

## *Supplementary Material*

# **Integrative Analysis of Fecal Metagenomics and Metabolomics in Bladder Cancer in a Chinese Population**

Chuan Qin, Zhenghao Chen, Rui Cao, Mingjun Shi and Ye Tian \*

Department of Urology, Beijing Friendship Hospital, Capital Medical University,  
Beijing 100068, China

\* Correspondence: youyitianye@126.com; Tel.: +86-010-63138377

**Table S1. List of top 35 microbiomes in terms of abundance.**

<b>Genus</b>	<b>Abundance trend</b>
Parabacteroides	Higher in EXP
Butyricicoccus	Higher in EXP
Megamonas	Higher in CON
Prevotella	Higher in CON
Fusobacterium	Higher in EXP
Eubacterium	Higher in CON
Dialister	Higher in CON
Veillonella	Higher in EXP
Escherichia	Higher in EXP
Anaerostipes	Higher in CON
Streptococcus	Higher in EXP
Fusicatenibacter	Higher in CON

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Bacteroides	Higher in EXP
Oscillibacter	Higher in CON
Lactobacillus	Higher in CON
Roseburia	Higher in CON
Megasphaera	Higher in CON
Gemmiger	Higher in CON
Ruminococcus	Higher in EXP
Phascolarctobacterium	Higher in EXP
Sutterella	Higher in CON
Romboutsia	Higher in CON
Faecalibacterium	Higher in CON
Bifidobacterium	Higher in CON
Coprococcus	Higher in CON
Paraprevotella	Higher in EXP
Collinsella	Higher in EXP
Clostridium	Higher in CON
Lachnoclostridium	Higher in EXP
Dorea	Higher in CON
Akkermansia	Higher in EXP
Alistipes	Higher in CON

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Subdoligranulum	Higher in CON
Bilophila	Higher in EXP
Blautia	Higher in CON
Species	Abundance trend
Bacteroides fragilis	Higher in EXP
Bacteroides thetaiotaomicron	Higher in EXP
Roseburia faecis	Higher in CON
Roseburia inulinivorans	Higher in CON
Faecalibacterium prausnitzii	Higher in CON
[Eubacterium] hallii	Higher in CON
Escherichia coli	Higher in EXP
Blautia wexlerae	Higher in CON
[Ruminococcus] torques	Higher in CON
[Eubacterium] rectale	Higher in EXP
Bifidobacterium adolescentis	Higher in CON
Bacteroides vulgatus	Higher in EXP
uncultured Ruminococcus sp.	Higher in CON
Blautia obeum	Higher in CON
Clostridium sp. CAG:7	Higher in EXP
uncultured Clostridium sp.	Higher in CON

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<i>Bifidobacterium longum</i>	Higher in EXP
<i>Dialister succinatiphilus</i>	Higher in CON
<i>Alistipes putredinis</i>	Higher in CON
<i>Bacteroides stercoris</i>	Higher in EXP
<i>Roseburia intestinalis</i>	Higher in CON
<i>Prevotella copri</i> CAG:164	Higher in CON
<i>Bacteroides ovatus</i>	Higher in CON
<i>Fusicatenibacter saccharivorans</i>	Higher in CON
<i>Akkermansia</i> sp. CAG:344	Higher in EXP
<i>Dorea longicatena</i>	Higher in CON
<i>Ruminococcus callidus</i>	Higher in EXP
<i>Bifidobacterium pseudocatenulatum</i>	Higher in CON
<i>Megamonas funiformis</i>	Higher in CON
<i>Bacteroides plebeius</i>	Higher in EXP
<i>Bacteroides dorei</i>	Higher in EXP
<i>Bacteroides coprocola</i>	Higher in CON
<i>Bacteroides uniformis</i>	Higher in EXP
<i>Prevotella copri</i>	Higher in CON
<i>Eubacterium</i> sp. CAG:38	Higher in EXP

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BLCA patients, EXP group; healthy individuals, CON group.

**Table S2. List of functional characterization of gut microbiota.**

<b>KEGG pathway</b>	<b>EXP relative abundance</b>	<b>CON relative abundance</b>
Organismal Systems; Immune system	0.000928	0.000973
Genetic Information Processing; Folding, sorting and degradation	0.008625	0.008780
Human Diseases; Cancers: Overview	0.002075	0.002042
Organismal Systems; Nervous system	0.000725	0.000660
Metabolism; Lipid metabolism	0.009825	0.009856
Human Diseases; Endocrine and metabolic diseases	0.001326	0.001403
Metabolism; Nucleotide metabolism	0.017829	0.018526
Human Diseases; Cardiovascular diseases	0.001040	0.001101
Cellular Processes; Cellular community - prokaryotes	0.011554	0.011921
Genetic Information Processing; Replication and repair	0.011273	0.011770
Cellular Processes; Transport and catabolism	0.002157	0.001922
Genetic Information Processing; Translation	0.019353	0.020376
Organismal Systems; Environmental adaptation	0.000752	0.000733

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Metabolism; Energy metabolism	0.019885	0.020447
Cellular Processes; Cell motility	0.002126	0.002373
Organismal Systems; Aging	0.001272	0.001327
Genetic Information Processing; Transcription	0.001031	0.001072
Metabolism; Metabolism of cofactors and vitamins	0.023138	0.023457
Environmental Information Processing; Signal transduction	0.009662	0.009675
Human Diseases; Neurodegenerative diseases	0.000403	0.000365
Metabolism; Glycan biosynthesis and metabolism	0.010453	0.010184
Metabolism; Carbohydrate metabolism	0.039645	0.040542
Organismal Systems; Digestive system	0.000498	0.000501
Human Diseases; Drug resistance: Antineoplastic	0.001292	0.001315
Human Diseases; Infectious diseases: Viral	0.000324	0.000320
Human Diseases; Drug resistance: Antimicrobial	0.005727	0.005662
Metabolism; Biosynthesis of other secondary metabolites	0.007913	0.007904
Metabolism; Metabolism of terpenoids and polyketides	0.005170	0.005238

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Metabolism; Metabolism of other amino acids	0.008116	0.008037
Metabolism; Amino acid metabolism	0.030106	0.030568
Environmental Information Processing; Membrane transport	0.020228	0.021590
Human Diseases; Infectious diseases: Bacterial	0.002343	0.002357
Metabolism; Xenobiotics biodegradation and metabolism	0.003032	0.003175
Cellular Processes; Cell growth and death	0.004911	0.005015
Organismal Systems; Endocrine system	0.002282	0.002359
<b>eggNOG pathway</b>	<b>EXP relative abundance</b>	<b>CON relative abundance</b>
Resolvase	0.002667	0.003035
Transporter	0.002213	0.002163
Integrase	0.002746	0.002642
Binding-protein-dependent transport systems inner membrane component	0.002713	0.003045
transposase	0.007272	0.007228
oxidoreductase	0.001693	0.001642
peptidase_	0.002346	0.002177
Transposase	0.005297	0.006012
Glycosyl transferase (Group 1	0.001749	0.001475

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ABC transporter (permease)	0.002362	0.002386
hydrolase family 43	0.001865	0.001684
radical SAM domain protein	0.002406	0.002516
Dehydrogenase	0.002745	0.002809
Hydrolase	0.002459	0.002451
helicase	0.002353	0.002495
AAA-ATPase	0.001627	0.001732
Ragb susd domain-containing protein	0.002919	0.002354
Transcriptional Regulator AraC Family	0.001952	0.001959
Glycosyl transferase, family 2	0.003903	0.003640
domain protein	0.005284	0.005281
membrane	0.001948	0.002067
Histidine kinase	0.011125	0.010771
Efflux transporter rnd family, mfp subunit	0.001896	0.001526
Membrane	0.007120	0.006665
acetyltransferase	0.003057	0.002800
hydrolase family 2	0.002524	0.002198
regulatoR	0.003367	0.003686
Methyltransferase	0.002679	0.002712

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RNA Polymerase	0.002477	0.002141
ATPase (AAA	0.001599	0.001866
hydrolase family 3	0.001669	0.001634
TonB dependent receptor	0.004881	0.003875
Mate efflux family protein	0.003663	0.003927
tonB-dependent Receptor	0.001983	0.001705
Transcriptional regulator	0.011444	0.012176
CAZy pathway	EXP relative abundance	CON relative abundance
amylase (EC 3.2.1.33)	0.001253	0.001430
dTDP-L-Rha: N-acetylglucosaminyl-PP-decaprenol &alpha_-1,3-L-rhamnosyl(...)	0.002248	0.002122
branching enzyme (EC 2.4.1.18)	0.001253	0.001424
pullulanase (EC 3.2.1.41)	0.001150	0.001337
sucrose phosphorylase (EC 2.4.1.7)	0.001150	0.001337
chitin oligosaccharide synthase (EC 2.4.1.-)	0.002248	0.002122
N-acetylgalactosaminyltransferase (EC 2.4.1.-)	0.002248	0.002122
hyaluronan synthase (EC 2.4.1.212)	0.002248	0.002122
UDP-Galf: galactofuranosyl-galactofuranosyl-rhamnosyl-N-acetylglucosam	0.002248	0.002122

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dolichyl-phosphate &beta;-glucosyltransferase (EC 2.4.1.117)	0.002248	0.002122
lysozyme (EC 3.2.1.17)	0.001510	0.001401
exo-&beta;-glucosaminidase (EC 3.2.1.165)	0.002537	0.002171
[inverting] exo-&alpha;-1,5-L-arabinanase (EC 3.2.1.-)	0.002385	0.002072
exo-1,3-1,4-glucanase (EC 3.2.1.-)	0.001401	0.001367
coniferin &beta;-glucosidase (EC 3.2.1.126)	0.001401	0.001367
dolichyl-phosphate &beta;-D-mannosyltransferase (EC 2.4.1.83)	0.002248	0.002122
isoprimeverose-producing oligoxyloglucan hydrolase (EC 3.2.1.120)	0.001401	0.001367
arabinanase (EC 3.2.1.99)	0.002385	0.002072
xylan 1,4-&beta;-xylosidase (EC 3.2.1.37)	0.001401	0.001367
exo-&alpha;-1,5-L-arabinofuranosidase (EC 3.2.1.-)	0.002385	0.002072
cellulose synthase (EC 2.4.1.12)	0.002248	0.002122
UDP-Galf: rhamnopyranosyl-N-acetylglucosaminyl-PP-decaprenol &beta;-1,(...)	0.002248	0.002122
xylanase (EC 3.2.1.8)	0.002477	0.002139
glucan 1,3-&beta;-glucosidase (EC 3.2.1.58)	0.001404	0.001369

N-acetylglucosaminyltransferase (EC 2.4.1.-)	0.002248	0.002122
neopullulanase (EC 3.2.1.135)	0.001150	0.001337
glucodextranase (EC 3.2.1.70)	0.001178	0.001356
acetyl xylan esterase (EC 3.1.1.72)	0.001510	0.001535
4-&alpha;-glucanotransferase (EC 2.4.1.25)	0.001253	0.001424
chitin synthase (EC 2.4.1.16)	0.002248	0.002122
galactan 1,3-&beta;-galactosidase (EC 3.2.1.145)	0.002385	0.002072
maltotriose-forming &alpha;-amylase (EC 3.2.1.116)	0.001150	0.001337
cyclomaltodextrinase (EC 3.2.1.54)	0.001253	0.001424
mannosylglycoprotein endo-&beta;-mannosidase (EC 3.2.1.152)	0.002151	0.001884
glucan 1,4-&beta;-glucosidase (EC 3.2.1.74)	0.001401	0.001367

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BLCA patients, EXP group; healthy individuals, CON group.

**Table S3. The KEGG pathway annotation results**

Map Name	Map ID	P value	FDR	RichFactor
Biosynthesis of unsaturated fatty acids	hsa01040	0.006	0.031	0.027
Linoleic acid metabolism	hsa00591	0.046	0.115	0.036

