Supplementary information

Title:

Highly Parallel SNP Genotyping Reveals High-resolution Landscape of Mono-allelic Ube3a Expression Associated with Locus-wide Antisense Transcription

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Supplementary Figure 1

Measurable SNP sites for the transcriptome-targeted assays

Measurable SNP sites, selected from the results of the genotyping assays (targeting genomic DNA from B6, MSM, and their reciprocal crosses), were visualized via the UCSC genome browser. “SNPs (Plus)” and “SNPs (Minus)” indicate sites which is able to detect the transcripts from plus and minus strand, respectively. SNP sites within the *Ube3a* locus are shown enlarged within the gray box.

Supplementary Figure 2

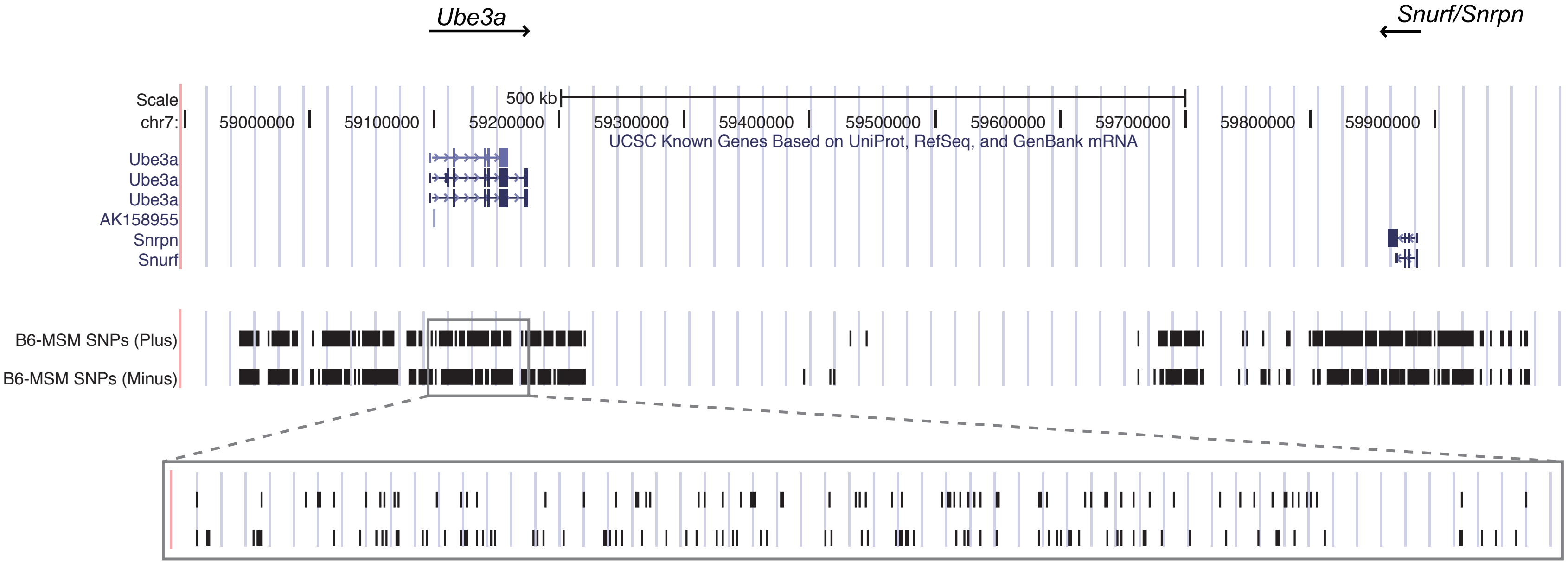
Balance of allelic expression of *Ube3a* in brain

Balance of allelic expression in the vicinity of *Ube3a* locus (plus-strand expression) was investigated by genomic segmentation analysis of **(A)** BM, and **(B)** MB hybrids. The x- and y-axis represent the genomic location of chromosome 7 and the signal intensity ratio between the B6 and MSM alleles, respectively. The blue lines indicate the segmented regions. The position of the *Ube3a* locus is indicated by the light blue box, and the horizontal arrow indicates the direction of transcription. Black and orange dashed lines indicate the genomic boundaries of the *Ube3a* locus and the computationally estimated transition site of the allelic balance, respectively. For genomic segmentation analysis we applied the circular binary segmentation algorithm to our dataset (the DNAcopy package from R was used). Non-expressed SNP sites were excluded from the analyses.

Supplementary Figure 3

Allelic balance of *Ube3a-ATS* expression in brain

Balance of allelic expression of *Ube3a-ATS* (minus-strand expression) was investigated by genomic segmentation analysis of **(A)** BM, and **(B)** MB hybrids. The x-axis and y-axis represent the genomic location of chromosome 7 and the signal intensity ratio between the B6 and MSM alleles, respectively. The pink lines designate segmented regions. The position of the *Ube3a* locus is indicated by the light blue box, and the horizontal arrow indicates the direction of transcription. Black dashed lines indicate the genomic boundaries of the *Ube3a* locus. For genomic segmentation analysis we applied the circular binary segmentation algorithm to our dataset (the DNAcopy package from R was used). Non-expressed SNP sites were excluded from the analyses.



Supplementary Figure 1
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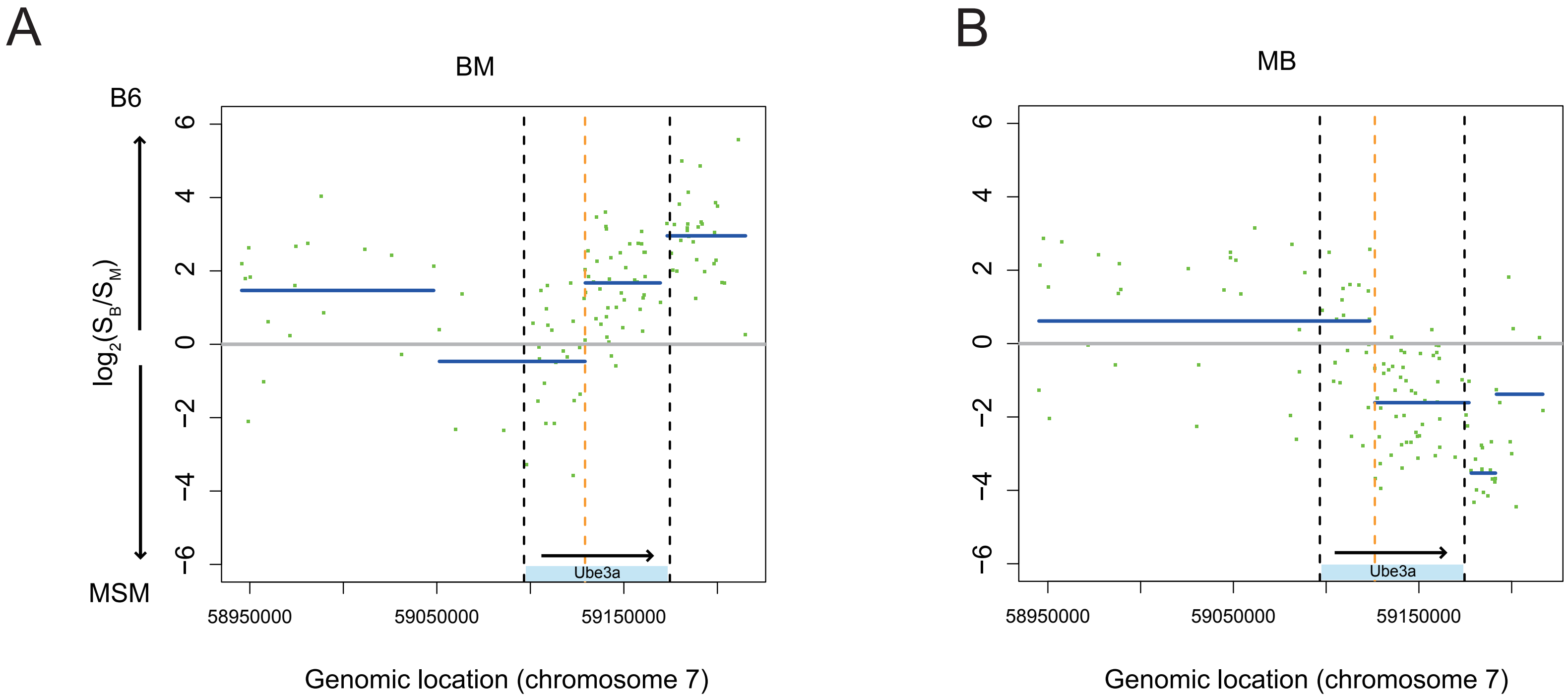

Supplementary Figure 2
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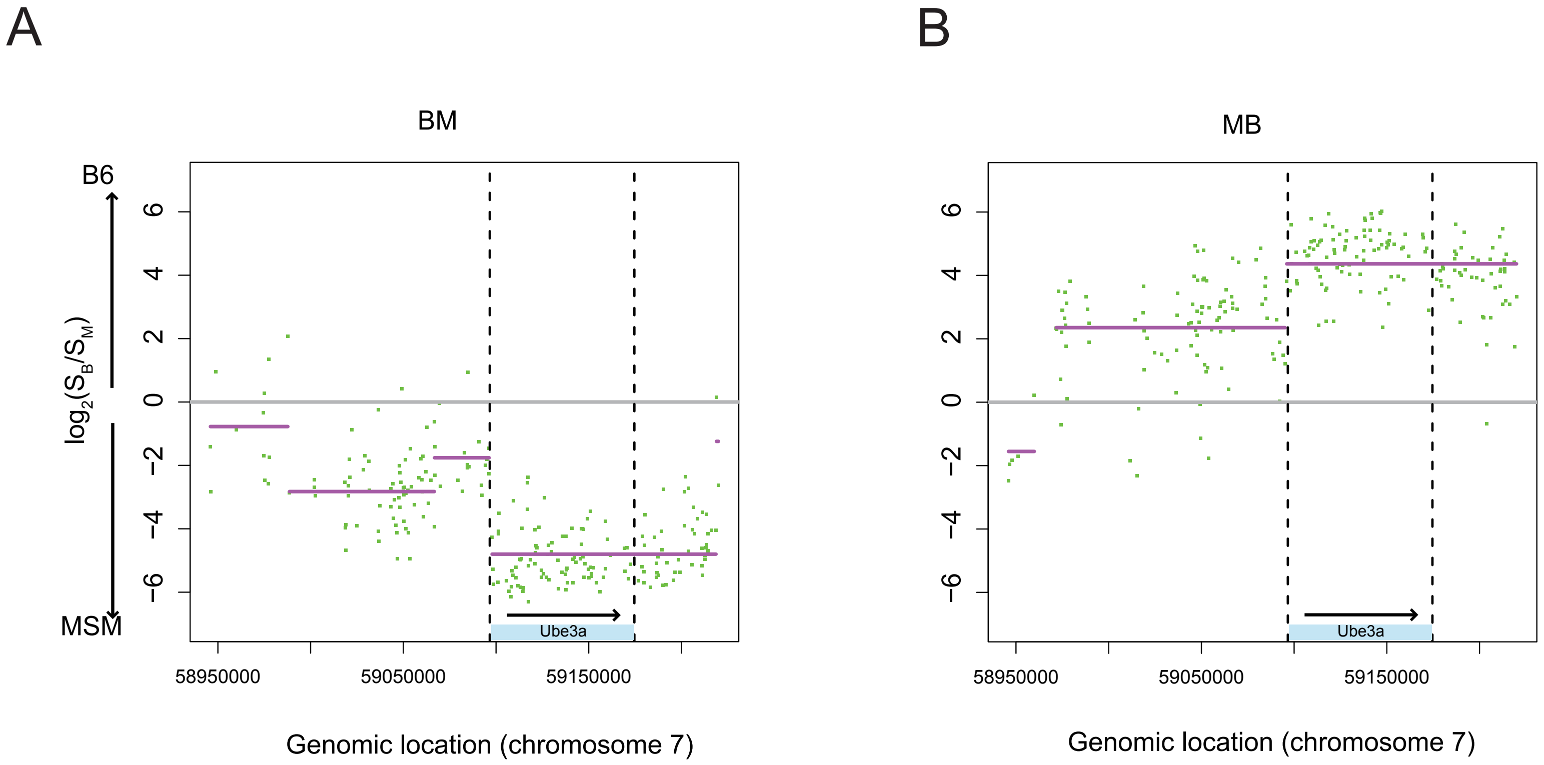

Supplementary Figure 3
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