The American Journal of Human Genetics, Volume *95*

Supplemental Data

Molecular Convergence of Neurodevelopmental Disorders

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Supplemental Figures:

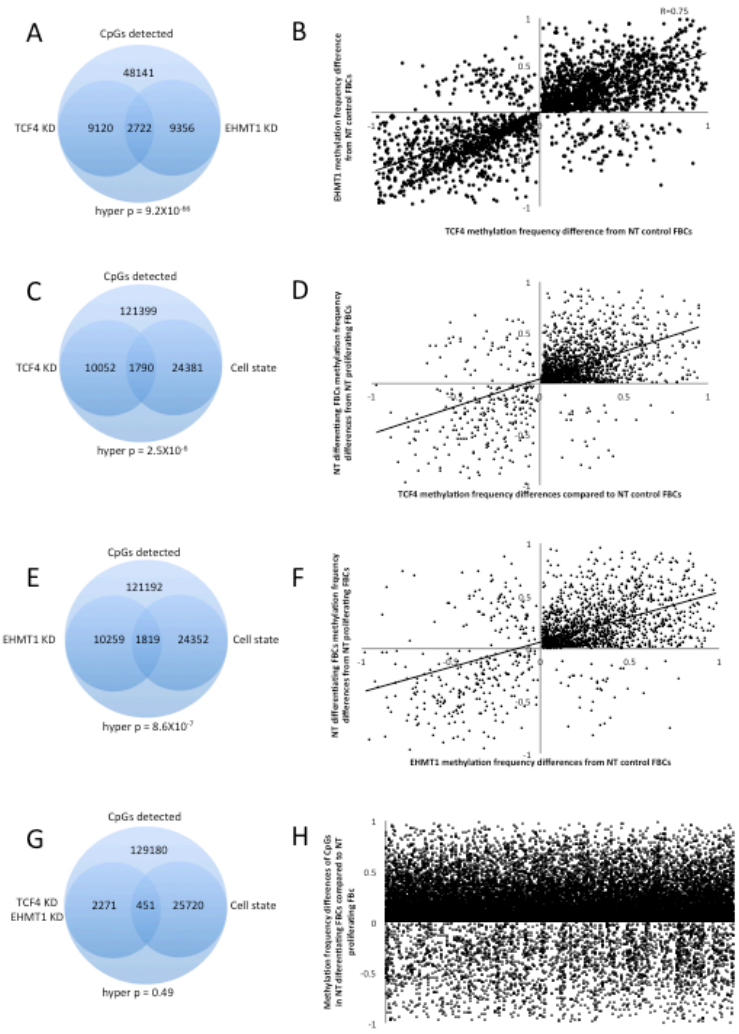

Figure S1. Analysis of differentially methylated single CpG sites in TCF4 KD, EHMT1 KD, and the cell state experiment. A and B) Significant overlap of differentially methylated CpGs in TCF4 KD and EHMT1 KD and correlation of methylation changes. C) CpG dinucleotides that show differential methylation in TCF4 KD show significant overlap with CpGs that show methylation differences in the cell state experiment (non-target proliferating FBCs compared to non-target differentiating FBCs). D) Common methylation differences observed in (C) show significant positive correlation with methylation patterns observed in differentiating FBCs. E) CpG dinucleotides that show differential methylation in EHMT1 KD show significant overlap with CpGs that show methylation differences in the cell state experiment (non-target proliferating FBCs compared to non-target differentiating FBCs). F) Common methylation differences observed in (E) show significant positive correlation with methylation patterns observed in differentiating FBCs. G) No significant overlap between single CpG methylation differences in TCF4 KD, EHMT1 KD, and the cell state experiments, suggesting that both TCF4 KD and EHMT1 show methylation differences more characteristic of the differentiating state, but that different CpGs are responsible for this effect. H) 86% of CpGs in the cell state experiment (non-target proliferating FBCs compared to non-target differentiating FBCs) are hypermethylated in differentiating FBCs.

% of Targets	% of Background
60.75%	28.03%
67.17%	34.69%
53.21%	24.65%
50.94%	24.43%
43.40%	19.15%
47.92%	23.90%
42.64%	22.51%

Figure S2. TCF4 *de novo* binding motifs. Motifs were calculating using all TCF4 peaks compared to 36930 background sequences using HOMER. Poly-A and poly-GA were the two most significant motifs (not shown).

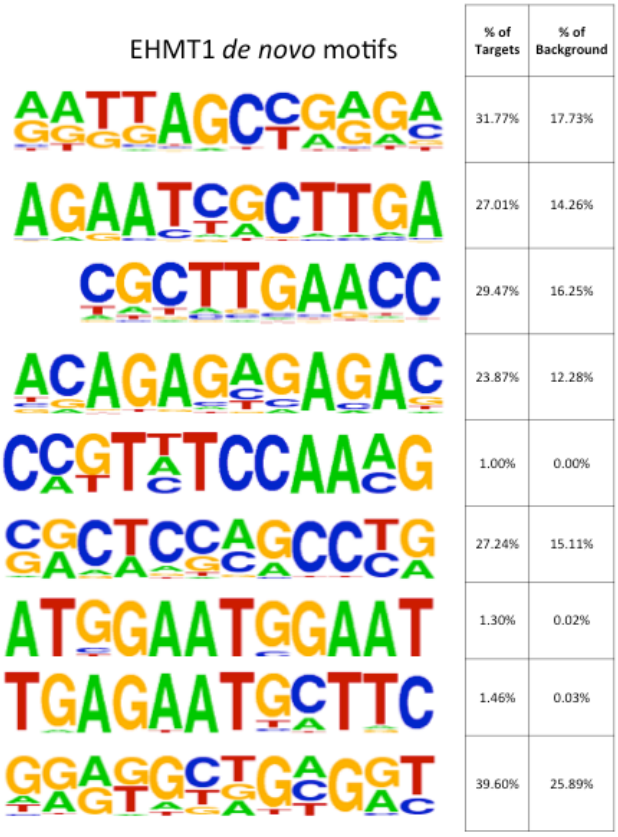

Figure S3. EHMT1 *de novo* binding motifs. Motifs were calculating using all EHMT1 peaks compared to 44896 background sequences using HOMER. Poly-A was the most significant motif (not shown).