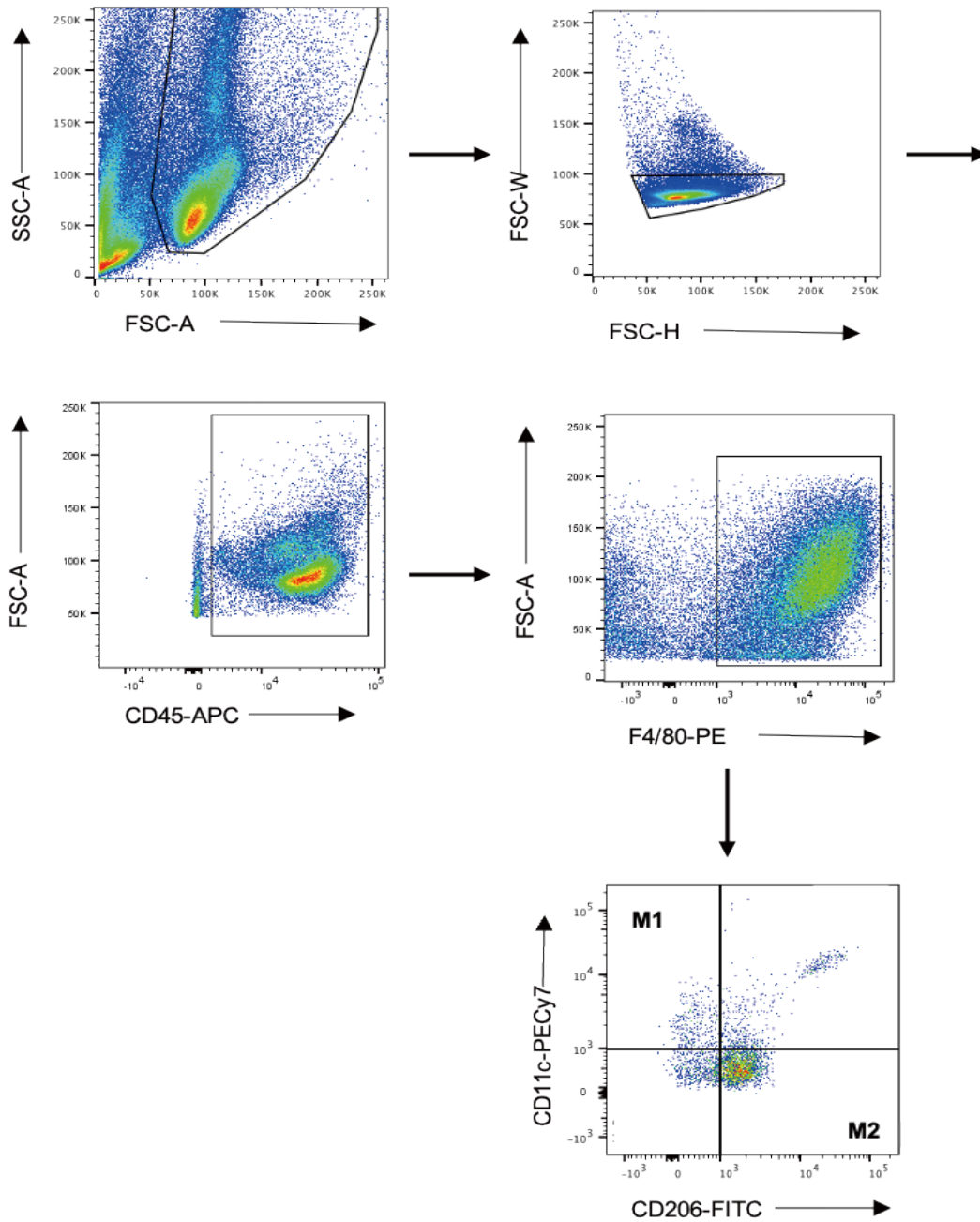


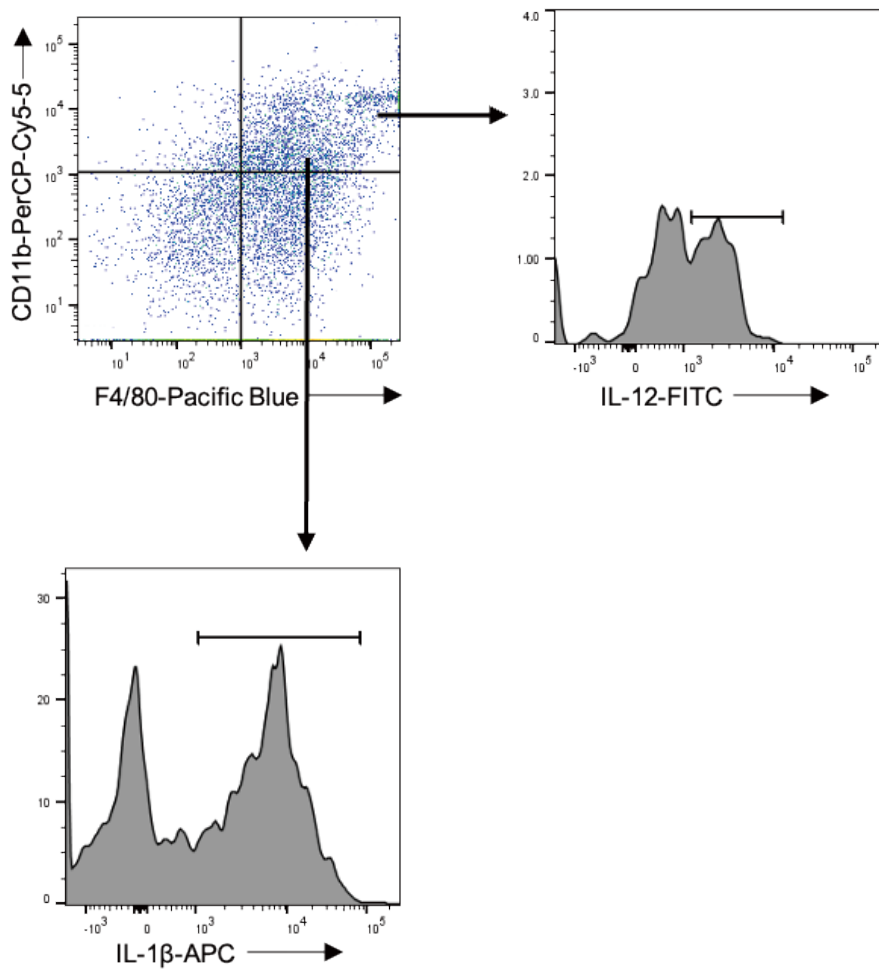
### Supplementary Figure 1. Strategy for innate lymphoid cells (ILCs)

Representative flow cytometry plots of liver CD45<sup>+</sup> Live & Dead<sup>-</sup> Lin<sup>-</sup> CD127<sup>+</sup> RORγ<sup>-</sup> GATA-3<sup>-</sup> T-bet<sup>+</sup> ILC1s, CD45<sup>+</sup> Live & Dead<sup>-</sup> Lin<sup>-</sup> CD127<sup>+</sup> RORγ<sup>-</sup> GATA-3<sup>+</sup> ILC2s and CD45<sup>+</sup> Live & Dead<sup>-</sup> Lin<sup>-</sup> CD127<sup>+</sup> RORγ<sup>+</sup> GATA-3<sup>-</sup> ILC3s in each group at 16-weeks of age.



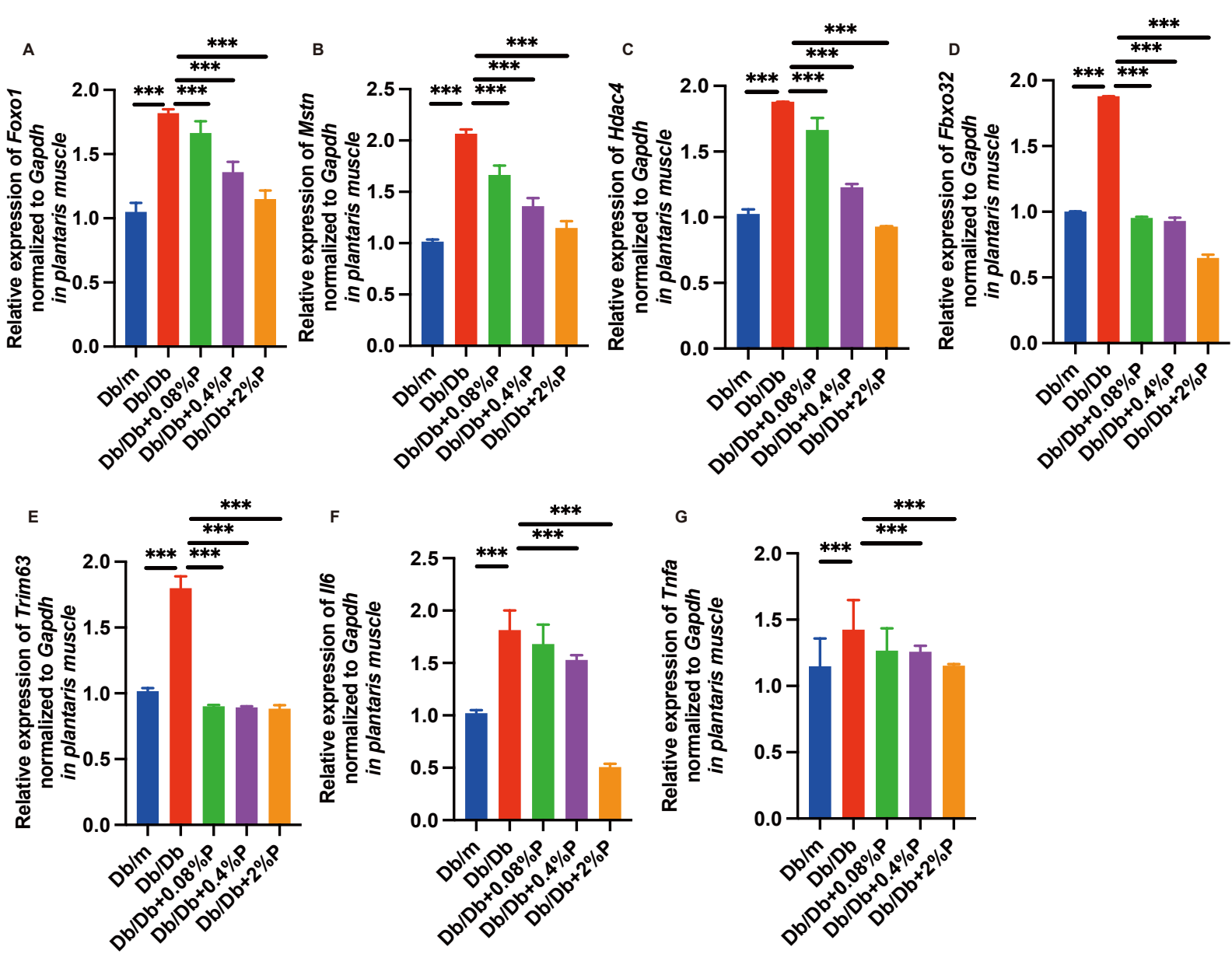
**Supplementary Figure 2. Strategy for macrophages**

Representative flow cytometry plots of liver CD45+ F4/80+ CD206- CD11c+ M1 macrophages and CD45+ F4/80+ CD206+ CD11c- M2 macrophages in each group at 16 weeks of age.



### Supplementary Figure 3. Strategy for macrophages

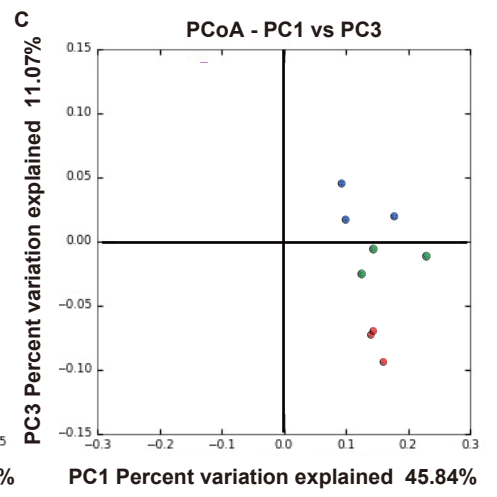
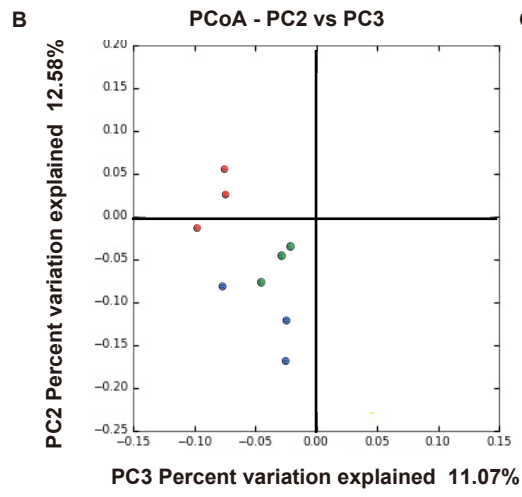
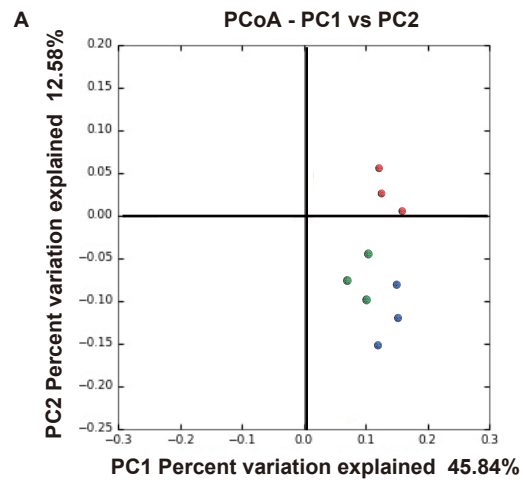
Representative flow cytometry plots of RAW264.7 cells F4/80+ CD11b+ IL12 cells and F4/80+ CD11b+ IL1 $\beta$  cells.



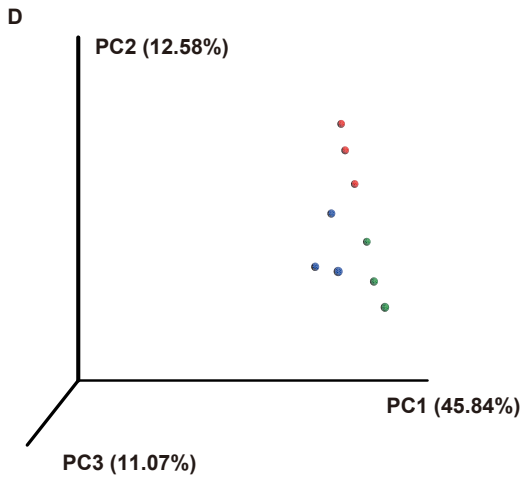
**Supplementary Figure 4. The gene expressions in plantaris muscle.**

The relative expression of mRNA (A) *Foxo1*, (B) *Mstn*, (C) *Hdac4*, (D) **Fbxo32**, (E) *Trim63*, (F) *Ilf6*, and (G) *Tnfa* of indicated genes in soleus muscle normalized to *Gapdh* (n=12).

Data have been represented in terms of mean ± SD values. \*\*\*p<0.001 by one-way ANOVA.



- Db/m
- Db/Db
- Db/Db+P

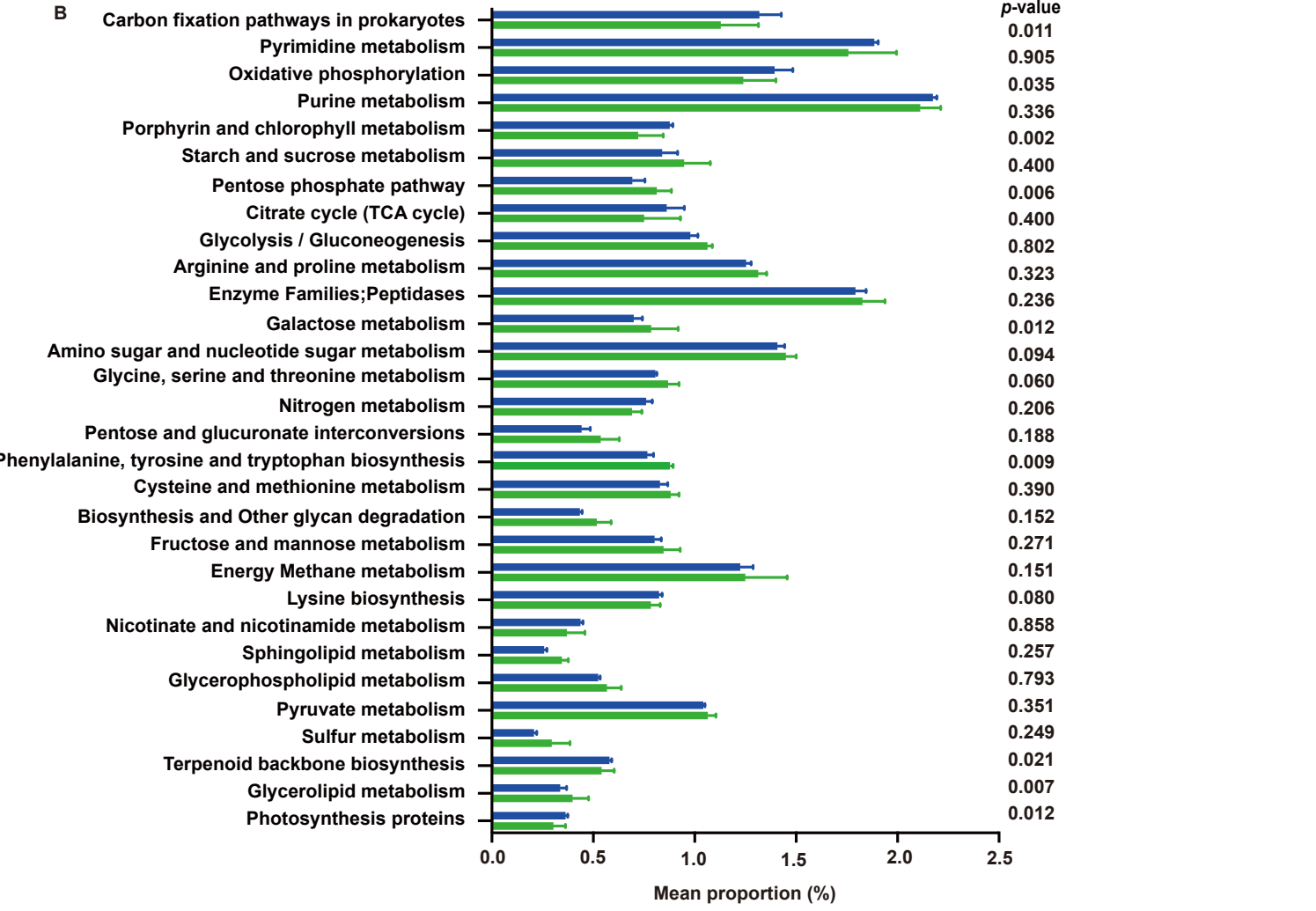
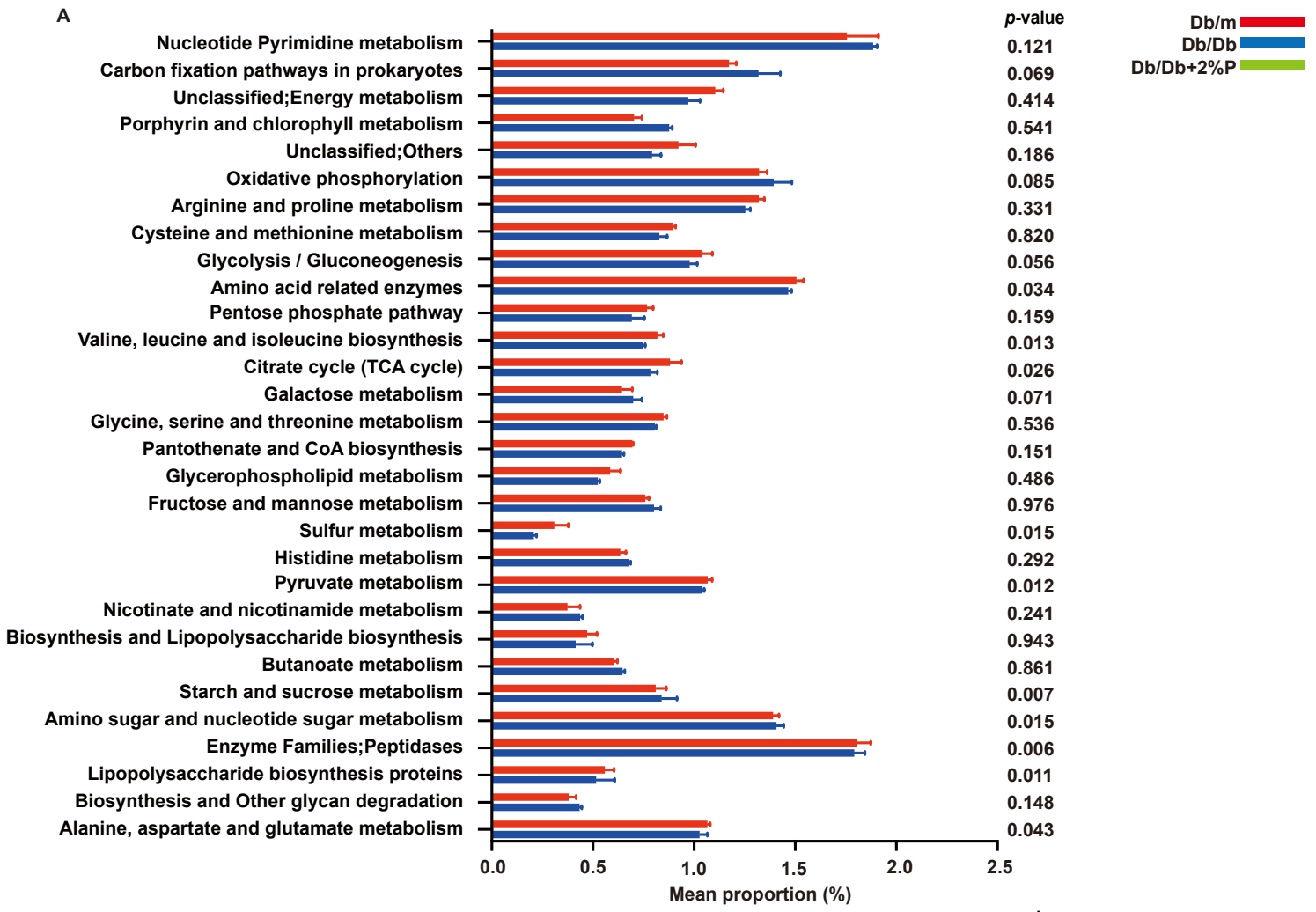


**Supplementary Figure 5. PCoA plots of gut microbiota of Db/m, Db/Db, and Eb/DB+2%P mice.**

Weighted PCoA plots were shown (n=3). (A) PC1 vs PC2, (B) PC2 vs PC3, and (C) PC1 vs PC3.

(D) Weighted beta-diversity with PERMANOVA test were shown (n=3).

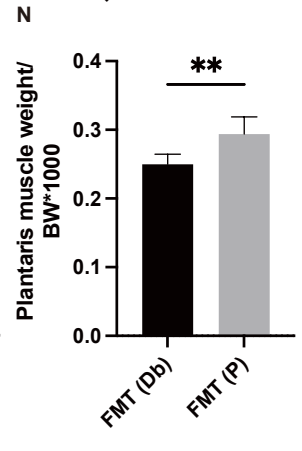
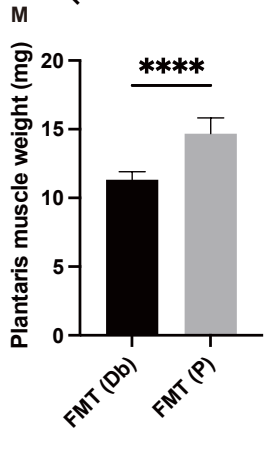
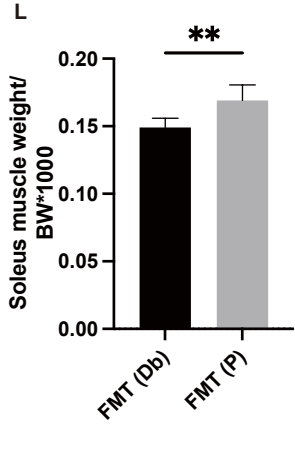
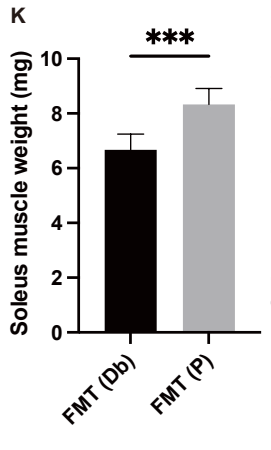
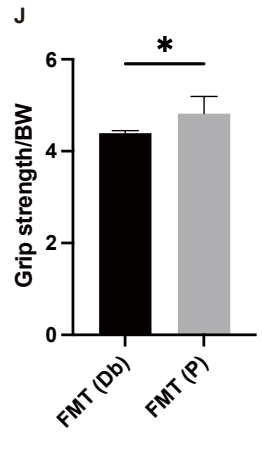
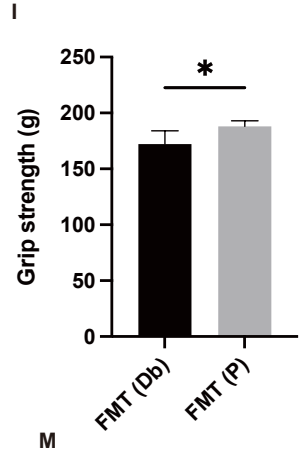
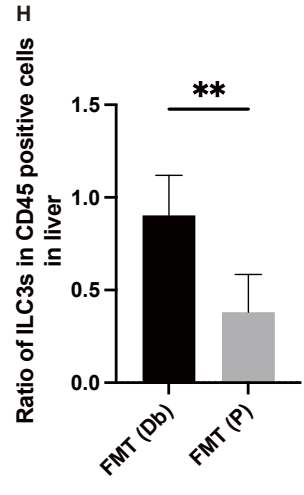
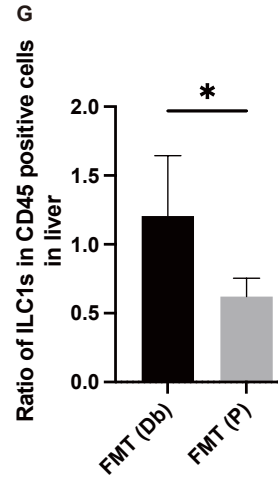
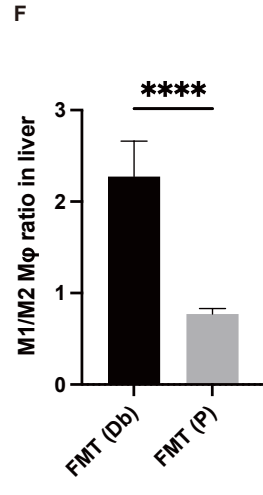
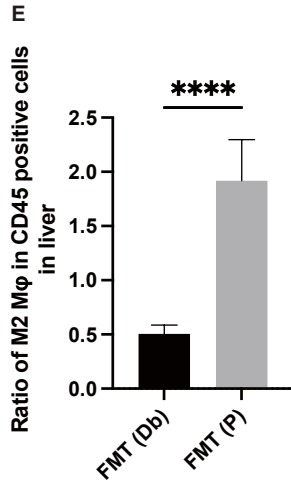
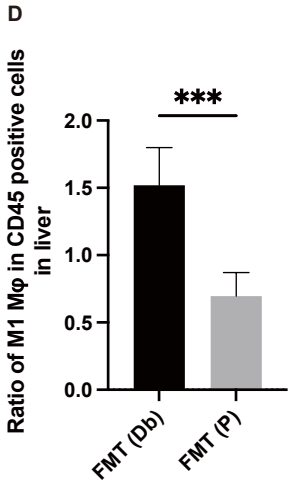
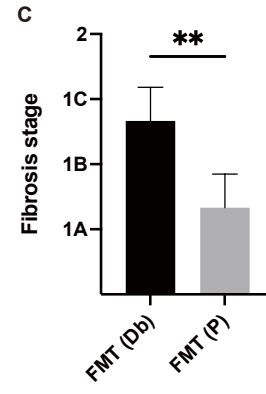
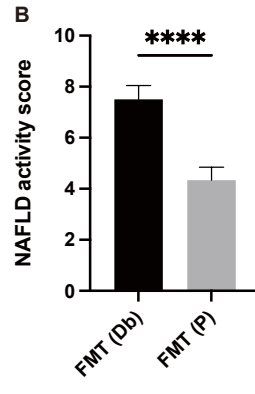
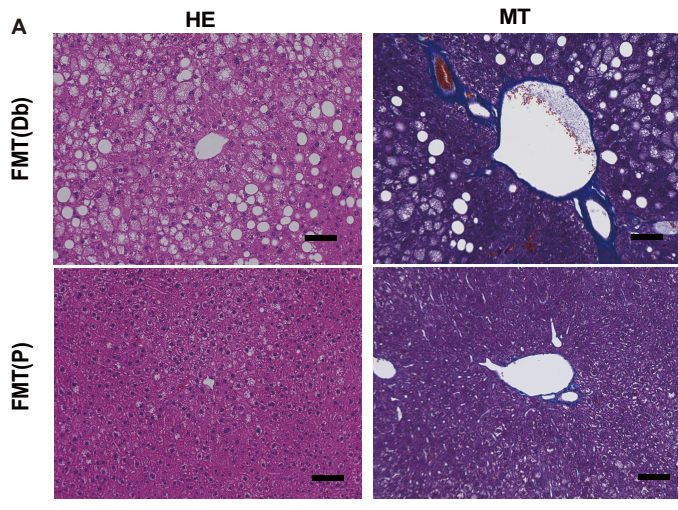
PCoA: Principal coordinate analysis, PERMANOVA: Permutational multivariate analysis of variance.



## Supplementary Figure 6. The functional profiles for gut microbiota.

(A and B) Change in metabolism profiles for the gut microbiota.

The degree of impairment in the gut microbial metabolism profile for Db/m mice, Db/Db mice, and Db/Db+2%P mice was assessed by the weighted average differences method, and the degree was ranked from top to bottom. The top 20 metabolism profiles for gut microbiota are shown, and the difference of these gut microbiota profiles was evaluated by unpaired t - tests. Histograms show the mean proportion of the relative abundance of metabolism profiles of gut microbiota (mean + standard deviation) and  $p$  - value by unpaired t - test is shown.





**Supplementary Figure 7. Fecal microbiota transplantation of Db/Db+2%P mice improved fatty liver, decreased the expression of genes related to inflammation, liver fibrosis, and fatty acid metabolism, and decreased the ratio of M1 macrophages, ILC1, and ILC3, and increased the ratio of M2 macrophages and ILC2, and increased the muscle strength and mass.**

(A) Representative images of hematoxylin & eosin- and Masson trichrome-stained liver sections.

Liver tissues were collected at 16-weeks of age. The scale bar shows 100  $\mu$ m.

(B and C) Nonalcoholic fatty liver disease (NAFLD) activity scores and the fibrosis stage

of NAFLD activity score (n = 6). Ratio of (D) M1 macrophages to CD45-positive cells,

(E) M2 macrophages to CD45-positive cells, (F) M1 to M2 macrophages, (G) ILC1s to CD45-positive cells,

(H) ILC3s to CD45-positive cells in the liver (n = 6 in each case). (I and J) Absolute and relative grip strength,

(K and L) absolute and relative soleus muscle weight, (M and N) absolute and relative plantaris muscle weight

in 16-weeks-old mice (n = 12 in each case).

Data are represented as the mean  $\pm$  SD values. Data were analyzed using unpaired t-test.

\*p<0.05, \*\*p<0.01, \*\*\*p<0.001.

FMT, fecal microbiota transplantation.