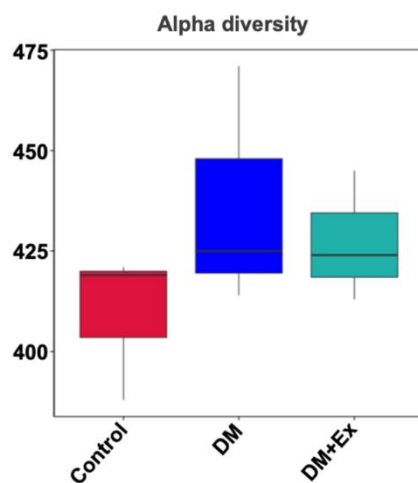


Figure S1. Indicator detection after establishment of T2DM model. (A) Body weight of mice in each group. (B) Fasting blood glucose in each group. (C) Insulin levels in mice of each group. (D) Glucose tolerance and (E) the area under glucose tolerance curve in each group. (F) Insulin tolerance and (G) the area under insulin tolerance curve in different groups. (H) Food intake in control mice and diabetic mice treated with or without exercise. * indicated the versus between control and DM. @ indicated the versus between DM+Ex and DM. * and @, $p < 0.05$. ** and @@, $p < 0.01$.

A



B

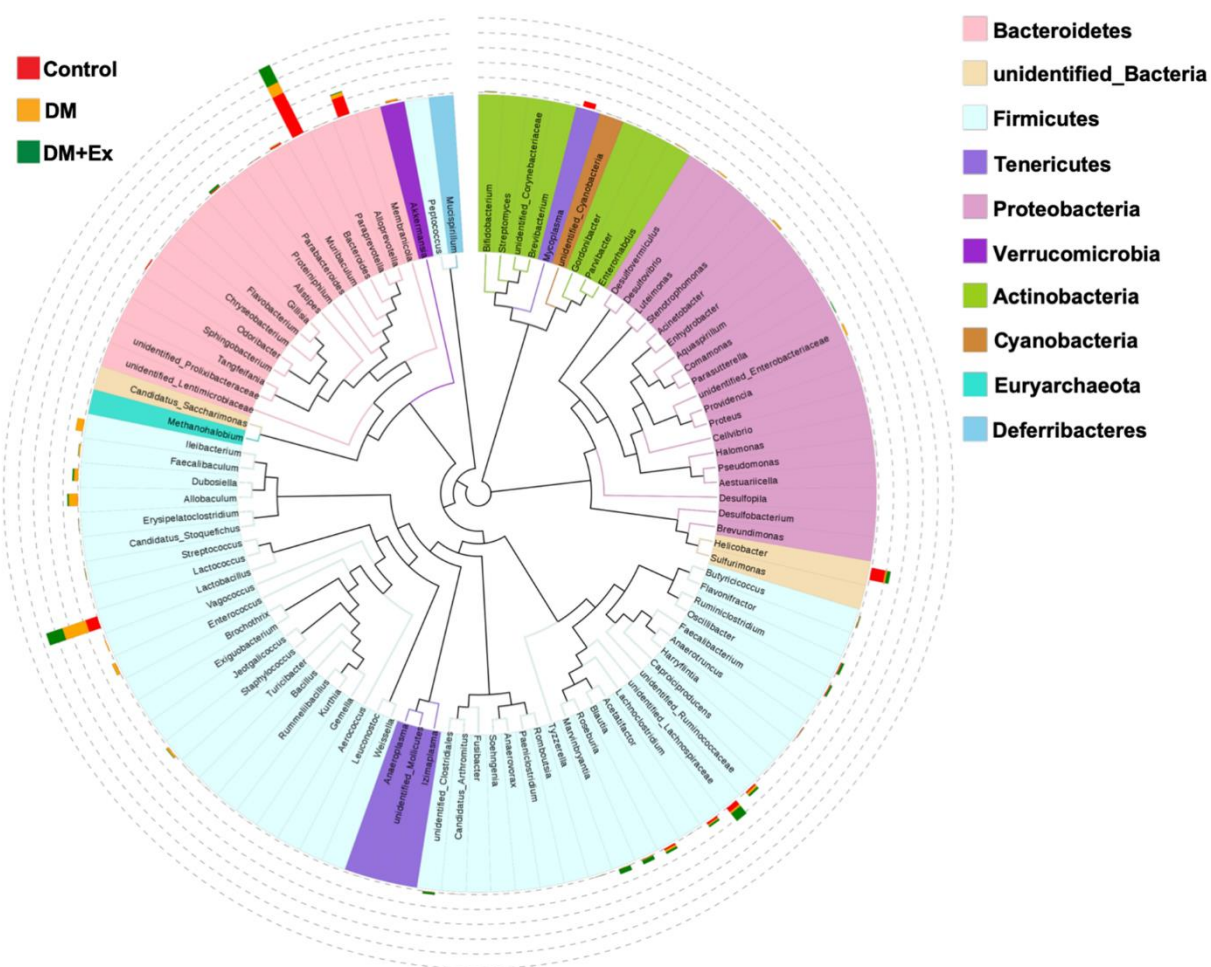


Figure S2. Analysis of intestinal flora sequencing results in each group. (A) Alpha diversity analysis. (B) Analysis of the genus-level species evolutionary tree results.

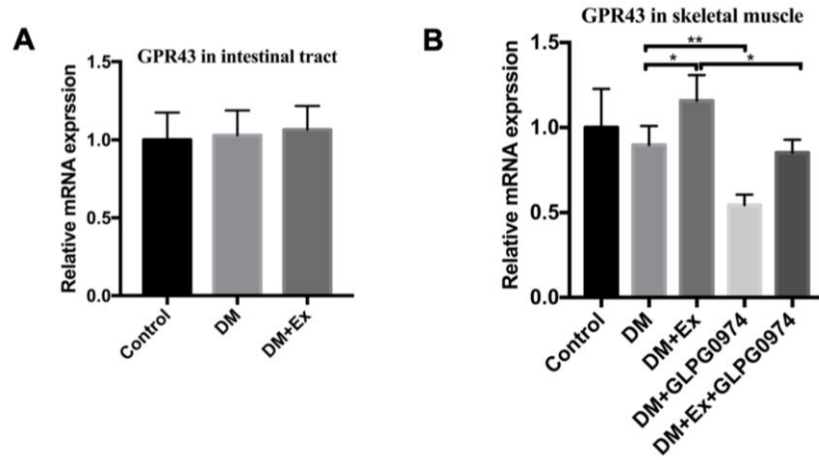


Figure S3. GPR43 expression in intestinal tract and skeletal muscle. (A) Detection of GPR43 expression in intestinal tract by RT-PCR. (B) Detection of GPR43 expression in skeletal muscle by ELISA. * $p < 0.05$. ** $p < 0.01$.

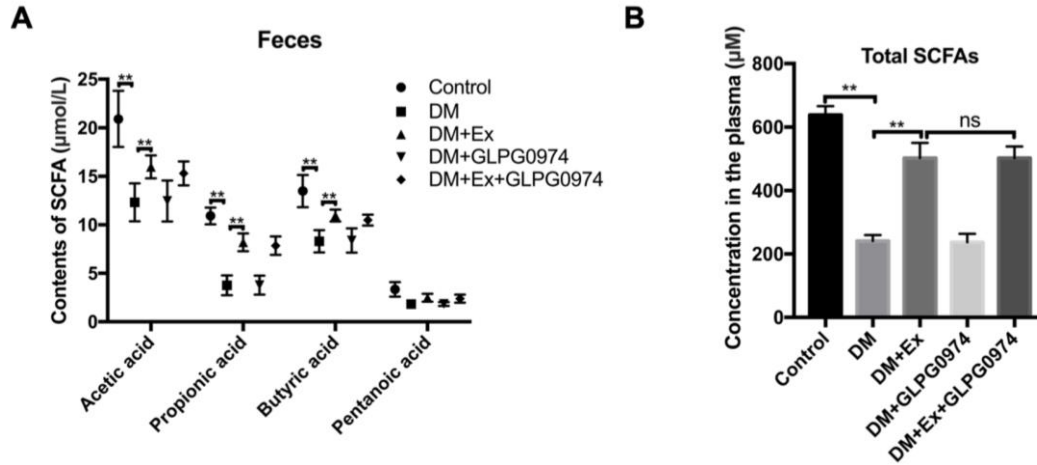


Figure S4. The addition of inhibitor GLPG0974 is independent of SCFA content in stool and plasma. (A) Detection of SCFAs content in stool of each group by GC. (B) Detection of total SCFAs concentration in plasma of mice by ELISA. * $p < 0.05$. ** $p < 0.01$.

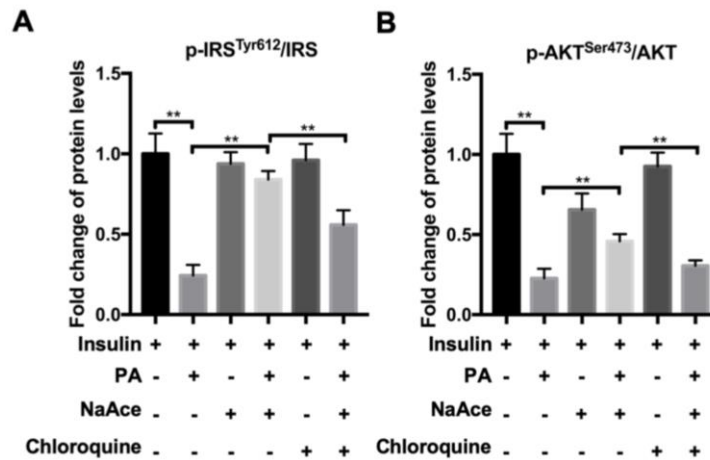


Figure S5. Quantitative analysis of protein levels in the Figure 5C. Semi-quantitative statistics of p-IRS^{Tyr612} (A) and p-AKT^{Ser473} (B) normalized to total IRS and AKT, respectively. ** $p < 0.01$.