Suppl Fig. 1

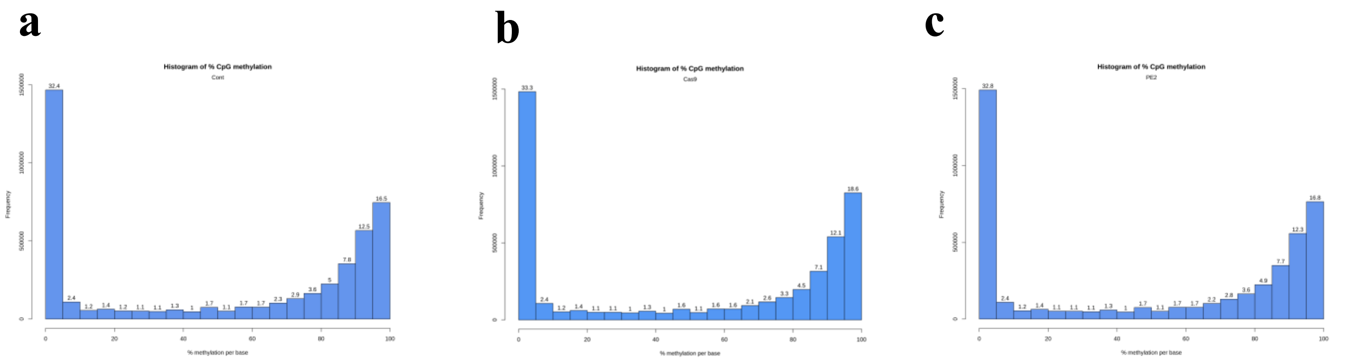

Figure 1. Methylation distribution. The methylation distribution in control (**a**), Cas9 (**b**) and PE2 (**c**).

Suppl Fig. 2

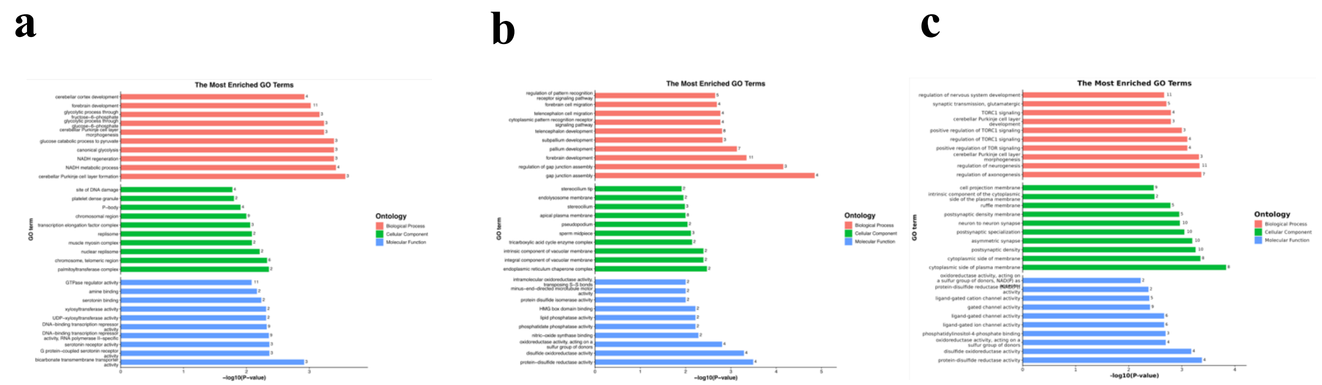

Figure 2. GO molecular function enrichment. The GO molecular function enrichment that relates to DMR in control vs. PE2 (**a**), PE2 vs. Cas9 (**b**) and control vs. Cas9 (**c**).

Suppl Fig. 3

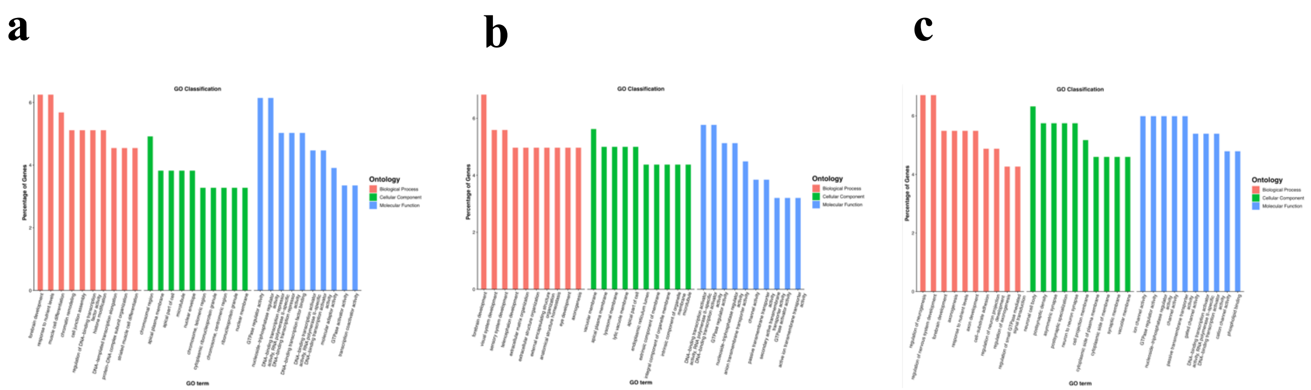

Figure 3. GO molecular function enrichment. (a) control vs. PE2 **(b)** PE2 vs. Cas9 **(c)** control vs. Cas9.

Suppl Fig. 4

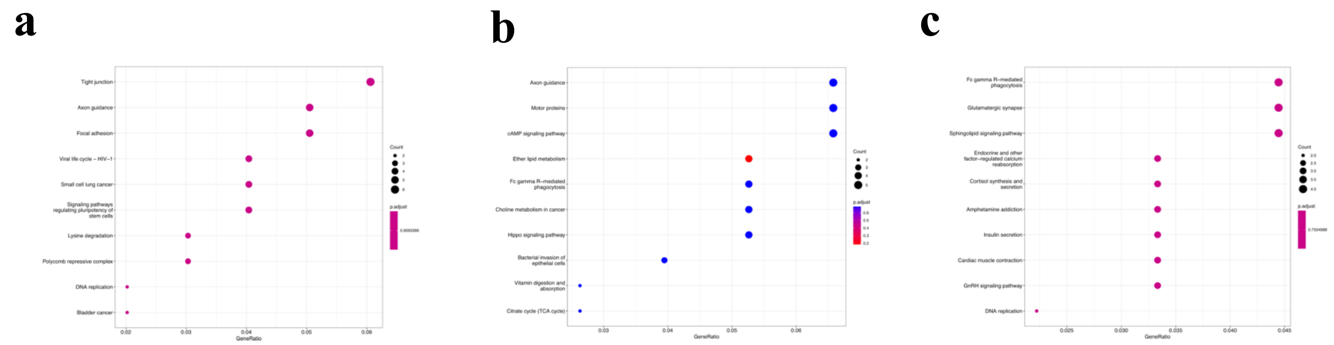

Figure 4. KEGG enrichment. The KEGG pathways analysis that relate to DMR in control vs. PE2 (**a**), PE2 vs. Cas9 (**b**) and control vs. Cas9 (**c**). The vertical axis represents the pathway name, and the horizontal axis represents the gene ratio (the ratio of the number of DMR related genes belonging to this KEGG pathway to the total number of genes belonging to this KEGG pathway). The size of the dot indicates the number of DMR related genes in the pathway, the color of the dot corresponds to a different q-value range, with deeper red shades indicating greater significance.