

genomic coordinate	pre-amplification primers		allele-specific primers			description
	forward	reverse	common Primer	C57 specific primer	JF1 specific primer	
66527171	TTAAGGGTCTATACCATCAAC	TTACCACAGTTTACCAGAAAAGG	TTAAGGGTCTATACCATCAAC	AAATTCACACTACTCCTCCCA T A	AAATTCACACTACTCCTCCCA A G	<i>Ube3A</i> intron2
66874979	GGTCACATGTAACCTGGAGAG	GCAATCACTGGAGCAATATTC	TGCTTAGTCTCGAAGCAATAG	TGAGTACTGAGCCGAGGA A T	TGAGTACTGAGCCGAGGA A A	
66922670	TAAAGAGACTAAATCTCCCAAG	ATGGTGGAAAGTAATAGTGCTCC	CTTTAATAGAGGAGATGAATGC	GGTGCTAATTTTCTGTGCAAT T G	GGTGCTAATTTTCTGTGCAAT A A	
67068825	TAGAAAGACCACAGGCACTC	CCTGGAAATGTTTGGGTCAC	ATTGGCCTCTTCTGTCTTTC	GGGTGTGTTGGTCTCCAGTT A G	GGGTGTGTTGGTCTCCAGTT A T	
67092368	CTAAAGACTCCACAGTCTAAAG	CAGTCCTCTATATGGCTTC	ACCTCAGCAGACTAGGTAAC	CTGTTGAGTCTTCAAGGA T C	CTGTTGAGTCTTCAAGGA T T	<i>Snrpn</i> exon10
67127862	GCAATAATGACATACCAGTGC	CACCAGGAATTAGAGGTIAG	CCAATGCTTGAAGTGAATGTC	ATGACATTTGCTCAAGCTAA G	ATGACATTTGCTCAAGCTAA T	
67149376	P1 AGAAAAACACCCACTAGCGC	GATAGAAAGTTCTGTGCCGC	CGGGATTTTGAACGTGTACTG	CACAGCCTTGGACAAGAG T	CACAGCCTTGGACAACAG A	<i>Snrpn</i> intron1 ; DMR IC
67150683	P2 CCCAAGTGATTGCAAGCATC	TCCTTAGTTTTCTCTTGCC	TCCTAAGAGCTGGAATTA C TG	GAGACAGGGCTTCTAAAT G	GAGACAGGGCTTCTAAAT T	<i>Snrpn</i> 5' upstream sequence ; DMR IC
67152575	AAATCTTACCACGTGGCTCG	TAACCACAGCGACCCCTATC	CCAAAGTAATGTAAAAGTGATGGG	AGAAGATGCTTTATCCTCAAAT T	AGAAGATGCTTTATCCTCAAAT A	<i>Snrpn</i> 5' upstream sequence ; IC
67154751	AACTTCTTTTGAGCCAGGCA	CAGGAAGGCTACACCGCTTA	CACCTCCAGGGGAGATAATTG	TAGCCAGTGCTACACAGAG A	TAGCCAGTGCTACACAGAG T	<i>Snrpn</i> 5' upstream sequence ; IC
67277796	GCTTCAGCAGCTGTCAAAGC	GATACTGGTGGGATTGTTGC	ACTCAAGTTAGTCGAGCTGAAACAG	AGCCTGAGGAAG A CAAA T GCTG	GCTGTAGCCTGAGGAAGAG A G	
67315352	CAGACTGGCAAACATGCACG	CAGACTGGCAAACATGCACG	AGAAACTGGGAGGTGCAAACTAC	GGATGGGA TAATTGCACTTGAGC	GGATGGGA AAAAATGCACTTGAA G	
67484602	TATTTCTGCAAGGGGGTTG	GCAAGGAAAGAGAATCTGCC	CCTATGTTCTCAGAAAGTCTGTGT	TATGGCATGTTTGTCTTAATGAG G	TATGGCAAAATGTCTTAATGAA A	
67570269	TAAATGTCAAGGGGGCAAAAG	AAGAGGCAGTCACCAITTAG	CCATTAITTCCTATGGCTG	GCAGAGAAATTCCTCAGAG T	GCAGAGAAATTCCTCAGAG G	
67832363	P3 CTCTAAAGGTGACTGCCTC	GCAACTGTGTGCAGGCTTCA	GGCAITCACTGAAGGCATTG	CAITTAACAGTTTCAGCTCTAGGA	CAITTAACAGTCTCAGCTGTAG T G	
67962860	GGGAGGGTCTTTCCTTACCA	TCCAACCTATTTCCCCACAC	TAAGGCTAGCTAGAGCTCAG	GAGAGACAATACTTCTAATAC C A	GAGAGACAATACTTCTAATAC A T	
68006896	P4 CATCTCAGCAGTGGTCTCAG	TCCTTTTGTGTGATGAGGTTG	TCTCTCACATGGGTCTATG	GATGCCCTACATCTGCAC T TG	GATGCCCTGCACTGCAC T TT	
68210034	P8 GTTACCTGACCATGATGACG	GCCTCATGAAACTGCACATGA	ACTCAGCCAGTCAGAGTAAC	GCCTGGTACAAACTGAA A GC	GCCTGGTACAAACTGAA C TA	
68265910	GCTTCTAATCAAGGTGGATG	TTCAAAACAGCATGAGCCAG	TTCTGGCTGATGTCAAACAG	GGCCCACTCGTATGTTTGA A	GGCCCACTCGTATGTTTGA G	
68416899	GTGAGAGAGAGTAAGTGCTC	TACCCTGCTCATGCTTTTTG	TAAGCTTATCCCTTGAAGAAAG	TGAGAGATAGGCTC AGAATG	ATAGGCTCAGAACAT TGGAATG	
68615493	CCAGAAAGTGAGTTTGGAGG	TGCTTCCCTTGCTGTGTGTG	CATCTACAGCATGAAGTAGAG	CTCCTCACGCTGTTTTACT T T	CTCCTCACGCTGTTTTACT T A	
68936232	GTGAAGCTGTCTGCTGAITC	TCACTGTGCTGCCCATGTG	CATGCAITGTTCTATGTTCATC	CCTGCAITTTGAGTATTT C TA	CCTGCAITTTGAGTATTT C TC	
68968981	ACAATGTAAGGAGATGGTGG	TTGAGGGCTTGTGTGTTCAA	CTGCTTGATGCACTGTGTT	TGTTCTAGTAATGTCAITGAG C TC	TGTTCTAGTAATGTCAITGAG C TA	
69117282	P9 ACCTGGTCCTTCAATCCTAG	TATTGAGGATGATATGGGGC	CTCTGATAACATGCCTGAATAC	CTATACTCTTCAACACAG C TC	CTATACTCTTCAACACAG C T	
69177824	CTGGAGAATGGAAGGAGTTGC	GGCTCTAACAGAGCATGAG	TAGACCTTCTGCTTCTTACAG	ACATGCCTCTAAGCAG T CC	ACATGCCTCTAAGCAG T CA	
69417859	CTACGAGTACCTTAAAGAACC	AGACTCACTGAGACACCAAC	AGGTGCATGGGTAAGAACAG	GGTCCAAAACATCAGGGAT T C	GGTCCAAAACATCAGGGAT A	
69493157	P5 CTCTTAACCACTGAACCAAG	GTGGAGACCAGCAGAGGAAG	CGGTGGAGACCAGCAGAG	ACGCATGCGCAATATCG C A	ACGCATGCGCAATATCG C G	<i>Ndn</i> 5' upstream sequence
69523461	P6 GATTACTCCGATGGCCAAGC	ATGATGGGTGGGAATGCAC	GACGGATCATAGGAGGTATCTG	GCAGGCCACTCAAC T GG	GCAGGCCACTCAAC T G	<i>Magel2</i> 5'UTR
69563167	TTCTCTGATGACCGTTGGC	CCACAAGTTAACAAGTGCAC	CATCACAAGTCATCAGTTGAC	GGCAATCTTTATGCAGTAT T GC	GGCAATCTTTATGCAGTAT A	<i>Mktn3</i> 3'UTR
69565295	P7 GCACCTGCCCATGCAGATAAT	GCACCTGCCCATGCAGATAAT	TTCTAAGTGCAGCTCTGAAC	CTGCAATGTATACAACCGAA A C	CTGCAATGTATACAACCGAA A T	<i>Mktn3</i> 5' upstream region
69593704	AAGACGCCAGCTCTAGGAAC	GGGTACAGAAACATAACTGAGA	GTCTTAGGGTTCCTATAAG	CTACAGAAACAATATCATG C G	CTACAGAAACAATATCATG C A	
69723428	AGAGCCATTCCCATGAGATC	TGGCTGAACCTCAAATCTC	CTCAAGATTACTTGGATTGATC	CACAAGATATGAGGACATAG C AT	CACAAGATATGAGGACATAG C AC	
69829104	GCCTGGCATTGCACATCTTG	TGGACCATGTGTCACACCTG	ACCCTGCCCATCTGCTAAC	GGAGCACTAGATGTG A CCCA	CAGGAGCACTAGATGTG T GG	
69916921	TTCCAAGCAATCAAGACCA	GATATCTATCATTTGGTCAACC	GAGATTGGGAGAAGTAGAAG	AGACTTGATGCAATATCTT A G	AGACTTGATGCAATATCTT A	
69971150	AATGGCTGAGCAGACAGCTG	CAAGGAGGGAGCATACATCC	CAAGGAGGGAGCATACATCC	CTGACTGATAACAACAGAG T G	CTGACTAATAACAACAGAG T A	
70094182	CATACTACTACTATTCACTAGG	TGCAGCTCACAACATCTTCC	GAGGACAATATGAAGTGAGAAC	GTAGAAACACTTGTCAITTT G TA	GTAGAAACACTTGTCAITTT G TA	

Table S1 : PCR primers used in allele-specific qPCR assays. The first column indicates the coordinates of the polymorphisms (NCBI build 37). For each genomic position, the second and third columns indicate the sequences of the forward and reverse primers used in the pre-amplification step. The three following columns indicate the sequences of the primers used in the allele-specific qPCR assays. Column 4 describes the primers that hybridize to both C57BL/6 and JF1/Ms genomes. Columns 5 and 6 describe the C57BL/6 and JF1/Ms allele-specific primers, respectively. Blue and red colors indicate polymorphisms. Nucleotides in bold correspond to additional mismatches introduced at the 3' end of several JF1-specific primers, to improve amplification specificity. The last column provides supplemental information about tested positions. P1 to P9 indicate the primers used in figure 2 C and in supplemental figure S14.