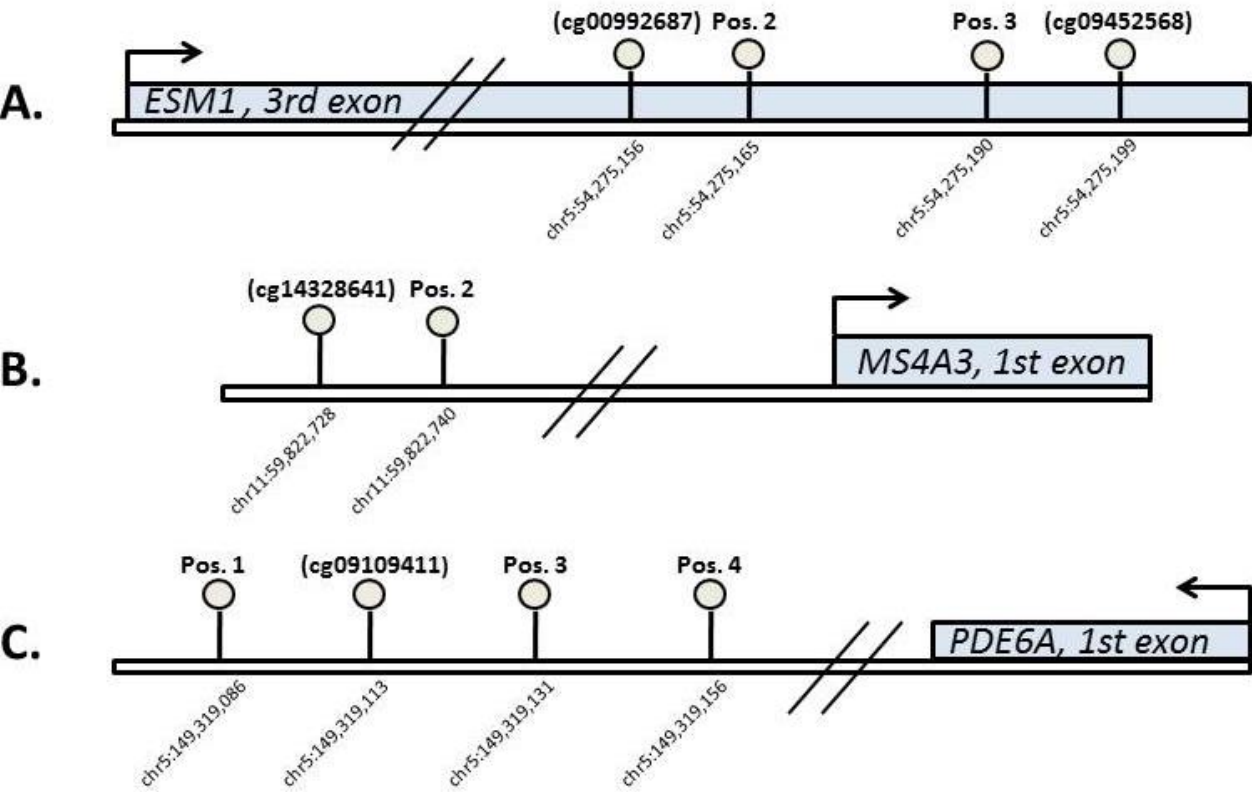
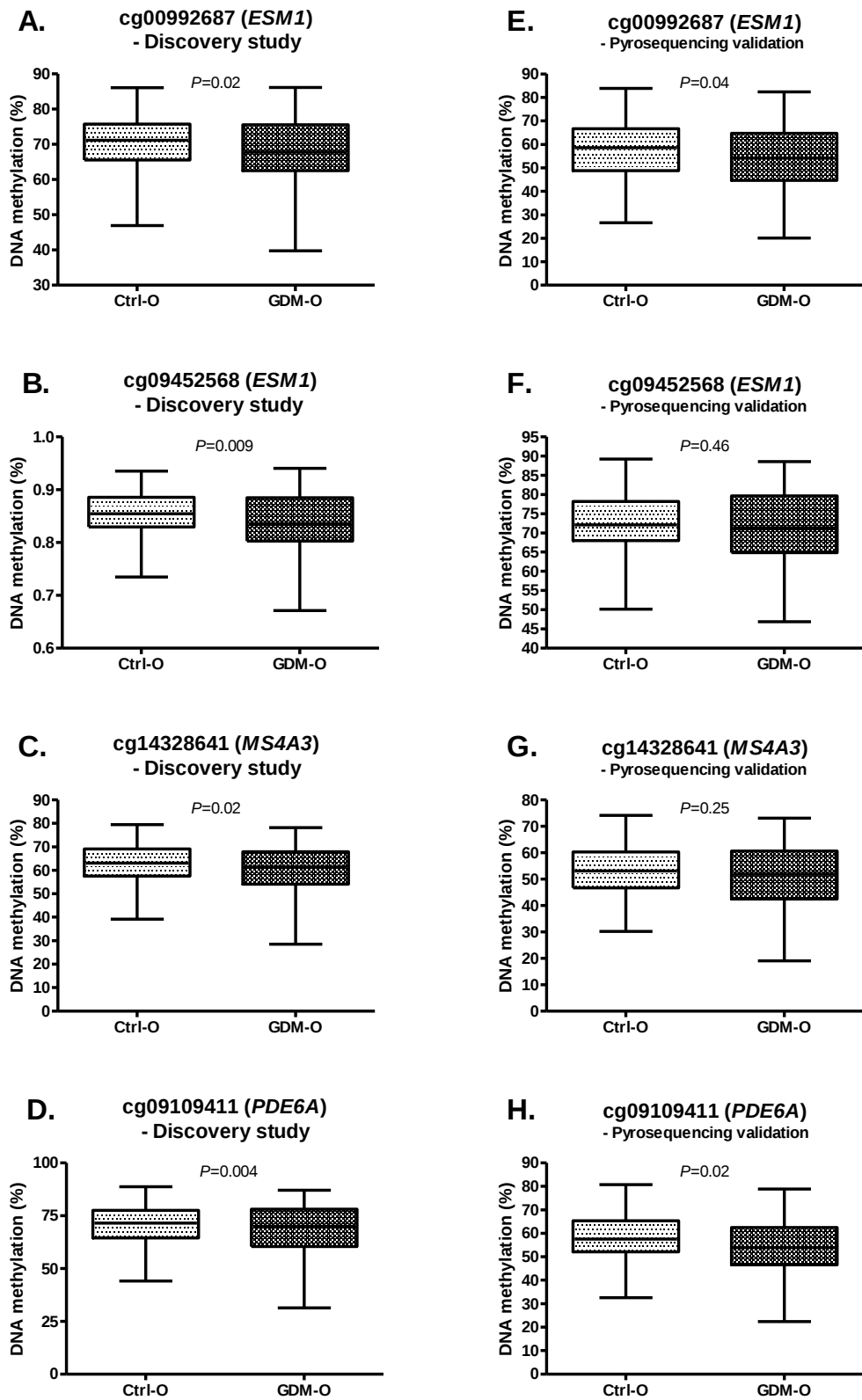


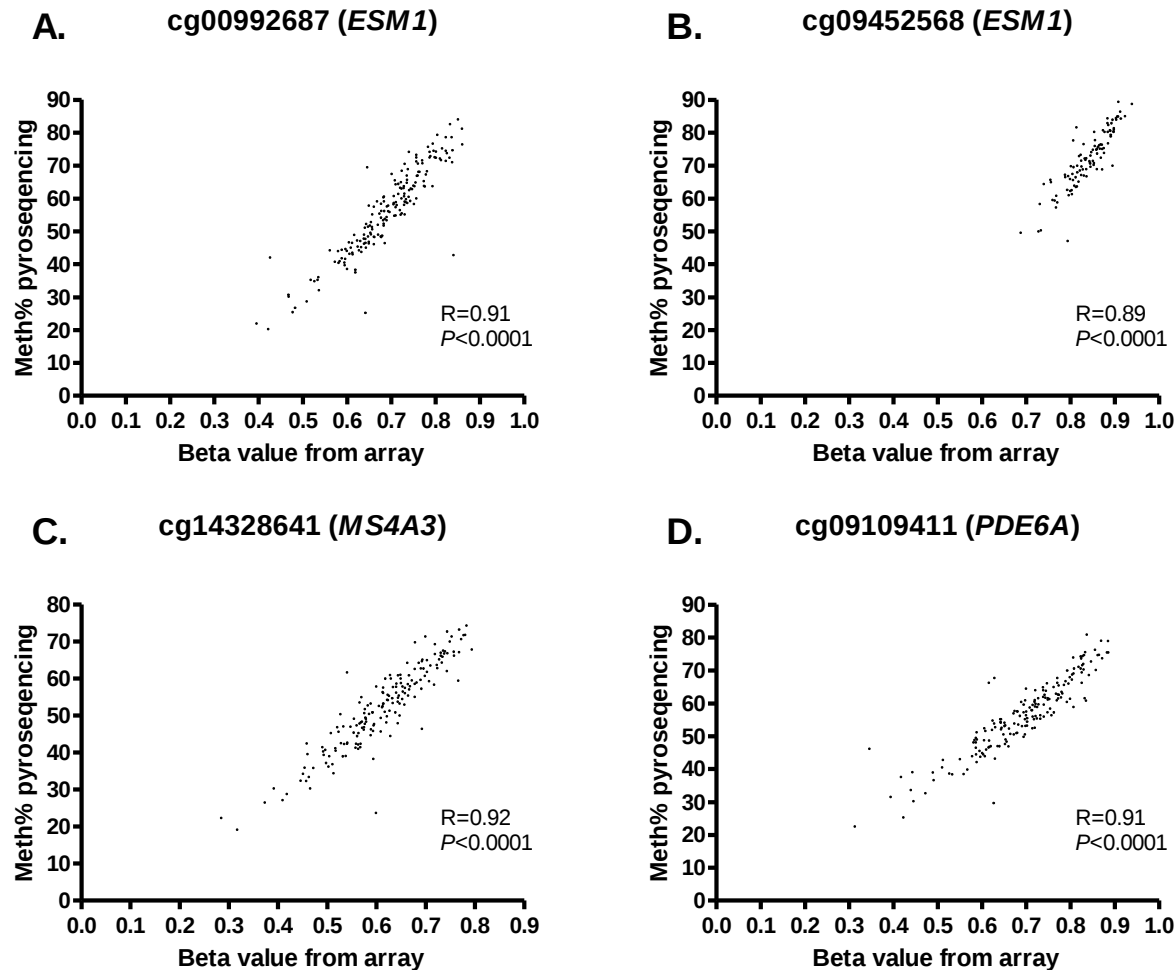
Supplementary Figure 1: Overview of pyrosequencing assay designs.



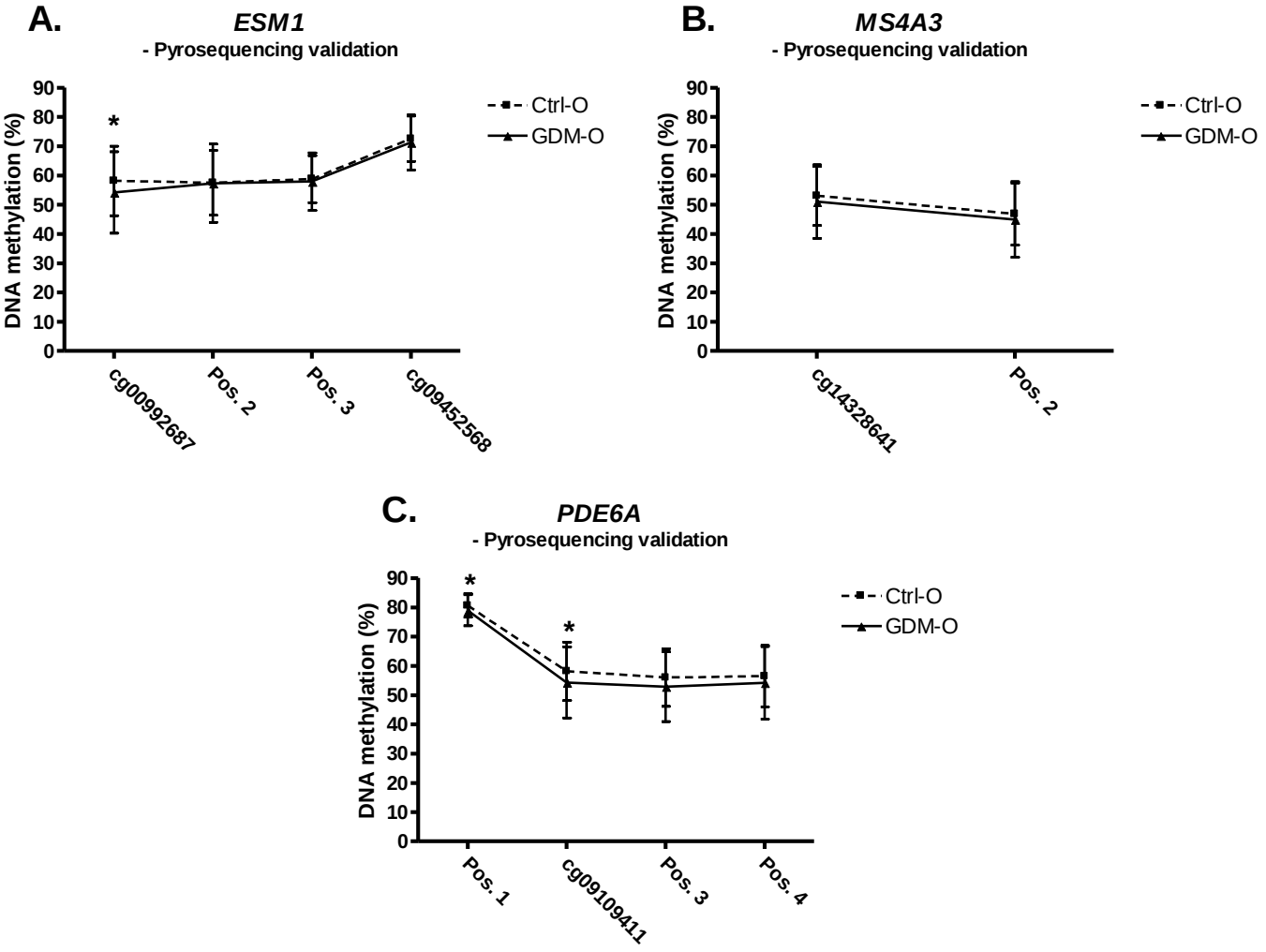
Supplementary Figure 2: DNA methylation levels measured using Infinium 450K array (A,B,C,D) and from the technical validation by pyrosequencing (E,F,G,H). Values are mean (SD) and *p*-values are calculated using Student's T-test. (*n*=186).



Supplementary Figure 3: Technical validation by pyrosequencing of Infinium 450K array data for A: cg00992687 (*ESM1*), B: cg09452568 (*ESM1*), C: cg14328641 (*MS4A3*) and D: cg09108411 (*PDE6A*). *p*-values are calculated using Pearson's correlations test. (*n*=186, except for cg09452568 where *n*=105).



Supplementary Figure 4: Technical validation of Infinium 450K array GDM versus control differences by pyrosequencing of specific CpG sites associated with A: ESM1, B: MS4A3 and C: PDE6A. Values are mean (SD) and *p*-values are calculated using Student's T-test. (*n*=186, except for cg09452568 where *n*=105).



Supplementary Figure 5: Cell count estimation using surrogate variable analysis. Values are mean (SD). ($n=186$).

