

## Supplementary Information for

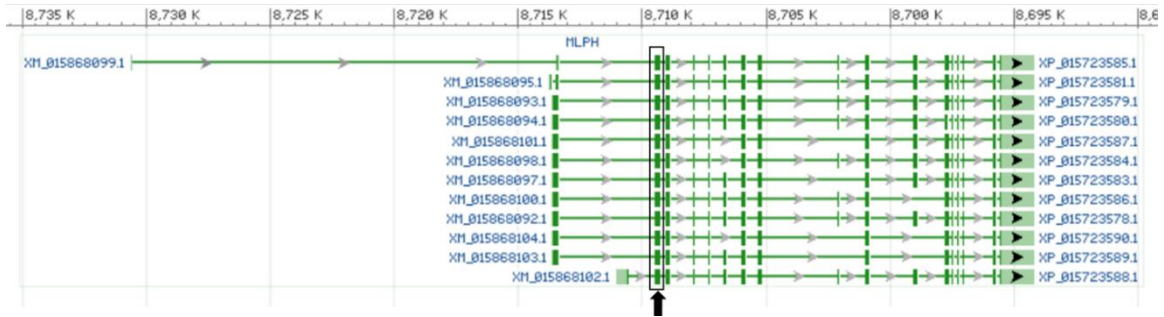
### **Direct delivery of adenoviral CRISPR/Cas9 vector into the blastoderm for generation of targeted gene knockout in quail**

Joonbum Lee, Jisi Ma, Kichoon Lee

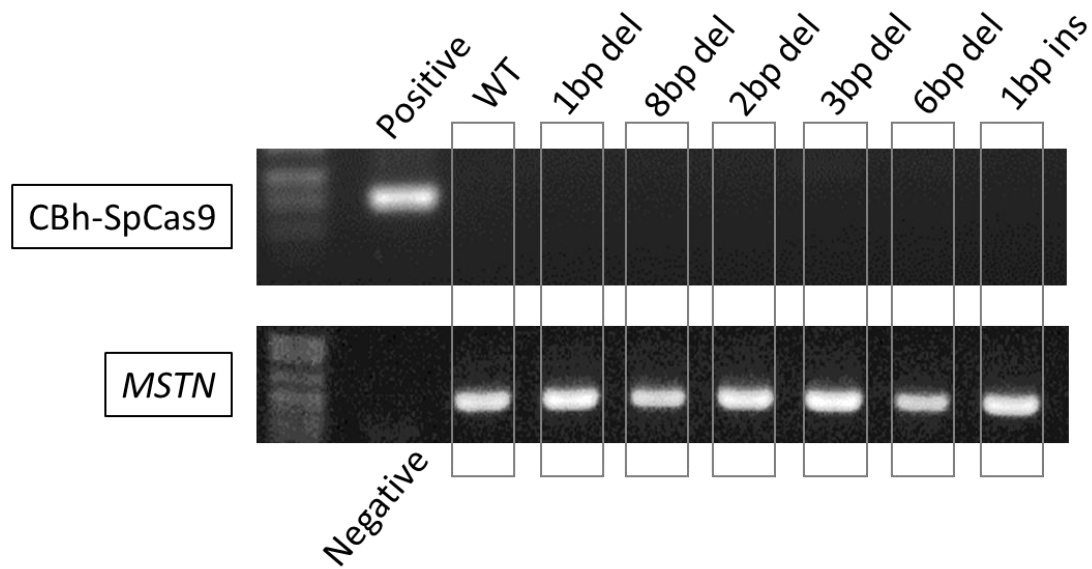
Corresponding to Kichoon Lee  
Email: [lee.2626@osu.edu](mailto:lee.2626@osu.edu)

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Figs. S1 to S3  
Tables S1 to S2

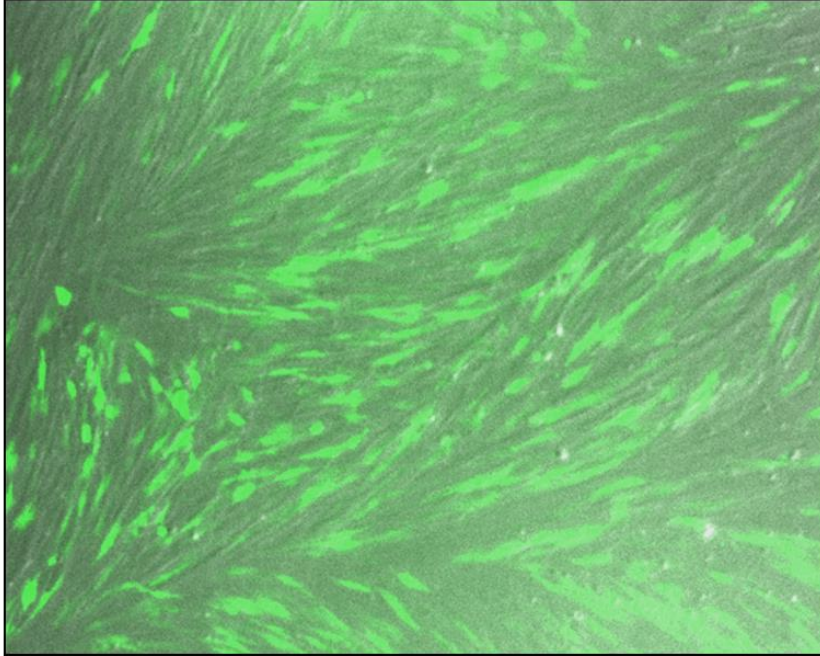


**Fig. S1. Diagrammatic representation of multiple transcripts of the Japanese quail *MLPH* gene and *MLPH* gRNA region.** A part of the ‘Genomic regions, transcripts, and products’ section was acquired from the NCBI Gene record for Japanese quail *MLPH* (Gene ID 107316507). The exons containing gRNA target sequences are boxed and directed by an arrow. Dark and light green boxes indicate translated and untranslated regions, respectively.



**Fig. S2. Detection of chromosomal integration of the viral vector into the host genome.** PCR amplification of a portion of the viral sequences, CBh promoter-Cas9, and the myostatin (*MSTN*) gene in all mutant quail genomic DNAs are shown. The adenoviral shuttle vector was used as a positive control and PCR master mix without genomic DNA was used as a negative control. Genomic DNA from wild-type quail (WT) was included to so that there was a negative control in viral vector detection and a positive control in *MSTN* gene amplification.

Bright Field + GFP



**Fig. S3. Adenovirus-mediated green fluorescent protein (GFP) gene expression in the primary turkey muscle cells.** Both GFP negative and positive cells are shown using a bright field with a fluorescent light microscopy.

**Table S1. Potential off-target sites of *MLPH* in Japanese quail genome.**

	Chromosome	Locus	Score	Sequence*	PAM	Direction
<i>MLPH</i>	7	8,709,348	46.1	AGGTGTAGAAGCGGCAATCC	AGG	-
off-target 1	3	51,763,707	30.2	CCTGAACTAAGCGGCAATCC	AGG	+
off-target 2	18	17,397	30.2	<u>TG</u> A <u>IT</u> GCTAAGCGGCAATCC	TGG	+
off-target 3	12	17,221,856	30.2	<u>TG</u> A <u>IT</u> GCTAAGCGGCAATCC	TGG	+
off-target 4	unplaced genomic scaffold	7,095	30.2	<u>TG</u> A <u>IT</u> GCTAAGCGGCAATCC	TGG	+
off-target 5	18	1,841,485	28.2	CTC <u>IT</u> TAGAAGCGGCAATAC	AGG	-
off-target 6	Z	402,850	28.2	CTAA <u>A</u> TCACAGCGGCAATCC	AGG	-

\*Identical nucleotides in potential off-target sites are underlined.

**Table S2. List of primers used in the present study.**

Purpose	Forward (5'-3')	Reverse (5'-3')
<i>MLPH</i>	GACCTGAAGTGCAAGATAGACCA	CTAGAAGAGCTGAATCCCCTTC
	CACCAGTCCCACCTGAATGAA	AGCTTGCAGGACAGCAGAAA
Off-target 1	CTCCCTCATTTTCTTCTGCTGTCTT	TCACTTGTAGGAAAGGCATTCTAGGA
Off-target 2	GAGGACTTACCTATTTGGGACTTGATATAT	ACGTGAAGCCAACCACTTCA
Off-target 3	GACGTAGCCCCGGGGTTT	CCGCCCCACCCCAAAT
Off-target 4	GGTGACGTAGCCCCATGGTCTT	GCTTCTATTTATTGCCCGCCACACA
Off-target 5	CACATCCCTCACAACCTCCCTCTT	GAACCTCCAGGCCTCTGCTATTT
Off-target 6	GGGAAGACAGCGCACTTATATTTATCAA	GAGCACTCAGAGGTTGGTGAAA
<i>MSTN</i>	TGTGATCGACAGGGCTTTAAC	CGCAGTTTGCTGAGGATTTGAA
CBh promoter-Cas9	GCTCTGACTGACCGCCTTACT	GTTGCCCAGCACCTTGAATT