(A) Analysis

PICRUSt2 Output: KO/EC/MetaCyc Abundance

R object: data.frame

Fun.	Sp_1	Sp_1	Sp_1
ko_1			
ko_2			
ko_3			

- compare_metagenome_results()
- compare_daa_results()
- ko2kegg_abundance()
- pathway_daa()
- pathway annotation()

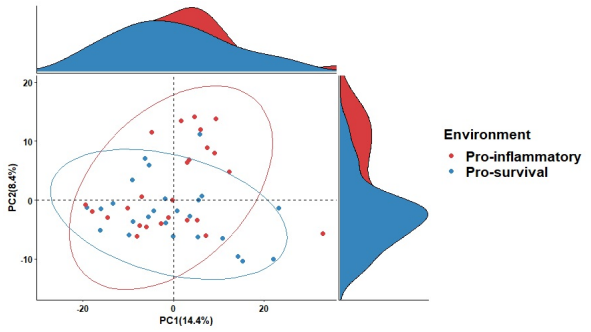
Annotated DA results Table

R object: data.frame

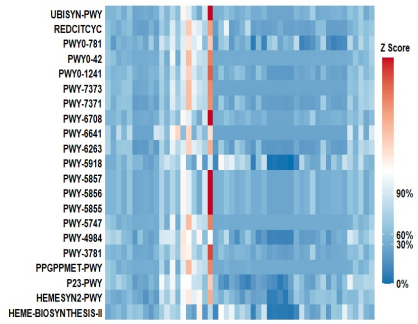
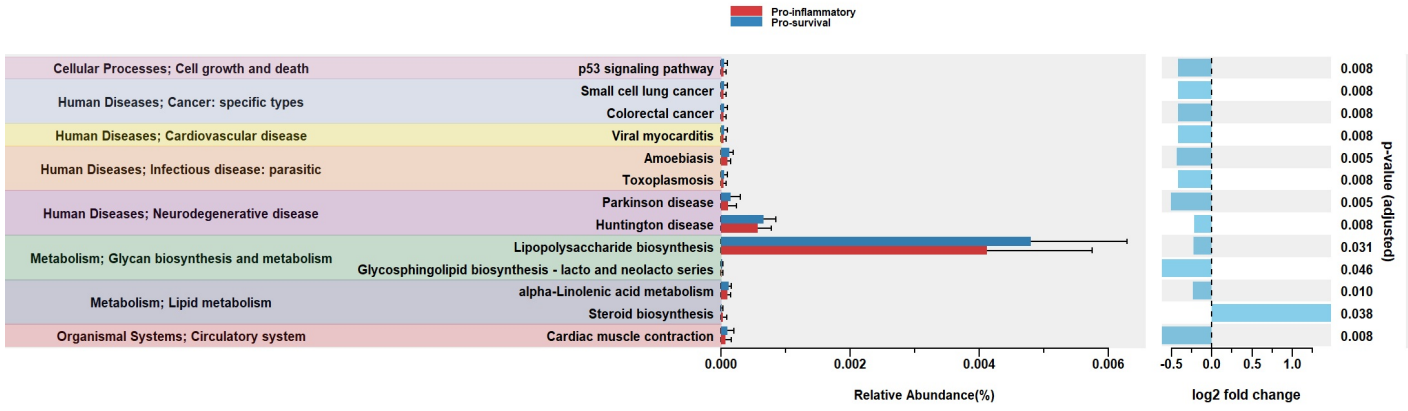
Pathway	name	class	p_adj
ko_1			
ko_2			
ko_3			

(B) Visualization

pathway_pca()



pathway_heatmap()



pathway_errorbar()