

## Responses of gut microbiota and metabolite profiles to sulfated polysaccharide from sea cucumber in humanized microbiota mice

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**Table S1** Data preprocessing statistics and quality control. A0 and C0 stand for fecal samples inoculation solution.

**Table S2** Alpha **diversity** analysis index (The amount of data selected during homogenization: cutoff = 71207). A0 and C0 stand for fecal samples inoculation solution.

**Fig. S1** Amount of microbiota in mice feces at day 5. Data are expressed as the mean  $\pm$  SD (n = 3).

**Fig. S2** Amount of microbiota in mice feces at day 20. Data are expressed as the mean  $\pm$  SD (n = 3).

**Fig. S3** The high-performance gel-permeation chromatography chromatograms of SCSPsj and d-SCSPsj.

**Fig. S4** The standard curve of SCFAs in GC was used for calculation. Acetic acid (Ace), propionic acid (Pro), butyric acid (But), isobutyric acid (Isobut), valeric Acid (Val) and

isovaleric acid (Isoval), 2-ethylbutyric acid was used as internal standard.

**Fig. S5** PCA of identified metabolites in serum samples at positive ion mode (A). Comparison of metabolites in serum samples at positive ion mode using OPLS-DA (B).

**Fig. S6** PCA of identified metabolites in serum samples at negative ion mode (A). Comparison of metabolites in serum samples at negative ion mode using OPLS-DA (B).

**Fig. S7** PCA of identified metabolites in cecal contents samples at positive ion mode (A). Comparison of metabolites in cecal contents samples at positive ion mode using OPLS-DA (B).

**Fig. S8** PCA of identified metabolites in cecal contents samples at negative ion mode (A). Comparison of metabolites in cecal contents samples at negative ion mode using OPLS-DA (B).

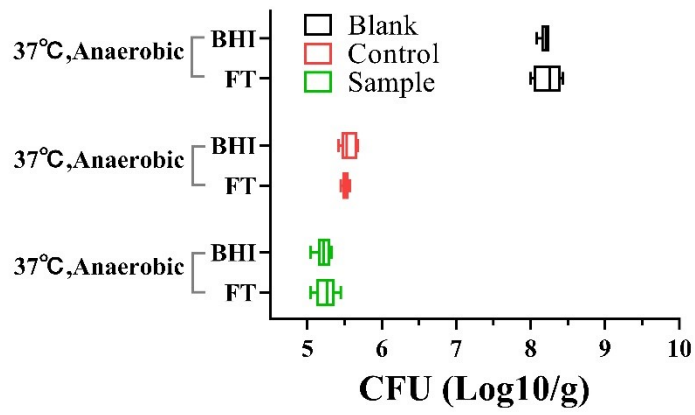
**Table S1** Data preprocessing statistics and quality control.

<b>Sample_name</b>	<b>Raw_reads(#)</b>	<b>Clean_Reads(#)</b>	<b>Base(nt)</b>	<b>AvgLen(nt)</b>	<b>Q20</b>	<b>GC%</b>	<b>Effective%</b>
Control1	83616	80030	20262050	253	89.19	54.88	95.71
Control2	84108	80172	20322964	253	90.3	52.49	95.32
Control3	88398	80171	20356051	253	89.67	50.36	90.69
Control4	82401	80141	20350125	253	89.92	52.35	97.26
Control5	83322	80062	20323245	253	90.77	50.46	96.09
Control6	82720	80220	20352970	253	89.6	49.92	96.98
Sample1	84956	80069	20322634	253	89.94	52.31	94.25
Sample2	86497	80097	20312539	253	89.1	52.69	92.6
Sample3	87239	80095	20310946	253	89.59	52.03	91.81
Sample4	82590	80194	20358421	253	89.64	52.36	97.1
Sample5	84223	80072	20323305	253	88.93	52.07	95.07
Sample6	83292	80202	20368176	253	89.38	52.58	96.29

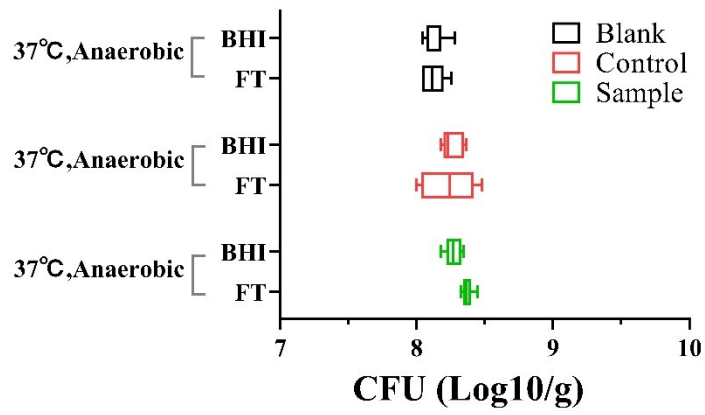
**Table S2** Alpha **diversity** analysis index (The amount of data selected during homogenization: cutoff = 73373).

<b>Sample Name</b>	<b>observed_species</b>	<b>shannon</b>	<b>simpson</b>	<b>chao1</b>	<b>ACE</b>	<b>goods_coverage</b>	<b>PD_whole_tree</b>
Control1	398	4.99	0.933	428.622	428.826	0.999	25.452
Control2	454	5.174	0.923	505.395	490.365	0.999	31.428
Control3	290	4.8	0.926	328.278	326.391	0.999	20.869
Control4	354	3.505	0.744	387.553	385.918	0.999	22.626
Control5	261	4.368	0.899	282.026	285.607	0.999	19.896
Control6	290	4.474	0.903	314.5	322.523	0.999	21.944
Sample1	422	4.268	0.867	459.196	456.04	0.999	28.926
Sample2	431	5.029	0.898	452.022	453.549	0.999	26.98
Sample3	459	5.329	0.933	488.216	485.167	0.999	28.544
Sample4	513	5.059	0.87	556.522	568.63	0.999	33.311
Sample5	372	3.717	0.755	392	394.446	0.999	23.554
Sample6	433	4.809	0.887	464.571	464.01	0.999	27.535

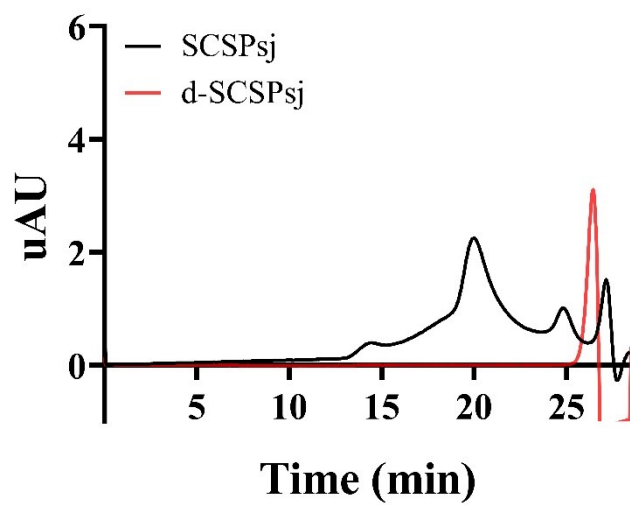
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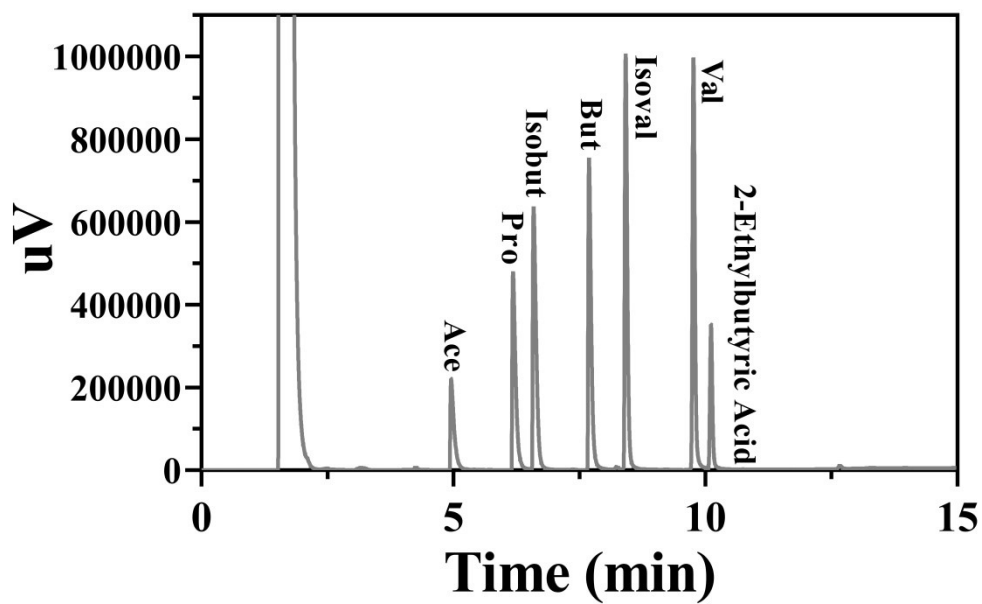
**Fig. S2** Amount of microbiota in mice feces at day 20. Data are expressed as the mean  $\pm$  SD (n = 3).



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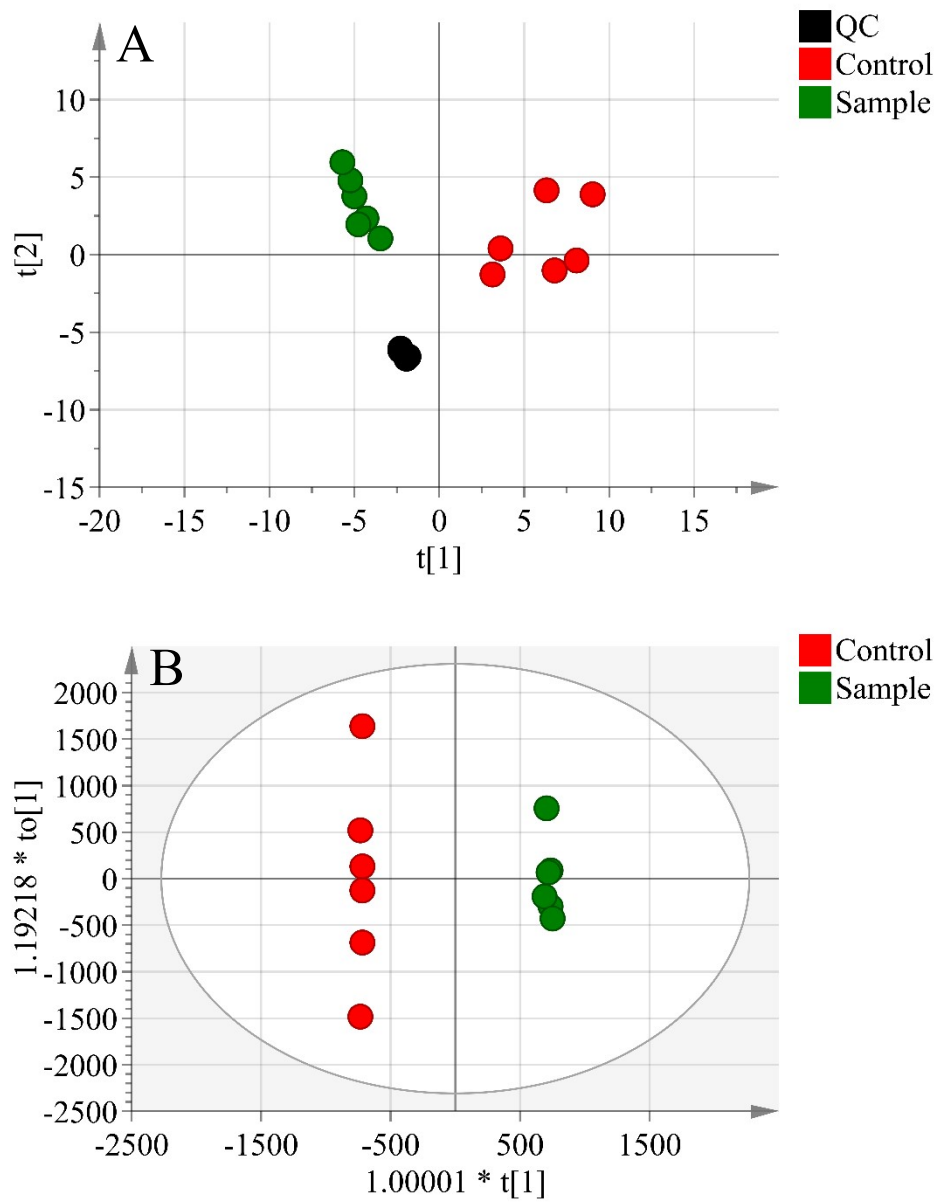


**Fig. S4** The standard curve of SCFAs in GC was used for calculation. Acetic acid (Ace), propionic acid (Pro), butyric acid (But), isobutyric acid (Isobut), valeric Acid (Val) and isovaleric acid (Isoval). 2-ethylbutyric acid was used as internal standard.

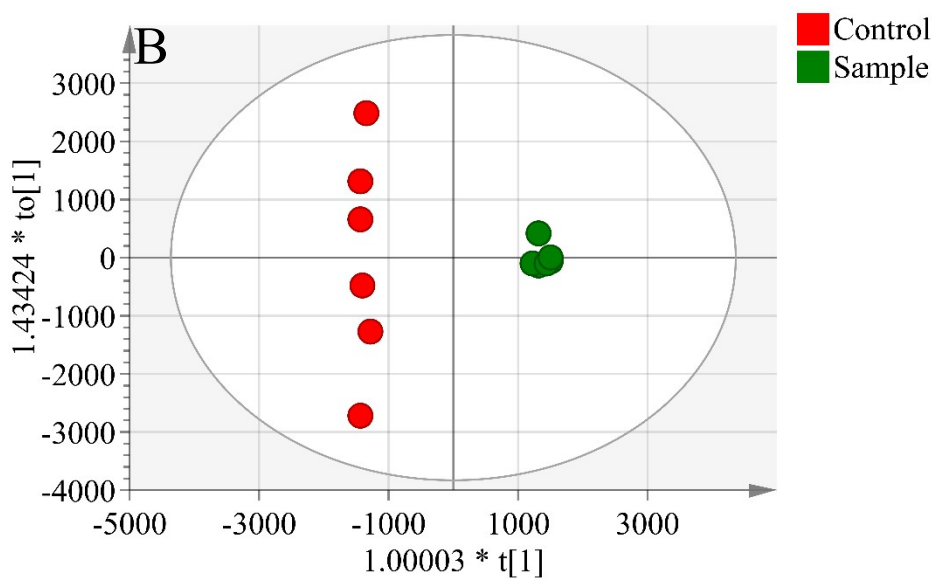
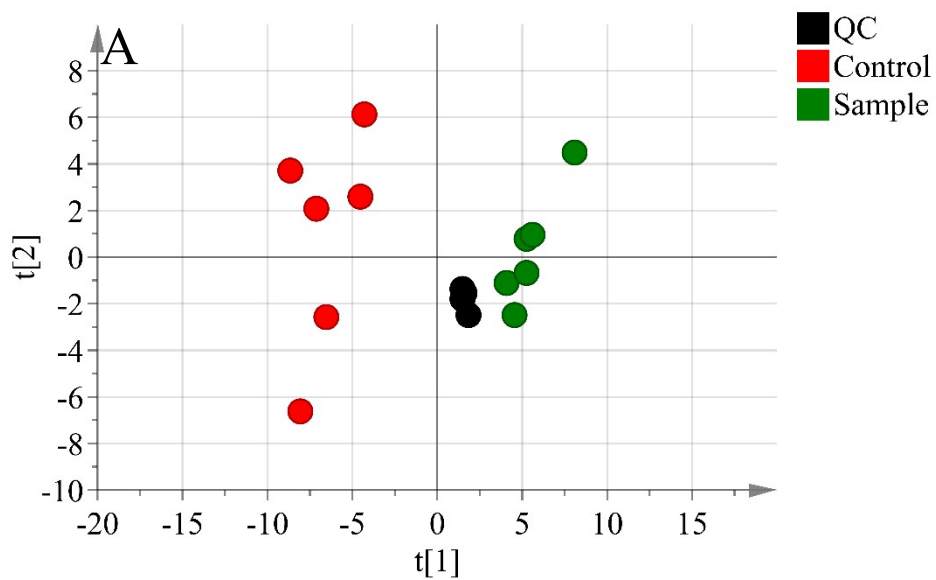




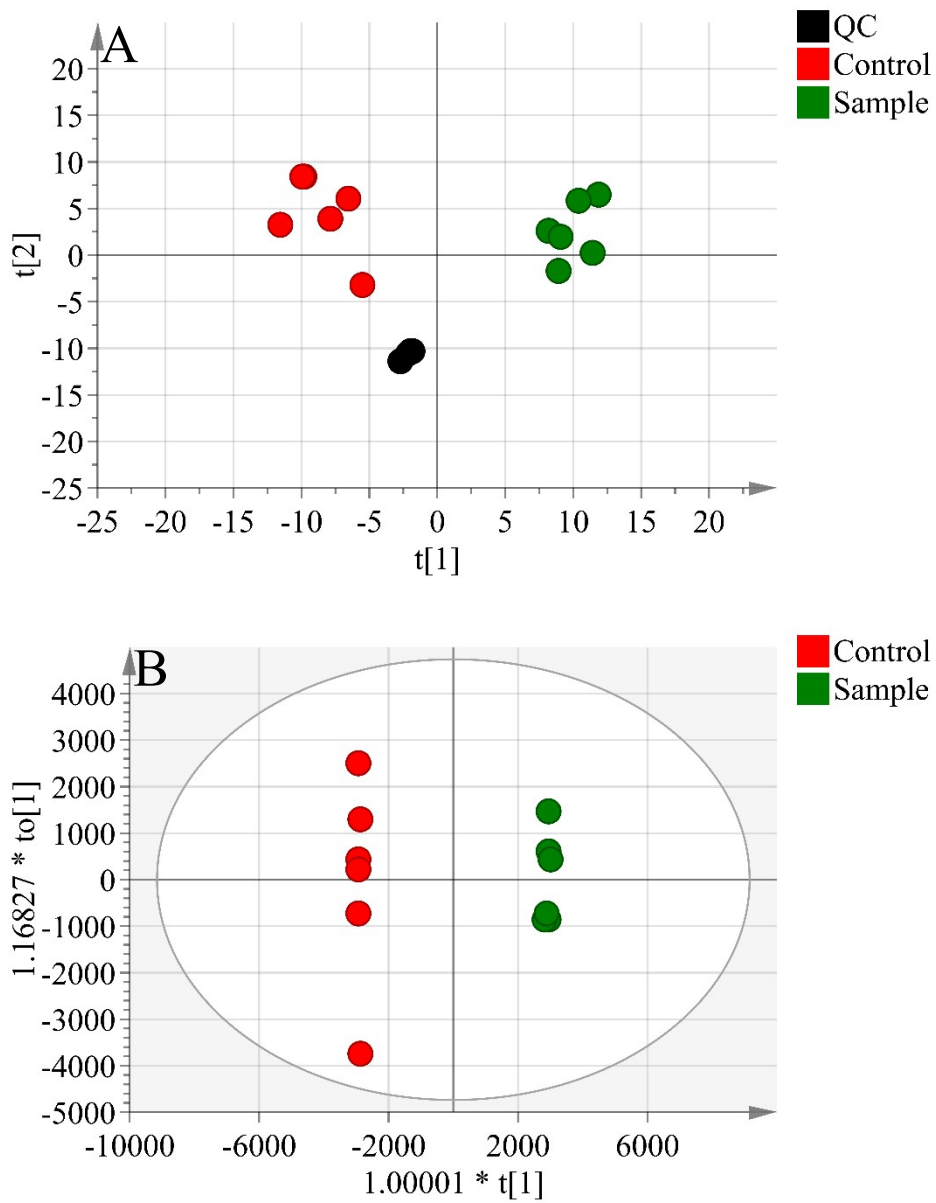
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