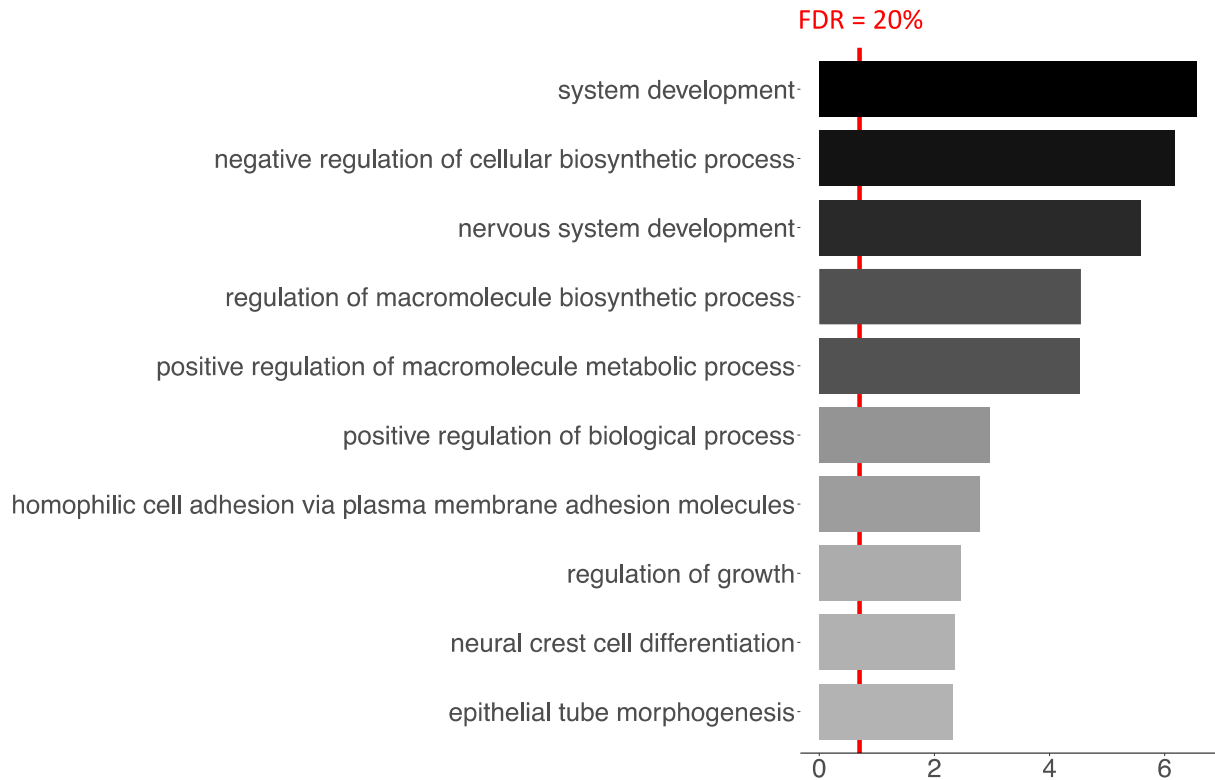




Supplementary Figure 5. *Top 10 enriched pathways for differentially methylated sites.* X axis shows $-\log_{10}(\text{FDR})$. Differential methylation sites were detected between each two time points, significant sites were selected if $\text{FDR} \leq 20\%$ and overlapping genes were the input for pathway analysis.