

1627555-1627762	1	CAAAC T GT TG ...CGAGGGGTAACCAAAAACCGAGTC CCTAAAAG GACCAACAAAAACACAC ACCA
1298951-1299182	1	TCA.....AAAGGAACAGAA G .AAAGTC GTAAAGGC.....ATGTGT CGG .GT CA
2317326-2317510	1	TACAG T .CGGTGA ACT CA CAAAAGGGGCGAA A ..AAAGTC ATAA TTGGTCAACTTT GC GT.....
266075-266302	1	GT CA C.....AAAAAG TCAACAGAG CA T CCCA
1336186-1336424	1	CAAAT TATCAAAGGA GGC CG GAGGAA GGTCAACGTAT CGC .CT CA
2261535-2261757	1	GGCAA AGG .AAAGTC ACAAAAAG TCGACAG CGT .CC CA
2373978-2374199	1	ACTCT TGAATAGACCAAA C .AAAGTC GT CAAAA AGGGTCACAAAAG CGCA AA AA
1279645-1279868	1	GAACCG CAAAGGCAGCAAAAGAAA AGCCAT ..CGGCGAA AGCCAAAGGGA CAT .CC CA
2363527-2363776	1	TACGG T .CGCGGA ACT GC CAAAGGA GGC GAA AG .AAAGC GACAAAAGAT CGTCGACAA AGCAT CC AA
659348-659617	1	TG CA GT.CGC CGAAC CG CA AGAGGGGGAGGG AC GAG AC .AAAGG CCAT .AAAAAGATAG TCGGAGGGGAT GT .CG CA
1401197-1401418	1	GAGGGCAAA AT .AAAGG CCATGAAAG GCAACAAAG CGT .TCC AA
10194-10372	1	TACAG T .CCC CAA ACTCT CGA ATGGGGGGGGGGCAAA AT .ATAGTC ACAAAAAG TCAAAGGGG CGC .TCC AA
671107-671355	1	..CAT T .CCCGA ATT TA CAAAGGGGGCAAG AG .GGGAC CAT ..AAAAAAAAG TCAACAAAG CGT .CC CA
707659-707892	1	CGCAA ACT GT CAAAGGGAGGCAAA AG .AAAGTC AC ..AAAAAAAAG TCGACAAAG CGT .CTCG CA
1782915-1783142	1	..CAG T .CGGCA ACT GT CAAAGGGGGCAAA C .AAAGTC AT ..AAAAAAG CCAACAAAG CGT .CT CA
148208-148428	1	TCA.....AAGGA GGC AAA AG .AAGGGT CACGAAAA ATCAAAGGGG ACGC .CC CA
527083-527339	1	TACAG T ACCC CAA AGCGT CAAAGGGGGCGGCAAA AG .AAAT CAT ..AAAAAAG TCGAGGACG CC CC CA
2320023-2320259	1	TCTCC AA ATCT CAAAGAGGGCAAA AG .AAAGTC AT AGGAA AAAAAGTCGGAGCGG CGT .CC CA
399024-399164	1	TG CA GT.CCGCA ACT GT CCAAGGA GC CAAAAGAAA.....AAAAAG TC GCAAGCCA ACA AAAAGAG TC .CC CA
196891-197139	1	TGCGG T .CTCTGGACCG CAAAGAGGGGCAAA AG .AAAGTC AT ..TAAAAAAG TGAAAGGAAT GT CC CA
659083-659327	1	TACAG C .CGGCA ACT T CAAAGGGGGCAAA A ..AAAGTC ATAAAAAG TCAACAAAG CGT .CC CA
756606-756849	1	TACAG T .CCC CTA ACTGT CAAAGGGGGCAAA C .AAAGTC ATAAAAAG TCAGGGGGG CGT .CC CG
1436862-1437108	1	TACAG T .CCC CAA ACTG CAAAGGGGGCAAA C .AAAGTC ATAAAAAG TCAGACG CAC GT.CC CA
349347-349598	1	TACAG T .TTT CA AT TG CA.....AATGG CA CAAA AG .AAAGTC AT ..AAAAAAG TCAGAGCGA CGT .CC CA
1732017-1732183	1	AAGGGGGGGCAAA C .AAAGTC ATAAAAAG TCAAAGGAT GT .CT TA
2316942-2317180	1	TACAG C .CGGTGA ACT CT AAAAGGGGGGGCAAA C .AAAGTC ATAAAAAG TCAAATAGAT GT .CC CA
662519-662768	1	TACAG T .CGGTGA ACT CT CAAAGGGGGC CA AA C .AAAGTC GTAAAAAG TCGAATAGAT GT .CC CA
2366989-2367235	1	TACAG T .TGGTGA ACT CT CAAAGGGGGGGCAAA C .AAAGTC ATAAAAAG TCAAAGGGG ACGT .CC CA
29444-29711	1	TACAG T .CCC CAA ACTCT CAT TGGGGGGGGGGGGGA AT .AAAGTC AT ..AAAAAAG CCAAAGGGG ACGT .CC CA
17707-17952	1	TACAG T .CCC CGA ACC TCAAAGGGGGGGCAAA AT .AAAGTC ATAAAAAG TCAAAGGGG ACGT .CC CA

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349347-349598
1732017-1732183
2316942-2317180
662519-662768
2366989-2367235
29444-29711
17707-17952

66 GGTATCGAGTGT.CTTGT.T.....TGGACTGCTGAG.GGGGAATGCGCCGACGCGA.....CGGCATC..CCAT...CTTTCT
48 CGCCTAATGTCT.GTTGT.T.....TCATATGTGTGGAACA AAAAGGGTATTGGCGC.....ACACTTGTGCGCG
60 CGTGCAAGATCTT.TTCACACGCAAAACTGTCTGCTTG.....GCGTCGACAAGAAAAATTTGTG....GGGACCT...GTCT.G
34 CGCATACAGGCC.ATTGT.T.....TTGCCTCGTTG..AAA..AATGGCAAACAGAATGG....GCGCAAAGAGACAT.CTATCTGA
52 TGCCTACAGCCT.GTCCG.T.....TTGATTGCTT..AGA..AAGTGC.....CGACAGCAGGCAT...GCCTTT
41 TTTTTCGCGGCC.TTCGC.T.....GTGCCTAGGTG..GGA..ATGCCCAAAAAGTCC.....CAACATTGGATAT...GTCTCA
60 .GTCTGCAGCCCA GTTGT.T.....CTGCCTGCTTG..AGCCTGAGCG.GAAAGCGT.....CGACAATAAACATGGCTTGTG
65 TGTCTGTGGCC.ATTGT.T.....TTATCTTTTA..ACA..ATTTGCAGACATT.....GGCGGTGAGGCGT...GCCCTG
71 CGCCTACAGCCC.GCCCT.T.....GTGCCTGCTTG..GGA..ATGCGCCAAAAGCGC.....CGACATCGGACAT...GCCAAAG
77 TGCACGCGAGCCC.GCTGCC.....TTGTCTGCTC..AAA..AATGGCAGGCATGCCGGGGGGGGGGGGCGAGACAT...GTCTGA
46 TGTCTACAGTCT.GCTAT.T.....TCCCGCGCTTG..GGA..ATGTGTCTAGAGTGC.....TGGCACCACAAACAT...ATTTC
73 TGTCTGTGGCCT.GCTGT.T.....TTGCCTTCTCG..GGC..ACATGCAAAAAGCGT.....TGACAACGGACAT...GTCTCA
68 TGTCTTCGACCC.ACTGT.T.....TTGTCCGCTT..AAA..AATGTAGACATAT.....GAGGGCGGGGCAT...GTCTGG
65 TGTCTGCGGCC.GTCATT.T.....TTGGCTGCTTG..GGA..AGGTGCCAGAGCGC.....CAACCGAGACAT...GTCTGG
66 TGTCTACAGCCC.GTTGT.T.....TTGCCTGCTTA..AAA..AATTATAGACAAAA.....TGGATAGGGACAT...GTCTGG
53 TGTGTGCAGTCT.GTTGT.C.....TTGCCTGCTCGAAAAAAAAGCACGGGCATCT.....GGTGGTGGGTTCAT...GTCTGG
70 TGCCCGCGGCC.GTTGT.T.....TTATCTGCTTA..AAAGGACATGTGGGCATGT.....GGGGCCGAGGCAT...GTCTGG
67 TGC GCGCGGTCC.GTTGC.T.....CTGTCTGCTTG..A.A..AATTGTGGACAAGC.....G..CGCGAGACAT...GCCTAA
73 TGTCTACAGCCC.GTTGT.G.....TTGCCGGCCCGA.AAA..ATGCGCAAAGGTGC.....CGACATTGGCCAT...GTCCCG
71 TGTCCCGAGCCC.GTTGT.T.....TTGTCTGCTTG..A.A..AATGGCGGACGCAC.....GGGTGCGGCGCAT...GCCCTGG
66 TGTCTACGGCCT.GCTAT.T.....TCGCCCTGCTTG..GCG..ATGCGCCAAAAGTGC.....CGACGCCAGGCAC...GCCCTCG
67 TGTCTACAGCCT.ATTGT.T.....TTGCCCGCTTG..GGA..ATGCGCCAAAAGTGC.....CGACACCAGACAT...G..TCG
67 TGTCTACAGCCT.GTTGT.T.....TTGCCCGCTTG..GGA..ATGCGCCAAAAGTGC.....CGACACCAGACAT...GTCTCA
69 TGTCTACAGCCT.GTTGTCT.....TTGTCTGCTTA..C.A..AATTCTAGACAAAT.....GGAGATGAGACAT...GTCTGC
9 TGTCCCGAGCCC.GTTGT.T.....TTGTCTGCTTG..AA..AAGTGTAGACAAAT.....GGATACGAGACAT...GTCTGA
67 TATCTACAGCCT.GTTGT.....TTGCCCTGTTGG..ATA..AACTGTGACAAAT.....GAAGATGAGACAT...ATAATGG
67 TGTCTACAGCCT.GTCGT.T.....TTGCCCGCTTG..AA..AATTGTAGACAAAT.....GGACATGGGACATGTCTGTCTGC
67 TGTCTACAGCCT.GTTGT.T.....TTGCCCGCTTG..AA..AATTGTGGACAAT.....GGACATGGGACAT...GTCTGC
75 TGTCTGCGAGCCC.GTTGT.T.....TTGTCTGCTTA..A.A..AATTGTAGACGTAC.....GGGGGCGAGATAT...GTCTGA
67 TGTCTACAGCCT.GTTGT.T.....TCGTCTGCTTA..A.A..AATTGTAGGCATAT.....GGGGGTGAGACAT...GTCTGA

1627555-1627762	135	...CGCCCGCGCGCGCGCGCGTCTGC...	TGAAATTCTGTCTGCGCAGACG...	ACACAACAGATTGTAGGCATTT.TTT.GGGGCG...
1298951-1299182	114	GCGTGGTGCGCCAATTG...	CGA.....TCTGACA...	AAGGAACAGACTGCAGACACTTTTTTGGAGCGATG
2317326-2317510	133	...CGGCAGTTGCGC..CAGACCGCC...	CAA.....GCAGGCA...	AAATTTGCGGTGTGTAGACACTT.....
266075-266302	107	...CGGC.ACTTTGG..GGCGTCTCCACA	CAC.....ACAGGCG...	GAACAATGCGATGTAGGCATCCATTT.GGATTGCTC
1336186-1336424	115	ATGCGTCTACTTCTG..CAAA.TTTT...	GAA.....GCGGCACAA.	AAACAGCAGGCTGTGTGGCAG.T.TTT.GTGACCTTT
2261535-2261757	109	ACCATAGGTCACGGTTGT...	CGA.....GCAGACA...	AAACAACGGACTGCAGACGCTT.TTT.GGGACGCTC
2373978-2374199	132	...ATAC.ACCCTCA..ATTT.TTTT...	CGA.....GCAGGTA...	AAACAACGGGACGCAACAC.T.TTC.AGGACGTCG
1279645-1279868	133	...GGGC.GCTTTTG..TGCA.TTCC...	CGA.....GCAGGCA...	AAACAATAGGCCGCAGACAT.T.TTT.TGGGCACTG
2363527-2363776	139	...CGAC.ATGTCTA..CATT.TTTT...	TGA.....GCAGATG...	AAACAAAAGGCCGCTAGACAC.T.TTT.GGGACGTCC
659348-659617	153	...CGAC.ATTTTGG..GGCA.....	CCG.....ACAGGCAA.	AAACAACAGGCTGTAGACGT.T.TTT.AGGATGCTT
1401197-1401418	114	GCATTG...CATTGTT...	TAG.....GCAGACA...	AGACAACAGGCTGTAGATAGTT.TTT.GCGATGTCG
10194-10372	141	...C..TTATGCGTC..TGCAATTTT...	TGA.....ACAGGCA...	AAACAACGGG.....
671107-671355	135	...TGGC.GCTCCCG..CGCA.TTCA...	CAA.....GCAGGCA...	AAACAACAGGCCGCTAGGCCGC.T.TTT.GGGACAGTT
707659-707892	134	...CCCTATATTTA..CATTTTTTT...	CGA.....GCAGGCAA.	AAACAGCAGACCCCTAGACACAT.TTG.GGGACATCC
1782915-1783142	134	...CGGT.ACTTTGA..CGCA.TCGC...	CAA.....GGAGGGC...	AAATAGCAGGTTGTGGGTGC.T.TTC.GGAACATCC
148208-148428	125	...CGGC.ACTTTTG..GCCA.TTCC...	CAA.....GCAGGCAA.	AAAGGACAGGCCGCAGGCCGC.T.TTT.GGGACGCGC
527083-527339	140	...CGGC.GCTTTCG..CGCA.TTCC...	CAG.....GCAGGCA...	AAACAACAGGCTGCAGATAC.T.TTT.AGGACGCTT
2320023-2320259	132	...CAGT.GCCTTTG..TGCC.CTCG...	CAA.....GCAGGGA...	AAACAACAGGCTGCAGACAC.C.TTT.GGGACGCCG
399024-399164				
196891-197139	138	...CGGC.ACTTTTG..CGCA.TTCC...	CAA.....GCAGGAAAAA	AAACAACAGCCTGTGGGCAC.T.TTT.GGGACGCTT
659083-659327	134	...C..C.ACCTGTC..TACATTTT...	CAA.....GCAGGCA...	AAACAACGGGATGTAGACAC.T.TTT.GGGACATCC
756606-756849	133	...C..C.ATTTGTC..TACAATTTT...	CAA.....GCAGGC...	AAACAACAGTCTGTAGACAC.T.TTT.GGGACGTCC
1436862-1437108	135	...C..C.ATTTGTC..TACAATTTT...	TAA.....GCGGGCA...	AAACAACGGTCTGTAGACAC.T.TTT.GGGACGTT
349347-349598	137	...TGGC.ACTTTGG..CGCA.TTCC...	CAA.....GTAGGCA...	AAAGAGCAGGCCGCTAGACAC.T.TTT.GGGACGCTT
1732017-1732183	76	...AGGC.ACTTTTG..CGCA.TGCC...	TAA.....GCAGGCA...	AAACAACTTGGCTGCCGACGC..TTT.CAGGACGCTT
2316942-2317180	134	...CGGC.ACTTTGG..CGCA.TCCC...	CAA.....GCAGGTG...	AAATAACGGGCTGTAGACAC..TTCTGGGACACCT
662519-662768	137	...CGGC.GCTTTAG..CGCA.TTCC...	CAA.....GCAGGCG...	AAATAGCAGGCTGTAGACAC.T.TTT.GGGACGCTT
2366989-2367235	134	...CGGC.GCTTTGG..CGCA.TTCC...	CAA.....GCAGGCG...	AAATAGCAGGCTGTAGACAC.T.TTT.GGGACGATT
29444-29711	142	...CGGC.ACTTTCG..CGCA.TTCC...	CAA.....GCAGGCA...	AAACAACGGGCTGCCAACAC.T.TTT.GGGACGTCC
17707-17952	134	...CGGC.ACTTTCG..CGCA.CTCC...	CAA.....GCGGACA...	AAACAACAGGCTGTAGACA..T.TTT.GGGACGCC

1627555-1627762			
1298951-1299182	185	C TTTTT GT T G T TTT C TTTTA ..TTCCTTTTTTTTT TT C G A G AGTCTGGGG A C....	
2317326-2317510			
266075-266302	182	TC C TT TT.. GT G G C CT T C TTAT C C ACCC G CT G G CAGTCTGGGG A C G TA	
1336186-1336424	190	T C TT C TT G C GAC CT TT T G TT TA G C CCCC A TT T G A GAGTT T G G CAAG T G C A	
2261535-2261757	178	C TTTT T .. GT G A TT T A T C T CA.....CCCC C TT T A A CAGTT T A G AC G A T CG T	
2373978-2374199	201	T G TT TTAG G ACAG T TT T TA TT TT.....	
1279645-1279868	202	T G TT TT.... AG CA TT TT C TT T G..... C CT C	
2363527-2363776	208	T CG C A.... AT G A TT T T C TT T T G T CCCC C CT G A C AGTT T G G CG A CT G ..	
659348-659617	219	T TTTT T TT T . AT G A T C TT C T C TT G ...CCTCC C CC T C T T G G CAGTT T G G CG G CT G ..	
1401197-1401418	179	T TTTT T AT C G C C T C TT T T G C CC C TT T G A CAGTT T G G GG A CT T TA	
10194-10372			
671107-671355	204	TT AT TT T.. A C G ACTTT C TT T T G T CCCC T TT G A C AAT T C G CG A CT G TA	
707659-707892	207	TTTT TT.... AT G A TT T TT C TT A GG..... T CC C TT T C G	
1782915-1783142	198	 AT G A CTTT G TT T T G C TCC C TT T G G CC G ACT G	
148208-148428	195	TTTT TT.... AT G A CTTT C TT T T G T CC T C TT T.....	
527083-527339	209	TTTT TTT A CA A CA A CTTT C TT T TA..... C TCC C CC C CA A CAGTT T G G GG A CT G CA	
2320023-2320259	201	TTTT TT T CT. AT G A CTTT C TT T T G C CC T C TT T G AA A GT T	
399024-399164			
196891-197139	210	TT C TT TT T .. GT G AC CT C C TT T T G C CCCC T TT G GG C AGTT T G.....	
659083-659327	202	TTTT TT.... AT G A CTTT T TT T T G C CCCC T TT G AG G GT T CA C CG A CT G TA	
756606-756849	200	TTTT TT.... AT G A CTTT G TT T T G C CCCC T TT G AT A GT T CG G AG G CT G TA	
1436862-1437108	203	TTTT TT.... AT G A CTTT G TT T T G C CCCC T TT G ACAGTT C GG C G A CT G TA	
349347-349598	206	TTTT TT.. AT G A CTTT T TT T T G C CCCC A TT T G A CG C TT T G G CG A CT G CA	
1732017-1732183	145	TTTT TT.... AT A AC CT TA TT TT G C TCC.....	
2316942-2317180	203	TTTT TT T .. AT G A CTTT C TT T T G C CCCC T TT G GCAGTT.....	
662519-662768	206	TTTT TT.... AT G A CTTT G TT T T G C CCCC T TT G AGAGTT C AC C G A CT G TA	
2366989-2367235	203	TTTT TT.... AT G A CTTT G TT T T G C CCCC T TT T G A AGAGTT C AC C G A CT G TA	
29444-29711	211	TTTT TTTT A TT G G CT G TA TT TT C GCTCCCC C CC C T C TT G ATAGTT T G C GG A CT A TA	
17707-17952	202	TTTT TT.... AT G A CTTT A TT T T G C CCCC T TT G AGAGTT C GG G A C T G TA	