

InDel Primers

SUCCESSFUL
UNSUCCESSFUL

Scaffold	C.r. Start	C.r. End	Primer 1	Primer 2	Approximate Annealing Temp. Primer 1	Approximate Annealing Temp. Primer 2	C.r. Product Size	S1-D2 Product Size	Insertion Size
1	202958	203725	AGAGGGCTGGATAAGAGATGTCCC	TTGTTGACCTGAAATGAGGATGGA	65	64	270	291	21
1	204522	204950	CCCCTTTAACACATCCCTCAACAC	TCTGGCAGACTCACTACAAGGTGC	64	65	457	491	34
1	461646	462227	GTGAGCACTGTACCATGGCGTAAG	CCAAACGTTTTAAGATACCGCCAA	65	65	482	529	47
1	467862	468587	GGGGTGTCAAGGATCAAGTAGGT	AACGTTCACTCATCAAAGTCGCT	64	65	218	239	21
1	624547	625117	ATACCACCCAGCTCACATCAACAA	GAGAAGAAGTGGCGGTTCAGAAA	64	65	121	150	29
1	1555648	1555948	ACGTCAACTGATGGACAGGAATGA	GTCTATATGGTAAGCCGTCTGGCG	65	65	442	488	46
1	1927302	1927565	GCTCAAGTTATCAGAGTGCCTGGA	GAAGCAGGCCTTGATATGAGATGG	64	65	363	480	117
2	91499	91955	GTCACCTCATGCGTCTTGTTGGAAG	TCATACGGCATGGACATGACTACA	65	64	386	434	48
2	767536	768213	CATTGGCTTGGAGTAAGTCAGCCT	GCGTAACGTGCGATGATGTGTAAT	64	65	438	532	94
2	802756	803055	ATGCTTGGGATGTAATAGGCCGTGT	ACCAAGGTGTACAATGCGTTCTGA	64	64	386	456	70
2	1044702	1045099	CAATGTCAAGGGCAAAACAATGAA	TGATTTTGACATGAGTTGGTTGGC	65	65	145	169	24
2	1172221	1172860	AGTATGTAGGTGGATGTGGCGGAT	AAAACGTATGCAAAGTGATCGTCC	64	64	115	142	27
2	1465727	1466382	GGACTTCAGAAGCAACTGGAGGAG	TAGTACTGCAATGCCGCTAATCC	64	65	486	526	40
2	1751729	1751990	ACAGTGGCAAGCACTGAATCCTC	GCTGGGTCTGAAAAGTGTGAAGT	65	65	281	309	28
3	107455	108188	TTGTTTGGTGCTCGTTATGCTGTT	TCAAAACCCGGAGAAACCTTTGTGT	64	65	144	184	40
3	308582	309170	TACAAGAACGGTTGGCTTCTCAT	AGTACGAAAAGTATGGGCTGAGCG	65	64	489	537	48
3	369810	370466	ATTTCCAGCAAGCTTGATCCATC	TGAACTTTAGCTAGCCCCAGCAG	64	65	216	245	29
3	751186	751876	GTCGAAGCTTGTCAAGTCCACACT	GTTGAAACATCAAGTGTGTTGCC	64	65	256	314	58
3	1011916	1012566	ACATTCTGATTCCGCCAGCTCTAC	AGGCGCCAGGTGATGATATGTAGT	64	65	219	250	31
4	959125	959845	TAGTACTGCCGAGATGGGGGTAGA	CCACTCTTTCATCTCACCTACGCA	65	64	129	149	20
4	987902	988712	AGCGTTTAACTCCGGTCCGTTAT	TGCGACAACCTTGACACTGTCTTCA	64	65	455	488	33
5	316270	316945	GCAGTGCAAAGTCAGACCACTT	GTTGGTACTGTGTGGGTTCTGAT	65	65	229	283	54
5	377296	378095	CAACATGTTTGCAGTCTAAAGCCG	AGAGCTCACATTCACAGCCAGCTA	64	64	420	503	83
5	586005	586813	GCCAACATATAACGGTCTTCCA	GCCTACGGCGTGATAAAAGTCATC	65	65	212	232	20
5	716136	717013	GGCACAGGTTGGGAACCTTGTAC	GGCTGCAGTTGTTGTTACGCTGT	64	64	193	226	33
5	1020583	1020996	AGTTTGGAGTTTACGGTCTCGTC	GCGCACAGTGAGTCGGTAGTGAT	65	64	324	387	63
6	214322	215174	TAGTCCATGCGTTTGGAGTAACA	TGCGGTAACCTCCGACATAATCCT	65	64	240	265	25
6	215631	215900	CAACAAGGATACCCTAGGAACCCC	GAAGAGAGCGACTTGCTGGGAG	64	65	374	454	80
6	561974	562828	CTGGAGTAATGACGTGTGGGTTTG	GTTGTGTAGGCACTCGTACAACCG	64	64	333	364	31
6	861749	862200	TAGCTGTAGATGAAGAGCATGGCG	CTTATGTCCATGGCACAACCATGT	64	65	347	500	153
6	919190	919844	GGTTGCCTGCATTACAACATTCAG	GTTGCTAACTCCTCCGAAAAACC	64	65	286	308	22
6	939029	939619	TGAGGTGTCTGAGTGTATAGCGGC	CGCACACAGTTCCTTAGATGCAGT	64	64	217	253	36
6	1290051	1290651	ATCGTCCGTAGACAGAACCCTCAG	GCTATAAGAGCATCCACAGCGAGG	64	65	469	526	57
7	1202895	1203375	CTGATTTGCTGTTGGACCAGACG	AAGAGCTGGATTATCGTCAGCAGC	65	65	435	533	98
9	724946	725502	AACCTCTTCCATACAAACACGC	CGTACATACATTCCGATTCAAGC	64	64	222	244	22
9	802158	802616	TCATGTACGAGAAGGAGCTCAACG	TTCCGATAGATGAATGGGAGCTGT	64	65	257	347	90
10	798971	799764	TGGTGTGTGTTTGGACAATGTTTG	AGAAATTGCAACCCAACCATCACT	64	64	203	225	22
11	416967	417727	TTGTAGTAGCGGGTGGTCTTTGCT	CGTCGCAACTCCTTTCATCAAGTA	65	64	142	163	21
12	148611	149033	CCGTAAATATGCACTGATGGGTGA	GGCATTGTCCAATAATGAGCCTTC	65	64	238	259	21
13	459165	459690	TGTCTTGCTTAGTCAGCACCTCG	CCCCTGACCCATAACTTACTGCAC	65	64	162	199	37
13	986155	986720	TGCCTGATTGGAGCGGATATACTT	CCCAAGTCAGTCCATACAACCTCC	65	65	275	295	20
14	348771	349466	TTTACGGTGCTTTTCTTTGGTCCG	GCCCCATCACAACCTCAAATCTC	65	65	209	231	22
14	723734	724333	TCTATTTTTGACCTGCATCCAGCA	ATGGGTAGCGATAACCTGTCCTGA	65	65	403	446	43

14	1023766	1024449	GGCACTCCATGCTCTAGGCTTTC	ATATCGGCAACAGCTCGGGAATAG	65	66	186	209	23
15	68571	69237	ATTGCTGACGTGCTCATGTTCATT	CAGTGACGTGCGAAACCAAGATAC	65	65	271	295	24
15	515941	516359	GGTTCTCGGGTTTCCTTGTITTTTC	ACCGTCACCTATGCACACACACTT	65	65	419	490	71
16	486143	486691	ATAATCAAATCAGACCACAGGGCG	GCATGTCAAGTAGACCCGGTTAGG	65	65	476	526	50
16	512589	513365	AAATGCAAACATGTGTTGTGGCTC	GCAGAATGGCTCCCCAGTCTACTA	65	64	413	507	94
16	752683	753511	TGTAGTGCAGTGTCTTGTGCTAGC	CTGTCTCTAACACCCGGAACCGTCT	64	64	301	338	37
16	1056884	1057293	GCTGCAAAGTGTCTATGCACAGGT	GAAGAGAGAGGGCCAAAGAGGAGT	64	64	154	188	34
18	444555	445038	CTATGCACAGCGATTCAAACCTTG	CAGTTGTCGTGTGAGGAACGACTT	65	64	306	378	72
18	585752	586505	GTAATGCCAGAAAGACCCCATCAG	CACATACATTGTCGCAGTCAAACG	65	64	494	529	35
18	847222	848121	CACTTTCAATGCAAGGTGTGCTCT	CTGCATTTCCGACAGAGTGTCTTG	64	65	252	275	23
19	421953	422331	TGCTACCGTATAACGGATGAGGCT	CAAAGCCTAGCAAAGGAGCTTGA	65	65	462	506	44
20	180752	181116	CGGCAGGATAATGAACAAAAGAGG	AGAACAGAAGCCACTGCACTCGTA	64	64	484	663	179
20	523721	524426	TCGCTGGGGTAGTTGTCTATGTGA	AAGGACAATCAGGACAAGGTGCTC	65	65	372	490	118
20	922658	922910	TAATCTCAACACATCCCTGCCTA	TAAAGGCCCTCCACTTTTACACCA	65	64	293	314	21
21	677564	678083	GCTGCAATCAATCATTTCCCTTTC	TTGCTGAACGCTACTACTGTTGGC	65	64	342	427	85
21	1015704	1016451	AGGTGTTCTGTTGCCATTATCT	CATCTATGTCACGTTTATCCCCAG	64	64	366	533	167
21	1056303	1056935	AGTTTTCTCCGCAATCCTATGGGT	TGCTTGTGTTGCTTGTGATGATGAA	65	64	150	313	163
23	117953	118423	CACCTATCACCTGTGGCGTACAAG	GCTCCCACTCGGTACGTAACACAC	64	65	185	210	25
23	954081	954911	GTGATAGGAGAGCCGCTGATCAAT	TGTCACCAAATGACGCTCTCTTC	64	64	362	407	45
26	234280	235088	CACATGAAGCCTCCTCACTCGAT	TGAGGAGGTGGTGTGCACTTTTT	65	65	284	308	24
26	431635	432335	CATACCATTTAGGTAACCGCCCCCT	GAATCATATTGCGAGGCTTGATGGG	65	64	249	269	20
26	432148	432532	TCAAGCCTCGAATATGATTAGCA	CGCTGCTCCAGCAGATGGACTC	65	68	205	225	20
26	698201	698860	ACATATCCCCTGAACGTGCTCTC	GATTTCTAGTGGAGGCGTGTGTT	65	64	422	459	37
26	745053	745917	TTGTAGGAAAAGGAGACGGGAAT	ACCAGTTGACTGCCTCCTCATTTTC	65	65	499	530	31
27	304755	305457	CTCAATAGCATGTGCTGGATTG	GCTGGATATTGTGAAGCAGCAAGA	65	64	492	526	34
27	652374	653059	TTGTACGAACATGGTTTGACGCT	TTGACCAAACATGCTCTCACTCTC	64	65	112	144	32
27	652996	653859	TTGAGAGTGAGAGCATGTTGGGTC	CTGATTGTGGGATTCTTGTAGCC	65	65	500	538	38
28	237729	237934	ATGGCCGCTCTCTCAACACTAATC	ATTATCAAAGCATACAAGGCCCCC	64	65	454	502	48
29	171983	172784	GTCCAACCTGTCTGACTTCCCCT	ATTTTCGTACGCCACGTGAAGAGTT	65	65	217	244	27
29	239257	239808	TAAAGCATCTACCAGGAAAGCCCA	GCGTAGAGTGTCTATCTTGGCTTCA	65	64	476	546	70
30	245178	245645	ACACCTGAAAGTCTGTGACCTGA	AACCTGCTCTCTCACTCACTCGAA	64	64	471	503	32
31	308030	308706	ATGAAGCTTCTTAGGAGTCGCGTG	ACAACGTATGACACATCGAGACGG	65	65	310	388	78
31	754580	754796	CGCAGGTTGTATGGCAGCTTAAC	TGCTGTGACCTCATACTCTTTGC	65	64	194	219	25
33	57308	57704	GTCGCACGACATGTGATAGTAGGG	GCACCAGACGGTGTGATAAGTGTG	64	65	279	315	36
33	409214	409938	TGCCATGTGCAACACAACAACCTTA	GTAGGGTTTACCTTAACGGCGGG	65	65	279	299	20
34	256984	257690	CTAGACCTGAGTGAGAGCCGAACC	AGTAGGGGGAATTGTTTGTGCCTT	64	65	382	526	144
35	310132	310557	ATGCCGAGCCAAATAACTTGTGTT	CTTGGGGATAAGAATTTGCGATG	64	64	362	406	44
35	608067	608350	CTGCGTGACTAAAACGAATGCAAC	ACATCCACTGTCTTACCCGCTTC	65	65	492	529	37
37	124694	125358	GCATGTGTGGTGTGTCATGTTT	GATTCGGCTCCAGAGCTTTGTCTA	64	65	297	331	34
37	254758	255276	TCTAAGTCCAGCTTCGCTTTGGTC	TATGACACTATCATCGTCCAGCGG	65	65	460	520	60
38	129613	130306	AACACCCAGACCTATTCTGCAACC	GAAGAGGCAGGTCTCGATTTGTA	64	64	246	266	20
40	40977	41311	GATGTTGGTAGAGTGTGCCGATTG	CTGCGCCCTCTTTCTTTCTTACT	64	65	172	200	28
40	494228	494906	AAAAGCTGTTGGCGTGTGTATGAA	ACTACGGTGGTCCCACAAAATCT	64	65	144	166	22
40	615014	615799	AATGCACGACTAGGGTAGGCAGAG	TTTCGTGAGCGTGTATGCAGTGTA	64	64	276	336	60
43	276084	276869	TTGCGGTTGTGGATTATGTGTTTC	CTTGTCAGTTAGTTTGTGCCCCC	65	65	421	455	34
46	454986	455818	GCATCGCTCTCTCAAAGCATGTAA	GTATTTTGTGTGCGGTCCAGGGTC	64	64	287	316	29
48	92338	92843	GGGGTCCGTGTGTTGTTTAGTA	TACGCTGTCCACTTCTGTATGTT	65	64	196	219	23
48	243024	243390	ATTGTAGTGGCATGGGATTGCT	TTCAATTCTACTCGTCCATTGCGA	64	65	226	257	31
49	429505	430255	TGACGTGCCTACTCGCTGATACTC	GTCATCATCCCTTCGCGTACTACC	64	65	495	556	61
49	551237	551584	GCCGTACTCGGTCTCAATCTAAGC	ACAACACAGAAAGAAAGCAGTGCC	64	64	119	144	25
50	593653	594433	CACATCACACCACACTGTTAAGCG	ATCCAGAATGATGCGTGAAAATGA	64	64	177	199	22

52	353630	354473	ATGCACGCATAACAATTGCAGAGT	ACGCAAACCTAGTGCAGGTGCT	64	65	129	153	24
53	302593	303318	ACATGAATTGCTTAGGCCGTTTTGT	TCATGAGCTGTCACTGCTTTGTGA	64	65	216	237	21
53	561092	561929	GTGAAGGAATGCCTTGTGGTGTT	CTAGAGCGCTTTCTCAGTTAGGCCG	64	64	350	381	31
54	410787	411428	CGCCATACAGGTGTCAATGTTCTC	GCCTTGGACTGAACACGTCTAGGT	64	65	408	444	36
55	279500	280325	AATCGGCTGTTTGTCAATGTGTACG	TTAGGTGCCTTACGACTCGTCCTC	65	64	353	392	39
56	395875	396424	ATCCTGGACACCTTGGAGTTGAAG	ACTGAGCCATAGCACAGCTCCTCT	64	65	403	501	98
57	11029	11279	CTACTGGGCAGGCTATGGTACTGG	TTATTGAAGACAAGCGCATCAGGA	65	65	190	218	28
57	123355	123996	CACTCAAATGATGCACTCGGAAC	GCCAGACCAGGCATTAGACAGATT	65	64	338	388	50
57	408860	409253	ATGCAGAGCAGAGAAATTCGGAGT	GTCATCTCCGACATCATCGACAAG	64	65	295	323	28
57	456676	457561	TACTCTATGCAGGAGAAGGCCGAG	TATAACCACCATCAATGCCAGCAG	65	65	489	519	30
58	242069	242478	CATGGCTTATGTGAAGAAACGACG	CCCAACACACTCAGTCAGCCATAC	64	65	240	263	23
59	27380	27993	TATTGAGGGCAGGGTATGAGTGGT	CACATCATGGACATGCTACGCTG	64	64	371	548	177
59	242009	242662	AATCAAAAAGCTTCGTGCCACATT	ATGGTTGGCTTATCGTTTTGCTGT	65	64	277	311	34
60	62687	63408	AACTAAAAATCTTATCGCCCCCG	TCTCTCCATCTTTGTCGTGGTGAC	65	64	281	301	20
61	527897	528547	GATGCATGCAGCCAAAATCAATAA	GCACTGCCTGGTTCTTCTTAGCAT	65	65	162	190	28
62	254823	255147	TATGCAAAGTACAGCACCCGATCA	TGTGTTGTACGAAGCTCACCATGA	65	64	256	360	104
63	159722	160326	TCATATTGAGCTTGAGGGCCAACT	GAAAGCTCTCGCTAGGTCAAGTGC	65	64	329	379	50
63	238867	239309	CTCCTGATTTTGTCTACTGCAAGA	CCACCAAGAACCTGTAAGGAGCAC	65	65	135	158	23
63	249701	250538	AGCACAAGTCAATGGTTCGCATTA	GCGTTTCATGCATTGATTCTTCTG	64	65	229	251	22
63	321911	322760	CTCACATGTAGTCAACGGTGGTGTG	GCCTTCAGATGCCATGCTCTTAGT	64	65	381	432	51
63	407037	407984	ACTGATCCAGGCTATTTGGTAGCG	CAGTATGTCGACCAGTCCCCAAAT	64	65	299	325	26
66	341868	342753	TGCCTACTCTGTGCAACAATACA	GTCGATGTTGATTGACGTTCTTGG	65	64	263	284	21
68	145612	146137	CCCAACGGTAAACACCTTCAAAAA	ATTGACTTCGGTTGTTGTGTCCCT	65	65	137	160	23
68	172241	172721	TTCTATTGTTGGTGTGGCAGGAGA	CAAACACAAATTTAAGCGTTGGCA	65	65	433	506	73
68	189954	190358	GGGTTTGATTGTTTGTGTACGGT	TACAATATTGCCGCTTTTGCACG	65	65	279	373	94
68	194690	195307	GCGTAGGCAGGATGCTTAGGTAGA	AACGTCTCAATGCTGCATCAGGTA	64	65	150	176	26
68	412853	413572	TTCCACTAGACCCTCCACTTCTGG	TGTAATGGAGAAGCGATGAGCTTG	64	64	245	268	23
69	237581	238253	ACGGACGGGTGCTTATTGATACTG	AATATGGCGTGGGGTAATCTTGTG	65	64	438	468	30
69	499527	500288	GCTAAGTAGCCCGCCTCAGCTAC	CACAGGTCTCATAACCAAGCAACG	64	65	193	215	22
71	209529	210213	TAATGCCACTACTGTCCGCTCTGA	GGCGGGGGAATAAAGTATTGCTAA	65	65	279	314	35
71	319657	320014	CATGCTACCCTTCTGATGCATGTC	AGTCCACAGAACCCTTGAACCC	65	65	483	521	38
73	88137	88453	CATAGCGGGGCTAACTTCATCACT	CTGACTATAGGAAGCGGTGGCTGT	64	64	331	426	95
75	372850	373664	AGATAAACACAATGGGGATGTGGG	GATTAGTGCAGCTTGCAGAAACACC	65	65	377	414	37
76	137460	137962	AGAGGTCAATTTATGTCGGTGCCT	TATTCATGCAGCTCAACCCAAAGA	65	65	424	517	93
77	105378	106296	GCAGGTGCATATGTCATCAGAAGG	CAGAGAGCAGGACGTTCCCTGA	65	66	118	144	26
79	194992	195501	TCACGAGCTCAGTCTACGAACCAC	ACTACAAGCACCCGGCTAGTGAAGG	65	64	363	422	59
79	208653	209061	ACCCTGCACAAAACATCGTGTAGA	CTGAAGCTTGGTGGGAAGGAAGAAA	64	65	323	479	156
80	78029	78884	CTGATCCAGGACTTGAATGACCCG	CCAAGTGCTTATTGGTCTCCAACC	65	65	346	385	39
80	310821	311134	TTTGAAGCACCTTCTCCAGCTTC	CCATTCGTGCGATAGGACTTTTT	65	64	465	516	51
87	53338	54065	CGGCTCAGGTAGTCAATCGAAGTT	CGTCAGATGAATGTTGTCCGTTTT	64	64	349	444	95
87	234125	234888	TGACGTGTTTTGGATATGAACAGGG	AGCACACCCTCCCCACATACTTTA	65	64	327	456	129
89	130109	130943	CAAGCTTGCCACCTGTACTACCAA	TTGATGTTGAGTCTTGGGTCGTGT	64	65	488	521	33
89	319078	319655	AGTTCTCGAAGTTTACTGGCGTGG	TATTCGAGCAGTTCAGCTCACACC	64	64	287	315	28
89	322286	323102	CAGCTCACAGGTCAATGACACTCA	AGTTCTCGAAGTTTACTGGCGTGG	64	64	272	302	30
89	350521	351090	GTTTGCACGACATGTATCAGGCTC	CGTGATGTAAGCTTTCGTGTTGGA	65	65	447	514	67
90	289778	290063	AGTAAAGAAAGGGCTGTGCTCACG	ATTGCATTCTGGGTTCTGAAGTT	65	65	276	384	108
91	26188	26511	CAGGAGGAGCGGTAGTATGGAGAA	CGTCGTATTCCGTCAATTTTGTG	64	64	343	377	34
93	342282	343148	AGTGTGTTGGCTAGTGTGGCAGTC	TCAAAACAGCTCTGCATCCACTTC	64	64	449	484	35
95	95838	96188	CTACCACCATCTGCCTGTTTACC	AAACTCATTCCACCTGCCAGTAA	64	65	411	499	88
95	301623	302316	CTCACACAAAGCACCCACCATATC	GAAGGAACCCCTGCAGTAGTACGGA	64	64	220	244	24
97	108656	109005	CCTGAGTGGGGTAAGGTAACATCG	CCCCTATCACCACAACCGACTTAT	64	64	229	250	21

97	186606	187051	AATGGAGTAAATGCTTATGCCCCC	TGCCCTTAGTCCAACAGTCACAAA	65	65	246	273	27
97	275060	275628	TTCCGGCATTGTGTATCACTTGG	GAAGGCGATACTCAGAGTGGCAGT	65	65	341	397	56
97	383531	384321	ATTCTATGCCACGGCAACGTATCT	CTAATGGCATGTATCGGACTGGTG	64	64	166	193	27
102	220248	221031	ATTTGAGTAGCTCCGGTCAGATGC	TAAGGTCACATCAACTCGCACACA	64	64	480	539	59
102	220731	221405	TAAGGTAACCTGCCCTGGCGCTTA	ATATCCCCTAAAGAATGGCTCGGA	64	64	478	623	145
104	250869	251361	TTCTTTTCGTTTGGATGCGAGTTT	TGGGGCACTTTGGTCATATACCTC	64	65	225	246	21
105	56756	57550	CCTACTAGATGTCAACGGCCAACC	TCTGGGGACGGATTCACTACTGTT	65	64	467	508	41
105	235680	236150	GCTGCTTCCAGTTC AAGTTGGTT	GAATAAGCACCCACGCCAATAGAC	64	64	156	214	58
108	59857	60113	ACTCATGATGCATCTTTGATTGCG	CACGGTGCCCTAATACACACGTAA	64	64	484	700	216
108	232131	232517	ACCACCTGCGTTCTATTGTGGAAT	AAAAATTACGTGCGAAAGAGGGGT	64	64	360	434	74
111	173768	174277	GAGTTCACAGGTCTACCAATGCC	GACTGACTTGCATCTAGCAGGGGT	65	65	394	435	41
112	300349	301169	GGTTGCCAACGTTAATTTGGTTTG	CCTCCCTACCACCTCTATGAGCCT	65	65	499	558	59
112	302169	302483	GTGGAAGCGTACATCGTCATCATC	TACTTCCGGGTGAGTTGATGGCT	64	65	474	522	48
114	115021	115380	AGGTGGCAGCGGCTATGTACTA	CAACTCCTTACCAGTTACCACGCC	65	65	279	299	20
115	212877	213421	GAACAGCAGGAAACAGTGACCTTT	GGTGATGCTGTAGCTTTTCGAGGAT	65	64	402	564	162
116	167684	168105	CAACCGGAATTTACTATGCCATGC	GTGTCCCAAGCCCAGACATGTAG	65	65	208	228	20
119	48169	48607	ACGCTCAAGCATGAAGACATGAAG	TGATCGTTCATTATCGCCTGTA	64	64	283	305	22
119	48518	48886	ACGCTCAAGCATGAAGACATGAAG	GGCCTAGGATTGTGATGTGAGGAG	64	65	358	419	61
123	52581	53432	CGCCACGCATTCTTGTACATACT	GCTATCGGCGTGGGTAAGTTACTG	65	65	497	536	39
127	39938	40274	AATGCTGTGTAGTTGTAGCACGGG	ATGTGTTTTTGGAACGAGCCCTAA	64	64	366	400	34
127	65174	65586	AAGGGCCTAAACATGCCTCATTCT	CCACCACCTGGACCTCATGTACTC	65	66	470	506	36
127	214586	215057	CTGTTAGCAGCAGTGGCCTAATCA	TTCTATTCTTCTCAGCCACCACCA	64	64	298	318	20
133	145594	146409	CACAAAACCGTTCTCTTCAAACC	CCGTAAGTTAAACGCACGCATGA	65	65	224	265	41
135	214039	214633	TATATATCGGCCTTGCCAAGCTGT	AGACTTGAGACAGACTCGCCCTGT	64	65	333	374	41
136	104253	104933	GTCACCTTCTCTACGCCTCACTC	AGAAATAAAAGGCTTCGCACAGCA	64	65	448	491	43
136	250068	250596	ACCCCAATCTCCAATAAAGCGAGT	CAGGTCCATTGATTCTTTCCATCC	65	64	257	281	24
137	122125	122409	ACAAAGCGTCAAATGTTGGTCTCA	GCACTAGAATAGAGCCACCGAGGA	65	65	413	480	67
139	11821	12243	TTGTCTTTGCATAGTGGCCACACA	GCAGGTGTTTTGGGTTCTCTTAC	64	64	276	300	24
139	181309	182142	GTATTGCAGTGTGGGAATGCAGAC	ACAGCATCACAGCTCATTCAAAGG	64	64	338	400	62
144	180150	180638	GACATTGTATGGTCTCAACCTGCG	CTGGTGACGTGATGTGTATGAAG	64	65	242	379	137
145	58273	59084	GGCAGCCACACTTATGACAACCTA	GGCGCAACATAGGAACATATTGGT	65	65	236	257	21
146	202453	203226	GACTCTTGCTCTTCACTGCAGCCT	ACTCTGGGCGATGAACCCTACAC	65	65	280	303	23
149	41629	41935	AACGCATATGGGCATCATCTCTCT	ATGCGAAAAAGATGACGTGATTGA	65	64	129	158	29
149	41934	42658	TCATGCACACTCCGTTTATCGACT	TTATGTGCATGCAAGGTATGGACC	65	65	184	206	22
151	114531	114979	CATACAGCAGAGTGTGTATGTGCG	AATATATAACGGTGCAAAACGCCG	65	64	271	296	25
151	114723	115331	ACCGTTATATATTGGCGGACCCTC	CAAGCTCTGCTCATTITGACGTGT	65	64	352	389	37
155	126432	126766	TCATTAGGTCTCAGGGAAACCAT	GCTTCAGGTGGTGTATGGTTGAGTT	65	65	130	151	21
158	153063	153516	TGACGTACTCGTAAGGAGTGGCTG	GCTTATTACGGCACCCAAAAGTTG	64	64	229	255	26
160	40962	41804	GTAGTCACGTAGCCTCGTGACGTC	TCCTGAACAGTCTGATCACTTGC	64	65	241	261	20
162	175231	175635	GCAGGAGGGTGACAGTATGACAGA	GATCACTTGTTTCGCACTGAGCCTA	64	64	366	418	52
170	152765	153522	GTGCTGGTGGGTTATCGTTTTCTT	GACAAGTGAGGTATGCATTACAGCG	64	65	254	275	21
171	157580	158207	GTCCTCGTCCAGTGTTTGATGTTG	TGCGCTTGATAACCTGCCTATTTT	65	64	313	348	35
186	141056	141627	TACTGCAACGGTAGCCGACCTAAT	CGCTATCTAGGCTTGGTGTATGGG	65	64	404	466	62
197	36738	37313	CAGTTTGCCACGTTACCAGTTCAG	GAGGATACCTGCGTACTTCGTCTGT	65	64	299	323	24
201	499	1140	AAACGCATTATCTGACGTTGGGAT	GGAGGTAATAGTCAGCGTGTGGG	64	65	313	346	33
301	11165	12035	GTGCCTTTATTGCTTGGAGTGTCC	AGCCACATGAACGGTGAAGGTT	65	65	193	218	25
328	16497	17136	TGTGGTCTCATTACAAATCCCCT	TACCTCAAGGCCATTTGGAACATC	64	65	279	306	27
329	31277	31953	GGTGAGACCGCATCACTGTGACTTT	ACATGCAGGTCTCTGCTGTGTCAT	64	65	260	282	22
336	7869	8530	AGCGTTGGACATGGAGCTAGTGAC	ATACACATCCGCGTACTGCACAAG	65	65	365	459	94
601	1190	2014	TCCTCTTCTACCAAATGGTGCAT	GTACAATGCGCTAAAGCACACACC	65	64	270	300	30
698	3444	4194	CAAATGAGTTAGCTGTCCGCATTG	AAAAGCCCTAACACTGCTGCACTC	65	65	243	271	28

882	3987	4529	GTAAAAGCATTGCAGGGGAGTCAG	AAGAGCTGCCTGGTCGCTATAATG	65	64	388	453	65
1097	438	800	CAAGAGACTGGTTGGTATGCATGG	TTGCAGCATACCGTACTCTTGGTC	64	64	497	536	39
1125	956	1417	TCGAGGGTAGACGTTGGGTAGGTA	GATGCTGATATGTGGCATGCTTTC	65	64	162	267	105
1220	3296	3932	GAAAAGCCAAAAGCTAAATGCACG	GCTTTGGACTAACCAGTTGCTGCT	65	65	390	446	56