Appendix A. Supplementary data

Supplementary materials

Table S1. Characteristics of the study cohort.

Characters	Non-GDM (n=709)	GDM (n=128)	P value
Descrptive measurements			
Prepregnant BMI			0.223
BMI<18.5	92 (13.0%)	18 (14.1%)	
18.5≤BMI＜25	560 (79.0%)	94 (73.4%)	
BMI≥25	57 (8.0%)	16 (12.5%)	
Multipara			0.076
No	504 (71.1%)	81 (63.3%)	
Yes	205 (28.9%)	47 (36.7%)	
Maternal age			<0.001
<30	439 (61.9%)	57 (44.5%)	
≥30	270 (38.1%)	71 (55.5%)	
Educational levels			0.245
High school or lower	67 (9.4%)	7 (5.5%)	
College	544 (76.7%)	106 (82.8%)	
Master degree or above	98 (13.8%)	15 (11.7%)	
BMI at enrollment			
BMI<18.5	58 (8.2%)	9 (7.0%)	
18.5≤BMI＜25	570 (80.4%)	100 (78.1%)	
BMI≥25	81 (11.4%)	19 (14.8%)	
SBP (mmHg)	108.27 (11.92)	109.35 (12.68)	0.349
DBP (mmHg)	65.62 (8.19)	67.59 (8.32)	0.371
Biochemistry			
OGTT0 (mmol/L)	4.20 (0.30)	4.48 (0.38)	<0.001
OGTT1 (mmol/L)	7.27 (1.27)	9.21 (1.27)	<0.001
OGTT2 (mmol/L)	6.30 (0.99)	8.20 (1.23)	<0.001
GLU (mmol/L)	4.29 (0.29)	4.52 (0.31)	<0.001
HbAlc (%)	4.92 (0.21)	5.05 (0.26)	<0.001
BUN (mmol/L)	2.75 (0.62)	2.74 (0.75)	0.828
CREA (μmol/L)	37.36 (5.70)	36.70 (5.41)	0.224
UA (μmol/L)	240.28 (44.62)	244.93 (47.71)	0.283
TP (g/L)	65.44 (3.15)	65.66 (3.48)	0.472
ALB (g/L)	38.63 (2.06)	38.50 (2.23)	0.503
CHOL (mmol/L)	5.81 (0.89)	5.76 (1.04)	0.604
TG (mmol/L)	2.16 (0.72)	2.38 (0.88)	0.009
ALT (U/L)	17.97 (11.94)	16.15 (11.10)	0.111
AST (U/L)	18.31 (6.44)	17.27 (6.21)	0.090
ALP (U/L)	46.51 (10.09)	46.89 (9.77)	0.691
LDH (U/L)	165.67 (26.97)	169.84 (38.74)	0.245
GGT (U/L)	15.65 (8.24)	15.49 (7.67)	0.840

TBIL (μmol/L)	7.58 (2.16)	7.85 (2.55)	0.274
DBIL (μmol/L)	2.17 (0.74)	2.28 (0.77)	0.143
TBA (μmol/L)	1.61 (1.18)	1.64 (1.20)	0.817
FMN (mmol/L)	1.81 (0.33)	1.82 (0.30)	0.724

Data presented are mean ± SD or n (%). The t-test and $\chi 2$ test were between the non-GDM group and GDM group.

BMI: body mass index; SBP: systolic blood pressure; DBP: diastolic blood pressure; OGTT: Oral Glucose Tolerance Test; HbA1: hemoglobin A1; BUN: blood urea nitrogen; CREA: creatinine; UA: uric acid; TP: total protein; ALB: albumin; CHOL: cholesterol; TG: triglyceride; ALT: alanine transaminase; AST: aspartate transaminase; ALP: alkaline phosphatase; LDH: lactic acid dehydrogenase; GGT: gamma-glutamyl transferase; TBIL: total bilirubin; DBIL: direct bilirubin; TBA: total bile acids; FMN: fructosamine.

Table S2. Serum trace element distribution of the study cohort.

Elements (μg/L)	LOD	>LOD (%)	Mean	GM	Percentile					Reference
					2.5	25	50	75	97.5	(2.5-97.5%)
Ag	0.01	100	0.22	0.15	0.04	0.09	0.13	0.19	1.19	—
As	0.14	99	0.83	0.62	0.20	0.41	0.61	0.91	2.53	0.3-6.4
Ba	6.48	5.7	5.13	4.83	4.58	4.58	4.58	4.58	11.61	—
Cd	0.09	11.1	0.07	0.07	0.06	0.06	0.06	0.06	0.17	0.07-0.46
Co	0.04	100	1.71	1.68	1.22	1.49	1.66	1.87	2.45	0.05-1.04
Cs	0.04	100	1.04	0.99	0.60	0.81	0.99	1.17	1.99	—
Cu	2.92	100	1700.82	1676.27	1151.94	1500.05	1668.64	1875.30	2310.30	1226-3435
Fe	59.92	100	1882.28	1731.34	895.53	1321.13	1623.33	2227.79	4098.67	592-2613
Hg	0.05	99.8	0.86	0.44	0.13	0.27	0.37	0.58	4.82	—
La	0.07	10.2	0.06	0.05	0.05	0.05	0.05	0.05	0.18	—
Mn	1.41	42.3	3.05	1.72	1.00	1.00	1.00	2.35	18.44	1.1-8.4
Mo	0.1	100	2.89	1.57	0.82	1.17	1.50	1.94	3.66	1.2-3.5
Nd	0.05	13.6	0.05	0.04	0.04	0.04	0.04	0.04	0.19	—
Ni	2.11	44.9	3.29	2.47	1.50	1.50	1.50	4.09	12.08	—
Pr	0.02	11.8	0.02	0.01	0.01	0.01	0.01	0.01	0.06	—
Rb	0.16	100	530.19	513.46	325.31	431.26	509.57	605.93	863.80	145-620
Sb	0.1	100	21.72	21.53	16.96	19.87	21.38	23.25	28.05	—
Sr	1.8	100	30.78	29.40	17.71	24.46	29.06	34.35	53.41	22.5-92.5
Tl	0.01	100	0.06	0.05	0.03	0.04	0.05	0.06	0.11	—
U	0.0109	28.4	0.01	0.01	0.01	0.01	0.01	0.01	0.06	—
V	0.15	79.7	1.78	1.07	0.10	0.44	1.96	2.46	3.96	0.23-2.56
Zn	87.97	100	651.39	614.19	402.43	514.33	595.18	699.74	1046.95	534-1026

GM: geometric mean. Reference values come from the dataset of serum trace element exposure levels of pregnant Chinese women at second trimester in China Nutrition and Health Survey 2010–2012.

Table S3. Association between single serum trace elements concentration and GDM related outcomes.

Elements (μg/L)	GDM		IGT		OGTT 0h		OGTT 1h		OGTT 2h	
	OR (95% CI)	P value	OR (95% CI)	P value	β (95% CI)	P value	β (95% CI)	P value	β (95% CI)	P value
Cu	2.05 (0.66, 6.44)	0.216	1.10 (0.37, 3.28)	0.865	0.13 (-0.003, 0.26)	0.055	0.20 (-0.37, 0.78)	0.483	0.40 (-0.09, 0.88)	0.110
Zn	0.79 (0.37, 1.58)	0.533	1.29 (0.67, 2.38)	0.426	-0.04 (-0.12, 0.04)	0.328	0.14 (-0.21, 0.48)	0.446	0.002 (-0.29, 0.30)	0.989
As	1.03 (0.77, 1.38)	0.839	1.27 (0.96, 1.67)	0.092	-0.03 (-0.06, 0.01)	0.090	-0.08 (-0.23, 0.07)	0.290	0.08 (-0.04, 0.21)	0.208
Mo	1.00 (0.67, 1.40)	0.995	0.99 (0.67, 1.361)	0.937	-0.004 (-0.05, 0.04)	0.846	0.02 (-0.17, 0.20)	0.843	-0.02 (-0.17, 0.14)	0.842
Hg	0.99 (0.79, 1.22)	0.911	1.15 (0.94, 1.40)	0.163	-0.002 (-0.03, 0.02)	0.884	0.07 (-0.00, 0.18)	0.215	0.06 (-0.03, 0.15)	0.216
Tl	1.13 (0.63, 1.96)	0.676	0.85 (0.47, 1.49)	0.577	-0.01 (-0.08, 0.05)	0.691	-0.004 (-0.33, 0.25)	0.788	-0.01 (-0.26, 0.24)	0.933
Fe	1.12 (0.69, 1.80)	0.651	0.96 (0.60, 1.54)	0.880	-0.002 (-0.06, 0.06)	0.994	0.14 (-0.11, 0.39)	0.265	0.02 (-0.19, 0.23)	0.873
Sr	0.73 (0.36, 1.45)	0.380	1.01 (0.51, 1.94)	0.973	-0.03 (-0.11, 0.05)	0.423	-0.30 (-0.64, 0.05)	0.092	-0.28 (-0.57, 0.01)	0.059
Ag	0.91 (0.71, 1.17)	0.484	1.07 (0.85, 1.35)	0.548	0.03 (0.002, 0.06)	0.038	0.05 (-0.08, 0.18)	0.416	0.08 (-0.03, 0.19)	0.167
Sb	0.84 (0.19, 3.58)	0.819	1.22 (0.29, 4.97)	0.787	0.04 (-0.13, 0.21)	0.620	-0.05 (-0.81, 0.70)	0.889	0.12 (-0.52, 0.76)	0.719
V	0.92 (0.80, 1.06)	0.256	0.91 (0.79, 1.04)	0.151	-0.001 (-0.02, 0.02)	0.947	-0.09 (-0.17, -0.02)	0.014	-0.05 (-0.11, 0.01)	0.125
Co	0.59 (0.20, 1.68)	0.329	0.64 (0.22, 1.78)	0.403	-0.03 (-0.15, 0.09)	0.628	-0.65 (-1.19, -0.12)	0.017	-0.28 (-0.73, 0.18)	0.232
Rb	1.16 (0.54, 2.47)	0.693	1.06 (0.50, 2.20)	0.880	-0.08 (-0.16, 0.01)	0.090	0.21 (-0.18, 0.60)	0.285	0.16 (-0.17, 0.50)	0.328
Cs	1.07 (0.56, 1.99)	0.843	1.29 (0.69, 2.36)	0.417	-0.09 (-0.17, -0.02)	0.017	0.24 (-0.09, 0.57)	0.150	0.20 (-0.08, 0.48)	0.167

OR: odds ratio; CI: confidence interval. Models were adjusted for maternal age, parity, pre-pregnant BMI and educational levels.

Table S4. Association between alpha diversity indexes and GDM related outcomes.

Diversity indices	GDM	
	OR (95% CI)	P value
Shannon	0.78 (0.62, 0.99)	0.037
Simpson	0.87 (0.74, 1.03)	0.105
Observed OTUs	0.74 (0.58, 0.93)	0.013
	IGT	
	OR (95% CI)	P value
Shannon	0.73 (0.58, 0.92)	0.008
Simpson	0.81 (0.69, 0.96)	0.014
Observed OTUs	0.76 (0.60 0.94)	0.015
	OGTT 0h	
	β (95% CI)	P value
Shannon	-0.03 (-0.05, 0.001)	0.059
Simpson	-0.01 (-0.03, 0.01)	0.301
Observed OTUs	-0.02 (-0.04, 0.004)	0.112
	OGTT 1h	
	β (95% CI)	P value
Shannon	-0.06 (-0.18, 0.06)	0.326
Simpson	-0.06 (-0.15, 0.04)	0.245
Observed OTUs	-0.06 (-0.16, 0.05)	0.266
	OGTT 2h	
	β (95% CI)	P value
Shannon	-0.13 (-0.24, -0.03)	0.012
Simpson	-0.11 (-0.19, -0.02)	0.011
Observed OTUs	-0.11 (-0.20, -0.03)	0.012

OR: odds ratio; CI: confidence interval. Models were adjusted for maternal age, parity, pre-pregnant BMI and educational levels.

Table S5. Composition of co-abundance groups (CAGs).

CAGs	Taxa
CAG1	D_0__Bacteria;D_1__Bacteroidetes;D_2__Bacteroidia;D_3__Bacteroidales;D_4__Bacteroidaceae;D_5__Bacteroides
CAG1	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Lachnospiraceae;D_5__[Eubacterium] ventriosum group
CAG1	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Lachnospiraceae;D_5__Lachnospiraceae UCG-010
CAG1	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Lachnospiraceae;Other
CAG1	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Ruminococcaceae;D_5__CAG-352
CAG1	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Ruminococcaceae;D_5__Faecalibacterium
CAG1	D_0__Bacteria;D_1__Firmicutes;D_2__Negativicutes;D_3__Selenomonadales;D_4__Acidaminococcaceae;D_5__Phascolarctobacterium
CAG1	D_0__Bacteria;D_1__Proteobacteria;D_2__Deltaproteobacteria;D_3__Desulfovibrionales;D_4__Desulfovibrionaceae;D_5__Bilophila
CAG2	D_0__Bacteria;D_1__Actinobacteria;D_2__Coriobacteriia;D_3__Coriobacteriales;D_4__Coriobacteriaceae;D_5__Collinsella
CAG2	D_0__Bacteria;D_1__Actinobacteria;D_2__Coriobacteriia;D_3__Coriobacteriales;D_4__Eggerthellaceae;D_5__Adlercreutzia
CAG2	D_0__Bacteria;D_1__Actinobacteria;D_2__Coriobacteriia;D_3__Coriobacteriales;D_4__Eggerthellaceae;Other
CAG2	D_0__Bacteria;D_1__Actinobacteria;D_2__Coriobacteriia;D_3__Coriobacteriales;Other;Other
CAG2	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Clostridiaceae 1;D_5__Clostridium sensu stricto 1
CAG2	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Clostridiaceae 1;Other
CAG2	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Ruminococcaceae;D_5__Ruminiclostridium 5
CAG2	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Ruminococcaceae;D_5__Ruminococcaceae UCG-004
CAG2	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Ruminococcaceae;D_5__Ruminococcus 2
CAG2	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Ruminococcaceae;D_5__Subdoligranulum
CAG3	D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Bifidobacteriales;D_4__Bifidobacteriaceae;D_5__Bifidobacterium
CAG3	D_0__Bacteria;D_1__Firmicutes;D_2__Bacilli;D_3__Lactobacillales;D_4__Enterococcaceae;D_5__Enterococcus
CAG3	D_0__Bacteria;D_1__Firmicutes;D_2__Bacilli;D_3__Lactobacillales;D_4__Lactobacillaceae;D_5__Lactobacillus
CAG3	D_0__Bacteria;D_1__Firmicutes;D_2__Bacilli;D_3__Lactobacillales;D_4__Leuconostocaceae;D_5__Weissella
CAG3	D_0__Bacteria;D_1__Firmicutes;D_2__Bacilli;D_3__Lactobacillales;D_4__Streptococcaceae;D_5__Lactococcus
CAG3	D_0__Bacteria;D_1__Firmicutes;D_2__Bacilli;D_3__Lactobacillales;D_4__Streptococcaceae;D_5__Streptococcus
CAG3	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Lachnospiraceae;D_5__[Eubacterium] hallii group
CAG3	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Lachnospiraceae;D_5__Blautia
CAG3	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Peptostreptococcaceae;Other
CAG3	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Ruminococcaceae;D_5__Ruminococcaceae UCG-013
CAG3	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Ruminococcaceae;D_5__UBA1819
CAG3	D_0__Bacteria;D_1__Firmicutes;D_2__Erysipelotrichia;D_3__Erysipelotrichales;D_4__Erysipelotrichaceae;D_5__Erysipelotrichaceae UCG-003

CAG3	D_0__Bacteria;D_1__Firmicutes;D_2__Erysipelotrichia;D_3__Erysipelotrichales;D_4__Erysipelotrichaceae;D_5__Turicibacter
CAG4	D_0__Bacteria;D_1__Actinobacteria;D_2__Coriobacteriia;D_3__Coriobacteriales;D_4__Eggerthellaceae;D_5__Eggerthella
CAG4	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Lachnospiraceae;D_5__Lachnoclostridium
CAG4	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Lachnospiraceae;D_5__Lachnospira
CAG4	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Lachnospiraceae;D_5__Tyzzerella 3
CAG4	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Ruminococcaceae;D_5__Butyricicoccus
CAG4	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Ruminococcaceae;D_5__Flavonifractor
CAG4	D_0__Bacteria;D_1__Firmicutes;D_2__Negativicutes;D_3__Selenomonadales;D_4__Veillonellaceae;D_5__Megasphaera
CAG4	D_0__Bacteria;D_1__Firmicutes;D_2__Negativicutes;D_3__Selenomonadales;D_4__Veillonellaceae;D_5__Veillonella
CAG4	D_0__Bacteria;D_1__Fusobacteria;D_2__Fusobacteriia;D_3__Fusobacteriales;D_4__Fusobacteriaceae;D_5__Fusobacterium
CAG4	D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Betaproteobacteriales;D_4__Burkholderiaceae;D_5__Parasutterella
CAG4	D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Enterobacteriales;D_4__Enterobacteriaceae;D_5__Enterobacter
CAG4	D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Enterobacteriales;D_4__Enterobacteriaceae;D_5__Escherichia-Shigella
CAG4	D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Enterobacteriales;D_4__Enterobacteriaceae;D_5__Klebsiella
CAG4	D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Enterobacteriales;D_4__Enterobacteriaceae;Other
CAG4	D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Pasteurellales;D_4__Pasteurellaceae;D_5__Haemophilus
CAG4	D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;Other;Other;Other
CAG5	D_0__Bacteria;D_1__Actinobacteria;D_2__Coriobacteriia;D_3__Coriobacteriales;D_4__Eggerthellaceae;D_5__Senegalimassilia
CAG5	D_0__Bacteria;D_1__Bacteroidetes;D_2__Bacteroidia;D_3__Bacteroidales;D_4__Muribaculaceae;D_5__metagenome
CAG5	D_0__Bacteria;D_1__Bacteroidetes;D_2__Bacteroidia;D_3__Bacteroidales;D_4__Prevotellaceae;D_5__Alloprevotella
CAG5	D_0__Bacteria;D_1__Bacteroidetes;D_2__Bacteroidia;D_3__Bacteroidales;D_4__Prevotellaceae;D_5__Prevotella 2
CAG5	D_0__Bacteria;D_1__Bacteroidetes;D_2__Bacteroidia;D_3__Bacteroidales;D_4__Prevotellaceae;D_5__Prevotella 7
CAG5	D_0__Bacteria;D_1__Bacteroidetes;D_2__Bacteroidia;D_3__Bacteroidales;D_4__Prevotellaceae;D_5__Prevotella 9
CAG5	D_0__Bacteria;D_1__Bacteroidetes;D_2__Bacteroidia;D_3__Bacteroidales;D_4__Prevotellaceae;D_5__Prevotellaceae NK3B31 group
CAG5	D_0__Bacteria;D_1__Bacteroidetes;D_2__Bacteroidia;D_3__Bacteroidales;D_4__Prevotellaceae;Other
CAG5	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Lachnospiraceae;D_5__[Eubacterium] ruminantium group
CAG5	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Lachnospiraceae;D_5__Coprococcus 2
CAG5	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Lachnospiraceae;D_5__Pseudobutyrivibrio
CAG5	D_0__Bacteria;D_1__Firmicutes;D_2__Erysipelotrichia;D_3__Erysipelotrichales;D_4__Erysipelotrichaceae;D_5__Catenibacterium
CAG5	D_0__Bacteria;D_1__Firmicutes;D_2__Erysipelotrichia;D_3__Erysipelotrichales;D_4__Erysipelotrichaceae;D_5__Holdemanella
CAG5	D_0__Bacteria;D_1__Firmicutes;D_2__Negativicutes;D_3__Selenomonadales;D_4__Veillonellaceae;D_5__Allisonella
CAG5	D_0__Bacteria;D_1__Firmicutes;D_2__Negativicutes;D_3__Selenomonadales;D_4__Veillonellaceae;D_5__Dialister
CAG5	D_0__Bacteria;D_1__Firmicutes;D_2__Negativicutes;D_3__Selenomonadales;D_4__Veillonellaceae;D_5__Megamonas

CAG5	D_0__Bacteria;D_1__Firmicutes;D_2__Negativicutes;D_3__Selenomonadales;D_4__Veillonellaceae;D_5__Mitsuokella
CAG6	D_0__Bacteria;D_1__Actinobacteria;D_2__Coriobacteriia;D_3__Coriobacteriales;D_4__Coriobacteriales Incertae Sedis;D_5__uncultured
CAG6	D_0__Bacteria;D_1__Bacteroidetes;D_2__Bacteroidia;D_3__Bacteroidales;D_4__Barnesiellaceae;D_5__Barnesiella
CAG6	D_0__Bacteria;D_1__Bacteroidetes;D_2__Bacteroidia;D_3__Bacteroidales;D_4__Marinifilaceae;D_5__Butyricimonas
CAG6	D_0__Bacteria;D_1__Bacteroidetes;D_2__Bacteroidia;D_3__Bacteroidales;D_4__Marinifilaceae;D_5__Odoribacter
CAG6	D_0__Bacteria;D_1__Bacteroidetes;D_2__Bacteroidia;D_3__Bacteroidales;D_4__Muribaculaceae;D_5__uncultured bacterium
CAG6	D_0__Bacteria;D_1__Bacteroidetes;D_2__Bacteroidia;D_3__Bacteroidales;D_4__Muribaculaceae;Other
CAG6	D_0__Bacteria;D_1__Bacteroidetes;D_2__Bacteroidia;D_3__Bacteroidales;D_4__Prevotellaceae;D_5__Paraprevotella
CAG6	D_0__Bacteria;D_1__Bacteroidetes;D_2__Bacteroidia;D_3__Bacteroidales;D_4__Rikenellaceae;D_5__Alistipes
CAG6	D_0__Bacteria;D_1__Bacteroidetes;D_2__Bacteroidia;D_3__Bacteroidales;D_4__Tannerellaceae;D_5__Parabacteroides
CAG6	D_0__Bacteria;D_1__Bacteroidetes;D_2__Bacteroidia;D_3__Bacteroidales;Other;Other
CAG6	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Christensenellaceae;D_5__Christensenellaceae R-7 group
CAG6	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Ruminococcaceae;D_5__[Eubacterium] coprostanoligenes group
CAG6	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Ruminococcaceae;D_5__Negativibacillus
CAG6	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Ruminococcaceae;D_5__Ruminiclostridium 6
CAG6	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Ruminococcaceae;D_5__Ruminococcaceae NK4A214 group
CAG6	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Ruminococcaceae;D_5__Ruminococcaceae UCG-002
CAG6	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Ruminococcaceae;D_5__Ruminococcaceae UCG-005
CAG6	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Ruminococcaceae;D_5__Ruminococcaceae UCG-010
CAG6	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Ruminococcaceae;D_5__Ruminococcaceae UCG-014
CAG6	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Ruminococcaceae;D_5__Ruminococcus 1
CAG6	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Ruminococcaceae;D_5__uncultured
CAG6	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Ruminococcaceae;Other
CAG6	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;Other;Other
CAG6	D_0__Bacteria;D_1__Proteobacteria;D_2__Deltaproteobacteria;D_3__Desulfovibrionales;D_4__Desulfovibrionaceae;D_5__Desulfovibrio
CAG6	D_0__Bacteria;D_1__Tenericutes;D_2__Mollicutes;D_3__Mollicutes RF39;Other;Other
CAG6	D_0__Bacteria;D_1__Verrucomicrobia;D_2__Verrucomicrobiae;D_3__Verrucomicrobiales;D_4__Akkermansiaceae;D_5__Akkermansia
CAG6	D_0__Bacteria;Other;Other;Other;Other;Other
CAG7	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Lachnospiraceae;D_5__[Ruminococcus] torques group
CAG7	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Lachnospiraceae;D_5__Agathobacter
CAG7	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Lachnospiraceae;D_5__Anaerostipes
CAG7	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Lachnospiraceae;D_5__Dorea
CAG7	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Lachnospiraceae;D_5__Fusicatenibacter

CAG7	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Lachnospiraceae;D_5__Lachnospiraceae NK4A136 group
CAG7	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Lachnospiraceae;D_5__Roseburia
CAG7	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Peptostreptococcaceae;D_5__Romboutsia
CAG7	D_0__Bacteria;D_1__Firmicutes;Other;Other;Other;Other

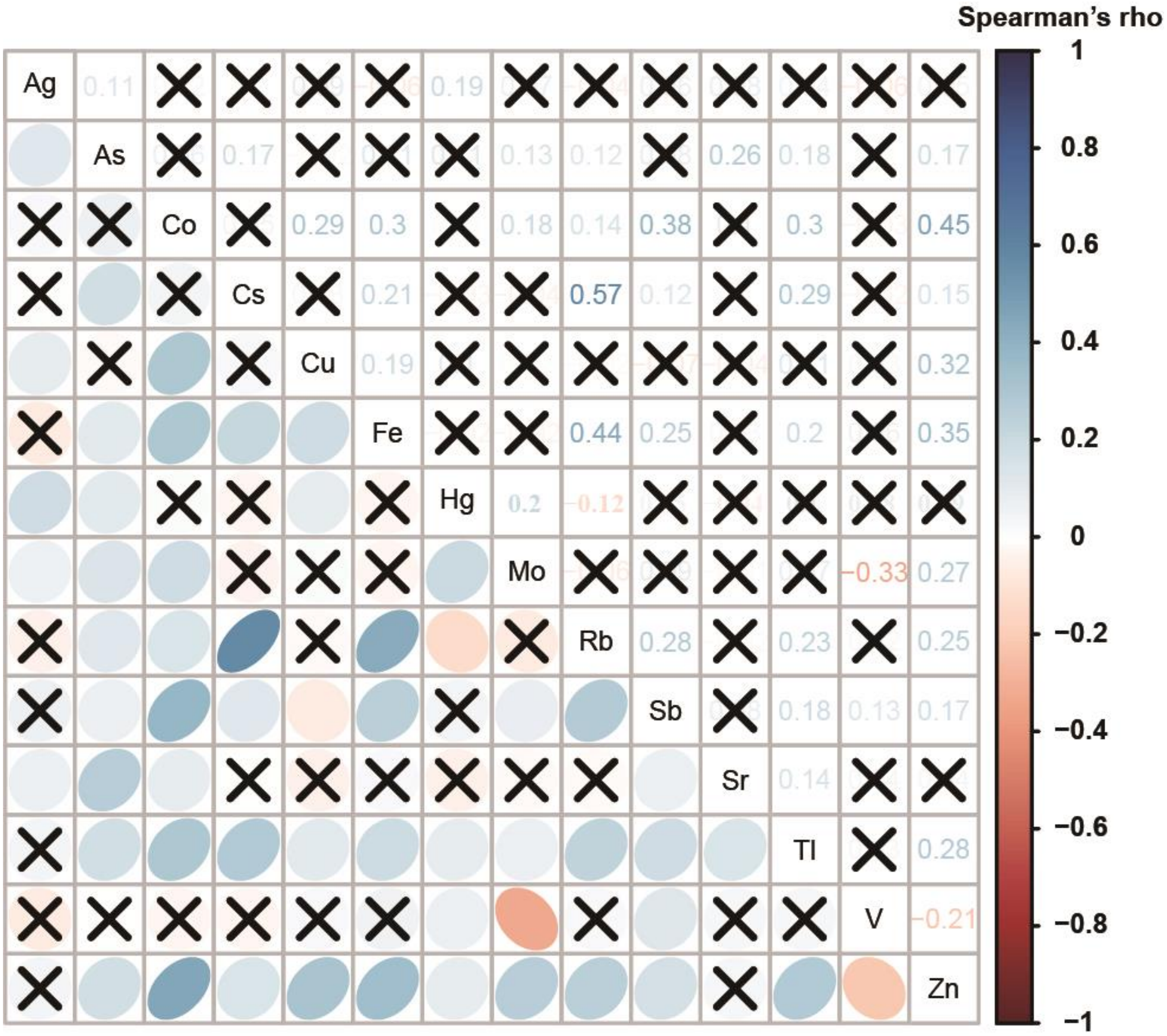

Fig. S1 Pairwise Spearman correlations among trace elements. Positive and negative correlations are indicated in blue and red, respectively (P value <0.05). Crosses indicate that the correlation was not statistically significant (P value ≥0.05).

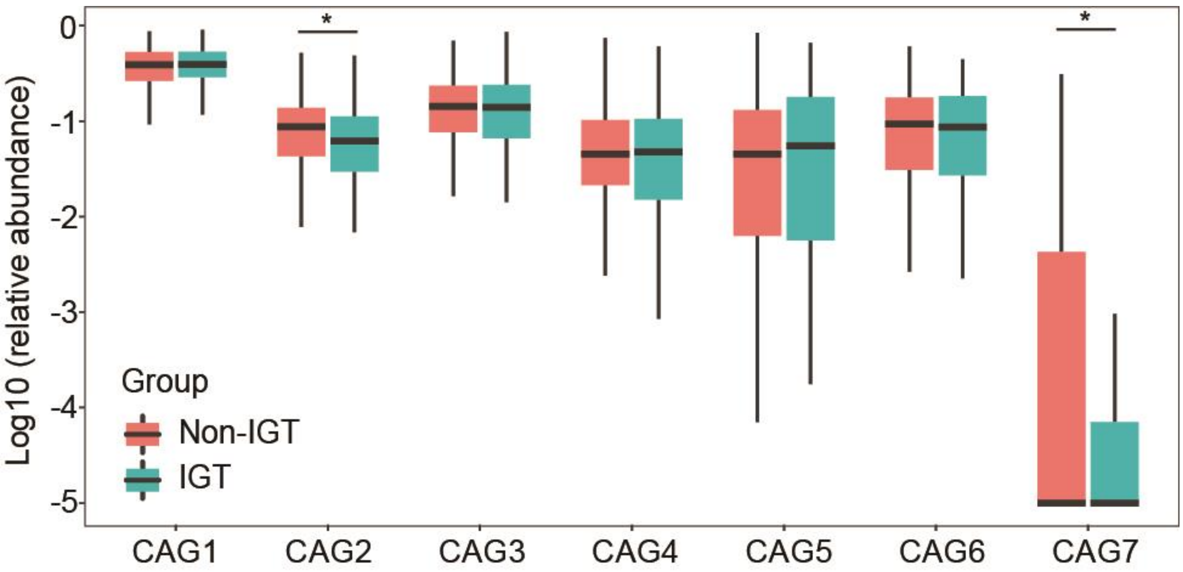

Fig. S2 Gut microbiota structure was associated with IGT and blood glucose levels. CAGs abundance in Non-IGT and IGT groups. Significance between groups was tested using Mann-Whitney U test. * indicates P-value <0.05.