Table S1. Characteristics of clinical samples and data.

Characteristics	Health (*n*=33)	Diabetes (*n*=53)	Stones (*n*=31)	Diastone (*n*=32)	Significant
Age	51.0±4.5	61.6±9.7	60.1±11.0	59.5±7.8	Nonsence[1]
Male	17 (51.5)	29 (54.7)	8 (25.8)	14 (43.8)	-
Total OTUs/group	2232	2246	1971	2009	-
ALT (U/L)	-	16.00±10.86	17.00±13.48	29.13±16.77	Sense[2a]
AST (U/L)	-	17.150±6.529	22.580±11.210	22.190±9.299	Sense[2b]
Blood glucose (mmol/L)	-	9.714±3.242	5.666±2.223	10.45±3.163	Sense[2c]
Total cholesterol (mmol/L)	-	4.257±1.079	4.643±0.754	4.802±1.009	Nonsence[2]
Triglyceride (mmol/L)	-	1.769±1.276	1.297±0.495	2.717±2.449	Sense[2d]
Total bile acids (umol/l)	-	-	3.244±1.899	5.641±2.625	Sense[2]

Data are presented as *n*, *n* (%) or mean ± standard deviation
1: AMOVA，2: Kruskal-Wallis nonparametric test. **P* <0.05 †*P* <0.01.
a: Diastone *vs.* Diabetes †
b: Diastone *vs.* Diabetes †, Stones *vs.* Diabetes *
c: Diastone *vs.* Stones †, Stones *vs.* Diabetes †
d: Diastone *vs.* Diabetes *, Diastone *vs.* Stones †

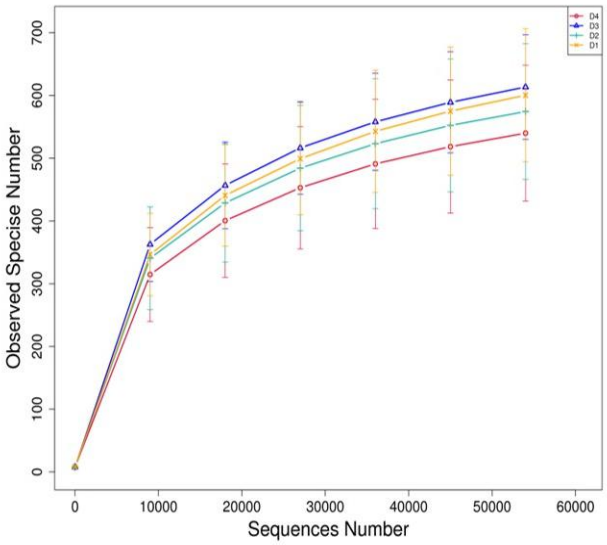
Table S2. Associations between clinical characteristics and gut microbiota.

Characteristics	Gut microbiota	Spearman's rho	p-Value
Blood glucose	*Fusobacteria*	–0.371†	<0.0001
	Tenericutes	0.272†	0.0060
	Oxyphotobacteria	0.344†	<0.0001
	Bacteroides	–0.271†	0.0060
	Faecalibacterium	–0.276†	0.0050
	Roseburia	–0.300†	0.0020
Total cholesterol	*Proteobacteria*	–0.209*	0.0400
	Actinobacteria	–0.200*	0.0500
	Megamonas	–0.231*	0.0230
	Unidentified Enterobacteriaceae	–0.296†	0.0030
Triglyceride	*Faecalibacterium*	–0.236*	0.0200
Total bile acid	*Tenericutes*	0.353*	0.0350

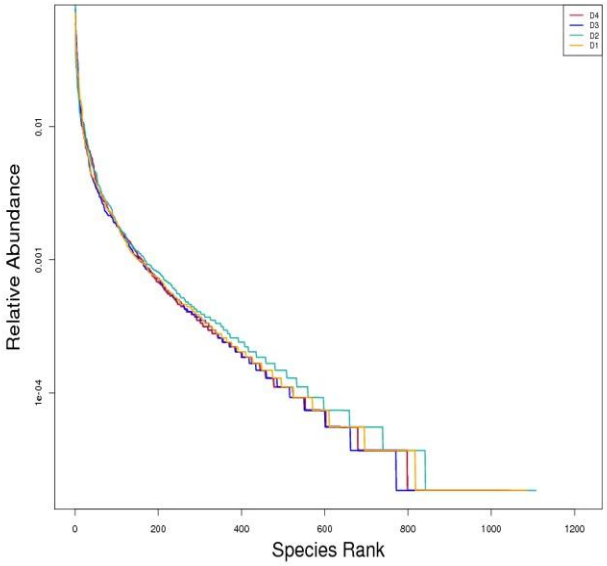
The top 10 phylum and genera were analyzed, the results with statistically significant were shown in the table.

*P <0.05 †P <0.01.

A


D4
D3
D2
D1
Observed Specise Number
0
100
200
300
400
500
600
700
0
10000
20000
30000
40000
50000
60000
Sequences Number

B


D4
D3
D2
D1
Relative Abundance
0.01
0.001
1e-04
0
200
400
600
800
1000
1200
Species Rank

C

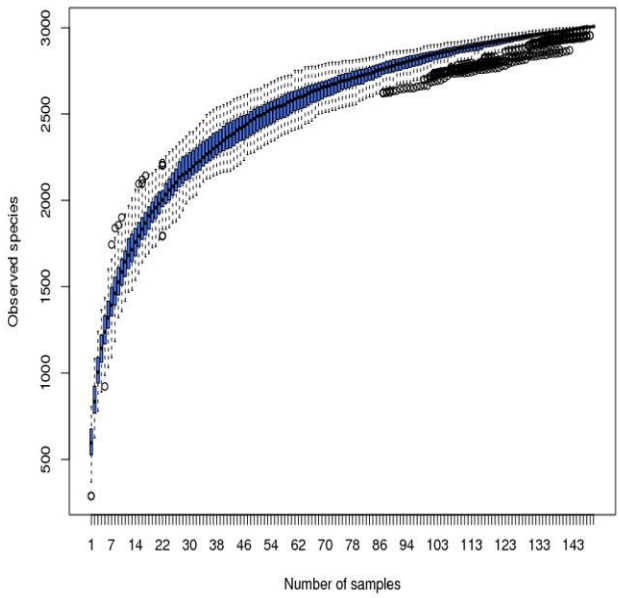

Observed species
500
1000
1500
2000
2500
3000
1 7 14 22 30 38 46 54 62 70 78 86 94 103 113 123 133 143
Number of samples

Figure S1. Quality analysis of sequencing data. A: Rarefaction curve was drawn to evaluate whether the sequencing depth of each sample was enough to reflect the microbial diversity, which directly reflects the rationality of the amount of sequencing data, and indirectly reflects the species richness of sample. When the curve tended to be flat, the sequencing depth was gradually reasonable. More data will only produce a small number of new species (OTUs). B: Rank abundance curve visually reflects the species richness and evenness of sample. In horizontal direction, the curve width reflects the species richness. In vertical direction, the curve smoothness reflects the species evenness. The flatter the curve, the more even of the species distribution. C: Species accumulation curve was drawn to evaluate whether the sample size was enough. The abscissa is sample size， the ordinate is number of OTUs after sampling. In a certain range, many species can be found in the community if the location of box plot shows a sharp rise along with the increase of sample size. When the location of box plot flattening out, the species will not significantly increase along with an increasing sample size.
D1: Healthy group; D2: Diabetes group; D3: Stones group; D4: Diastone group.

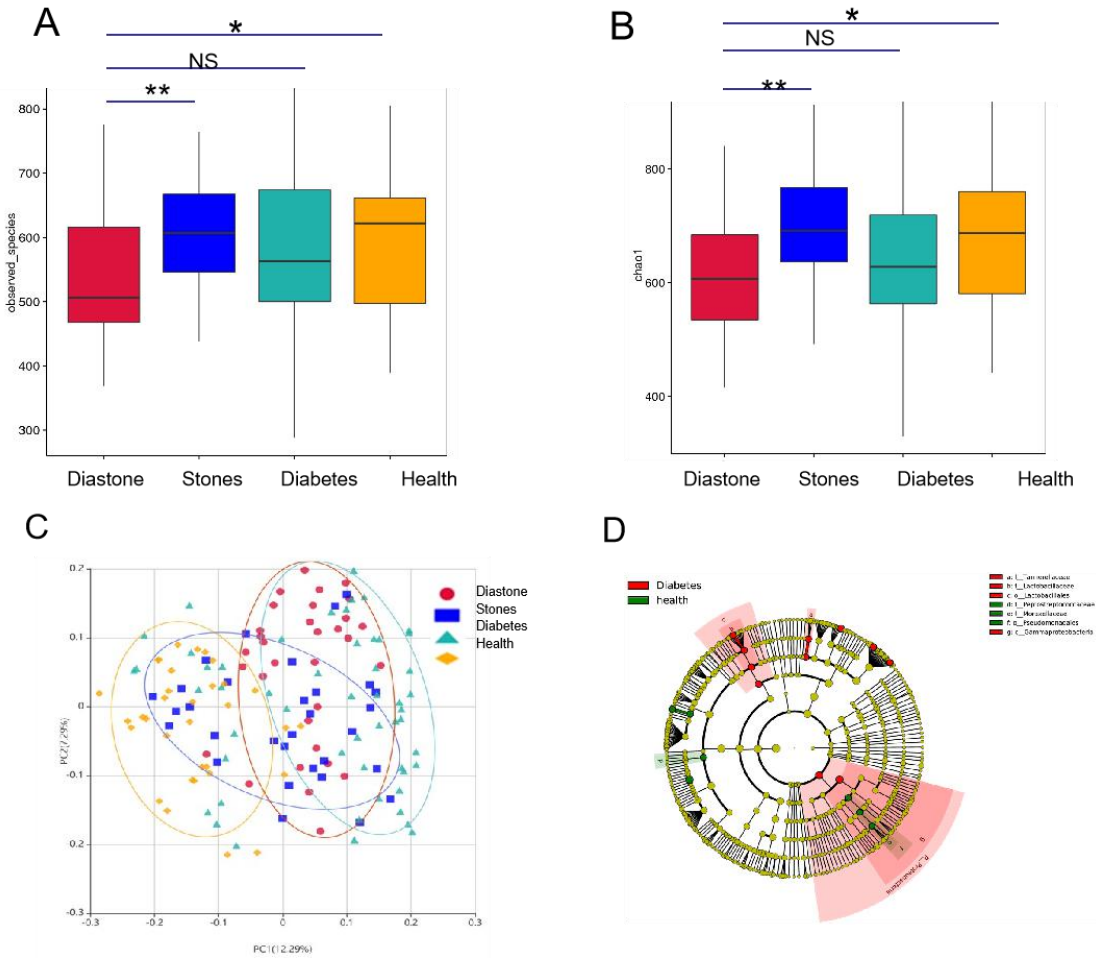


Figure S2 The gut microbial characteristics among 4 groups.
A. The observed species among 4 groups.

B. B. The chao indexes among 4 groups.
C. PcoA analysis in 4 groups.
D. LEfSe analysis between Health group and Diabetes group.
(Wilcoxon rank-sum test, *P <0.05, †P <0.01; NS: Nonsense, LDA score:3.5)

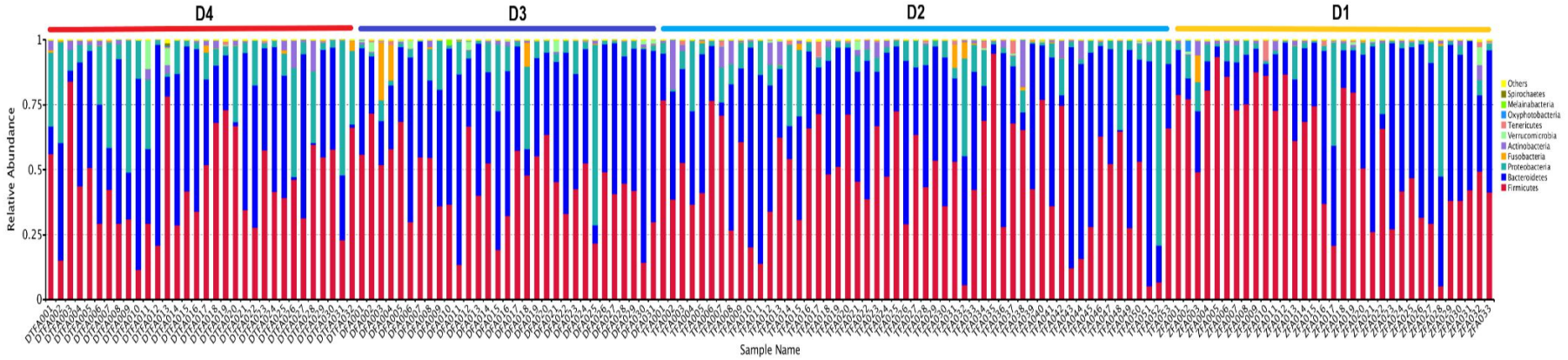

D4
D3
D2
D1
Relative Abundance
1
0.75
0.5
0.25
0
Sample Name
Others
Spirochaetes
Melainabacteria
Oxyphotobacteria
Tenericutes
Verrucomicrobia
Actinobacteria
Fusobacteria
Proteobacteria
Bacteroidetes
Firmicutes

Figure S3. Relative abundance of species at the phylum level. The top 10 species with the highest abundance at phylum level were selected. A column-like cumulative graph of the relative abundance of species was generated to visually view the relative abundance of species and their proportions for all samples.
D1: Healthy group, ZFA001-033; D2: Diabetes group, TFA001-053; D3: Stones group, DFA001-031; D4: Diastone group, DTFA001-032.