

Figure S2.

Seq. Frag.	1	2	3	4	5	6	7	8	9										
<i>M. famulus</i>	C A	C T C	G A	C G G C	G G C C G T	G T T T A A C G C C C A	T T C T C G G G C T G G G	T C C C A G A A A	G G G G T A T T G G C C										
C57BL/6J	C A	C T C	G A	C G G C	G G C C G T	G T T T A A C G C C C A	T T C T C G G G C T G G G	T C C C A G A A A	G G G G T A T T G G C C										
RIIIS/J	C A	C T C	G A	C G G C	G G C C G T	G T T T A A C G C C C A	T T C T C G G G C T G G G	T C C C A G A A A	G G G G T A T T G G C C										
D03_a	.	.	.	T A A	A A T T T C A G C C C G T	T T G	G	C A	T C A	A	A	G G G	G A A	G G G	G A G	G G G	G A G	G G G	G A G
D03_b	.	.	.	T A A	A A T T T C A G C C C G T	T T G	G	C A	T C A	A	A	G G G	G A A	G G G	G A G	G G G	G A G	G G G	G A G
D06_a	.	[A]	.	T A A	A A T T T C A G C C C G T	T T G	G	C A	T C A	A	A	G G G	G A A	G G G	G A G	G G G	G A G	G G G	G A G
D06_b	.	[A]	.	T A A	A A T T T C A G C C C G T	T T G	G	C A	T C A	A	A	G G G	G A A	G G G	G A G	G G G	G A G	G G G	G A G
D25_a	.	(A)	.	T A A	A A T T T C A G C C C G T	T T G	G	C A	T C A	A	A	G G G	G A A	G G G	G A G	G G G	G A G	G G G	G A G
D25_b	.	(A)	.	T A A	A A T T T C A G C C C G T	T T G	G	C A	T C A	A	A	G G G	G A A	G G G	G A G	G G G	G A G	G G G	G A G
D30_a	.	A	.	T A A	A A T T T C A G C C C G T	T T G	G	C A	T C A	A	A	G G G	G A A	G G G	G A G	G G G	G A G	G G G	G A G
D30_b	.	A	.	T A A	A A T T T C A G C C C G T	T T G	G	C A	T C A	A	A	G G G	G A A	G G G	G A G	G G G	G A G	G G G	G A G
D40_a	.	A	.	T A A	A A T T T C A G C C C G T	T T G	G	C A	T C A	A	A	G G G	G A A	G G G	G A G	G G G	G A G	G G G	G A G
D40_b	.	A	.	T A A	A A T T T C A G C C C G T	T T G	G	C A	T C A	A	A	G G G	G A A	G G G	G A G	G G G	G A G	G G G	G A G
D42_a	(.)	(G)	(G)	T A A	A A T T T C A G C C C G T	T T G	G	C A	T C A	A	A	G G G	G A A	G G G	G A G	G G G	G A G	G G G	G A G
D42_b	(A)	(G)	(G)	T A A	A A T T T C A G C C C G T	T T G	G	C A	T C A	A	A	G G G	G A A	G G G	G A G	G G G	G A G	G G G	G A G
D44_a	(.)	(G)	(G)	T A A	A A T T T C A G C C C G T	T T G	G	C A	T C A	A	A	G G G	G A A	G G G	G A G	G G G	G A G	G G G	G A G
D44_b	(A)	(G)	(G)	T A A	A A T T T C A G C C C G T	T T G	G	C A	T C A	A	A	G G G	G A A	G G G	G A G	G G G	G A G	G G G	G A G
D57_a	(.)	(G)	(G)	T A A	A A T T T C A G C C C G T	T T G	G	C A	T C A	A	A	G G G	G A A	G G G	G A G	G G G	G A G	G G G	G A G
D57_b	(A)	(G)	(G)	T A A	A A T T T C A G C C C G T	T T G	G	C A	T C A	A	A	G G G	G A A	G G G	G A G	G G G	G A G	G G G	G A G
MC06_a	(.)	(G)	(G)	T A A	A A T T T C A G C C C G T	T T G	G	C A	T C A	A	A	G G G	G A A	G G G	G A G	G G G	G A G	G G G	G A G
MC06_b	(A)	(G)	(G)	T A A	A A T T T C A G C C C G T	T T G	G	C A	T C A	A	A	G G G	G A A	G G G	G A G	G G G	G A G	G G G	G A G
MC17_a	(.)	(G)	(G)	T A A	A A T T T C A G C C C G T	T T G	G	C A	T C A	A	A	G G G	G A A	G G G	G A G	G G G	G A G	G G G	G A G
MC17_b	(A)	(G)	(G)	T A A	A A T T T C A G C C C G T	T T G	G	C A	T C A	A	A	G G G	G A A	G G G	G A G	G G G	G A G	G G G	G A G
MC41_a	(G)	(G)	(G)	T A A	A A T T T C A G C C C G T	T T G	G	C A	T C A	A	A	G G G	G A A	G G G	G A G	G G G	G A G	G G G	G A G
MC41_b	[G]	[G]	[G]	T A A	A A T T T C A G C C C G T	T T G	G	C A	T C A	A	A	G G G	G A A	G G G	G A G	G G G	G A G	G G G	G A G
MC45_a	(.)	(G)	(G)	T A A	A A T T T C A G C C C G T	T T G	G	C A	T C A	A	A	G G G	G A A	G G G	G A G	G G G	G A G	G G G	G A G
MC45_b	(A)	(G)	(G)	T A A	A A T T T C A G C C C G T	T T G	G	C A	T C A	A	A	G G G	G A A	G G G	G A G	G G G	G A G	G G G	G A G
MC50_a	(.)	(G)	(G)	T A A	A A T T T C A G C C C G T	T T G	G	C A	T C A	A	A	G G G	G A A	G G G	G A G	G G G	G A G	G G G	G A G
MC50_b	(A)	(G)	(G)	T A A	A A T T T C A G C C C G T	T T G	G	C A	T C A	A	A	G G G	G A A	G G G	G A G	G G G	G A G	G G G	G A G
MC55_a	(.)	(G)	(G)	T A A	A A T T T C A G C C C G T	T T G	G	C A	T C A	A	A	G G G	G A A	G G G	G A G	G G G	G A G	G G G	G A G
MC55_b	(A)	(G)	(G)	T A A	A A T T T C A G C C C G T	T T G	G	C A	T C A	A	A	G G G	G A A	G G G	G A G	G G G	G A G	G G G	G A G
MC74_a	(.)	(G)	(G)	T A A	A A T T T C A G C C C G T	T T G	G	C A	T C A	A	A	G G G	G A A	G G G	G A G	G G G	G A G	G G G	G A G
MC74_b	(A)	(G)	(G)	T A A	A A T T T C A G C C C G T	T T G	G	C A	T C A	A	A	G G G	G A A	G G G	G A G	G G G	G A G	G G G	G A G
MC81_a	(.)	(G)	(G)	T A A	A A T T T C A G C C C G T	T T G	G	C A	T C A	A	A	G G G	G A A	G G G	G A G	G G G	G A G	G G G	G A G
MC81_b	(A)	(G)	(G)	T A A	A A T T T C A G C C C G T	T T G	G	C A	T C A	A	A	G G G	G A A	G G G	G A G	G G G	G A G	G G G	G A G
Rel. Pos.	-55	-38	-29	-19	-10	-1	4.2	20	41										

- = SNPS distinguishing RIIIS/J from C57BL/6J inbred strain
- = Missing Data
- ( ) = Uncertain (<90%) haplotypic phase
- [ ] = Uncertain (<90%) predicted genotype
- = Genotype prediction not applicable to missing outgroup data

**Figure S2. Summary of polymorphic sites across *B4galnt2* gene region and haplotypic phase.** Phase was determined by PHASE version 2.1 (Stephens *et al.*, 2001; Stephens and Donnelly, 2003). “D” is the identifier for individuals from the German population, “MC” is the identifier for individuals from the French population. For polymorphic sites where outgroup data was obtainable, the derived state of the polymorphic site is displayed as a letter.