

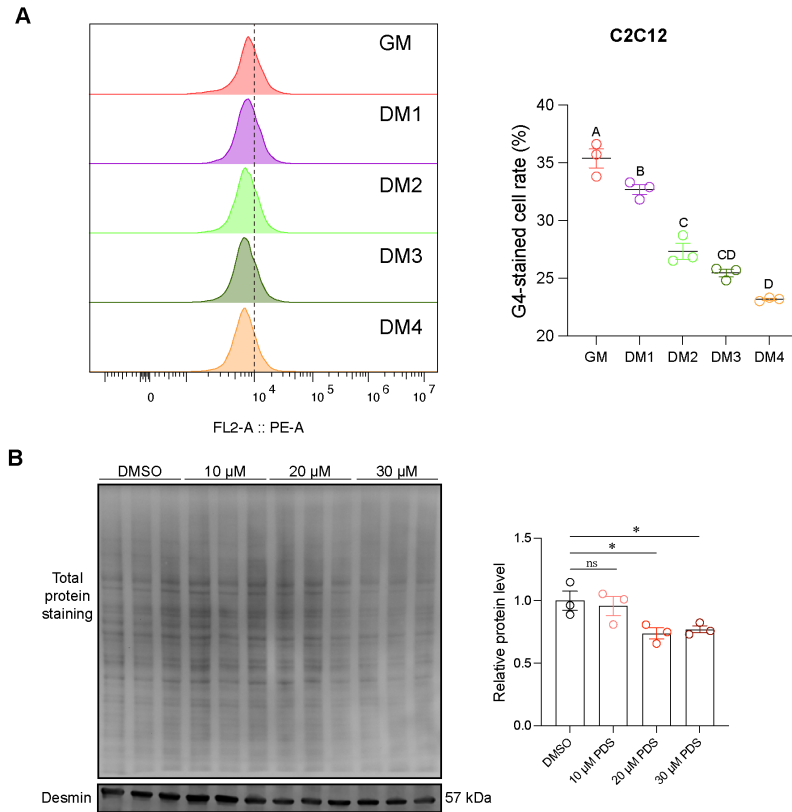


Figure S1. G4 density during myoblast differentiation and PDS effect on Desmin. (A) Mouse myoblast cells (C2C12) treated with GM, DM for 24 h (DM1), 48 h (DM2), 72 h (DM3), and 96 h (DM4) were collected and performed G4-immunofluorescence staining ($n = 3$). The G4-stained cells proportion was quantified in a flow cytometry. Fluorescence value $\geq 10^4$ was considered as the threshold for G4 positive cells. Ordinary one-way ANOVA was used to analyze the difference among groups. Different letters represent $P < 0.05$. (B) Western blot was performed to quantify the effect of PDS at Desmin protein level ($n = 3$). Loaded total proteins were considered as the normalization for Desmin. ImageJ was used to measure the protein gray value. Student's T-test was used to analyze the difference among groups. * represents $P < 0.05$.

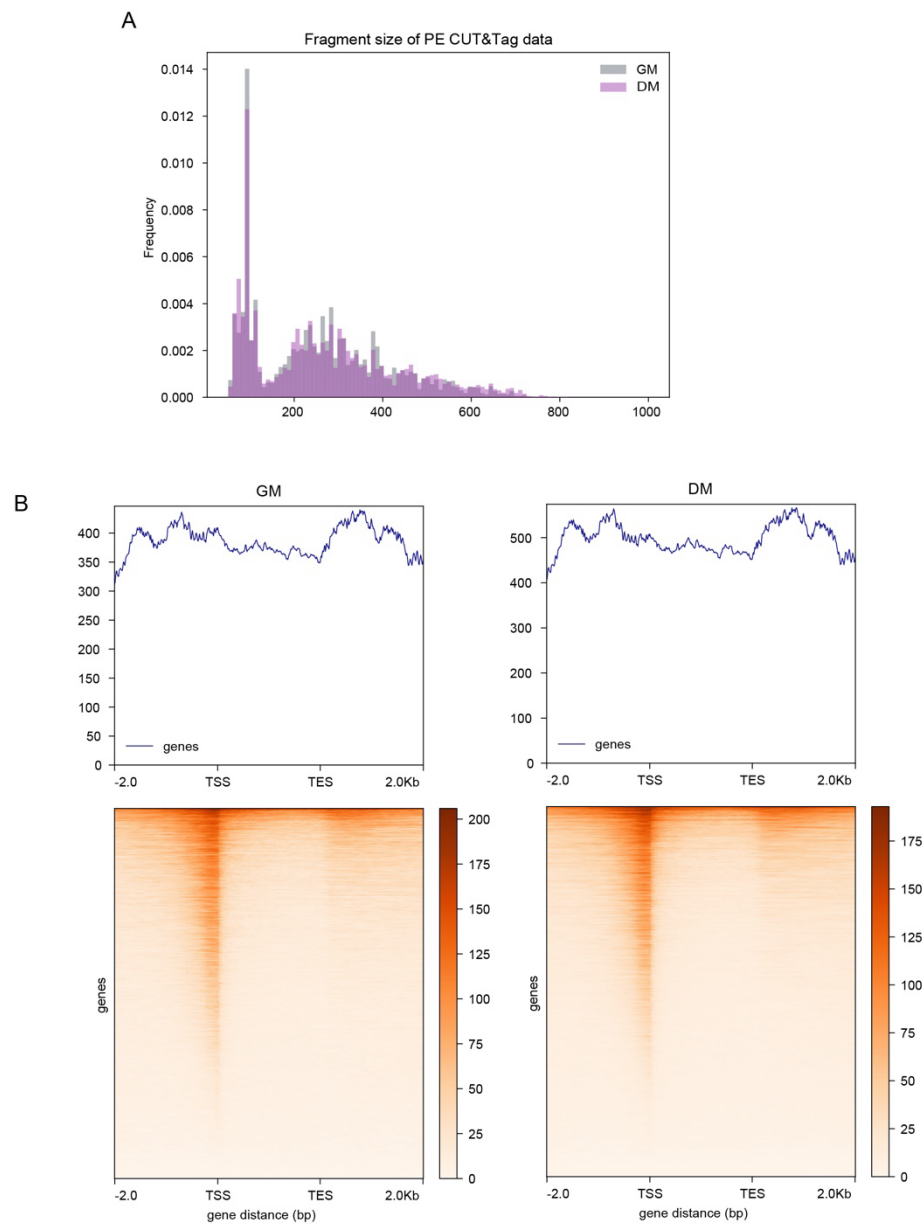


Figure S2. G4 Cut & Tag products size and distribution. (A) Fragment size for Cut & Tag products. (B) The distribution of Cut & Tag products.



Figure S3. G4 PQSs schematic diagram in *MyoD1* promoter.

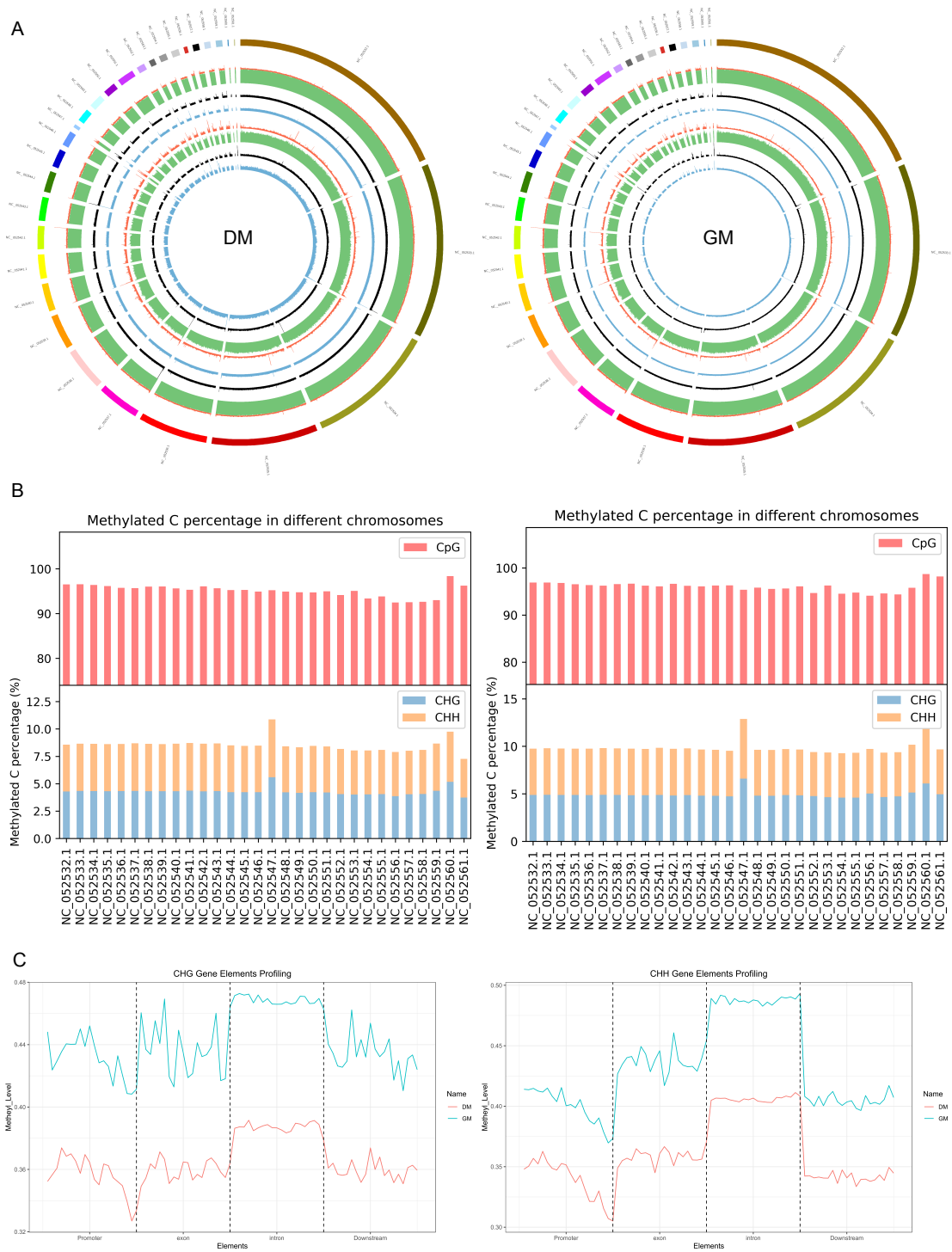


Figure S4. CpG-, CHH- and CHG-type methyl modification distribution information. (A) The circos diagrams at chromosomes level for DM and GM. (B) The methylated C percentage for CpG, CHH and CHG. (C) The CHG- and CHH-type methylation element profiling.

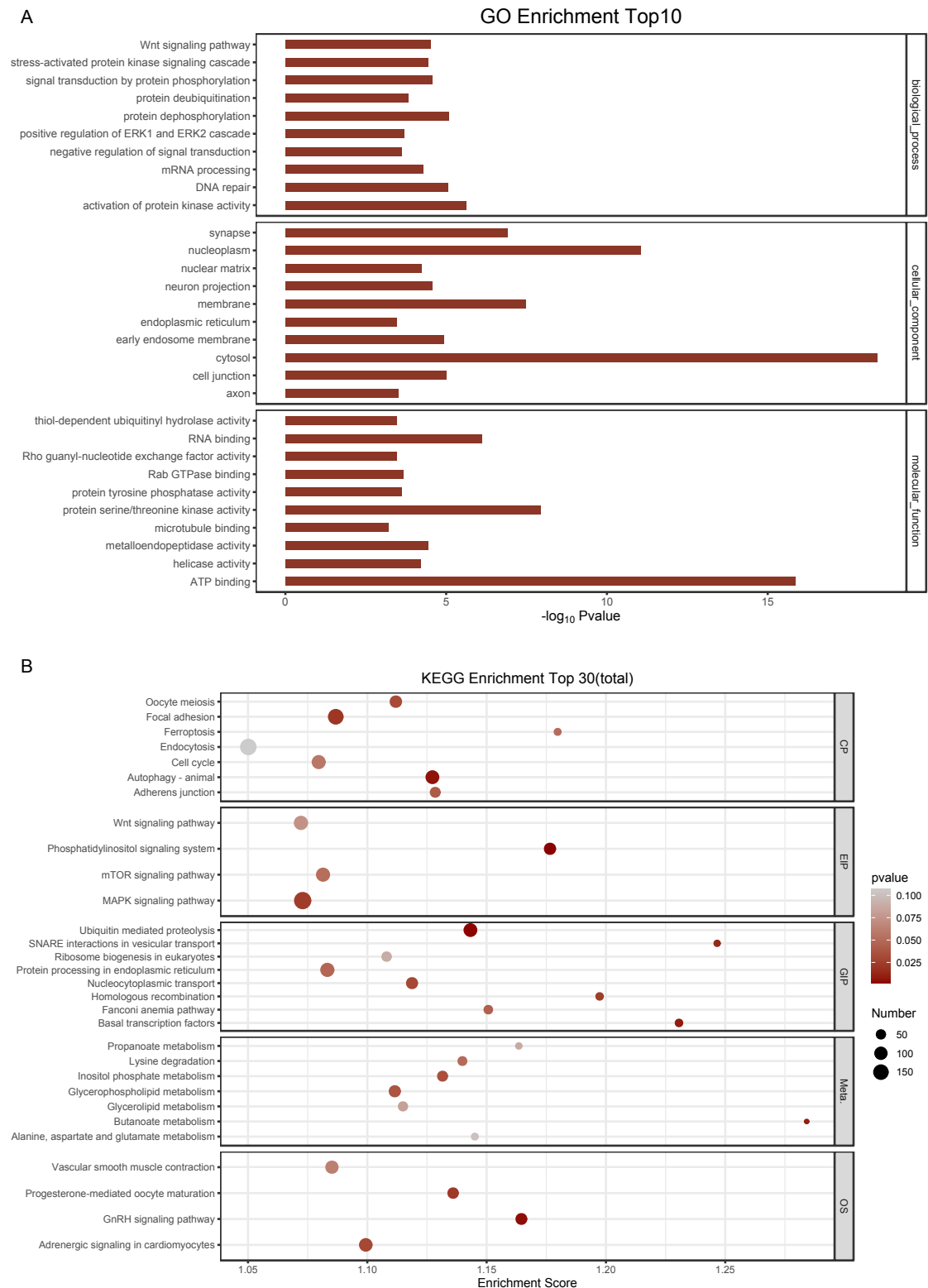


Figure S5. The GO and KEGG enrichment analysis for DMRs. (A) The top 10 GO terms for DMRs. (B) The top 30 KEGG pathways for DMRs.

PLA2G4A

NC_052539.1: 10,031,036-10,138,865

5'-**GGGGGG**AGGC**GGG**TGACTCACGGC**GGG**-3'
10,138,924-10,138,950



Figure S6. PQSs prediction for *PLA2G4A*.