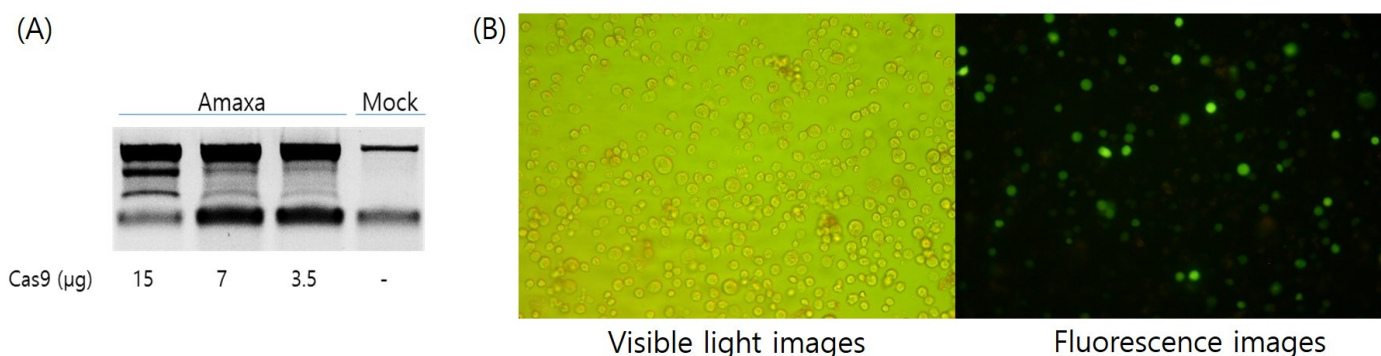


Article

Generation of a Dystrophin Mutant in Dog by Nuclear Transfer Using CRISPR/Cas9-Mediated Somatic Cells



Supplemental Figure S1. Genome editing in Canine fetal fibroblast via RNP delivery. (A) Mutations were detected by T7E1 assay. A mixture of Cas9 protein and in vitro transcribed sgRNA (20 μg) was transfected into 2x10⁵ cells. (B) Fibroblasts expressing green fluorescence protein transiently(original magnification 100X).

Total Sequences	With both indicator sequences	More than minimum frequency	Insertions	Deletions	Indel frequency	HDR frequency
71232	51673	51396	0	51396	51396 (100.0%)	0 (0.0%)

ID	Sequence	Length	Count	Type	HDR
1	<div><div>TGAGCTGGGTCCGACAATCAACTCGTAATTATCCACAGGTTAATGTCATTAACTTCCACCACAGCTGGTCTGTTGGCTGGGCTTT</div><div> </div><div>TGAGCTGGGTCCGAC-----ATGGCTGGGCTTT</div><div>GAACGCTCTCATCCACAGTCTATAGGTAAGGAGACCACTGAGATATTGACTAATT</div><div> </div><div>GAACGCTCTCATCCACAGTCTATAGGTAAGGAGACCACTGAGATATTGACTAATT</div></div>	83	47491	Del	N/A
2	<div><div>TGAGCTGGGTCCGACAATCAACTCGTAATTATCCACAGGTTAATGTCATTAACTTCCACCACAGCTGGTCTGTTGGCTGGGCTTT</div><div> </div><div>TGAGCTGGGTCCGAC-----ATGGCTGGGCTTT</div><div>GAACGCTCTCATCCACAGTCTATAGGTAAGGAGACCACTGAGATATTGACTAATT</div><div> </div><div>GAACGCTCTCATCCACAGTCTATAGGTAAGGAGACCACTGAGATATTGACTAATT</div></div>	83	120	Del	N/A
3	<div><div>TGAGCTGGGTCCGACAATCAACTCGTAATTATCCACAGGTTAATGTCATTAACTTCCACCACAGCTGGTCTGTTGGCTGGGCTTT</div><div> </div><div>TGAGCTGGGTCCGAC-----ATGGCTGGGCTTT</div><div>GAACGCTCTCATCCACAGTCTATAGGTAAGGAGACCACTGAGATATTGACTAATT</div><div> </div><div>GAACGCTCTCATCCACAGTCTATAGGTAAGGAGACCACTGAGATATTGACTAATT</div></div>	83	100	Del	N/A

Supplemental Figure S2. Targeted mutagenesis in dog cells by CRISPR/Cas9. The result of deep sequencing of mutant dog cells. Target Sequence of the sgRNA is underlined within the genomic sequence of DMD gene. Red boxes represent a protospacer-adjacent motif (PAM) sequence.

Mismatch 0 ; 1 / Mismatch 1 ; 0 / Mismatch 2 ; 2 / Mismatch 3 ; 16

	Target	Chromosome	Position	Direction	Mismatches	
1	crRNA: TTCACCACCAGCTGGTCTGANGG DNA: cTctCCACCAGCTGGTCTGgGGG	chr24	22878368	+	3	
2	crRNA: TTCACCACCAGCTGGTCTGANGG DNA: TTCACCTCCAGCTGtTCTaATGG	chr8	29061641	+	3	
3	crRNA: TTCACCACCAGCTGGTCTGANGG DNA: TTCACaAgCAGCTGGaCTGAGGG	chr12	4938755	+	3	
4	crRNA: TTCACCACCAGCTGGTCTGANGG DNA: TTCACCACattCTGGTCTGAAGG	chr3	26238745	+	3	
5	crRNA: TTCACCACCAGCTGGTCTGANGG DNA: TTCACCACCACcCTGGcCTGATGG	chr3	50964839	-	2	
6	crRNA: TTCACCACCAGCTGGTCTGANGG DNA: cGcCCACCAGCTGGTCTGACGG	chr3	57426757	+	3	
7	crRNA: TTCACCACCAGCTGGTCTGANGG DNA: TTCACCcCCAGCTGaTCTGgGGG	chr3	62735685	+	3	
8	crRNA: TTCACCACCAGCTGGTCTGANGG DNA: TTCACCAGcAGCTGGTaTgTGG	chr3	73060142	+	3	
9	crRNA: TTCACCACCAGCTGGTCTGANGG DNA: aTCAGcACCAGCTGGcCTGAGGG	chr25	45357425	-	3	
10	crRNA: TTCACCACCAGCTGGTCTGANGG DNA: TTCACCACCACacGGTCTGAAGG	chr1	16905540	-	3	
11	crRNA: TTCACCACCAGCTGGTCTGANGG DNA: TTCACCACCAGCTGGaCaGATGG	chr1	35850847	+	2	
12	crRNA: TTCACCACCAGCTGGTCTGANGG DNA: TTCACCACCAGCTGGaggGATGG	chr1	1.13E+08	-	3	
13	crRNA: TTCACCACCAGCTGGTCTGANGG DNA: TTCAGcAtCAGCTGGcCTGACGG	chr33	17707648	+	3	
14	crRNA: TTCACCACCAGCTGGTCTGANGG DNA: TTCACCAtCAGcGGTCTGtAGG	chr20	56928844	+	3	
	crRNA: TTCACCACCAGCTGGTCTGANGG DNA: TTCACCACCAGCTGGTCTGATGG	chrX	27933928	-	0	On target
15	crRNA: TTCACCACCAGCTGGTCTGANGG DNA: aTCACCACCAGCTGagCTGAAGG	chrX	1.06E+08	+	3	
16	crRNA: TTCACCACCAGCTGGTCTGANGG DNA: aTCACCACCAGCTGagCTGAAGG	chrX	1.06E+08	-	3	
17	crRNA: TTCACCACCAGCTGGTCTGANGG DNA: TTCACCACCAGCTGGagaGATGG	chr18	50645543	+	3	
18	crRNA: TTCACCACCAGCTGGTCTGANGG DNA: TgCACCACCAGCaGGTCTGcAGG	chr28	32426415	-	3	

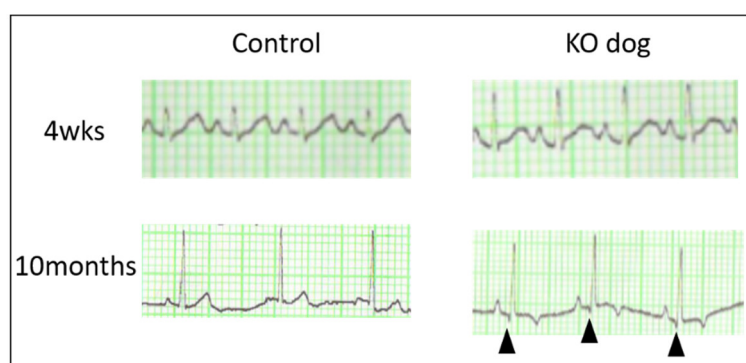
Supplemental Figure S3. Potential off-target sites with up to 3 mismatches, relative to the wild-type sequence.

Off-target Analysis

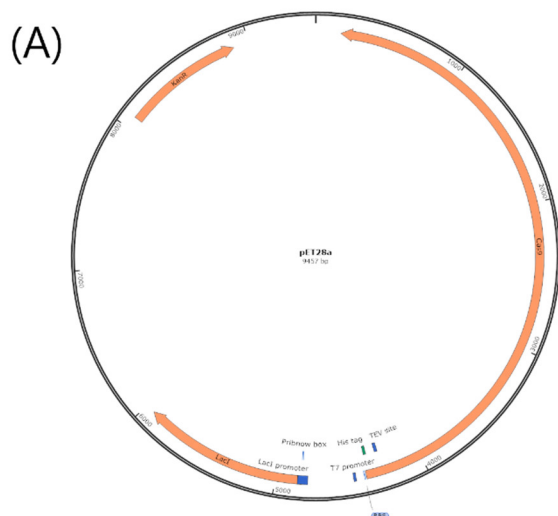
	Total Sequences	With both indicator sequences	More than minimum frequency	Insertions	Deletions	Indel frequency
1	13213	11325	10553	0	68	68 (0.6%)
2	14376	13779	13442	0	7	7 (0.1%)
3	12183	11326	10835	0	9	9 (0.1%)
4	15741	15231	14892	0	18	18 (0.1%)
5	15043	14459	14088	0	2	2 (0.0%)
6	14224	12056	11843	0	4	4 (0.0%)
7	11372	10141	9789	0	3	3 (0.0%)
8	12832	12439	12244	0	2	2 (0.0%)
9	330652	11629	11439	0	2	2 (0.0%)
10	339871	8548	8240	0	2	2 (0.0%)
11	336445	9669	9364	0	0	0 (0.0%)
12	295067	8274	8135	0	0	0 (0.0%)
13	245902	9766	9577	0	0	0 (0.0%)
14	280667	9419	8966	0	0	0 (0.0%)
15	256539	10355	10007	0	0	0 (0.0%)
16	235573	9310	8534	0	0	0 (0.0%)
17	337899	8469	8107	0	0	0 (0.0%)
18	373015	7996	7691	0	0	0 (0.0%)

#6	1	GTTTGTGTTAGCCGCCCCACCAAGCTGGTCTGACGGCCAGGTCCTATGCTCGCTCTTGCTGGCCATCCATTCCCCAGCA	78	6126	WT or Sub
		GTTTGTGTTAGCCTCCCCACCAAGCTGGTCTGACGGCCAGGTCCTATGCTCGCTCTTGCTGGCCATCCATTCCCCAGCA			
#6	2	GTTTGTGTTAGCCGCCCCACCAAGCTGGTCTGACGGCCAGGTCCTATGCTCGCTCTTGCTGGCCATCCATTCCCCAGCA	78	4872	WT or Sub
		GTTTGTGTTAGCCGCCCCACCAAGCTGGTCTGACGGCCAGGTCCTATGCTCGCTCTTGCTGGCCATCCATTCCCCAGCA			

Supplemental Figure S4. No off-target mutations at candidate sites in dystrophin mutant dog. Indel frequencies at potential off-target sites were analyzed using targeted deep sequencing. Off-target candidate #6 had 1 bp substituted allele which is pre-existed SNP not caused by CRISPR/Cas9.



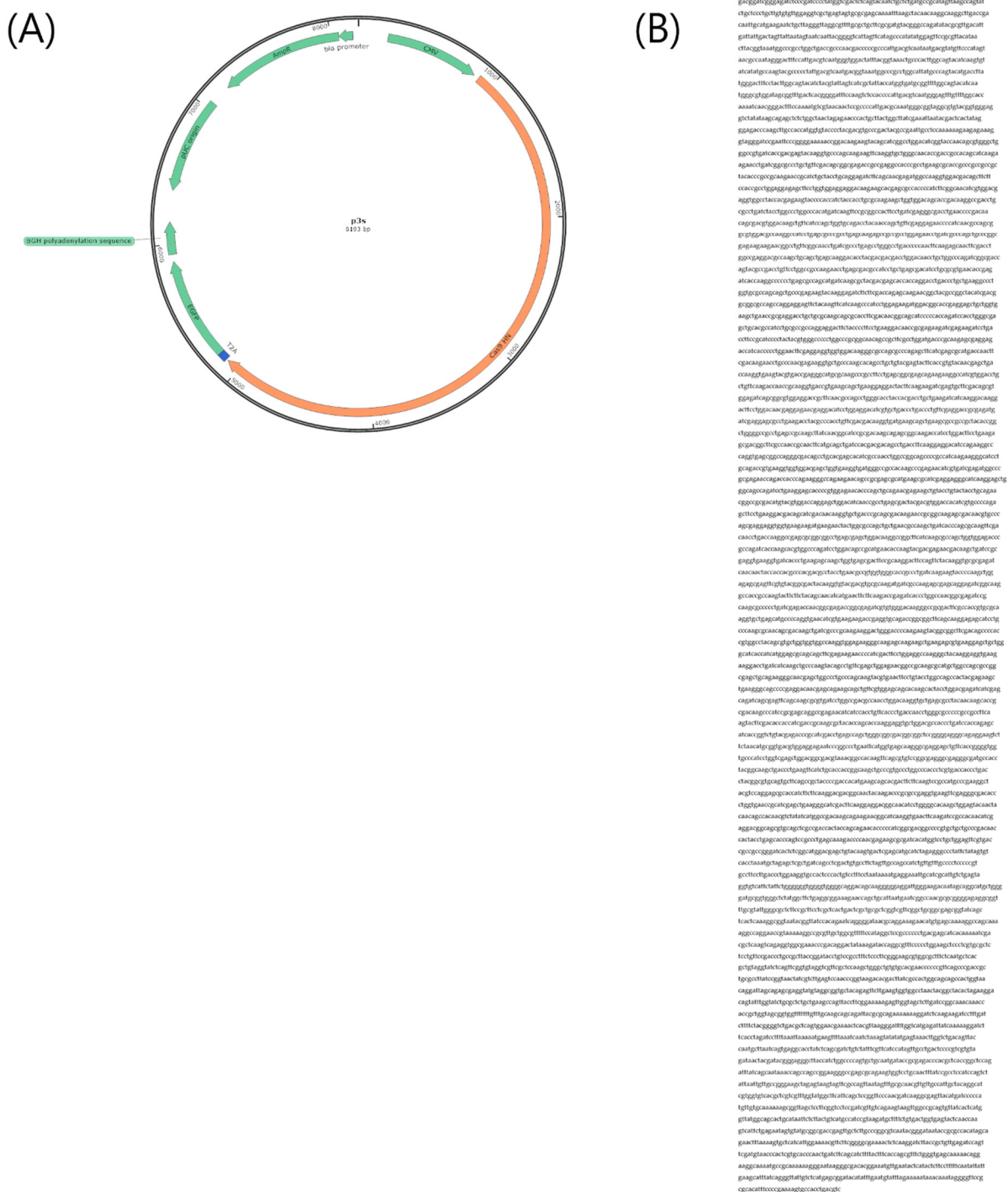
Supplemental Figure S5. Electrocardiogram changes according to age in normal and *dystrophin* mutant dogs. Arrows indicate the Q wave in the dystrophin mutant dog.



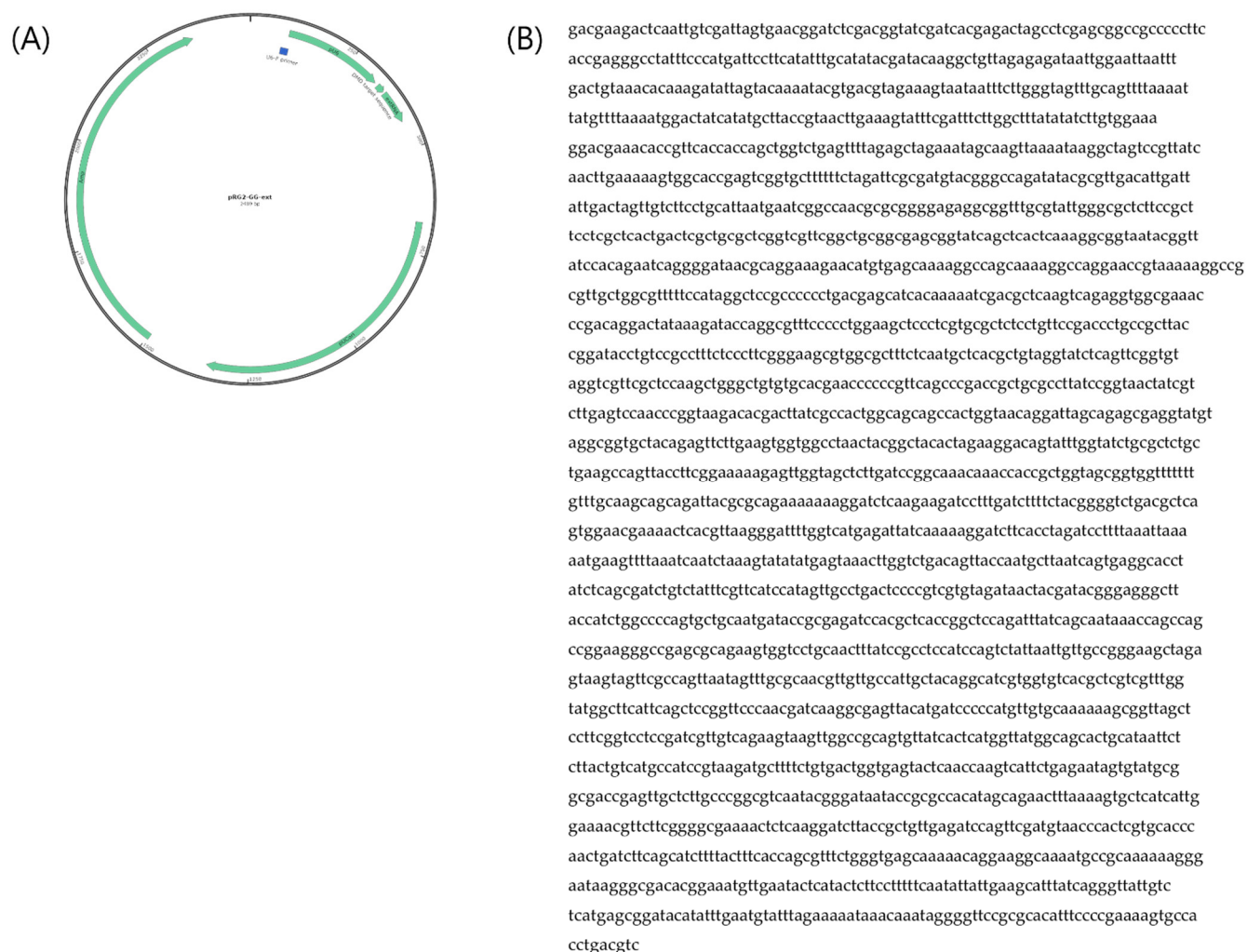
(B)

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Supplemental Figure S6. pET vector. (A) vector map (B) vector sequence



Supplemental Figure S7. p3s-Cas9-2A-GFP vector vector. (A) vector map (B) vector sequence



Supplemental Figure S8. pRG2-sgRNA vector. (A) vector map (B) vector sequence

Supplemental Table S1. Parameters of MRI sequences.

	T1 Axial	T1 Axial CE	T2 Coronal	T2 Axial	T2 IDEAL
Sequence	FSE	FSE	FSE	FSE	FSE
FOV (cm)	18 × 18	18 × 18	18 × 18	18 × 18	18 × 18
Slice thickness(mm)	3	3	3	3	3
Interslice gap (mm)	0.3	0.3	0.3	0.3	0.3
Relaxation time (ms)	759	1478	4315	5313	7313
Echo time (ms)	10.1	10.1	71.6	71.8	66.6
Matrix	256 × 192	256 × 192	256 × 192	256 × 192	256 × 224
Nex	4.00	4.00	4.00	4.00	3.00

CE, contrast enhanced; FSE, fast spin echo; FOV, field of view

Supplemental Table S2. T2 values of each hind-limb muscle

T2 values	Control dog	<i>Dystrophin</i> mutant dog
Rectus femoris	38.1	62.8
Vastus lateralis	36.7	41.9
Vastus medialis	41.5	45.4
Biceps femoris	40	39.5
Semitendinosus	37.3	41.4
Semimembranosus	37.1	40.6
Adductor magnus	40.3	49.3
Mean ± SD	38.7 ± 1.9	45.8 ± 8.2

SD, standard deviation

Supplemental Table S3. List of primers used for targeted deep sequencing

Primers used for T7E1 assay and Deep Sequencing of on-target site	
Fwd_1st	GACACCTACCAATCAGAGTAGATTCC
Rev_1st	CAGTGGATAGTCAGATCAGTATGG
Fwd_2nd	GAATGGACTCCGTCCTGGTAG
Rev_2nd	GAAATGAGCTGGAACCACACTGG
Fwd_DS	ACACTCTTTCCCTACACGACGCTCTTCCGATCTTGGATTGCAACAAACCAACA
Rev_DS	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTTGAACCACACTGGTGAAAA
Primers used for Deep Sequencing of off-target site	
DogDMD_Off_1_O_F	AGGACACCCAGGTCCTTACC
DogDMD_Off_1_O_R	CCACTGTGTTCTTCCCAGGT
DogDMD_Off_2_O_F	TGCACCTGGTCTTAGCTCCT
DogDMD_Off_2_O_R	TCCTCCTTCTGCCTGTGTCT
DogDMD_Off_3_O_F	GACTCAATCCCAGGTCTCCA
DogDMD_Off_3_O_R	CCATTTTCGGCAGAAAATCAT
DogDMD_Off_4_O_F	GCTGGATCCTGGGTAGACAA
DogDMD_Off_4_O_R	CCAATGTGGGACTTGATCCT
DogDMD_Off_5_O_F	TCACCTAGGCATGCATTCAA
DogDMD_Off_5_O_R	CCCCCTGGTTGACTAATGTG
DogDMD_Off_6_O_F	CAGCTCTGAAGGACCACACA
DogDMD_Off_6_O_R	CAGCAGGTAAACACCAAGCA
DogDMD_Off_7_O_F	CATGGAGGACACGATGCTAA
DogDMD_Off_7_O_R	GTGCAGGCAGCAACTTGTA
DogDMD_Off_8_O_F	AAACTCCTTTTTTGGGGCCTA
DogDMD_Off_8_O_R	TCCTCCTCTCATCTGGGCTA
DogDMD_Off_9_O_F	GGGATTTTGTTCCTCAAGGTT
DogDMD_Off_9_O_R	GAGAAGAATTTGGGGGAAGC
DogDMD_Off_10_O_F	AACCGCAAACCAATACAAGG
DogDMD_Off_10_O_R	GGGAAAGACAGACCTTCACG
DogDMD_Off_11_O_F	TAGGGTTGCCATCACAAGGT
DogDMD_Off_11_O_R	TCAGGAATGTCCTGGCTCT
DogDMD_Off_12_O_F	AGAGTACATGGCCTGGATGG
DogDMD_Off_12_O_R	GATGGAGACTGGGCTCTCTG
DogDMD_Off_13_O_F	TCCCATGAAAGAGGATCCAG
DogDMD_Off_13_O_R	TGTGTGGTCTCCCTGTGTA
DogDMD_Off_14_O_F	TTGCAGTGGTGGAGAGAGTG
DogDMD_Off_14_O_R	TGTGGGTCACAGAACTGGAA
DogDMD_Off_15_O_F	TTGGTTTGGTTGGTGCAGTA
DogDMD_Off_15_O_R	CAGTTGACGGCAGTTGAGAA
DogDMD_Off_16_O_F	CAGTTGATGGCAGTTGAGAA
DogDMD_Off_16_O_R	TTGGTTTGGTTGGTGCAGTA
DogDMD_Off_17_O_F	CCATCCATCATCCTTTGCTT
DogDMD_Off_17_O_R	TGAAAGCGTTTTGCAGATTG
DogDMD_Off_18_O_F	GCTTCTTGGAGGAGCAACAC
DogDMD_Off_18_O_R	CAGGGAACAGGCTGTGGTAT
DogDMD_Off_1_i_F	CCAGGACAGCAGGAAGAAAG
DogDMD_Off_1_i_R	GCCTCCTGGTGGATTATGAA
DogDMD_Off_2_i_F	CCTCTTGATGAGTCCCATTGA
DogDMD_Off_2_i_R	GGGAAACTTTTGTTCCTTT

DogDMD_Off_3_i_F	CTCACTTCAGGCTTGCCTCT
DogDMD_Off_3_i_R	TCCCCTCACCTTGACTTCAG
DogDMD_Off_4_i_F	TGCCTTAACCATTTCTATCCTCA
DogDMD_Off_4_i_R	GCGTCCCCCTGTTTAATCTT
DogDMD_Off_5_i_F	TTCTACCCAAAGCAGCCACT
DogDMD_Off_5_i_R	TCCAAACCTTTCCTTGTGCT
DogDMD_Off_6_i_F	CCTGTGGTCTGGTGACATTG
DogDMD_Off_6_i_R	CACACCTGACACTTGGCTGT
DogDMD_Off_7_i_F	CAAGCCAGACACAAAAGCAA
DogDMD_Off_7_i_R	CACCCAATGCCTAGCTCTTC
DogDMD_Off_8_i_F	AGGAAAAGTTGGGACGGTCT
DogDMD_Off_8_i_R	CAGGTTCTACCTCGCTCTG
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DogDMD_Off_9_i_R	TGTGTGGATCAGAGCAGAGG
DogDMD_Off_10_i_F	CCCCAGTCACTGATCCCTTA
DogDMD_Off_10_i_R	GAGCTCACGGCTGGACTTAC
DogDMD_Off_11_i_F	CTTTTGAGGCTTCCCTCCTT
DogDMD_Off_11_i_R	GACACTGCACTGTGGCATT
DogDMD_Off_12_i_F	GGGTCTTCGCATCTATGTGT
DogDMD_Off_12_i_R	CCCTTCTTTCTTTCCCCATC
DogDMD_Off_13_i_F	CATCCCTGAACACTCCTGGT
DogDMD_Off_13_i_R	CAGGTTTGGAGGATCTTGGA
DogDMD_Off_14_i_F	CTGGGAGACACTGTGCGTAG
DogDMD_Off_14_i_R	GAGGGAAACGGACAGCACTA
DogDMD_Off_15_i_F	CCTGTCAAAGGTGGAAGCAT
DogDMD_Off_15_i_R	TCACGCCAGTCATTTCTGAG
DogDMD_Off_16_i_F	TCACACCAGTCATTTCTGAG
DogDMD_Off_16_i_R	CCTGTCAAAGGTGGAAGCAT
DogDMD_Off_17_i_F	CTGTCCCTGCACCCCTATTA
DogDMD_Off_17_i_R	CCCAGCTCTTGTCTGGATGT
DogDMD_Off_18_i_F	CCCTCGTCTCCAACAAATA
DogDMD_Off_18_i_R	GGGGTCACACACCAGGTACT
DogDMD_Off_1_DS_F	ACACTCTTTCCCTACACGACGCTCTTCCGATCTGACCAGAATCCAAGCCTCCT
DogDMD_Off_1_DS_R	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTCTGGACTGGTCAACTCAGCA
DogDMD_Off_2_DS_F	ACACTCTTTCCCTACACGACGCTCTTCCGATCTCAAAGACCTGGGATTCCAAA
DogDMD_Off_2_DS_R	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTTTTCATTTAACTCAAACACAACG
DogDMD_Off_3_DS_F	ACACTCTTTCCCTACACGACGCTCTTCCGATCTGGTGTCCCTGTCTCAAGGTT
DogDMD_Off_3_DS_R	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGATGGGTACAAAGGGCTGT
DogDMD_Off_4_DS_F	ACACTCTTTCCCTACACGACGCTCTTCCGATCTGGAAGAGAGAGAGAGGGGAAA
DogDMD_Off_4_DS_R	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGATTTGGCTCTTTGGCTGAA
DogDMD_Off_5_DS_F	ACACTCTTTCCCTACACGACGCTCTTCCGATCTGCATTTTCTCTAAATGCCAGA
DogDMD_Off_5_DS_R	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTTCCATTGGGGTAAAGACTGG
DogDMD_Off_6_DS_F	ACACTCTTTCCCTACACGACGCTCTTCCGATCTCTGGCCAAGGTTCTGTTTGT
DogDMD_Off_6_DS_R	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTTGTGTGTCTGGGCTGAGTTC
DogDMD_Off_7_DS_F	ACACTCTTTCCCTACACGACGCTCTTCCGATCTGGGATGGAGTGCCAGTTTAA
DogDMD_Off_7_DS_R	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTCAGGGAGTCCAACACAGGAC
DogDMD_Off_8_DS_F	ACACTCTTTCCCTACACGACGCTCTTCCGATCTTCACAGCAAACACTACCCCAA
DogDMD_Off_8_DS_R	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTAGGCTTGCCAGTGAAACATC
DogDMD_Off_9_DS_F	ACACTCTTTCCCTACACGACGCTCTTCCGATCTCCTCTTGCTCCAAAGCTGTC

DogDMD_Off_9_DS_R	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGCTGGTAGGCTGCTCATCTC
DogDMD_Off_10_DS_F	ACACTCTTTCCCTACACGACGCTCTTCCGATCTCAAAGCCAGAAGATGGAAGC
DogDMD_Off_10_DS_R	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGGTGACCACCCTGGTTTCTA
DogDMD_Off_11_DS_F	ACACTCTTTCCCTACACGACGCTCTTCCGATCTGTCAGACCTGCAGCAGACAA
DogDMD_Off_11_DS_R	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGGGGGCTTTAGTCAGGGTAG
DogDMD_Off_12_DS_F	ACACTCTTTCCCTACACGACGCTCTTCCGATCTAGGTCAGTGGGTACCTGTGC
DogDMD_Off_12_DS_R	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTATCTATCCACCCCTCCCATCC
DogDMD_Off_13_DS_F	ACACTCTTTCCCTACACGACGCTCTTCCGATCTACCCCTGGCTTGTACCCATTT
DogDMD_Off_13_DS_R	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTAGTGCAAGCTGGAGTGTCTT
DogDMD_Off_14_DS_F	ACACTCTTTCCCTACACGACGCTCTTCCGATCTGGTTTACCTGCGTCCTCTCA
DogDMD_Off_14_DS_R	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTCCCCCAGAAACACAGCTAAG
DogDMD_Off_15_DS_F	ACACTCTTTCCCTACACGACGCTCTTCCGATCTGAAAAGCAGGCTCCCTGTAA
DogDMD_Off_15_DS_R	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTCATGTGAAAGTGGAGGTCCATA
DogDMD_Off_16_DS_F	ACACTCTTTCCCTACACGACGCTCTTCCGATCTCATGTGAAAGTGGAGGTCCATA
DogDMD_Off_16_DS_R	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGAAAAGCAGGCTCCCTGTAA
DogDMD_Off_17_DS_F	ACACTCTTTCCCTACACGACGCTCTTCCGATCTGGCTGGGCCCTACTCACTAT
DogDMD_Off_17_DS_R	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTGTCCATCTCATGGCTCGTCT
DogDMD_Off_18_DS_F	ACACTCTTTCCCTACACGACGCTCTTCCGATCTGAGCCACTTGGTCTCCTCTG
DogDMD_Off_18_DS_R	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTTCTCCATGCAGTCCTCACAC