

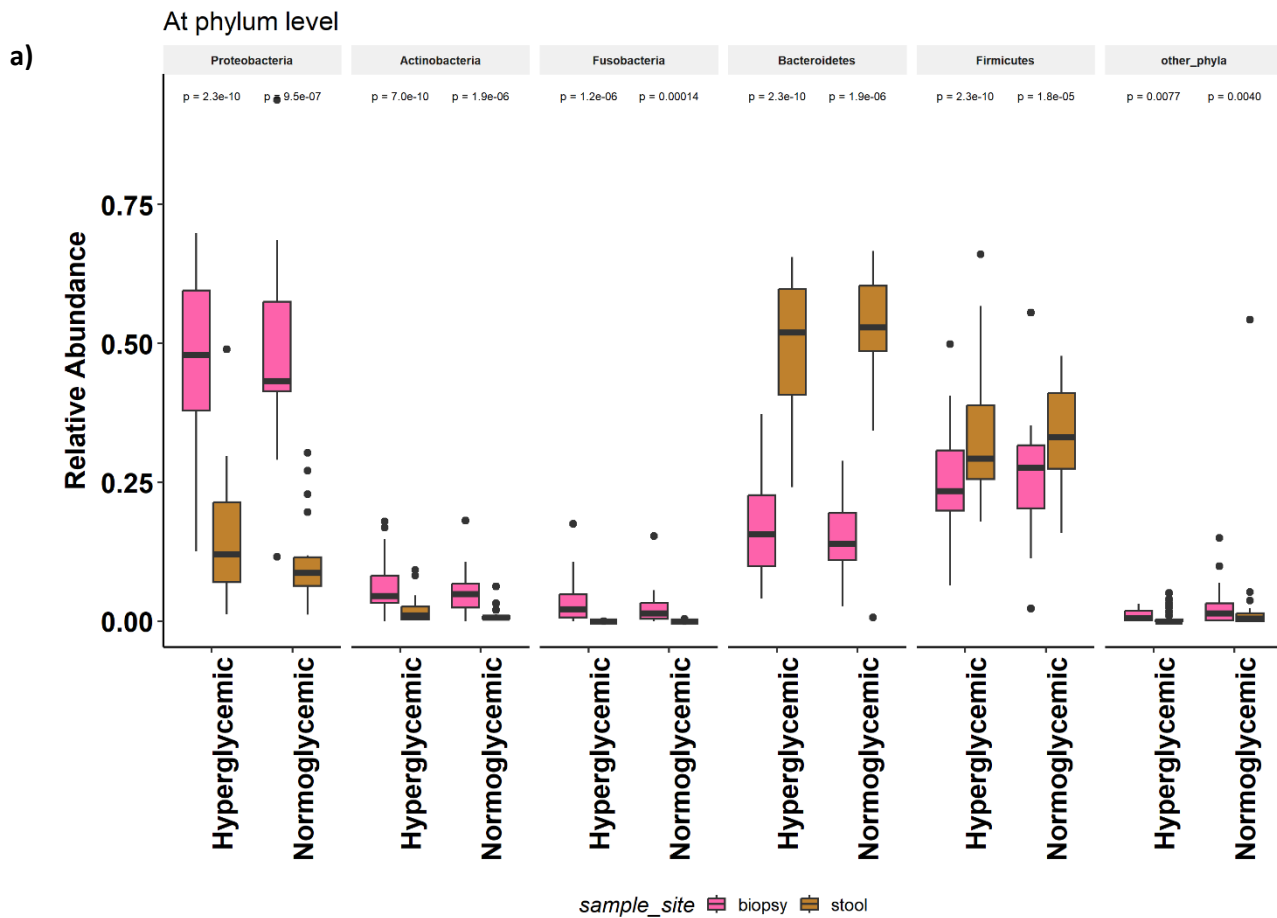
Supplementary Information

Hyperglycemia is associated with duodenal dysbiosis and altered duodenal microenvironment

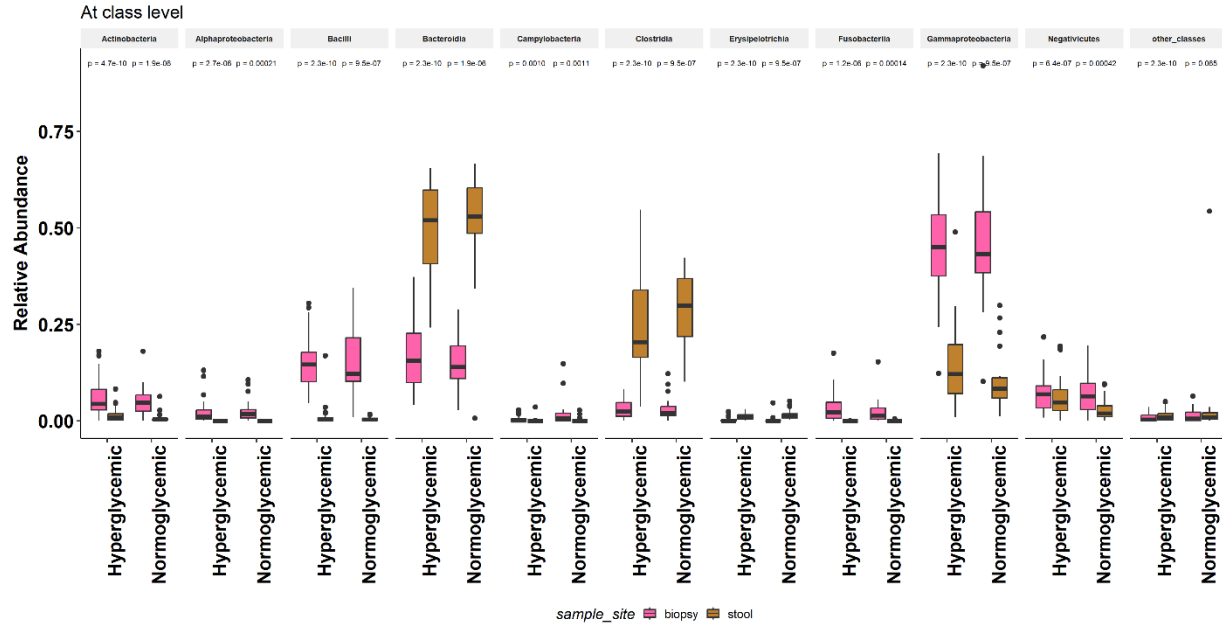
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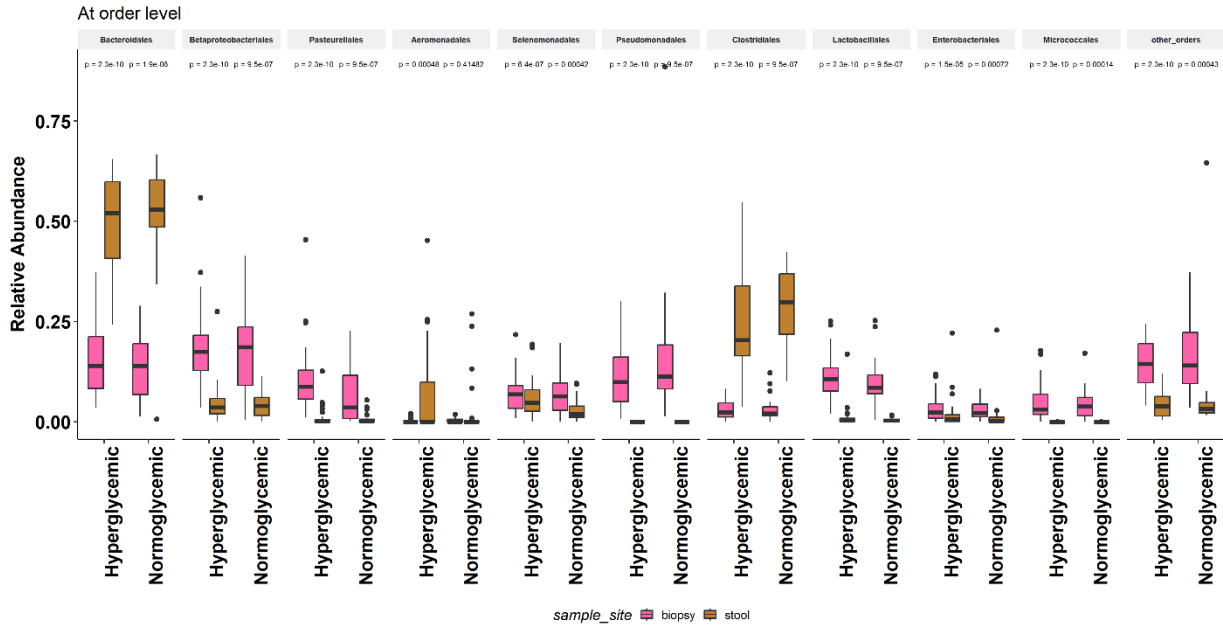
Supplementary Figures



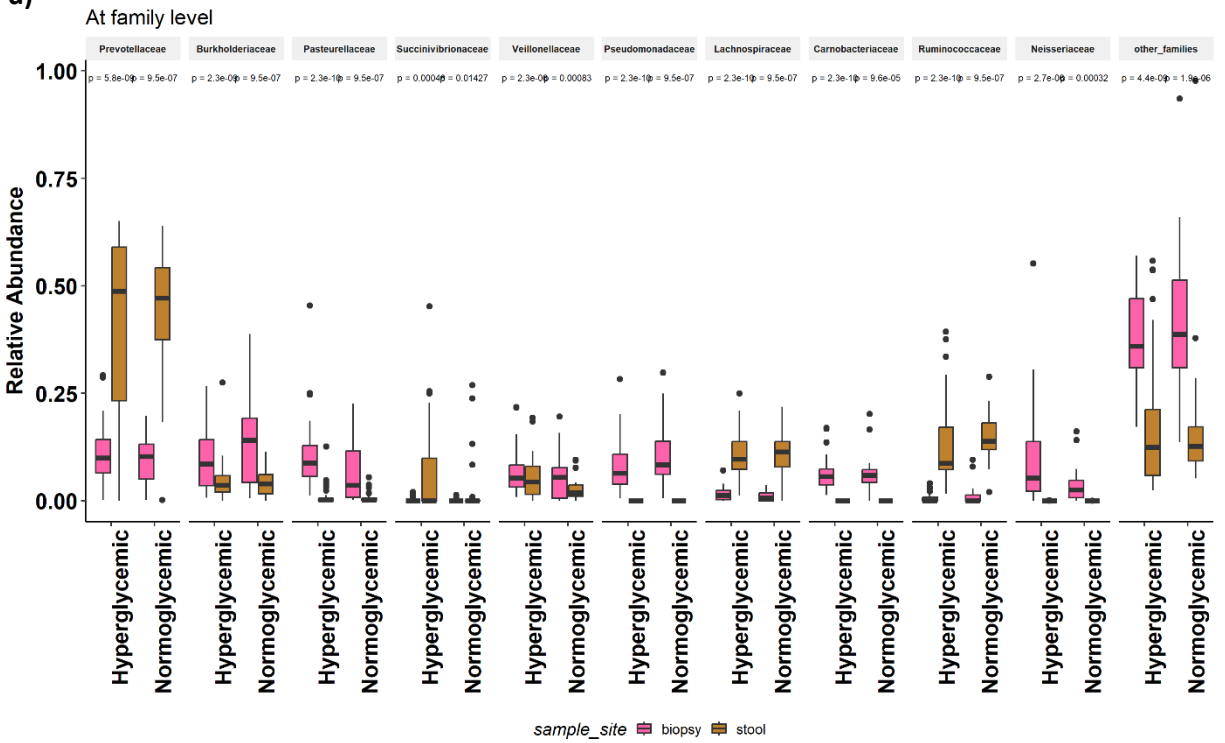
b)



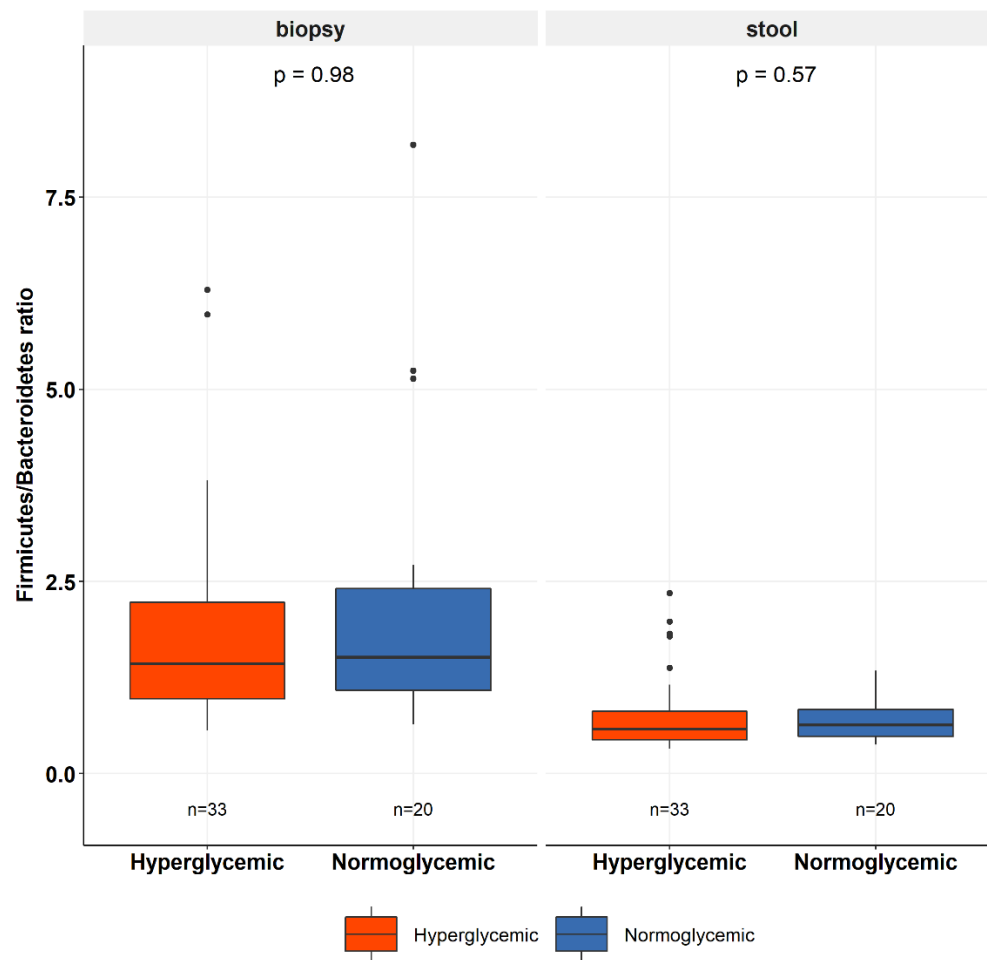
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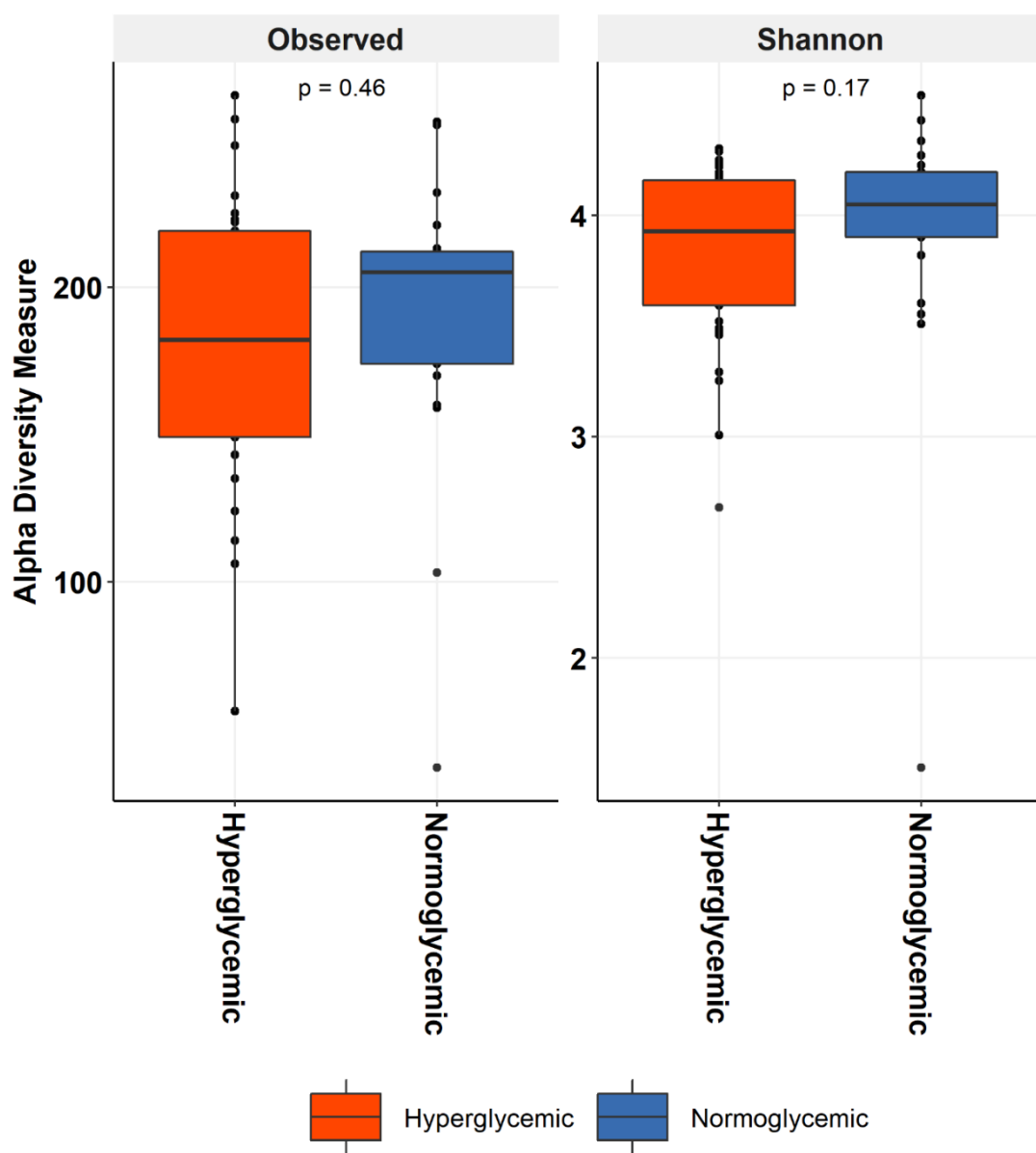
d)



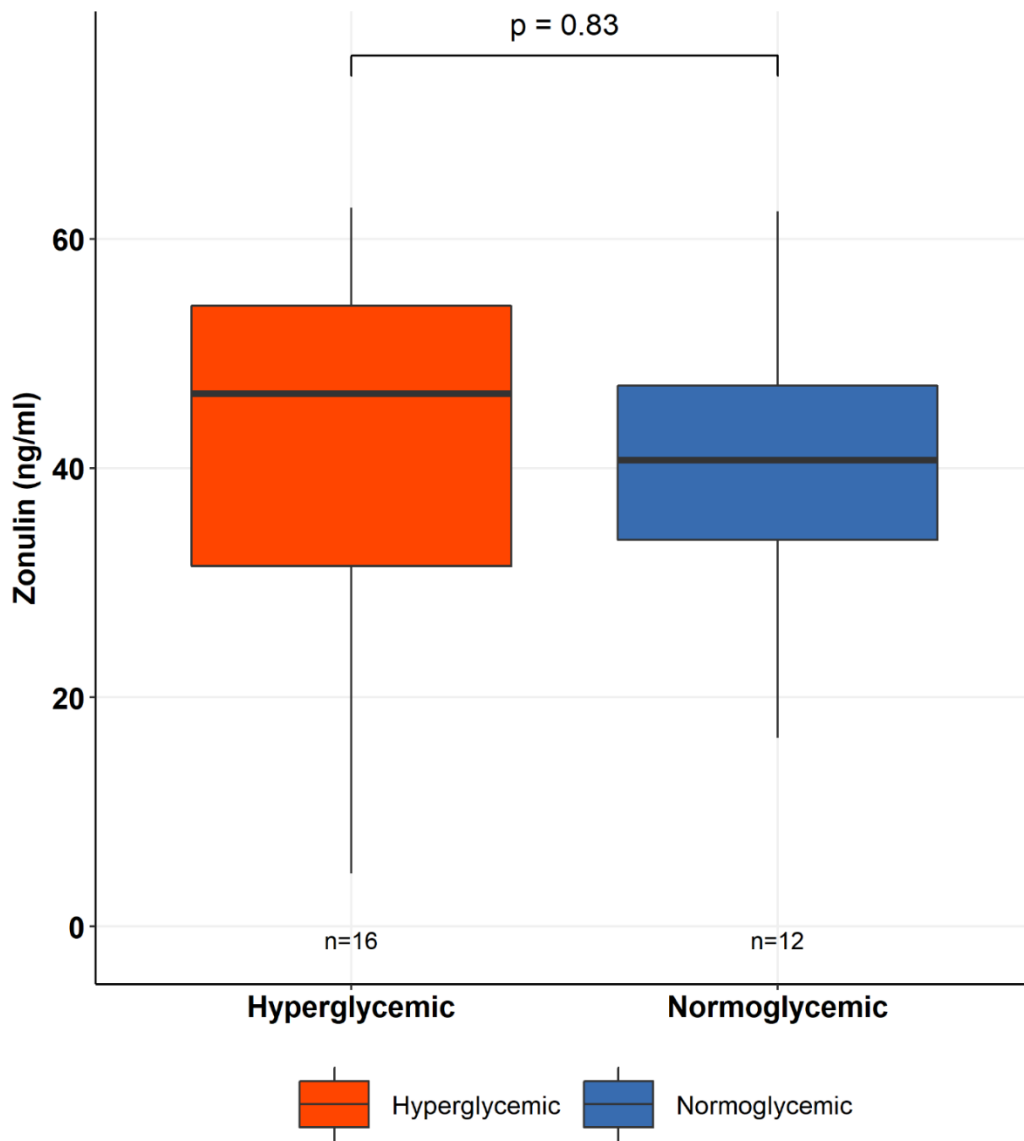
Supplementary Figure 1: Boxplot showing the comparison of top taxa between hyperglycemics and normoglycemics group in stool and duodenum samples at **a)** Phylum **b)** Class **c)** Order and **d)** Family level.



Supplementary Figure 2: Boxplot showing the comparison of Firmicutes to Bacteroidetes ratio between hyperglycemics and normoglycemics group, segregated by sample site.

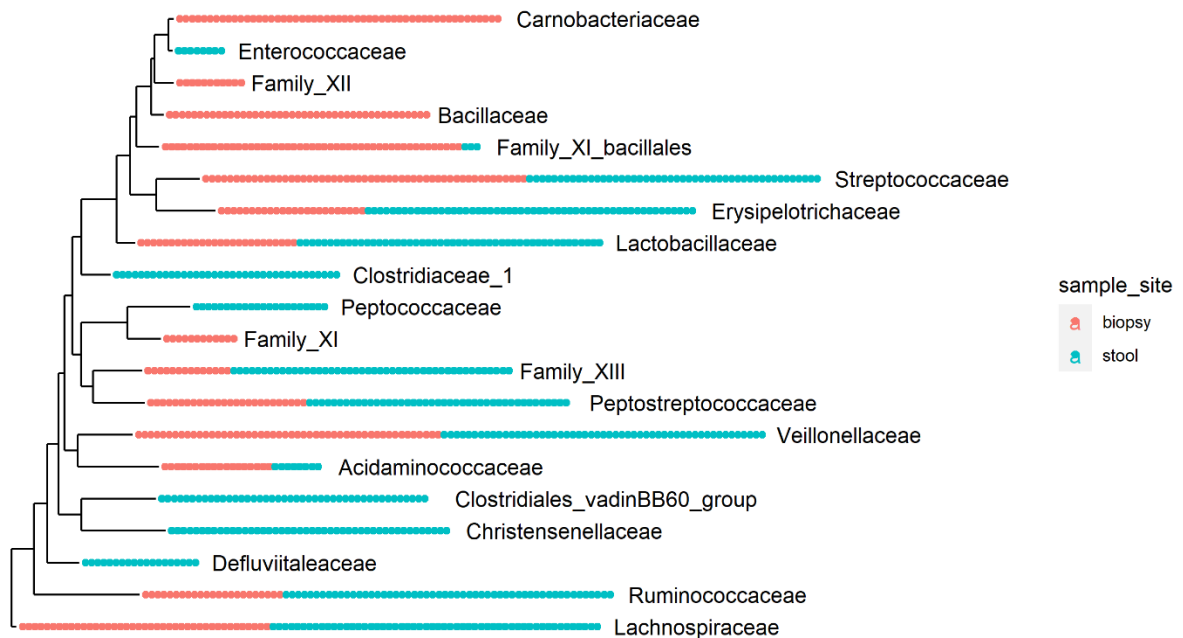


Supplementary Figure 3: Boxplot showing the comparison of alpha diversity (Observed richness and Shannon Diversity) between hyperglycemics and normoglycemics group in stool samples.



Supplementary Figure 4: Boxplot comparing the serum zonulin in hyperglycemics and normoglycemics group.

Supplementary Figure 6: Correlation plot showing the significant spearman correlation between clinical indicators with differentially abundant species and predicted metabolic pathways. Only significant values ($p < 0.05$) are shown.



Supplementary Figure 7: Phylogenetic tree showing the taxa that belong to Firmicutes phylum prevalent in stool and biopsy samples.

SUPPLEMENTARY TABLES

Supplementary Table 1: Table depicting differentially abundant species in biopsy compared to stool, analyzed using DESeq2 package.

	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj
Carnobacterium_maltaromaticum	1613.455734	-15.42078984	0.451980867	-34.11823588	3.96E-255	1.87E-253
Serratia_NA	1148.879907	-14.93697107	0.454171163	-32.88841804	3.22E-237	1.22E-235
Granulicatella_elegans	478.1497192	-30	0.919822352	-32.61499348	2.51E-233	7.92E-232
Stenotrophomonas_NA	275.2207093	-30	0.953713282	-31.45599474	3.48E-217	9.38E-216
Acinetobacter_NA	363.384368	-30	1.052574894	-28.50153483	1.12E-178	2.65E-177
Prevotella_nanceiensis	214.7459924	-30	1.067896861	-28.09260061	1.21E-173	2.53E-172
Sphingomonas_NA	439.8343998	-30	1.089555031	-27.53417601	6.85E-167	1.29E-165
Acinetobacter_johnsonii	535.4017573	-30	1.100107179	-27.27007021	9.61E-164	1.65E-162
Peptostreptococcus_stomatis	114.6630347	-29.85709389	1.145166477	-26.07227376	7.52E-150	1.18E-148
Porphyromonas_pasteri	324.7825	-30	1.197650456	-25.04904487	1.79E-138	2.60E-137
Gemella_NA	990.4518472	-14.65444836	0.628465258	-23.31783367	2.92E-120	3.25E-119
Bacillus_NA	254.921879	-30	1.295151784	-23.16330825	1.07E-118	1.12E-117
Prevotella_salivae	118.627363	-29.89616974	1.291260476	-23.15270257	1.37E-118	1.36E-117
Prevotella_melaninogenica	1072.714281	-14.8122896	0.65915845	-22.47151591	7.89E-112	7.45E-111
Lactobacillus_iners	206.1762066	-30	1.341449414	-22.36386977	8.85E-111	7.96E-110
Alcaligenes_faecalis	421.6215973	-30	1.389861713	-21.58488123	2.49E-103	2.05E-102
Corynebacterium_NA	102.8778318	-29.44931695	1.38082406	-21.32734922	6.33E-101	4.98E-100
Prevotella_histicola	187.8930393	-30	1.449001999	-20.70390518	3.19E-95	2.32E-94
Chryseobacterium_hominis	287.4101051	-30	1.469085312	-20.42086988	1.09E-92	7.64E-92
Phascolarctobacterium_faecium	404.7961298	-30	1.495143478	-20.06496396	1.49E-89	1.01E-88
Burkholderia_NA	160.3486125	-30	1.502215486	-19.97050375	9.94E-89	6.48E-88
Acinetobacter_bouvetii	251.868882	-30	1.546784691	-19.39507171	8.49E-84	5.35E-83
Prevotella_nigrescens	175.3361093	-29.3181995	1.537369589	-19.07036519	4.45E-81	2.71E-80
Neisseria_NA	2639.790751	-13.25825462	0.708998551	-18.69997422	4.95E-78	2.93E-77
Prevotella_NA	146.2953126	-30	1.643535769	-18.25332954	1.95E-74	1.11E-73
Gemella_morbilorum	90.09176658	-29.56606759	1.685854563	-17.53773323	7.38E-69	4.10E-68
Pseudonocardia_NA	92.51599136	-29.58122533	1.686963799	-17.5351868	7.72E-69	4.17E-68
Lachnoanaerobaculum_cf.	139.8399966	-30	1.719822193	-17.44366372	3.85E-68	1.96E-67
Prevotella_pallens	143.4741594	-30	1.802073871	-16.64748626	3.16E-62	1.49E-61
Streptococcus_NA	1288.141872	-7.856333751	0.472731033	-16.61903536	5.07E-62	2.28E-61
Fusobacterium_periodonticum	802.3212583	-13.39308519	0.80934851	-16.54798276	1.66E-61	7.11E-61
Fusobacterium_NA	60.13797789	-29.00018404	1.837130481	-15.78558754	3.91E-56	1.61E-55
Exiguobacterium_NA	93.9292709	-29.59374569	1.990087922	-14.87057198	5.12E-50	2.01E-49
Capnocytophaga_leadbetteri	37.20137672	-28.32123657	1.922715898	-14.72980828	4.15E-49	1.60E-48
Ochrobactrum_NA	87.50530846	-29.40021638	2.003761851	-14.67251029	9.67E-49	3.66E-48
Proteus_NA	102.7977377	-29.62629526	2.026283981	-14.62099861	2.06E-48	7.65E-48
Fusobacterium_nucleatum	375.0341906	-13.54910286	0.959634909	-14.11901832	2.90E-45	1.05E-44
Pseudonocardia_carboxydivorans	97.79473919	-29.69716414	2.143529984	-13.85432645	1.20E-43	4.27E-43
Providencia_NA	44.86608333	-28.59697134	2.070271795	-13.81314831	2.12E-43	7.43E-43
Flectobacillus_roseus	58.87670973	-28.86927361	2.095238131	-13.77851671	3.43E-43	1.18E-42
Pelomonas_NA	68.64555161	-29.1779978	2.168407593	-13.45595629	2.84E-41	9.42E-41
Nesterenkonia_xinjiangensis	89.32684545	-28.73295187	2.135778785	-13.45314977	2.95E-41	9.61E-41
Dialister_pneumosintes	46.35766155	-28.67180868	2.195996331	-13.05640099	5.84E-39	1.84E-38
Parvimonas_micra	25.76149898	-27.85563488	2.152176028	-12.94300955	2.57E-38	7.84E-38
Dolosigranulum_pigrum	27.93147186	-26.3956479	2.14570487	-12.30162091	8.88E-35	2.62E-34
Paracoccus_sphaerophysae	24.52192918	-27.7470726	2.28313361	-12.15306563	5.53E-34	1.61E-33
Streptococcus_cristatus	132.9406896	-8.015062225	0.6682081	-11.99485942	3.78E-33	1.08E-32
Oribacterium_parvum	32.62892972	-28.05738122	2.349879871	-11.93992151	7.33E-33	2.07E-32
Acinetobacter_haemolyticus	71.60401651	-29.02334051	2.445810645	-11.86655253	1.77E-32	4.91E-32
Stomatobaculum_longum	17.83171979	-27.33197519	2.312198458	-11.8207739	3.05E-32	8.35E-32
Leptotrichia_wadei	28.32265857	-27.72891664	2.346230959	-11.81849406	3.13E-32	8.46E-32
Rothia_NA	16.89007888	-27.27510674	2.442020039	-11.16907572	5.78E-29	1.52E-28
Rothia_mucilaginosa	1159.448647	-11.71296593	1.056327093	-11.0883892	1.43E-28	3.70E-28
Helicobacter_pylori	47.24198418	-28.63895592	2.866459959	-9.991053889	1.67E-23	4.04E-23
Curtobacterium_NA	44.27261809	-28.57125516	2.903894399	-9.838944268	7.65E-23	1.81E-22
Oribacterium_sinus	103.2842734	-13.46948536	1.371437281	-9.821437368	9.10E-23	2.12E-22
Prevotella_shahii	18.36636785	-27.09735969	2.808180291	-9.649437318	4.94E-22	1.14E-21
Acinetobacter_junii	27.30241135	-27.89110205	2.906844911	-9.594974245	8.39E-22	1.89E-21
Porphyromonas_endodontalis	16.97955892	-27.268738	2.899279565	-9.405349636	5.19E-21	1.14E-20

Rothia_NA	16.89007888	-27.27510674	2.442020039	-11.16907572	5.78E-29	1.52E-28
Rothia_mucilaginosa	1159.448647	-11.71296593	1.056327093	-11.0883892	1.43E-28	3.70E-28
Helicobacter_pylori	47.24198418	-28.63895592	2.866459959	-9.991053889	1.67E-23	4.04E-23
Curtobacterium_NA	44.27261809	-28.57125516	2.903894399	-9.838944268	7.65E-23	1.81E-22
Oribacterium_sinus	103.2842734	-13.46948536	1.371437281	-9.821437368	9.10E-23	2.12E-22
Prevotella_shahii	18.36636785	-27.09735969	2.808180291	-9.649437318	4.94E-22	1.14E-21
Acinetobacter_junii	27.30241135	-27.89110205	2.906844911	-9.594974245	8.39E-22	1.89E-21
Porphyromonas_endodontalis	16.97955892	-27.268738	2.899279565	-9.405349636	5.19E-21	1.14E-20
Rothia_dentocariosa	140.1632573	-13.85055073	1.581318622	-8.758861459	1.97E-18	4.19E-18
Gemella_sanguinis	115.7511191	-11.22117885	1.326874586	-8.456849627	2.75E-17	5.77E-17
Aggregatibacter_segnis	207.3884124	-11.38721119	1.356277688	-8.395929017	4.62E-17	9.50E-17
Haemophilus_NA	1939.86755	-4.189205334	0.532777286	-7.862957834	3.75E-15	7.54E-15
Campylobacter_NA	59.90669661	-13.67337056	1.753925607	-7.79586689	6.40E-15	1.26E-14
Lactococcus_NA	123.3397881	-13.62437548	1.755835954	-7.75948086	8.53E-15	1.66E-14
Campylobacter_conciscus	134.5041413	-7.786888575	1.099671197	-7.081106242	1.43E-12	2.70E-12
Neisseria_subflava	335.7335687	-11.89549808	1.887943513	-6.300770121	2.96E-10	5.38E-10
Veillonella_atypica	824.2826995	-5.724553032	0.921302955	-6.213540295	5.18E-10	9.32E-10
Veillonella_NA	352.5651384	-5.823437399	0.938429031	-6.205517097	5.45E-10	9.72E-10
Veillonella_dispar	653.6443592	-5.196364972	0.878158074	-5.917345777	3.27E-09	5.62E-09
Veillonella_rogosae	110.424345	-7.382600896	1.500881265	-4.918844061	8.71E-07	1.44E-06
Megasphaera_micronuciformis	98.12758218	-8.803019524	1.884871609	-4.67035499	3.01E-06	4.90E-06
Veillonella_tobetsuensis	138.9414678	-8.199866944	1.756641522	-4.667922762	3.04E-06	4.91E-06
Neisseria_mucosa	106.8569018	-9.11482682	2.196094729	-4.150470696	3.32E-05	5.31E-05
Aeromonas_NA	23.49732955	-8.643822068	2.16163101	-3.99875003	6.37E-05	0.000100293
Haemophilus_parainfluenzae	346.4111515	-3.448816388	0.891279002	-3.869513789	0.000109053	0.000164888
Haemophilus_sputorum	127.7660454	-7.109530254	2.039316088	-3.486232612	0.000489875	0.000712203
Dialister_invisus	7.330159539	-7.2930326	2.170748239	-3.35968606	0.000780311	0.001117263
Eubacterium_brachy	13.64647513	-8.22577768	2.482167638	-3.313949289	0.000919882	0.001307201
Eubacterium_sulci	9.992952977	-8.040796885	2.472437996	-3.252173319	0.001145262	0.001615332
Filifactor_alocis	16.76446414	-8.7908782	2.810641688	-3.127712166	0.001761726	0.002448281
Veillonella_parvula	43.00541196	-5.768775965	1.846595722	-3.124005918	0.001784069	0.002461233
Micrococcus_lylae	16.57247425	-8.665786718	2.801357445	-3.09342413	0.001978611	0.002709837
Corynebacterium_mucifaciens	8.874001242	-7.706656296	2.899307752	-2.658102194	0.007858206	0.01053334
Gemella_paraahaemolysans	9.963204523	-7.19071259	2.899787577	-2.479737705	0.013147906	0.017377302
Lautropia_mirabilis	7.723067996	-7.166182689	2.899175681	-2.471800083	0.013443467	0.017644551
Klebsiella_pneumoniae	12.06023979	-7.137240904	2.900283398	-2.460877068	0.013859785	0.017941776
Sphingobacterium_alimentarium	12.1270314	-7.144140212	2.900270707	-2.463266686	0.013767747	0.017941776
Luteimonas_tolerans	5.541083629	-6.900207768	2.900308963	-2.379128519	0.017353624	0.022311803
Gordonia_NA	5.275590278	-6.822875995	2.900429045	-2.352367835	0.018654318	0.023822068
Methylobacterium_jeotgali	6.13660632	-6.588822507	2.901207529	-2.271062115	0.023143218	0.029160455
Microbacterium_NA	1.523695446	-5.35494037	2.509655274	-2.133735428	0.032864444	0.041134967
Brachybacterium_muris	4.918158808	-6.178363207	2.901698297	-2.129223156	0.033235802	0.041326096
Actinomyces_odontolyticus	3.36722039	-5.982874887	2.893968504	-2.067360055	0.038700239	0.047806178

Supplementary Table 2: Table depicting differentially abundant species in stool compared to biopsy, analysed using DESeq2 package.

	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj
Megasphaera_NA	197.5746702	27.03893545	1.127025843	23.99140678	3.42E-127	4.62E-126
Bacteroides_uniformis	70.33650864	23.13321169	0.97078811	23.8293109	1.66E-125	2.09E-124
Faecalibacterium_prausnitzii	235.1771634	9.954791384	0.421594959	23.61221637	2.89E-123	3.41E-122
Ruminococcus_bromii	35.18817687	24.77288594	1.114620267	22.22540417	1.95E-109	1.68E-108
Bifidobacterium_longum	30.50077264	24.51312347	1.161268106	21.10892682	6.59E-99	4.98E-98
Dorea_longicatena	29.5130339	6.954800201	0.396881311	17.52362734	9.46E-69	4.97E-68
Bacteroides_thetaiotaomicron	30.29770029	24.24740749	1.415270599	17.13270063	8.46E-66	4.21E-65
Alistipes_putredinis	23.84087191	24.18623168	1.43852452	16.8132217	1.95E-63	9.46E-63
Faecalibacterium_NA	108.287534	8.81950205	0.530216284	16.63378196	3.97E-62	1.83E-61
Lactobacillus_delbrueckii	9.439956684	22.95635989	1.382670896	16.6029096	6.64E-62	2.92E-61
Blautia_NA	25.89055506	6.760554335	0.409870484	16.49436736	4.03E-61	1.69E-60
Prevotella_copri	243.3688704	10.00747256	0.654546725	15.28916451	9.03E-53	3.63E-52
Blautia_massiliensis	20.93315762	6.464491017	0.473938522	13.6399358	2.32E-42	7.82E-42
Eubacterium_eligens	49.49645181	7.677029748	0.580593626	13.22272483	6.49E-40	2.08E-39
Roseburia_faecis	136.432762	9.129075081	0.701402076	13.0154663	9.99E-39	3.10E-38
Coprococcus_comes	18.48642867	6.209643127	0.503401593	12.33536646	5.84E-35	1.75E-34
Butyrivibrio_crossotus	22.65067886	23.97173654	2.070847533	11.57580949	5.47E-31	1.45E-30
Coprococcus_catus	16.33295302	5.985453853	0.557719857	10.73200779	7.20E-27	1.84E-26
Sutterella_wadsworthensis	103.1952044	8.769149082	0.82713759	10.60180216	2.92E-26	7.37E-26
Eubacterium_hallii	9.108093599	5.231137872	0.495985417	10.54695903	5.25E-26	1.30E-25
Bacteroides_NA	61.24535127	7.754113147	0.767825068	10.09880176	5.59E-24	1.37E-23
Mitsuokella_multacida	9.108265629	22.66709676	2.276442089	9.957247263	2.34E-23	5.61E-23
Fusicatenibacter_saccharivorans	10.90111414	5.403805549	0.560529176	9.640542858	5.39E-22	1.23E-21
Bacteroides_stercoris	40.84392257	24.84622467	2.637401321	9.420722009	4.48E-21	9.96E-21
Roseburia_inulinivorans	96.18501909	6.659552645	0.744733978	8.942189887	3.82E-19	8.29E-19
Odoribacter_splanchnicus	58.20607526	7.943501626	0.890955833	8.915707527	4.85E-19	1.04E-18
Mitsuokella_jalaludinii	67.8773135	7.981479732	0.950466063	8.397437891	4.56E-17	9.48E-17
Blautia_obeum	16.49929952	5.836516561	0.733517214	7.956891054	1.76E-15	3.59E-15
Ruminococcus_NA	7.217012626	4.925614034	0.627504297	7.849530368	4.18E-15	8.31E-15
Romboutsia_NA	12.89168029	5.75828144	0.749010182	7.687854685	1.50E-14	2.89E-14
Blautia_faecis	5.805876017	4.571122993	0.63127693	7.241074046	4.45E-13	8.50E-13
Slackia_isoflavoniconvertens	4.566723141	4.227291432	0.608482063	6.947273692	3.72E-12	6.97E-12
Coprococcus_eutactus	36.11758925	6.953475939	1.056723041	6.580225537	4.70E-11	8.70E-11
Roseburia_hominis	17.82179239	6.208449452	0.977595747	6.350732879	2.14E-10	3.93E-10
Bilophila_wadsworthia	23.30945385	6.60360946	1.06996704	6.171787737	6.75E-10	1.19E-09
Roseburia_intestinalis	22.96937726	6.590765895	1.090574619	6.0433883	1.51E-09	2.64E-09
Alistipes_obesi	23.24895376	6.620499325	1.109417901	5.967543265	2.41E-09	4.18E-09
Alistipes_senegalensis	19.74596863	6.350694678	1.077009217	5.89660198	3.71E-09	6.32E-09
Anaerostipes_hadrus	5.230760655	4.458208804	0.762657981	5.845620072	5.05E-09	8.52E-09
Holdemanella_biformis	15.17594023	5.968628946	1.202433381	4.963791792	6.91E-07	1.16E-06
Lactobacillus_ruminis	115.8026381	4.527815631	0.922440517	4.90851773	9.18E-07	1.51E-06
Ruminococcus_callidus	5.998896335	4.664045909	1.134493162	4.111127385	3.94E-05	6.25E-05
Dorea_formicigenerans	10.17736589	2.348375489	0.595885723	3.940982977	8.11E-05	0.000126752
Flavonifractor_plautii	5.292811925	4.472615289	1.140117985	3.922940739	8.75E-05	0.000135514
Clostridium_NA	3.832864782	4.021133524	1.026617405	3.916876437	8.97E-05	0.000137837
Ruminococcus_bicirculans	8.034208248	5.084247005	1.300836615	3.908443956	9.29E-05	0.000141586
Lachnospiraceae_bacterium	4.589092292	4.155891908	1.080310514	3.846942017	0.000119601	0.000179402
Allisonella_histaminiformans	6.833264595	4.681266652	1.235301777	3.789573318	0.000150906	0.000224577
Parasutterella_excrementihominis	6.322664811	4.548133825	1.24152455	3.663345862	0.000248942	0.000367578
Bifidobacterium_NA	211.9075037	2.635239217	0.722158391	3.649115276	0.000263145	0.000385538
Parabacteroides_distasonis	22.57697765	2.950428975	0.876472179	3.366255135	0.000761962	0.001099319
Intestinibacter_bartlettii	3.035093413	3.654111323	1.124689883	3.24899457	0.001158137	0.001621392
Escherichia/Shigella_NA	280.3165491	2.433914347	0.802090093	3.034465042	0.002409627	0.003276399
Alistipes_shahii	5.754964555	4.411673322	1.608029704	2.743527257	0.0060783	0.008205705
Klebsiella_NA	20.15517261	3.951550477	1.504537497	2.626422063	0.008628775	0.011484778
Bifidobacterium_angulatum	5.417323415	4.460479096	1.918217259	2.325325286	0.020054573	0.025438351

Supplementary Table 3: Table depicting the Spearman correlations of zonulin with anthropometric variables and bacterial load.

Variable	Correlation Coefficient	95% CI	p value
Height (m)	-0.46	1.59, 1.66	0.012
Weight (Kg)	0.48	69.5, 78.6	0.009
Body Mass Index (Kg/m ²)	0.65	26.0, 30.8	0.0001
Waist Circumference (in.)	0.47	38.0, 41.7	0.009
Hip Circumference (in.)	0.53	39.2, 42.3	0.003
Total Bacterial Count (/ng of DNA)	0.36	474.1, 2354.4	0.061 (#0.03, one-sided)

