

Supplementary materials

Table S1.

Effect of SFF on diversity of gut microbiota in HFD/STZ-induced diabetic mice.

	NC	DC	DC+SFF
observed_species	486±78.83*	411.6±58.63	433.6±46.21
shannon	5.34±0.49	5.18±0.77	5.43±0.61
simpson	0.93±0.02	0.92±0.03	0.93±0.03
chao1	516.44±72.98**	455.02±56.27	473.88±69.17*
ace	527.97±71.09**	462.90±54.62	481.18±47.07*
goods_coverage	0.998±0.00018	0.998±0.00023	0.998±0.00024

Data are expressed as mean ± SD. * Indicates significantly different from the DC group at the * $P < 0.05$, ** $P < 0.01$ level.

Supplementary figure captions

Figure S1. SFF remodels the structure of gut microbiota in HFD/STZ-induced diabetic mice. (A) PCoA score plot of gut microbiota at the genus level; (B) NMDS score plot of gut microbiota.

Figure S2. SFF regulates the gut microbial community at genus level. Comparison of relative abundance of gut microbial community at genus level, including *Ruminiclostridium*, *Blautia*, *Faecalibaculum*, *Bacteroides*, *Parabacteroides*, *Enterococcus*, *Desulfovibrio* and *Romboutsia* are shown. ‘*’, ‘**’ and ‘***’ indicate significantly different from the DC group at the $P < 0.05$, $P < 0.01$ and $P < 0.001$ levels, respectively.

Figure S3. SFF improves the gut integrity in HFD/STZ-induced mice. The plasma lipopolysaccharide (LPS). * Indicates significantly different from the DC group at the * $P < 0.05$ level.

Figure S4. Spearman's correlation between gut microbiota and T2DM-related indexes (Genus). Good's coverage and the genus with significant correlations are shown.

Figure S5. Effect of SFF on the colonic metabolite profile of the diabetic mice. Box plot visualizations of the relative abundances of (R)-carnitine and choline metabolites in DC+SFF and DC groups. * $P < 0.05$, compared to DC group.