

Table S2: SNPs used for analysis of monoallelic expression in F1 progeny of Castaneous male and C57BL/6 female mice

Gene	SNP	Position	BL/6 allele	Cast allele	Primers	Expressed allele
<i>Dlk1</i>	NES17644873	chr12:110,698,537	T	C	(F) AGTATAACAGCGGCGAGGAG (R) AGCTCTAAGGAACCCCGGTA	C
<i>Gtl2</i>	NES17649632	chr12:110,797,703	T	C	(F) CACAGAGCACACAGTCACCA (R) GGATTAACGATCCACCAGCA	T
	NES17649638	chr12:110,797,931	A	C		A
<i>H19</i>	Szabo & Mann ⁶⁸	chr7:149,761,689	A	C	(F) AGGAATCTGCTCCAAGGTGA (R) GCATTGCCAAAGAGGTTTACA	A
<i>Igf2</i>	Szabo & Mann ⁶⁸	chr7:149,839,519	C	T	(F) TCCGAGAGGGACGTGTCTAC (R) GGGTGTCAATTGGGTTGTTT	T
<i>Peg3</i>	NES16164957	chr7:6,659,876	G	A	(F) CAAAGACTTTCACTCTCATCACA (R) GGCAGGAATCATTATGTATAGGG	A
	NES16164959	chr7:6,659,966	T	G		G

SNPs are named according to Perlegen IDs (<http://mouse.perlegen.com/mouse/browser.html>) as previously reported [1]. Positions are based on the mm9 (NCBI37) assembly of the mouse genome. Note that the alleles listed here reflect the (+) strand, whereas the sequencing traces for *H19*, *Igf2* and *Peg3* (shown in Fig. S1) reflect the (-) strand.

Reference for table S2

1. Frazer KA, Eskin E, Kang HM, Bogue MA, Hinds DA, et al. (2007) A sequence-based variation map of 8.27 million SNPs in inbred mouse strains. *Nature* 448: 1050-1053.