```
result/
|-- 00.RawData/                                  【Raw reads and merged reads】
|      |-- Sample_Name/                          【Raw data and merged pair-end reads for each sample】
|      |      |--*_1.fq.gz                       【Read 1 sequences with barcode and primer removed】
|      |      |--*_2.fq.gz                       【Read 2 sequences with barcode and primer removed】
|      |      |--*.raw_1.fq.gz                   【Read 1 sequences with barcodes and primers】
|      |      |--*.raw_2.fq.gz                   【Read 2 sequences with barcodes and primers】
|      |      `--*.extendedFrags.fastq           【Raw Tags after reads merging】
|      |-- SampleSeq_info.xls                    【List of barcodes and primers】
|      `-- assembl_stat.xls                      【Statistical form for reads merging process of all samples】
|-- 01.CleanData/                                【Quality-controlled tags information】
|      |-- Sample_Name/                          【Results of quality control for each sample】
|      |      |--*.fastq                         【Clean tags(FASTQ format)】
|      |      |--*.fna                           【Clean tags(FASTA format)】
|      |      `-- histograms.txt                 【Length distribution of clean tags】
|      `-- QCstat.xls                            【Statistical table for data pre-processing and quality control】
|-- 02.OTUanalysis/                              【OTUs Clustering and Species Annotation】
|      |-- OTUs.fasta                            【OTUs representative sequences (FASTA format)】
|      |-- OTUs.tax_assignments.txt              【Species annotation results of OTUs】
|      |-- all_rep_set_tax_assignments.krona.html 【Krona taxonomy visualization】
|      |-- OTUs.tre                              【OTUs phylogenetic tree】
|      |-- otu_table_even.biom                   【Absolute abundance after normalization (Biom format)】
|      |-- taxa_abundance/                       【Species abundance information for each sample】
|      |      |-- evenabs/                       【Absolute abundance after normalization】
|      |      |      |-- otu_table.absolute.xls  【OTUs' absolute abundance】
|      |      |      `-- otu_table.*.absolute.xls 【OTUs' absolute abundance summarized at each taxonomic level】
|      |      `-- relative/                      【Relative abundance after normalization】
|      |             |-- otu_table.relative.xls  【OTUs' relative abundance】
|      |             `-- otu_table.*.relative.xls 【OTUs' relative abundance summarized at each taxonomic level】
|      |-- taxa_stat/                            【OTUs' statistical results】
|      |      |-- Classified_stat.{png,svg}      【Tags abundance layout at each taxonomic level】
|      |      |-- classified_stat.xls            【Statistical form of tags'  number annotated at each taxonomic level】
|      |      |-- Sample_Tags-OTUs_dis.{png,svg} 【Tags distribution and OTU analysis layout】
|      |      `-- Tags_stat.xls                  【Statistical table of tags number and OTUs number】
|      |-- taxa_charts_html/                     【Species annotation results in html format】
|      |      |-- area_charts.html               【Area chart of species annotation results】
|      |      |-- bar_charts.html                【Bar plot of species annotation results】
|      |      |-- pie_charts.html                【Pie chart of species annotation results】
|      |      |-- charts/                        【Pictures used in the webpage】
|      |      |-- css/                           【Configuring file of webpage】
|      |      `-- js/                            【Configuring file of webpage】
|      |-- top10/                                【Top 10 species abundance layout at each taxonomic level】
|      |-- taxa_heatmap/                         【Heatmap of clustering of species annotation】
|      |      |-- cluster/                       【Species abundance heatmap at taxonomic levels(phylum,class,family,genus)】
|      |      `-- OTU_heatmap/                   【OTUs heatmap result】
|      |-- taxa_tree/                            【Taxon composition profile】
|      |      |-- *.taxtree.{png,svg}            【Taxon composition profile for each sample】
|      |      `-- all.taxtree.{png,svg}          【Taxon Taxon composition profile for all samples】
|      |-- GraPhlan/                             【GraPhlan results】
|      |      |-- graphlan.{png,pdf}             【Figures generated by GraPhlan】
|      |-- genus_evolutionary_tree/              【Phylogenetic tree at genus level】
|      |      `-- genus_100.tree.{pdf,png,svg}   【Phylogenetic tree for top 100 genus】
|      |-- ternaryplot/                          【Ternaryplot analysis among 3 samples(or groups)】
|      |      `-- *-*-*                          【Ternaryplot analysis results for each Comparison at each taxonomic level】
|--03.AlphaDiversity/                            【Alpha Diversity】
|      |-- observed_species.{pdf,png}            【Pictures of rarefaction curves】
|      |-- group_observed_species.{pdf,png}      【Rarefaction curves for groups】
|      |-- plot_observed_species.txt             【Data used for plotting rarefaction curves】
|      |-- rank_abundance.{pdf,png}              【Pictures of rank abundance curve】
|      |-- group_rank_abundance.{pdf,png}        【Rank abundance curve for groups】
|      |-- alpha_diversity_index.xls             【Tables of alpha diversity indices】
|      |-- alpha_rarefaction_plots/              【Results of alpha diversity analysis in html format】
|      |-- venn_figure/                          【Venn diagram】
|      |-- Flower_figure/                        【Flower diagram】
|      |-- Specaccum/                            【Species accumulation curve】
|      |      |-- specaccum.{png,pdf}            【Pictures of species accumulation curve】
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|   |-- Alpha_div/                          【Box plots for comparison of alpha diversity indices among groups】
|   |   |-- ACE/
|   |   |   |-- ACE.{png,pdf}               【Box plots for ACE index】
|   |   |   |-- ACE_Tukey.txt               【Multi-group variation analysis of ACE index】
|   |   |   `-- ACE_wilcox.txt              【Non-parametric wilcox test of ACE index】
|   |   |-- chao1/
|   |   |   |-- chao1.{png,pdf}             【Box plots for chao1 index】
|   |   |   |-- chao1_Tukey.txt             【Multi-group variation analysis of chao1 index】
|   |   |   |-- chao1_wilcox.txt            【Non-parametric wilcox test of ACE index】
|   |   |-- goods_coverage/
|   |   |   |-- goods_coverage.{png,pdf}    【Box plots for the good' s coverage index】
|   |   |   |-- goods_coverage_Tukey.txt    【Multi-group variation analysis of the good' s coverage index】
|   |   |   |-- goods_coverage_wilcox.txt   【Non-parametric wilcox test of goods_coverage index】
|   |   |-- observed_species/
|   |   |   |-- observed_species.{png,pdf}  【Box plots for observed_species index】
|   |   |   |-- observed_species_Tukey.txt  【Multi-group variation analysis of observed_species index】
|   |   |   |-- observed_species_wilcox.txt 【Non-parametric wilcox test of observed_species index】
|   |   |-- Shannon/
|   |   |   |-- shannon.{png,pdf}           【Box plots for observed_species index】
|   |   |   |-- shannon_Tukey.txt           【Multi-group variation analysis of observed_species index 】
|   |   |   |-- shannon_wilcox.txt          【Non-parametric wilcox test of observed_species index】
|   |   |-- simpson/
|   |   |   |-- simpson.{png,pdf}           【Box plots for simpson index】
|   |   |   |-- simpson_Tukey.txt           【Analysis of variance of simpson index among groups】
|   |   |   |-- simpson_wilcox.txt          【Non parametric Wilcox test of simpson index among groups】
|   |   |-- PD_whole_tree/
|   |   |   |-- PD_whole_tree.{png.pdf}     【Box plots for PD_whole_tree index】
|   |   |   |-- PD_whole_tree_Tukey.txt     【Analysis of variance of PD_whole_tree index among groups】
|   |   |   `-- PD_whole_tree_wilcox.txt    【Non parametric Wilcox test of PD_whole_tree index among groups】
|-- 04.BetaDiversity/                       【Beta Diversity Analysis】
|   |-- Beta_div/                           【Box plots for comparison of Beta Diversity】
|   |   |--weighted_unifrac.{png,pdf}       【Box plots of Beta Diversity indices based on weigted unifrac distances】
|   |   |--weighted_unifrac_TukeyHSD.txt    【Analysis of variance among groups based on weighted unifrac distance】
|   |   |--weighted_unifrac_wilcox.txt      【Non parametric wilcon test based on weighted unifrac distances】
|   |   |--unweighted_unifrac.{png,pdf}     【Box plots of Beta Diversity indices based on unweigted unifrac distances】
|   |   |--unweighted_unifrac_TukeyHSD.txt  【Analysis of variance among groups based on unweighted unifrac distance】
|   |   |--unweighted_unifrac_wilcox.txt    【Analysis of variance among groups based on unweighted unifrac distance】
|   |-- beta_div_heatmap/                   【heat map of unifrac distances】
|   |   |-- beta_diversity.heatmap.{png,svg}    【Heatmap of weighted and unweighted unifrac distances】
|   |   |-- beta_diversity.heatmap.UnW.{png,svg}【Heatmap of unweighted unifrac distances】
|   |   |-- beta_diversity.heatmap.W.{png,svg}  【Heatmap of weighted unifrac distances】
|   |   |-- unweighted_unifrac_sorted_otu_table.txt【Unweighted unifrac distances】
|   |   `-- weighted_unifrac_sorted_otu_table.txt【weighted unifrac distances】
|   |-- PCA                                 【Result of Principle Component Analysis(PCA)】
|   |   |-- PCA12_2.{png,pdf}               【PCA results with sample names】
|   |   |-- PCA12.{png,pdf}                 【PCA results without labeling sample names】
|   |   |-- pca.csv                         【Statistical table for each principle component】
|   |   |-- PCA_stat_correlation1.txt        【Statistical table of the first principle component】
|   |   `-- PCA_stat_correlation2.txt        【Statistical table of the second principle component】
|   |-- PCoA/                               【Principal Co-ordinates Analysis(PCoA)】
|   |   |-- unweighted_unifrac/             【PCoA results based on unweighted unifrac distances】
|   |   |   |-- {*.png, *.pdf}              【PCoA figures based on unweighted unifrac distances】
|   |   |   |-- unweighted_unifrac_dm.txt   【Profiling matrix of unweighted unifrac distances】
|   |   |   `-- unweighted_unifrac_pc.txt   【Profiling component coordinates statistical table】
|   |   |-- weighted_unifrac/               【PCoA results based on weighted unifrac distances】
|   |   |   |-- {*.png, *.pdf}              【PCoA figures plotted with paired component】
|   |   |   |-- weighted_unifrac_dm.txt     【Profiling matrix of weighted unifrac distances】
|   |   |   `-- weighted_unifrac_pc.txt     【Profiling component coordinates statistical table】
|   |   |-- binary_jaccard_dm.txt           【Profiling matrix of binary_jaccard distances】
|   |   |-- binary_jaccard_pc.txt           【Profiling component coordinates statistical table】
|   |   |-- bray_curtis_dm.txt              【Profiling matrix of bray_curtis distances】
|   |   `-- bray_curtis_pc.txt              【Profiling component coordinates statistical table】
|   |-- Tree/                               【Phylogenetic tree】
|   |   |-- unweighted_unifrac/             【Clustering results based on unweighted unifrac distances】
|   |   |   |-- unweighted_unifrac.{png,pdf}【Figures of UPGMA tree based on unweighted unifrac distances】
|   |   |       |-- sorted_otu_table_upgma.tre【Files of UPGMA tree based on unweighted unifrac distances, viewed with MEGA software】
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|   |       `-- UPGMA.UnW.tree.{png,svg}        【UPGMA cluster tree of unweighted unifrac distance combining with top10 phyla distribution】
|   |   `-- weighted_unifrac/                   【Clustering results based on weighted unifrac distances】
|   |       |-- sorted_otu_table_upgma.tre      【Files of UPGMA tree based on weighted unifrac distances, viewed with MEGA software】
|   |       |-- weighted_unifrac.{pdf,png}      【Figures of UPGMA tree based on weighted unifrac distances】
|   |       `-- UPGMA.W.tree.{png,svg}          【UPGMA cluster tree of unweighted unifrac distance combining with top10 phyla distribution】
|   |-- NMDS/                                   【Non-Metric Multi-Dimensional Scaling(NMDS)】
|   |   |-- NMDS.{png,pdf}                      【NMDS figures with sample name labeled】
|   |   |-- NMDS2.{png,pdf}                     【NMDS figures without sample names】
|   |   `-- NMDS_scores.txt                     【Profiling component coordinates statistical table】
|   |-- LEfSe/                                  【Linear discriminant analysis (LDA) effect size analysis】
|   |   |-- */LDA.*.{png,pdf}                   【Linear discriminant analysis (LDA) effect size bar plot】
|   |   |-- */LDA.*.tree.{png,pdf}              【Figures of Cladogram】
|   |   |-- */LDA.*.res                         【Statistical results of LEfSe analysis】
|   |   `-- */biomarkers_raw_images/            【Figures comparing relative abundance of each biomarker among groups】
|   |-- MetaStat/                               【MetaStats analysis】
|   |   |-- */*.test.xls                        【MetaStats results at taxonomic level】
|   |   |-- */*.psig.xls                        【MetaStats results with p value less than 0.05】
|   |   |-- */*.qsig.xls                        【MetaStats results with q value less than 0.05】
|   |   |-- */*.cluster.*.diff.{png,pdf,txt}    【Heatmap analysis for species with significant differences among groups】
|   |   |-- */boxplot                           【Box plot for species with significant differences among groups】
|   |   `-- */PCA                               【PCA analysis for species with significant differences among groups】
|   |-- Anosim/                                 【Analysis of similarities(ANOSIM)】
|   |   |-- stat_anosim.txt                     【Results of ANOSIM】
|   |   `-- *.{png,pdf}                         【Box plot for ANOSIM】
|   |-- Adonis/                                 【Permutational Multivariate Analysis of Variance Using Distance Matrices】
|   |   `-- bray_adonis.txt                     【Results of ADONIS】
|   |-- Amova/                                  【Analysis of molecular variance】
|   |   `-- stat_amova.txt                      【Result of AMOVA】
|   |-- MRPP/                                   【Multiple Response Permutation Procedure (MRPP)】
|   |   `-- stat_mrpp.txt                       【Results of MRPP】
|   |-- t.test_bar_plot/                        【T-test analysis for species with significant differences among groups】
|   |   |-- */*-VS-*. {png,svg}                 【Bar plots for species with significant differences among groups at each taxonomic level】
|   |   |-- */*-VS-*.xls                        【Statistical results for species with significant differences among groups at each taxonomic level】
|   |   |-- */*-VS-*.psig.xls                   【Statistical results with p value less than 0.05】
|   |-- Environmen_factor/                      【Analysis with environment factors】
|   |   |-- mantel_test/                        【mantel_test analysis】
|   |   |-- spearman/                           【Spearman analysis】
|   |   |-- VPA/                                【Variance partitioning canonical correspondence analysis】
|   |   `-- multiCCA/                           【Canonical correspondence analysis】
|-- 05.WebShow/                                 【Results' comprehensive demonstration in the format of webpage】
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