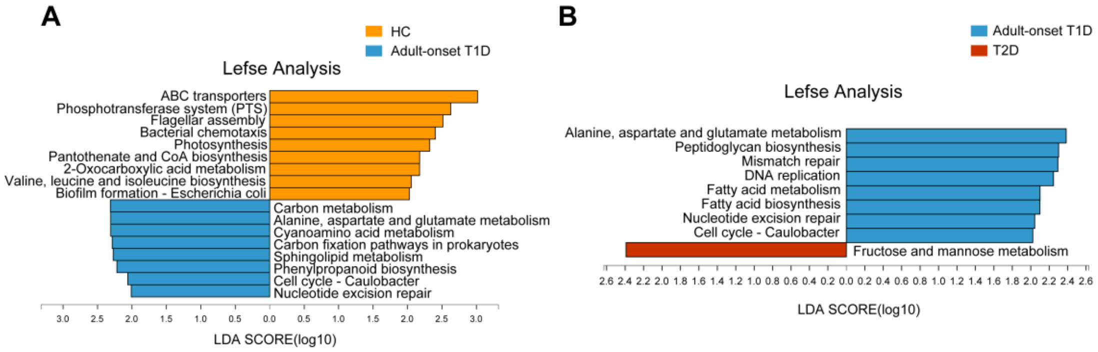
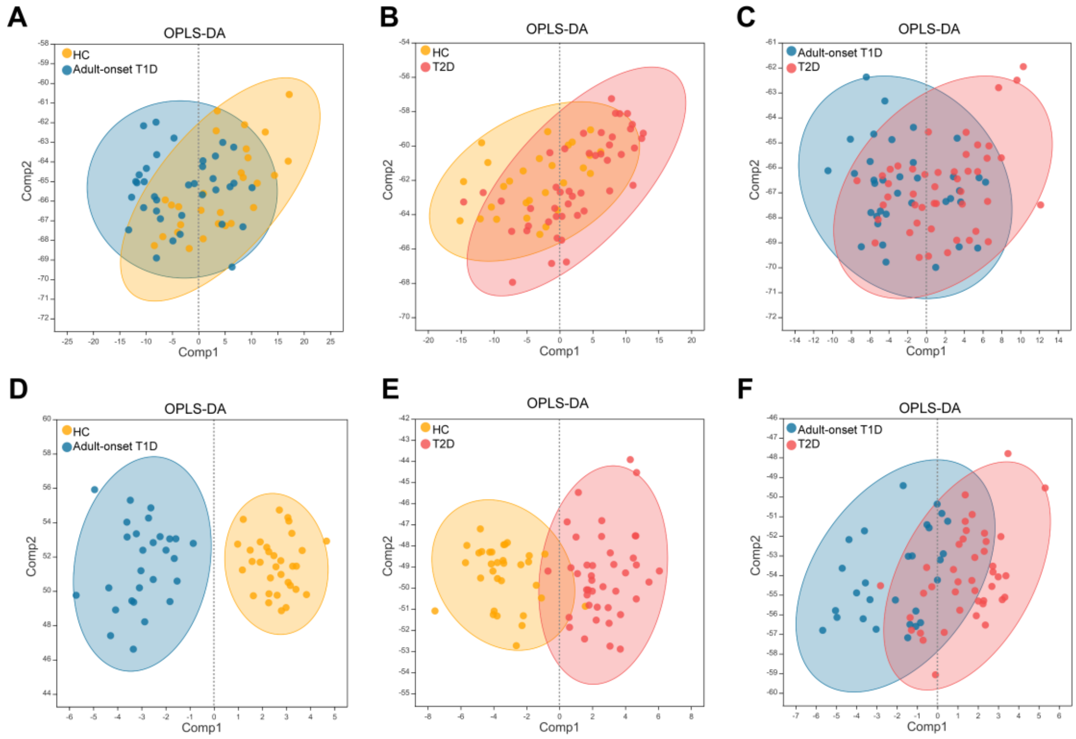
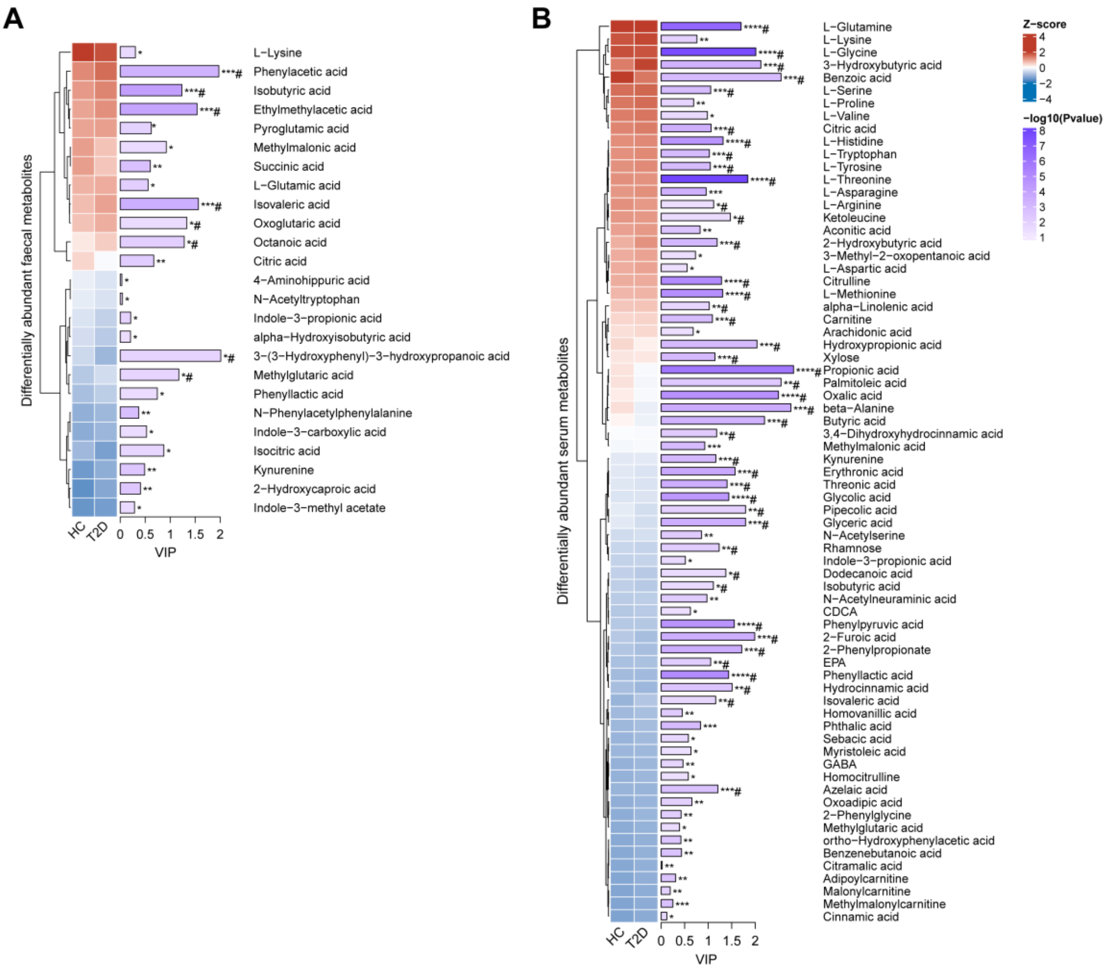


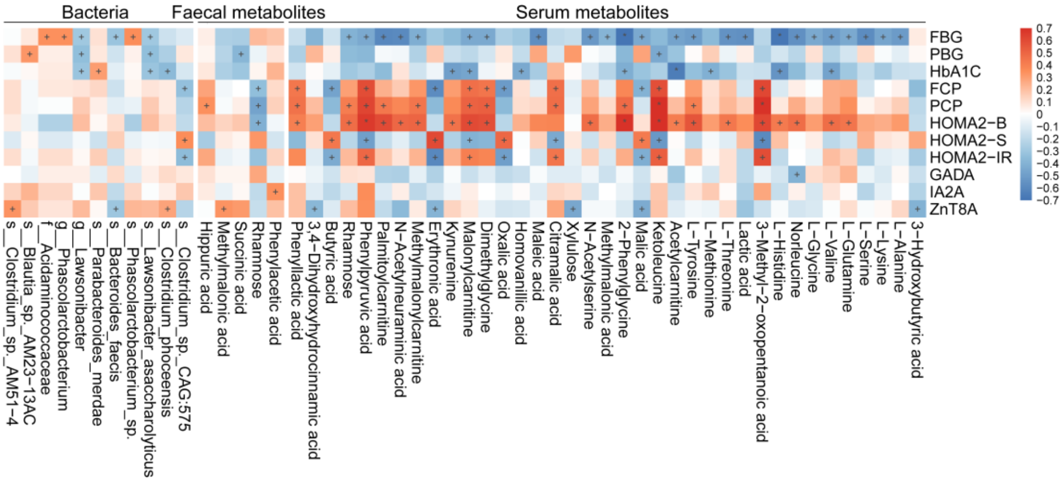
Supplementary Figure 1. Gut microbiota functional alterations in adult-onset T1D. KEGG pathway analysis of differentially abundant gut microbiota between patients with adult-onset T1D and HCs (A) and between patients with adult-onset T1D and T2D (B). Pathways with LDA value > 2 and *P* < 0.05 were considered differentially abundant. Abbreviations: KEGG, Kyoto Encyclopedia of Genes and Genomes; HC, healthy control; T1D, type 1 diabetes; T2D, type 2 diabetes; LDA, linear discriminant analysis.



Supplementary Figure 2. Faecal/serum metabolome profiles assessed by OPLS-DA. (A-C) Comparisons of the faecal metabolome between the three study groups. (D-F) Comparisons of the serum metabolome between the three study groups. Abbreviations: OPLS-DA, orthogonal partial least squares discriminant analysis; HC, healthy control; T1D, type 1 diabetes; T2D, type 2 diabetes.



Supplementary Figure 3. Differentially abundant faecal/serum metabolites in patients with T2D. (A, B) Differentially abundant faecal/serum metabolites identified by OPLS-DA between T2D patients and HCs. The relative abundance was transformed into Z scores. Altered metabolites were identified by the OPLS-DA. $^{*}P_{fdr} < 0.1$, $^{**}P_{fdr} < 0.05$, $^{***}P_{fdr} < 0.01$, $^{****}P_{fdr} < 0.001$, $^{\#}$VIP > 1. Abbreviations: OPLS-DA, orthogonal partial least squares discriminant analysis; VIP, variable influence on projection; HC, healthy control; T1D, type 1 diabetes; T2D, type 2 diabetes.



Supplementary Figure 4. Interactions of disease-related taxa/metabolites and host clinical parameters in adult-onset T1D. Associations of differentially abundant taxa or faecal/serum metabolites and clinical parameters in patients with adult-onset T1D. Correlations were calculated with Spearman's correlation analysis. $^{+}P < 0.05$, $^{*}P_{fdr} < 0.1$. Abbreviations: FBG, fasting blood glucose; PBG, postprandial blood glucose; HbA1c, haemoglobin A1c; FCP, fasting C-peptide; PCP, postprandial C-peptide; HOMA2-B, homoeostasis model assessment 2 estimates of β-cell function; HOMA2-S, homoeostasis model assessment 2 estimates of insulin sensitivity; HOMA2-IR, homoeostasis model assessment 2 estimates of insulin resistance; GADA, glutamic acid decarboxylase antibody; IA-2A, insulinoma-associated protein 2 antibody; ZnT8A, zinc transporter 8 antibody; AUC, area under the curve.

Supplementary Table 1. Demographics and baseline characteristics of discovery set and validation set.

	Discovery set				**Validation set**			
Variable	Healthy controls (n = 36)	adult-onset T1D (n = 51)	T2D (n = 56)	*P* value between all groups	Healthy controls (n = 28)	adult-onset T1D (n = 27)	T2D (n = 20)	*P* value between all groups
Age (years)	43.0 (28.5-52.0)	40.0 (32.0-48.0)	45.5 (35.0-52.0)	0.249	37.5 (30.0, 52.5)	34.5 (31.2, 45.8)	43.0 (40.8, 52.0)	0.073
Diabetes duration (months)	/	8.0 (3.0-22.0)	3.0 (1.0-10) $^{\#}$	0.006	/	30.0 (8.2-52.0)	20.5 (8.0-48.0)	0.847
Male/female (n)	17/19	35/16	38/18	0.078	13/15	10/17	7/13	0.674
BMI (kg/m^2)	22.8 ± 2.2	20.9 ± 2.5*	24.6 ± 3.7 $^{*\#}$	< 0.001	23.3 ± 4.2	21.4 ± 2.6	29.9 ± 5.0 $^{*\#}$	< 0.001
FBG (mmol/L)	4.8 (4.6-5.2)	7.9 (5.1-10.3) *	7.3 (5.9-10.0) *	< 0.001	4.7 (4.4-4.9)	6.8 (6.0-8.0) *	7.7 (6.3-8.5) *	< 0.001
PBG (mmol/L)	5.7 (4.8-6.7)	14.8 (11.5-18.2) *	14.1 (10.1-17.7) *	< 0.001	/	15.8 (13.8-18.7)	13.4 (12.3-16.0)	0.103
HbA1c (%)	5.4 (5.2-5.6)	8.7 (7.0-10.5) *	8.4 (6.2-10.4) *	< 0.001	5.6 (5.4-5.8)	7.2 (6.4-8.5) *	6.0 (5.7-8.9) *	< 0.001
FCP (pmol/L)	409.6 (345.0-610.3)	135.1 (36.0-220.4) *	524.2 (262.8-689.8) $^{\#}$	< 0.001	354.7 (309.5-462.0)	103.3 (61.7-201.6) *	764.8 (591.7-927.5) $^{\#}$	< 0.001
PCP (pmol/L)	1772.7 (1225.8-2492.5)	277.5 (60.6-648.1) *	1229.3 (750.5-2200.8) $^{\#}$	< 0.001	/	347.0 (160.5-744.3)	1571.6 (1285.1-2350.5) $^{\#}$	< 0.001

Data are presented as the mean ± SD or median (interquartile range). Chi-squared tests and analysis of variance (ANOVA) with the post hoc correction using the Fisher's lease significant difference method were used as appropriate, or a Kruskal-Wallis test between multiple groups with Bonferroni correction was applied. *versus HC, $P < 0.05$; $^{\#}$versus adult-onset T1D, $P < 0.05$. Abbreviations: T1D, type 1 diabetes; T2D, type 2 diabetes; BMI, body mass index; FBG, fasting blood glucose; PBG, postprandial blood glucose; HbA1c, heamoglobin A1c; FCP, fasting C-peptide; PCP, postprandial C-peptide.

Supplementary Table 2. The bacteria differentially abundance between patients with adult-onset T1D and HC.

Species	Mean relative abundance		Lefse Analysis	
	HC	Adult-onset T1D	LDA score	FDR
f__Acidaminococcaceae	3.07E-03	4.71E-03	2.9648	0.3448
f__Acidaminococcaceae.g__Phascolarctobacterium	3.07E-03	4.71E-03	2.9648	0.2226
f__Acidaminococcaceae.g__Phascolarctobacterium.s__Phascolarctobacterium_sp_	1.72E-04	2.52E-04	2.0214	0.2663
f__Acidaminococcaceae.g__Phascolarctobacterium.s__Phascolarctobacterium_succinatutens	4.97E-04	7.95E-04	2.3671	0.2751
f__Bacteroidaceae.g__Bacteroides.s__Bacteroides_cellulosilyticus	1.17E-03	2.66E-03	3.0256	0.0628
f__Bacteroidaceae.g__Bacteroides.s__Bacteroides_faecis	6.27E-04	6.96E-04	2.1385	0.2640
f__Bacteroidaceae.g__Bacteroides.s__Bacteroides_fluxus	4.06E-04	9.93E-04	2.7220	0.1093
f__Bacteroidaceae.g__Bacteroides.s__Bacteroides_intestinalis	1.21E-03	2.42E-03	2.9830	0.0628
f__Bacteroidaceae.g__Bacteroides.s__Bacteroides_sp_	2.41E-03	1.20E-03	2.9334	0.1645
f__Bacteroidaceae.g__Bacteroides.s__Bacteroides_sp__4_1_36	2.84E-04	6.42E-04	2.4257	0.0953
f__Bacteroidaceae.g__Bacteroides.s__Bacteroides_sp__A1C1	7.00E-05	1.31E-04	2.4150	0.1923
f__Bacteroidaceae.g__Bacteroides.s__Bacteroides_sp__AF26_10BH	3.09E-05	8.08E-05	2.2587	0.0628
f__Bacteroidaceae.g__Bacteroides.s__Bacteroides_sp__AF34_31BH	1.79E-04	3.35E-04	2.2126	0.1923
f__Bacteroidaceae.g__Bacteroides.s__Bacteroides_sp__AR29	1.01E-04	2.39E-04	2.0988	0.0953
f__Bacteroidaceae.g__Bacteroides.s__Bacteroides_sp__D20	3.37E-04	7.19E-04	2.4247	0.1645
f__Bacteroidaceae.g__Bacteroides.s__Bacteroides_stercoris_CAG_120	4.38E-04	9.39E-04	2.4917	0.2595
f__Bacteroidaceae.g__Bacteroides.s__Bacteroides_thetaiotaomicron	5.55E-03	9.86E-03	3.3565	0.2595
f__Bacteroidaceae.g__Bacteroides.s__Bacteroides_uniformis	7.00E-03	1.52E-02	3.7333	0.1093
f__Bacteroidaceae.g__Bacteroides.s__Bacteroides_uniformis_CAG_3	1.28E-04	2.89E-04	2.1855	0.0953
f__Bifidobacteriaceae.g__Bifidobacterium.s__Bifidobacterium_bifidum	1.36E-04	1.95E-04	2.2933	0.2061
f__Clostridiaceae.g__Clostridium.s__Clostridium_disporicum	9.59E-04	2.43E-05	2.6103	0.2542

f__Clostridiaceae.g__Clostridium.s__Clostridium_phoceensis	7.14E-05	1.32E-04	2.1757	0.1893
f__Clostridiaceae.g__Clostridium.s__Clostridium_sp__AF28_12	2.34E-04	1.36E-04	2.2039	0.2127
f__Clostridiaceae.g__Clostridium.s__Clostridium_sp__AM25_23AC	3.50E-04	1.84E-04	2.2477	0.1645
f__Clostridiaceae.g__Clostridium.s__Clostridium_sp__AM51_4	2.54E-04	1.35E-04	2.2455	0.1893
f__Clostridiaceae.g__Clostridium.s__Clostridium_sp__CAG_354	1.03E-05	2.14E-05	2.6970	0.2640
f__Clostridiaceae.g__Clostridium.s__Clostridium_sp__CAG_571	2.78E-05	6.50E-05	2.3411	0.1645
f__Clostridiaceae.g__Clostridium.s__Clostridium_sp__CAG_575	2.79E-05	4.01E-05	2.4128	0.2397
f__Clostridiaceae.g__Clostridium.s__Clostridium_sp__SS2_1	4.22E-04	2.52E-04	2.0755	0.2595
f__Clostridiaceae.g__unclassified_f__Clostridiaceae.s__Clostridiaceae_bacterium_TF01_6	2.86E-04	1.78E-04	2.1405	0.2127
f__Eggerthellaceae.g__Eggerthella	2.32E-05	8.12E-05	2.0708	0.1512
f__Eggerthellaceae.g__Eggerthella.s__Eggerthella_sp__CAG_298	2.32E-05	8.12E-05	2.0708	0.1893
f__Erysipelotrichaceae.g__Catenibacterium	1.69E-04	4.17E-04	2.2907	0.0644
f__Erysipelotrichaceae.g__Catenibacterium.s__Catenibacterium_mitsuokai	1.69E-04	4.17E-04	2.2907	0.0628
f__Eubacteriaceae.g__Eubacterium.s__Eubacterium_rectale_CAG_36	1.81E-04	5.31E-05	2.2481	0.1085
f__Eubacteriaceae.g__Eubacterium.s__Eubacterium_sp__41_20	1.78E-04	5.60E-05	2.1721	0.1093
f__Eubacteriaceae.g__Eubacterium.s__Eubacterium_sp__CAG_180	6.34E-04	6.04E-04	2.3948	0.2077
f__Eubacteriaceae.g__Eubacterium.s__Eubacterium_sp__CAG_251	2.58E-04	6.18E-04	2.4294	0.2640
f__Lachnospiraceae	1.42E-01	9.30E-02	4.4290	0.1932
f__Lachnospiraceae.g__Anaerostipes	4.22E-03	2.28E-03	2.9950	0.2131
f__Lachnospiraceae.g__Anaerostipes.s__Anaerostipes_hadrus	4.22E-03	2.28E-03	2.9950	0.2542
f__Lachnospiraceae.g__Blautia.s__Blautia_sp__AF14_40	7.38E-05	4.32E-05	2.3732	0.2127
f__Lachnospiraceae.g__Blautia.s__Blautia_sp__AF32_4BH	2.22E-04	1.03E-04	2.1938	0.2678
f__Lachnospiraceae.g__Blautia.s__Blautia_sp__AM23_13AC	2.21E-04	1.12E-04	2.1302	0.2640
f__Lachnospiraceae.g__Blautia.s__Blautia_sp__CAG_37	3.74E-04	2.16E-04	2.1897	0.1645
f__Lachnospiraceae.g__Blautia.s__Blautia_sp__OF09_25XD	1.16E-04	5.46E-05	2.2041	0.2595
f__Lachnospiraceae.g__Enterocloster.s__Enterocloster_asparagiformis	8.95E-05	2.52E-04	2.4579	0.0628

f__Lachnospiraceae.g__Roseburia.s__Roseburia_intestinalis	9.21E-03	4.25E-03	3.4721	0.2068
f__Lachnospiraceae.g__Roseburia.s__Roseburia_intestinalis_CAG_13	2.65E-04	1.24E-04	2.2140	0.2127
f__Lachnospiraceae.g__Roseburia.s__Roseburia_inulinivorans	1.17E-02	6.02E-03	3.4868	0.2186
f__Lachnospiraceae.g__unclassified_f__Lachnospiraceae	4.23E-02	2.20E-02	4.0579	0.0926
f__Lachnospiraceae.g__unclassified_f__Lachnospiraceae.s___Eubacterium__rectale	2.14E-02	7.51E-03	3.9070	0.0923
f__Lachnospiraceae.g__unclassified_f__Lachnospiraceae.s__Lachnospiraceae_bacterium_2_1_58FAA	8.95E-05	4.36E-05	2.3705	0.1645
f__Lachnospiraceae.g__unclassified_f__Lachnospiraceae.s__Lachnospiraceae_bacterium_AM26_1LB	2.41E-04	1.19E-04	2.0599	0.2678
f__Lachnospiraceae.g__unclassified_f__Lachnospiraceae.s__unclassified_f__Lachnospiraceae	1.52E-02	7.38E-03	3.6305	0.0923
f__Odoribacteraceae.g__Butyricimonas	9.27E-04	1.88E-03	2.7167	0.1512
f__Odoribacteraceae.g__Butyricimonas.s__Butyricimonas_virosa	9.27E-04	1.88E-03	2.7167	0.1893
f__Odoribacteraceae.g__Odoribacter.s__Odoribacter_laneus	1.57E-05	2.77E-05	2.5694	0.0923
f__Odoribacteraceae.g__unclassified_f__Odoribacteraceae	1.59E-04	3.04E-04	2.0405	0.0926
f__Odoribacteraceae.g__unclassified_f__Odoribacteraceae.s__unclassified_f__Odoribacteraceae	1.59E-04	3.04E-04	2.0405	0.1070
f__Oscillospiraceae	3.42E-03	7.92E-03	3.4752	0.3448
f__Oscillospiraceae.g__Oscillibacter	3.00E-03	7.41E-03	3.4649	0.2226
f__Oscillospiraceae.g__Oscillibacter.s__Oscillibacter_sp_	1.34E-03	4.70E-03	3.3430	0.1893
f__Oscillospiraceae.g__Oscillibacter.s__unclassified_g__Oscillibacter	1.53E-04	2.13E-04	2.0726	0.1645
f__Oscillospiraceae.g__Oscillibacter.s__uncultured_Oscillibacter_sp_	9.67E-05	1.38E-04	2.1009	0.1645
f__Peptostreptococcaceae.g__Romboutsia	1.84E-03	2.51E-04	2.9368	0.1123
f__Peptostreptococcaceae.g__Romboutsia.s__Romboutsia_timonensis	1.84E-03	2.51E-04	2.9368	0.1382
f__Prevotellaceae.g__Prevotella.s__Prevotella_bivia	2.92E-04	3.79E-04	2.1927	0.2640
f__Rikenellaceae.g__Alistipes.s__Alistipes_finegoldii	8.96E-04	1.38E-03	2.5993	0.2640
f__Rikenellaceae.g__Alistipes.s__Alistipes_senegalensis	2.82E-04	5.15E-04	2.2412	0.0628
f__Rikenellaceae.g__Alistipes.s__Alistipes_shahii	1.58E-03	2.02E-03	2.7077	0.1070
f__Rikenellaceae.g__Alistipes.s__Alistipes_sp__AF14_19	2.87E-04	3.47E-04	2.0950	0.2054
f__Rikenellaceae.g__Alistipes.s__Alistipes_sp__HGB5	2.71E-04	4.31E-04	2.1785	0.1893

f__Rikenellaceae.g__Alistipes.s__unclassified_g__Alistipes	4.07E-03	5.67E-03	3.1700	0.1893
f__Rikenellaceae.g__unclassified_f__Rikenellaceae	7.84E-04	4.91E-04	2.3014	0.1294
f__Rikenellaceae.g__unclassified_f__Rikenellaceae.s__Rikenellaceae_bacterium	7.84E-04	4.91E-04	2.3014	0.1645
f__Ruminococcaceae.g__Anaerotruncus	3.97E-04	5.24E-04	2.1297	0.1512
f__Ruminococcaceae.g__Anaerotruncus.s__Anaerotruncus_colihominis	3.97E-04	5.24E-04	2.1297	0.2054
f__Ruminococcaceae.g__Faecalibacterium.s__uncultured_Faecalibacterium_sp_	7.57E-04	5.60E-04	2.2006	0.2559
f__Ruminococcaceae.g__Massilimaliae	1.83E-05	5.32E-05	2.2059	0.0926
f__Ruminococcaceae.g__Massilimaliae.s__Massilimaliae_massiliensis	1.83E-05	5.32E-05	2.2059	0.1085
f__Ruminococcaceae.g__Ruminococcus.s___Ruminococcus__gnavus_CAG_126	3.61E-05	1.13E-05	2.6911	0.1893
f__Ruminococcaceae.g__Ruminococcus.s__Ruminococcus_sp__AM45_9BH	3.74E-05	2.14E-05	2.8698	0.1893
f__Ruminococcaceae.g__Ruminococcus.s__unclassified_g__Ruminococcus	1.30E-02	8.56E-03	3.4539	0.2542
f__Ruminococcaceae.g__unclassified_f__Ruminococcaceae	5.75E-03	9.24E-03	3.4014	0.1274
f__Ruminococcaceae.g__unclassified_f__Ruminococcaceae.s__Ruminococcaceae_bacterium	4.15E-03	7.46E-03	3.3686	0.1093
f__Ruminococcaceae.g__unclassified_f__Ruminococcaceae.s__unclassified_f__Ruminococcaceae	7.14E-04	7.51E-04	2.1955	0.1645
f__Tannerellaceae	1.27E-02	1.42E-02	3.3216	0.2703
f__Tannerellaceae.g__Parabacteroides	1.27E-02	1.40E-02	3.3066	0.1512
f__Tannerellaceae.g__Parabacteroides.s__Parabacteroides_johnsonii	5.91E-04	1.27E-03	2.8290	0.2751
f__Tannerellaceae.g__Parabacteroides.s__Parabacteroides_merdae	2.91E-03	5.72E-03	3.3139	0.1551
f__unclassified_o__Clostridiales.g__Evtepia	2.58E-04	5.97E-04	2.4512	0.1512
f__unclassified_o__Clostridiales.g__Evtepia.s__Evtepia_gabavorous	2.58E-04	5.97E-04	2.4512	0.2042
f__unclassified_o__Clostridiales.g__Intestinimonas	1.91E-04	4.69E-04	2.3257	0.1123
f__unclassified_o__Clostridiales.g__Intestinimonas.s__Intestinimonas_butyriciproducens	1.91E-04	4.69E-04	2.3257	0.1364
f__unclassified_o__Clostridiales.g__Lawsonibacter	1.28E-04	2.29E-04	2.0810	0.1682
f__unclassified_o__Clostridiales.g__Lawsonibacter.s__Lawsonibacter_asaccharolyticus	1.28E-04	2.29E-04	2.0810	0.2127
f__unclassified_o__Clostridiales.g__unclassified_o__Clostridiales.s__Clostridiales_bacterium	4.08E-03	1.14E-02	3.6865	0.1085
f__unclassified_p__Firmicutes.g__unclassified_p__Firmicutes.s__Firmicutes_bacterium_AF12_30	2.34E-04	7.85E-05	2.2576	0.1070

f__unclassified_p__Firmicutes.g__unclassified_p__Firmicutes.s__Firmicutes_bacterium_CAG_114	7.66E-05	1.47E-04	2.1954	0.2542
f__unclassified_p__Firmicutes.g__unclassified_p__Firmicutes.s__Firmicutes_bacterium_CAG_137	9.08E-05	2.32E-04	2.0756	0.2542
f__unclassified_p__Firmicutes.g__unclassified_p__Firmicutes.s__Firmicutes_bacterium_CAG_341	1.38E-04	6.29E-04	2.5903	0.1085

Abbreviations: HC, healthy control; T1D, type 1 diabetes; LDA, linear discriminant analysis; FDR, false discovery rate.

Supplementary Table 3. The bacteria differentially abundance between patients with T2D and HC.

Species	Mean relative abundance		Lefse Analysis	
	HC	T2D	LDA score	FDR
f__Bacteroidaceae	1.61E-01	2.27E-01	4.5818	0.2678
f__Bacteroidaceae.g__Bacteroides	1.60E-01	2.26E-01	4.5788	0.2766
f__Bacteroidaceae.g__Bacteroides.s__Bacteroides_cellulosilyticus	1.17E-03	2.66E-03	3.0660	0.1280
f__Bacteroidaceae.g__Bacteroides.s__Bacteroides_clarus	5.25E-04	8.35E-04	2.4712	0.1886
f__Bacteroidaceae.g__Bacteroides.s__Bacteroides_eggerthii	1.10E-03	3.28E-03	3.0868	0.2585
f__Bacteroidaceae.g__Bacteroides.s__Bacteroides_fluxus	4.06E-04	9.93E-04	2.3775	0.2715
f__Bacteroidaceae.g__Bacteroides.s__Bacteroides_intestinalis	1.21E-03	2.42E-03	3.2382	0.0894
f__Bacteroidaceae.g__Bacteroides.s__Bacteroides_oleiciplenus	1.84E-04	6.34E-04	2.5234	0.1280
f__Bacteroidaceae.g__Bacteroides.s__Bacteroides_salyersiae	7.43E-04	2.25E-03	2.9794	0.1453
f__Bacteroidaceae.g__Bacteroides.s__Bacteroides_sp__1_1_14	1.53E-04	2.69E-04	2.6328	0.2832
f__Bacteroidaceae.g__Bacteroides.s__Bacteroides_sp__4_1_36	2.84E-04	6.42E-04	2.4789	0.1949
f__Bacteroidaceae.g__Bacteroides.s__Bacteroides_sp__A1C1	7.00E-05	1.31E-04	2.8499	0.1818
f__Bacteroidaceae.g__Bacteroides.s__Bacteroides_sp__AF26_10BH	3.09E-05	8.08E-05	2.7388	0.1948
f__Bacteroidaceae.g__Bacteroides.s__Bacteroides_sp__AR29	1.01E-04	2.39E-04	2.5009	0.2715
f__Bacteroidaceae.g__Bacteroides.s__Bacteroides_sp__D20	3.37E-04	7.19E-04	2.4254	0.2597
f__Bacteroidaceae.g__Bacteroides.s__Bacteroides_uniformis	7.00E-03	1.52E-02	3.6183	0.1948
f__Bacteroidaceae.g__Bacteroides.s__Bacteroides_uniformis_CAG_3	1.28E-04	2.89E-04	2.4617	0.1280
f__Bacteroidaceae.g__Bacteroides.s__uncultured_Bacteroides_sp_	6.23E-04	8.22E-04	2.5061	0.1886
f__Bifidobacteriaceae.g__Bifidobacterium.s__Bifidobacterium_bifidum	1.36E-04	1.95E-04	2.3776	0.2715
f__Clostridiaceae.g__Butyricicoccus	2.21E-03	2.08E-03	2.5832	0.2613
f__Clostridiaceae.g__Butyricicoccus.s__Butyricicoccus_sp__AF10_3	9.67E-05	6.24E-05	2.8167	0.1453
f__Clostridiaceae.g__Butyricicoccus.s__Butyricicoccus_sp__AM27_36	2.05E-04	1.88E-04	2.5992	0.2658

f__Clostridiaceae.g__Butyricicoccus.s__Butyricicoccus_sp__AM28_25	2.22E-04	2.18E-04	2.6231	0.1917
f__Clostridiaceae.g__Butyricicoccus.s__uncultured_Butyricicoccus_sp_	1.99E-04	1.66E-04	2.6091	0.1755
f__Clostridiaceae.g__Clostridium.s__Clostridium_sp__27_14	8.86E-05	1.19E-04	2.4868	0.1948
f__Clostridiaceae.g__Clostridium.s__Clostridium_sp__AM51_4	2.54E-04	1.35E-04	2.5247	0.2585
f__Clostridiaceae.g__Clostridium.s__Clostridium_sp__SS2_1	4.22E-04	2.52E-04	2.3542	0.1362
f__Clostridiaceae.g__Clostridium.s__Clostridium_sp__TF06_15AC	1.01E-04	6.62E-05	2.8375	0.2832
f__Clostridiaceae.g__Clostridium.s__uncultured_Clostridium_sp_	3.02E-03	2.46E-03	2.6853	0.2715
f__Desulfovibrionaceae	1.13E-03	2.11E-03	2.8709	0.2198
f__Desulfovibrionaceae.g__Bilophila	1.13E-03	2.11E-03	2.8709	0.1886
f__Desulfovibrionaceae.g__Bilophila.s__Bilophila_sp__4_1_30	1.56E-04	3.18E-04	2.6017	0.1518
f__Desulfovibrionaceae.g__Bilophila.s__Bilophila_wadsworthia	7.84E-04	1.43E-03	2.7034	0.1948
f__Desulfovibrionaceae.g__Bilophila.s__unclassified_g__Bilophila	1.95E-04	3.67E-04	2.3373	0.1781
f__Erysipelotrichaceae.g__Catenibacterium	1.69E-04	4.17E-04	2.4815	0.0801
f__Erysipelotrichaceae.g__Catenibacterium.s__Catenibacterium_mitsuokai	1.69E-04	4.17E-04	2.4815	0.1280
f__Eubacteriaceae.g__Eubacterium.s__Eubacterium_rectale_CAG_36	1.81E-04	5.31E-05	2.7300	0.1948
f__Eubacteriaceae.g__Eubacterium.s__Eubacterium_sp_	5.95E-03	3.11E-03	3.3105	0.2832
f__Eubacteriaceae.g__Eubacterium.s__Eubacterium_sp__36_13	2.30E-03	8.41E-04	3.0604	0.1610
f__Eubacteriaceae.g__Eubacterium.s__Eubacterium_sp__41_20	1.78E-04	5.60E-05	2.9218	0.1280
f__Eubacteriaceae.g__Eubacterium.s__Eubacterium_sp__CAG_86	1.28E-03	4.60E-04	2.8291	0.1886
f__Lachnospiraceae	1.42E-01	9.30E-02	4.4745	0.0616
f__Lachnospiraceae.g__Anaerostipes	4.22E-03	2.28E-03	3.1184	0.1886
f__Lachnospiraceae.g__Anaerostipes.s__Anaerostipes_hadrus	4.22E-03	2.28E-03	3.1184	0.1886
f__Lachnospiraceae.g__Blautia.s__Blautia_sp__CAG_37	3.74E-04	2.16E-04	2.4918	0.1917
f__Lachnospiraceae.g__Mediterraneibacter.s__Mediterraneibacter_butyricigenes	9.03E-05	7.94E-05	3.1273	0.2715
f__Lachnospiraceae.g__Roseburia	4.13E-02	2.77E-02	3.9926	0.1886
f__Lachnospiraceae.g__Roseburia.s__Roseburia_faecis	3.43E-03	2.70E-03	2.8277	0.2038

f__Lachnospiraceae.g__Roseburia.s__Roseburia_intestinalis	9.21E-03	4.25E-03	3.5894	0.1518
f__Lachnospiraceae.g__Roseburia.s__Roseburia_intestinalis_CAG_13	2.65E-04	1.24E-04	2.4986	0.1818
f__Lachnospiraceae.g__Roseburia.s__Roseburia_sp__AM23_20	8.46E-04	7.41E-04	2.6077	0.1280
f__Lachnospiraceae.g__Roseburia.s__Roseburia_sp__MUC_MUC_530_WT_4D	8.71E-05	7.28E-05	2.9640	0.1631
f__Lachnospiraceae.g__Roseburia.s__Roseburia_sp__OF03_24	7.85E-04	7.10E-04	2.5685	0.1280
f__Lachnospiraceae.g__Roseburia.s__Roseburia_sp__TF10_5	2.23E-03	1.74E-03	2.6361	0.2832
f__Lachnospiraceae.g__Roseburia.s__unclassified_g__Roseburia	6.87E-03	5.38E-03	3.1885	0.1290
f__Lachnospiraceae.g__unclassified_f__Lachnospiraceae	4.23E-02	2.20E-02	4.0952	0.0385
f__Lachnospiraceae.g__unclassified_f__Lachnospiraceae.s___Eubacterium__rectale	2.14E-02	7.51E-03	3.9211	0.1280
f__Lachnospiraceae.g__unclassified_f__Lachnospiraceae.s__Lachnospiraceae_bacterium_5_1_63FAA	2.00E-04	1.20E-04	2.4412	0.2832
f__Lachnospiraceae.g__unclassified_f__Lachnospiraceae.s__Lachnospiraceae_bacterium_AM26_1LB	2.41E-04	1.19E-04	2.4225	0.2585
f__Lachnospiraceae.g__unclassified_f__Lachnospiraceae.s__unclassified_f__Lachnospiraceae	1.52E-02	7.38E-03	3.5871	0.1280
f__Odoribacteraceae.g__Odoribacter.s__Odoribacter_laneus	1.57E-05	2.77E-05	3.0212	0.1280
f__Peptostreptococcaceae.g__Romboutsia	1.84E-03	2.51E-04	2.9088	0.2613
f__Peptostreptococcaceae.g__Romboutsia.s__Romboutsia_timonensis	1.84E-03	2.51E-04	2.9088	0.2267
f__Prevotellaceae.g__Prevotella.s__Prevotella_bivia	2.92E-04	3.79E-04	2.4477	0.2887
f__Ruminococcaceae.g__Agathobaculum	3.18E-04	2.63E-04	2.3763	0.0336
f__Ruminococcaceae.g__Agathobaculum.s__Agathobaculum_butyriciproducens	3.18E-04	2.63E-04	2.3763	0.0894
f__Ruminococcaceae.g__Faecalibacterium	5.48E-02	4.36E-02	4.1068	0.0336
f__Ruminococcaceae.g__Faecalibacterium.s__Faecalibacterium_prausnitzii	3.64E-02	2.75E-02	3.9625	0.0894
f__Ruminococcaceae.g__Faecalibacterium.s__Faecalibacterium_sp_	2.49E-03	1.82E-03	2.7738	0.1132
f__Ruminococcaceae.g__Faecalibacterium.s__Faecalibacterium_sp__AF10_46	5.57E-04	3.67E-04	2.3403	0.1280
f__Ruminococcaceae.g__Faecalibacterium.s__Faecalibacterium_sp__AF27_11BH	4.95E-04	3.34E-04	2.3405	0.1280
f__Ruminococcaceae.g__Faecalibacterium.s__Faecalibacterium_sp__AF28_13AC	3.04E-05	3.64E-05	3.1619	0.1280
f__Ruminococcaceae.g__Faecalibacterium.s__Faecalibacterium_sp__AM43_5AT	6.08E-04	4.21E-04	2.2648	0.1290
f__Ruminococcaceae.g__Faecalibacterium.s__Faecalibacterium_sp__OM04_11BH	2.76E-04	1.92E-04	2.3960	0.1948

f__Ruminococcaceae.g__Faecalibacterium.s__unclassified_g__Faecalibacterium	1.10E-02	9.68E-03	3.4103	0.0894
f__Ruminococcaceae.g__Faecalibacterium.s__uncultured_Faecalibacterium_sp_	7.57E-04	5.60E-04	2.3249	0.1280
f__Ruminococcaceae.g__Flavonifractor	1.19E-03	1.56E-03	2.8108	0.2766
f__Ruminococcaceae.g__Flavonifractor.s__Flavonifractor_plautii	1.19E-03	1.56E-03	2.8108	0.2726
f__Ruminococcaceae.g__Subdoligranulum.s__Subdoligranulum_sp__OF01_18	1.34E-04	1.96E-04	2.5081	0.2832
f__Tannerellaceae	1.27E-02	1.42E-02	3.3107	0.2225
f__Tannerellaceae.g__Parabacteroides	1.27E-02	1.40E-02	3.3053	0.2613
f__unclassified_o__Clostridiales.g__unclassified_o__Clostridiales.s___Bacteroides__pectinophilus	2.12E-04	1.56E-04	2.8481	0.1280
f__unclassified_o__Clostridiales.g__unclassified_o__Clostridiales.s__Clostridiales_bacterium_36_14	1.84E-04	1.27E-04	2.9128	0.1755
f__unclassified_o__Clostridiales.g__unclassified_o__Clostridiales.s__Clostridiales_bacterium_Nov_37_41	9.03E-05	6.87E-05	2.8225	0.2591
f__unclassified_p__Firmicutes.g__unclassified_p__Firmicutes.s__Firmicutes_bacterium_AF12_30	2.34E-04	7.85E-05	2.5140	0.1280
f__unclassified_p__Firmicutes.g__unclassified_p__Firmicutes.s__Firmicutes_bacterium_AF16_15	8.23E-05	9.42E-05	2.7039	0.2036

Abbreviations: HC, healthy control; T2D, type 2 diabetes; LDA, linear discriminant analysis; FDR, false discovery rate.

Supplementary Table 4. The viruses differentially abundance between patients with adult-onset T1D and HC.

Species	**Mean relative abundance**		**Lefse Analysis**	
	HC	**Adult-onset T1D**	**LDA score**	**FDR**
f__Myoviridae.g__Punavirus	1.24E-06	3.59E-08	4.3120	0.1077
f__Myoviridae.g__Punavirus.s__Salmonella_virus_SJ46	1.24E-06	3.59E-08	4.3301	0.2399
f__Myoviridae.g__unclassified_f__Myoviridae.s__Myoviridae_sp_	1.11E-07	4.41E-06	3.5316	0.3648
f__unclassified_o__Caudovirales	5.95E-06	1.84E-06	4.4898	0.0132
f__unclassified_o__Caudovirales.g__unclassified_o__Caudovirales	5.95E-06	1.84E-06	4.5041	0.0291
f__unclassified_o__Caudovirales.g__unclassified_o__Caudovirales.s__uncultured_Caudovirales_phage	5.95E-06	1.84E-06	4.5018	0.0648

Abbreviations: HC, healthy control; T1D, type 1 diabetes; LDA, linear discriminant analysis; FDR, false discovery rate.

Supplementary Table 5. The viruses differentially abundance between patients with T2D and HC.

Species	**Mean relative abundance**		**Lefse Analysis**	
	HC	**T2D**	**LDA score**	**FDR**
f__Herpesviridae	4.97E-07	9.62E-08	3.7804	0.1258
f__Herpesviridae.g__Varicellovirus	4.97E-07	9.62E-08	3.7394	0.2347
f__Herpesviridae.g__Varicellovirus.s__Human_alphaherpesvirus_3	4.97E-07	9.62E-08	3.8048	0.4149
f__Siphoviridae.g__Cequinquevirus	4.53E-07	1.78E-06	3.6772	0.2436
f__Siphoviridae.g__unclassified_f__Siphoviridae.s__Butyrivibrio_virus_Bo_Finn	1.72E-07	0.00E+00	3.5552	0.4149

Abbreviations: HC, healthy control; T2D, type 2 diabetes; LDA, linear discriminant analysis; FDR, false discovery rate.

Supplementary Table 6. The fungi differentially abundance between patients with T2D and HC.

Species	Mean relative abundance		Lefse Analysis	
	HC	**T2D**	**LDA score**	**FDR**
f__Metschnikowiaceae	4.66E-08	2.77E-08	4.5086	0.0468
f__Metschnikowiaceae.g__Clavispora	1.51E-07	1.49E-08	4.4814	0.0510
f__Metschnikowiaceae.g__Clavispora.s___Candida__intermedia	4.66E-08	2.77E-08	4.4850	0.0510
f__Venturiaceae	4.66E-08	2.77E-08	4.2474	0.0468
f__Venturiaceae.g__Venturia_f__Venturiaceae	1.51E-07	1.49E-08	4.2670	0.0510
f__Venturiaceae.g__Venturia_f__Venturiaceae.s__Venturia_nashicola	1.51E-07	1.49E-08	4.2427	0.0510

Abbreviations: HC, healthy control; T2D, type 2 diabetes; LDA, linear discriminant analysis; FDR, false discovery rate.

Supplementary Table 7. The faecal metabolites differentially abundance between patients with adult-onset T1D and HC.

Metabolite	**VIP**	***P* value**	**FDR**	**FC (Adult-onset T1D/HC)**
Sarcosine	1.0433	0.0101	0.0712	0.8623
Creatine	1.7973	0.0072	0.0705	0.7215
Gallic acid	1.8367	0.0324	0.0997	0.7846
4-Hydroxybenzoic acid	0.9846	0.0181	0.0736	0.8275
Hippuric acid	0.4254	0.0335	0.0997	0.7389
Ethylmethylacetic acid	0.8342	0.0061	0.0698	1.0862
Phenylacetic acid	1.0808	0.0162	0.0736	1.1069
Indole-3-carboxylic acid	0.3030	0.0195	0.0749	1.1982
N-Acetyltryptophan	0.2978	0.0218	0.0793	0.9269
Cinnamic acid	0.1841	0.0039	0.0698	1.1772
N-Phenylacetylphenylalanine	0.2216	0.0114	0.0712	1.0450
Azelaic acid	0.5411	0.0324	0.0997	1.1106
Methylmalonic acid	0.9015	0.0144	0.0736	0.8842
4-Aminohippuric acid	0.1637	0.0144	0.0736	0.9367
Rhamnose	0.7296	0.0150	0.0736	0.9335
3-(3-Hydroxyphenyl)-3-hydroxypropanoic acid	1.9112	0.0061	0.0698	0.6564
Isobutyric acid	0.6761	0.0039	0.0698	1.0791
Isovaleric acid	0.9735	0.0045	0.0698	1.1190
Octanoic acid	1.1355	0.0013	0.0698	1.1818
Succinic acid	0.5980	0.0082	0.0705	0.8935
Isocitric acid	0.9234	0.0347	0.0997	0.6549
Malonic acid	1.3757	0.0281	0.0971	0.8595
Phenyllactic acid	0.7032	0.0114	0.0712	1.2326

Abbreviations: HC, healthy control; T1D, type 1 diabetes; VIP, variable importance in projection; FDR, false discovery rate; FC, fold change.

Supplementary Table 8. The faecal metabolites differentially abundance between patients with T2D and HC.

Metabolite	**VIP**	***P* value**	**FDR**	**FC (T2D/HC)**
L-Lysine	0.3040	0.0233	0.0847	0.9768
Indole-3-methyl acetate	0.2862	0.0271	0.0889	1.1406
Ethylmethylacetic acid	1.5378	0.0001	0.0031	1.0953
2-Hydroxycaproic acid	0.4059	0.0041	0.0314	1.5668
Phenylacetic acid	1.9738	0.0005	0.0073	1.1152
Indole-3-carboxylic acid	0.5278	0.0351	0.0967	1.1325
N-Acetyltryptophan	0.0464	0.0248	0.0855	0.9366
Indole-3-propionic acid	0.2104	0.0121	0.0596	0.8652
N-Phenylacetylphenylalanine	0.3707	0.0018	0.0209	1.1174
Methylmalonic acid	0.9217	0.0331	0.0952	0.8908
Pyroglutamic acid	0.6225	0.0117	0.0596	1.0387
4-Aminohippuric acid	0.0344	0.0156	0.0674	0.9274
alpha-Hydroxyisobutyric acid	0.2061	0.0371	0.0984	0.8427
3-(3-Hydroxyphenyl)-3-hydroxypropanoic acid	2.0115	0.0147	0.0674	0.6980
Isobutyric acid	1.2348	0.0001	0.0025	1.0921
Isovaleric acid	1.5643	0.0004	0.0061	1.1268
Methylglutaric acid	1.1718	0.0167	0.0676	1.2166
Citric acid	0.6716	0.0070	0.0485	0.8169
Oxoglutaric acid	1.3334	0.0322	0.0952	1.1017
Octanoic acid	1.2804	0.0090	0.0515	1.1383
Succinic acid	0.6032	0.0021	0.0211	0.8848
Isocitric acid	0.8737	0.0177	0.0680	0.6741
Kynurenine	0.4901	0.0041	0.0314	1.3907
L-Glutamic acid	0.5571	0.0084	0.0515	1.0433
Phenyllactic acid	0.7417	0.0331	0.0952	1.1608

Abbreviations: HC, healthy control; T2D, type 2 diabetes; VIP, variable importance in projection; FDR, false discovery rate; FC, fold change.

Supplementary Table 9. The serum metabolites differentially abundance between patients with adult-onset T1D and HC.

Metabolite	**VIP**	***P* value**	**FDR**	**FC (Adult-onset T1D/HC)**
Benzoic acid	3.3690	0.0001	0.0017	0.7515
3-Hydroxybutyric acid	3.2314	0.0000	0.0006	1.2358
3,4-Dihydroxyhydrocinnamic acid	2.7390	0.0000	0.0000	0.6825
Butyric acid	2.4838	0.0015	0.0130	0.6953
Propionic acid	2.2024	0.0008	0.0085	0.7698
Hydroxypropionic acid	1.9033	0.0196	0.0568	0.8109
Acetic acid	1.8626	0.0050	0.0283	1.1613
Pyruvic acid	1.8143	0.0085	0.0345	0.9411
Carnitine	1.8008	0.0000	0.0006	0.8908
Lactic acid	1.7849	0.0001	0.0016	0.9503
L-Aspartic acid	1.7596	0.0001	0.0017	0.8978
N-Methylnicotinamide	1.6482	0.0043	0.0280	1.3654
Oxalic acid	1.5105	0.0289	0.0773	0.8524
L-Tyrosine	1.4999	0.0000	0.0004	0.9454
Kynurenine	1.4849	0.0003	0.0042	0.8477
L-Glutamic acid	1.4744	0.0161	0.0475	0.9071
Phenyllactic acid	1.4265	0.0001	0.0013	0.5917
Erythronic acid	1.3846	0.0068	0.0313	0.8366
Creatine	1.3704	0.0097	0.0345	0.9143
Ketoleucine	1.3343	0.0131	0.0412	0.9232
Glyceric acid	1.3225	0.0278	0.0759	0.8312
L-Histidine	1.3003	0.0003	0.0041	0.9566
Dimethylglycine	1.2901	0.0142	0.0429	0.8514
Ribulose	1.2403	0.0016	0.0130	0.8899
L-Threonine	1.2389	0.0072	0.0313	0.9503
Pyroglutamic acid	1.2356	0.0075	0.0313	0.9213
Methylmalonic acid	1.2332	0.0052	0.0283	0.9032
L-Glutamine	1.2164	0.0007	0.0082	0.9700
Azelaic acid	1.2158	0.0075	0.0313	0.5117
Malic acid	1.2013	0.0136	0.0421	0.9129
N-Acetylneuraminic acid	1.1795	0.0022	0.0175	0.8098
3-Methyl-2-oxopentanoic acid	1.1514	0.0221	0.0627	0.9520
Xylose	1.1443	0.0323	0.0818	0.9095
Phenylpyruvic acid	1.1273	0.0024	0.0183	0.7919
Rhamnose	1.0981	0.0115	0.0381	0.7818
Xylulose	1.0864	0.0060	0.0283	0.8964
Acetylcarnitine	1.0675	0.0093	0.0345	0.9392
L-Methionine	1.0404	0.0010	0.0098	0.9500
L-Glycine	1.0260	0.0050	0.0283	0.9637
Isovaleric acid	1.0238	0.0335	0.0834	1.6044

Maleic acid	0.9899	0.0097	0.0345	0.8840
L-Tryptophan	0.9755	0.0055	0.0283	0.9568
Phthalic acid	0.8608	0.0007	0.0082	0.8255
L-Valine	0.8194	0.0097	0.0345	0.9691
N-Acetylserine	0.8054	0.0048	0.0283	0.8998
Norleucine	0.7597	0.0097	0.0345	0.9605
L-Serine	0.7390	0.0057	0.0283	0.9730
L-Lysine	0.7174	0.0106	0.0358	0.9791
Palmitoylcarnitine	0.6617	0.0028	0.0191	0.8066
Homovanillic acid	0.5834	0.0028	0.0191	0.8560
L-Leucine	0.5818	0.0323	0.0818	0.9818
L-Asparagine	0.5652	0.0131	0.0412	0.9764
2-Phenylglycine	0.3858	0.0300	0.0788	0.9055
Malonylcarnitine	0.2015	0.0102	0.0351	0.8480
Citramalic acid	0.1592	0.0387	0.0948	0.8962
L-Alanine	0.1310	0.0238	0.0664	1.0166
Methylmalonylcarnitine	0.1306	0.0060	0.0283	0.8214

Abbreviations: HC, healthy control; T1D, type 1 diabetes; VIP, variable importance in projection; FDR, false discovery rate; FC, fold change.

Supplementary Table 10. The serum metabolites differentially abundance between patients with T2D and HC.

Metabolite	VIP	*P* value	FDR	FC (T2D/HC)
Propionic acid	2.8122	0.0000	0.0000	0.6747
beta-Alanine	2.7575	0.0003	0.0028	0.5721
Palmitoleic acid	2.5492	0.0052	0.0179	0.6441
Benzoic acid	2.5476	0.0013	0.0059	0.7696
Oxalic acid	2.4934	0.0000	0.0003	0.7161
Butyric acid	2.1964	0.0006	0.0036	0.6956
3-Hydroxybutyric acid	2.1198	0.0005	0.0035	1.1427
Hydroxypropionic acid	2.0373	0.0011	0.0058	0.7583
L-Glycine	2.0123	0.0000	0.0000	0.9246
2-Furoic acid	1.9885	0.0004	0.0028	0.5044
L-Threonine	1.8416	0.0000	0.0000	0.9213
Pipecolic acid	1.7939	0.0101	0.0286	0.6824
Glyceric acid	1.7924	0.0003	0.0028	0.7006
2-Phenylpropionate	1.7126	0.0003	0.0028	0.5461
L-Glutamine	1.6986	0.0000	0.0000	0.9577
Erythronic acid	1.5709	0.0002	0.0020	0.7834
Phenylpyruvic acid	1.5551	0.0000	0.0003	0.7358
Hydrocinnamic acid	1.5076	0.0034	0.0124	0.4392
Ketoleucine	1.4722	0.0333	0.0738	0.9189
Glycolic acid	1.4371	0.0000	0.0005	0.8528
Phenyllactic acid	1.4351	0.0000	0.0002	0.6238
Threonic acid	1.4017	0.0003	0.0028	0.8038
Dodecanoic acid	1.3757	0.0342	0.0747	0.6531
L-Histidine	1.3153	0.0000	0.0003	0.9534
L-Methionine	1.3082	0.0000	0.0003	0.9348
Citrulline	1.2824	0.0000	0.0002	0.9325
Rhamnose	1.2319	0.0091	0.0270	0.7752
Azelaic acid	1.2068	0.0024	0.0096	0.5094
2-Hydroxybutyric acid	1.1893	0.0009	0.0054	1.0680
3,4-Dihydroxyhydrocinnamic acid	1.1794	0.0063	0.0205	0.8675
Kynurenine	1.1622	0.0010	0.0058	0.8770
Isovaleric acid	1.1589	0.0182	0.0452	1.4892
Xylose	1.1440	0.0011	0.0058	0.8896
L-Arginine	1.1161	0.0448	0.0908	0.8967
Isobutyric acid	1.1104	0.0273	0.0626	0.6817
Carnitine	1.0910	0.0015	0.0065	0.9313
Citric acid	1.0626	0.0004	0.0030	0.9629
L-Serine	1.0541	0.0012	0.0058	0.9633
EPA	1.0533	0.0073	0.0224	0.7244
L-Tyrosine	1.0464	0.0012	0.0058	0.9612
L-Tryptophan	1.0262	0.0012	0.0058	0.9608

alpha-Linolenic acid	1.0246	0.0171	0.0433	0.9245
L-Valine	0.9822	0.0258	0.0601	0.9662
N-Acetylneuraminic acid	0.9746	0.0068	0.0214	0.8336
L-Asparagine	0.9575	0.0005	0.0033	0.9655
Methylmalonic acid	0.9276	0.0013	0.0059	0.9002
N-Acetylserine	0.8597	0.0061	0.0203	0.8825
Phthalic acid	0.8392	0.0013	0.0059	0.8477
Aconitic acid	0.8275	0.0029	0.0113	0.9624
L-Lysine	0.7617	0.0114	0.0312	0.9784
3-Methyl-2-oxopentanoic acid	0.7293	0.0436	0.0898	0.9645
L-Proline	0.6912	0.0171	0.0433	0.9785
Arachidonic acid	0.6804	0.0392	0.0843	0.9507
Oxoadipic acid	0.6543	0.0101	0.0286	0.7859
Myristoleic acid	0.6358	0.0425	0.0887	0.6852
CDCA	0.6219	0.0413	0.0876	0.8332
Sebacic acid	0.5789	0.0211	0.0516	0.8150
Homocitrulline	0.5787	0.0485	0.0956	0.8161
L-Aspartic acid	0.5535	0.0472	0.0944	0.9653
Indole-3-propionic acid	0.5156	0.0237	0.0570	0.8315
GABA	0.4649	0.0156	0.0418	0.8327
Homovanillic acid	0.4507	0.0061	0.0203	0.8732
Benzenebutanoic acid	0.4341	0.0026	0.0104	0.8410
2-Phenylglycine	0.4235	0.0080	0.0242	0.8978
ortho-Hydroxyphenylacetic acid	0.4199	0.0036	0.0129	0.7693
Methylglutaric acid	0.3905	0.0281	0.0634	0.8012
Adipoylcarnitine	0.3074	0.0032	0.0118	0.8527
Methylmalonylcarnitine	0.2495	0.0024	0.0096	0.7344
Malonylcarnitine	0.1930	0.0114	0.0312	0.8835
Cinnamic acid	0.1204	0.0251	0.0594	0.7892
Citramalic acid	0.0233	0.0171	0.0433	0.9563

Abbreviations: HC, healthy control; T2D, type 2 diabetes; VIP, variable importance in projection; FDR, false discovery rate; FC, fold change.

Supplementary Table 11. The performances of all prediction models.

Random Forest Analysis
Patients with adult-onset T1D vs HC & patients with adult-onset T1D vs patients with T2D
Model 1: microbiome (6 species)
Model 2: faecal metabolome (6 faecal metabolites)
Model 3: microbiome (6 species) + faecal metabolome (6 faecal metabolites)

Features		
Model 1	**Model 2**	**Model 3**
[Eubacterium] rectale Parabacteroides johnsonii Clostridium sp. CAG:575 Flavonifractor plautii Bacteroides stercoris CAG:120 Firmicutes bacterium AF16-15	Kynurenine Citric acid Indole-3-propionic acid L-Lysine N-Phenylacetylphenylalanine Octanoic acid	Model 1 + Model 2
Discovery: Adult-onset T1D vs HC: AUC = 0.931 Adult-onset T1D vs T2D: AUC = 0.932	Discovery: Adult-onset T1D vs HC: AUC = 0.836 Adult-onset T1D vs T2D: AUC = 0.844	Discovery: Adult-onset T1D vs HC: AUC = 0.988 Adult-onset T1D vs T2D: AUC = 0.981
Validation: Adult-onset T1D vs HC: AUC = 0.729 Adult-onset T1D vs T2D: AUC = 0.784	Validation: Adult-onset T1D vs HC: AUC = 0.657 Adult-onset T1D vs T2D: AUC = 0.644	Validation: Adult-onset T1D vs HC: AUC = 0.824 Adult-onset T1D vs T2D: AUC = 0.812

Abbreviations: HC, healthy control; T1D, type 1 diabetes; T2D, type 2 diabetes; AUC: area under curve.