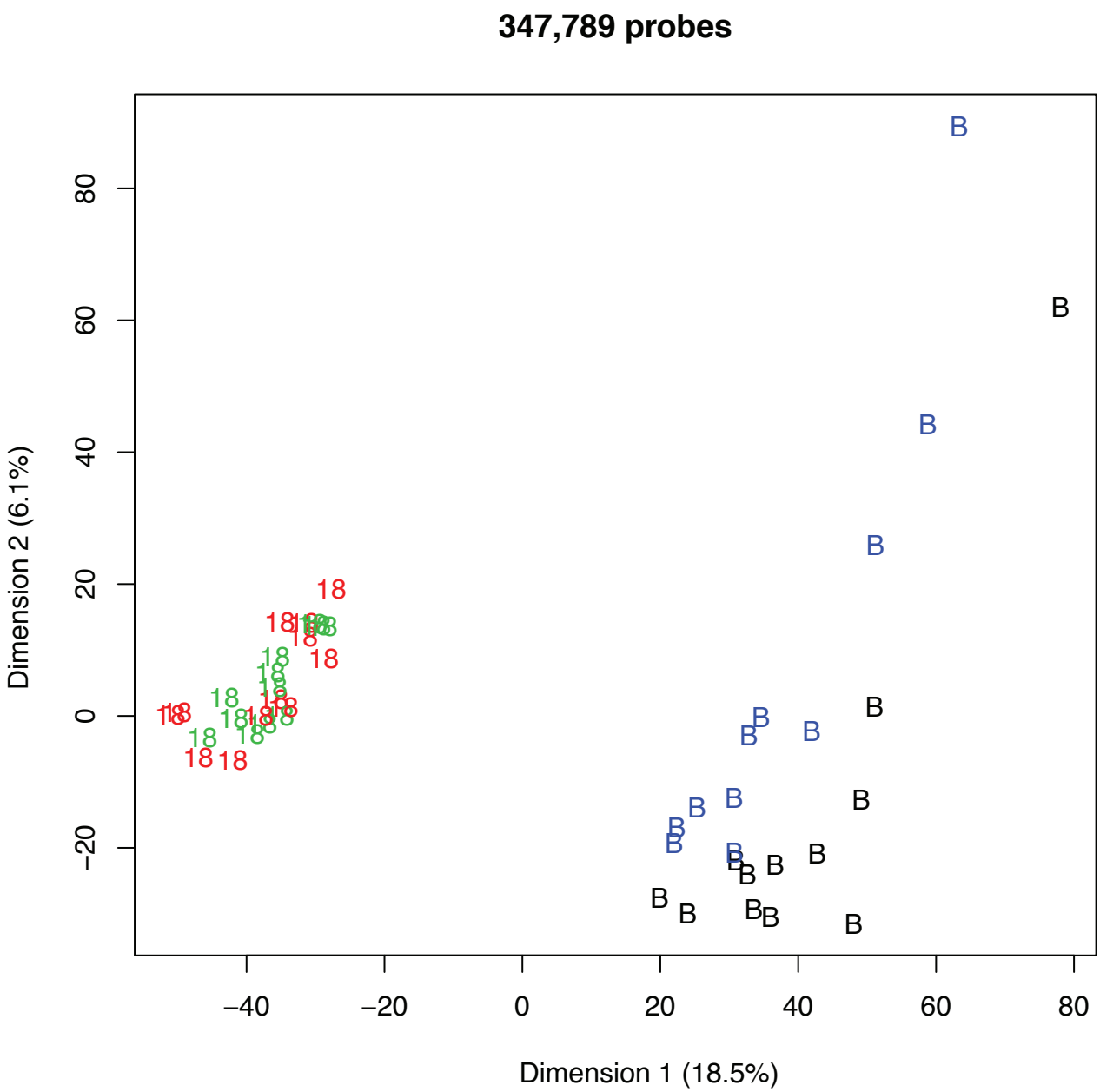


Figure S1. Multidimensional scaling plot of DNA methylation data from all samples and all 347,789 probes

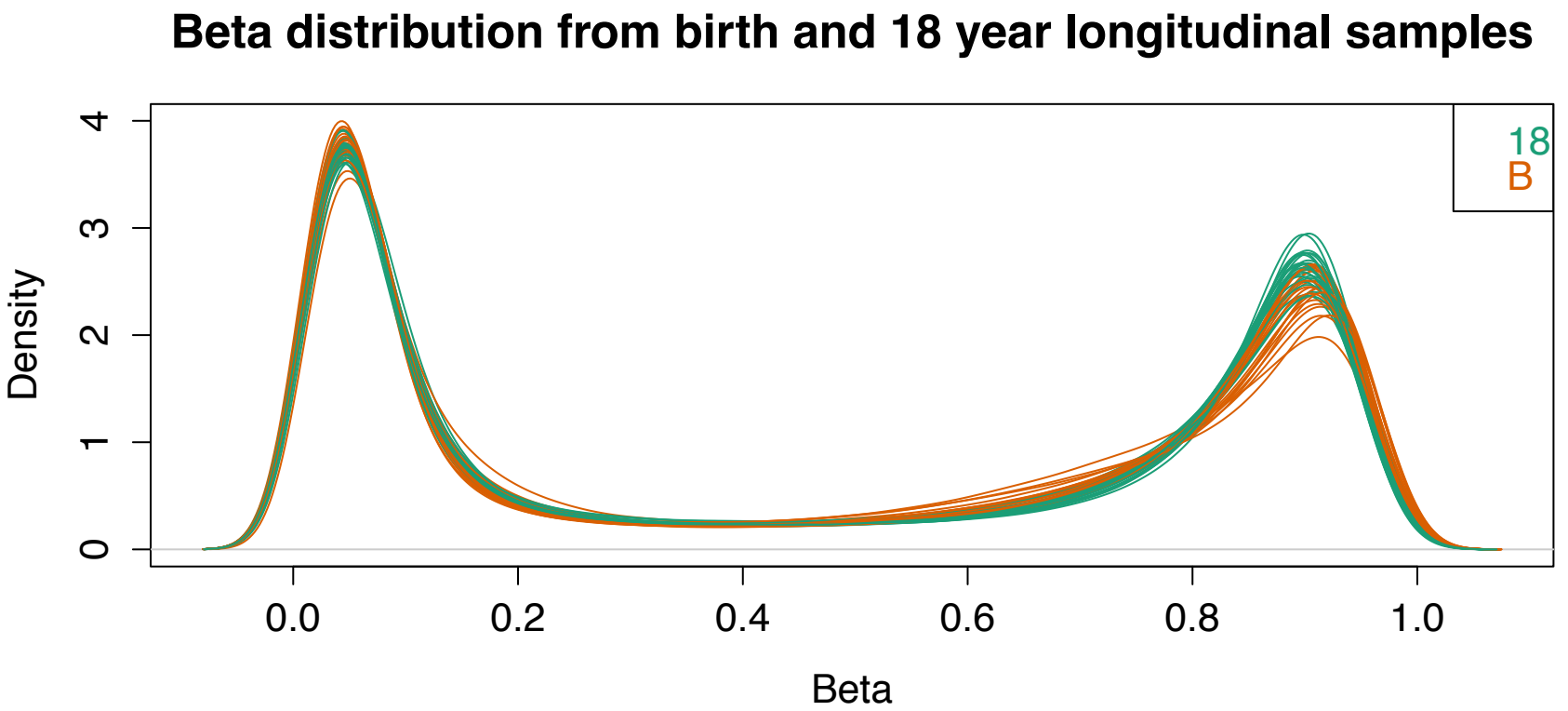
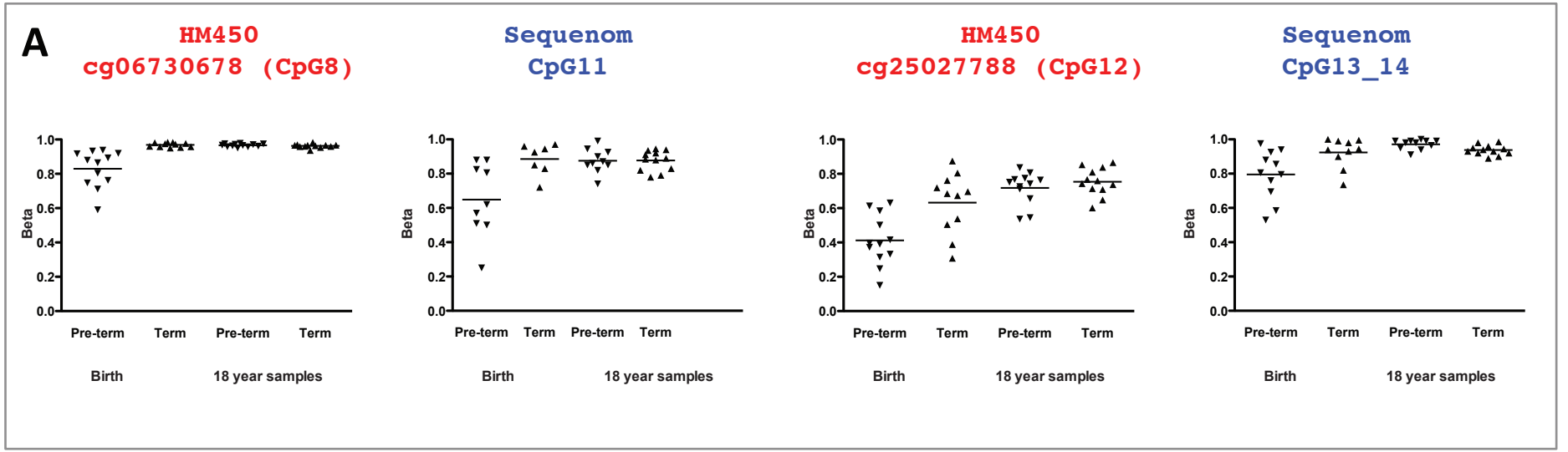


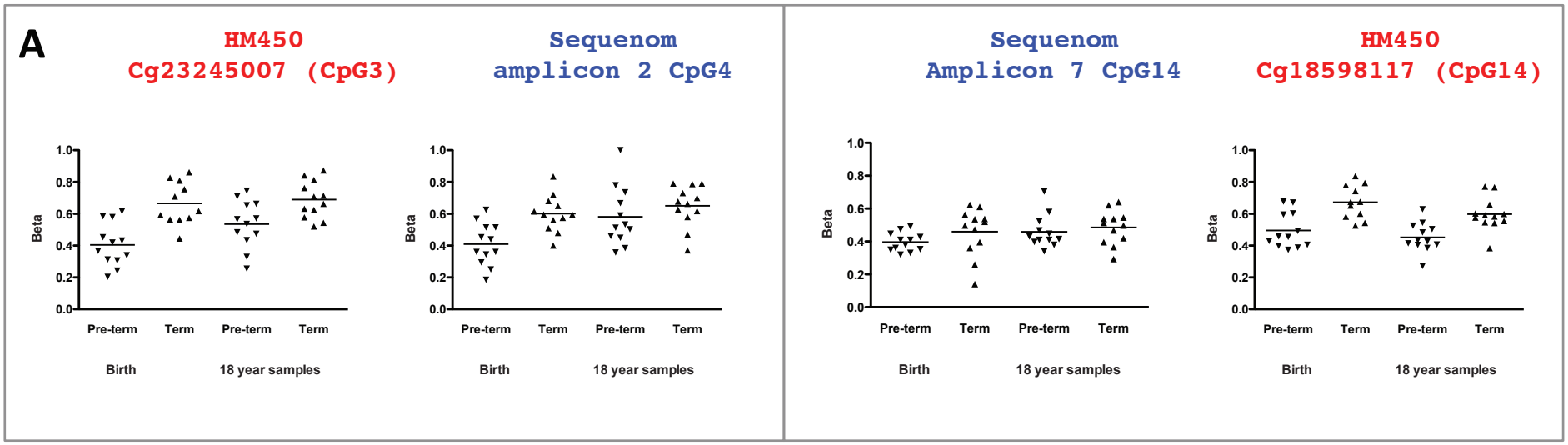
Figure S2. Beta distribution plots coloured by sample age



B

TGCCTC**CG**GAACGCACTGCACTAATGTGGAGACCTCGAGATTCTG**CG**AGGTCCCTGCCTTGCCCC**CG**GGTTCACATACTCATG**CGCG**GGTTGAG

Figure S3. Sequenom validation of VWF gene body enhancer birth-DMP



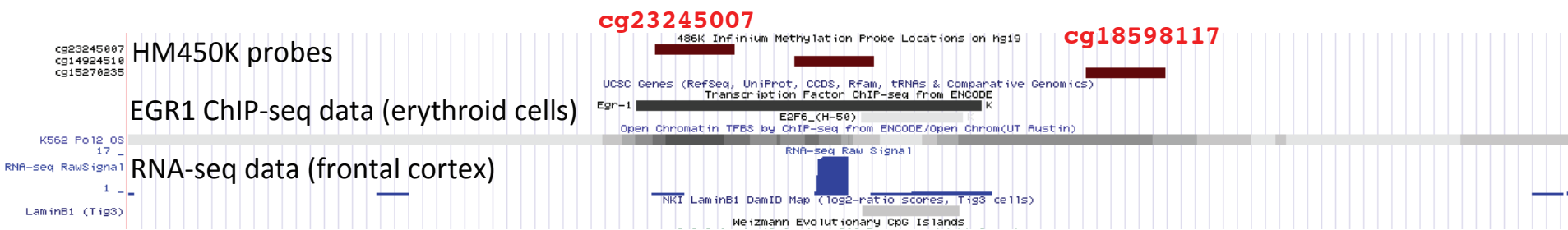
B

Amplicon 2

CCTGAACCGGGGCACAGGACACAGGACTAGGGTGGAAGGCGGCATGAGACTACGCGCACAGGAAAGACCC

Amplicon 7

CGCTGATGCAGAGCGCGGGGGCGCAGGTTAAACCTAAAGGGGGGAAGCTTTTCGGGGCAGAACAGACAACG



C

CGCCGCCCCCGACCCCGTGCA

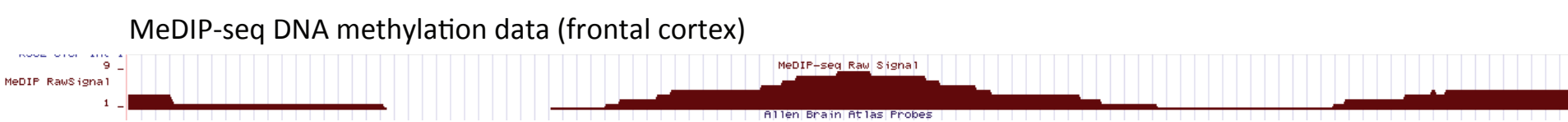
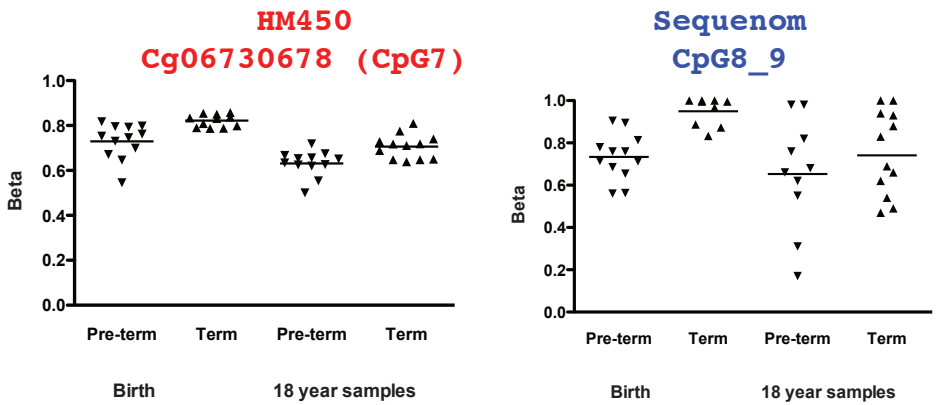


Figure S4. Sequenom validation of candidate long-term preterm-DMPs flanking tandem EGR1 consensus sites and genomic landmark context

A



B

CCACGCGGGGTCCGGCCTGGGATCCAGGCTAAGGGCCGGCGGAAGAGGCCCCAATGGGGCGGTGACCCCAGCCTCGCCCGA

Figure S5. Sequenom validation of *TINAGL* 3'UTR candidate long term preterm-DMP