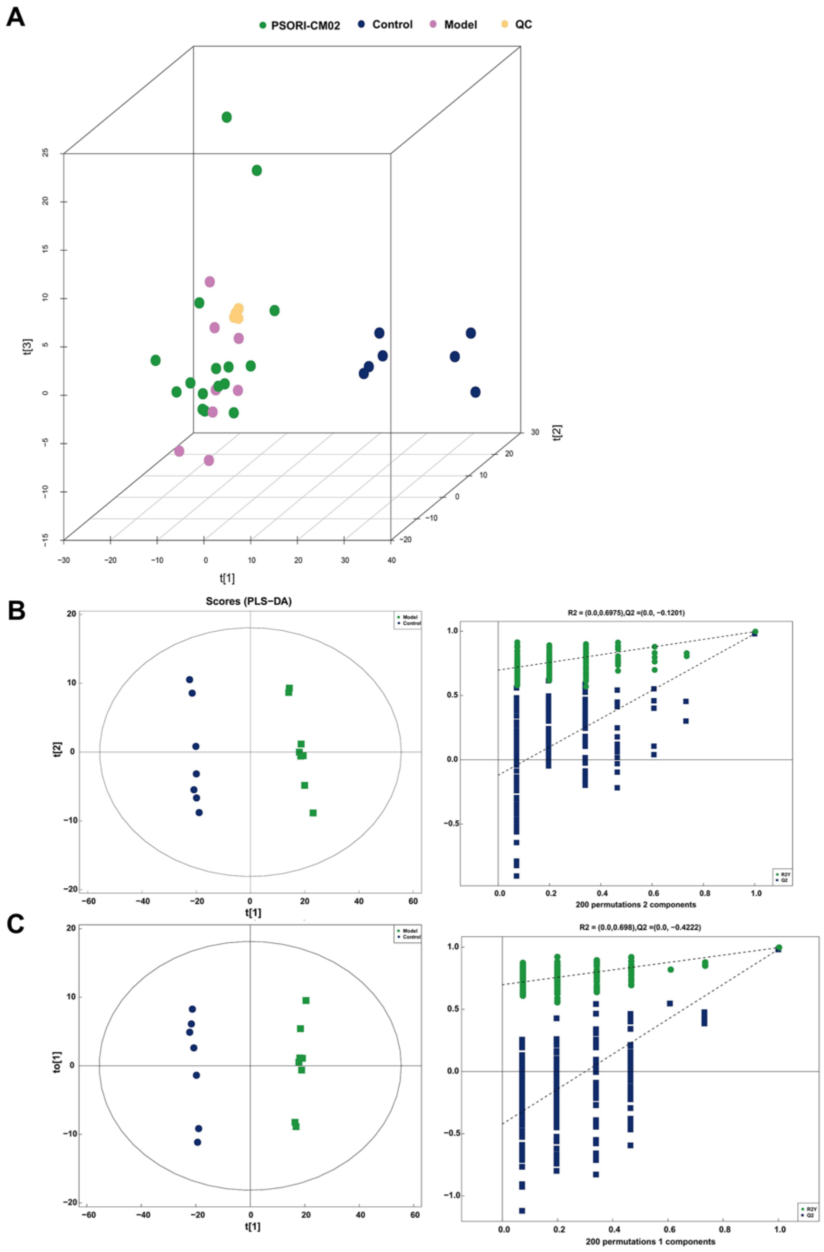
Supplementary Table 1 Baseline of clinical samples.

Baseline	Healthy controls (n=9)	Psoriasis (n=9)
Age (mean±SD)	39.52±10.31	42.26±11.24
Gender (male/female)	5/4	5/4
PASI	-	7.71±3.85

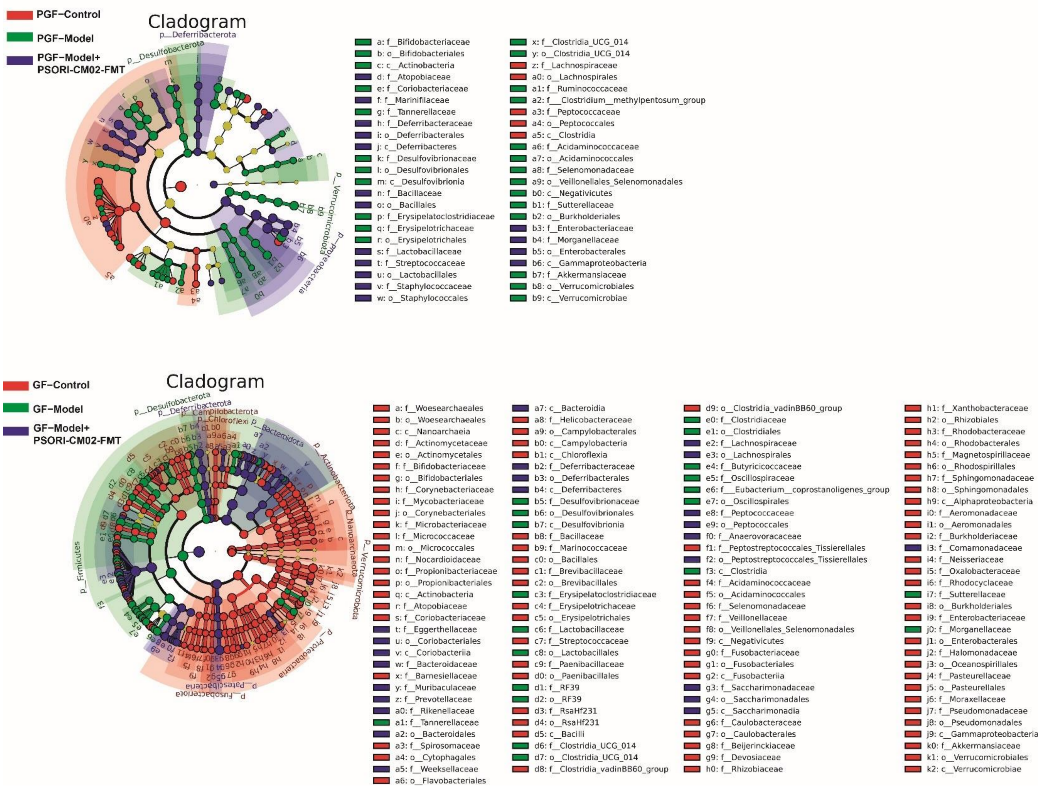
SD, standard deviation; PASI, psoriasis area, and severity index.

Supplementary Table 2 Sequence of primers.

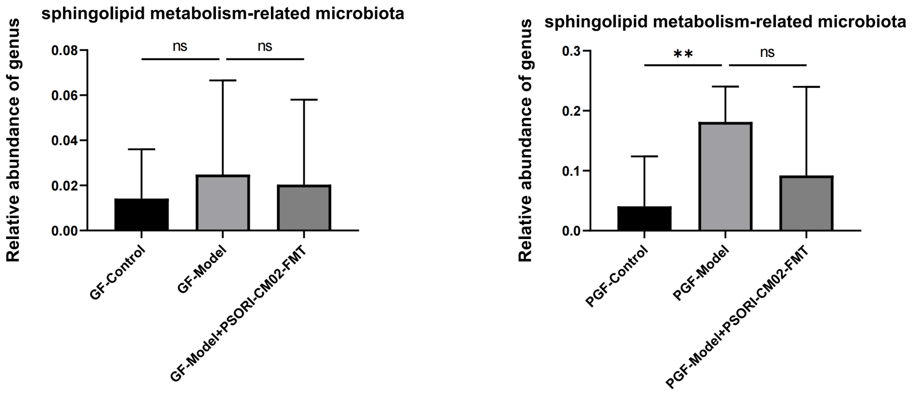
Name	**Forward**	**Reverse**
Flg	5’-TACTGGTGCTAAAGCTGGCAA-3’	5’-CCACCATGCCTCCGTCTAAG -3’
Krt 14	5’-GCAGTATCCGATCTCTTCATGC-3’	5’-GGCCCTCGAATCCTCTGACT-3’
Krt 10	5’-CGGAAACGAGAAGGTGACCA-3’	5’-GCACGTTGGCATTGTCAGTT-3’
β-actin	5’-GGCTGTATTCCCCTCCATCG-3’	5’-CCAGTTGGTAACAATGCCATGT-3’



Supplementary Figure 1. (A) PCA score plots derived from mice in the control, model, MTX, and PSORI-CM02 groups and quality control samples. (B) PLS-DA score plot and validation of the corresponding PLS-DA model through permutation analysis. (C) OPLS-DA score plot and validation of the corresponding OPLS-DA model through permutation analysis. R^2 represents the explained variance, whereas Q^2 indicates the predictive capability of the model. QC, quality control; PCA, principal component analysis; PLS-DA, partial least squares discriminant analysis; OPLS-DA, orthogonal partial least squares discriminant analysis.



Supplementary Figure 2. Cladogram of the LEfSe analysis results from PGF and GF mice. SPF, Specific pathogen-free; PGF, pseudo germ-free; GF, germ-free; FMT, fecal microbiota transplantation; LEfSe, linear discriminant analysis effect size.



Supplementary Figure 3. The total relative abundance of sphingolipid metabolism-related microbiome species at the genus level in GF and PGF mice. PGF, pseudo germ-free; GF, germ-free; FMT, fecal microbiota transplantation; $^{**}p < 0.01$, ns, not significant, compared with the model group.