

	10	20	30	40	50	60
31_Pabe	ATGGGCAGCCGGCCCCG	CAGCCCCAGCGCCTTCCCT	TGCGCCCTGGTGGGGAC	CAGCAGCCAGGAGG		
21_Ptro	ATGGTCAGCCGGCCCCG	CAGCCCCAGCGCCTTCCCT	TGAGCCCTGGTGGGGAC	CAGCAGCCAGGAGG		
38_Ogar	ATGGGCAGTCGACCCCC	GAAGCCCCAGCGCCGGCCCCG	CACCCCTGGTGGGAGAC	CCGCAGCCCGGAGG		
24_Mmul	ATGGGCAGCCGGCCCCG	CAGCCCCAGAGCTCGCCCT	TGCGCCCTGGTGGGGAC	CAGCGGCCAGGAGG		
68_Hsap	ATGGTCAGCCGGCCCCG	CAGCCCCAGCGCCTTCCCT	TGCTCCCTGGTGGGGAC	CAGCAGCCAGGAGG		
88_Mmul	ATGGGCAGCCGGCCCCG	CAGTCCCAGCGCCTTGCCCT	TGCGCCCTGGTGGGGAC	CAGCAGCCAGGAGG		
04_Mmul	ATGGGCAGCCGGCCCCG	CAGCCCCAGCGCCTTGCCCT	TGCGCCCTGGTGGGGGAC	CAGCAGCCAGGAGG		
53_Cjac	ATGGGCAGCCGACCCCC	GACCCCCAGCGCCTTGCCCT	TGCGCCCTGGTGGGGAT	CGCAGCCAGGAGG		
86_Nleu	ATGGGCAGCCGGCCCCG	CAGCCCCAGCGCCTTCCCT	TGCGCCCTGGTGGGGAC	CAGCAGCCAGGAGG		
06_Cjac	ATGGGCAGCCGACCCCC	GACCCCCAGCGCCTTGCCCT	TGCGCCCTGGTGGGGAC	CAGCAGCCAGGAGG		
05_Ogar	ATGGGCAGACGACCCCC	GAAGCCCCAGCGCCGGCCA	ACGCACCCCTGGTGGGGAC	CCGCAGCCCGGAGG		
61_Ggor	ATGGGCAGCCGGCCCCG	CAGCCCCAGCGCCTTGCCCT	TGCGCCCTGGTGGGGAC	CAGCAGCCAGGAGG		
32_Pabe	ATGGGCAGCCGGCCCCG	CAGCCCCGGCGCCTTCCCT	TGCGCCCTGGTGGGGAC	CAGCAGCCAGGAGG		
28_Ptro	ATGGGCAGCCGGCCCTG	CAGCCCCAGCGCCTTGCCCT	TGCGCCCTGGGGGGGAC	CAGCAGCCAGGAGG		
49_Hsap	ATGGGCAGCCGGCCCCG	CAGCCCCAGCGCCTTCCCT	TGCGCCCTGGTGGGGAC	CAGCAGCCAGGAGG		
48_Hsap	ATGGGCAGCCGGCCCTG	CAGCCCCAGCGCCTTGCCCT	TGCGCCCTGGTGGGGAC	CAGCAGCCAGGAGG		
67_Ptro	ATGGGCAGCCGGCCCCG	CAGCCCCAGCGCCTTCCCT	TGAGCCCTGGTGGGGAC	CAGCAGCCAGGAGG		
88_Nleu	ATGGGCAGCCGGCCCCG	CAGCCCCAGCGCCTTGCCCT	TGCGCCCTGGTGGGGAC	CAGCAGCCAGGAGG		
33_Pabe	ATGGGCAGCCGGCCCCG	CAGCCCCAGCGCCTTGCCCT	TGCGCCCTGGTGGGGGAC	CAGCAGCCAGGAGG		
31_Ggor	ATGGGCAGCCGGCCCCG	CAGCCCCAGTGCCTGCCTT	TGCGCCCTGGTGGGGAC	CAGCAGCCAGGAGG		
87_Nleu	ATGAGCAGCCGGCCCCG	CAGCCCCAGCGCCTTGCCCT	TGCGCCCTGGTGGTGG	---GAGCAACCAGGAGG		

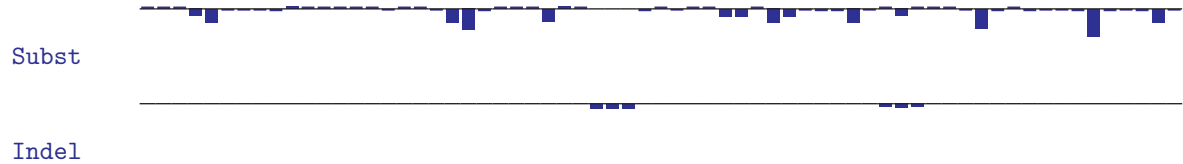


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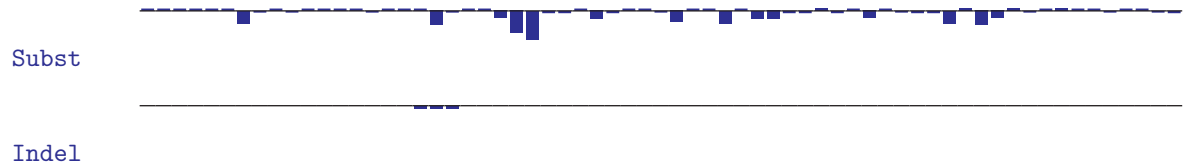


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	70	80	90	100	110	120	130
31_Pabe	A	C	C	C	G	C	C
21_Ptro	A	C	C	C	G	C	C
38_Ogar	A	C	C	C	G	C	C
24_Mmul	A	C	C	C	G	C	C
68_Hsap	A	C	C	C	G	C	C
88_Mmul	A	C	C	A	G	C	C
04_Mmul	A	C	C	G	C	C	C
53_Cjac	A	C	C	G	A	C	C
86_Nleu	A	C	C	C	G	C	C
06_Cjac	A	C	C	G	C	C	C
05_Ogar	A	C	C	G	C	C	C
61_Ggor	A	C	C	G	C	C	C
32_Pabe	A	C	C	G	C	C	C
28_Ptro	A	C	C	A	G	C	C
49_Hsap	A	C	C	G	C	C	C
48_Hsap	A	C	C	A	G	C	C
67_Ptro	A	C	C	G	C	C	C
88_Nleu	A	C	C	A	G	C	C
33_Pabe	A	C	C	A	G	C	C
31_Ggor	A	C	C	A	G	C	C
87_Nleu	A	C	C	C	G	C	C



	140	150	160	170	180	190
31_Pabe	CCAGCCTGGAAGACCCGGCGGGGACCCCGCCGTGGGCGCGCTCACCGCCGTAGTGGTCCCTGGCC					
21_Ptro	CCAGCCTGGAAGACCCGGCGGGGGGACCCGGCCGTGGACGGGCTCACCTCCATAGTGGTCCCTGGCC					
38_Ogar	CCAGCCTGGAAGACTCGGTGGGGCCCTCGACCGCGGACACCCTTACCTCCGTCCGTGGTCCCTGGCC					
24_Mmul	CCAGCCTGGAAGACCCG---GGGACCCCGCCGTGGGCGCGCTCACCTCCGTAGTGGTCCCTGGCC					
68_Hsap	CCAGCCTGGAAGACCCGGCGGGGGACCCGGCCGTGGACGGGCTCACCTCCATAGTGGTCCCTGGCC					
88_Mmul	CCAGCCCGGAAGACCCGGCGGGGATCCCGCCGTGGACGGGCTCACCTCCGTGGTGGTCCCTGGCC					
04_Mmul	CCAGCCTGGAAGACCCGGTGGGGATCCCGCCGTGGGCGCGGTCATCTCCGTGGTGGTCCCTGGCC					
53_Cjac	CCAGCCTAGGAGACCCGGTGGGGGCCCCGGCCGGGGACTCGCTCACCTTCGTGATGGTCCCTGGCC					
86_Nleu	CCAGCCTGGAAGACCCGGCAGGAACCCCGCCGTGGGCGCGCTCACCTCCGTAGTCCGTCCCTGGCC					
06_Cjac	CCAGCCTGGAAGACCCGGCGGGGGCTCCAGCCGGGACGGGCTCATCTTCGTGGTGGTCCCTGGCT					
05_Ogar	CCAGCCTGGAAGACTCGGCGGGGACCCCGACCCCGGACGTCCTCACCTCAGTCCGTGGTCCCTGGCC					
61_Ggor	CCAGCCTGGAAGACCCGGCGGGGACCCCGCCATGGGCGCGCTCACCTCCATAGTGGTCCCTGGCC					
32_Pabe	CCAGCCTGGAAGACCCGGCGGGGGGCCCCGGCCGTGGACGTGCTCACCTCCATAGTGGTCCCTGGCC					
28_Ptro	CCAGCCCGGAAGACCCGGCGGGGACCCCGCCGTGGACGGGCTCACCTCCATGATGGTCCCTGGAC					
49_Hsap	CCAGCCTGGAAGACCCGGCGGGTACCCCGCCGTGGGCGCGCTCACCTCCATAGTGGTCCCTGGCC					
48_Hsap	CCAGCCCGGAAGACCCGGCGGGGACCCCGCCGTGGACGGGCTCACCTCCATGGTGGTCCCTGGAC					
67_Ptro	CCAGCCTGGAAGACCCGGCGGGTACCCCGCCGTGGACGGGCTCACCTCCATAGTGGTCCCGGCC					
88_Nleu	CCAGCCCGGAAGACCCGGCGGGGACCCCGCCGTGGACGGGCTCACCTCCGTGGTGGTCCCTGGCC					
33_Pabe	CCAGCCTGGAAGACCCGGCGGGGACCCCGCCGTGGACGGGCTCACCTCCGTGGTGGTCCCTGGCC					
31_Ggor	CCAGCCCGGAAGACCCGGCGGGGACCCCGCCGTGGACGGGCTCACCTCCATAGTGGTCCCTGGCC					
87_Nleu	CCAGCCTGGAAGACCCGGCGGGGGCCCCGGCCGTGGACGGGCTCACCTCCATAGTGGTCCCTGGCC					



	200	210	220	230	240	250	260
31_Pabe	GCGGGCTGTGCCCTGCGTGTGCCCTGGACGACGTCGACCTTGTGCTGGAGCTCCCGCCAACGTC						
21_Ptro	GCGGGCTGTGCCCTGCGTGTGCCCTGGACGACGTCGACCTGGTGCTGGAGCCCGCACCACGTC						
38_Ogar	GCGGGCTGTGCCCTTGAAGTGCCCCCTGGACGACGTCGACCTGGTGCTGGAGCCCGCACCACGTC						
24_Mmul	GCGGGCTGTGCCCTGCGTGTGCCCTGGACGACGTTGACCTGGTGCTAGAGCCCGCACCACGTC						
68_Hsap	GCGGGCTGTGCCCTGCGTGTGCCCTGGACGACGTCGACCTGGTGCTGGAGCCCGCACCACGTC						
88_Mmul	GCGGGCTGTGCCCTGCGTGTGCCCTGGAGAACGTCGACCTGGTGCTGGAGCTCCGCGCCAATGTC						
	ACAGGCTGTGCCCTGCGTGTGCCCTGGACACCGTCGACCTGGTGCTGGAGCTCCCGCCGACATC						
53_Cjac	GCGGGCAGTTCCCTGAAGGTGTCCCTGAACGACGACAACTGGTGCTGGTGCCCGCGCCACGTC						
86_Nleu	GCGGGCTGTGCCCTGCGTGTGCCACTGGACGACGTCGACCTGGTACTGGAGCTCCCGCCAACGTC						
06_Cjac	GAGGGCTGTGCCCTGAAGGTGTCCCGGGACGACGTTGACCTGGTGCTGGAGCCCGCGCCACGTC						
05_Ogar	GCGGGCTGTGCCCTTGAAGTGCCCCCTGGACGACGTCGACCTGGTGCTGGAGCCCGCACCACGTC						
61_Ggor	GCGGGCTGTGCCCTGCGTGTGCCCTGGACGACGTCGACCTGGTGCTGGAGCTCCCGCCAACGTC						
32_Pabe	GCGGGCTGTGCCCTGCGTGTGCCCTGGACGACGTCGACCTTGTGCTGGAGCCCGCACCACGTC						
28_Ptro	GCGGGCTGTGCCCTGCGTGTGCCCTGGAGGACGTCGACCTGGTGCTGGAGCTCCGCGCCAATGTC						
49_Hsap	GCGGGCTGTGCCCTGCGTGTGCCCTGGACGACGTCGACCTGGTGCTGGAGCTCCCGCCAACGTC						
48_Hsap	GCGGGCTGTGCCCTGCGTGTGCCCTGGAGGACGTCGACCTGGTGCTGGAGCTCCGCGCCAATGTC						
67_Ptro	GCGGGCTGTGCCCTGCGTGTGCCCTGGACGACGTCGACCTGGTGCTGGAGCTCCCGCCAACGTC						
88_Nleu	GCAGGCTGTACCTTGCGTGTGACCTGGAGGACGTCGACTTGGTGCTGGAGCTCCGCGCCAATGTC						
33_Pabe	GCGGGCTGTGCCCTGCGTGTGCCCTGGAGGACGTCGACCTGGTGCTGGAGCTCCGCGCCAATGTC						
31_Ggor	GCGGGCTGTGCCCTGCGTGTGCCCTGGATGACGTCGACCTGGTGCTGGAGCCCGCACCACGTC						
87_Nleu	GCGGGCTGTGCCCTGCGTGTGCTCCTGGACGACATCGACCTGGTGCTGGAGCCCGCAGCAACGTC						



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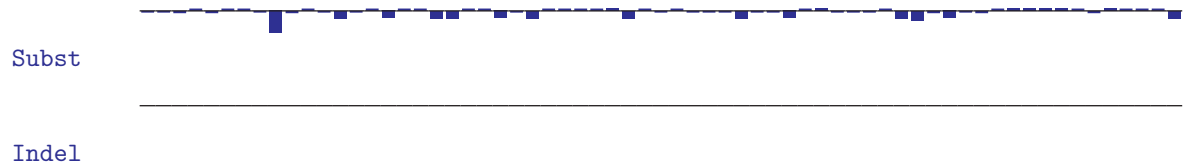
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31_Pabe	GATCCTGCGAGTGTCTCTCGATGGACACACCCCTCATCCTGATCCCCGAGGTCCCTCCTGAGCTCCG					
21_Ptro	GATCCTGCGAGTGTCTCTCGGTGGACACACCCCTCATCCTGATCCCCAGAGGTCCCTCCTGAGCTCCG					
38_Ogar	AGTCCTGCAAGTATCCTTCGAAGGGCACACCCCTCATCCTGGTCCCCGAGGTCCCTCCTAGGGTCCG					
24_Mmul	GATCCTGCGAGTGTCTCTCGGTGGACACACCCCTCATCCTGATCCCCGAGGTCCCTCCTGAGCTCCG					
68_Hsap	GATCCTGCGAGTGTCTCTCGGTGGACACACCCCTCATCCTGATCCCCAGAGGTCCCTCCTGAGCTCCG					
88_Mmul	GGTCCTGCGAGTGTCTCTTGGTGGACACACCCCTCATCCTGATCCCCGAGGTCCCTCCTAAGCTCCG					
04_Mmul	GATCCTGCGAGTGTCTCTCGGTGGACACACCCCTCATCCTGATCCCCGAGGTCCCTCCTGAGCTCCG					
53_Cjac	GATCATGCGAGTGTCTCTCGGTGGACACACCCCTCTTCCTGATCCCCGAGGTCCCTCCTGAGCTCCC					
86_Nleu	GATCCTGCGAGTGTCTCTCGATGGACACACCCCTCATCCTGATCCCCGAGGTCCCCCTGAGCTCTG					
06_Cjac	GATCATA CGAGTGTCTCTCGGTGGACAAAACCCCTCTTCCTGATCTCCGAGGTGTTCTGAGCTCCG					
05_Ogar	AGTCCTGCAAGTATCCTTCGAAGGGCACACCCCTCATCCTGGTCCCCGAGGTCCCTCCTAGGCTTGG					
61_Ggor	GATCCTGCGAGTGTCTCTCGATGGACACACCCCTCATCCTGATCCCCGAGGTCCCTCCTGAGCTCTG					
32_Pabe	GATCCTGCGAGTGTCTCTCGATGGACACACCCCTCATCCTTATCCCCGAGGTCCCTCCTGAGCTCCG					
28_Ptro	GGTCCTGCGAGTGTCTCTTGGTGGACACACCCCTCATCGTGATCCCCGAGGTCCCTCCTGAGCTCCG					
49_Hsap	GATCCTGCGAGTGTCTCTCGATGGACACACCCCTCATCCTGATCCCAGAGGTCCCTCCTGAGCTCTG					
48_Hsap	GGTCCTGCGAGTGTCTCTTGGTGGACACACCCCTCATCGTGATCCCCGAGGTCCCTCCTGAGCTCCG					
67_Ptro	GATCCTGCGAGTGTCTCTCGATGGACACACCCCTCATCCTGATCCCCGAGGTCCCTCCTGAGCTCTG					
88_Nleu	GGTCCTGCGAGTGTCTCTCGGTGGACACGCCCTCATCGTGATCCCCGAGGTCCCTCCTGAGCTCTG					
33_Pabe	GGTCCTGCGAGTGTCTCTCGGTGGACACACCCCTCATCGTGATCCCCGAGGTCCCTCCTGAGCTCCG					
31_Ggor	GATCCTGCGAGTGTCTCTCGGTGGACACACCCCTCATCCTGATCCCAGAGGTCCCTCCTGAGCTCCG					
87_Nleu	GATCCTGCGAGTGTCTCTCGGTGGACACACCCCTCATCCTGATCCCCGAGGTCCCTCCTGAGCTCCG					



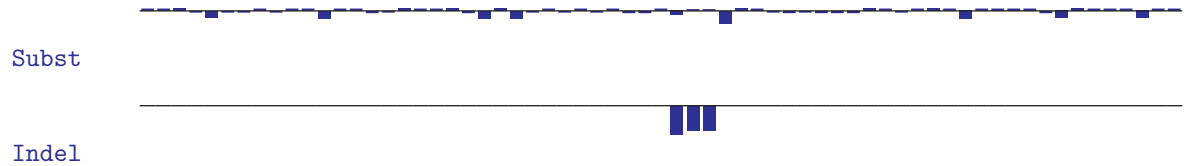
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	330	340	350	360	370	380	390
31_Pabe	T	C	G	A	C	G	C
21_Ptro	T	C	G	A	C	G	C
38_Ogar	T	C	G	A	C	A	C
24_Mmul	T	C	G	A	C	G	C
68_Hsap	T	C	G	A	C	G	C
88_Mmul	T	C	G	A	C	G	C
04_Mmul	T	T	G	A	C	G	A
53_Cjac	T	C	G	A	C	G	C
86_Nleu	T	C	G	A	C	G	C
06_Cjac	T	C	G	A	C	G	C
05_Ogar	T	C	A	A	G	A	T
61_Ggor	T	C	G	A	C	G	C
32_Pabe	T	C	G	A	C	G	C
28_Ptro	T	C	G	A	C	G	C
49_Hsap	T	C	G	A	C	G	C
48_Hsap	T	C	G	A	C	G	C
67_Ptro	T	C	G	A	C	G	C
88_Nleu	T	C	G	A	C	G	C
33_Pabe	G	C	G	A	C	G	C
31_Ggor	T	C	G	A	C	G	C
87_Nleu	T	C	G	A	C	G	C



	400	410	420	430	440	450
31_Pabe	GCTCTCAGGGAGGACGTCGTCGTCGAGCAGGAAGTCTTCTGCGCATCTGTCCCAGAGATCGCCGC					
21_Ptro	GCTGTCAGGGAGGACGTCGTCGTCGAGCTGGAA---	TTCTGCGCATCTGTCTCAGAGATCGCCGC				
38_Ogar	GCTCCTGGGGAGGAAATCGTCCTTGAGCAGCCATTCTTCCTCGAGTCTGTCCCAGAGATCGCCGC					
24_Mmul	GCTCTCAGGGAGGACGTCGTCGTCGAGCTGGAA---	TTCTGTGCATCTGTCCCAGAGATCGCCGC				
68_Hsap	GCTGTCAGGGAGGACGTCGTCGTCGAGCTGGAA---	TTCTGCGCATCTGTCCCAGAGATCGCCGC				
88_Mmul	GCTCACGGGGAAGACGTCGTCGTCAGCAGGAAGTCTTCTGCGCATCTGTCCCAGAGATCGCTGC					
04_Mmul	GCTCTCAGAGAGGACGTCGTCGTCGAGCAGGAAGTCTTCTGCGCATCTGTCCCAGAGATCGCCGC					
53_Cjac	GCTCTCGGGGAGGACGTCGTCGTCGAGCAGGAA---	TTCTGCGCATCTGTCCCAGAGGTCGCCGC				
86_Nleu	GCTCTCAGGGAGGACGTCGTCGTCGAGCAGGAA---	GTCTGCGCATCTGTCCCAGAGATCGCCGC				
06_Cjac	GCTCTCGGGGAGGACGTCGTAGTCGAGCAGGAA---	TTCTGCGCATCTGTCCCAGAGGTCGCCGC				
05_Ogar	GCTCCTGGGGAGGAAATCGTCCTCGAGCAGCCATTCTTCCTCACATCTGTCTCAGAGATCGCCGC					
61_Ggor	GCTCTCAGGGAGGACGTCGTCGTTGAGCAGGAAGTCTTCTGCGCATCTGTCCCAGAGATCGCCGC					
32_Pabe	GCTCTCAGGGAGGACGTCGTCGTCGAGCTGGAA---	TTCTGCGCATCTGTCCCAGAGATCGCCGC				
28_Ptro	GCTCACGGGGAAGACGTCGTCGTCGAGCAGGAAGTCTTCTGCGCATCTGTCCCAGAGATCGCTGC					
49_Hsap	GCTCTCAGGGAGGACGTCGTCGTTGAGCAGGAAGTCTTCTGCGCATCTGTCCCAGAGATCGCCGC					
48_Hsap	GCTCACGGGGAAGACGTCGTCGTCGAGCAGGAA---	GTCTGCGCATCTGTCCCAGAGATCGCTGC				
67_Ptro	GCTCTCAGGGAGGACGTCGTCGTTGAGCAGGAAGTCTTCTGCGCATCTGTCCCAGAGATCGCCGC					
88_Nleu	GCTCACGGGGAAGACGTCGTCCTTCGAGCAGGAA---	GTCTGCGCATCTGTCCCAGAGATCGCTGC				
33_Pabe	GCTCACGGGGAAGACGTCGTCGTCGAGCAGGAAGTCTTCTGCGCATCTGTCCCAGAGATCGCCGC					
31_Ggor	GCTGTCAGGGAGGACGTCGTCGTCGAGCTGGAA---	TTCTGCGCATCTGTCCCAGAGATCGCCGC				
87_Nleu	GCTCTCAGGGAGGACGTCGTCGTCGACCTGGAA---	TTCTGCGCATCCGTCCCAGAGTTCCGCCGC				



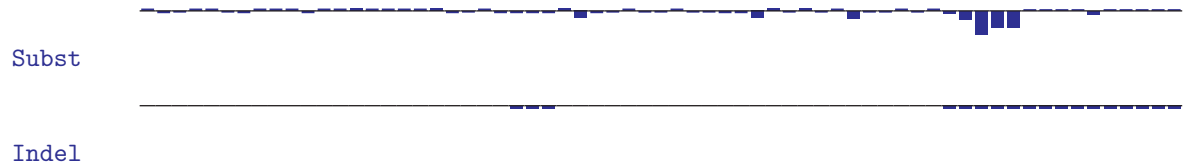
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31_Pabe	CCAGGAAGAGGCC	TACGAGGAGGAC	GCGGACCTTC	GAGTTCCCGGAG	CTCCGGAGGGAC	TCCGCGAG	
21_Ptro	CCAGGAAGAGGCC	TACGAGGAGGAT	GCGGACCCCGAG	TTCCCGGAGCT	CCGGATGGACT	CCCCAA	
38_Ogar	CCAAAAGGGGGC	TTCCACGACGAC	GCTGAGCCCC	TTCTGTCAGGCG	CCCCGGATGGAA	CCCTCCAG	
24_Mmul	CCAGGAAGAGGCC	TACGAGGAGGAG	GCGGACCCCGAG	TTCTTGGAGCT	CCGGATGGACT	CCCCAA	
68_Hsap	CCAGGAAGAGGCC	TACGAGGAGGAC	GCGGACCCCGAG	TTCCCGGAGCT	CCGGATGGACT	CCCCAA	
88_Mmul	CCAGGAAGAGGCC	TACGAGGAGGAC	GCGGACTCTGA	ATTCCCGGAG	CTCCGCATGGACT	CCGCAT	
04_Mmul	CCAGGAAGAGGCC	TACGAGGAGGAG	GCGGACCCCGAG	TTCCCGGAGCT	CCGGATGGACT	CCCCAA	
53_Cjac	CCAGGAGGAGGT	GTTACGAGGAGG	ACGCGGACTCCG	AGTTCCAGGAG	CTCTGGATGGACT	CCCCAG	
86_Nleu	CCAGGAAGAGGCC	TACGAGGAGGAC	GCGGACCGCGAG	TTTCCCGGAG	CTCCGGATGGAC	GCGCGCAG	
06_Cjac	CCAGGAGGAGGT	GTTACGAGGAGG	ACGCGGACTCCG	AGTTCCAGGAG	CTCTGGATGGACT	CCCCAG	
05_Ogar	CCAAAAGGGGGC	TTCCACGAGGAC	ACGGAGCCCC	TACGTCCCTGGAG	CCCCGGATGGAA	CCCTCCAG	
61_Ggor	CCAGGAAGAGGCC	TACGAGGAGGAC	GCGGACCCCGAG	TTCCCGGAGCT	CCAGATGGACT	CCGCAG	
32_Pabe	CCAGGAAGAGGCC	TACGAGGAGGAC	GCGGACCCCGAG	TTCCCGGAGCT	CCGGATGGACT	CCCCAA	
28_Ptro	CGAGGAAGAGGCC	TACGAGGAGGAC	GCGGACTCTGAG	TTCCCGGAGCT	CTGGATGGACT	CCGCAG	
49_Hsap	CCAGGAAGAGGCC	TACGAGGAGGAC	GCGGACCCCGAG	TTTCCCGGAG	CTCCAGATGGACT	CCGCAG	
48_Hsap	CGAGGAAGAGGCC	TACGAGGAGGAC	GCGGACTCTGAG	TTCCCGGAGCT	CTGGATGGACT	CCGCAG	
67_Ptro	CCAGGAAGAGGCC	TACGAGGAGGAC	GCGGACCCCGAG	TTTCCCGGAG	CTCCAGATGGACT	CCGCAG	
88_Nleu	CCAGGAAGAGGCC	TACGAGAAGGAC	GCGGACTCTGA	ATTCCCGGAG	CTCTGGATGGACT	CCGCAG	
33_Pabe	CCAGGAAGAGGCC	TACGGGGAGGAC	GCGGACTCTGA	ATTTCCCGGAG	CTCTGGATGGACT	CCGCAG	
31_Ggor	CCAGGAAGAGGCC	TACGAGGAGGAC	GCGGACCCCGAG	TTCCCGGAGCT	CCGGATGGACT	CCCCAG	
87_Nleu	CCAGGAAGAGGCC	TACGAGGAGGAC	GCGGACCCCGAG	TTCCCGGTGCT	GCGGATGGACT	CCCCAA	



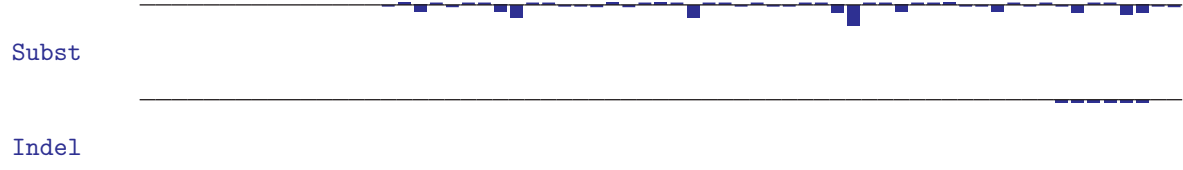
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	530	540	550	560	570	580
31_Pabe	CCAGCTCAGCCGCTGGGCTCTACTCCTCCGCTAGAAAGTATGTTTCAGCCCCCTACCGGGAGGGCCCC					
21_Ptro	CCGGCTCAGCCGCTGGGCTCTACCCCTCCCTCTAGAAGTATGTTTCATCCCCCTACCGGGAGGGCCCC					
38_Ogar	CTGGCTTAGCTGCTGGGCTCCAGCCATCTGCTAGAAGGGTGTCCGGCCCC-----					
24_Mmul	CCGGCTCAGCCGCTGGGCTCTACCCCTCCGCTAGAAAGTATGTTTCAGCCCCCTACCGGGAGGGCCCC					
68_Hsap	CCGGCTCAGCCGCTGGGCTCTACCCCTCCCTCTAGAAGTATGTTTCATCCCCCTACCGGGAGGGCCCC					
88_Mmul	CCGGCTCAGCCGCTGGGCTCTACCCCTCCGCTAGAAAGTATGTTTCAGCCCCCTATCCGGGAGGGCCCC					
04_Mmul	CCGGCTCAGCCGCTGGGCTATACCCCTTCGCTAGTGGTGTGTTTCAGTCTCTACCGGGAGGGCCCC					
53_Cjac	CCGGCTCAGCCGCTGGGCTCTACCACTCCGCTAGAAGTATGTTTCGGCCCCCTACCGAGGAGAGCCCC					
86_Nleu	CCGGCTCAGCCGCTGGGCTCTACTCCTCCGCTAGAAAGTATGTTTCAGCCCCCTGTTGGGAGGGCCCC					
06_Cjac	CCGGCTCAGCCGCTGGGCTCTACCCCTCCGCTAGAAAGTATATTCGGCCCCCTACCGGGAGGGCCCC					
05_Ogar	CCGGCTCAGCCGCTGGGCTCCAGCCCCCTCCGCTAGAAAGGTGTCCAGCCCC-----					
61_Ggor	CCGGCTCAGCCGCTGGGCTCTACTCCTCCGCTAGAAAGTATGTTTCAGCCCCCTACCGGGAGGGCCCC					
32_Pabe	CCGGCTCAGCCGCTGGGCTCTACCCCTCCCTCTAGAAGTATGTTTCAGCCCCCTATTGGGAGGGCCCC					
28_Ptro	CCGGCTCAGCCGCTGGGCTCTACCCCTCCGCTAGAAAGTATGTTTCAGCCCCCTACCGGGAGGGCCCC					
49_Hsap	CCGGCTCAGCCGCTGGGCTCTACTCCTCCGCCAGAAGTATGTTTCAGCCCCCTACCGGGAGGGCCCC					
48_Hsap	CCGGCTCAGCCGCTGGGCTCTACCCCTCCGCTAGAAAGTATGTTTCAGCCCCCTACCGGGAGGGCCCC					
67_Ptro	CCGGCTCAGCCGCTGGGCTCTAC---TCCGCCAGAAGTATGTTTCAGCCCCCTACCGGGAGGGCCCC					
88_Nleu	CCGGCCCCAGCCGCTGGGCTCTACCCCTCCGCTAGAAGTATGTTTCAGCCCCCTACCGGGAGGGCCCC					
33_Pabe	CCGGCTCAGCCGCTGGGCTCTACCCCTCCGCTAGAAAGTATGTTTCAGCCCCCTACCGGGAGGGCCCC					
31_Ggor	CCGGCTCAGCCGCTGGGCTCTACCCCTCCCTCTGGAAGTATGTTTCATCCCCCTACCGGGAGGGCCCC					
87_Nleu	CCGGCTCAGCCGCTGGGCTCTACCCCTTCTCTAGAAGTATGTTTCAGCCCCCTGTTGGGAGGGCCCC					



	590	600	610	620	630	640	650
31_Pabe	NNNNNNNNNNNNNNN	ATCCCAGAA	CCCTGTGCTCT	TGGCCCCCA	CCCCAGTTC	CAGAGAGAC	ACTC
21_Ptro	NNNNNNNNNNNNNNN	ATCCCAGAA	CCCTGTGCTCT	TGGCCCCCA	CCCCAGTTC	CAGAGAGAC	CGCTC
38_Ogar	NNNNNNNNNNNNNNN	ATCCCAGAA	CCCTGTGCTCT	TGGCCCCCA	CCCCAGTTC	CAGAGAGAC	CGCTC
24_Mmul	NNNNNNNNNNNNNNN	ATCCCAGAA	CCCTGTGCTCT	TGGCCCCCA	CCCCAGTTC	GGAG	-----AG
68_Hsap	NNNNNNNNNNNNNNN	ATCCCAGAA	CCCTGTGCTCT	TGGCCCCCA	CCCCAGTTC	CAGAGAGAC	CGTTC
88_Mmul	NNNNNNNNNNNNNNN	ATCCCAGGG	CCCTGTGCTCT	TGGCCCCCA	CCCCAGTTC	CAGAGAGAC	CGCTC
04_Mmul	NNNNNNNNNNNNNNN	ATCCCAGGG	CCCTGTGCTCT	TGGCCCCCA	CCCCAGTTC	CAGAGAGAC	CTCTC
53_Cjac	NNNNNNNNNNNNNNN	ATCCCAGAG	CCCTGTGCTCT	TGGCCCCCA	CCCCAGTTC	CAGAGAGAC	CGCTC
86_Nleu	NNNNNNNNNNNNNNN	ATCCCAGAA	CCCTGTGCTCT	TGGCCCCCA	CCCCAGTTC	GGAGAGAC	CGCTC
06_Cjac	NNNNNNNNNNNNNNN	ATCCCAGAG	CCCTGTGCTCT	TGGCCCCCA	CCCCAGTTC	CAGAGAGAC	CGCTC
05_Ogar	NNNNNNNNNNNNNNN	ATCCCAGAA	CCCTGTGCTCT	TGGCCCCCA	CCCCAGTTC	CAGAGAGAC	CGATC
61_Ggor	NNNNNNNNNNNNNNN	ATCCCAGAA	CCCTGTGCTCT	TGGCCCCCA	CCCCAGTTC	CAGAGAGAC	ACTC
32_Pabe	NNNNNNNNNNNNNNN	ATCCCAGAA	CCCTGTGCTCT	TGGCCCCCA	CCCCAGTTC	CAGAGAGAC	CGCTC
28_Ptro	NNNNNNNNNNNNNNN	ATCCGAGGG	CCCTGTGCTCT	TGGCCCCCA	CCCCAGTTC	CAGAGAGAC	CGCTC
49_Hsap	NNNNNNNNNNNNNNN	ATCCCAGAA	CCCTGTGCTCT	TGGCCCCCA	CCCCAGTTC	CAGAGAGAC	ACTC
48_Hsap	NNNNNNNNNNNNNNN	ATCCGAGGG	CCCTGTGCTCT	TGGCCCCCA	CCCCAGTTC	CAGAGAGAC	CGCTC
67_Ptro	NNNNNNNNNNNNNNN	ATCCCAGAA	CCCTGTGCTCT	TGGCCCCCA	CCCCAGTTC	CAGAGAGAC	ACTC
88_Nleu	NNNNNNNNNNNNNNN	ATCCGAGGG	CCCTGTGCTCT	TGGCCCCCA	CCCCAGTTC	CAGAGAGAC	CGCTC
33_Pabe	NNNNNNNNNNNNNNN	ATCCGAGGG	CCCTGTGCTCT	TGGCCCCCA	CCCCAGTTC	CAGAGAGAC	CGCTC
31_Ggor	NNNNNNNNNNNNNNN	ATCCCAGAA	CCCTGTGCTCT	TGGCCCCCA	CCCCAGTTC	CAGAGAGAC	CGCTC
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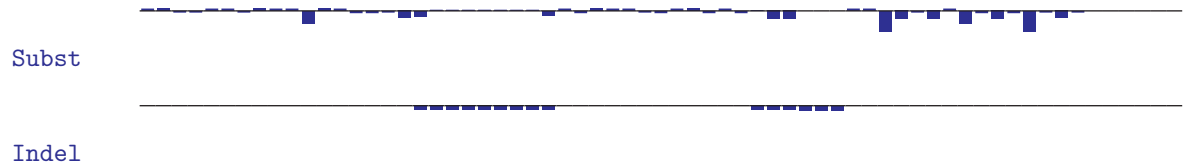
	660	670	680	690	700	710
31_Pabe	TCCACGCCCCATCTTCGACCCGGAGTTCCACCTTCTGGAGCCTGTCCCCAGCTCACCTCTCCAAAC					
21_Ptro	TCCACGCCCCATCTTTGACCTGGAATTCCGCGCTTCTGGAGCCTGTCCCCAGCTCACCTCTCCAAAC					
38_Ogar	CCCCAAACCCCATGTTTGACCTGGAATTCCACCTTCTGGAGCCTTTCCCCAGCTCACCACTCCAAAC					
24_Mmul	CGTACGCCCCGTCTTCGACCCGGAATTCCACCTTCTGGAGCCTGTCCCCAGCTCACCTCTCCAAAC					
68_Hsap	TCCACGCCCCATCTTTGACCTGGAATTCCGCGCTTCTGGAGCCTGTCCCCAGCTCACCTCTCCAAAC					
88_Mmul	TCCAAGCCCCATCTTCGACCCGGAATTCCACCTTCTGGAGCCTGTCCCCAGCTCACCTCTCCAAAC					
04_Mmul	TCCACGCCCCATCTTCGACCCAGAATTCCACCTTCTGGAGCCTGTCCCCAGCTCACCTCTCCAAAC					
53_Cjac	TCCACGCCCCAACTGCGACCCAGGAATTCCACTTTCTGGAGCCTGTTCCTCCACCTCACCTCTGCAAC					
86_Nleu	TCCACGCCCCATCTTCGACCCGGAATTCCGCGCTTCTGGAACTGTCCCCAGCTCACCTCTCCAAAC					
06_Cjac	TCCACGCCCCATCTGCGACCCAGGAATTCCACTTTCTGGAGCCTGTTCCTCCAGCTCACCTCTCCAAAC					
05_Ogar	CCCCAAACCCCATGTTTCGACCTGGAATTCCACCTTCTGGAGCCTTTCCCCAGCTCACCACTCCAAAC					
61_Ggor	TCCAGGCCCCTTCTTCGACCCGGAATTCCGCGCTTCTGGAGCCTGTCCCCAGCTCACCTCTCCAAAC					
32_Pabe	TCCACGCCCCATCTTCGACCTGGAATTCCGCGCTTCTGGAGCCTGTCCCCAGCTCACCTCTCCAAAC					
28_Ptro	TCCACGCCCCATCTTCGACCTGGAATTCCACTTTCTGGAGCCTGTCCCCAGCTCACCTCTCCAAAC					
49_Hsap	TCCAGGCCCCTTCTTCGACCCGGAATTCCGCGCTTCTGGAGCCTGTCCCCAGCTCACCTCTCCAAAC					
48_Hsap	TCCACGCCCCATCTTCGACCTGGAATTCCACTTTCTGGAGCCTGTCCCCAGCTCACCTCTCCAAAC					
67_Ptro	TCCAGGCCCCTTCTTCGACCCGGAATTCCGCGCTTCTGGAGCCTGTCCCCAGCTCACCTCTCCAAAC					
88_Nleu	TCCACGCCCCATCTTCGACCTGGAATTCCACCTTCTGGAGCCTGTCCCCAGCTCACCTCTTCAAC					
33_Pabe	TCCACGCCCCATTTTCGACCTGGAATTCCACTTTCTGGAGCCTGTCCCCAGCTCACCTCTCCAAA					
31_Ggor	TCCACGCCCCACCTTTGACCTGGAATTCCGCGCTTCTGGAGCCTGTCCCCAGCTCACCTCTCCAAAC					
87_Nleu	TCCATGCCCCATCTTCGACCTCGAATTCCGCGCTTCTGCAGCCTGTCCCCAGCTCACCTCTCCAAAC					



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	720	730	740	750	760	770	780
31_Pabe	CTCTACCTCCCTCTCCGCGCGTGGGGAGTCCAGGTCCC	-----	CACGCGCACCCGCCGNNNNNN				
21_Ptro	CTCTACCTCCCTCTCCGTGCGTGGGGAGTCCAGGTCCC	-----	CACGCGCGCTCGCCGNNNNNN				
38_Ogar	CTCTACCTCCCTTCTCCA	-----	AGTCCAAGTCCACGTCCCCACGCGCGACCCAGAGNNNNNN				
24_Mmul	CTCTACCTCCCTCTCCGCGCGTGGGGAGTCCAGGTCCC	-----	CACGCTCGCCCGCCGNNNNNN				
68_Hsap	CTCTACCTCCCTCTCCGTGCGTGGGGAGTCCAGGTCCC	-----	CACGCGCGCTCGCCGNNNNNN				
88_Mmul	CTCCACCTCCCTCTCCA	-----	AGTCCGGGTCCC-----CACGAGCGCCCGGAGNNNNNN				
04_Mmul	CTCTACCTCCCTCTCCGCGCGTGGGGAGTCCAGGTCCC	-----	CATGCGCGCCACCTNNNNNN				
53_Cjac	CTCTACCTCCCTCTCTG	-----	AGTCCAGGTCCC-----CAAGCGCGCCAGAGNNNNNN				
86_Nleu	CTCTACTTCCCTCTCCGCGCGTGGGGAGTCCAGGTCCC	-----	CACGCGCACCCGCTGNNNNNN				
06_Cjac	CTCTACCTCCCTCTTCG	-----	AGTCCAGGTCCC-----CACACGCGCCGGGAGNNNNNN				
05_Ogar	CTCTACCTCCCTTCCCCA	-----	AATCCAGGTTCCCAC-----CACACACGCTCTGAGNNNNNN				
61_Ggor	CTCTACCTCCCTCTCCGCGCGTGGGGAGTCCAGGTCCC	-----	CACGCGCACCCGCCGNNNNNN				
32_Pabe	CTCTACCTCCGTCTCCGTGCGTGGGGAGTCCAGGTCCC	-----	CACGCGCACCCGCCGNNNNNN				
28_Ptro	CTCTACCTCCCTCTCCG	-----	AGTCCAGGTCCC-----CACGCGCGCCCGGAGNNNNNN				
49_Hsap	CTCTACCTCCCTCTCCGCGCGTGGGGAGTCCAGGTCCC	-----	CACGCGCACCCGCCGNNNNNN				
48_Hsap	CTCTACCTCCCTCTCCG	-----	AGTCCAGGTCCC-----CACGCGCGCCCGGAGNNNNNN				
67_Ptro	CTCTACCTCCCTCTCCGCGCGTGGGGAGTCCAGGTCCC	-----	CACGCGCGCCCGCCGNNNNNN				
88_Nleu	CTCTACCTCCCTCTCCG	-----	AGTCCAGGTCCC-----CACGCGCGCCCGGAGNNNNNN				
33_Pabe	CTCTACCTCCGTCTCCG	-----	AGTCCAGGTCCC-----CACGCGCGCCCGGAGNNNNNN				
31_Ggor	CTCTACCTCCCTCTCCGTGCGTGGGGAGTCCAGGTCCC	-----	CATGCGCGCTCGCCGNNNNNN				
87_Nleu	CTTTACCTCCCTCTCCGTGCGTGGGAAGTCCAGGTCCC	-----	CAAGCGCGCCCGCCGNNNNNN				



	790	800	810	820	830
31_Pabe	NNNCTCCCGAAACGCCCTCCGTGCAAGGCCCGCAGACGACTGTTCCAGGAA				
21_Ptro	NNNCTCCCGGAACGCCCTCCGTGCAAGGCCCGGAGACGCCGTGTTCCAGGCA				
38_Ogar	NNNCACTCTCCTCAGCCTCCGTGCAAGGCCCGGAGATGCTTGTTCGGAA				
24_Mmul	NNNCTACCAGAACGCCCTCAGTGAAGGCCCGGAGACGCCGTGTTCCAGGCA				
68_Hsap	NNNCTCCCGGAACGCCCTCCGTGCAAGGCCCGGAGACGCCGTGTTCCAGGCA				
88_Mmul	NNNCTCCCAGAGCGCCCTCCGTGCAAGGCCCGGAGACGCCGTGTTCCAGGAA				
04_Mmul	NNNCTCCCGGAACGCCCTCCGTGCAAGGCCCGCAGACGACTGTTCCAGGAA				
53_Cjac	NNNCTCCCAGAGCGCCCTCTGTGCAAGGCCCGGAGACGACTGTTTCAGGAA				
86_Nleu	NNNCTCCCGAAACGCCCTCCATGCAAGGCCCGCAGACGACTGTTCCAGGAA				
06_Cjac	NNNCTCCCAGAGCGCCCTCCGTGCAAGGCCCGGAGACGACTGTTTCAGGAA				
05_Ogar	NNNCGCTCTCCCCGCCCTCCCTGTAAGGCCCGGAGAAGTTTGTTCAGGAA				
61_Ggor	NNNCTCCCGAAACGCCCTCCGTGCAAGGCCCGCAGACGACTGTTCCAGGAA				
32_Pabe	NNNCTCCCGGAACGCCCTCCGTGCAAGGCCCGCAGACGACTGTTCCAGGCA				
28_Ptro	NNNCTCCCAGAGCGCCCTCCGTGCAAGGTCCGAAGACGCCGTGTTCCAGGAA				
49_Hsap	NNNCTCCCGAAACGCCCTCCGTGCAAGGCCCGCAGACGACTGTTCCAGGAA				
48_Hsap	NNNCTCCCAGAGCGCCCTCCGTGCAAGGTCCGAAGACGCCGTGTTCCAGGAA				
67_Ptro	NNNCTCCCGAAACGCCCTCCGTGCAAGGCCCGCAGACGACTGTTCCAGGAA				
88_Nleu	NNNCTCCCAGAGCGCCCTCCGTGCAAGGCCCGGAGACGCCGTGTTCCAGGAA				
33_Pabe	NNNCTCCCAGAGCGCCCTCCGTGCAAGGCCCGGAGACGCCGTGTTCCAGGAA				
31_Ggor	NNNCTCCCGGAACGCCCTCCGTGCAAGGCCCGCAGACGCCGTGTTCCAGGCA				
87_Nleu	NNNCTCCCGGAACGCCCTCTGTGCAAGGCCCGGAGACGCCGTGTTCCAGGCA				



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