

Table. S1 Fold changes of selected bacteria at genus level.

OTU ID	Mean ± SD of Control	Mean ± SD of PS	Fold of PS / Control	Significance (Control, PS)	Mean ± SD of PS + C3G	Fold of PS / PS + C3G	Significance (PS, PS+C3G)
g__Alistipes	0.03156±0.01631	0.00902±0.00325	0.2857	$p < 0.05$	0.01664±0.02117	1.8457	$p > 0.05$
g__Dubosiella	0.08909±0.04760	0.00337±0.00300	0.0378	$p < 0.05$	0.05535±0.04369	16.4461	$p < 0.05$
g__Ileibacterium	0.0000±0.00000	0.01728±0.03983	∞	$p < 0.05$	0.0000±0.00000	0.0000	$p < 0.05$
g__Helicobacter	0.00675±0.00875	0.01696±0.01072	2.5136	$p < 0.05$	0.00885±0.00712	0.5218	$p > 0.05$
g__Desulfovibrio	0.01003±0.01274	0.01915±0.01428	1.9099	$p > 0.05$	0.00802±0.00525	0.4187	$p < 0.05$
g__norank_f__Oscillospiraceae	0.00685±0.00792	0.01384±0.01078	2.0207	$p > 0.05$	0.00943±0.00657	0.6811	$p > 0.05$
g__Lachnoclostridium	0.00269±0.00339	0.00646±0.00544	2.3996	$p > 0.05$	0.00508±0.00329	0.7870	$p > 0.05$
g__Lachnospiraceae_UCG-006	0.00085±0.00142	0.01382±0.01491	16.2644	$p < 0.05$	0.00133±0.00118	0.0960	$p < 0.05$
g__norank_f__Lachnospiraceae	0.00444±0.00618	0.01972±0.01135	4.4403	$p < 0.05$	0.01595±0.00968	0.8085	$p > 0.05$
g__unclassified_f__Lachnospiraceae	0.01283±0.01273	0.03847±0.01891	2.9972	$p < 0.05$	0.03157±0.01960	0.8207	$p > 0.05$
g__Lachnospiraceae_NK4A136_group	0.01283±0.01411	0.08035±0.04519	6.2623	$p < 0.05$	0.06526±0.0555	0.8122	$p > 0.05$
g__Roseburia	0.00297±0.00362	0.00953±0.00597	3.2105	$p < 0.05$	0.00598±0.00507	0.6278	$p > 0.05$
g__Marvinbryantia	0.00122±0.00082	0.00090±0.00100	0.7398	$p > 0.05$	0.00243±0.00362	2.6905	$p > 0.05$
g__Prevotellaceae_NK3B31_group	0.02363±0.04095	0.00005±0.00001	0.0019	$p > 0.05$	0.00006±0.00016	1.2910	$p > 0.05$
g__Prevotellaceae_UCG-001	0.0000±0.0001	0.01755±0.03764	5995.2392	$p > 0.05$	0.00005±0.00009	0.0028	$p > 0.05$
g__Parasutterella	0.0101±	0.0001±	0.0142	$p < 0.05$	0.00401±0.00204	28.0714	$p < 0.05$