGGCATTTCGCATCGAGGATCTGCCAACTTCAGAAAAGCACAGTCCATGGCGCAAGAACAAA						
89_Hsap	TGTAACAGGCATTTCGCATCGAGGATCTGCCAACTTCAGAAAAGCACAGTCCACGCGCAAGAACAAA						
93_Ggor	TGTAACAGGCATTTCGCATCGAGGATCTGCCAACTTCAGAAAAGCACAGTCCACGCGCAAGAACAAA						
14_Mmur	TACAGCGAGCCCTGACATCGAGGATCTGCCAA	CCCTGGGAAAAGCACGGTCCCTGCCAAAGAAGAAA					
67_Ogar	TGTGACAGACCCCTCATGTCTGAGGATCAGCCAACTGCAGAAAAGCACAGTCCACGCCCCAAAGAAGGC-						
38_Nleu	TGCCCTCCCAGTTTGTAGTCAGGGGAAAAGCGGAACTAGTGACACCAAGTCCACGCGCAAGAACAAA						
27_Cjac	TGTGACCGACATTGGCCCCGAGGATCTGCCAACTCCAGAAAAGCACAGCGCACCCCGAAGAAGGAA						
98_Mmul	TGTAACAGACATTTCACATCGAGGATCTGCCAA	CCCCAGAAAAGCACAGTCCACGCCCCAAGGACAAA					
41_Ptro	TGTAACAGGCATTTCGCATCGAGGATCTGCCAACTTCAGAAAAGCACAGTCCACGCGCAAGAACAAA						
93_Tsyr	TGTAACAGATGTTCCCCCTGAGGATCGGCCAA	CCCCAGAAAAGCACAGTCCATGCCCAGGAAGGAA					



Subst



Indel

	530	540	550	560	570	580
51_Pabe	GTCCAAGCG	CCACAGCCT	CAAACGT	TGGCCACCAGT	CACTCCACGGAGAAAG	TGGATGGAGACACA
89_Hsap	GTCCAAGCG	CCACAGCCT	CAAACGT	TGGCCACCAGT	CACTCCACGGAGAAAG	TGGATGGAGACACA
93_Ggor	GTCCAAGCG	CCACAGCCT	CAAACGT	TGGCCACCAGT	CACTCCACGGAGAAAG	TAGATGGAGACACA
14_Mmur	GCCAGAGCACC	ACAGTCCCCAAT	GTGGCGACC	AGCCGCTCCACAGAT	AAAAGTGGGTGGAGAGACA	
67_Ogar	--CAGAGC	ACCCCCGT	CCCCAAGGGAGAT	GACGAGTCACTCT	GGGGAGAAAGTGGGGGGAGAGACC	
38_Nleu	GTCCAAGCG	CCACAGCCT	CAAACGT	TGGCCACCAGT	CACTCCACGGAGAAAG	TGGATGGAGACACA
27_Cjac	GTCCGAGCACC	ACAACTC	AAACAT	TGGCAACCAGT	CACTCCAGGGAGAAAG	TGGATGGAGAGACA
98_Mmul	GTCCGAGCACC	ACAGCCT	CAAATGT	TGGCAACCAGT	CACTCCACAGACAAAAGTGGATGGAGACACA	
41_Ptro	GTCCAAGCG	CCACAGCCT	CAAACGT	TGGCCACCAGT	CACTCCACGGAGAAAG	TGGATGGAGACACA
93_Tsyr	GTCAGAGTACC	ACAGCTTCAGACGT	AGCAACTAGTCACTCCAT	GGAGAAAGTGGGTGGAGAGACA		



Subst



Indel

	590	600	610	620	630	640	650
51_Pabe	CAGACAACAGTT	GAGAAAAGAT	TGGTTTGGCAACAGT	GACCCCTGGTTGGAAATCATAGTTGGGGTCTT			
89_Hsap	CAGACAACAGTT	GAGAAAAGAT	TGGTTTGTCAACAGT	GACCCCTGGTTGGAAATCATAGTTGGGGTCTT			
93_Ggor	CAGACAACAGTT	GAGAAAAGAT	TGGTTTGGCAACAGT	GACCCCTGGTTGGAAATCATAGTTGGGGTCTT			
14_Mmur	CGGGTAACAGTT	GACAAAGAT	TGGTTTGGCAGACAGT	GACCCCTGGTTGGAAATCATAGTTGGGGTCTT			
67_Ogar	CAGACAACAGTT	GAGAAAAGAT	TGGTTTGGCAGCGGT	GACCCCTGGTTGGAAATCATAGTTGGGGTCTT			
38_Nleu	CAGACAACAGTT	GAGAAAAGAT	TGGTTTGGCAACAGT	GACCCCTGGTTGGAAATCATAGTTGGGGTCTT			
27_Cjac	CAGATAACAGTT	GACAAAGAT	TGGTTTGGCAACAGT	GACCCCTGGTTGGAAATTAATAGTTGGAGTCTT			
98_Mmul	CAGACAGCAATT	GAGAAAAGAT	TGGTTTGGCGACAGT	GACCCCTAGTTGGAAATCATCGTCGGGGTCTT			
41_Ptro	CAGACAACAGTT	GAGAAAAGAT	TGGTTTGGCAACAGT	GACCCCTGGTTGGAAATCATAGTTGGGGTCTT			
93_Tsyr	CAAAACAACAA	TTGAGAAAAGAT	TGGTTTGGCGACAGT	GACCCCTGGTTGGAAATTAATAGTTGGGGTCTT			

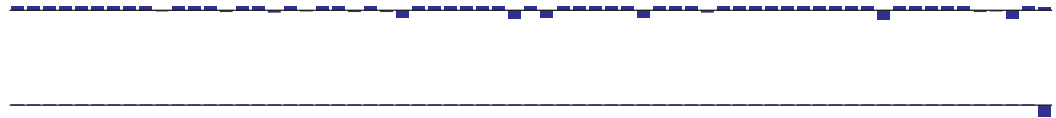


Subst



Indel

	660	670	680	690	700	710																																																										
51_Pabe	A	C	T	A	G	C	C	A	T	T	G	G	C	T	T	C	A	T	T	G	G	T	G	G	A	A	T	C	A	T	C	G	T	T	G	T	T	A	T	G	C	G	A	A	A	A	A	T	G	T	C	G	G	G	A	A	G	G	T	A	C	T		
89_Hsap	A	C	T	A	G	C	C	A	T	C	G	G	C	T	T	C	A	T	T	G	G	T	G	C	A	A	T	C	A	T	C	G	T	T	G	T	T	A	T	G	C	G	A	A	A	A	A	T	G	T	C	G	G	G	A	A	G	G	T	A	C	T		
93_Ggor	A	C	T	A	G	C	C	A	T	C	G	G	C	T	T	C	A	T	T	G	G	T	G	C	A	A	T	C	A	T	C	G	T	T	G	T	T	A	T	G	C	G	A	A	A	A	A	T	G	T	C	G	G	G	A	A	G	G	T	A	C	T		
14_Mmur	A	C	T	A	G	C	C	A	T	T	G	G	C	T	C	C	T	T	G	G	C	G	G	A	T	C	A	T	C	A	T	T	G	T	G	G	T	A	T	G	A	G	A	A	A	A	A	T	G	T	C	G	G	G	A	A	G	A	T	A	C	T		
67_Ogar	A	C	T	A	G	C	C	A	T	T	G	G	C	T	T	C	C	T	T	G	G	T	G	G	G	A	T	C	A	T	C	A	T	T	G	T	G	G	T	A	T	G	C	G	A	A	A	A	A	T	G	T	C	T	G	G	A	A	G	G	T	A	C	T
38_Nleu	A	C	T	A	G	C	C	A	T	T	G	G	C	T	T	C	A	T	C	G	G	T	G	G	A	T	C	A	T	C	A	T	T	G	T	G	G	T	A	T	G	C	G	A	A	A	A	A	T	G	T	C	G	G	G	A	A	G	G	T	A	C	-	
27_Cjac	A	C	T	A	G	C	C	A	T	T	G	G	C	T	T	C	A	T	T	G	G	T	G	G	A	T	C	A	T	C	G	T	T	G	T	T	A	T	G	C	G	A	A	A	A	A	T	G	T	C	G	G	G	A	A	G	G	C	C	-				
98_Mmul	A	C	T	A	G	C	C	A	T	T	G	G	C	T	T	C	A	T	T	G	G	T	G	G	G	A	T	C	A	T	C	G	T	T	G	T	G	T	A	T	G	C	G	A	A	A	A	A	T	G	T	C	G	G	G	A	A	G	G	T	A	C	T	
41_Ptro	A	C	T	A	G	C	C	A	T	C	G	G	C	T	T	C	A	T	T	G	G	T	G	G	A	T	C	A	T	C	G	T	T	G	T	G	T	A	T	G	C	G	A	A	A	A	A	T	G	T	C	G	G	G	A	A	G	G	T	A	C	T		
93_Tsyr	A	C	T	A	G	C	C	A	T	T	G	G	C	T	T	C	A	T	T	G	G	T	G	G	G	A	T	C	A	T	C	A	T	T	G	T	G	T	A	T	G	C	G	A	A	A	A	A	T	G	T	C	C	G	G	A	A	G	T	T	C	T		



Indel

	720				
51_Pabe	C	G	C	C	C
89_Hsap	C	G	C	C	C
93_Ggor	C	G	C	C	C
14_Mmur	C	A	C	C	C
67_Ogar	C	G	-	-	-
38_Nleu	-	-	-	-	-
27_Cjac	-	-	-	-	-
98_Mmul	C	G	-	-	-
41_Ptro	C	G	C	C	C
93_Tsyr	C	G	C	C	C



Subst



Indel