

Supplementary Table 1. Analysis of functional gene differences in disease and healthy sample through flower microbiota

Description	D1D	D2D	D3D	H1D	H2D	H3D	Mean_D	Mean_H	Foldchange
	Down								
Glycogen_degradation_II_eukaryotic	0	0	0	16.8433	8.2993	2.6773	0	9.2733	0
Nicotinate_degradation_I	1.4799	0	0	4.3636	8.7273	249.9415	0.4933	87.67746667	0.005626303
Superpathway_of_glycol_metabolism_and_degradation	8.5471	9.8771	48.7547	680.8891	1,242.44	836.99	22.39297	920.1077333	0.024337331
Methylphosphonate_degradation_I	70.8167	78.038	131.4629	841.8954	1,535.42	1215.198	93.4392	1,197.50	0.078028245
D_galactarate_degradation_I	37.234	88.2589	105.0655	682.0341	1,243.52	858.7213	76.8528	928.0908333	0.082807412
Superpathway_of_D_glucarate_and_D_galactarate_degradation	37.234	88.2589	105.0655	682.0341	1,243.52	858.7213	76.8528	928.0908333	0.082807412
D_glucarate_degradation_I	39.4394	92.8564	105.891	683.0239	1,245.49	895.2025	79.3956	941.2404	0.084352095
Bifidobacterium_shunt	74.9897	189.7022	88.15	721.8532	1,317.05	1050.082	117.614	1,029.66	0.114226001
L_rhamnose_degradation_I	109.5272	119.8057	111.2272	681.0356	1,241.52	804.9778	113.52	909.1779333	0.124860084
Superpathway_of_hexuronide_and_hexuronate_degradation	82.1343	153.7027	165.7893	767.3652	1,398.98	952.0202	133.8754	1,039.46	0.128793735
Superpathway_of_beta_D_glucuronide_and_D_glucuronate_degradation	72.8889	170.3847	190.3714	818.0922	1,491.31	982.1389	144.5483	1,097.18	0.131745451
4_Deoxy_L_threo_hex_4_enopyranuronate_degradation	149.9864	137.6688	160.0506	778.8274	1,419.86	947.9047	149.2353	1,048.86	0.142282775
Superpathway_of_L_arginine_and_L_ornithine_degradation	66.341	180.8046	261.7949	819.3737	1,493.89	1,059.69	169.6468	1,124.32	0.150888532
Superpathway_of_L_arginine_putrescine_and_4_aminobutanoate_degradation	66.341	180.8046	261.7949	819.3737	1,493.89	1,059.69	169.6468	1,124.32	0.150888532
D_galacturonate_degradation_I	156.8958	171.6254	176.6284	759.8056	1,385.65	1,082.03	168.3832	1,075.83	0.156514953
Myo_chiro_and_scillo_inositol_degradation	582.04	720.05	586.04	2721.55	4,963.88	3,269.19	629.3767	3651.54	0.172359242
Glyoxylate_cycle	181.9387	249.0169	219.5371	685.0707	1,249.52	1,038.58	216.8309	991.0586667	0.218787149
D_fructuronate_degradation	284.3514	290.7694	278.2142	911.1783	1,661.59	1,263.61	284.445	1,278.79	0.222432235
Taxadiene_biosynthesis_engineered	386.6094	352.7598	158.7768	746.7521	1,361.73	1,098.42	299.382	1,068.97	0.280066714
Superpathway_of_glyoxylate_bypass_and_TCA	338.6479	446.4721	381.5669	880.3398	1,605.53	1,308.43	388.8956	1,264.77	0.307484111
Adenosine_nucleotides_degradation_II	667.7844	661.4066	328.938	1157.249	2,107.49	1,717.17	552.7097	1,660.64	0.332829591
Enterobactin_biosynthesis	266.9397	340.4448	317.9411	679.5809	1,239.01	758.1324	308.4419	892.2408667	0.345693498
dTDP_L_rhamnose_biosynthesis_I	496.3579	362.0573	245.4327	657.7932	1,210.15	1,320.35	367.9493	1062.7667	0.346218319
Ketogluconate_metabolism	19.2158	81.946	49.6872	12.3868	19.9984	372.8298	50.283	135.0716667	0.372269042
Aromatic_biogenic_amine_degradation_bacteria	72.8716	38.7746	5.8197	5.3231	10.6441	290.3324	39.1553	102.0998667	0.383500011
Urea_cycle	256.793	77.6539	50.8787	257.3973	431.0299	297.8706	128.4419	328.7659333	0.390678758
Cis_vaccenate_biosynthesis	907.4302	975.5726	768.0065	1575.61	2,876.05	2,214.68	883.6698	2,222.12	0.397670386
Palmitoleate_biosynthesis_I_from_5Z_dodec_5_enoate	848.9285	939.378	753.2941	1475.148	2,692.33	2,066.50	847.2002	2,077.99	0.407700854
Superpathway_of_glycolysis_pyruvate_dehydrogenase_TCA_and_glyoxylate_bypass	465.1258	584.4952	486.6881	879.9718	1,604.99	1,264.90	512.103	1,249.95	0.409698465
Fatty_acid_elongation___saturated	893.5567	974.167	774.9377	1490.953	2,720.95	2,114.95	880.8871	2,108.95	0.417689671
Oleate_biosynthesis_IV_anaerobic	882.4206	973.1091	777.1325	1471.402	2,685.24	2,073.57	877.5541	2,076.74	0.42256385
Gondoate_biosynthesis_anaerobic	924.9952	977.0519	775.6136	1491.67	2,721.74	2,116.48	892.5536	2,109.96	0.423018393
5Z_dodec_5_enoate_biosynthesis	867.9971	971.7022	780.0784	1446.119	2,639.06	2,020.85	873.2592	2,035.34	0.429047806
Photorespiration	128.6871	82.893	15.762	10.5649	21.1106	479.6967	75.7807	170.4574	0.444572662
Superpathway_of_glycolysis_and_Entner_Doudoroff	601.7125	580.3755	493.8645	844.1473	1,540.14	1,203.33	558.6508	1,195.87	0.467148938
NAD_biosynthesis_I_from_aspartate	470.0568	494.7447	403.6556	684.18	1,247.53	989.8	456.1524	973.8366667	0.468407467
Myo_inositol_degradation_I	554.9015	643.5241	524.8216	864.3783	1,574.99	1,219.78	574.4157	1219.7163	0.470942082
L_methionine_biosynthesis_III	216.9527	149.4119	89.1009	17.9473	35.8844	909.1925	151.8218	321.0080667	0.472953328

O_antigen_building_blocks_biosynthesis_E_coli	551.3711	495.9398	358.7122	657.4467	1,206.88	1,080.63	468.6744	981.6527667	0.477433959
TCA_cycle_IV_2_oxoglutarate_decarboxylase	555.5908	692.0818	563.3017	903.721	1,647.56	1,185.25	603.6581	1245.5108	0.484667094
Guanosine_nucleotides_degradation_III	749.2974	806.1873	634.875	1034.668	1,885.27	1,510.11	730.1199	1,476.68	0.494432029
Purine_nucleotides_degradation_II_aerobic	762.1269	773.1455	463.7452	984.1029	1,792.98	1,233.57	666.3392	1,336.88	0.498427399
Stearate_biosynthesis_II_bacteria_and_plants	789.9481	882.29	692.028	1073.525	1,958.85	1,703.47	788.0887	1,578.61	0.499228163
8_Amino_7_oxononanoate_biosynthesis_I	805.343	891.7191	700.7174	1128.146	2,058.04	1,614.44	799.2598	1,600.21	0.499472641

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Aerobactin_biosynthesis	1.8972	7.9734	54.4952	2.9967	2.7718	0.8931	21.45527	2.220533333	9.662213282
Protocatechuate_degradation_II_ortho_cleavage_pathway	142.6431	78.6018	65.7177	6.6096	6.892	12.4836	95.6542	8.661733333	11.04330927
Sulfoglycolysis	2.5	5.91	53.4669	2.25	2.08	0.67	20.62563	1.666666667	12.37538
4_Methylcatechol_degradation_ortho_cleavage	1.2389	26.0336	31.3589	0	0	2.63	19.5438	0.876666667	22.29330798
Superpathway_of_salicylate_degradation	1.7228	28.7661	29.0886	0	0	2.5915	19.85917	0.863833333	22.98958132
Toluene_degradation_III_aerobic_via_p_cresol	1.971	34.7276	42.9894	0	0	3.3684	26.56267	1.1228	23.65752286
2_Methylcitrate_cycle_I	90.7506	57.9908	48.1072	0	0	6.1755	65.6162	2.0585	31.87573476
Norspermidine_biosynthesis	99.5679	17.8855	7.475	0	0	3.7459	41.6428	1.248633333	33.35070344
Aromatic_compounds_degradation_via_beta_ketoadipate	78.2373	42.8723	29.0553	0	0	3.7299	50.05497	1.2433	40.25976568
Catechol_degradation_III_ortho_cleavage_pathway	78.2373	42.8723	29.0553	0	0	3.7299	50.05497	1.2433	40.25976568
Superpathway_of_methylglyoxal_degradation	149.4395	249.8585	164.0321	5.9438	5.187	1.6731	187.7767	4.267966667	43.9967588
Catechol_degradation_to_beta_ketoadipate	79.9474	42.4789	24.4614	0	0	3.3214	48.96257	1.107133333	44.22463419
4_Hydroxyphenylacetate_degradation	57.553	25.874	76.4629	0	0	2.9163	53.29663	0.9721	54.82628673
Arginine_ornithine_and_proline_interconversion	82.2291	55.2845	164.5582	0	0	4.9677	100.6906	1.6559	60.80717435
Hexitol_fermentation_to_lactate_formate_ethanol_and_acetate	732.0107	846.4765	684.4469	10.5969	12.8135	2.6756	754.3114	8.695333333	86.74898796
L_glutamate_and_L_glutamine_biosynthesis	268.6585	226.5845	244.4965	0	0	7.4676	246.5798	2.4892	99.05987198
Superpathway_of_23_butanediol_biosynthesis	131.5191	232.8105	183.7835	0.5598	0	0	182.7044	0.1866	979.1230797
Methylgallate_degradation	479.8345	562.4967	424.007	0.175	0	0	488.7794	0.058333333	8379.075429
Gallate_degradation_I	438.1	528.1781	395.3	0.14	0	0	453.8594	0.046666667	9725.557857
Gallate_degradation_II	438.1	528.1781	395.3	0.14	0	0	453.8594	0.046666667	9725.557857
Superpathway_of_RR_butanediol_biosynthesis	766.9682	738.95	542.3899	0.21	0	0	682.7694	0.07	9753.848095
14_Dihydroxy_2_naphthoate_biosynthesis_I	23.9388	75.5631	100.4207	0	0	0	66.64087	0	-
3_Phenylpropanoate_and_3_3_hydroxyphenylpropanoate_degradation	2.9392	11.4828	39.7297	0	0	0	18.05057	0	-
3_Phenylpropanoate_and_3_3_hydroxyphenylpropanoate_degradation_to_2_oxopent_4_enoate	0.7454	3.1383	22.0677	0	0	0	8.650467	0	-
3_Phenylpropanoate_degradation	32.2443	15.3451	39.04	0	0	0	28.87647	0	-
Acetyl_CoA_fermentation_to_butanoate_II	0.888	3.9414	30.3344	0	0	0	11.72127	0	-
Adenosylcobalamin_biosynthesis_I_early_cobalt_insertion	4.0369	14.4042	51.5062	0	0	0	23.31577	0	-
Adenosylcobalamin_biosynthesis_II_late_cobalt_incorporation	19.3238	39.638	29.0918	0	0	0	29.3512	0	-
Allantoin_degradation_IV_anaerobic	0	5.3796	5.4865	0	0	0	3.622033	0	-
Androstenedione_degradation	3.3379	0	0	0	0	0	1.112633	0	-
Catechol_degradation_I_meta_cleavage_pathway	101.8021	28.9758	19.5798	0	0	0	50.11923	0	-
Cinnamate_and_3_hydroxycinnamate_degradation_to_2_oxopent_4_enoate	0.7454	3.1383	22.0677	0	0	0	8.650467	0	-
CobIIyrate_ac_diamide_biosynthesis_I_early_cobalt_insertion	2.7418	9.9984	41.6601	0	0	0	18.13343	0	-
Ectoine_biosynthesis	0	4.9831	0	0	0	0	1.661033	0	-
Formaldehyde_assimilation_II_RuMP_Cycle	226.939	46.4227	23.5137	0	0	0	98.95847	0	-

Formaldehyde_oxidation_I	178.5288	34.8773	17.6271	0	0	0	77.01107	0	-
Fucose_degradation	78.3486	17.628	34.9155	0	0	0	43.6307	0	-
Heterolactic_fermentation	67.3238	175.1732	79.5485	0	0	0	107.3485	0	-
Incomplete_reductive_TCA_cycle	59.3113	148.3498	76.5861	0	0	0	94.74907	0	-
Isopropanol_biosynthesis	32.4409	21.8721	9.7159	0	0	0	21.34297	0	-
L_12_propanediol_degradation	2.9981	12.9885	120.4462	0	0	0	45.4776	0	-
L_isoleucine_biosynthesis_IV	169.0387	152.3855	209.3149	0	0	0	176.913	0	-
L_tryptophan_degradation_to_2_amino_3_carboxymuconate_semialdehyde	1.2212	9.9933	12.1039	0	0	0	7.7728	0	-
Mannan_degradation	124.9541	37.3763	16.7357	0	0	0	59.6887	0	-
NAD_biosynthesis_II_from_tryptophan	1.3113	12.811	15.209	0	0	0	9.7771	0	-
Nitrate_reduction_I_denitrification	31.5	10.4348	10	0	0	0	17.3116	0	-
Palmitate_biosynthesis_II_bacteria_and_plants	32.7863	0	0	0	0	0	10.92877	0	-
Phenylacetate_degradation_I_aerobic	4.1085	15.1598	88.6886	0	0	0	35.98563	0	-
Pyruvate_fermentation_to_acetate_and_lactate_II	240.8081	146.7197	164.3929	0	0	0	183.9736	0	-
Pyruvate_fermentation_to_acetone	32.4409	21.8721	9.7159	0	0	0	21.34297	0	-
S_methyl_5_thio_alpha_D_ribose_1_phosphate_degradation	121.5145	23.6036	9.9073	0	0	0	51.67513	0	-
Superpathway_of_chorismate_metabolism	69.5457	196.6775	234.99	0	0	0	167.0711	0	-
Superpathway_of_demethylmenaquinol_6_biosynthesis_I	20.6248	68.1444	92.5929	0	0	0	60.45403	0	-
Superpathway_of_demethylmenaquinol_8_biosynthesis	22.1064	72.6223	98.0906	0	0	0	64.2731	0	-
Superpathway_of_demethylmenaquinol_9_biosynthesis	20.6248	68.1444	92.5929	0	0	0	60.45403	0	-
Superpathway_of_fucose_and_rhamnose_degradation	27.7595	22.8322	55.2612	0	0	0	35.2843	0	-
Superpathway_of_glucose_and_xylose_degradation	453.5723	409.4444	273.467	0	0	0	378.8279	0	-
Superpathway_of_glycerol_degradation_to_13_propanediol	2.9626	9.5377	71.7029	0	0	0	28.06773	0	-
Superpathway_of_heme_biosynthesis_from_glycine	203.8321	45.7011	19.4711	0	0	0	89.6681	0	-
Superpathway_of_hexitol_degradation_bacteria	344.4022	401.2173	346.9415	0	0	0	364.187	0	-
Superpathway_of_L_threonine_metabolism	3.0544	11.1433	78.5336	0	0	0	30.91043	0	-
Superpathway_of_L_tryptophan_biosynthesis	5.9586	19.6345	161.1447	0	0	0	62.24593	0	-
Superpathway_of_lipopolysaccharide_biosynthesis	10.1424	11.4162	93.5947	0	0	0	38.38443	0	-
Superpathway_of_menaquinol_10_biosynthesis	30.4895	97.6423	128.2319	0	0	0	85.45457	0	-
Superpathway_of_menaquinol_11_biosynthesis	30.9588	98.6705	129.2656	0	0	0	86.2983	0	-
Superpathway_of_menaquinol_12_biosynthesis	30.9588	98.6705	129.2656	0	0	0	86.2983	0	-
Superpathway_of_menaquinol_13_biosynthesis	30.9588	98.6705	129.2656	0	0	0	86.2983	0	-
Superpathway_of_menaquinol_6_biosynthesis_I	30.4895	97.6423	128.2319	0	0	0	85.45457	0	-
Superpathway_of_menaquinol_7_biosynthesis	32.3932	97.6423	128.2319	0	0	0	86.08913	0	-
Superpathway_of_menaquinol_8_biosynthesis_I	32.6457	103.7534	135.2297	0	0	0	90.54293	0	-
Superpathway_of_menaquinol_8_biosynthesis_II	155.3324	31.2039	13.1501	0	0	0	66.56213	0	-
Superpathway_of_menaquinol_9_biosynthesis	30.4895	97.6423	128.2319	0	0	0	85.45457	0	-
Superpathway_of_N_acetylglucosamine_N_acetylmannosamine_and_N_acetylneuraminate_deg	3.723	11.8655	92.4085	0	0	0	35.999	0	-
Superpathway_of_N_acetylneuraminate_degradation	12.4639	38.7812	234.1535	0	0	0	95.13287	0	-
Superpathway_of_phenylethylamine_degradation	3.8995	14.1052	80.4341	0	0	0	32.81293	0	-
Superpathway_of_phylloquinol_biosynthesis	26.6661	77.8836	98.5689	0	0	0	67.7062	0	-
Superpathway_of_polyamine_biosynthesis_II	127.642	171.1203	94.4637	0	0	0	131.0753	0	-

Superpathway_of_sulfolactate_degradation	0	4.9764	0	0	0	0	1.6588	0	-
Superpathway_of_sulfur_oxidation_Acidianus_ambivalens	67.17	12	5	0	0	0	28.05667	0	-
Superpathway_of_thiamin_diphosphate_biosynthesis_I	196.7008	427.1066	412.388	0	0	0	345.3985	0	-
Superpathway_of_thiamin_diphosphate_biosynthesis_II	366.0404	380.4134	353.8352	0	0	0	366.763	0	-
Syringate_degradation	559.7288	621.734	473.1302	0	0	0	551.531	0	-
Thiazole_biosynthesis_I_E_coli	53.1605	164.4886	205.1995	0	0	0	140.9495	0	-
Thiazole_biosynthesis_II_Bacillus	141.8175	133.0431	145.3558	0	0	0	140.0721	0	-
Toluene_degradation_I_aerobic_via_o_cresol	127.4377	87.6088	48.1855	0	0	0	87.744	0	-
Toluene_degradation_II_aerobic_via_4_methylcatechol	127.4377	87.6088	48.1855	0	0	0	87.744	0	-
Toluene_degradation_IV_aerobic_via_catechol	1.4868	15.2456	17.4846	0	0	0	11.40567	0	-

Disease is indicated by D and healthy samples by H. Each was performed in 3 iterations.