Table 2. Primer sequences of markers used for mapping key deletion endpoints

Deletion	**Marker**	**Forward primer sequence (5’→3’)**	**Reverse primer sequence (5’→3’)**
11Pu (prox)	**jmjdc2c-ex18**	CTGATAAGGCCCCAGAATCA	ACCACGTAAGGCCAGTCATC
	jmjdc2c-ex22	TAGGTTCCTTCGACCCTGTG	TGGGGTCAAACAAATGACTG
8Pub (prox)	**8Pub74.9**	TGCAAATGATGGTGAAGAGG	CCATAATGCAAGACCCCACT
	8Pub75.1	GCACAAGAGACCTGGGAGAC	TTTCCTCAGGATCCTCTCCA
11R30M (dist)	**286H15**	AGTCAGCTGAGACCACAGGAG	GAATTGACGGGAAGTCACAG
	D4Rck140	CATGATCTGGCTGCTGCG	GAATTCACTTCACAGCTA
9R75VH (dist)	**Nfibex4lge**	AGATGCATTCAGAGCGTGTC	TGAGCGTTACAGAACACAAGG
	Nfib5'	GCTCGCAGCAAAGTTTCG	AGATGCCCAAGAAAATCTTCC
46UTHc (dist)	**Frem1iii-ex4**	AACGGAAGGCCAAAATATCC	TTGGGGTCCATTTTGTGAAT
	DEPC2-823	AGGCGCAACATTAAGTTCTATC	TGGGTCCTAATGATGTCCTTTC
8Pub (distl)	**Novel2(Bnc2)**	TTTGGTCAACAGTTTTACGATGC	TGCACCAGGAACAGTTTATTTG
	D4Jkn1	GGACCGGGCTACATAGAGAAG	CTATATCTCTTACTAATTTCTTAAGTG
9R75VH (prox)	**8Pub75.1**	As above	As above
	8Pub75.4	CACAAGCCATAAAACCAGGA	TTGTGAACTGGGAAGCACAC
46UTHc (prox)	**r77.3**	TGCACACAATAAAGTTGAAAGG	TGTGGAGACTCTCAGGAAAACA
	129L11	GGGCCTTTTACTCTGGTGAC*	ATTTGTTTCCCCTGCAAACC
173G (dist))	**395J04-SP6**	GGGTTGTGGGTTCTCAGTG*	CTAGCTAGCGTTTCGTGCAG
	395J04-10k	GGAATGGCGAGAGAAATGAA	GTCTCAGCAAGCCTGACCTC
1THO-IV (dist)	**395J04-10k**	As above	As above
	s79.48	GTGAGTGTGTGGGGGACTTT	TCCCTGCTCCTATTGCATCT

Primer sequences used in PCR to amplify sequences from C3H, 101, *Mus spretus*, and deletion/*spretus* heterozygous DNA. The amplified fragments were subsequently sequenced by using the same primers; SNPs were identified between laboratory strains and *M. spretus* and presence or absence of these SNPs in the heterozygous samples used to identify extent of deletions.

*Two primers are not present with 100% identity in the sequence assembly in Vega. The equivalent sequences in Vega are: 129L11, GGGCCTTTTCATCTGGTGAC; 395J04-SP6, GGGTTGTGGGTTTCTCAGTG.