

Supplementary tables

Table S1. Alpha diversity indices of gut microbiota in NS controls, OS and RS patients.

Alpha diversity indices	NS controls		OS patients		RS patients		P value		
	Mean	SD	Mean	SD	Mean	SD	NS-OS	NS-RS	OS-RS
Ace	784.340	275.020	900.780	248.900	959.150	93.543	0.003	0.001	0.540
Chao	716.000	259.260	827.950	235.630	839.610	154.020	0.009	0.051	0.616
Shannon	4.306	0.847	4.290	0.978	4.272	0.804	0.595	0.722	0.669
Simpson	0.051	0.046	0.076	0.107	0.056	0.033	0.546	0.225	0.607

NS, non-kidney stone. OS, occasional stone. RS, recurrent stone. SD, standard deviation.

Table S2. Higher bacteria genera in NS controls, OS and RS patients by LEfSe analysis.

Groups	Bacteria (counts, /10,000)	LDA score	P value
NS controls	g_Blautia (448)	3.930	0.006
	g_Coprococcus_2 (59)	3.573	0.011
	g_Eubacterium_hallii_group (167)	3.560	0.003
	g_Fusicatenibacter (89)	3.511	0.004
	g_unclassified_f_Peptostreptococcaceae (95)	3.340	0.010
	g_unclassified_f_Lachnospiraceae (86)	3.338	0.000
	g_Ruminococcaceae_UCG_005 (19)	2.798	0.021
	g_Adlercreutzia (15)	2.776	0.004
	g_Lachnospiraceae_ND3007_group (10)	2.616	0.042
	g_Marvinbryantia (13)	2.446	0.002
OS patients	g_Lachnoclostridium (150)	3.499	0.025
	g_Acinetobacter (28)	3.309	0.000
	g_unclassified_p_Firmicutes (9)	2.989	0.000
	g_Empedobacter (9)	2.943	0.000
	g_Pseudomonas (54)	2.878	0.003
	g_Cellulosilyticum (7)	2.756	0.000
	g_Synechococcus (14)	2.568	0.029
	g_Cetobacterium (12)	2.474	0.013
	g_Ruminococcaceae_UCG_009 (1)	2.419	0.006
	g_Nocardia (1)	2.390	0.000
RS patients	g_Litoricola (1)	2.218	0.035
	g_norank_f_Eubacteriaceae (1)	2.192	0.002
	g_Eubaacterium (1)	2.166	0.003
	g_Rhodococcus (4)	2.164	0.050
	g_Leuconostoc (6)	2.137	0.007
	g_Pedomicrobium (1)	2.090	0.019
	g_Oceanobacillus (3)	2.052	0.003
	g_Ruminococcus_gnavus_group (57)	3.307	0.027
	g_Tyzzerella_4 (16)	2.905	0.004
	g_Prevotellaceae_UCG_001 (23)	2.504	0.041
	g_Mangrovibacter (2)	2.340	0.013
	g_Flavonifractor (5)	2.249	0.019
	g_Halomonas (9)	2.231	0.000
	g_Peptoniphilus (1)	2.210	0.003
	g_Geobacter (3)	2.166	0.000
	g_unclassified_f_Planococcaceae (6)	2.154	0.006
	g_Photobacterium (2)	2.153	0.010
	g_An aerosalibacter (2)	2.143	0.000
	g_Brevinema (4)	2.100	0.000
	g_Lysinibacillus (3)	2.071	0.016
	g_Clostridium_sensu_stricto_18 (2)	2.070	0.014
	g_Paracoccus (4)	2.068	0.006
	g_Candidatus_Brocadia (1)	2.065	0.035

g_Syntrophobacter (1)	2.064	0.037
g_Halothiobacillus (1)	2.042	0.021
g_Fructobacillus (3)	2.006	0.021
g_Hafnia_Obesumbacterium (2)	2.005	0.013
g_Clostridium_sensu_stricto_6 (3)	2.000	0.002

NS, non-kidney stone. OS, occasional stone. RS, recurrent stone. LDA, linear discriminant analysis. LEfSe, linear discriminant analysis Effect Size.

Table S3. Higher bacteria genera in NS controls and kidney stone patients by LEfSe analysis.

Group	Bacteria (counts, /10,000)	LDA score	P value
NS controls	g_Blautia (448)	3.921	0.014
	g_An aerostipes (127)	3.598	0.010
	g_Coprococcus_2 (59)	3.478	0.004
	g_Fusicatenibacter (89)	3.458	0.021
	g_Eubacterium_hallii_group (167)	3.413	0.004
	g_unclassified_f_Peptostreptococcaceae (95)	3.348	0.002
	g_unclassified_f_Lachnospiraceae (86)	3.278	0.000
	g_Fusobacterium (55)	3.197	0.023
	g_Dorea (78)	3.115	0.027
	g_Ruminococcus_1 (43)	3.103	0.019
	g_Adlercreutzia (15)	2.706	0.001
	g_Marvinbryantia (13)	2.415	0.001
	g_norank_f_Coriobacteriaceae (5)	2.400	0.038
	g_Lachnospiraceae_FCS020_group (7)	2.310	0.005
	g_Coprococcus_3 (28)	2.310	0.045
OS+RS patients	g_Megamonas (424)	3.862	0.024
	g_Lachnoclostridium (150)	3.484	0.007
	g_Acinetobacter (28)	3.205	0.000
	g_Ruminococcus_gnavus_group (57)	3.157	0.007
	g_Parabacteroides (48)	3.145	0.043
	g_Enterococcus (61)	3.011	0.050
	g_Pseudomonas (54)	2.959	0.001
	g_Weissella (34)	2.953	0.010
	g_unclassified_p_Firmicutes (9)	2.821	0.000
	g_Empedobacter (9)	2.808	0.000
	g_Tyzzerella_4 (16)	2.719	0.001
	g_Erysipelatoclostridium (8)	2.684	0.012
	g_Cellulosilyticum (7)	2.610	0.000
	g_Prevotella_2 (15)	2.605	0.002
	g_Prevotellaceae_UCG_001 (23)	2.582	0.012
	g_Flavobacterium (8)	2.547	0.010
	g_Staphylococcus (27)	2.533	0.049
	g_Synechococcus (14)	2.522	0.008
	g_norank_f_Ruminococcaceae (19)	2.457	0.028

g_Sutterella (6)	2.441	0.027
g_Cetobacterium (12)	2.294	0.003
g_Peptoclostridium (6)	2.275	0.018
g_Ruminiclostridium_9 (8)	2.248	0.012
g_Variibacter (10)	2.203	0.020
g_Bradyrhizobium (11)	2.201	0.030
g_Sulfuricurvum (9)	2.174	0.025
g_Halomonas (9)	2.136	0.000
g_norank_f_Xanthobacteraceae (5)	2.133	0.008
g_Nocardia (1)	2.095	0.000
g_Paenisporesarcina (2)	2.094	0.013
g_Leuconostoc (6)	2.088	0.002
g_norank_f_Porphyromonadaceae (11)	2.071	0.025
g_Ralstonia (2)	2.068	0.006
g_Ruminococcaceae_UCG_009	2.062	0.002
g_Geobacter (3)	2.058	0.000
g_Eubacterium (1)	2.048	0.017
g_Streptomyces (7)	2.032	0.041
g_Atopobium (1)	2.009	0.002
g_Rhodococcus (4)	2.003	0.015
g_Aquabacterium (3)	2.003	0.022

NS, non-kidney stone. OS, occasional stone. RS, recurrent stone. LDA, linear discriminant analysis. LEfSe, linear discriminant analysis Effect Size.

Table S4. Potential factors associated with the gut microbiota after propensity score match.

Factors	NS controls (n=24)	KS patients (n=24)	P value	Standardized difference
Gender (male), n (%)	16 (66.7)	14 (58.3)	0.766	0.015
Age (year), mean (standard deviation)	50.83 (8.70)	50.08 (12.86)	0.814	0.008
Fat (More-Fat), n (%)	9 (37.5)	10 (41.7)	1	0.015
Red meat (>100 G/Day), n (%)	4 (16.7)	5 (20.8)	1	0.046
Milk (>250 MI/Day), n (%)	5 (20.8)	4 (16.7)	1	0.025
Fruit (>200 G/Day), n (%)	8 (33.3)	8 (33.3)	1	<0.001
Sitting time (>4 H/Day), n (%)	13 (54.2)	11 (45.8)	0.773	0.081
Sleeping time (<6 H/Day), n (%)	20 (83.3)	21 (87.5)	1	0.073
Smoking (Yes), n (%)	11 (45.8)	11 (45.8)	1	0.038
Family history of stone (Yes), n (%)	4 (16.7)	6 (25.0)	0.722	0.047
Hypertension (Yes), n (%)	2 (8.3)	2 (8.3)	1	0.02
NAFLD (Yes), n (%)	3 (12.5)	4 (16.7)	1	0.018

Table S5. Higher bacteria genera in NS controls and kidney stone patients by LEfSe analysis after propensity score match.

Group	Pathways	LDA score	P value
NS controls	g_Blautia	4.024	0.025
	g_Eubacterium_hallii_group	3.805	0.006
	g_unclassified_f_Peptostreptococcaceae	3.466	0.017
	g_unclassified_f_Lachnospiraceae	3.176	0.047
	g_Collinsella	3.176	0.009
	g_Fusicatenibacter	3.176	0.049
	g_Adlercreutzia	3.039	0.003
	g_Dorea	2.987	0.043
	g_Ruminococcus_gauvrauuii_group	2.638	0.014
	g_Coprococcus_1	2.509	0.029
OS+RS patients	g_Moryella	2.346	0.013
	g_Howardella	2.285	0.037
	g_Lachnoclostridium	3.692	0.012
	g_Acinetobacter	3.496	0.024
	g_unclassified_p_Firmicutes	3.212	0.003
	g_Empedobacter	3.078	0.000
	g_Erysipelatoclostridium	3.040	0.029
	g_Cellulosilyticum	2.880	0.009
	g_Cetobacterium	2.740	0.039
	g_Defluviitoga	2.548	0.046
	g_Enterorhabdus	2.491	0.016
	g_Gillisia	2.458	0.011
	g_Flavonifractor	2.409	0.002
	g_Microbacterium	2.368	0.047
	g_Nocardia	2.342	0.027
	g_norank_f_Xanthobacteraceae	2.340	0.031
	g_Mycoplasma	2.339	0.024
	g_Litoricola	2.300	0.026
	g_Halomonas	2.275	0.021
	g_Peptoniphilus	2.255	0.035
	g_Eubacterium	2.230	0.045
	g_norank_f_Eubacteriaceae	2.213	0.004
	g_Brevundimonas	2.204	0.046
	g_Bosea	2.202	0.014
	g_Clostridium_sensu_stricto_18	2.190	0.027
	g_Geobacter	2.189	0.017
	g_Paracoccus	2.175	0.019
	g_Brevinema	2.159	0.012
	g_Fructobacillus	2.145	0.028

NS, non-kidney stone. OS, occasional stone. RS, recurrent stone. LDA, linear discriminant analysis. LEfSe, linear discriminant analysis Effect Size.

Table S6. Fecal SCFAs level in NS controls, OS and RS patients.

SCFAs	Concentration of SCFAs			P value
	NS controls ($\mu\text{g}/\text{mg}$)	OS patients ($\mu\text{g}/\text{mg}$)	RS patients ($\mu\text{g}/\text{mg}$)	
Acetic acid	21.4393(10.1007)	44.6567(36.9926)	55.4854(22.6412)	<0.001
Propionic acid	0.0792(0.0517)	0.0762(0.0548)	0.0876(0.0463)	>0.05
Propionic acid-2-methyl	0.0069(0.0068)	0.0055(0.0048)	0.0069(0.0059)	>0.05
Butyric acid	0.0892(0.062)	0.091(0.0498)	0.0906(0.0682)	>0.05
Butanoic acid-3-methyl	0.0061(0.0078)	0.0054(0.0051)	0.0057(0.0079)	>0.05
Pentanoic acid	0.0087(0.0133)	0.0061(0.0107)	0.0031(0.0093)	>0.05
Hexanoic acid	0.0007(0.0008)	0.0007(0.0005)	0.0005(0.0004)	0.0375

SCFAs, short chain fatty acids. NS, non-kidney stone. OS, occasional stone. RS, recurrent stone.