Table S2 part I

DMR coordinates	Genomic position	Evidence for a role in *cis* regulation from ENCODE (*51*)
DMR1 MMU12:19181482-19182200	CpG island, multiple homologous copies as part of a segmental duplication.	- ESC DNaseI hypersensitivity (HS)
DMR2 MMU12:111666100-111666400	CpG island 57.8kb upstream of *Ppp2r5c* (*52*)	- Heart (8 weeks): H3K36m3 - Liver (8 weeks): H3K36m3
DMR3 MMU15:78370350-78370800	CpG island in last exon of *Sstr3* (*52*).	- Cerebellum (8 weeks): H3K4m1 - C2C12 myocytes: Myogenin bound - Heart (8 week): H3K36m3, Pol2 bound
DMR4 MMU1:39654450-39655100	Intergenic	Immediately 5' of a region enriched in: - Cerebellum (8 weeks): H3K4m1, DNaseI HS - Cerebrum (8 weeks): DNaseI HS - Liver (8 weeks): H3K4m1, H3K36m3
DMR5 MMU3:142351001-142351500	Intergenic	- G1E: DNase I HS - CH12: H3K9me3 - Erythroblast H3K9me3 - Megakaryocyte H3K27me3 - Liver (8 weeks) H3K27me3 - Heart (8weeks) H3K27me3
DMR6 MMU17:39984601-39985700	In *Rn45S* coding region	- Liver, Heart, Cerebellum (all at 8 weeks): H3K4me1, H3K4me3, H3K27me3, H3K36me3 - Cerebellum, heart (8 weeks): CTCF binding - Cerebellum, cerebrum, whole brain and ES-CJ7: DNAse I HS
DMR7 MMU10:80033801-80034300	Intergenic	- Cerebellum (8weeks) H3K4me1, H3K27ac, Pol2 - Heart (8weeks): H3K4me1 - Liver E14.5: H3K4me1 H3K4me3, H3K27a, H3K79me2 - MEL: H3K4m1, H3K4me3, H3K27a M3K36m3, Pol2 - GIE: DNAseI HS - CH12 cells: H3K4me3/pol2 - Erythroblasts and megakaryocytes: H3K4me1 M3K4me3
DMR8 MMU7: 137835001-137836500	Intron of *Tacc2*	- Cerebellum H3K4m3, H3K27me3, H3K27ac - Cerebrum, whole brain E14.5 and 8weeks DNAse I HS - ES-CJ7 DNAse I HS - Heart E14.5 H3K4m1, Heart 8w H3K4m3, H3K27me3 H3K79m3, CTCF and Pol2 binding - Liver (8weeks): H3K79me2 - CH12: H3K36me3 - Megakaryocyte H3K36m3
DMR9: MMU7:53354201-53354900	Exon1 of *Kcnj11*	- Cerebellum H3K4m1, H3K27ac - Heart E14.5 H3K4m1, Heart 8w H39ac, H3K27ac H3K27m3, CTCF and Pol2 binding - Liver (8weeks): H3K27me3 - CH12: H3K27me3 - Megakaryocyte H3K9m3, H3k27m3
DMR10: MU11:33922001-33922500	Intergenic	- CH12: H3K9me3 - Megakaryocyte H3K4m1
DMR11: MMU14:75925601-75926100	Exon2 of *Siah3*	- Heart 8w H3K27m3 - Liver E.14.5 H3K4m1, H3K4m3, H3K27ac, H3K36m3 - MEL H3K4m1, H3K4m3, H3K9ac, H3K27ac, H3K36m3, p300 and Pol2 binding, DNaseI HS - Erythroblast H3K4m1 - MEL H3K4m3, H3K9m3, H3K27m3
DMR12: MMU5:26397201-26397700	Intergenic	- GIE: DNAseI HS - CH12 H3K9m3 - Erythroblast H3K27m3 - Megakaryocyte H3K27m3 - ES-CJ7 DNaseI HS

Table S2 part II

DMR coordinates	**Genomic position**	**Evidence for a role in *cis* regulation from ENCODE (*51*)**
DMR13: MMU2:172688001-172688500	Intergenic	- Cerebellum H3K4m3 - Cerebrum and brain DNaseI HS - Heart E14.5 H3K4m1, H3K27a. 8weeks: H3K27m3 - Liver H3K27m3 - G1E DNaseI HS - CH12 J3K9m3, H3K27m3 - ES-CJ7 DNaseI HS
DMR14:MMU12:107752401-107752500	Intergenic	- CH12 H3K9m3 - Erythroblast H3K9m3 - Megakaryocyte H3K9m3
DMR15: MMU11:46390601-46391100	Exon 3 *Bc053393*	
DMR16: MMU7: 10836601-10837100	Intergenic	- Megakaryocyte H3K9m3
DMR17:MMU10:120699201-120699700	Intergenic	- MEL H3K4m1, H3K36m3 - Megakaryocyte H3K9m3

Table S2: Analysis of validated DMRs using the ENCODE (*51*) datasets suggests cell-type specific enrichment of histone modifications and transcription factor binding characteristic of a role in *cis* regulation of transcription.