

SEQ ID NO:	Chromosome	Protospacer (cRNA)	Cut site coordinate	Score
1	chr2	CCGAAGCCCGGGUCAUCCGG	9555543	83
2	chr2	CUGACGCUGCAGUUUAAAGG	9490227	82
3	chr2	UGGCGCCGAAGGGAUCACAG	9490422	82
4	chr2	UGGGGCCGAAUAUAACAUAAG	9535838	80
5	chr2	UCUCCUAUUCCUGACCAGCG	9555577	80
6	chr2	UUGGAGCUGCUGGCGCCGAA	9490412	78
7	chr2	AGCGACUGCACGUUGAAGGA	9505183	78
8	chr2	CAACAGCGACUGCACGUUGA	9505187	78
9	chr2	AGUUUGUGGGAACUCGAGGG	9505265	78
10	chr2	AGCAGAAUGUGCCCCGAAUG	9510046	78
11	chr2	GUAGCGGGGCCGGAACAUG	9555605	78
12	chr2	GCGAUUAAUGCUACUUGCAA	9502195	77
13	chr2	UAAAGUUUGUGGGAACUCGA	9505268	77
14	chr2	GGACUUCUUCACUGGACACG	9536706	77
15	chr2	CCGCGACCUCCGGAUGACCC	9555537	77
16	chr2	AUGCAUCCCUUUCUGCGAGA	9497149	76
17	chr2	AAGUAGCAUUAUUCGCCUCC	9502214	76
18	chr2	CCCUCCUGGUCCUCAUUCG	9510047	76
19	chr2	UAGCUUUAUUAUAGCCCAGUU	9517975	76
20	chr2	GGUCUUUACCGAGUCUCUGG	9555517	76
21	chr2	CAGCACGAAAGGAACCACGC	9555575	76
22	chr2	CACAGACUCACAUUUGGACG	9490334	75
23	chr2	GUGAUCGCCACUCACAGCUA	9510008	75
24	chr2	AACGUUCAGUACUUGAUGUC	9536808	75
25	chr2	CUGGCGCCGAAGGGAUCACA	9490421	74
26	chr2	CGUCGAAUUGCUGAGCAGCA	9490499	74
27	chr2	CUGGGUCUUUACCGAGUCUC	9555514	74
28	chr2	CAGCGUGGUUCCUUUCGUGC	9555562	74
29	chr2	GGUCGCGGCGCCAGCACGAA	9555564	74
30	chr2	CAACAUCGUUGGGUCUGUCC	9492953	73
31	chr2	GUCACAAAUCCUACUGUAC	9494660	73
32	chr2	AAUGCAUCCCUUUCUGCGAG	9497150	73
33	chr2	GGGCACUCACUGCUAUUACC	9497247	73
34	chr2	AUAAAGUUUGUGGGAACUCG	9505269	73
35	chr2	GCGUUCUUGAAAACACUCCU	9505308	73
36	chr2	GGAGCAGAACAUGAUCCGGA	9510072	73
37	chr2	CCAAUUCAUAGAUUGUAACC	9510118	73
38	chr2	CAUCUAUCGGAACACUUCAU	9523295	73
39	chr2	CAUCGCUUCUACAGAUACA	9526150	73
40	chr2	UCAUCGCUUCUACAGAUACA	9526151	73
41	chr2	UUCUUCACUGGACACGUGGU	9536702	73
42	chr2	GUCUUUACCGAGUCUCUGGU	9555518	73
43	chr2	CAAAUGUGAGAAACGAGUAC	9493806	72
44	chr2	UGCUGUUCUCCUCUCGCAGAA	9497154	72
45	chr2	UGGGCUAGAACCCUAGAGUC	9535912	72
46	chr2	GCCGCGACCUCCGGAUGACC	9555538	72
47	chr2	CGUGCUGGCGCCGCGACCUC	9555547	72
48	chr2	CGAAAGGAACACGCUGGUC	9555580	72

FIG. 1

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
49	chr21	CUGCCGGUUGGCAUCGUACG	26840497	84
50	chr21	UACAUGUGCUGGCUGCAUCG	26840439	82
51	chr21	UGUGUCCAGUCACCGCUAUG	26842640	82
52	chr21	CGACGUCGGCGGCACGUGCG	26844362	82
53	chr21	GGAGACUGUUCGAGAACGUG	26840005	81
54	chr21	UGGCCGUGUCGGACGCACUC	26844807	81
55	chr21	AUGCAGCGAGCUGUGCCCGA	26844937	81
56	chr21	GACUGUUCGAGAACGUGCGG	26840002	80
57	chr21	GCGCGUGGUCCCCGUGUCCCG	26844747	80
58	chr21	GUACGCUGGCGUCUCACCAA	26839654	79
59	chr21	GUUCUCGAACAGUCUCCCA	26840023	79
60	chr21	UCAAACCAACACUUCCCGU	26840361	79
61	chr21	GCACCUCGUACGAUGCCAAC	26840488	79
62	chr21	GCUUGUGGCAGACCAGUCGA	26842610	79
63	chr21	GGUUUCCACAUAGCGGUGAC	26842647	79
64	chr21	GCCGCUUCCGGAAACCGACC	26844599	79
65	chr21	GCUUCACGCUCCAGAACGUG	26844642	79
66	chr21	CGGCUUCACGCUCCAGAACG	26844644	79
67	chr21	CUGGCCGUGUCGGACGCACU	26844808	79
68	chr21	CUUGCGCCUUCGGAACCCCU	26844933	79
69	chr21	GGUGAGACGCCAGCGUACUU	26839671	78
70	chr21	UGUUCGAGAACGUGCGGUGG	26839999	78
71	chr21	AACCAACACUUCCCGUGGG	26840358	78
72	chr21	GUGUACCGGCACCUCUGGUG	26840394	78
73	chr21	GGUGUACCGGCACCUCUGGU	26840395	78
74	chr21	GUCAUCCACGAUGAACAGAA	26842468	78
75	chr21	CCGGCCCCUUCUGUUAUCG	26842475	78
76	chr21	UCCGCUUUCACAGUCGGCCG	26844337	78
77	chr21	AAUCGGCAGGGCGACGUCGG	26844373	78
78	chr21	CGGAUUCGGCAGGGCGACGU	26844376	78
79	chr21	GGUGGCGAGGCGCUCGUGG	26844462	78
80	chr21	GCGCCCGAGUGCGUCCGACA	26844816	78
81	chr21	AAUGCAGCGAGCUGUGCCCG	26844938	78
82	chr21	CCGCUGUUUCACUUCGAUGU	26838232	77
83	chr21	GAGGAGUCCAGUACACGAUG	26839980	77
84	chr21	UGUAAACUGGCACUGCCGGU	26840485	77
85	chr21	CAUGUGGCAUGUUAAACACG	26841159	77
86	chr21	UCGUAAUUCAGUUAGCCUGG	26842505	77
87	chr21	GCUGGGGUGUUUGUACAAUC	26842542	77
88	chr21	GGGUCGUGGACGACGAGCCC	26844342	77
89	chr21	CCUGCCGAUUCGCGCCGAGG	26844398	77
90	chr21	AGCCUCUGCGAGGGCGUGCG	26844520	77
91	chr21	ACGUUCUGGAGCGUGAAGCC	26844658	77
92	chr21	ACUCGGGCGCCCCUCCGAGG	26844791	77
93	chr21	GCAAGCUGGGCAGCGACAUG	26844903	77
94	chr21	CCAACAUCGAAGUGAAACAG	26838220	76
95	chr21	GAAUGGAUUCCCAAGUACGC	26839668	76
96	chr21	AGGAGUCCAGUACACGAUGA	26839979	76

FIG. 2

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
97	chr21	GUAGACGUGCAGGAUCCGUG	26965830	85
98	chr21	GUUUCGCAGCUGGCGCGCGG	26965777	84
99	chr21	AGAAAAGGGGCGCGUGUACG	26965847	82
100	chr21	CGGAGCCACUGCUUCUAUCG	26965996	82
101	chr21	UCGUCUACGCGGGCGGCCGG	26966106	82
102	chr21	GUAAUUCGUCUGCGUCCGG	26930013	81
103	chr21	GGACUGGUCCAAGAGCUGCG	26965683	81
104	chr21	CGAAACCCCGCGUCCACAC	26965748	81
105	chr21	CUGCACGUCUACACCCGCGA	26965807	81
106	chr21	CCUGGAGCGAGAUGGUUCGG	26966072	81
107	chr21	GCCAUGAUUCAGGUGACCGA	26930056	80
108	chr21	ACAACGGACGCUACUGCACA	26932915	80
109	chr21	UGGAUGUCUGUGCUCGCCUG	26934606	80
110	chr21	AUGGCGCGGUUGUAUGGCCG	26965540	80
111	chr21	UGGCUGACGCGUCCAUGGCG	26965554	80
112	chr21	AACCCCGCGUCCACACCGG	26965745	80
113	chr21	CUGGAGCGAGAUGGUUCGGU	26966071	80
114	chr21	AUCGACCAACUCUACUCCGG	26966146	80
115	chr21	CAUGGGCUACUCUGCCACGA	26924369	79
116	chr21	CUAUAGCGGUUGGAGCCACA	26924408	79
117	chr21	ACGUGGUGAGGAUUCUGAA	26924589	79
118	chr21	CAGUAAGGGUACACUGACG	26924606	79
119	chr21	ACUUGGGAGCAGCGUACCAU	26932861	79
120	chr21	GCGGUGGAAGGGACGCCUUG	26934532	79
121	chr21	UGGUGUGCUGUGGUACGCCA	26934586	79
122	chr21	UGGCAUCGUAGGUCUGUCCU	26934692	79
123	chr21	CCGGCCAUACAACCGCGCCA	26965554	79
124	chr21	UCCGCUCUCUCGCCCUGG	26965651	79
125	chr21	CCGGCGCACAGCAACCCGAG	26965708	79
126	chr21	UGUACGGGGAUGGGUCCGCA	26965833	79
127	chr21	AGUAAUUCGUCUGCGUCCG	26930014	78
128	chr21	GUACUCCGUGUGUCCCGGCA	26934626	78
129	chr21	UCUGGUGGCUGACGCGUCCA	26965559	78
130	chr21	CCAGUGCUGCGCGUCCGCUC	26965706	78
131	chr21	GUGCGCCGGAGCAUGCUCGU	26965734	78
132	chr21	AUGCUCGUGGGCCUCCGGUG	26965746	78
133	chr21	GAAGAAAAGGGGCGCGUGUA	26965849	78
134	chr21	ACCCUAAAGCCACUGCUGCG	26965885	78
135	chr21	GGCUACCUUGUCUACGCGGG	26966113	78
136	chr21	GGUGGGCUACCUCGUCUACG	26966117	78
137	chr21	CUACUCCGGCGGCGGCAAGG	26966135	78
138	chr21	ACUAUAGCGGUUGGAGCCAC	26924409	77
139	chr21	CUUGGGAGCAGCGUACCAUU	26932862	77
140	chr21	GGGAGCAGCGUACCAUUGGG	26932865	77
141	chr21	AACAACGGACGCUACUGCAC	26932916	77
142	chr21	ACGUCAAGCCAUGGCAACUG	26933027	77
143	chr21	CUAUUUCAGACGUCAAGCCA	26933036	77
144	chr21	AGUACUCAGGCCCGAAUGUC	26934656	77

FIG. 3

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
145	chr11	CGACGCGACAUCCAACCGAG	10305767	84
146	chr11	CGCUCGGUUGGAUGUCGCGU	10305780	82
147	chr11	UCACGUCAGCGAGCCCGGUG	10306011	82
148	chr11	GCGCUUGACUCGGAUGCGGG	10306348	82
149	chr11	CUGCCGCUUCGGGACGUGCA	10306427	82
150	chr11	CUUCACGUCAGCGAGCCCGG	10306013	80
151	chr11	GUAGCGCUUGACUCGGAUGC	10306351	80
152	chr11	GCACCGUGCACGUCCCCAAG	10306418	80
153	chr11	CUAGGAAGGCGAGCGAACCC	10305735	79
154	chr11	ACAAGGACAACGUCGCCCC	10306492	79
155	chr11	UGGGGAGCACUCCACUCGG	10306614	79
156	chr11	AGCGGUGUCAGCGCCUAGGA	10305749	78
157	chr11	AUUCGGCCCCAGGACAUGAA	10306069	78
158	chr11	CCUGUCUUCGGGGCUUCGAG	10306082	78
159	chr11	GUGGGGAGCACUCCACUCG	10306615	78
160	chr11	GAGCGAACCCAGGUACAUCA	10305725	77
161	chr11	UCCUAGGCGCUGACACCGCU	10305764	77
162	chr11	AGGCGCUGACACCGCUCGGU	10305768	77
163	chr11	CACCGGGCUCGCUGACGUGA	10306026	77
164	chr11	GGUAGCGCUUGACUCGGAUG	10306352	77
165	chr11	AGGGCGUAGUUACCUGUCUU	10306094	76
166	chr11	CGCCGGCGGCCGUGACCCUG	10306515	76
167	chr11	UCCGUCGCCCUAUGUACCU	10305730	75
168	chr11	UUCACGUCAGCGAGCCCGGU	10306012	75
169	chr11	GGCGUAGUUACCUGUCUUCG	10306092	75
170	chr11	CAUCCGGACUGCUGCGGGCG	10306325	75
171	chr11	UCUGGCGGUAGCGCUUGACU	10306358	75
172	chr11	ACCGAGCGGUGUCAGCGCCU	10305753	74
173	chr11	CCUGGGGCGCGAAUAAGGGUC	10306047	74
174	chr11	CCAGACCCUUAUUCGGCCCC	10306059	74
175	chr11	UAUUCGGCCCCAGGACAUGA	10306068	74
176	chr11	GCGCCGGCGGGCGUAGCCCU	10306516	74
177	chr11	UUCUAAGCCACAAGCACACG	10306595	74
178	chr11	GGGAGCACUCCACUCGGGG	10306612	74
179	chr11	ACCCAGGUACAUCAGGGCGA	10305719	73
180	chr11	AUAAGUGGGCUCUGAGUCGU	10305971	73
181	chr11	CUGGGGCCGAAUAAGGGUCU	10306046	73
182	chr11	AUCCGGACUGCUGCGGGCGG	10306324	73
183	chr11	ACUCGGAUGCGGGCGGCAUC	10306341	73
184	chr11	AGCGGCAGCCAAAGCUCGGG	10306400	73
185	chr11	GGCCUUCACGUCAGCGAGCC	10306016	72
186	chr11	UCAUGUCCUGGGGCCGAAUA	10306053	72
187	chr11	CACCAGAGUCCGACCCGGGC	10306558	72
188	chr11	AGUGGGGAGCACUCCACUC	10306616	72
189	chr11	UUCGUCGCCCUGAUGUACC	10305729	71
190	chr11	CAGAGCCCACUUAUCCACC	10305950	71
191	chr11	AAUAAGUGGGCUCUGAGUCG	10305970	71
192	chr11	CAUGUCCUGGGGCCGAAUAA	10306052	71

FIG. 4

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
193	chr1	GCUGUGCUGUGGUUCCGUGA	116392921	81
194	chr1	CAGGAACGGCCGCCCGUGGA	116395233	81
195	chr1	GCGGCCGUUCCUGAUGCCGU	116395255	81
196	chr1	GCCAAGGCCUGCGUAGUACA	116397909	81
197	chr1	UACCUAGGACUCGUUCUCCG	116393709	80
198	chr1	GCAUCAGGAACGGCCGCCCG	116395237	80
199	chr1	GUAGACAACAAUACCACGUG	116389447	79
200	chr1	UAUCAUCGUAGCCAAUGUGC	116389679	79
201	chr1	AUCGUAGCCAAUGUGCCGGA	116389683	79
202	chr1	GGUCAUCCAGUCCACUCGG	116400948	79
203	chr1	UGACCGCUGGAUCAACGAUG	116400978	79
204	chr1	AUCAUCAGGCGACGCCUGG	116403971	79
205	chr1	UCUUUUUAAGGCACCGCACG	116389446	78
206	chr1	AGCACUUCGACAUUUGCCCA	116395259	78
207	chr1	CGUUGGGACCAUCUCGCGCC	116387322	77
208	chr1	UUCUGAUUCACCAGUGAGCG	116388917	77
209	chr1	GUGGAUAACUCCUCGCUCAC	116388919	77
210	chr1	CAGCAAACCUUCCGGCACA	116389678	77
211	chr1	CGCCCGUGGAGGGUCAAUCA	116395223	77
212	chr1	UCAGGAACGGCCGCCCGUGG	116395234	77
213	chr1	CAUGAUUGACCCUCCACGGG	116395236	77
214	chr1	CAAACAUUCCACUACCACUG	116399040	77
215	chr1	GAAUGAGCGGCUGAUCAGCA	116399523	77
216	chr1	GCUGAGAUCCUGGCGCGAGA	116387326	76
217	chr1	GUGGUAUUGUUGUCUACACU	116389465	76
218	chr1	GACACUACUGCCAAACGCA	116390238	76
219	chr1	UGUUGGGGCUCCGAUGUGUU	116393554	76
220	chr1	CACCACGAUACUGACGAAGA	116401178	76
221	chr1	AGAGGAUCAACUUACUUGAG	116401653	76
222	chr1	AAUGCCCAUAAUACCGCCA	116403973	76
223	chr1	CUCAUCAUCAGGCGACGCC	116403968	76
224	chr1	GACAAAGCGUCUGGUACCU	116388244	75
225	chr1	UAUCCACAUAUCACGGGUG	116389574	75
226	chr1	UGAUGAAGGGCGCCCCAGAA	116393597	75
227	chr1	UCUGGGGUAGGGUGCUAUCG	116398628	75
228	chr1	UCACCUUUGGGCCUCCGAG	116400948	75
229	chr1	ACGAUGUGGAAGACAGCUAC	116400992	75
230	chr1	CAGAGGAUCAACUUACUUGA	116401654	75
231	chr1	CUCCAAUAGGCGUUCUGAA	116393678	74
232	chr1	AUCACUGCCGUGUACUACGC	116397904	74
233	chr1	CUCUACUCCAGUCACAAUUG	116398768	74
234	chr1	GAGUGGACUGGGAUGACCGC	116400965	74
235	chr1	CCAGAGGAUCAACUUACUUG	116401655	74
236	chr1	GAAUGCCCAUAAUACCGCC	116403974	74
237	chr1	CUCACCAUUUCGAAUCACAA	116388647	73
238	chr1	AGGCAAUGUCCUCGUCUCC	116388978	73
239	chr1	CGUGGUAUUGUUGUCUACAC	116389464	73
240	chr1	CCUCAAGCCAGGUGUACUCA	116389625	73

FIG. 5

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
241	chr11	GAACUACCCAGUCGUACGUG	27657922	82
242	chr11	ACACGCUCAGCUCCCCUCGG	27658161	80
243	chr11	AACUACCCAGUCGUACGUGC	27657921	79
244	chr11	UAUUAGUGAGUGGGUAACGG	27658119	79
245	chr11	UCAUGCCAUACAGAAGCGUG	27674165	79
246	chr11	GGUAGACGCCAAAACAUGUG	27674187	79
247	chr11	AAGGGCCCGCACGUACGACU	27657928	78
248	chr11	ACGACUGGGUAGUUCGGCAC	27657942	78
249	chr11	CGACUGGGUAGUUCGGCACU	27657943	78
250	chr11	CUCUGACCCUGCCCGCCGAG	27658161	78
251	chr11	AGAGUGGCGCCGGACCCUCA	27658192	78
252	chr11	UCCCAUGGGUCCGCACACCU	27658458	78
253	chr11	UCUACCCACACGCUUCUGUA	27674158	78
254	chr11	GUACGUGCGGGCCCUUACCA	27657909	76
255	chr11	AGUGGACAUGUCGGGCGGGA	27658080	76
256	chr11	UUGACUACUGAGCAUACCC	27658285	76
257	chr11	UGUGUACCUCCACGUUUCAG	27674103	76
258	chr11	CGAGACCAAGUGCAAUCCCA	27658002	75
259	chr11	ACUGCAGUGGACAUGUCGGG	27658085	75
260	chr11	ACUCUGACCCUGCCCGCCGA	27658162	75
261	chr11	ACGCAGACUUGUACACGUCC	27658291	75
262	chr11	GGGACUCUGGAGAGCGUGAA	27658427	75
263	chr11	ACCCAGGUGUGCGGACCCAU	27658447	75
264	chr11	UGUUAAAUUCACUGAAACG	27674106	75
265	chr11	CAUGCCAUAACAGAAGCGUGU	27674166	75
266	chr11	UAAGGGCCCGCACGUACGAC	27657927	74
267	chr11	GAAUUGGCUGGCGAUUCAUA	27657874	73
268	chr11	CUGCAGUGGACAUGUCGGGC	27658084	73
269	chr11	AUGGGUCCGCACACCUUGGU	27658462	73
270	chr11	GCACGUACGACUGGGUAGUU	27657936	72
271	chr11	GUCCCAUGGGUCCGCACACC	27658457	72
272	chr11	GGAUUAACCUUGUGCACUCA	27674256	72
273	chr11	UACCCAGGUGUGCGGACCCA	27658448	71
274	chr11	GUAACCCAUGGGAUUGCACU	27658009	70
275	chr11	GGACUCUGGAGAGCGUGAAU	27658426	70
276	chr11	GAAGCAAACAUCCGAGGACA	27658481	70
277	chr11	ACACGUGAUAAGAAGAGCUGU	27658356	69
278	chr11	CACGCUCUCCAGAGUCCCAU	27658444	69
279	chr11	GCUCAGUAGUCAAGUGCCUU	27658263	68
280	chr11	UGUGCGGACCCAUGGGACUC	27658440	68
281	chr11	CUUCAUUGGGCCGAACUUUC	27658338	66

FIG. 6

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
282	chr11	UACCGCACCGCUUAGAUCUG	14968983	80
283	chr11	CCAACCCCAAUUGCAGUUUG	14968901	77
284	chr11	CAUGCUGGGCACAUACACGC	14968935	77
285	chr11	UUCUGGGGCAUGCUAACAUG	14968826	76
286	chr11	UUACCGCACCGCUUAGAUCU	14968982	76
287	chr11	AAUCUGAGUACUUGCAUGCU	14968949	75
288	chr11	AGCCCCAGAUCUAAGCGGUG	14968973	74
289	chr11	CGCUUCGUCCUCACUGAGCG	14970038	74
290	chr11	GCAUGCUAACAUGAGGGCGA	14968833	73
291	chr11	AAGGGAUAUGUCCAGCGACU	14968851	73
292	chr11	AUGGUCUCUCUCCAAGUCGC	14968852	73
293	chr11	GUUCCCCAAACUGCAAUUG	14968893	73
294	chr11	UAAUCUGAGUACUUGCAUGC	14968950	73
295	chr11	UCGUCCUCACUGAGCGUGGC	14970042	73
296	chr11	GGACGAAGCGCGCCUCCUGC	14970013	71
297	chr11	CGUCCUCACUGAGCGUGGCC	14970043	71
298	chr11	AUUACCGCACCGCUUAGAUC	14968981	70
299	chr11	CUCCAACCCCAAUUGCAGUU	14968899	69
300	chr11	CGUUCSCCCAAACUGCAAUU	14968894	66
301	chr11	CCCCAAACUGCAAUUGGGGU	14968889	65

FIG. 7

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
302	chr11	CGCGUCCUCUUUACUGAGUG	15075095	78
303	chr11	UAUCUUGGUCCUGUACCAGG	15074774	77
304	chr11	ACCUGAAUGGCGCCGCCUGG	15074789	77
305	chr11	UAUUGGCUGGACCUACCUGA	14978358	76
306	chr11	CCCGGCCACACUCAGUAAAG	15075102	76
307	chr11	CCUUUACAGAGAGGCGGCAU	15074718	74
308	chr11	CAGCCGAUGAGUCACACAGG	15077323	73
309	chr11	AAAGAGGCUAACCUUCAGGU	14978359	72
310	chr11	CAGUAUCUUGGUCCUGUACC	15074771	72
311	chr11	AUCUUGGUCCUGUACCAGGC	15074775	72
312	chr11	UGCCAGCCGAUGAGUCACAC	15077326	70
313	chr11	AGGCUUGCUGAGCAGAUCA	15077360	70
314	chr11	AUCCUUCUUUACAGAGAGG	15074712	69
315	chr11	AGAGGACGCGCGCCUCCUGC	15075120	69
316	chr11	GCUUUGGAACCCACAUUGGU	15077394	69
317	chr11	CAACUUCGUGCCCACCAAUG	15077396	69
318	chr11	GUCCCUGCGCGCCUGCCAA	15077416	69

FIG. 8

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
319	chr2	GUGGGUGUUAACAUUACACU	187380496	80
320	chr2	UGUACAGAUUGGAUUCGCU	187352265	77
321	chr2	CCUACACACACUCAUUGUGG	187360654	76
322	chr2	AUCCGUGUCCAUAUUAUGGUC	187379006	76
323	chr2	GACAUACCUUCACUUUCUCG	187380477	76
324	chr2	CUGAUUCCAUGGCGACCUGA	187352174	75
325	chr2	GCAAUGGCAUGUAUACAAGC	187359253	75
326	chr2	CGUUUACUGCAACAGAACCU	187380769	75
327	chr2	CCUGAGGACUCAAUUCAGUU	187383258	75
328	chr2	UUAGGAGCCUAAGUUGCCAA	187363489	74
329	chr2	UACCUGACCAUAUUGGACA	187378996	74
330	chr2	CGUGGGUGUUAACAUUACAC	187380495	73
331	chr2	UGUGAGAGCUACUCUUAUCU	187352223	71
332	chr2	GCACAUCCUUAUGCACUUC	187352118	70
333	chr2	UGCUGGAACGAUGUUGCAGC	187380735	70
334	chr2	GCGUUUACUGCAACAGAACC	187380770	70
335	chr2	CACUGCAGUGGCCAACAACC	187363401	69
336	chr2	GGCUACUAAGGCCUGGUUGU	187363402	69
337	chr2	GCAUCACUGCUUAUCUCGCU	187378963	68
338	chr2	AGACAAUCCGUGUCCAUAUA	187379001	68
339	chr2	GCCAUACCUUGGAAGUGCAUA	187352124	67
340	chr2	GGACAGUCAUGACUAUAACC	187346277	66

FIG. 9

SEQ ID NO:	Chromosome:	Protospacer (crRNA)	Cut site coordinate	Score
341	chr17	CAGCCACCUUCAUCCCCAA	34255407	74
342	chr17	GUUAUAACAGCAGGUGACUG	34256239	74
343	chr17	AGCGAGCCCUUGGGGAAUGA	34255401	73
344	chr17	UUGCUUGUCCAGGUGGUCCA	34256789	73
345	chr17	UAUGAGCAGCAGGCACAGAA	34255371	72
346	chr17	GGCGGCAGAGACUUUCAUGC	34255350	71
347	chr17	UACCUGGCUGAGCGAGCCCU	34255411	71
348	chr17	GCAGCCACCUUCAUCCCCA	34255406	71
349	chr17	AUAGGAAGAUCUCAGUGCAG	34256281	71
350	chr17	GAGCAGCAGGCACAGAAGGG	34255368	70
351	chr17	CCUGGCUGAGCGAGCCCUUG	34255409	70
352	chr17	ACCUGGCUGAGCGAGCCCUU	34255410	70
353	chr17	AAGUUAUAACAGCAGGUGAC	34256241	70
354	chr17	GAGCCCUUGGGGAAUGAAGG	34255398	69
355	chr17	AGUUAUAACAGCAGGUGACU	34256240	69
356	chr17	GUGUUCAAGUCUUCGGAGUU	34256814	69
357	chr17	AUUGGUGAAGUUAUAACAGC	34256248	68

FIG. 10

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
358	chr17	AUUCUGUGGAAUCUGCCGGG	36089253	69
359	chr17	CCUGGAGCUGAGUGCCUGAG	36088673	67
360	chr17	UCUGGACCCACUCCUCACUG	36088721	66
361	chr17	ACUGGCACUUACAUGACACC	36089188	65
362	chr17	ACUCACGUGAUGCAGAGAAC	36089997	65
363	chr17	GGUCUGUGCUGACCCCAGUG	36088721	64
364	chr17	CCUAACCAAGCGAAGCCGGC	36088742	64
365	chr17	GACUGGCACUUACAUGACAC	36089187	64
366	chr17	GUGCUGACCCCAGUGAGGAG	36088716	63
367	chr17	GCUUCCUAACCAAGCGAAGC	36088746	63
368	chr17	ACAGACCUGCCGGCUUCGCU	36088749	62
369	chr17	CCUGCCGGCUUCGCUUGGUU	36088754	62
370	chr17	AGAGAGCCAUGGUGCAGAGG	36090024	62
371	chr17	GGUGCAGAGGAGGACAGCAA	36090034	62
372	chr17	UCACCUGCUCAGAAUCAUGC	36090057	62
373	chr17	UAGUCAGCUAUGAAAUUCUG	36089239	61
374	chr17	GAAAUUCUGUGGAAUCUGCC	36089250	61

FIG. 11

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
375	chr17	CUGAGACUCACACGACUGCU	35878534	71
376	chr17	AGGUACCAUGAAGGUCUCCG	35880295	71
377	chr17	UAUGACUCCCGGCUGAACAA	35875570	69
378	chr17	GUAUGACUCCCGGCUGAACA	35875571	69
379	chr17	GACUCACACGACUGCUGGGU	35878538	69
380	chr17	UACUCCUUGAUGUGGGCACG	35878584	69
381	chr17	UAGCAAUGAGGAUGACAGCG	35880280	69
382	chr17	CUGGGUUGGCACACACUUGG	35872441	68
383	chr17	UCUUUGGCAUCCUUGACCUG	35875637	68
384	chr17	CUCUCCACAGGUACCAUGA	35880304	68
385	chr17	UACCCACCCGCUCCUUGAA	35872271	67
386	chr17	GGUAGAAUCUGGGCCCUUCA	35872270	67
387	chr17	UCUCUGGGUUGGCACACACU	35872438	67
388	chr17	AUACUCCUUGAUGUGGGCAC	35878583	67
389	chr17	GGUGUGGUGUCCGAGGAAUC	35878638	67
390	chr17	UCAAGACCAGGACUUACAUG	35880230	67
391	chr17	AGACCAGGACUUACAUGGGG	35880233	67

FIG. 12

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
392	chr17	ACAUACAUUACAGCUUCCCG	34271252	79
393	chr17	GUCCUGGACCCACUUCUGUG	34271740	75
394	chr17	CCGGGGACAGUGGCUACUGG	34271235	74
395	chr17	CCUGGACCCACUUCUGUGUG	34271738	72
396	chr17	UCCUGGACCCACUUCUGUGU	34271739	72
397	chr17	CUGGCUGAGCAAGCCCCUGG	34270349	71
398	chr17	UUACAGCUUCCCGGGGACAG	34271245	71
399	chr17	ACAGAUCUCCUUGUCCAGUU	34271710	71
400	chr17	CACCAGUAGCCACUGUCCCC	34271248	70
401	chr17	CAGCUGCUUUCAGCCCCCAG	34270348	69
402	chr17	GUCCAUUGAGGGUGUGUCCU	34271103	69
403	chr17	AGUCCAUUGAGGGUGUGUCC	34271104	69
404	chr17	ACAAGAAGAAAAGUCCAUUG	34271115	69
405	chr17	GACCCAGGACACACCCUCAA	34271113	69
406	chr17	UUCCCGGGGACAGUGGCUAC	34271238	69
407	chr17	CCACCAGUAGCCACUGUCCC	34271247	69
408	chr17	CCAGGUGCUUCAUAAAGUCC	34271756	69

FIG. 13

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
409	chr2	CUUCUGAUUCGCCGCAGAGG	227813970	79
410	chr2	GUGCUGCUACUCCACCUCUG	227813971	78
411	chr2	ACACGGCAGCUGGCCAAUGA	227815542	77
412	chr2	AUGUCAGUGUAACAUACCUG	227816384	77
413	chr2	UACCUUCUGAUUCGCCGCAG	227813973	76
414	chr2	CAAACUCUUGGUACAGCACA	227813915	72
415	chr2	GCGCAAUCCAAAACAGACU	227816353	72
416	chr2	AAUUUAUUGUGGGCUUCACA	227815525	71
417	chr2	CGCAAUCCAAAACAGACUU	227816354	70
418	chr2	CUGUACCAAGAGUUUGCUCC	227813934	69
419	chr2	AGCAGCCAGGAGCAAACUCU	227813927	68
420	chr2	GCACUGACAUCAAAGCAGCC	227813940	68
421	chr2	CACCUCUGCGGCGAAUCAGA	227813983	68
422	chr2	UGUGGGCUUCACACGGCAGC	227815532	68
423	chr2	AUUGAUGUCACAGCCUUCAU	227815543	68
424	chr2	AGCAACUUUGACUGCUGUCU	227815476	65
425	chr2	GUGAAGCCCACAAUAAUJU	227815509	64

FIG. 14

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
426	chr6	CGAACGUCCAUGCUGCACAG	131950425	84
427	chr6	AAGACUCGACUCACCCGCGA	131950295	83
428	chr6	CUUGAACUCCACCGGCAGGG	131949413	81
429	chr6	ACCGUACCACCGAAGAUGCA	131950524	81
430	chr6	GACCCAUGCACCCGCACAA	131950828	81
431	chr6	GAAGACUCGACUCACCCGCG	131950294	80
432	chr6	GGUGGUACGGUGUACCGCAG	131950500	80
433	chr6	UCUGGAAGGACUCUCCGCU	131950498	80
434	chr6	CGGGUCGCAUGGGUCGCGCU	131950848	79
435	chr6	GUUCAAGUGCCCUGACGGCG	131949385	78
436	chr6	GGGGGUGCAGCAUCGGCCGU	131949446	78
437	chr6	CGAGCCCAAGGACCAACCG	131950315	78
438	chr6	CUGCAGUUCUGGCCGACGGC	131950987	78
439	chr6	GCGGACGGGGCCCAUACUGG	131951160	78
440	chr6	UAUGAUUAGAGCCAACUGCC	131950106	77
441	chr6	UGCUCUCGCAGCUUACCGAC	131950154	77
442	chr6	UCCGGGACAGUUGUAAUGGC	131949338	76
443	chr6	GUUGUCAUUGGUAACCCGGG	131950044	76
444	chr6	GGGCAGGCCCAACCACGGUU	131950315	76
445	chr6	ACGAACGUCCAUGCUGCACA	131950424	76
446	chr6	CCCGCUGCAGUUCUGGCCGA	131950983	76
447	chr6	UCAGGGCACUUGAACUCCAC	131949405	75
448	chr6	UUCUGUGGAGUAUGUACCGA	131949450	75
449	chr6	AGAGCCGCCUGUGCAUGGUC	131949987	75
450	chr6	GGCGUUGUCAUUGGUAACCC	131950041	75
451	chr6	GGCCAAACGUGUCUCCAGU	131950151	75
452	chr6	AGCUUGACCCUCCUCGGGAA	131950383	75
453	chr6	AGCACGAGGCUCACGCCCGC	131950924	75
454	chr6	GACGGGGCCCAUACUGGCGG	131951163	75
455	chr6	AGCUCGGUAUGUCUUAUGC	131949488	74
456	chr6	CGCAAGGCCUGACCAUGCAC	131949992	74
457	chr6	UACCGACUGGAAGACACGUU	131950141	74
458	chr6	GCUUGACCCUCCUCGGGAAG	131950384	74
459	chr6	GACGAACGUCCAUGCUGCAC	131950423	74
460	chr6	CCAGUGCACGUGCCUGGACG	131950450	74
461	chr6	CAAGUACCAGUGCACGUGCC	131950456	74
462	chr6	UCCCUGCAUCUUCGGUGGUA	131950513	74
463	chr6	UCCCCGGCCAACCGCAAGAU	131950786	74
464	chr6	CGGUGCACACGCCGAUCUUG	131950787	74
465	chr6	ACGCCGAUCUUGCGGUUGGC	131950795	74
466	chr6	AUUCUGUCACUUCGGCUCCC	131950802	74
467	chr6	ACCAUGACCGCCGCCAGUUA	131951158	74
468	chr6	AACCAUGACCGCCGCCAGUA	131951159	74
469	chr6	UGUCUCCGGGACAGUUGUAA	131949334	73
470	chr6	CCCAAGGACCAACCGUGGU	131950311	73
471	chr6	CAGCUUGACCCUCCUCGGGA	131950382	73
472	chr6	CGCAAGAUCGGCGUGUGCAC	131950774	73
473	chr6	CGACCCAUGCACCCGCACA	131950829	73

FIG. 15

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
474	chr17	GGAGCGCCGGAUGUGCCGAC	40554804	80
475	chr17	ACGCAACUUUGAGCGCAACA	40555103	80
476	chr17	CAUCAGCAUUGACCGCUACG	40555415	80
477	chr17	AGGCAGAAGAGUCGCCUAUG	40554744	79
478	chr17	CCGGCGCUCCUCCAUGAGUG	40554779	79
479	chr17	GCCGCGCUGUAGGCCAGAA	40555540	78
480	chr17	GAGGUCACGGACGAUUACAU	40555783	78
481	chr17	GCGCUCCUCCAUGAGUGUGG	40554776	77
482	chr17	UCCCUUCUGGGCCUACAGCG	40555529	77
483	chr17	GAGCAGGUAGGUAUCGGUCA	40555602	77
484	chr17	CCGUGACCUCAUCUUGACAC	40555808	77
485	chr17	GCGGAACUUGACGCCGAUGA	40554894	76
486	chr17	UAGGCCACGAAACAAUGA	40555677	76
487	chr17	CAGGCAGAAGAGUCGCCUAU	40554743	75
488	chr17	GCCAGGACCACCCCAUUGUA	40555042	75
489	chr17	CUACGACGUCACCUACAGCC	40554941	74
490	chr17	GGUCUCGGCCUCCACACUCA	40554780	73
491	chr17	CCGAUGAAGGCGUACAAGAA	40554907	73
492	chr17	UGCGCUCAAAGUUGCGUGCC	40555121	73
493	chr17	CUACAGCGCGGCCAAGUCCU	40555517	73
494	chr17	UGAUGGAGUACAUGAUAGGG	40555694	73
495	chr17	CCACACUCAUGGAGGAGCGC	40554791	72
496	chr17	CAUCAAGGUGAUCAUCGCUG	40555079	72
497	chr17	UCGUGGGCCUACUGGGCAAU	40555653	72
498	chr17	ACGUGCGGAACUUUAAAGCC	40555707	72
499	chr17	GUUGACGCAGCAGCGGACGC	40554930	71
500	chr17	CCAGGACUUGGCCGCGCUGU	40555530	71
501	chr17	AAAGUUCGCGACGUCCUUCU	40555728	71
502	chr17	UGUUGAAGUUGGCCACCGUC	40555019	70
503	chr17	CCGCUACGUGGCCAUCGUCC	40555403	70
504	chr17	GAAACCAAUGAAAAGCGUGC	40558924	70
505	chr17	CAGGCUGUAGGUGACGUCGU	40554954	69
506	chr17	CCUACAGCGCGGCCAAGUCC	40555518	69
507	chr17	GUACUCCAUCAUUUGUUUCG	40555670	69
508	chr17	CGAUGAAGGCGUACAAGAAA	40554908	68
509	chr17	UCUUCAGCUGCCCUACAAU	40555041	68
510	chr17	ACCAAUGAAAAGCGUGCUGG	40558921	68
511	chr17	ACCACCAGCACGCUUUUCAU	40558932	68
512	chr17	GUUGAAGUUGGCCACCGUCU	40555020	67
513	chr17	UCCUCUGGAGGUCACUGUAC	40555292	67
514	chr17	UACUCCAUCAUUUGUUUCGU	40555669	67
515	chr17	CCUUUCUUGUACGCCUUCAU	40554895	66
516	chr17	AUUUGUUUCGUGGGCCUACU	40555660	66
517	chr17	CACAGCGAUGAUCACCUUGA	40555092	65

FIG. 16

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
518	chr7	GAGUGAAGAGCGGCUCACGG	66152236	81
519	chr7	CCGGCGAGCACCUUGGCGCG	66114862	78
520	chr7	CCGCGCGCCAAGGUGCUCGC	66114850	76
521	chr7	CAAGCUCCCGGCAUGCAGCG	66114834	75
522	chr7	UCAGGACUCUGGUGCCUGCA	66134309	75
523	chr7	CCACAGCAGUCACAGGCCGG	66145472	75
524	chr7	GGGAUCGCCGCGCUGCAUGC	66114829	74
525	chr7	GGUGCCAGCUCCGCGCGCCA	66114860	74
526	chr7	GGCGAUCCCGGCGAGCACCU	66114855	74
527	chr7	UGCUCUUCUCAGUAACUACG	66127736	74
528	chr7	UGGCACCUUGGCGCUGUUGG	66114888	72
529	chr7	UGGAUCUCCACAGCAGUCAC	66145479	72
530	chr7	AGAGAGUGAAGAGCGGCUCA	66152233	72
531	chr7	CGCCGCCACCAACAGCGCCA	66114881	71
532	chr7	GGCGCGCGGAGCUGGCACCU	66114876	70
533	chr7	ACAUAUCAAAAACACCAUGC	66134307	70
534	chr7	GCAGAAUGCUGGUGACGGUG	66152266	70

FIG. 17

SEQ ID NO.	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
535	chr4	AGAGAGCAGCGCGGGCCAUG	73869472	76
536	chr4	ACCUUCUGCGCGCCGGCCAG	73869555	74
537	chr4	GAGCCACACUCAAGAAUGGG	73869922	74
538	chr4	CUAUGGGGGAUGCAGGAUUG	73869941	74
539	chr4	GCACUGGCAGCGCAGUUCAG	73869686	73
540	chr4	GAGAGAGCAGCGCGGGCCAU	73869473	72
541	chr4	AGUGCCACUCGCAGGAGCCG	73869512	72
542	chr4	UUCUUCCCUAGGAGCGUCCG	73869675	72
543	chr4	ACUUCGGUUUGGGCGCAGUG	73869772	72
544	chr4	CGCGCCGGCCAGCGGCUACC	73869547	71
545	chr4	GAUGAUUUUCUUAACUAUGG	73869955	71
546	chr4	CUGGCCGGCGCGCAGCAGGU	73869570	70
547	chr4	CUUGGGGUGAAUUCCUGCA	73869716	69
548	chr4	AGUGUGAACGUGAAGUCCCC	73869760	69
549	chr4	GGGCGGCGGAGAGAGCAGCG	73869481	68
550	chr4	GGAGCAGCAGUGCCACUCGC	73869520	68
551	chr4	UGCUCUGGUAGCCGCUGGC	73869555	68

FIG. 18

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
552	chr4	UCUUAACCAUGGGCGAUGCG	74098643	85
553	chr4	UCUCAACCCCGCAUCGCCCA	74098637	78
554	chr4	UUUCUUAACCAUGGGCGAUG	74098641	74
555	chr4	CAGCGCAGUUCAGUGGCCAG	74098912	74
556	chr4	UUCUUAACCAUGGGCGAUGC	74098642	73
557	chr4	AGAGCGUGGCGCGGGCCAUG	74099119	73
558	chr4	ACUUCGGUUUGGGCGCAGUG	74098819	72
559	chr4	GCACUGGCAGCGCAGUUCAG	74098905	72
560	chr4	UUCUUCUUAGGAGCGCCCC	74098916	72
561	chr4	CAAGAACAUCCAAAGUGUGA	74098844	70
562	chr4	CUUGAGGUGAAUUCCCUGCA	74098875	70
563	chr4	AGUGUGAAGGUGAAGUCCCC	74098831	69
564	chr4	ACCUGCUGCGCGCCGGCUGG	74099036	69
565	chr4	GGGACCCACCUGCUGCGCGC	74099029	68
566	chr4	GAGAGCGUGGCGCGGGCCAU	74099118	68
567	chr4	GGGCGAGACUUACAUGACUU	74098803	67
568	chr4	CAGUGCUUGCAGACCCUGCA	74098876	67

FIG. 19

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
569	chr4	UCUGAACCAUGGGGGAUGCG	74038135	81
570	chr4	AGUGUGAAUGUAAGGUCCCC	74038322	78
571	chr4	CAGGGGGAGCACCAACUGAC	74037263	76
572	chr4	GAUGAUUUUCUGAACCAUGG	74038127	74
573	chr4	UUCUUCCCUAGGAGCGUCCG	74038407	74
574	chr4	ACUUCGGUUUGGGCGCAGUG	74038310	72
575	chr4	UCUCAACCCCGCAUCCCCCA	74038129	71
576	chr4	CGAUGAUUUUCUGAACCAUG	74038126	71
577	chr4	ACAUCCAAAGUGUGAAUGUA	74038330	71
578	chr4	GGGACCUUACAUUCACACUU	74038338	71
579	chr4	CAGUGCUUGCAGACACUGCA	74038367	71
580	chr4	GCAGCGCAGUUCAGUGACCA	74038402	71
581	chr4	AGAGCGUGGCGUGGGCCAUG	74038610	71
582	chr4	ACCUGCUGCGCGCCGGCUGG	74038527	69
583	chr4	UCGAUGAUUUUCUGAACCAU	74038125	68
584	chr4	GGGACCCACCUGCUGCGCGC	74038520	68
585	chr4	GAGAGCGUGGCGUGGGCCAU	74038609	68

FIG. 20

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
586	chr4	UUUGGGAUGAACUCCUUGCG	73998282	79
587	chr4	ACAAGGAGCUCGAAGGACCG	73998544	79
588	chr4	AAUCUGCAAGUGUUCGCCAU	73998238	78
589	chr4	AGCGCGCACAAAGGAGCUCGA	73998537	77
590	chr4	CAUAGGCCCCACAGUGCUGCA	73998221	76
591	chr4	CAGCCAGGGCCCAUCGCCAG	73998477	76
592	chr4	GUUUGUUUACAGACCACGCA	73998283	75
593	chr4	GCUCGAAGGACCGGGGACAC	73998551	75
594	chr4	AGGCCACAGUGCUGCAAGG	73998218	74
595	chr4	GCGCUCUCACCGCUGGCGAU	73998480	74
596	chr4	GCGCCAUGCGCUCUCACCGC	73998473	73
597	chr4	GCACAAGGAGCUCGAAGGAC	73998542	73
598	chr4	AGCUCGAAGGACCGGGGACA	73998550	73
599	chr4	AGCCUCCCUGAAGAACGGGA	73998078	71
600	chr4	CUUGGAGCACUGUGGGCCUA	73998234	71
601	chr4	CACAAGGAGCUCGAAGGACC	73998543	69
602	chr4	ACUUCCACCUUGGAGCACUG	73998226	68

FIG. 21

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
603	chr4	UGGAGCACUGCGGGGCCUGCG	73837066	79
604	chr4	AGGAGCUCUCAACCGCUGGCG	73836854	77
605	chr4	GAGCUCUCACCGCUGGCGAG	73836852	76
606	chr4	CCGCCGGGGCCCCUCGCCAG	73836855	76
607	chr4	CGCAGGCCCGCAGUGCUGCA	73837081	76
608	chr4	ACACGGGCCCGCGCGGCUGGA	73836765	74
609	chr4	GCCCGAAGGACCCGGGACAC	73836781	74
610	chr4	AGCGCGCACAAGGAGCCCGA	73836795	74
611	chr4	CUUGGAGCACUGCGGGGCCUG	73837068	74
612	chr4	AGGCCCGCAGUGCUGCAAGG	73837084	74
613	chr4	ACAAGGAGCCCGAAGGACCC	73836788	73
614	chr4	GCAGUUUACCAAUCGUUUUG	73837036	73
615	chr4	AAACUGCAGGUGUUCGCCGC	73837064	73
616	chr4	GUGCCAGGAGCUCUCAACCGC	73836859	72
617	chr4	CAAAACGAUUGGUAAACUGC	73837051	72
618	chr4	AGCCCGAAGGACCCGGGACA	73836782	71
619	chr4	CAGCCGCGCGGCCCGUGUCC	73836782	70

FIG. 22

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
620	chr4	AUUUCUGUGUUGGCGCAGUG	73741657	79
621	chr4	CUAAGUUCUUUAGCACUCCU	73741558	71
622	chr4	UGUAAACAUGACUCCAAGC	73740669	70
623	chr4	CAACAGGUGCAGUUUUGCCA	73741553	70
624	chr4	CAAGAGAGCCACGGCCAGCU	73740671	69
625	chr4	GAACUGAGAGUGAUUGAGAG	73741645	69
626	chr4	CAUGACUCCAAGCUGGCCG	73740675	68
627	chr4	CAGAGCUGCAGAAAUCAGGA	73740698	68
628	chr4	UGAUGGAAGAGAGCUCUGUC	73741978	68
629	chr4	AGAGCUCUGUCUGGACCCCA	73741987	68
630	chr4	AAAUUUGGGGUGGAAAGGUU	73741604	67
631	chr4	UCUGGACCCCAAGGAAAACU	73741996	67
632	chr4	UCUGCACCCAGUUUCCUUG	73741990	66
633	chr4	GUUCUUUGAUAAAUUUGGGG	73741614	65
634	chr4	GAAGGCUGCCAAGAGAGCCA	73740680	64
635	chr4	CACACAGAGCUGCAGAAAUC	73740702	64
636	chr4	AUUUCUGCAGCUCUGUGUGA	73740718	63

FIG. 23

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
637	chr2	UUCCAGUCCAGUUUGCUAUG	218164649	76
638	chr2	ACUGACCCAGAAGCGUCACU	218164760	76
639	chr2	GCGCCGCAACAACAUCCGCC	218164361	75
640	chr2	GGGCCUUAAACAGUGUACGC	218164532	75
641	chr2	GCGAAAAUUUUGGCCGAUGA	218164290	74
642	chr2	GUCUCAGUUUCUAGCAUACA	218165122	74
643	chr2	GACCUCAUAGCAAACUGGAC	218164659	72
644	chr2	GAUGGUAAGCCUGGCGGAAA	218164691	72
645	chr2	AUCGGCCAAAAUUUUCGCCA	218164273	71
646	chr2	UGUGAGCGCCGCAACAACAU	218164366	71
647	chr2	CGGAUCCUGCCUCACACCUU	218164588	71
648	chr2	CUUGACCAAGUGACGCUUCU	218164767	71
649	chr2	UGUCUCAGUUUCUAGCAUAC	218165121	71
650	chr2	AGCGCCGCAACAACAUCCGC	218164362	70
651	chr2	GGGCCCCGGCCGAUGUUGUUG	218164370	70
652	chr2	ACUUGACCAAGUGACGCUUC	218164766	70
653	chr2	UCCAGUUUGCUAUGAGGUCC	218164643	69
654	chr2	CAACAACAUCGGCCGGGCCC	218164355	68
655	chr2	CCAUGGAUUCUCAAGAUGC	218164256	65

FIG. 24

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
656	chr2	GCUACUGGCCUGCAUCAGUG	218135223	78
657	chr2	UGGAUGAGUAGACGGUCCUU	218135355	78
658	chr2	GAGCCCGGUCGAUGUGAUUG	218135670	78
659	chr2	AAGGAUGCCCAGAAUCUCGG	218135699	77
660	chr2	UGUUAGCCCAGCCUGCUAUG	218135391	76
661	chr2	GAUGUGAUJGCGGCGCUCAC	218135660	76
662	chr2	GCGCCGCAAUCACAUCGACC	218135679	76
663	chr2	UAAGAUGACCAGCAUCACGA	218135006	75
664	chr2	ACUGACCCAGAAGCGCUACU	218135280	75
665	chr2	CAGGCUCAGCAGGAAUACCA	218134973	74
666	chr2	AAGGAAGUCAACUUCUAUAG	218135194	74
667	chr2	CAUGUAUAGCUAGAAUCUUG	218135781	74
668	chr2	UGUGGUCAUUAUCUAUGCCC	218134968	73
669	chr2	GUCCUUCGGAAAAGUAAGAC	218135341	73
670	chr2	GGGCCUUAACAGCGUACGC	218135508	73
671	chr2	AUUGGCCAGAAGUUUCGCCA	218135767	73
672	chr2	UAUACAUGGCUUGAUCAGCA	218135808	73

FIG. 25

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
673	chr4	GAUGUGACGCCGCGGCCCGG	122826823	85
674	chr4	CGGACAGAAGAGCGGCCGAG	122826997	81
675	chr4	CGGCUGUACUGCAAAAACGG	122827282	81
676	chr4	GCGGGUCGGCACUCACUGUG	122827351	81
677	chr4	CGGGUCGGCACUCACUGUGA	122827350	80
678	chr4	GAAAUACACCAGUUGGUAUG	122892299	80
679	chr4	AUGUGGCACUGAAACGAACU	122892316	80
680	chr4	CCGGGAUCCCGUUGCAACCG	122826858	79
681	chr4	UUCACGGAUGGGUGUCUCCG	122826919	79
682	chr4	AUUAGCGGACGCGGUGCCCG	122826853	78
683	chr4	GCGGCUGUACUGCAAAAACG	122827281	78
684	chr4	AUGUAGAAGAUGUGACGCCG	122826815	77
685	chr4	GGGUGCCAGAUUAGCGGACG	122826844	77
686	chr4	CGGGAUCCCGUUGCAACCGC	122826857	77
687	chr4	CGCGGUUGCAACGGGAUCCC	122826871	77
688	chr4	GUCUCCGCGGACGCCGCCUG	122826906	77
689	chr4	CCCCGUAACUCGGCCGUCG	122827311	77
690	chr4	GACCCCGUAACUCGGCCGU	122827313	77
691	chr4	CCCCGACGGCCGAGUUGACG	122827323	77
692	chr4	GCGGUGCCCGCGGUUGCAAC	122826863	76
693	chr4	AAGAGCGGCCGAGCGGCUCG	122827004	76
694	chr4	GCUGCCGCCAUCCUCGGGCA	122827211	76
695	chr4	UCCGCUAAUCUGGCACCCGC	122826827	75
696	chr4	CCGCGGUUGCAACGGGAUCC	122826870	75
697	chr4	GGGACCUGGGUUCACGGAU	122826930	75
698	chr4	GACACCAUCCGUGAACCCC	122826938	75
699	chr4	UUUUGCAGUACAGCCGCUUG	122827263	75
700	chr4	UUCCUGCGCAUCCACCCCGA	122827309	75
701	chr4	CGGCCGAGUUGACGGGGUCC	122827329	75
702	chr4	UAUGUGGCACUGAAACGAAC	122892315	75
703	chr4	CCCGGCGGGUGCCAGAUUAG	122826838	74
704	chr4	CGCCGGCUCGCCGCGCACCA	122826969	74
705	chr4	GCCGGCUCGCCGCGCACCAG	122826970	74
706	chr4	UCGGCCGCUCUUCUGUCCGC	122826981	74
707	chr4	CGUCAACUCGGCCGUCGGGG	122827308	74
708	chr4	ACGGCCGAGUUGACGGGGUC	122827328	74
709	chr4	CGAACUGGGCAGUAUAAACU	122892330	74
710	chr4	AUCUGGCACCCGCCGGGCCG	122826820	73
711	chr4	ACCCCGUAACUCGGCCGUC	122827312	73
712	chr4	UCUCCCGGACCCCGUAACU	122827320	73
713	chr4	CACCCCGACGGCCGAGUUGA	122827321	73
714	chr4	ACCCCGACGGCCGAGUUGAC	122827322	73
715	chr4	GAAGAUGUGACGCCGCGGCC	122826820	72
716	chr4	CCGCUAAUCUGGCACCCGCC	122826826	72
717	chr4	CGCGGUGCCCGCGGUUGCAA	122826862	72
718	chr4	CUCUCCCCAGGCGGCGUCCG	122826914	72
719	chr4	CGGCCGAGCGGCUCGAGGCU	122827009	72
720	chr4	GCCGCUUGGGGUCCUUGAAG	122827251	72

FIG. 26

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
721	chr8	UGUGGUGAAUGUCCCGUGCG	38414822	84
722	chr8	UGAGGAAUGAUCCCAUUCGG	38424414	82
723	chr8	CCAGUGGCUAAAAGCACAUUCG	38424567	82
724	chr8	CAACCGCACCCGCAUCACAG	38429795	82
725	chr8	GCAUGGUUGACCGUUCUGGA	38421801	81
726	chr8	GUGAAGCUAACCAGUCUGCG	38423058	81
727	chr8	GAACUCCACGUUGCUACCCA	38424637	81
728	chr8	AGGAAACCAUCCAUGGUCGA	38412452	80
729	chr8	GAGCUCUACGUGCUCUCAG	38413728	80
730	chr8	GGAAGACCUGGACCGCAUCG	38413940	80
731	chr8	UUCUCCAAGGAAACCGGUG	38412422	79
732	chr8	GGCCCAGCAGCCAUCGACCA	38412450	79
733	chr8	GCGCCUCUACUGCAUGGAUG	38412500	79
734	chr8	AUACUCCACGAUGACAUACA	38416052	79
735	chr8	ACCCAACCGUGUGACCAAAG	38417893	79
736	chr8	CGCAGGGGAGUAUACGUGCU	38421856	79
737	chr8	GAAGGAGACCACUGUCUCGG	38424453	79
738	chr8	GUUGCCCCGCAACAAAACAG	38424648	79
739	chr8	ACCGGCCCAUCCUGCAAGCA	38424670	79
740	chr8	UUUUAACCAGCGCAGUGUG	38427982	79
741	chr8	CAGCAGCCAUCGACCAUGGA	38412446	78
742	chr8	AUCCAUGCAGUAGAGGCGCU	38412484	78
743	chr8	UGCCCAGCGCCUCUACUGCA	38412494	78
744	chr8	AUCGUGGAGUAUGCCUCCAA	38416029	78
745	chr8	GAGCAUCCCUCUGCGCAGAC	38419543	78
746	chr8	AUACUCCCCUGCGUCCUCAA	38421878	78
747	chr8	CAACGUGGAGUUAUGUGUA	38424615	78
748	chr8	GGUGUAGUUGCCCUUGUCAG	38426197	78
749	chr8	AUUUUUAACCAGCGCAGUG	38427980	78
750	chr8	AAGCAUCUCACCGAAAUCCC	38440354	78
751	chr8	UCCCCGACCUUGCCUGAACA	38457360	78
752	chr8	CGGCCUAGCGGUGCAGAGUG	38457395	78
753	chr8	GUUUCUCCAAGGAAACCGG	38412424	77
754	chr8	AGCGCCUCUACUGCAUGGAU	38412499	77
755	chr8	CAUUUGCAGGUGGUCUUUCG	38414281	77
756	chr8	UAGCAGACUUUGGCCUCGCA	38414823	77
757	chr8	UACUCCACGAUGACAUACAA	38416053	77
758	chr8	UCAGAGACCCCUGCUAGCAU	38418290	77
759	chr8	GAUGACCGACCCACCAUGC	38419649	77
760	chr8	AGUGUCUCACGCAUACGGUU	38428353	77
761	chr8	CAGCCACACUCUGCACCGCU	38457386	77
762	chr8	GAAGACGGAUCCUCCCCUG	38413726	76
763	chr8	UCCUCGGGCUUACAGCUCGU	38414156	76
764	chr8	GAUCCGGUCAAAUAAUGCCU	38414596	76
765	chr8	AGGUCCCUUGUAUGUCAUCG	38416045	76
766	chr8	AAGUAUUUUUACCUGUCCCG	38418233	76
767	chr8	GUGGGACUCCCAUGCUAGCA	38418286	76
768	chr8	UUGGUUUUUGUCCAGCAUUCG	38423172	76

FIG. 27

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
769	chr2	AUGGUGGUAGUAGCAACCAA	112781695	81
770	chr2	UAUGUAAUGCAGCAGCCGUG	112779528	80
771	chr2	GGUAGUAGCAACCAACGGGA	112781690	78
772	chr2	GGCCAUCGCCAAUGACUCAG	112781612	77
773	chr2	UGGUGGUAGUAGCAACCAAC	112781694	77
774	chr2	CUUCUUCAGAACCUUCCCGU	112781691	75
775	chr2	AGCUAUGGCCCACUCCAUGA	112781791	75
776	chr2	AGCCGUGAGGUACUGAUCAU	112779541	74
777	chr2	GAGAUACCCAAAACCAUCAC	112775241	72
778	chr2	CUCGAAUUAUACUUUGAUUG	112779564	72
779	chr2	GAUACUGGAAAACCAGGCGU	112775071	71
780	chr2	UUUGAUUGAGGGCGUCAUUC	112779576	71
781	chr2	GCUCUCCUUGAAGGUAAGCU	112781730	71
782	chr2	UGAGACUCCAGACCUACGCC	112775071	70
783	chr2	GGGUGCUUAUAAGUCAUCAA	112778081	69
784	chr2	GCACCCAUGUCAAAUUUCAC	112778110	69
785	chr2	UUCCUCUGAGUCAUUGGCGA	112781622	69
786	chr2	GGCUGCUGCAUUAACAUAUUC	112779510	65

FIG. 28

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
787	chr2	CAUGGCCACAACAACUGACG	112833479	80
788	chr2	GUGCAGUUCAGUGAUCGUAC	112832771	79
789	chr2	CUUCGACACAUGGGAUAACG	112832799	79
790	chr2	GAUCACUGAACUGCACGCUC	112832752	77
791	chr2	GGUGGUCGGAGAUUCGUAGC	112833526	77
792	chr2	UCCGACCACCACUACAGCAA	112833501	75
793	chr2	CUCCGACCACCACUACAGCA	112833502	75
794	chr2	GAGGUGCUGAUGUACCAGUU	112830466	74
795	chr2	CUUAUCAUCUUUCAACACGC	112831327	73
796	chr2	AUCACUGAACUGCACGCUCC	112832751	72
797	chr2	AUCAUUUCACUGGCGAGCUC	112836212	72
798	chr2	AACCUAUCUUCUUCGACACA	112832809	71
799	chr2	UGGUGAAGUCAGUUAUAUCC	112830398	70
800	chr2	AGAGGUGCUGAUGUACCAGU	112830465	70
801	chr2	CAUCUUUCAACACGCAGGAC	112831332	70
802	chr2	GCAGGCCGCGUCAGUUGUUG	112833472	70
803	chr2	AGUUUAUCCUGGCCGCCUU	112830408	69
804	chr2	UGAUGUACCAGUUGGGGAAC	112830473	68
805	chr2	UGAUAAGCCCACUCUACAGC	112831299	65

FIG. 29

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
806	chr2	UUCAGGACAUUACUUAUUGCG	102164999	80
807	chr2	UGGGGCUAUCCGCUGGUCAG	102176596	80
808	chr2	GUGUAAAGUCCCCUGACCAG	102176593	79
809	chr2	UGGUCAGGGGACUUUACACA	102176609	79
810	chr2	AUGGGGCUAUCCGCUGGUCA	102176595	78
811	chr2	ACCACAUGCCAGUCCAGCGA	102176673	78
812	chr2	ACUUCUCCAUGCUACCCGAG	102176753	78
813	chr2	UGGAAGGGAUGACUACGUUG	102175637	77
814	chr2	AGAAACAUGGGGCUAUCCGC	102176589	77
815	chr2	GAAGGUGACCGUCGCUGGAC	102176669	77
816	chr2	AAGCAGAAACUACCCGUUGC	102165220	76
817	chr2	GCAAGCAAUAUCCUAUUACC	102166254	76
818	chr2	GAGCCCAGCUAAUGAGACAA	102168646	76
819	chr2	CUGGUCAGGGGACUUUACAC	102176608	76
820	chr2	GAGGCUUGUUCUGUAGAUAC	102164910	75
821	chr2	CAAGCAAUAUCCUAUUACCC	102166255	75
822	chr2	AUACAGUAUAUAUGCGUCAU	102175498	75
823	chr2	UAGAUGAAGGUGACCGUCGC	102176674	75
824	chr2	CAUGGGGCUAUCCGCUGGUC	102176594	74
825	chr2	GAGAGGCUCACGUGCCUCUC	102176751	74
826	chr2	GACAUUACUUAUUGCGUGGUA	102165004	73
827	chr2	UAUGGAAGGGAUGACUACGU	102175635	73
828	chr2	AUGGAAGGGAUGACUACGUU	102175636	73
829	chr2	UAGUGGCUGGUGACAGUAAC	102176701	73
830	chr2	CUACCCGUUGCAGGAGACGG	102165229	72
831	chr2	AGUAAGCAAUGUCACUCAAC	102171840	71
832	chr2	AAUAGUCUCCCCUAGCACU	102171897	71
833	chr2	CACGUGCCUCUCGGGUAGCA	102176759	70
834	chr2	CCUGAAUCCUCCACCUUAGC	102164970	69
835	chr2	AAUUCUAUUACCCGGGUAU	102166253	69
836	chr2	GGGUAGUUUCUGCUUAAUA	102165200	68
837	chr2	AGUUGAGUGACAUUGC UUAC	102171854	68
838	chr2	UAAUAGUCUCCCCUAGCAC	102171898	67
839	chr2	UUA AUGAAUUAUUCGAUUC	102176552	67

FIG. 30

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
840	chr3	GUCUGGAUCACGUUCAAGG	190656257	82
841	chr3	AUAGUCGUUUUGACACUGGA	190609151	81
842	chr3	ACUGGGGACUAGACACCAUG	190604157	80
843	chr3	CCAGAACGCUGCGAUGACUG	190604141	79
844	chr3	CAUUCUCCAAAACUCCACGG	190645774	79
845	chr3	GACGUUGAUGUUGCCCCGAG	190648469	79
846	chr3	CGGUCUAGCAGUGAUGAGCA	190648669	79
847	chr3	CCUUACUAAUAGCGGUUCUCG	190604329	78
848	chr3	CUAGAAAAUAUGGCCUCUCG	190648468	78
849	chr3	AGUGAUAGUCGGUUUGACAC	190609155	77
850	chr3	UCUGAUGGAUUCUCGCAAUG	190627380	77
851	chr3	UUUGUAUUACUGACCCUCCG	190645772	77
852	chr3	AGCCCCAACUACGUGCUGCA	190648414	77
853	chr3	GCACAAUGUCCAAGCACCGA	190656350	77
854	chr3	AGUGGGCACUUGAUGCGAGC	190604192	76
855	chr3	AUCAGGCUACCUUAACAUGC	190604406	76
856	chr3	GGAGCUACUCAUUCUUGUA	190627344	76
857	chr3	UUGAUGUCACCAUUAACGAA	190627445	76
858	chr3	UUGACCGAGACAGUCUGCCU	190645833	76
859	chr3	GGCACAUGUCCAAGCACCG	190656349	76
860	chr3	CAGCUGGCCUUACUCUGAUC	190604268	75
861	chr3	UACUAAUGCGGUUCUCGGGG	190604326	75
862	chr3	AAACUAAAAUAGACCGUACA	190627345	75
863	chr3	GAUCUGGUAUUGGACUAGGC	190604284	74
864	chr3	ACCGACUACACUUGGUAUA	190609177	74
865	chr3	AUUCUCCAAAACUCCACGGA	190645773	74
866	chr3	UUCCUGGAGCACGUAGUUG	190648404	74
867	chr3	GCGGUCUAGCAGUGAUGAGC	190648668	74
868	chr3	CAUUGCCACCAAGCUCAUUG	190656036	74
869	chr3	GUAUUGGACUAGGCAGGACC	190604290	73
870	chr3	UAGGCAGGACCGGGACCUUG	190604299	73
871	chr3	UGGAUUCUCGCAUUGAGGUU	190627385	73
872	chr3	UCAGUCUGGAUCACGUUCA	190656254	73
873	chr3	GGUGCUUGGACAUUGUGCCU	190656333	73
874	chr3	GGAGGACUUCCUUCGGUGCU	190656347	73
875	chr3	CCCCGAGAACCGCAUUAUA	190604341	72
876	chr3	UAUAGUUGCCAGUGUCAUUG	190604383	72
877	chr3	GACGUACGUUUCAUCUCACC	190620413	72
878	chr3	GAUCCAGACUGAUGUCAGAC	190656231	72
879	chr3	GGGAGCAGGGGUUCCAAUC	190656521	72
880	chr3	UCCAGAACGCUGCGAUGACU	190604140	71
881	chr3	GCAACUAUACCUUGCAUGUUA	190604409	71
882	chr3	CCCAUGAUACCUUUCGUUAA	190627442	71
883	chr3	UUUGACCGAGACAGUCUGCC	190645832	71
884	chr3	AGUUGGGGCUUAGAACAACC	190648389	71
885	chr3	GGUUCCUGGAGCACGUAGU	190648406	71
886	chr3	CGGUGCUCACGGUCAUUA	190648565	71
887	chr3	UCAUCACUGCUAGACCGCCU	190648651	71

FIG. 31

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
888	chr5	ACUGCUGUGCAGUCGCACCC	132679802	82
889	chr5	UGGGCUUUGUAGGCGAGUCG	132677859	81
890	chr5	UGUGCCGGCAACUUUGUCCA	132674116	80
891	chr5	GGGACGGCUUCUUACCUUGG	132674504	80
892	chr5	GCUUUGUAGGCGAGUCGAGG	132677856	79
893	chr5	GGAAGCCAACCAGAGUACGU	132682520	79
894	chr5	AGUUGCCGGCACAUAGCUAGC	132674094	76
895	chr5	UGAUAU CGCACUUGUGUCCG	132674121	76
896	chr5	GUUUUCCAACGUACUCUGGU	132682513	76
897	chr5	GAUGUCUGUUACGGUCAACU	132674474	75
898	chr5	UGAGAAGGACACUCGCUGCC	132679796	75
899	chr5	GUGUCCGUGGACAAAGUUGC	132674108	74
900	chr5	GUAGGCGAGUCGAGGUGGAA	132677851	74
901	chr5	UGUAGGCGAGUCGAGGUGGA	132677852	74
902	chr5	ACGGCUCGACAGGAACCUCU	132679871	74
903	chr5	CAAGUGCGAUUACACCUUAC	132674142	73
904	chr5	GAUUCCUGAAACGGCUCGAC	132679861	71
905	chr5	CGACUGCACAGCAGUUCCAC	132679822	70
906	chr5	AGAAGUUUUCCAACGUACUC	132682517	70
907	chr5	AACGGCUCGACAGGAACCUC	132679870	68
908	chr5	CAACUCGGUGCACAGAGUCU	132674459	67
909	chr5	GGUUCCUGUCGAGCCGUUUC	132679853	66
910	chr5	AGCUGAUCCGAUUCCUGAAA	132679852	66
911	chr5	UGUCGAGCCGUUUCAGGAAU	132679847	65

FIG. 32

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
912	chr7	AUUCGUUCUGAAGAGGUGAG	22727565	78
913	chr7	CAAAUUCGGUACAUCUCGA	22727607	78
914	chr7	CAUUCCCUCAACUUGGUGUG	22729691	77
915	chr7	UCAGGGCUGAGAUGCCGUCG	22727609	76
916	chr7	CUUCCAAUCUGGAUUCAAUG	22728802	76
917	chr7	GGAGAAGGCAACUGGACCGA	22727452	75
918	chr7	CAUCUCAGCCCUGAGAAAGG	22727630	75
919	chr7	GUACCUCAUUGAAUCCAGAU	22728793	75
920	chr7	ACAUUUGCCGAAGAGCCCUC	22731554	75
921	chr7	ACAGUGUCCUGGACAACUCA	22729730	74
922	chr7	CACACCAAGUUGAGGGAAUG	22729676	73
923	chr7	UCUUCCCCCACACCAAGUUG	22729684	73
924	chr7	GUGUCCUCAUUCCCUCAACU	22729684	73
925	chr7	GACAGUGUCCUGGACAACUC	22729729	73
926	chr7	GGAAGGCAGCAGGCAACACC	22727486	72
927	chr7	CAUGUGUGAAAGCAGCAAAG	22728727	72
928	chr7	CUUCCCCCACACCAAGUUGA	22729683	72

FIG. 33

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
929	chr1	CGTGACTCTGACCTGCCCCGG	154429253	79
930	chr1	AGCUGCCCCAAAGAGUACGG	154465195	76
931	chr1	UCGAGGUUUUGUCAGACCCC	154465287	74
932	chr1	GCGUGACUCUGACCUGCCCCG	154429252	72
933	chr1	UCGGUGCAGCUCCACGACUC	154429380	72
934	chr1	CUGCCAGUUAGCAGUCCCCGG	154434602	72
935	chr1	GACACUACUGGCGACGCACA	154434638	72
936	chr1	UGUGCGUCGCCAGUAGUGUC	154434652	72
937	chr1	GUCAUCCACGACGCCUGGAG	154436010	72
938	chr1	ACGACGCCUGGAGCGGCCUG	154436017	72
939	chr1	AAUGCAGAGGAGCGUUCCGA	154454551	72
940	chr1	AUCUGGUCGGUUGUGGCUCG	154465304	71
941	chr1	CUGAUGUCAUAAGGGCUCCG	154465336	71
942	chr1	CACCCCAUCCUGACGACAA	154430579	70
943	chr1	UGCCAGUUAGCAGUCCCCGGA	154434603	70
944	chr1	UGCAUCCGCCGUACUCUUUG	154465201	70
945	chr1	AGCUCAGAUUACGGGCUGAA	154435127	69
946	chr1	ACCUGUCCAAGGCGUGCCCA	154436096	69
947	chr1	UCAGGCCGCUCCAGGCGUCG	154436004	69
948	chr1	UGAUGUCAUAAGGGCUCCGU	154465335	69
949	chr1	AACUAUUCAUGCUACCGGGC	154429404	68
950	chr1	CACGUGCCUCAGGCCGCUCC	154436012	68
951	chr1	AGAGGAGCGUUCCGAAGGCC	154454546	68
952	chr1	GGAGCCGUGCCAGUAUUCCC	154434563	67
953	chr1	CUCCGGGACUGCUAACUGGC	154434590	67
954	chr1	UACGGUUUGAGCUCAGAUAU	154435118	67
955	chr1	AGCCAGCAGCGCGCAGCCGA	154405643	66
956	chr1	CAGCCUUUGUCGUCAGGGAU	154430571	66
957	chr1	CUCCUCCGGGACUGCUAAC	154434594	66
958	chr1	CGGAGGCCAUGGGCACGCCU	154436101	66
959	chr1	GUGGACACCUCGUUCUCAGC	154448145	66
960	chr1	CCUGCGCAGGGCAGCGCCUU	154405698	65
961	chr1	AUGUGCGUCGCCAGUAGUGU	154434651	65
962	chr1	CCGUGGCCAGAAACCCCGC	154435043	65
963	chr1	CAUGCAUCCGCCGUACUCUU	154465199	65

FIG. 34

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
964	chr5	CCACAGACUGUACGGCAAGG	55941103	83
965	chr5	UAUUCUACCGUGGUACACAG	55941547	83
966	chr5	GAACUACUAGUCCUUCACUG	55941085	81
967	chr5	CACUGUCCAGUAUUCUACCG	55941557	81
968	chr5	UCUUAUUAGGUGCGAUGCA	55954828	81
969	chr5	UAAGCAAACAGGCACGACUA	55947566	79
970	chr5	GUGCAUCGCACCUAUUUAAG	55954814	79
971	chr5	GGUGGAAUGGACUACUCCAA	55954923	79
972	chr5	AACUGUACAACUCGUGUGGA	55957213	78
973	chr5	GCGGCUACAUGCCUCAGUGA	55941084	77
974	chr5	AGACUUGGACUGACGGAACU	55941527	77
975	chr5	GACUAGUGACACAUUGUACA	55951541	77
976	chr5	AAGCACCCUGUAUCACAGAC	55954855	77
977	chr5	ACAGAACUGUACAACUCGUG	55957217	77
978	chr5	GUUUAGGAUUCGCUGUAUGA	55960470	76
979	chr5	CUUCCAAAGGACCUACUGUU	55952055	75
980	chr5	UGUGUACCACGGUAGAAUAC	55941563	74
981	chr5	GGACCAAAGAUGCCUCAACU	55963363	74
982	chr5	CAAUGUGUCACUAGUCAAAAG	55951560	73
983	chr5	GCCAGGUUAUACCUCUAAAU	55954816	73
984	chr5	CCUGGUCCAUCAGCAUUAUAC	55952305	72
985	chr5	ACUCGGAUCUUGAGAAGACU	55941512	71
986	chr5	UGUCCGAACAGUAGGUCCUU	55952064	71
987	chr5	UGGACUUACGAGCUUGUUUA	55952258	71
988	chr5	AUGGAGGCUGCGACUGAUGA	55941145	70
989	chr5	CACAUUGUACAUGGUACGAA	55951532	69
990	chr5	CACCCAAAGCAUGUUAUCUU	55954954	66

FIG. 35

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
991	chr1	UUGCCUGGUCCUCCUGACUG	206772395	75
992	chr1	AGGCGCAUGUGAACUCCCUG	206770951	74
993	chr1	CGGAGAUCUCGAAGCAUGUU	206772319	74
994	chr1	GAAGAUGUCAAACUCACUCA	206768698	73
995	chr1	GGCGCAUGUGAACUCCCUGG	206770950	73
996	chr1	AAGGCGCAUGUGAACUCCCU	206770952	73
997	chr1	CAAGGCGCAUGUGAACUCCC	206770953	73
998	chr1	GCGCCGUAGCCUCAGCCUGA	206770927	72
999	chr1	GGUCUUCAGGUUCUCCCCCA	206770948	71
1000	chr1	GGGUCUUGGUUCUCAGCUUG	206770994	71
1001	chr1	GAUGAUCCAGUUUUACCUGG	206771013	71
1002	chr1	AAACUGGAUCAUCUCAGACA	206771035	71
1003	chr1	GGAUCAUCUCAGACAAGGCU	206771040	71
1004	chr1	UCGUAUUCUUAUUGUCAUGU	206768659	70
1005	chr1	UGGCCCUACCCCAGUCAGG	206772398	70
1006	chr1	GAACCAAGACCCAGACAUCA	206770971	69
1007	chr1	UCACAUGCGCCUUGAUGUCU	206770974	69

FIG. 36

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
1008	chr11	GCGCCGCCAGCAGCACUACG	11798648	82
1009	chr11	UGGCAUUCCAGGGUUACCUG	117999243	82
1010	chr11	UCGCUUCCCGAAGUAACAAG	117994104	81
1011	chr11	GCGCCGCACAUACAGCUGGA	117995669	81
1012	chr11	UGGGUAGCUGAAUCUUCGG	117993295	80
1013	chr11	CUGGUUCCACUGUCCCGUUG	117999441	79
1014	chr11	GCUGGUUCCACUGUCCCGUU	117999442	78
1015	chr11	CGUCUUGGCUCAGACGCUCA	117986530	77
1016	chr11	UGC GGUAAGGUCAUAGGACA	117989491	77
1017	chr11	GUUUCCCGGCACCUUGCGAA	117993387	77
1018	chr11	AGGCCUCCUCAUCAAGCGGG	117998788	77
1019	chr11	GCAAGCCUGCCUCAUCAACC	117999349	77
1020	chr11	CUUCAAAACACACAGACGGA	117988403	76
1021	chr11	CUGCGGUAAGGUCAUAGGAC	117989492	76
1022	chr11	GUAUGAGAUUGCCAUCGCA	117993388	76
1023	chr11	GAUUGCCAUCGCAAGGUGC	117993394	76
1024	chr11	UUACUUCGGGAAGCGACAGA	117994085	76
1025	chr11	CUCCUCAUCAAGCGGGUGGA	117998784	76
1026	chr11	UACGAGGCACGGCAGCAUCC	117986468	75
1027	chr11	GCCAGCAGCACUACGAGGCA	117986479	75
1028	chr11	GUCGCUUCCCGAAGUAACAA	117994103	75
1029	chr11	GCUAUGAAGUGGCGCUCCUG	117988498	74
1030	chr11	GGUCACUGCGGUAAGGUCAU	117989497	74
1031	chr11	GGUCCAAGGUCACUGCGGUA	117989504	74
1032	chr11	UCGGGAAGAUUCAGCUACCC	117993309	74
1033	chr11	UGUCGCUUCCCGAAGUAACA	117994102	74
1034	chr11	ACACAGGGUGGCUCGGCCUU	117999167	74
1035	chr11	GAAGAAUCGCCCUUGACAGA	117999314	74
1036	chr11	CCAGGCAUCUCCGAAUUUG	117999331	74
1037	chr11	CGAGUCACUCACUUGACUGC	117999628	74
1038	chr11	CAGGAGCGCCACUUCAUAGC	117988483	73
1039	chr11	ACCUGGUAUCUCCUCAGGUA	117989442	73
1040	chr11	AUUGCCAUCGCAAGGUGCC	117993395	73
1041	chr11	AAGCGACAGAUUGGUUUCACC	117994075	73
1042	chr11	CGGAGCCCUCGCCUACUGCC	117995658	73
1043	chr11	CACCAUCCACCCGCUUGAUG	117998794	73
1044	chr11	GGCUGGUUCCACUGUCCCGU	117999443	73
1045	chr11	AGGAGUGACCAUUCUUCAGU	117999464	73
1046	chr11	AGCUCCAGUCAGAUAUUCCC	117999508	73
1047	chr11	UUGGACCUGUACCACAGCAA	117989532	72
1048	chr11	UCAUUUGCGGGGGCCAUCUU	117993320	72
1049	chr11	CAAGGUGCCGGGAAACUUCA	117993406	72
1050	chr11	GGCGCCGCACAUACAGCUGG	117995670	72
1051	chr11	CAUCCACCCGCUUGAUGAGG	117998797	72
1052	chr11	UGGCCCCGGUAGCCAUUGCUG	117989531	71
1053	chr11	UGUACCACAGCAUUGGCUAC	117989539	71
1054	chr11	CCCCCAGGCUGACAGAACGC	117998944	71
1055	chr11	ACCAGGCAUCUCCCGAAUUU	117999332	70

FIG. 37

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
1056	chr21	UCACAGCUCAGUACCUAAGG	33268516	78
1057	chr21	UGAGAAAUCACAUUCCGUCA	33276636	78
1058	chr21	UGUGAGCAAACAACCCAUGA	33283237	78
1059	chr21	AUCUCAGGGCUUACCGUCAU	33283238	77
1060	chr21	CACAGCUCAGUACCUAAGGU	33268517	76
1061	chr21	CUUGUAAACGCACCACAGCA	33288190	76
1062	chr21	CCCAGCGUCCGUCCAUGGCG	33266469	75
1063	chr21	UUGAGAAUGAAUACGAAACU	33279844	75
1064	chr21	GAUGACGGCCACCAUCCAGG	33288118	75
1065	chr21	UCGGCUGCUUCGCCUUGCUG	33288190	75
1066	chr21	AAUAAGUUGUCCAUGGCUCC	33283140	74
1067	chr21	CAUCUCAGGGCUUACCGUCA	33283239	74
1068	chr21	AUUCUCAUCCGACAAUGGAA	33296229	74
1069	chr21	CUUUCACAGCUCAGUACCUA	33268513	73
1070	chr21	CAAGGUGUGGUCACCAUACU	33276666	72
1071	chr21	UUAGCCAUAUUGGACCCCC	33279765	72
1072	chr21	CUUAUUGUGUUAAGUUCGA	33283169	72
1073	chr21	UCCCCAGCUUUGUCCGAUC	33283186	72
1074	chr21	UUCCUGAUCGGAACAAAGCU	33283196	71
1075	chr21	CGUCCAUGGCGUGGAGCCUU	33266478	70
1076	chr21	GGACUUAUAAUGUGCAAUAC	33279892	70
1077	chr21	ACUUAUUGUGUUAAGUUCG	33283168	70
1078	chr21	CAUCCAGGGGGUCCAAUAA	33279757	69
1079	chr21	GUGACCACACCUUGAGAGUC	33276687	68
1080	chr21	CCGUCCAUGGCGUGGAGCCU	33266477	67
1081	chr21	CUUCCUGAUCGGAACAAAGC	33283195	67
1082	chr21	AGUACUUCUACUUGCAUUC	33279771	66

FIG. 38

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
1083	chr5	UGUCCGAGACACCAAAAUCG	132660209	79
1084	chr5	GCAGCCUGACACGUUGAUCA	132659748	78
1085	chr5	GAGCGGAUUCUGCCCGCACA	132659812	78
1086	chr5	GCAAGUGAGAGCAAUGACCG	132658250	77
1087	chr5	GAAUCCCUGAUCAACGUGUC	132659756	77
1088	chr5	GGUGUCUCGGACAUGCAAGC	132660187	76
1089	chr5	UGGUCAACAAAAGCGCCAUG	132658230	75
1090	chr5	CAUGGCGCUUUUGUUGACCA	132658245	75
1091	chr5	GCCCGCACAAAGGUCUCAGCU	132659823	75
1092	chr5	CCGAGACACCAAAAUCGAGG	132660212	75
1093	chr5	GAGCAGGUCCUUUACAAACU	132660223	74
1094	chr5	UGGAGCAUCAACCUGACAGC	132659462	73
1095	chr5	AAACUGGGCCACCUCGAUUU	132660208	72
1096	chr5	CACGUUGAUCAGGGAUUCCA	132659739	70
1097	chr5	UGCCCGCACAAAGGUCUCAGC	132659822	70
1098	chr5	UGCAGCCUGACACGUUGAUC	132659749	69
1099	chr5	UUAAAGAAACUUUUUCGCGA	132660264	69
1100	chr5	GCUAGCCGACACUCACCUUC	132658359	67
1101	chr5	CGAGGUGGCCAGUUUGUAA	132660227	67
1102	chr5	UUUAAAGAAACUUUUUCGCG	132660263	67
1103	chr5	GAAUCCGCUCAGCAUCCUCU	132659787	65
1104	chr5	CCACCUCGAUUUUGGUGUCU	132660200	65

FIG. 39

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
1105	chrX	UGGACAUGGAAUCCACCCGA	118741093	81
1106	chrX	UAACAUGGUUAUGUAGAGUG	118773899	80
1107	chrX	AUGGACAUGGAAUCCACCCG	118741092	79
1108	chrX	AUAGUGCCUUUAACUCCCG	118758238	79
1109	chrX	CGAGGGUCGCACUCACCCGU	118727725	78
1110	chrX	UAGAAGUACCCCUGAAUGAG	118746999	78
1111	chrX	GUCGCACUCACCCGUAGGCG	118727720	76
1112	chrX	CGGGACUGGUAAUCCUCCA	118749736	76
1113	chrX	AGUAUAGUUAGUGUCGGGAC	118749750	76
1114	chrX	UUUGAGCUGGCUCCCUCGGG	118741093	75
1115	chrX	CAAUUUGAGCUGGCUCCCUC	118741096	75
1116	chrX	CCAGCUCAAUUGUAGUCUA	118741118	75
1117	chrX	UCGGGACUGGUAAUCCUCC	118749737	75
1118	chrX	AUUGUUCAGUCAUCGUCGC	118773937	74
1119	chrX	GGACUUCUAAAACUUACCAC	118758242	73
1120	chrX	GUGGAAUUGCGCUUCUUACC	118773880	73
1121	chrX	GAGACACUCAAAUUGUCAC	118741033	72
1122	chrX	AUUGCACCUGCGACGAUGAC	118773931	71
1123	chrX	CACUCUCAUUGGUGCUACAC	118747030	70
1124	chrX	CCAUAGACUACAAUUGAGC	118741106	69
1125	chrX	UGAUGACCUAAUUGUGCAAU	118761198	69
1126	chrX	CACAUAAUGUUUUCUACGUA	118761290	69
1127	chrX	CUGACUGUGUCAAAGUAUC	118766882	69
1128	chrX	GGCGGGGGCGCCGCGCCUAC	118727722	67
1129	chrX	AACUUACCACGGGAAGUUAA	118758232	67
1130	chrX	UCUAUUGAACGACGAGUUUC	118746968	66

FIG. 40

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
1131	chrX	UCUUCGAUAGGUCUUCACCU	115005315	74
1132	chrX	GCUGAAAUGGAGCAUACCUU	115009591	74
1133	chrX	UCAAGAAGUACACCUAUGCC	115013810	74
1134	chrX	GAACUAAAAUACCGAAACAU	115015691	73
1135	chrX	AUUGCUCAGAUGACGGAAUU	115007968	71
1136	chrX	CUUGCUGGAUAGGUCCCAA	115009587	71
1137	chrX	CGAGUAAAAGUAAGAUAGAC	115009647	71
1138	chrX	CCUGGGCAGAAACUACUUAU	115014439	71
1139	chrX	AUAGUGGAUCCCGGAUACUU	115015781	71
1140	chrX	AGGAUGCAGAUUUUCCCUAUU	115010748	70
1141	chrX	UAGAGAUAAACCUAAGUAUCC	115015784	70
1142	chrX	UCUUCAGACACCGAGAUAAA	115017180	70
1143	chrX	CUACGUUUCUGGCUACCAUU	115005272	69
1144	chrX	GUAGCAAAGUUUUCUUCGAU	115005303	69
1145	chrX	GUAAGAUAGACUGGCGGCAA	115009656	69
1146	chrX	GCUUUCGUUUGCUUGGCUAU	115017249	67
1147	chrX	AGAAAACUUUGCUACGUUUC	115005283	65

FIG. 41

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
1148	chr6	UGCAGGACUCACCACCAAUG	52186453	80
1149	chr6	GGUUGACCAUCACAGUCCGG	52187703	80
1150	chr6	AGGUUGACCAUCACAGUCCG	52187704	79
1151	chr6	GGAUCGGUUGUAGUAAUCUG	52187768	79
1152	chr6	UCCCCUCUGCAGCCGCAAUG	52189060	79
1153	chr6	AGAGAUCCUGGUCCUGCGCA	52189192	79
1154	chr6	GGCCACAUGGUGGACAAUCG	52189272	78
1155	chr6	GAACUUCCCCCGGACUGUGA	52187709	77
1156	chr6	GAGAAGAUACUGGUGUCCGU	52189247	77
1157	chr6	ACAACCGAUCCACCUCACCU	52187792	76
1158	chr6	UGGGCUGCAUCAACGCUGAU	52189131	76
1159	chr6	CAUCAACGCUGAUGGGAACG	52189138	76
1160	chr6	CACCCCGAUUGUCCACCAUG	52189282	75
1161	chr6	UUGGGCUGCAUCAACGCUGA	52189130	74
1162	chr6	AAGAGAUCCUGGUCCUGCGC	52189191	74
1163	chr6	CAGUAUCUUCUCCAGCCGGA	52189224	74
1164	chr6	GUGGACAAUCGGGGUGACAC	52189263	73
1165	chr6	GAGGCAAAGUGCCGCCACUU	52189112	72
1166	chr6	UAGGCCACAUGGUGGACAAU	52189274	72
1167	chr6	CAGCGUUGAUGCAGCCCAAG	52189114	71
1168	chr6	AUCACAAUCCCACGAAUCC	52187665	69
1169	chr6	CUUCCGGCUGGAGAAGAUAC	52189237	69
1170	chr6	UUGGGCAUCCUGGAUUUCGU	52187661	68
1171	chr6	GUAGUAAUCUGAGGACCUUU	52187759	67
1172	chr6	GGAGGCAAAGUGCCGCCACU	52189111	67
1173	chr6	UGGUAAUUGGUAAUCCGGUUA	52187733	66

FIG. 42

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
1174	chr22	GUGUGACGUUGGAUCGCUUG	17103516	84
1175	chr22	UUCACGAUGCCGGUUCGCCG	17109058	84
1176	chr22	CAUUUCCGUGAGUCCCUUG	17109635	82
1177	chr22	UCCAUUCGAUGUGAGCCACG	17097911	81
1178	chr22	ACAAGGAGACCUUGUUCGCCG	17097908	81
1179	chr22	CGUCCCCGACCUUGUUCGGCG	17108772	81
1180	chr22	AGACCCACACACGCCCUACG	17109564	81
1181	chr22	ACUCGGGCUUGGACACGAUG	17109788	81
1182	chr22	UCGCAGGGAGGCGCCACCCG	17085176	80
1183	chr22	GCCAGCAUCCUGUACCUCGA	17098791	80
1184	chr22	GUGGGACCCCAACAUCACCG	17102163	80
1185	chr22	GCAGAGUUACCGCAGGUAUG	17102295	80
1186	chr22	CAGUUCUGUCUACCGCCUG	17108434	80
1187	chr22	CGUAGUCUGCUACUUCAGCG	17108733	80
1188	chr22	GGGCCGCAUGCACCGCGUAG	17108868	80
1189	chr22	UGUCGGGGGACAACUACCUG	17108894	80
1190	chr22	ACUCGGGCACCGUCAGCCAG	17109277	80
1191	chr22	GGUCAGGGUCAACCACAAAG	17100377	79
1192	chr22	AUGGGUAGAUUCGUUCCACA	17102210	79
1193	chr22	AAACAGUCGCGGAGUGUCUG	17104766	79
1194	chr22	CCCGCGGCACGCGCGCCAAG	17108579	79
1195	chr22	GCGACCACGGAAGCCCGUG	17108642	79
1196	chr22	CCCCCGACAGCUCCCCUACG	17108868	79
1197	chr22	CGGGCCGCAUGCACCGCGUA	17108867	79
1198	chr22	UGGCUGACGGUGCCGCAGUC	17109293	79
1199	chr22	AGGAGGUCAGGAGACGCCAU	17109421	79
1200	chr22	GCGAGAGCAUCAAGCCUUCG	17109465	79
1201	chr22	CCAUUUCCGUGAGUCCCUUG	17109636	79
1202	chr22	GGGAGCAGACCAGCGCCCGG	17085207	78
1203	chr22	CACGUCGAGUCUACCGGCU	17085227	78
1204	chr22	ACCUGAGCUCAUGCAUGGCG	17102028	78
1205	chr22	GCACAUGCACCACAUACCUG	17102298	78
1206	chr22	GCGUAGAGUGAGUGUGACGU	17103527	78
1207	chr22	CCCGCUCAUGGACAGGUUCG	17108805	78
1208	chr22	GCUCAUGGACAGGUUCGAGG	17108808	78
1209	chr22	CCGGGCCGCAUGCACCGCGU	17108866	78
1210	chr22	AUUCGAACCAGUCGGGACAG	17108961	78
1211	chr22	GGGCGCCCGCUUCACGAUGC	17109068	78
1212	chr22	CGCCAGUGCCAGCCGGACUG	17109293	78
1213	chr22	GACGUGAGGGAGCACCUCGA	17109463	78
1214	chr22	GGGCUGCAGUAGACCCGCCA	17109534	78
1215	chr22	UCCUCCUCGUAGGGCGUGUG	17109556	78
1216	chr22	CCGGUGGUCCAGGAGUCGCA	17085191	77
1217	chr22	UCCCCGUGGCUCACAUCGAA	17097922	77
1218	chr22	CAGAUAAUCUGCACCCUCG	17098793	77
1219	chr22	AGCCAGCAUCCUGUACCUCG	17098790	77
1220	chr22	GCUGUGUUCUUAACCGCCUG	17098883	77
1221	chr22	UGAUGAACCAGUACCCAC	17105868	77

FIG. 43

SEQ ID NO.	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
1222	chr11	CUUAUAAUAAUAUGGUCCG	112148723	79
1223	chr11	UUUUUCAGAUAAUGCACCC	112148728	75
1224	chr11	UUUGAAUCUUAUCAUACGA	112143710	74
1225	chr11	AUAGUUACAGCCAUACCUCU	112148681	73
1226	chr11	AUGACUGAUUCUGACUGUAG	112150076	72
1227	chr11	GAAUCCUCCUGAUACAUC	112143795	71
1228	chr11	GUUCCUUGAUGUUUUCAGG	112143803	71
1229	chr11	AGAUAGCCAGCCUAGAGGUA	112148679	71
1230	chr11	CAAGUUCUCUUAUUGACCA	112150121	71
1231	chr11	GCAUCUUUUUAUCAUGUCCU	112143747	70
1232	chr11	AAGGCUCAGUCUUACCUUAA	112148605	70
1233	chr11	UUACAGCCAUACCUCUAGGC	112148685	70
1234	chr11	UCAGUCAUAUCUUCAAUAG	112150103	70
1235	chr11	UUCUUUCAGAGAAGUGUCCC	112143752	69
1236	chr11	UAUAAAGAUAGCCAGCCUAG	112148684	69
1237	chr11	CAAAUAGAGGCCGAUUUCCU	112150116	69
1238	chr11	UGCAUCUUUUUAUCAUGUCC	112143746	68

FIG. 44

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
1239	chr2	ACGCCGAGUUUGAAGAUCAG	102375976	80
1240	chr2	UUCACGUCCCCACAUUACUG	102367852	75
1241	chr2	AUCAUGCAAAGCAAUUCUCG	102367989	75
1242	chr2	AACGCCGAGUUUGAAGAUCA	102375975	75
1243	chr2	UGUAAUUUAUUGGAUGUUCG	102384941	74
1244	chr2	GCAGACAUGGCUGAUAUCCC	102390072	74
1245	chr2	ACUUCCGGUUCGUCUCUACC	102396844	73
1246	chr2	CAAGCCAGGUAGAGACGAAC	102396852	73
1247	chr2	UAUAAGCACCCAAAGGGUCA	102362685	72
1248	chr2	CCCCUUCAACCACAGUAAUG	102367849	72
1249	chr2	CCCUUCAACCACAGUAAUGU	102367848	71
1250	chr2	CCCCACAUAUCUGUGGUUGA	102367859	71
1251	chr2	GAGAAUUAACCCUUGACCCUU	102362688	70
1252	chr2	UCGGCGUUCUUCUUUAUCGU	102375948	70
1253	chr2	AGAUCGCAGUAAUAUAGUUC	102381635	70
1254	chr2	GGGUAAUUCUCUACAAUUA	102362664	69
1255	chr2	GCAAUUCUCGAGGAACUCCU	102367979	69
1256	chr2	CGGCGUUCUUCUUUAUCGUU	102375947	69
1257	chr2	ACUGCAACAUGGUUAAGCUU	102381657	69
1258	chr2	CUCUUGUGAAGACGUGGCCU	102390077	69
1259	chr2	CCUGUGUCAUUAACUCAAC	102368030	68
1260	chr2	GAACGCCGAGUUUGAAGAUC	102375974	68
1261	chr2	CCUCUUGUGAAGACGUGGCC	102390078	67
1262	chr2	CAAUUCUCGAGGAACUCCUU	102367978	66

FIG. 45

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
1263	chr2	AGGUCGUUACUACCCAUGAA	102423959	80
1264	chr2	AAGGAGCAACCGAAUCGUAG	102437252	80
1265	chr2	AGCAAGGAUCAGACGCUUGG	102447203	80
1266	chr2	UCUAAUGGAUCUCCAUUCGA	102424007	79
1267	chr2	UCCAGCGGUAACCGUGUACA	102424410	79
1268	chr2	GAGCAAGGAUCAGACGCUUG	102447202	79
1269	chr2	UAGGUCGUUACUACCCAUGA	102423960	78
1270	chr2	AUGUGAUGCGGAAUACUCAC	102424301	78
1271	chr2	GUACCGGACCUACCAGAGCA	102447187	78
1272	chr2	ACGACCUAUCUGAUGUCCAA	102423987	77
1273	chr2	CCCAGAAUUAUUCACCCCUG	102424089	77
1274	chr2	ACCUUGUACCAGGUUACCGC	102424399	77
1275	chr2	AGUCGGAUACUGUGAGUUCG	102437323	77
1276	chr2	UGGUACCAACAACCUUCGAA	102424007	75
1277	chr2	ACCCAGAAUUAUUCACCCCU	102424090	75
1278	chr2	GUUGUUCAAGUGAGAACCAU	102437358	75
1279	chr2	AAAACUCUCAGGGAUUCACG	102452083	75
1280	chr2	GAUCUCCAUUCGAAGGUUGU	102424000	74
1281	chr2	UUCGAAUGGAGAUCCAUAUAG	102424021	74
1282	chr2	AGAUAUUCUGGAUCCUGUCG	102441351	73
1283	chr2	AAGCACGAUUUGGCUUUGAA	102443241	73
1284	chr2	GCUUGGCACCAUCGGGACCC	102447106	73
1285	chr2	GAGGGCACUCGCCGCCAGCA	102447120	73
1286	chr2	UUUCAAUCCAGUGCCUGUAG	102447142	73
1287	chr2	CGGGAGAACAUGCUCUGUU	102423285	72
1288	chr2	CGUUACUACCCAUGAAGGGC	102423955	72
1289	chr2	GACCCAGAAUUAUUCACCCC	102424091	72
1290	chr2	GCUACAUCAUAGGGGCUCCU	102424231	72
1291	chr2	AAACUUCAUCCACUACGAUU	102437249	72
1292	chr2	UCACUCAGCGUGAUCUUCGC	102445262	72
1293	chr2	AGAGCUUUUUUCACGAGAUG	102451956	72
1294	chr2	ACCAGCUCAGAAUUAACCUU	102452107	72
1295	chr2	CCCCAGGGGUGAAUAAUUCU	102424101	71
1296	chr2	GGAUCCUGUCGAGGACACAC	102441360	71
1297	chr2	UCUCAGUACCUAGGCGAAA	102443319	71
1298	chr2	CGGCGAGUGCCCUCUUCUAC	102447141	71
1299	chr2	UUGAAAUAGUGCUGCUGUAC	102447171	71
1300	chr2	CAAGCGUCUGAUCCUUGCUC	102447187	71
1301	chr2	AGAGCAAGGAUCAGACGCUU	102447201	71
1302	chr2	AAGCCUCUCCAAGUAACUGU	102451989	71
1303	chr2	UUCUUUCAGUUGGACGGACU	102445313	70
1304	chr2	CUGGGUCCAUUGACAUAUUU	102451833	70
1305	chr2	AGGCAUGUGGUAGCGCAUUU	102452044	70
1306	chr2	GUUGCAGGAGAGCGAAUUA	102423328	69
1307	chr2	CACAAAGUCCAGCGGUAACC	102424403	69
1308	chr2	GCUUUGCAGCUAAUAGUUAA	102443210	69
1309	chr2	AUUAGCUGCAAAGCACGAUU	102443231	69
1310	chr2	ACUGGGUCCAUUGACAUAUU	102451834	69

FIG. 46

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
1311	chr11	UGUGCUACACGGAUACCCCA	102791447	82
1312	chr11	GAUGCUAUAAACUACGAUUCG	102795203	82
1313	chr11	GCGCACAAAUCCCUUCUACC	102792712	78
1314	chr11	AGAUGUGUUUGCUCCCAGCG	102797282	78
1315	chr11	CUCCCAUUCUACUGAUUUCG	102795538	76
1316	chr11	AACACAUCUGACCUACAGGU	102797256	76
1317	chr11	GAGCUCAACUUCGCGGUAGA	102792713	75
1318	chr11	UGAUGCUAUAAACUACGAUUC	102795204	75
1319	chr11	UCACUGAGGGGAACCCUCGC	102797284	75
1320	chr11	GAUGGCAUCCAAGCCAUUA	102795456	74
1321	chr11	UCGUUUUAUUAUUAUUAUACC	102790805	73
1322	chr11	GAUUGGCAGGGAAUAAGUAC	102791487	73
1323	chr11	AGCUCAACUUCGCGGUAGAA	102792714	73
1324	chr11	UUGAUGCUAUAAACUACGAUU	102795205	73
1325	chr11	CUUACUGUCACACGCUUUUG	102795247	73
1326	chr11	UACCCUAGCUACACCUUCAG	102795507	73
1327	chr11	CACCACUGAAGGUGUAGCUA	102795517	73
1328	chr11	UAUAAACGAUCUAUGGAUCC	102790779	72
1329	chr11	UGAUGAAUAUAAACGAUCUA	102790786	72
1330	chr11	GCAAGAUGUGGACUUAGUCC	102797992	72
1331	chr11	AAUCGUAGUUUAUAGCAUCAA	102795220	71
1332	chr11	CAUACUCACCAUAUAUGGCU	102795460	71
1333	chr11	UCACCACUGAAGGUGUAGCU	102795516	71
1334	chr11	AAACCGGACUUCUUCUCUGU	102792629	70
1335	chr11	UGGUGAUGUUCAGCUAGCUC	102795487	70
1336	chr11	AGCCCCGAUAUCAGUAGAAU	102795548	70
1337	chr11	CUAAUAGCUGGUUUAACUGC	102790426	69
1338	chr11	AGCUUACUGUCACACGCUUU	102795245	68
1339	chr11	GCUUACUGUCACACGCUUUU	102795246	68
1340	chr11	UGAGCAUCCCCUCCAUAUACC	102796719	67
1341	chr11	GCUAUCAUUUUGGGAUAACC	102790773	66
1342	chr11	CACACGCUUUUGGGGUUUGU	102795255	66
1343	chr11	UGGCUUACCUCUGAAAUUGU	102796673	66

FIG. 47

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
1344	chr16	GUCGCGGUCGUAGUCCUCAG	55488671	84
1345	chr16	CCGCUGGUGCGGCACCACUG	55488669	83
1346	chr16	ACAUCUGGGUUGCCGCAGCG	55483058	82
1347	chr16	GAUUCGAGAAAACCGCAGUG	55484104	82
1348	chr16	GCCAGGGAGCGCUACGAUGG	55479481	81
1349	chr16	AUGGAGGCGCUAAUGGCCCG	55479497	81
1350	chr16	GAUGAUGGGCGACGGCGCGG	55479567	81
1351	chr16	UACGAUGAUGACCGCAAGUG	55489802	81
1352	chr16	ACCAUGCGGAAGCCACGCUG	55483058	80
1353	chr16	GUCCGUCCUUAACCGUCAAAG	55485320	80
1354	chr16	UCCUUCAGCGUUGCCGCCCA	55488557	80
1355	chr16	CUUGAUGAUGGGCGACGGCG	55479570	79
1356	chr16	ACCAGCGGUAGCCAUCCGUG	55488642	79
1357	chr16	CUUGGGGUACCCUCGCUCCA	55498324	79
1358	chr16	GCCGCCUGCAGGUCCACGA	55502870	79
1359	chr16	GAUGCCGUCGUGGACCUGCA	55502878	79
1360	chr16	UUGUCCCACUUGGGCUUGCG	55483100	78
1361	chr16	GAGUCCGUCCUUAACCGUCAA	55485322	78
1362	chr16	GACGAUGAGCUAUGGACCUU	55485411	78
1363	chr16	ACCAUGGGCGGCAACGCUGA	55488568	78
1364	chr16	ACGGAUGGCUACCGCUGGUG	55488658	78
1365	chr16	ACCACAUCUUUCCGUCACUG	55489750	78
1366	chr16	CUACGAUGAUGACCGCAAGU	55489801	78
1367	chr16	GAUGGCAUCGCUCAGAUCCG	55493264	78
1368	chr16	AAAGAUUGAUGCGGUUAUCG	55497024	78
1369	chr16	CGACGGCAUCCAGGUUAUCG	55502853	78
1370	chr16	GCCGCAGCGUGGCUUCCGCA	55483047	77
1371	chr16	UGACGAUGAGCUAUGGACCU	55485410	77
1372	chr16	UUAGUGGUCCGUGUGAAGUA	55485617	77
1373	chr16	AGUGGCACCCACCGGUCUCA	55488711	77
1374	chr16	GCCGCAGUGACGGAAGAUG	55489761	77
1375	chr16	AGGGCCUCGUACCUUGGUCA	55489819	77
1376	chr16	CAAACUCGUGGGCUGCCACG	55491819	77
1377	chr16	CAUGGCGUGGCCAAACUCGU	55491830	77
1378	chr16	UCCACUCGCUGGACAUCAGG	55498368	77
1379	chr16	UAAAGGCGGCAUCCACUCGC	55498379	77
1380	chr16	AUGGCCCGGGGCGCGCUCAC	55479509	76
1381	chr16	GCGCGCUCACGGGUCCCCUG	55479519	76
1382	chr16	UCGCCGGGAACUUGAUGAU	55479581	76
1383	chr16	UGGCUUCCGCAUGGUCUCGA	55483038	76
1384	chr16	UGGAUUCGAGAAAACCGCAG	55484106	76
1385	chr16	CGGUUUUCUCGAAUCCAUGA	55484124	76
1386	chr16	UGAAGUAUGGGAACGCCGAU	55485630	76
1387	chr16	GAAGUAUGGGAACGCCGAUG	55485631	76
1388	chr16	CCUCAGUGGUGCCGCACCAG	55488657	76
1389	chr16	UACGACCGCGACAAGAAGUA	55488694	76
1390	chr16	GCUCCCGGAAAAGAUUGAUG	55497015	76
1391	chr16	GCUUGGGGUACCCUCGCUCC	55498325	76

FIG. 48

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
1392	chr11	GUACGAGCUGGAUACCCAAG	102838661	82
1393	chr11	AAUCCUACUGUUGCUGUGCG	102843515	81
1394	chr11	CACGGUUGGAGGGAAACCUA	102838642	80
1395	chr11	CUUGCUGAGUAACUUAUAUG	102839149	80
1396	chr11	CAGGUUCCGUGGGUACCAGG	102840222	80
1397	chr11	UAUGCGGCAUCCACGCCUGA	102839165	79
1398	chr11	UCGAUUUCCUCACGGUUGG	102838631	77
1399	chr11	UGCUCAGCCUAUCCAUAUGGA	102843487	77
1400	chr11	CGAUUUUCCUCACGGUUGGA	102838632	76
1401	chr11	AAUCAAUUCUGGGCUAUCAG	102838691	76
1402	chr11	GCGCAUACCUCCAGAGUGU	102842775	76
1403	chr11	UCACGGUUGGAGGGAAACCU	102838641	75
1404	chr11	ACUUUUGGCGCAAUCCUC	102839224	75
1405	chr11	GAGACAGGCGGAACCGAGUC	102840479	75
1406	chr11	UACCUGAACAAGGUUCAUGC	102843456	75
1407	chr11	GCAUCGAUUUCCUCACGGU	102838628	74
1408	chr11	CGCAUAUGAAGUUACUAGCA	102839136	74
1409	chr11	UCUGGAGGGACAGGUUCCGU	102840212	74
1410	chr11	UGGGCAUCUCCAUAUAUCCC	102842209	73
1411	chr11	GAAGCUGGACUCCGACACUC	102842774	73
1412	chr11	UGCAGCUCCAUCCAAUGGAU	102843492	73
1413	chr11	UCACAGUUGGCUGGCGUCCC	102840188	72
1414	chr11	UUCUGGAGGGACAGGUUCCG	102840211	70
1415	chr11	GCAUGGGCCAAAACAUUUC	102842245	69
1416	chr11	GUUCUGAAGUGACCAACAUC	102842734	68
1417	chr11	CACCAGCAUGAACCUUGUUC	102843446	66

FIG. 49

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
1418	chr11	CGAUGAGGAUGAACGCUGGA	102524956	82
1419	chr11	AUGAUUGGCUUUGCGCGAGG	102527528	79
1420	chr11	AUCAUGAUUGGCUUUGCGCG	102527531	79
1421	chr11	AAUCGAUCCACUGUAAUAUG	102527642	79
1422	chr11	AGACUUACCGCAUAUUACAG	102527637	78
1423	chr11	GUUCAUGAGUUGCAGCAUAC	102523386	77
1424	chr11	AGUGGAUCGAUUAGUGUCAA	102527619	77
1425	chr11	GCAGUGAUGUAUCCAACCUA	102523310	76
1426	chr11	UGAUGGGCCAGGAAACACGC	102525025	76
1427	chr11	CAUCACUGCAUUAGGAUCAG	102523336	75
1428	chr11	UGGACGGAUGGUAGCAGUCU	102524940	75
1429	chr11	AGGAGAUGCUCACUUCGAUG	102524971	75
1430	chr11	CUGCAUUUUUCUAUGACGC	102527860	72
1431	chr11	GGGACUCCUACCCAUUUGAU	102525041	71
1432	chr11	CUUCCAAAGUGGUCACCUAC	102527761	71
1433	chr11	GGGGACUCCUACCCAUUUGA	102525042	70
1434	chr11	UCUGCAUUUUUCUAUGACG	102527859	69
1435	chr11	UCCUACCCAUUUGAUGGGCC	102525036	68
1436	chr11	AGUGAGUAUUCUGCAACAUC	102527819	66

FIG. 50

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
1437	chr11	GAUGCUAUCACCACACUCCG	102716331	80
1438	chr11	GCAACCAGUAUCAGUCUACA	102722625	78
1439	chr11	UCAAUUGCUUGGACGCUGCU	102714630	77
1440	chr11	AGUUAGUGCGUUCCCACUUG	102722456	77
1441	chr11	AUGAUGAAAAAGCCUCGCUG	102722506	77
1442	chr11	UGUGACGGGGAAGCCAAAUG	102722540	77
1443	chr11	CAGCCUGUAUACCAGUUGGA	102715363	76
1444	chr11	UUGGUCCAGUAGGUUGGAUA	102716401	76
1445	chr11	CUCCCUCAAGAUGACAUCGA	102718436	76
1446	chr11	GUAGACUGAUACUGGUUGCU	102722641	76
1447	chr11	AAGUAUUUCUCCACGGAGUG	102716333	75
1448	chr11	AUGCCAUCGAUGUCAUCUUG	102718445	75
1449	chr11	CUUGAUUAACUUAUCUUGCGG	102721404	75
1450	chr11	ACCCUAGAGAUUAUACCUGU	102722430	75
1451	chr11	GGUGGUUUUAUGUUAACCCC	102722470	75
1452	chr11	UAAGCAGCCUGUAUACCAGU	102715359	74
1453	chr11	AGCAUAGUUGGGAUACAUCA	102718495	74
1454	chr11	CCCAAGGAUUAUCAAACUA	102714645	73
1455	chr11	AACGCACUAACUUGACCUAC	102722433	73
1456	chr11	GGUUAUCCCAAAAGCAUAUC	102713809	72
1457	chr11	GAUAUGCUUUUUGGGAUAACC	102713824	72
1458	chr11	AUCCCUUCCAACUGGUUAUAC	102715354	72
1459	chr11	AAGUUAGUGCGUUCCCACUU	102722455	72
1460	chr11	UUUUUUGGGUUGAAUGUGACG	102722553	72
1461	chr11	UGCCAUCGAUGUCAUCUUGA	102718446	71
1462	chr11	CAAGUUAGUGCGUUCCCACU	102722454	71
1463	chr11	AAACAGCUGCGUCAAUUGCU	102714619	70
1464	chr11	AUUGACAGGCAACCAAUACU	102714700	70
1465	chr11	CCGUUAGGUACUUCUGGAGA	102715427	70
1466	chr11	AAUGUCAAAACUGGGGUCAC	102716366	70
1467	chr11	CUUGGUCCAGUAGGUUGGAU	102716400	70
1468	chr11	GUAUCCCAACUAUGCUUUCA	102718476	70
1469	chr11	GGCAUGAGCAAGGAUUCCA	102721491	70
1470	chr11	GUUUACGUUACCUCAGAAU	102714562	68
1471	chr11	GUCAAUUGCUUGGACGCUGC	102714629	68
1472	chr11	UACUUAUCUUGCGGAGGUGU	102721410	68
1473	chr11	AGAUCAAUUGCGUAAUAUCU	102713429	67
1474	chr11	UUUCCUACUUAACGUUCUUGC	102713759	66

FIG. 51

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
1475	chr11	CAAGUUCAUGAGCAGCAACG	102776758	83
1476	chr11	GUACAAGCAGGUUAUCCAAG	102772957	80
1477	chr11	UCACAUCAUCUUGCGAAAGG	102776650	80
1478	chr11	UUGCAGCGGACAAAUACUGG	102772851	78
1479	chr11	AUCUUGCGAAAGGCGGAACU	102776657	77
1480	chr11	AGUCAUCAGCUAUUAGUCUA	102772074	76
1481	chr11	GAGCUGAAGUGACCAACGUC	102779566	74
1482	chr11	UCCAAGAGGCAUCCAUACCC	102772943	73
1483	chr11	AUUUUUGGCGAAGAUCAC	102775302	73
1484	chr11	GCUGGCAUCUCAGAUCCTGA	102776369	73
1485	chr11	AAGUCAUCAGCUAUUAGUCU	102772073	72
1486	chr11	CACCAGGGGUUCCUCAGUAG	102776407	72
1487	chr11	CAUUCACAUCAUCUUGCGAA	102776647	72
1488	chr11	CCUUUCCUGGCAUGCCGAAG	102779532	71
1489	chr11	AAAGUACUACAACCUCGAAA	102779717	71
1490	chr11	CUCCAACAAGGAUCUUGCCC	102780491	71
1491	chr11	CUGCAUAUGAAGUUAACAGC	102775215	70
1492	chr11	UGCCUCUACUGAGGAACCCC	102776397	70
1493	chr11	UACCUGGGCAAGAUCUUGU	102780501	70
1494	chr11	UCAACCUUAGGCUAACUCC	102772049	69
1495	chr11	UCUUUGCAGCGGACAAAUAC	102772854	68
1496	chr11	UGGGUUUCCUCCAACCAUA	102772923	67
1497	chr11	CAUCUUGCGAAAGGCGGAAC	102776656	67

FIG. 52

SEQ ID NO.	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
1498	chr11	CACACCUGACAUGAACCGUG	102871923	81
1499	chr11	CUCUCUGCUGAUGACAUACG	102867930	80
1500	chr11	AAGUAGGUCCUAUAAAAACG	102865817	79
1501	chr11	AUGAUGCACGCACCUCGAUG	102872942	79
1502	chr11	AGUAGGUCCUAUAAAAACGU	102865818	78
1503	chr11	UCAGUGUUUUGGUGAUACGU	102863143	77
1504	chr11	UGUCAGGAUUUGGCAAGCGU	102867372	77
1505	chr11	CGUGGCAUUCAGUCCCUGUA	102867912	77
1506	chr11	UGGCCAUUCUAGUGAUCCAA	102868000	77
1507	chr11	AGGAUGUUGACUACGCAAUC	102871903	77
1508	chr11	ACAUCGGGGACUCCACAUCG	102872942	77
1509	chr11	UAAUCAGUUUGGGAUAACCA	102864220	76
1510	chr11	GUGGGGAACAUUACGGCCUU	102867996	76
1511	chr11	CAUACACCAACGUUACCUGU	102872866	76
1512	chr11	UUUGAUGCUGUCACUACCGU	102867302	75
1513	chr11	UUGGUGGUUUUUGCCCGUGG	102871808	75
1514	chr11	UGCCAGGGGGGCGCCGUAUGG	102872890	75
1515	chr11	CCCUGAAAUGAUGGACAUCG	102872928	75
1516	chr11	GCAACUGGACACAUCUACCC	102872967	74
1517	chr11	GAGGUGCGUGCAUCUCC	102872961	74
1518	chr11	GUAAUCAGUUUGGGAUAACC	102864219	73
1519	chr11	UUUUGAUGCUGUCACUACCG	102867303	73
1520	chr11	CGGCCUUUGGAUCACUAGAA	102868009	73
1521	chr11	ACUAGAAUGGCCAAGACCUA	102868022	73
1522	chr11	AUUUCGAUGAGGACGAAUUC	102871615	73
1523	chr11	GGGUAACAUUACUCCAUAUCU	102871884	73
1524	chr11	AGGGGAUGCACAUUUCGAUG	102871626	72
1525	chr11	UUGCGUAGUCAACAUCUCA	102871920	72
1526	chr11	ACAUCCUCACGGUUCAUGUC	102871931	72
1527	chr11	AAAUGCCAGGGGGGCGCCGUA	102872893	72
1528	chr11	CCCGAUUCCUUGGAAGUUCU	102864197	71
1529	chr11	UUAUGGCCAACCUGCCAUC	102866373	71
1530	chr11	CUCACUGCUGUUCACGAGAU	102868038	71
1531	chr11	CCCCGAUGUCCAUAUUUCA	102872916	71
1532	chr11	AAGAAUUAACUCACCAUAC	102867910	70
1533	chr11	CCUGAACAGCUCUACAAGCC	102874867	70
1534	chr11	UUUUGGUGAUACGUUGGAGU	102863149	68
1535	chr11	CAAUUUUAGGCCCGAUUCCU	102864187	68
1536	chr11	CACGAGAUUGGCCAUUCCUU	102868026	68
1537	chr11	UCCCCGAUGUCCAUAUUUC	102872917	68
1538	chr11	GGCAAGCGUUGGUUCUCUUU	102867383	66
1539	chr11	GCAAGCGUUGGUUCUCUUUU	102867384	65
1540	chr11	CUAGCCCAUGCUUUUGGACC	102871661	65
1541	chr11	UGGUUUUUGCCCGUGGAGGU	102871804	65

FIG. 53

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
1542	chr11	AAUUUUUACCAGACUUCACGA	102954498	74
1543	chr11	GAUGCCAUUACCAGUCUCCG	102950139	73
1544	chr11	CUUAGGUCUUGACCACUCCA	102952113	72
1545	chr11	CUACCAUCCUACAAAUCUCG	102955459	71
1546	chr11	UUCUUCGGCUUAGAGGUGAC	102955377	70
1547	chr11	CUGGCAUGACGCGAACAAUA	102944305	70
1548	chr11	UGGACCAUUUAAGAGUUCGA	102955287	70
1549	chr11	UAGGAUUGGUAGUAUGAUCUC	102955482	70
1550	chr11	UUCCCGCGAGAUUUUGUAGGA	102955467	69
1551	chr11	UAUGCAGCAUCAAUACGGUU	102949079	69
1552	chr11	UACCAUCCUACAAAUCUCGC	102955458	69
1553	chr11	CCGAGUUACCAUAGAGAGAC	102952019	69
1554	chr11	GGCCAGAGGGCCCAUCAAAU	102954259	68
1555	chr11	UUCUCGGAGCCUCUCAGUCA	102955420	68
1556	chr11	CUUGUUGCUGCGCAUGAGUU	102952142	68
1557	chr11	ACCUGGACAAGUAGUUCCAA	102954160	68
1558	chr11	AAAGUGGCUUUUGCCGGUGU	102952071	68
1559	chr11	GCGACUUCUACCCAUUUGAU	102954258	67
1560	chr11	CCUCCUGGGCCAAAUUAUGG	102954208	67
1561	chr11	AGCAAUGCCAUCGUGAAGUC	102954502	67
1562	chr11	AUAUGCAGCAUCAAUACGGU	102949078	67
1563	chr11	ACAUCAGGAACCCCGCAUCU	102955328	67
1564	chr11	AGGAUUCCCGCGAGAUUUUGU	102955463	66
1565	chr11	UUUCCUAUCUACACCUACAC	102952073	66
1566	chr11	GAUACUCUACCUCUGCAAAC	102955592	65
1567	chr11	CUUGGAGUGGUCAAGACCUA	102952125	65
1568	chr11	AAAUCUCGCGGGAAUCCUGA	102955447	65

FIG. 54

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
1569	chr11	ACUGCUUCUCGACAUCUCCG	19055436	80
1570	chr11	GUUUCCUACCAGCCCGACCA	19056276	79
1571	chr11	AGUGAAGGAUGCUUCCGUCA	19055449	78
1572	chr11	CGACCGCUGACAGGUGUCUG	19055975	76
1573	chr11	UUGAUUUCAUCACUGCAGCG	19055838	75
1574	chr11	GUAGGCACAGGUCAUCACAG	19056081	75
1575	chr11	CAGUGAAGGAUGCUUCCGUC	19055450	74
1576	chr11	GCUGAGGUGGAUCACAGUGA	19055464	74
1577	chr11	CUACUGCUGAGCAUCUUGGA	19055914	74
1578	chr11	CCGCCCCAGACACCUUGUCAG	19055966	74
1579	chr11	AGACUGCUUCUCGACAUCUC	19055434	73
1580	chr11	UCAGCAUGCUCAGGCCUGCA	19056059	73
1581	chr11	GAGCAUGGAUCCAACCACCC	19056389	73
1582	chr11	GACUGCUUCUCGACAUCUCC	19055435	72
1583	chr11	ACAUCUCCGGGGUGCCCUGA	19055447	72
1584	chr11	CCUAAUAUUAUGGAUCUGGA	19055654	72
1585	chr11	CGGCGGCAGCGAUACCAGAU	19055998	72

FIG. 55

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
1586	chr1	GACCCAAUCCCGUUGACAG	115286238	80
1587	chr1	GAUCUGGACUUCGAGGUCGG	115286475	80
1588	chr1	UGGGUGCUAAACAGCACACG	115286538	80
1589	chr1	CGAUAGCUGCACGCGUGGCG	115286606	79
1590	chr1	GCGAUAGCUGCACGCGUGGC	115286607	78
1591	chr1	AGCGGCGAUAGCUGCACGCG	115286611	78
1592	chr1	GCGGUUUAUCCGGAUAGAU	115286119	77
1593	chr1	CUUGACAAAGGUGUGAGUCG	115286186	77
1594	chr1	GCCCCGGCACCCGCUGUCAA	115286240	77
1595	chr1	ACACCGAGAAUUCGCCCCUG	115286407	77
1596	chr1	GGCGAUAGCUGCACGCGUGG	115286608	77
1597	chr1	UUUUCUGAUCGGCAUACAGG	115286746	77
1598	chr1	AUCUAUCCGGAUAAACCGCC	115286135	76
1599	chr1	CUUUGUCAAGGCGCUGACCA	115286161	76
1600	chr1	GUGUGACAGUGUCAGCGUGU	115286374	76
1601	chr1	UAAACAGCACACGGGGUGAA	115286545	76
1602	chr1	GCAGACCCGCAACAUUACUG	115286584	76
1603	chr1	ACACACAGGCCGUAUCUAUC	115286122	75
1604	chr1	CAUGGUCAGCGCCUUGACAA	115286174	75
1605	chr1	CCCGUUGACAGCGGGUGCCG	115286229	75
1606	chr1	GCAACAUUACUGUGGACCCC	115286576	74
1607	chr1	AUGCUGAAGUUUAGUCCAGU	115286687	74
1608	chr1	UGUCAACGGGAUUUGGGUCC	115286254	73
1609	chr1	GCCGCUUUUUAAACAGCCUG	115286572	73
1610	chr1	AGCUUUUCUGAUCGGCAUAC	115286749	73
1611	chr1	ACCCAAAUCCCGUUGACAGC	115286237	72
1612	chr1	GGGAUUUGGGUCCCGGCACU	115286261	72
1613	chr1	CAGGAUCUGGACUUCGAGGU	115286478	72
1614	chr1	GUGCAGCUAUCGCCGCUGCC	115286629	72
1615	chr1	GGGGCAUUGACUCAAGCAC	115286210	71
1616	chr1	ACCCGCUGUCAACGGGAUUU	115286248	71
1617	chr1	AAUUCGCCCCUGUGGAAGAU	115286415	71
1618	chr1	UCGCCGCUUUUUAAACAGCC	115286570	71
1619	chr1	UCCCGUUGACAGCGGGUGCC	115286230	70
1620	chr1	CCCCGGCACCCGCUGUCAAC	115286241	70
1621	chr1	GUGGUGCUGCCCCCUUCAAC	115286456	70
1622	chr1	AUCCCGUUGACAGCGGGUGC	115286231	69
1623	chr1	CACCCGCUGUCAACGGGAUU	115286247	69
1624	chr1	CUUCCACAGGGGCGAAUUCU	115286398	69
1625	chr1	AGGCUGCCUGGCGGUUUAUC	115286129	68
1626	chr1	UGCAGCUAUCGCCGCUGCCG	115286630	68
1627	chr1	CGUGCAGCUAUCGCCGCUGC	115286628	67
1628	chr1	CGCCGCUUUUUAAACAGCCU	115286571	65

FIG. 56

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
1629	chr17	UGAGACGACUGGGCGCUGCG	49506455	85
1630	chr17	GAGCAUGUCGGCGCCGUGCG	49506386	84
1631	chr17	UUGCAAGCAGGGCGCGAACG	49512873	83
1632	chr17	GUGUCCUCGCACACGGUGCA	49506591	82
1633	chr17	CAAGCAGAACACCGUGUGCG	49506527	81
1634	chr17	AGACCUCAUAGCCAGCACGG	49510523	81
1635	chr17	UCGCUUGGAUUCGGCGCAGGG	49512938	81
1636	chr17	AGCUUCUCAACGGCUCUGCG	49512788	80
1637	chr17	ACGGUCUGGUUUGGCUCCACA	49502167	79
1638	chr17	AGGCGUGACGUUCUCCGACG	49506314	79
1639	chr17	CAAGCCGUGCACCGAGUGCG	49506356	79
1640	chr17	GCGUCGUCGGCCUCCACGCA	49506387	79
1641	chr17	CAUGUCGGCGCCGUGCGUGG	49506389	79
1642	chr17	CGAGGCGUGCCGCGUGUGCG	49506473	79
1643	chr17	CGACGGCACGUUUUCCGACG	49506557	79
1644	chr17	UCCCAGCCCGUGGUGACCCG	49510575	79
1645	chr17	GACAGGGAUGAGGUUGUCGG	49510588	79
1646	chr17	GCUUCUCAACGGCUCUGCGG	49512789	79
1647	chr17	CCCCGGUUGGGCUCACACCG	49513004	79
1648	chr17	GGCGCGGCCCGUCCAUUGCG	49495443	78
1649	chr17	CAGCAGGCGCGGCCCGUCCA	49495448	78
1650	chr17	GCCACGGGCCGCGCCAUGGA	49495447	78
1651	chr17	CUCGGUCGCGCUCACCACGU	49506316	78
1652	chr17	AGCCCCACGCACUCGGUGCA	49506348	78
1653	chr17	AGCCGUGCACCGAGUGCGUG	49506358	78
1654	chr17	GCCGUAGGCGCAGCGGCACA	49506409	78
1655	chr17	CUGCGCCUACGGCUACUACC	49506431	78
1656	chr17	CGUCGGAUACGUGCCGUCG	49506542	78
1657	chr17	CUCGUCGGAUACGUGCCGU	49506544	78
1658	chr17	GCGCUCGGUGUCCUCGCACA	49506598	78
1659	chr17	CGAGGUCGGCUCGCUUGGAUG	49512948	78
1660	chr17	CAUCCAGCGAGCCGACCUCG	49512963	78
1661	chr17	GGUGCACGGCUUGCACGGCU	49506334	77
1662	chr17	AAGCCGUGCACCGAGUGCGU	49506357	77
1663	chr17	GUCGGGGCACUCCUCGCACA	49506526	77
1664	chr17	GUGUGGACCGUGUAAUCCAA	49510427	77
1665	chr17	GCUUGCAAGCAGGGCGCGAA	49512875	77
1666	chr17	GGGUGGCCAGCUUGCAAGC	49512885	77
1667	chr17	GGGCUCACACACGGUCUGGU	49502177	76
1668	chr17	GGUAGUAGCCGUAGGCGCAG	49506416	76
1669	chr17	GUGUGCGAGGAGUGCCCCGA	49506540	76
1670	chr17	ACCGUGUAAUCCAACGGCCA	49510421	76
1671	chr17	GCAGCCCUCAAGGGUGACGG	49512721	76
1672	chr17	GGUGGCCAGCUUGCAAGCA	49512884	76
1673	chr17	GGCUCGCUUGGAUGCGGCGCA	49512941	76
1674	chr17	UCUCCACGAGGUCGGCUCGC	49512954	76
1675	chr17	CCGAGCCCGCCUCGCACACG	49506470	75
1676	chr17	GGCGUGCCGCGUGUGCGAGG	49506476	75

FIG. 57

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
1677	chr12	AUCACGGCGGAAACGGUACG	5494630	86
1678	chr12	UGGCGAACAGAACAUACACGG	5494617	85
1679	chr12	UCAUCGGCCAUCGACAUUCG	5494718	83
1680	chr12	AGAGACGCUACAACUCACCG	5494518	82
1681	chr12	GCGGAGCAUAAGAGUCACCG	5494649	82
1682	chr12	GAGACGCUACAACUCACCGC	5494519	81
1683	chr12	CACAUACCGAGUACUCCCCU	5494654	81
1684	chr12	GGAGCAUAAGAGUCACCGAG	5494651	81
1685	chr12	CGGAGCAUAAGAGUCACCGA	5494650	80
1686	chr12	UGAAGUCAGUGCUCGGACGU	5494884	80
1687	chr12	UCGGUGUCCAUUGCAAUCAC	5494469	79
1688	chr12	CCCGCCCUUGUAUCUCAUGG	5494573	79
1689	chr12	AUGUUCUGUUCGCCACCG	5494597	79
1690	chr12	GGAUUACGUGGGCAGCCCCG	5494594	79
1691	chr12	GAAGCCAGGCCGCUAAAAA	5494820	78
1692	chr12	GCCGGUAAAAACGGUUGCA	5494828	78
1693	chr12	ACAAUAAACUCUGGGCUGG	5494923	78
1694	chr12	GUAUCUCAUGGAGGAUUACG	5494582	77
1695	chr12	AUAUUUCUCGCUUAUCUCCG	5494253	76
1696	chr12	GUAAUCCUCCAUGAGAUACA	5494566	76
1697	chr12	UUACGUGGGCAGCCCCGUGG	5494597	76
1698	chr12	GUGGGUGACCGACAAGUCAU	5494702	76
1699	chr12	CUGGUGUCCCCGAAUGUCGA	5494713	76
1700	chr12	CAUCGACAUUCGGGGACACC	5494726	76
1701	chr12	UUUUUAUGAAACGCGAUGUA	5494798	76
1702	chr12	GCAACCGUUUUUGACCGGCC	5494812	76
1703	chr12	GGGGUAUUGAUGAUAAACAC	5494848	76
1704	chr12	CAGUGCUCGGACGUAGGUUU	5494878	76
1705	chr12	UCAGUGCUCGGACGUAGGUU	5494879	76
1706	chr12	UCUCGACAAGGCACACACAC	5494953	76
1707	chr12	AUUCAGCCGGUGAUUGCAA	5494474	75
1708	chr12	GCCCCCGCCCUUGUAUCUCA	5494570	75
1709	chr12	CUCCAUGAGAUACAAGGGCG	5494560	74
1710	chr12	GAGUCACCGAGGGGAGUACU	5494660	74
1711	chr12	GUCGAUGGCCGAUGACUUGU	5494698	74
1712	chr12	CCGGUAAAAACGGUUGCAG	5494829	74
1713	chr12	UCAGAGAACAUAACUCGU	5494916	74
1714	chr12	UGAUGUUCUGUUCGCCACCA	5494599	73
1715	chr12	CCCCUGCAACCGUUUUUGAC	5494817	73
1716	chr12	UCCAUGAGAUACAAGGGCGG	5494559	72
1717	chr12	AGUCAUCGGCCAUCGACAUU	5494716	72
1718	chr12	GGCCGGUAAAAACGGUUGC	5494827	72
1719	chr12	GCUUAUCUCCGUGGCAUCCA	5494262	71
1720	chr12	UGUCCAUUGCAAUACCGGC	5494465	71
1721	chr12	GGACACCAGGUCACGGUGCU	5494739	71
1722	chr12	UCUCCGAUUUUUCUCGACA	5494965	71
1723	chr12	UACCGUGGCAAAAGUAACCA	5432328	70
1724	chr12	ACAGAACAUCACGGCGGAAA	5494623	70

FIG. 58

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
1725	chr19	GCGCCACGCAAGUCCACAG	49061667	84
1726	chr19	CGGACCGCUGUGGACUUGCG	49061659	82
1727	chr19	CUUCUUUGAAACCCGCUGCA	49061576	79
1728	chr19	CCUAGACAGGACUACUCGGG	49061865	79
1729	chr19	UGUGGACUUGCGUGGGCGCG	49061651	78
1730	chr19	GGACCGCUGUGGACUUGCGU	49061658	78
1731	chr19	AAACUGCACCAGCGAGUCGU	49061730	78
1732	chr19	CAGUUUCGCUCACCCCACGC	49061759	78
1733	chr19	CUGCAAGGCUGAUAACGCUG	49061561	76
1734	chr19	CACGCAAGUCCACAGCGGUC	49061672	76
1735	chr19	UGGGACUCAAUUGGCACACU	49061941	76
1736	chr19	ACUGCACCAGCGAGUCGUCG	49061728	75
1737	chr19	UUGGGACUCAAUUGGCACAC	49061940	75
1738	chr19	AGCUCACCCCGACGACUCGC	49061734	74
1739	chr19	UUUCAAGAAGUACUGGCGG	49061600	73
1740	chr19	UCAAGAAGUACUGGCGGAG	49061602	73
1741	chr19	CGGCCAACCGCAGCCGGCGU	49061760	72
1742	chr19	GUGCCCCGGCCAACCGCAGC	49061766	72
1743	chr19	AGCGUUAUCAGCCUUGCAGC	49061577	71
1744	chr19	AGCGGGUUUCAAGAAGUAC	49061594	71
1745	chr19	AGCGAGUCGUCGGGGUGAGC	49061720	70
1746	chr19	AACUGCACCAGCGAGUCGUC	49061729	70

FIG. 59

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
1747	chr1	UGGCUAGCCAGGUCGUGCG	156879222	85
1748	chr1	CCGUCCGCCUCGCAGCAUCG	156860935	84
1749	chr1	CUUUGAGUAUAUGCGGCACG	156876548	82
1750	chr1	GCAAUCGACUGCAUCACGCA	156881474	82
1751	chr1	GGCGCCGCCGCGAUGCUGCG	156860940	81
1752	chr1	ACGGAGACCACUCUUCACGA	156864735	81
1753	chr1	CGGCAGCCAAUGAGACCGUG	156873803	81
1754	chr1	GCCCACUAGACAGUUGCGUG	156879276	81
1755	chr1	GUACCAGCUCUCCAACACGG	156880153	81
1756	chr1	CAGGAAGAACGUGACGUGCU	156871699	80
1757	chr1	UGAUGGCGUAGACCUCUGGU	156881512	80
1758	chr1	GAGAGACUCCAGAGCGUUGA	156866923	79
1759	chr1	CCCUUUCGAGUUAACCCCG	156873942	79
1760	chr1	CUUCUUCGGCGUCUGCACCG	156876506	79
1761	chr1	UCACCACCGAGAGCGACGUG	156880080	79
1762	chr1	GGCAAUCGACUGCAUCACGC	156881473	79
1763	chr1	UCUAGCAGCCCAGCAACUGCA	156842147	78
1764	chr1	GCCGCCGCGAUGCUGCGAGG	156860943	78
1765	chr1	GAAGAGUGGUCUCCGUUUCG	156864754	78
1766	chr1	CCAGGUGCCCAUGCCUCGG	156868541	78
1767	chr1	GCGCAGACACCCGUGCCGCA	156873806	78
1768	chr1	GUUGCCGUUGUUGACGUGGG	156873839	78
1769	chr1	CCGGGACAUCGUGCUCUAGU	156876116	78
1770	chr1	UCGGCAGGACUCCAGCGUG	156876443	78
1771	chr1	CGGUACAGGAUGCUCUCGGG	156880040	78
1772	chr1	AUGAUGGCGUAGACCUCUGG	156881513	78
1773	chr1	AGGUCUUCUCACCAUCACCG	156868642	77
1774	chr1	UUACGGUACAGGAUGCUCUC	156880043	77
1775	chr1	GCUCCACACGUCGUCUCUGG	156880071	77
1776	chr1	GUACCAGGGCUGCUUGCCGU	156880122	77
1777	chr1	CAGAGGUCUACGCCAUCAUG	156881529	77
1778	chr1	CGCAGUCCCGAGGAGCCGUG	156861063	76
1779	chr1	UCGCAGUCCCGAGGAGCCGU	156861064	76
1780	chr1	CCUCGGGACUGCGAUGCACC	156861085	76
1781	chr1	CCCAGCACCAUCGUGAAGAG	156864740	76
1782	chr1	ACUCACAGGCGACUGAGCCG	156864788	76
1783	chr1	GGGCACCUGGACCUUCAGCG	156868516	76
1784	chr1	GUCGUCCCCACAUCACCG	156868543	76
1785	chr1	GAAGCUGGUCUCAUUGAGCA	156873746	76
1786	chr1	CAACGGCAACUACACGCUGC	156873864	76
1787	chr1	GCAGUCUCCUUCUCGCCGUG	156874396	76
1788	chr1	CGGUGGUGAACUACGGUAC	156880054	76
1789	chr1	AGUUGCGGGCUGCUAGAUCU	156842165	75
1790	chr1	GACUGCGAUGCACCCGGGAU	156861091	75
1791	chr1	CGGACACUCACAGCUCAGUC	156861140	75
1792	chr1	AUCUGGAGCUCGUGAUCUG	156864400	75
1793	chr1	AGGCAUCUGGCGCCACGAAA	156864754	75
1794	chr1	GGCACCUGGACCUUCAGCGU	156868515	75

FIG. 60

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
1795	chr9	GUCGCUGCACCAGAUCCGAG	84670872	83
1796	chr9	AUUACGUACAAUGCACAGUG	84724348	83
1797	chr9	GCUUCAGUGGUUCUAUAACG	84727759	81
1798	chr9	AUCAUCAUUGCUGAUAAACGG	84867254	81
1799	chr9	ACGCAAGGACUCCACCGUG	84948505	81
1800	chr9	ACCAAUCACACGGAGUACCA	84727826	80
1801	chr9	GCCCCAGAGCCGCGCCAUGG	84670782	79
1802	chr9	ACCACUGAAGCGCUGGUUUG	84727735	79
1803	chr9	GGUUUUUAUCAGUGACGUCUG	84745038	79
1804	chr9	CAAGUUCUAUGGCGUCUGCG	84948565	79
1805	chr9	AUCGCGGUGCACGAAGUGCU	84955404	79
1806	chr9	GUCAGUGCUGUACACGUCCC	84955491	79
1807	chr9	CAUUGUGUGGCCACCGACCU	85020206	79
1808	chr9	ACCCCAAACAGCGCUUCAG	84727746	78
1809	chr9	GCCGUGGUACUCCGUGUGAU	84727815	78
1810	chr9	AACUGCAGCGAAUGACAUCG	84744997	78
1811	chr9	CACCGAGAGAUGUCCCGAC	84745059	78
1812	chr9	ACGUCACUGAUAAAACCGGU	84745056	78
1813	chr9	UGUGGUGGUGAUUGCGUCUG	84752011	78
1814	chr9	GUUCUAUGGCGUCUGCGUGG	84948568	78
1815	chr9	GACUGCGUCAGUUCGUGGG	84955328	78
1816	chr9	CUGCGACUGCGUCAGUCCG	84955332	78
1817	chr9	GGCUGAGGGCAACCCGCCCA	84955327	78
1818	chr9	UAUAGCCCAGCAGAUCCGCG	84955375	78
1819	chr9	CAUGUACAGGAAAUUCACGA	85020273	78
1820	chr9	GUACCAGCUGUCAAACAAUG	85020360	78
1821	chr9	GGUGAUAGAGUGUAUCACUC	85021268	78
1822	chr9	GCACUGCAUUUGCAGGACGU	84670850	77
1823	chr9	CGACCCUUCUCCUGGCAUCG	84670903	77
1824	chr9	CGUCACUGAUAAAACCGGUC	84745057	77
1825	chr9	CGCCAGGUAGACCAUGCCCG	84955380	77
1826	chr9	GUACAGCACUGACUACUACA	84955513	77
1827	chr9	GCAUUGUGUGGCCACCGACC	85020207	77
1828	chr9	UCACGACGGAAAGCGACGUC	85020287	77
1829	chr9	AAGGUGGCAUGGACCCGCCA	84670780	76
1830	chr9	CAUGCCCGCGGCGAUCUGCU	84955368	76
1831	chr9	AGUCAGUGCUGUACACGUCC	84955492	76
1832	chr9	ACCUCUGGGGGCACGUGCG	85021296	76
1833	chr9	GCGACCCCGCACGUGCCCCC	85021304	76
1834	chr9	GGCAUGGACCCGCCAUGGCG	84670785	75
1835	chr9	CAUCGUGGCAUUUCCGAGAU	84670918	75
1836	chr9	GUAUUGGGAUGUUGGUAACC	84723690	75
1837	chr9	GCGCUUCAGUGGUUCUAUAA	84727757	75
1838	chr9	AACCGGUCGGGAACAUCUCU	84745069	75
1839	chr9	ACUGCGUCAGUUCGUGGGC	84955327	75
1840	chr9	UGCGACUGCGUCAGUCCGU	84955331	75
1841	chr9	CCAGCAGAUCCGCGGGCA	84955381	75
1842	chr9	AAUGCAGUGCCUCUCGGAUC	84670875	74

FIG. 61

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
1843	chr2	GCCUGCCAGGAGGCUAACUA	237877264	79
1844	chr2	UCCAUCCGCAGGAGCUACA	237911533	78
1845	chr2	AGUAGCGGCCAUGCACUGCC	237911620	78
1846	chr2	CUGGCAGAGCAAGCGCACUG	237911767	78
1847	chr2	GCGCACUGAGGGCAUUGUGU	237911779	78
1848	chr2	ACCGUAGUUAGCCUCCUGGC	237877253	77
1849	chr2	UGGCAGAGCAAGCGCACUGA	237911768	77
1850	chr2	GGGCACCGUAGUUAGCCUCC	237877257	75
1851	chr2	ACACCACAGCGUCUCCCCGA	237877325	75
1852	chr2	AGGCCGUCGGGGAGACGCUG	237877334	74
1853	chr2	GAGACGCUGUGGUGUGACUG	237877345	74
1854	chr2	CGACUGCACCUGGCACAUGG	237911563	74
1855	chr2	GUGAUGGGGACCACGAUGAA	237911702	74
1856	chr2	GCGCCGCGGGAGGCGGCACA	237859691	73
1857	chr2	AGUGGUCAUGAAGAGGUGAU	237877229	73
1858	chr2	AGGUUCUCCUGGCAGUGCA	237911624	73
1859	chr2	GGGUAGAGGAUGCUGCCGGG	237911681	73

FIG. 62

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
1860	chr2	GUCACCCGGUCAUAGGAAGG	165991323	80
1861	chr2	AAAGAGCUGCAUGCCGACCA	166038003	80
1862	chr2	CGUCAUUGGAUAGUGCUGCA	166041284	80
1863	chr2	GUGUCGUCGGGGCACAAACA	166043887	80
1864	chr2	CUGAGUCAUUGAGUCGAAACA	166047671	80
1865	chr2	CCGGGUGACAAAGCCAAUUG	165991297	79
1866	chr2	CAGCUUUAGAGGGCGAGCAA	166043970	79
1867	chr2	UUUGUCACCCGUGCAUAGGA	165991320	78
1868	chr2	GCGUGGGAGUUGACAAUCAC	166037946	78
1869	chr2	UGGCGAGUCCAAGUUCUACC	166039478	78
1870	chr2	AGAACUUGGACUCGCCAAUG	166039460	77
1871	chr2	UGGCUUUGUCACCCGGUCAU	165991316	76
1872	chr2	UUAACACCACAACUGGUGAC	166002609	76
1873	chr2	AAAGACGAUUAAGACGAUGU	166012236	76
1874	chr2	UUGUGUUCGCGUGCUGUGU	166037877	76
1875	chr2	AACUGAAGGUCCACCAACCA	166043752	76
1876	chr2	UCCCGAUGCAACUCAGUUCA	165991810	75
1877	chr2	GGGUGGCUUACUGUUGAGAA	165992075	75
1878	chr2	GGUACAGUCACAGUAAGACU	166036147	75
1879	chr2	CAUGGAGCACUAUCCAAUGA	166041271	75
1880	chr2	GACCCUAAUAAAGUUAACCC	165992034	74
1881	chr2	GUCAAACCGUCACCAGUUG	166002615	74
1882	chr2	UGUAGAAGAACAGCCCGUAG	166015654	74
1883	chr2	UUAAGUGGGUACAUACCACU	166037777	74
1884	chr2	ACGCUUAGCCUGGUAGAACU	166039474	74
1885	chr2	UCAGUUCUACAUCGCCUGU	166043723	74
1886	chr2	CAGUAGGUAUCCCGGAUGC	166043820	74
1887	chr2	ACGGCUCUCGUUAUCCUCAA	166043917	74
1888	chr2	CUUGUUUCGACUAAUGACUC	166047658	74
1889	chr2	CUGAAUUCGUCUCAAUGCU	166052878	74
1890	chr2	CAAUGAGUAACCCUCCUGAU	166056430	74
1891	chr2	UGGUAGUCACAUUUCACUC	165994301	73
1892	chr2	AGCUGUCCAACAGGCGAUGU	166043729	73
1893	chr2	UGGCAGUGUUUCCAGCGAAU	166043800	73
1894	chr2	AUGACCUACUGGUCUGACUC	166043844	73
1895	chr2	UGCGUCUCUCUCCGUGUCGU	166043874	73
1896	chr2	CAUUUUGUCACGCAUCAAUC	165994268	72
1897	chr2	CAGAUUGAUGCGUGACAAAA	165994281	72
1898	chr2	CUUUAGUAGUGAAUCGGAUC	166036067	72
1899	chr2	CAGCAUCCGGGAUGACCUAC	166043833	72
1900	chr2	UUGUUUGUGCCCCGACGACA	166043873	72
1901	chr2	CGUCUCUCUCCGUGUCGUCG	166043876	72
1902	chr2	UAGUCUUUGUUGAGCAUCCG	166044035	72
1903	chr2	UGUCAUUCGGUUCUUCAA	166045090	72
1904	chr2	ACUCUUGGAACUACUUAAG	166045243	72
1905	chr2	GGAUGCUCUACGAAUACAGA	165991612	71
1906	chr2	UCCGAAUAGUUGAACAUAAAC	166013797	71
1907	chr2	UGGUACAGUCACAGUAAGAC	166036146	71

FIG. 63

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
1908	chr2	UUUGGUCACACUAUCAUACG	165389729	83
1909	chr2	UUGGUCACACUAUCAUACGA	165389728	80
1910	chr2	CAGCUUCAGAGGUCGAGCAA	165323235	79
1911	chr2	AUCCAUCCAUCCCUAAAACG	165377603	79
1912	chr2	CUCUUGUUUGCGUUUCAACG	165389504	79
1913	chr2	AGAGAUGUUUGAUGUAAGCG	165374845	78
1914	chr2	GUCACACUAUCAUACGAGGG	165389725	78
1915	chr2	UUGAGUCAUGAGACGAAAUA	165313717	77
1916	chr2	GGAGCCACGGAUGCUCAGUA	165323162	77
1917	chr2	GGUAGAAGGGCCCCCGACCA	165323453	77
1918	chr2	UAUGGAGCACUAUCCCAUGA	165331528	77
1919	chr2	AUGAUUGUGAACUCCACGC	165344756	77
1920	chr2	GAUAUUGGAGCUCCCGCCGA	165365199	77
1921	chr2	GGUAGCGUCUGUAAGCCCUC	165389547	77
1922	chr2	CCAGUCUGGAGGGUUACUCA	165307906	76
1923	chr2	CUCUCCAAGACGCAACAGUA	165323202	76
1924	chr2	ACUGCUGAACUGCUCGCUCA	165331530	76
1925	chr2	AGUUCUCCGAUCAUUCGCGC	165342465	76
1926	chr2	AUCAUACGAGGUGGAGACG	165389717	76
1927	chr2	CAGUCAGUGCUGGUACCGCC	165295847	75
1928	chr2	UGUAGGCCUGAAGACCAUUG	165310335	75
1929	chr2	CUGCUGAACUGCUCGCUCAU	165331529	75
1930	chr2	CCAUGAGUAACCCUCCAGAC	165307918	74
1931	chr2	CUAAGCGUGUUUGCGCUAAU	165310417	74
1932	chr2	UAGUCCUJACUGAGCAUCCG	165323170	74
1933	chr2	GCACGAACAGAGAGUCUCUU	165323307	74
1934	chr2	UGGUGUGGUCUCCUGGUCG	165323454	74
1935	chr2	UUGAGAGCAAUCAAACUGCC	165374898	74
1936	chr2	CGUUUCAACGUGGUCGUAAU	165389494	74
1937	chr2	GCGUUGUUCAAUAGCAGCAA	165295890	73
1938	chr2	GAGACCCAAACAGGAACGCA	165295945	73
1939	chr2	ACGGGAUCCAUGGAUUGGU	165308767	73
1940	chr2	AAAUGACAGAGUCCGAAAAU	165315661	73
1941	chr2	CUCGCCCUCUGUUGCGUCU	165323194	73
1942	chr2	UCUCUCCAAGACGCAACAGU	165323201	73
1943	chr2	CAUAGCGCUGUGGACUGCAA	165323434	73
1944	chr2	CUGCUGAAAGUGGGUUGCAUA	165370239	73
1945	chr2	GCUCUCCAUCUGUAUUCGA	165389433	73
1946	chr2	AAUUUACCAGCCGGAUGAU	165342459	72
1947	chr2	GCGUGGGAGUUCACAAUCAU	165344741	72
1948	chr2	GCAUACUCACAUAACAACUC	165370292	72
1949	chr2	AACUUUGAUAAACGUAGGACU	165374939	72
1950	chr2	CACGUUGAAACGCAAACAAG	165389517	72
1951	chr2	GUAGGCCUGAAGACCAUUGU	165310336	71
1952	chr2	GGGUAGAAGGGCCCCCGACC	165323454	71
1953	chr2	AUUCAGCAGCGAGUCAGUA	165354652	71
1954	chr2	UGUCUUCAGAUUCCGAUUUU	165315661	70
1955	chr2	GCAUGGUGGGCAUUUCUGUC	165331347	70

FIG. 64

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
1956	chr2	CCGUUGUCAUGUUACACAG	165097400	81
1957	chr2	AUGGUGGAAACGGAUGACCA	165092414	80
1958	chr2	CCUAGACAUUACGUGCUGCU	165154646	80
1959	chr2	CUCUUGGCAAGCAAGCUCGG	165097317	79
1960	chr2	UCAAAAGCAGAAUCGCUUGG	165162677	79
1961	chr2	GACCAAGCUCCAUUAAACUG	165131305	78
1962	chr2	GUUGAUCCGGGACAAAACUA	165092392	77
1963	chr2	AGUCAUGGGGUAGUGCUCCA	165137932	77
1964	chr2	AACCGGGAUAAGGCUCUUAAG	165100332	76
1965	chr2	CUAGGGUCAUGUAUUUGCCC	165092409	75
1966	chr2	GUGCUCACAAUACUGUAGC	165113887	75
1967	chr2	GAUGUUGUUCUACCCCGAGA	165115519	75
1968	chr2	CAGUUUCAGAGGUCGGGCAA	165140919	75
1969	chr2	CAGUCUCUCUUGAGUAUCCG	165140984	75
1970	chr2	UCAUGAGUCGAAAUAAGAGAC	165155811	75
1971	chr2	UCAAGACUCUGAAAGUUCGA	165163849	75
1972	chr2	GACCCUGACACAAUUCACCC	165090957	74
1973	chr2	AAUGAACACUAGGUUGAUCC	165092380	74
1974	chr2	CUAUCUUGCACUGCUUCAAG	165097256	74
1975	chr2	CCUUCUCAGUAGUGGUGCAU	165113820	74
1976	chr2	CAAUUGGCACUGUGACGGUG	165127725	74
1977	chr2	UCCAGUACCUACACCACUGG	165127810	74
1978	chr2	UGUACUGCGAUCAUUCAGAC	165131248	74
1979	chr2	UUACGUUUCUUCGUGAUCCA	165164429	74
1980	chr2	GAUGGUGGAAACGGAUGACC	165092415	73
1981	chr2	AGAGCCUUAUCCCGGUUUGA	165100314	73
1982	chr2	CCAAUGCACCACUACUGAGA	165113832	73
1983	chr2	UGUUUUGCUAUUUGCGUCUUG	165140962	73
1984	chr2	UUCAAAAGCAGAAUCGCUUG	165162676	73
1985	chr2	UACUCCACUAAACCCUGUU	165170464	73
1986	chr2	CUGCCAGGGUGAAUUGUGUC	165090966	72
1987	chr2	UCUUACUGCUGGGCGAGGUA	165094385	72
1988	chr2	ACCCGAAGAAGACCUUAAAC	165115478	72
1989	chr2	ACGCAACAGUAACGUUAGUC	165140793	72
1990	chr2	GACCUCUAAGAGCCUUAUCC	165100322	71
1991	chr2	UCGGUGCCAUCAAAUCAUUA	165100361	71
1992	chr2	AGCCUCAGUUUAAUGGAGCU	165131295	71
1993	chr2	GACAGAAAUGUCCGCCAUGC	165138085	71
1994	chr2	UCAGCUCUAACGUCACCUAC	165140672	71
1995	chr2	CUCAUUUGGACCUUACCAAC	165155763	71
1996	chr2	ACCCAAAACACGCUUUGUAA	165090584	70
1997	chr2	ACUACUACUUCACUAUAGGC	165092299	70
1998	chr2	GGUUGAUCCGGGACAAAACU	165092391	70
1999	chr2	CAGAAAGCUUCUUUACCGAC	165162795	70
2000	chr2	CUUACUGCUGGGCGAGGUUAU	165094386	69
2001	chr2	CCGGAAGCUUGUUUACUGA	165115459	69
2002	chr2	ACCACCAGUGGUGUAGGUAC	165127799	69
2003	chr2	CAUUUGAAGACAGCGAAAGC	165140854	69

FIG. 65

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
2004	chr17	GCGGAUCACACGGAACAGCG	63941946	85
2005	chr17	UAUGGAACUGCUGCGCCCCG	63961351	85
2006	chr17	GUGUUGGUGUCGUUGAACGG	63968201	85
2007	chr17	GGGACGCCGGACCCACUAUG	63940869	84
2008	chr17	AGGGCACUGUCCCGAUUCGA	63947057	82
2009	chr17	CGUCUCCGCAUCCUGUGCG	63957262	82
2010	chr17	CAUGGUAUGCCAACGACACG	63968092	82
2011	chr17	GUUGGUGUCGUUGAACGGCG	63968203	82
2012	chr17	UGUCCUGCGGCUGAUCCGCG	63941894	81
2013	chr17	GAUGAACAUAGCUGAACAGCG	63972224	81
2014	chr17	CGUGUCCUGCGGCUGAUCCG	63941896	80
2015	chr17	GAGGGCACUGUCCCGAUUCG	63947058	80
2016	chr17	GACGAGUCCCAUCAUAGAG	63949511	80
2017	chr17	GCCCAACUUGAUGCGCCCGA	63951798	80
2018	chr17	CAGCCUGGACACAUCGCAAG	63963737	80
2019	chr17	UCAGGGCUGAAGACGAUCGU	63968342	80
2020	chr17	CUUCAGCGUAGUCAGGCGCG	63972379	80
2021	chr17	CCGCGCCUGACUACGCUGAA	63972393	80
2022	chr17	CUACGGAGACCCCCCGCCGG	63972624	80
2023	chr17	GAUCUACGGAGACCCCCCGC	63972627	80
2024	chr17	CCUGUUCGAGAUCACCACGU	63941681	79
2025	chr17	CACGCCCAAUCCGCGCCAGG	63941927	79
2026	chr17	GAAGUGGUGGACUCUGCGCA	63948693	79
2027	chr17	AGCUGACUACAAGCCCCCGG	63949464	79
2028	chr17	CGACCUGGAGAUGCCCACCG	63951467	79
2029	chr17	UCGGACUCCUCGGAGGCGAU	63951499	79
2030	chr17	GCGCGGCAGGUUGCAGUCCA	63957332	79
2031	chr17	GCUUUUGUGUACCAGACGGA	63959270	79
2032	chr17	CUAGGCCUGGCCAACGUACA	63959298	79
2033	chr17	CCCUACGAGUAUUUCCAGCA	63959367	79
2034	chr17	GAUCGUCAUGGACCCGUUCG	63961302	79
2035	chr17	AUGAGUGCAUCAAGACCGGG	63966209	79
2036	chr17	CCAAUCAAGGUAUCGUUGG	63968062	79
2037	chr17	CGUGUCAUUGCUGUACCACG	63968179	79
2038	chr17	GUCAGGGCUGAAGACGAUCG	63968343	79
2039	chr17	CUCAUCAAGAUACUGGCCCG	63971799	79
2040	chr17	GGGAUGCCGAUGACCUCCGG	63972623	79
2041	chr17	GAUGCCGAUGACCUCCGGCG	63972625	79
2042	chr17	AUGUACCGCCACAGCCACGA	63941008	78
2043	chr17	AGAUCAGAGGGCCUACCGC	63941067	78
2044	chr17	UUGGGCUUGGCAAUCCUCAG	63941329	78
2045	chr17	CGGAUCACACGGAACAGCGU	63941947	78
2046	chr17	CGAAGGCCUGCUUCGUCACG	63943065	78
2047	chr17	CCUAUCCACUAUACUUAGG	63943848	78
2048	chr17	UGAGAGGUUCGACAUCUCCG	63945478	78
2049	chr17	GAUGUCGAACCUCUCAGAGG	63945497	78
2050	chr17	GUCCCGAUUCGAGGGCAUGA	63947049	78
2051	chr17	CAUCUCGCCAUCCUCAUCCG	63951837	78

FIG. 66

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
2052	chr3	GUGCAUCUCAGGCCGACUGG	38579381	83
2053	chr3	AGUUCGCACCUUGGAUCACUG	38609742	82
2054	chr3	AGUCGGCGAGAUCUUCACUG	38550379	81
2055	chr3	GAUGAGGCCUCUCGCUCAG	38550545	81
2056	chr3	UCGACAUACUUGGUCCAGGG	38622417	81
2057	chr3	AGCGAUAAACCUCAGGUGCG	38550402	80
2058	chr3	CCGCACCUUGAGGUUAUCGC	38550416	80
2059	chr3	ACUCCGGCGCAAGCACGAAG	38550670	80
2060	chr3	UUCGUGCUUGCGCCGGAGUG	38550686	80
2061	chr3	ACUUGUAUACCCACCCACGA	38554282	80
2062	chr3	GUGGUGUCCACCGCACAGCA	38575429	80
2063	chr3	UGGGCGAGACGGUUCAGCA	38597933	80
2064	chr3	AUCUACACACGGAGCCUGGG	38599005	80
2065	chr3	CUUCCACCCCAUCCGGAGAG	38630338	80
2066	chr3	CCAACAGCAAUGGCUCUCGG	38551157	79
2067	chr3	CUGUGGAUGUCCAUAAGCA	38597870	79
2068	chr3	AUGCUCGCGCGCUGGAACG	38604033	79
2069	chr3	CGUGGUCGCAAUGGCCUAUG	38606042	79
2070	chr3	UGGCUGCAGGACAUGUCCGG	38606802	79
2071	chr3	CGGCACCAACGGCUCCGUGG	38609787	79
2072	chr3	CCAGGCCGAGGCUCACACGA	38550326	78
2073	chr3	CACCUUGAGGUUAUCGCUGG	38550419	78
2074	chr3	UGGGGACCGCAUCCAUGCA	38550823	78
2075	chr3	CGCAUCCUCAGACUGAUCCG	38551461	78
2076	chr3	GCGAGACGGUUCAGCAUGG	38597936	78
2077	chr3	ACUCUUCGCGCUGAUGACGC	38606700	78
2078	chr3	UUUAGGCACCGGUAGCCUC	38606798	78
2079	chr3	CAACGGCACCAACGGCUCCG	38609790	78
2080	chr3	AUGGCGGUGAAGGUGUACCU	38620971	78
2081	chr3	CACUCGACAUACUUGGUCCA	38622414	78
2082	chr3	AGGCUCACACGAUGGACUCA	38550334	77
2083	chr3	GAUGACUCGGAAGAGCGUCG	38551514	77
2084	chr3	CGGAGAAUUGUACUGGACCA	38560205	77
2085	chr3	UCCCAAACUCCCCGCAAAG	38560325	77
2086	chr3	UGGGCCCCAUCAAGUCACUG	38562474	77
2087	chr3	CUUCGAGGACAUCUACCUAG	38566563	77
2088	chr3	CAAGACCUGCUACCACAUCG	38575361	77
2089	chr3	GUGCUCACGAUGUGGUAGC	38575368	77
2090	chr3	CAUUACCUCACCGCACCCUG	38579345	77
2091	chr3	CCCUACUACUACUCCAACA	38587502	77
2092	chr3	UCCGUGUGUAGAUGGCUUCG	38598983	77
2093	chr3	UCCUCGAGCCAUCUACACA	38598994	77
2094	chr3	CACUCAGACCACGCCAUCGG	38599040	77
2095	chr3	GCUAGAGACCCGCCAGACA	38603716	77
2096	chr3	GGAGGGCUACCGGUGCCUAA	38606784	77
2097	chr3	CGCAACUUCACAGCGCUCAA	38609807	77
2098	chr3	CUCUGCCAUGCGCUUCUCGA	38633235	77
2099	chr3	UGUAGUCAGACCCCCGCACC	38550403	76

FIG. 67

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
2100	chr12	UGUCUUUCGAGUGUUGUGCG	51765927	84
2101	chr12	CGUGAAGCGCAACAGCACGG	51721835	83
2102	chr12	CUCCUGCUUUGCGACGCAGUG	51807154	83
2103	chr12	UCUGUCCUUCGCCCCGUAGG	51745975	82
2104	chr12	GCAGAUUGGAAGAGCGGUUCG	51807104	82
2105	chr12	CUGAGUCUAGCAGACGUGGA	51762643	81
2106	chr12	GUACCCGUACAGUCAAGUUG	51769235	81
2107	chr12	GUCCUGCAGCGUGCCUACCG	51807204	81
2108	chr12	GAACAGCUGCAGUCCGAUCA	51699665	80
2109	chr12	CGCGGAUGACGAGCACAGCA	51721676	80
2110	chr12	CAGCUACCGAUGACAGUGUA	51721942	80
2111	chr12	AUUCGCGUGGAUGUCUGCAC	51769114	80
2112	chr12	GGGUACCCGUACAGUCAAGU	51769237	80
2113	chr12	ACCUAGUUCGAGUAGCCCA	51780682	80
2114	chr12	GAGUUUGCCUUUCAUCUACG	51663023	79
2115	chr12	GAUUCUGUCCUUCGCCCCGU	51745978	79
2116	chr12	GGUACCCGUACAGUCAAGUU	51769236	79
2117	chr12	GUGCUGCCAGGUCAACAUCG	51770565	79
2118	chr12	UGCAGCUGUAUUCGCGGA	51788744	79
2119	chr12	ACCGGGGACAUUUGGCAAGG	51807220	79
2120	chr12	GGGAUGUCCCCGUAGAUGAA	51663018	78
2121	chr12	UCCUGACUGGUCGAAGAAUG	51686451	78
2122	chr12	CAGGAGACGCCCGCCGAUGU	51721885	78
2123	chr12	ACCAAUUAGCCUCCUACGGG	51745978	78
2124	chr12	AUUAGCCUCCUACGGGCGGA	51745982	78
2125	chr12	GGCCACUUUAAGCAGCGUG	51769040	78
2126	chr12	GCCUGGGCUACUCGGAACU	51780693	78
2127	chr12	GCCUAGAUAAAGGAACACCA	51806668	78
2128	chr12	CAUUGAACUGGGUGGCAUCG	51806879	78
2129	chr12	AACCACACUGCGUCGCAAGC	51807164	78
2130	chr12	GUGCAAAGGAAAGACGUAAC	51706557	77
2131	chr12	GUAGCUGCUCCGGCGCUCGC	51721735	77
2132	chr12	UGUAGCUGCUCCGGCGCUCG	51721736	77
2133	chr12	GGCGUGGUGUCCCUCAUCGG	51721866	77
2134	chr12	GUAGGAGGCUAAUUGGUCCA	51745960	77
2135	chr12	ACUGAGUCUAGCAGACGUGG	51762642	77
2136	chr12	GUGUGUCUGCAAGAUAACC	51765852	77
2137	chr12	AGUCAUGCAUAUGCCAGCGA	51765873	77
2138	chr12	UCAGUGAUCCGUAUCAAGAA	51768978	77
2139	chr12	AACUGUAUCGCCAAUCACAC	51769107	77
2140	chr12	GGUGCAGACAUCCACCGGAA	51769128	77
2141	chr12	AGCAGCGAGUCGGAUCCUGA	51769320	77
2142	chr12	GAGCAGGGUACGAAUCCCUU	51806392	77
2143	chr12	AGCCUAGAUAAAGGAACACCC	51806667	77
2144	chr12	UGACUGCCAUCGGCCUUUGG	51662931	76
2145	chr12	GUCCUCCCGAUGACUGCCAU	51662941	76
2146	chr12	ACAUUCUUCGACCAGUCAGG	51686437	76
2147	chr12	UCUGUUGUCUGGCAGCCGAA	51706668	76

FIG. 68

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
2148	chr2	AGGAAACCGUGACCCAUUCUG	166228834	80
2149	chr2	GGCUGAGCGUCCAUCAACCA	166284536	80
2150	chr2	AUAGGCGAGCACAUGAAAAG	166286359	80
2151	chr2	UAUGCCCUUCGACACCAAGG	166286391	80
2152	chr2	CGUGUGUAGUCAGUGUCCAG	166293364	80
2153	chr2	CGAAUCCUACGUCUAGUCAA	166199767	79
2154	chr2	AAAGCCAAUUCUCGACCAG	166204364	79
2155	chr2	GUGUCCGAAGGGAUUUAAUG	166233407	79
2156	chr2	GUCGUUGUGAAUGCACUCAU	166228955	78
2157	chr2	UUGGGUCAUUAAGCCUAAACA	166293275	78
2158	chr2	CCACCAUUGCUGCCGGUGAA	166284585	77
2159	chr2	CCGUUCACCGGCAGCAUUGG	166284597	77
2160	chr2	GUUCACCGGCAGCAUUGGUG	166284599	77
2161	chr2	CUUAUAGACGUUACCGCUUA	166198926	76
2162	chr2	GCCAAGUUAACAUAGAGUCA	166242615	76
2163	chr2	UGACAGUGCCAAUUGCACCU	166272473	76
2164	chr2	GGGCUGAGCGUCCAUCAACC	166284535	76
2165	chr2	GAGGUUGUCUACCCCAUUC	166286340	76
2166	chr2	UCACUUUUCUUCGUGACCCG	166305829	76
2167	chr2	CCAUGAAUAACCCACCGGAC	166306529	76
2168	chr2	CCAGUCCGGUGGGUUAUUCA	166306541	76
2169	chr2	CAGCAAUGCGUUGUUCAAUG	166311689	76
2170	chr2	AUGUUAGUCAAAAUGUGCGA	166228756	75
2171	chr2	UAAAGCUCUCAGUGUCCGAA	166233396	75
2172	chr2	CUGUGCAUUUUCCCGUUCAC	166284585	75
2173	chr2	CGUUCACCGGCAGCAUUGGU	166284598	75
2174	chr2	UGUUACUGCUGCGUCGUCC	166284640	75
2175	chr2	GUUACUGCUGCGUCGUCCU	166284641	75
2176	chr2	UUACUGCUGCGUCGUCCUG	166284642	75
2177	chr2	ACCUUGGUGUCGAAGGGCAU	166286377	75
2178	chr2	AGUGUAUUAACACCACAGAU	166228834	74
2179	chr2	UUAAGCUCUCAGUGUCCGA	166233395	74
2180	chr2	AGUUCUGCGAUCAUUCAGAC	166278144	74
2181	chr2	GUUUCACCUUGGUGUCGAA	166286383	74
2182	chr2	UCGACAUUUUUGGUCCAGUC	166306527	74
2183	chr2	UUGCUCUUUUGACUAGACGU	166199774	73
2184	chr2	AAAAGCCAAUUCUCGACCA	166204365	73
2185	chr2	GCAAAACAUUCGGAACGAUU	166228799	73
2186	chr2	UAUGAAUUCGAUGAGCCAG	166251785	73
2187	chr2	AGUUUCCACCUUGGUGUCGA	166286384	73
2188	chr2	GCCUAGCCCUUCGACACCA	166286388	73
2189	chr2	AGCUCGUGUAGCCAUAAUCA	166293325	73
2190	chr2	UCGUGACCCGUGGAACUGGC	166305819	73
2191	chr2	ACAUUUUUGGUCCAGUCCGG	166306530	73
2192	chr2	ACUACUACUUCACUGUAGGA	166204000	72
2193	chr2	CUAGGUCAAAUUAUACAUCCU	166204212	72
2194	chr2	UCUGGCUCAUCGGAUUUCAU	166251799	72
2195	chr2	UUUUCCAAUUCGGAUUCCCC	166272468	72

FIG. 69

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
2196	chr3	GUGACACUCUCAUAGGACGG	38697463	83
2197	chr3	UAGUUUCGAGGGAUCCAAUG	38793997	83
2198	chr3	UUCGAACCCUUCGCGCUCUG	38713999	82
2199	chr3	UCAUCGCUAAUCCGACUGUG	38726716	82
2200	chr3	UGUAGUCACCAUGGCGUAUG	38756765	82
2201	chr3	GUGACUCCGGAGUAAAGCGA	38793967	82
2202	chr3	CAAGACUUGCUACCGUAUCG	38722322	81
2203	chr3	GCACUUAACCUCAAGGACGG	38750082	81
2204	chr3	CUAUGUGCUGCACCUCUCCA	38697611	80
2205	chr3	GAAUGUCCUAGGAGAAUCCG	38697776	80
2206	chr3	GCACAGCAAUAGAUCUCCGU	38763571	80
2207	chr3	GGCACAGCAAUAGAUCUCCG	38763572	80
2208	chr3	GGGGCAAGCUCACUAGUGGG	38752255	79
2209	chr3	ACUAGCCCGGCGUUUCCAG	38752491	79
2210	chr3	AGGUUAAAGGUGAUCCAUG	38755912	79
2211	chr3	GCUCCAGCAGAACUGAUCG	38793787	79
2212	chr3	AGGCUGGAGUGUUCUCACUA	38697349	78
2213	chr3	UGACACUCUCAUAGGACGGU	38697464	78
2214	chr3	GUGCAGCACAUAGCUCCGAU	38697633	78
2215	chr3	UUCUUGCUUCCAUCGGAGAG	38697684	78
2216	chr3	AGACUGAUCCGAGCGGCCAA	38698450	78
2217	chr3	UGCAGCUGUUGAUUCCCGGG	38710848	78
2218	chr3	GGAUACCACCAAGAGUCCA	38722364	78
2219	chr3	CAUCGCUAAUCCGACUGUGU	38726715	78
2220	chr3	CACCAUCACCUUGUGCAUCG	38742373	78
2221	chr3	UCUCAACAGGCAUUCGAUGC	38750176	78
2222	chr3	GGAGACCACGAAAGCCAUCG	38752375	78
2223	chr3	UGGUUGUAAGGAUCAGAGCG	38755815	78
2224	chr3	GGCCCGAGUGGCACUAAACC	38792129	78
2225	chr3	UCCGUUCUACAGCACACACC	38793745	78
2226	chr3	GUAUGGAGCUGAUUGCCCCU	38697360	77
2227	chr3	GGCAAUCAGCUCCAUAUCUG	38697378	77
2228	chr3	AGGUGCAUCAACUAUACCGA	38712308	77
2229	chr3	CAGUGGCCGCAGAGCGCGAA	38714005	77
2230	chr3	CAGAGCGCGAAGGGUUCGAA	38714014	77
2231	chr3	CAGCGGGGCCAGUCUUAUG	38728710	77
2232	chr3	UGUUACGGUAGUUUCCCCU	38728753	77
2233	chr3	GGAGCAUGGCUUCGAAGGUA	38742322	77
2234	chr3	AUCAUAACCUCGUCUUAUGA	38750077	77
2235	chr3	GCAAGCUCACUAGUGGGCGG	38752258	77
2236	chr3	GAGUGAGAUUUCUCGGCCAG	38752443	77
2237	chr3	GCUCCCCGAUCAGUUCUGCU	38793796	77
2238	chr3	GGGAGCUCACCAUAGAACUU	38793816	77
2239	chr3	CAACUCCGUCGCUUUACUC	38793961	77
2240	chr3	GGUCAACAUGCAACCCAAGU	38709599	76
2241	chr3	UCACAAUCGACAAAGGUACA	38712288	76
2242	chr3	CGAGAUGCUGCUUAAGUGGG	38718720	76
2243	chr3	GGUUGGCAAGCAGCUCCUAG	38728756	76

FIG. 70

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
2244	chr3	UCCGGACUCUACGAGCACUG	38872234	81
2245	chr3	GGUAUUCGCAUCCUCUGCG	38896951	81
2246	chr3	UUCACCGCUAGGGUACUCGG	38846988	80
2247	chr3	CCAAUCAUGCCUGACGCCCA	38894646	80
2248	chr3	UUUACGGCACUGGCACAUGG	38896996	80
2249	chr3	AGAGCCACCGAGUACCCUAG	38846996	79
2250	chr3	UUCGGCCAAUCCGAGCCAAG	38847670	79
2251	chr3	ACAAUUCUGAAGAGCGUCGG	38847693	79
2252	chr3	CAAUUCUGAAGAGCGUCGGA	38847694	79
2253	chr3	UUACCACUUGCAGCAGAGCG	38871458	79
2254	chr3	CAGUGCUCGUAGAGUCCGGA	38872249	79
2255	chr3	AGUAGAGCCCAGUAGUACGC	38909187	79
2256	chr3	GUAGAGCCCAGUAGUACGCA	38909188	79
2257	chr3	GAAGAGCUGCUGACCUACCA	38921160	79
2258	chr3	AACACACGGAAGGUACGCAG	38925464	79
2259	chr3	UGAAGAUCGCCUCCACUGCA	38847025	78
2260	chr3	GCGACAUCAUCAGAGCAAAG	38847607	78
2261	chr3	GAUGCGGAUACCACUAGGA	38896973	78
2262	chr3	ACUGCGUGUUAUGGCUACA	38945457	78
2263	chr3	AUUGUCCGCUUGGCUCGGAU	38847663	77
2264	chr3	UGUUUACGGCACUGGCACAU	38896998	77
2265	chr3	UUGGGUCAUCAGCCGGAACA	38910110	77
2266	chr3	CUUCUUCACAGAGCGUAGCA	38921229	77
2267	chr3	GAACACACGGAAGGUACGCA	38925463	77
2268	chr3	GGUUCAUACAACUUCUUGAG	38846919	76
2269	chr3	CGGACAAUUCUGAAGAGCGU	38847690	76
2270	chr3	GUGGUGGUCAAUGCUCUCAU	38871691	76
2271	chr3	AACUGGGACAGCGCACGAAG	38872223	76
2272	chr3	GCCUCAGUGCUCGUAGAGUC	38872245	76
2273	chr3	AGGUUCCACCAAUGACCCA	38883335	76
2274	chr3	CUGC UUCCAUGCUGUAGCG	38883360	76
2275	chr3	GACUUGGUUGGCACCACUUG	38894612	76
2276	chr3	UGGCAUCCAAGUACCUUGUG	38904041	76
2277	chr3	GGGGGCAACAGUCCACACG	38904040	76
2278	chr3	GGAAUGUCGCCAUAGAGCUU	38950171	76
2279	chr3	GAAGCGGAUUGCCAUCCAAA	38950262	76
2280	chr3	UUUGGCUUUGCGACACGCAA	38847099	75
2281	chr3	UUUGGUAGCAGGUUUUCCGC	38883315	75
2282	chr3	CUCUUGUCCACGCUACAGCA	38883365	75
2283	chr3	GACCAUACAGGAUCCCCGAA	38886129	75
2284	chr3	CCUAGGAAAAUACCUUUCG	38886128	75
2285	chr3	AGCACUGGAUCGAUUCGCGC	38894849	75
2286	chr3	GUUUACGGCACUGGCACAUG	38896997	75
2287	chr3	GCCGUAAACAUGAGACUGUC	38897023	75
2288	chr3	GCCUCGGCGAAAGUAGUGGU	38900013	75
2289	chr3	UCUUAACGCACAGCCACUGG	38904022	75
2290	chr3	UGAACCUGAAAUGCAUCUCG	38921115	75
2291	chr3	UCAGGUCUGAAGGUCAUCGU	38921242	75

FIG. 71

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
2292	chr7	GUACGACAGCGACCAGAUCA	97732731	76
2293	chr7	UUCUUCUGCAAACAGCUGAG	97732658	73
2294	chr7	AUCUUCUGCAGAGAAUCGCC	97733765	73
2295	chr7	UUA AUGGGCAAACGGGAUGC	97733815	73
2296	chr7	ACCAUAAAGAGCCUUUAACA	97734277	73
2297	chr7	CUUUGGAUUA AUGGGCAAAC	97733808	72
2298	chr7	GCCCUGUUAAGGCUCUUUA	97734288	71
2299	chr7	AAAAGACUGCCAAGGCCACG	97732626	70
2300	chr7	UCUCUGCAGAAGAUUCUCAA	97733744	70
2301	chr7	AUCUGAAUUACUGGUCCGAC	97732709	69
2302	chr7	UGUUUUCAGUGGCUUAUGAA	97739882	69
2303	chr7	GGCCACGAGGAUUUUC AUGU	97732613	68
2304	chr7	CUGGUCGCGUCGUACCAGU	97732712	68
2305	chr7	GAAGGGGCCUCACCUUGAUC	97732731	68
2306	chr7	GGGCUCCGGCAGUUC CUCCU	97733723	68
2307	chr7	CCAAUGAUGAUCUGAAUUAC	97732700	67
2308	chr7	GGCCACUUGUUUUUCAAUUG	97734256	66

FIG. 72

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
2309	chr12	UUACCCUAUUCUGCUCUCGG	57012391	83
2310	chr12	CUGCUCUCGGGGGAUACUUG	57012401	79
2311	chr12	UAUCCCCCGAGAGCAGAAUA	57012382	76
2312	chr12	GCAAUCCCUCCAGAGAUGAG	57013622	75
2313	chr12	GUAGAGAUCUGGAUCCUCU	57013671	75
2314	chr12	UCACAUCCGUAGGAGAGUCU	57012452	74
2315	chr12	CAGCCUAGCUCAGAGCUUUG	57015742	74
2316	chr12	GUAUCCCCCGAGAGCAGAAU	57012383	73
2317	chr12	CUUUACCCUAGACUCUCCUA	57012446	73
2318	chr12	UUCUCUUGAUUCACAUCCGU	57012442	73
2319	chr12	AGGGGAGACUUACCUUGCUG	57015688	73
2320	chr12	CUUACCCUAUUCUGCUCUCG	57012390	72
2321	chr12	UGAGCCAGGCUAGCACAGGU	57013578	72
2322	chr12	AAAAGCCACUCAUCUCUGGA	57013615	72
2323	chr12	GAGCUUUGGGGCUGUCUGUA	57015730	72
2324	chr12	UUGCUCUCCAGGCACCAUG	57015797	72
2325	chr12	AGAGGAGCGUCCAGCCAGGU	57012822	71

FIG. 73

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
2326	chr2	UCAGCGCCGGCGACUAUGAG	75049662	83
2327	chr2	CUGGGUCUGGAGAUACCGGG	75049638	82
2328	chr2	AAUGGAUAACGUCCUCCCGG	75198918	82
2329	chr2	UUGCUCGUGGUAGCGGUCAG	75053640	81
2330	chr2	GUGGUUGAGUAGUAGCCUG	75120663	81
2331	chr2	CAUCAGCGCCGGCGACUAUG	75049664	80
2332	chr2	UAGUCGCCGGCGCUGAUGAA	75049681	79
2333	chr2	UGGCUAUGCAUACACCGUAG	75053687	79
2334	chr2	CACGAACUGAUUGGGUJCCG	75198874	79
2335	chr2	AUCAGCGCCGGCGACUAUGA	75049663	78
2336	chr2	UCGCUCUCCAGGUUCCGUCU	75049717	78
2337	chr2	CCGUAGUGGGAAUCACACUA	75053673	78
2338	chr2	CCAUAGUGUGAUUCCACUA	75053685	78
2339	chr2	GAGUCGUGUGCAUGAUCGAA	75120611	78
2340	chr2	UGGUUGAGUAGUAGCCUGG	75120664	78
2341	chr2	GGCCGUAGUACCAUUCGUUG	75198648	78
2342	chr2	GGUGAACCUGGCCUUCGCGG	75198705	78
2343	chr2	CCGUGUAGGCAGCUGCCAA	75198831	78
2344	chr2	AGAGGUCUGAGUCCACCGGG	75198918	78
2345	chr2	CUUGAAGCCCAGACGGAACC	75049722	77
2346	chr2	GCUUGGCAGAGACUUGCUCG	75053627	77
2347	chr2	AUCAUGCACACGACUCUGCU	75120630	77
2348	chr2	GGUACCACAAUGACCGUGU	75198817	77
2349	chr2	CGUAGUGGGAAUCACACUAU	75053672	76
2350	chr2	CUGGCGAAGACAGCGGCGAU	75198596	76
2351	chr2	GGAGUCCCCGGGAUCUCAC	75053661	75
2352	chr2	UAUCUACUCCAUGACGGCUG	75198561	75
2353	chr2	CCUAUGCUGUCCACAACGAA	75198646	75
2354	chr2	AGCCAUGGAGGCCUCCGCGA	75198706	75
2355	chr2	UCCAGCCCCUCAUAGUCGC	75049668	74
2356	chr2	UCUACUGCUGCCUCAAUGAC	75051255	74
2357	chr2	GGCUAUGCAUACACCGUAGU	75053686	74
2358	chr2	GGCUGGUUGCACGAACUGAU	75198865	74
2359	chr2	GCUGGUUGCACGAACUGAUU	75198866	74
2360	chr2	AGUCGCCGGCGCUGAUGAAG	75049682	73
2361	chr2	UGUGUACAAAGUCAGCCGCC	75049598	72
2362	chr2	CGCCGGCGACUAUGAGGGGC	75049658	72
2363	chr2	UGCUGCCCCUUAUCAGCGC	75049675	72
2364	chr2	CUCGCUCUCCAGGUUCCGUC	75049718	72
2365	chr2	GGGAUCCUCACCUGUCAUUG	75051257	72
2366	chr2	GGUCAAAAUGAUGAUUGUCG	75051428	72
2367	chr2	AUGUAUGAUGGCCAUGUACC	75120767	72
2368	chr2	AUCAAAAGGCCACAGCCGUCA	75198565	72
2369	chr2	AGCUGCCUACACGGUCAUUG	75198810	72
2370	chr2	UGGGCUUCAAGCAUGCCUUC	75049698	71
2371	chr2	CUGUGGUUGAGUAGUAGCCC	75120661	71
2372	chr2	AGCCGUCAUGGAGUAGAUAC	75198577	71
2373	chr2	GUCCACAACGAAUGGUACUA	75198638	71

FIG. 74

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
2374	chr10	CAUCUACUUCCUGCCGCUCG	69409034	80
2375	chr10	GCUACAAACAUCACCGCGAG	69409033	80
2376	chr10	AGAUGAGGGCGAUCACCACG	69409064	80
2377	chr10	GUGACACCUUGUUGACUCUCG	69404984	79
2378	chr10	GUGCCCGGACAUCAGGCGCA	69408961	79
2379	chr10	GGGUGCCACCAAGUGCGUGG	69414987	79
2380	chr10	CCAGGCCACCACGCACUUGG	69414994	79
2381	chr10	GGAUCAUCCUGGCCCAUCGG	69416140	79
2382	chr10	GACGAUGGCAUUACCCGUCA	69416179	79
2383	chr10	GGCGUCCCCAGGAUGGAUCA	69404885	78
2384	chr10	CCCCUCCGAGGCUACCAGUG	69404914	78
2385	chr10	UGAGGGCGAUCACCACGAGG	69409067	78
2386	chr10	GCCUGGCCCGAAGACAGCGG	69414965	77
2387	chr10	GACUGUGCGCAUCCUCCGAU	69416140	77
2388	chr10	AGUCAACAGGUGUCACACUA	69404965	76
2389	chr10	GCAAUAACCGCCUUGGUGCU	69415091	76
2390	chr10	ACCAUAGCCCUGAUCCAUC	69404890	75
2391	chr10	CCGGAAUCCAGAGCGAAACC	69405083	75
2392	chr10	CGGAAUCCAGAGCGAAACCU	69405084	75
2393	chr10	GCACCGUGCGCCUGAUGUCC	69408970	75
2394	chr10	UCAUCGGCCUCACGCUCUGG	69408990	75
2395	chr10	CGUGAGGCCGAUGACGCUGU	69409011	75
2396	chr10	UCCACCGUACCAUGGACCA	69415007	75
2397	chr10	UGACCGCCAUUGCUGCCGAC	69415936	75
2398	chr10	AUGCCCGUGGUGUUGCUCUC	69416273	75
2399	chr10	UCGAGCUUAUCUUCUUGGU	69405030	74
2400	chr10	GGCACCGUGCGCCUGAUGUC	69408969	74
2401	chr10	CUGCGCGCCUCCAGAGCGUG	69408995	74
2402	chr10	UUGCCUGUGCGCAGCAAUGG	69415945	74
2403	chr10	UGACUGUGCGCAUCCUCCGA	69416139	74
2404	chr10	GCCCCUCCGAGGCUACCAG	69404916	73
2405	chr10	CGCUCUCCCCAGGUUUCGCUC	69405078	73
2406	chr10	GAUGCCAGCAAUAACCGCCU	69415084	73
2407	chr10	GGGCGUCCCCAGGAUGGAUC	69404886	72
2408	chr10	CCCCACUGGUAGCCUCGGAG	69404926	72
2409	chr10	ACCUGUUGACUCUCGUGGAG	69404989	72
2410	chr10	CCACGCACUUGGUGGCACCC	69415002	72
2411	chr10	ACCCUGGUCCAUGGUGACGG	69415018	72
2412	chr10	CAACUACUUCAUCGUCAAUC	69416103	72
2413	chr10	UGCUGAUCCUCCGAUGGGCC	69416145	72
2414	chr10	CCCCUCCGAGGCUACCAGU	69404915	71
2415	chr10	CAGCUCGAGCUUAUCUCCU	69405026	71
2416	chr10	GCGCGCAGUGCCCGGACAUC	69408968	71
2417	chr10	UUUGUAGCCUACAGCGUCAU	69409006	71
2418	chr10	UCCCCAGAGGCCUACAGG	69414945	71
2419	chr10	GCCCCCGCUGUCUUCGGGCC	69414976	71
2420	chr10	UCCCCACUGGUAGCCUCGGA	69404925	70
2421	chr10	CUCCACCGUACCAUGGACC	69415008	70

FIG. 75

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
2422	chr4	UCUACGCGCUUCAUAGCGAG	103719228	82
2423	chr4	CAGAGCGCGAUGCGCCAGGA	103719430	82
2424	chr4	GGGGUCAAACACGACUGUCA	103589852	80
2425	chr4	GCAGAAACCUGGAUAGACGG	103719640	80
2426	chr4	UAUGUACACCGUGACCAGAA	103589866	79
2427	chr4	UUGCCGGUUUGGAUGAAACC	103589906	79
2428	chr4	CUACUCCAUGACGGCCAUUG	103719140	79
2429	chr4	CCGGUUUGGAUGAAACCUGG	103589909	78
2430	chr4	GGACGGCUGCACGAACUGGU	103719447	78
2431	chr4	CGCCCCGGCAGCUAGCGAGG	103719597	78
2432	chr4	CUGCUC AUGAUACUUGUCAC	103656229	77
2433	chr4	AUUGACCAACGUGUUGAAGG	103719267	77
2434	chr4	GCGCUCUGGUCCCUGGCGUA	103719403	77
2435	chr4	ACAGGCAGUCCCAGCGCGGA	103719508	77
2436	chr4	CAGGCAGUCCCAGCGCGGAA	103719509	77
2437	chr4	ACAAAGCAGAGAGUACGGCC	103658265	76
2438	chr4	AGUACGGCCUGGCAUGACUU	103658276	76
2439	chr4	CUGGCGAACACAGCUGUGAU	103719178	76
2440	chr4	UUCCGCGCUGGGACUGCCUG	103719494	76
2441	chr4	UGGUGGUGUCUGCAUCGUUG	103589833	75
2442	chr4	GAGCUCUAGCUCAUCAUAGC	103589936	75
2443	chr4	UGACGGCCAUUGCGGUGGAC	103719132	75
2444	chr4	CUCCAUGACGGCCAUUGCGG	103719137	75
2445	chr4	UCCUCACCUGUCCACCGCAA	103719138	75
2446	chr4	GCGCAUCGCGCUCUGGUCCC	103719410	75
2447	chr4	CACCACCACACCAUACGCCA	103719405	75
2448	chr4	ACCAGUUCGUGCAGCCGUCC	103719432	75
2449	chr4	GGACCAGAGCGCGAUGCGCC	103719426	75
2450	chr4	GCCAGGACGGCUGCACGAAC	103719443	75
2451	chr4	CUGCAACUGCUGGACCAAGC	103719535	75
2452	chr4	CCACGGGGGCAGUUGAGACU	103719561	75
2453	chr4	GAAACCUGGAUAGACGGGGG	103719637	75
2454	chr4	CAAGUAUCAUGAGCAGCUAA	103656210	74
2455	chr4	GACAGUCCUCAUGCGCUUGU	103719336	74
2456	chr4	AGGCAGUCCCAGCGCGGAAG	103719510	74
2457	chr4	GGCCGCCCCGGCAGCUAGCG	103719594	74
2458	chr4	CCAACGAUGCAGACACCACC	103589819	73
2459	chr4	CUGGUGGUGUCUGCAUCGUU	103589832	73
2460	chr4	UACAUACUGCUUUGCCGGUU	103589895	73
2461	chr4	GUCCACCGCAAUGGCCGUCA	103719147	73
2462	chr4	UCCUGGCCCAAGCGCAUG	103719330	73
2463	chr4	UGACAGUCCUCAUGCGCUUG	103719335	73
2464	chr4	CGGUGUACAUACUGCUUUGC	103589890	72
2465	chr4	UACUUGUCACAGGUAUCUCC	103656239	72
2466	chr4	CAUGGCCGCCUUAACACGU	103719260	72
2467	chr4	GCUGCACGAACUGGUUGGUG	103719452	72
2468	chr4	GACCGCCUCGCUAGCUGCCG	103719587	72
2469	chr4	UGACCGCCUCGCUAGCUGCC	103719588	72

FIG. 76

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
2470	chrX	GUAGACGAACCGGAUGUCAG	47585241	84
2471	chrX	GAAUUGCAGAAGGCCGUCUG	47583511	83
2472	chrX	GCGCGGCCUAGCAACCACGA	47585396	82
2473	chrX	CAGGUCCCACAACCGCAGCG	47585311	81
2474	chrX	GGCGCGGCCUAGCAACCACG	47585395	81
2475	chrX	UCAUCAGGGCCAAGUUCGUG	47584953	80
2476	chrX	GGUUGCUAGGCCGCGCCCCA	47585377	80
2477	chrX	CUCAUAACGCUGGUUAUAAGG	47584983	79
2478	chrX	CAAUGAGAAACUCCUCGCUG	47585311	79
2479	chrX	AAUUGCAGAAGGCCGUCUGU	47583510	78
2480	chrX	UCCGCAGACACUCUCCAUGG	47585268	78
2481	chrX	AUCAGAGCCUCGCCCCUUCG	47585398	78
2482	chrX	GAUCUCAUAACGCUGGUUAUA	47584986	77
2483	chrX	CGCGGCCUAGCAACCACGAG	47585397	77
2484	chrX	GCGGCCUAGCAACCACGAGG	47585398	77
2485	chrX	ACCGAGGUCGGAUUGCAGA	47583521	76
2486	chrX	GUAUCCGCAGACACUCUCCA	47585271	76
2487	chrX	AGUCAUCAGGGCCAAGUUCG	47584951	75
2488	chrX	UCAUCUUGAUCUCAUAACGC	47584993	75
2489	chrX	UGGCGGGGGUGUAGACGAAC	47585251	75
2490	chrX	GGGUGAGGACUCACCGAGGU	47583533	74
2491	chrX	UAGGGGAUGCCGCUGACAUC	47585244	74
2492	chrX	CGCAGACACUCUCCAUGGCG	47585266	74
2493	chrX	UUCACCAAGACCUACACUGU	47585646	74
2494	chrX	UCAGGCUAUCUGGGACCGCA	47586674	74
2495	chrX	UUCUGGUGUCCCCACGAACU	47584950	73
2496	chrX	GUCAUCAGGGCCAAGUUCGU	47584952	73
2497	chrX	UGGUUGCUAGGCCGCGCCCC	47585378	73
2498	chrX	GUUCGUCUACACCCCGCCA	47585266	72
2499	chrX	GUGUCUGCGGAUACUCCAC	47585292	72
2500	chrX	CUCGCCCCCUCGUGGUUGCU	47585390	72
2501	chrX	UAAAGGGUUCCAAGCCUAG	47585227	71
2502	chrX	GCAGACACUCUCCAUGGCGG	47585265	71
2503	chrX	GAAACUCCUCGCUGCGGUUG	47585305	71
2504	chrX	CUAGCAACCACGAGGGGGCG	47585403	71
2505	chrX	CUGAGCUUAGCUCAGCGCCG	47585622	71
2506	chrX	AACGCUGGUAUAAGGUGGUC	47584978	70
2507	chrX	AUAAAGGGUUCCAAGCCUUA	47585226	68
2508	chrX	AAACUCCUCGCUGCGGUUGU	47585304	68
2509	chrX	CGGGCAGGAUUCAGGCUAUC	47586684	66

FIG. 77

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
2510	chr22	AUGAUGGCAAGAUGUACACG	32858043	82
2511	chr22	CACGAUGAGCCCCGAGCCAAG	32802011	81
2512	chr22	GUGUAGACCAGCGUGCCGAA	32849501	80
2513	chr22	GGUGUAGACCAGCGUGCCGA	32849502	79
2514	chr22	GACUCUCGGAAGCUUCCGUA	32857295	79
2515	chr22	UUGAUGAUGCUUUUAUCCGG	32859344	79
2516	chr22	GCACGAUGAGCCCCGAGCCAA	32802012	78
2517	chr22	CGUAUGGAUGUACUGCACAU	32857279	78
2518	chr22	UACGCCUGCAUCCGGCAGAA	32859302	78
2519	chr22	CAGCAGCGGCAAUGACCCCU	32802008	77
2520	chr22	CCUGUAGGUCGCGUCUAUGA	32858027	77
2521	chr22	CCGGAUGCAGGCGUAGUGUU	32859282	77
2522	chr22	GAUGAUGCUUUUAUCCGGGG	32859342	77
2523	chr22	UGAUGAUGCUUUUAUCCGGG	32859343	77
2524	chr22	AUUGAUGAUGCUUUUAUCCG	32859345	77
2525	chr22	CCAGGAGCGCUUACCGAUGU	32802119	76
2526	chr22	UUUUGCCACAGAUGUACCG	32857254	76
2527	chr22	CACGGGGCUGUGCAACUUCG	32858059	76
2528	chr22	UGCAGGCGUAGUGUUUGGAC	32859277	76
2529	chr22	CUACGCCUGCAUCCGGCAGA	32859301	76
2530	chr22	CGGCAAUGACCCCUUGGCUC	32802014	75
2531	chr22	GGGCGAGCAUGUGCACGCCU	32802068	75
2532	chr22	CCGUAUGGAUGUACUGCACA	32857280	75
2533	chr22	AUAGUUCAGCCCCUUGCGCU	32858094	75
2534	chr22	UUACCUUGCAGUUACAACCC	32858125	75
2535	chr22	GUACCGAGGAUGGGCCCCCC	32859340	75
2536	chr22	AGCACGAUGAGCCCGAGCCA	32802013	74
2537	chr22	GCGGCAAUGACCCCUUGGCU	32802013	74
2538	chr22	GCCUUCUGCAACUCCGACAU	32802118	74
2539	chr22	GUAUGGAUGUACUGCACAUG	32857278	74
2540	chr22	GGUCCAGAGACACUCGUUCU	32859222	74
2541	chr22	GCCGCCCUUCUGCCGGAUGC	32859294	74
2542	chr22	GGAGGGGCCCCUUCGGCACGC	32849506	73
2543	chr22	GGCUGUGCAACUUCGUGGAG	32858064	73
2544	chr22	UGUGCAACUUCGUGGAGAGG	32858067	73
2545	chr22	GCUGAACUAUCGGUAUACCC	32858119	73
2546	chr22	AGUGUUUGGACUGGUAGCCA	32859268	73
2547	chr22	ACUGCAGCUGGUACCGAGGA	32859330	73
2548	chr22	CUCGGGCUCAUCGUGCUCCU	32802031	72
2549	chr22	GUUGGCCAUUACCGUCAGC	32857355	72
2550	chr22	UCACCCUCUCCCAGCGCAAG	32858097	72
2551	chr22	CCAAACACUACGCCUGCAUC	32859294	72
2552	chr22	ACCGAUGUCGGAGUUGCAGA	32802107	71
2553	chr22	GAUAGUUCAGCCCCUUGCGC	32858095	70
2554	chr22	GUAGCCAGGGUAACCGAAAU	32859255	70
2555	chr22	UGCAGUAGCCGCCCUUCUGC	32859301	70
2556	chr22	UAUCCGGGGGGGCCCAUCCU	32859331	70
2557	chr22	CUGCAGCUGGUACCGAGGAU	32859331	70

FIG. 78

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
2558	chr6	UUUGGGAUCAUUGCCCUGUG	31577534	68
2559	chr6	CAGCAAACCCUCAAGCUGAG	31577130	67
2560	chr6	GGUGUGGGUGAGGAGCACAU	31577283	67
2561	chr6	GGCUACAGGCUUGUCACUCG	31576787	66
2562	chr6	UCUGGUAGGAGACGGCGAUG	31577311	66
2563	chr6	GGCGCUCSCCAAGAAGACAG	31575803	65
2564	chr6	GCGCUCSCCAAGAAGACAGG	31575804	65
2565	chr6	AAGCACCGCCUGGAGCCCUG	31575816	65
2566	chr6	UUGGAGUGAUCGGCCCCCAG	31575916	65
2567	chr6	CCAGGAGGGCAUUGGCCCGG	31577158	65
2568	chr6	GUGCAGCAGGCAGAAGAGCG	31575880	64
2569	chr6	CCAGAGGGCUGAUUAGAGAG	31576550	64
2570	chr6	GUGGGUGAGGAGCACAUGGG	31577280	64
2571	chr6	GCUGAGGAACAAGCACCGCC	31575826	63
2572	chr6	UGGAGUGAUCGGCCCCCAGA	31575917	63
2573	chr6	UGAUUAGAGAGAGGUCCCUG	31576541	63
2574	chr6	GCUGAGAGAUAAACCAGCUGG	31577206	63

FIG. 79

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
2575	chr12	GGUGGGAUAUACCCCUCAG	6334210	77
2576	chr12	GUGGACCGGGACACCGUGUG	6333467	77
2577	chr12	CCACGGCGUACAGCGUCGCG	6329609	77
2578	chr12	UAAUGUAUCGCUACCAACGG	6330625	75
2579	chr12	AGAGGUGCACGGUCCCAUUG	6333386	74
2580	chr12	AAAGUUGGGACAGUCACCGG	6329930	74
2581	chr12	AGGUGGCACCACCCUAUCAG	6329880	74
2582	chr12	GGUGGCACCACCCUAUCAGG	6329879	74
2583	chr12	UGCGCUGGAAGGAAUUCGUG	6329557	74
2584	chr12	GAAUCCUUCACGCGCAACG	6329574	73
2585	chr12	ACAGCAUGCUGGCGACCUUG	6329461	73
2586	chr12	UUGGUGGGAUAUACCCCUC	6334212	72
2587	chr12	GACCAGUCCAAUAACCCUG	6334207	72
2588	chr12	AGAGCUUGGACUCCACCGU	6330623	72
2589	chr12	CUUUGCGGCUCGCCGAGAG	6329900	72
2590	chr12	AAUCCUUCACGCGCAACGG	6329575	72
2591	chr12	UGGACUGGUCCCUACCUAG	6334183	71
2592	chr12	CAGCUGCUCCAAUAGCCGAA	6333742	71
2593	chr12	GUUUAAUGUAUCGCUACCAA	6330628	71
2594	chr12	GGGUCAGCCCCUGAUAGGG	6329883	71
2595	chr12	CGCGACGCUGUACGCCGUGG	6329595	71
2596	chr12	UGAGCGACCACGAGAUCAU	6329524	71
2597	chr12	UCCAGCGUGGCCUCGCGCCG	6329440	71
2598	chr12	GACAUCGAGGAGGCGCUUUG	6329357	71
2599	chr12	UGGUGGGAUAUACCCUCA	6334211	70
2600	chr12	UGGACAGUCAUUGUACAAGU	6333856	70
2601	chr12	AGGAACUACUACUAAGCCCC	6330038	70
2602	chr12	CUGCGGGGAGCCGCAAAGUU	6329916	70
2603	chr12	CGGUGACUGUCCCAACUUUG	6329915	70
2604	chr12	CGGGGGCACGUUCUCCACCA	6329592	70
2605	chr12	ACGAAUCCUUCACGCGCAA	6329572	70
2606	chr12	CGUGCCCCCGUUGCGCUGGA	6329568	70
2607	chr12	AAUACAGCAUGCUGGCGACC	6329464	70
2608	chr12	CGAGGGCUGUCGCAAGGAUG	6329863	69
2609	chr12	GAGGUGGCACCACCCUAUCA	6329881	69
2610	chr12	AAGUCCAAGCUCUACUCCA	6330602	69
2611	chr12	UGCAGCCACACCGGUGUCC	6333473	69
2612	chr12	ACCAGUCCAAUAACCCUGA	6334208	69
2613	chr12	CGAGGCGCAAUACAGCAUGC	6329472	69
2614	chr12	ACCACGGCGUACAGCGUCGC	6329608	69
2615	chr12	UACUUGUACAAUGACUGUCC	6333843	69
2616	chr12	CACCACGGCGUACAGCGUCG	6329607	69
2617	chr12	GAACGGGCGCUGCCUGCGCG	6329490	69
2618	chr12	GCGAGGGCUGUCGCAAGGAU	6329862	69
2619	chr12	AGCUGCUCCAAUAGCCGAAA	6333741	68
2620	chr12	CUCACCAAUGGAGUAGAGCU	6330609	68
2621	chr12	ACAGUACCCGGGGGUAUAGG	6329939	68
2622	chr12	UGCAGUCCGUAUCCUGCCCC	6333831	68

FIG. 80

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
2623	chr1	CGUGUUGGAGAACGUCCCCG	12192472	82
2624	chr1	UUGCCUGCCGAUAAGGCCCG	12201990	82
2625	chr1	GUGGGGCCUGCAAAUAUCCG	12192502	80
2626	chr1	GUGCUGCAGCAAAUGCUCGC	12188890	79
2627	chr1	CCCGGGCGGCACUUGCAGCAG	12191886	79
2628	chr1	GGGGACCUGCUCGUCCUUCG	12206883	79
2629	chr1	CUCCAGUCCGACGCCAGCG	12167119	78
2630	chr1	GUACUGCGCGCUGAGCAAGC	12191855	78
2631	chr1	AGGAACUGAAACAUCAGACG	12192446	78
2632	chr1	GUAACGUGGUGGCCAUCCCU	12192882	78
2633	chr1	GAUAAGGCCCGGGUACACA	12201999	78
2634	chr1	GCCUGUGGCUGGUUCCGAGU	12202098	78
2635	chr1	UGCCUGUGGCUGGUUCCGAG	12202099	78
2636	chr1	GGCAUUUACACCCUACGCC	12188815	77
2637	chr1	UCUCGCUGCUCUAGACCAGG	12191777	77
2638	chr1	GCGGUUCUGUCCCCGAGUGC	12191797	77
2639	chr1	GUCGUGUUGGAGAACGUCCC	12192474	77
2640	chr1	CCACCCGGAGUAUGGCCCCA	12192942	77
2641	chr1	CACCCGGAGUAUGGCCCCAG	12192943	77
2642	chr1	CGUCCUUCGGGGACUCCGAG	12206872	77
2643	chr1	GGAGUCACACACGGUGUCCG	12190992	76
2644	chr1	GAGAACGUCCCCGGGGCACA	12192465	76
2645	chr1	UCGUGUUGGAGAACGUCCCC	12192473	76
2646	chr1	ACUUGCCUGCCGAUAAGGCC	12201988	76
2647	chr1	CAGACGGCGACGGGCGCCAU	12167094	75
2648	chr1	CUCCAACACGACUUAUCCA	12192497	75
2649	chr1	CUGGGGCCAUACUCCGGGUG	12192928	75
2650	chr1	CCUGGGGCCAUACUCCGGGU	12192929	75
2651	chr1	CACGUCCOCCACCCGGAGUA	12192934	75
2652	chr1	GGGGUAAGUGUACUGCCCCU	12192946	75
2653	chr1	CCCACCCGGAGUAUGGCCCC	12192941	75
2654	chr1	CUUGCCUGCCGAUAAGGCC	12201989	75
2655	chr1	CUCGUCCUUCGGGGACUCCG	12206874	75
2656	chr1	CGUAGGGUGUAAAUGCCACC	12188797	74
2657	chr1	CCGCUGCGCAAGUGCCGCC	12191898	74
2658	chr1	AGGACUCAGCUACUCACAUC	12192524	74
2659	chr1	GAUGGCCACCACGUUACAGC	12192864	74
2660	chr1	UGUAACGUGGUGGCCAUCCC	12192881	74
2661	chr1	CCCUGGGGCCAUACUCCGGG	12192930	74
2662	chr1	ACUUCUUGCGACUUAACCAAC	12193097	74
2663	chr1	GCCUUAUCGGCAGGCAAGUG	12201972	74
2664	chr1	GUACCCCGGGCCUUAUCGGC	12201981	74
2665	chr1	CGAUAAAGGCCCGGGUACAC	12201998	74
2666	chr1	UGGACAGAAGGGCGCCACU	12202096	74
2667	chr1	AGCCCAGAGCUCCAGUCCGA	12167128	73
2668	chr1	CUCCCGGGCUCCGGGGCGUA	12188813	73
2669	chr1	GCUCAGCGCGCAGUACCAGC	12191836	73
2670	chr1	GGCGACUUCGCUCUCCAGU	12193094	73

FIG. 81

SEQ ID NO:	Chromosome	Protospacer (crRNA)	Cut site coordinate	Score
2671	chr11	GUGCACGAUCUGAUGCCCCGG	102110999	82
2672	chr11	UCAGAUCGUGCACGUCCGCG	102111021	82
2673	chr11	GCACGAUCUGAUGCCCCGGCG	102110997	81
2674	chr11	GGUCGGUCUCCGAGUCCCCG	102111024	81
2675	chr11	CAUCAGAUCGUGCACGUCCG	102111019	79
2676	chr11	UGUUGGUAACUGGCUACGCA	102223634	79
2677	chr11	GGGCAACGAGGUUACCUGUC	102111167	78
2678	chr11	GGGGCAACGAGGUUACCUGU	102111168	78
2679	chr11	GGUUGCCCCGGGUCCGGACGG	102110938	77
2680	chr11	ACGAGGUUACCUGUCGGGAG	102111162	77
2681	chr11	ACGAUCUGAUGCCCCGGCGGG	102110995	76
2682	chr11	GGGCUCCGGCGGCUUGAAGA	102111134	76
2683	chr11	GUGUUGGUAACUGGCUACGC	102223635	76
2684	chr11	GGAAGUCAUCUGGGGUUCGA	102227537	76
2685	chr11	AUCAGAUCGUGCACGUCCGC	102111020	75
2686	chr11	CGGGGACUCGGAGACCGACC	102111039	75
2687	chr11	AUGAACCUUUACCAAAACGA	102186126	75
2688	chr11	GAUGAACCUUUACCAAAACG	102186127	75
2689	chr11	GCCGGUUGCCCCGGGUCCGGA	102110941	74
2690	chr11	GCCGUCCGGACCCGGGCAAC	102110952	74
2691	chr11	UGCACGAUCUGAUGCCCCGGC	102110998	74
2692	chr11	GACGUGCACGAUCUGAUGCC	102111002	74
2693	chr11	GGACUCGGAGACCGACCUGG	102111042	74
2694	chr11	CGAGGUUACCUGUCGGGAGU	102111161	74
2695	chr11	ACCCGGGCAACCGGCACCCG	102110961	73
2696	chr11	GCCCAAUCCACUCCCGAC	102111165	73
2697	chr11	CGAUCAGACAACAACAUGGC	102162479	73
2698	chr11	AGCCACAGGGAGGCGUCAU	102205972	73
2699	chr11	GUUGAAGAGCGCCUCCAGGU	102111041	72
2700	chr11	GGGGCACGUUGGCCGUCUUG	102111075	72
2701	chr11	ACAUCGAUCAGACAACAACA	102162475	72
2702	chr11	AACGGUUCUGCUGUGAGGGC	102229729	72
2703	chr11	GUUGCCCCGGGUCCGGACGGC	102110937	71
2704	chr11	UGGGGCACGUUGGCCGUCUU	102111076	71
2705	chr11	GGGUGCCGGUUGCCCCGGGUC	102110945	70
2706	chr11	CAGGGCCCGCCGUCCGGACC	102110944	70
2707	chr11	AGGGCCCGCCGUCCGGACCC	102110945	70
2708	chr11	CGACUCCUUCUUAAGCCGC	102111141	70
2709	chr11	UAAUAGGCCAGUACUGAUGC	102114155	70
2710	chr11	GGGGGCUGUGACGUUCAUCU	102162511	70
2711	chr11	CACGAUCUGAUGCCCCGGCGG	102110996	69
2712	chr11	CCAAGGCUUGACCCUCGUUU	102186127	69
2713	chr11	GCCGCGGGUGCCGGUUGCCC	102110950	68
2714	chr11	CGUGCACGUCCGCGGGGACU	102111027	68
2715	chr11	AAUAUGAUGAACUCGGCUUC	102162567	68
2716	chr11	CGCCGCGGGUGCCGGUUGCC	102110951	67
2717	chr11	GCUCAGAUCCUUCCUUAAC	102223748	67
2718	chr11	CUGGGGCACGUUGGCCGUCU	102111077	65

FIG. 82

Human IL1A (IL1A-001; GRCh38)									
#	crRNA sequence	Target		On-target score*	Off-target score**	Precision score***	Frameshift %****	Combined score^	
		Exon #	Strand						
sg235	CAGAGACAGATGATCAATGG	3	-	69.5	67	0.57	93.7	72.6	SEQ ID NO: 2719 SEQ ID NO: 2720
sg236	GCCATAGCTTACATGATAGA	4	-	53.9	76.9	0.65	93.9	78.6	

Machine-Learning (inDelphi) Predictions	
Top genotype	Repair outcome†
insA (35.3%)	TACCTGATTTCAGAGACAGATGATCAA {A}TGGAGGAACGTCTTCTTCATTTTCA
insT (56%)	ATGGAGTGGGCCCATACCTTACATGAT {T}AGAAGGATTCTGTGAGGAAGGAAAA

Empirical data: ICE, day 10 post-nucleofection			
KO score	Top genotype	inDelphi	Repair outcome
		rank	
99%	insA (99%)	1st	TACCTGATTTCAGAGACAGATGATCAA {A}TGGAGGAACGTCTTCTTCATTTTCA
48%	insT (32%)	1st	ATGGAGTGGGCCCATAGCTTACATGAT {T}AGAAGGATTCTGTGAGGAAGGAAAA

FIG. 83A

Human IL1B (IL1B-201; GRCh38)

#	crRNA sequence	Target		On-target score*	Off-target score**	Precision score***	Frameshift g****	Combined score^	
		Exon #	Strand						
sg237	TGATGGCCCTAAACAGATGA	3	+	60.9	66.7	0.57	80	67.9	SEQ ID NO: 2721
sg238	GGTGGTCGGAGATTCGTAGC	4	-	58.3	49.3	0.6	86.3	65.2	SEQ ID NO: 2722
sg248	ACCTATCTTCTTCGACACAT	5	+	61.7	86.5	0.65	89.9	80.5	SEQ ID NO: 2723
sg249	CTTCGACACATGGGATAACG	5	+	68.2	93.8	0.52	75.3	73.7	SEQ ID NO: 2724
sg250	GTGCAGTTCAGTCGTAC	5	-	64.4	91	0.48	83.9	74.3	SEQ ID NO: 2725

Machine-Learning (inDelphi) Predictions	
Top genotype	Repair outcome†
insA (33.3%)	CTTTGAAGCTGATGGCCCTAAACAGA {A}TGAAGGTAAGACTATGGGTTTAACTC
insT (51.5%)	TGCTGTAGTGGTGGTTCGGAGATTCGT {T}AGCTGGATGCCGCCATCCAGAGGGCA
insA (51.9%)	CATTTCAGAACCTATCTTCTCGACA {A}CATGGGATAACGAGGCTTATGTGCAC
insA (33.4%)	ACCTATCTTCTTCGACACATGGGATA {A}ACGAGGCTTATGTGCACGATGCACCT
insT (18.3%)	TCCCGGAGCGTGCAGTTCAGTCGTG {T}TACAGGTGCATCGTGCACATAAAGCCT

Empirical data: ICE, day 10 (*day 3) post-nucleofection		
KO score	Top genotype	inDelphi rank
66%	insA (40%)	1st
0%	wild-type	NA
3%*	CAdel (3%)*	2nd
33%*	insA (22%)*	1st
81%*	Gdel (55%)*	8th
		Repair outcome
		CTTTGAAGCTGATGGCCCTAAACAGA {A}TGAAGGTAAGACTATGGGTTTAACTC
		TGCTGTAGTGGTGGTTCGGAGATTCGT AGCTGGATGCCGCCATCCAGAGGGCA
		CATTTCAGAACCTATCTTCTCGACA ---TGGGATAACGAGGCTTATGTGCAC
		ACCTATCTTCTTCGACACATGGGATA {A}ACGAGGCTTATGTGCACGATGCACCT
		TCCCGGAGCGTGCAGTTCAGTCGTGATC- TACAGGTGCATCGTGCACATAAAGCCT

FIG. 83B

Canine IL1A (IL1A-201; CanFam3.1)									
#	crRNA sequence	Target		On-target score*	Off-target score**	Precision score***	Frameshift %****	Combined score^	
		Exon #	Strand						
sg239	TGACCATCTCTCTGGAATC	3	+	49.5	57.7	0.55	78.3	63.7	SEQ ID NO: 2726
sg240	GACATCCGAGCTTACCTTCA	4	+	43.8	41.8	0.61	87.2	63.3	SEQ ID NO: 2727
sg251	AGTATAGTTCGACAAACAGG	5	+	72.1	85.1	0.49	77.6	70.6	SEQ ID NO: 2728
sg252	TCTGTATGCAGCATCATG	5	-	68.4	66.6	0.48	90.4	68.3	SEQ ID NO: 2729

Machine-Learning (inDelphi) Predictions	
Top genotype	Repair outcome†
insA (35.2%)	TTCTGAAATTGACCATCTCTCTCTGA {A}ATCAGGTAAGTAAATGACTGCAATTC
insT (52.7%)	AATCTCAAAGAGATGCCAGCTTACCT {T}TCAAAGGAAAATGTGGTAGTGGTGGCA
insC (30.6%)	CTCAATCAAAGTATAGTTCGACAAAC {C}AGGAGGAAATTACCTCATGACTGCTG
insC (20.4%)	CATCCAAATCTGTGTAATGCAGCAGTC {C}ATGAGGTAATTTCCTCCTGTTTGTCG

Empirical data: ICE, day 10 post-nucleofection			
KO score	Top genotype	inDelphi rank	Repair outcome
	90% insA (56%)	1st	TTCTGAAATTGACCATCTCTCTCTGA {A}ATCAGGTAAGTAAATGACTGCAATTC
	97% insT (57%)	1st	AATCTCAAAGAGATGCCAGCTTACCT {T}TCAAAGGAAAATGTGGTAGTGGTGGCA

FIG. 83C

Canine IL1B (IL1B-201; CanFam3.1)									
		Target							
	crRNA sequence	Exon #	Strand	On-target score*	Off-target score**	Precision score***	Frameshift %****	Combined score^	
sg241	TGATGGCCCTGGAAATGTGA	3	+	66.1	51.5	0.53	91.2	65.2	SEQ ID NO: 2731
sg242	ACTCTTGTTACAGAGCTGGT	4	-	68.9	62	0.64	84	70	SEQ ID NO: 2732

Machine-Learning (inDelphi) Predictions	
Top genotype	Repair outcome†
insT (22.9%)	CTTTGAAGCTGATGGCCCTGGAAATG {T}TGAAGGTGAGACCATGGGCTTAGCTC
insT (56.4%)	ATGCCCTCAGACTCTTGTACAGAGCT {T}GGTGGGAGACTTGCAACTGGATGCCC

Empirical data: ICE, day 10 post-nucleofection			
KO score	Top genotype	inDelphi rank	Repair outcome
	99% delTG (95%)	2nd	CTTTGAAGCTGATGGCCCTGGAAATG ---AAGGTGAGACCATGGGCTTAGCTC
	99% insT (99%)	1st	ATGCCCTCAGACTCTTGTACAGAGCT {T}GGTGGGAGACTTGCAACTGGATGCCC

FIG. 83D

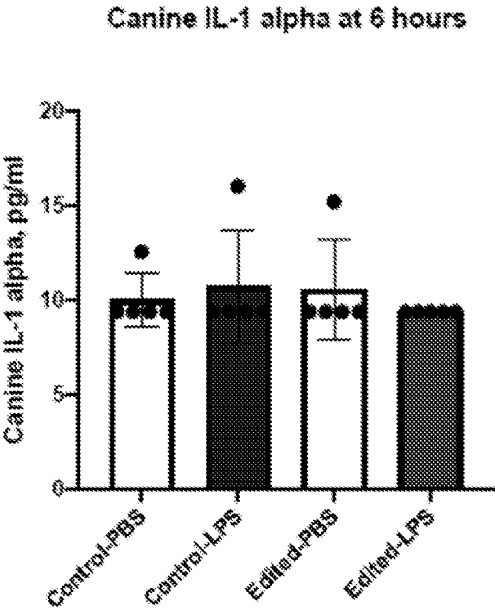


FIG. 84A

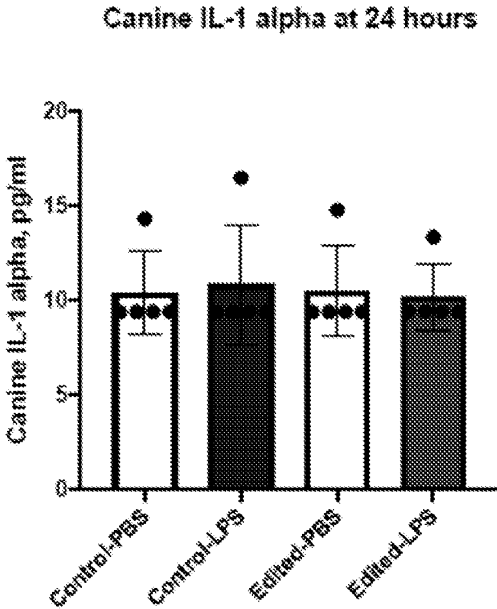


FIG. 84B

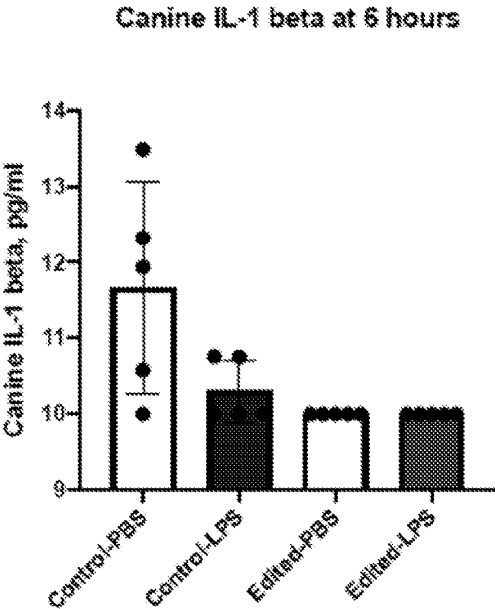


FIG. 84C

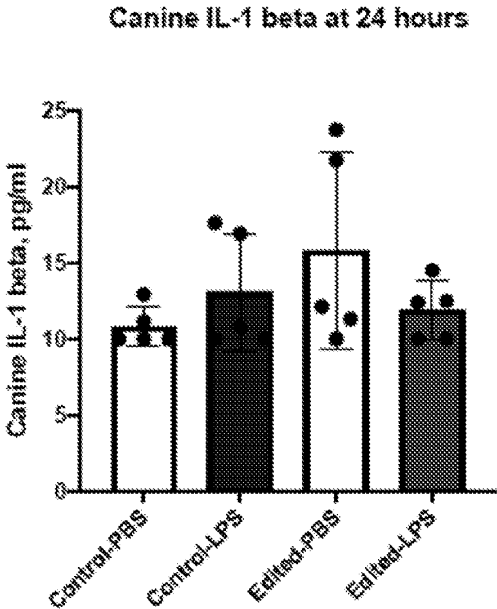


FIG. 84D

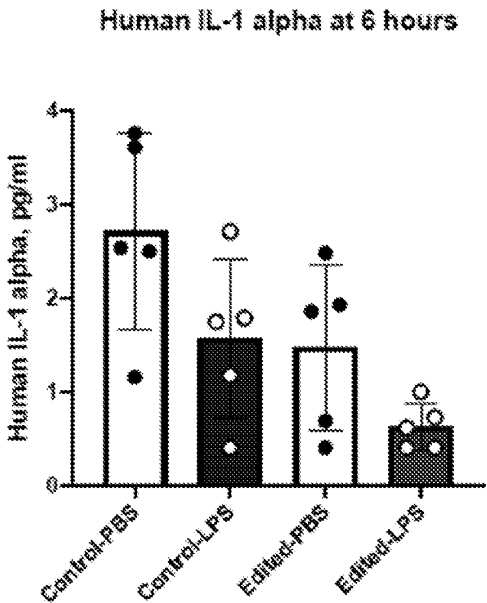


FIG. 85A

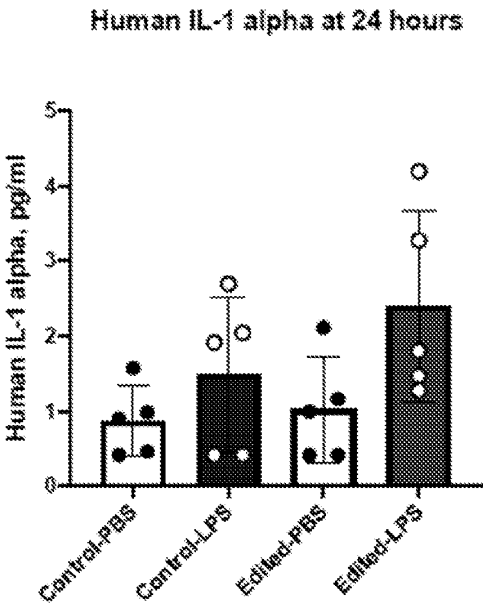


FIG. 85B

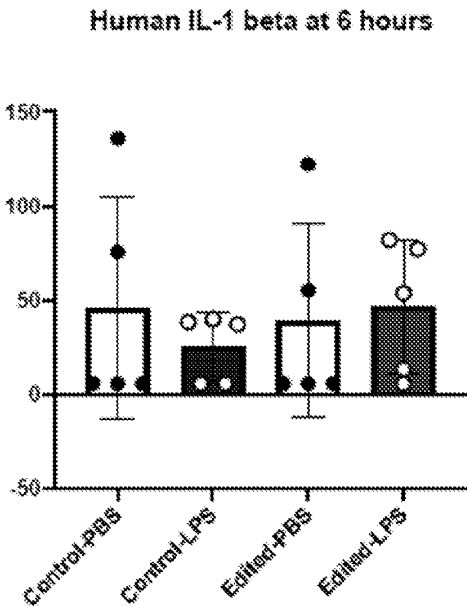


FIG. 85C

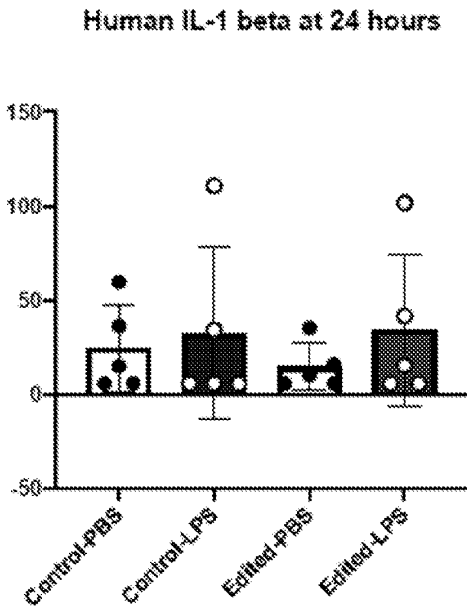


FIG. 85D

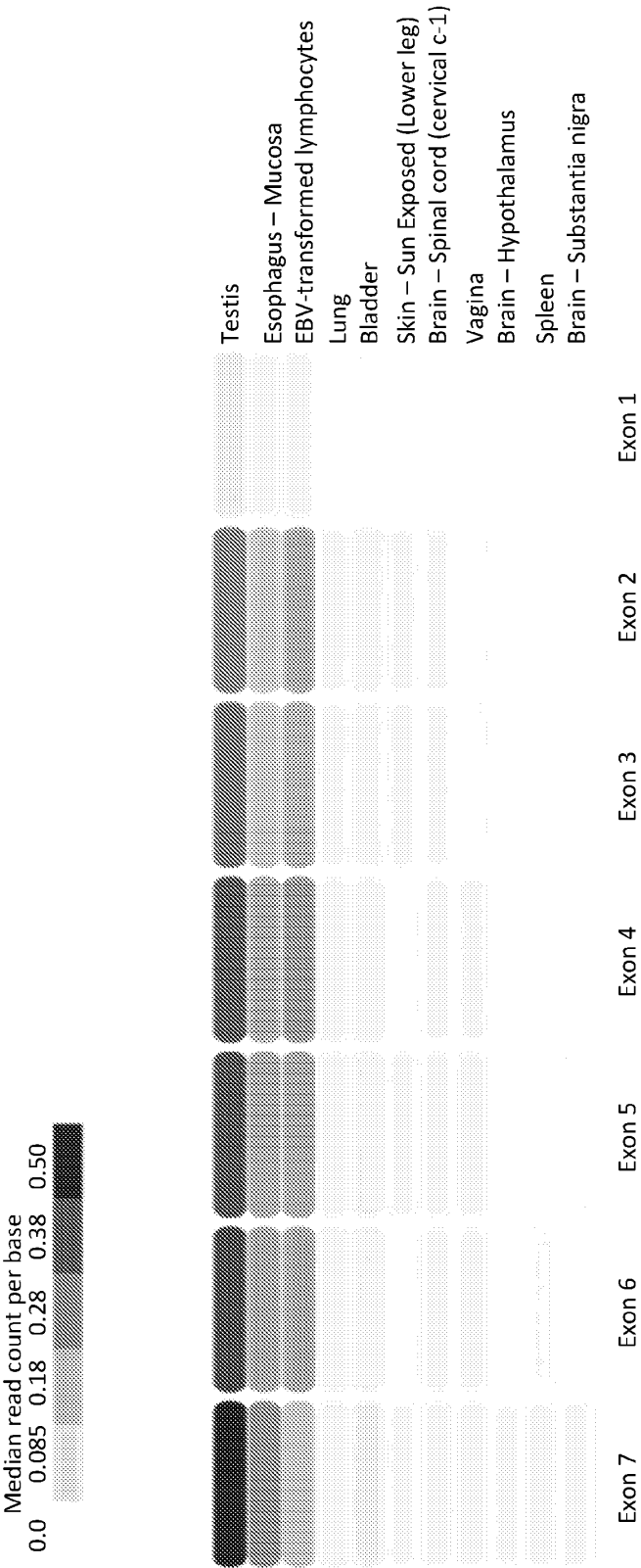


FIG. 86

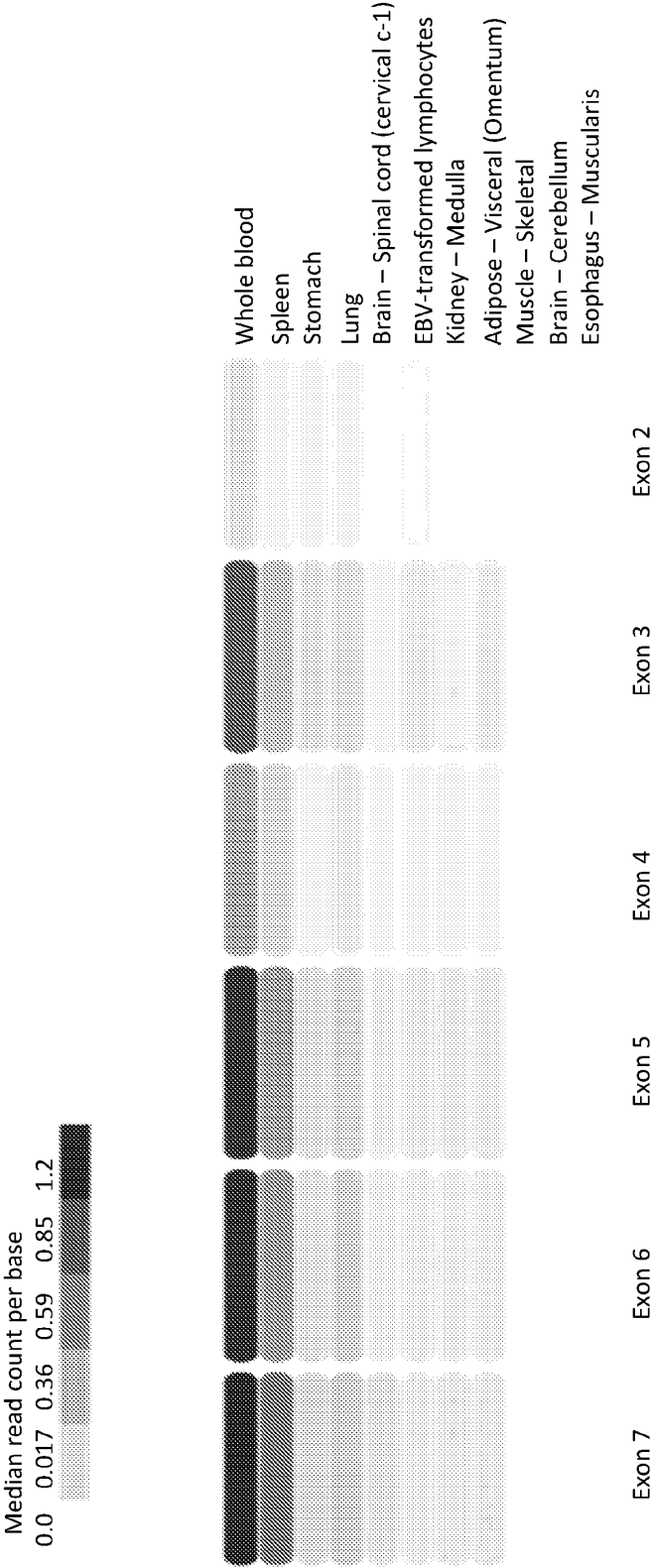


FIG. 87

Single guide RNA (sgRNA)		Target			On-target	InDelphi Predictions		Off-Targets	
#	Target sequence	Exon #	Strand	Domain		AA	Precision		Recall
Human IL-1A (IL1A-001; GRCh38)									
235	CAGAGACAGATGATCAATGG	3	-	Interleukin-1 propeptide (1-109 aa)	25	0.68	0.57	94%	0-0-0-11-232 (0-0-0-2-1)
236	GCCATAGCTTACATGATAGA	4	-	Interleukin-1 propeptide (1-109 aa)	36	0.52	0.65	94%	0-0-0-14-133 (0-0-0-2-3)
Human IL-1B (IL1B-201; GRCh38)									
237	TGATGGCCCTAAACAGATGA	3	+	Interleukin-1 propeptide (1-103 aa)	32	0.55	0.57	80%	0-0-7-21-180 (0-0-2-7-2)
238	GGTGGTCGGAGATTCTGTAGC	4	-	Interleukin-1 propeptide (1-103 aa)	50	0.57	0.6	86%	0-0-1-1-20 (0-0-0-0-0)
248	ACCTATCTTCTTCGACACAT	5	+	Interleukin-1 propeptide (1-103 aa)	107	0.63	0.65	90%	0-0-0-15-140 (0-0-0-0-0)
249	CTTCGACACATGGGATAACG	5	+		110	0.66	0.52	75%	0-0-0-1-36 (0-0-0-0-0)
250	GTGCAGTTCAGTGATCGTAC	5	-		119/120	0.64	0.48	84%	0-0-0-2-27 (0-0-0-0-0)
259	CATGGCCACAACAACACTGACG	4	-	Interleukin-1 propeptide (1-103 aa)	66	0.67	0.46	79%	0-0-1-3-74 (0-0-0-0-2)
260	AGGTCCTGGAAGGAGCACTG	4	-	Interleukin-1 propeptide (1-103 aa)	33/34	0.79	0.64	92%	0-0-14-4-377 (0-0-4-3-12)

FIG. 88

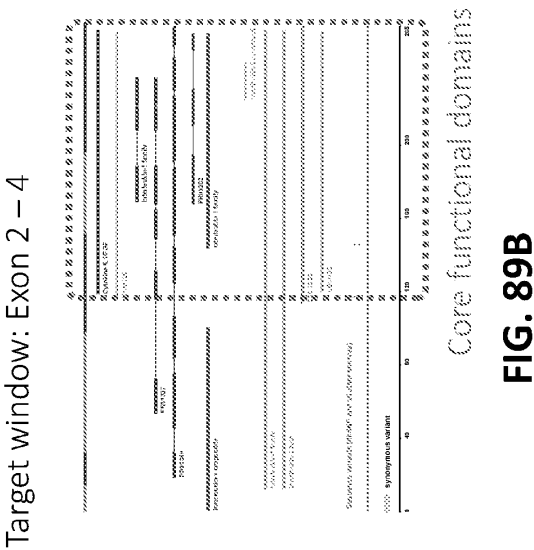
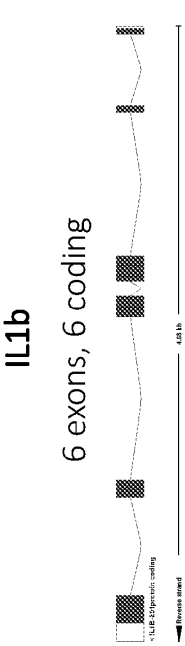


FIG. 89B

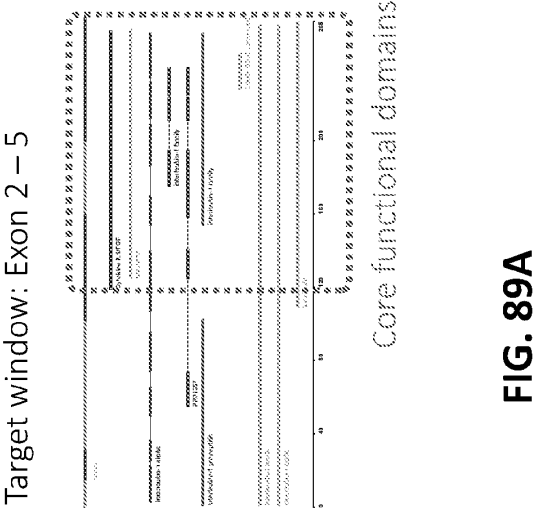
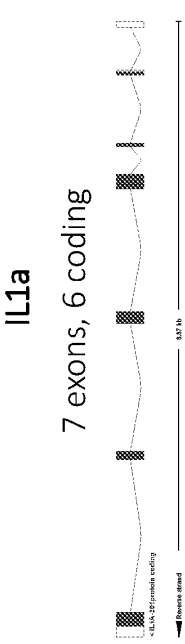


FIG. 89A

Single guide RNA (sgRNA)		Target			On-target	InDelphi Predictions	Off-Targets		
#	Target sequence	Exon #	Strand	Domain	AA	Score	Precision	Frameshift	0-1-2-3-4 mismatches (seed only)
Canine IL-1A (IL1A-201; CanFam3.1)									
239	TGACCATCTCTCTCTGAATC	3	+	Interleukin-1 propeptide (1-103 aa)	31	0.50	0.55	78%	0-0-2-24-451 (0-0-0-4-5)
240	GACATCCCAGCTTACCTTCA	4	+	Interleukin-1 propeptide (1-103 aa)	63	0.44	0.61	87%	0-0-0-12-123 (0-0-0-3-3)
251	AGTATAGTTCGACAAACAGG	5	+	Cytokine IL1/FGF (122-260 aa)	144	0.72	0.49	78%	0-0-0-2-39 (0-0-0-0-0)
252	TCTGTAATGCAGCAGTCATG	5	-	Cytokine IL1/FGF (122-260 aa)	150	0.68	0.48	90%	0-1-0-8-159 (0-0-0-0-4)
Canine IL-1B (IL1B-201; CanFam3.1)									
241	TGATGGCCCTGGAAATGTGA	3	+	Interleukin-1 propeptide (1-103 aa)	32	0.66	0.53	91%	0-0-1-29-183 (0-0-0-6-7)
242	ACTCTTGTACAGAGCTGGT	4	-	Interleukin-1 propeptide (1-103 aa)	56	0.69	0.64	84%	0-0-2-8-130 (0-0-1-3-3)

FIG. 90

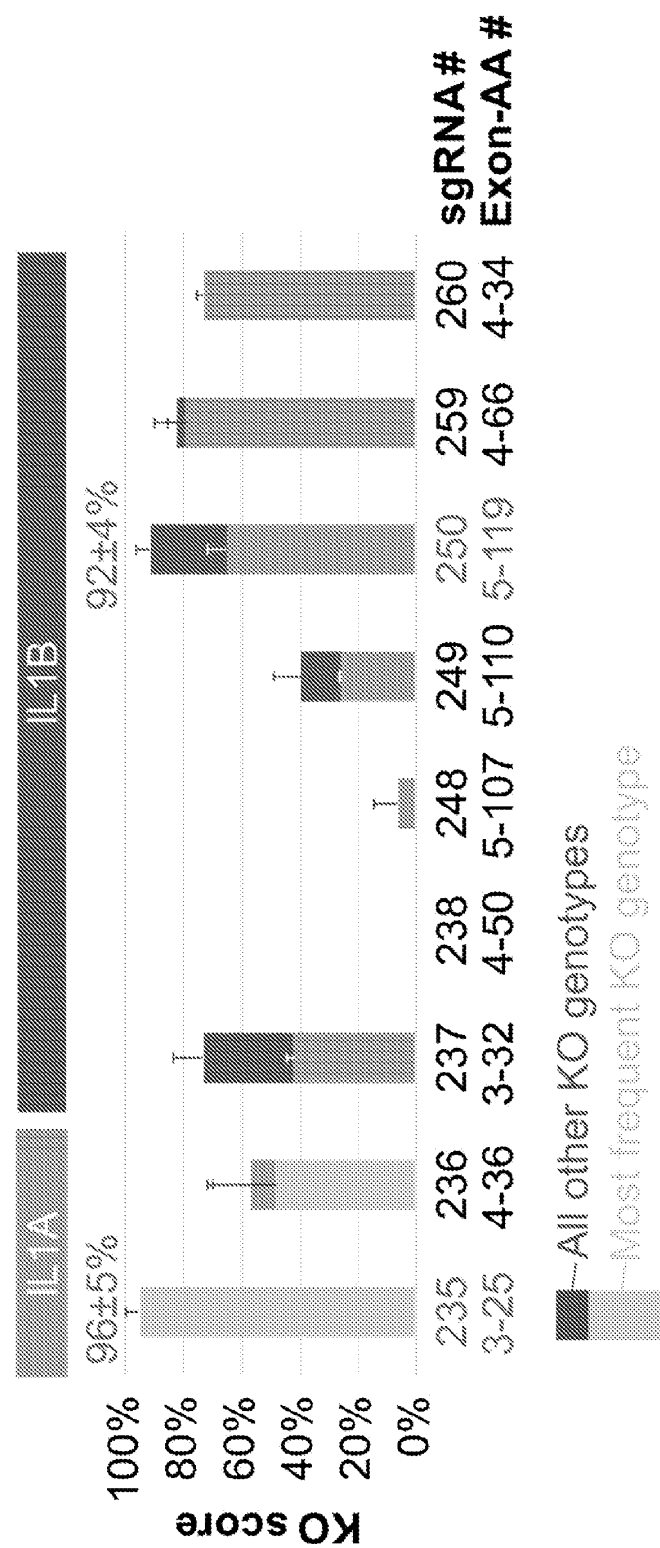


FIG. 91A

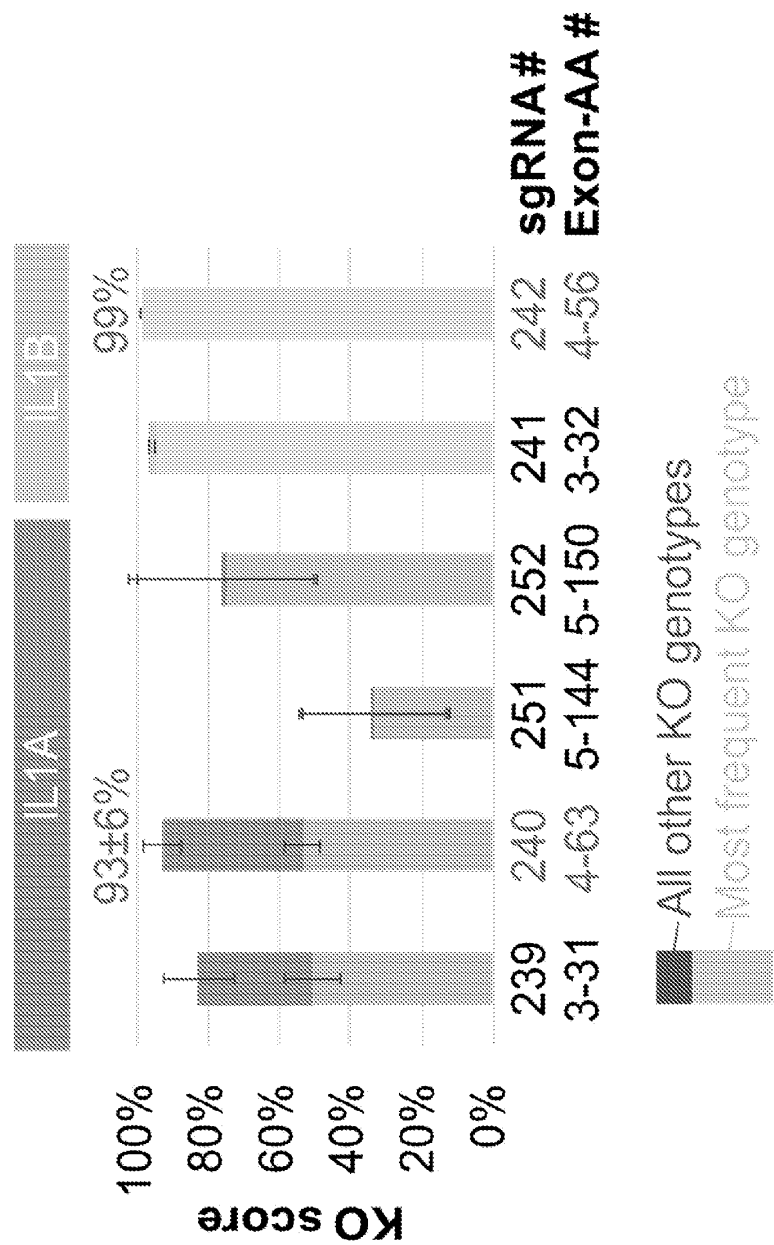


FIG. 91B

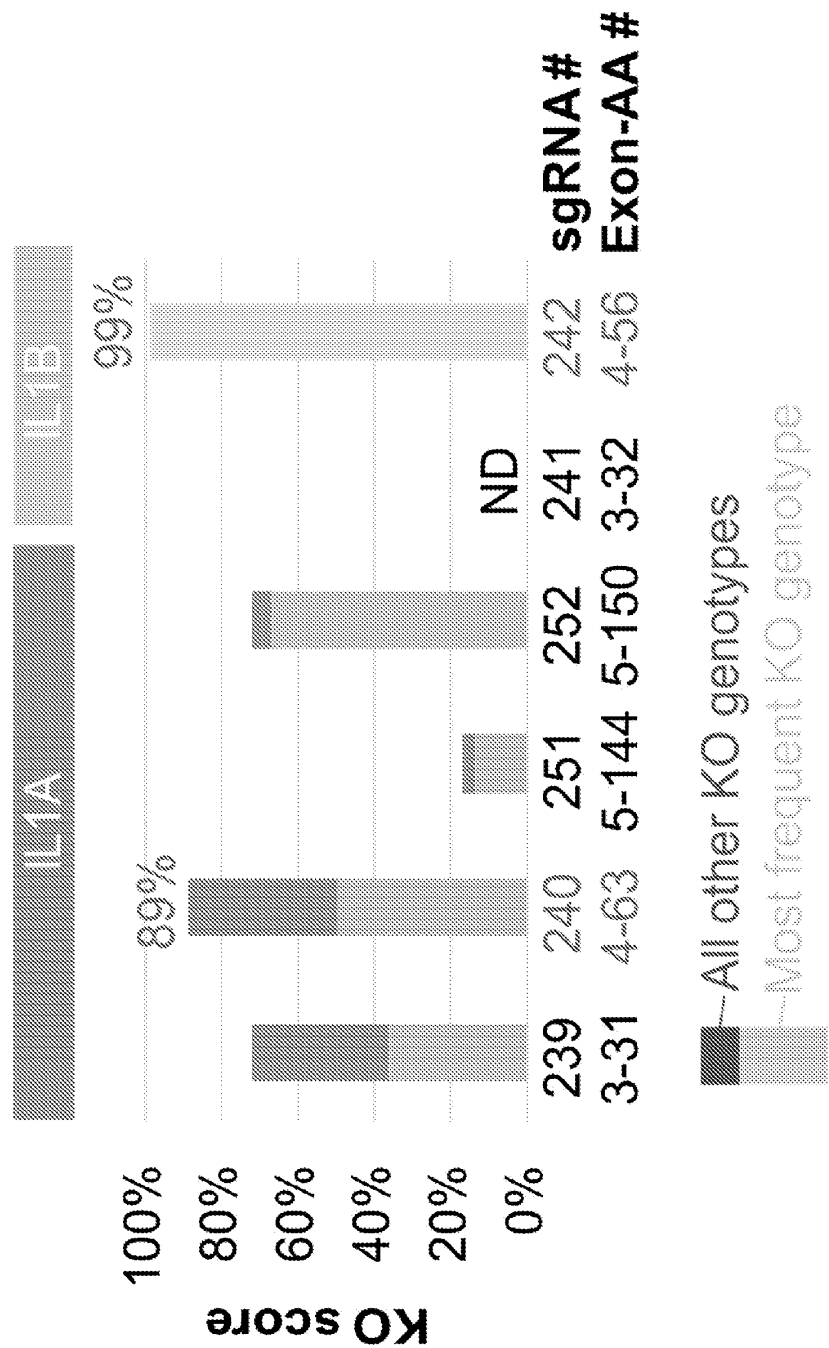


FIG. 91C

In silico predicted off-targets of sgRNA #240 in the dog (*Canis familiaris*) genome

Off-target	Sequence (Seed)	PAM	Score	Gene	Chromosome	Strand	Position	Mismatches	On-target	Editing efficiency
	GACATCCCGAGCTTACCTTCA	AGG	100	IL1A	chr17	-1	36977152	0	TRUE	97%
#1	CACATCCCGAGCTTACCTTCA	CGG	1.67322207	IncRNA	chr27	1	34712401	3	FALSE	0%
#2	TAAATAGCAGCTTACCTTCA	CAG	1.54205034		chr35	-1	18871859	3	FALSE	0%
#3	GAGATCCCGAGCTTACCTTCA	GAG	1.32551887		chr10	-1	2693301	4	FALSE	0%

In silico predicted off-targets of sgRNA #242 in the dog (*Canis familiaris*) genome

Off-target	Sequence (Seed)	PAM	Score	Gene	Chromosome	Strand	Position	Mismatches	On-target	Editing efficiency
	ACTCTTGTTACAGAGCTGGT	GGG	100	IL1B	chr17	1	37022194	0	TRUE	99%
#1	ACTCTTGTTACAGAGCTGGT	CAG	6.16161972		chr33	-1	20234937	2	FALSE	0%
#2	CCTCATGTTACAGAGCTGGT	GGG	2.76564774		chr1	-1	47541563	3	FALSE	99%
#3	GTGCTTGTTACAGAGCTGGT	GGG	2.32143742		chr26	-1	32323843	3	FALSE	25%

FIG. 92

On-target	Off-target #2	Off-target #3
Day 2	99%	0%
Day 10	99%	0%

FIG. 93A

On-target	Off-target #2	Off-target #3
day 2	99%	0%
day 10	99%	6%

FIG. 93B

CHONDROCYTES						
Single guide RNA (sgRNA)		Inference of CRISPR edits from Sanger traces (ICE), day 8-10 post-nucleofection				
#	Target sequence	Exon #	KO score	Top genotype	Predicted	Edit
Human IL-1A (IL1A-001; GRCh38)						
235	CAGAGACAGATGATCAATGG	3	96±5%	insA	96±5%	ATTCAGAGACAGATGATCAA {A} TGGAGGAAC
236	GCCATAGCTTACATGATAGA	4	57±13%	insT	49±23%	TGGCCCATAGCTTACATGAT {T} AGAAGGATTT
Human IL-1B (IL1B-201; GRCh38)						
237	TGATGGCCCTAAACAGATGA	3	74±11%	insA	42±3%	AGGTGATGGCCCTAAACAGGA {A} TGAAGGTAAG
238	GGTGGTCGGAGATTCGTAGC	4	0%	wt	0%	AGTGGTGGTCGGAGATTCGT AGCTGGATGCGGC
248	ACCTATCTTCTTCGACACAT	5	6±8%	delCA	6±8%	AGAACCTATCTTCTTCGACA ---TGGGATAACGA
249	CTTCGACACATGGGATAACG	5	40±9%	insA	26±0%	CTTCTTCGACACATGGGATA {A} ACGAGGCTTA
250	GTGCAGTTCAGTGCATCGTAC	5	92±4%	delG	66±6%	AGCGTGCAGTTCAGTGCATC- TACAGGTGCATCG
259	CAITGGCCACAACAACCTGACG	4	83±8%	delG	80±6%	GTCCATGGCCACAACAACCT- ACGCGGCGCTGCGT
260	AGGTCTCTGGAAGGAGCACTG	4	74±2%	insA	74±2%	TCCAGGTCTCTGGAAGGAGCA {A} CTGCGGAGAG

FIG. 94A

CHONDROCYTES						
Single guide RNA (sgRNA)		Inference of CRISPR edits from Sanger traces (ICE), day 8-10 post-nucleofection				
#	Target sequence	Exon #	KO score	Top genotype	Predicted	Edit
Canine IL-1A (IL1A-201; CanFam3.1)						
239	TGACCATCTCTCTCTGAATC	3	83±10%	insA	51±8%	35%
240	GACATCCAGCTTACCTTCA	4	93±6%	insT/delT	54±5%	53%
251	AGTATAGTTCGACAAACAGG	5	34±21%	insC	33±21%	31%
252	TCTGTAAATGCAGCAGTCATG	5	77±26%	insC	75±25%	20%
Canine IL-1B (IL1B-201; CanFam3.1)						
241	TGATGGCCCTGGAAATGTGA	3	99%	delTG	95%	17%
242	ACTCTTTGTTACAGAGCTGGT	4	99±0%	insT	99±0%	56%

FIG. 94B

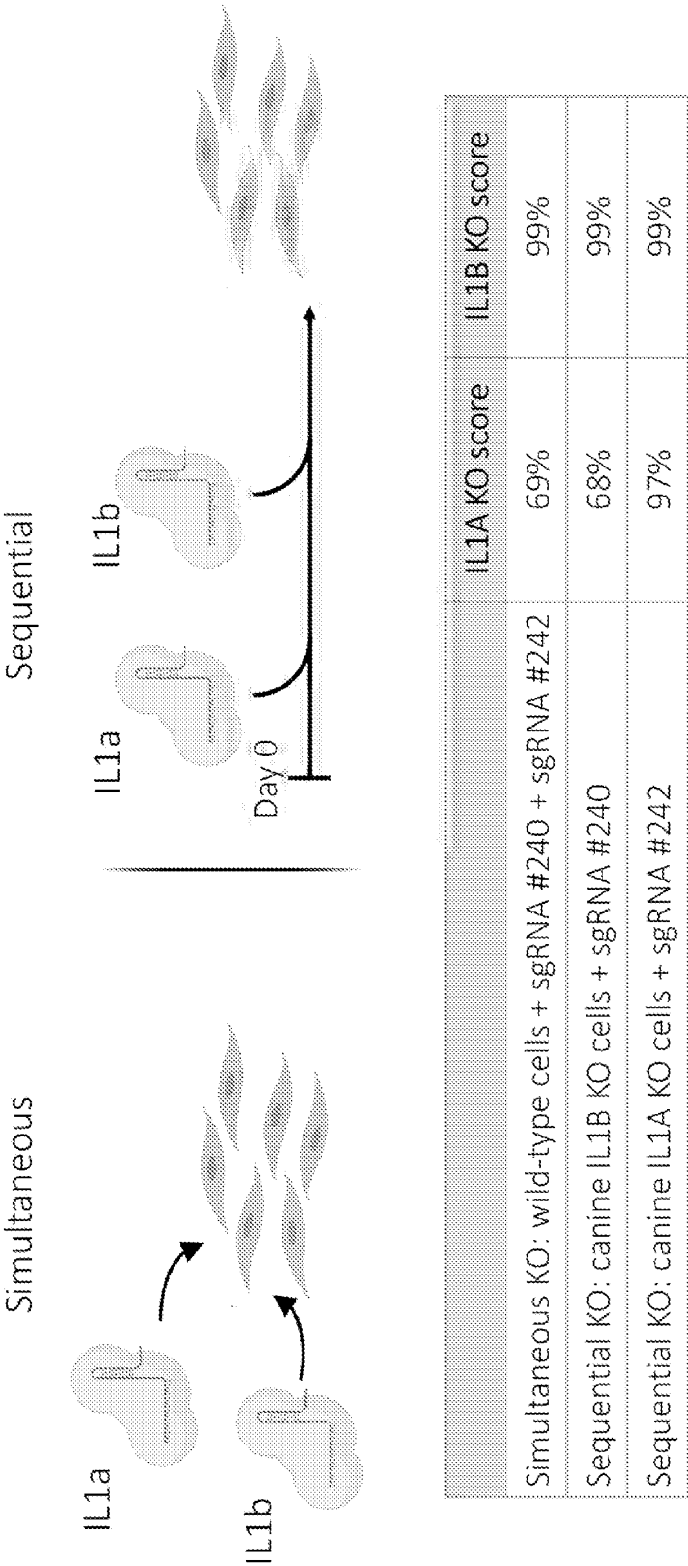


FIG. 95

FIG. 96B