Species-level exploration of the gut microbiome in the leaf-eating Presbytis monkeys reflected the effects of anthropogenic activity and specialized dietary niches: conservation on the fourth biodiversity level

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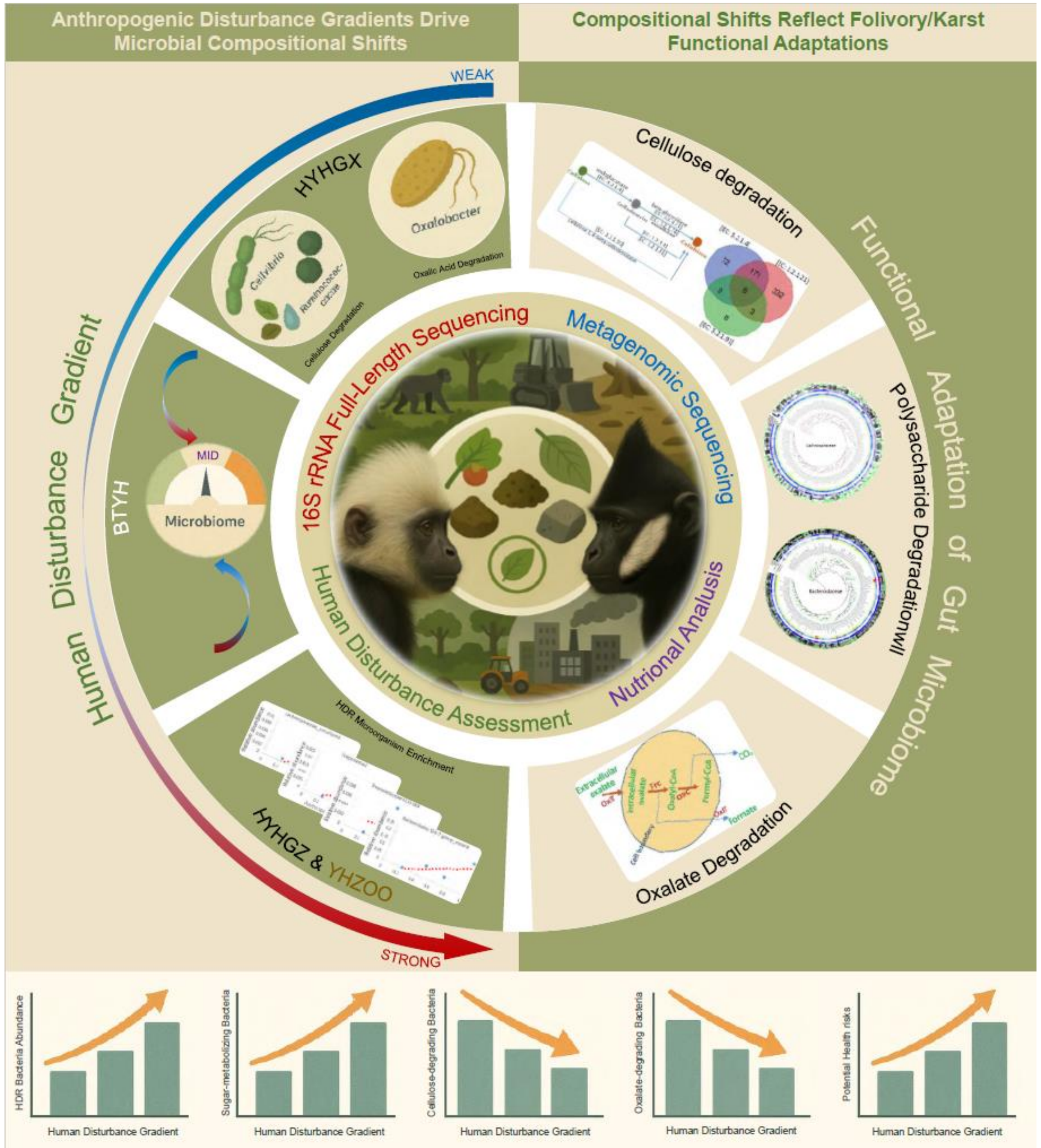
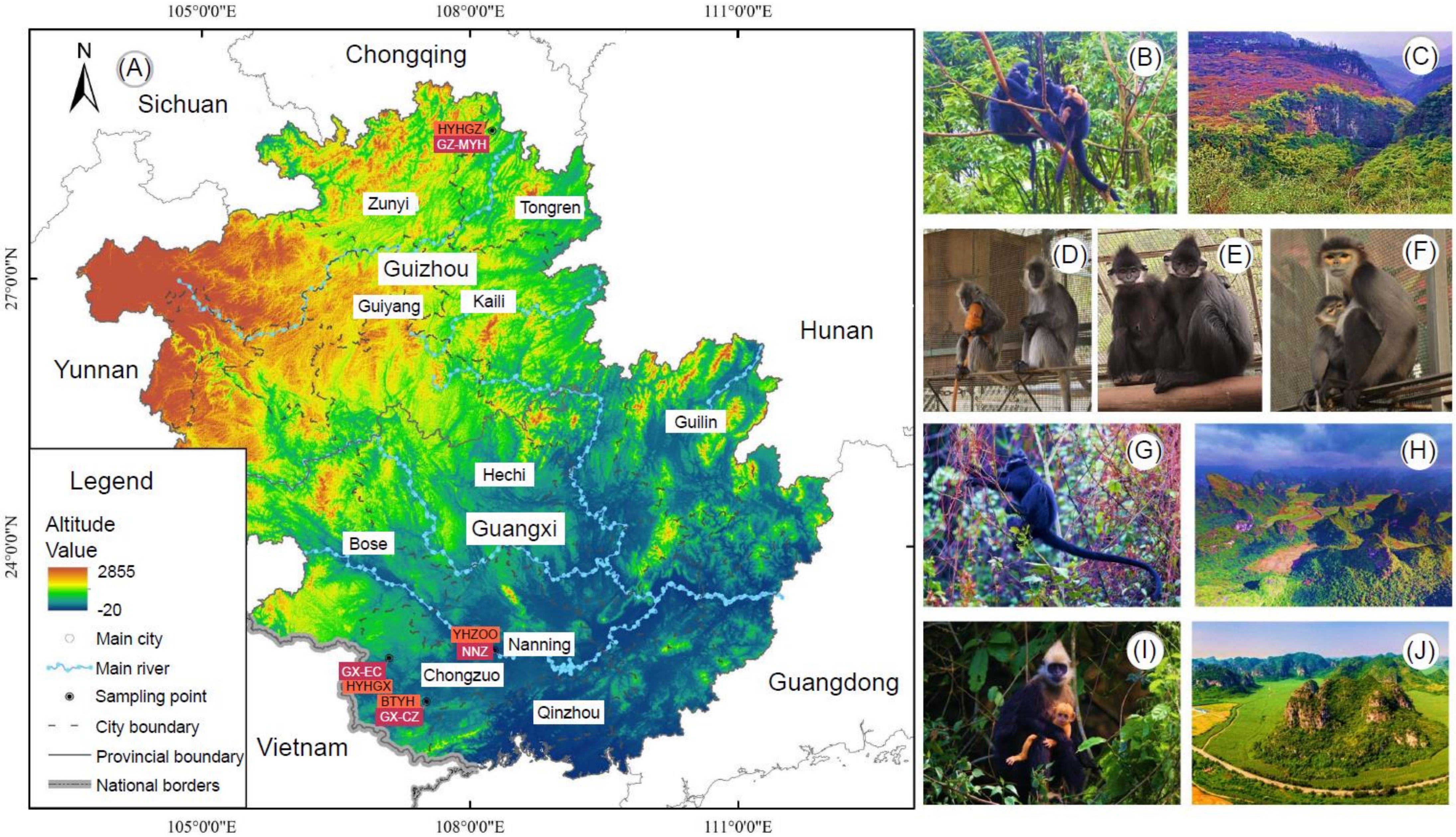
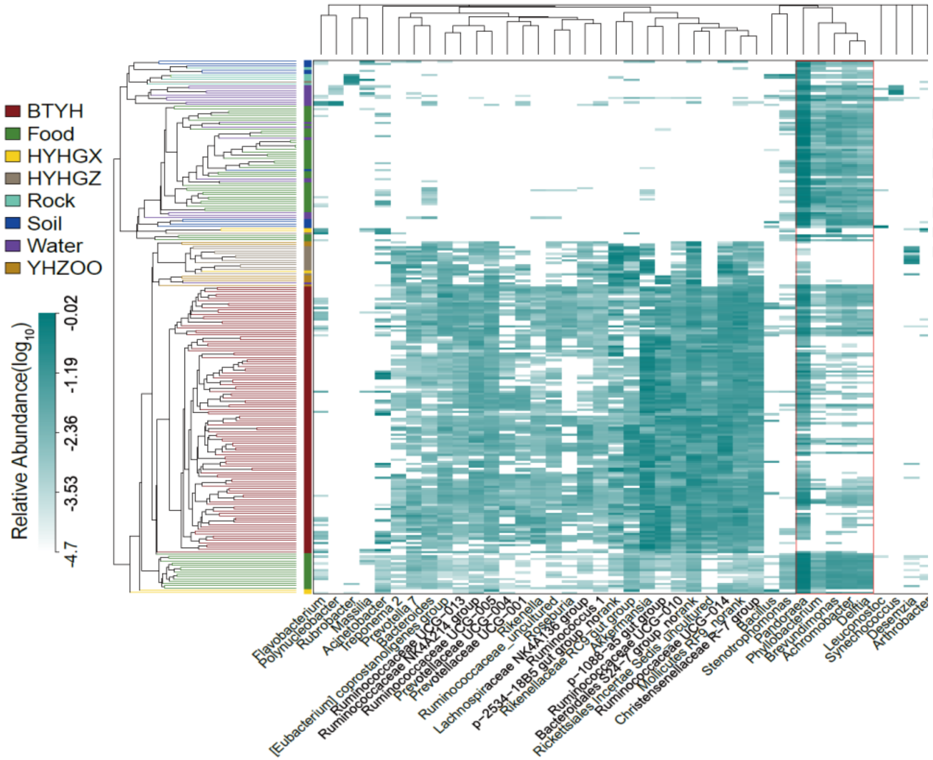
Introduction



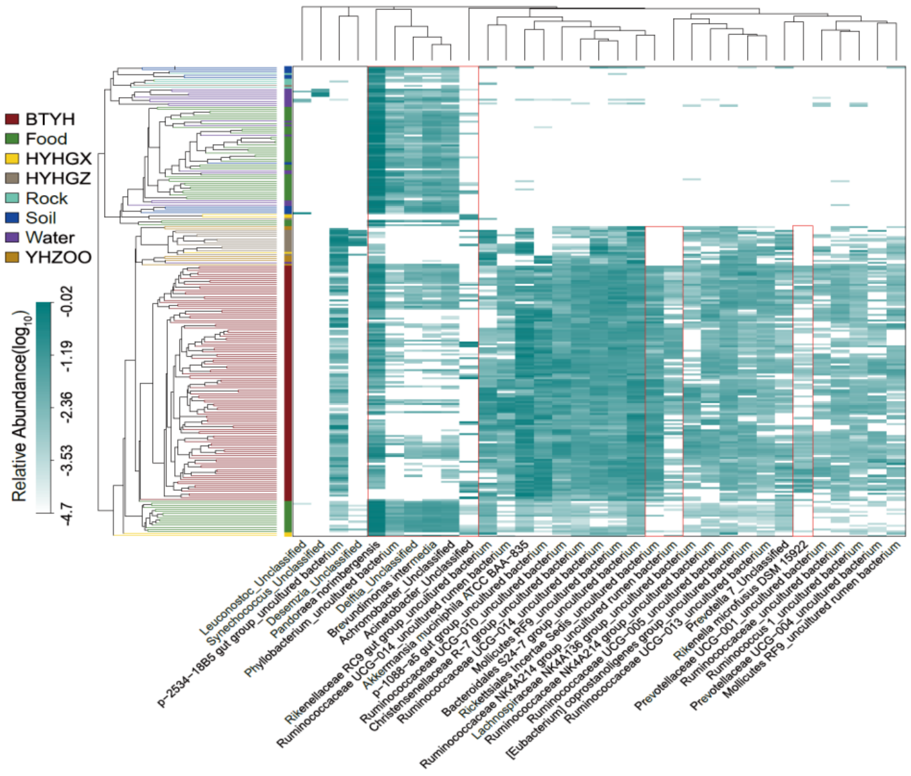
Highlights


105°0'0"E
108°0'0"E
111°0'0"E
27°0'0"N
24°0'0"N
N
(A)
Chongqing
Sichuan
HYHGZ
GZ-MYH
Zunyi
Tongren
Guizhou
Guiyang
Kaili
Yunnan
Hunan
Guilin
Hechi
Guangxi
Bose
YHZOO
NNZ
Nanning
GX-EC
HYHGX
Chongzuo
BTYH
GX-CZ
Qinzhou
Guangdong
Vietnam
Legend
Altitude Value
2855
-20
Main city
Main river
Sampling point
City boundary
Provincial boundary
National borders
(B)
(C)
(D)
(E)
(F)
(G)
(H)
(I)
(J)

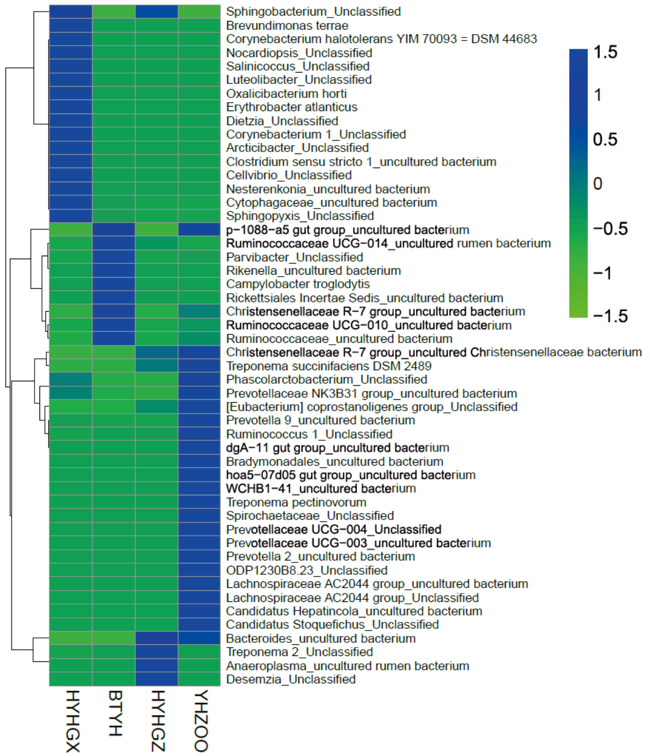
Case 1:The between-group differences in microbial community structure are significant



Dominant Genera Composition

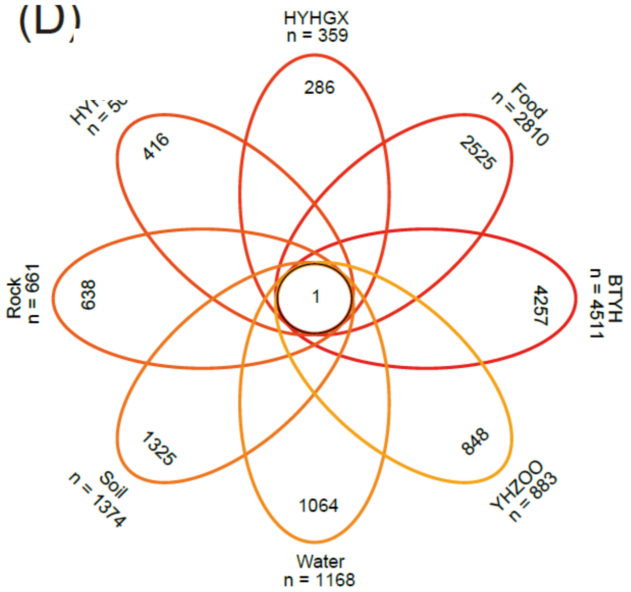


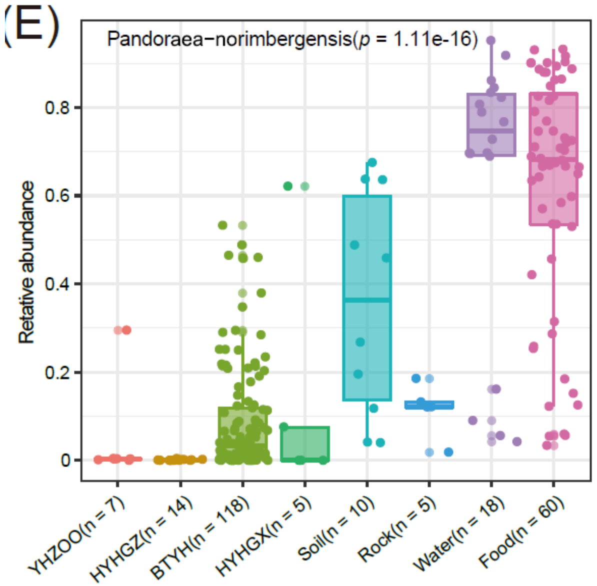
Dominant Species Composition



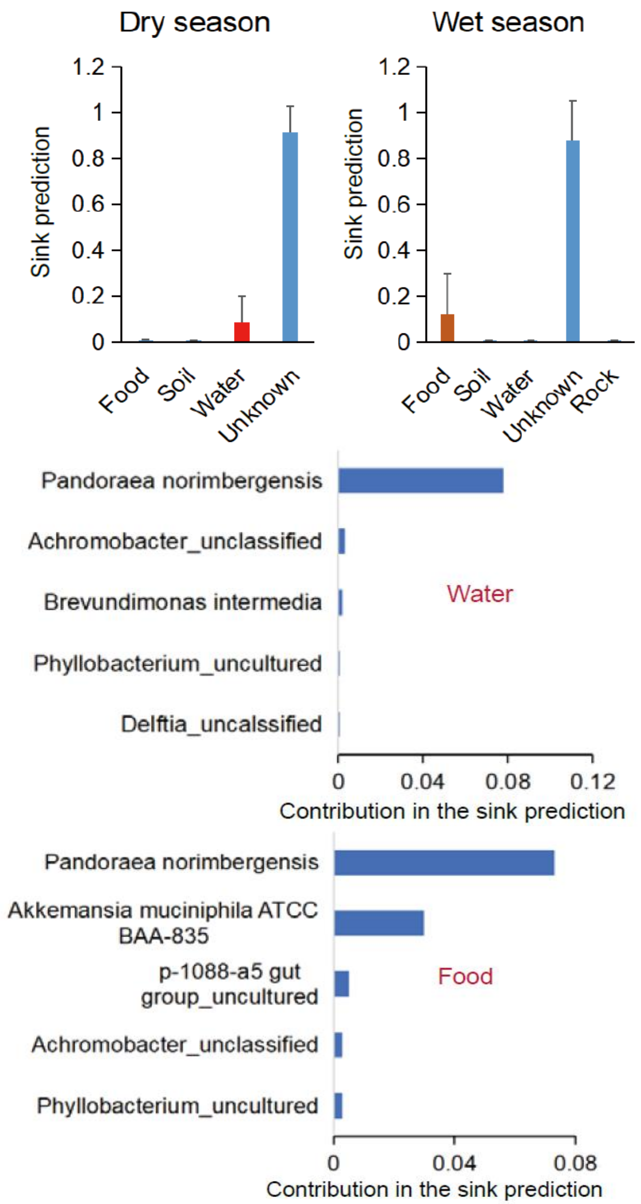
Top 50 Differential Species Composition

Case 2: Host environment influences gut microbial community structure

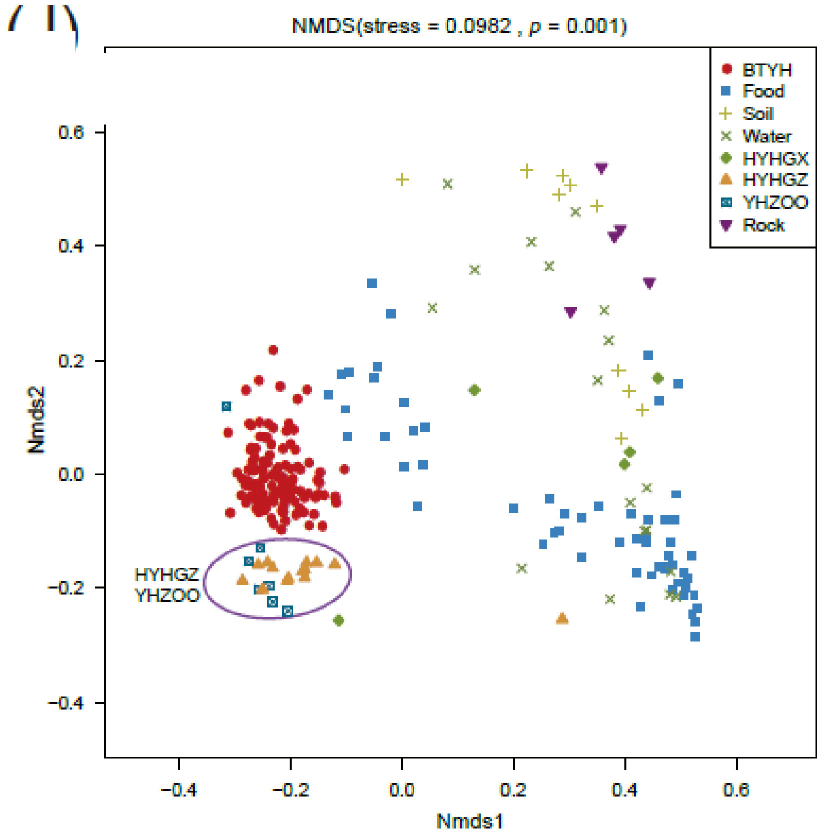




Core ASV
Pandoraea norimbergensis



The main environmental contribution of *P. norimbergensis*

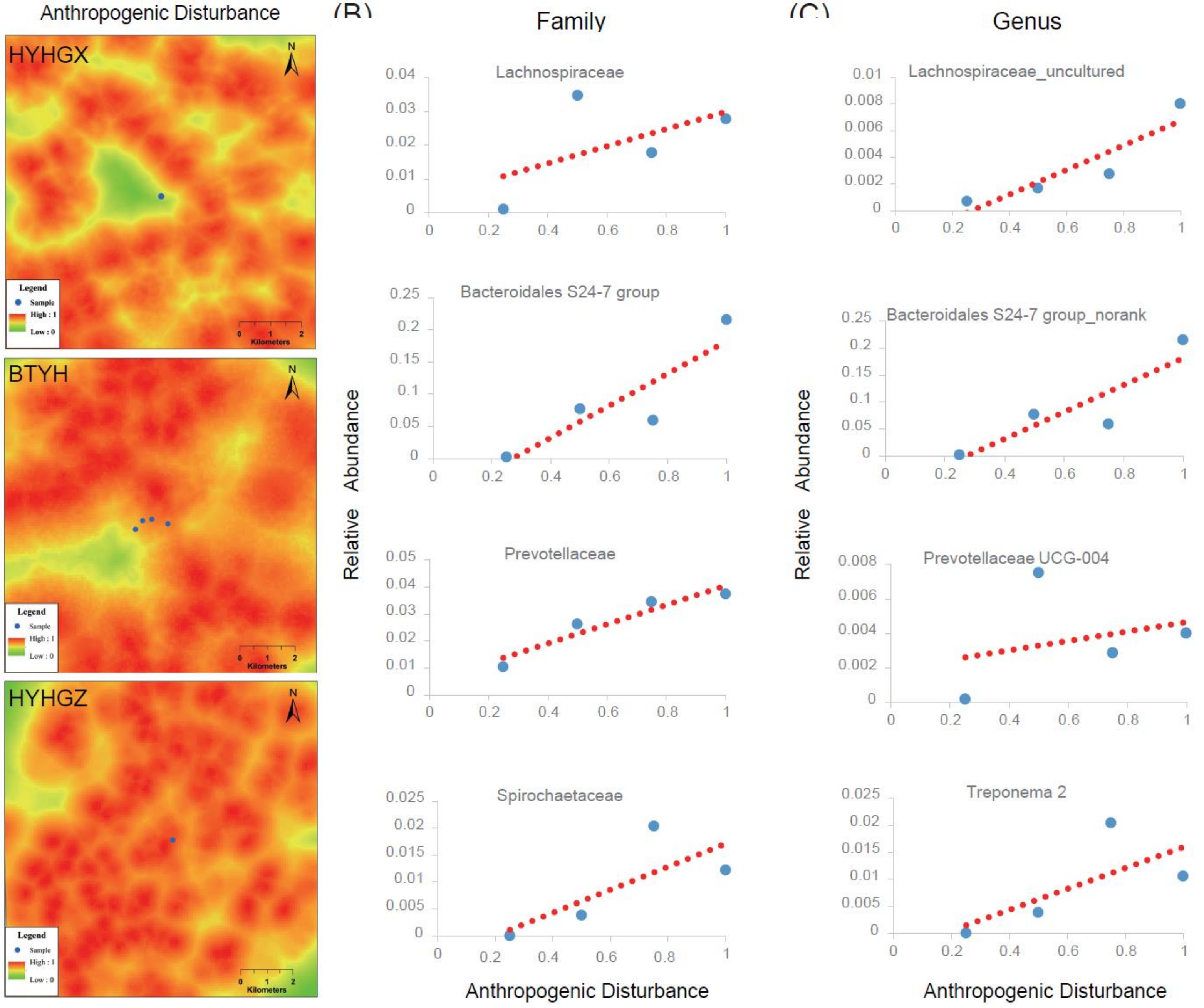


HYHGZ and YHZOO show more similar community composition

Case 3:Human disturbance drives enrichment of HDR microbes

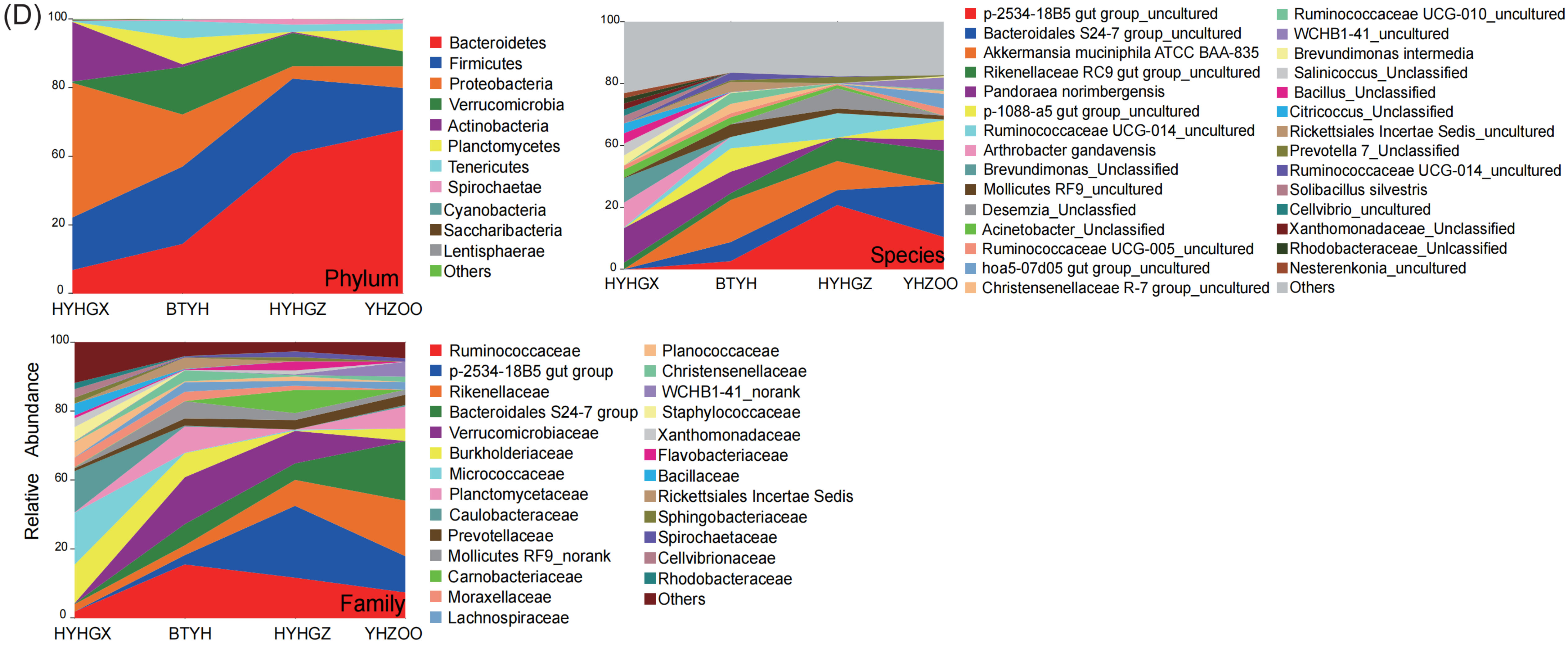
Human disturbance gradient

- HYHGX（Low）
- BTYH（Medium）
- HYHGZ（High）
- YHZOO（Stronget）

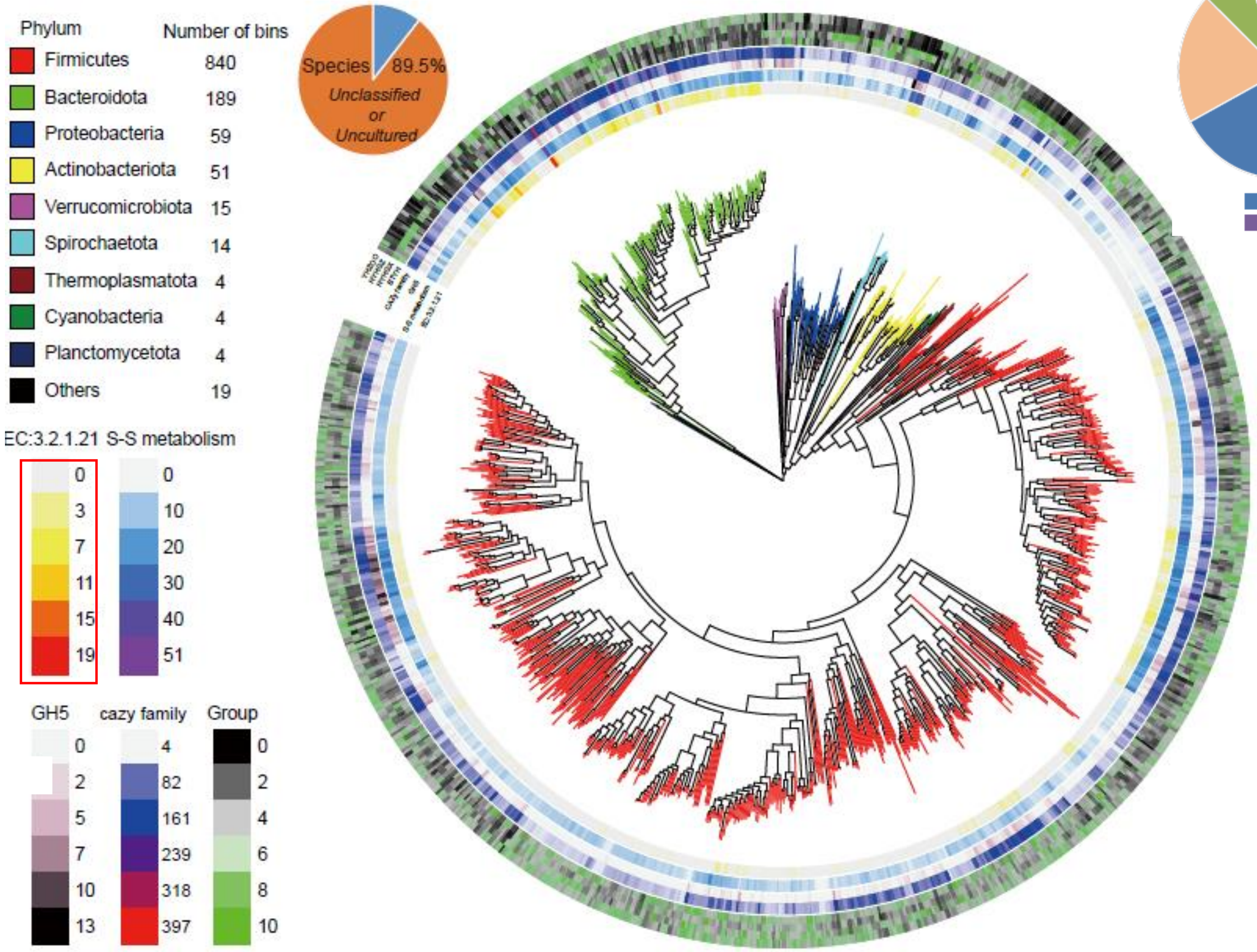


Human disturbance–related (HDR) gut microbial taxa increase significantly with disturbance intensity

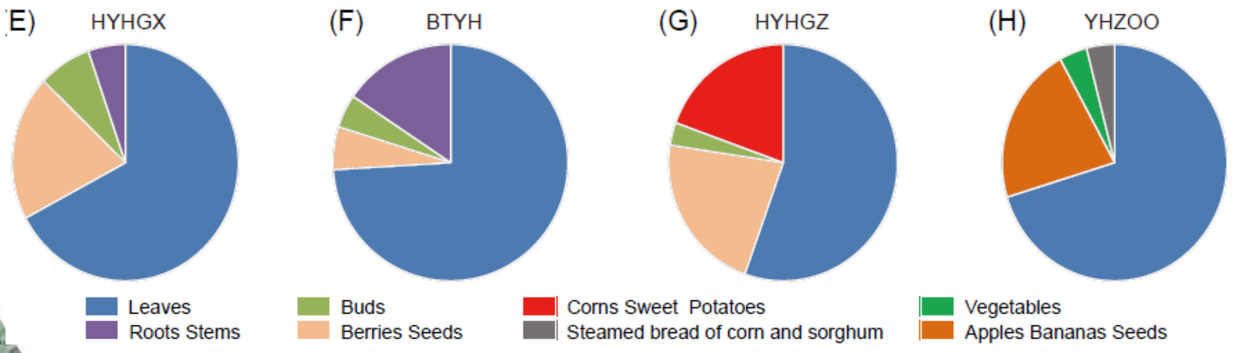
Case 3:Human disturbance drives enrichment of HDR microbes



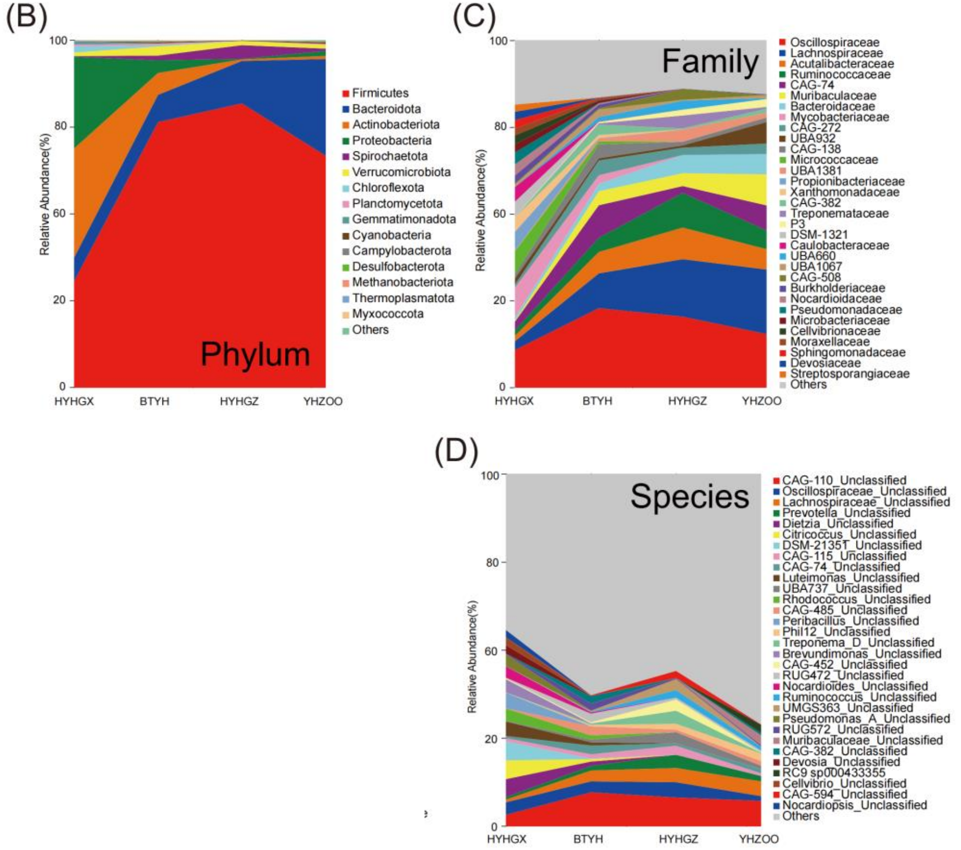
Case 4: Cellulose degradation function



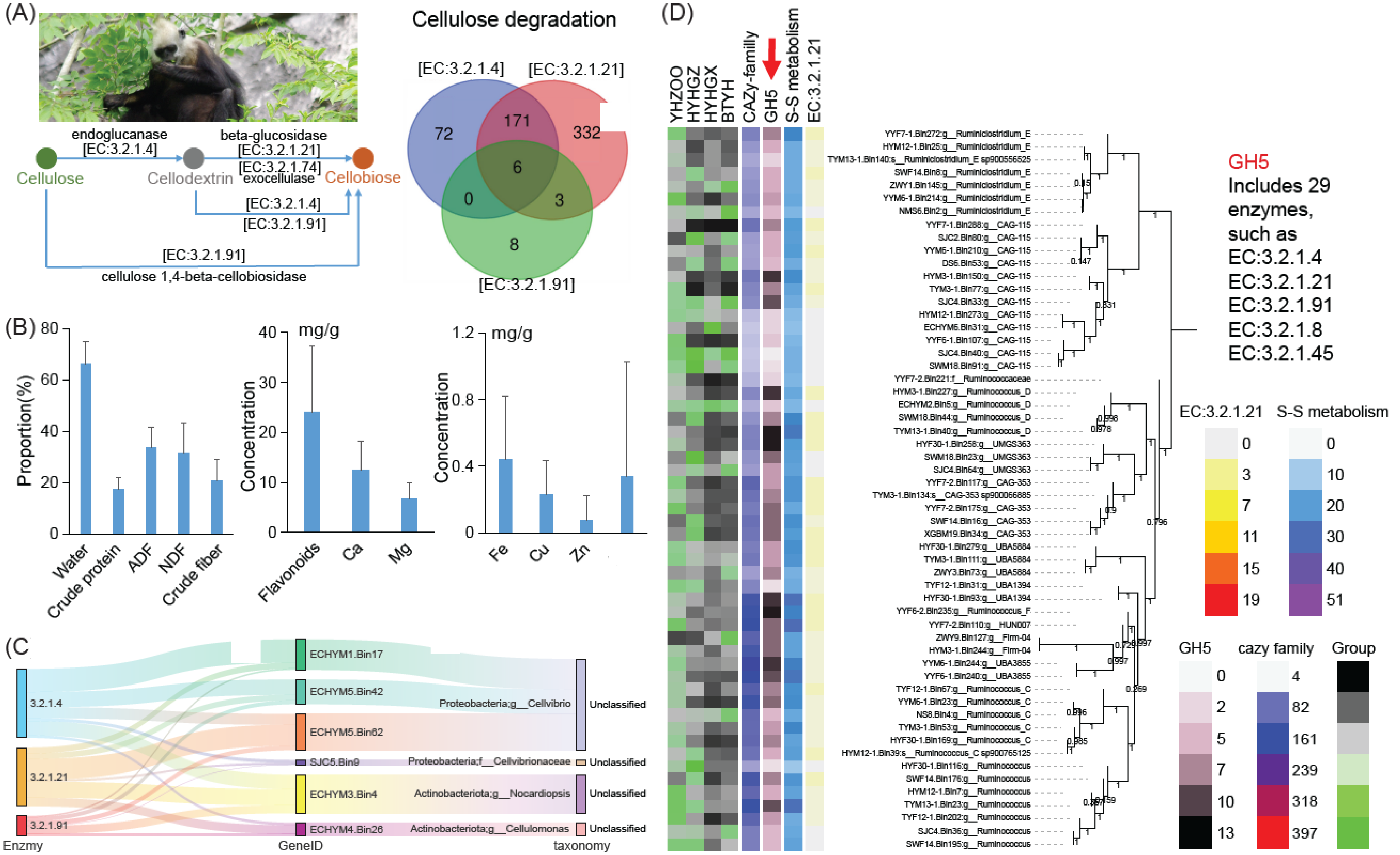
1,199 high-quality non-redundant MAGs



Based on feeding/feeding-record data



Case 4: Cellulose degradation function



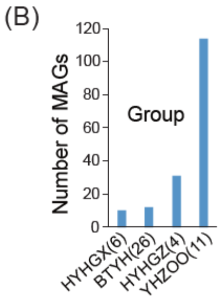
GH5
Includes 29 enzymes, such as
EC:3.2.1.4
EC:3.2.1.21
EC:3.2.1.91
EC:3.2.1.8
EC:3.2.1.45

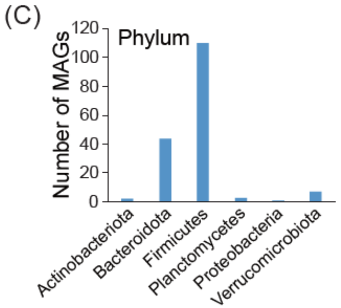
1,199 MAGs reveal potential roles in cellulose degradation

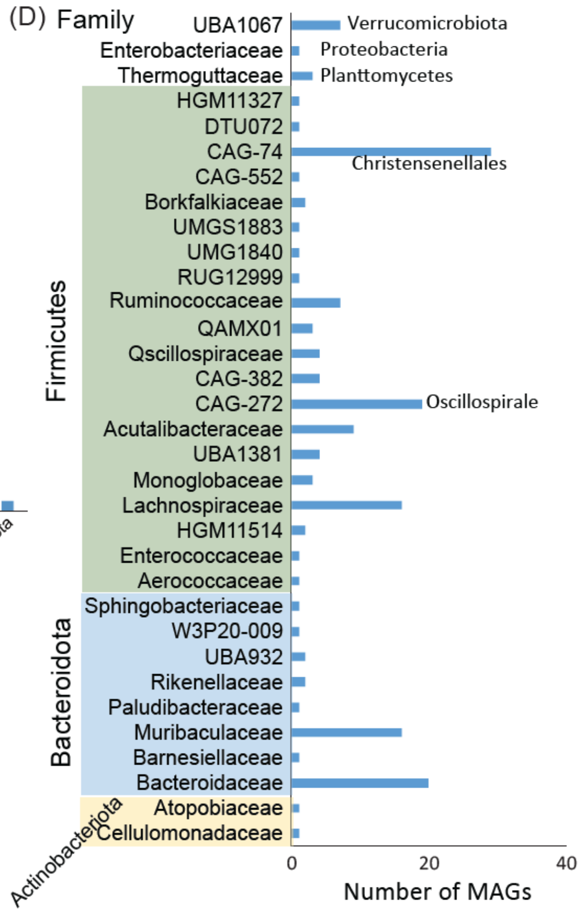
Case 5: Degradation Potential of Dietary Polysaccharides and Host Glycans

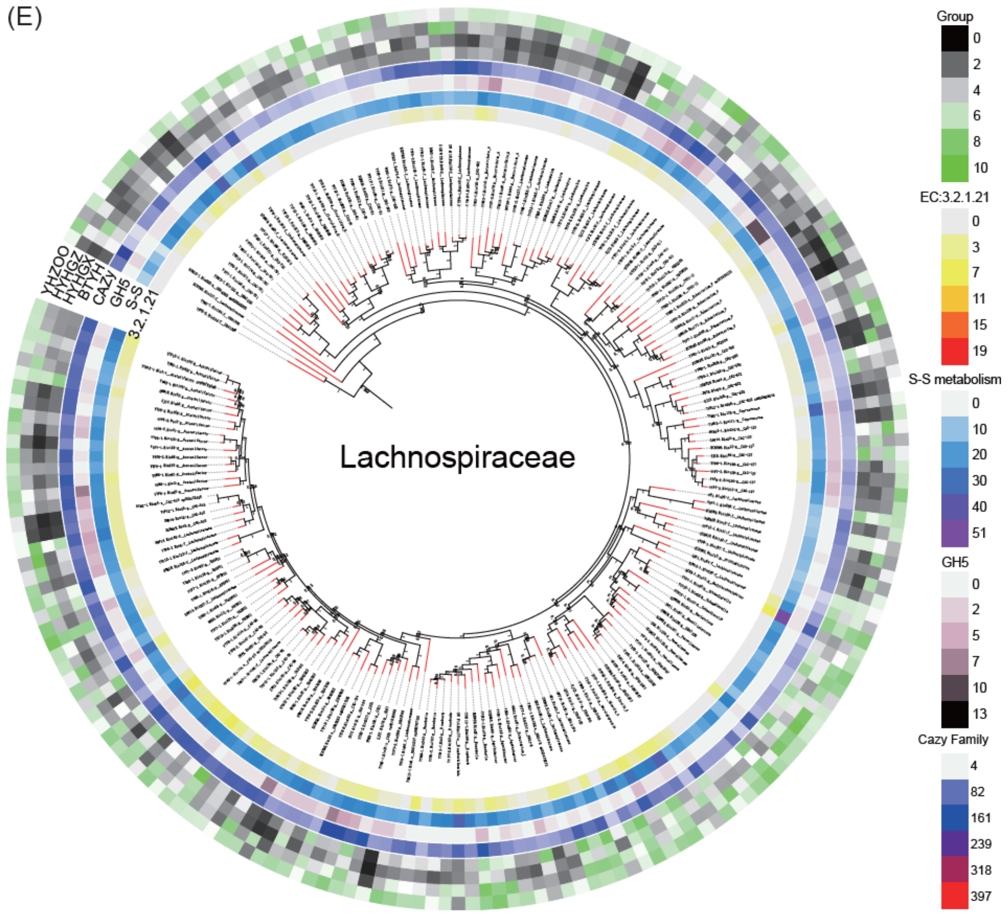
(A)

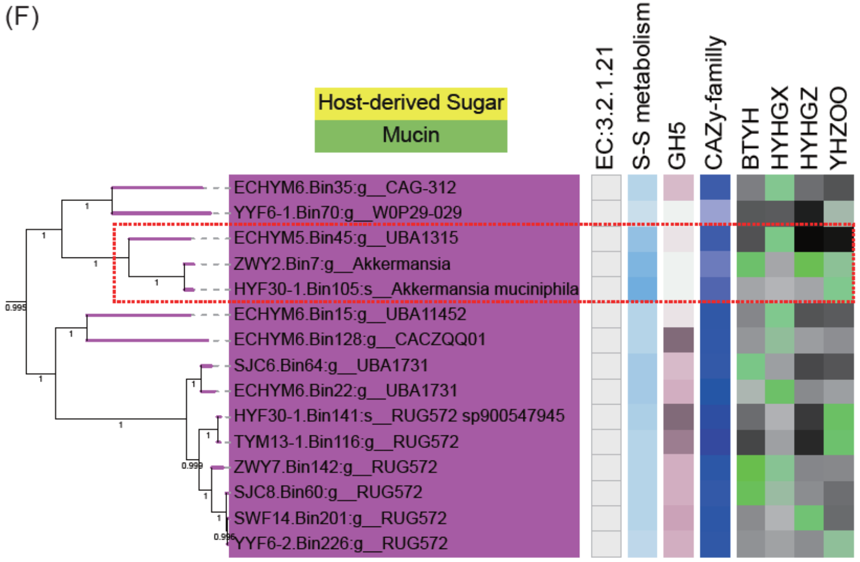
Major diet-derived polysaccharides	Microbial carbohydrate-degrading enzymes activities
Starch	GH13,GH31,GH97
Inulin	GH32,GH91
Pectin	GH28,GH8,CE12,PL1,PL9
Cellulose	GH1,GH3,GH5,GH8,GH9,GH44,GH48
Arabinoxylan	GH3,GH5,GH11,GH43,GH51,GH67,GH115,CE1,CE2,CE4,CE6,CE7,GH44,GH48



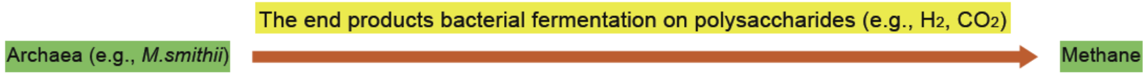








(G)



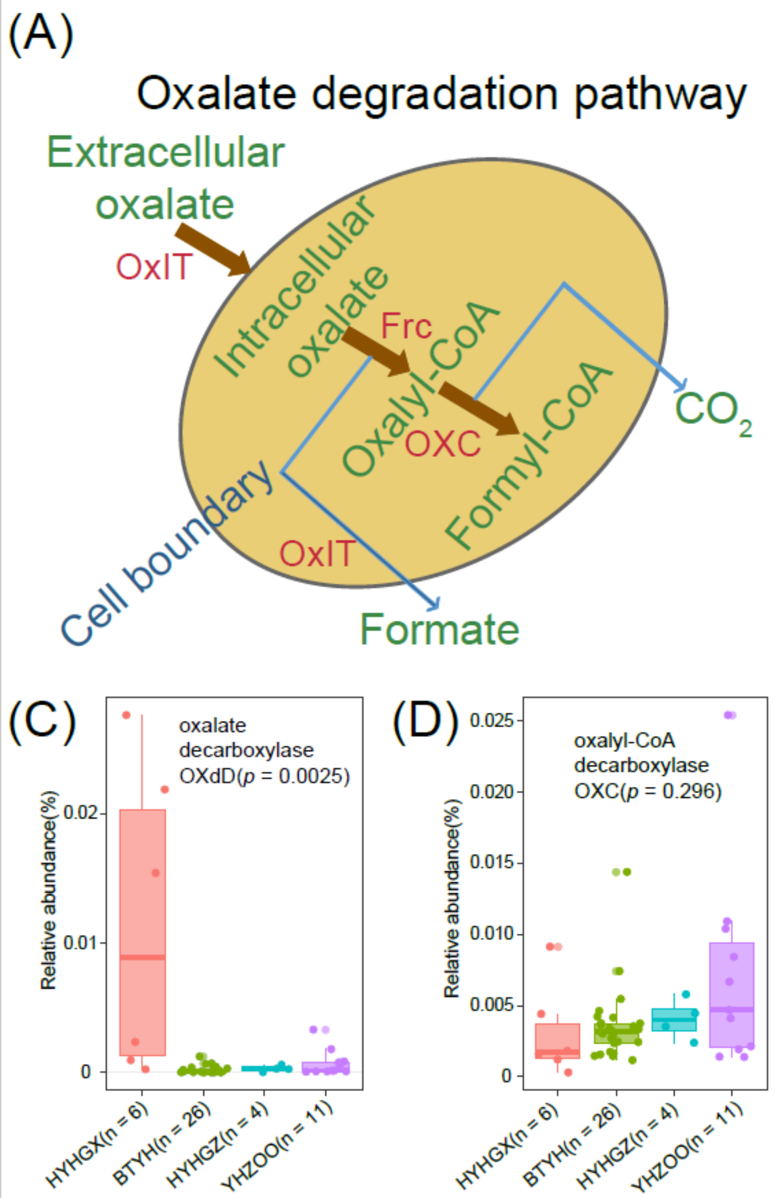
The end products bacterial fermentation on polysaccharides (e.g., H_2, CO_2)

Archaea (e.g., *M.smithii*) → Methane

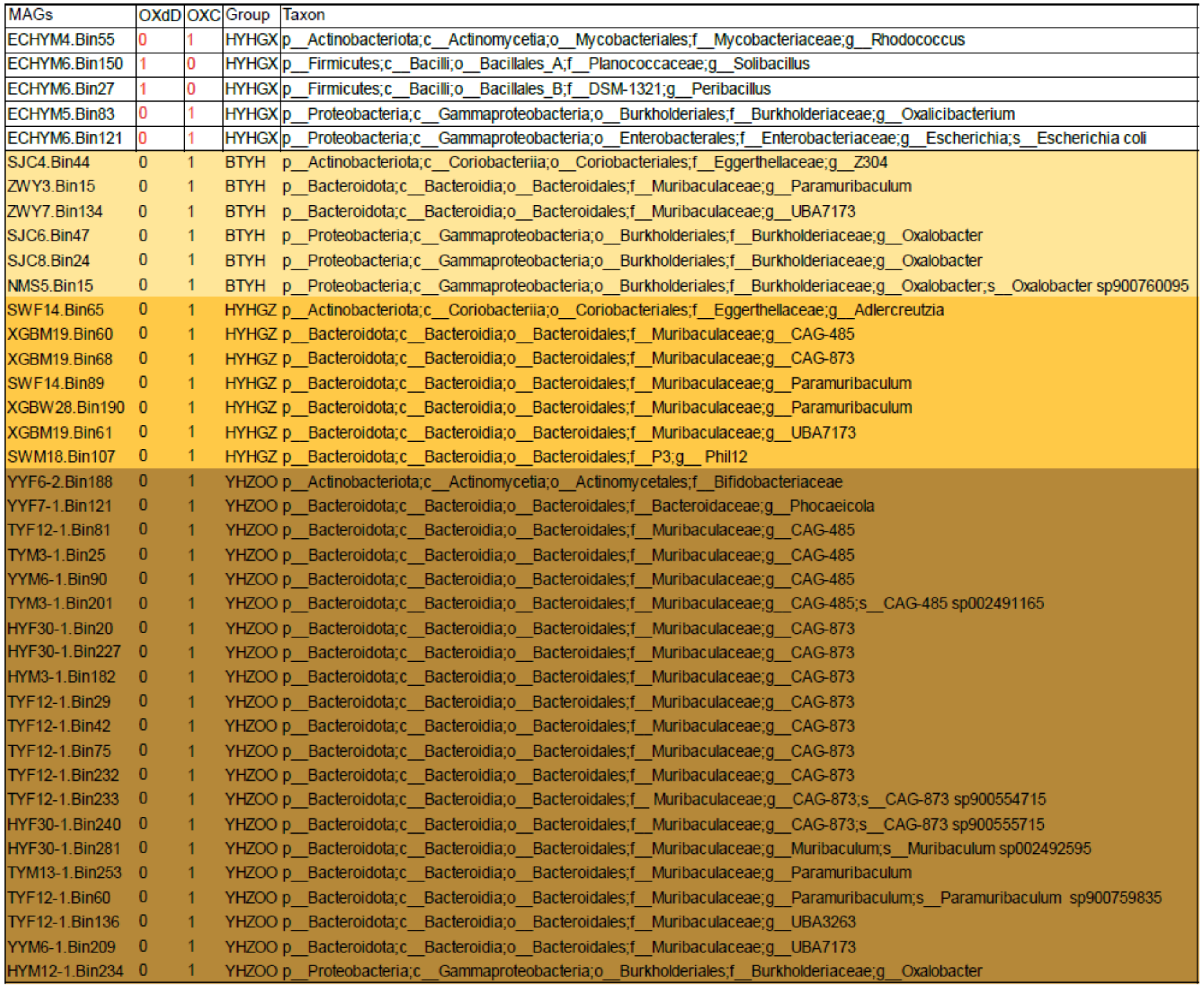
ZWY9.Bin28	d__Archaea;p__Methanobacteriota;c__Methanobacteria;o__Methanobacteriales;f__Methanobacteriaceae;g__Methanobrevibacter_A
HYM12-1.Bin159	d__Archaea;p__Methanobacteriota;c__Methanobacteria;o__Methanobacteriales;f__Methanobacteriaceae;g__Methanobrevibacter_A;s__Methanobrevibacter_A smithii
ECHYM6.Bin135	d__Archaea;p__Thermoplasmatota;c__Thermoplasmata;o__Methanomassiliicoccales;f__Methanomethylophilaceae;g__Methanomethylophilus
YYF7-1.Bin179	d__Archaea;p__Thermoplasmatota;c__Thermoplasmata;o__Methanomassiliicoccales;f__Methanomethylophilaceae;g__MX-02;s__MX-02 sp006954405
SJC6.Bin162	d__Archaea;p__Thermoplasmatota;c__Thermoplasmata;o__Methanomassiliicoccales;f__Methanomethylophilaceae;g__UBA71
ECHYM6.Bin109	d__Archaea;p__Thermoplasmatota;c__Thermoplasmata;o__Methanomassiliicoccales;f__Methanomethylophilaceae;g__UBA71

Potential Role of MAGs in Polysaccharide & Glycan Degradation

Case 6: Oxalate Degradation Function and Adaptation



(B)



MAGs	OXdD	OXC	Group	Taxon
ECHYM4.Bin55	0	1	HYHGX	p__Actinobacteriota;c__Actinomycetia;o__Mycobacteriales;f__Mycobacteriaceae;g__Rhodococcus
ECHYM6.Bin150	1	0	HYHGX	p__Firmicutes;c__Bacilli;o__Bacillales_A;f__Planococcaceae;g__Solibacillus
ECHYM6.Bin27	1	0	HYHGX	p__Firmicutes;c__Bacilli;o__Bacillales_B;f__DSM-1321;g__Peribacillus
ECHYM5.Bin83	0	1	HYHGX	p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Burkholderiaceae;g__Oxalicibacterium
ECHYM6.Bin121	0	1	HYHGX	p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacterales;f__Enterobacteriaceae;g__Escherichia;s__Escherichia coli
SJC4.Bin44	0	1	BTYH	p__Actinobacteriota;c__Coriobacteriia;o__Coriobacteriales;f__Eggerthellaceae;g__Z304
ZWY3.Bin15	0	1	BTYH	p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Muribaculaceae;g__Paramuribaculum
ZWY7.Bin134	0	1	BTYH	p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Muribaculaceae;g__UBA7173
SJC6.Bin47	0	1	BTYH	p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Burkholderiaceae;g__Oxalobacter
SJC8.Bin24	0	1	BTYH	p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Burkholderiaceae;g__Oxalobacter
NMS5.Bin15	0	1	BTYH	p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Burkholderiaceae;g__Oxalobacter;s__Oxalobacter sp900760095
SWF14.Bin65	0	1	HYHGZ	p__Actinobacteriota;c__Coriobacteriia;o__Coriobacteriales;f__Eggerthellaceae;g__Adlercreutzia
XGBM19.Bin60	0	1	HYHGZ	p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Muribaculaceae;g__CAG-485
XGBM19.Bin68	0	1	HYHGZ	p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Muribaculaceae;g__CAG-873
SWF14.Bin89	0	1	HYHGZ	p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Muribaculaceae;g__Paramuribaculum
XGBW28.Bin190	0	1	HYHGZ	p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Muribaculaceae;g__Paramuribaculum
XGBM19.Bin61	0	1	HYHGZ	p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Muribaculaceae;g__UBA7173
SWM18.Bin107	0	1	HYHGZ	p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__P3;g__ Phil12
YYF6-2.Bin188	0	1	YHZOO	p__Actinobacteriota;c__Actinomycetia;o__Actinomycetales;f__Bifidobacteriaceae
YYF7-1.Bin121	0	1	YHZOO	p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Phocaeicola
TYF12-1.Bin81	0	1	YHZOO	p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Muribaculaceae;g__CAG-485
TYM3-1.Bin25	0	1	YHZOO	p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Muribaculaceae;g__CAG-485
YYM6-1.Bin90	0	1	YHZOO	p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Muribaculaceae;g__CAG-485
TYM3-1.Bin201	0	1	YHZOO	p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Muribaculaceae;g__CAG-485;s__CAG-485 sp002491165
HYF30-1.Bin20	0	1	YHZOO	p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Muribaculaceae;g__CAG-873
HYF30-1.Bin227	0	1	YHZOO	p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Muribaculaceae;g__CAG-873
HYM3-1.Bin182	0	1	YHZOO	p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Muribaculaceae;g__CAG-873
TYF12-1.Bin29	0	1	YHZOO	p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Muribaculaceae;g__CAG-873
TYF12-1.Bin42	0	1	YHZOO	p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Muribaculaceae;g__CAG-873
TYF12-1.Bin75	0	1	YHZOO	p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Muribaculaceae;g__CAG-873
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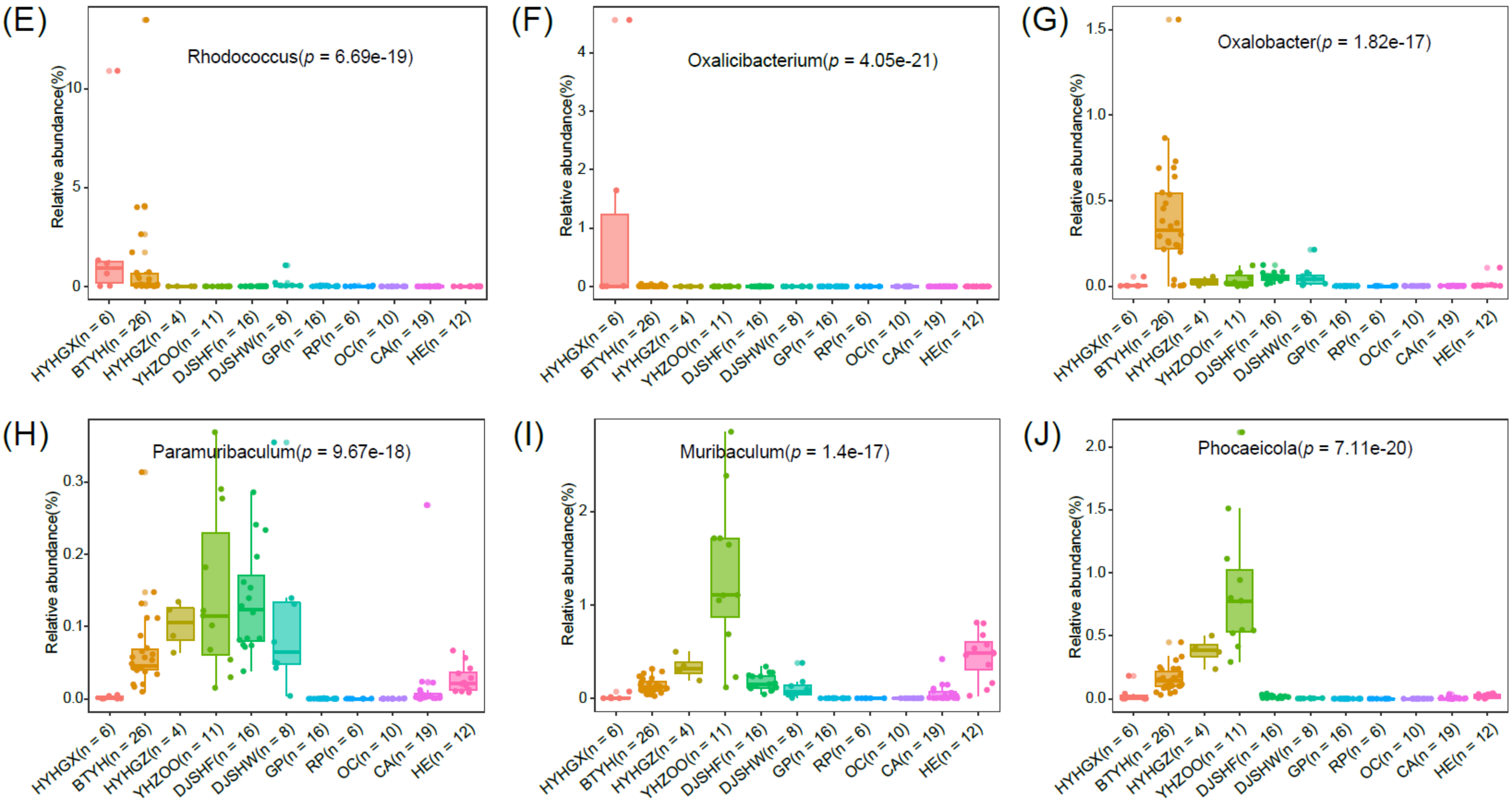
HYF30-1.Bin240	0	1	YHZOO	p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Muribaculaceae;g__CAG-873;s__CAG-873 sp900555715
HYF30-1.Bin281	0	1	YHZOO	p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Muribaculaceae;g__Muribaculum;s__Muribaculum sp002492595
TYM13-1.Bin253	0	1	YHZOO	p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Muribaculaceae;g__Paramuribaculum
TYF12-1.Bin60	0	1	YHZOO	p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Muribaculaceae;g__Paramuribaculum;s__Paramuribaculum sp900759835
TYF12-1.Bin136	0	1	YHZOO	p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Muribaculaceae;g__UBA3263
YYM6-1.Bin209	0	1	YHZOO	p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Muribaculaceae;g__UBA7173
HYM12-1.Bin234	0	1	YHZOO	p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales;f__Burkholderiaceae;g__Oxalobacter

Potential Role of Langur Gut Microbiome-Associated MAGs in Oxalate Degradation

Case 6: Oxalate Degradation Function and Adaptation



Potential Role of Langur Gut Microbiome-Associated MAGs in Oxalate Degradation

Summary

- Significant differences in gut microbial diversity and functions across langur populations.

- With increasing human disturbance, we found a significant enrichment of human disturbance-related microbes in langurs, suggesting that human activities are directly driving the “humanization” of their gut microbiota.

- The langur gut microbiome not only degrades polysaccharides but also supports oxalate metabolism and mucin utilization. These functions provide adaptive strategies that help langurs in karst limestone regions cope with high-fiber and oxalate-rich diets.

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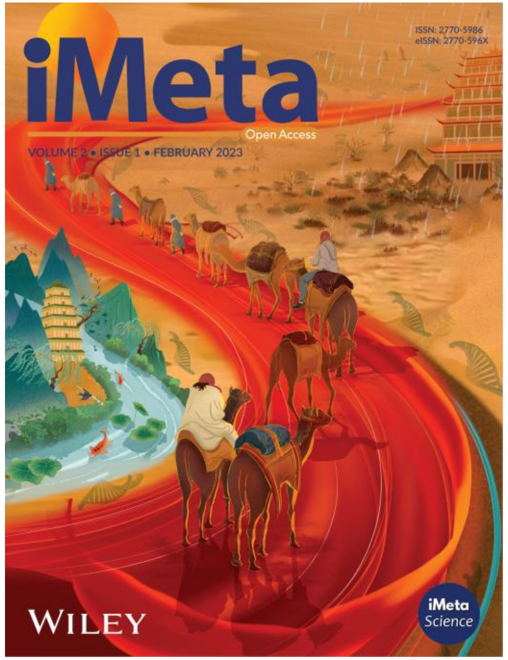

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