

Article Title: Integrated omics analysis reveals the alteration of gut microbiota and fecal metabolites in *Cervus elaphus kansuensis*

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Supplemental Table S1: General characteristics of 16S rDNA sequencing

CRD				WRD			
Samples	Raw tags	Effective tags	ASVs	Samples	Raw tags	Effective tags	ASVs
C1	110,435	62,021	1,608	W1	101,297	63,916	1,374
C2	104,703	58,579	1,569	W2	102,579	65,779	1,273
C3	101,725	62,202	1,580	W3	105,724	69,542	1,294
C4	102,471	61,627	1,508	W4	114,024	71,645	1,267
C5	99,123	56,717	1,459	W5	83,665	48,339	945
C6	107,389	64,691	1,567	W6	74,832	44,425	833
C7	116,317	67,213	1,650	W7	102,870	63,449	1,261
C8	107,645	64,350	1,171	W8	81,717	50,562	981
C9	103,295	68,031	1,645	W9	107,226	63,848	1,358
C10	102,882	62,093	1,477	W10	100,488	69,919	1,315
C11	103,334	55,695	1,392	W11	114,428	70,355	1,302
C12	109,557	63,007	1,577	W12	87,503	53,777	749
C13	107,085	56,320	1,563	W13	81,848	47,747	996
C14	105,037	59,644	1,491	W14	79,109	46,495	849
C15	99,636	59,933	1,636	W15	111,907	60,195	1,306
C16	111,427	62,233	1,506	W16	80,701	48,632	784
C17	114,035	65,666	1,560	W17	90,168	65,245	508
C18	74,990	45,163	866	W18	64,053	40,988	796
C19	112,979	68,196	1,613	W19	106,106	67,270	1,201
C20	103,949	58,423	1,451				
C21	100,109	57,734	1,463				
C22	103,097	63,058	1,467				

Supplemental Table S2: Statistics of 16S rDNA sequencing

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Supplemental Table S3: Relative abundance of gut microbiota detected by 16S rDNA sequencing after homogenization at phylum level

Taxonomy	WRD	CRD	Tax_detail
<i>Firmicutes</i>	0.70075	0.620228	k__Bacteria;p__Firmicutes;
<i>Bacteroidota</i>	0.235322	0.321706	k__Bacteria;p__Bacteroidota;
<i>Proteobacteria</i>	0.021647	0.009687	k__Bacteria;p__Proteobacteria;
<i>Euryarchaeota</i>	0.012481	0.010964	k__Archaea;p__Euryarchaeota;
<i>Actinobacteriota</i>	0.012271	0.004946	k__Bacteria;p__Actinobacteriota;
<i>Verrucomicrobiota</i>	0.001194	0.011572	k__Bacteria;p__Verrucomicrobiota;
<i>Spirochaetota</i>	0.002811	0.008532	k__Bacteria;p__Spirochaetota;
<i>Desulfobacterota</i>	0.001502	0.006118	k__Bacteria;p__Desulfobacterota;
<i>Patescibacteria</i>	0.00273	0.001536	k__Bacteria;p__Patescibacteria;
<i>Cyanobacteria</i>	0.001264	0.002785	k__Bacteria;p__Cyanobacteria;
<i>Campilobacterota</i>	0.000945	0.000582	k__Bacteria;p__Campilobacterota;
<i>Acidobacteriota</i>	0.001711	0	k__Bacteria;p__Acidobacteriota;
<i>Chloroflexi</i>	0.001706	0.000004	k__Bacteria;p__Chloroflexi;
<i>Nitrospirota</i>	0.001417	0.000009	k__Bacteria;p__Nitrospirota;
<i>Myxococcota</i>	0.000814	0.00004	k__Bacteria;p__Myxococcota;
<i>Elusimicrobiota</i>	0.000305	0.00074	k__Bacteria;p__Elusimicrobiota;
<i>Gemmatimonadota</i>	0.000277	0.000019	k__Bacteria;p__Gemmatimonadota;
<i>Fibrobacterota</i>	0.000231	0.000136	k__Bacteria;p__Fibrobacterota;
<i>Deferribacterota</i>	0.000153	0.000212	k__Bacteria;p__Deferribacterota;
<i>Armatimonadota</i>	0.000206	0.000003	k__Bacteria;p__Armatimonadota;
<i>Halobacterota</i>	0.000003	0.000046	k__Archaea;p__Halobacterota;
<i>SAR324_clade(Marine_group_B)</i>	0.000055	0.00004	k__Bacteria;p__SAR324_clade(Marine_group_B);
<i>Thermoplasmatota</i>	0	0.000062	k__Archaea;p__Thermoplasmatota;
<i>Latescibacterota</i>	0.000033	0	k__Bacteria;p__Latescibacterota;
<i>Bdellovibrionota</i>	0.00002	0.000011	k__Bacteria;p__Bdellovibrionota;
<i>NB1-j</i>	0.000023	0	k__Bacteria;p__NB1-j;
<i>WPS-2</i>	0.000044	0	k__Bacteria;p__WPS-2;
<i>Zixibacteria</i>	0.000017	0	k__Bacteria;p__Zixibacteria;
<i>Synergistota</i>	0	0.000016	k__Bacteria;p__Synergistota;
Others	0.000066	0.000005	Others

Supplemental Table S4: Relative abundance of gut microbiota detected by 16S rDNA sequencing after homogenization at genus level

Taxonomy	WRD	CRD
Others	0.192426	0.182979
UCG-005	0.138798	0.127736
Rikenellaceae_RC9_gut_group	0.086585	0.117099
UCG-010	0.084722	0.11039
Eubacterium_coprostanoligenes_group	0.04903	0.049079
Christensenellaceae_R-7_group	0.036849	0.035573
Bacteroides	0.02914	0.035518
Alistipes	0.023091	0.034067
Monoglobus	0.028429	0.025419
Bacteroidales_RF16_group	0.007626	0.022234
Clostridia_UCG-014	0.025421	0.015964
dqA-11_gut_group	0.02123	0.015631
Prevotellaceae_UCG-003	0.002147	0.015183
UCG-009	0.007902	0.012313
Prevotellaceae_UCG-004	0.020025	0.011599
Akkermansia	0.001061	0.01133
Methanobrevibacter	0.011362	0.010853
Romboutsia	0.00966	0.009456
Muribaculaceae	0.014665	0.008524
Treponema	0.002785	0.008338
Clostridia_vadinBB60_group	0.007118	0.00829
F082	0.000674	0.00784
NK4A214_group	0.007435	0.007359
UCG-002	0.001999	0.006794
Ruminococcus	0.00636	0.00612
Mailhella	0.001297	0.005837
Oscillibacter	0.003528	0.005159
Lachnospiraceae_UCG-010	0.00275	0.005088
Paeniclostridium	0.000422	0.00476
Family_XIII_AD3011_group	0.001677	0.004628
p-2534-18B5_gut_group	0.000117	0.003939
p-251-o5	0.004855	0.003912
Candidatus_Soleaferrea	0.002897	0.002969
Clostridium_sensu_stricto_1	0.000588	0.002802
Phascolarctobacterium	0.00098	0.002502
Gastranaerophilales	0.001088	0.002401
Incertae_Sedis	0.002072	0.002296
RF39	0.002166	0.002285
Agathobacter	0.00709	0.001785
Papillibacter	0.000772	0.001679
Bacillus	0.041751	0.001641
Lachnospiraceae_NK3A20_group	0.000239	0.001617
Eubacterium_ruminantium_group	0.001213	0.001613
Hydrogenoanaerobacterium	0.0006	0.001565
Candidatus_Saccharimonas	0.000616	0.001536
Prevotellaceae_UCG-001	0.000541	0.001439
Izomoplasmatales	0.001074	0.001186
Turicibacter	0.001184	0.00118
Dorea	0.000953	0.001104
Anaerorhabdus_furcosa_group	0.000859	0.001085
Olsenella	0.000186	0.001053
Anaerovorax	0.000473	0.001032
Ruminococcaceae	0.00142	0.000955
Cellulosilyticum	0.000048	0.000931
Defluviitaleaceae_UCG-011	0.000703	0.000885
Terrisporobacter	0.000461	0.000827
Pseudomonas	0.000258	0.000789
Elusimicrobium	0.000294	0.00074
Eubacterium_ventriosum_group	0.000178	0.000727
Prevotella	0.002111	0.000723
Arthrobacter	0.004535	0.000718
Eubacterium_nodatum_group	0.000934	0.00068
Bacteroidales_UCG-001	0.000028	0.00068
Sporichthyaceae	0.000073	0.000648
Pygmaibacter	0.000692	0.000644
Lachnospiraceae_NK4A136_group	0.001491	0.000637
Alloprevotella	0.000278	0.000623
Flavobacterium	0.000147	0.000619
Rheinheimera	0.000139	0.000613
M2PB4-65_termite_group	0.000014	0.000598
Saccharofermentans	0.000248	0.000557
Oscillospiraceae	0.000263	0.000547
Pseudarcobacter	0.000061	0.000528
Eubacterium_siraeum_group	0.001575	0.000507
Colidextribacter	0.000947	0.000499
Odoribacter	0.000167	0.000471
Lactobacillus	0.002807	0.000464
Parasutterella	0.000613	0.000448
Oscillospira	0.000838	0.000441
Lysinibacillus	0.019453	0.000437
Acetitumaculum	0.000091	0.000436
Escherichia-Shigella	0.000073	0.000433
Sphingorhabdus	0.000069	0.000402
Eubacterium_brachy_group	0.001108	0.000375
hgcI_clade	0.000052	0.000366
Parabacteroides	0.000058	0.000351
Incertae_Sedis	0.000041	0.000335
V9D2013_group	0.000063	0.000331
Clostridium_sensu_stricto_6	0.000003	0.000323
Sutterella	0.000022	0.000286
DNF00809	0.00023	0.000282
Rikenella	0.000044	0.000281
qir-aah93h0	0.000009	0.000274

<i>Eubacterium_hallii_group</i>	0.000102	0.000271
<i>Aeromonas</i>	0.00012	0.00027
<i>Bacteroidales</i>	0.000011	0.000265
<i>Paludicola</i>	0.000102	0.000263
<i>Mogibacterium</i>	0.000144	0.000258
<i>Caulobacter</i>	0.000067	0.000246
<i>Limnohabitans</i>	0.000034	0.000242
<i>Moryella</i>	0.000134	0.000236
<i>Solibacillus</i>	0.013153	0.000228
<i>Negativibacillus</i>	0.000352	0.000227
<i>Polynucleobacter</i>	0.000016	0.000225
<i>Lachnospiraceae_UCG-002</i>	0.000078	0.000223
<i>Chloroplast</i>	0.000147	0.000221
<i>Corynebacterium</i>	0.000016	0.000221
<i>XBB1006</i>	0.000061	0.00022
<i>Coprococcus</i>	0.000053	0.00022
<i>Mucispirillum</i>	0.000153	0.000212
<i>Prevotellaceae_Ga6A1_group</i>	0.000003	0.000211
<i>Succinivibrio</i>	0.000019	0.000209
<i>Candidatus_Planktophila</i>	0.000028	0.000204
<i>Shewanella</i>	0.000025	0.0002
<i>Lachnospiraceae_NK4B4_group</i>	0.000102	0.000192
<i>Enterorhabdus</i>	0.000131	0.000185
<i>Polaromonas</i>	0.000041	0.000184
<i>Pedobacter</i>	0.000022	0.000179
<i>Tuzzarella</i>	0.000095	0.000178
<i>Brevundimonas</i>	0.000053	0.000174
<i>Algoriphagus</i>	0.000027	0.000174
<i>Caproiciproducens</i>	0.000106	0.000173
<i>Catenibacillus</i>	0	0.000166
<i>Eubacterium_xylanophilum_group</i>	0.000283	0.000158
<i>Acinetobacter</i>	0.005385	0.000155
<i>Family_XIII_UCG-001</i>	0.000139	0.000154
<i>Desulfovibrio</i>	0.000088	0.000151
<i>Roseburia</i>	0.000994	0.000147
<i>Blautia</i>	0.000184	0.000147
<i>GWE2-31-10</i>	0.000003	0.000143
<i>Sediminibacterium</i>	0.000011	0.000142
<i>Cyanobium_PCC-6307</i>	0.000019	0.000138
<i>Fibrobacter</i>	0.000231	0.000136
<i>Klebsiella</i>	0	0.000131
<i>UCG-007</i>	0.000086	0.000126
<i>Rhodoferrax</i>	0.000038	0.000123
<i>DTU014</i>	0.000009	0.000123
<i>Clostridium_methylpentosum_group</i>	0.000044	0.000119
<i>UCG-004</i>	0.000095	0.000115
<i>Frisingicoccus</i>	0.000103	0.000113
<i>Salinicoccus</i>	0.000005	0.000101
<i>Bifidobacterium</i>	0.000089	0.000099
<i>Methanospaera</i>	0.001119	0.000096
<i>Ruminiclostridium</i>	0.00003	0.000094
<i>Peptococcus</i>	0.000019	0.000094
<i>UKL13-1</i>	0	0.000094
<i>Pseudarcicella</i>	0.000014	0.000092
<i>Faecalibacterium</i>	0.000217	0.000089
<i>Dubosiella</i>	0.000145	0.000089
<i>Coriobacteriaceae_UCG-002</i>	0.00003	0.000089
<i>Intestinimonas</i>	0.000303	0.000086
<i>Aeriscardovia</i>	0.000006	0.000084
<i>Succiniclaticum</i>	0.000003	0.000084
<i>Candidatus_Limnoluna</i>	0	0.00008
<i>Ruminobacter</i>	0.000003	0.000078
<i>Dechloromonas</i>	0.0004	0.000077
<i>Mitochondria</i>	0.000022	0.000077
<i>Lachnospiraceae_AC2044_group</i>	0.000013	0.000077
<i>Candidatus_Planktoluna</i>	0.000013	0.000073
<i>Parvibacter</i>	0.000286	0.00007
<i>Hydrogenophaga</i>	0.000355	0.000067
<i>Psychrobacillus</i>	0.004936	0.000066
<i>Allobaculum</i>	0.000038	0.000066
<i>Rhodobacter</i>	0.000423	0.000063
<i>Dinghuibacter</i>	0.000028	0.000063
<i>Howardella</i>	0.000014	0.000063
<i>Victivallaceae</i>	0.000006	0.000063
<i>Incertae_Sedis</i>	0	0.000063
<i>Planococcus</i>	0.000003	0.000062
<i>GKS98_freshwater_group</i>	0.000006	0.000059
<i>WCHB1-41</i>	0.000002	0.000058
<i>Erysipelatoclostridium</i>	0.00015	0.000057
<i>Acetobacter</i>	0.000009	0.000057
<i>Sanguibacteroides</i>	0.000005	0.000055
<i>Candidatus_Aquirestis</i>	0	0.000055
<i>Rurimicrobium</i>	0.000002	0.000054
<i>CL500-29_marine_group</i>	0.000144	0.000053
<i>Butyrivibrio</i>	0.000011	0.000049
<i>Anaerotruncus</i>	0.000208	0.000047
<i>Lacihabitans</i>	0.000003	0.000046
<i>Methanocorpusculum</i>	0.000003	0.000046
<i>Novosphingobium</i>	0.000134	0.000045
<i>Atopobium</i>	0.000067	0.000045
<i>Erysipelothrix</i>	0.000009	0.000043
<i>Citricoccus</i>	0	0.000043
<i>SAR324_clade(Marine_group_B)</i>	0.000055	0.00004
<i>Sphaerochaeta</i>	0.000002	0.00004
<i>NS11-12_marine_group</i>	0	0.00004
<i>Prevotellaceae_NK3B31_group</i>	0.000041	0.000039

env.OPS_17	0.000006	0.000039
Fluviicola	0.000006	0.000036
Acidovorax	0.00032	0.000035
OLB12	0.000156	0.000035
Roseomonas	0.000041	0.000035
Dielma	0.000333	0.000034
Flavonifractor	0.000213	0.000034
Erysipelotrichaceae	0.000209	0.000032
Kocuria	0	0.000032
EMP-G18	0.000092	0.000031
Luteolibacter	0.000006	0.000031
Enteractinococcus	0.000003	0.000031
Methylotenera	0	0.000031
Tabrizicola	0	0.000031
Paraprevotella	0.000103	0.000028
Hyphomonas	0.000019	0.000028
Campylobacter	0	0.000028
Arenimonas	0.000111	0.000027
hoa5-07d05_gut_group	0.000014	0.000027
Lachnospiraceae_XPB1014_group	0.000006	0.000027
Malikia	0	0.000027
Salinimicrobium	0	0.000027
Candidatus_Aquiluna	0	0.000027
Helicobacter	0.000838	0.000026
Anaeroplasma	0.000405	0.000026
Breznakia	0.000045	0.000026
Kapobacteriales	0.00003	0.000026
Solitalea	0.000008	0.000026
Lactococcus	0.000005	0.000026
MWH-CFBk5	0	0.000026
Muribaculum	0.000203	0.000023
Lachnospiraceae_UCG-001	0.000181	0.000023
LD29	0.000005	0.000023
Ignavibacterium	0	0.000023
Pantoea	0.000713	0.000022
Microcystis_PCC-7914	0	0.000019
Comamonas	0.000506	0.000018
Lachnospira	0.000297	0.000018
Denitratisona	0.000158	0.000018
PeM15	0.000084	0.000018
Caldicoprobacter	0	0.000018
Paludibacter	0	0.000016
Marvinbryantia	0.000073	0.000015
Anaerofustis	0.000006	0.000015
Pseudorhodobacter	0	0.000015
Rhodococcus	0.000392	0.000013
Solobacterium	0.000095	0.000013
Streptococcus	0.000045	0.000013
Cerasicoccus	0.000033	0.000013
Victivallis	0.000005	0.000013
Sandarakinorhabdus	0.000003	0.000013
Faecalitalea	0	0.000013
UCG-001	0.000048	0.000012
Sulfuritalea	0.000048	0.000012
Anaerovibrio	0.000008	0.000012
Ornithinimicrobium	0	0.000012
OC31	0	0.000012
COB_P4-1_termite_group	0	0.000012
Lachnospiraceae_UCG-006	0.000016	0.000011
OM27_clade	0.000006	0.000011
Desulfatiglans	0	0.000011
Lysobacter	0.00002	0.000009
Harryflintia	0.000014	0.000009
Phenylobacterium	0.000008	0.000009
Ileibacterium	0.000006	0.000009
Bilophila	0.000002	0.000009
Garicola	0	0.000009
Jeotgalicoccus	0	0.000009
Ferruginibacter	0.000266	0.000008
Syntrophococcus	0.000014	0.000008
Hirschia	0.000008	0.000008
Paenisporosarcina	0.000006	0.000008
Thiobacillus	0	0.000008
Vogesella	0	0.000008
Tyzzerella	0	0.000008
BSV26	0	0.000008
Sulfurifustis	0	0.000007
Rhodovastum	0	0.000007
UCG-008	0	0.000007
Georgenia	0	0.000007
Oceanobacillus	0	0.000007
Clostridium_sensu_stricto_13	0	0.000007
Eubacterium	0	0.000007
Catenibacterium	0	0.000007
Ornithinibacillus	0	0.000007
Sericytochromatia	0	0.000007
LD-RB-34	0	0.000007
Ellin6067	0.000158	0.000005
P3OB-42	0.000042	0.000005
Erysipelotrichaceae_UCG-009	0.000005	0.000005
Laceyella	0	0.000005
Aliicoccus	0	0.000005
Anaerosporobacter	0	0.000005
Altererythrobacter	0	0.000005
Aliidiomarina	0	0.000005
Sva0081_sediment_group	0	0.000005

<i>Bacteroidales_BS11_gut_group</i>	0	0.000005
<i>Hoeflea</i>	0	0.000005
<i>Brevibacillus</i>	0	0.000005
<i>Isoptericola</i>	0	0.000005
<i>Blrii41</i>	0	0.000005
<i>Acetatifactor</i>	0	0.000005
<i>Paenibacillus</i>	0.00065	0.000004
<i>Terrimonas</i>	0.000241	0.000004
<i>A0839</i>	0.000064	0.000004
<i>Butyricoccus</i>	0.000059	0.000004
<i>Candidatus_Stoquefichus</i>	0.000016	0.000004
<i>Devosia</i>	0.000006	0.000004
<i>Undibacterium</i>	0.000006	0.000004
<i>Eubacterium_oxidoreducens_group</i>	0.000005	0.000004
<i>Pelagibacterium</i>	0.000002	0.000004
<i>Christensenellaceae</i>	0	0.000004
<i>Azospirillum</i>	0	0.000004
<i>Atopostipes</i>	0	0.000004
<i>Cellvibrio</i>	0	0.000004
<i>Luteimonas</i>	0	0.000004
<i>GCA-900066575</i>	0.000252	0.000003
<i>Nocardioidea</i>	0.000147	0.000003
<i>Armatimonas</i>	0.000005	0.000003
<i>Aliihoeflea</i>	0	0.000003
<i>CAG-352</i>	0	0.000003
<i>Halomonas</i>	0.000011	0.000001
<i>Aureimonas</i>	0.000005	0.000001
<i>Micropruina</i>	0.002322	0
<i>Nitrospira</i>	0.001417	0
<i>Saccharimonadales</i>	0.001361	0
<i>Dokdonella</i>	0.001241	0
<i>Ahniella</i>	0.000655	0
<i>Zoogloea</i>	0.000598	0
<i>Nakamurella</i>	0.000586	0
<i>Tessaracoccus</i>	0.000497	0
<i>TM7a</i>	0.000484	0
<i>SWB02</i>	0.000366	0
<i>Pseudoxanthomonas</i>	0.000305	0
<i>Ottowia</i>	0.000302	0
<i>Nitrosomonas</i>	0.000302	0
<i>DS-100</i>	0.000295	0
<i>Amaricoccus</i>	0.00028	0
<i>Haliangium</i>	0.000248	0
<i>Subgroup_17</i>	0.000239	0
<i>Thauera</i>	0.000236	0
<i>JG1_0001001-H03</i>	0.000223	0
<i>UTCFX1</i>	0.000206	0
<i>Fimbriimonadaceae</i>	0.000202	0
<i>Trichococcus</i>	0.0002	0
<i>IMCC26207</i>	0.000184	0
<i>Paracoccus</i>	0.000183	0
<i>Hyphomicrobium</i>	0.000178	0
<i>SC-I-84</i>	0.000173	0
<i>Candidatus_Alysiosphaera</i>	0.000173	0
<i>Ferribacterium</i>	0.000166	0
<i>PHOS-HE36</i>	0.000163	0
<i>Kineosphaera</i>	0.000153	0
<i>Candidatus_Accumulibacter</i>	0.000152	0
<i>Vicinamibacteraceae</i>	0.00015	0
<i>Candidatus_Competibacter</i>	0.000145	0
<i>Microbacterium</i>	0.000136	0
<i>Pseudoflavonifractor</i>	0.000131	0
<i>Subgroup_10</i>	0.000131	0
<i>Bradyrhizobium</i>	0.000117	0
<i>OLB14</i>	0.000113	0
<i>ASF356</i>	0.000111	0
<i>Bryobacter</i>	0.000102	0
<i>A4b</i>	0.000102	0
<i>AAP99</i>	0.0001	0
<i>AKYH767</i>	0.000097	0
<i>Cellulomonas</i>	0.000091	0
<i>RBG-13-54-9</i>	0.000078	0
<i>Defluviococcus</i>	0.000077	0
<i>SJA-28</i>	0.000073	0
<i>Gemmobacter</i>	0.000072	0
<i>Thermomonas</i>	0.000072	0
<i>Nannocystis</i>	0.000069	0
<i>Mesorhizobium</i>	0.000069	0
<i>NS9_marine_group</i>	0.000067	0
<i>UBA1819</i>	0.000066	0
<i>Aeromonadales</i>	0.000064	0
<i>Kouleothrix</i>	0.000063	0
<i>BD1-7_clade</i>	0.000058	0
<i>Clostridium_sensu_stricto_3</i>	0.000056	0
<i>Polyangium</i>	0.000056	0
<i>Azospira</i>	0.000055	0
<i>Massilia</i>	0.000053	0
<i>Mycobacterium</i>	0.000053	0
<i>Aquimonas</i>	0.000052	0
<i>Micromonospora</i>	0.000052	0
<i>Defluviimonas</i>	0.00005	0
<i>Aquabacterium</i>	0.00005	0
<i>Arcobacter</i>	0.000047	0
<i>DEV007</i>	0.000047	0
<i>Sandaracinus</i>	0.000047	0
<i>mle1-27</i>	0.000045	0

<i>Pajaroellobacter</i>	0.000045	0
<i>Iamia</i>	0.000044	0
WPS-2	0.000044	0
<i>Propioniciclava</i>	0.000042	0
<i>Oerskovia</i>	0.000036	0
<i>Latescibacterota</i>	0.000033	0
IMCC26256	0.000033	0
<i>Proteiniclasticum</i>	0.00003	0
<i>Longivirga</i>	0.000028	0
<i>Inhella</i>	0.000027	0
<i>Shinella</i>	0.000027	0
Amb-16S-1323	0.000027	0
<i>Bosea</i>	0.000027	0
UCG-003	0.000025	0
<i>Lachnospiraceae_FCS020_group</i>	0.000025	0
SBR1031	0.000025	0
<i>Candidatus_Contendobacter</i>	0.000023	0
<i>Methylocystis</i>	0.000023	0
NB1-j	0.000023	0
Subgroup_7	0.000023	0
<i>Stella</i>	0.000023	0
JG30-KF-CM45	0.000023	0
CCM19a	0.000023	0
C10-SB1A	0.000023	0
<i>Mycetocola</i>	0.000022	0
966-1	0.000022	0
<i>Turneriella</i>	0.000022	0
<i>Psychrobacter</i>	0.00002	0
<i>Oikopleura</i>	0.000019	0
<i>Acetoanaerobium</i>	0.000019	0
<i>Coprobacillus</i>	0.000019	0
<i>Zixibacteria</i>	0.000017	0
<i>Pedomicrobium</i>	0.000017	0
<i>Flexilinea</i>	0.000017	0
<i>Lautropia</i>	0.000016	0
<i>Enhydrobacter</i>	0.000014	0
<i>Hahella</i>	0.000014	0
Bfidi19	0.000014	0
<i>Bdellovibrio</i>	0.000014	0
<i>Cloacibacterium</i>	0.000014	0
<i>Macellibacteroides</i>	0.000014	0
<i>Sandaracinobacter</i>	0.000014	0
<i>Candidatus_Jidaibacter</i>	0.000014	0
<i>Aridibacter</i>	0.000013	0
<i>Dermatophilaceae</i>	0.000013	0
Elev-16S-1166	0.000013	0
<i>Piscinibacter</i>	0.000013	0
<i>Thiothrix</i>	0.000013	0
A21b	0.000011	0
<i>Candidatus_Obscuribacter</i>	0.000011	0
MVP-88	0.000011	0
<i>Proteocatella</i>	0.000011	0
OLB8	0.000011	0
<i>Plasticumulans</i>	0.000009	0
LWQ8	0.000009	0
<i>Mumia</i>	0.000009	0
<i>Clostridium_sensu_stricto_5</i>	0.000009	0
<i>Longilinea</i>	0.000008	0
<i>Pannonibacter</i>	0.000008	0
<i>Prosthecoibacter</i>	0.000008	0
A2	0.000008	0
<i>Blastococcus</i>	0.000008	0
37-13	0.000008	0
PB19	0.000008	0
<i>Crenothrix</i>	0.000006	0
<i>Phaselicystis</i>	0.000006	0
<i>Methylophilus</i>	0.000006	0
<i>Collinsella</i>	0.000006	0
<i>Schwartzia</i>	0.000005	0
<i>Pseudobutyrvibrio</i>	0.000005	0
<i>Absconditabacteriales_(SR1)</i>	0.000005	0
<i>Selenomonas</i>	0.000005	0
<i>Quinella</i>	0.000005	0
<i>Oribacterium</i>	0.000003	0

Supplemental Table S5: *T*-test of gut microbiota in captive and wild *Cervus elaphus kansuensis* at phylum level

Taxa	Average (C)	SD (C)	Average (W)	SD (W)	<i>P</i> _value	<i>Q</i> _values	Interval lower	Interval upper
k__Bacteria;p__Firmicutes;	0.62044	0.034241	0.700926	0.04343	1.83E-07	-0.03505	0.055387	0.105585
k__Bacteria;p__Bacteroidota;	0.321488	0.025311	0.23526	0.067591	2.74E-05	-0.03505	-0.12025	-0.05221
k__Bacteria;p__Proteobacteria;	0.009679	0.008408	0.021544	0.024064	0.053209	-0.03505	-0.00018	0.02391
k__Archaea;p__Euryarchaeota;	0.010956	0.006303	0.012461	0.01161	0.61808	-0.03505	-0.00462	0.007628
k__Bacteria;p__Actinobacteriota;	0.004947	0.003316	0.012267	0.015168	0.052871	-0.03505	-0.0001	0.014739
k__Bacteria;p__Verrucomicrobiota;	0.011605	0.01035	0.001192	0.001418	0.000119	-0.03505	-0.01504	-0.00579
k__Bacteria;p__Spirochaetota;	0.008535	0.006372	0.002819	0.005093	0.002818	-0.03505	-0.00934	-0.00209
k__Bacteria;p__Desulfobacterota;	0.006095	0.002779	0.001499	0.000914	8.89E-08	-0.03505	-0.00589	-0.0033
k__Bacteria;p__Patescibacteria;	0.00154	0.000849	0.002722	0.004217	0.244259	-0.03505	-0.00088	0.003241
k__Bacteria;p__Campilobacterota;	0.000579	0.001005	0.000952	0.00223	0.507982	-0.03505	-0.00077	0.001517
k__Bacteria;p__Cyanobacteria;	0.002784	0.002165	0.001272	0.001336	0.009814	-0.03505	-0.00264	-0.00039
k__Bacteria;p__Acidobacteriota;	0	0	0.0017	0.002486	0.008018	-0.03505	0.000502	0.002899
k__Bacteria;p__Chloroflexi;	4.05E-06	1.39E-05	0.001717	0.002349	0.005199	-0.03505	0.000581	0.002846
k__Bacteria;p__Nitrospirota;	1.35E-05	3.52E-05	0.001416	0.002085	0.008933	-0.03505	0.000397	0.002408
k__Bacteria;p__Myxococcota;	4.59E-05	0.00011	0.000808	0.001286	0.018977	-0.03505	0.000141	0.001383
k__Bacteria;p__Elusimicrobiota;	0.000738	0.000565	0.000294	0.000312	0.003211	-0.03505	-0.00073	-0.00016
k__Bacteria;p__Gemmatimonadota;	1.62E-05	5.16E-05	0.000277	0.000458	0.023772	-0.03505	3.88E-05	0.000482
k__Bacteria;p__Fibrobacterota;	0.000136	0.000175	0.000239	0.0005	0.40316	-0.03505	-0.00015	0.000353
k__Bacteria;p__Deferribacterota;	0.000206	0.000329	0.000152	0.000287	0.571447	-0.03505	-0.00025	0.00014
k__Bacteria;p__Armatimonadota;	5.40E-06	1.97E-05	0.000213	0.000344	0.017196	-0.03505	4.13E-05	0.000373
k__Archaea;p__Halobacterota;	4.86E-05	0.000115	4.69E-06	2.04E-05	0.093199	-0.03505	-9.58E-05	7.96E-06
k__Bacteria;p__SAR324_clade(Marine_group_B);	4.59E-05	7.14E-05	5.63E-05	0.000102	0.713373	-0.03505	-4.67E-05	6.74E-05

k__Archaea;p__Thermoplasmatota;	6.34E-05	8.90E-05	0	0	0.003078	-0.03505	-0.0001	-2.40E-05
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Supplemental Table S6: General characteristics of metagenomic sequencing data

Sample ID	Raw data	Clean data	Effective (%)	ORFs NO.	Integrity ORFs	Total length (Mbp)	Average length (bp)	GC
C17	6,608.30	6,597.13	99.831	502,941	123,924 (24.64 %)	279.9	556.52	47.1
C18	5,902.33	5,890.88	99.806	405,168	104,961 (25.91 %)	224.06	553.02	44.5
C19	6,671.23	6,656.41	99.778	507,213	139,382 (27.48 %)	283.06	558.08	44.66
W17	6,320.78	6,315.53	99.917	485,651	161,574 (33.27 %)	260.21	535.79	50.25
W18	6,671.93	6,652.07	99.702	573,031	166,493 (29.05 %)	317.02	553.23	46.3
W19	6,745.71	6,728.67	99.747	541,816		307.48	567.51	46.31

Supplemental Table S7: All differential gut microbiota at genus level based on metagenomic sequencing

Taxa	Mean (group 1)	standard error (group 1)	Mean (group 2)	standard error (group 2)	P value	Q value
f Prevotellaceae:g Paraprevotella	0.013103322	0.000147986	0.002110989	0.000586958	0.000124	0.165747
f Chromatiaceae:g Allochromatium	0	0	2.43E-06	2.44E-07	0.000628	0.165747
f Staphylococcaceae:g Macrococcus	6.57E-07	1.60E-07	3.50E-06	2.37E-07	0.000666	0.165747
f Erysipelotrichaceae:g Allobaculum	0.000723546	4.37E-05	0.000109777	4.66E-05	0.000705	0.165747
f Prevotellaceae:g Alloprevotella	0.00090268	1.69E-05	0.000188663	7.50E-05	0.000784	0.165747
f Synergistaceae:g Thermovirga	2.15E-06	2.33E-07	0	0	0.000823	0.165747
f Cellvibrionaceae:g Cellvibrio	3.75E-06	2.59E-07	2.76E-07	2.76E-07	0.000861	0.165747
f Chitinophagaceae:g Chitinophaga	0.000177543	8.68E-06	9.20E-05	4.38E-06	0.000945	0.165747
f Saprospiraceae:g Saprospira	8.07E-06	9.27E-07	1.07E-07	7.00E-08	0.001025	0.165747
f Flavobacteriaceae:g Gillisia	2.73E-05	2.03E-06	8.15E-06	1.06E-06	0.001154	0.165747
f Budviciaceae:g Leminorella	2.88E-06	3.36E-07	4.27E-08	4.27E-08	0.001192	0.165747
f Flavobacteriaceae:g Polaribacter	8.58E-05	7.03E-06	2.49E-05	2.61E-06	0.001498	0.173312
f Kordiimonadaceae:g Kordiimonas	8.56E-06	3.27E-07	1.23E-06	8.66E-07	0.001536	0.173312
f Prevotellaceae:g Prevotellamassilia	0.000268921	6.07E-06	6.46E-05	2.64E-05	0.001617	0.173312
f Flavobacteriaceae:g Maribacter	6.49E-05	6.80E-06	1.47E-05	1.05E-06	0.001782	0.173312
f Salinivirgaceae:g Salinivirga	8.38E-05	7.92E-06	1.35E-05	5.74E-06	0.001952	0.173312
f Flammeovirgaceae:g Marivirga	3.58E-05	1.36E-06	1.45E-05	2.64E-06	0.00199	0.173312
f Siphoviridae:g P70virus	0	0	1.55E-06	2.21E-07	0.002117	0.173312
f Podoviridae:g Cba41virus	1.10E-06	7.87E-07	7.20E-06	4.23E-07	0.002246	0.173312
f Desulfobacteriaceae:g Desulfatirhabdium	4.79E-06	5.54E-07	3.57E-07	3.57E-07	0.002284	0.173312
f Cellulomonadaceae:g Paraoskovia	4.56E-07	4.56E-07	4.77E-06	5.00E-07	0.002502	0.173312
f Unclassified:g Candidatus Aditrix	4.45E-06	6.94E-07	3.97E-08	3.97E-08	0.002583	0.173312
f Acidaminococcaceae:g Phascolarctobacterium	0.004660239	0.000486723	0.000764635	0.000391394	0.002662	0.173312
f Rhodocyclaceae:g Candidatus Dactylopiobacterium	4.46E-06	6.67E-07	3.12E-07	1.57E-07	0.002832	0.173312
f Erysipelotrichaceae:g Egerthia	7.52E-06	5.08E-07	1.32E-05	8.04E-07	0.002962	0.173312
f Carnobacteriaceae:g Jeotgallibaca	7.41E-06	4.94E-08	2.09E-06	9.07E-07	0.003085	0.173312
f Halomonadaceae:g Chromohalobacter	1.96E-06	3.37E-07	0	0	0.003209	0.173312
f Mesocaciditogaceae:g Mesocaciditoga	3.08E-06	2.87E-07	6.70E-07	3.15E-07	0.003371	0.173312
f Bacillaceae:g Pontibacillus	1.34E-05	1.31E-06	6.86E-05	9.90E-06	0.003643	0.173312
f Unclassified:g Candidatus Fonsibacter	1.49E-06	2.63E-07	3.49E-08	3.49E-08	0.003818	0.173312
f Halobacteroidaceae:g Candidatus Frackibacter	5.55E-06	4.93E-07	1.76E-05	2.17E-06	0.00399	0.173312
f Flavobacteriaceae:g Chryseobacterium	0.000441008	2.69E-05	0.000282223	1.22E-05	0.004074	0.173312
f Pectobacteriaceae:g Pectobacterium	1.46E-06	1.13E-07	3.06E-06	2.79E-07	0.004282	0.173312
f Planctomycetaceae:g Mariniblastus	2.68E-06	2.15E-07	7.59E-07	2.98E-07	0.004411	0.173312
f Rhodospirillaceae:g Nisaea	2.19E-06	4.24E-07	3.23E-08	3.23E-08	0.004716	0.173312
f Chitinophagaceae:g Parafilimonas	6.78E-06	7.00E-07	1.41E-06	8.07E-07	0.004754	0.173312
f Crocintomicaceae:g Fluviicola	9.59E-05	1.35E-05	1.60E-05	8.62E-06	0.004933	0.173312
f Halobacteroidaceae:g Selenihalanaerobacter	2.83E-06	3.71E-07	5.32E-07	2.79E-07	0.005067	0.173312
f Prolixibacteraceae:g Tangiafeiana	5.80E-05	2.45E-06	1.88E-05	7.59E-06	0.005233	0.173312
f Schleiferiaceae:g Schleiferia	5.96E-06	8.54E-07	1.02E-06	5.33E-07	0.005271	0.173312
f Idiomarinaceae:g Idiomarina	9.49E-06	8.97E-07	3.38E-06	8.71E-07	0.005407	0.173312
f Flavobacteriaceae:g Riemerella	2.11E-05	9.09E-08	3.07E-05	1.97E-06	0.005446	0.173312
f Flavobacteriaceae:g Winogradskyella	2.22E-05	3.14E-06	6.76E-06	5.70E-07	0.005565	0.173312
f Chlamydiaceae:g Chlamydia	0.000822852	0.00020969	0.002424575	0.000256187	0.005603	0.173312
f Lentimicrobiaceae:g Lentimicrobium	0.001017613	0.000187655	8.85E-05	4.88E-05	0.005687	0.173312
f Sporocadaceae:g Pestalotiopsis	0	0	2.52E-06	5.28E-07	0.005725	0.173312
f Flavobacteriaceae:g Aequorivita	8.82E-05	7.11E-06	3.80E-05	7.93E-06	0.005985	0.173312
f Methanobacteriaceae:g Methanospaera	3.08E-05	8.43E-06	0.000604211	0.000121429	0.006023	0.173312
f Thermoanaerobacteraceae:g Thermacetogenium	1.82E-05	3.28E-06	1.96E-06	1.03E-06	0.006061	0.173312
f Unclassified:g Phocaeicola	3.87E-05	1.90E-06	1.78E-05	4.06E-06	0.006189	0.173312
f Desulfovibrionaceae:g Bilophila	8.59E-05	9.84E-06	3.23E-05	6.01E-06	0.006227	0.173312
f Desulfobulbaceae:g Desulfobulbus	1.77E-06	3.85E-07	0	0	0.006305	0.173312
f Thermoanaerobacteraceae:g Desulfovirgula	2.71E-06	2.75E-07	6.55E-07	3.58E-07	0.00643	0.173312
f Rubricoccaceae:g Rubrivirga	1.31E-07	1.31E-07	2.01E-06	3.92E-07	0.006468	0.173312
f Thermodesulfobacteriaceae:g Thermodesulfobacterium	1.04E-06	7.13E-07	4.47E-06	2.74E-07	0.006546	0.173312
f Lentisphaeraceae:g Lentisphaera	8.45E-06	8.88E-07	1.96E-06	1.15E-06	0.00663	0.173312
f Ruminococcaceae:g Bittarella	1.53E-05	1.25E-06	2.99E-05	3.05E-06	0.006668	0.173312
f Glomeraceae:g Rhizopagus	7.27E-07	6.48E-07	9.37E-06	1.85E-06	0.006706	0.173312
f Erysipelotrichaceae:g Turicibacter	0.000262125	9.87E-06	0.000123911	3.00E-05	0.00679	0.173312
f Paenibacillaceae:g Saccharibacillus	1.50E-05	1.44E-06	3.03E-05	3.19E-06	0.006828	0.173312
f Synergistaceae:g Aminiphilus	3.68E-07	3.68E-07	3.05E-06	4.95E-07	0.006911	0.173312
f Hvellaceae:g Pleurocapsa	1.25E-06	2.91E-07	0	0	0.007275	0.179495
f Holosporaceae:g Holospora	1.74E-06	4.08E-07	1.22E-08	1.22E-08	0.007458	0.181091
f Haloferaceae:g Haloferax	0	0	1.09E-06	2.67E-07	0.007887	0.18497
f Coxiellaceae:g Candidatus Berkiella	1.74E-06	4.26E-07	0	0	0.007968	0.18497
f Desulfovibrionaceae:g Mailhella	0.001236471	0.000280725	8.83E-05	4.24E-05	0.008253	0.18497
f Marinilibacillaceae:g Labilibacter	0.000104741	4.11E-06	4.30E-05	1.48E-05	0.00833	0.18497
f Sphingomonadaceae:g Sphingorhabdus	8.47E-07	1.93E-07	4.70E-08	4.70E-08	0.008368	0.18497
f Unclassified:g Candidatus Planktophila	1.61E-06	3.96E-07	3.67E-08	3.67E-08	0.008626	0.18497
f Dysgonomonadaceae:g Dysgonomonas	0.001275463	0.000115199	0.00061779	0.000121893	0.008878	0.18497
f Flavobacteriaceae:g Psychrosereps	6.12E-05	1.20E-05	9.88E-06	5.36E-06	0.009004	0.18497
f Cytophagaceae:g Dyadobacter	9.38E-05	6.77E-06	5.49E-05	7.49E-06	0.009353	0.18497
f Flavobacteriaceae:g Arenibacter	6.39E-05	1.07E-05	1.92E-05	4.53E-06	0.009391	0.18497
f Cytophagaceae:g Flexibacter	2.36E-05	4.19E-06	4.83E-06	2.53E-06	0.009429	0.18497
f Rikenellaceae:g Rikenella	0.000174023	1.66E-05	6.61E-05	2.27E-05	0.009467	0.18497
f Unclassified:g Chloracidobacterium	1.94E-06	5.07E-07	0	0	0.009551	0.18497
f Rhizobiaceae:g Agrobacterium	3.60E-06	1.13E-06	1.25E-05	2.06E-06	0.009632	0.18497
f Desulfobacteriaceae:g Desulfatibacillum	1.19E-05	1.16E-06	3.68E-06	1.85E-06	0.009856	0.18497
f Ectothiorhodospiraceae:g Ectothiorhodospira	1.20E-06	3.19E-07	0	0	0.010072	0.18497
f Desulfovibrionaceae:g Desulfovibrio	0.000180012	5.44E-06	8.99E-05	2.34E-05	0.0102	0.18497
f Leptotrichiaceae:g Leptotrichia	5.51E-05	1.98E-06	4.48E-05	1.90E-06	0.010321	0.18497
f Porphyromonadaceae:g Sanquibacteroides	7.13E-05	8.81E-06	2.63E-05	8.29E-06	0.010446	0.18497
f Myxococcaceae:g Myxococcus	1.90E-06	8.96E-07	6.37E-06	8.10E-07	0.010622	0.18497
f Nitrospiraceae:g Candidatus Maanetobacterium	6.69E-07	4.22E-07	9.09E-06	2.25E-06	0.010756	0.18497
f Flammeovirgaceae:g Fulvivirga	4.61E-05	8.67E-06	9.76E-06	4.72E-06	0.010795	0.18497
f Hymenobacteraceae:g Pontibacter	8.72E-05	1.27E-05	3.89E-05	3.48E-06	0.010876	0.18497
f Methylococcaceae:g Methyloglobulus	2.31E-06	5.20E-07	3.05E-07	1.72E-07	0.010914	0.18497
f Flavobacteriaceae:g Psychroflexus	2.71E-05	2.28E-06	1.20E-05	3.42E-06	0.010952	0.18497
f Rhodobacteraceae:g Phaeobacter	7.49E-06	1.95E-06	3.67E-07	1.11E-07	0.01099	0.18497
f Rikenellaceae:g Millionella	0.00022548	1.08E-05	0.000107488	3.07E-05	0.011198	0.18497
f Chitinophagaceae:g Niabella	9.52E-05	1.70E-05	2.71E-05	8.08E-06	0.011363	0.18497
f Archaeoglobaceae:g Archaeoglobus	9.48E-07	4.87E-07	3.31E-06	4.43E-07	0.011633	0.18497
f Saccharospirillaceae:g Reinekea	1.53E-06	2.93E-07	3.02E-07	1.82E-07	0.011759	0.18497
f Halomonadaceae:g Candidatus Carsonella	1.27E-06	3.34E-07	5.94E-08	5.94E-08	0.011797	0.18497
f Unclassified:g Thermosulfidibacter	0	0	2.35E-06	6.60E-07	0.011888	0.18497
f Chitinophagaceae:g Flavosolibacter	2.00E-05	4.56E-06	3.03E-06	1.36E-06	0.011926	0.18497
f Flavobacteriaceae:g Alaibacter	1.49E-05	2.76E-06	4.80E-06	6.38E-07	0.011964	0.18497
f Lachnospiraceae:g Eisenbergiella	0.00017781	9.57E-06	6.82E-05	2.93E-05	0.012003	0.18497
f Piscirickettsiaceae:g Sulfurivirga	3.61E-06	8.94E-07	3.91E-07	1.33E-07	0.012041	0.18497
f Cyclobacteriaceae:g Cyclobacterium	5.06E-05	3.16E-06	2.02E-05	7.96E-06	0.012248	0.18497
f Thermoanaerobacteraceae:g Moorella	1.75E-05	1.44E-06	2.94E-05	3.04E-06	0.012329	0.18497
f Erysipelotrichaceae:g Merdibacter	3.61E-05	3.72E-06	1.20E-05	5.72E-06	0.012413	0.18497
f Flavobacteriaceae:g Aquimarinia	7.17E-05	9.03E-06	3.00E-05	7.67E-06	0.012495	0.18497

f Rhodobiaceae:g Tepidicaulis	2.77E-06	4.02E-07	7.93E-07	3.97E-07	0.012575	0.18497
f Balneolaceae:g Gracilimonas	4.93E-08	4.93E-08	1.94E-06	5.43E-07	0.013	0.188797
f Chromobacteriaceae:g Jeongeupia	6.42E-06	1.67E-06	5.60E-07	2.42E-07	0.013082	0.188797
f Methylococcaceae:g Methylosarcina	1.81E-06	5.28E-07	0	0	0.013527	0.190344
f Eubacteriaceae:g Anaerofustis	5.21E-05	2.16E-06	0.000110387	1.69E-05	0.013565	0.190344
f Acidaminococcaceae:g Succinospira	7.37E-06	1.63E-06	1.49E-06	5.49E-07	0.013649	0.190344
f Bacillaceae:g Salipaludibacillus	4.98E-07	4.98E-07	6.21E-06	1.60E-06	0.013687	0.190344
f Selenomonadaceae:g Anaerovibrio	3.52E-05	7.69E-06	6.18E-05	1.38E-06	0.013853	0.190916
f Prolixibacteraceae:g Draconibacterium	0.000214685	3.11E-05	8.68E-05	2.12E-05	0.014015	0.191424
f Ruminococcaceae:g Agathobaculum	0.000265862	1.32E-05	0.000110439	4.41E-05	0.014223	0.191942
f Rhodospirillaceae:g Oceanibaculum	6.10E-06	3.78E-07	2.07E-06	1.13E-06	0.014304	0.191942
f Erwiniaceae:g Phaseolibacter	0	0	7.18E-07	2.15E-07	0.014576	0.193899
f Debaryomycetaceae:g Yamadazyma	3.30E-07	9.95E-08	0	0	0.014962	0.19425
f Micromonosporaceae:g Catenuloplanes	1.28E-06	8.19E-07	6.13E-06	1.22E-06	0.015135	0.19425
f Unclassified:g Leptothrix	1.43E-06	4.34E-07	0	0	0.015265	0.19425
f Opitutaceae:g Cephalotococcus	2.92E-06	8.01E-07	2.40E-07	1.62E-07	0.01539	0.19425
f Barnesiellaceae:g Barnesiella	0.001874033	0.000190114	0.000808768	0.000262859	0.015481	0.19425
f Lactobacillaceae:g Pediococcus	3.08E-06	9.41E-07	1.43E-05	3.29E-06	0.015519	0.19425
f Nostocaceae:g Richelia	1.53E-06	4.70E-07	0	0	0.015937	0.19425
f Myoviridae:g Cp8virus	1.31E-06	4.03E-07	0	0	0.015975	0.19425
f Desulfobacteraceae:g Desulfococcus	1.23E-05	3.33E-06	1.29E-06	6.74E-07	0.016102	0.19425
f Cytophagaceae:g Emticia	4.07E-05	9.04E-06	1.07E-05	2.27E-06	0.01614	0.19425
f Acetobacteraceae:g Gluconobacter	1.44E-06	4.49E-07	0	0	0.016179	0.19425
f Carnobacteriaceae:g Alkalibacterium	1.81E-05	1.25E-06	2.75E-05	2.63E-06	0.016217	0.19425
f Cyclobacteriaceae:g Echinicola	1.64E-05	2.60E-06	5.44E-06	2.23E-06	0.016297	0.19425
f Enterococcaceae:g Vagococcus	5.08E-06	1.27E-06	6.40E-07	5.64E-07	0.016423	0.19425
f Cyclobacteriaceae:g Algoriphagus	0.000140151	1.42E-05	5.90E-05	2.12E-05	0.016507	0.19425
f Enterococcaceae:g Enterococcus	0.0002502	2.31E-06	0.000453796	6.41E-05	0.016818	0.196331
f Selenomonadaceae:g Selenomonas	0.000316382	8.93E-06	0.000680203	0.000114873	0.016987	0.196331
f Porphyromonadaceae:g Petrimonas	0.000216136	1.19E-05	9.67E-05	3.60E-05	0.017069	0.196331
f Methanobacteriaceae:g Methanobacterium	3.26E-05	7.20E-06	9.74E-05	1.94E-05	0.017243	0.19685
f Odoribacteraceae:g Butyrivimonas	0.001901956	9.56E-05	0.000952319	0.000290101	0.017639	0.198801
f Flavobacteriaceae:g Cloacibacterium	3.00E-05	7.74E-06	5.36E-06	2.15E-06	0.018164	0.198801
f Desulfotomaculaceae:g Desulfotomaculum	9.88E-06	1.70E-06	4.23E-06	7.20E-07	0.018244	0.198801
f Sneathiellaceae:g Sneathiella	1.33E-06	4.34E-07	0	0	0.018282	0.198801
f Flavobacteriaceae:g Salegentibacter	3.59E-05	6.02E-06	1.32E-05	4.39E-06	0.018366	0.198801
f Methanoregulaceae:g Methanosphaerula	1.79E-06	5.89E-07	0	0	0.01849	0.198801
f Neisseriaceae:g Alysia	1.53E-06	4.39E-07	1.69E-07	9.64E-08	0.018581	0.198801
f Hyphomonadaceae:g Maricaulis	1.39E-07	1.39E-07	1.37E-06	3.84E-07	0.018711	0.198801
f Peptostreptococcaceae:g Clostridioides	0.000170339	1.12E-05	0.000337173	5.41E-05	0.018749	0.198801
f Rikenellaceae:g Mucinivorans	0.000426894	1.42E-05	0.000212596	5.85E-05	0.019033	0.198801
f Flavobacteriaceae:g Spongibacterium	3.53E-07	3.53E-07	2.03E-06	4.38E-07	0.019117	0.198801
f Pasteurellaceae:g Rodentibacter	1.72E-05	3.74E-06	5.23E-06	1.41E-06	0.019155	0.198801
f Marinilabiliaceae:g Saccharicrinis	2.55E-05	3.07E-06	1.04E-05	3.99E-06	0.019194	0.198801
f Prolixibacteraceae:g Sunxiuqinia	0.000120171	1.64E-05	5.41E-05	1.51E-05	0.019535	0.198801
f Sclerotiniaceae:g Botrytis	0	0	1.00E-05	3.38E-06	0.019573	0.198801
f Lactobacillaceae:g Lactobacillus	0.000240399	3.21E-06	0.000438868	6.69E-05	0.019612	0.198801
f Crocinitomaculaceae:g Crocinitomix	3.55E-05	7.86E-06	9.15E-06	4.17E-06	0.019909	0.198801
f Clostridiaceae:g Clostridiisalibacter	3.72E-05	1.05E-06	1.58E-05	7.17E-06	0.020213	0.198801
f Carnobacteriaceae:g Desemzia	1.11E-06	4.43E-07	3.59E-06	7.22E-07	0.020293	0.198801
f Unclassified:g Hydrogenimonas	1.49E-06	5.09E-07	0	0	0.020331	0.198801
f Cyclobacteriaceae:g Belliella	1.56E-05	2.67E-06	5.48E-06	2.19E-06	0.020415	0.198801
f Flavobacteriaceae:g Mesonia	2.09E-05	5.49E-06	4.53E-06	1.22E-06	0.020683	0.198801
f Tannerellaceae:g Parabacteroides	0.007361119	0.000647167	0.003581468	0.001127887	0.020893	0.198801
f Actinomycetaceae:g Varibaculum	3.44E-05	4.24E-06	1.51E-05	5.16E-06	0.021287	0.198801
f Flavobacteriaceae:g Tenacibaculum	6.25E-05	4.94E-06	2.93E-05	1.04E-05	0.021371	0.198801
f Hyphomonadaceae:g Robiginitomaculum	2.85E-06	8.73E-07	7.16E-06	1.22E-06	0.021409	0.198801
f Porphyromonadaceae:g Porphyromonas	0.001197301	9.51E-05	0.000615863	0.000178246	0.021447	0.198801
f Odoribacteraceae:g Odoribacter	0.001483515	0.000171947	0.000713218	0.000205255	0.021531	0.198801
f Spirochaetaceae:g Marispirachaeta	1.70E-05	2.58E-06	6.49E-06	2.60E-06	0.021657	0.198801
f Gemmataceae:g Zavarzinella	9.55E-07	4.78E-07	4.39E-06	1.10E-06	0.021737	0.198801
f Unclassified:g Candidatus Symbiothrix	0.000242518	7.05E-06	0.000157629	2.87E-05	0.021775	0.198801
f Sporomusaceae:g Pelosinus	1.89E-05	2.78E-06	4.02E-05	6.89E-06	0.021859	0.198801
f Vibrionaceae:g Grimontia	2.63E-06	9.17E-07	0	0	0.022029	0.198801
f Pseudonocardiaceae:g Actinokineospora	2.22E-07	2.22E-07	3.16E-06	1.00E-06	0.022067	0.198801
f Sporomusaceae:g Anaeromusa	2.29E-05	4.73E-06	6.64E-06	3.17E-06	0.022144	0.198801
f Methylophilaceae:g Methylophilus	1.73E-06	4.81E-07	2.21E-07	2.21E-07	0.022225	0.198801
f Schizoporaceae:g Schizopora	4.08E-06	1.14E-06	6.88E-07	3.46E-07	0.022362	0.198801
f Flavobacteriaceae:g Capnocytophaga	0.000292611	2.83E-05	0.000171319	3.18E-05	0.022485	0.198801
f Neisseriaceae:g Amantcinitium	1.02E-06	3.04E-07	1.08E-07	1.08E-07	0.022696	0.198801
f Siphoviridae:g Sextacivirus	1.08E-06	8.29E-07	5.56E-06	1.35E-06	0.022823	0.198801
f Synechococcaceae:g Dactylococcopsis	1.71E-06	5.89E-07	3.93E-08	3.93E-08	0.022905	0.198801
f Myoviridae:g Msw3virus	2.50E-08	2.50E-08	2.51E-06	8.78E-07	0.022943	0.198801
f Deferribacteraceae:g Geovibrio	4.37E-06	1.20E-06	7.36E-07	4.75E-07	0.023021	0.198801
f Alteromonadaceae:g Alteromonas	6.86E-06	1.96E-07	1.33E-05	2.28E-06	0.023194	0.198801
f Choanephoraceae:g Choanephora	0	0	1.74E-06	6.22E-07	0.023321	0.198801
f Sporomusaceae:g Anaerospomusa	1.69E-05	2.05E-06	6.54E-06	3.09E-06	0.023451	0.198801
f Methanosarcinaceae:g Methanolobus	4.47E-06	7.21E-07	2.00E-06	5.09E-07	0.023529	0.198801
f Unclassified:g Candidatus Izimiplasma	7.76E-05	1.85E-05	0.000166519	2.60E-05	0.023699	0.198801
f Peptoniphilaceae:g Anaerococcus	2.79E-05	4.62E-06	4.25E-05	2.54E-06	0.023782	0.198801
f Chlorobiaceae:g Chlorobaculum	8.95E-06	2.75E-06	1.26E-06	4.00E-07	0.024132	0.200633
f Hyphomicrobiaceae:g Cucumbibacter	0	0	6.88E-07	2.50E-07	0.024526	0.202393
f Rhodobacteraceae:g Maribius	1.62E-06	5.90E-07	0	0	0.024608	0.202393
f Unclassified:g Candidatus Vecturithrix	1.05E-05	2.05E-06	1.79E-05	1.76E-06	0.024917	0.203061
f Halobacteriaceae:g Haladaptatus	1.01E-06	5.11E-07	3.10E-06	5.65E-07	0.024955	0.203061
f Sphingobacteriaceae:g Solitalea	5.69E-05	1.76E-05	7.92E-06	3.90E-06	0.02526	0.203684
f Flavobacteriaceae:g Galbibacter	5.95E-06	1.48E-06	1.26E-06	8.94E-07	0.025298	0.203684
f Porphyromonadaceae:g Lascolabacillus	7.99E-05	1.80E-05	2.72E-05	7.41E-06	0.025589	0.204949
f Leptospiraceae:g Turnerella	1.50E-06	2.03E-08	6.26E-07	3.26E-07	0.026118	0.206564
f Eggerthellaceae:g Gordonibacter	4.92E-05	8.57E-06	9.01E-05	1.26E-05	0.026156	0.206564
f Legionellaceae:g Legionella	1.55E-05	2.97E-06	6.77E-06	1.31E-06	0.026331	0.206564
f Eggerthellaceae:g Cryptobacterium	4.13E-06	8.02E-07	1.72E-05	4.86E-06	0.026784	0.206564
f Flavobacteriaceae:g Gaetbulibacter	8.76E-06	1.83E-06	2.88E-06	1.25E-06	0.026911	0.206564
f Prevotellaceae:g Prevotella	0.040816396	0.00162042	0.023349739	0.00640132	0.027119	0.206564
f Desulfobacteraceae:g Candidatus Magnetomorum	9.01E-06	2.83E-06	1.33E-06	6.85E-07	0.02729	0.206564
f Bacillaceae:g Amphibacillus	1.03E-05	3.78E-06	2.05E-05	7.31E-07	0.027371	0.206564
f Prolixibacteraceae:g Prolixibacter	8.51E-05	2.14E-05	2.47E-05	8.35E-06	0.027494	0.206564
f Flavobacteriaceae:g Wenyinzhuanqia	1.74E-05	2.70E-06	8.82E-06	1.87E-06	0.027532	0.206564
f Thermodesulfobacteriaceae:g Thermosulfurimonas	5.08E-06	1.40E-06	1.39E-06	6.70E-08	0.027708	0.206564
f Unclassified:g Pseudohongiella	1.13E-06	4.30E-07	0	0	0.027746	0.206564
f Porphyromonadaceae:g Fermentimonas	9.40E-05	1.27E-05	4.39E-05	1.43E-05	0.027784	0.206564
f Colwelliaceae:g Thalassotalea	2.99E-06	1.01E-06	2.82E-07	2.17E-07	0.027875	0.206564
f Flavobacteriaceae:g Lutibacter	9.39E-05	1.61E-05	4.25E-05	1.12E-05	0.027913	0.206564
f Coleofasciculaceae:g Geitlerinema	6.70E-07	2.56E-07	0	0	0.027951	0.206564
f Solibacteraceae:g Candidatus Solibacter	8.64E-07	2.08E-07	2.45E-06	5.74E-07	0.028456	0.209281
f Peptostreptococcaceae:g Paenicostridium	6.86E-05	1.34E-06	0.000225249	6.02E-05	0.028684	0.20995
f Cryomorphaceae:g Owenweeksia	3.79E-05	7.81E-06	1.49E-05	4.14E-06	0.028859	0.210226

f Rhodobacteraceae:g Pannonibacter	1.18E-06	3.57E-07	1.64E-07	1.64E-07	0.029124	0.211149
f Methanomicrobiaceae:g Methanofollis	2.98E-06	1.06E-06	2.01E-07	2.01E-07	0.029306	0.211468
f Bacillaceae:g Bacillus	0.001816245	0.000396949	0.092243501	0.035257906	0.029609	0.212306
f Halofaracaceae:g Halobellus	1.43E-06	3.01E-07	2.98E-06	5.26E-07	0.0297	0.212306
f Cytophagaceae:g Runella	2.28E-05	3.08E-06	1.29E-05	2.34E-06	0.029871	0.212537
f Synergistaceae:g Aminomonas	3.57E-06	8.81E-07	9.22E-07	5.57E-07	0.030179	0.212951
f Peptostreptococcaceae:g Asaccharospora	7.65E-06	1.23E-06	1.78E-05	3.82E-06	0.030217	0.212951
f Rickettsiaceae:g Rickettsia	8.62E-06	8.24E-07	3.98E-06	1.63E-06	0.030347	0.212951
f Chitinophagaceae:g Sediminibacterium	1.51E-05	4.35E-06	3.65E-06	1.22E-06	0.0308	0.214742
f Pasteurellaceae:g Chelonobacter	4.18E-06	1.36E-06	6.01E-07	3.66E-07	0.030883	0.214742
f Methylothermaceae:g Methylohalobius	1.45E-06	5.83E-07	0	0	0.031895	0.220778
f Rhodospirillaceae:g Thalassospira	3.76E-05	7.04E-06	1.32E-05	6.83E-06	0.032113	0.221286
f Yersiniaceae:g Ewingella	5.14E-08	5.14E-08	7.11E-07	2.62E-07	0.032627	0.223411
f Marinifilaceae:g Marinifilum	6.96E-05	1.89E-05	1.96E-05	7.43E-06	0.032838	0.223411
f Spirochaetaceae:g Alkalispirochaeta	3.17E-06	4.85E-07	1.94E-06	1.26E-07	0.032922	0.223411
f Bacteroidaceae:g Bacteroides	0.133964951	0.010246608	0.071565603	0.02322556	0.033006	0.223411
f Bacteroidaceae:g Anaerorhabdus	0.000158152	2.58E-05	6.26E-05	2.91E-05	0.033174	0.22356
f Bacillaceae:g Salibacterium	2.23E-06	1.76E-06	1.11E-05	3.15E-06	0.033722	0.224783
f Acidobacteriaceae:g Acidobacterium	1.62E-06	1.87E-07	6.67E-07	3.40E-07	0.03376	0.224783
f Oceanospirillaceae:g Marinobacterium	1.23E-06	3.65E-07	3.99E-06	1.07E-06	0.033926	0.224783
f Streptomyetaceae:g Kitasatospora	2.24E-06	5.34E-07	6.79E-06	1.79E-06	0.034216	0.224783
f Rhodobiaceae:g Afifella	1.76E-06	4.18E-07	4.06E-07	3.71E-07	0.034518	0.224783
f Methanomassiliococcaceae:g Candidatus Methanomethylophilus	4.79E-05	1.54E-05	8.98E-06	4.58E-06	0.034556	0.224783
f Unclassified:g Candidatus Azobacteroides	7.82E-06	2.63E-06	1.00E-06	1.00E-06	0.034731	0.224783
f Tannerellaceae:g Tannerella	0.000957134	0.000153259	0.000444847	0.000146239	0.034903	0.224783
f Desulfomicrobiaceae:g Desulfomicrobium	5.60E-06	1.91E-06	7.65E-07	6.02E-07	0.034941	0.224783
f Unclassified:g Fenollaria	5.57E-06	1.87E-06	8.87E-07	5.30E-07	0.035151	0.224783
f Thiotrichaceae:g Beggiatoa	8.22E-06	1.85E-06	3.36E-06	7.98E-07	0.035189	0.224783
f Neisseriaceae:g Snodgrassella	5.02E-06	1.02E-06	1.78E-06	8.76E-07	0.035227	0.224783
f Succinivibrionaceae:g Ruminobacter	2.68E-05	1.01E-06	1.37E-05	5.38E-06	0.035266	0.224783
f Thermoanaerobacterales Family III. Incertae Sedis:g Thermovenabulum	1.75E-06	9.02E-07	7.03E-06	2.02E-06	0.035482	0.226686
f Fusobacteriaceae:g Psychrilybacter	2.73E-06	9.50E-07	4.53E-07	1.20E-07	0.035881	0.226686
f Listeriaceae:g Listeria	4.65E-05	5.59E-06	0.000145294	4.13E-05	0.036009	0.226686
f Chamaesiphonaceae:g Chamaesiphon	9.74E-07	4.12E-07	0	0	0.036312	0.227517
f Hyphomicrobiaceae:g Filomicrobium	2.54E-06	7.48E-07	6.19E-07	3.20E-07	0.036529	0.227517
f Veillonellaceae:g Veillonella	8.22E-05	8.05E-06	0.000287861	8.67E-05	0.036659	0.227517
f Flavobacteriaceae:g Seonamhaeicola	1.36E-05	3.80E-06	3.69E-06	1.85E-06	0.037025	0.227517
f Balneolaceae:g Aliifodinibius	7.72E-06	1.15E-06	3.06E-06	1.62E-06	0.037064	0.227517
f Lachnospiraceae:g Lachnoanaerobaculum	5.18E-05	5.41E-06	3.59E-05	4.06E-06	0.037102	0.227517
f Rhodobacteraceae:g Jannaschia	1.15E-06	3.36E-07	2.13E-07	2.13E-07	0.037182	0.227517
f Rhodospirillaceae:g Magnetospirillum	2.90E-05	6.81E-06	1.23E-05	2.12E-06	0.037348	0.227622
f Cytophagaceae:g Spirosoma	8.05E-05	1.03E-05	5.14E-05	6.99E-06	0.037986	0.230596
f Thermoanaerobacterales Family III. Incertae Sedis:g Thermosediminibacter	3.14E-06	6.70E-07	8.50E-06	2.20E-06	0.038293	0.23103
f Ectothiorhodospiraceae:g Halorhodospira	2.03E-06	1.80E-07	5.93E-07	5.93E-07	0.03842	0.23103
f Ustilaginaceae:g Ustilago	0	0	2.67E-06	1.15E-06	0.038511	0.23103
f Bacillaceae:g Anoxybacillus	3.13E-05	1.09E-05	0.00020641	7.50E-05	0.039082	0.233537
f Flammeovirgaceae:g Fabibacter	1.89E-05	6.46E-06	3.50E-06	1.75E-06	0.039255	0.233663
f Natriabaceae:g Natronorubrum	0	0	6.37E-07	2.77E-07	0.039601	0.234
f Flavobacteriaceae:g Bizionia	2.52E-05	9.35E-06	3.43E-06	1.49E-06	0.039809	0.2347
f Sordariaceae:g Sordaria	0	0	3.61E-06	1.58E-06	0.03989	0.2347
f Clavicipitaceae:g Metarhizium	6.87E-08	6.87E-08	9.21E-06	4.00E-06	0.04011	0.235089
f Unclassified:g Neofamilia	4.89E-06	3.34E-07	2.62E-06	9.39E-07	0.040288	0.23523
f Unclassified:g Ndongabacter	1.34E-05	1.83E-06	6.15E-06	2.60E-06	0.04055	0.235865
f Pseudobacteriovoracaceae:g Pseudobacteriovorax	7.01E-06	1.63E-06	2.30E-06	1.28E-06	0.041132	0.237901
f Unclassified:g Sulfurovum	1.03E-05	2.97E-06	3.15E-06	1.00E-06	0.041212	0.237901
f Synergistaceae:g Cloacibacillus	8.18E-05	7.98E-06	4.45E-05	1.45E-05	0.041608	0.23818
f Chromatiaceae:g Thiohalocapsa	1.70E-06	7.20E-07	7.31E-08	7.31E-08	0.041689	0.23818
f Actinomycetaceae:g Actinobaculum	0	0	2.73E-06	1.21E-06	0.041727	0.23818
f Erysipelotrichaceae:g Solobacterium	3.59E-05	3.63E-06	7.93E-05	1.90E-05	0.042124	0.238629
f Cyclobacteriaceae:g Lunatimonas	4.94E-06	1.27E-06	1.77E-06	6.18E-07	0.042162	0.238629
f Bacillaceae:g Terribacillus	7.45E-06	2.65E-06	6.08E-05	2.37E-05	0.042421	0.238629
f Ruminococcaceae:g Papillibacter	0.000307285	2.15E-05	0.000144862	6.93E-05	0.042504	0.238629
f Aerococcaceae:g Eremococcus	4.12E-06	4.84E-07	9.87E-06	2.52E-06	0.042586	0.238629
f Kosmotogaceae:g Kosmotoga	5.62E-06	1.02E-06	1.60E-06	1.49E-06	0.043155	0.23875
f Coriobacteriaceae:g Olequesella	2.28E-06	3.61E-07	1.35E-06	2.09E-07	0.043193	0.23875
f Ruminococcaceae:g Sporobacter	0.0006793	5.27E-05	0.000363547	0.000132284	0.043328	0.23875
f Unclassified:g Thermoflexibacter	6.04E-05	2.27E-05	9.13E-06	4.52E-06	0.043452	0.23875
f Cytophagaceae:g Ohtaekwangia	2.06E-05	6.95E-06	4.69E-06	1.77E-06	0.043578	0.23875
f Selenomonadaceae:g Centipeda	1.10E-06	7.26E-07	3.97E-06	1.08E-06	0.043802	0.23875
f Enterobacteriaceae:g Enterobacter	2.91E-06	6.57E-07	7.29E-06	1.87E-06	0.043928	0.23875
f Tolypothrichaceae:g Hassallia	2.21E-05	8.33E-06	3.49E-06	1.13E-06	0.044009	0.23875
f Nitrosomonadaceae:g Nitrosomonas	2.75E-05	8.26E-06	8.71E-06	2.12E-06	0.044345	0.23875
f Streptococcaceae:g Streptococcus	0.000266195	2.48E-05	0.000353067	3.07E-05	0.044384	0.23875
f Flavobacteriaceae:g Crocettalea	1.51E-06	6.60E-07	5.30E-08	5.30E-08	0.044475	0.23875
f Paenibacillaceae:g Cohnella	6.19E-05	1.26E-05	0.000124991	2.59E-05	0.044552	0.23875
f Enterococcaceae:g Bavariococcus	5.59E-06	2.08E-06	8.93E-07	5.01E-07	0.044636	0.23875
f Rhodobacteraceae:g Donahicola	1.01E-06	4.45E-07	3.45E-08	3.45E-08	0.045145	0.239997
f Bernardetiaceae:g Hugenholtzia	3.78E-05	9.93E-06	1.34E-05	5.11E-06	0.045183	0.239997
f Caldilineaceae:g Litorilinea	2.57E-06	6.86E-07	7.97E-07	4.45E-07	0.045758	0.241631
f Flavobacteriaceae:g Bergeyella	2.03E-05	5.27E-06	6.80E-06	3.37E-06	0.045883	0.241631
f Sordariaceae:g Neurospora	0	0	8.84E-06	4.09E-06	0.045964	0.241631
f Halococcaceae:g Halococcus	4.89E-07	4.89E-07	2.29E-06	6.86E-07	0.046546	0.242391
f Peptococcaceae:g Desulfotomaculum	0.000122808	4.56E-06	0.000203325	3.73E-05	0.046628	0.242391
f Rhodobacteraceae:g Oceanicella	6.60E-07	2.57E-07	8.21E-08	8.21E-08	0.046709	0.242391
f Ophiostomataceae:g Sporothrix	0	0	4.86E-06	2.28E-06	0.046933	0.242391
f Ruminococcaceae:g Massilimalia	0.000563335	3.60E-05	0.000284571	0.000125872	0.047054	0.242391
f Rickettsiaceae:g Orientia	9.93E-07	4.66E-07	0	0	0.047134	0.242391
f Kosmotogaceae:g Mesotoga	9.05E-06	5.51E-07	5.94E-06	1.36E-06	0.047218	0.242391
f Flavobacteriaceae:g Olleya	7.57E-06	3.08E-06	9.67E-07	4.20E-07	0.04743	0.242663
f Rhizobiaceae:g Neorhizobium	0	0	9.48E-07	4.48E-07	0.047691	0.242963
f Propionibacteriaceae:g Acidipropionibacterium	1.11E-06	5.18E-07	5.12E-06	1.82E-06	0.047864	0.242963
f Alcaligenaceae:g Pelistega	1.23E-06	2.67E-07	3.89E-07	2.95E-07	0.048086	0.242963
f Gemmatocaceae:g Gemmata	1.46E-05	3.57E-06	5.56E-06	2.34E-06	0.048124	0.242963
f Colwelliaceae:g Thalassomonas	3.97E-08	3.97E-08	2.64E-06	1.24E-06	0.048622	0.244671
f Rhodobacteraceae:g Litoreibacter	3.40E-06	9.67E-07	1.03E-06	5.92E-07	0.049735	0.249227
f Gallionellaceae:g Gallionella	9.92E-07	4.76E-07	0	0	0.049859	0.249227

Supplemental Table S8: All fecal metabolites detected by LC-MS/MS

Compound ID	Name	Other name(s), synonym(s)	Formula	Molecular weight	E ₁ (nmol)	n _D 20	n _D 40	n _D 60	n _D 80	n _D 100	n _D 120	n _D 140	n _D 160	n _D 180	n _D 200	n _D 220	n _D 240	n _D 260	n _D 280	n _D 300	n _D 320	n _D 340	n _D 360	n _D 380	n _D 400	n _D 420	n _D 440	n _D 460	n _D 480	n _D 500	n _D 520	n _D 540	n _D 560	n _D 580	n _D 600	n _D 620	n _D 640	n _D 660	n _D 680	n _D 700	n _D 720	n _D 740	n _D 760	n _D 780	n _D 800	n _D 820	n _D 840	n _D 860	n _D 880	n _D 900	n _D 920	n _D 940	n _D 960	n _D 980	n _D 1000	n _D 1020	n _D 1040	n _D 1060	n _D 1080	n _D 1100	n _D 1120	n _D 1140	n _D 1160	n _D 1180	n _D 1200	n _D 1220	n _D 1240	n _D 1260	n _D 1280	n _D 1300	n _D 1320	n _D 1340	n _D 1360	n _D 1380	n _D 1400	n _D 1420	n _D 1440	n _D 1460	n _D 1480	n _D 1500	n _D 1520	n _D 1540	n _D 1560	n _D 1580	n _D 1600	n _D 1620	n _D 1640	n _D 1660	n _D 1680	n _D 1700	n _D 1720	n _D 1740	n _D 1760	n _D 1780	n _D 1800	n _D 1820	n _D 1840	n _D 1860	n _D 1880	n _D 1900	n _D 1920	n _D 1940	n _D 1960	n _D 1980	n _D 2000	n _D 2020	n _D 2040	n _D 2060	n _D 2080	n _D 2100	n _D 2120	n _D 2140	n _D 2160	n _D 2180	n _D 2200	n _D 2220	n _D 2240	n _D 2260	n _D 2280	n _D 2300	n _D 2320	n _D 2340	n _D 2360	n _D 2380	n _D 2400	n _D 2420	n _D 2440	n _D 2460	n _D 2480	n _D 2500	n _D 2520	n _D 2540	n _D 2560	n _D 2580	n _D 2600	n _D 2620	n _D 2640	n _D 2660	n _D 2680	n _D 2700	n _D 2720	n _D 2740	n _D 2760	n _D 2780	n _D 2800	n _D 2820	n _D 2840	n _D 2860	n _D 2880	n _D 2900	n _D 2920	n _D 2940	n _D 2960	n _D 2980	n _D 3000	n _D 3020	n _D 3040	n _D 3060	n _D 3080	n _D 3100	n _D 3120	n _D 3140	n _D 3160	n _D 3180	n _D 3200	n _D 3220	n _D 3240	n _D 3260	n _D 3280	n _D 3300	n _D 3320	n _D 3340	n _D 3360	n _D 3380	n _D 3400	n _D 3420	n _D 3440	n _D 3460	n _D 3480	n _D 3500	n _D 3520	n _D 3540	n _D 3560	n _D 3580	n _D 3600	n _D 3620	n _D 3640	n _D 3660	n _D 3680	n _D 3700	n _D 3720	n _D 3740	n _D 3760	n _D 3780	n _D 3800	n _D 3820	n _D 3840	n _D 3860	n _D 3880	n _D 3900	n _D 3920	n _D 3940	n _D 3960	n _D 3980	n _D 4000	n _D 4020	n _D 4040	n _D 4060	n _D 4080	n _D 4100	n _D 4120	n _D 4140	n _D 4160	n _D 4180	n _D 4200	n _D 4220	n _D 4240	n _D 4260	n _D 4280	n _D 4300	n _D 4320	n _D 4340	n _D 4360	n _D 4380	n _D 4400	n _D 4420	n _D 4440	n _D 4460	n _D 4480	n _D 4500	n _D 4520	n _D 4540	n _D 4560	n _D 4580	n _D 4600	n _D 4620	n _D 4640	n _D 4660	n _D 4680	n _D 4700	n _D 4720	n _D 4740	n _D 4760	n _D 4780	n _D 4800	n _D 4820	n _D 4840	n _D 4860	n _D 4880	n _D 4900	n _D 4920	n _D 4940	n _D 4960	n _D 4980	n _D 5000	n _D 5020	n _D 5040	n _D 5060	n _D 5080	n _D 5100	n _D 5120</
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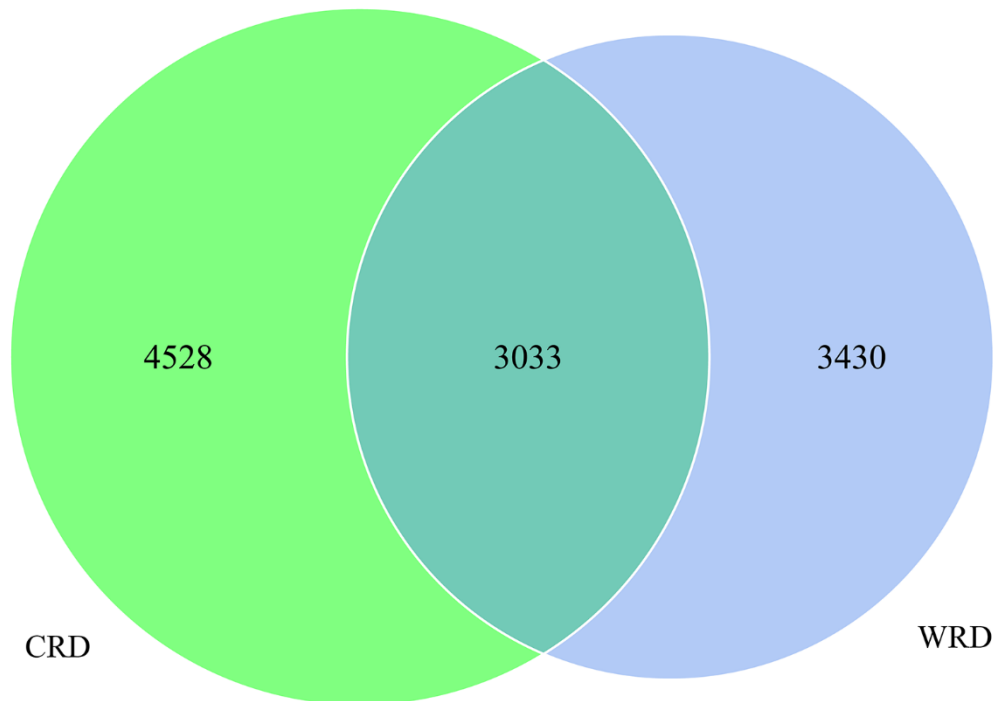
[illegible]

Com_3360_pos	Homo-Gamma-Linolenic Acid	--	C20 H34 O2	306.2557	7.973	307.2636	1062995.45	12163130.26	12324734.35	15027107.3	8.93321.639	676489.872	2008860.19	26466794.69	1878579.33	2435572.34	25185020.19	25208467.87	15081224.67	14851154.15	16116346.25
Com_3407_pos	KKK	--	C18 H38 N6 O4	366.8074	6.481	363.3182	2628329.84	3121415.778	1853313.365	2112151.78	191847.283	216051.681	239865.265	5795817.066	17113375.99	29695401.04	4796237.308	1897995.45	1765277.87	4811813.44	16537936.76
Com_3419_pos	Acetyl-L-glutamine	--	C10 H19 N O5	201.13549	1.348	204.12274	17102825.97	1731407.927	1731407.927	1731407.927	1731407.927	1731407.927	1731407.927	1731407.927	1731407.927	1731407.927	1731407.927	1731407.927	1731407.927	1731407.927	1731407.927
Com_3438_pos	2,4,4-trihydroxyphenylacetamide	--	C8 H9 N O3	159.03993	0.975	160.04723	330989.049	490986.514	490986.514	490986.514	490986.514	490986.514	490986.514	490986.514	490986.514	490986.514	490986.514	490986.514	490986.514	490986.514	490986.514
Com_3478_pos	3-(3,4-dihydroxy-1-methyl-2-propenyl)-5-hydroxybenzyl-2-methyl-2-oxo-3-oxobutanoate	--	C13 H21 O13	236.1263	1.055	231.13358	4668796.388	5837631.81	4294716.561	497367.586	726830.211	399393.614	251761.629	331403.869	331403.869	331403.869	331403.869	331403.869	331403.869	331403.869	331403.869
Com_3525_pos	5-mono-phosphoryl-2-oxo-3-oxobutanoate	--	C10 H17 O13	236.1263	1.055	231.13358	4668796.388	5837631.81	4294716.561	497367.586	726830.211	399393.614	251761.629	331403.869	331403.869	331403.869	331403.869	331403.869	331403.869	331403.869	331403.869
Com_3535_pos	3-Amino-1,2,4-triazole	--	C2 H3 N3	69.06267	0.521	69.06267	433103.013	433103.013	433103.013	433103.013	433103.013	433103.013	433103.013	433103.013	433103.013	433103.013	433103.013	433103.013	433103.013	433103.013	433103.013
Com_3546_pos	1,4-Oxalotetraol (reduced)	--	C10 H17 O13	236.1263	1.055	231.13358	4668796.388	5837631.81	4294716.561	497367.586	726830.211	399393.614	251761.629	331403.869	331403.869	331403.869	331403.869	331403.869	331403.869	331403.869	331403.869
Com_3554_pos	3-Amino-1,2,4-triazole	--	C2 H3 N3	69.06267	0.521	69.06267	433103.013	433103.013	433103.013	433103.013	433103.013	433103.013	433103.013	433103.013	433103.013	433103.013	433103.013	433103.013	433103.013	433103.013	433103.013
Com_3572_pos	Oxetanol-4	--	C2 H4 O2	58.0423	0.418	57.24076	1385440.81	140311.209	140311.209	140311.209	140311.209	140311.209	140311.209	140311.209	140311.209	140311.209	140311.209	140311.209	140311.209	140311.209	140311.209
Com_3578_pos	Nb-Adeno-1,4-lysine	--	C18 H34 N2 O5	338.11725	1.88	339.12441	1891248.7	1891248.7	1891248.7	1891248.7	1891248.7	1891248.7	1891248.7	1891248.7	1891248.7	1891248.7	1891248.7	1891248.7	1891248.7	1891248.7	1891248.7
Com_3597_pos	S-Adeno-1,4-lysine	--	C18 H34 N2 O5	338.11725	1.88	339.12441	1891248.7	1891248.7	1891248.7	1891248.7	1891248.7	1891248.7	1891248.7	1891248.7	1891248.7	1891248.7	1891248.7	1891248.7	1891248.7	1891248.7	1891248.7
Com_3617_pos	4,4-dihydroxy-1,5-dimethyl-2-oxo-3-oxobutanoate	--	C13 H21 O13	236.1263	1.055	231.13358	4668796.388	5837631.81	4294716.561	497367.586	726830.211	399393.614	251761.629	331403.869	331403.869	331403.869	331403.869	331403.869	331403.869	331403.869	331403.869
Com_3620_pos	2-Amino-3-oxobutanoate	--	C10 H17 O13	236.1263	1.055	231.13358	4668796.388	5837631.81	4294716.561	497367.586	726830.211	399393.614	251761.629	331403.869	331403.869	331403.869	331403.869	331403.869	331403.869	331403.869	331403.869
Com_3636_pos	3-Amino-1,2,4-triazole	--	C2 H3 N3	69.06267	0.521	69.06267	433103.013	433103.013	433103.013	433103.013	433103.013	433103.013	433103.013	433103.013	433103.013	433103.013	433103.013	433103.013	433103.013	433103.013	433103.013
Com_3668_pos	Tetranol-1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29,30,31,32,33,34,35,36,37,38,39,40,41,42,43,44,45,46,47,48,49,50,51,52,53,54,55,56,57,58,59,60,61,62,63,64,65,66,67,68,69,70,71,72,73,74,75,76,77,78,79,80,81,82,83,84,85,86,87,88,89,90,91,92,93,94,95,96,97,98,99,100,101,102,103,104,105,106,107,108,109,110,111,112,113,114,115,116,117,118,119,120,121,122,123,124,125,126,127,128,129,130,131,132,133,134,135,136,137,138,139,140,141,142,143,144,145,146,147,148,149,150,151,152,153,154,155,156,157,158,159,160,161,162,163,164,165,166,167,168,169,170,171,172,173,174,175,176,177,178,179,180,181,182,183,184,185,186,187,188,189,190,191,192,193,194,195,196,197,198,199,200,201,202,203,204,205,206,207,208,209,210,211,212,213,214,215,216,217,218,219,220,221,222,223,224,225,226,227,228,229,230,231,232,233,234,235,236,237,238,239,240,241,242,243,244,245,246,247,248,249,250,251,252,253,254,255,256,257,258,259,260,261,262,263,264,265,266,267,268,269,270,271,272,273,274,275,276,277,278,279,280,281,282,283,284,285,286,287,288,289,290,291,292,293,294,295,296,297,298,299,300,301,302,303,304,305,306,307,308,309,310,311,312,313,314,315,316,317,318,319,320,321,322,323,324,325,326,327,328,329,330,331,332,333,334,335,336,337,338,339,340,341,342,343,344,345,346,347,348,349,350,351,352,353,354,355,356,357,358,359,360,361,362,363,364,365,366,367,368,369,370,371,372,373,374,375,376,377,378,379,380,381,382,383,384,385,386,387,388,389,390,391,392,393,394,395,396,397,398,399,400,401,402,403,404,405,406,407,408,409,410,411,412,413,414,415,416,417,418,419,420,421,422,423,424,425,426,427,428,429,430,431,432,433,434,435,436,437,438,439,440,441,442,443,444,445,446,447,448,449,450,451,452,453,454,455,456,457,458,459,460,461,462,463,464,465,466,467,468,469,470,471,472,473,474,475,476,477,478,479,480,481,482,483,484,485,486,487,488,489,490,491,492,493,494,495,496,497,498,499,500,501,502,503,504,505,506,507,508,509,510,511,512,513,514,515,516,517,518,519,520,521,522,523,524,525,526,527,528,529,530,531,532,533,534,535,536,537,538,539,540,541,542,543,544,545,546,547,548,549,550,551,552,553,554,555,556,557,558,559,560,561,562,563,564,565,566,567,568,569,570,571,572,573,574,575,576,577,578,579,580,581,582,583,584,585,586,587,588,589,590,591,592,593,594,595,596,597,598,599,600,601,602,603,604,605,606,607,608,609,610,611,612,613,614,615,616,617,618,619,620,621,622,623,624,625,626,627,628,629,630,631,632,633,634,635,636,637,638,639,640,641,642,643,644,645,646,647,648,649,650,651,652,653,654,655,656,657,658,659,660,661,662,663,664,665,666,667,668,669,670,671,672,673,674,675,676,677,678,679,680,681,682,683,684,685,686,687,688,689,690,691,692,693,694,695,696,697,698,699,700,701,702,703,704,705,706,707,708,709,710,711,712,713,714,715,716,717,718,719,720,721,722,723,724,725,726,727,728,729,730,731,732,733,734,735,736,737,738,739,740,741,742,743,744,745,746,747,748,749,750,751,752,753,754,755,756,757,758,759,760,761,762,763,764,765,766,767,768,769,770,771,772,773,774,775,776,777,778,779,780,781,782,783,784,785,786,787,788,789,790,791,792,793,794,795,796,797,798,799,800,801,802,803,804,805,806,807,808,809,810,811,812,813,814,815,816,817,818,819,820,821,822,823,824,825,826,827,828,829,830,831,832,833,834,835,836,837,838,839,840,841,842,843,844,845,846,847,848,849,850,851,852,853,854,855,856,857,858,859,860,861,862,863,864,865,866,867,868,869,870,871,872,873,874,875,876,877,878,879,880,881,882,883,884,885,886,887,888,889,890,891,892,893,894,895,896,897,898,899,900,901,902,903,904,905,906,907,908,909,910,911,912,913,914,915,916,917,918,919,920,921,922,923,924,925,926,927,928,929,930,931,932,933,934,935,936,937,938,939,940,941,942,943,944,945,946,947,948,949,950,951,952,953,954,955,956,957,958,959,960,961,962,963,964,965,966,967,968,969,970,971,972,973,974,975,976,977,978,979,980,981,982,983,984,985,986,987,988,989,990,991,992,993,994,995,996,997,998,999,1000,1001,1002,1003,1004,1005,1006,1007,1008,1009,1010,1011,1012,1013,1014,1015,1016,1017,1018,1019,1020,1021,1022,1023,1024,1025,1026,1027,1028,1029,1030,1031,1032,1033,1034,1035,1036,1037,1038,1039,1040,1041,1042,1043,1044,1045,1046,1047,1048,1049,1050,1051,1052,1053,1054,1055,1056,1057,1058,1059,1060,1061,1062,1063,1064,1065,1066,1067,1068,1069,1070,1071,1072,1073,1074,1075,1076,1077,1078,1079,1080,1081,1082,1083,1084,1085,1086,1087,1088,1089,1090,1091,1092,1093,1094,1095,1096,1097,1098,1099,1100,1101,1102,1103,1104,1105,1106,1107,1108,1109,1110,1111,1112,1113,1114,1115,1116,1117,1118,1119,1120,1121,1122,1123,1124,1125,1126,1127,1128,1129,1130,1131,1132,1133,1134,1135,1136,1137,1138,1139,1140,1141,1142,1143,1144,1145,1146,1147,1148,1149,1150,1151,1152,1153,1154,1155,1156,1157,1158,1159,1160,1161,1162,1163,1164,1165,1166,1167,1168,1169,1170,1171,1172,1173,1174,1175,1176,1177,1178,1179,1180,1181,1182,1183,1184,1185,1186,1187,1188,1189,1190,1191,1192,1193,1194,1195,1196,1197,1198,1199,1200,1201,1202,1203,1204,1205,1206,1207,1208,1209,1210,1211,1212,1213,1214,1215,1216,1217,1218,1219,1220,1221,1222,1223,1224,1225,1226,1227,1228,1229,1230,1231,1232,1233,1234,1235,1236,1237,1238,1239,1240,1241,1242,1243,1244,1245,1246,1247,1248,1249,1250,1251,1252,1253,1254,1255,1256,1257,1258,1259,1260,1261,1262,1263,1264,1265,1266,1267,1268,1269,1270,1271,1272,1273,1274,1275,1276,1277,1278,1279,1280,1281,1282,1283,1284,1285,1286,1287,1288,1289,1290,1291,1292,1293,1294,1295,1296,1297,1298,1299,1300,1301,1302,1303,1304,1305,1306,1307,1308,1309,1310,1311,1312,1313,1314,1315,1316,1317,1318,1319,1320,1321,1322,1323,1324,1325,1326,1327,1328,1329,1330,1331,1332,1333,1334,1335,1336,1337,1338,1339,1340,1341,1342,1343,1344,1345,1346,1347,1348,1349,1350,1351,1352,1353,1354,1355,1356,1357,1358,1359,1360,1361,1362,1363,1364,1365,1366,1367,1368,1369,1370,1371,1372,1373,1374,1375,1376,1377,1378,1379,1380,1381,1382,1383,1384,1385,1386,1387,1388,1389,1390,1391,1392,1393,1394,1395,1396,1397,1398,1399,1400,1401,1402,1403,1404,1405,1406,1407,1408,1409,1410,1411,1412,1413,1414,1415,1416,1417,1418,1419,1420,1421,1422,1423,1424,1425,1426,1427,1428,1429,1430,1431,1432,1433,1434,1435,1436,1437,1438,1439,1440,1441,1442,1443,1444,1445,1446,1447,1448,1449,1450,1451,1452,1453,1454,1455,1456,1457,1458,1459,1460,1461,1462,1463,1464,1465,1466,1467,1468,1469,1470,1471,1472,1473,1474,1475,1476,1477,1478,1479,1480,1481,1482,1483,1484,1485,1486,1487,1488,1489,1490,1491,1492,1493,1494,1495,1496,1497,1498,1499,1500,1501,1502,1503,1504,1505,1506,1507,1508,1509,1510,1511,1512,1513,1514,1515,1516,1517,1518,1519,1520,1521,1522,1523,1524,1525,1526,1527,1528,1529,1530,1531,1532,1533,1534,1535,1536,1537,1538,1539,1540,1541,1542,1543,1544,1545,1546,1547,1548,1549,1550,1551,1552,1553,1554,1555,1556,1557,1558,1559,1560,1561,1562,1563,1564,1565,1566,1567,1568,1569,1570,1571,1572,1573,1574,1575,1576,1577,1578,1579,1580,1581,1582,1583,1584,1585,1586,1587,1588,1589,1590,1591,1592,1593,1594,1595,1596,1597,1598,1599,1600,1601,1602,1603,1604,1605,1606,1607,1608,1609,1610,1611,1612,1613,1614,1615,1616,1617,1618,1619,1620,1621,1622,1623,1624,1625,1626,1627,1628,1629,1630,1631,1632,1633,1634,1635,1636,1637,1638,1639,1640,1641,1642,1643,1644,1645,1646,1647,1648,1649,1650,1651,1652,1653,1654,1655,1656,1657,1658,1659,1660,1661,1662,1663,1664,1665,1666,1667,1668,1669,1670,1671,1672,1673,1674,1675,1676,1677,1678,1679,1680,1681,1682,1683,1684,1685,1686,1687,1688,1689,1690,1691,1692,1693,1694,1695,1696,1697,1698,1699,1700,1701,1702,1703,1704,1705,1706,1707,1708,1709,1710,1711,1712,1713,1714,1715,1716,1717,1718,1719,1720,1721,1722,1723,1724,1725,1726,1727,1728,1729,1730,1731,1732,1733,1734,1735,1736,1737,1738,1739,1740,																				

Crom. 685b	Egagone methyl ester	Egagone methyl ester; Methyl egagone	C10 H17 N O 1	199.1268	1.37	200.1274	1240441.58	13873539.83	15606761.51	1427959.52	13012902.82	1067308.55	4221773.141	4627177.65	4454809.156	5276055.285	5287575.265	4016044.58	8417091.27	9609234.72	1024732.52
Crom. 690b	4-acetyl-2-ethoxybenzoic acid/Phenacetinic acid	4-acetyl-2-ethoxybenzoic acid/Phenacetinic acid	C12 H13 O 7	266.0873	5.23	297.0964	1606501.32	1608273.25	8143242.07	2335.889	906919.726	781095.07	4517614.73	3537295.95	4525091.614	4444000.036	629488.796	432506.16	4513358.79	519075.08	504774.182
Crom. 691b	Palmitoylthiamineamide	Palmitoylthiamineamide; Palmitad	C17 H31 N O 2	299.2814	9.27	300.2894	7621318.24	916401.89	344844.317	338084.19	120831.13	160603.86	114939.112	912918.718	2083929.23	707334.196	1764291.67	799121.18	682406.01	477793.55	4807420.931
Crom. 694b	4-ethylthio-1-phenyl-3-oxo-2-butanone-5-ol	4-ethylthio-1-phenyl-3-oxo-2-butanone-5-ol	C17 H18 N 2	304.0764	1.22	305.0865	1270753.74	1010222.93	148755.12	137085.26	223907.05	386675.09	912918.718	912922.25	736617.09	1362949.47	841947.98	427252.72	459945.95	410757.956	
Crom. 697a	2-deoxythymine-6-phosphate	C6 H13 O 11 P 8	240.0475	1.85	245.0419	70545.1446	726000.87	70781.781	658580.062	103455.35	854961.843	478422.19	84230.245	271804.018	4609818.4	4053630.452	1110993.78	1526707.87	152794.852	171373.841	
Crom. 698a	1,2-bis(4-hydroxyphenyl)-2,2,6,6-tetramethyl-1,3-dioxane-4,5-dione	Dioxinone	C18 H18 N 2 O 4	326.3317	1.54	327.3387	134235.12	176081.72	134235.12	176081.72	134235.12	176081.72	134235.12	176081.72	134235.12	176081.72	134235.12	176081.72	134235.12	176081.72	134235.12
Crom. 705a	Lupeol	Lupeol	C19 H40 O 7 P	422.3535	8.59	426.2613	6110562.58	125000.87	610601.294	512626.44	98483.25	139063.21	135628.84	7338.5225	448481.4427	458481.4427	36559.3685	56899.3685	388941.94	579940.97	459494.174
Crom. 710b	6,6-dimethyl-3-oxo-2-thiophene-5-ylidene-2-thiophene-3-carboxylic acid/Isocoumaric acid	Isocoumaric acid	C17 H12 N 4 O 2	307.1784	5.02	308.1858	1551799.96	1797051.8	1468064.25	1230977.17	1010042.3	1139206.76	144665.74	258154.098	216030.78	243493.971	144665.74	740748.85	579634.42	620070.338	
Crom. 715b	Acetylcholine	Acetylcholine	C18 H31 N O 2	341.0575	1.26	342.0645	293127.596	454345.75	6195624.75	378185.52	1040989.7	351578.06	1040989.7	351578.06	1040989.7	351578.06	1040989.7	351578.06	1040989.7	351578.06	1040989.7
Crom. 718a	Cholesterol	Cholesterol	C21 H34 O 2	386.5392	1.45	387.5462	874940.393	650589.127	51062.69	445155.74	96260.313	723319.239	872024.849	806969.614	913296.611	8718929.236	612784.848	599024.485	954513.3	9601810.511	
Crom. 722a	2-oxo-3-oxo-2-thiophene-5-ylidene-2-thiophene-3-carboxylic acid/Isocoumaric acid	Isocoumaric acid	C18 H18 N 2 O 4	326.3317	1.54	327.3387	134235.12	176081.72	134235.12	176081.72	134235.12	176081.72	134235.12	176081.72	134235.12	176081.72	134235.12	176081.72	134235.12	176081.72	134235.12
Crom. 724a	2-Ethylthio-4-hydroxybenzoate	C14 H19 O 7	300.0831	1.149	301.0164	666557.91	94290.26	217808.65	70781.781	658580.062	103455.35	854961.843	478422.19	84230.245	271804.018	4609818.4	4053630.452	1110993.78	1526707.87	171373.841	
Crom. 725a	Methylthio-2-ethylthio-4-hydroxybenzoate	C14 H19 O 7	300.0831	1.149	301.0164	666557.91	94290.26	217808.65	70781.781	658580.062	103455.35	854961.843	478422.19	84230.245	271804.018	4609818.4	4053630.452	1110993.78	1526707.87	171373.841	
Crom. 726a	Methylthio-2-ethylthio-4-hydroxybenzoate	C14 H19 O 7	300.0831	1.149	301.0164	666557.91	94290.26	217808.65	70781.781	658580.062	103455.35	854961.843	478422.19	84230.245	271804.018	4609818.4	4053630.452	1110993.78	1526707.87	171373.841	
Crom. 727a	Methylthio-2-ethylthio-4-hydroxybenzoate	C14 H19 O 7	300.0831	1.149	301.0164	666557.91	94290.26	217808.65	70781.781	658580.062	103455.35	854961.843	478422.19	84230.245	271804.018	4609818.4	4053630.452	1110993.78	1526707.87	171373.841	
Crom. 728a	Methylthio-2-ethylthio-4-hydroxybenzoate	C14 H19 O 7	300.0831	1.149	301.0164	666557.91	94290.26	217808.65	70781.781	658580.062	103455.35	854961.843	478422.19	84230.245	271804.018	4609818.4	4053630.452	1110993.78	1526707.87	171373.841	
Crom. 729a	Methylthio-2-ethylthio-4-hydroxybenzoate	C14 H19 O 7	300.0831	1.149	301.0164	666557.91	94290.26	217808.65	70781.781	658580.062	103455.35	854961.843	478422.19	84230.245	271804.018	4609818.4	4053630.452	1110993.78	1526707.87	171373.841	
Crom. 730a	Methylthio-2-ethylthio-4-hydroxybenzoate	C14 H19 O 7	300.0831	1.149	301.0164	666557.91	94290.26	217808.65	70781.781	658580.062	103455.35	854961.843	478422.19	84230.245	271804.018	4609818.4	4053630.452	1110993.78	1526707.87	171373.841	
Crom. 731a	Methylthio-2-ethylthio-4-hydroxybenzoate	C14 H19 O 7	300.0831	1.149	301.0164	666557.91	94290.26	217808.65	70781.781	658580.062	103455.35	854961.843	478422.19	84230.245	271804.018	4609818.4	4053630.452	1110993.78	1526707.87	171373.841	
Crom. 732a	Methylthio-2-ethylthio-4-hydroxybenzoate	C14 H19 O 7	300.0831	1.149	301.0164	666557.91	94290.26	217808.65	70781.781	658580.062	103455.35	854961.843	478422.19	84230.245	271804.018	4609818.4	4053630.452	1110993.78	1526707.87	171373.841	
Crom. 733a	Methylthio-2-ethylthio-4-hydroxybenzoate	C14 H19 O 7	300.0831	1.149	301.0164	666557.91	94290.26	217808.65	70781.781	658580.062	103455.35	854961.843	478422.19	84230.245	271804.018	4609818.4	4053630.452	1110993.78	1526707.87	171373.841	
Crom. 734a	Methylthio-2-ethylthio-4-hydroxybenzoate	C14 H19 O 7	300.0831	1.149	301.0164	666557.91	94290.26	217808.65	70781.781	658580.062	103455.35	854961.843	478422.19	84230.245	271804.018	4609818.4	4053630.452	1110993.78	1526707.87	171373.841	
Crom. 735a	Methylthio-2-ethylthio-4-hydroxybenzoate	C14 H19 O 7	300.0831	1.149	301.0164	666557.91	94290.26	217808.65	70781.781	658580.062	103455.35	854961.843	478422.19	84230.245	271804.018	4609818.4	4053630.452	1110993.78	1526707.87	171373.841	
Crom. 736a	Methylthio-2-ethylthio-4-hydroxybenzoate	C14 H19 O 7	300.0831	1.149	301.0164	666557.91	94290.26	217808.65	70781.781	658580.062	103455.35	854961.843	478422.19	84230.245	271804.018	4609818.4	4053630.452	1110993.78	1526707.87	171373.841	
Crom. 737a	Methylthio-2-ethylthio-4-hydroxybenzoate	C14 H19 O 7	300.0831	1.149	301.0164	666557.91	94290.26	217808.65	70781.781	658580.062	103455.35	854961.843	478422.19	84230.245	271804.018	4609818.4	4053630.452	1110993.78	1526707.87	171373.841	
Crom. 738a	Methylthio-2-ethylthio-4-hydroxybenzoate	C14 H19 O 7	300.0831	1.149	301.0164	666557.91	94290.26	217808.65	70781.781	658580.062	103455.35	854961.843	478422.19	84230.245	271804.018	4609818.4	4053630.452	1110993.78	1526707.87	171373.841	
Crom. 739a	Methylthio-2-ethylthio-4-hydroxybenzoate	C14 H19 O 7	300.0831	1.149	301.0164	666557.91	94290.26	217808.65	70781.781	658580.062	103455.35	854961.843	478422.19	84230.245	271804.018	4609818.4	4053630.452	1110993.78	1526707.87	171373.841	
Crom. 740a	Methylthio-2-ethylthio-4-hydroxybenzoate	C14 H19 O 7	300.0831	1.149	301.0164	666557.91	94290.26	217808.65	70781.781	658580.062	103455.35	854961.843	478422.19	84230.245	271804.018	4609818.4	4053630.452	1110993.78	1526707.87	171373.841	
Crom. 741a	Methylthio-2-ethylthio-4-hydroxybenzoate	C14 H19 O 7	300.0831	1.149	301.0164	666557.91	94290.26	217808.65	70781.781	658580.062	103455.35	854961.843	478422.19	84230.245	271804.018	4609818.4	4053630.452	1110993.78	1526707.87	171373.841	
Crom. 742a	Methylthio-2-ethylthio-4-hydroxybenzoate	C14 H19 O 7	300.0831	1.149	301.0164	666557.91	94290.26	217808.65	70781.781	658580.062	103455.35	854961.843	478422.19	84230.245	271804.018	4609818.4	4053630.452	1110993.78	1526707.87	171373.841	
Crom. 743a	Methylthio-2-ethylthio-4-hydroxybenzoate	C14 H19 O 7	300.0831	1.149	301.0164	666557.91	94290.26	217808.65	70781.781	658580.062	103455.35	854961.843	478422.19	84230.245	271804.018	4609818.4	4053630.452	1110993.78	1526707.87	171373.841	
Crom. 744a	Methylthio-2-ethylthio-4-hydroxybenzoate	C14 H19 O 7	300.0831	1.149	301.0164	666557.91	94290.26	217808.65	70781.781	658580.062	103455.35	854961.843	478422.19	84230.245	271804.018	4609818.4	4053630.452	1110993.78	1526707.87	171373.841	
Crom. 745a	Methylthio-2-ethylthio-4-hydroxybenzoate	C14 H19 O 7	300.0831	1.149	301.0164	666557.91	94290.26	217808.65	70781.781	658580.062	103455.35	854961.843	478422.19	84230.245	271804.018	4609818.4	4053630.452	1110993.78	1526707.87	171373.841	
Crom. 746a	Methylthio-2-ethylthio-4-hydroxybenzoate	C14 H19 O 7	300.0831	1.149	301.0164	666557.91	94290.26	217808.65	70781.781	658580.062	103455.35	854961.843	478422.19	84230.245	271804.018	4609818.4	4053630.452	1110993.78	1526707.87	171373.841	
Crom. 747a	Methylthio-2-ethylthio-4-hydroxybenzoate	C14 H19 O 7	300.0831	1.149	301.0164	666557.91	94290.26	217808.65	70781.781	658580.062	103455.35	854961.843	478422.19	84230.245	271804.018	4609818.4	4053630.452	1110993.78	1526707.87	171373.841	
Crom. 748a	Methylthio-2-ethylthio-4-hydroxybenzoate	C14 H19 O 7	300.0831	1.149	301.0164	666557.91	94290.26	217808.65	70781.781	658580.062	103455.35	854961.843	478422.19	84230.245	271804.018	4609818.4	4053630.452	1110993.78	1526707.87	171373.841	
Crom. 749a	Methylthio-2-ethylthio-4-hydroxybenzoate	C14 H19 O 7	300.0831	1.149	301.0164	666557.91	94290.26	217808.65	70781.781	658580.062	103455.35	854961.843	478422.19	84230.245	271804.018	4609818.4	4053630.452	1110993.78	1526707.87	171373.841	
Crom. 750a	Methylthio-2-ethylthio-4-hydroxybenzoate	C14 H19 O 7	300.0831	1.149	301.0164	666557.91	94290.26	217808.65	70781.781	658580.062	103455.35	854961.843	478422.19	84230.245	271804.018	4609818.4	4053630.452	1110993.78	1526707.87	171373.841	
Crom. 751a	Methylthio-2-ethylthio-4-hydroxybenzoate	C14 H19 O 7	300.0831	1.149	301.0164	666557.91	94290.26	217808.65	70781.781	658580.062	103455.35	854961.843	478422.19	84230.245	271804.018	4609818.4	4053630.452	1110993.78	1526707.87	171373.841	
Crom. 752a	Methylthio-2-ethylthio-4-hydroxybenzoate	C14 H19 O 7	300.0831	1.149	301.0164	666557.91	94290.26	217808.65	70781.781	658580.062	103455.35	854961.843	478422.19	84230.245	271804.018	4609818.4	4053630.452	1110993.78	1526707.87	171373.841	
Crom. 753a	Methylthio-2-ethylthio-4-hydroxybenzoate	C14 H19 O 7	300.0831	1.149	301.0164	666557.91	94290.26														

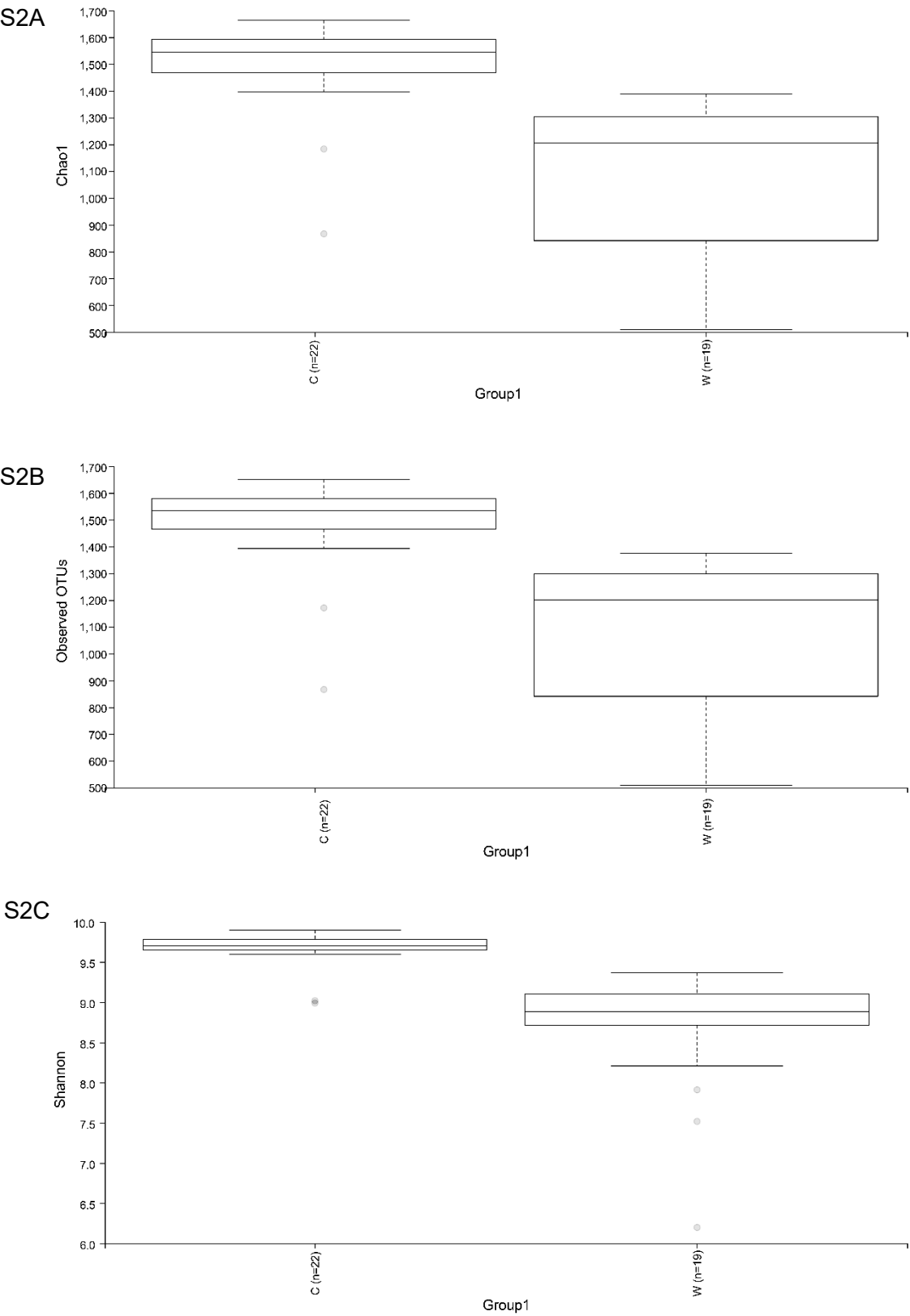
Com 8551_pos	Boc-beta-cyano-L-alanine	--	C9 H14 N2 O4	214.09501	1.366	215.10236	7222498.359	10518866.43	8466968.495	8118589.05	10095470.24	9572379.037	2213414.8	2081726.755	2101141.135	1987038.197	7459332.902	2848767.883	5453456.161	4893835.815	5540000.985
Com 8928_pos	4-Hydroxyproline, Acid	--	C5 H9 N2 O3	136.20735	5.581	137.21106	5480138.387	1000000.71	7797534.477	8685759.047	1006735.59	9077663.514	4335066.078	2938356.612	4454318.384	5717075.877	1589501.071	3442859.59	4586915.085	6645678.387	6132542.317
Com 9432_pos	gamma-Glutamylmethionine	--	C10 H18 N2 O5 S	278.09356	4.794	279.10086	8699010.099	1418706.757	5569917.478	3416033.337	2999766.43	10918948.09	7628159217	7332852684	107099.8183	1358159769	7849644818	8812646146	1282453349	1445174620	1301991446
Com 9803_pos	N-Acetyl-L-glutrylalanine	--	C11 H17 N O3	207.08932	8.758	208.09654	7242654.114	8518486.326	8109277.185	6043581.685	6544768.310	7792341.41	5227407.227	4899782.352	5657747.218	4511484.41	6294495.334	5464811.45	5264701.196	555081758	5866253.66
Com 10261_pos	Protein-L-lysine	--	C10 H19 N O3	217.13117	4.953	218.13844	5435019.453	7606216.108	6695826.813	6211379.515	8114997.653	3011331.955	1018770.777	1178070.392	1075262.499	1921501.539	1541078.616	1260533.401	3487970.627	4705950.965	7974376.111
Com 10421_pos	4-Oxoretinol	--	C20 H28 O2	300.20836	0.752	301.2157	2627444.925	4064019.629	3511716.58	3287218.247	4303782.941	4449843.514	3660775.489	2916726.82	3524081.441	4895677.042	1148004.77	2641307.438	3153170.107	2090137.227	3506700.653
Com 10961_pos	L-Methionine	--	C11 H15 N O2 S	297.10742	4.752	298.11463	5980380.293	3178939.995	4331885.664	4530401.629	7015245.443	7676553.327	655650.565	2362648.877	1696848.882	1260077.75	950913.329	1927701.306	2678421.176	2795672.034	3255386.649
Com_11033_pos	Hydrocortisone acetate	Cortisol 21-acetate; Hydrocortisone acetate; Cortfil	C23 H32 O6	404.21838	5.75	405.2258	6558929.418	7554815.316	2582208.514	5754247.208	4554641.477	6334315.404	1816004.904	1640289.48	1726214.256	2538019.102	1799912.91	1552165.282	3404724.666	2864343.057	3230545.076
Com_11288_pos	Pregnenolone	Fingonolone; 5-Pregna- Bata-20-one; Stera- Hydroxyprog-5-en-20-one	C21 H32 O2	316.23992	9.736	317.2471	1292663.364	1643103.486	1650030.582	1426914.313	2050599.412	1708482.658	2799236.072	2688745.377	2953607.304	4084119.294	1777556.474	3246227.435	2455749.397	2238451.369	2243293.6
Com_12720_pos	Meningione	--	C31 H40 O2	444.30259	8.279	445.3171	852560.085	803138.544	1080326.324	1139872.049	1015211.088	1750691.4	2200445.621	1549036.866	1797860.439	156662.502	2605108.301	2108422.35	1174048.58	1178007.89	1126248.864
Com_13520_pos	Pro-Pn	Meningione; Vitamin K2	C14 H18 N2 O3	282.13165	5.721	283.1384	2666403.524	1938615.983	3024361.982	1994475.681	2178014.076	2180803.351	14314453.584	1070885.5	1108792.809	1616466.75	872645.7731	1252171.077	1668486.585	1772018.11	1616829.922

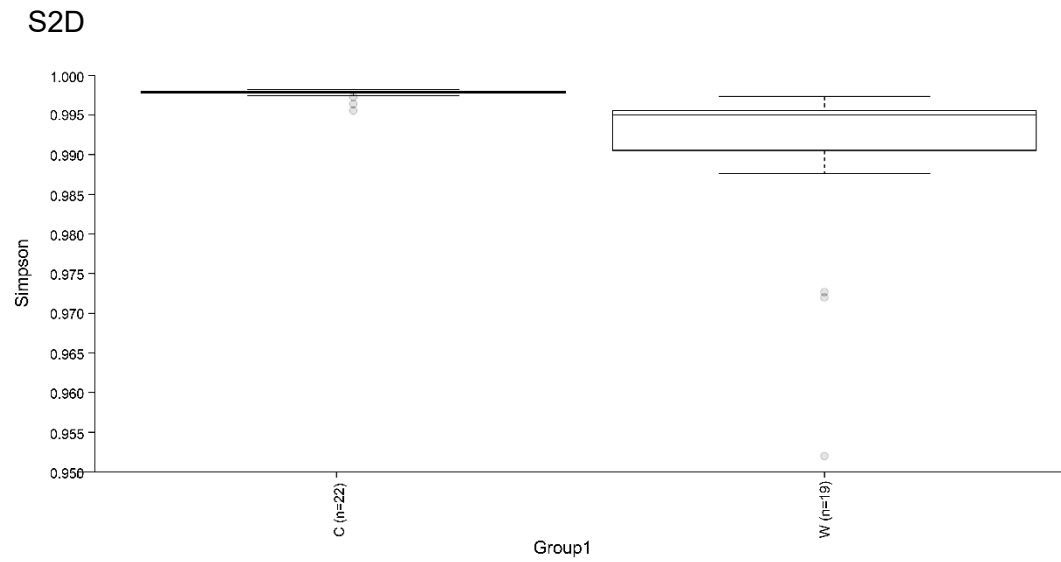
Supplemental Figure S1 Venn diagram of ASVs detected in captive and wild *Cervus elaphus kansuensis* based on 16S rDNA sequencing.



Supplemental Figure S1 Venn diagram of ASVs detected in captive and wild *Cervus elaphus kansuensis* based on 16S rDNA sequencing. Each circle represents a group of samples, and the numbers in the overlapping part of the circles represent the number of ASVs shared between different groups, while the numbers without overlapping part represent the number of ASVs specific to each group. There were 3,033 ASVs detected both in CRD and WRD. Otherwise, there were 4,528 and 3,430 specific ASVs detected in CRD and WRD, respectively.

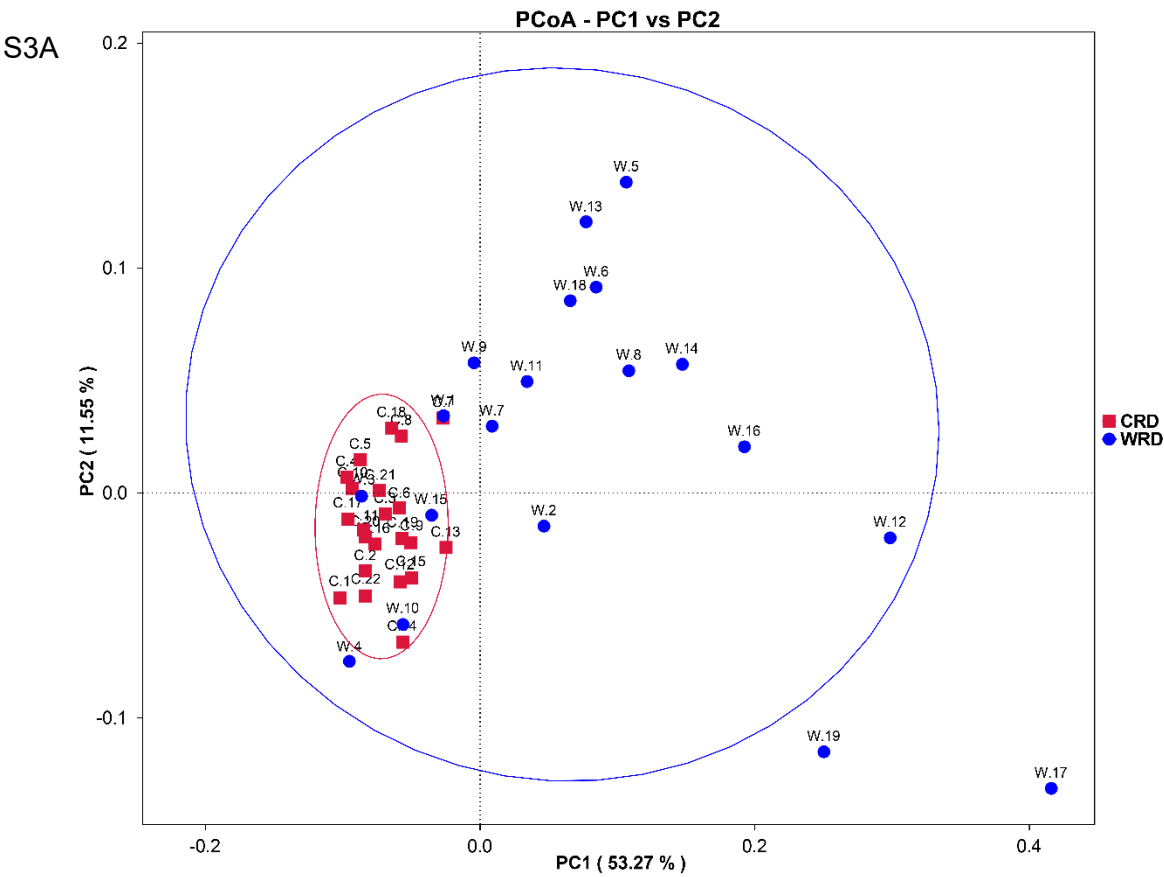
Supplemental Figure S2 Boxplots of alpha diversity of gut microbiota detected by 16S rDNA sequencing.



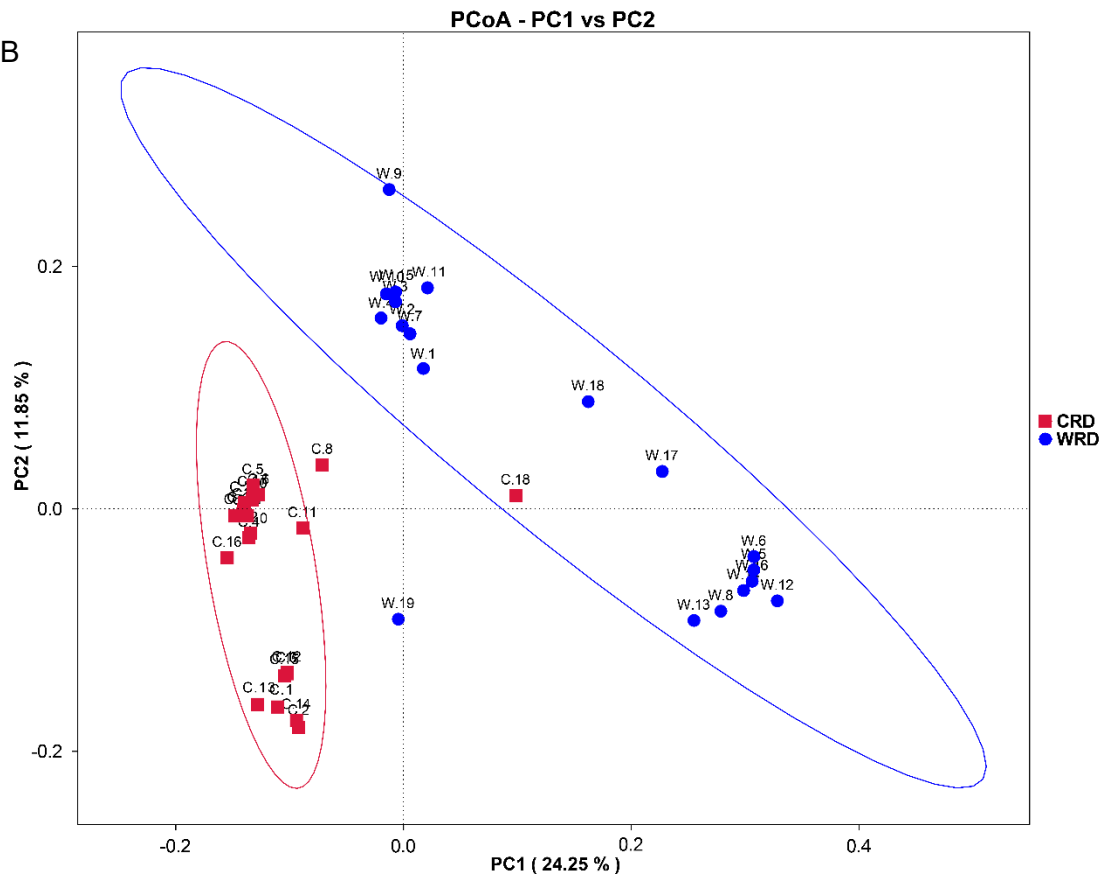


Supplemental Figure S2 Boxplots of alpha diversity of gut microbiota detected by 16S rDNA sequencing. **S2A.** Boxplot of Chao1 index. **S2B.** Boxplot of Observed OUTs index. **S2C.** Boxplot of Shannon index. **S2D.** Boxplot of Simpson index.

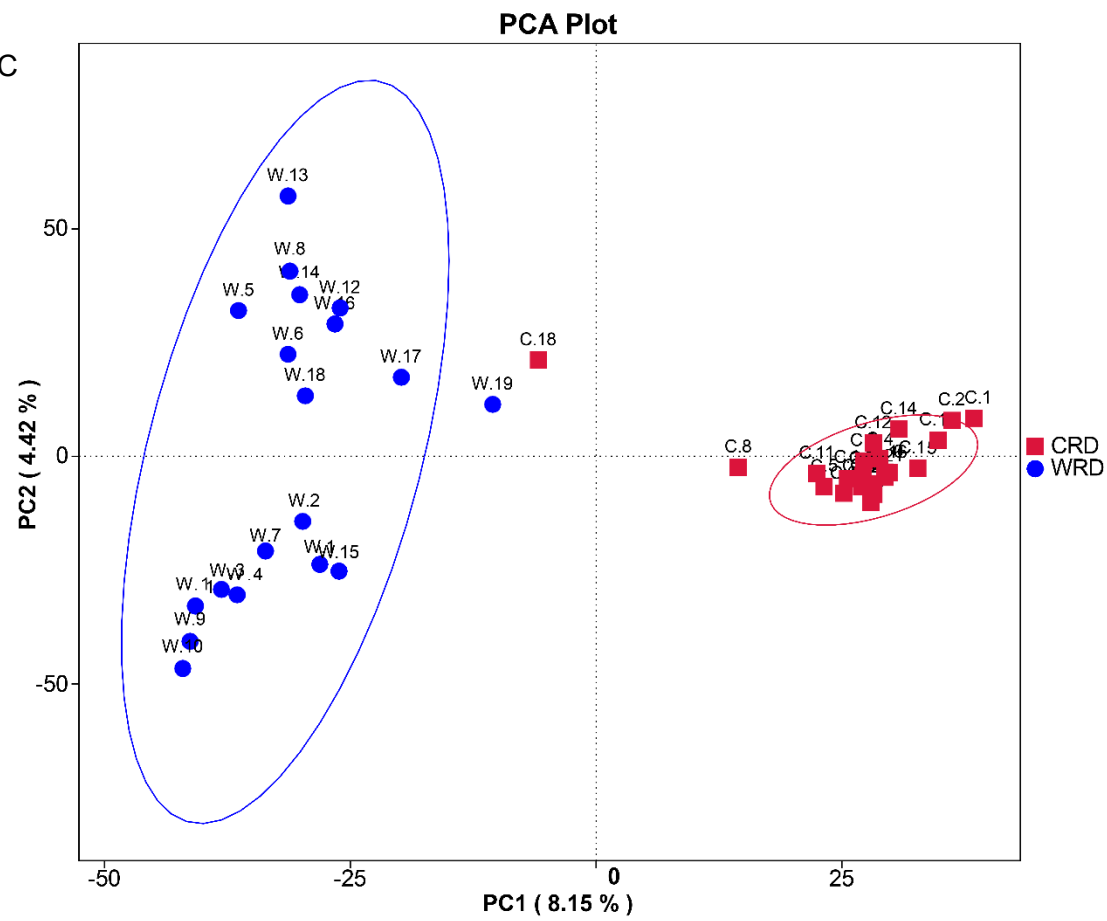
Supplemental Figure S3 PCoA and PCA analysis of gut microbiota detected by 16S rDNA sequencing.



S3B

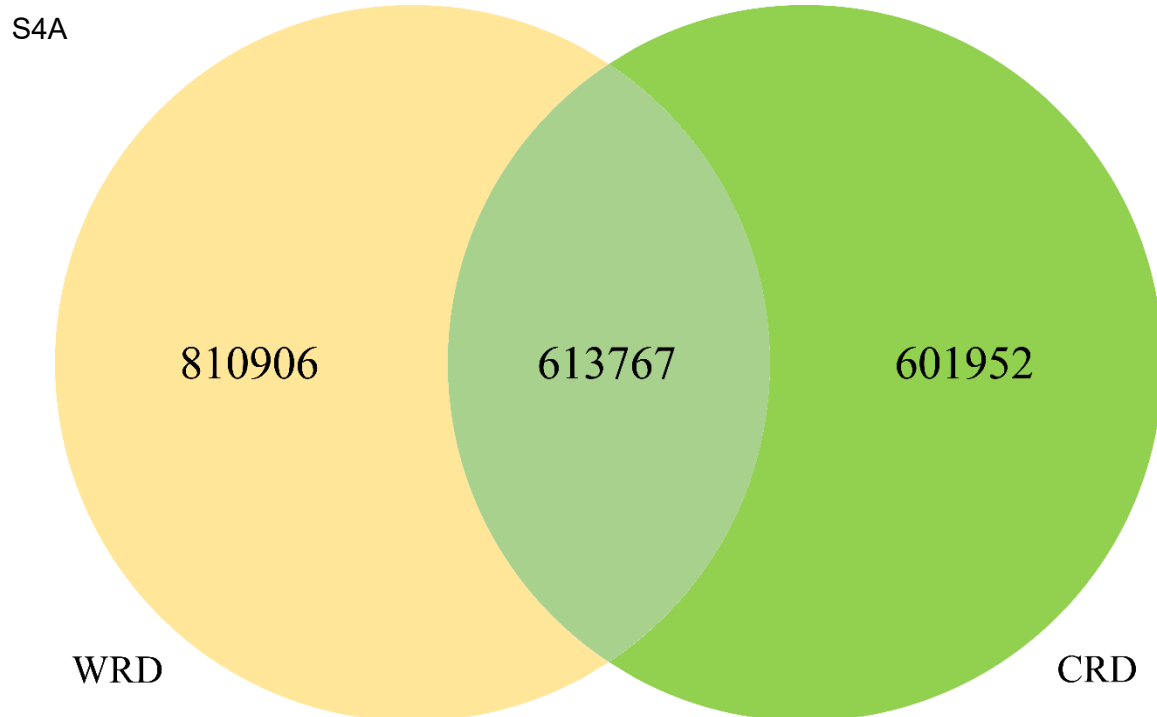


S3C

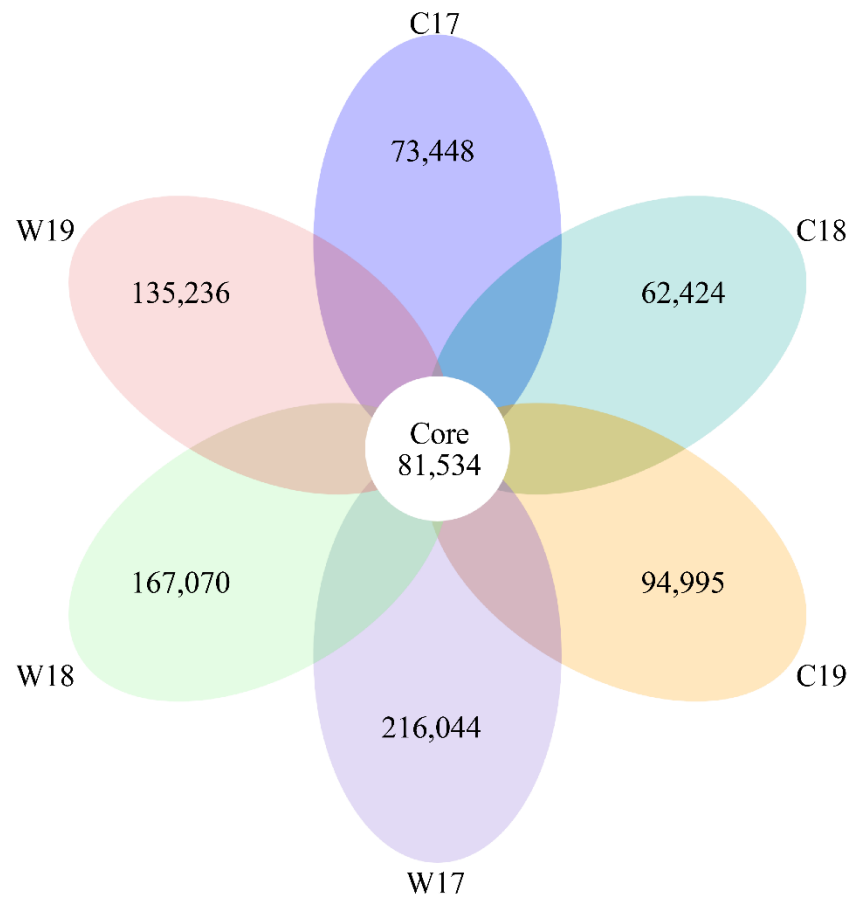


Supplemental Figure S3 PCoA and PCA analysis of gut microbiota detected by 16S rDNA sequencing. **S3A.** PCoA analysis with weighted unifrac. **S3B.** PCoA analysis with unweighted unifrac. **S3C.** PCA analysis of gut microbiota detected by 16S rDNA sequencing. PCoA analysis (**S3A, S3B**) was made based on Weighted unifrac distance and Unweighted unifrac distance, and the principal coordinate combination with the largest contribution was selected for presentation. The results showed that the microbial community structure of samples within the CRD and WRD groups was very similar, but the microbial community structure of the two groups was significantly different, and the samples of the two groups could be clearly clustered into two clusters at the PC1 level. PCA analysis is also an important method to reflect the differences in microbial composition between samples. Figure **S3C** showed similar results to figure **S3A, S3B**, and CRD and WRD groups can be clearly distinguished at the PC1 level, with samples within the two groups being closer together and samples between the two groups being farther apart

Supplemental Figure S4 (A) Venn and (B) flower diagram of genes detected by metagenomic sequencing.



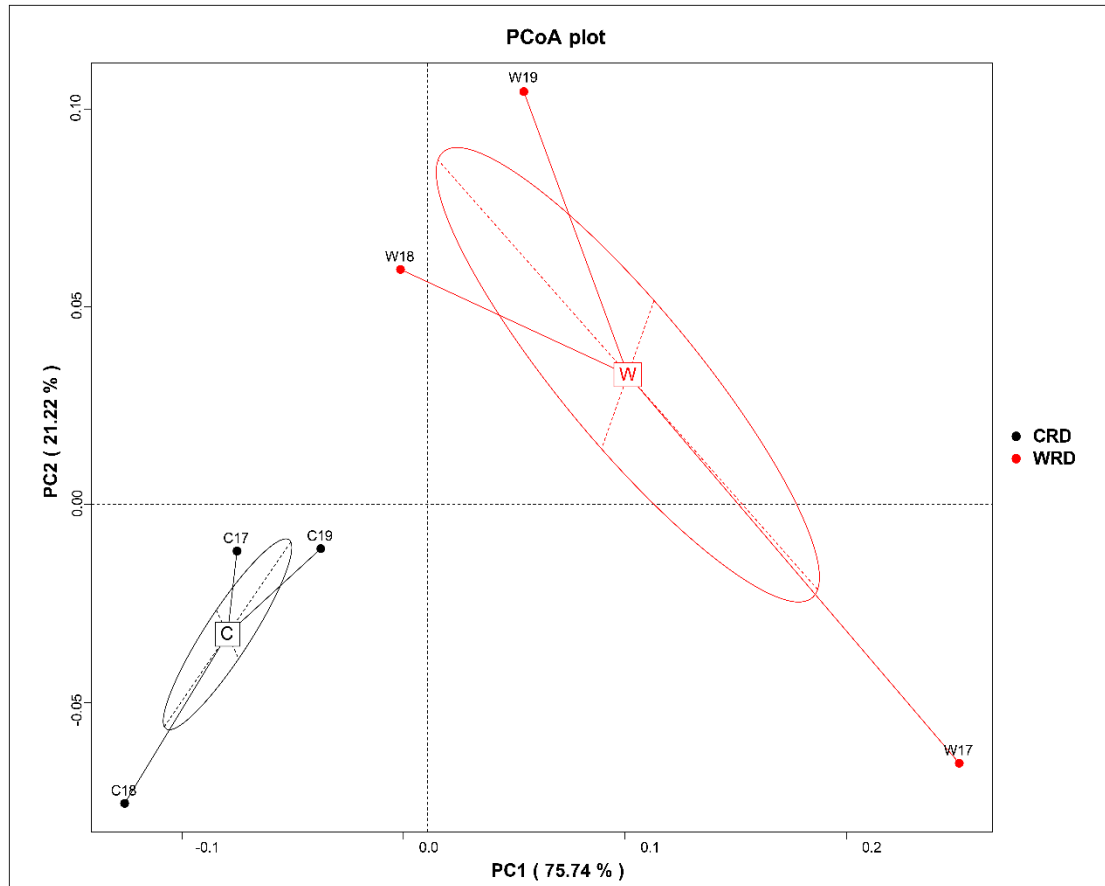
S4B



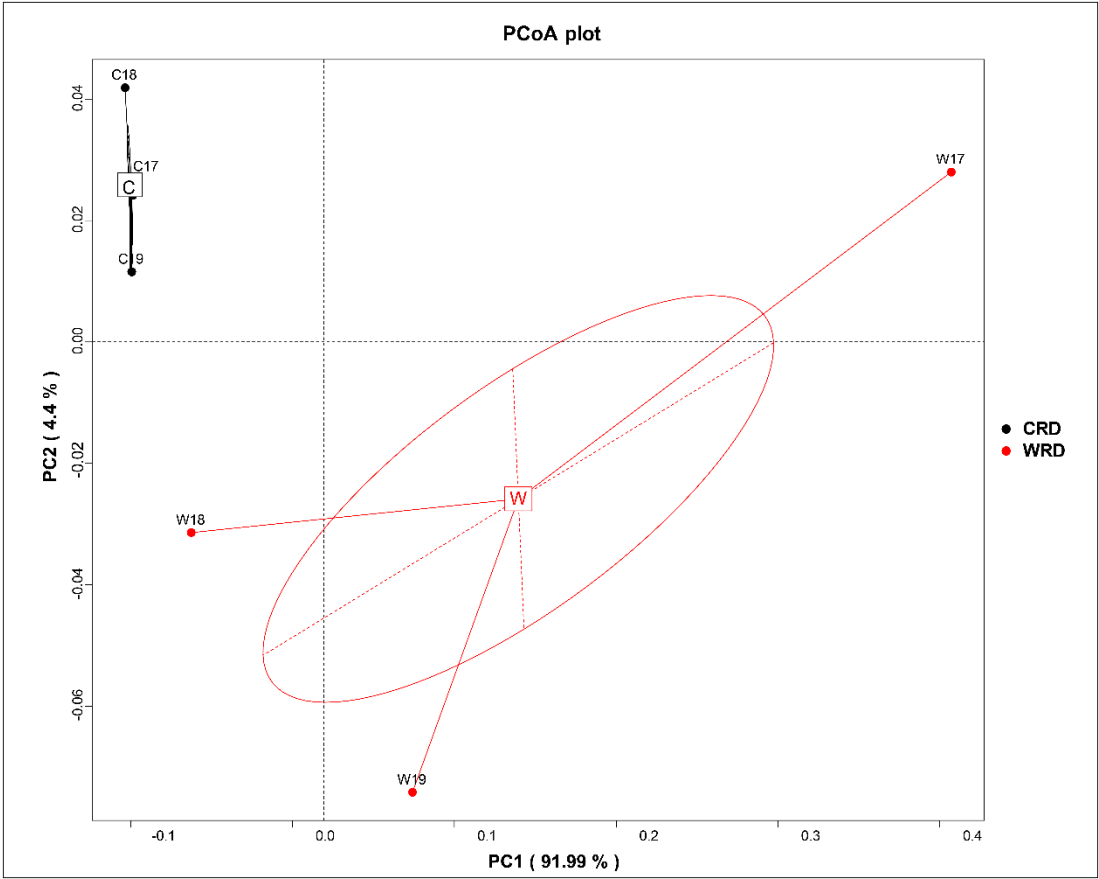
Supplemental Figure S4 Venn and flower diagrams of genes detected by metagenomic sequencing. **S4A.** Venn diagram of genes detected in captive and wild *Cervus elaphus kansuensis*. **S4B.** Flower diagram of genes detected in each sample.

Supplemental Figure S5 (A) PCoA and (B) PCA analysis of gut microbiota detected by metagenomic sequencing.

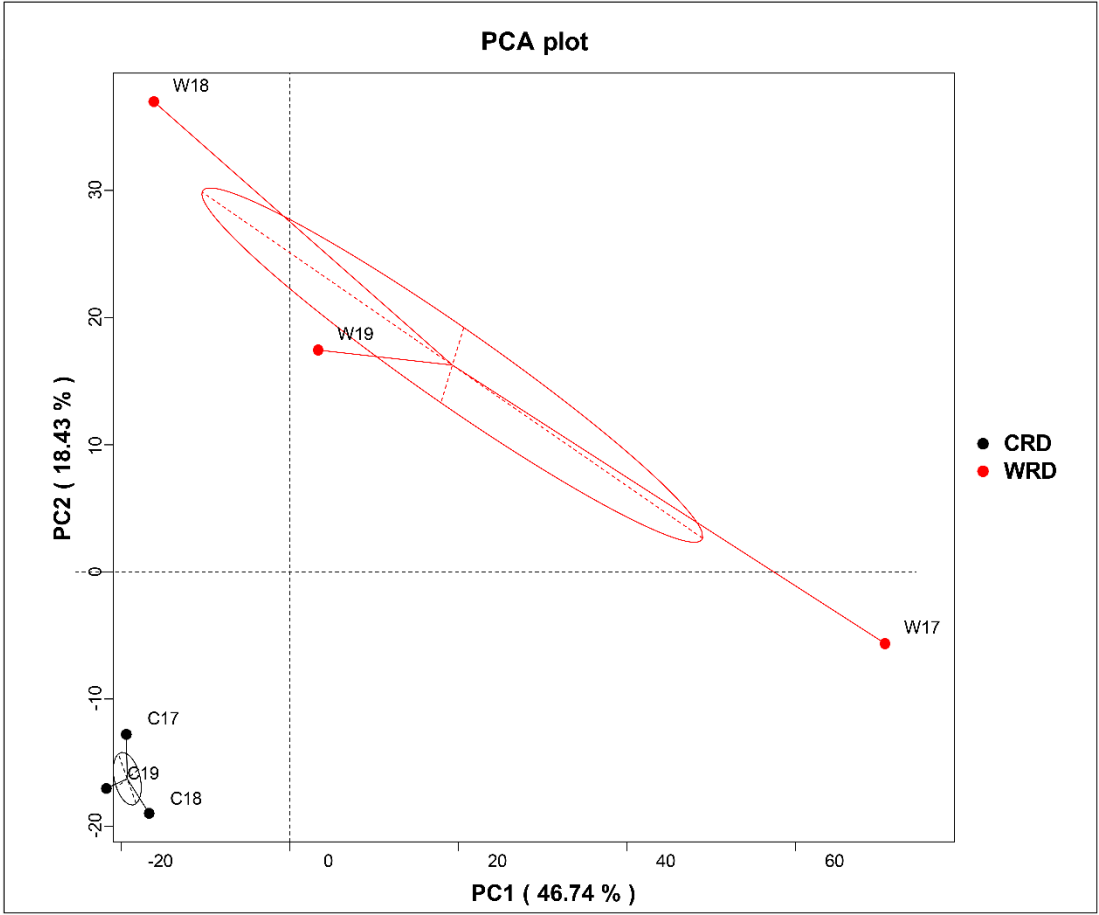
S5A



S5B

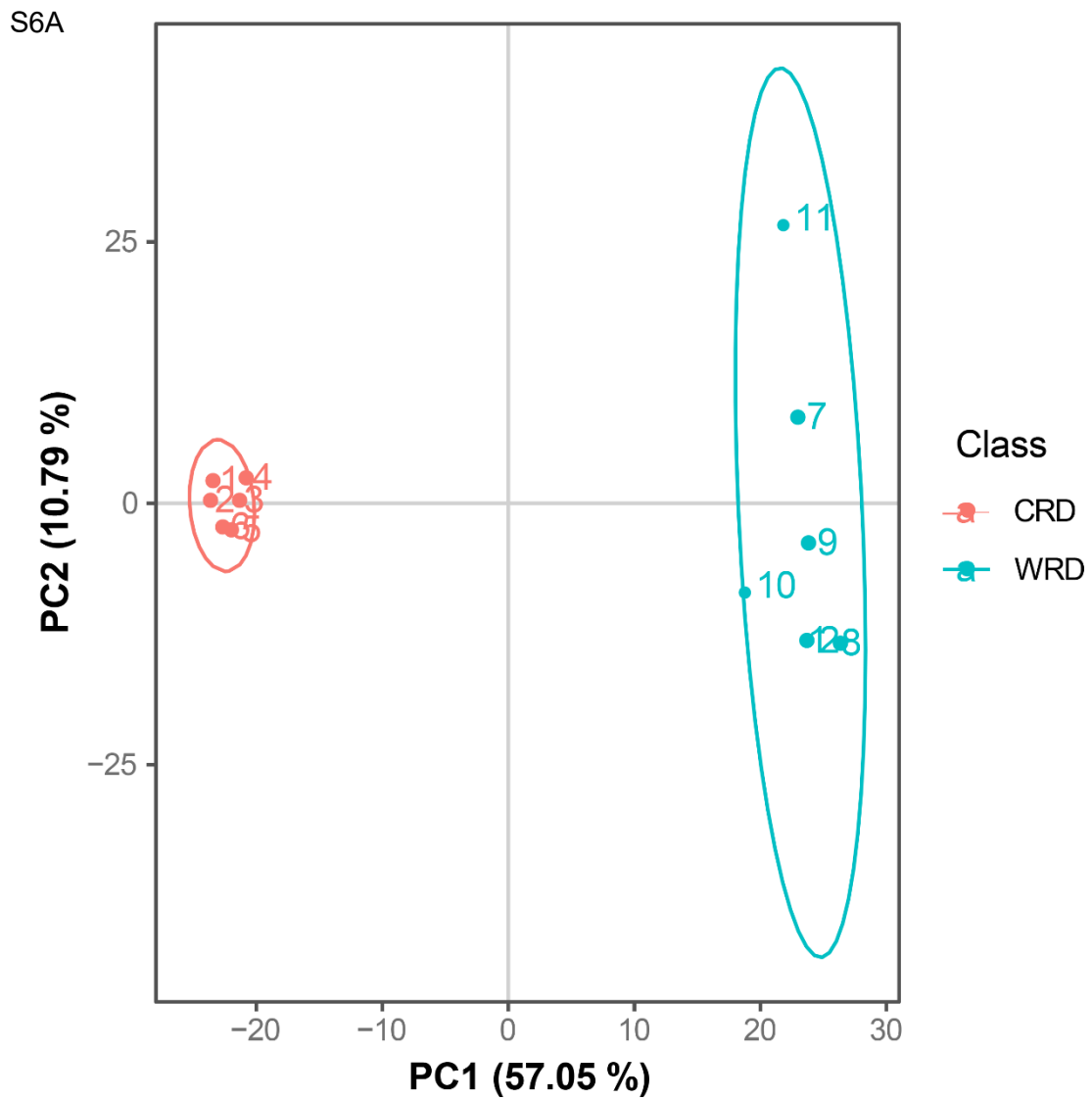


S5C



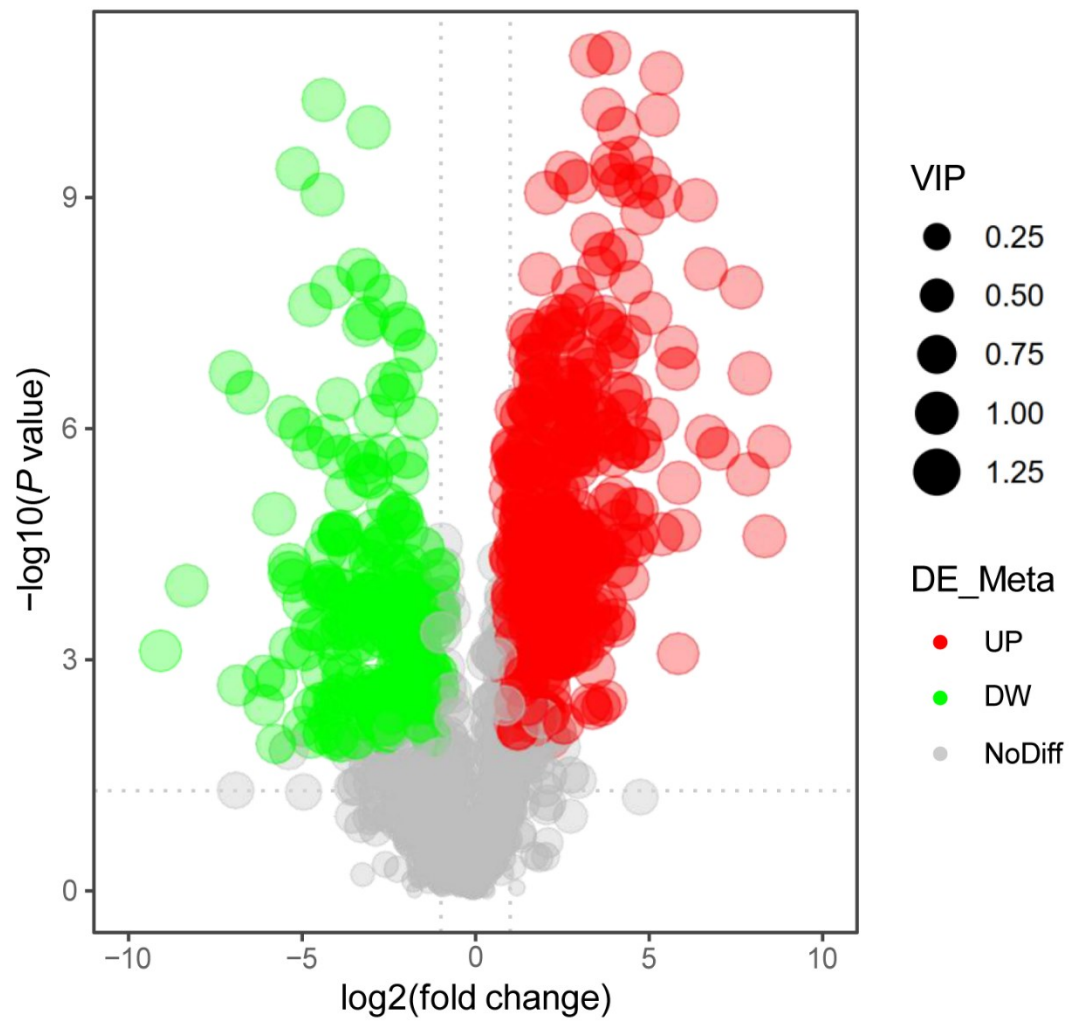
Supplemental Figure S5 PCoA and PCA analysis of gut microbiota detected by metagenomic sequencing. **S5A.** PCoA analysis of gut microbiota at phylum level. **S5B.** PCoA analysis of gut microbiota at genus level. **S5C.** PCA analysis of gut microbiota detected by metagenomic sequencing. The results of PCoA analysis (**S5A, S5B**) showed that the microbial community structure of samples within the CRD and WRD groups was relatively similar, but the microbial community structure of the two groups was significantly different, and the samples of the two groups could be clearly clustered into two clusters at the PC1 level. The microbial community structure of samples in CRD group was relatively similar, while it in WRD group was relatively different. Figure **S5C** showed similar results to figure **S5A, S5B**, and CRD and WRD groups can be clearly distinguished at the PC2 level, with samples within the CRD group being closer together, while samples within the WRD group being farther apart. PCoA and PCA analysis showed that the gut microbial composition of captive red deer is more similar, whereas it varies more among different individuals of wild red deer.

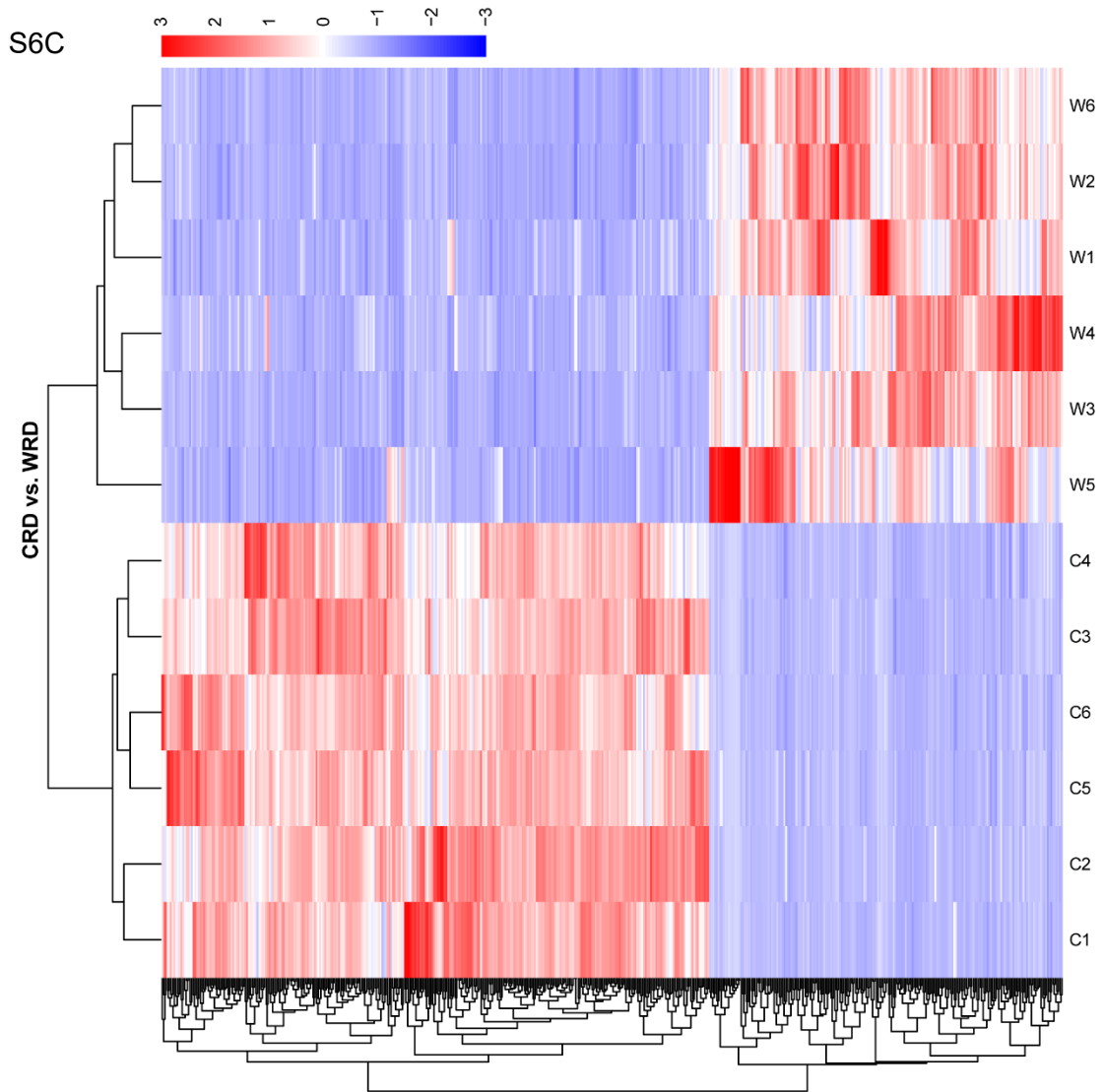
Supplemental Figure S6 PCA and differential analysis of fecal metabolites detected in captive and wild *Cervus elaphus kansuensis* based on LC-MS/MS.



S6B

CRD vs. WRD

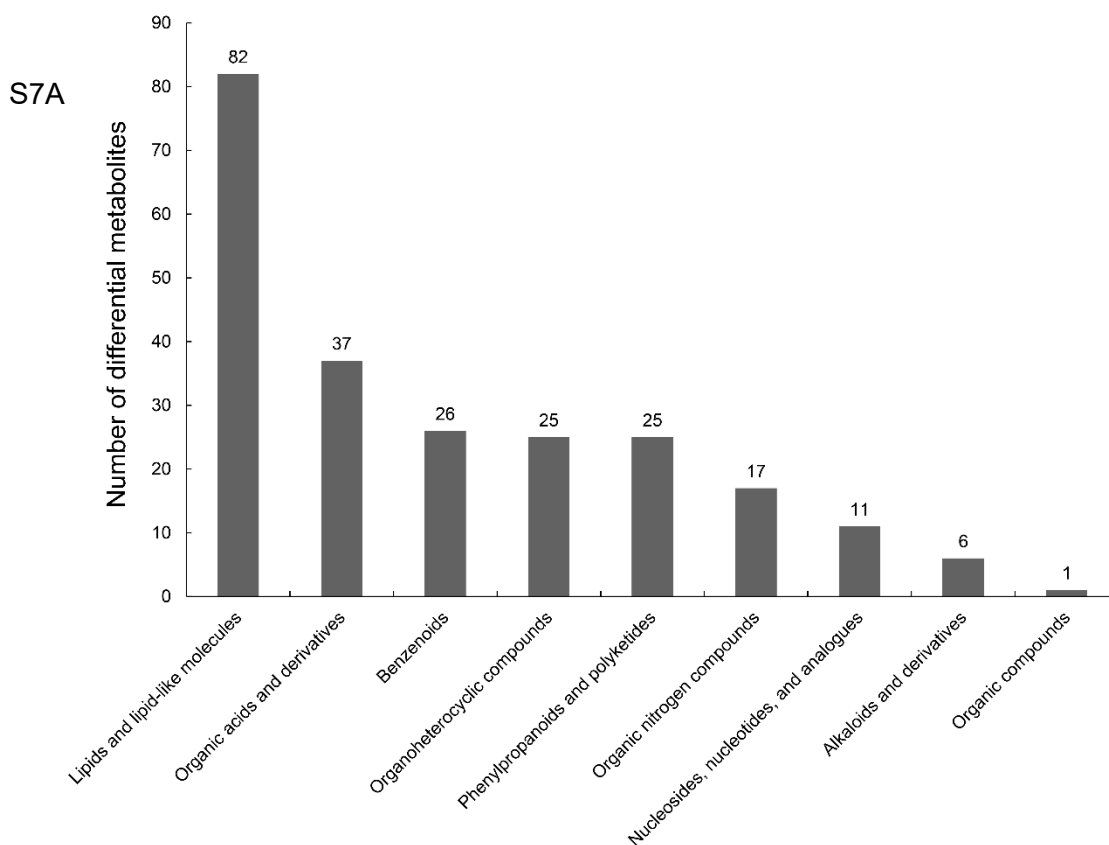


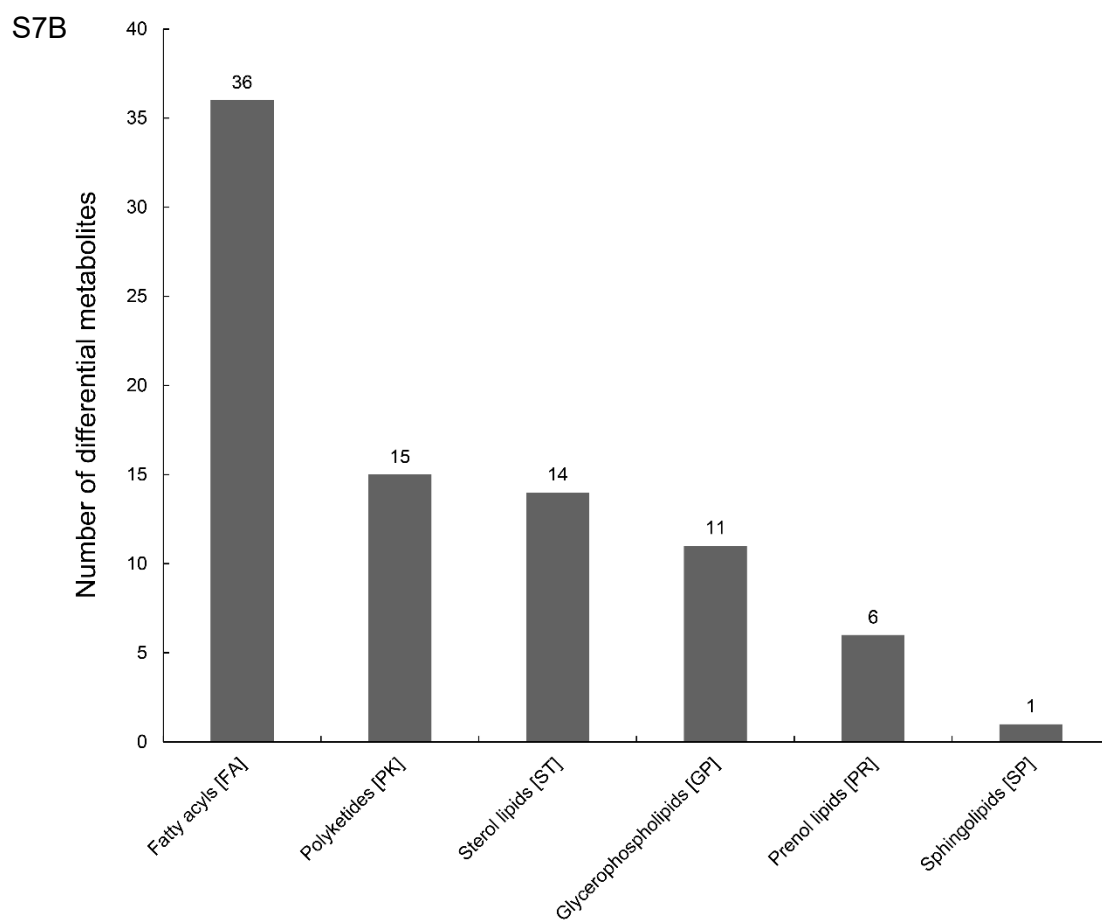


Supplemental Figure S6 PCA and differential analysis of fecal metabolites detected in captive and wild *Cervus elaphus kansuensis* based on LC-MS/MS. **S6A.** PCA analysis of gut microbiota detected by LC-MS/MS. PCA method was used to analyze the difference of fecal metabolites between the two groups. The results showed that the CRD and WRD groups were significantly clustered into two clusters, and the fecal metabolites of the two groups could be distinguished at the PC1 level. **S6B.** Volcano plot of differential metabolites. There were 549 differential metabolites were screened between CRD and WRD. Among them, 336 differential metabolites were significantly

upregulated in CRD, while 213 differential metabolites were significantly downregulated in CRD compared with WRD. **S6C.** Heat map of differential metabolites. Hierarchical clustering analysis of differential metabolites showed that the expression patterns of metabolites in the samples within the CRD and WRD groups differed less, whereas the expression patterns of metabolites between the two groups were more different.

Supplemental Figure S7 Annotation of differential fecal metabolites detected in captive and wild *Cervus elaphus kansuensis*. **S7A.** HMDB annotation of differential metabolites. **S7B.** Lipdmaps annotation of differential metabolites.





Supplemental Figure S7 Annotation of differential fecal metabolites detected in captive and wild *Cervus elaphus kansuensis*. **S7A.** HMDB annotation of differential metabolites. Most differential metabolites were annotated to "Lipids and lipid-like molecules". **S7B.** Lipdmaps annotation of differential metabolites. Most differential metabolites were annotated to "Fatty acyls [FA]".