

**S3 Table. List of epiphenotypes, coverage corrections and transformations applied.**

<b>Trait</b>	<b>N° of outliers removed</b>	<b>Coverage correction</b>	<b>Transformation applied</b>
mCG_global	4	yes	none
mCHG_global	3	yes	none
mCHH_global	0	yes	none
CG_GBM	4	yes	INT
CHG_GBM	0	no	INT
CHH_GBM	0	no	INT
CG_intergenic	5	yes	none
CHG_intergenic	0	yes	gaussianize
CHH_intergenic	0	yes	gaussianize
mCG_TEs	2	no	gaussianise
mCHG_TEs	0	no	none
mCHH_TEs	0	no	none
mCG_prom	5	yes	none
mCHG_prom	1	yes	INT
mCHH_prom	1	no	INT
CG_GBM_more5met	4	yes	none
CHG_GBM_more5met	0	yes	none
CHH_GBM_more5met	0	yes	none