

Supplementary tables

Table S1 The relative abundance of the top 15 bacteria of the gut microbiota in the CON, T2DM, and DN groups at the phylum level (% $\bar{x}\pm s$)

phylum	CON	T2DM	DN	P 值
<i>Bacteroidetes</i>	61.94±22.73	60.30±26.01	67.64±14.37	0.881
<i>Firmicutes</i>	28.98±16.40	27.42±18.80	24.15±9.97	0.729
<i>Proteobacteria</i>	5.11±7.94	8.79±9.49	4.27±5.29	0.525
<i>Actinobacteria</i>	0.34±0.26	1.47±2.30	1.07±1.18	0.443
<i>Candidatus_Melainabacteria</i>	0.55±1.03	0.32±0.99	0.06±0.08	0.245
<i>Uroviricota</i>	0.53±1.29	0.04±0.04	0.16±0.29	0.564
<i>Fusobacteria</i>	0.35±1.24	0.16±0.51	0.01±0.01	0.198
<i>Tenericutes</i>	0.24±0.63	0.02±0.06	0.15±0.19	0.167
<i>Verrucomicrobia</i>	0.10±0.17	0.05±0.04	0.18±0.32	0.889
<i>Euryarchaeota</i>	0.02±0.02	0.02±0.04	0.16±0.26	0.054
<i>Lentisphaerae</i>	0.00±0.00	0.00±0.00	0.10±0.35	0.196
<i>Chlamydiae</i>	0.05±0.13	0.01±0.01	0.01±0.01	0.295
<i>Synergistetes</i>	0.00±0.01	0.05±0.17	0.00±0.01	0.090
<i>Spirochaetes</i>	0.01±0.01	0.01±0.01	0.01±0.02	0.590
<i>Crenarchaeota</i>	0.02±0.07	0.00±0.00	0.00±0.00	0.111

Table S2 The relative abundance of the top 15 bacteria of the gut microbiota in the CON, T2DM, and DN groups at the genus level (% , $\bar{x}\pm s$)

genus	CON	T2DM	DN	<i>P</i> 值
<i>Bacteroides</i>	17.94±14.18	26.67±17.41	29.22±15.23	0.109
<i>Prevotella</i>	27.31±30.01	11.35±20.20	16.28±21.11	0.429
<i>Phocaeicola</i>	10.13±8.80	12.80±9.26	9.59±7.42	0.538
<i>Faecalibacterium</i>	6.50±5.02	7.81±6.89	3.78±2.51	0.169
<i>Alistipes</i>	1.91±1.88	2.71±2.90	4.74±5.01	0.339
<i>Parabacteroides</i>	1.88±1.15	3.94±3.56	3.28±1.90	0.066
<i>Clostridium</i>	2.82±2.27	2.09±1.84	2.48±1.68	0.679
<i>Roseburia</i>	2.39±2.00	2.30±2.72	1.62±0.86	0.585
<i>Eubacterium</i>	1.98±1.37	2.02±2.67	1.66±2.31	0.417
<i>Escherichia</i>	2.07±6.21	2.63±4.62	0.61±0.66	0.052
<i>Ruminococcus</i>	1.60±0.89	1.10±0.99	1.63±1.08	0.156
<i>Klebsiella</i>	0.46±0.68	2.87±5.67	0.60±1.00	0.199
<i>Blautia</i>	1.03±0.79	1.12±1.06	1.00±0.75	0.942
<i>Lachnospira</i>	0.90±0.61	0.95±1.02	0.68±1.67*	0.022
<i>Bifidobacterium</i>	0.20±0.19	1.03±2.12	0.77±0.99	0.606

**P*<0.05, compared with CON groups

Table S3 The relative abundance of the top 15 bacteria of the gut microbiota in the CON, T2DM, and DN groups at the species level (% , $\bar{x}\pm s$)

species	CON	T2DM	DN	P 值
<i>Prevotella copri</i>	22.13±25.77	8.24±16.86	11.08±18.47	0.197
<i>Phocaeicola vulgatus</i>	3.76±3.47	6.30±4.25	4.88±3.59	0.230
<i>Faecalibacterium prausnitzii</i>	4.31±3.38	5.12±4.31	2.56±1.66	0.177
<i>Phocaeicola plebeius</i>	4.40±6.30	3.06±5.33	1.89±4.81	0.374
<i>Bacteroides uniformis</i>	1.91±2.19	2.88±2.92	4.19±2.40	0.064
<i>Bacteroides ovatus</i>	1.89±2.31	2.98±3.02	2.73±2.32	0.379
<i>Bacteroides fragilis</i>	2.47±6.46	3.25±5.56*	1.24±0.66	0.034
<i>Bacteroides stercoris</i>	0.88±1.14	1.52±2.04	3.31±3.74*	0.031
<i>Escherichia coli</i>	2.06±6.17	2.62±4.59	0.61±0.66	0.051
<i>Phocaeicola dorei</i>	1.20±0.87	2.22±1.36	1.68±1.19	0.161
<i>Bacteroides xylanisolvens</i>	1.07±1.16	2.03±2.64	1.34±1.02	0.552
<i>Bacteroides thetaiotaomicron</i>	1.21±1.34	1.40±1.18	1.58±1.06	0.292
<i>Bacteroides caccae</i>	0.69±0.59	1.31±1.34	1.29±0.92	0.115
<i>Parabacteroides merdae</i>	0.64±0.44	1.33±1.48	0.98±0.65	0.316
<i>Parabacteroides distasonis</i>	0.52±0.35	1.05±0.80	1.06±0.71	0.606
<i>[Eubacterium]_rectale</i>	0.01±0.01	0.01±0.01	0.01±0.01	0.239
<i>Lachnospiraceae_bacterium</i>	0.01±0.01	0.01±0.00	0.01±0.01	0.386
<i>Prevotella_sp.</i>	0.01±0.01	0.00±0.01	0.01±0.01	0.184
<i>Bacteroides_sp.</i>	0.00±0.00	0.01±0.01	0.01±0.01	0.750
<i>Eubacterium_sp.</i>	0.01±0.01	0.01±0.01	0.01±0.01	0.266
<i>Phocaeicola_coprocola</i>	0.00±0.00	0.01±0.01	0.01±0.01	0.975
<i>Clostridia_bacterium</i>	0.01±0.01	0.00±0.00	0.01±0.01	0.309

<i>Klebsiella_pneumoniae</i>	0.00±0.00	0.01±0.03	0.00±0.01	0.166
<i>Ruminococcaceae_bacterium</i>	0.01±0.01	0.00±0.00	0.01±0.00	0.154
<i>Lachnospira_eligens</i>	0.01±0.01	0.01±0.01	0.00±0.01	0.090
<i>Alistipes_putredinis</i>	0.00±0.00	0.00±0.01	0.01±0.02	0.149
<i>Faecalibacterium_sp.</i>	0.01±0.00	0.01±0.01	0.00±0.00	0.124
<i>Roseburia_inulinivorans</i>	0.01±0.01	0.00±0.01	0.00±0.00	0.167
<i>Bacteroides_eggerthii</i>	0.00±0.00	0.00±0.00	0.01±0.01*	0.042
<i>Bacteroides_cellulosilyticus</i>	0.00±0.00	0.00±0.00	0.01±0.02	0.220

* $P < 0.05$, compared with CON groups

Table S4 AUC and 95%CI of renal function related indexes distinguishing DN from CON and T2DM

Parameters	CON-DN		T2DM-DN	
	AUC	95%CI	AUC	95%CI
ACR	0.881	0.718 - 1.000	0.826	0.647 - 1.000
ALB	0.815	0.622 - 1.000	0.785	0.592 - 0.977
UCR	0.839	0.642 - 1.000	0.757	0.556 - 0.957
UA	0.929	0.830 - 1.000	0.635	0.402 - 0.869
UREA	0.738	0.532 - 0.944	0.583	0.338 - 0.829
SCR	0.637	0.416 - 0.857	0.520	0.277 - 0.764
BUN/CR	0.518	0.285 - 0.750	0.524	0.282 - 0.766