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

Introductory paragraph

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

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

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

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

Congenital muscular dystrophy 1A (MDC1A) is an autosomal recessive neuromuscular disease associated with a high degree of morbidity and mortality in early childhood [1]. It is caused by mutations in the *LAMA2* gene encoding Laminin α2 chain (LAMA2), which interacts with the β1 and γ1 chains to form the heterotrimer Laminin-211, an extracellular matrix protein (reviewed in [3]). Laminin-211 interacts with α-dystroglycan and α7β1 integrin in skeletal muscle and Schwann cells, providing the necessary roles such as survival and stability of myotubes, as well as proper neurite growth, axon myelination and migration of Schwann cells. Lack of Laminin-211 in MDC1A causes degeneration of skeletal muscle and impaired Schwann cell differentiation, resulting in a cascade of secondary events including apoptosis/necrosis of muscle fibers, inflammation, and fibrosis, which ultimately precipitate the disease. Despite significant advances in our understanding of MDC1A pathophysiology, currently, there is no cure.

Due to the genetic nature of the disease, gene therapy is a promising treatment option for MDC1A. The large size of *LAMA2* transcript, however, presents a challenge with respect to gene delivery. We have recently overcome this challenge by using CRISPR/Cas9 technology to correct a mutation in *Lama2* gene *in vivo* [4]*.* We focused on dy^{2J}/dy^{2J} mouse model, which harbors a splice site mutation in *Lama2* causing spontaneous exon skipping and truncation of N-terminal domain of the protein [5]. We developed an exon inclusion strategy to correct the splice mutation, leading to restoration of full-length Lama2. This study established the first direct correction of the primary genetic defect underlying MDC1A in an *in vivo* model.

To date, there are over 350 reported pathogenic nonsense-, missense-, splice site- and deletion mutations in the *LAMA2* gene. Given the variety of MDC1A-causing genomic alterations, CRISPR/Cas9-mediated gene editing strategies would require design and thorough analysis of multiple sgRNAs specific for each individual mutation. Moreover, safety concerns regarding CRISPR/Cas9's potential mutagenic nature and the presence of off-target effects after gene editing remain, which together may prove to be challenging from a safety and regulatory point-of-view. In contrast, the attenuation of disease pathogenicity by targeted modulation of disease modifier gene expression would be a potentially safer alternative and beneficial to all individuals with MDC1A.

One of the strongest reported disease modifiers for MDC1A is Laminin-α1 protein, which is structurally similar to Laminin-α2 (**Fig. 1a**). However, Laminin-α1 is not expressed in skeletal muscles or Schwann cells. A series of studies previously demonstrated that transgenic expression of *Lama1*, encoding Laminin-α1, rescued both myopathy and peripheral neuropathy in *dy*^{2j}/*dy*^{2j} [6] and *dy*^{3K}/*dy*^{3K} [2,7-10]; the latter also showed increased lifespan. Although these studies firmly established compensatory function of Laminin-α1 in MDC1A, utilization of this modifier as a postnatal gene therapy is hampered by the size of *Lama1* cDNA, which exceeds the 4.7 kb packaging capacity of AAV vectors. Advances in CRISPR/Cas9 technologies have provided opportunities for regulating gene expression and creating epigenetic alterations without introducing DNA double-strand breaks (DSBs); commonly termed CRISPR transcriptional activation/inhibition system. The strategy utilizes nuclease-deficient Cas9 (dCas9), which is unable to cleave DNA due to mutations within the nuclease domains, but still retains the ability to specifically bind to DNA when guided by a single guide RNA (sgRNA) [11,12]. Using the originally described *S. pyogenes* (*Sp*) dCas9 fused to multiple copies of the VP16 transcriptional activator, our group and others have demonstrated utilization of the CRISPR/dCas9 system to upregulate expression of modifier genes *in vitro* [11-14]. A major challenge for *in vivo* applications lies in the large size of *Sp*dCas9 and its transcriptional activator fusion derivatives that exceed AAV genome packaging capacity. To accommodate this limitation, we sought to adapt the transcriptional upregulation system and utilize a significantly smaller Cas9 protein derived from *S. aureus* (*Sa*)[15] to upregulate MDC1A modifier *Lama1*. We hypothesized that CRISPR/dCas9-mediated transcriptional upregulation of *Lama1* would be sufficient to compensate for the lack of *Lama2* and ameliorate disease phenotypes in *dy*^{2j}/*dy*^{2j} mice.

First, we mutagenized *Sa*Cas9 endonuclease catalytic residues (D10A, N580A) to create *Sa*dCas9 and then fused it to transcriptional activators VP64 (four copies of VP16) on both N- and C-termini (**Fig. S1**). We tested the ability of the system, denoted as *Sa*dCas9-2xVP64, to upregulate the expression of minCMV-driven *tdTomato* gene in 293T cells [16]. In the absence of the *Sa*dCas9-2xVP64, the expression of *tdTomato* was undetectable due to the low baseline activity of minCMV promoter (**Fig. S1a, b**). In the presence of *Sa*dCas9-2xVP64 in combination with an sgRNA targeting the minCMV locus, we observed high *tdTomato* fluorescence signal (**Fig. S1c, d**), indicating the general applicability of this system to modulate expression of a gene of interest.

Subsequently, we tailored the system to upregulate *Lama1* expression and designed five sgRNAs, denoted as g1 to g5, within the 500 nucleotides region immediately upstream of the *Lama1* transcription start site (**Figs. 1b, c**). When co-expressed with *Sa*dCas9-VP64 in C2C12 murine myoblasts, 3 out of 5 sgRNAs, namely g1, g2, and g5 consistently induced significant increase of *Lama1* transcript expression (**Figs. 1d, e**).

Although all sgRNAs were designed to target a chromatin-accessible region derived from DNAse1 hypersensitivity- and assay for transposase-accessible chromatin (ATAC-Seq) sites (**Fig. 1b**), g3 and g4 failed to increase expression of *Lama1* above the basal level. This corroborates previously reported findings that chromatin accessibility is not a reliable predictor of successful gene activation [12,17,18]. Nonetheless, the sgRNA closest to the transcription start site, g1, and the combination of the three most optimum sgRNAs (g1, g2, g5) resulted in a robust increase in Lama1 protein expression in *dy*^{2j}/*dy*^{2j}-derived myoblasts (**Figs. 1f, 1g**), warranting further investigation *in vivo*.

We then treated 3-week-old *dy*^{2j}/*dy*^{2j} mice with an AAV9 carrying FLAG-tagged *Sa*dCas9-2xVP64 in the absence of sgRNA (no guide) or with g1 (single guide) or a combination of g1, g2 and g5 (three guides) (**Fig. 2a**). Due to the packaging capacity of the AAV, the dCas9-2xVP64 and the three guides were split into two vectors (**Fig. 2a**). Each mouse received a single intramuscular injection of 7.5×10^{11} viral genomes of AAV9, which was doubled to 1.5×10^{12} viral genomes total for the three guide cohort, in the right *tibialis anterior* (TA) and was sacrificed 4 weeks post injection. FLAG expression was detected by western blot in all *Sa*dCas9-2xVP64-injected right TA muscles, however, only those injected with guide-containing constructs showed Lama1 upregulation (**Fig. 2b**). Similarly, immunofluorescence staining revealed sarcolemmal expression of Lama1 (**Fig. 2c**, upper), indicating proper protein localization. Furthermore, H&E staining exhibited considerably improved muscle architecture (**Fig. 2c**, lower) in the single- and three guide treatment groups, as compared to the no guide controls.

Next, we sought to investigate whether upregulation of *Lama1* could be achieved systemically *in vivo* and, if administered into pre-symptomatic neonatal *dy*^{2j}/*dy*^{2j} mice, would prevent the manifestation of dystrophic pathophysiology and paralysis. AAV9 particles carrying either no guide or a combination of three guides were injected into the temporal vein of 2-day-old (P2) *dy*^{2j}/*dy*^{2j} mice (**Fig. 3a**). Seven weeks post injection, the animals that received the three guides treatment showed an absence of classical hindlimb contracture, unlike the control group (**Fig. 3b; Supplementary videos 1** and **2**). Western blot, immunofluorescence and H&E staining of TA and gastrocnemius muscles demonstrated robust expression of Lama1 on the sarcolemmal membrane (**Fig. 3c, 3d**), leading to ~50% reduction of fibrosis (**Figs. 3e**, **3f, S2**).

We subsequently examined the ability of *Lama1* upregulation to reverse established muscular and peripheral nerve dysfunctions by initiating the treatment at 3 weeks of age, when paralysis was already apparent [19,20] (**Fig. 4a**). We first tested three different doses, ranging from 7.5×10^{10} to 3×10^{11} viral genome/gram of mouse per AAV9, which was doubled for the three guide cohorts due to the utilization of two vectors, and found that the highest dose resulted in homogeneous Lama1-positive fibers (**Fig. S3a**), significant improvement of muscle function and mobility (**Figs. S3b, S3c**). Longitudinal measurement of animal mobility and stand-up activity in a non-invasive open field activity assay showed significant difference between no guide and three guides-treated mice starting at 5 and 6 weeks old, respectively, which was sustained over time (**Figs. 4b, 4c**). Furthermore, specific tetanic force, which measures the aggregate torque produced by the dorsi flexor muscles, was also improved in the three guides-treated mice (**Fig. 4d**). In line with this finding, we observed a significant increase in nerve conduction velocity, which indicates restoration of the myelination defect and contributes to neuromuscular functionality (**Fig. 4e**). The absence of paralysis in the hind limbs and markedly improved movement of the mice were evident at the end of the treatment regimen (**Supplementary videos 3, 4**).

Molecular analysis of the treated mice revealed strong Lama1 expression by immunostaining and western blot (**Figs. 4f, 4g, S4**), which was accompanied by normalization of α4 chain of the laminin subunit (**Figs. S5, S6**) [6], significant improvement in muscle histopathology (**Fig. 4h**) and approximately 50% reduction in the fibrotic area (**Fig. 4i**) compared to the no guide control group. There was a trend towards larger fibers in the treated mice, although it did not reach statistical significance due to the large variation between animals (**Fig. 4j**). In addition, upregulation of Lama1 was also observed in the endoneurium of sciatic nerves and resulted in restoration of myelination defect (**Figs. 4k, S7**), supporting the improvement of nerve conduction velocity and lack of paralysis in the mice (**Fig. 4e**, **Supplementary videos 3, 4**). Quantification of the AAV genome copy number revealed accumulation of most of the viral genome in the liver, which is expected from intravenous delivery. Nevertheless, approximately 1.11±0.4 and 34.1±4.3 copies/diploid genome of the viral genome were detected in the sciatic nerves and skeletal muscles, respectively (**Fig. S8**). Remarkably, even relatively low transduction efficiency in sciatic nerves was sufficient for functionally significant upregulation of Lama1 expression.

Finally, we investigated the genome wide effects of CRISPR/dCas9-mediated Lama1 upregulation by performing RNA-sequencing on quadriceps muscles isolated from mice treated with AAV9 carrying no guide and three guides (**Figs. S9, S10, Supplemental**

Tables 1-3). Age-matched wildtype and *dy*^{2j}/*dy*^{2j} mice served as controls. We observed a 3.6-log$_2$fold upregulation of Lama1 (defined by a false discovery rate, FDR <0.05) when comparing the mice treated with AAV9 carrying no guide and three guides (**Fig. S9a**). The transcriptional change was even higher at 9-log$_2$fold when comparing untreated *dy*^{2j}/*dy*^{2j} with three guide-treated *dy*^{2j}/*dy*^{2j} (**Fig. S9b, S9c**). Hierarchical clustering between groups revealed clustering between wildtype and three guides, whereas the untreated cohort was clustered together with no guide-treated mice (**Figs. S9d, S10**). We also computationally predicted 704 potential off-target binding sites for the three sgRNAs targeting *Lama1* promoter in the mouse genome, selected based on the presence of a 6bp PAM-proximal seed sequence and fewer than ten total mismatches to the cognate target sequence (**Supplemental Tables 4-5**). None of the top 100 genes contained a predicted off-target site within 60 kilobases of the gene body, with the average distance from off-target site to the gene body being 2.2 megabases. Taken together, our results provide strong evidence of the robustness and durability of CRISPR/dCas9-mediated Lama1 upregulation for the treatment of MDC1A. Additionally, we show the therapeutic promise of the strategy for reversal of dystrophic feature in skeletal muscle and peripheral neuropathy in *dy*^{2j}/*dy*^{2j} mouse model of MDC1A, which ultimately halts progression of the disease, without any confounding off-target effects.

One challenge in developing a therapy for MDC1A is that the heterogeneity of mutations often leads to variable disease severity and progression. Therefore, there is an urgent need to develop a universal, mutation-independent strategy that provides a treatment approach for all patients with MDC1A. Our study establishes a framework in which CRISPR/dCas9 transcriptional upregulation of a disease modifier gene, such as *Lama1,* ameliorates disease symptoms *in vivo* and has the potential to be applied to all MDC1A patients, irrespective of their mutations.

Advances have been made towards elucidating MDC1A pathogenesis due to the availability of several mouse models with absent or reduced *Lama2* expression. Yet, an important question in the development of therapeutics and clinical trials in MDC1A is the reversibility of symptoms caused by muscle fibrosis and nerve abnormalities. This issue has been challenging to address in patients[21], however, the ability to modify gene expression in postnatal animals allowed us to address this question and begin to investigate the therapeutic window of intervention.

We have previously demonstrated that an early intervention using CRISPR/Cas9-mediated correction of a splicing defect resulted in robust Lama2 restoration and prevention of disease manifestation [4]. Here we showed that upregulation of *Lama1*, when initiated at pre-disease-onset, leads to similar prevention. Importantly, when the therapeutic intervention was initiated at older age, significant rescue of the phenotypes was attainable, indicating that post-symptomatic treatment provides a significant benefit in the dy^{2j}/dy^{2j} mouse model.

In addition to *Lama1* upregulation described in this study, a number of disease modifying strategies are currently being explored in MDC1A animal models, including treatment with miniaturized agrin [22-24] and laminin-α1 LN-domain nidogen-1 (αLNNd) [25-27]. While the efficacy of αLNNd has only been explored in transgenic mice, AAV-mediated delivery of mini agrin has been shown to normalize most histopathological parameters in skeletal muscle, and improve myelination and regeneration of Schwann cells of the peripheral nerves [22,24]. Despite the observed phenotypic improvement, the mini agrin-treated mice still have a lower survival rate compared to wild-type animals expressing full-length agrin, suggesting the potential shortcoming of the shortened version of agrin, which may be overcome by its full-length form in native glycosylation state [25]. It is important to note that many preclinical studies in MDC1A were carried out in the more severe dy^{W}/dy^{W} mouse model. Therefore, as a follow up on our study, it will be important to evaluate our approach in the dy^{W}/dy^{W} mice to assess critical parameter such as survival, which is not possible in the *dy*^{2j}/*dy*^{2j} mouse model due to its near-normal life span. Overall, our approach in combining the CRISPR/dCas9-mediated transcriptional upregulation and AAV9 as a delivery vehicle can be translated to many other disease modifiers, such as agrin, as well as conditions where modulation of disease modifiers is required within both skeletal muscles and peripheral nerves.

In fact, neuromuscular disorders have provided excellent examples to demonstrate the role of disease modifiers (recently reviewed in [28]). Beyond MDC1A, several studies have demonstrated that upregulation of *Lama1* stabilizes the sarcolemmal membrane in dystrophin-deficient mouse models [29]. The most advanced approach is via delivery of Laminin-111 protein, although the efficacy remains low and the need to produce a large amount of bioactive protein is challenging [29]. In addition, the utilization of CRISPR/dCas9 system to upregulate Lama1 in *mdx* mice has been achieved locally via electroporation, which is not easily translatable into clinical settings [30]. Our strategy of employing AAV-mediated *S. aureus* dCas9 to upregulate *Lama1 in vivo* may be tested further as a potential therapy in the context of Duchenne muscular dystrophy.

In addition, since the CRISPR/dCas9-mediated transcriptional modulation acts directly on the endogenous locus, it may be used in conjunction with a mutation-correction approach where the level of restoration of the defective gene is suboptimal, therefore necessitating further amplification to reach therapeutic efficacy [4,31-36].

A very recent study by Liao *et al* described utilization of the CRISPR/Cas9 system to recruit MCP:P65:HSF1 transcriptional activation complex to induce expression of target genes in skeletal muscle, kidney and liver tissues [18]. This resulted in phenotypic augmentation such as enhanced muscle mass and substantial improvement in disease pathophysiology, thereby highlighting the feasibility of using CRISPR/dCas9-mediated transcriptional activation as a possible therapeutic modality. However, their study relied almost exclusively on a Cas9-expressing transgenic mouse model or local intramuscular treatments, and therefore it is difficult to extrapolate the efficacy of this strategy to disease-relevant models. In contrast, we successfully demonstrated robust upregulation of Lama1 after systemic delivery of therapeutic components in a relevant mouse model of disease that does not constitutively express Cas9.

Finally, the modular nature of the CRISPR/dCas9 system can be utilized to not only to upregulate, but also to downregulate target gene expression. The latter can be achieved by coupling dCas9 with transcriptional repressor such as Kruppel-associated box (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.

Methods

Engineering of activation constructs

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

Cell Culture

Primary myoblasts were isolated from the Extensor Digitorum Longus (EDL) Muscle of *dy*^{2J}/*dy*^{2J} mice, as previously described[40] and maintained in DMEM supplemented with 1% chicken embryo extract (GeminiBioscience), 10% horse serum, 1% penicillin/streptomycin and 1% L-glutamine (all from Gibco, unless indicated otherwise). HEK293 and C2C12 cells where maintained in DMEM supplemented with 10% FBS, 1% penicillin/streptomycin and 1% L-glutamine (all from Gibco). All cells were maintained at 37^{o}C with 5% CO_2.

Transfection of HEK293T cells was performed as previously described[2]. C2C12 and *dy*^{2J}/*dy*^{2J} cells were transfected in 12-well plates using the Neon Transfection System (Invitrogen). 400,000 cells were electroporated with 1.5 µg of DNA utilizing optimization program 16 (pulse voltage: 1400V, pulse width: 20ms, pulse number: 2). Cells were grown for 72 hours, after which RNA or protein was subsequently collected for protein analysis and guide screening.

Animals, virus production and injections

dy^{2j}/*dy*^{2j} mice were purchased from the Jackson Laboratory and maintained in the Toronto Center for Phenogenomics. Both male and female were used in the analyses. All animal experiments were performed according to Animal Use Protocol number 20-0305. *Sa*dCas9-2xVP64, single guide and three guides plasmids (**Fig. 2a, Supplemental Table S6**) were packaged into AAV9 vectors by Vigene Biosciences as previously described [3]. For intramuscular and temporal vein injection into neonatal pups, the dose of $7.5x10^{11}$ viral genomes each was used. Due to the limitation in packaging capacity, two AAVs were needed for the three guides cohort (**Fig. 2a**), therefore the total virus injected was $1.5x10^{12}$ viral genomes per animal. Injection volume was brought to 50 µl with 1XPBS (Gibco).

For the tail vein injection in young, 3 week old mice, three different doses were initially tested: $7.5x10^{10}$, $1.5x10^{11}$ and $3x10^{11}$ viral genomes per gram of mouse (**Fig. S3**). Similar to the intramuscular and temporal vein injections, two AAVs were needed for the three guides cohort, therefore the total dose used in experiments described in **Figs. 4, S4-S10** was $6x10^{11}$ viral genomes per gram of mouse. Injection volume was brought to 100 µl with 1XPBS (Gibco).

RNA isolation, guide screening and RT-PCR

RNA was isolated from cultured cells and mouse tissue sections, and cDNA synthesis was performed as previously described[3]. PCR amplification was utilized to assess the efficiency of each guide in upregulating *Lama1* expression using a primer in *Lama1* exon 55 (RDC 1919) and a second primer spanning the junction of exons 55 and 56 (RDC 1920). Sequences are listed in **Supplemental Table S6**.

qPCR utilizing Fast SYBR green Master Mix (Qiagen) on a Step One Plus Real Time PCR (Applied Biosystems) was performed. *Lama1* expression was analyzed using a primer in *Lama1* exon 55 (RDC 1919) and one spanning the junction of exons 55 and 56 (RDC 1920). Primers against endogenous Gapdh (RDC 345 and 346) were used as an internal control. ΔΔCt was analyzed to assess fold changes between treated and untreated samples.

Protein Isolation and western blot

Protein was isolated from dy^{2j}/dy^{2j} myoblasts and C2C12 cells by adding 150 µl of a 1:1 part solution of RIPA homogenizing buffer (50-mM Tris HCl pH 7.4, 150-nM NaCl, 1-mM EDTA) and RIPA double-detergent buffer (2% deoxycholate, 2% NP40, 2% Triton X-100 in RIPA homogenizing buffer) supplemented with protease-inhibitor cocktail (Roche). Cells were subsequently scraped from the bottom of each well, collected and incubated on ice for 30 min. Cells then centrifuged at 12000xg for 15 min at 4°C and the supernatant was collected and stored at -80°C. Protein from mouse tissue sections was collected as previously described[3]. Whole protein concentration was measured using

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

Immunofluorescence and H&E staining

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

Toluidine blue staining and electron microscopy

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

Open field and *in vivo* muscle force assays

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

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

Nerve conduction velocity

Mice were anesthetized with urethane (1.2 mg/g i.p.) and underwent a tracheotomy to maintain their airway but were not artificially ventilated. Core body temperature was maintained at 34-36.5˚C using a feedback-controlled heating pad (TR-200; Fine Science Tools). The sciatic nerve was exposed at two locations via incisions (~15 mm) above the left knee (site #1) and along the sacral region of the vertebral column (site #2). After separating the nerve from adjacent tissue, a bipolar hook electrode was applied to the nerve at each site. Each electrode comprised two chlorided silver wires (0.01″ diameter, A-M systems) placed ~1 mm apart and bent at the tip to form hooks, and attached to a stimulator (Model DS3, Digitimer Ltd). Stimulating electrodes were insulated from underlying tissue using a small piece of plastic paraffin film. Stimulus duration was fixed at 20 μs and current intensity was varied. Stimulus timing was controlled by computer using a Power1401 computer interface and Signal v5 software (Cambridge Electronic Design, CED). The compound muscle action potential (CMAP) was recorded using needle electrodes (~30 G, BD *PrecisionGlide*™), one inserted into the gastrocnemius muscle and the other (reference) electrode inserted into the Achilles tendon. The CMAP signal was amplified, low-pass filtered at 10 Hz and high-pass filtered at 1 kHz (DAM 80, World Precision Instruments), and digitized at 40 kHz using the Power1401 and Signal v5 software (CED). To calculate conduction velocity (CV) from CMAP responses, the sciatic nerve was stimulated at just-maximal intensity (beyond which there is no change in CMAP amplitude or latency) three times at site #1 and again three times at site #2. Nerve conduction velocity was calculated as the difference between average CMAP latencies for each stimulation site divided by the length of nerve (7.5-10 mm) separating the sites.

Vector genome quantification

Evaluation of AAV genome distribution was performed as previously published [42] with a few modifications. Genomic DNA was extracted from tibialis anterior, sciatic nerve, and liver of treated mice using Qiagen Blood and Tissue Kit. 90 ng of DNA was amplified using primers located in between the two inverted tandem repeats (ITRs) (RDC 1687, RDC 1679, **Supplemental Table S7**) using Fast SYBR green master mix (Qiagen) on a Step One Plus Real Time PCR (Applied Biosystems). The Ct value of each reaction was converted to viral genome copy number by interpolating against the copy number of standard curve of a known plasmid containing the sgRNA cassette (RDC 362). The amount of DNA input (90 ng per tissue) was used as a conversion factor to diploid genome (7 picogram DNA = 1 diploid genome).

RNA-Sequencing

Total RNA was isolated from quadriceps muscles using RNeasy kit (Qiagen) and quantified using Qubit RNA HS assay (Thermo Fisher Scientific). RNA-Sequencing was performed by the Centre for Applied Genetics in Toronto using the Illumina HiSeq 2500 system, producing 120bp paired-end reads. Raw transcript reads were aligned to the GRCm38 mouse genome (mm10) using HISAT2 [43]. HTSeq was used to determine the absolute number of read counts for each gene [44]. Only genes with at least 1 read per million in at least three replicates were kept for downstream analysis. Normalization and differential expression analysis was completed using the R packages limma, v3.36.3 and edgeR, v.3.22.3 [45]. Differentially expressed genes were defined as genes with a more than twofold change and adjusted $P < 0.05$. Off-target analysis was conducted using a list of 704 computationally predicted using Cas-OFFinder [46]. Using the Bedtools suite "closest" function, each of the top 100 differentially expressed genes was matched to the nearest off-target loci to determine the shortest distance from off-target loci to differentially expressed gene body.

Statistical Analysis

GraphPad Prism (GraphPad software) was utilized to preform all statistical analyses. Two-tailed Student' t-tests to evaluate statistical significance between two groups was preformed. Significance was considered to be $P < 0.05$.

Data availability

The authors declare that the main data supporting the findings of this study are available within the article and its Supplementary Information files. Extra data are available from the corresponding authors upon request.

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Author contributions

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., E.H., R.K., K.M.P., R.M., performed the experiments, D.A.B., K.I.G., M.D., S.A.P. 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. analyzed data, D.U.K, E.A.I., R.D.C. supervised the study, D.U.K. wrote the manuscript with inputs from the other authors. All authors provided feedback and agreed on the final manuscript.

Figure legends

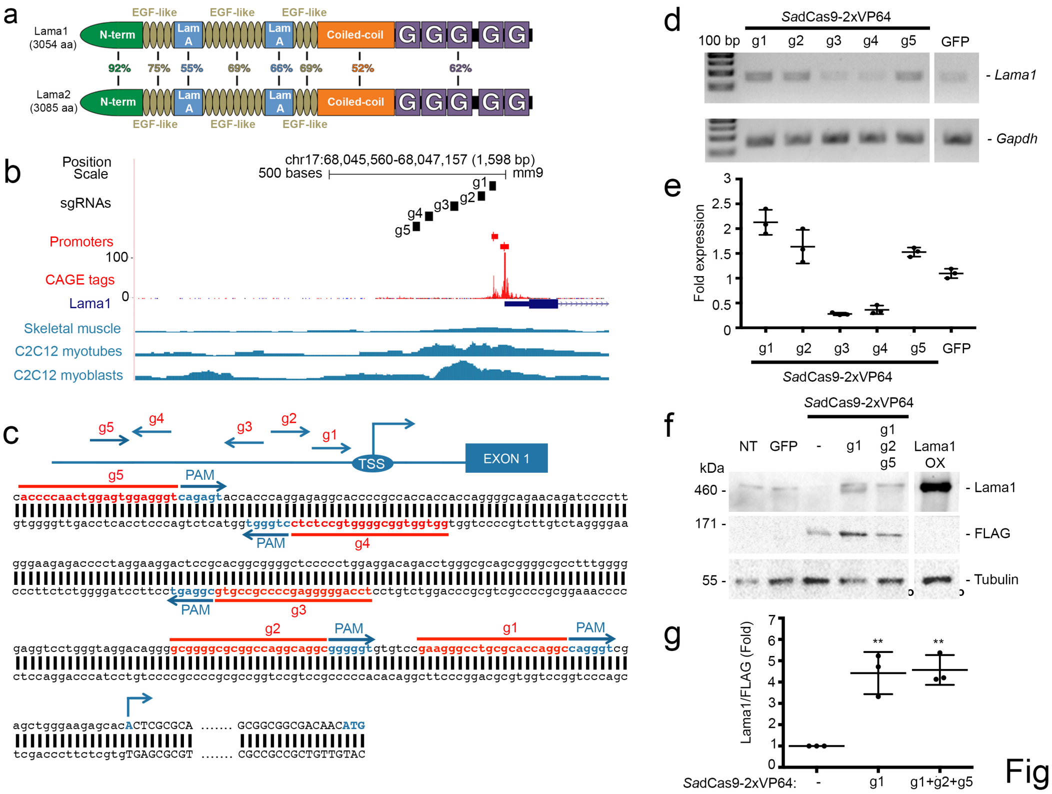

Figure 1

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

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

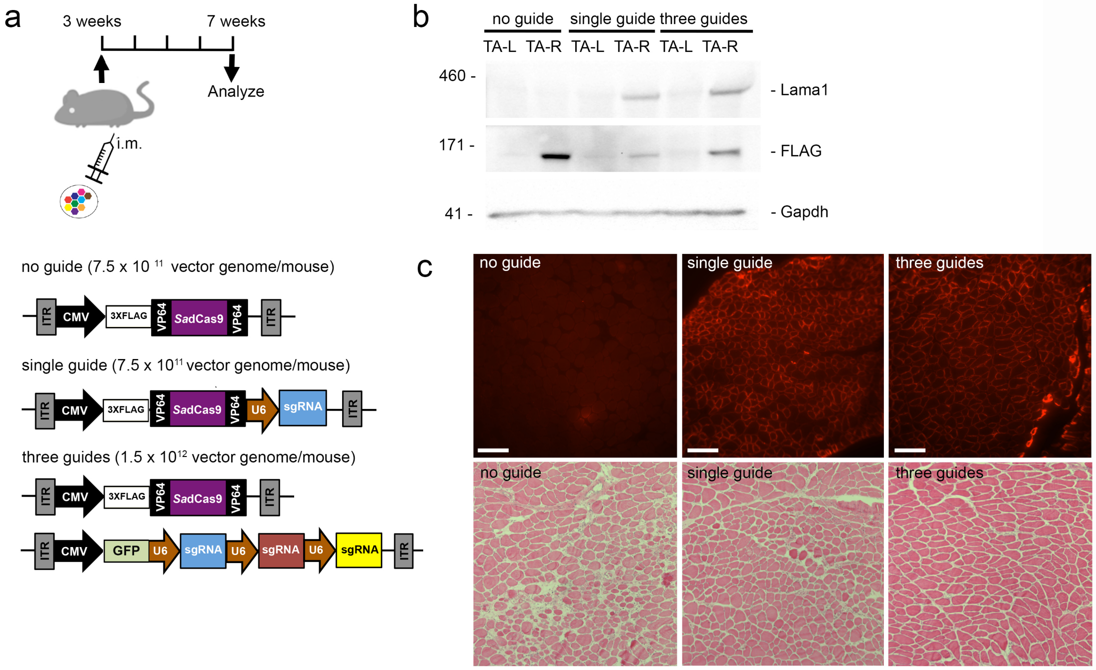

Figure 2

Fig. 2. Upregulation of Lama1 in *tibialis anterior* (TA) muscles of dy^{2j}/dy^{2j} mice following intramuscular administration. (**a**) Right TA muscles of 3-week old dy^{2j}/dy^{2j} mice were injected with AAV9-carrying no guide (n=4; 7.5x10^{11} viral genomes), single guide (n=4; 7.5x10^{11} viral genomes) or three guides (n=4; split into two vectors, thus total dose was 2x7.5x10^{11} viral genomes). ITR: Inverted Terminal Repeats. CMV and U6 promoters are depicted in arrows. Left TA muscles serve as control. (**b**) Western blot analysis on Lama1, FLAG-tagged *Sad*Cas9, and Gapdh expression. (**c**) Immunofluorescence (upper) and H&E (lower) stainings on cross-sections of right TA muscles from each treatment group. Scale bar: 50 μm. Representative images from one animal per treatment group are shown.

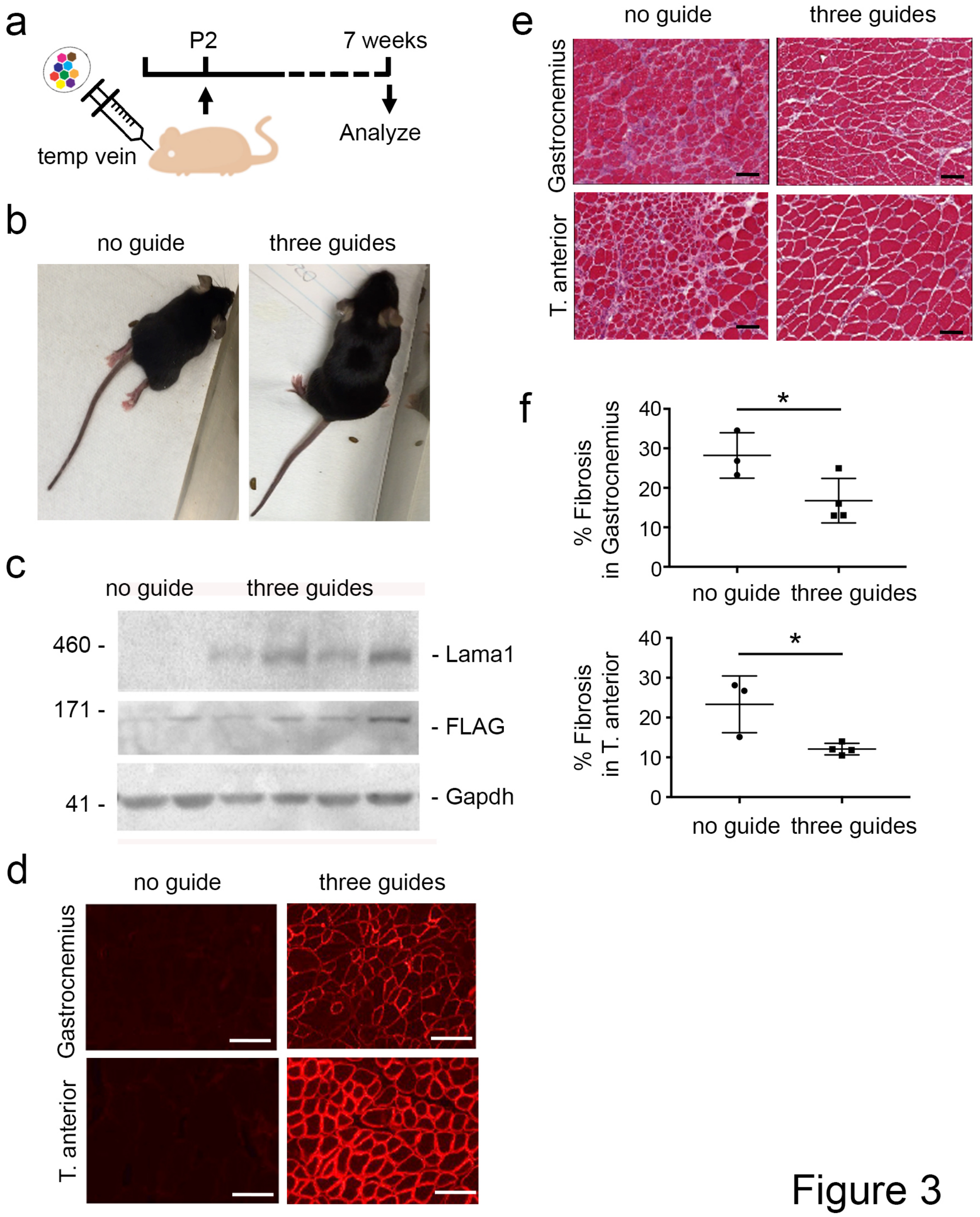

Figure 3

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

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

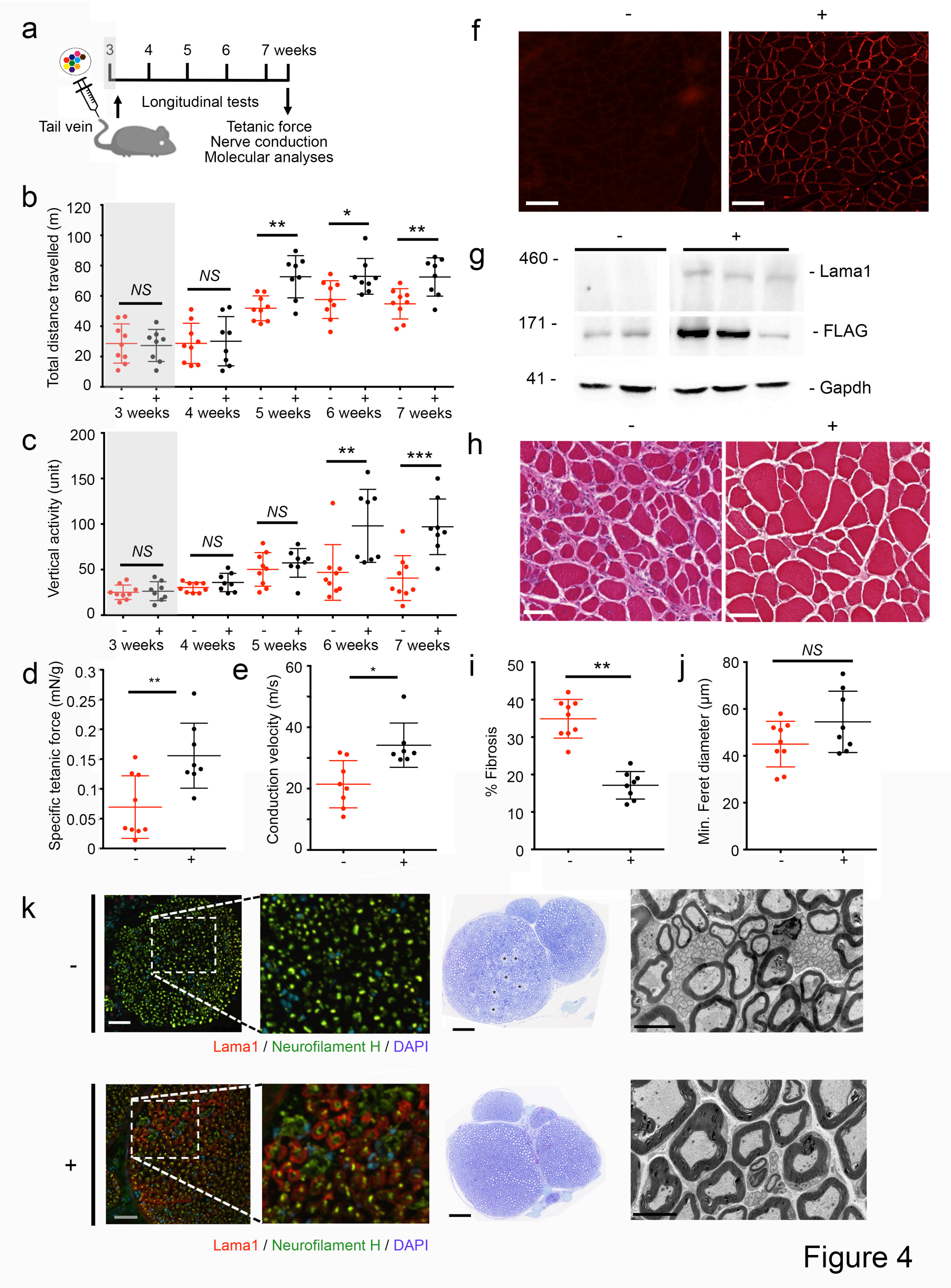

Figure 4

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

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

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Extended data/supplementary figures

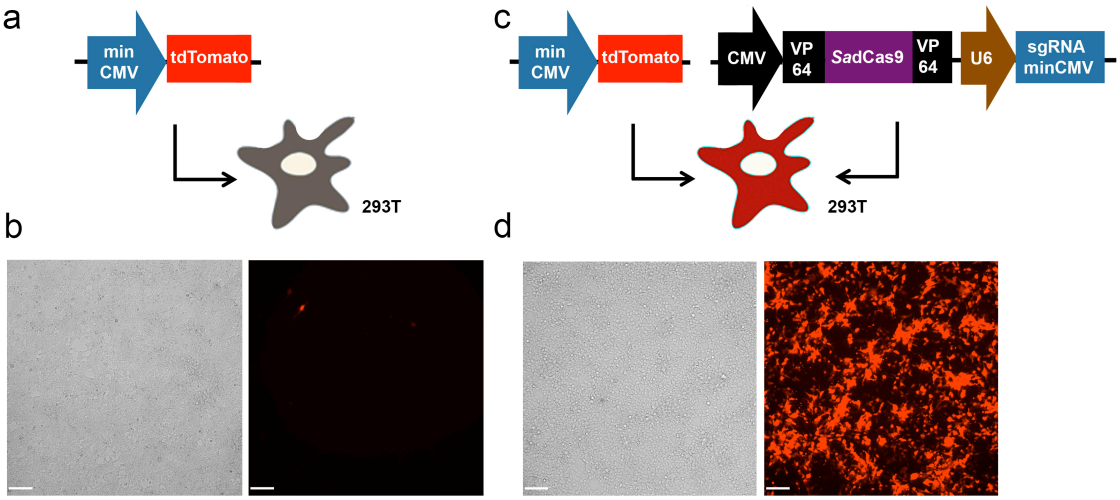

Figure S1

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.

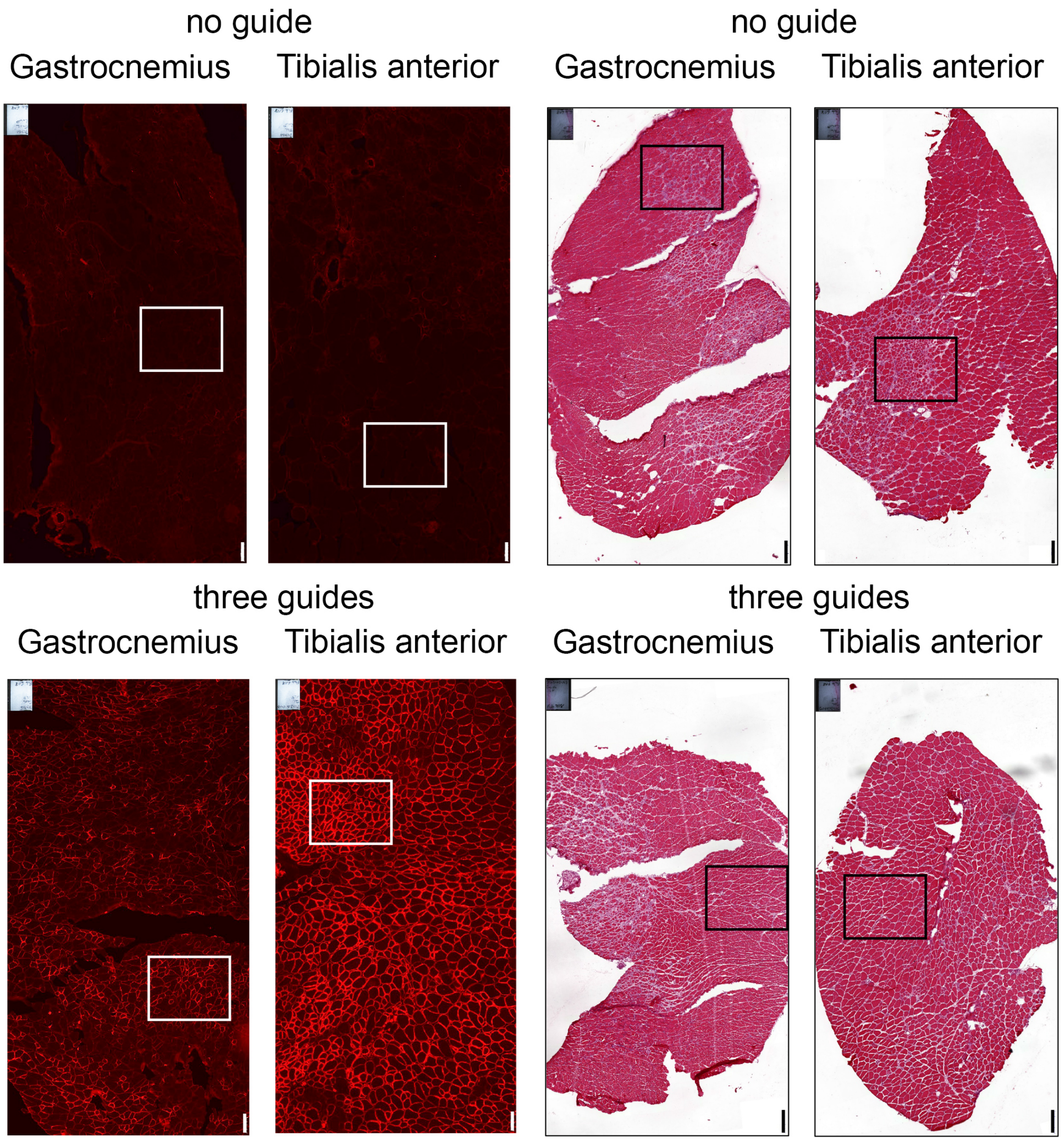

Figure S2

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.

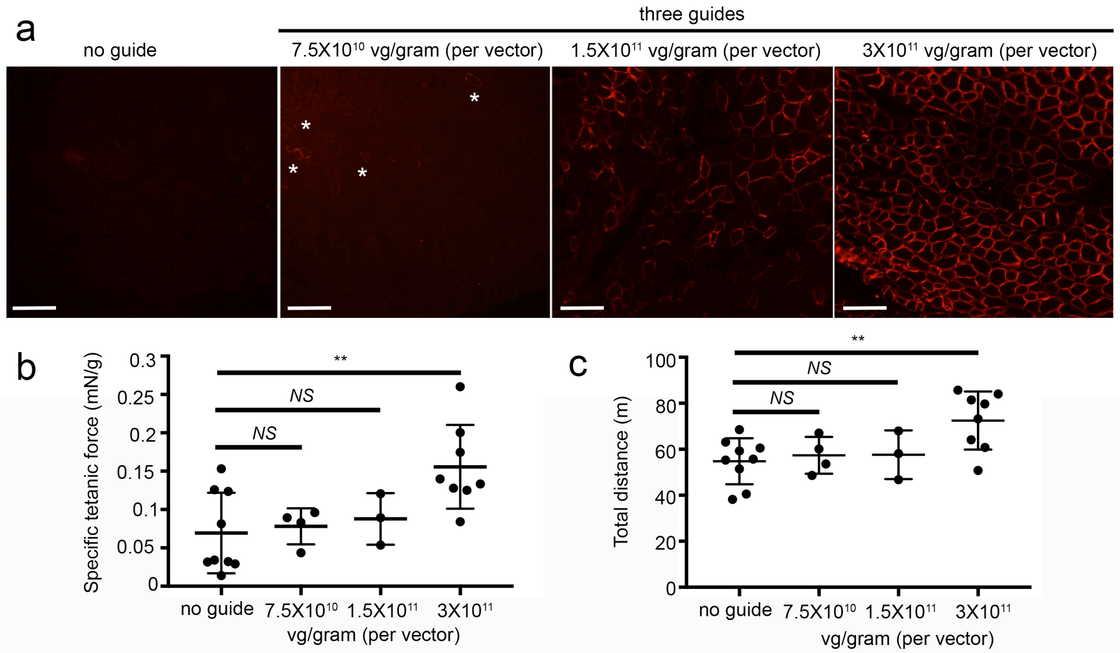

Figure S3

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.

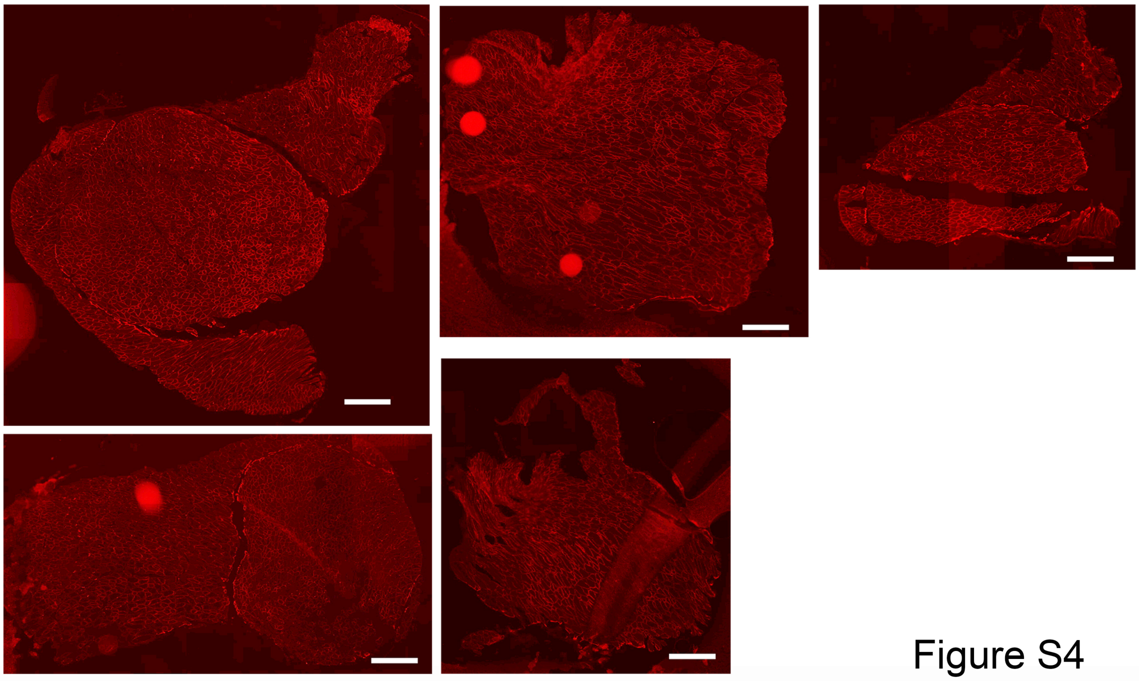

Figure S4

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.

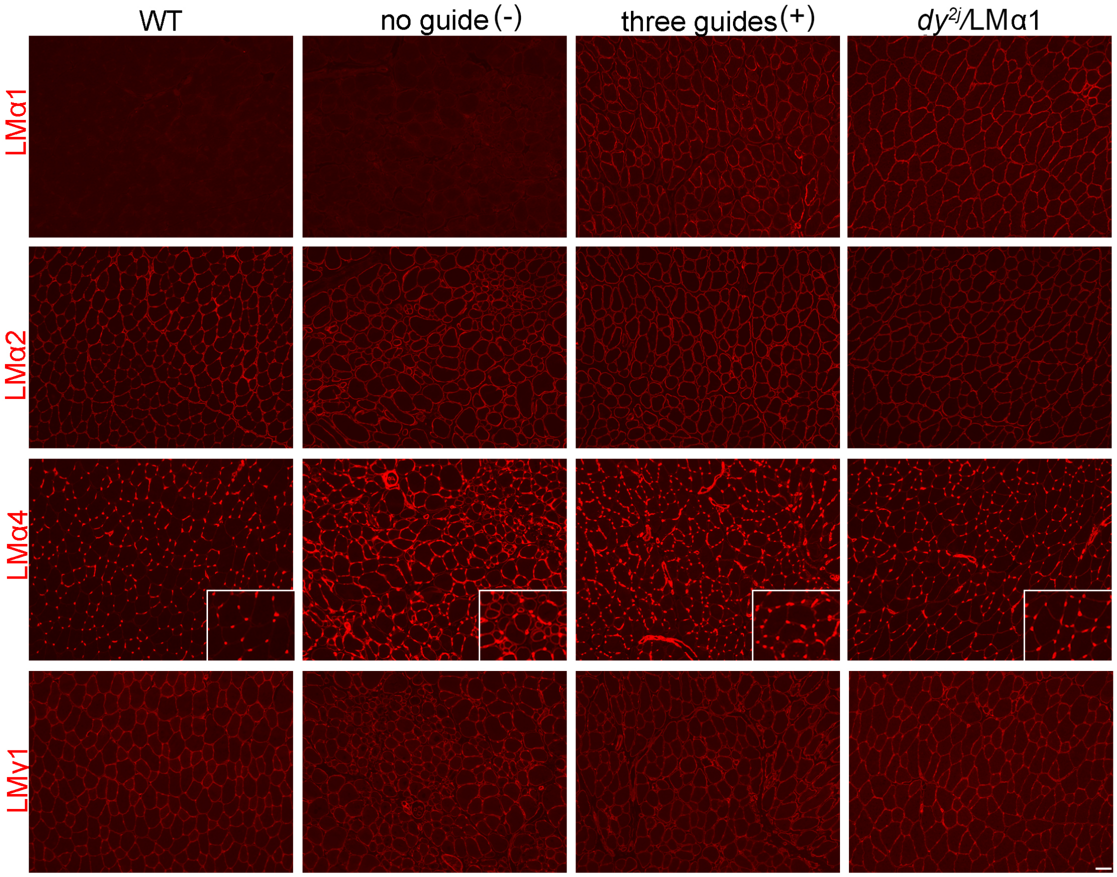

Figure S5

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.

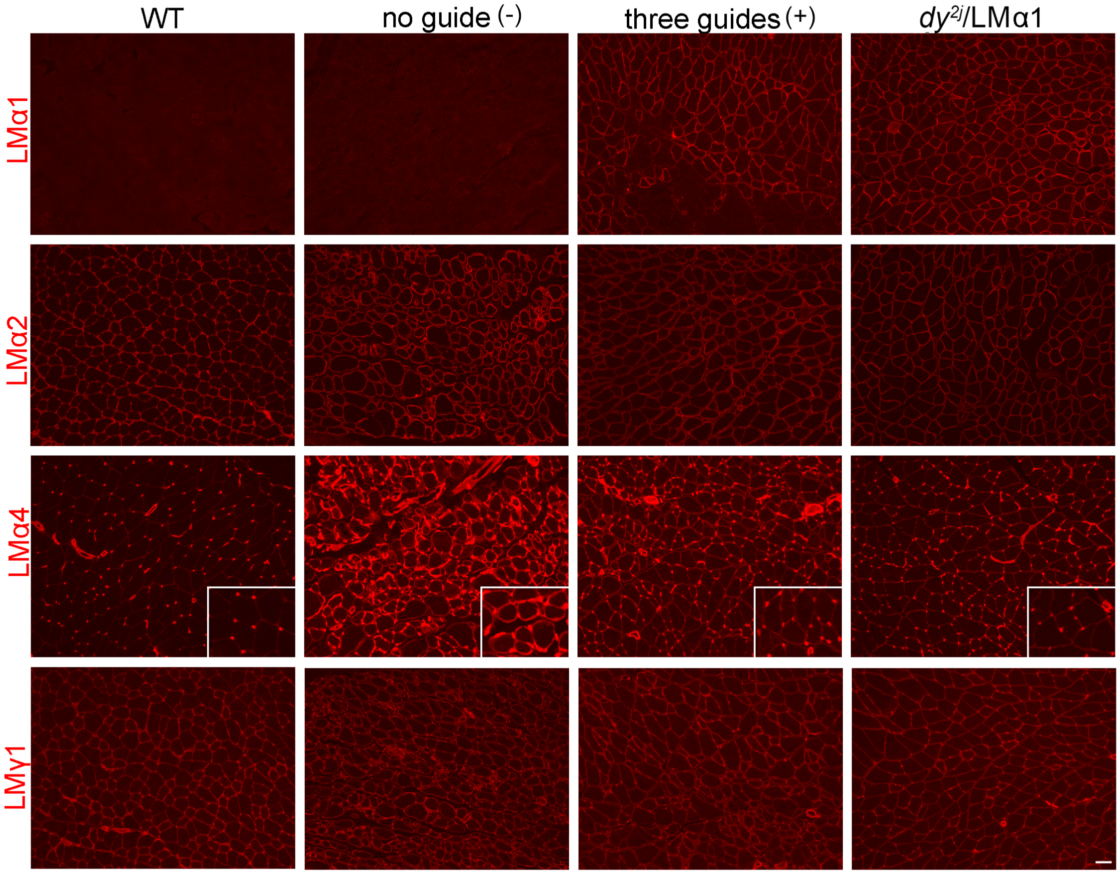

Figure S6

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.

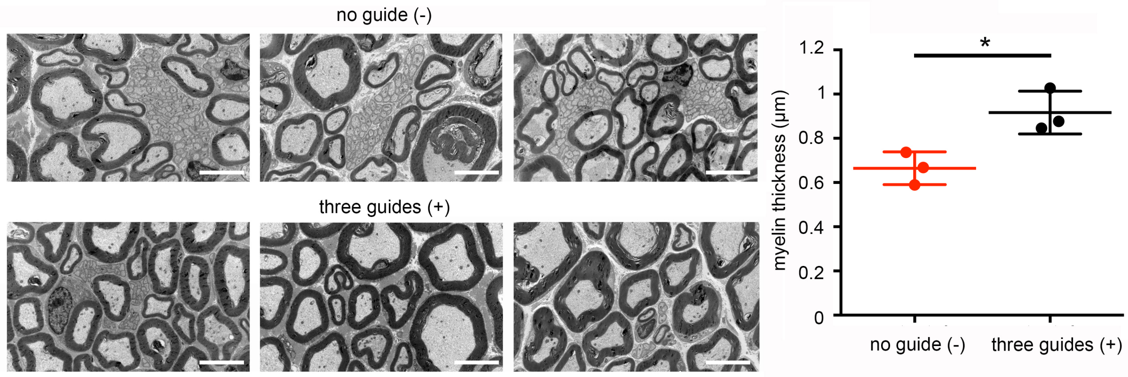

Figure S7

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.

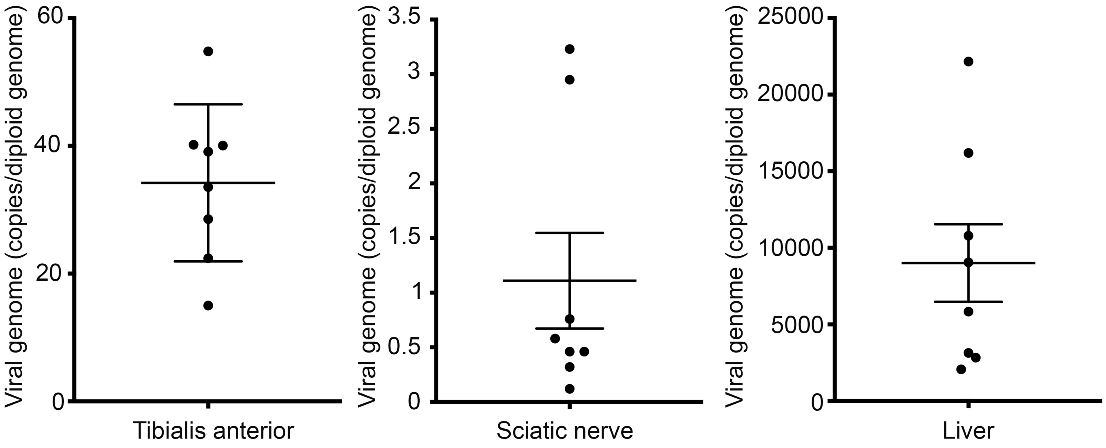

Figure S8

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.

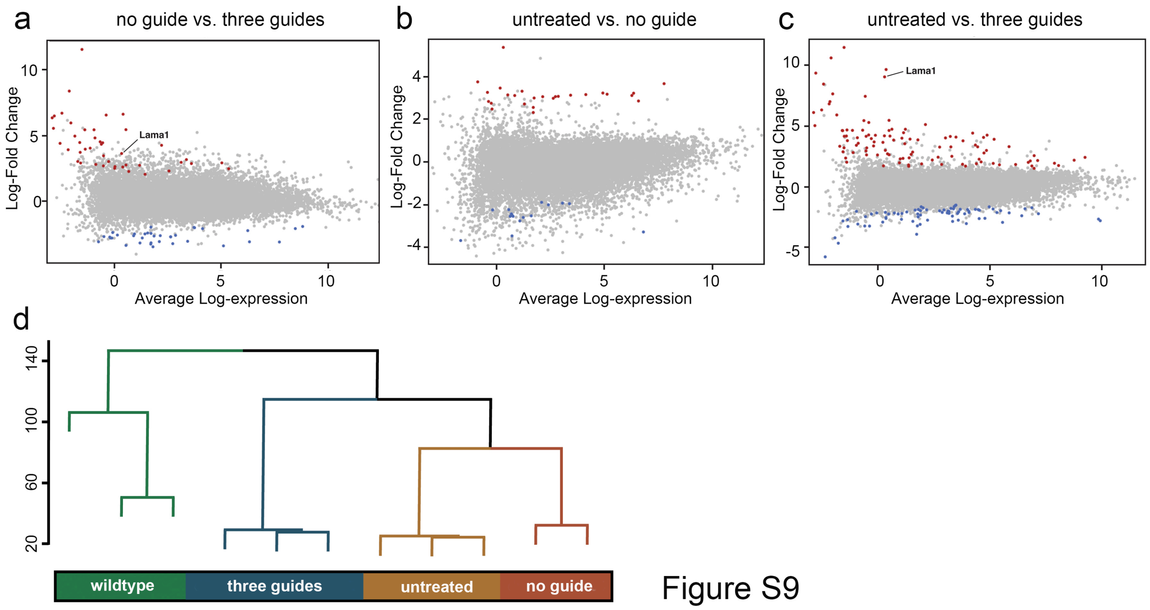

Figure S9

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**).

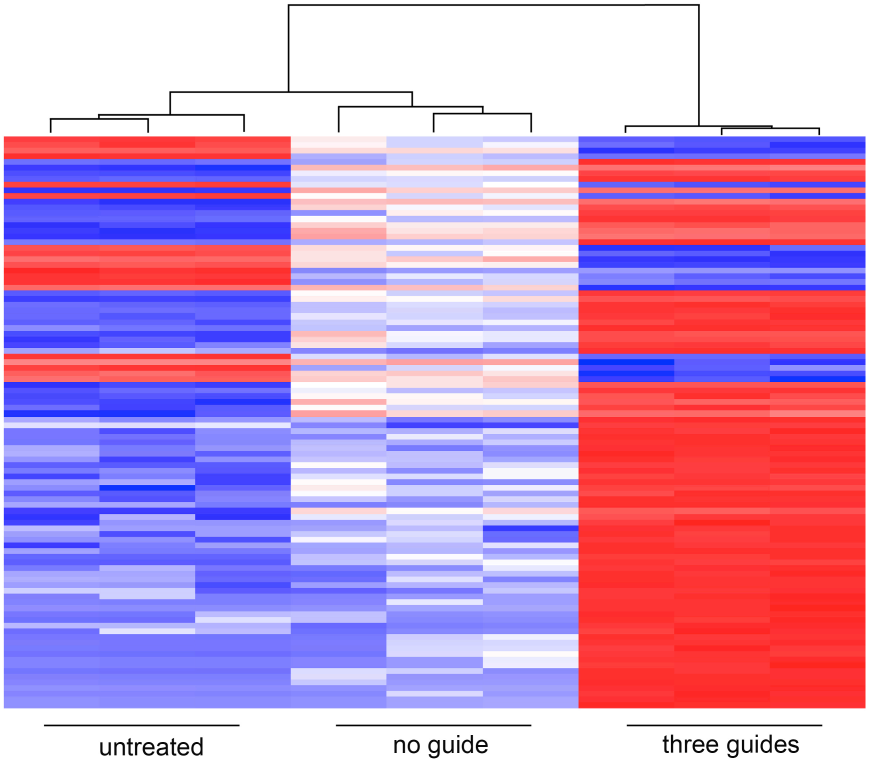

Figure S10

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	agggGCGaGGaGCaGCCcaGCAGGCCTGAGT	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	CAggtAtGtGttacCGCACCAGGCTGGAGT	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	gACtcACtCtAAtgGGgGTGGAGGGTGGGGGT	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	83290352	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	CAtgGtaGGGgGCtatCtGGCAGGCTGGGGT	+	9
11	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr1	82782223	gACaGgAGctCaTGtGacCCAGGCTAGGAT	+	9
12	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr1	87661823	ggCCagGGaGCagGGCCtGGCAGGCCAGGAT	-	8
13	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr1	90031346	agtCctAGctgCTGCGCcCCAGGCCTGGAT	-	9
14	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr1	91995313	gAaCtCtGGGCaCtGCtctGCAGGCTGGGAT	+	9
15	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr1	92235646	CtgtGtAGacCCTcCtCtCCAGGCATGAGT	+	9
16	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr1	109694154	ggttGgaCtCcACgGGAGTGGAGGGTGGGGGT	+	9
17	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr1	126488448	CAagGtGGGGaGCatggtGGCAGGCAGGAGT	-	9
18	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr1	134277663	CttgGcActtCCTGgGgACCAGGCAGGAAT	-	9
19	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr1	135031972	ttCtGAcctcCaTGgGCACCAGGCATGAAT	-	9
20	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr1	141104237	CAagGACaaCcAaTGtAGgGGAGGGTTGGAGT	-	8
21	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr1	156757803	agttGAAGGGtCaGCaggCCAGGCCAGGAT	+	9
22	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr1	157391498	aACattggCCAAaTGGtGaGGAGGGTGTGGAT	+	9
23	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr1	159690336	CAgCcAtctGCCTtCcatCCAGGCCTGGAT	-	9
24	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr1	161901532	CACgGtgtGtgCTcaGaACCAGGCTGGAGT	+	9
25	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr1	165282075	aACCcCGGGctGgGGgggcGCAGGCCGGGGT	+	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	CcCaGAgGGGCtgcaGggCCAGGCTTGAAT	-	9
33	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr1	181119150	acCCactGaGCCatCtCACCAGGCTCGGAT	+	9
34	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr1	182612878	gAtgGAgGaGgCaGCtCtCCAGGCCTGAGT	-	9
35	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr1	182861831	CtttGAAGtGaCaGaGgcCCAGGCCTGAGT	-	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	CcCtcCGcaGCGCtttCtGGCAGGCTGGGGT	+	9
41	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr2	25995977	CACCacccctttCgGCcCACCAGGCCTGAAT	+	9
42	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr2	28820200	aACtGAtGtcCaTGCcttCCAGGCATGAGT	-	9
43	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr2	31672867	CAgCccAGGcCCaGCtgcCCAGGCAGGGAT	-	8
44	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr2	32697101	tACtGAAGctCCTGtctgCCAGGCAAGGAT	-	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	CtgCcctttcCCTGtGCACCAGGCAGGAAT	+	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	actCGAAGccCgTcCtCcCCAGGCTAGAGT	+	9
70	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr2	131044485	CAggGCaGGGCagGGCagGGCAGGCCAGAGT	+	7
71	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr2	160732046	ggagGCGGGcaGgcGCgAGGCAGGCCGGAGT	-	9
72	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr2	160802250	CAtgGAAcGaCCaGtGCcCCAGGCGTGGAT	+	7
73	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr2	162278982	CAggcAAaaGgCTGtGtcCCAGGCAGGAGT	+	9
74	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr2	163475692	ggCaGgGcaGgGCaGgCAGGCAGGCCAGAGT	+	9
75	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr2	164089776	aACtGttCaaAACgGagGTGGAGGGTGGGGGT	+	9
76	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr2	164638656	CAggGtGctGgGaGGCCAGGCAGGCATGGGT	-	7
77	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr2	164852526	CAggGcAGatCtgGaGgACCAGGCCAGAGT	+	9
78	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr2	168045391	acCCaccGaGCCatCtCACCAGGCTGGAAT	+	9
79	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr2	170015101	gAagGcAGGGaaTcCtCcCCAGGCTGGGGT	+	9
80	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr2	179934167	CtCCGAgGGGttTGCaggCCAGGCAGGGGT	-	7
81	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr2	180232667	tgCgGAgGaGCtTGCcacCCAGGCAAGAGT	-	9
82	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr3	10144068	CtgCcAAaGcCaTGttCgCCAGGCTCGAGT	-	9
83	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr3	11083365	CtCCacctGGCCTcCctgCCAGGCTAGGGT	+	9
84	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr3	18621066	CtCgctgGGGCCTtCcCACCAGGCCTGGAT	+	7
85	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr3	19951663	CAtgGtGGGGgaCGtgatGGCAGGCAGGAAT	-	9
86	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr3	27671606	aAgCcaGaGGaGCcGgCtGGCAGGCAGGAAT	+	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	CcCtccctGcaCTGCGCtCCAGGCATGAGT	+	9
92	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr3	55076356	CtCCcAAGtGCtaGaatcCCAGGCTCGAAT	+	9
93	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr3	67982882	CACtGCaGtGaatGGCaAtGCAGGCGAGGGT	+	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	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr3	115947255	CACactGaGaCtacaCCAGGCAGGCAGGGAT	-	9
102	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr3	116858057	gACaGAgaGGagaCcCACCAGGCAAGAAT	-	9
103	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr3	117437453	CcaaaAAtaGCCatCcCACCAGGCTAGGGT	-	9
104	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr3	119127176	CAaaGAtGGGgaaGaaCtCCAGGCTGGGAT	-	9
105	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr3	127683845	CAtCcACagCcctgaGAGTGGAGGGTTGGAAT	+	9
106	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr3	130060315	CctCGgtccGCGCGGgagGGCAGGCCTGGAT	+	9
107	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr3	130325786	agCaacAGcctCTGCcCACCAGGCATGGGT	+	9
108	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr3	131136757	gggaGaGGGaCcCtGaCAGGCAGGCAGGGAT	-	9
109	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr3	131471626	CAttcAccccCCaGCGCACCAGGCTTGGAT	-	8
110	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr3	147117145	CcatGAtGGaCCaGCatcCCAGGCCAGAGT	-	9
111	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr3	153279735	aAtgGgGGGGgGgGcaCtGGCAGGCTAGGAT	+	9
112	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr3	153488946	CAgCtaGaGtgcCaGgCAGGCAGGCGTGAGT	+	9
113	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr3	154251972	ttCCtAAGtcCCccaGCtCCAGGCCTGAGT	+	9
114	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr4	8570745	CAggcaGGcagGCaGgCAGGCAGGCAGGGAT	-	9
115	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr4	18028813	CAggcaGGcagGCaGgCAGGCAGGCATGAGT	-	9
116	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr4	24631445	CAtCGCtacctGCcaaCAGGCAGGCTGGGGT	-	9
117	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr4	31636941	CtaCtgagCCtgCTGcAGTGGAGGGTCAGAAT	+	9
118	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr4	33716488	CtaCtAcctGaCTGgGaACCAGGCTTGGGT	-	9
119	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr4	37047240	CtCattgGGGCCTtCcCACCAGGCCTGGAT	-	7
120	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr4	37063381	CtCtcAgGtctCTtCtCACCAGGCCTGAGT	-	9
121	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr4	38565722	gcCatCcaGGCagGGtCAGGCAGGCATGAGT	-	9
122	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr4	41633043	CAaCcAcGGtgCTcaGCtCCAGGCTAGAAT	+	8
123	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr4	43536337	CAgCaCtGGctGCtGtaAtGCAGGCCTGGGT	+	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	53545042	aACaGAgCtgAcCTGGAtatGAGGGTATGAAT	-	9
129	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr4	56611614	CAgacAAGGaCCctttCcCCAGGCCAGGGT	-	9
130	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr4	57847249	CAgCagAGGGgCcGCattCCAGGCCTGAAT	-	8
131	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr4	63232225	CAgaGAAGGGCtgaactcCCAGGCTAGAGT	+	9
132	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr4	65387392	gAaaGCaGGGgagaGgCAGGCAGGCAGGGGT	+	9
133	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr4	103500698	tAtaGAtGtGgCTaCctACCAGGCCAGGAT	+	9
134	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr4	107496668	CcCacaGctGaGCccCCAGGCAGGCAGGGAT	-	9
135	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr4	108025417	aACCcCaGGGtGgGGgCgGGCAGGCTTGAGT	-	7
136	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr4	109850272	CACCtgAtatCaTGgcCtCCAGGCTGGGAT	-	9
137	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr4	114586084	CAagGAaCCCAAtTcaAcaaGAGGGTGAGAAT	-	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	tcCtGAtGGGCCatCtttCCAGGCCTGGGT	+	9
147	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr4	130857621	CACCcAgGGcCCccaGtACCAGGCAGGGAT	+	7

148	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr4	131189393	CgtCGAAGcagCaGCaggCCAGGCGTGAAT	-	9
149	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr4	134999167	aACgGCGcaGgGtGaCtAaGCAGGCGAGAAT	-	9
150	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr4	136262995	aACCccAGcaCCTcataACCAGGCAGGGAT	+	9
151	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr4	137673872	tcCCtggGGcCCaGCaCcCCAGGCTGGAAT	-	9
152	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr4	137772074	CAtCGcAtGaggaGtcCACCAGGCTTGGGT	-	9
153	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr4	139074698	tggCGgtGGcCCgGgGCcCCAGGCTGGGGT	+	9
154	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr4	139216803	tACaGatGaGaGCaGCCccGCAGGCAGGAAT	+	9
155	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr4	139965800	gggCaAAGGtCCaGCGgtCCAGGCGAGGGT	+	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	CACtcCtGGGtGCtttagGGCAGGCCAGGGT	-	9
163	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr4	149864826	CAgtGttGcctGgGGgCAGGCAGGCCTGGAT	+	9
164	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr4	150622270	CAggcaGGcagGCaGgCAGGCAGGCAGGGAT	-	9
165	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr4	151267812	agCaGAAGGaggTGtGagCCAGGCTGGGAT	-	9
166	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr4	152045043	CAgtGtGaGcCGtGGagAGGCAGGCAGGGGT	+	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	CACCagAGatCtTGCagACCAGGCGGGAGT	-	7
173	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr5	35318901	CAgacAaaCCAcaaGGgGTGGAGGGTGGGGAT	+	9
174	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr5	44180103	tAgtGAAaGGCCTGaGgACCAGGCAAGAAT	-	6
175	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr5	53788779	CtCCaaGttGCcatGCaAGGCAGGCATGGGT	+	9
176	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr5	74171504	ggCCGtGGGGgGtGGgggGGCAGGCAAGAAT	-	8
177	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr5	101591226	CAggtttGGGCggGCaCgCCAGGCAAGGAT	+	9
178	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr5	103409544	CtCtGggaGagCTGgGaACCAGGCTTGGGT	-	9
179	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr5	104770100	tAtgtcCCCgAcCTGGgcTGGAGGGTGGGGGT	-	9
180	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr5	106464301	aAatGgGaGcCGCGcaCAGGCAGGCTAGGGT	-	8
181	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr5	112718721	CACaGgCattggCaGGAGTGGAGGGTGGGGGT	-	8
182	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr5	113162833	CttCGgAGaGCtcGCtttCCAGGCAGGGGT	-	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	tcCCcAgGGctCTGtttACCAGGCATGGAT	+	9
192	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr5	128632023	CAgCaAtGccCCaGtcCtCCAGGCTGGGGT	-	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	CACtctGGGtgGttcCCAtGCAGGCAAGAGT	+	9
204	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr5	144881996	tAgtGAgtttgCTGaGCACCAGGCAAGAGT	+	9
205	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr5	145646342	aggCtgGGGagtaGGCCAGGCAGGCTAGAAT	+	9
206	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr5	150589492	tACtGcCCaggggTGGgGTGGAGGGTGGGGGT	+	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	atCCatcaGGgCTGCagACCAGGCCAGGAT	+	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	aAggcAgGtGCCacCaCACCAGGCTAGAAT	+	9
221	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr6	72989175	CAgCGctGcagCTGCtCgCCAGGCTGGAAT	-	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	CcttGcAGGGgCTGtGCtCCAGGCTGGGGT	-	7
229	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr6	90965675	aACtGAgGctCCaaaGaACCAGGCTAGGAT	+	9
230	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr6	102677674	CcCtGcAGGtttTtgGCACCAGGCTGGGAT	+	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	121129290	CtCCcAAatGCtgGgGttCCAGGCGTGAAT	+	9
287	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr6	122781164	gACaaaGGGGtGCGGtggGGCAGGCTGGGGT	+	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	gggCcatGGcaGaGGCCAGGCAGGCCGGGAT	+	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	gACtcgGGGtCtaGGgtAGGCAGGCGGGGAT	+	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	CAgacttctcCCTGCtCACCAGGCTGGAGT	-	9
314	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr7	81778798	CAtaGcAGtGCggGtGgACCAGGCTGGAAT	+	8
315	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr7	82771251	gggCcacGGcaGaGGCCAGGCAGGCCGGGAT	-	9
316	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr7	82771352	gggCcacGGcaGaGGCCAGGCAGGCCGGGAT	-	9
317	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr7	82771740	gggCcacGGcaGaGGCCAGGCAGGCCGGGAT	-	9
318	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr7	82771840	aggCcacGGcaGaGGCCAGGCAGGCCGGGAT	-	9
319	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr7	87666635	tACCtAgaacCtTGgGCACCAGGCTGGAAT	-	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	CAgaGACCCatAgTGGgtgtGAGGGTGAGGAT	-	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	gctCtcAGGtCCTtCtCACCAGGCCAGGGT	+	8
335	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr7	138607181	CtCCccAtctCCTcCagACCAGGCAGGGAT	+	9
336	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr7	140220561	CAggGccGGaCCatCtCtCCAGGCAGGGGT	-	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	CAggcaGGcagGCaGgCAGGCAGGCAGGGGT	+	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	CAagtgtGtcCaaGGCCAGGCAGGCCAGGAT	+	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	gACaGtGGtGatatGCtAGGCAGGCGTGAGT	-	9
365	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr8	119428002	CcCCaCtGGGCagGatCAGGCAGGCCTGGAT	-	7
366	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr8	120068314	CACCccAGGGCCTctGtgCCAGGCGGGGGT	+	6
367	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr8	120860571	CctaGgAGGcgCTGgcCACCAGGCTGGGAT	-	8
368	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr8	120974936	atgaGAAGGGaCaGCcagCCAGGCTTGGAT	+	9
369	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr8	123041378	CtgCGgGGtGCGgaGgCgcGCAGGCCCGAGT	-	9
370	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr8	125191189	tAtCaAccaGCgTGCtaACCAGGCCTGGAT	-	9
371	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr8	125596642	CAtgGcAGGctCTGtttcCCAGGCTGGAGT	+	9
372	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr8	126158536	CcCaGggctGCCTGCatACCAGGCAAGAAT	-	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	CAtCctttccCCaGgGCACCAGGCAGGGAT	+	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	ataCaAAacGCCTaCGtgCCAGGCATGGAT	+	9
385	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr9	46913410	aACaaAgGGGCCTGgGaACCAGGCCAGGGT	+	6
386	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr9	49513721	CcaCtgGGattGaGGaCAGGCAGGCAAGGGT	-	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	CtCCcAgCtCctCaGaAGaGGAGGGTTAGAGT	-	9
392	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr9	64028355	aACtGctGaGCCatCtCtCCAGGCCTGGAT	-	9
393	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr9	64321431	agCCGaGatGtGCaGCCAGGCAGGCAGGGGT	+	7
394	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr9	64764207	agagGAAtGGCtTtgtCACCAGGCCAGAGT	-	9
395	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr9	65128873	CACgcCaGGtgagGGggAGGCAGGCGGGGGT	+	9
396	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr9	69433414	aACCGttGaGCCacCtCtCCAGGCCTGGGT	-	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	CtCatAtCCCAtCTcaAGcaGAGGGTTGGGAT	+	9
402	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr9	96972110	CACCGtAGccatgGCaCtCCAGGCAGGGGT	+	8
403	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr9	98534790	gAtCtgGGGGtGgtGCagGGCAGGCTGGGGT	-	9
404	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr9	106552854	CACCagtGtGCCTcgcCACCAGGCCTGGAT	+	7
405	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr9	106652201	aAaCtgAGcctCTGCtgACCAGGCTGGGGT	+	9
406	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr9	107279877	CAgCtcCCCCAttctcAGgGGAGGGTGGGGGT	-	9
407	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr9	109104664	CAggcaaGtGCagGGgCAGGCAGGCAAGGGT	-	9
408	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr9	111481582	CcCaGtGGttCcCGGatgGGCAGGCAGGGAT	+	9
409	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr9	115956828	CAagGACaCacAgTGcAGgGGAGGGTCAGAAT	-	8
410	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr9	119029882	CcCCatcctGtCTGgGCtCCAGGCTGGAGT	+	9
411	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr9	119972855	gACCGgaaGctGgGaCCtGGCAGGCTGGGGT	+	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	CACatAcaGGaggagGCACCAGGCCGGGGT	+	9
418	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr10	29217098	CAgtttAGGGCCTGaGatCCAGGCTTGGGT	+	7
419	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr10	29534725	CAgCcAAGGttCccgGagCCAGGCGGGAAT	+	9
420	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr10	33182172	CAgCtAgaGaCaTGaGCtCCAGGCGGGGGT	-	8
421	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr10	39018711	atCtGAgGtGatTGtGtACCAGGCTAGGGT	+	9
422	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr10	39514838	tgaacAAGGGCaTGaGaACCAGGCAGGAGT	+	8
423	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr10	62424916	CcaacAAGGcCaTcCaCtCCAGGCTGGGAT	+	9
424	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr10	62820798	gAgacAgGGGCCTGaGttCCAGGCTAGAGT	+	8
425	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr10	70037110	tggaaCGtGGtcCtGCCAGGCAGGCTGGGAT	+	9
426	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr10	70815707	CAgtGACCtCtctgGGgaTGGAGGGTGGGGAT	-	9
427	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr10	73100122	CtCtGCGGGaCcCGGgCtaGCAGGCAGGGGT	+	7
428	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr10	78196582	CAggtCtGtGCcaGGCCAGGCAGGCAGGAAT	-	7
429	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr10	79623512	tAgtGAgtGGgCTGCcCtCCAGGCCGGGGT	+	8
430	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr10	79653456	CACCcAAGctCCTGtGCtCCAGGCTGGAAT	+	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	acCCattGaGCCatCtCACCAGGCCAGGGT	+	9
436	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr10	128913811	CcCCGAAcacgCTaCagcCCAGGCTGGGAT	-	9
437	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr11	5252790	gctCagtgCtgACTGGAGTGGAGGGTGAGGGT	-	9
438	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr11	7421018	CttttAAtGGgaTGaGCcCCAGGCTGGGAT	-	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	atCtGCGGctgGgGtaCAGGCAGGCAAGAAT	+	9

448	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr11	59896272	tAtaGAAGGatgTGtGggCCAGGCGGGGAT	-	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	CACaGAtGttCCTGtGagCCAGGCCTGAAT	+	7
456	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr11	63130471	CACtGctCttAACaGGtagGGAGGGTGTGGAT	+	9
457	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr11	63934474	ggCtGCaGGGCtgaGCCttGCAGGCTAGGGT	+	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	CAggattGGGCCTcCGagCCAGGCTGGGAT	-	8
464	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr11	85710844	CAgtGgGGGagGgGGgggGGCAGGCCTGAGT	-	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	atCCcAAaGGCCaGacacCCAGGCTGGGAT	-	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	gACaGgCgCtAcCTtGAcaGGAGGGTAGGGGT	-	9
478	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr11	103603781	gAgtaAAaaGgCTGgcCACCAGGCCTGAGT	+	9
479	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr11	106263794	CtCaGCcccctGCaGgCAGGCAGGCCTGAGT	-	9
480	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr11	106361263	aACaGAAGGcaggaCGtcCCAGGCTTGGAT	-	9
481	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr11	107538125	CtaaGAgGGtaCacgGCACCAGGCATGGGT	+	9
482	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr11	109785130	acCaGgAGGaCCctGCgCCAGGCCTGAGT	-	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	ttCtGtctGGtCTGCaCtCCAGGCTTGGGT	-	9
492	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr12	21518525	CtgtGtAGaaCtTGCtCACCAGGCTGGAAT	-	8
493	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr12	24731791	CAtCtttGGGCtgGagCAaGCAGGCCAGAGT	-	9
494	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr12	29120532	atCCtcCCtggACaGGgGTGGAGGGTGGGAGT	-	9
495	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr12	30913970	acCtttGGGcaGaGGCaAGGCAGGCAGGGAT	+	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	CACtGgtGGGCcgGtCCcaGCAGGCAGGAAT	+	8
506	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr12	82553117	CACtGaGcacgGCaGCatGGCAGGCAGGGGT	-	9
507	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr12	86359817	tAtgcAtGGttCTGgGtACCAGGCCAGGGT	-	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	gACaGtGGGcCGgtGCCtGGCAGGCTTGAGT	-	7
514	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr13	13964861	CAtCaggacGCCctgGCACCAGGCCCGGAT	-	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	CACtcaGtGGgGCaGaCttGCAGGCCAGAGT	+	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	tgCaGcCCCtcACTGGaTGGAGGGTTAGAGT	-	8
535	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr13	73820815	CACaccAGGGagatgGCACCAGGCTTGGAT	-	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	CACCcCaGcGgGaGtgCAGGCAGGCATGGAT	+	7
543	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr13	111052405	CtggGaGtGGgGaGGCCtGGCAGGCTGGGGT	-	8
544	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr13	112723361	aAtCcaGGaGCaaGaCCAGGCAGGCCTGGGT	+	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	CtagGAAGtagCTGgGatCCAGGCCAGGAT	+	9
550	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr14	25304711	CtgCcAcaGGCCctCaCACCAGGCCGGAAT	-	8
551	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr14	25773733	CtCCacCagCccCTGGAGaaGAGGGTAGGGAT	-	9
552	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr14	26531551	CAggGgAGaGCCactGCACCAGGCACGAGT	+	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	CACCcttcGGCagtGCCtGGCAGGCCGGGAT	+	8
566	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr14	72181539	CACCcAAcaGCCatgatgCCAGGCTAGAGT	-	9
567	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr14	74495784	CAagGAAGcaCtTGttacCCAGGCAGGAAT	-	9
568	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr14	75613804	aAgCtgAGGGCagGaaCtCCAGGCAGGAAT	-	9
569	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr14	76617123	ttCCaAAGGaCCaagGatCCAGGCACGGGT	-	9
570	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr14	78674124	CAtgcaGGcagGCaGgCAGGCAGGCAGGAGT	+	9
571	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr14	80562162	CtCtacAtGaCCTGgGagCCAGGCTTGGAT	-	9
572	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr14	81843636	CcCtGAcctGCtTGaGttCCAGGCCTGAAT	+	9
573	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr14	94725726	gcCaaAAGtGCtTtgGgACCAGGCAAGAAT	+	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	CtCtGAtctcCaTGgGCACCAGGCATGAAT	+	8
580	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr15	4538774	aACCGctGaGCCatCtCtCCAGGCATGAAT	+	8
581	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr15	4930962	gAgtcAAGGtCtTagGCACCAGGCCTGGGT	-	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	CACaGCcctGtGtGGgtAtGCAGGCGGGGAT	-	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	aACtGtAGaGCaaGCGttCCAGGCAGGGAT	-	8
592	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr15	76378269	aAgacAAGcaCCacCaCACCAGGCAAGAAT	-	9
593	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr15	78664606	CctCtAaCCtAgCTGGAccaGAGGGTGGGAAT	-	9
594	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr15	78796591	CtgCtgCCCCAgCTtcAGacGAGGGTGTGGAT	-	9
595	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr15	78858217	tgCCaccGtGCCacCGCACCAGGCTAGGGT	-	8
596	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr15	79502867	aACCGAAGacCgacCaggCCAGGCTGGGAT	-	9
597	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr15	79996883	CAgCagGGaaCatGttCAGGCAGGCTAGGGT	-	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	CgggGcAGGagCTGCagtCCAGGCATGGGT	+	9
603	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr15	91397763	gAgaGgaGGGaGaGGCCAtGCAGGCATGGGT	-	8
604	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr15	93336955	CggCGCGGGtCaCGtgCgcGCAGGCAGGAGT	-	8
605	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr15	98968874	aACCaCaGtGCtCGGgagtGCAGGCTGGAAT	-	9
606	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr15	100768206	CACaGgGtcGgaaGGCtgGGCAGGCCTGGGT	-	9
607	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr15	102364355	CtCtGAActGCCcctcCcCCAGGCACGAGT	+	9
608	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr16	4084975	CcagGctGGGgCTGCatACCAGGCTGGGAT	+	8
609	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr16	7296055	tAaaagGaGGaGaaGCCAGGCAGGCAAGAGT	-	9
610	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr16	8237459	tgCaGAAGaGatTctGCcCCAGGCAGGAAT	-	9
611	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr16	29714613	gACtGActGGtCgGaGatCCAGGCCAGAGT	+	9
612	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr16	31520231	tggtGtGGGGCagGGCggGGCAGGCTGGGGT	-	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	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr16	95653807	CAagcaaGGcaGCatCCAGGCAGGCATGGAT	-	9
621	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr16	96257044	CAggcaGGcagGCaGgCAGGCAGGCAGGAAT	+	9
622	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr17	4989255	ttCtGAActcCCTGgcCACCAGGCACGAAT	+	8
623	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr17	7239340	CtCCatCCaCAgCTGGgGcGGAGGGTGAGGGT	-	7
624	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr17	11393387	CACCatCaCtgtgTttAGTGGAGGGTGAGGAT	-	9
625	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr17	11877092	CtCCagAGacaaTGgGaACCAGGCAGGAAT	-	9
626	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr17	13208284	CAtCctGcaGCGaaGCtAaGCAGGCAGGAGT	-	9
627	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr17	19402027	aACCtttgCtAAgaGaAGTGGAGGGTGAGAGT	+	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	CcCaGgAGGcCtaGaGttCCAGGCAGGAGT	-	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	CcCCcCccccCcCcGgCAGGCAGGCTCGAAT	-	9
640	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr17	47802371	gAaCtgAaGGgCTGCaggCCAGGCCAGGAT	-	9
641	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr17	48006368	gcCtGtAGGcttgGCaCACCAGGCAGGGGT	+	9
642	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr17	48814087	ggagaAAaGGtaTGCcCACCAGGCCTGGGT	-	9
643	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr17	49030382	gAgtGCtGGagGaGGCtAcGCAGGCAGGGAT	+	9
644	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr17	50325041	gACtatAGGtCtgaaGCACCAGGCTAGAGT	+	9
645	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr17	51539790	tgaCacgGGtgCTGaGCACCAGGCTCGAGT	+	9
646	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr17	56895029	ggCaGgGGctCaCGGCCAGGCAGGCAGGAGT	+	7
647	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr17	67696999	tgCtcACCCCAACTGGAGTGGAGGGTCAGAGT	+	4
648	CACCGCGGGGCGCGGCCAGGCAGGCNNNNNN	chr17	67697184	agggGCGGGGCGCGGCCAGGCAGGCGGGGGT	+	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	CgttGAAGtGtCTGCtgcCCAGGCCTGGGT	-	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	gACtcACtCtAAtgGGgGTGGAGGGTGGGGGT	+	8
673	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr18	75554852	atCtGAcaGGgCTGCctgCCAGGCGGGGGT	+	9
674	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr18	75587686	CgCtcctttGCCTGgcCACCAGGCTGGGGT	+	9
675	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr18	77003914	CAggtAAaGGtCaGaGggCCAGGCCTGGGT	-	9
676	CACCGACCCCAACTGGAGTGGAGGGTNNNNNN	chr18	80290043	gAggacCCggAgCTGGAGTGGAGGGTCAGAGT	+	8
677	CACCGAAGGGCCTGCGCACCAGGCNNNNNN	chr18	82033084	aAaCcctGtGCtTGCtgACCAGGCATGGAT	+	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	gACgGCaGaGCctGGCtttGCAGGCAGGGGT	-	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	CAgatAtGaGtCTtCatACCAGGCCTGGAT	-	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	tACtGCaaGtCGgtGCCAtGCAGGCAGGAGT	-	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	CACCGTCCCCTCCACCCCACAGTG	AAGAAT
	tdTomato sgRNA Bottom	AAACCACTGTGGGGTGGAGGGGAC	
	Lama1 sgRNA1 Top	CACCGAAGGGCCTGCGCACCAGGC	CAGGGT
	Lama1 sgRNA1 Bottom	AAACGCCTGGTGCGCAGGCCCTTC	
	Lama1 sgRNA2 Top	CACCGCGGGGCGCGGCCAGGCAGGC	GGGGGT
	Lama1 sgRNA2 Bottom	AAACGCCTGCCTGGCCGCGCCCCGC	
	Lama1 sgRNA3 Top	CACCGTCCAGGGGGAGCCCCGCCGTG	CGGAGT
	Lama1 sgRNA3 Bottom	AAACCACGGCGGGGCTCCCCCTGGAC	
	Lama1 sgRNA4 Top	CACCGGTGGTGGCGGGGTGCCTCTC	CTGGGT
	Lama1 sgRNA4 Bottom	AAACGAGAGGCACCCCGCCACCACC	
	Lama1 sgRNA5 Top	CACCGACCCCAACTGGAGTGGAGGGT	CAGAGT
	Lama1 sgRNA5 Bottom	AAACACCCTCCACTCCAGTTGGGGTC	