Supplementary Table 1 | Richness and diversity estimators in the NC, HG, HF, and M cohorts[a].

Parameter	NC	HG	HF	M
Number of tags	132523±2979[†‡]	129279±3709[§]	104564±1046[†§]	117713±5745[‡]
Number of OTUs	2309	1578	1043	1454
Chao1	915.79[*,†,‡]	536.99[*,§]	337.69[†,§]	464.75[‡]
Shannon index	5.8395[†]	5.2318	4.967[†]	5.214
Simpson index	0.9416	0.9298	0.9259	0.9304
PD_whole tree	49.117[*,†,‡]	27.182[*,§]	22.313[†,§]	26.96[‡]
Observed_species	667.72[*,†,‡]	395.66[*,§]	281.31[†,§]	354.3[‡]

[a]HG, gestational diabetes mellitus; HF, hyperlipidemia; M, gestational diabetes mellitus plus hyperlipidemia; OTU, operational taxonomic units.

[b]The operational taxonomic units (OTUs) were defined based on a similarity threshold of 97%; Independent t-test was used to test for significant differences (p < 0.05) in each variable between the four cohorts. [*], [†], [‡] and [§] indicate significant differences between the NC and HG cohorts, between the NC and HF cohorts, between the NC and M cohorts, and between HG and HF cohorts, respectively. The parameters were calculated using QIIME software.

Supplementary Table 2 | Phylum-level relative abundance of bacteria in fecal samples of NC, HG, HF and M cohorts.

	mean_NC	mean_HG	mean_HF	mean_M	Kruskal.test
Actinobacteria	0.035322	0.021067	0.050202	0.03071	0.004082
Verrucomicrobia	0.000479	0.008284	0.007298	0.004111	0.001986

Significant differences were calculated using the Kruskal test by R. A significant difference between the groups was considered at $P < 0.05$.

Supplementary Table 3 | Genus-level relative abundance of bacteria in fecal samples of NC, HG, HF and M cohorts.

	mean_NC	mean_HG	mean_HF	mean_M	Kruskal.test
Streptococcus	0.002419	0.001865	0.003089	0.009571	0.000576
Faecalibacterium	0.136772	0.067333	0.089484	0.069898	0.009032
Veillonella	0.001268	0.000564	0.001833	0.008154	0.000439
Prevotella	7.71E-05	0.0029	0.001412	0.003131	0.001562
Haemophilus	0.000269	0.000496	0.000778	0.005828	0.000394
Actinomyces	6.82E-05	0.000233	0.000327	0.003236	1.36E-05
Akkermansia	0.000277	0.008265	0.006419	0.003619	0.000635

Significant differences were calculated using the Kruskal test by R. A significant difference between the groups was considered at $P < 0.05$.

Supplemetary Table 4 | Gut microbiota abundance (phylum) and their correlation with clinical characteristics and biochemical variables in in the NC, HG, HF, and M cohorts.

	FPG	2hPG	TG	TC	HDL	LDL
Firmicutes	0.1051	-0.0513	-0.04651	-0.1084	0.07876	-0.1710
Proteobacteria	-0.0690	-0.1561	0.03583	0.3408*	-0.2561	0.3734*
Bacteroidetes	-0.0320	0.1740	0.0006	-0.01731	0.001429	0.0558
Actinobacteria	-0.2277	-0.3155*	0.1114	0.0734	-0.1221	0.02204
Verrucomicrobia	-0.0466	-0.05321	-0.03252	0.1199	0.1352	0.08451
Tenericutes	-0.0234	-0.03199	0.1671	0.1990	-0.03193	0.2782

Data are Spearman correlation coefficients. Significant correlations shown in boldface. *P < 0.05.

Supplementary Table 5 | P-value of significant plasma lipids of NC, HG, HF and M cohorts.

Compound Name	Group1	Group2	P-value	Compound Name	Group1	Group2	P-value	Compound Name	Group1	Group2	P-value
3-Dehydrocarnitine	M	NC	0.0035	6-Hexanoyl-D-erythro-sphingosine	M	HF	0.0000	6-Hexanoyl-D-erythro-sphingosine	M	HG	0.0003
6-Hexanoyl-D-erythro-sphingosine	M	NC	0.0001	ArachidoylEthanolamide	M	HF	0.0002	ArachidoylEthanolamide	M	HG	0.0006
ArachidoylEthanolamide	M	NC	0.0008	CER	M	HF	0.0000	CER	M	HG	0.0001
CER	M	NC	0.0002	cPA	M	HF	0.0056	DG	M	HG	0.0005
Che	M	NC	0.0039	DG	M	HF	0.0000	Eicosanoicacid	M	HG	0.0042
DG	M	NC	0.0006	Eicosanoicacid	M	HF	0.0027	FA	M	HG	0.0048
dMePE	M	NC	0.0070	FA	M	HF	0.0007	Hexadecanamide	M	HG	0.0000
Eicosanoicacid	M	NC	0.0044	Hexadecanamide	M	HF	0.0000	LdMePE	M	HG	0.0005
FA	M	NC	0.0106	LdMePE	M	HF	0.0014	LPA	M	HG	0.0005
Hexadecanamide	M	NC	0.0000	LPA	M	HF	0.0001	LPC	M	HG	0.0243
LdMePE	M	NC	0.0005	LPC	M	HF	0.0471	LPEt	M	HG	0.0011
LPA	M	NC	0.0006	LPEt	M	HF	0.0113	LPG	M	HG	0.0027
LPC	M	NC	0.0193	LPI	M	HF	0.0010	LPI	M	HG	0.0100
LPEt	M	NC	0.0023	MG	M	HF	0.0016	LPS	M	HG	0.0067
LPG	M	NC	0.0013	N-hexadecyl-ethanolamine	M	HF	0.0092	MG	M	HG	0.0054
LPI	M	NC	0.0047	OAHFA	M	HF	0.0000	N-hexadecyl-ethanolamine	M	HG	0.0048
MG	M	NC	0.0028	Octadecanoicacid	M	HF	0.0042	OAHFA	M	HG	0.0001

Metabolite				Metabolite				Metabolite			
N-hexadecyl-ethanolamine	M	NC	0.0018	PAF	M	HF	0.0055	Octadecanoicacid	M	HG	0.0346
OAHFA	M	NC	0.0001	PC	M	HF	0.0055	PAF	M	HG	0.0001
Octadecanoicacid	M	NC	0.0013	PEt	M	HF	0.0008	PC	M	HG	0.0008
PAF	M	NC	0.0001	PG	M	HF	0.0005	PE	M	HG	0.0202
PC	M	NC	0.0079	PI	M	HF	0.0002	PEt	M	HG	0.0001
PE	M	NC	0.0010	PIP	M	HF	0.0025	PG	M	HG	0.0002
PEt	M	NC	0.0002	PIP3	M	HF	0.0093	PI	M	HG	0.0002
PG	M	NC	0.0000	PS	M	HF	0.0091	PIP	M	HG	0.0044
phSM	M	NC	0.0006	So	M	HF	0.0009	PIP3	M	HG	0.0156
PI	M	NC	0.0000	TG	M	HF	0.0001	PS	M	HG	0.0034
PIP	M	NC	0.0015					SM	M	HG	0.0074
SM	M	NC	0.0045					So	M	HG	0.0021
So	M	NC	0.0007					TG	M	HG	0.0000
TG	M	NC	0.0000								

Significant differences were calculated using the ANOVA test. A significant difference between the groups was considered at $P < 0.01$.

Supplemetary Table 6 | Gut microbiota abundance (phylum) and their correlation with lipid classes variables in in the M cohort.

	3-Dehydrocarnitine	CER	DG	cPA	Hexadecanamide	Octadecanoicacid	PEt	PIP3	PC	So	SM
Firmicutes	0.6247*	0.6843*	0.5893*	-	0.6313*	0.6378*	0.6434*	0.7909**		-	-
Bacteroidetes	-0.5975*	-0.7636**	-6.3645*	-0.5990*	-0.6943*		-0.7510**	-0.7694**	-0.5853*		
Actinobacteria	-	-	-	-	-	-	-	-	-	-0.5899*	
Tenericutes	-	-	-	-	-	-	-	-	-	-	-0.6222*

Data are Spearman correlation coefficients. Significant correlations shown in boldface. *P < 0.05; **P < 0.01.