



食叶猴肠道微生物组的物种水平研究揭示人类活动与食性特化的影响：论生物多样性第四层级的保护

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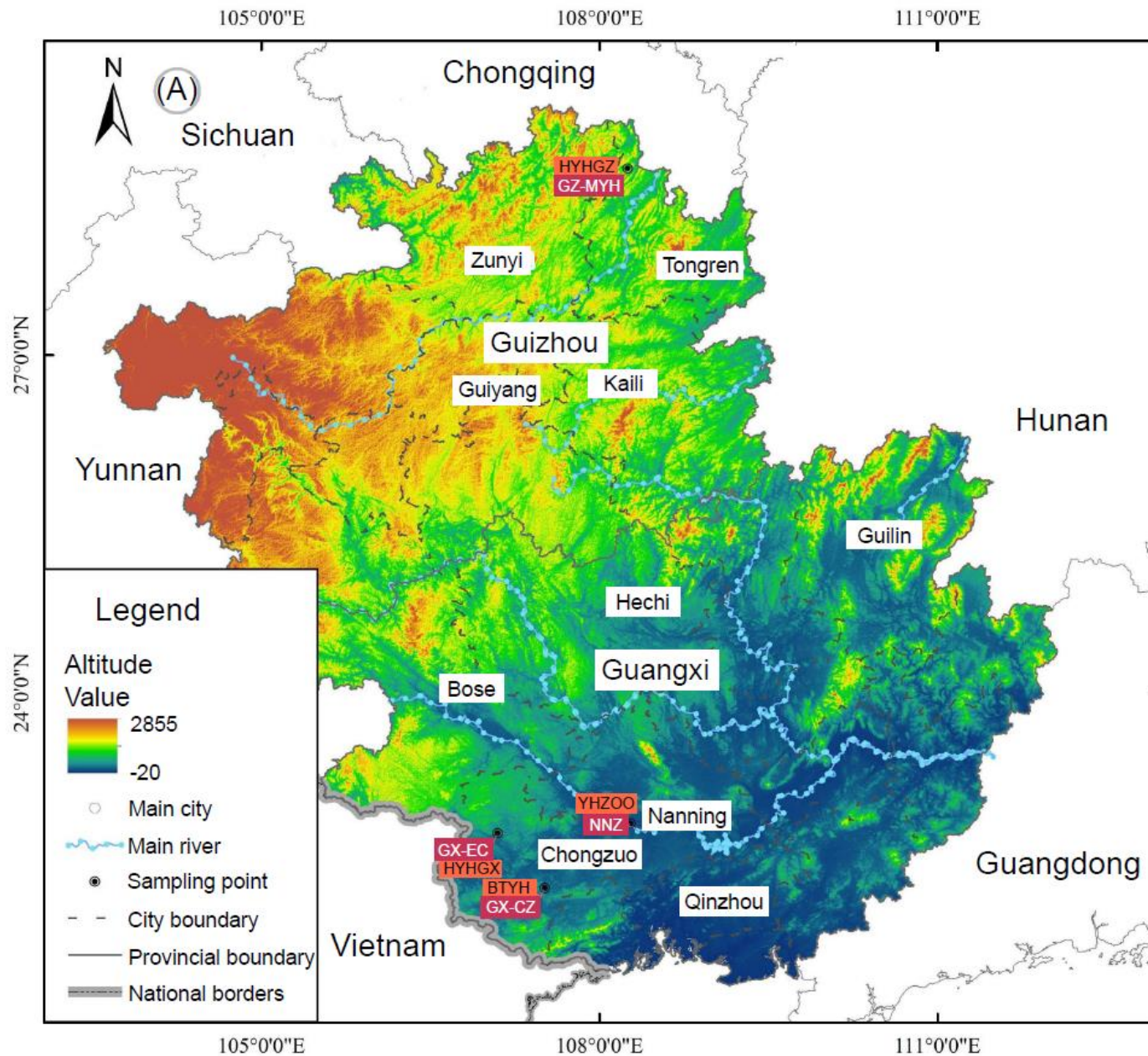
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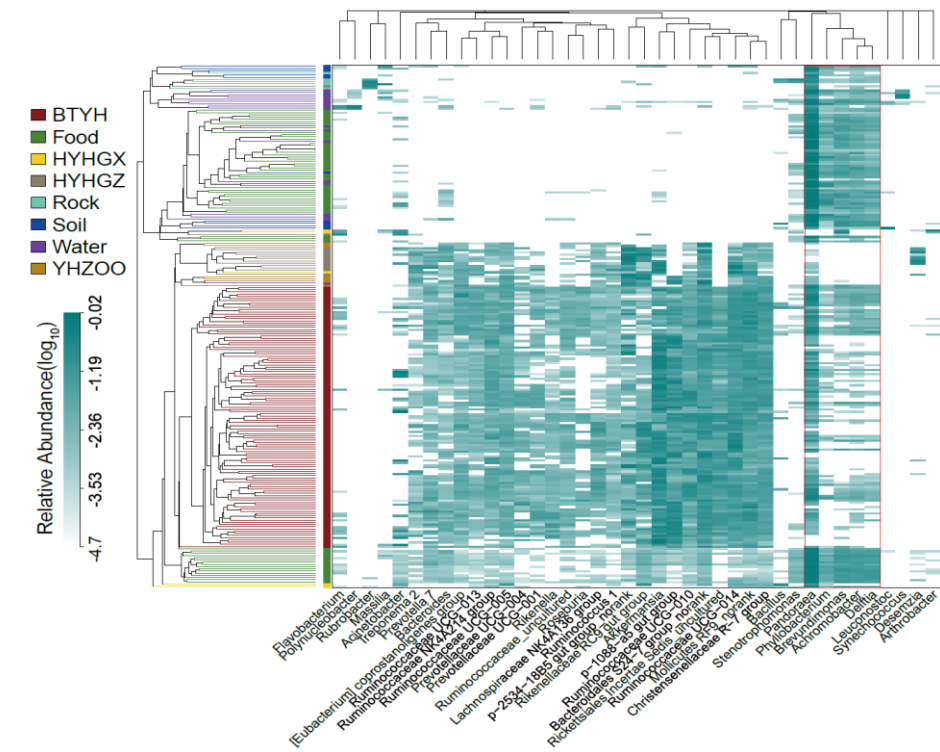
Qihai Zhou, Qiuyan Guo, Xinyuan Cui, Tao Meng, Zhuting Pang, Song Wang, Hua Chen, et al. 2025. Species-level exploration of the gut microbiome in the leaf-eating Presbytis monkeys reflected the effects of anthropogenic activity and specialized dietary niches: conservation on the fourth biodiversity level. *iMetaOmics* 2: e70051. <https://doi.org/10.1002/imo2.70051>

亮点

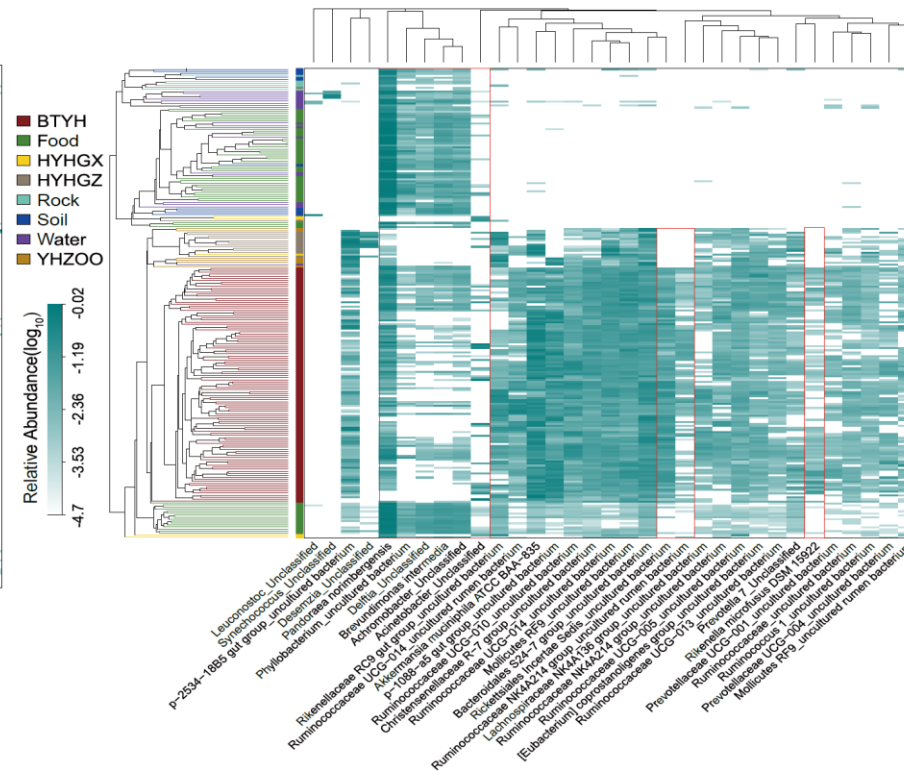




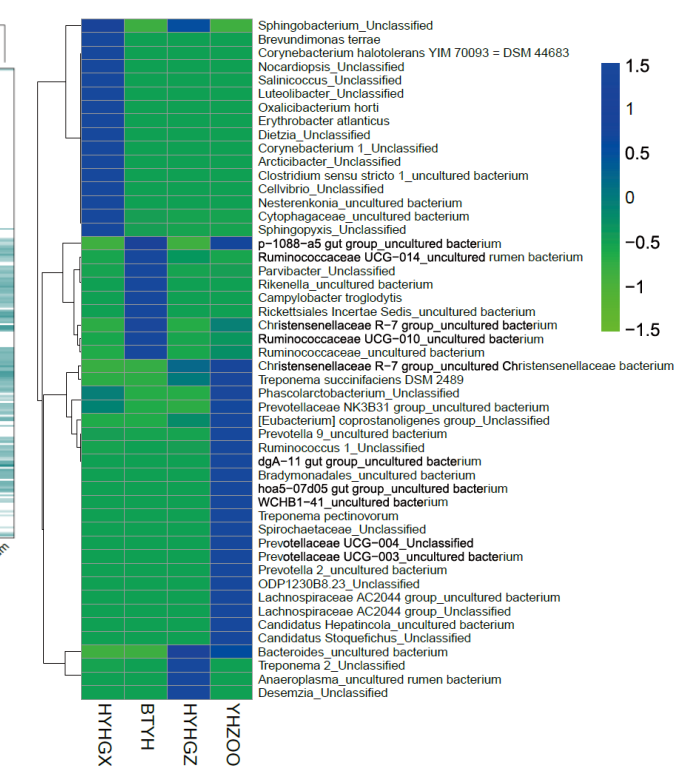
结果1:微生物群落结构的组间差异性显著



优势菌属组成

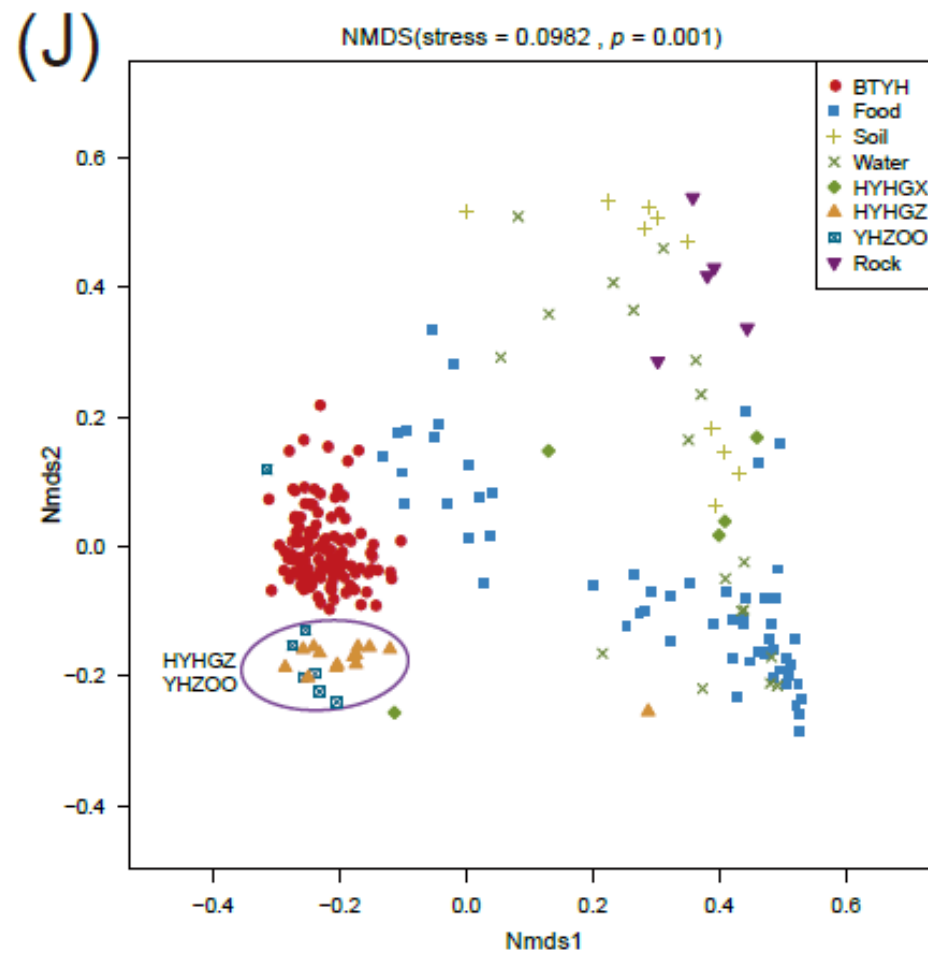
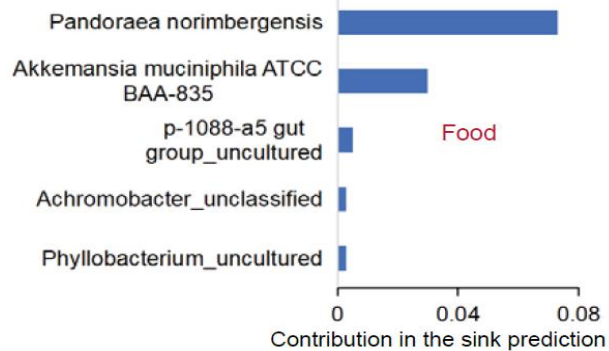
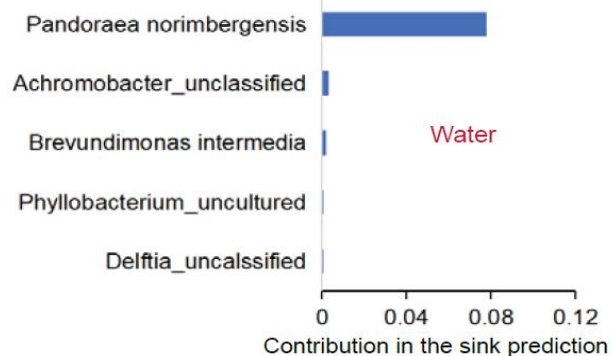
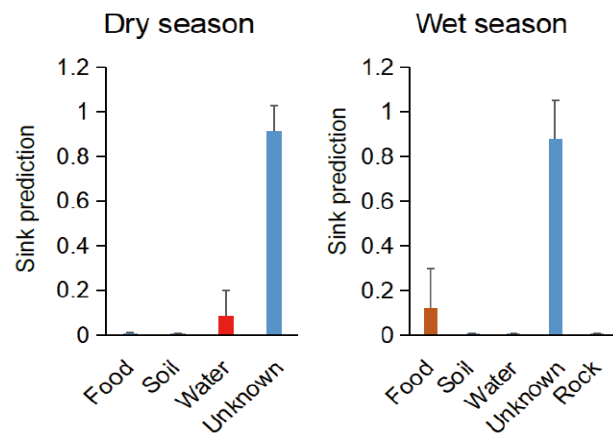
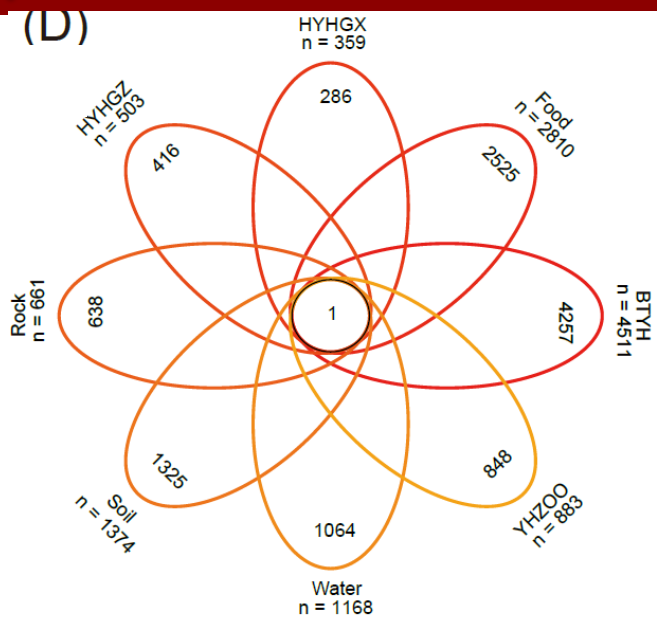


优势菌种组成

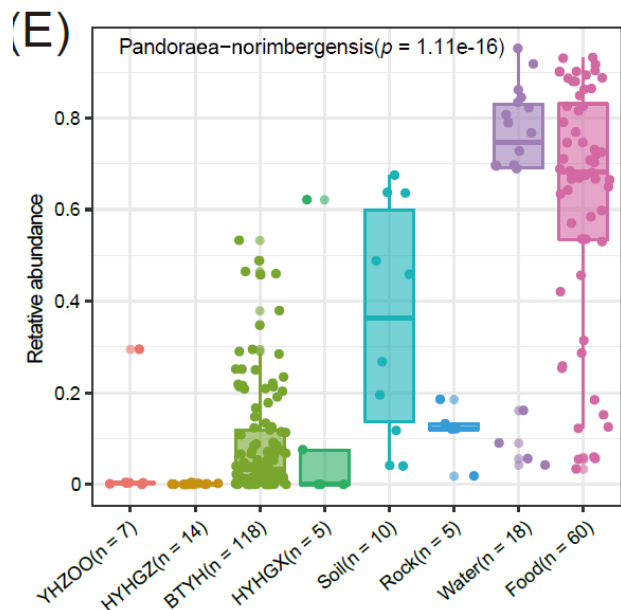


显著差异的Top50物种组成

结果2:宿主环境影响肠道微生物群落结构



HYHGZ和YHZOO群落组成更相似



核心ASV—*Pandoraaea norimbergensis*

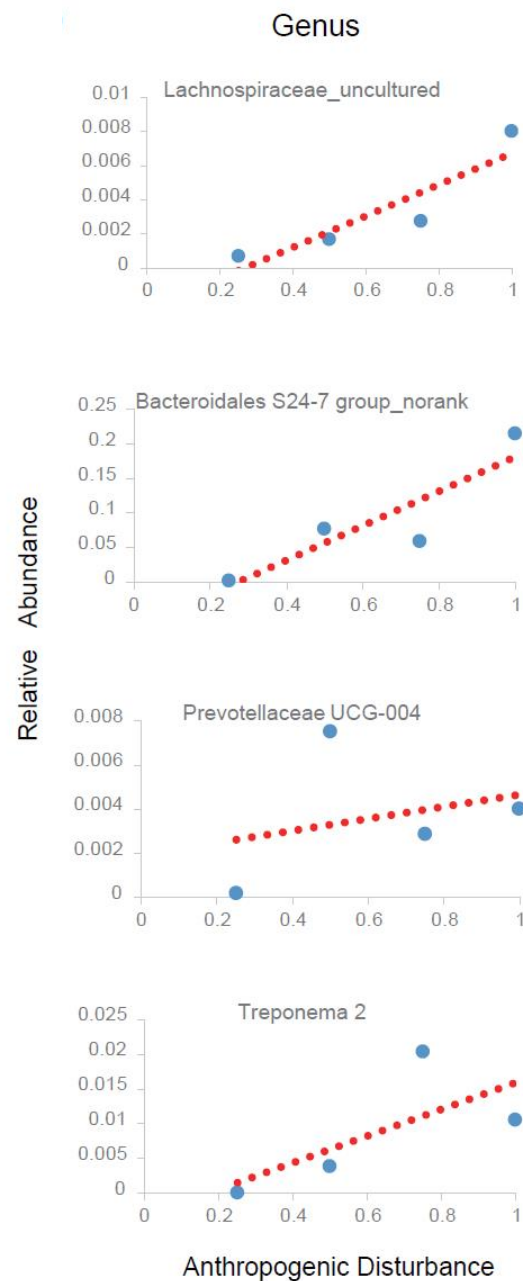
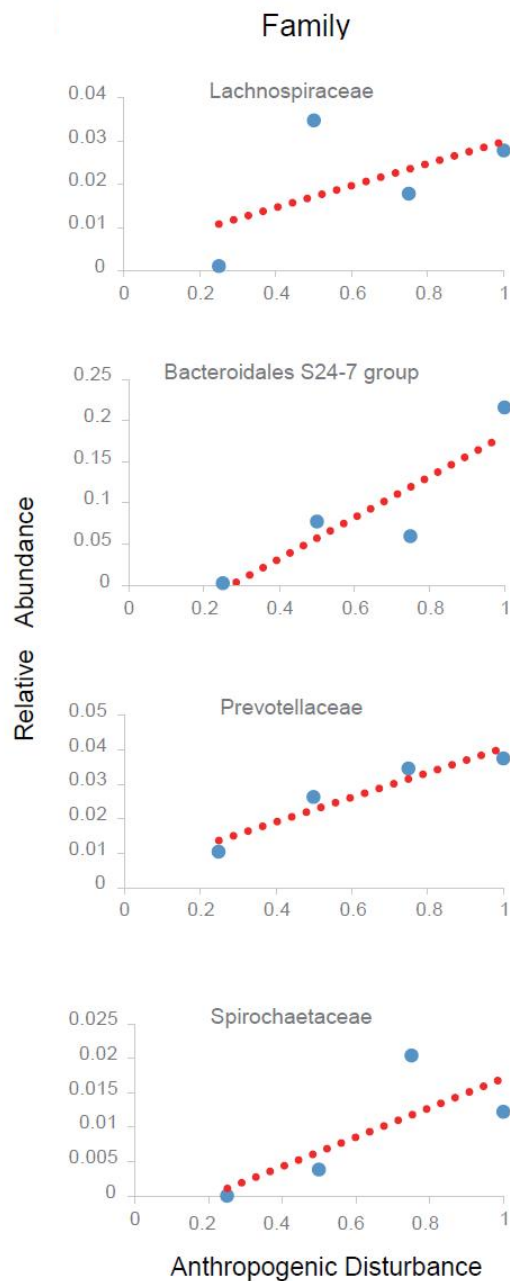
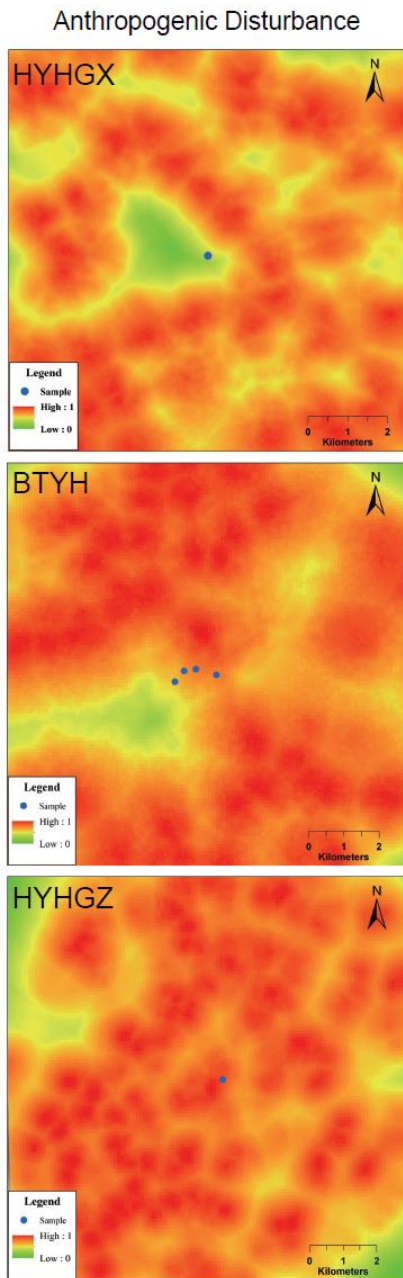
*P. Norimbergensis*的主要环境贡献



结果3:人类干扰驱动HDR微生物富集

人类干扰分级

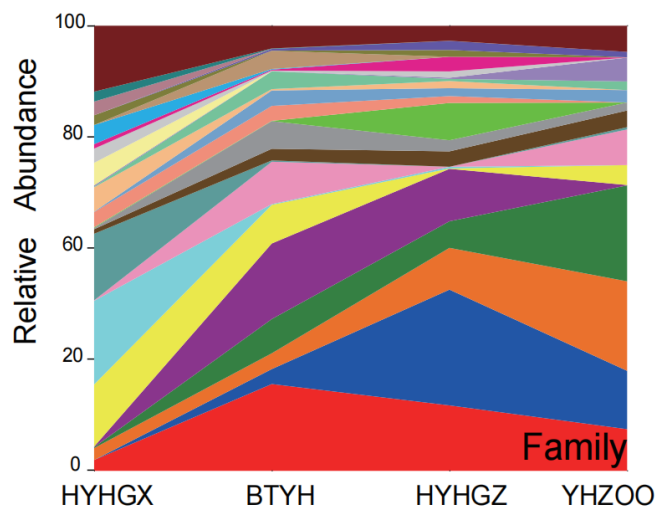
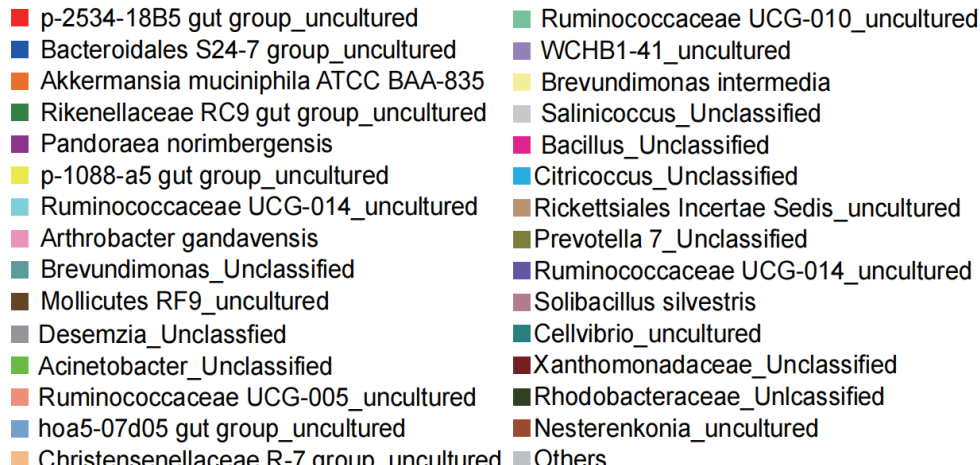
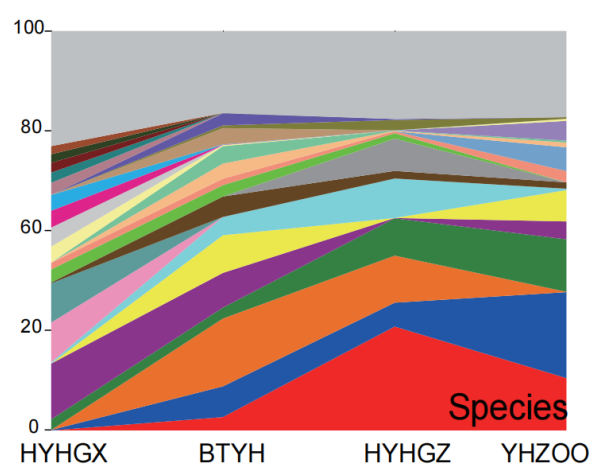
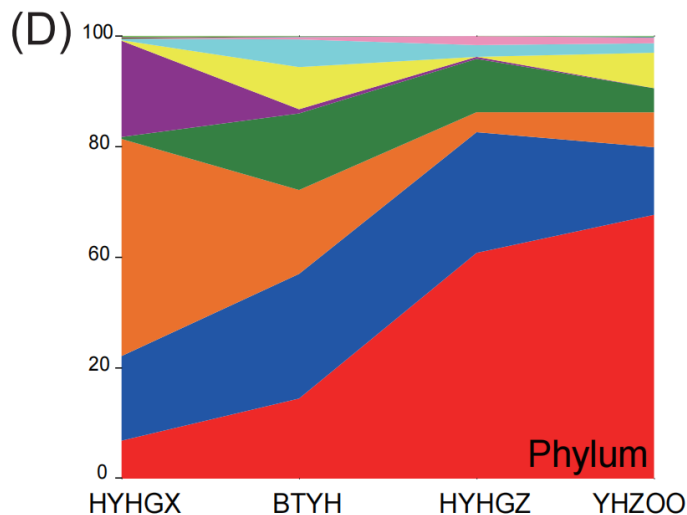
- HYHGX (低)
- BTYH (中)
- HYHGZ (高)
- YHZOO (最强)



人类相关微生物类群
(HDR) 随人类干扰强度显著增加



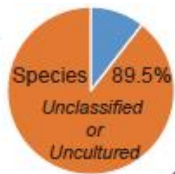
结果3:人类干扰驱动HDR微生物富集



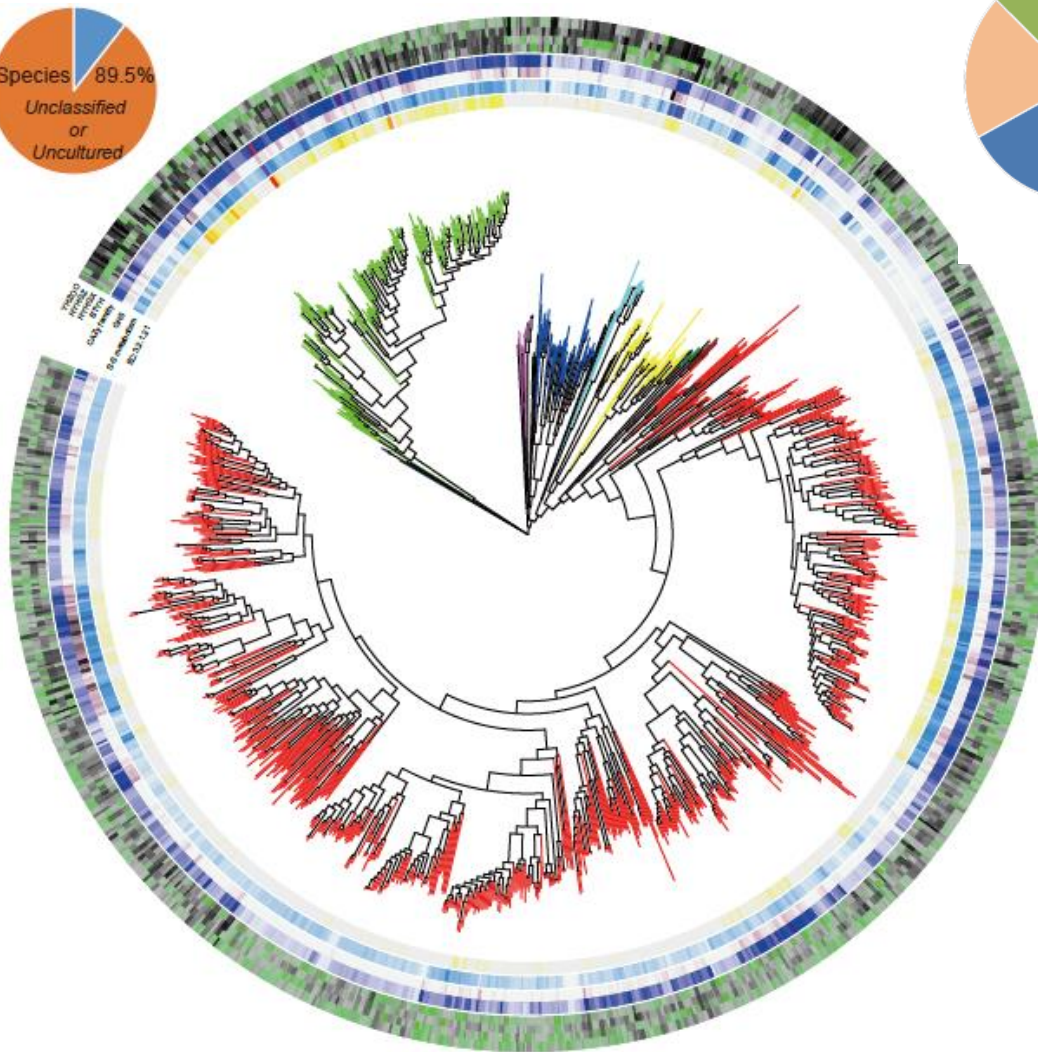
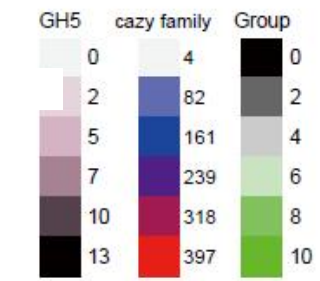
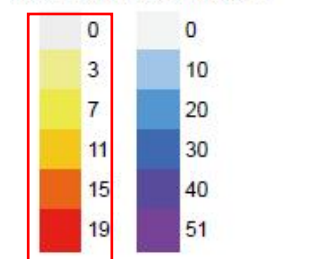
结果4:纤维素降解功能



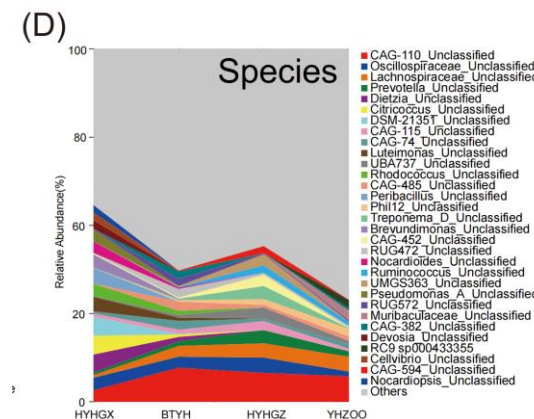
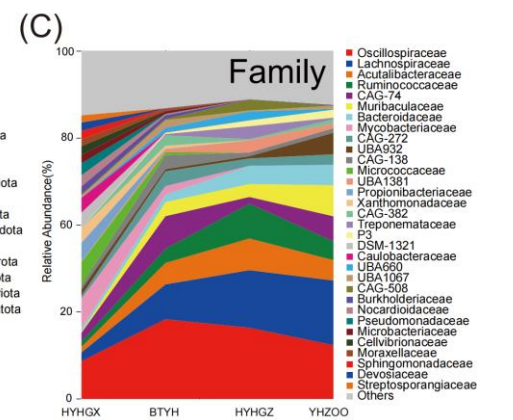
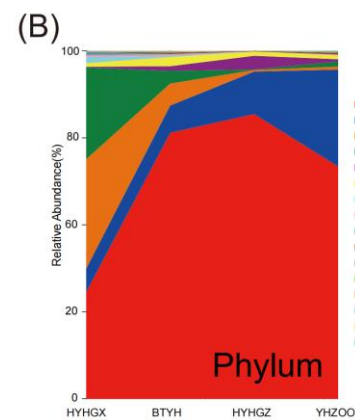
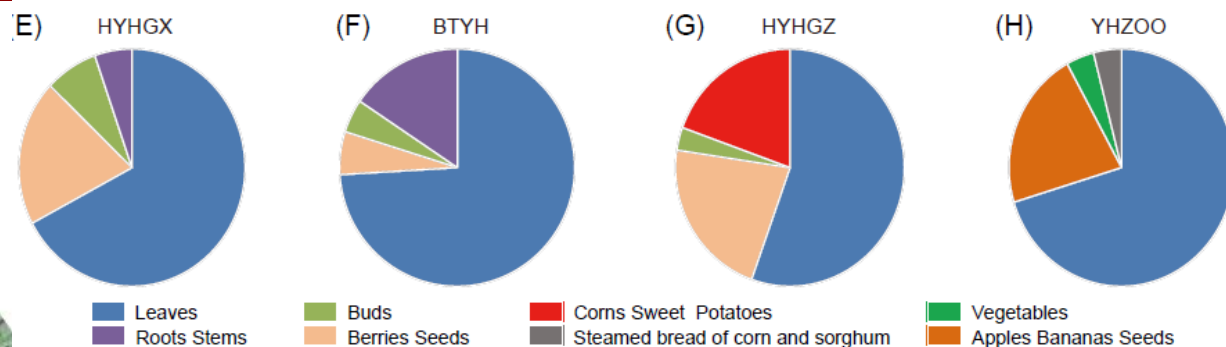
Phylum	Number of bins
Firmicutes	840
Bacteroidota	189
Proteobacteria	59
Actinobacteriota	51
Verrucomicrobiota	15
Spirochaetota	14
Thermoplasmata	4
Cyanobacteria	4
Planctomycetota	4
Others	19



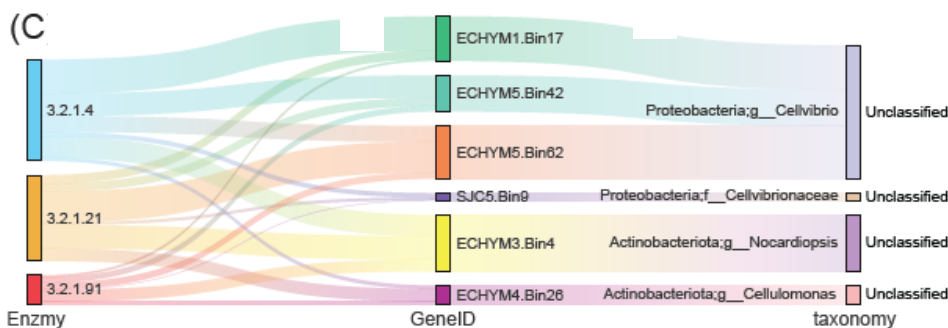
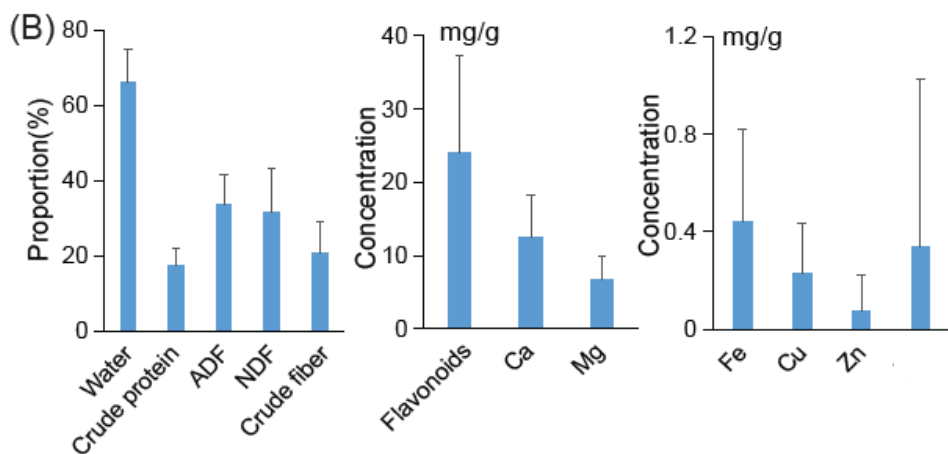
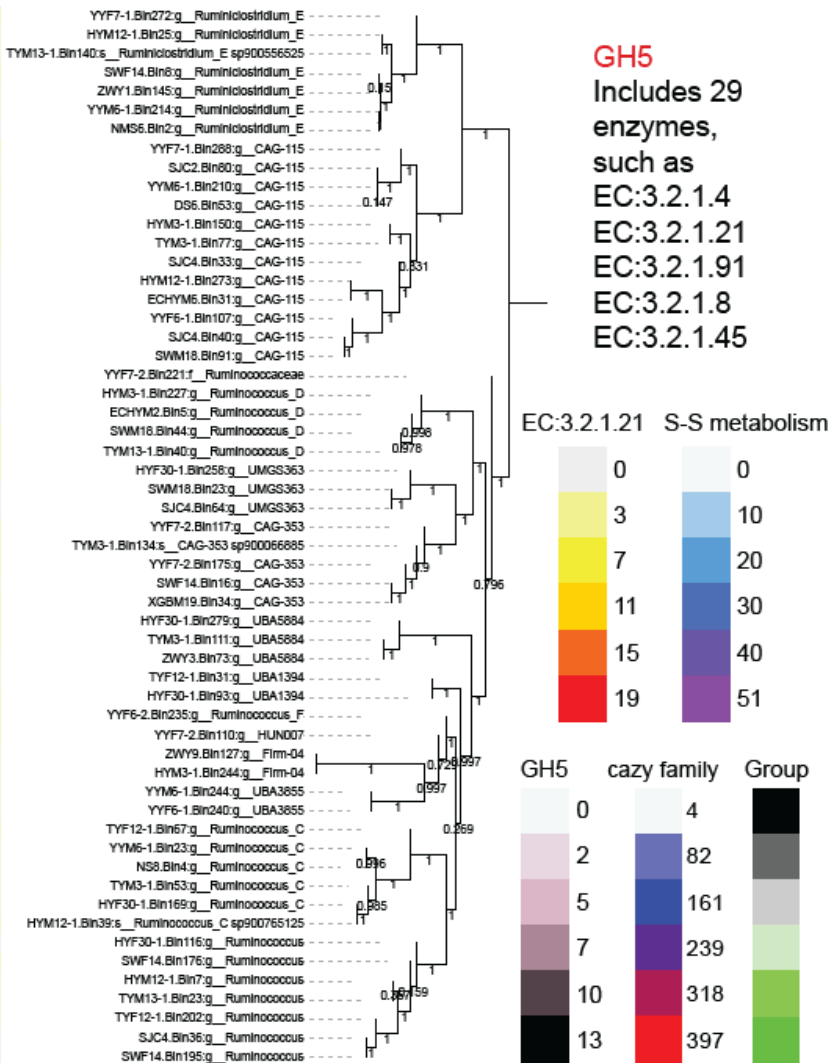
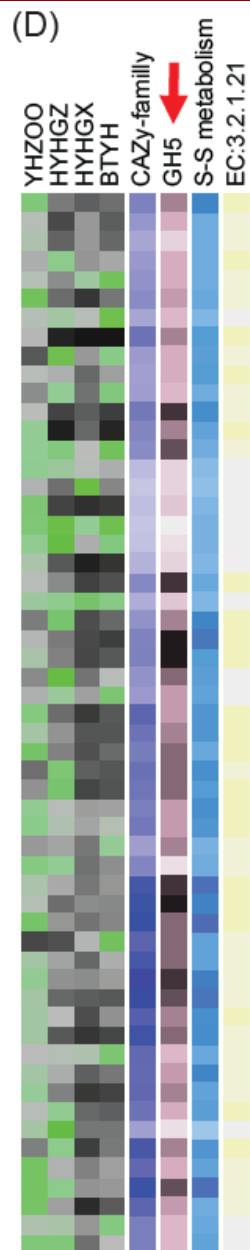
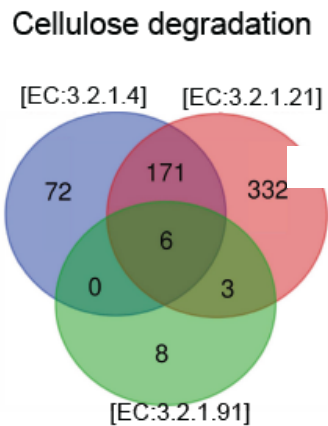
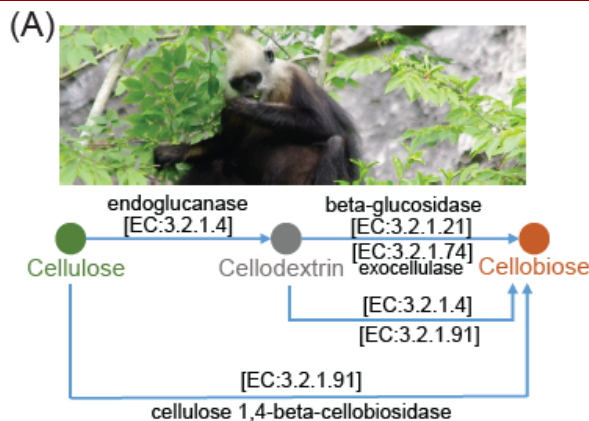
EC:3.2.1.21 S-S metabolism



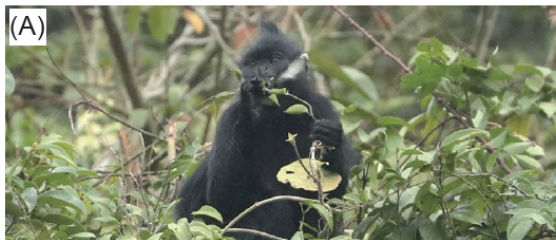
1,199 MAGs



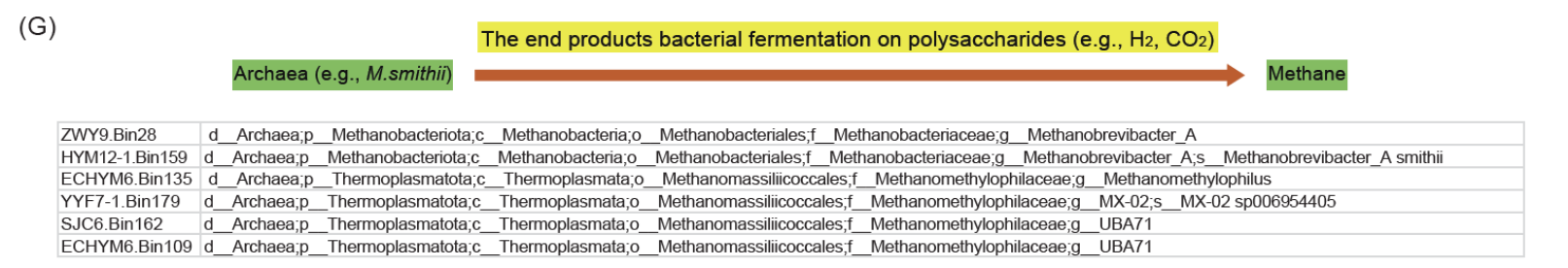
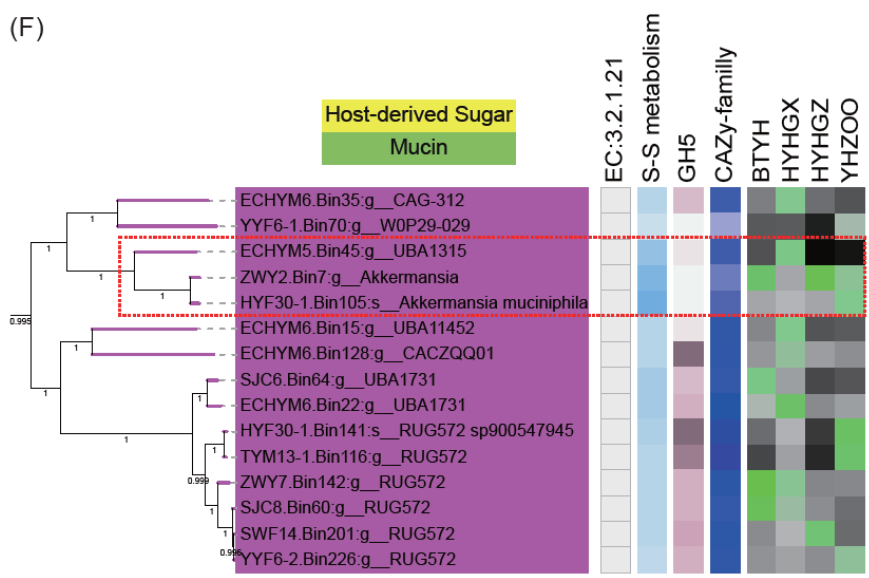
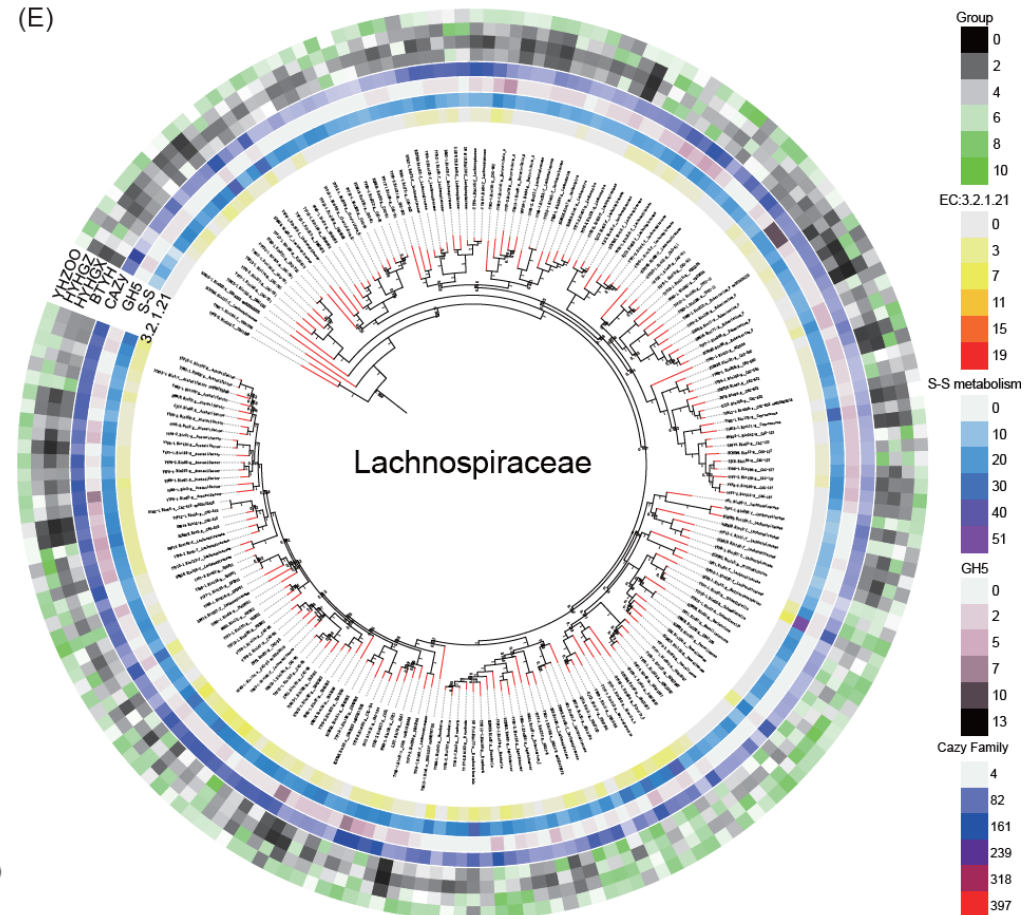
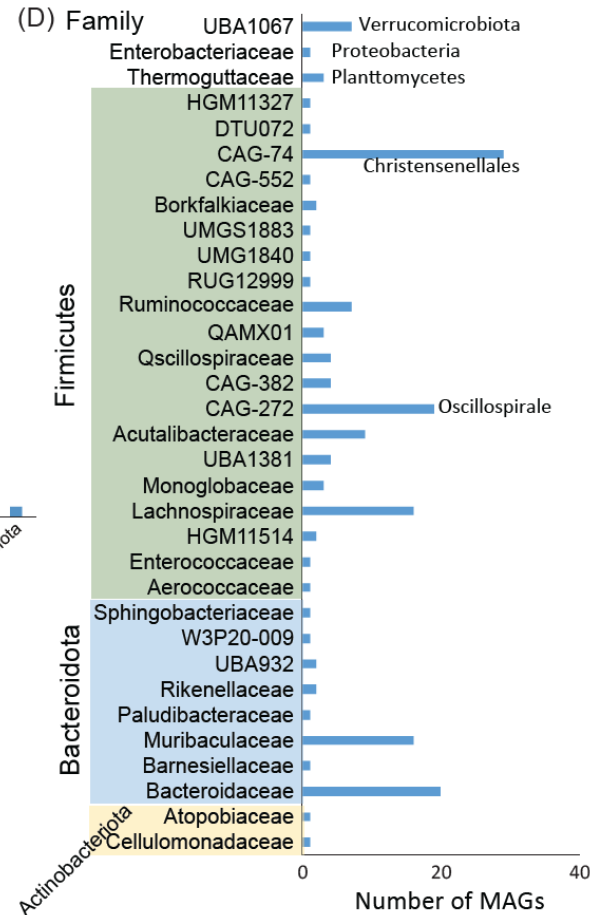
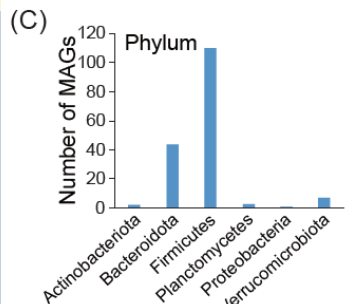
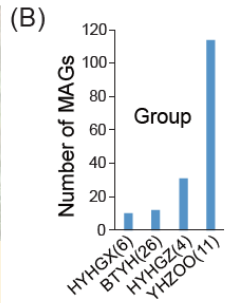
结果4:纤维素降解功能



结果5：饮食多糖与宿主糖链的微生物降解潜力



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

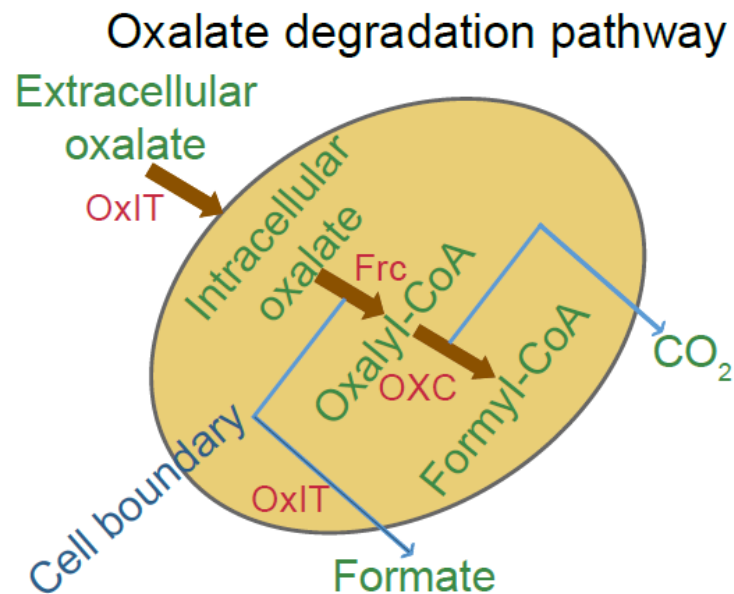


叶猴肠道微生物相关MAGs在多糖及糖链降解中的潜在作用



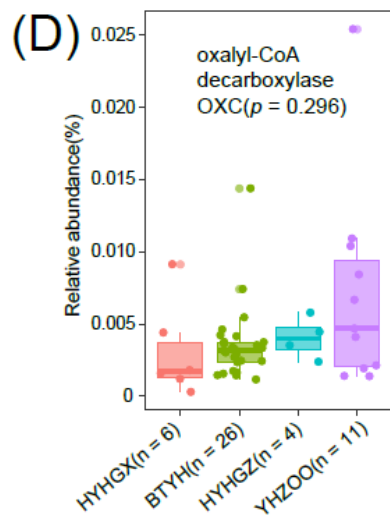
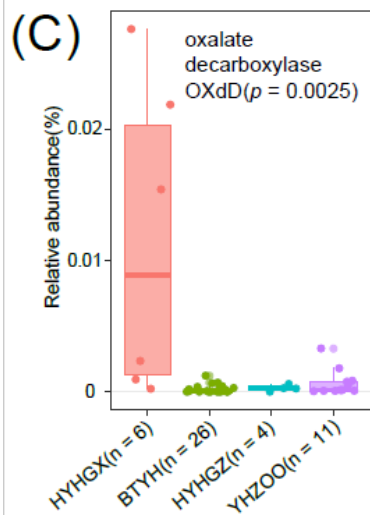
结果6:草酸降解功能与适应性

(A) Oxalate degradation pathway



(B)

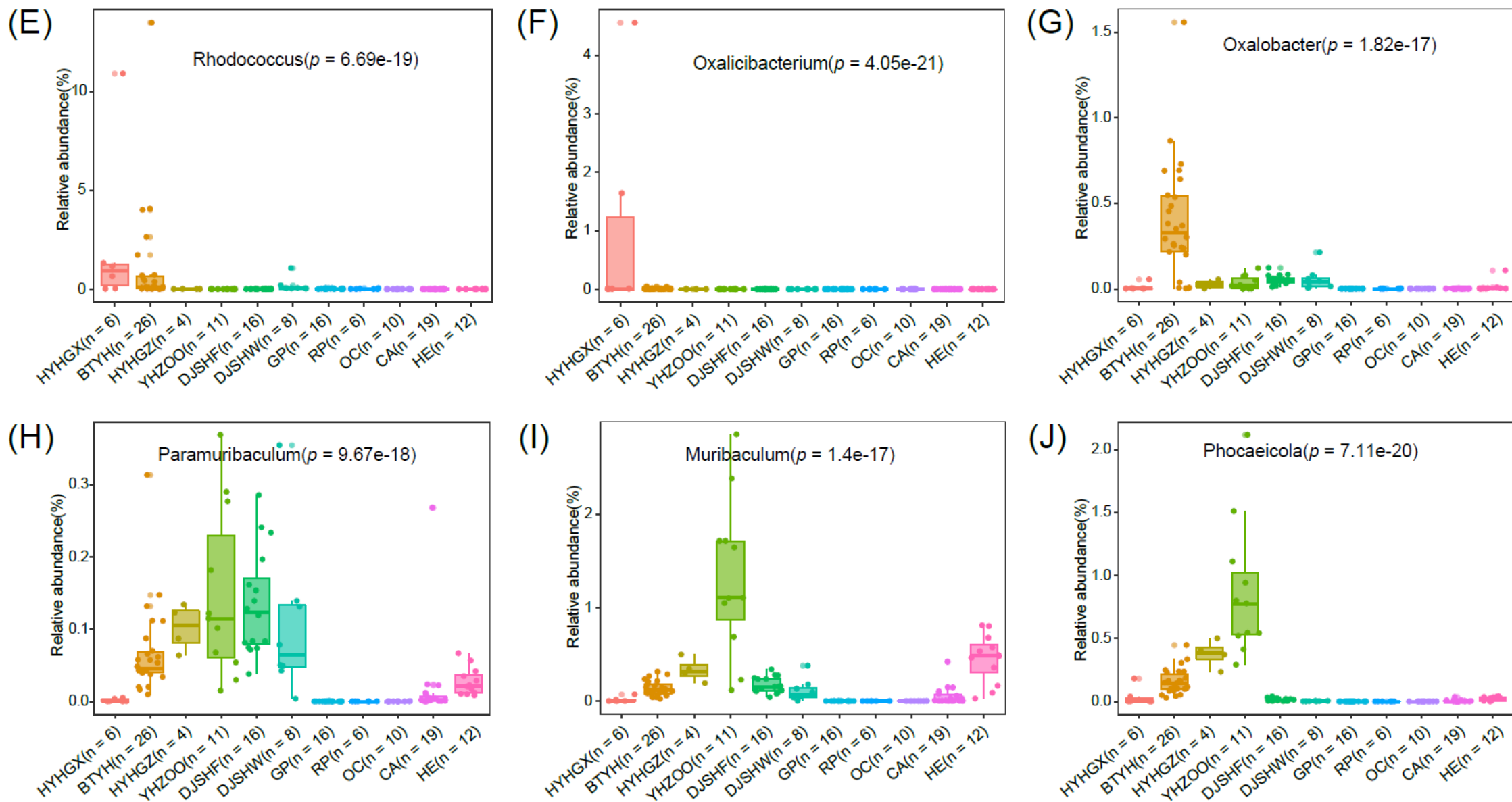
MAGs	OXdD	OXC	Group	Taxon
ECHYM4.Bin55	0	1	HYHGX	p_Actinobacteriota;c_Actinomycetia;o_Mycobacteriales;f_Mycobacteriaceae;g_Rhodococcus
ECHYM6.Bin150	1	0	HYHGX	p_Firmicutes;c_Bacilli;o_Bacillales_A;f_Planococcaceae;g_Solibacillus
ECHYM6.Bin27	1	0	HYHGX	p_Firmicutes;c_Bacilli;o_Bacillales_B;f_DSM-1321;g_Peribacillus
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
TYF12-1.Bin232	0	1	YHZOO	p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Muribaculaceae;g_CAG-873
TYF12-1.Bin233	0	1	YHZOO	p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Muribaculaceae;g_CAG-873;s_CAG-873 sp900554715
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



叶猴肠道微生物相关MAGs在草酸盐降解中的潜在作用



结果6:草酸降解功能与适应性



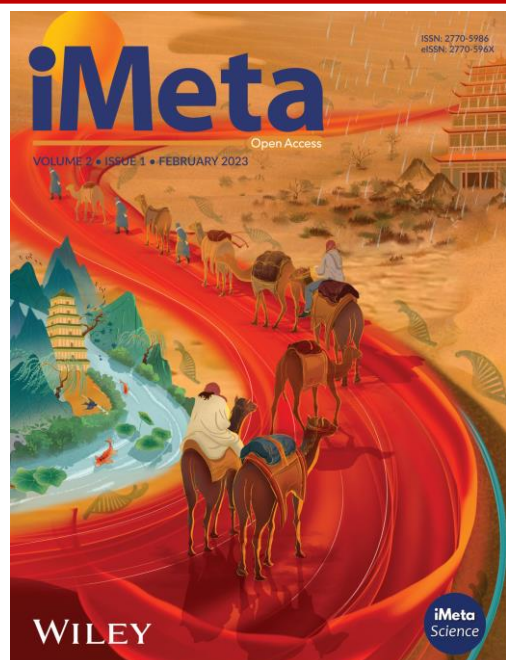
叶猴肠道微生物相关MAGs在草酸盐降解中的潜在作用



总结

- ❑ 不同叶猴群体，肠道微生物多样性与功能存在显著差异。
- ❑ 随着人类干扰强度增加，会导致人源相关菌群（HDR）在叶猴群体中显著富集
- ❑ 肠道微生物组具备多糖降解、草酸代谢和黏蛋白利用等功能，为喀斯特石灰岩地区的叶猴了提供适应性解决方案以应对高纤维饮食和高草酸胁迫

Qihai Zhou, Qiuyan Guo, Xinyuan Cui, Tao Meng, Zhuting Pang, Song Wang, Hua Chen, et al. 2025. 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. *iMetaOmics* 2: e70051. <https://doi.org/10.1002/imo2.70051>



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