	forward primer	$\sim$	TALEN A off-si	te	TALEN B of	ff-site				_	reverse prime
57BL/6 DBA/2	CCAACCACCCATGGCTTCT	таттатосто	CTTCATTCAAGCCGAA	GCGAGATTAGGTG	CCGGGAGATGTC	ATATTAAGGTGCCTGCTTGCATGA	AGGACTTGAGTCTGGAT	TCTCAGTGTCCAT	GTAGAGGCCAGGCT	GATGATGTGT	GTATGCTACCCCAG
FVB/N ounder				••••							
Off-sit	te 3										
Off-sit	te 3 forward primer					TALEN A off-site	TALEN B	off-sit <u>e/</u>	reverse pri:	mer	
C57BL/6	forward primer		TATGAACAACACAG <mark>G</mark> A	AGATCCCATGGAG	SAAGGAGTGAGGG	TALEN A off-site					
Off-sit	forward primer		TATGAACAACACAG	AGATCCCATGGAG	SAAGGAGTGAGGG						

Figure S6 Nucleotide polymorphisms in TALEN-Fus15 off-target sites 1 and 3.

Sequencing of HRMA PCR products revealed single nucleotide polymorphisms between wildtype C57BL/6 controls and mutant founder animals in the TALEN-Fus15 off-site 1 (A) and off-site 3 (B). These polymorphisms were identified as strain polymorphisms, resulting from the mixed genetic backgrounds (C57BL/6, DBA/2, and FVB/N) of founders. Predicted TALEN off-target binding sites and HRMA primer binding sites are indicated.