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Table S1 Potential faecal biomarkers in *Radix Scrophulariae*-treated rats.

No.	Rt_m/z	Compound ID	VIP	ion mode	Formula	Description	Pathways
1	1.39_136.0399	HMDB00157	1.3164	pos	C5H4N4O	Hypoxanthine	Purine metabolism
2	0.99_153.0411	HMDB00292	1.7322	pos	C5H4N4O2	Xanthine	Purine metabolism, Caffeine metabolism
3	13.41_280.2406	HMDB00673	2.3958	neg	C18H32O2	Linoleic acid	Linoleic acid metabolism
4	3.97_164.0477	HMDB02035	1.1405	neg	C9H8O3	4-Hydroxycinnamic acid	Ubiquinone and other terpenoid-quinone biosynthesis, Phenylalanine metabolism
5	1.44_268.0804	HMDB00195	1.6379	neg	C10H12N4O5	Inosine	Purine metabolism
6	6.68_408.2877	HMDB00619	14.5787	neg	C24H40O5	Cholic acid	Primary bile acid biosynthesis
7	0.66_221.0900	HMDB00215	2.3694	neg	C8H15NO6	N-Acetyl-D-glucosamine	Amino sugar and nucleotide sugar metabolism
8	7.84_595.3498	HMDB04157	1.4764	neg	C33H48N4O6	L-Urobilinogen	Porphyrin and chlorophyll metabolism
9	1.64_304.0773	HMDB00133	1.3461	neg	C10H13N5O5	Guanosine	Purine metabolism
10	1.08_289.0675	HMDB00296	2.8402	neg	C9H12N2O6	Uridine	Pyrimidine metabolism

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Table S2. Fingerprint pathway in normal rats treated with *Radix Scrophulariae* determined using MetPA analysis.

Pathway name	Total	Expected	Hits	Raw p	-log(p)	Holm adjust	FDR	Impact
Purine metabolism	92	0.72622	4	0.0049847	5.3014	0.39878	0.39878	0.05662
Linoleic acid metabolism	15	0.1184	1	0.11239	2.1858	1	1	0.65625
Caffeine metabolism	21	0.16577	1	0.1539	1.8714	1	1	0.0305
Ubiquinone and other terpenoid-quinone biosynthesis	36	0.28417	1	0.24979	1.3871	1	1	0.0337
Phenylalanine metabolism	45	0.35521	1	0.30228	1.1964	1	1	0.01193
Primary bile acid biosynthesis	47	0.371	1	0.31346	1.1601	1	1	0.00027
Pyrimidine metabolism	60	0.47362	1	0.38211	0.96204	1	1	0.02061
Amino sugar and nucleotide sugar metabolism	88	0.69464	1	0.50854	0.67622	1	1	0.01122
Porphyrin and chlorophyll metabolism	104	0.82094	1	0.56934	0.56328	1	1	0.00167

Note: Total is the total number of compounds in the pathway; Hits is the exact number of matches in the uploaded tag data; Raw p is the original P value obtained by path analysis; Impact is the path influence value obtained by topological analysis.

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Table S3. Taxonomic comparisons between the control group and *Radix Scrophulariae* group at the genus level

OTU	Mean abundance- Radix Scrophulariae (%)	Mean abundance-control (%)	p-value	q-value
Corynebacterium	0.0042	0.1447	0.000056	0.005009
Dehalobacterium	0.0172	0.0806	0.000289	0.013023
Brevundimonas	0	0.0284	0.000678	0.02037
Rhodococcus	0	0.0451	0.001589	0.035814
Ruminococcus	1.3414	8.5845	0.002022	0.036465
Prevotella	0.2085	12.1782	0.003189	0.047919
Butyricimonas	0.0792	0.0142	0.0055	0.070841
Enhydrobacter	0.0032	0.0312	0.0086	0.096923
Rothia	0.0118	0	0.009844	0.097811
Facklamia	0.1055	0.0293	0.010944	0.097811
Lactobacillus	26.1461	13.7453	0.211067	0.528106
Neisseria	0	0.0056	0.011933	0.097811
Lactococcus	0.0287	0.0035	0.014078	0.105772

Flavobacterium	0	0.0126	0.016967	0.117672
Geobacillus	0.0455	0.0024	0.022067	0.134774
Burkholderia	0.0634	0.0018	0.022422	0.134774
Acinetobacter	0.009	0.0618	0.025	0.140781
Odoribacter	0.1373	0.0053	0.026544	0.140781
Anaerobiospirillum	0.0046	0.0428	0.034833	0.174478
Zea	0.0054	0	0.042644	0.202362
Sediminibacterium	0.2641	0.0503	0.049778	0.224401

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