A mutation-independent approach via transcriptional upregulation of a disease modifier gene rescues muscular dystrophy *in vivo*

Dwi U. Kemaladewi[1,*], Prabhpreet S. Bassi[1,2,*], Steven Erwood[1,2], Dhekra Al-Basha[3, 4], Kinga I. Gawlik[5], Kyle Lindsay[1], Ella Hyatt[1], Rebekah Kember[1], Kara M. Place[1], Ryan M. Marks[1], Madeleine Durbeej[5], Steven A. Prescott[3,4,6], Evgueni A. Ivakine[1,**], Ronald D. Cohn[1,2,7,**]

[1]Program in Genetics and Genome Biology, the Hospital for Sick Children Research Institute, Toronto, Canada
[2]Department of Molecular Genetics, University of Toronto, Canada
[3]Program in Neuroscience and Mental Health, the Hospital for Sick Children Research Institute, Toronto, Canada
[4]Department of Physiology, University of Toronto, Canada
[5]Unit of Muscle Biology, Department of Experimental Medical Science, Lund University, Lund, Sweden
[6]Institute of Biomaterials and Biomedical Engineering, University of Toronto, Canada
[7]Department of Pediatrics, the Hospital for Sick Children, Toronto, Canada
*These authors contributed equally to this work
**These authors contributed equally to this work

24 **Introductory paragraph**

25 Identification of genetic modifiers has provided critically important insights into the
26 pathogenesis and heterogeneity of disease phenotypes in individuals affected by
27 neuromuscular disorders (NMDs). Targeting modifier genes to improve disease
28 phenotypes could be especially beneficial in cases where the causative genes are large,
29 structurally complex and the mutations are heterogeneous. Here, we report a mutation-
30 independent strategy to upregulate expression of a compensatory disease-modifying
31 gene in Congenital Muscular Dystrophy type 1A (MDC1A) using a CRISPR/dCas9-
32 based transcriptional activation system.

33 MDC1A is caused by nonfunctional Laminin α2, which compromises muscle fibers
34 stability and axon myelination in peripheral nerves [1]. Transgenic overexpression of
35 *Lama1*, encoding a structurally similar protein Laminin α1, ameliorates muscle wasting
36 and paralysis in the MDC1A mouse models, demonstrating its important role as a
37 disease modifier [2]. Yet, upregulation of *Lama1* as a postnatal gene therapy is hampered
38 by its large size, which exceeds the current genome packaging capacity of clinically
39 relevant delivery vehicles such as adeno-associated viral vectors (AAVs).

40 In this study, we use the CRISPR/dCas9-based transcriptional activation system to
41 upregulate *Lama1*. This system is comprised of catalytically inactive *S. aureus* Cas9
42 (dCas9) fused to VP64 transactivation domains and sgRNAs targeting the *Lama1*
43 promoter. We first demonstrate robust upregulation of *Lama1* in myoblasts, and
44 following AAV9-mediated intramuscular delivery, in skeletal muscles of dy^{2j}/dy^{2j} mouse
45 model of MDC1A.

46 We therefore assessed whether systemic upregulation of *Lama1* would yield therapeutic
47 benefits in dy^{2j}/dy^{2j} mice. When the intervention was started early in pre-symptomatic
48 dy^{2j}/dy^{2j} mice, *Lama1* upregulation prevented muscle fibrosis and hindlimb paralysis. An
49 important question for future therapeutic approaches for a variety of disorders relates to
50 the therapeutic window and phenotypic reversibility. This is particularly true for muscular
51 dystrophies as it has long been hypothesized that fibrotic changes in skeletal muscle
52 represent an irreversible disease state that would impair any therapeutic intervention at
53 advanced stages of the disease. Here, we demonstrate that dystrophic features and
54 disease progression were significantly improved and reversed when the treatment was
55 initiated in symptomatic 3-week old dy^{2j}/dy^{2j} mice with already-apparent hind limb
56 paralysis and significant muscle fibrosis.

Collectively, our data demonstrate the feasibility and therapeutic benefit of CRISPR/dCas9-mediated modulation of a disease modifier gene, which opens up an entirely new and mutation-independent treatment approach for all MDC1A patients. Moreover, this treatment strategy provides evidence that muscle fibrosis can be reversible to some degree, thus extending the therapeutic window for this disorder. Our data provide a proof-of-concept strategy that can be applied to a variety of disease modifier genes and a powerful therapeutic approach for various inherited and acquired diseases.

67 Congenital muscular dystrophy 1A (MDC1A) is an autosomal recessive neuromuscular
68 disease associated with a high degree of morbidity and mortality in early childhood [1]. It is
69 caused by mutations in the *LAMA2* gene encoding Laminin α2 chain (LAMA2), which
70 interacts with the β1 and γ1 chains to form the heterotrimer Laminin-211, an extracellular
71 matrix protein (reviewed in [3]). Laminin-211 interacts with α-dystroglycan and α7β1
72 integrin in skeletal muscle and Schwann cells, providing the necessary roles such as
73 survival and stability of myotubes, as well as proper neurite growth, axon myelination
74 and migration of Schwann cells. Lack of Laminin-211 in MDC1A causes degeneration of
75 skeletal muscle and impaired Schwann cell differentiation, resulting in a cascade of
76 secondary events including apoptosis/necrosis of muscle fibers, inflammation, and
77 fibrosis, which ultimately precipitate the disease. Despite significant advances in our
78 understanding of MDC1A pathophysiology, currently, there is no cure.
79 Due to the genetic nature of the disease, gene therapy is a promising treatment option
80 for MDC1A. The large size of *LAMA2* transcript, however, presents a challenge with
81 respect to gene delivery. We have recently overcome this challenge by using
82 CRISPR/Cas9 technology to correct a mutation in *Lama2* gene *in vivo* [4]. We focused on
83 dy^{2j}/dy^{2j} mouse model, which harbors a splice site mutation in *Lama2* causing
84 spontaneous exon skipping and truncation of N-terminal domain of the protein [5]. We
85 developed an exon inclusion strategy to correct the splice mutation, leading to
86 restoration of full-length Lama2. This study established the first direct correction of the
87 primary genetic defect underlying MDC1A in an *in vivo* model.
88 To date, there are over 350 reported pathogenic nonsense-, missense-, splice site- and
89 deletion mutations in the *LAMA2* gene. Given the variety of MDC1A-causing genomic
90 alterations, CRISPR/Cas9-mediated gene editing strategies would require design and
91 thorough analysis of multiple sgRNAs specific for each individual mutation. Moreover,
92 safety concerns regarding CRISPR/Cas9's potential mutagenic nature and the presence
93 of off-target effects after gene editing remain, which together may prove to be
94 challenging from a safety and regulatory point-of-view. In contrast, the attenuation of
95 disease pathogenicity by targeted modulation of disease modifier gene expression would
96 be a potentially safer alternative and beneficial to all individuals with MDC1A.
97 One of the strongest reported disease modifiers for MDC1A is Laminin-α1 protein, which
98 is structurally similar to Laminin-α2 (**Fig. 1a**). However, Laminin-α1 is not expressed in
99 skeletal muscles or Schwann cells. A series of studies previously demonstrated that
100 transgenic expression of *Lama1*, encoding Laminin-α1, rescued both myopathy and

101 peripheral neuropathy in *dy*^{2j}/*dy*^{2j} [6] and *dy*^{3K}/*dy*^{3K} [2,7-10]; the latter also showed increased
102 lifespan. Although these studies firmly established compensatory function of Laminin-α1
103 in MDC1A, utilization of this modifier as a postnatal gene therapy is hampered by the
104 size of *Lama1* cDNA, which exceeds the 4.7 kb packaging capacity of AAV vectors.
105 Advances in CRISPR/Cas9 technologies have provided opportunities for regulating gene
106 expression and creating epigenetic alterations without introducing DNA double-strand
107 breaks (DSBs); commonly termed CRISPR transcriptional activation/inhibition system.
108 The strategy utilizes nuclease-deficient Cas9 (dCas9), which is unable to cleave DNA
109 due to mutations within the nuclease domains, but still retains the ability to specifically
110 bind to DNA when guided by a single guide RNA (sgRNA) [11,12]. Using the originally
111 described *S. pyogenes* (*Sp*) dCas9 fused to multiple copies of the VP16 transcriptional
112 activator, our group and others have demonstrated utilization of the CRISPR/dCas9
113 system to upregulate expression of modifier genes *in vitro* [11-14]. A major challenge for *in*
114 *vivo* applications lies in the large size of *Sp*dCas9 and its transcriptional activator fusion
115 derivatives that exceed AAV genome packaging capacity. To accommodate this
116 limitation, we sought to adapt the transcriptional upregulation system and utilize a
117 significantly smaller Cas9 protein derived from *S. aureus* (*Sa*)[15] to upregulate MDC1A
118 modifier *Lama1*. We hypothesized that CRISPR/dCas9-mediated transcriptional
119 upregulation of *Lama1* would be sufficient to compensate for the lack of *Lama2* and
120 ameliorate disease phenotypes in *dy*^{2j}/*dy*^{2j} mice.
121 First, we mutagenized *Sa*Cas9 endonuclease catalytic residues (D10A, N580A) to
122 create *Sa*dCas9 and then fused it to transcriptional activators VP64 (four copies of
123 VP16) on both N- and C-termini (**Fig. S1**). We tested the ability of the system, denoted
124 as *Sa*dCas9-2xVP64, to upregulate the expression of minCMV-driven *tdTomato* gene in
125 293T cells [16]. In the absence of the *Sa*dCas9-2xVP64, the expression of *tdTomato* was
126 undetectable due to the low baseline activity of minCMV promoter (**Fig. S1a, b**). In the
127 presence of *Sa*dCas9-2xVP64 in combination with an sgRNA targeting the minCMV
128 locus, we observed high *tdTomato* fluorescence signal (**Fig. S1c, d**), indicating the
129 general applicability of this system to modulate expression of a gene of interest.
130 Subsequently, we tailored the system to upregulate *Lama1* expression and designed five
131 sgRNAs, denoted as g1 to g5, within the 500 nucleotides region immediately upstream
132 of the *Lama1* transcription start site (**Figs. 1b, c**). When co-expressed with *Sa*dCas9-
133 VP64 in C2C12 murine myoblasts, 3 out of 5 sgRNAs, namely g1, g2, and g5
134 consistently induced significant increase of *Lama1* transcript expression (**Figs. 1d, e**).

135 Although all sgRNAs were designed to target a chromatin-accessible region derived
136 from DNAse1 hypersensitivity- and assay for transposase-accessible chromatin (ATAC-
137 Seq) sites (**Fig. 1b**), g3 and g4 failed to increase expression of *Lama1* above the basal
138 level. This corroborates previously reported findings that chromatin accessibility is not a
139 reliable predictor of successful gene activation [12,17,18]. Nonetheless, the sgRNA closest to
140 the transcription start site, g1, and the combination of the three most optimum sgRNAs
141 (g1, g2, g5) resulted in a robust increase in Lama1 protein expression in dy^{2j}/dy^{2j}-derived
142 myoblasts (**Figs. 1f, 1g**), warranting further investigation *in vivo*.
143 We then treated 3-week-old dy^{2j}/dy^{2j} mice with an AAV9 carrying FLAG-tagged
144 *Sa*dCas9-2xVP64 in the absence of sgRNA (no guide) or with g1 (single guide) or a
145 combination of g1, g2 and g5 (three guides) (**Fig. 2a**). Due to the packaging capacity of
146 the AAV, the dCas9-2xVP64 and the three guides were split into two vectors (**Fig. 2a**).
147 Each mouse received a single intramuscular injection of 7.5×10^{11} viral genomes of
148 AAV9, which was doubled to 1.5×10^{12} viral genomes total for the three guide cohort, in
149 the right *tibialis anterior* (TA) and was sacrificed 4 weeks post injection. FLAG
150 expression was detected by western blot in all *Sa*dCas9-2xVP64-injected right TA
151 muscles, however, only those injected with guide-containing constructs showed Lama1
152 upregulation (**Fig. 2b**). Similarly, immunofluorescence staining revealed sarcolemmal
153 expression of Lama1 (**Fig. 2c**, upper), indicating proper protein localization.
154 Furthermore, H&E staining exhibited considerably improved muscle architecture (**Fig.
155 2c**, lower) in the single- and three guide treatment groups, as compared to the no guide
156 controls.
157 Next, we sought to investigate whether upregulation of *Lama1* could be achieved
158 systemically *in vivo* and, if administered into pre-symptomatic neonatal dy^{2j}/dy^{2j} mice,
159 would prevent the manifestation of dystrophic pathophysiology and paralysis. AAV9
160 particles carrying either no guide or a combination of three guides were injected into the
161 temporal vein of 2-day-old (P2) dy^{2j}/dy^{2j} mice (**Fig. 3a**). Seven weeks post injection, the
162 animals that received the three guides treatment showed an absence of classical
163 hindlimb contracture, unlike the control group (**Fig. 3b; Supplementary videos 1** and
164 **2**). Western blot, immunofluorescence and H&E staining of TA and gastrocnemius
165 muscles demonstrated robust expression of Lama1 on the sarcolemmal membrane (**Fig.
166 3c, 3d**), leading to ~50% reduction of fibrosis (**Figs. 3e**, **3f, S2**).
167 We subsequently examined the ability of *Lama1* upregulation to reverse established
168 muscular and peripheral nerve dysfunctions by initiating the treatment at 3 weeks of age,

169 when paralysis was already apparent [19,20] (**Fig. 4a**). We first tested three different doses,
170 ranging from $7.5x10^{10}$ to $3x10^{11}$ viral genome/gram of mouse per AAV9, which was
171 doubled for the three guide cohorts due to the utilization of two vectors, and found that
172 the highest dose resulted in homogeneous Lama1-positive fibers (**Fig. S3a**), significant
173 improvement of muscle function and mobility (**Figs. S3b, S3c**). Longitudinal
174 measurement of animal mobility and stand-up activity in a non-invasive open field
175 activity assay showed significant difference between no guide and three guides-treated
176 mice starting at 5 and 6 weeks old, respectively, which was sustained over time (**Figs.**
177 **4b, 4c**). Furthermore, specific tetanic force, which measures the aggregate torque
178 produced by the dorsi flexor muscles, was also improved in the three guides-treated
179 mice (**Fig. 4d**). In line with this finding, we observed a significant increase in nerve
180 conduction velocity, which indicates restoration of the myelination defect and contributes
181 to neuromuscular functionality (**Fig. 4e**). The absence of paralysis in the hind limbs and
182 markedly improved movement of the mice were evident at the end of the treatment
183 regimen (**Supplementary videos 3, 4**).
184 Molecular analysis of the treated mice revealed strong Lama1 expression by
185 immunostaining and western blot (**Figs. 4f, 4g, S4**), which was accompanied by
186 normalization of α4 chain of the laminin subunit (**Figs. S5, S6**) [6], significant improvement
187 in muscle histopathology (**Fig. 4h**) and approximately 50% reduction in the fibrotic area
188 (**Fig. 4i**) compared to the no guide control group. There was a trend towards larger fibers
189 in the treated mice, although it did not reach statistical significance due to the large
190 variation between animals (**Fig. 4j**). In addition, upregulation of Lama1 was also
191 observed in the endoneurium of sciatic nerves and resulted in restoration of myelination
192 defect (**Figs. 4k, S7**), supporting the improvement of nerve conduction velocity and lack
193 of paralysis in the mice (**Fig. 4e**, **Supplementary videos 3, 4**). Quantification of the AAV
194 genome copy number revealed accumulation of most of the viral genome in the liver,
195 which is expected from intravenous delivery. Nevertheless, approximately 1.11±0.4 and
196 34.1±4.3 copies/diploid genome of the viral genome were detected in the sciatic nerves
197 and skeletal muscles, respectively (**Fig. S8**). Remarkably, even relatively low
198 transduction efficiency in sciatic nerves was sufficient for functionally significant
199 upregulation of Lama1 expression.
200 Finally, we investigated the genome wide effects of CRISPR/dCas9-mediated Lama1
201 upregulation by performing RNA-sequencing on quadriceps muscles isolated from mice
202 treated with AAV9 carrying no guide and three guides (**Figs. S9, S10, Supplemental**

203 **Tables 1-3**). Age-matched wildtype and *dy*^{2j}/*dy*^{2j} mice served as controls. We observed
204 a 3.6-$\log_2$fold upregulation of Lama1 (defined by a false discovery rate, FDR <0.05)
205 when comparing the mice treated with AAV9 carrying no guide and three guides (**Fig.**
206 **S9a**). The transcriptional change was even higher at 9-$\log_2$fold when comparing
207 untreated *dy*^{2j}/*dy*^{2j} with three guide-treated *dy*^{2j}/*dy*^{2j} (**Fig. S9b, S9c**). Hierarchical
208 clustering between groups revealed clustering between wildtype and three guides,
209 whereas the untreated cohort was clustered together with no guide-treated mice (**Figs.**
210 **S9d, S10**). We also computationally predicted 704 potential off-target binding sites for
211 the three sgRNAs targeting *Lama1* promoter in the mouse genome, selected based on
212 the presence of a 6bp PAM-proximal seed sequence and fewer than ten total
213 mismatches to the cognate target sequence (**Supplemental Tables 4-5**). None of the
214 top 100 genes contained a predicted off-target site within 60 kilobases of the gene body,
215 with the average distance from off-target site to the gene body being 2.2 megabases.
216 Taken together, our results provide strong evidence of the robustness and durability of
217 CRISPR/dCas9-mediated Lama1 upregulation for the treatment of MDC1A. Additionally,
218 we show the therapeutic promise of the strategy for reversal of dystrophic feature in
219 skeletal muscle and peripheral neuropathy in *dy*^{2j}/*dy*^{2j} mouse model of MDC1A, which
220 ultimately halts progression of the disease, without any confounding off-target effects.
221

222 One challenge in developing a therapy for MDC1A is that the heterogeneity of mutations
223 often leads to variable disease severity and progression. Therefore, there is an urgent
224 need to develop a universal, mutation-independent strategy that provides a treatment
225 approach for all patients with MDC1A. Our study establishes a framework in which
226 CRISPR/dCas9 transcriptional upregulation of a disease modifier gene, such as *Lama1,*
227 ameliorates disease symptoms *in vivo* and has the potential to be applied to all MDC1A
228 patients, irrespective of their mutations.
229 Advances have been made towards elucidating MDC1A pathogenesis due to the
230 availability of several mouse models with absent or reduced *Lama2* expression. Yet, an
231 important question in the development of therapeutics and clinical trials in MDC1A is the
232 reversibility of symptoms caused by muscle fibrosis and nerve abnormalities. This issue
233 has been challenging to address in patients[21], however, the ability to modify gene
234 expression in postnatal animals allowed us to address this question and begin to
235 investigate the therapeutic window of intervention.
236 We have previously demonstrated that an early intervention using CRISPR/Cas9-
237 mediated correction of a splicing defect resulted in robust Lama2 restoration and
238 prevention of disease manifestation [4]. Here we showed that upregulation of *Lama1*,
239 when initiated at pre-disease-onset, leads to similar prevention. Importantly, when the
240 therapeutic intervention was initiated at older age, significant rescue of the phenotypes
241 was attainable, indicating that post-symptomatic treatment provides a significant benefit
242 in the dy^{2j}/dy^{2j} mouse model.
243 In addition to *Lama1* upregulation described in this study, a number of disease modifying
244 strategies are currently being explored in MDC1A animal models, including treatment
245 with miniaturized agrin [22-24] and laminin-α1 LN-domain nidogen-1 (αLNNd) [25-27]. While
246 the efficacy of αLNNd has only been explored in transgenic mice, AAV-mediated delivery
247 of mini agrin has been shown to normalize most histopathological parameters in skeletal
248 muscle, and improve myelination and regeneration of Schwann cells of the peripheral
249 nerves [22,24]. Despite the observed phenotypic improvement, the mini agrin-treated mice
250 still have a lower survival rate compared to wild-type animals expressing full-length
251 agrin, suggesting the potential shortcoming of the shortened version of agrin, which may
252 be overcome by its full-length form in native glycosylation state [25]. It is important to note
253 that many preclinical studies in MDC1A were carried out in the more severe dy^{W}/dy^{W}
254 mouse model. Therefore, as a follow up on our study, it will be important to evaluate our
255 approach in the dy^{W}/dy^{W} mice to assess critical parameter such as survival, which is not

256 possible in the *dy^{2j}/dy^{2j}* mouse model due to its near-normal life span. Overall, our
257 approach in combining the CRISPR/dCas9-mediated transcriptional upregulation and
258 AAV9 as a delivery vehicle can be translated to many other disease modifiers, such as
259 agrin, as well as conditions where modulation of disease modifiers is required within
260 both skeletal muscles and peripheral nerves.
261 In fact, neuromuscular disorders have provided excellent examples to demonstrate the
262 role of disease modifiers (recently reviewed in [28]). Beyond MDC1A, several studies have
263 demonstrated that upregulation of *Lama1* stabilizes the sarcolemmal membrane in
264 dystrophin-deficient mouse models [29]. The most advanced approach is via delivery of
265 Laminin-111 protein, although the efficacy remains low and the need to produce a large
266 amount of bioactive protein is challenging [29]. In addition, the utilization of CRISPR/dCas9
267 system to upregulate Lama1 in *mdx* mice has been achieved locally via electroporation,
268 which is not easily translatable into clinical settings [30]. Our strategy of employing AAV-
269 mediated *S. aureus* dCas9 to upregulate *Lama1 in vivo* may be tested further as a
270 potential therapy in the context of Duchenne muscular dystrophy.
271 In addition, since the CRISPR/dCas9-mediated transcriptional modulation acts directly
272 on the endogenous locus, it may be used in conjunction with a mutation-correction
273 approach where the level of restoration of the defective gene is suboptimal, therefore
274 necessitating further amplification to reach therapeutic efficacy [4,31-36].
275 A very recent study by Liao *et al* described utilization of the CRISPR/Cas9 system to
276 recruit MCP:P65:HSF1 transcriptional activation complex to induce expression of target
277 genes in skeletal muscle, kidney and liver tissues [18]. This resulted in phenotypic
278 augmentation such as enhanced muscle mass and substantial improvement in disease
279 pathophysiology, thereby highlighting the feasibility of using CRISPR/dCas9-mediated
280 transcriptional activation as a possible therapeutic modality. However, their study relied
281 almost exclusively on a Cas9-expressing transgenic mouse model or local intramuscular
282 treatments, and therefore it is difficult to extrapolate the efficacy of this strategy to
283 disease-relevant models. In contrast, we successfully demonstrated robust upregulation
284 of Lama1 after systemic delivery of therapeutic components in a relevant mouse model
285 of disease that does not constitutively express Cas9.
286 Finally, the modular nature of the CRISPR/dCas9 system can be utilized to not only to
287 upregulate, but also to downregulate target gene expression. The latter can be achieved
288 by coupling dCas9 with transcriptional repressor such as Kruppel-associated box
289 (KRAB) [17,37]. A very recent study described that following sarcolemmal injury, the muscle

membrane resealing process is greatly improved upon the deletion of Osteopontin, which acts in a concerted fashion with protective modifiers such as Latent TGF-β binding protein (LTBP4) and Annexins 1 and 6 [38,39]. The combinatorial effects of such modifiers, whether they are additive, synergistic or even opposing in action, represent a new paradigm for lessening disease phenotypes. A foreseeable application of CRISPR/dCas9-mediated modulation is in the upregulation of protective disease modifier genes, such as Lama1 or LTBP4, with concurrent downregulation of detrimental genes, such as Osteopontin, providing a combinatorial therapeutic approach.

In summary, our study establishes a framework to utilize CRISPR/dCas9 to modulate gene expression of disease modifiers that should be considered as a mutation-independent therapeutic strategy not only to MDC1A, but also to various other inherited and acquired diseases.

302 **Methods**

303

304 **Engineering of activation constructs**

305 A fragment containing a catalytically inactive *SaCas9* coupled to two flanking VP64
306 transactivator domains was synthesized by BioBasic Canada and cloned into pX601
307 (Addgene 61591) using AgeI and EcoRI directional cloning to generate 3XFLAG-VP64-
308 SadCas9 (D10A/N580A)-NLS-VP64 plasmid (**Figs. 2a, S11, Supplemental Table S6**).
309 Each sgRNA **(Supplemental Table S6)** was subsequently introduced using BsaI
310 directional cloning. To generate the three guides only construct (**Fig. 2a**), a fragment
311 containing three repetitive regions of U6 promoter and *S. aureus* guide scaffold was
312 assembled, with short linkers in between each region (BioBasic Canada). The fragment
313 was cloned into KpnI and NotI sites of a pX601-derivative plasmid.

314

315 **Cell Culture**

316 Primary myoblasts were isolated from the Extensor Digitorum Longus (EDL) Muscle of
317 dy^{2J}/dy^{2J} mice, as previously described [40] and maintained in DMEM supplemented with
318 1% chicken embryo extract (GeminiBioscience), 10% horse serum, 1%
319 penicillin/streptomycin and 1% L-glutamine (all from Gibco, unless indicated otherwise).
320 HEK293 and C2C12 cells where maintained in DMEM supplemented with 10% FBS, 1%
321 penicillin/streptomycin and 1% L-glutamine (all from Gibco). All cells were maintained at
322 37°C with 5% CO_2.
323 Transfection of HEK293T cells was performed as previously described[2]. C2C12 and
324 dy^{2J}/dy^{2J} cells were transfected in 12-well plates using the Neon Transfection System
325 (Invitrogen). 400,000 cells were electroporated with 1.5 µg of DNA utilizing optimization
326 program 16 (pulse voltage: 1400V, pulse width: 20ms, pulse number: 2). Cells were
327 grown for 72 hours, after which RNA or protein was subsequently collected for protein
328 analysis and guide screening.

329

330 **Animals, virus production and injections**

331 dy^{2j}/dy^{2j} mice were purchased from the Jackson Laboratory and maintained in the
332 Toronto Center for Phenogenomics. Both male and female were used in the analyses.
333 All animal experiments were performed according to Animal Use Protocol number 20-
334 0305. *Sa*dCas9-2xVP64, single guide and three guides plasmids (**Fig. 2a,**
335 **Supplemental Table S6**) were packaged into AAV9 vectors by Vigene Biosciences as

336 previously described [3]. For intramuscular and temporal vein injection into neonatal pups,
337 the dose of $7.5x10^{11}$ viral genomes each was used. Due to the limitation in packaging
338 capacity, two AAVs were needed for the three guides cohort (**Fig. 2a**), therefore the total
339 virus injected was $1.5x10^{12}$ viral genomes per animal. Injection volume was brought to
340 50 µl with 1XPBS (Gibco).
341 For the tail vein injection in young, 3 week old mice, three different doses were initially
342 tested: $7.5x10^{10}$, $1.5x10^{11}$ and $3x10^{11}$ viral genomes per gram of mouse (**Fig. S3**).
343 Similar to the intramuscular and temporal vein injections, two AAVs were needed for the
344 three guides cohort, therefore the total dose used in experiments described in **Figs. 4,**
345 **S4-S10** was $6x10^{11}$ viral genomes per gram of mouse. Injection volume was brought to
346 100 µl with 1XPBS (Gibco).
347
348 **RNA isolation, guide screening and RT-PCR**
349 RNA was isolated from cultured cells and mouse tissue sections, and cDNA synthesis
350 was performed as previously described[3]. PCR amplification was utilized to assess the
351 efficiency of each guide in upregulating *Lama1* expression using a primer in *Lama1* exon
352 55 (RDC 1919) and a second primer spanning the junction of exons 55 and 56 (RDC
353 1920). Sequences are listed in **Supplemental Table S6**.
354 qPCR utilizing Fast SYBR green Master Mix (Qiagen) on a Step One Plus Real Time
355 PCR (Applied Biosystems) was performed. *Lama1* expression was analyzed using a
356 primer in *Lama1* exon 55 (RDC 1919) and one spanning the junction of exons 55 and 56
357 (RDC 1920). Primers against endogenous Gapdh (RDC 345 and 346) were used as an
358 internal control. ΔΔCt was analyzed to assess fold changes between treated and
359 untreated samples.
360
361 **Protein Isolation and western blot**
362 Protein was isolated from dy^{2j}/dy^{2j} myoblasts and C2C12 cells by adding 150 µl of a 1:1
363 part solution of RIPA homogenizing buffer (50-mM Tris HCl pH 7.4, 150-nM NaCl, 1-mM
364 EDTA) and RIPA double-detergent buffer (2% deoxycholate, 2% NP40, 2% Triton X-100
365 in RIPA homogenizing buffer) supplemented with protease-inhibitor cocktail (Roche).
366 Cells were subsequently scraped from the bottom of each well, collected and incubated
367 on ice for 30 min. Cells then centrifuged at 12000xg for 15 min at $4^{o}C$ and the
368 supernatant was collected and stored at $-80^{o}C$. Protein from mouse tissue sections was
369 collected as previously described[3]. Whole protein concentration was measured using

370 Pierce BCA protein assay kit according to the manufacturer's protocol (Thermo Fisher
371 Scientific). Western blot was performed as previously described[3]. Primary antibodies
372 used were rabbit Anti-LNα1 E3 (a gift from Dr. Peter Yurchenco, 0.6 µg/ml), mouse
373 monoclonal M2 anti-Flag (Sigma Aldrich F1804, 1:1000) and rabbit polyclonal anti-
374 GAPDH (Santa Cruz sc-25778, 1:5000).

375 **Immunofluorescence and H&E staining**

376 Muscles and nerves were sectioned at 8 µm thickness and processed for
377 immunofluorescence analyses according to standard procedures. Antibodies used for
378 immunofluorescence staining were rat monoclonal against Laminin α1 (mAb200,
379 Durbeej Lab, 1:20), α2 (4H8-2, Sigma, 1:500), γ1 chain (clone A5, Thermo Fisher
380 Scientific), rabbit polyclonal against Laminin α4 chain (kindly provided by Dr. Sasaki),
381 mouse monoclonal against NF-H (Biolegend SMI 31, 1:1000), goat polyclonal anti-rat
382 Alexa Fluor 555 (Thermo Fisher Scientific, 1:250) and goat polyclonal anti-mouse Alexa
383 Fluor 488 (Thermo Fisher Scientific, 1:250). H&E staining was performed as previously
384 described [4]. Both immunofluorescence and H&E slides were scanned with the 3Dhistech
385 Pannoramic 250 Flash II digital scanner and analyzed with CaseViewer software, with
386 the exception of **Figs. S5**, **S6,** which were analyzed with a Zeiss Axioplan fluorescence
387 microscope (Carl Zeiss) and images were captured using an ORCA 1394 ER digital
388 camera (Hamamatsu Photonics) and Open Lab software version 4 (Improvision).
389

390 **Toluidine blue staining and electron microscopy**

391 Freshly isolated mouse sciatic nerves were halved and fixed in a solution of 2%
392 paraformaldehyde and 2.5% glutaraldehyde in 0.1M sodium cacodylate buffer until
393 further use. For embedding, the specimens were rinsed with the 0.1M sodium
394 cacodylate buffer, post-fixed in 1% osmium tetroxide in the washing buffer, dehydrated
395 in a graded ethanol series followed by propylene oxide, and embedded in Quetol-Spurr
396 resin overnight at 65^0C. Sections of 90nm thickness were cut on a Leica EM UC7
397 ultramicrotome, stained with uranyl acetate and lead citrate, and imaged on a FEI Tecnai
398 20 electron microscope at 4400-, 10,000-, and 44,000X magnifications. The same 90nm
399 sections were stained with toluidine blue and imaged on a Leica DM-2000. All reagents
400 were purchased from Electron Microscopy Sciences. Quantification of myelin thickness
401 was measured using ImageJ from at least 14 random axons per field (at least 5 fields
402 per animal) [41].

403 **Open field and *in vivo* muscle force assays**

404 Open field activity test and assessment of *in vivo* muscle force were performed on tail
405 vein injected cohorts at the Lunenfeld-Tanenbaum Research Institute's Centre for
406 Modeling Human Disease Mouse Phenotyping Facility. For the open field test, mice
407 were placed in the frontal center of a transparent Plexiglas open field (41.25 cm × 41.25
408 cm × 31.25 cm) illuminated by 200 lx. A trained operator, who is unaware of the nature
409 of the projects and treatments, performed experiments. The VersaMax Animal Activity
410 Monitoring System recorded vertical activities and total distance travelled for 20 minutes
411 per animal.

412 *In vivo* muscle contraction test was performed using 1300A: 3-in-1 Whole Animal
413 System and analyzed using Dynamic muscle control/analysis (DMC/DMA) High
414 throughput software suite (Aurora Scientific). The mice were anaesthetised with
415 intraperitoneal injection of ketamine/xylazine cocktail at 100 mg/kg and 10 mg/kg of body
416 weight, respectively. Contractile output was measured via percutaneous electrodes that
417 stimulate specific nerves innervating the plantar flexors. Specific tetanic force (200 ms of
418 0.5-ms pulses at 125 Hz) was recorded and corrected to body weight.

419

420 **Nerve conduction velocity**

421 Mice were anesthetized with urethane (1.2 mg/g i.p.) and underwent a tracheotomy to
422 maintain their airway but were not artificially ventilated. Core body temperature was
423 maintained at 34-36.5˚C using a feedback-controlled heating pad (TR-200; Fine Science
424 Tools). The sciatic nerve was exposed at two locations via incisions (~15 mm) above the
425 left knee (site #1) and along the sacral region of the vertebral column (site #2). After
426 separating the nerve from adjacent tissue, a bipolar hook electrode was applied to the
427 nerve at each site. Each electrode comprised two chlorided silver wires (0.01″ diameter,
428 A-M systems) placed ~1 mm apart and bent at the tip to form hooks, and attached to a
429 stimulator (Model DS3, Digitimer Ltd). Stimulating electrodes were insulated from
430 underlying tissue using a small piece of plastic paraffin film. Stimulus duration was fixed
431 at 20 μs and current intensity was varied. Stimulus timing was controlled by computer
432 using a Power1401 computer interface and Signal v5 software (Cambridge Electronic
433 Design, CED). The compound muscle action potential (CMAP) was recorded using
434 needle electrodes (~30 G, BD *PrecisionGlide*™), one inserted into the gastrocnemius
435 muscle and the other (reference) electrode inserted into the Achilles tendon. The CMAP
436 signal was amplified, low-pass filtered at 10 Hz and high-pass filtered at 1 kHz (DAM 80,

437 World Precision Instruments), and digitized at 40 kHz using the Power1401 and Signal
438 v5 software (CED). To calculate conduction velocity (CV) from CMAP responses, the
439 sciatic nerve was stimulated at just-maximal intensity (beyond which there is no change
440 in CMAP amplitude or latency) three times at site #1 and again three times at site #2.
441 Nerve conduction velocity was calculated as the difference between average CMAP
442 latencies for each stimulation site divided by the length of nerve (7.5-10 mm) separating
443 the sites.
444
445 **Vector genome quantification**
446 Evaluation of AAV genome distribution was performed as previously published [42] with a
447 few modifications. Genomic DNA was extracted from tibialis anterior, sciatic nerve, and
448 liver of treated mice using Qiagen Blood and Tissue Kit. 90 ng of DNA was amplified
449 using primers located in between the two inverted tandem repeats (ITRs) (RDC 1687,
450 RDC 1679, **Supplemental Table S7**) using Fast SYBR green master mix (Qiagen) on a
451 Step One Plus Real Time PCR (Applied Biosystems). The Ct value of each reaction was
452 converted to viral genome copy number by interpolating against the copy number of
453 standard curve of a known plasmid containing the sgRNA cassette (RDC 362). The
454 amount of DNA input (90 ng per tissue) was used as a conversion factor to diploid
455 genome (7 picogram DNA = 1 diploid genome).
456
457 **RNA-Sequencing**
458 Total RNA was isolated from quadriceps muscles using RNeasy kit (Qiagen) and
459 quantified using Qubit RNA HS assay (Thermo Fisher Scientific). RNA-Sequencing was
460 performed by the Centre for Applied Genetics in Toronto using the Illumina HiSeq 2500
461 system, producing 120bp paired-end reads. Raw transcript reads were aligned to the
462 GRCm38 mouse genome (mm10) using HISAT2 [43]. HTSeq was used to determine the
463 absolute number of read counts for each gene [44]. Only genes with at least 1 read per
464 million in at least three replicates were kept for downstream analysis. Normalization and
465 differential expression analysis was completed using the R packages limma, v3.36.3 and
466 edgeR, v.3.22.3 [45]. Differentially expressed genes were defined as genes with a more
467 than twofold change and adjusted $P < 0.05$. Off-target analysis was conducted using a
468 list of 704 computationally predicted using Cas-OFFinder [46]. Using the Bedtools suite
469 “closest” function, each of the top 100 differentially expressed genes was matched to the

470 nearest off-target loci to determine the shortest distance from off-target loci to
471 differentially expressed gene body.
472
473 **Statistical Analysis**
474 GraphPad Prism (GraphPad software) was utilized to preform all statistical analyses.
475 Two-tailed Student' t-tests to evaluate statistical significance between two groups was
476 preformed. Significance was considered to be $P < 0.05$.
477
478 **Data availability**
479 The authors declare that the main data supporting the findings of this study are available
480 within the article and its Supplementary Information files. Extra data are available from
481 the corresponding authors upon request.
482
483 **Acknowledgements**
484 The Cohn lab members are gratefully acknowledged for the technical support and critical
485 input in this study. We thank P. Yurchenco (Rutgers University) for providing critical
486 reagents in this study, C. Rand (Aurora Scientific), I. Vukobradovic (Clinical Phenotyping
487 Core, Centre for Modeling Human Disease), R. Smith (Prescott Lab) for assistance with
488 functional and behavioral studies, D. Holmyard (Nanoscale Biomedical Imaging Facility)
489 for electron microscopy analysis and S. Pereira (The Centre for Applied Genomics) for
490 genomic data acquisition.
491 This work was supported by AFM-Telethon, Cure CMD, Muscular Dystrophy Association
492 (to D.U.K), Rare Disease Foundation Microgrant (to P.S.B. and S.E.), SickKids
493 Restracomp (to S.E.), CIHR Summer Studentship (to R.M.), Natural Sciences and
494 Engineering Research Council of Canada, Canadian Institute for Health Research,
495 SickKids Foundation and R.S. McLaughlin Foundation Chair in Pediatrics (to R.D.C).
496
497 **Author contributions**
498 D.U.K., E.A.I., R.D.C. conceived the study, D.U.K., P.S.B., S.E., D.A.B., K.I.G., K.L.,
499 E.H., R.K., K.M.P., R.M., performed the experiments, D.A.B., K.I.G., M.D., S.A.P.
500 provided critical reagents, D.U.K., P.S.B, S.E., D.A.B, K.I.G, S.A.P., E.A.I, R.D.C.
501 analyzed data, D.U.K, E.A.I., R.D.C. supervised the study, D.U.K. wrote the manuscript
502 with inputs from the other authors. All authors provided feedback and agreed on the final
503 manuscript.
504

Figure legends

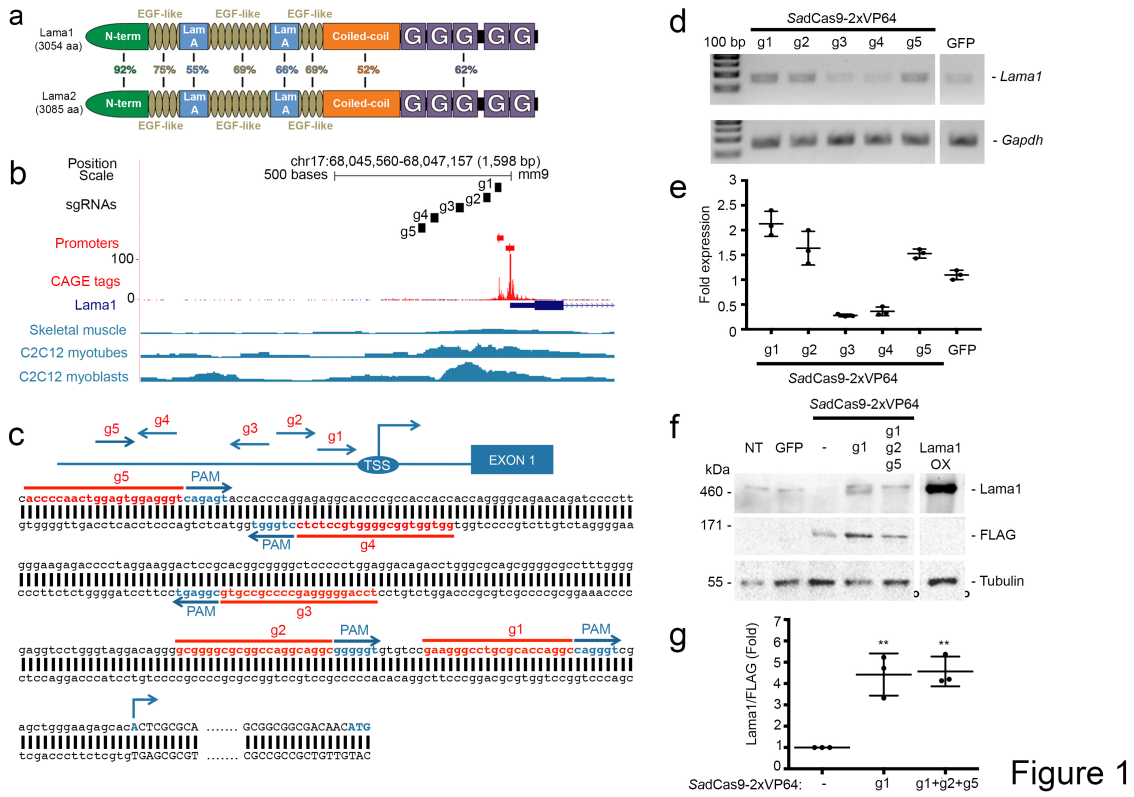


Fig. 1. *Sa*dCas9-2xVP64-mediated upregulation of *Lama1 in vitro*. (**a**) Lama1 and Lama2 protein alignment. Total amino acid (aa) and percentage similarity between each domain are indicated. (**b**) Analyses of Lama1 proximal promoter. Five sgRNAs (g1-g5) were designed in the proximal promoter region of Lama1 immediately upstream of the transcription start site (TSS), as indicated by CAGE tags (red). Chromatin accessibility in skeletal muscle tissue and cells (retrieved using Digital DNase footprinting and ATAC-Seq) are shown in blue. Data were plotted according to positions from the UCSC Genome Browser. (**c**) Positions of the five sgRNAs relative to *Lama1* TSS. Arrowheads indicate the direction of each sgRNA. Sequences of each sgRNA (red) are immediately downstream (5') of *Sa* PAM sequences (NNGRRT) (in blue). ATG indicates translation start site. (**d-e**) C2C12 myoblasts were transfected with a plasmid containing *Sa*dCas9-2xVP64 and the corresponding sgRNA(s) targeting *Lama1*, and 72 hours post-transfection, analyzed by (**d**) RT-PCR and (**e**) qRT-PCR. Single and combination of optimal sgRNAs were transfected into dy^{2j}/dy^{2j} myoblasts and Lama1 protein expression was assessed by western blot (**f**). FLAG expression serves as transfection control and used to (**g**) normalize Lama1 upregulation by densitometry analysis. Data are presented

524 as mean ± standard deviation from at least three independent experiments. Statistical
525 analysis was performed using Student's *t*-test. ***P*<0.01.

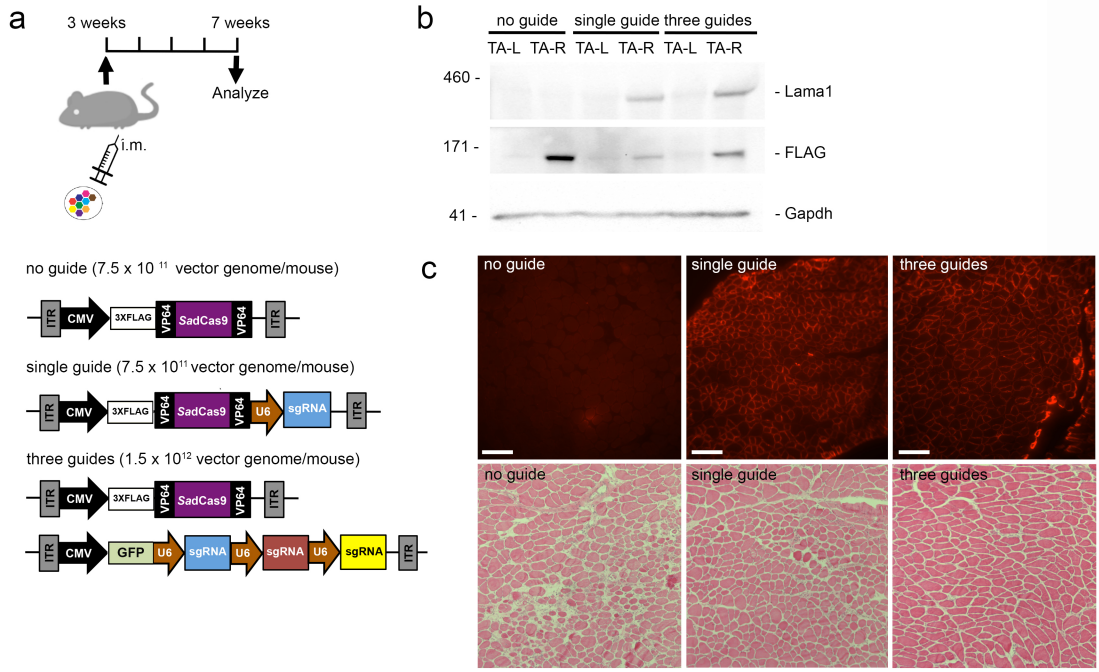


Figure 2

526

527 **Fig. 2. Upregulation of Lama1 in *tibialis anterior* (TA) muscles of dy^{2j}/dy^{2j} mice**
528 **following intramuscular administration.** (**a**) Right TA muscles of 3-week old dy^{2j}/dy^{2j}
529 mice were injected with AAV9-carrying no guide (n=4; 7.5×10^{11} viral genomes), single
530 guide (n=4; 7.5×10^{11} viral genomes) or three guides (n=4; split into two vectors, thus
531 total dose was $2 \times 7.5 \times 10^{11}$ viral genomes). ITR: Inverted Terminal Repeats. CMV and U6
532 promoters are depicted in arrows. Left TA muscles serve as control. (**b**) Western blot
533 analysis on Lama1, FLAG-tagged *Sa*dCas9, and Gapdh expression. (**c**)
534 Immunofluorescence (upper) and H&E (lower) stainings on cross-sections of right TA
535 muscles from each treatment group. Scale bar: 50 μm. Representative images from one
536 animal per treatment group are shown.

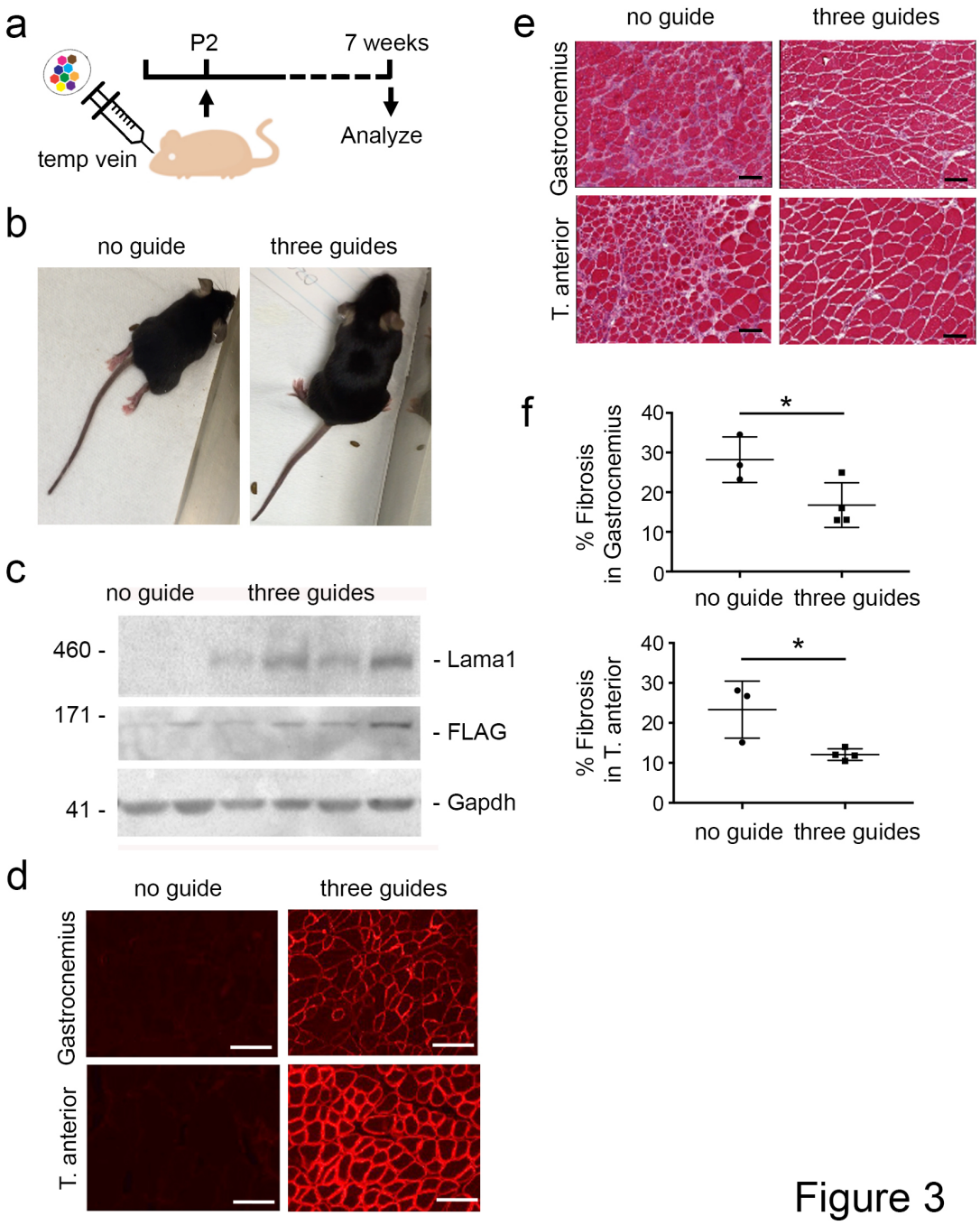
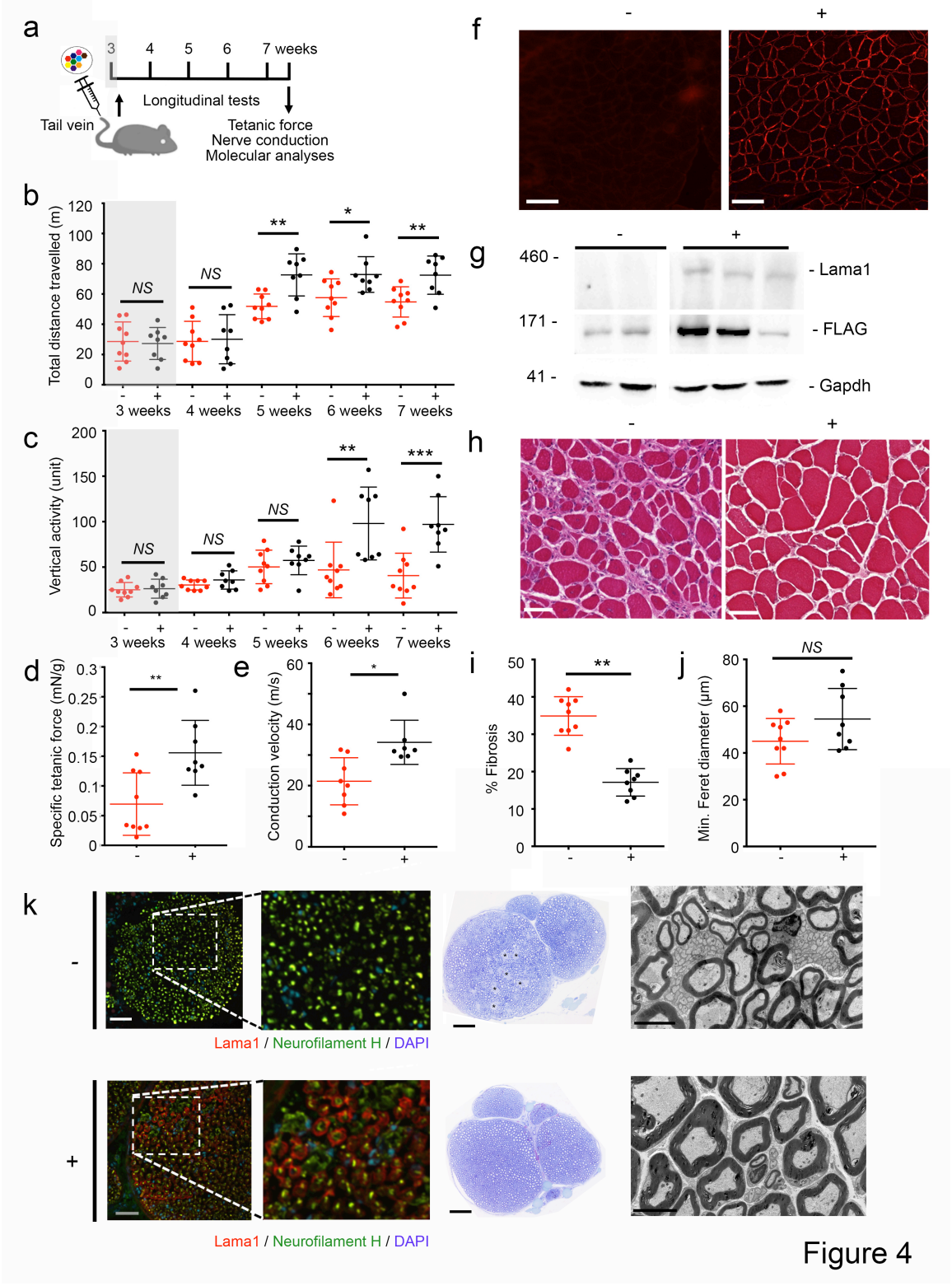


Figure 3

537

538 **Fig. 3. Early intervention to upregulate Lama1 prevents disease progression in**
539 ***dy^{2j}/dy^{2j}* mice.** (**a**) Two-day-old neonatal *dy^{2j}/dy^{2j}* mice were injected with AAV9 carrying
540 no guide (n=3; 7.5x10^{11} viral genomes) or three guides (n=4; split into two vectors, thus
541 total dose was 2x7.5x10^{11} viral genomes) via temporal vein and sacrificed 7 weeks later.
542 (**b**) Photographs of *dy^{2j}/dy^{2j}* from both treatment groups prior to sacrificing. Note the

543 difference in hindlimb contractures. Lama1 expression was analyzed by (**c**) western blot
544 and (**d**) immunofluorescence staining, and general histopathology was evaluated by (**e**)
545 H&E staining. The muscle groups analyzed are indicated on each panel, except on (**c**),
546 which shows tibialis anterior (TA) muscles. Scale bars: 100 μm (**d**), 200 μm (**e**). (**f**) The
547 percentage of fibrosis from gastrocnemius (upper) and TA (lower) muscles are
548 calculated and presented as mean ± standard deviation. Statistical analysis was
549 performed using Student's *t*-test. *$P<0.05$.
550
551



552

553 **Fig. 4. Upregulation of Lama1 in older dy^{2j}/dy^{2j} mice halts disease progression.**

554 (**a**) Three-week old *dy^{2J}/dy^{2J}* mice were injected with AAV9 carrying no guide (denoted as
555 -; n=9; 3x10^{11} viral genomes/gram) or three guides (denoted as +; n=6; split into two
556 vectors, thus total dose was 2x3x10^{11} viral genomes/gram) via tail vein. Grey box
557 represents period before treatment. (**b, c**) Open field activity assay was performed
558 weekly, before (grey-shaded) and after treatment, and the mice were tested for (**d**)
559 muscle contractile and (**e**) nerve conduction velocity at the end of the treatment regimen,
560 prior to molecular analyses of the tissues. (**f**) Immunofluorescence staining and (**g**)
561 western blot to analyze Lama1 expression and (**h**) H&E staining to quantify (**i**) fibrosis
562 and (**j**) fiber size were performed on gastrocnemius muscles. (**k**) Sciatic nerves were
563 stained for Lama1 (red) and Neurofilament H (green) (left). Nuclei were counterstained
564 by DAPI (blue). Higher magnification images from the dotted area are shown.
565 Representative toluidine blue staining (middle) and electron micrograph (right) are
566 shown. Asterisks indicate region of amyelinated axon fibers. Scale bars: 100 μm (**f**), 50
567 μm (**h**), and 200 μm (**k**). Data are presented as mean ± standard deviation. Statistical
568 analysis was performed using Student's *t*-test. *P<0.05. **P<0.01.

569

570

571 **References**

572

573 1. Dowling, J. J., H, D. G., Cohn, R. D., Campbell, C. Treating pediatric neuromuscular
574 disorders: The future is now. *American journal of medical genetics. Part A* 2017.
575 2. Gawlik, K., Miyagoe-Suzuki, Y., Ekblom, P., Takeda, S., Durbeej, M. Laminin alpha1
576 chain reduces muscular dystrophy in laminin alpha2 chain deficient mice. *Human*
577 *molecular genetics* 13:16. 2004.
578 3. Yurchenco, P. D., McKee, K. K., Reinhard, J. R., Ruegg, M. A. Laminin-deficient
579 muscular dystrophy: Molecular pathogenesis and structural repair strategies. *Matrix*
580 *biology : journal of the International Society for Matrix Biology* 2017.
581 4. Kemaladewi, D. U., Maino, E., Hyatt, E., Hou, H., Ding, M., Place, K. M., Zhu, X.,
582 Bassi, P., Baghestani, Z., Deshwar, A. G., Merico, D., Xiong, H. Y., Frey, B. J.,
583 Wilson, M. D., Ivakine, E. A., Cohn, R. D. Correction of a splicing defect in a mouse
584 model of congenital muscular dystrophy type 1A using a homology-directed-repair-
585 independent mechanism. *Nat Medicine.* 23:8. 2017.
586 5. Sunada, Y., Bernier, S. M., Utani, A., Yamada, Y., Campbell, K. P. Identification of a
587 novel mutant transcript of laminin alpha 2 chain gene responsible for muscular
588 dystrophy and dysmyelination in dy2J mice. *Human molecular genetics* 4:6. 1995.
589 6. Gawlik, K. I., Harandi, V. M., Cheong, R. Y., Petersen, A., Durbeej, M. Laminin alpha1
590 reduces muscular dystrophy in dy(2J) mice. *Matrix biology : journal of the*
591 *International Society for Matrix Biology* 2018.
592 7. Gawlik, K. I., Li, J. Y., Petersen, A., Durbeej, M. Laminin alpha1 chain improves
593 laminin alpha2 chain deficient peripheral neuropathy. *Human molecular genetics*
594 15:18. 2006.

595 8. Gawlik, K. I., Mayer, U., Blomberg, K., Sonnenberg, A., Ekblom, P., Durbeej, M.
596 Laminin alpha1 chain mediated reduction of laminin alpha2 chain deficient muscular
597 dystrophy involves integrin alpha7beta1 and dystroglycan. *FEBS letters* 580:7. 2006.
598 9. Gawlik, K. I., Akerlund, M., Carmignac, V., Elamaa, H., Durbeej, M. Distinct roles for
599 laminin globular domains in laminin alpha1 chain mediated rescue of murine laminin
600 alpha2 chain deficiency. *PloS one* 5:7. 2010.
601 10. Gawlik, K. I., Durbeej, M. Transgenic overexpression of laminin alpha1 chain in
602 laminin alpha2 chain-deficient mice rescues the disease throughout the lifespan.
603 *Muscle & nerve* 42:1. 2010.
604 11. Maeder, M. L., Linder, S. J., Cascio, V. M., Fu, Y., Ho, Q. H., Joung, J. K. CRISPR
605 RNA-guided activation of endogenous human genes. *Nature methods* 10:10. 2013.
606 12. Perez-Pinera, P., Kocak, D. D., Vockley, C. M., Adler, A. F., Kabadi, A. M., Polstein,
607 L. R., Thakore, P. I., Glass, K. A., Ousterout, D. G., Leong, K. W., Guilak, F.,
608 Crawford, G. E., Reddy, T. E., Gersbach, C. A. RNA-guided gene activation by
609 CRISPR-Cas9-based transcription factors. *Nature methods* 10:10. 2013.
610 13. Gonzalez, S., Fernando, R. N., Perrin-Tricaud, C., Tricaud, N. In vivo introduction of
611 transgenes into mouse sciatic nerve cells in situ using viral vectors. *Nature protocols*
612 9:5. 2014.
613 14. Wojtal, D., Kemaladewi, D. U., Malam, Z., Abdullah, S., Wong, T. W., Hyatt, E.,
614 Baghestani, Z., Pereira, S., Stavropoulos, J., Mouly, V., Mamchaoui, K., Muntoni, F.,
615 Voit, T., Gonorazky, H. D., Dowling, J. J., Wilson, M. D., Mendoza-Londono, R.,
616 Ivakine, E. A., Cohn, R. D. Spell Checking Nature: Versatility of CRISPR/Cas9 for
617 Developing Treatments for Inherited Disorders. *Am J Hum Genet* 98:1. 2016.
618 15. Ran, F. A., Cong, L., Yan, W. X., Scott, D. A., Gootenberg, J. S., Kriz, A. J., Zetsche,
619 B., Shalem, O., Wu, X., Makarova, K. S., Koonin, E. V., Sharp, P. A., Zhang, F. In
620 vivo genome editing using Staphylococcus aureus Cas9. *Nature* 520:7546. 2015.
621 16. Esvelt, K. M., Mali, P., Braff, J. L., Moosburner, M., Yaung, S. J., Church, G. M.
622 Orthogonal Cas9 proteins for RNA-guided gene regulation and editing. *Nature*
623 *methods* 10:11. 2013.
624 17. Qi, L. S., Larson, M. H., Gilbert, L. A., Doudna, J. A., Weissman, J. S., Arkin, A. P.,
625 Lim, W. A. Repurposing CRISPR as an RNA-guided platform for sequence-specific
626 control of gene expression. *Cell* 152:5. 2013.
627 18. Liao, H. K., Hatanaka, F., Araoka, T., Reddy, P., Wu, M. Z., Sui, Y., Yamauchi, T.,
628 Sakurai, M., O'Keefe, D. D., Nunez-Delicado, E., Guillen, P., Campistol, J. M., Wu, C.
629 J., Lu, L. F., Esteban, C. R., Izpisua Belmonte, J. C. In Vivo Target Gene Activation
630 via CRISPR/Cas9-Mediated Trans-epigenetic Modulation. *Cell* 171:7. 2017.
631 19. Pasteuning-Vuhman, S., Putker, K., Tanganyika-de Winter, C. L., Boertje-van der
632 Meulen, J. W., van Vliet, L., Overzier, M., Plomp, J. J., Aartsma-Rus, A., van Putten,
633 M. Natural disease history of the dy2J mouse model of laminin alpha2 (merosin)-
634 deficient congenital muscular dystrophy. *PloS one* 13:5. 2018.
635 20. Kemaladewi, D. U., Benjamin, J., Hyatt, E., Ivakine, E. A., Cohn, R. D. Increased
636 polyamine as protective disease modifier in Congenital Muscular Dystrophy. *Human*
637 *molecular genetics* 2018.
638 21. Bonnemann, C. G., Wang, C. H., Quijano-Roy, S., Deconinck, N., Bertini, E.,
639 Ferreiro, A., Muntoni, F., Sewry, C., Beroud, C., Mathews, K. D., Moore, S. A., Bellini,
640 J., Rutkowski, A., North, K. N., Members of International Standard of Care Committee
641 for Congenital Muscular, D. Diagnostic approach to the congenital muscular
642 dystrophies. *Neuromuscular disorders : NMD* 24:4. 2014.
643 22. Qiao, C., Li, J., Zhu, T., Draviam, R., Watkins, S., Ye, X., Chen, C., Li, J., Xiao, X.
644 Amelioration of laminin-alpha2-deficient congenital muscular dystrophy by somatic

645 gene transfer of miniagrin. *Proceedings of the National Academy of Sciences of the*
646 *United States of America* 102:34. 2005.
647 23. Bentzinger, C. F., Barzaghi, P., Lin, S., Ruegg, M. A. Overexpression of mini-agrin in
648 skeletal muscle increases muscle integrity and regenerative capacity in laminin-
649 alpha2-deficient mice. *FASEB journal : official publication of the Federation of*
650 *American Societies for Experimental Biology* 19:8. 2005.
651 24. Qiao, C., Dai, Y., Nikolova, V. D., Jin, Q., Li, J., Xiao, B., Li, J., Moy, S. S., Xiao, X.
652 Amelioration of Muscle and Nerve Pathology in LAMA2 Muscular Dystrophy by AAV9-
653 Mini-Agrin. *Molecular Therapy* 9:2018.
654 25. Meinen, S., Barzaghi, P., Lin, S., Lochmuller, H., Ruegg, M. A. Linker molecules
655 between laminins and dystroglycan ameliorate laminin-alpha2-deficient muscular
656 dystrophy at all disease stages. *The Journal of cell biology* 176:7. 2007.
657 26. Reinhard, J. R., Lin, S., McKee, K. K., Meinen, S., Crosson, S. C., Sury, M., Hobbs,
658 S., Maier, G., Yurchenco, P. D., Ruegg, M. A. Linker proteins restore basement
659 membrane and correct LAMA2-related muscular dystrophy in mice. *Science*
660 *translational medicine* 9:396. 2017.
661 27. McKee, K. K., Crosson, S. C., Meinen, S., Reinhard, J. R., Ruegg, M. A., Yurchenco,
662 P. D. Chimeric protein repair of laminin polymerization ameliorates muscular
663 dystrophy phenotype. *The Journal of clinical investigation* 127:3. 2017.
664 28. Hightower, R. M., Alexander, M. S. Genetic modifiers of Duchenne and
665 facioscapulohumeral muscular dystrophies. *Muscle & nerve* 57:1. 2018.
666 29. Rooney, J. E., Gurpur, P. B., Burkin, D. J. Laminin-111 protein therapy prevents
667 muscle disease in the mdx mouse model for Duchenne muscular dystrophy.
668 *Proceedings of the National Academy of Sciences of the United States of America*
669 106:19. 2009.
670 30. Perrin, A., Rousseau, J., Tremblay, J. P. Increased Expression of Laminin Subunit
671 Alpha 1 Chain by dCas9-VP160. *Molecular therapy. Nucleic acids* 6:2017.
672 31. Yuan, J., Ma, Y., Huang, T., Chen, Y., Peng, Y., Li, B., Li, J., Zhang, Y., Song, B.,
673 Sun, X., Ding, Q., Song, Y., Chang, X. Genetic Modulation of RNA Splicing with a
674 CRISPR-Guided Cytidine Deaminase. *Molecular cell* 72:2. 2018.
675 32. Villiger, L., Grisch-Chan, H. M., Lindsay, H., Ringnalda, F., Pogliano, C. B., Allegri,
676 G., Fingerhut, R., Haberle, J., Matos, J., Robinson, M. D., Thony, B., Schwank, G.
677 Treatment of a metabolic liver disease by in vivo genome base editing in adult mice.
678 *Nature medicine* 24:10. 2018.
679 33. Bengtsson, N. E., Hall, J. K., Odom, G. L., Phelps, M. P., Andrus, C. R., Hawkins, R.
680 D., Hauschka, S. D., Chamberlain, J. R., Chamberlain, J. S. Muscle-specific
681 CRISPR/Cas9 dystrophin gene editing ameliorates pathophysiology in a mouse
682 model for Duchenne muscular dystrophy. *Nature communications* 8:2017.
683 34. Nelson, C. E., Hakim, C. H., Ousterout, D. G., Thakore, P. I., Moreb, E. A., Rivera,
684 R. M., Madhavan, S., Pan, X., Ran, F. A., Yan, W. X., Asokan, A., Zhang, F., Duan,
685 D., Gersbach, C. A. In vivo genome editing improves muscle function in a mouse
686 model of Duchenne muscular dystrophy. *Science* 2015.
687 35. Tabebordbar, M., Zhu, K., Cheng, J. K., Chew, W. L., Widrick, J. J., Yan, W. X.,
688 Maesner, C., Wu, E. Y., Xiao, R., Ran, F. A., Cong, L., Zhang, F., Vandenberghe, L.
689 H., Church, G. M., Wagers, A. J. In vivo gene editing in dystrophic mouse muscle and
690 muscle stem cells. *Science* 2015.
691 36. Long, C., Amoasii, L., Mireault, A. A., McAnally, J. R., Li, H., Sanchez-Ortiz, E.,
692 Bhattacharyya, S., Shelton, J. M., Bassel-Duby, R., Olson, E. N. Postnatal genome
693 editing partially restores dystrophin expression in a mouse model of muscular
694 dystrophy. *Science* 2015.

37. Thakore, P. I., D'Ippolito, A. M., Song, L., Safi, A., Shivakumar, N. K., Kabadi, A. M., Reddy, T. E., Crawford, G. E., Gersbach, C. A. Highly specific epigenome editing by CRISPR-Cas9 repressors for silencing of distal regulatory elements. *Nature methods* 12:12. 2015.
38. Lamar, K. M., Bogdanovich, S., Gardner, B. B., Gao, Q. Q., Miller, T., Earley, J. U., Hadhazy, M., Vo, A. H., Wren, L., Molkentin, J. D., McNally, E. M. Overexpression of Latent TGFbeta Binding Protein 4 in Muscle Ameliorates Muscular Dystrophy through Myostatin and TGFbeta. *PLoS genetics* 12:5. 2016.
39. Quattrocelli, M., Capote, J., Ohiri, J. C., Warner, J. L., Vo, A. H., Earley, J. U., Hadhazy, M., Demonbreun, A. R., Spencer, M. J., McNally, E. M. Genetic modifiers of muscular dystrophy act on sarcolemmal resealing and recovery from injury. *PLoS genetics* 13:10. 2017.
40. Kemaladewi, D. U., de Gorter, D. J., Aartsma-Rus, A., van Ommen, G. J., ten Dijke, P., t Hoen, P. A., Hoogaars, W. M. Cell-type specific regulation of myostatin signaling. *FASEB journal : official publication of the Federation of American Societies for Experimental Biology* 26:4. 2012.
41. Zhang, Y., Argaw, A. T., Gurfein, B. T., Zameer, A., Snyder, B. J., Ge, C., Lu, Q. R., Rowitch, D. H., Raine, C. S., Brosnan, C. F., John, G. R. Notch1 signaling plays a role in regulating precursor differentiation during CNS remyelination. *Proceedings of the National Academy of Sciences of the United States of America* 106:45. 2009.
42. Hakim, C. H., Wasala, N. B., Pan, X., Kodippili, K., Yue, Y., Zhang, K., Yao, G., Haffner, B., Duan, S. X., Ramos, J., Schneider, J. S., Yang, N. N., Chamberlain, J. S., Duan, D. A Five-Repeat Micro-Dystrophin Gene Ameliorated Dystrophic Phenotype in the Severe DBA/2J-mdx Model of Duchenne Muscular Dystrophy. *Molecular therapy. Methods & clinical development* 6:2017.
43. Kim, D., Langmead, B., Salzberg, S. L. HISAT: a fast spliced aligner with low memory requirements. *Nature methods* 12:4. 2015.
44. Anders, S., Pyl, P. T., Huber, W. HTSeq--a Python framework to work with high-throughput sequencing data. *Bioinformatics* 31:2. 2015.
45. Ritchie, M. E., Phipson, B., Wu, D., Hu, Y., Law, C. W., Shi, W., Smyth, G. K. limma powers differential expression analyses for RNA-sequencing and microarray studies. *Nucleic acids research* 43:7. 2015.
46. Bae, S., Park, J., Kim, J. S. Cas-OFFinder: a fast and versatile algorithm that searches for potential off-target sites of Cas9 RNA-guided endonucleases. *Bioinformatics* 30:10. 2014.

Extended data/supplementary figures

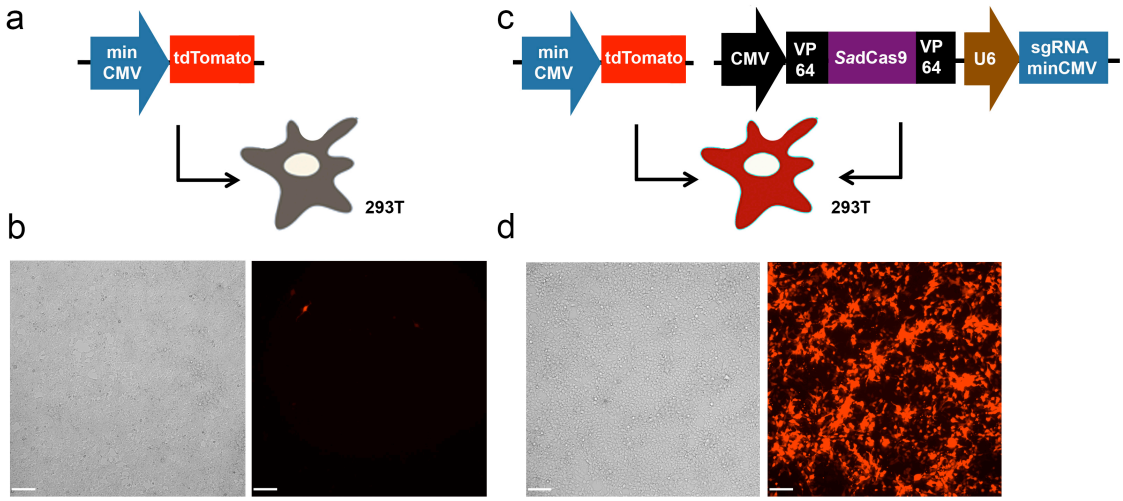


Figure S1

Fig. S1. ***Sa*dCas9-2xVP64 enhances expression of minCMV-driven *tdTomato in vitro*.** HEK293T was transfected with (**a**,**b**) a plasmid containing minCMV-driven *tdTomato* gene only, or (**c**,**d**) in combination with a plasmid containing *Sa*dCas9-2xVP64 and a sgRNA targeting the minCMV promoter. (**b**,**d**) Cells were imaged for *tdTomato* expression by fluorescent microscopy. Scale bar: 50 μm.

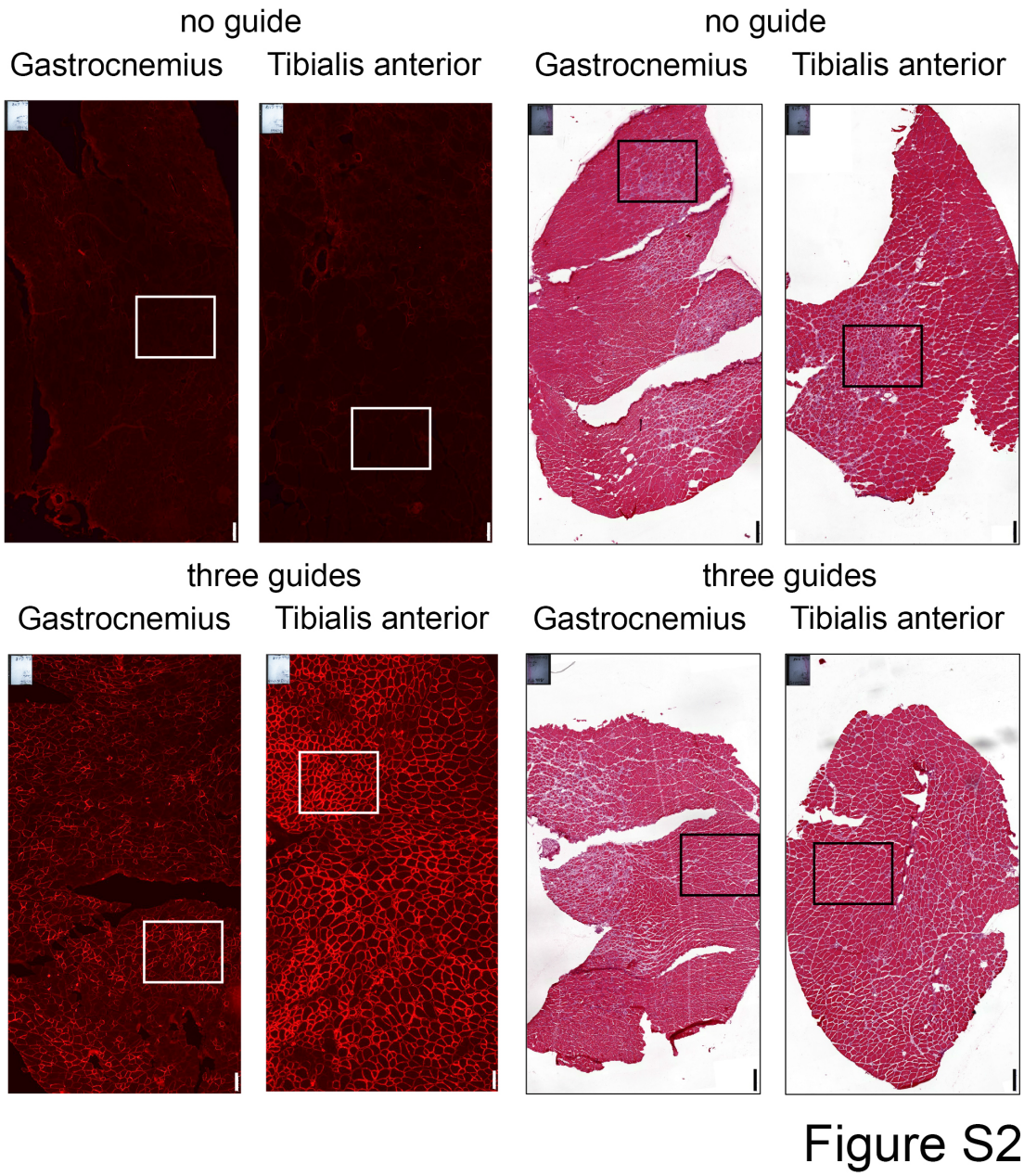


Fig. S2. Expression of Lama1 and muscle architecture following early intervention in neonatal *dy^{2j}/dy^{2j}* mice. Lower magnification of immunofluorescence and H&E staining images of Fig. 3 in the main manuscript.

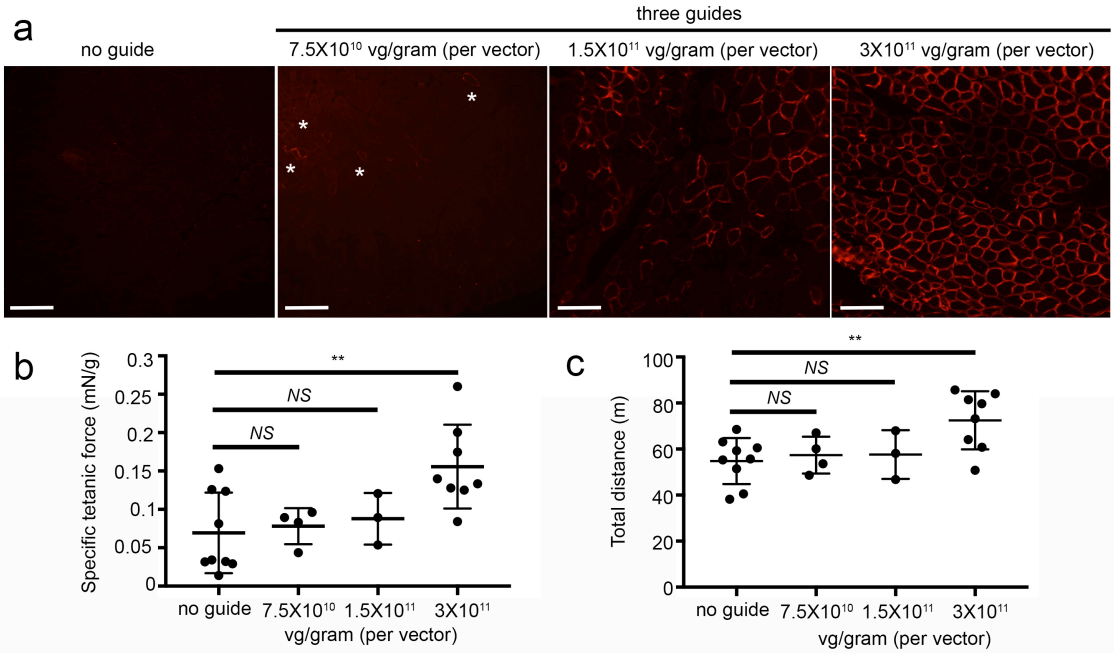


Figure S3

Fig. S3. Upregulation of Lama1 corresponds to improvement of muscle functions. Three-weeks old dy^{2j}/dy^{2j} mice were injected systemically via tail vein with different doses of AAV9: $7.5x10^{10}$, $1.5x10^{11}$, or $3x10^{11}$ viral genome (vg)/gram of mouse. Two AAVs were necessary for the three guide cohort, therefore the total doses of virus injected was $1.5x10^{11}$, $3x10^{11}$, and $6x10^{11}$ viral genomes/gram of mouse. TA muscles isolated four weeks later were stained for Lama1 expression (**a**). Asterisks indicate Lama1-positive fibers in the low dose cohort. Scale bar: 100 µm. *In vivo* contractile force assay (**b**) and open field test (**c**) performed in the end of the treatment regimen. Data are presented as average ± standard deviation. Statistical analysis was performed using one-way ANOVA. *NS:* not significant. $^{**}P<0.01$.

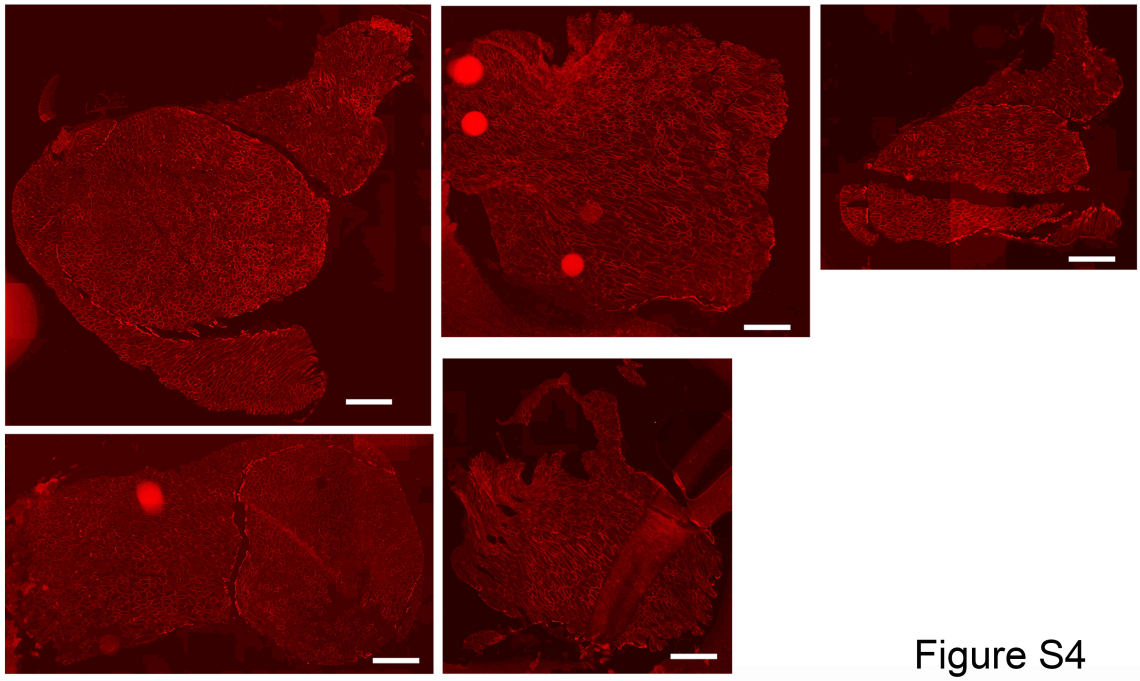


Fig. S4. Representative images of Lama1-positive muscle sections

Mice were injected systemically with three guides at the age of three weeks old via tail vein, and sacrificed at the age of 11-12 weeks old. Muscles were stained for Lama1 expression (red). Scale bar: 500 μm.

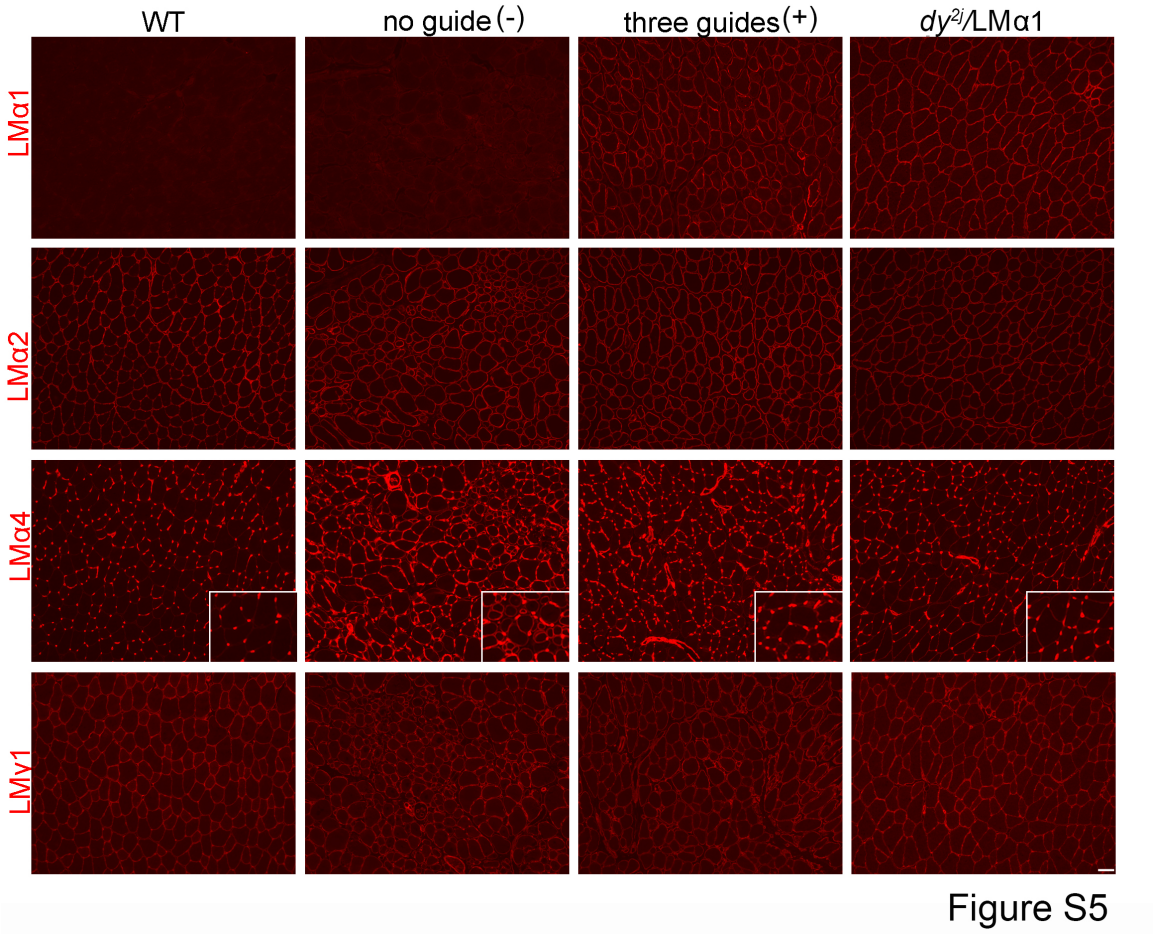


Fig. S5. Expression of Laminin (LM) subunits in tibialis anterior muscles. Expression of LM subunits in tibialis anterior from wild-type, dy^{2j}/dy^{2j} (intravenously injected with AAV carrying no guide or three guides) and dy^{2j}/LMα1 (with transgenic overexpression of LMα1) mice (n=3 for each group). Expression of LMα1 chain in tibialis anterior is comparable between dy^{2j}/dy^{2j} AAV-three guide-treated mice and transgenic mice. No major differences in expression of LMα2 and LMγ1 were detected between the groups. LMα4 chain is upregulated in muscle from dy^{2j}/dy^{2j} AAV-no guide-treated mice and its expression is partially normalized in muscle from dy^{2j}/dy^{2j} AAV-three guide treated mice. Scale bar: 50μm.

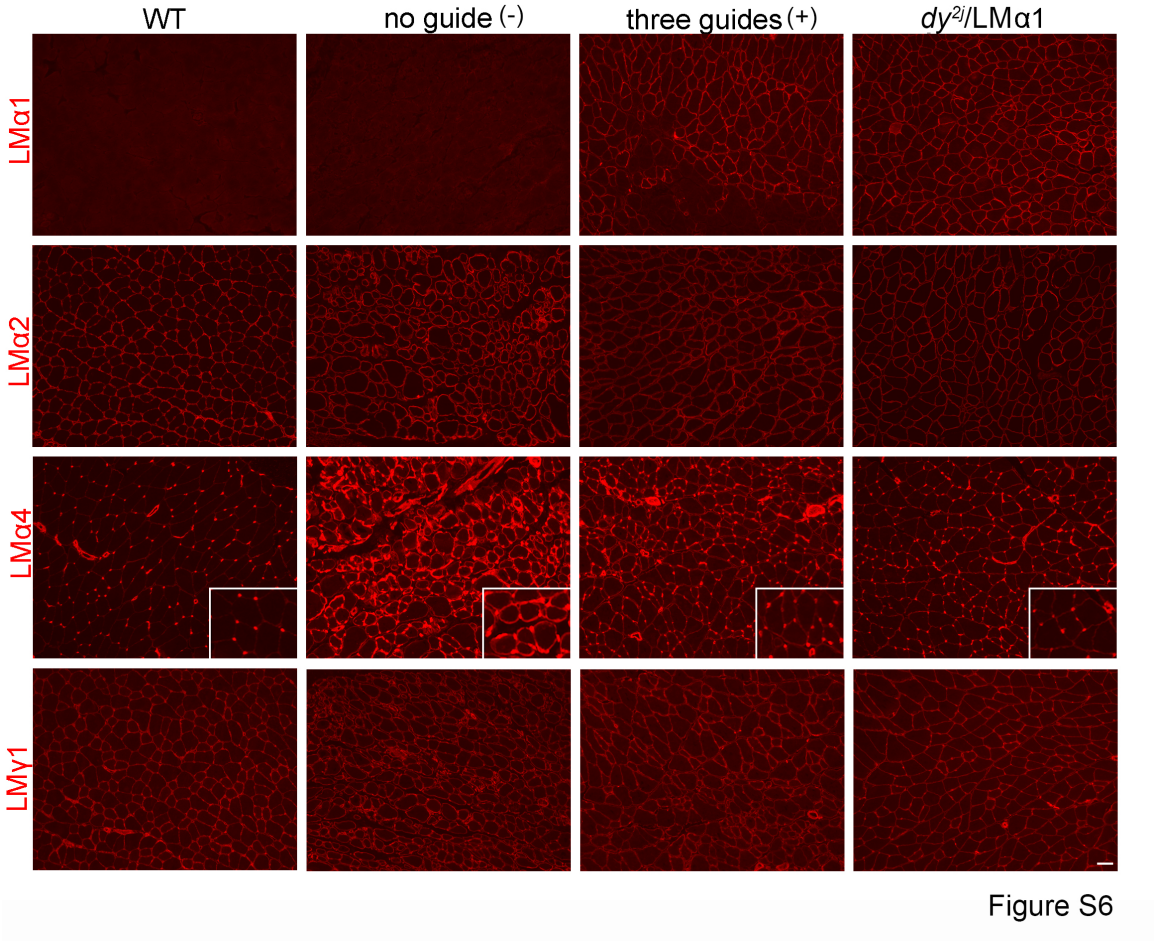


Fig. S6. Expression of Laminin (LM) subunits in gastrocnemius muscles.

Expression of LM subunits in tibialis anterior from wild-type, dy^{2j}/dy^{2j} (intravenously injected with AAV carrying no guide or three guides) and dy^{2j}/LMα1 (with transgenic overexpression of LMα1) mice (n=3 for each group). Expression of LMα1 chain in tibialis anterior is comparable between dy^{2j}/dy^{2j} AAV-three guide-treated mice and transgenic mice. No major differences in expression of LMα2 and LMγ1 were detected between the groups. LMα4 chain is upregulated in muscle from dy^{2j}/dy^{2j} AAV-no guide-treated mice and its expression is partially normalized in muscle from dy^{2j}/dy^{2j} AAV-three guide treated mice. Scale bar: 50μm.

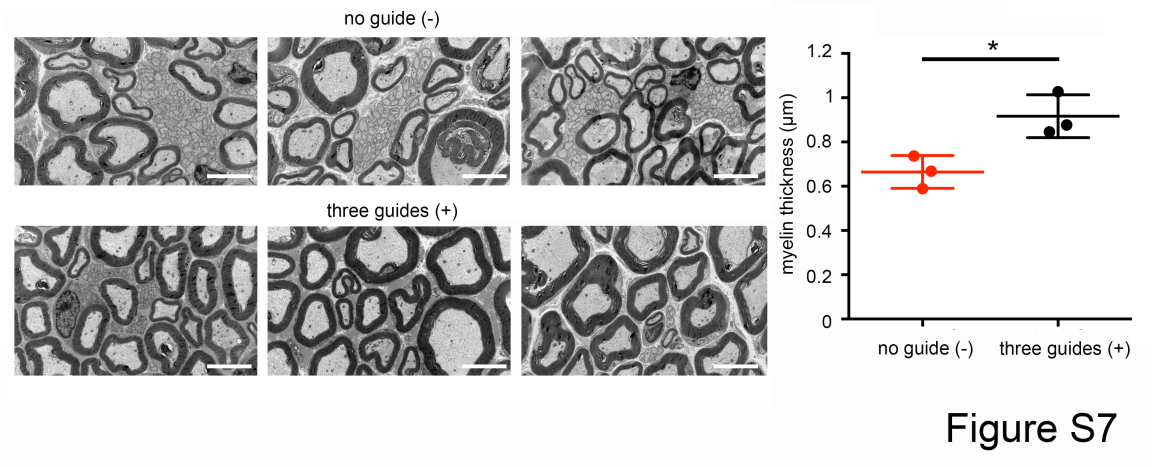


Fig. S7. Myelination of sciatic nerves.

Electron microscopy images of sciatic nerves isolated from dy^{2j}/dy^{2j} mice injected with AAV carrying no guide or three guides (n=3 for each group). Myelin thickness was quantified using ImageJ and presented as average ± standard deviation. Statistical analysis was performed using Student's *t*-test. $^{*}P<0.05$. Scale bar: 5 μm.

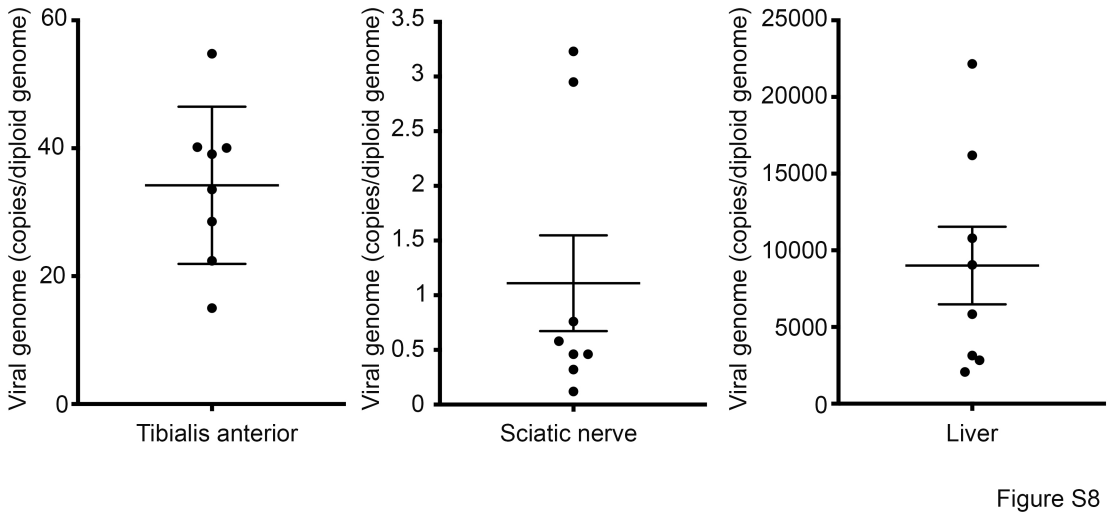


Fig. S8. Quantitative evaluation of AAV genome distribution.

Genomic DNA isolated from tibialis anterior muscle, sciatic nerve and liver of dy2j mice injected with AAV carrying three guides (n=8) was amplified for the presence of viral genome by qPCR. Data are presented as average ± SEM.

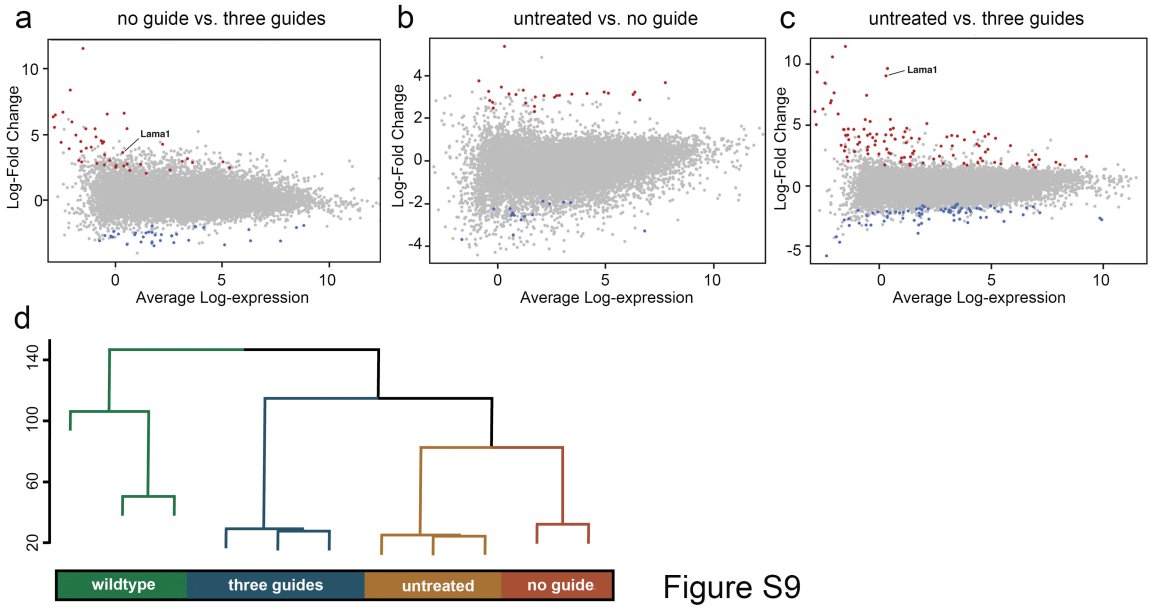


Figure S9

Fig. S9. Genome-wide analysis of gene expression of *Sa*dCas9-VP64-treated *dy^{2j}/dy^{2j}* mice.

Differential expression analysis derived from RNA-Sequencing results from the quadriceps of treated and untreated mice (**a-c**), comparing SadCas9-2xVP64 alone and SadCas9-2xVP64 with three guides targeting Lama1 (**a**), untreated to SadCas9-2xVP64 alone (**b**), and untreated to SadCas9-2xVP64 with three guides targeting Lama1 (**c**). Gene significantly differentially expressed, (FDR < 0.05), are coloured. Red data points indicate a log-fold change greater than one, while blue data points indicate a log-fold change less than one. Hierarchical clustering was performed on the normalized counts-per-million expression data (**d**).

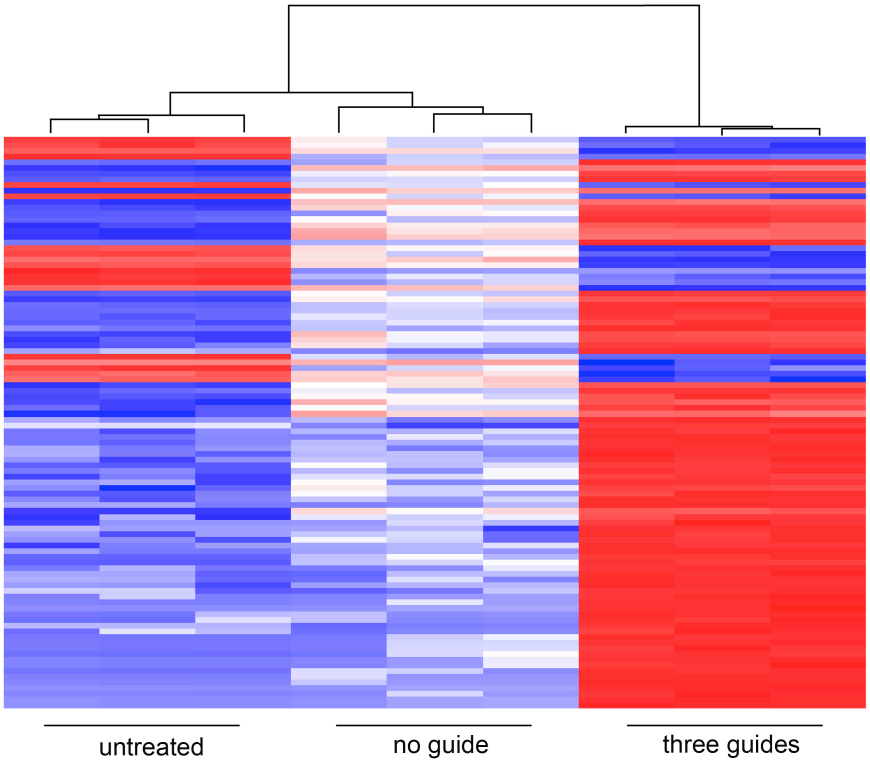


Figure S10

Fig. S10. Top 100 differentially expressed genes.

Heatmap illustrating normalized log-CPM values for the top 100 genes differentially expressed in SadCas9-2xVP64 with three guide treated quadriceps versus untreated quadriceps. Red indicates higher expression while blue indicates lower expression.

Start 3X FLAG

M - DYKDHDGDYKDHDIDYKDDDDK - HGPRA -

VP64

DALDDFDLDMLGSDALDDFDLDMLGSDALDDFDLDMLGSDALDDFDLDM -

NLS

VN - PKKKRKV - GIHGVPAA -

D10A

SadCas9

KRNYILGLA*IGITSVGYGIIDYETRDVIDAGVRLFKEANVENNEGRRSKRGARRL

KRRRRHRIQRVKKLLFDYNLLTDHSELSGINPYEARVKGLSQKLSEEEFSAALLHLAK

RRGVHNVNEVEEDTGNELSTKEQISRNSKALEEKYVAELQLERLKKDGEVRGSINRF

KTSDYVKEAKQLLKVQKAYHQLDQSFIDTYIDLLETRRTYYEGPGEGSPFGWKDIKE

WYEMLMGHCTYFPEELRSVKYAYNADLYNALNDLNNLVITRDENEKLEYYEKFQIIEN

VFKQKKKPTLKQIAKEILVNEEDIKGYRVTSTGKPEFTNLKVYHDIKDITARKEIIENAEL

LDQIAKILTIYQSSEDIQEELTNLNSELTQEEIEQISNLKGYTGTHNLSLKAINLILDELWH

TNDNQIAIFNRLKLVPKKVDLSQQKEIPTTLVDDFILSPVVKRSFIQSIKVINAIIKKYGLP

NDIIIELAREKNSKDAQKMINEMQKRNRQTNERIEEIIRTTGKENAKYLIEKIKLHDMQE

N580A

GKCLYSLEAIPLEDLLNNPFNYEVDHIIPRSVSFDNSFNNKVLVKQEEA*SKKGNRTPF

QYLSSSDSKISYETFKKHILNLAKGKGRISKTKKEYLLEERDINRFSVQKDFINRNLVDT

RYATRGLMNLLRSYFRVNNLDVKVKSINGGFTSFLRRKWKFKKERNKGYKHHAEDA

LIIANADFIFKEWKKLDKAKKVMENQMFEEKQAESMPEIETEQEYKEIFITPHQIKHIKD

FKDYKYSHRVDKKPNRELINDTLYSTRKDDKGNTLIVNNLNGLYDKDNDKLKKLINKS

PEKLLMYHHDPQTYQKLKLIMEQYGDEKNPLYKYYEETGNYLTKYSKKDNGPVIKKIK

YYGNKLNAHLDITDDYPNSRNKVVKLSLKPYRFDVYLDNGVYKFVTVKNLDVIKKENY

YEVNSKCYEEAKKLKKISNQAEFIASFYNNDLIKINGELYRVIGVNNDLLNRIEVNMIDIT

YREYLENMNDKRPPRIIKTIASKTQSIKKYSTDILGNLYEVKSKKHPQIIKKG -

NLS

KRPAATKKAGQAKKKK - GS -

VP64

DALDDFDLDMLGSDALDDFDLDMLGSDALDDFDLDMLGSDALD DFDLDML

Fig. S11. Protein encoded in the *Sa*dCas9-VP64 transcriptional activator plasmid. Different domains are annotated accordingly. Amino acids encoding *Sa*dCas9 are in bold and italic, and the mutated residues D10A and N580A are indicated in red asterisk (*). NLS: Nuclear localization signal.

Supplemental video legends

Video S1. Phenotype of control *dy^{2j}/dy^{2j}* mouse following early intervention.

The *dy^{2j}/dy^{2j}* mouse was injected with AAV9 containing *Sa*dCas9-2xVP64 (no guide) at P2 (pre-symptomatic stage) via temporal vein and video was taken at the age of 7-week old. Hind limb paralysis, contracture and kyphosis resulting from lack of functional *Lama2* and compensatory *Lama1* are apparent.

Video S2. Phenotype of treated *dy^{2j}/dy^{2j}* mouse following early intervention.

The *dy^{2j}/dy^{2j}* mouse was injected with AAV9 containing *Sa*dCas9-2xVP64 and sgRNAs targeting *Lama1* proximal promoter (three guides) at P2 (pre-symptomatic stage) via temporal vein and video was taken at the age of 7-week old. Upregulation of compensatory *Lama1* expression ameliorates the hind limb paralysis, contracture and kyphosis.

Video S3. Phenotype of control *dy^{2j}/dy^{2j}* mouse following intervention at symptomatic stage.

The *dy^{2j}/dy^{2j}* mouse was injected with AAV9 containing *Sa*dCas9-2xVP64 (no guide) at 3-week old (pre-symptomatic stage) via tail vein. Video was taken at the age of 7-week old. Hind limb paralysis, contracture and kyphosis resulting from lack of functional *Lama2* and compensatory *Lama1* are apparent.

Video S4. Phenotype of treated *dy^{2j}/dy^{2j}* mouse following intervention at symptomatic stage.

The *dy^{2j}/dy^{2j}* mouse was injected with AAV9 containing *Sa*dCas9-2xVP64 and sgRNAs targeting *Lama1* proximal promoter (three guides) at 3-week old (pre-symptomatic stage) via tail vein. Video was taken at the age of 7-week old. Dystrophic features and disease progression were significantly improved and partially reversed following upregulation of *Lama1*.

Supplemental tables

Supplemental table 1. Top 100 genes differentially expressed in “SadCas9-2xVP64 + three guides” compared to “untreated”

Supplemental table 2. Top 100 genes differentially expressed in “SadCas9-2xVP64 + three guides” compared to “SadCas9-2xVP64 + no guide”

Supplemental table 3. Top 100 genes differentially expressed in “SadCas9-2xVP64 + no guide” compared to “untreated”

Supplemental table 4. Analysis showing distance from off-target site to differentially expressed gene body

Supplemental table 5. List of computationally predicted off-target sites

Supplemental table 6. Primers, plasmids and sgRNAs used in this study

Supplemental Table 1. Top 100 genes differentially expressed in "SadCas9-2xVP64 + three guides" compared to "untreated"

SYMBOL	TXCHROM	logFC	AveExpr	t	P.Value	adj.P.Val
Ces1c	chr8	8.06720501	-4.0858727	25.0852651	7.60E-11	1.10E-06
1810053B23	chr16	10.5369617	-2.0993569	17.6475033	2.81E-09	6.76E-06
Fabp1	chr6	7.92790193	-3.3988185	18.7401814	1.44E-09	6.76E-06
1700003G13	chr9	7.85466761	-3.8132313	17.9773962	2.19E-09	6.76E-06
Cyp2c69	chr19	6.79884139	-4.4022125	17.5155103	2.77E-09	6.76E-06
Slc7a4	chr16	5.42020681	0.54904376	17.737618	2.38E-09	6.76E-06
Ttr	chr18	8.97781797	-3.6645933	17.0207698	3.88E-09	7.51E-06
Apoa2	chr1	5.40091384	-0.6005275	16.7716387	4.16E-09	7.51E-06
Lama1	chr17	8.98321051	0.34708087	15.7290019	8.52E-09	1.37E-05
Apob	chr12	7.80234986	-3.4299405	15.0813327	1.26E-08	1.82E-05
Tat	chr8	5.3144494	-3.9814489	14.66332	1.58E-08	2.07E-05
Serpina1c	chr12	8.1709174	-3.2361681	14.3754788	2.04E-08	2.27E-05
Fam25c	chr14	7.39071119	-0.5378939	14.4492017	1.90E-08	2.27E-05
Serpina3k	chr12	9.29387622	-2.7989697	13.9984407	2.72E-08	2.81E-05
Igfbp1	chr11	6.69308056	-4.2970164	13.6072358	3.38E-08	3.26E-05
Mup3	chr4	7.59035385	-2.0248159	13.5095555	3.70E-08	3.35E-05
Rdh7	chr10	6.12757345	-4.306269	12.9783192	5.31E-08	4.07E-05
Gys2	chr6	4.5777154	-1.5679355	13.0234776	5.00E-08	4.07E-05
Wnt4	chr4	4.20831956	5.03311767	12.9293649	5.35E-08	4.07E-05
Gc	chr5	8.24180382	-3.5843802	12.9381073	5.75E-08	4.07E-05
Klrg2	chr6	4.59908759	-1.1223193	12.8010591	5.92E-08	4.07E-05
Srrm4os	chr5	4.04588484	3.61138985	12.4826437	7.52E-08	4.94E-05
Mat1a	chr14	7.36113899	-3.7343781	12.3707009	8.71E-08	5.47E-05
Alb	chr5	9.586285	0.41592462	12.2174291	1.04E-07	6.01E-05
Serpina1a	chr12	6.95305368	-3.6425688	12.1347225	1.04E-07	6.01E-05
Azgp1	chr5	6.86136461	-4.0619138	11.9945852	1.16E-07	6.46E-05
Fgb	chr3	7.48821994	-3.1735567	11.6312338	1.59E-07	8.50E-05
Cidea	chr18	5.07510399	2.21493926	11.4830743	1.71E-07	8.82E-05
9030619P08	chr15	3.92341807	-0.2600478	11.3463138	1.89E-07	9.42E-05
Fgg	chr3	7.33395248	-3.4152783	11.1329778	2.41E-07	0.00011613
Mmd2	chr5	6.67105341	-3.3145461	11.0364562	2.58E-07	0.00012028
Cyp3a11	chr5	8.17360921	-3.6630995	10.8836274	3.06E-07	0.00013811
Slc27a2	chr2	6.6827	-3.1819203	10.7687412	3.26E-07	0.00014295
Ambp	chr4	6.13758126	-3.4506026	10.6633966	3.54E-07	0.00015057
Fga	chr3	7.62720297	-3.9076478	10.5588289	4.03E-07	0.00016636
Samd11	chr4	4.11178696	-0.4979967	10.4245456	4.25E-07	0.00017075
Fabp4	chr3	2.15462805	9.01447477	10.3115148	4.68E-07	0.00018279
Ighg1	chr12	8.46471745	-3.4389537	10.3557091	4.95E-07	0.00018754
Lctl	chr9	4.2237416	-0.3808795	10.2088981	5.19E-07	0.00018754
Pvalb	chr15	2.52928689	12.8626777	10.2161746	5.11E-07	0.00018754
Apoa5	chr9	6.60004476	-4.1263676	10.219239	5.36E-07	0.00018765
Vps13c	chr9	-2.1668504	3.212495	-10.146085	5.45E-07	0.00018765
Gm4841	chr18	3.86778458	5.35415478	9.78492273	7.72E-07	0.00025932
Prkar2b	chr12	3.97928004	3.13121334	9.7483776	8.00E-07	0.00026274
Pdpr	chr8	-2.203443	3.29044627	-9.4808172	1.03E-06	0.00033107
Hhipl1	chr12	-2.7573871	2.31203806	-9.4137394	1.10E-06	0.00034623
Epn3	chr11	4.58955952	-1.5891827	9.3486758	1.19E-06	0.00036635
Aldh1a7	chr19	3.50528717	1.27190747	9.26652168	1.28E-06	0.00038529
Apoa1	chr9	8.39321713	-2.4434213	9.24069066	1.44E-06	0.00042593
Aspg	chr12	4.61360624	-0.6564861	9.09955804	1.53E-06	0.00044273
Adgrd1	chr5	-2.427791	3.44722048	-8.9858424	1.70E-06	0.00048062
Kng1	chr16	5.95942358	-3.7065193	8.99480646	1.75E-06	0.00048561
Ucp1	chr8	11.3963873	-1.5055582	9.07259957	1.85E-06	0.000504
Cps1	chr1	5.87067733	-3.3848414	8.82056311	2.09E-06	0.00055915
Sfrp4	chr13	-3.0424407	4.08490344	-8.7250934	2.23E-06	0.00058511
Jmjd1c	chr10	-3.2313535	1.84643433	-8.5191608	2.77E-06	0.00071562
Orm2	chr4	6.27368915	-2.5305119	8.54126641	2.83E-06	0.00071836
Atp6v1g1	chr4	1.90407218	8.11437097	8.46629447	2.93E-06	0.00072976
NA	NA	3.54327015	-0.8576183	8.37633903	3.24E-06	0.00079375
Elovl6	chr3	3.24419618	3.37792107	8.22580012	3.81E-06	0.0009186
Plg	chr17	4.98742747	-2.84041	8.16368792	4.16E-06	0.00098659
Pzp	chr6	6.39214719	-3.2228911	8.11448596	4.53E-06	0.00105615
Thrsp	chr7	3.26554164	6.03631914	7.85593444	5.77E-06	0.00131835
Gfpt2	chr11	-2.0366124	3.28844052	-7.8437333	5.84E-06	0.00131835
Bhmt	chr13	6.2546489	-3.2262881	7.78687551	6.55E-06	0.00145525
Apoc3	chr9	6.95422106	-2.1511746	7.78192704	6.70E-06	0.00146687
Proca1	chr11	2.63255929	1.56171029	7.68968505	6.97E-06	0.00150381
Hpd	chr5	6.45914605	-3.386459	7.69200292	7.34E-06	0.00156002
Pcsk6	chr7	-1.8922339	4.14311915	-7.6077764	7.67E-06	0.00160525
Dnajb13	chr7	5.86226504	-1.8392095	7.50871687	8.97E-06	0.0018516
NA	NA	-2.8570014	1.63865163	-7.4503139	9.23E-06	0.00187895
Myo5b	chr18	2.30425852	1.18853647	7.43398437	9.40E-06	0.00188746
Fam213b	chr4	2.52777314	7.1852214	7.33239481	1.06E-05	0.00210163
Aldob	chr4	6.06208644	-2.8991635	7.31447554	1.14E-05	0.0021888
Uox	chr3	5.46798424	-3.8910942	7.31419174	1.12E-05	0.0021888
NA	NA	-3.0351581	12.8448432	-7.2578878	1.16E-05	0.00221053
Mrln	chr10	1.89226589	5.31305923	7.19570826	1.25E-05	0.00234855
Me1	chr9	1.9768026	6.91692293	7.13418269	1.35E-05	0.00243628
Agbl1	chr7	-2.0885962	1.3608529	-7.1465611	1.33E-05	0.00243628
NA	NA	-2.9421529	5.7414647	-7.1386369	1.34E-05	0.00243628
NA	NA	-2.8056988	10.2088761	-7.0774684	1.45E-05	0.00258145
Trpm1	chr7	2.96315703	0.3806044	7.01294075	1.57E-05	0.00276221
Cst6	chr19	2.23495652	4.66958372	7.00007046	1.59E-05	0.00276912
Igtp	chr11	1.86743947	4.54464325	6.89217296	1.82E-05	0.00312869
NA	NA	4.69385795	0.68222882	6.84250559	1.97E-05	0.00331558
Med12	chrX	-2.8614945	3.45721138	-6.8346408	1.96E-05	0.00331558
Serpina1d	chr12	6.32897767	-3.6602287	6.8549536	2.01E-05	0.00334534
NA	NA	4.3761592	4.3735629	6.78718488	2.11E-05	0.00342487
Kcnk3	chr5	3.81800932	1.86995833	6.77998928	2.11E-05	0.00342487
Car5b	chrX	2.17094632	2.52751196	6.69419221	2.34E-05	0.00374934
Aldh1a2	chr9	-3.9155062	1.81350194	-6.6857214	2.38E-05	0.0037799
Grem2	chr1	2.40181819	2.79352205	6.59957294	2.64E-05	0.00414096
Ces1d	chr8	4.10023518	3.35125626	6.59264986	2.69E-05	0.00417708
Ston1	chr17	-2.2562933	0.96729497	-6.573946	2.72E-05	0.00418839
Hpx	chr7	4.63301432	-1.3730015	6.56670755	2.80E-05	0.0042629
Apoh	chr11	2.91855783	-0.5038737	6.52074789	2.92E-05	0.00432487
Ces5a	chr8	2.60133348	0.55171618	6.51934336	2.93E-05	0.00432487
Dpp6	chr5	-2.9196681	0.2619482	-6.5178887	2.93E-05	0.00432487
NA	NA	-3.2449209	-0.3411066	-6.4875991	3.06E-05	0.00445983
Hist1h4i	chr13	1.82127787	3.91078129	6.41227049	3.36E-05	0.00485751

Supplemental Table 2. Top 100 genes differentially expressed in "SadCas9-2xVP64 + three guides" compared to "SadCas9-2xVP64 no guide"

SYMBOL	TXCHROM	logFC	AveExpr	t	P.Value	adj.P.Val
Ces1c	chr8	7.68192528	-4.0858727	23.7177026	1.33E-10	1.92E-06
Tat	chr8	6.51413216	-3.9814489	18.7406265	1.40E-09	1.01E-05
Slc7a4	chr16	5.42395906	0.54904376	16.666776	4.43E-09	1.30E-05
Cyp2c69	chr19	6.41356165	-4.4022125	16.3517656	5.46E-09	1.30E-05
Fabp1	chr6	7.01430136	-3.3988185	16.2688646	5.82E-09	1.30E-05
1810053B23	chr16	8.36567269	-2.0993569	16.2583139	6.04E-09	1.30E-05
Ttr	chr18	8.59253823	-3.6645933	16.1987709	6.30E-09	1.30E-05
Apoa2	chr1	4.31309488	-0.6005275	13.99838	2.46E-08	4.44E-05
1700003G13	chr9	6.16709101	-3.8132313	13.5514729	3.48E-08	5.59E-05
Rdh7	chr10	6.27061455	-4.306269	13.3403682	4.07E-08	5.88E-05
Apob	chr12	6.36042846	-3.4299405	11.8844821	1.26E-07	0.00015264
Alb	chr5	6.60124813	0.41592462	11.8383922	1.31E-07	0.00015264
Gc	chr5	7.61086889	-3.5843802	11.8108876	1.37E-07	0.00015264
Mup3	chr4	5.93703811	-2.0248159	11.5983687	1.58E-07	0.00016265
Igfbp1	chr11	5.77947999	-4.2970164	11.4236063	1.82E-07	0.00017145
Serpina1a	chr12	6.56777394	-3.6425688	11.3493672	1.97E-07	0.00017145
Fam25c	chr14	4.42384018	-0.5378939	11.2759968	2.02E-07	0.00017145
Klrg2	chr6	4.01555522	-1.1223193	11.016482	2.51E-07	0.000195
Serpina1c	chr12	6.4833408	-3.2361681	10.992408	2.67E-07	0.000195
Fgg	chr3	7.23133838	-3.4152783	10.9526164	2.81E-07	0.000195
Fgb	chr3	7.10294021	-3.1735567	10.9405546	2.83E-07	0.000195
Kif1a	chr1	-3.2035885	1.72216362	-10.578571	3.68E-07	0.0002416
Lama1	chr17	3.60580481	0.34708087	10.3369068	4.59E-07	0.00028082
Serpina3k	chr12	6.46825197	-2.7989697	10.3674744	4.66E-07	0.00028082
Kng1	chr16	6.59377507	-3.7065193	10.145317	5.74E-07	0.00033198
Fga	chr3	7.24192323	-3.9076478	9.94497979	7.04E-07	0.00039142
Cidea	chr18	4.23425211	2.21493926	9.56079601	9.62E-07	0.00050767
Mat1a	chr14	5.91921759	-3.7343781	9.56655238	9.84E-07	0.00050767
Cyp3a11	chr5	7.26000864	-3.6630995	9.49753456	1.09E-06	0.00054116
Cadm4	chr7	-3.0854364	3.43404374	-9.3112336	1.22E-06	0.00058834
Slc27a2	chr2	5.77735647	-3.1819203	9.16142955	1.47E-06	0.00068446
Ucp1	chr8	11.5394284	-1.5055582	9.19742703	1.63E-06	0.00073752
Myo5b	chr18	2.70815964	1.18853647	8.91782918	1.82E-06	0.00079698
Mbp	chr18	-3.1241971	6.32564126	-8.796965	2.07E-06	0.00087745
Uox	chr3	6.38500137	-3.8910942	8.81536963	2.13E-06	0.00087745
NA	NA	7.30546168	-3.4389537	8.74748808	2.33E-06	0.00093426
Prx	chr7	-3.432919	5.10990804	-8.6589476	2.39E-06	0.00093426
Mpz	chr1	-3.1391767	7.72442679	-8.5709125	2.62E-06	0.00095901
Samd11	chr4	3.4319878	-0.4979967	8.53270285	2.74E-06	0.00095901
Apoa5	chr9	5.68644419	-4.1263676	8.55205544	2.76E-06	0.00095901
Azgp1	chr5	5.17378801	-4.0619138	8.54116051	2.77E-06	0.00095901
Ambp	chr4	5.00265745	-3.4506026	8.53232871	2.79E-06	0.00095901
Aspg	chr12	4.49864426	-0.6564861	8.45164468	3.02E-06	0.00101368
9030619P08	chr15	2.99612235	-0.2600478	8.36658783	3.27E-06	0.00105887
Sbsn	chr7	-2.6633714	0.90905622	-8.3572564	3.30E-06	0.00105887
Plg	chr17	5.52507799	-2.84041	8.36109263	3.39E-06	0.00106392
Cldn19	chr4	-3.2653338	2.7388015	-8.2964238	3.53E-06	0.00108534
Gys2	chr6	2.88423499	-1.5679355	8.17357339	4.04E-06	0.00121478
Ahsg	chr16	5.41354129	-0.9425466	8.11597943	4.43E-06	0.00130544
Wnt4	chr4	2.89310387	5.03311767	8.06192403	4.57E-06	0.00132035
Srrm4os	chr5	2.83746235	3.61138985	8.01069135	4.84E-06	0.00137073
Apoa1	chr9	6.68102512	-2.4434213	7.80253925	6.50E-06	0.0018055
Elovl6	chr3	3.14304008	3.37792107	7.70931392	6.83E-06	0.00186108
G6pc	chr11	5.60315183	-3.3951407	7.70806009	7.06E-06	0.00187982
Cps1	chr1	5.23974239	-3.3848414	7.6779702	7.26E-06	0.00187982
Aldob	chr4	6.32598423	-2.8991635	7.69579537	7.29E-06	0.00187982
Arg1	chr10	4.44362967	-1.6097834	7.59014941	7.93E-06	0.00201138
Epn3	chr11	3.69453485	-1.5891827	7.53325568	8.41E-06	0.00209514
Hba-a1	NA	-2.2700334	6.2456611	-7.4965888	8.73E-06	0.00213896
Ddn	chr15	-3.398565	0.55130958	-7.2073462	1.24E-05	0.00298201
Fa2h	chr8	-3.2130863	1.20608522	-7.032031	1.53E-05	0.00363058
Cadm3	chr1	-2.051734	3.75756436	-6.9210036	1.75E-05	0.00403033
Ppp1r3b	chr8	2.57692007	0.40173032	6.92011989	1.76E-05	0.00403033
Pzp	chr6	5.50500956	-3.2228911	6.84788224	1.99E-05	0.00449761
Nfasc	chr1	-2.6849138	1.86436923	-6.7931454	2.06E-05	0.00458172
Orm2	chr4	4.38077136	-2.5305119	6.70807897	2.33E-05	0.00506111
Sox10	chr15	-3.2987824	1.71005186	-6.6733195	2.41E-05	0.00506111
Hpx	chr7	5.41271902	-1.3730015	6.697118	2.41E-05	0.00506111
Prkar2b	chr12	2.93206413	3.13121334	6.65445212	2.46E-05	0.00506111
Bmp7	chr2	-2.8365493	-0.1703501	-6.65022	2.47E-05	0.00506111
Ces5a	chr8	2.72830868	0.55171618	6.64349268	2.49E-05	0.00506111
Serpina1d	chr12	6.18935314	-3.6602287	6.67534697	2.52E-05	0.00506111
Dnajb13	chr7	4.93453349	-1.8392095	6.49479192	3.09E-05	0.00612482
Serpinc1	chr1	3.93724606	-1.3533652	6.28356394	4.02E-05	0.0078515
Dact2	chr17	-2.5238997	0.9490797	-6.1621573	4.69E-05	0.00902999
NA	NA	2.77363083	-0.8576183	6.1509308	4.76E-05	0.0090517
Hpd	chr5	5.36870724	-3.386459	6.15556143	4.90E-05	0.0091922
Acsm3	chr7	4.79325628	-0.8979803	6.08513137	5.32E-05	0.00985906
Dusp15	chr2	-2.832713	1.31355423	-5.9744195	6.05E-05	0.0110674
Mag	chr7	-2.4835744	1.72185278	-5.8808295	6.88E-05	0.01242024
2310008N11	chr8	2.47762951	0.0223978	5.78103716	7.90E-05	0.0140903
Aph1c	chr9	2.02542717	1.4446743	5.69597944	8.90E-05	0.01567068
Alas2	chrX	-2.7381939	2.63862482	-5.6882468	9.00E-05	0.01567068
Aldh1a2	chr9	-3.5045852	1.81350194	-5.619936	9.96E-05	0.01713352
Rasgef1c	chr11	-2.7268056	-0.4788461	-5.5831253	0.00010446	0.01760109
Slc9b2	chr3	2.60867469	0.03741035	5.58003047	0.00010488	0.01760109
Sptbn5	NA	-3.1073231	2.1100215	-5.5741903	0.00010597	0.01760109
Apoh	chr11	2.6612831	-0.5038737	5.5623464	0.00010758	0.01766438
Pllp	chr8	-2.6544819	2.15418714	-5.5538324	0.00010889	0.01767908
Mgat3	chr15	-2.522372	1.43835928	-5.538076	0.00011133	0.01787536
Spen	chr4	-2.0266173	3.73200949	-5.4989035	0.0001177	0.01857554
Mup11	chr4	6.5359933	-0.3747465	5.54577617	0.00011827	0.01857554
Hbb-bt	NA	-2.1214318	4.13274184	-5.4147076	0.00013289	0.02043237
Kif19a	chr11	-2.4525954	1.56428869	-5.414812	0.00013292	0.02043237
Hepacam	chr9	-3.1235403	-0.7331738	-5.3921781	0.00013769	0.02094399
9130230L23	chr5	2.99937564	-1.7029617	5.3379434	0.00014889	0.0224111
Apoc3	chr9	3.89375921	-2.1511746	5.21346237	0.00018033	0.02686402
Scube1	chr15	-2.61022	0.15037746	-5.1910997	0.00018445	0.02719675
Gal3st1	chr11	-2.7637327	-0.2060749	-5.1771827	0.00018838	0.02749575
Gm4841	chr18	2.44516047	5.35415478	5.13981561	0.00019895	0.02874825

Supplemental Table 3. Top 100 genes differentially expressed in SadCas9-2xVP64-no guide compared to "untreated"

SYMBOL	TXCHROM	logFC	AveExpr	t	P.Value	adj.P.Val
Hba-a1	NA	3.12223892	6.2456611	12.331034	8.43E-08	0.00121768
Mpz	chr1	3.67608141	7.72442679	10.6882893	3.34E-07	0.00241497
Hbb-bt	NA	3.16484723	4.13274184	9.89369815	6.93E-07	0.00244925
Hba-a2	chr11	3.23794544	4.91567042	9.85619618	7.18E-07	0.00244925
Cadm4	chr7	3.13536782	3.43404374	9.68323067	8.47E-07	0.00244925
Mbp	chr18	3.22961817	6.32564126	9.26281665	1.28E-06	0.00308948
Lama1	chr17	5.3774057	0.34708087	8.31143772	3.57E-06	0.0073592
Hbb-bs	chr7	2.8634898	6.55027296	8.1395833	4.19E-06	0.00756795
Prx	chr7	3.18266127	5.10990804	7.96374203	5.11E-06	0.00765789
Cldn19	chr4	3.06808525	2.7388015	7.89212771	5.53E-06	0.00765789
Tlr13	chrX	-2.5987846	1.26055872	-7.8376704	5.88E-06	0.00765789
1700001O22Rik	chr2	3.76078395	-0.8282985	7.77422963	6.36E-06	0.00765789
Ccl2	chr11	-2.7593297	1.1058906	-7.6753655	7.09E-06	0.00788188
Mx1	chr16	-3.4609353	0.74527914	-7.5588781	8.15E-06	0.00804522
Fa2h	chr8	3.32272314	1.20608522	7.53694641	8.35E-06	0.00804522
C5ar1	chr7	-1.8891035	2.10571941	-7.258534	1.16E-05	0.01013989
Kif1a	chr1	2.32436318	1.72216362	7.23538702	1.19E-05	0.01013989
Fam178b	chr1	3.0042875	1.76045364	7.10719561	1.40E-05	0.01120779
Ddn	chr15	3.14993822	0.55130958	6.92964353	1.74E-05	0.01322915
Lctl	chr9	3.26770545	-0.3808795	6.88735709	1.83E-05	0.01325713
Pllp	chr8	3.06580561	2.15418714	6.82876119	1.97E-05	0.01357527
Lrrc15	chr16	-2.4883765	0.74755506	-6.7582519	2.15E-05	0.01414289
NA	NA	-1.9501553	3.38202652	-6.6526	2.46E-05	0.01547083
Alas2	chrX	2.9899336	2.63862482	6.51840873	2.93E-05	0.01765268
Xist	chrX	-3.2767212	6.77693285	-6.4385364	3.26E-05	0.01864379
Ncmap	chr4	3.08130356	2.86901463	6.39750506	3.43E-05	0.01864379
Gjb1	chrX	3.46954089	0.2018106	6.38853084	3.48E-05	0.01864379
Mag	chr7	2.56287891	1.72185278	6.33342043	3.73E-05	0.01922711
Snca	chr6	3.12063457	0.87022355	6.30932249	3.86E-05	0.01922711
Il1rl1	chr1	-2.5405179	0.79307145	-6.2535459	4.15E-05	0.01968275
Pvalb	chr15	1.9371664	12.8626777	6.2397791	4.22E-05	0.01968275
Dusp15	chr2	2.72326203	1.31355423	5.89258602	6.77E-05	0.02962619
Adam12	chr7	-2.0037212	2.41708454	-5.8606882	7.07E-05	0.02962619
Ccl7	chr11	-2.540678	0.66322051	-5.838118	7.30E-05	0.02962619
Cd300lb	chr11	-2.4326089	0.71920982	-5.8322784	7.35E-05	0.02962619
Bmp7	chr2	2.48796642	-0.1703501	5.82971426	7.38E-05	0.02962619
Arg1	chr10	-3.6796601	-1.6097834	-5.8042644	7.70E-05	0.03006634
Sfrp1	chr8	-1.9250563	3.06171827	-5.6945804	8.91E-05	0.03389067
Aoah	chr13	-2.230976	0.59804822	-5.5991203	0.00010202	0.0377995
Msr1	chr8	-2.5214491	1.6301269	-5.5421659	0.00011069	0.03942958
Cmtm5	chr14	2.84161366	-0.3319268	5.5243583	0.00011364	0.03942958
Clec4d	chr6	-2.2426926	-0.1450714	-5.5175924	0.0001146	0.03942958
Mmd2	chr5	4.10127424	-3.3145461	5.35972024	0.00014594	0.04854376
Gal3st1	chr11	2.75795131	-0.2060749	5.34218678	0.00014781	0.04854376
Sbspon	chr1	2.22808049	0.44090614	5.22117943	0.00017632	0.05546403
Adamts6	chr13	-2.4536128	1.59657982	-5.2204485	0.00017656	0.05546403
Hhipl1	chr12	-1.9118394	2.31203806	-5.2007135	0.00018171	0.05586471
Hepacam	chr9	2.91504751	-0.7331738	5.16779439	0.00019114	0.0575421
F2rl1	chr13	-2.2231625	1.71289475	-5.1068931	0.00020888	0.06109392
Gm42067	NA	1.85312529	2.04012111	5.09877039	0.0002114	0.06109392
Adcy7	chr8	-1.881753	4.6834493	-5.0461447	0.00022871	0.06480185
Kif19a	chr11	2.27988907	1.56428869	5.02136549	0.00023743	0.06597873
Tlr8	chrX	-4.0365645	-1.2570211	-4.9449509	0.00027029	0.07369187
Smox	chr2	1.81483923	5.4987099	4.89994085	0.00028521	0.07513181
C3ar1	chr6	-3.095913	2.52727176	-4.897357	0.00028728	0.07513181
Eps8l1	chr7	-2.4924048	2.20261789	-4.8867435	0.00029117	0.07513181
Adgre1	chr17	-1.5575189	3.45468859	-4.8714084	0.00029787	0.07551336
Sfrp4	chr13	-2.0811203	4.08490344	-4.8359387	0.00031448	0.07742878
Slfn4	chr11	-2.7773743	-1.1861611	-4.8334332	0.00031615	0.07742878
Lilr4b	chr10	-3.0117057	2.19904976	-4.7560936	0.00035649	0.08523435
NA	NA	2.2188592	1.46909467	4.74477333	0.00036179	0.08523435
Dupd1	chr14	1.83532553	6.3387283	4.73767715	0.00036571	0.08523435
Cdh1	chr8	2.69435584	0.15753197	4.7105409	0.00038186	0.08758428
Cfap100	chr6	2.68467385	-0.1085207	4.65308887	0.00041746	0.09425372
Chil3	chr3	-4.4041995	-0.8908455	-4.6368929	0.00043783	0.09733231
NA	NA	-2.032801	1.63865163	-4.5516428	0.00048859	0.10697147
Ms4a7	chr19	-2.0914278	2.7993614	-4.4397996	0.0005829	0.12571458
Pmp22	chr11	1.97966029	7.02265612	4.41974373	0.00060171	0.12720169
Sox10	chr15	2.30301682	1.71005186	4.41400578	0.0006074	0.12720169
Tnc	chr4	-2.1869894	6.29769631	-4.323846	0.00070125	0.14475757
Dclre1c	chr2	-1.798468	1.83339495	-4.2666147	0.00076856	0.15522687
Ccl6	chr11	-1.8144934	4.30576424	-4.2626793	0.00077345	0.15522687
A930016O22Rik	chr7	1.77831878	7.34616069	4.2491595	0.00079047	0.15646948
Spire2	chr8	2.46586051	-0.8626346	4.23290116	0.00081207	0.15857376
Pdpr	chr8	-1.5137564	3.29044627	-4.2177999	0.00083148	0.1601984
Ms4a4a	chr19	-3.3012903	2.04305875	-4.2086143	0.0008496	0.16153672
Retnla	chr16	1.70702394	3.83252031	4.18081523	0.00088276	0.16566021
Igsf6	chr7	-2.1161057	1.14725297	-4.1698631	0.00089871	0.16649164
Bmper	chr9	-2.3781522	3.01926601	-4.1196582	0.00097551	0.17808689
Kcnmb4	chr10	2.06573485	-0.0707184	4.1071686	0.00099511	0.17808689
Cenpi	chrX	-3.2736233	-0.9010077	-4.1092747	0.00099827	0.17808689
Tfec	chr6	-2.4975075	-0.9890424	-4.0905242	0.00102332	0.18032955
Ccr1	chr9	-3.5459938	0.74382016	-4.0436169	0.00111601	0.19199831
Serpine1	chr5	-1.6929341	4.20045863	-4.0366477	0.00111654	0.19199831
G530011O06Rik	chrX	-3.0056326	0.28110767	-4.0255271	0.00114176	0.19199831
Ptger2	chr14	-2.2297542	-0.7377989	-4.0227253	0.00114269	0.19199831
Lilrb4a	chr10	-4.0994493	0.16994375	-3.9912293	0.00123047	0.20437115
Rnf180	chr13	-1.9538557	-0.0378799	-3.9618891	0.00126259	0.20522254
Ccl12	chr11	-2.0439673	-0.1216011	-3.9612473	0.001264	0.20522254
Jmjd1c	chr10	-1.8859772	1.84643433	-3.942432	0.00130374	0.20875585
Myh4	chr11	1.82246949	13.9035537	3.93272021	0.00132479	0.20875585
Cd33	chr7	-2.5021255	1.96787566	-3.931379	0.0013291	0.20875585
Fam25c	chr14	2.96687101	-0.5378939	3.90989754	0.00138126	0.21461452
Ccr5	chr9	-3.1584851	1.7062355	-3.9018754	0.0014026	0.21561211
Sostdc1	chr12	2.54871926	-0.5067107	3.88711315	0.00143042	0.21757481
Ccnb1	chr13	-2.1828154	0.91827463	-3.8617101	0.0014905	0.22309683
Nuf2	chr1	-2.3761242	0.99193462	-3.8590906	0.00149761	0.22309683
Fgf16	chrX	-2.4858276	0.08167528	-3.850861	0.00151877	0.22347127
Naip6	chr13	-3.0919726	-0.73325	-3.8332285	0.00157101	0.22347127

Supplemental Table 4. Analysis showing distance from off-target site to differentially expressed gene body

SYMBOL	TXCHROM	logFC	adj.P.Val	Gene start (bp)	Gene end (bp)	Off-Target Sequence	Chromosome	Site (bp)	to Gene (bp)	matches	Strand	Lama1 Guide
Ces1c	chr8	8.06720501	1.10E-06	93099015	93131283	agggGCGaGaGaGCaGCCcaGCAGGCCTGAGT	chr8	90241651	2857364	9	+	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN
Slc7a4	chr16	5.42020681	6.76E-06	17572018	17583214	tgCaGAAGaGatTctGCcCCAGGCAGGAAT	chr16	8237459	9334559	9	-	CACCGAAGGGCCTGCGCACCAGGCNNNNNN
Fabp1	chr6	7.92790193	6.76E-06	71199827	71205023	CAgCGctGcagCTGCtCgCCAGGCTGGAAT	chr6	72989175	1784152	8	-	CACCGAAGGGCCTGCGCACCAGGCNNNNNN
1700003G13Rik	chr9	7.85466761	6.76E-06	45318265	45322079	ataCaAAacGCCTaCGtgCCAGGCATGGAT	chr9	43733430	1584835	9	+	CACCGAAGGGCCTGCGCACCAGGCNNNNNN
Cyp2c69	chr19	6.79884139	6.76E-06	39842660	39886769	gACgGCaGaGCctGGCtttGCAGGCAGGGGT	chr19	40318577	431808	9	-	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN
1810053B23Rik	chr16	10.5369617	6.76E-06	93342504	93366668	CACtGTAGatCCctCtgcCCAGGCTGGGGT	chr16	93058037	284467	9	+	CACCGAAGGGCCTGCGCACCAGGCNNNNNN
Apoa2	chr1	5.40091384	7.51E-06	171225054	171226379	tggCaCcGGGCGaGGCggaGCAGGCATGAGT	chr1	171081055	143999	9	+	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN
Ttr	chr18	8.97781797	7.51E-06	20665250	20674324	tAtgGCaGcagGCaGgCAGGCAGGCAAGAGT	chr18	24331496	3657172	9	-	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN
Lama1	chr17	8.98321051	1.37E-05	67697265	67822645	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Apob	chr12	7.80234986	1.82E-05	7977648	8016835	CAggcgGGcagGCaGgCAGGCAGGCTGGGGT	chr12	8858012	841177	9	+	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN
Tat	chr8	5.3144494	2.07E-05	109990437	109999803	aACCtctGaGCCatCtCtCCAGGCCTGAGT	chr8	110878472	878669	9	-	CACCGAAGGGCCTGCGCACCAGGCNNNNNN
Fam25c	chr14	7.39071119	2.27E-05	34351881	34355433	aACtGACCCCAgtgGGctgGGAGGGTGGGAGT	chr14	32562154	1789727	8	+	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN
Serpina1c	chr12	8.1709174	2.27E-05	103894926	103904887	ttCacACttgAAtTGGAGgGGAGGGTGGGGGT	chr12	105870943	1966056	9	+	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN
Serpina3k	chr12	9.29387622	2.81E-05	104338486	104346144	ttCacACttgAAtTGGAGgGGAGGGTGGGGGT	chr12	105870943	1524799	9	+	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN
Igfbp1	chr11	6.69308056	3.26E-05	7197782	7202546	CttttAatGGgaTGaGCcCCAGGCTGGGAT	chr11	7421018	218472	9	-	CACCGAAGGGCCTGCGCACCAGGCNNNNNN
Mup3	chr4	7.59035385	3.35E-05	62083476	62087342	CAgaGAAGGGCtgaactcCCAGGCTAGAGT	chr4	63232225	1144883	9	+	CACCGAAGGGCCTGCGCACCAGGCNNNNNN
Gys2	chr6	4.5777154	4.07E-05	142422613	142473109	CAggtAtGttacCGCACCAGGCTGGAGT	chr6	143140787	667678	9	-	CACCGAAGGGCCTGCGCACCAGGCNNNNNN
Wnt4	chr4	4.20831956	4.07E-05	137277489	137299726	tcCCtggGGcCCaGCaCcCCAGGCTGGAAT	chr4	137673872	374146	9	-	CACCGAAGGGCCTGCGCACCAGGCNNNNNN
Rdh7	chr10	6.12757345	4.07E-05	127884028	127888817	CcCCGAAcacgCTaCagcCCAGGCTGGGAT	chr10	128913811	1024994	9	-	CACCGAAGGGCCTGCGCACCAGGCNNNNNN
Gc	chr5	8.24180382	4.07E-05	89417522	89457898	CAggtttGGGCggGCaCgCCAGGCAAGGAT	chr5	101591226	12133328	9	+	CACCGAAGGGCCTGCGCACCAGGCNNNNNN
Klrg2	chr6	4.59908759	4.07E-05	38625693	38637242	CgggcgGtcGgGCGGgCAGGCAGGCGGGGGT	chr6	38551799	73894	9	-	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN
Srrm4os	chr5	4.04588484	4.94E-05	116438720	116465487	CcCaGACttCctgTGGAGaGGAGGGTCAGAGT	chr5	116290065	148655	8	-	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN
Mat1a	chr14	7.36113899	5.47E-05	41105035	41124412	gACCaCtGGGCtaGtgCAGGCAGGCAAGGGT	chr14	41192606	68194	7	+	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN
Alb	chr5	9.586285	6.01E-05	90460897	90476602	CAggtttGGGCggGCaCgCCAGGCAAGGAT	chr5	101591226	11114624	9	+	CACCGAAGGGCCTGCGCACCAGGCNNNNNN
Serpina1a	chr12	6.95305368	6.01E-05	103853589	103863562	ttCacACttgAAtTGGAGgGGAGGGTGGGGGT	chr12	105870943	2007381	9	+	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN
Azgp1	chr5	6.86136461	6.46E-05	137981520	137990233	CAgtaAAGGctCctgGCACCAGGCCTGAAT	chr5	139375397	1385164	8	-	CACCGAAGGGCCTGCGCACCAGGCNNNNNN
Fgb	chr3	7.48821994	8.50E-05	83040141	83049863	CACCagctGagCTaCaCtCCAGGCCAGAAT	chr3	87805463	4755600	9	+	CACCGAAGGGCCTGCGCACCAGGCNNNNNN
Cidea	chr18	5.07510399	8.82E-05	67343564	67367794	gACtcACtCtAAtggGGgGTGGAGGGTGGGGGT	chr18	69341102	1973308	8	+	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN
9030619P08Rik	chr15	3.92341807	9.42E-05	75427606	75431829	aACtGtAGaGCaaGCGttCCAGGCAGGGAT	chr15	76107757	675928	8	-	CACCGAAGGGCCTGCGCACCAGGCNNNNNN
Fgg	chr3	7.33395248	0.00011613	83007724	83015049	CACCagctGagCTaCaCtCCAGGCCAGAAT	chr3	87805463	4790414	9	+	CACCGAAGGGCCTGCGCACCAGGCNNNNNN
Mmd2	chr5	6.67105341	0.00012028	142562358	142608800	CtttGAAGGGagaGgaaACCAGGCCTGGGT	chr5	142010113	552245	9	-	CACCGAAGGGCCTGCGCACCAGGCNNNNNN
Cyp3a11	chr5	8.17360921	0.00013811	145854426	145879964	aggCtgGGGagtaGGCCAGGCAGGCTAGAAT	chr5	145646342	208084	9	+	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN
Slc27a2	chr2	6.6827	0.00014295	126552407	126588243	CtCCtACCCactCaGagGaGGAGGGTTGGGGT	chr2	126819405	231162	9	-	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN
Ambp	chr4	6.13758126	0.00015057	63143275	63154799	CAgaGAAGGGCtgaactcCCAGGCTAGAGT	chr4	63232225	77426	9	+	CACCGAAGGGCCTGCGCACCAGGCNNNNNN
Fga	chr3	7.62720297	0.00016636	83026076	83033627	CACCagctGagCTaCaCtCCAGGCCAGAAT	chr3	87805463	4771836	9	+	CACCGAAGGGCCTGCGCACCAGGCNNNNNN
Samd11	chr4	4.11178696	0.00017075	156246966	156255657	CACaGCactGGgaaaaCAGGCAGGCAGGAGT	chr4	155503906	743060	9	-	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN
Fabp4	chr3	2.15462805	0.00018279	10204088	10208576	CtgCcAAaGcCaTGttCgCCAGGCTCGAGT	chr3	10144068	60020	9	-	CACCGAAGGGCCTGCGCACCAGGCNNNNNN
Pvalb	chr15	2.52928689	0.00018754	78191114	78206400	CctCtAaCCtAgCTGGAccaGAGGGTGGGAAT	chr15	78664606	458206	9	-	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN
Lctl	chr9	4.2237416	0.00018754	64117147	64138118	aACtGctGaGCCatCtCtCCAGGCCTGGAT	chr9	64028355	88792	9	-	CACCGAAGGGCCTGCGCACCAGGCNNNNNN
NA	NA	8.46471745	0.00018754	113325240	113330523	CgCCatAGtGaCTGaagACCAGGCATGAAT	chr12	118303251	4972728	8	+	CACCGAAGGGCCTGCGCACCAGGCNNNNNN
Apoa5	chr9	6.60004476	0.00018765	46268633	46271919	aACaaAgGGGCCTGgGaACCAGGCCAGGGT	chr9	46913410	641491	6	+	CACCGAAGGGCCTGCGCACCAGGCNNNNNN
Vps13c	chr9	-2.1668504	0.00018765	67840396	67995638	aACCGttGaGCCacCtCtCCAGGCCTGGGT	chr9	69433414	1437776	8	-	CACCGAAGGGCCTGCGCACCAGGCNNNNNN
Gm4841	chr18	3.86778458	0.00025932	60268301	60273267	tAtCGgAaaGCCTGCtCcCCAGGCTAGGAT	chr18	61821232	1547965	7	+	CACCGAAGGGCCTGCGCACCAGGCNNNNNN
Prkar2b	chr12	3.97928004	0.00026274	31958476	32061296	acCtttGGGcaGaGGCaAGGCAGGCAGGGAT	chr12	30913970	1044506	9	+	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN
Pdpr	chr8	-2.203443	0.00033107	111094630	111137074	aACCtctGaGCCatCtCtCCAGGCCTGAGT	chr8	110878472	216158	9	-	CACCGAAGGGCCTGCGCACCAGGCNNNNNN
Hhipl1	chr12	-2.7573871	0.00034623	108306270	108330869	tgaCtCGGtGtcCaGaCAGGCAGGCATGGAT	chr12	106527437	1778833	9	-	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN
Epn3	chr11	4.58955952	0.00036635	94489599	94499974	CACacACaCacACaGtAGaGGAGGGTTGGGGT	chr11	95563937	1063963	8	-	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN
Aldh1a7	chr19	3.50528717	0.00038529	20692953	20727562	attCGAAGGGCtccaGttCCAGGCAAGGGT	chr19	17118070	3574883	9	-	CACCGAAGGGCCTGCGCACCAGGCNNNNNN
Apoa1	chr9	8.39321713	0.00042593	46228580	46230466	aACaaAgGGGCCTGgGaACCAGGCCAGGGT	chr9	46913410	682944	6	+	CACCGAAGGGCCTGCGCACCAGGCNNNNNN
Aspg	chr12	4.61360624	0.00044273	112106679	112127559	tgaCtCGGtGtcCaGaCAGGCAGGCATGGAT	chr12	106527437	5579242	9	-	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN
Adgrd1	chr5	-2.427791	0.00048062	129096750	129204599	CAgCaAtGccCCaGtcCtCCAGGCTGGGGT	chr5	128632023	464727	9	-	CACCGAAGGGCCTGCGCACCAGGCNNNNNN
Kng1	chr16	5.95942358	0.00048561	23057865	23082078	gACtGActGGtCgGaGatCCAGGCCAGAGT	chr16	29714613	6632535	9	+	CACCGAAGGGCCTGCGCACCAGGCNNNNNN
Ucp1	chr8	11.3963873	0.000504	83298352	83298452	ggtaGAtCCCAcCTcaAGTGGAGGGTAAGAGT	chr8	80336949	2953403	8	-	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN
Cps1	chr1	5.87067733	0.00055915	67123026	67231259	CAtgGtaGGGgGCtatCtGGCAGGCTGGGGT	chr1	74579710	7348451	9	+	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN
Sfrp4	chr13	-3.0424407	0.00058511	19623104	19632994	gACaaAAGtGCtTGgtggCCAGGCTAGGAT	chr13	20914228	1281234	9	-	CACCGAAGGGCCTGCGCACCAGGCNNNNNN
Jmjd1c	chr10	-3.2313535	0.00071562	67096125	67256326	tggaaCGtGGtcCtGCCAGGCAGGCTGGGAT	chr10	70037110	2780784	9	+	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN
Orm2	chr4	6.27368915	0.00071836	63362449	63365878	CAgaGAAGGGCtgaactcCCAGGCTAGAGT	chr4	63232225	130224	9	+	CACCGAAGGGCCTGCGCACCAGGCNNNNNN
Atp6v1g1	chr4	1.90407218	0.00072976	63544772	63550750	CAgaGAAGGGCtgaactcCCAGGCTAGAGT	chr4	63232225	312547	9	+	CACCGAAGGGCCTGCGCACCAGGCNNNNNN
NA	NA	3.54327015	0.00079375	21753529	21800773	CAtgGtGGGGgaCGtgatGGCAGGCAGGAAT	chr3	19951663	1801866	9	-	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN
Elovl6	chr3	3.24419618	0.0009186	129532355	129638495	CctCGgtccGCGCGGgagGGCAGGCCTGGAT	chr3	130060315	421820	9	+	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN
Plg	chr17	4.98742747	0.00098659	12378609	12419384	CtCCagAGacaaTGgGaACCAGGCAGGAAT	chr17	11877092	501517	9	-	CACCGAAGGGCCTGCGCACCAGGCNNNNNN
Pzp	chr6	6.39214719	0.00105615	128483567	128526720	gACaaaGGGGtGCGGtggGGCAGGCTGGGGT	chr6	122781164	5702403	8	+	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN
Gfpt2	chr11	-2.0366124	0.00131835	49794178	49838613	gAtCttgGGttCTGgGtACCAGGCTAGGGT	chr11	48443528	1350650	9	-	CACCGAAGGGCCTGCGCACCAGGCNNNNNN
Thrsp	chr7	3.26554164	0.00131835	97412938	97417730	gACtagtGGGgcaGGaCAGGCAGGCTGGGGT	chr7	98123842	706112	9	+	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN
Bhmt	chr13	6.2546489	0.00145525	93616675	93637961	CcCCtAcaGGtgaGgaCACCAGGCGAGAGT	chr13	93929752	291791	9	-	CACCGAAGGGCCTGCGCACCAGGCNNNNNN
Apoc3	chr9	6.95422106	0.00146687	46232933	46235636	aACaaAgGGGCCTGgGaACCAGGCCAGGGT	chr9	46913410	677774	6	+	CACCGAAGGGCCTGCGCACCAGGCNNNNNN
Proca1	chr11	2.63255929	0.00150381	78193392	78205763	tgtaaAAaGGCaTGtGCACCAGGCGTGGGT	chr11	80531260	2325497	8	+	CACCGAAGGGCCTGCGCACCAGGCNNNNNN
Hpd	chr5	6.45914605	0.00156002	123171807	123182727	tcCCcAgGGctCTGtttACCAGGCATGGAT	chr5	120699033	2472774	9	+	CACCGAAGGGCCTGCGCACCAGGCNNNNNN
Pcsk6	chr7	-1.8922339	0.00160525	65861734	66050386	tAggGgAatGCCaGgcCACCAGGCAGGAGT	chr7	68123824	2073438	9	+	CACCGAAGGGCCTGCGCACCAGGCNNNNNN
Dnajb13	chr7	5.86226504	0.0018516	100501716	100514960	aAgaGAgaGcCCTGCtggCCAGGCGTGGAT	chr7	101044600	529640	9	-	CACCGAAGGGCCTGCGCACCAGGCNNNNNN
NA	NA	-2.8570014	0.00187895	59672814	59676700	CAggcaGGcagGCaGgCAGGCAGGCATGAGT	chr9	60247801	571101	9	+	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN
Myo5b	chr18	2.30425852	0.00188746	74440936	74771493	atCtGAcaGGgCTGCctgCCAGGCGGGGGT	chr18	75554852	783359	9	+	CACCGAAGGGCCTGCGCACCAGGCNNNNNN
Fam213b	chr4	2.52777314	0.00210163	154895504	154899135	CAggcaGGcagGCaGgCAGGCAGGCAGGAGT	chr4	154517734	377770	9	-	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN
Uox	chr3	5.46798424	0.0021888	146570426	146632305	CcatGAtGGaCCaGCatcCCAGGCCAGAGT	chr3	147117145	484840	9	-	CACCGAAGGGCCTGCGCACCAGGCNNNNNN
Aldob	chr4	6.06208644	0.0021888	49535995	49549546	CAggcaGGcagGCaGgCAGGCAGGCAAGAAT	chr4	49152862	383133	9	-	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN
NA	NA	-3.0351581	0.00221053	39846958	39848788	gcCCcAgGGcCCcGaGtgCCAGGCAGGGGT	chr17	35138694	4708264	9	-	CACCGAAGGGCCTGCGCACCAGGCNNNNNN
Mrln	chr10	1.89226589	0.00234855	70204664	70219711	tggaaCGtGGtcCtGCCAGGCAGGCTGGGAT	chr10	70037110	167554	9	+	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN
Agbl1	chr7	-2.0885962	0.00243628	76229887	77124698	CACCaCaGGcCctGagaAaGCAGGCTAGGGT	chr7	79214171	2089473	9	+	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN
Me1	chr9	1.9768026	0.00243628	86581371	86695953	CACCGcccaaCCcGCcagCCAGGCTGGGAT	chr9	87740633	1044680	9	-	CACCGAAGGGCCTGCGCACCAGGCNNNNNN
NA	NA	-2.9421529	0.00243628	56223715	56223771	CcCCGcAGGGCtcagGgACCAGGCTTGAGT	chr9	57503743	1279972	7	+	CACCGAAGGGCCTGCGCACCAGGCNNNNNN
NA	NA	-2.8056988	0.00258145	11144125	11144181	tgCaGAAGaGatTctGCcCCAGGCAGGAAT	chr16	8237459	2906666	9	-	CACCGAAGGGCCTGCGCACCAGGCNNNNNN
Trpm1	chr7	2.96315703	0.00276221	64153835	64269775	aggCctGGGGtGgGGagAGGCAGGCCTGGGT	chr7	65989742	1719967	9	-	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN
Cst6	chr19	2.23495652	0.00276912	5344705	5349574	CtCCtctGGGCtgctGgACCAGGCAGGGGT	chr19	10291798	4942224	9	+	CACCGAAGGGCCTGCGCACCAGGCNNNNNN
Igtp	chr11	1.86743947	0.00312869	58199556	58207591	gggCcgGGGaaGCaGgCAGGCAGGCAGGAGT	chr11	59079498	871907	9	-	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN
Med12	chrX	-2.8614945	0.00331558	101274030	101297465	tttaGAggtCAgaTGGAGTGGAGGGTGGGGGT	chrX	95671635	5602395	9	-	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN
NA	NA	4.69385795	0.00331558	50717670	50718915	gAtCttgGGttCTGgGtACCAGGCTAGGGT	chr11	48443528	2274142	9	-	CACCGAAGGGCCTGCGCACCAGGCNNNNNN
Serpina1d	chr12	6.32897767	0.00334534	103763594	103773592	ttCacACttgAAtTGGAGgGGAGGGTGGGGGT	chr12	105870943	2097351	9	+	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN
Kcnk3	chr5	3.81800932	0.00342487	30588170	30625271	CACtcAtGGcCaaGCctgCCAGGCCAGAGT	chr5	30885535	260264	9	-	CACCGAAGGGCCTGCGCACCAGGCNNNNNN
NA	NA	4.3761592	0.00342487	180370491	180385885	tgCgGAgGaGCtTGCcacCCAGGCAAGAGT	chr2	180232667	137824	9	-	CACCGAAGGGCCTGCGCACCAGGCNNNNNN
Car5b	chrX	2.17094632	0.00374934	163976822	164027997	gAggGCttGGgGCtGggAGGCAGGCTTGAAT	chrX	167049748	3021751	9	+	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN
Aldh1a2	chr9	-3.9155062	0.0037799	71215789	71296243	aACCGttGaGCCacCtCtCCAGGCCTGGGT	chr9	69433414	1782375	8	-	CACCGAAGGGCCTGCGCACCAGGCNNNNNN
Grem2	chr1	2.40181819	0.00414096	174833785	174921819	tggCaCcGGGCGaGGCggaGCAGGCATGAGT	chr1	171081055	3752730	9	+	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN
Ces1d	chr8	4.10023518	0.00417708	93166068	93197838	agggGCGaGGaGCaGCCcaGCAGGCCTGAGT	chr8	90241651	2924417	9	+	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN
Ston1	chr17	-2.2562933	0.00418839	88597684	88662586	CttaGtCgCCcACaGGgGTGGAGGGTTAGGAT	chr17	84059032	4538652	8	+	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN
Hpx	chr7	4.63301432	0.0042629	105591613	105600137	CACtGggGaGCagGgtCcCCAGGCCGGGGT	chr7	101349375	4242238	9	-	CACCGAAGGGCCTGCGCACCAGGCNNNNNN
Apoh	chr11	2.91855783	0.00432487	108343354	108414396	CtaaGAgGGtaCacgGCACCAGGCATGGGT	chr11	107538125	805229	9	+	CACCGAAGGGCCTGCGCACCAGGCNNNNNN
Ces5a	chr8	2.60133348	0.00432487	93499064	93535830	agggGCGaGGaGCaGCCcaGCAGGCCTGAGT	chr8	90241651	3257413	9	+	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN
Dpp6	chr5	-2.9196681	0.00432487	26817203	27727505	CACtcAtGGcCaaGCctgCCAGGCCAGAGT	chr5	30885535	3158030	9	-	CACCGAAGGGCCTGCGCACCAGGCNNNNNN
NA	NA	-3.2449209	0.00445983	72691549	72695050	aACCGttGaGCCacCtCtCCAGGCCTGGGT	chr9	69433414	3258135	8	-	CACCGAAGGGCCTGCGCACCAGGCNNNNNN
Hist1h4i	chr13	1.82127787	0.00485751	22040636	22041362	gACaaAAGtGCtTGgtggCCAGGCTAGGAT	chr13	20914228	1126408	9	-	CACCGAAGGGCCTGCGCACCAGGCNNNNNN

Supplemental Table 5. List of computationally predicted off-target sites

Number	Lama1 Guide	Chromosome	Off-Target Loci	Off-Target Sequence	Strand	Mismatches
1	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr1	16312174	CcCaagCtCtgAgTGaAGTGGAGGGTGGGAAT	+	9
2	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr1	21512452	CACaGAgGacaaTGCttcCCAGGCTCGAGT	-	9
3	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr1	38624595	CtaCtAAGttCCgGgatACCAGGCATGGGT	-	9
4	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr1	52143894	ggCaGAAGacCaTGaGttCCAGGCCAGAGT	-	9
5	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr1	55058127	CctCGAAGattCacaGtACCAGGCATGAGT	+	9
6	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr1	57263402	ggaCaAAGGcCtTGCcCtCCAGGCACGAGT	-	8
7	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr1	57936493	CAgtGaGGGatGCacaCAGGCAGGCAAGGGT	-	8
8	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr1	57936538	CAgtGaGGGatGCacaCAGGCAGGCAAGGGT	-	8
9	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr1	57936626	CAgtGaGGGatGCacaCAGGCAGGCAAGGGT	-	8
10	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr1	74579710	CAtgGtaGGGgGCtatCtGGCAGGCTCGGGT	+	9
11	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr1	82782223	gACaGgAGctCaTGtGacCCAGGCTAGGAT	+	9
12	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr1	87661823	ggCCagGGaGCagGGCCtGGCAGGCCAGGAT	-	8
13	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr1	90031346	agtCCAGCctgCTGCGCcCCAGGCCTGGAT	-	9
14	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr1	91995313	gAaCtCtGGGCaCtGCtctGCAGGCTGGGAT	+	9
15	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr1	92235646	CTgtGtAGacCCTcCtCtCCCAGGCATGAGT	+	9
16	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr1	109694154	ggttGgaCtCcACgGGAGTGGAGGGTGGGGGT	+	9
17	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr1	126488448	CAagGtGGGGaGCattggtGGCAGGCAGGAGT	-	9
18	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr1	134277663	CttgGcActtCCTGgGgACCAGGCAGGAAT	-	9
19	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr1	135031972	tCtGAcctcCaTGgGCACCAGGCATGAAT	-	9
20	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr1	141104237	CAagGACaaCAaTGtAGaGGAGGGTTGGAGT	-	8
21	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr1	156757803	agttGAAGGGtCaGaggCCAGGCCAGGAT	+	9
22	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr1	157391498	aACattggCCAAaTGGtGaGGAGGGTGTGGAT	+	9
23	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr1	159690336	CAgCcAtctGCCTtCcatCCAGGCCTGGAT	-	9
24	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr1	161901532	CACgGtgtGtgCTcaGaACCAGGCTGGAGT	+	9
25	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr1	165282075	aACCcCGGGCtGgCGGggcGCAGGCCGGGGT	+	9
26	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr1	171065806	tggCaCcGGGCGaGGCggaGCAGGCATGAGT	+	9
27	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr1	171073441	tggCaCcGGGCGaGGCggaGCAGGCATGAGT	+	9
28	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr1	171081055	tggCaCcGGGCGaGGCggaGCAGGCATGAGT	+	9
29	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr1	179669168	agaatAagaCgACTGGAGTGGAGGGTGGGGGT	-	9
30	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr1	179800672	aAaaaCGGGGaaaGGCtAGGCAGGCTGGAGT	+	8
31	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr1	180373924	CAgCcAttGGCCgagGtgCCAGGCGAGAGT	+	9
32	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr1	180487362	CcCaGAgGGGCtgcaGggCCAGGCCTTGAAT	-	9
33	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr1	181119150	acCCactGaGCCatCtCACCAGGCTCGGAT	+	9
34	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr1	182612878	gAtgGAgGaGgCaGCtCtCCAGGCCTGAGT	-	9
35	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr1	182861831	CttGAAGtGaCaGaGgcCCAGGCCTGAGT	-	9
36	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr1	185442646	aACCcgAGGctgTGgtgACCAGGCAGGAGT	+	9
37	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr1	185927332	CtgaGgAGGaaaTGaaCACCAGGCTTGAGT	+	9
38	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr2	6479941	CctCagAcaGCCTtCtCgCCAGGCAGGGGT	+	9
39	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr2	17447051	CtggcCtGGGaaCaGCCAtGCAGGCAAGAAT	+	9
40	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr2	25429065	CcCtcCGcaGCGCttCtGGCAGGCTGGGGT	+	9
41	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr2	25995977	CACCaccccttCgGcCCACCAGGCCTGAAT	+	9
42	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr2	28820200	aACCtGAtGtcCaTGCcttCCAGGCATGAGT	-	9
43	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr2	31672867	CAgCccAGGcCCaGCtgcCCAGGCAGGGAT	-	8
44	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr2	32697101	tACtGAAGctCCTGttctgCCAGGCAAGGAT	-	8
45	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr2	33173673	gtgaGAAGGaaCaGCGatCCAGGCAAGGGT	-	9
46	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr2	33490722	CcCtaggCCCAgCctGAGTcGAGGGTTTGGGT	+	9
47	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr2	33501232	CACCcAtGGagtgtgGCACCAGGCAGGGGT	+	8
48	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr2	33953091	CAaCtcAGaGCCctgGagCCAGGCCTGGGT	-	9
49	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr2	34575773	CAgCtcAGcaCgcaCaCACCAGGCATGGAT	-	9
50	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr2	47931225	CtgCccttttCCTGtGCACCAGGCAGGAAT	+	9
51	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr2	49708239	CctaccgtGGCtTGaGCACCAGGCCAGAGT	+	9
52	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr2	57240174	aACCcctGaGCCatCtCtCCAGGCCAGGAT	+	9
53	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr2	70248762	gcCCGAgGaGCCTGgGagCCAGGCCAGAAT	+	7
54	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr2	73434966	agCCatttCgAACTGatGTGGAGGGTGGGGGT	+	9
55	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr2	82053716	tcCCGgCCCCggCTGcgGctGAGGGTGCGGGT	+	9
56	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr2	84996827	CtaaGAgGatCCTGtaCcCCAGGCTAGGGT	-	9
57	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr2	85792786	agCCGCacGcaGCtGaaAGGCAGGCTGGGGT	-	9
58	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr2	93064802	CAgCactGtttgTGgGCACCAGGCTAGGAT	-	9
59	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr2	93611661	agggGtGaGcatCGGCCAGGCAGGCAAGAAT	+	9
60	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr2	93645694	CAgCtgAGaGagTGCaggCCAGGCCAGAGT	+	9
61	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr2	105006767	CACaGAgGacaaTGCttcCCAGGCTCGAGT	-	9
62	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr2	105127350	CAgCcAgGcGtCctCGggCCAGGCCAGGAT	+	9
63	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr2	108600572	CtCtGtgaCCtggTGGAGgGGAGGGTCAGAGT	+	9
64	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr2	117143318	tACtacAGGaCgTGgtCACCAGGCTGGGGT	-	8
65	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr2	119080155	ttCtGActacCCaGgGCACCAGGCATGAAT	+	9
66	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr2	126819405	CtCCtACCCactCaGagGaGGAGGGTTGGGGT	-	9
67	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr2	127089292	CAggcaGGcagGCaGgCAGGCAGGCTAGGGT	+	9
68	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr2	130267469	CtttGgActcCaTGgGCACCAGGCATGGAT	-	9
69	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr2	130564058	actCGAAGccCgTcCtcCCAGGCTAGAGT	+	9
70	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr2	131044485	CAggGCaGGGCCagGGCagGGCAGGCCAGAGT	+	7
71	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr2	160732046	ggagGCGGGcaGgcGCgAGGCAGGCCGGAGT	-	9
72	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr2	160802250	CAtgGAAcGaCaGtGCcCCAGGCGTGGAT	+	7
73	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr2	162278982	CAggcAAaaGgCTGtGtcCCAGGCAGGAGT	+	9
74	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr2	163475692	ggCaGgGcaGgCaGgCAGGCAGGCCAGAGT	+	9
75	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr2	164089776	aACtGttCaaAACgGagGTGGAGGGTGGGGGT	+	9
76	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr2	164638656	CAggGtGctGgGaGGCCAGGCAGGCATGGGT	-	7
77	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr2	164852526	CAggGcAGatCtgGaGgACCAGGCCAGAGT	+	9
78	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr2	168045391	acCCaccGaGCCatCtCACCAGGCCTGGAAT	+	9
79	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr2	170015101	gAagGcAGGGaaTctCccCCAGGCTGGGGT	+	9
80	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr2	179934167	CtCCGAgGGGttTGcaggCCAGGCCAGGGGT	-	7
81	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr2	180232667	tgCgGAgGaGCtTGCcacCCAGGCAAGAGT	-	9
82	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr3	10144068	CtgCcAAaGcCaTGttCgCCAGGCTCGAGT	-	9
83	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr3	11083365	CtCCacctGGCCTcCctgCCAGGCTAGGGT	+	9
84	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr3	18621066	CtCgctgGGGCCTcCcCACCAGGCCTGGAT	+	7
85	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr3	19951663	CAtgGtGGGGgaCGtgatGGCAGGCAGGAAT	-	9
86	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr3	27671606	aAgCcaGaGGaGCcGgCGGCCAGGCAGGAAT	+	9
87	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr3	34729203	ttCaGAaCCacAtaGGAGTGGAGGGTGGGGAT	+	8
88	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr3	38817310	CcggGaGGaGgaCGGgCAGGCAGGCATGAGT	-	8
89	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr3	48238520	CAgtGACttgAtgTGcAGgGGAGGGTTGGAAT	+	9
90	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr3	51795944	CctCGAaaGGCCccgatgCCAGGCAGGGGT	+	9
91	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr3	52184374	CcCtccctGcaCTGGCtCCCAGGCATGAGT	+	9
92	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr3	55076356	CtCCcAAGtGCtaGaatcCCAGGCTCGAAT	+	9
93	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr3	67982882	CACtGCAGtGaatGGCaatGCAGGCGAGGGGT	+	8
94	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr3	68213723	aACCactGGGCCTtCtCtCCAGGCCTGGAT	-	7
95	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr3	69549643	CtCCcAAGtcCtTcaGtgCCAGGCATGGAT	+	9
96	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr3	87805463	CACCagctGagCTaCaCtCCAGGCCAGAAT	+	9
97	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr3	89380504	CACCaggacGCCctgaCACCAGGCCTGGAT	-	9
98	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr3	89931273	aACCaaGGcagGCaGgCAGGCAGGCAGGAAT	+	8
99	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr3	98329680	CACCGcAGGtttcagGCcCCAGGCAAGAGT	+	8
100	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr3	108428269	gACCtggaGGCCTGgttcCCAGGCTCGGGT	-	9
101	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr3	115947255	CACactGaGaCtacaCCAGGCAGGCAGGGAT	-	9
102	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr3	116858057	gACaGAgaGGagagCcCACCAGGCAAGAAT	-	9
103	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr3	117437453	CcaaaAAtaGCCatCcCACCAGGCTAGGGT	-	9
104	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr3	119127176	CAaaGAtGGGgaaGaaCtCCAGGCCTGGGAT	-	9
105	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr3	127683845	CAtCcCAgCccctgaGAGTGGAGGGTTGGAAT	+	9
106	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr3	130060315	CctCGgtccGCGCGGgagGGCAGGCCTGGAT	+	9
107	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr3	130325786	agCaacAGcctCTGCcCACCAGGCATGGGT	+	9
108	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr3	131136757	gggaGaGGGaCCctGaCAGGCAGGCAGGGAT	-	9
109	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr3	131471626	CAttcAcccCCaGCGCACCAGGCTTGGAT	-	8
110	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr3	147117145	CcatGAtGGaCCaGCatcCCAGGCCAGAGT	-	9
111	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr3	153279735	aAtgGgGGGGgGgGcaCtGGCAGGCTAGGAT	+	9
112	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr3	153488946	CAgCtaGaGtgcCaGgCAGGCAGGCGTGAGT	+	9
113	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr3	154251972	ttCCtAAGtcCCccaGCtCCCAGGCCTGAGT	+	9
114	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr4	8570745	CAggcaGGcagGCaGgCAGGCAGGCAGGGAT	-	9
115	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr4	18028813	CAggcaGGcagGCaGgCAGGCAGGCATGAGT	-	9
116	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr4	24631445	CACCGCtacctGCcaaCAGGCAGGCTGGGGT	-	9
117	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr4	31636941	CtaCtgagCCtgCTGcAGTGGAGGGTCAGAAT	+	9
118	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr4	33716488	CtaCtAcctGaCTGgGaACCAGGCTTGGGT	-	9
119	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr4	37047240	CtCattgGGGCCTtCcCACCAGGCCTGGAT	-	7
120	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr4	37063381	CtCtcAgGtcTCTcCtCACCAGGCCTGAGT	-	9
121	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr4	38565722	gcCatCcaGGCagGGtCAGGCAGGCATGAGT	-	9
122	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr4	41633043	CAaCcAcGGtgCTcaGCtCCAGGCTAGAAT	+	8
123	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr4	43536337	CAgCaCtGGctGGCGtaAtGCAGGCCTGGGT	-	9
124	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr4	43631260	CtggGAgGtcCCTggGCgCCAGGCAGGGGT	+	8
125	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr4	46610409	CtCtGCaaGGCtCtGCagtGCAGGCTGGGGT	-	9
126	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr4	48029877	gAagtAAaGGgCTGgGtgCCAGGCTTGGGT	-	9
127	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr4	49152862	CAggcaGGcagGCaGgCAGGCAGGCAAGAAT	-	9
128	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr4	51545042	aACaGAgCtgAcCTGGAtatGAGGGTATGAAT	-	9
129	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr4	56611614	CAgcaAGGaCCcttCcCCAGGCCAGGGT	-	9
130	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr4	57847249	CAgCagAGGGgCcGCattCCAGGCCTGAAT	-	8
131	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr4	63232225	CAgaGAAGGGCtgaactcCCAGGCTAGAGT	+	9
132	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr4	65387392	gAaaGCaGGGagagGgCAGGCAGGCAGGGGT	+	9
133	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr4	103500698	tAtaGAtGtGgCTaCctACCAGGCCAGGAT	+	9
134	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr4	107496668	CcCacaGctGaGCccCCAGGCAGGCAGGGAT	-	9
135	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr4	108025417	aACCcCaGGGtGgGGgCgGGCAGGCTTGAGT	-	7
136	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr4	109850272	CACCtgAtatCatTGgcCtCCAGGCTGGGAT	-	9
137	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr4	114586084	CAagGAatCCAAtTcaAcaaGAGGGTGAGAAT	-	9
138	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr4	114597689	CAaCtgGaGGagGaaCgAGGCAGGCAGGGGT	-	9
139	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr4	118003033	ggatGccaGGCaTGCaCACCAGGCCAGAGT	-	9
140	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr4	119990866	aAaaGggctGaCTGgGCACCAGGCATGGAT	+	9
141	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr4	120748899	aAtgcAtCCCAgCTGGgcaGGAGGGTAAGGGT	-	9
142	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr4	123704443	CAgttgAtGGagTGaGaACCAGGCTGGAGT	+	9
143	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr4	124586574	CtCaGCGGGGCttaGggAGGCAGGCATGAAT	-	7
144	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr4	125077860	CACCCAgGGctgctCaCcCCAGGCAGGGAT	+	9
145	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr4	125972352	gtgCctGctGaGCGGCCAtGCAGGCCTGAGT	+	9
146	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr4	127560300	tcCtGAtGGGCCatCttCCAGGCCTGGGT	+	9
147	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr4	130857621	CACCCAgGGcCCccaGtACCAGGCCAGGGAT	+	7

148	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr4	131189393	CgtCGAAGcagCaGCaggCCAGGCGTGAAT	-	9
149	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr4	134999167	aACgGCGCacGgGtGaCtAaGCAGGCGAGAAT	-	9
150	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr4	136262995	aACCccAGcaCCTcataACCAGGCAGGGAT	+	9
151	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr4	137673872	tcCCtggGGcCCaGCaCccCCAGGCTGGAAT	-	9
152	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr4	137772074	CAtCGcAtGaggaGtcCACCAGGCTTGGGT	-	9
153	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr4	139074698	tggCGgtGGcCCgGgGCcCCAGGCTGGGGT	+	9
154	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr4	139216803	tACaGatGaGaGGCaGCCccGCAGGCAGGAAT	+	9
155	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr4	139965800	ggaCCAAGGtCCaGCCgtCCAGGCGAGGGGT	+	8
156	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr4	141365262	CtgacCctGGgacTGCCAGGCAGGCACGGGT	+	9
157	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr4	141383300	CtCCcAgGGtgCgGgagACCAGGCCAGGGT	-	9
158	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr4	142030832	CACaGAgttaCaaGgGaACCAGGCTTGGGT	+	9
159	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr4	144538231	gcgCtgGGGtgGCtcCCAGGCAGGCAAGAAT	+	9
160	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr4	148214494	tttCaAgcctCCTGCaCACCAGGCTTGAGT	+	9
161	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr4	148325578	CcCCGgGaGatGgaGaCAGGCAGGCTGGGGT	-	8
162	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr4	149607546	CACtcCtGGGGGCttagGGCAGGCCAGGGGT	-	9
163	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr4	149864826	CAgtGttGcctGgGGgCAGGCAGGCCTGGAT	+	9
164	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr4	150622270	CAggcaGGcagGCaGgCAGGCAGGCAGGGAT	-	9
165	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr4	151267812	agCaGAAGGaggTGtGagCCAGGCTGGGAT	-	9
166	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr4	152045043	CAgtGtGaGcCGtGGagAGGCAGGGCAGGGGT	+	8
167	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr4	154277939	CACCcActtaCCTGaGggCCAGGCCAGAGT	-	8
168	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr4	154517734	CAggcaGGcagGCaGgCAGGCAGGCAGGAGT	-	9
169	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr4	155503906	CACaGCactGgGaaaaCAGGCAGGCAGGAGT	-	9
170	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr5	27387510	CAgaGAAaGaCttagaCACCAGGCCTGAGT	+	8
171	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr5	30885535	CACtcAtGGcCaaGCctgCCAGGCCAGAGT	-	9
172	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr5	33371717	CACCagAGatCtTGCagACCAGGCGGGGAGT	-	7
173	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr5	35318901	CAgacAaaCCAcaaGGgGTGGAGGGTGGGGAT	+	9
174	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr5	44180103	tAgtGAAaGGCCTGaGgACCAGGCAAGAAT	-	6
175	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr5	53788779	CtCCaaGttGCcatGCaAGGCAGGCATGGGT	+	9
176	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr5	74171504	ggCCGtGGGGgGtGGggGGCAGGCAAGAAT		8
177	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr5	101591226	CAggttGGGCgagGCaCgCCAGGCAAGGAT	+	9
178	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr5	103409544	CtCtGggaGagCTGgGaACCAGGCTTGGGT	-	9
179	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr5	104770100	tAtgtcCCCgAcCTGGgcTGGAGGGTGGGGGT	-	9
180	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr5	106464301	aAatGgSaGcCGCGcaCAGGCAGGCTAGGGT	-	8
181	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr5	112718721	CACaGgCattggCaGGAGTGGAGGGTGGGGGT	-	8
182	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr5	113162833	CttCGgAGaGCtcGCttCCAGGCAGGGGT	-	9
183	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr5	114333628	CAggcaGGcagGCaGgCAGGCAGGCAGGAGT	-	9
184	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr5	114478328	CACCccAtGGtCacactACCAGGCCCGGGT	+	9
185	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr5	115355261	CtCCcaaGGcCagctCCAGGCAGGCTCGGGT	+	9
186	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr5	116290065	CcCaGACttCctgTGGAGaGGAGGGTCAGAGT	-	8
187	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr5	117135722	CtgCtgGGGGCagGGgCAGGCAGGCAGGGGT	+	7
188	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr5	117269617	CAgCcAAGGGCgcagGagCCAGGCTGGGGT	-	8
189	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr5	117683710	CtgCatGGGaaGCaGagAGGCAGGCAGGAGT	+	9
190	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr5	118120829	CtCaGAAaGGtCacaGCACCAGGCCAGGGT	-	7
191	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr5	120699033	tcCCcAgGGctCTGttAACCAGGCATGGAT	+	9
192	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr5	128632023	CAgCaAGccCCaGtcCtCCAGGCTGGGGT	-	9
193	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr5	130038096	ggCtGaGGGtCctGGgCAGGCAGGCAGGGAT	+	8
194	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr5	130617222	CACCctGcaGtagGcaCAGGCAGGCAGGGAT	-	9
195	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr5	130707876	CAaaGAtCCCtcCaGGAGgaGAGGGTTGGGGT	-	8
196	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr5	131687101	ggCaaAAtGGCCTtCtgtCCAGGCAGGGGT	+	9
197	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr5	135171823	ttCtGAccttCCTGgGCACCAGGCATGAAT	-	8
198	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr5	135494493	CACCacAGGcCtTGgGggCCAGGCCAGGGT	+	7
199	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr5	139375397	CAgtaAAGGctCctgGCACCAGGCCTGAAT	+	8
200	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr5	140670603	agCCGaatGctGaGGgCAGGCAGGCCGGGGT	-	9
201	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr5	140705034	CtCaGCGGGcgagGcgCAcGCAGGCCGGGGT	+	9
202	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr5	142010113	CtttGAAGGGagaGgaaACCAGGCCTGGGT	-	9
203	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr5	144069950	CACtctGGGtgGttcCCAtGCACCAAGAGT	+	9
204	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr5	144881996	tAgtGAgtttgCTGaGCACCAGGCAAGAGT	+	9
205	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr5	145646342	aggCtgGGGagtaGGCCAGGCAGGCTAGAAT	+	9
206	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr5	150585492	tACGcCCaggggTGGggTGGAGGGTGGGGGT	+	9
207	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr6	7817896	CACCatgGtcCCaGaGgcCCAGGCCTGGGT	+	9
208	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr6	8130590	gACCccaCtCAACaGGgGTGGAGGGTGGGGGT	-	7
209	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr6	23963904	CAtCacCaCCAtCaGtAcTtGAGGGTTTGAAT	-	9
210	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr6	28205878	gACCagGGGGCTgGataAGGCAGGCAGGGAT	-	8
211	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr6	36376167	gAaaGtGGGcgtCGGgCAGGCAGGCAGGGAT	-	8
212	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr6	38551799	CGggcgGtcGgGCGGgCAGGCAGGCGGGGGT	-	9
213	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr6	38889460	CACtGcCaggAAtgGctGTGGAGGGTTGGGGT	+	9
214	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr6	48559713	aCCatcaGGgCTGCagACCAGGCCAGGAT	+	9
215	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr6	48713013	CACaGcAGGaCCctgcagCCAGGCTCGGAT	-	9
216	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr6	50539773	CACCtAgGaaCacagGCcCCAGGCAGGGGT	-	9
217	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr6	51484037	CtCttAAcGtCtTcaGCACCAGGCCAGGAT	-	8
218	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr6	53608068	CcCaGcAGcagtTtCcCACCAGGCCAGGGT	-	9
219	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr6	58019878	tACtGgaatGCcaGGgCAGGCAGGCAGGAGT	-	9
220	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr6	61969456	aAggcAgGtGCCaCaCACCAGGCTAGAAT	+	9
221	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr6	72989175	CAgCGctGcaggTGGCtCgCCAGGCTGGAAT		8
222	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr6	82041470	CggtGGGaaGCGCGGggAGGCAGGCAAGAGT	+	8
223	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr6	82876617	ttCtGAtcttCtTGaGCACCAGGCGTGAAT	-	9
224	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr6	84215450	CAgaGaaaaGCtgGGCtAGGCAGGCTGGAAT	-	9
225	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr6	84365790	CcggGAtGGaCCTaaGCtCCAGGCCAGAGT	+	8
226	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr6	88476970	CgCtGCtctGtGCtGaCAaGCAGGCAGGGGT	-	9
227	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr6	90579818	aACCtACaCCcAgcatAGTaGAGGGTCTGGGT	-	9
228	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr6	90599564	CctttGcAGGGgCTGtGCtCCAGGCTGGGGT	-	7
229	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr6	90965675	aACtGAgGctCCaaaGaACCAGGCTAGGAT	+	9
230	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr6	102677674	CcCtGcAGGttTTgGCACCAGGCTGGGAT	+	8
231	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr6	103070900	CAgaGAAGGagagGacCcCCAGGCCTGGGT	+	9
232	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr6	106128458	aACaGgaGGGtGaaGtaAGGCAGGCAAGAGT	+	9
233	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr6	114497631	CcCtGcAaaGCCTaCatcCCAGGCGGGAGT	-	9
234	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr6	114500055	CcCtGcAaaGCCTaCatcCCAGGCGGGAGT	-	9
235	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr6	114502461	CcCtGcAaaGCCTaCatcCCAGGCGGGAGT	-	9
236	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr6	114504796	CcCtGcAaaGCCTaCatcCCAGGCGGGAGT	-	9
237	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr6	114507158	CcCtGcAaaGCCTaCatcCCAGGCGGGAGT	-	9
238	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr6	114509496	CcCtGcAaaGCCTaCatcCCAGGCGGGAGT	-	9
239	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr6	114511902	CcCtGcAaaGCCTaCatcCCAGGCGGGAGT	-	9
240	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr6	114516740	CcCtGcAaaGCCTaCatcCCAGGCGGGAGT	-	9
241	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr6	114519171	CcCtGcAaaGCCTaCatcCCAGGCGGGAGT	-	9
242	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr6	114521580	CcCtGcAaaGCCTaCatcCCAGGCGGGAGT	-	9
243	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr6	114524014	CcCtGcAaaGCCTaCatcCCAGGCGGGAGT	-	9
244	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr6	114526435	CcCtGcAaaGCCTaCatcCCAGGCGGGAGT	-	9
245	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr6	114528873	CcCtGcAaaGCCTaCatcCCAGGCGGGAGT	-	9
246	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr6	114531255	CcCtGcAaaGCCTaCatcCCAGGCGGGAGT	-	9
247	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr6	114533590	CcCtGcAaaGCCTaCatcCCAGGCGGGAGT	-	9
248	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr6	114538443	CcCtGcAaaGCCTaCatcCCAGGCGGGAGT	-	9
249	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr6	114540895	CcCtGcAaaGCCTaCatcCCAGGCGGGAGT	-	9
250	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr6	114543319	CcCtGcAaaGCCTaCatcCCAGGCTGGAGT	-	9
251	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr6	114545728	CcCtGcAaaGCCTaCatcCCAGGCTGGAGT	-	9
252	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr6	114548173	CcCtGcAaaGCCTaCatcCCAGGCGGGAGT	-	9
253	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr6	114550576	CcCtGcAaaGCCTaCatcCCAGGCGGGAGT	-	9
254	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr6	114553012	CcCtGcAaaGCCTaCatcCCAGGCGGGAGT	-	9
255	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr6	114555469	CcCtGcAaaGCCTaCatcCCAGGCTGGAGT	-	9
256	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr6	114557855	CcCtGcAaaGCCTaCatcCCAGGCGGGAGT	-	9
257	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr6	114562789	CcCtGcAaaGCCTaCatcCCAGGCGGGAGT	-	9
258	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr6	114565230	CcCtGcAaaGCCTaCatcCCAGGCGGGAGT	-	9
259	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr6	114567670	CcCtGcAaaGCCTaCatcCCAGGCAGGAGT	-	9
260	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr6	114572637	CcCtGcAaaGCCTaCatcCCAGGCGGGAGT	-	9
261	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr6	114575099	CcCtGcAaaGCCTaCatcCCAGGCTGGAGT	-	9
262	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr6	114577576	CcCtGcAaaGCCTaCatcCCAGGCGGGAGT	-	9
263	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr6	114580077	CcCtGcAaaGCCTaCatcCCAGGCAGGAGT	-	9
264	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr6	114582448	CcCtGcAaaGCCTaCatcCCAGGCGGGAGT	-	9
265	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr6	114584789	CcCtGcAaaGCCTaCatcCCAGGCGGGAGT	-	9
266	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr6	114587247	CcCtGcAaaGCCTaCatcCCAGGCGGGAGT	-	9
267	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr6	114589689	CcCtGcAaaGCCTaCatcCCAGGCGGGAGT	-	9
268	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr6	114592134	CcCtGcAaaGCCTaCatcCCAGGCGGGAGT	-	9
269	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr6	114594587	CcCtGcAaaGCCTaCatcCCAGGCGGGAGT	-	9
270	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr6	114597072	CcCtGcAaaGCCTaCatcCCAGGCGGGAGT	-	9
271	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr6	114599522	CcCtGcAaaGCCTaCatcCCAGGCGGGAGT	-	9
272	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr6	114604544	CcCtGcAaaGCCTaCatcCCAGGCGGGAGT	-	9
273	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr6	114607031	CcCtGcAaaGCCTaCatcCCAGGCGGGAGT	-	9
274	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr6	114609485	CcCtGcAaaGCCTaCatcCCAGGCGGGAGT	-	9
275	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr6	114611909	CcCtGcAaaGCCTaCatcCCAGGCGGGAGT	-	9
276	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr6	114614367	CcCtGcAaaGCCTaCatcCCAGGCGGGAGT	-	9
277	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr6	114616880	CcCtGcAaaGCCTaCatcCCAGGCGGGAGT	-	9
278	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr6	114619300	CcCtGcAaaGCCTaCatcCCAGGCGGGAGT	-	9
279	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr6	114621800	CcCtGcAaaGCCTaCatcCCAGGCGGGAGT	-	9
280	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr6	114624302	CcCtGcAaaGCCTaCatcCCAGGCGGGAGT	-	9
281	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr6	114626747	CcCtGcAaaGCCTaCatcCCAGGCGGGAGT	-	9
282	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr6	114629180	CcCtGcAaaGCCTaCatcCCAGGCGGGAGT	-	9
283	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr6	114634160	CcCtGcAaaGCCTaCatcCCAGGCGGGAGT	-	9
284	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr6	114636655	CcCtGcAaaGCCTaCatcCCAGGCAGGAGT	-	9
285	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr6	120382670	ttCgctgGGGCCTtCcCACCAGGCCTGGAT	+	8
286	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr6	121125250	CtCCcAatGCtgGgtGttCCAGGCGTGAAT	+	9
287	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr6	122781164	gACaaaGGGGtGCGggGGCAGCTGGGGGT	+	8
288	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr6	138794597	CACttgAtGtCCTGtcatCCAGGCAGGAAT	+	9
289	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr6	140579138	aACCtctGaGCCatCtCtCCAGGCCAGAGT	+	9
290	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr6	143140787	CAggtAtGtGttacCGCACCAGGCTGGAGT	-	9
291	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr6	145140036	CggCagcatGCtTGaGCACCAGGCACGGGT	+	9
292	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr6	146971083	gcagGAgtGGCCTtCcCtCCAGGCCTGAAT	+	9
293	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr7	4324706	CgCgctgGGaCCTtCcCACCAGGCCTGGGT	-	8
294	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr7	4745749	CAgCtcctGcCCTGCGCtCCAGGCTAGGGT	+	7
295	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr7	7277683	ggaCCatGGcaGaGCCAGGCAGGCCGGGAT	+	9
296	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr7	29038770	CgCCccAtaGaCcagGCACCAGGCTGGAAT	-	9
297	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr7	29514402	CAgaGCtGacaGCaGCCcaGCAGGCCAGGAT	+	9

298	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr7	31150434	acCCGcAGGcaCaGgtgACCAGGCAGGAGT	+	9
299	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr7	36838074	CAaCGtgGGagCTGgGagCCAGGCTTGGAT	+	8
300	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr7	36848608	CttCcaaGGGCaCtGaCAtGCAGGCCTGAGT	-	9
301	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr7	37092813	CACCtcAtttCCcagaCACCAGGCATGGGT	+	9
302	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr7	38123045	CAgCcactGaaGgGGCtAGGCAGGCTGGGGT	-	9
303	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr7	44972182	ttagGAAGGGCCTGgaaACCAGGCAGGGAT	-	7
304	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr7	65989742	aggCctGGGGtGgGGagAGGCAGGCCTGGGT	-	9
305	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr7	68123824	tAggGgAatGCCaGgcCACCAGGCAGGAGT	+	9
306	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr7	79214171	CACCaCaGGcCctGagaAaGCAGGCTAGGGT	+	9
307	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr7	79459583	acCtGcAGaGCCaGtcCACCAGGCTAGGGT	+	8
308	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr7	79792951	gACtcgCGGCCtaGGgtAGGCAGGCGCGGGAT	+	9
309	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr7	79801854	CAggcCaGGGCaaGGCCcaGCAGGCCTGGGT	-	8
310	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr7	80062652	CtgCGCaGaGCtCaGCactGCAGGCTGGGAT	-	9
311	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr7	80994047	gcCCGccGaGCCccCGgCCCAGGCAGGGAT	+	9
312	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr7	81468367	gACaGgtGGGCCTctaatCCAGGCCTGGGT	-	9
313	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr7	81578428	CAgatctctCCTGCtCACCAGGCTGGAGT	-	9
314	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr7	81778798	CAtaGcAGtGCggGtGgACCAGGCTGGAAT	+	8
315	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr7	82771251	ggaCcacGGcaGaGGCCAGGCAGGCCGGGAT	-	9
316	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr7	82771352	ggaCcacGGcaGaGGCCAGGCAGGCCGGGAT	-	9
317	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr7	82771740	ggaCcacGGcaGaGGCCAGGCAGGCCGGGAT	-	9
318	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr7	82771840	aggCcacGGcaGaGGCCAGGCAGGCCGGGAT	-	9
319	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr7	87666635	tACCtAgaacCTGgGCACCAGGCTGGAAT	-	8
320	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr7	98123842	gACtagtGGGgcaGGaCAGGCAGGCTGGGGT	+	9
321	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr7	98430866	gACtcAAGGtgCaGaGagCCAGGCTAGAGT	-	9
322	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr7	101044600	aAgaGAgaGcCCTGCtggCCAGGCGTGGAT	-	9
323	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr7	101349375	CACtGggGaGCagGgtCcCCAGGCCGGGGT	-	9
324	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr7	111678449	CAtCtAcGGGaagGtGaACCAGGCTAGAAT	+	8
325	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr7	111695318	ggaaGCtGGGCattGgCAGGCAGGCATGAAT	-	9
326	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr7	112773259	CtCgGAAGcaCCatCtCtCCAGGCCAGAGT	-	8
327	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr7	113018110	CAgaGACCCctAgTGGggtGAGGGTGAGGAT	-	9
328	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr7	114634101	CtaaGCtGGGgGCacACAGGCAGGCAAGGAT	+	8
329	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr7	116158895	gttaGAgaGcCCTGaGtACCAGGCAAGGAT	-	9
330	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr7	117001776	CACacAtaGGCagGCaCACCAGGCATGAAT	+	7
331	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr7	117002279	CACacAcaGGCaTaCaCACCAGGCATGAAT	+	7
332	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr7	127341234	gcagtAAGaGCtTGaGCtCCAGGCCAGGGT	+	9
333	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr7	134130658	CtgtGAAGaGCtgtCttACCAGGCAGGGGT	+	9
334	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr7	135510409	gctCtcAGGtCTtCCACCAGGCCAGGGT	+	8
335	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr7	138607181	CtCCccAtctCCTcCagACCAGGCAGGGAT	+	9
336	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr7	140220561	CAggGccGGaCCatCtCtCCAGGCCAGGGGT	-	9
337	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr7	141310786	CAggGAAGctgCTGtGacCCAGGCGAGAAT	-	8
338	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr7	142624194	CcCaGatGGGCaCGGgCAtGCAGGCAAGGAT	+	7
339	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr7	142960249	CtCCtAAGctCCatCttgCCAGGCTGGGAT	+	9
340	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr7	144513026	ttCtGAcctcCtTGgGCACCAGGCATGAGT	+	9
341	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr7	145295097	CACaGAtCCCAcagGccTTGGAGGGTCTGGGT	+	8
342	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr8	3624632	CtgcTtGGaGCagaGaCAGGCAGGCATGAAT	+	9
343	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr8	12853787	CAgaGgCCtggACcGGgGTGGAGGGTGAGGGT	-	8
344	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr8	14039525	tcCCcAtctctCTGCtCACCAGGCATGAGT	+	9
345	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr8	25201736	CggCGgcGcGCGgcGCgcGGCAGGCGCGGAT	-	9
346	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr8	26974740	gACaGgatGtCcCGGCtgGGCAGGCTAGGGT	-	9
347	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr8	31922609	CAgCacgGGGCtTctcCtCCAGGCTTGAGT	+	9
348	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr8	44554008	CAggcaGGcagGCaGgCAGGCAGGGCAGGGGT	+	9
349	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr8	45054404	tgCtaAaaCCAAgTaGAGTGGAGGGTTGGGAT	+	8
350	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr8	46650495	CcCgGCaGGcaGgGGatAGGCAGGCCTGAGT	+	8
351	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr8	47635899	CtCCaAAaaGCCgGgatgCCAGGCGCGAGT	-	9
352	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr8	68838281	CAaCGCGctGCtCcGCCctGCAGGCAGGGAT	-	7
353	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr8	70155798	CgCtGtgGGtgCTGgGaACCAGGCTTGAGT	+	8
354	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr8	71352363	actCGttaGcCGtGtCCAGGCAGGCCTGGGT	+	9
355	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr8	78585857	CAagtgGtcCaaGGCCAGGCAGGCCAGGAT	+	9
356	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr8	80336949	ggtaGAtCCCAcCTcaAGTGGAGGGTAAGAGT	+	8
357	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr8	90241651	aggGGCGaGGaGCaGCCcaGCAGGCCTGAGT	+	9
358	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr8	101340162	CcCCaCtGGGaGttcCCAtGCAGGCGAGAGT	-	8
359	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr8	104182220	gcCtGACCaaggCTaGtGTGGAGGGTTTGAAT	+	9
360	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr8	104985257	CAtttcAaaGtCTGgaCACCAGGCAAGGAT	-	9
361	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr8	105462123	gACtGcAGatgCTGgGtcCCAGGCCAGAGT	+	9
362	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr8	108867868	gACaacgGaGCCTGacCtCCAGGCTTGGGT	-	9
363	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr8	110878472	aACCtcTGaGCCatCtCtCCAGGCCTGAGT	-	9
364	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr8	114816077	gACaGtGtGtGatatGCtAGGCCAGGCGTGAGT	-	9
365	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr8	119428002	CcCCaCtGGGCagGatCAGGCAGGCCTGGAT	-	7
366	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr8	120068314	CACCccAGGGCCTctGtgCCAGGCGGGGGT	+	6
367	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr8	120860571	CctaGgAGGcgCTGgcCACCAGGCTGGGAT	-	8
368	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr8	120974936	atgaGAAGGGaCaGCcagGCCAGGCTTGGAT	+	9
369	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr8	123041378	CtgCGGGGtGCGgaGgCgcGCAGGCCCGAGT	-	9
370	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr8	125191189	tAtCaAccaGCgTGCtaACCAGGCCTGGAT	-	9
371	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr8	125596642	CAtgGcAGGctCTGttcCCAGGCTGGAGT	+	9
372	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr8	126158536	CcCaGggatGCCTGCatACCAGGCAAGAAT	-	8
373	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr9	6221347	CcaaGAgtGGCCcaCtCACCAGGCAGGGAT	+	8
374	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr9	14751175	gAgCaActGGaacGaGCACCAGGCACGGGT	-	9
375	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr9	21916518	ttCtGctGaGtCTctGCACCAGGCATGGGT	+	9
376	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr9	22034827	CACCctCatgcACaaGAGTtGAGGGTTGGGGT	-	9
377	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr9	22617858	gACtaAAGattCccaGCACCAGGCATGGGT	+	9
378	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr9	23028171	CAtCtttcCCCaGgGCACCAGGCAGGGGAT	+	9
379	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr9	23128294	CAggGaGGcagGCaGgCAGGCAGGCAGGGAT	+	8
380	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr9	26613462	gAaCaACCtgAgCTcctGTGGAGGGTCTGAAT	-	9
381	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr9	37851492	gACaGAagCCtgtTGGAGTtGAGGGTTGGGAT	+	8
382	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr9	40241455	CAaaGCcaGcaGCaGaCAGGCAGGCTGGGGT	+	8
383	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr9	42855882	CAtCccAGGctacaCaCACCAGGCCTGAGT	+	9
384	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr9	43733430	ataCaAAacGCCTaCGtgCCCAGGCATGGAT	+	9
385	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr9	46913410	aACaaAgGGGCCTGgGaACCAGGCCAGGGT	+	6
386	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr9	49513721	CaaCtgGGattGaGGaCAGGCAGGCAAGGGT	-	9
387	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr9	52736360	CAagcAAGGaCacGtGCACCAGGCTTGAGT	+	7
388	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr9	53321364	CtgtGACCaggACTGGAGgtGAGGGTAAGAGT	+	8
389	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr9	57503743	CcCCGcAGGGCtcagGgACCAGGCTTGAGT	+	7
390	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr9	60247801	CAggcaGGcagGCaGgCAGGCAGGCATGAGT	+	9
391	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr9	63184373	CtCCcAgCtCctCaGaaGaGGGAGGGTTAGAGT	-	9
392	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr9	64028355	aACtGctGaGCCatCtCtCCAGGCCTGGAT	-	9
393	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr9	64321431	agCCGaGatGtGCaGCCAGGCAGGCACGGGGT	-	7
394	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr9	64764207	agagGAAtGGCTTgtCACCAGGCCAGAGT	-	9
395	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr9	65128873	CACgcCaGGtgagGGgaAGGCAGGCGGGGGT	+	9
396	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr9	69433414	aACCGttGaGCCacCtCtCCCAGGCCTGGGT	-	8
397	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr9	77945476	tACacAgCggcACTGGAcTGGAGGGTCTGAGT	+	8
398	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr9	86648571	aACtGtGGGagGCaGtCcaGCAGGCAAGGGT	+	9
399	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr9	87740633	CACCGcccaaCCcGCcagCCAGGCTGGGAT	-	9
400	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr9	90022393	aAttatAGGtCCaGgcCACCAGGCCTGGAT	-	9
401	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr9	96933684	CtCatAtCCCAcTcaAGcaGAGGGTTGGGAT	+	9
402	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr9	96972110	CACCGtAGccatgGaCaCtCCAGGCAGGGGT	+	8
403	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr9	98534790	gAtCtgGGGGtGgtGCagGGCAGGCTGGGGT	-	9
404	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr9	106552854	CACCagtGtGCCTgcCACCAGGCCTGGAT	+	7
405	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr9	106652201	aaaCtgAGcctCTGCtgACCAGGCTGGGGT	+	9
406	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr9	107279877	CAgCtcCCCCAttctcAGgGGAGGGTGGGGGT	-	9
407	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr9	109104664	CAggcaGtGCagGGgCAGGCAGGCAAGGGT	-	9
408	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr9	111481582	CcCaGtGGtnCCCGtatgGGCAGGCAGGGAT	+	9
409	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr9	115956828	CAagGACaCacAgTGcAGgGGAGGGTCAGAAT	-	8
410	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr9	119029882	CcCCatcctGtCTGgGCtCCAGGCTGGAGT	+	9
411	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr9	119972855	gACCGgaaGctGgGaCCtGGCCAGGCTGGGGT	+	9
412	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr10	3754863	gACaGCaaGGCcCtGgtAGGCAGGCAAGAAT	-	8
413	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr10	4744761	CACaGtaGGcaGtaGgtAGGCAGGCAAGAAT	-	9
414	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr10	5147787	gACCaAAGGcgtTtgcCACCAGGCCTGGAT	+	8
415	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr10	10301849	aACaGAgCaCActTGctGTtGAGGGTTTGGGT	+	9
416	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr10	12721008	gACCaAcctGaaTGCcCACCAGGCAAGGAT	+	8
417	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr10	21806329	CACatAcaGGaggaaGCACCAGGCCGGGGT	+	9
418	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr10	29217098	CAgtttAGGGCCTGaGatCCAGGCTTGGGT	+	7
419	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr10	29534725	CAgCcAAGGttCccgGagCCAGGCGGGGAAT	+	9
420	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr10	33182172	CAgCtAgaGaCaTGaGCtCCAGGCGGGGGT	-	8
421	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr10	39018711	atCtGAgGtGatTGtGtACCAGGCTAGGGT	+	9
422	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr10	39514838	tgaacAAGGGCaTGaGaACCAGGCAGGAGT	+	8
423	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr10	62424916	CaaacAAGGcCaTcCaCtCCCAGGCCTGGGAT	+	9
424	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr10	62820798	gAgacAgGGGCCTGaGttCCAGGCTAGAGT	+	8
425	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr10	70037110	tggaaCGtGGtcCtGCCAGGCAGGCTGGGAT	+	9
426	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr10	70815707	CAgtGACCtCtctgGGgaTGGAGGGTGGGGAT	-	9
427	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr10	73100122	CtCtGCGGGaCcCGgCtaGCAGGCAGGGGT	+	7
428	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr10	78196582	CAggtCtGtGCcaGGCCAGGCAGGCAGGAAT	-	7
429	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr10	79623512	tAgtGAgtGGgCTGCcCtCCAGGCCGGGGT	+	8
430	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr10	79653456	CACCcAAGctCCTGtGCCCAGGCTGGAAT	+	5
431	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr10	79923552	gAgtGAAGGtgCacaCCACCAGGCCTGGGT	+	9
432	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr10	93675226	CAggcaGGcagGCaGgCAGGCAGGCAGGAAT	+	9
433	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr10	117606251	CAagaAcaGGCCTGCaagCCAGGCGTGGGT	+	8
434	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr10	120694625	ttgCaAttGGCCaGCGCtCCAGGCATGAAT	-	8
435	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr10	120758425	acCCattGaGCCatCtCtCACCAGGCCAGGGT	+	9
436	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr10	128913811	CcCCGAAcacgCTaCagCCAGGCTGGGAT	-	9
437	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr11	5252790	gctCagtgCCACTGGAGTGGAGGGTGAGGGT	-	9
438	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr11	7421018	CtttAtGGgaTGaGCcCCAGGCTGGGAT	-	9
439	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr11	8717499	CAgtGaGGGGCagcagtAGGCAGGCATGAGT	-	9
440	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr11	20371071	aAagGCaGGGaaaGctCAGGCAGGCTGGAGT	-	9
441	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr11	26961809	ggCacAgactCCTGCtCACCAGGCAAGAAT	-	9
442	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr11	46510386	CcCtGCaGGaaagGGCCAtGCAGGCCTGGGT	-	8
443	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr11	46553375	CcCtGCaGGGtaaGGaCAtGCAGGCCTGGGT	-	8
444	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr11	48088143	tAgCcAaCtCAAgTGaAGcaGAGGGTCAGAAT	+	9
445	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr11	48443528	gAtCttgGGttCTGgGtACCAGGCTAGGGT	-	9
446	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr11	59079498	gggCcgGGGaaGCaGgCAGGCAGGCAGGAGT	-	9
447	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr11	59889465	atCtGCGGctgGGtaCAGGCAGGCAAGAAT	+	9

448	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr11	59896272	tAtaGAAGGatgTGtGggCCAGGCGGGGGAT	-	9
449	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr11	60597089	aAttaAAGGtgtTtCcCACCAGGCCTGGAT	-	9
450	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr11	60606291	aAttaAAGGtgtTtCcCACCAGGCCTGGAT	-	9
451	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr11	60615501	aAttaAAGGtgtTtCcCACCAGGCCTGGAT	-	9
452	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr11	60624712	aAttaAAGGtgtTtCcCACCAGGCCTGGAT	-	9
453	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr11	60647231	aAttaAAGGtgtTtCcCACCAGGCCTGGAT	-	9
454	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr11	60662842	aAttaAAGGtgtTtCcCACCAGGCCTGGAT	-	9
455	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr11	61537636	CACaGAtGHtCCTGtGagCCAGGCCTGAAT	+	7
456	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr11	63130471	CACtGctCttAACaGGtagGGAGGGTGTGGAT	+	9
457	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr11	63934474	ggCtGCaGGGCtgaGCCHGCAGGCTAGGGT	+	9
458	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr11	67966116	CAtCcAAGtGCtgGaattCCAGGCTTGAGT	+	9
459	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr11	69565321	CcagGAAGtGagaGaaCACCAGGCACGAAT	+	9
460	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr11	72136055	gctCGgAGacgCTGCGggCCAGGCAGGGAT	+	9
461	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr11	80531260	tgtaaAAaGGCaTGtGCACCAGGCGTGGGT	+	8
462	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr11	81781637	CAggcaGGcagGCaGgCAGGCAGGCAGGAAT	+	9
463	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr11	83327345	CAggattGGGCCTcCGaggCCAGGCTGGGAT	-	8
464	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr11	85710844	CAgtGgGGGagGgGGggGGCAGGCCTGAGT	-	9
465	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr11	85735263	ggCaGAgGGattTtCaCACCAGGCAAGAGT	+	9
466	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr11	85812147	CAtCtAgGatgCTtgGCcCCAGGCAAGGAT	+	9
467	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr11	88504549	gcCtGcAGGGCCctCtCgCCAGGCCTGAAT	-	8
468	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr11	91269261	aAtacACtaCAcCTaGAGaGGAGGGTCTGGAT	+	9
469	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr11	95563937	CACaCACaCacACaGtAGaGGAGGGTTGGGGT		8
470	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr11	95941986	CAgCcttGGGgacaaGCACCAGGCATGGGT	+	9
471	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr11	98350092	CcCCcACtCgAgCTtcAGgtGAGGGTAGGGGT	+	9
472	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr11	98385431	atCCcAAaGGCCaGacaccCCAGGCTGGGAT	-	9
473	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr11	98498863	CACgcgGaaGaGCGagCAaGCAGGCTTGGGT	+	9
474	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr11	98562560	CctCcAtcacCCTGgGtACCAGGCTTGGGT	+	9
475	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr11	99060618	CtgCtgGGGGCtgccCaAGGCAGGCTTGGGT	+	9
476	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr11	102217537	CACtGCcaGGaGgGaCCAaGCAGGCATGGGT	+	7
477	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr11	102769375	gACaGgCgCAcCTtGAccGGAGGGTAGGGGT		9
478	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr11	103603781	gAgtaAAatGgCTGgcCACCAGGCCTGAGT	+	9
479	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr11	106263794	CtCaGCcccctGCaGgCAGGCAGGCCTGAGT	-	9
480	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr11	106361263	aACaGAAGGcaggacGtcCCAGGCTTGGAT	-	9
481	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr11	107538125	CtaaGAgGGtaCacgGCACCAGGCATGGGT	+	9
482	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr11	109785130	acCaGgAGGaCCcctGCgCCAGGCCTGAGT	-	9
483	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr11	112270871	aACCactGaGCCaaCtCtCCAGGCATGGAT	+	9
484	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr11	113070859	gACtGActGtCCctgGCACCAGGCTGGAAT	+	8
485	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr11	114783454	CcCCatctGaCCTcaGaACCAGGCAGGAGT	+	9
486	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr11	118668890	tgCCGcAGaagCTGgGCtCCAGGCCCGAGT	+	8
487	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr11	119033522	CtCCccAcaGCCTGacatCCAGGCCTGAGT	-	9
488	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr11	120476342	CACaGgcaGtaagGcCCAGGCAGGCCAGGGT	-	9
489	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr12	8858012	CAggcgGGcagGCaGgCAGGCAGGCTGGGGT	+	9
490	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr12	16663830	gAgCtACCaCAcTTGaAGgGGAGGGTCTGGGT	+	8
491	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr12	17699510	tCtGtctGGtCTGCaCtCCAGGCTTGGGT	-	9
492	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr12	21518525	CTgtGAGaaCtTGCCACCAGGCTGGAAT	-	8
493	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr12	24731791	CAtCHtGGGCtgGagCAaGCAGGCCAGAGT	-	9
494	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr12	29120532	atCCtcCCtggACaGGgGTGGAGGGTGGGAGT	-	9
495	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr12	30913970	acCtttGGGCcaGaGGCaAGGCAGGCAGGGAT	+	9
496	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr12	35936480	ggaaGAgCCCAcCTccAGTaGAGGGTCAGAGT	-	9
497	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr12	37539562	ttCCaAtaGcCCTGtGgtCCAGGCCAGGGT	+	9
498	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr12	42531226	CACtaAtGtatCatgGCACCAGGCAGGGGT	-	9
499	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr12	51566130	CAtCcCtGcagGaaGgCAGGCAGGCAGGGGT	-	9
500	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr12	55776121	tACaaAAGaGCCTttcatCCAGGCTCGGGT	-	9
501	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr12	66290707	CAggcAAGGaCtgGtGggCCAGGCAGGGGT	+	9
502	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr12	71433917	gAgaGaaaGctGCaGCCAGGCAGGCTGGGGT	+	9
503	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr12	79049689	CcaaGAAGGctgTGtGttCCAGGCAGGAGT	-	9
504	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr12	79061547	gACCcAgaGGtCTctaaACCAGGCCAGAAT	+	9
505	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr12	82263332	CACtGgtGGGCcgGtCCaGCAGGCAGGAAT	+	8
506	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr12	82553117	CACtGaGcacgGCaGCaHGGCAGGCAGGGGT	-	9
507	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr12	86359817	tAtgcAtGGtCTGgGtACCAGGCCAGGGT	-	9
508	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr12	86621523	tAagGaaGaGCaCGcCgAGGCAGGCTGGGAT	+	9
509	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr12	100325518	gACtGgtGaGtCTGaGacCCAGGCCAGGGT	-	9
510	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr12	105870943	ttCacACttgAAtTGGAGgGGAGGGTGGGGGT	+	9
511	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr12	106527437	tgaCtCGGtGtcCaGaCAGGCAGGCATGGAT	-	9
512	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr12	118303251	CgCCatAGtGaCTGaagACCAGGCATGAAT	+	8
513	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr13	12179663	gACaGtGGcCGgtGCCtGGCAGGCTTGAGT	-	7
514	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr13	13964861	CAtCaggacGCCctgGCACCCAGGCCCGGAT	-	9
515	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr13	20914228	gACaaAAGtGCtTGgtggCCAGGCTAGGAT	-	9
516	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr13	24919802	CtCtttAaaGCtTGCaaACCAGGCGGGAAT	-	9
517	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr13	34206479	CAgacCtGGGaaaGGtCAaGCAGGCCTGGGT	-	9
518	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr13	37149519	tAgacAAGGGaCacCatACCAGGCTTGAAT	-	9
519	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr13	42979866	agCCagAaGGCgcGtGCtCCAGGCAAGAGT	-	9
520	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr13	43421634	tAggcAAGGGCtgcgGCtCCAGGCCTGAGT	-	9
521	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr13	44055834	CCCCGtGtGaaGaaGtaAGGCAGGCTGGGGT	-	9
522	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr13	44229402	gAgaGAAGGGaaTGaGggCCAGGCTGGAGT	+	8
523	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr13	48697316	CAgaGAAGccaCTcttCACCAGGCAGGAAT	-	8
524	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr13	51868399	CtCtGcctGGtCTGgtCcCCAGGCCAGGGT	+	9
525	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr13	52045981	CAgCaAcaGGgaaaCaCACCAGGCAGGGAT	+	9
526	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr13	52833465	CAttcgAGGtgCTGgaCACCAGGCTTGGGT	+	8
527	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr13	53100751	CAggcaGGcagGCaGgCAGGCAGGCAGGAAT	-	9
528	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr13	54440068	CAgCagcaGGCaCaGgCgGGCAGGCCAGAGT	-	9
529	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr13	55391654	CACtaGtGGgGCaGacGtGCAGGCCAGAGT	+	9
530	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr13	59899317	CACaatcaGGCacaCaCACCAGGCATGAAT	+	9
531	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr13	70126600	atCaGAAacGaCTctGaACCAGGCATGGGT	-	9
532	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr13	71070085	aAagGaaGGcCagGcCCAGGCAGGCCTGAGT	+	9
533	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr13	72366003	CACCGgctccCCcGaGgcCCAGGCCCGAGT	-	9
534	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr13	73239443	tgCaGcCCCtcACTGGgaTGGAGGGTTAGAGT	-	8
535	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr13	73820815	CACaccAGGGagtgGCACCAGGCTTGGAT	-	8
536	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr13	93929752	CcCCtAcaGGtgaGgaCACCAGGCGAGAGT	-	9
537	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr13	98475919	CcaCGgAGGcaagGatCACCAGGCCAGGGT	+	9
538	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr13	98754007	CAgCaCaGGGgagGaggAGGCAGGCCAGAGT	+	9
539	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr13	100689073	ggCaagGtGGgGaGGgCAGGCAGGCAAGAGT	-	9
540	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr13	101994963	tAagGAAGcaatTGaGaACCAGGCAAGGGT	+	9
541	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr13	102681498	CcCCtcAGGtCtTtgGtACCAGGCTTGGAT	-	8
542	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr13	105444228	CACCCaGcGgGaGtgCAGGCAGGCATGGAT	+	7
543	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr13	111052405	CtggGaGtGGgGaGGCCtGGCAGGCTGGGGT	-	8
544	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr13	112723361	aAtCaGGaGCaaGaCCAGGCAGGCCTGGGT	+	8
545	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr13	114136231	CACacACaCacACgGGgGTGGAGGGTAGGGAT	-	7
546	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr14	11910722	CAggcaGGcagGCaGgCAGGCAGGCAGGAAT	+	9
547	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr14	12509076	CAtCaAAGGGtaTaCttgCCAGGCAAGAAT	+	8
548	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr14	14986067	CACCcaattGCagGGCttGGCAGGCAGGAAT	-	9
549	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr14	23975031	CtagGAAGtagCTGgGatCCAGGCCAGGGAT	+	9
550	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr14	25304711	CtgCcAcaGGCCctCaCACCAGGCCGGAAT	-	8
551	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr14	25773733	CtCCatCaaCccCCTGGAGaaGAGGGTAGGGAT	-	9
552	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr14	26531551	CAggGgAGaGCCactGCACCAGGCACAGAGT	+	7
553	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr14	28440110	CAgacaGGcagGCaGgCAGGCAGGCAAGAGT	-	9
554	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr14	30082011	CAggcaGGcagGCaGgCAGGCAGGCACGGGT	-	9
555	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr14	30612628	CACgtggtGGCtTGCctcCCAGGCCAGGAT	-	9
556	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr14	32562154	aACtGACCCCAgtgGGctgGGAGGGTGGGAGT	+	8
557	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr14	41192606	gACCaCtGGGCtaGtgCAGGCAGGCAAGGGT	+	7
558	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr14	53622914	CAggcaGGcagGCaGgCAGGCAGGCATGGAT	+	9
559	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr14	57798611	CcCCGAgGacgCaGCcCgCCAGGCCCGGGT	-	8
560	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr14	62300124	aAagGAAGGGtgTGtcCACCAGGCCAGAGT	+	7
561	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr14	63493007	CtgCcAgaGcCaTGCtCACCAGGCCAGAGT	-	8
562	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr14	63703799	aAgCGcAGGcCacGCctACCAGGCAAGAAT	-	8
563	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr14	66153763	CAatGAtGctCCaGCaacCCAGGCTGGGGT	+	9
564	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr14	70861731	CAggcaGGcagGCaGgCAGGCAGGCAGGGAT	+	9
565	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr14	70895904	CACCcttcGGCagGCCtGGCAGGCCGGGAT	+	8
566	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr14	72181539	CACCcAAcaGCCatgatgCCAGGCTAGAGT	-	9
567	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr14	74495784	CAagGAAGcaCtTGttacCCAGGCCAGGAAT	-	9
568	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr14	75613804	aAgCtgAGGGCagGaaCtCCAGGCCAGGAAT	-	9
569	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr14	76617123	ttCCaAAGGaCCaagGatCCAGGCACGGGT	-	9
570	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr14	78674124	CAtgcaGGcagGCaGgCAGGCAGGCAGGAGT	+	9
571	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr14	80562162	CtCtacAtGaCCTGgGagCCAGGCTTGGAT	-	9
572	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr14	81843636	CcCtGAccGCtTGaGttCCAGGCCTGAAT	+	9
573	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr14	94725726	gcCaaAAGtGCtTgGgACCAGGCAAGAAT	+	9
574	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr14	96951751	ggCCtCaGGGtGtaGggAGGCAGGCAGGGGT	+	9
575	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr14	98168981	CgCCGctGctCCcGgcCgCCAGGCTGGGGT	+	9
576	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr14	102124710	CtagGACtggAgaTGGaaTGGAGGGTGAGGAT	+	9
577	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr14	105341431	tcCCaCaGGaaGCGaCCctGCAGGCTTGAGT	+	9
578	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr14	118049261	aAggcAtGcGCCacCaCACCAGGCAAGAAT	-	9
579	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr14	121666531	CtCtGAtctCaTGgGCACCAGGCATGAAT	+	8
580	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr15	4538774	aACCGtGaGCCatCtCtCCAGGCCATGAAT	+	9
581	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr15	4930962	gAgtcAAGGtCTagGCACCAGGCCTGGGT	-	8
582	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr15	12809175	CcCtGAgttcCCacCcCACCAGGCGTGAAT	-	9
583	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr15	35255002	CACaGCtGGGgaCaaaatGGCAGGCGAGAAT	+	9
584	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr15	37068666	CcaCtcAGaGCCTtgGtcCCAGGCTAGGAT	+	9
585	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr15	54799982	CtCCttgGcctCTtgGCACCAGGCTGGGGT	+	9
586	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr15	59540985	CACaGCccGtCGtGGgtAtGCAGGCGGGGAT	-	9
587	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr15	63954610	CAgtGAAGacaCactGtACCAGGCTAGAAT	-	9
588	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr15	65109882	CAttataGtGaGCaGCaAGGCAGGCAGGGAT	+	9
589	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr15	73035793	CAtgcaGGcagGCaGgCAGGCAGGCAGGAAT	+	9
590	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr15	74723850	CAggGCtGcttGtGGCCAaGCAGGCCAGAGT	+	8
591	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr15	76107757	aACtGtAGaGCCaaGCGttCCAGGCCAGGGAT	-	8
592	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr15	76378269	aAgacAAGcaCCacCaCACCAGGCAAGAAT	-	9
593	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr15	78664606	CctCtAaCCtAgCTGGAccaGAGGGTGGGAAT	-	9
594	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr15	78796591	CtgCgCCCCAgCTtcAGacAGGGTGTGGAT	-	9
595	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr15	78858217	tgCCaccGtGCCacCGCACCAGGCTAGGGT	-	8
596	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr15	79502867	aACCGAAGacCgacCaggCCAGGCTGGGAT	-	9
597	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr15	79996883	CAgCagGGaaCatGthCAGGCAGGCTAGGGT	-	9

598	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr15	80070079	atCCtAAttcCCTGtGttCCAGGCCGGAGT	+	9
599	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr15	82373520	CAtCGgtGGGaGgGGaggGGCAGGCTGGGGT	-	8
600	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr15	83401238	CcCtGcAcctCCTGCatgCCAGGCAGGAGT	-	9
601	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr15	87721010	aACCatAtGcagTGCaCACCAGGCCTGAAT	-	8
602	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr15	87978712	CgggGcAGGagCTGCagtCCAGGCCATGGGT	+	9
603	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr15	91397763	gAgaGgaGGGaGaGGCCAtGCAGGCATGGGT	-	8
604	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr15	93336955	CggCGCGGGtCaCGtCgcGCAGGCAGGAGT	-	8
605	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr15	98968874	aACCaCaGtGCtCGgagtGCAGGCTGGAAT	-	9
606	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr15	100768206	CACaGgGtcGgaaGGCtgGGCAGGCCTGGGT	-	9
607	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr15	102364355	CtCtGAactGCCccctcCcCCAGGCACGAGT	+	9
608	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr16	4084975	CcagGctGGGgCTGCatACCAGGCTGGGAT	+	8
609	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr16	7296055	tAaaagGaGGaGaaGCCAGGCAGGCAAGAGT	-	9
610	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr16	8237459	tgCaGAAGaGatTctGCcCCAGGCAGGAAT	-	9
611	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr16	29714613	gAtCGActGGtCgGaGatCCAGGCCAGAGT	+	9
612	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr16	31520231	tggtGtGGGGCGagGGCggGGCAGGCTGGGGT	-	9
613	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr16	32741027	aAaCacAGGGagcGCGtgCCAGGCACGAGT	+	9
614	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr16	47648456	acCCactGaGCCatCtCACCAGGCCGGAAT	+	9
615	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr16	51781482	CttCGtAtttgCTGCctACCAGGCAGGAAT	-	9
616	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr16	76599263	gAtaGAAGaGatgGCGagCCAGGCAGGAAT	-	9
617	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr16	86523901	tAtgGtAGGGCtaGgGacCCAGGCATGGGT	-	9
618	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr16	92296678	agCCGAgGaGCagGCaCtCCAGGCCAGAGT	+	8
619	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr16	93058037	CACtGtAGatCCctCtgcCCAGGCTGGGGT	+	9
620	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr16	95653807	CAagcaaGGcaGCatCCAGGCCAGGCATGGAT	-	9
621	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr16	96257044	CAggcaGGcaggCaGgCAGGCAGGCAGGAAT	+	9
622	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr17	4989255	ttCtGAActcCCTGgcCACCAGGCACGAAT	+	8
623	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr17	7239340	CtCCatCcCAgCTGGgGcGGAGGGTGAGGGT	-	7
624	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr17	11393387	CACCatCaCtgtgTttAGTGGAGGGTGAGGAT	-	9
625	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr17	11877092	CtCCagAGacaaTGgGaACCAGGCAGGAAT	-	9
626	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr17	13208284	CAtCctGcaGCGaaGCtAaGCAGGCAGGAGT	-	9
627	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr17	19402027	aACCtttgCAAgcGaAGTGGAGGGTGAGAGT	+	9
628	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr17	19703962	tttaGAagtCAtgTGGAGTGGAGGGTGGGGAT	+	9
629	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr17	25328971	CAgCaggcaGgCTGgGaACCAGGCGAGAAT	+	9
630	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr17	25489501	gACaaAgGGGgtTcCtgACCAGGCAAGAGT	-	9
631	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr17	26100322	CAgCaaGtaaCcCGaCCtGGCAGGCAGGAGT	-	9
632	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr17	27598481	CACCttCCCCtAgcaGcGcaGAGGGTGGGAGT	-	9
633	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr17	30701492	CcCaGgAGGcCtaGgGttCCAGGCAGGAGT	-	9
634	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr17	32217864	CAagGaGaGtCcCtGtgAGGCAGGCAGGGGT	-	9
635	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr17	35138694	gcCCcAgGGcCCcGaGtgCCAGGCAGGGGT	-	9
636	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr17	45530371	ttCCtCcttGaGCtGCCtGGCAGGCTAGAGT	+	9
637	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr17	46452848	CACtagttGGCaTGgGgtCCAGGCAAGAGT	-	9
638	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr17	46626496	tgCCctcGccCCTGtGtACCAGGCCTGAAT	+	9
639	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr17	47754264	CcCCcCcccCcCcGgCAGGCAGGCTCGAAT	-	9
640	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr17	47802371	gAaCtgAaGGgCTGCaggCCAGGCCAGGAT	-	9
641	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr17	48006368	gcCtGtAGGcttgGCaCACCAGGCAGGGGT	+	9
642	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr17	48814087	ggagaAAGGtaTGCcCACCAGGCCTGGGT	-	9
643	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr17	49030382	gAgtGCtGGagGaGGCtArGCAGGCAGGGAT	+	9
644	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr17	50325041	gACtatAGGtCtgaaGCACCAGGCTAGAGT	+	9
645	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr17	51539790	tgaCacgGGtgCTGaGCACCAGGCTCGAGT	+	9
646	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr17	56895029	ggCaGGgGGrtCaCGGCCAGGCAGGCAGGAGT	+	7
647	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr17	67696999	tgCtcACCCCAACTGGAGTGGAGGGTCAGAGT	+	4
648	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr17	67697184	aggGCGGGGCGCGGCCAGGCAGGCGGGGGT	+	4
649	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr17	67697217	gtCCGAAGGGCCTGCGCACCAGGCCAGGGT	+	2
650	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr17	74246645	CAggcaGGcaggCaGgCAGGCAGGCAGGAAT	+	9
651	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr17	79698437	CcCgGAAaacaCTGtGgACCAGGCTTGGGT	-	8
652	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr17	79899281	gggCtatGGcCGaGGCCAGGCAGGCCGGGGT	-	8
653	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr17	80755465	ttCtGAAGGGCtgcCaagCCAGGCAAGAAT	+	9
654	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr17	84059032	CttaGtCgCCcACaGGgGTGGAGGGTTAGGAT	+	8
655	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr18	8664611	CgtGAAGtGtCTGCtgcCCAGGCCTGGGT	-	8
656	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr18	11055089	ttCgaAgGGtCCTGCtggCCAGGCAGGAGT	-	9
657	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr18	24331496	tAtgGCaGcagGCaGgCAGGCAGGCAAGAGT	-	9
658	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr18	24884321	aAaCaAAGGctCTGtctcCCAGGCAGGGAT	+	9
659	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr18	25534154	CcagGcCtgtAACaGGgGTGGAGGGTAGGGAT	+	9
660	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr18	26105816	CtttGtGGctgGCaGgCAGGCAGGCAGGAGT	+	9
661	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr18	30166283	CctgtAAataCCTGCcCcCCAGGCTGGGAT	+	9
662	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr18	31955429	gttCagAGGGaCTGtGaACCAGGCTTGAAT	-	8
663	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr18	34436822	ggCtGAgGGaCCatCaCACCAGGCAGGGAT	+	8
664	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr18	34777262	CcgCaccGtGCCgGCcCtCCAGGCCCGAGT	-	9
665	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr18	35956458	acCCagGaGagGCaGgCAGGCAGGCATGGAT	-	9
666	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr18	35989110	CtCCcAAGaGggctCtgACCAGGCCTGAGT	-	9
667	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr18	37969479	CgCCGcAGGagtgGgGtACCAGGCGAGAAT	-	8
668	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr18	42626305	ttCtcAgGaGCCTGaGCACCAGGCCAGGAT	-	7
669	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr18	49749340	CAggGCaaGcaGtaGgCAGGCAGGCATGGAT	+	9
670	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr18	61821232	tAtCGgAaaGCCTGCtCcCCAGGCTAGGAT	+	7
671	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr18	62058979	CAggcaGGcaggCaGgCAGGCAGGCAGGGAT	+	9
672	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr18	69341102	gACtcACtCAtAtgGGgGTGGAGGGTGGGGGT	+	8
673	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr18	75554852	atCtGAcaGGgCTGCctgCCAGGCGGGGGGT	+	9
674	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr18	75587686	CgCtccttttGCCTGgcCACCAGGCTGGGGT	+	9
675	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr18	77003914	CAggtAAaGGtCaGaGggCCAGGCCTGGGT	-	9
676	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr18	80290043	gAggacCCggAgCTGGAGTGGAGGGTCAGAGT	+	8
677	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr18	82033084	aAaCccttGtGCTTGCtgACCAGGCATGGAT	+	9
678	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr18	85484016	ttCtGAgctcCaTGgGCACCAGGCATGGAT	+	9
679	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr19	10291798	CtCCtctGGGCtgctGgACCAGGCAGGGGT	+	9
680	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr19	10473650	gACaGcAGGtgCTGaGagCCAGGCTAGAGT	+	8
681	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr19	15509500	CAggGAActtCCTGacatCCAGGCTGGGAT	-	9
682	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr19	17118070	attCGAAGGGCtccaGttCCAGGCAAGGGT	-	9
683	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr19	24509474	CACgcAgGGGCCaGCtCcCCAGGCAAGAAT	+	6
684	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr19	28869299	CAtCGAtctGtCTcaGgcCCAGGCATGAGT	-	9
685	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr19	40318577	gACgGcaGaGCctGGCttGCAGGCAGGGGT	-	9
686	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr19	44682710	CAaCGgaGcaaGgGGtCAGGCAGGCTTGGGT	+	8
687	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr19	44999000	CtaCGgtGGtgGCcaCCAtGCAGGCATGGAT	-	9
688	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr19	45711447	CACCccttctgCTcCtCACCAGGCCCGAGT	-	9
689	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr19	46443869	gAgtGcAGGGCaTaaagACCAGGCTGGAGT	+	9
690	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr19	49875622	CACtcCtacagGCaGgCAGGCAGGCAAGGGT	+	9
691	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr19	55342092	CACCGAcacaCCgGCaCcCCAGGCTGGGGT	-	7
692	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr19	55693963	gAgaGAtGccCCTGgcCCCCAGGCAGGAGT	+	9
693	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr19	56185078	CAgaAtGaGtCTtCatACCAGGCCTGGAT	-	9
694	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr19	59026211	ttCCacAGGGtCaGCtgtCCAGGCGAGAGT	-	9
695	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chrX	41941542	CAtCatGGtGgGaaGCatGGCAGGCATGGGT	-	9
696	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chrX	48055904	CAggcAtGtGtCacCaCACCAGGCAGGGAT	+	9
697	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chrX	49387738	CtgaGcAGGGgCTGaagACCAGGCGGGGGT	+	8
698	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chrX	56575516	CAtCtctGaGtCTtCtCACCAGGCATGGAT	+	8
699	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chrX	60893103	CcCCGCaGctCcCGGCgctGCAGGCAAGAGT	-	8
700	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chrX	89419565	aggacAAGGGaaTGgGCtCCAGGCAGGAAT	-	9
701	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chrX	93284620	gACCGacaccCGCaGCgAcGCAGGCGAGGGT	+	9
702	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chrX	95412272	tACtGCaaGtCCgtGCCAtGCAGGCAGGAGT	-	8
703	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chrX	95671635	tttaGAggtCAgaTGGAGTGGAGGGTGGGGGT	-	9
704	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chrX	167049748	gAggGCttGGgGCtGggAGGCAGGCTTGAAT	+	9

Supplemental Table 6. Primers, plasmids and sgRNAs used in this study

	Name	Sequences (5' to 3')	ID Number
Primers	U6_gRNA_PCR_F	GAG GGC CTA TTT CCC ATG ATT CCT	RDC 255
	dTomato_guide_B	AAA CCA CTG TGG GGT GGA GGG GAC	RDC 1194
	mGAPDH F	TGTTTGTGATGGGTGTGAACC	RDC 345
	mGAPDH R	ACTGTGGTCATGAGCCCTTC	RDC 346
	Lama1 Primer FW	GGAAGGTTACAAAGTTCGATTGG	RDC 977
	Lama1 Primer RV	ACGTGAAATAAGACCTTGCCATC	RDC 978
	Lama1 qPCR 1 KL F	TTTCTTTGAAGGAAGCGGATATG	RDC 1918
	Lama1 qPCR 2 KL F	TGGGTCCATTAACAGAAGGAAAG	RDC 1919
	Lama1 qPCR 2 KL R	ATGGGTGAAGTCCAAAAGTTGAG	RDC 1920
	Vector genome F	ATGGTGAGCAAGGGCGAGG	RDC 1687
	Vector genome R	AGCTTGCCGTAGGTGGCATC	RDC 1679

	Name	ID number
Plasmids	minCMV-tdTomato	RDC 262
	px601 SadCas9-VP64	RDC 153
	3-guide casettes	RDC 367

	Name	Sequences (5' to 3')	PAM
sgRNAs	*tdTomato* sgRNA Top *tdTomato* sgRNA Bottom	CACCGTCCCCTCCACCCCACAGTG AAACCACTGTGGGGTGGAGGGGAC	AAGAAT
	Lama1 sgRNA1 Top *Lama1* sgRNA1 Bottom	CACCGAAGGGCCTGCGCACCAGGC AAACGCCTGGTGCGCAGGCCCTTC	CAGGGT
	Lama1 sgRNA2 Top *Lama1* sgRNA2 Bottom	CACCGCGGGGCGCGGCCAGGCAGGC AAACGCCTGCCTGGCCGCGCCCCGC	GGGGGT
	Lama1 sgRNA3 Top *Lama1* sgRNA3 Bottom	CACCGTCCAGGGGGAGCCCCGCCGTG AAACCACGGCGGGGCTCCCCCTGGAC	CGGAGT
	Lama1 sgRNA4 Top *Lama1* sgRNA4 Bottom	CACCGGTGGTGGCGGGGTGCCTCTC AAACGAGAGGCACCCCGCCACCACC	CTGGGT
	Lama1 sgRNA5 Top *Lama1* sgRNA5 Bottom	CACCGACCCCAACTGGAGTGGAGGGT AAACACCCTCCACTCCAGTTGGGGTC	CAGAGT