

Supplementary Tables

Table 1. Primer information for q-PCR for each mutation candidate

Primer ID	Sequence	Chr	Strands*	Position	
s893-1-F1	TGTGATTGGATGACTGGGCCTTGG	10	+	121,957,974	121,957,997
s893-1-R1	CCGCTCTTACTTTAAGGCCTGCC	10	-	121,958,037	121,958,059
s984-1-F1	AGGCTGAGCCTACCATGAAAGAGG	6	+	90,647,379	90,647,402
s984-1-R1	TCTCTCACTCTCCAAGCCAACC	6	-	90,647,464	90,647,486
s390-1-F1	TCAACACCTGCACCACAATGGG	6	+	101,122,351	101,122,372
s390-1-R1	CTTATCCCAGCAACTCATGACC	6	-	101,122,405	101,122,427
s1290-2-F2	AGAAAGACTGGGGTACACTTGGG	7	+	57,058,398	57,058,420
s1290-2-R2	TCTTCAGCACCAGCTGACTTCC	7	-	57,058,453	57,058,474
s280-1-F1	ACTCGTACTAGCTGAGGGTCTTGG	9	+	34,296,862	34,296,885
s280-1-R1	TTCCGAAGGGAAACCCACAGTTCC	9	-	34,296,945	34,296,968
L400-1-F3	TGTCTGGAGGGTCCAAGTTAAACC	13	+	101,637,639	101,637,662
L400-1-R1	CAGTATCTGAACATCAGGTTTCAGGG	13	-	101,637,701	101,637,725

“+” denotes strand read from centromere to telomere and “-” the opposite direction.

Table 2. Identification of parental origins of two mutations by SNP analyses

Mouse ID	SNP ID	SNP location (NCBI, Build 37)	SNP			Observed bases
			C3H/HeJ	C57BL/6J	JF1	
B6C3-4G-4	rs31214087	Chr6 99,507,214	T	T	C	T
	rs31214089	Chr6 99,507,319	A	A	G	A
	rs31214091	Chr6 99,507,350	G	G	A	G
	rs31214093	Chr6 99,507,469	T	T	C	T
B6C3-4G-5	rs37142080	Chr7 58,626,316	T	T	G	T
	rs36718055	Chr7 58,627,057	A	G	C	A