

Description of Additional Supplementary Files

Data S1. Genome-wide list of bimodal methylation regions by sample

Data S2. Known imprinted DMR coordinates, with regions of biallelic methylation masked

Data S3. List of SNPs associated with cell-type-specific ASMs

Data S4. Genome-wide list of SNPs associated with parental ASMs

Data S5. Novel parental-ASM participant information

Data S6. Novel parental-ASM locus and primer information

Data S7. Summary data of trio data families genotyping and methylation status.

Data S8. Transcription factor enrichment analysis (ReMap)

Data S9. Chromatin states enrichment analysis (chromHMM)

Data S10. All imprinted genes with parental ASM regions and known imprinted DMRs

Data S11. Genes exhibiting tissue-specific imprinting, tissue-specific bimodality

Data S12. Fold-change biased genes vs expressed genes in relevant tissue

Data S13. Genes found with significant associations by Hofmeister et al.

Data S14. PanelApp Genomic imprinting panel associations with parental ASM

Data S15. Allelically biased genes associated with phenotypes and disease

Data S16. Tissue-specific escape from imprinting near tissue-specific unmethylated regions

Data S17. Raw sequencing counts, per trio participant, split by variant allele