

Supplementary Table 16. *Significantly differentially methylated regions* . Columns are: 'Contrast', the comparison where differential methylation region(DMR) identified and formatted as case groups versus reference groups; 'Chr', 'Start', and 'End', genomic position of DMRs(hg19); 'Gene', genes overlapped with the DMR; 'Mean_Beta_Ref' and 'Mean_Beta_Case', mean methylation beta value in reference groups and case groups; 'Diff_beta', difference in mean methylation beta level in case groups compared to reference groups; 'P' and 'FWER', raw P value and family-wise error rate.

Contrast	Chr	Start	End	Gene	P	FWER
T2_VS_T0	chr9	135,754,117	135,754,163	AK8;C9orf9;C9orf98	1.60E-04	0.109
T3_VS_T0	chr2	219,924,408	219,925,065	IHH	2.94E-05	0.114
T3_VS_T2	chr2	219,924,695	219,925,251	IHH	2.79E-05	0.136
T3_VS_T2	chr1	16,085,237	16,085,984	FBLIM1	1.26E-04	0.136
T3_VS_T2	chr15	75,165,338	75,165,821	SCAMP2	2.65E-04	0.136