```
|-- 00.RawData                                          【Raw reads】
|    |-- sample                                         【Raw reads for each sample】
|    |    |-- -- *1.fq.gz                               【Read 1 sequences】
|    |    `-- -- *2.fq.gz                               【Read 2 sequences】
|-- 01.CleanData                                        【Quality-controlled data information】
|    |-- novototal.QCstat.info.xls                      【Statistical table for data quality control】
|    |-- total.QCstat.info.xls                          【Detailed statistical table for data quality control】
|    |-- total.*.NonHostQCstat.info.xls                 【Statistical table for host related data quality control】
|    `-- Sample                                         【Results of quality control for each sample】
|         |-- -- *.fq1.gz                               【Read 1 sequences after quality control (FASTQ format)】
|         |-- -- *.fq2.gz                               【Read 2 sequences after quality control (FASTQ format)】
|         |-- -- *.nohost.fq1.gz                        【Read 1 sequences after filtering host related (FASTQ format)】
|         |-- -- *.nohost.fq2.gz                        【Read 2 sequences after filtering host related (FASTQ format)】
|         |-- -- *.qual.png                             【Distribution of Sequencing Quality】
|         `-- *.base.png                                【Distribution of A/T/G/C Base】
|-- 02.Assembly                                         【Assembly results】
|    |-- total.scaftigs.stat.info.xls                   【Statistical table for Scaftigs(>=500bp)】
|    |-- total.scafSeq.stat.info.xls                    【Statistical table for Scaffold(>=500bp)】
|    `-- Sample                                         【Assembly result of each sample】
|         |-- *.scafSeq.fa                              【Scaffold sequence(FASTA format)】
|         |-- *.scafSeq.500.ss.txt                      【Statistical table for scaffold】
|         |-- *.scaftigs.fa                             【Scaftigs sequence(FASTA format, >=500bp)】
|         |-- *.scaftigs.500.ss.txt                     【Statistical table for scaftigs(>=500bp)】
|         |-- *.len.png                                 【Distribution of the length of Scaftigs(PNG format)】
|         `-- *.len.svg                                 【Distribution of the length of Scaftigs(SVG format)】
|-- 03.GenePredict                                      【Gene predict results and abundance statistics】
|    |-- GenePredict                                    【Gene predict results】
|    |    `-- Sample                                    【Gene predict results of each sample】
|    |         |-- *.CDS.fa                             【Gene results(FASTA format)】
|    |         |-- *.protein.fa                         【Protein results(FASTA format)】
|    |         |-- *.mgm.gff                            【Gene predict results (GFF format)】
|    |         |-- *.CDS.fa.stat.xls                    【Statistical table for predicted genes】
|    |         |-- *.CDS.fa.integrity.stat.xls          【Statistical table for integrity of predicted genes】
|    |         `-- *.CDS.fa.len.{png|svg|xls}           【Distribution of the length of predicted genes(PNG, SVG & XLS format)】
|    |-- UniqGenes                                      【Dereplication】
|    |    |-- Unigenes.CDS.cdhit.fa                     【Gene results after dereplication(FASTA format)】
|    |    |-- Unigenes.CDS.cdhit.fa.integrity.stat.xls  【Statistical table for integrity of genes after dereplication】
|    |    |-- Unigenes.CDS.cdhit.fa.len.{png|svg|xls}   【Distribution of the length of genes after dereplication】
|    |    |-- Unigenes.CDS.cdhit.fa.stat.xls            【Statistical table for genes after dereplication】
|    |    |-- Unigenes.protein.fa                       【Protein results before dereplication(FASTA format)】
|    |    |-- Unigenes.protein.cdhit.fa                 【Protein results after dereplication(FASTA format)】
|    |    |-- Unigenes.protein.cdhit.fa.len.xls         【Distribution of the length of proteins after dereplication】
|    |    `-- Unigenes.protein.table.txt               【Statistical table for cluster result of unigenes】
|    |-- GeneStat                                       【Statistic analysis of genes】
|    |    |-- core_pan                                  【Core-pan analysis】
|    |    |-- correlation                               【Correlation analysis】
|    |    |-- genebox                                   【Box plot of genes among groups】
|    |    `-- venn                                      【Venn diagram】
|    `-- GeneTable                                      【Gene abundance analysis】
|    |    `-- Sample                                    【Reads Mapping Results of each samples】
|    |         |-- coverage_depth.png                   【Depth distribution(PNG format)】
|    |         |-- coverage_depth.svg                   【Depth distribution(SVG format)】
|    |         |-- coverage.depth.table.xls             【Statistical table for reads mapping】
|    |         |-- *.PE.soap                            【Paired reads after soap alignment】
|    |         |-- *.SE.soap                            【Unpaired reads after soap alignment】
|    |         `-- soap.coverage.depthsingle            【Depth distribution of single base】
|    |    `-- Total                                     【Gene abundance tables for all samples】
|    |         |-- Unigenes.readsNum.xls                【Statistical table for mapping reads of genes】
|    |         |-- Unigenes.readsNum.even.tree          【Phylogenetic tree(Bray-Curtis distance) of genes after normalization】
|    |         |-- Unigenes.readsNum.relative.xls       【Statistical table for reletive abundance】
|    |         |-- Unigenes.readsNum.screening.fa       【Protein sequence after filted by number of mapping reads(FASTA format, >=2)】
|    |         `-- Unigenes.readsNum.even.xls           【Statistical table for abundance after normalization】
|-- 04.TaxAnnotation                                    【Taxonomy annotation results】
|    |-- MAT                                            【Array of taxonomy annotation abundance】
|    |    |-- Absolute                                  【Absolute abundance】
|    |    |    `-- Unigenes.absolute.{k,p,c,o,f,g,s}.xls 【Array of absolute abundance at each taxonomic level】
|    |    `-- Relative                                  【Relative abundance】
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| | `-- Unigenes.relative.{k,p,c,o,f,g,s}.xls	【Array of relative abundance at each taxonomic level】
| |-- GeneNums	【Statistics for numbers of annotated genes】
| | `-- Unigenes.absolute.{k,p,c,o,f,g,s}.xls	【Statistics for numbers of annotated genes at each taxonomic level】
| |-- GeneNums.BetweenSamples/	【Statistics for numbers of annotated genes in different samples】
| | `-- Unigenes.absolute.{k,p,c,o,f,g,s}.xls	【Array of annotated numbers in different samples at each taxonomic level】
| |-- GeneNums.BetweenSamples.heatmap/	【Heatmap analysis of gene numbers in different samples】
| | `—-{kingdom,phylum,class,order,family,genus,species}	【Heatmap analysis of gene numbers at each taxonomic level】
| | `-- {k,p,c,o,f,g,s}.genenum.heatmap.txt	【Statistical table for gene numbers at each taxonomic level】
| | `-- {k,p,c,o,f,g,s}.genenum.heatmap.txt.{png,pdf}	【Heatmap of gene numbers at each taxonomic level(PNG & PDF format)】
| |-- MicroNR_Anno	【Annotation results by MicroNR database】
| | |-- Unigenes.lca.tax.detail.xls	【Detailed results of LCA annotation】
| | |-- Unigenes.lca.tax.xls	【Results of LCA annotation】
| | |-- Unigenes.m8.tax.xls	【Blast m8 result added tax id and tax rank】
| | `—-Unigenes.screening.m8.xls	【Blast m8 result after filtered by e_value(e >= e_min*10)】
| |-- Cluster_Tree	【Sample cluster result】
| | |-- figure	【Sample cluster result at each taxonomic level】
| | | `-- Bar.tree.{k,p,c,o,f,g,s}10.png	【Sample cluster figures at each taxonomic level(PNG & PDF format)】
| | `-- table	【Statistical table for cluster analysis】
| |-- heatmap	【Heatmap of gene abundance】
| | |-- figure	【Heatmap of gene abundance】
| | `-- table	【Statistical table for heatmap analysis】
| |-- PCA	【PCA analysis results】
| | `—-{kingdom,phylum,class,order,family,genus,species}	【PCA analysis results at each taxonomic level】
| | |-- PCA12_2.pdf(png)	【PCA result without sample names(PNG & PDF format)】
| | |-- PCA12.pdf	【PCA result with sample names(PNG & PDF format)】
| | |-- pca.csv	【Statistical table for PCA analysis】
| | |-- PCA_stat_correlation1.txt	【Statistical table for PCA1 analysis】
| | `-- PCA_stat_correlation2.txt	【Statistical table for PCA2 analysis】
| |—-MetaStats	【MetaStats results】
| | `—-{kingdom,phylum,class,order,family,genus,species}	【MetaStats results at each taxonomic level】
| | |—-boxplot	【Box plots of species with significant difference】
| | |—-PCA	【PCA analysis result for species with significant difference】
| | |—-cluster.*.diff.{png,pdf|txt}	【Heatmap analysis result for species with significant difference】
| | |—-A-vs-B.test.xls	【Statistical table for MetaStats】
| | |—-A-vs-B.qsig.xls	【Statistical table for MetaStats(q_value <0.05)】
| | |—-A-vs-B.Psig.xls	【Statistical table for MetaStats(p_value <0.05)】
| | |—-*_diff_relative.xls	【Relative abundance of species with significant difference】
| | `—-{k,p,c,o,f,g,s}_qsig.xls	【Statistical table for species with significant difference(q_value <0.05)】
| |—-Krona	【Krona taxonomy visualization】
| `-- top	【Top 10 species at each taxonomic level】
| |-- figure	【Bar plots for top 10 species at each taxonomic level(PNG & SVG format)】
| `-- table	【Statistical table for top 10 species at each taxonomic level】
|-- 05.FunctionAnnotation	【Function annotation results】
| |-- CAZy	【Results based on CAZy database 】
| | |-- CAZy_Anno	【Annotation results based on CAZy database】
| | | |-- cazy.unigenes.num.pdf(png,txt)	【Statistical results for annotated genes at level 1(PDF, PNG & TXT format)】
| | | |-- Unigenes.blast.m8.filter.anno.xls	【Annotation results of filtered blast.m8 result】
| | | |-- Unigenes.blast.m8.filter.xls	【Blast.m8 result after filtered】
| | | |-- Unigenes.level1.bar.png(svg)	【Bar plot for relative abundance at level 1 of CAZy(PNG & SVG format)】
| | | |-- Unigenes.level1.bar.tree.png(svg)	【Cluster result of annotation at level 1 of CAZy(PNG & SVG format)】
| | |--CAZy_MAT	【CAZy annotation abundance】
| | | |-- Absolute	【Absolute abundance of CAZy annotation at level 1, level 2 and ec level】
| | | `-- Relative	【Relative abundance of CAZy annotation at level 1, level 2 and ec level】
| | |--GeneNums	【Statistics for numbers of CAZy annotation at level 1, level 2 and ec level】
| | |--GeneNums.BetweenSamples	【Statistics for annotated numbers in different samples at each level】
| | |--GeneNums.BetweenSamples.heatmap	【Heatmap analysis of annotated genes at each level】
| | |--heatmap	【Cluster heatmap of annotated genes at each level】
| | |--MetaStats	【Metastat analysis at each level】
| | | |-- EC	【Metastat analysis at EC level】
| | | |-- level1	【Metastat analysis at level 1】
| | | `-- level2	【Metastat analysis at level 2】
| | |-- PCA	【PCA analysis at each level】
| | | |-- ec	【PCA analysis at EC level】
| | | |-- level1	【PCA analysis at level 1】
| | | `-- level2	【PCA analysis at level 2】
| |-- eggNOG	【Results based on eggNOG database】
| | |--eggNOG_Anno	【Annotation results based on eggNOG database】

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|   |   |   |-- eggNOG.unigenes.num.pdf(png,txt)        【Statistical results for annotated genes at level 1(PDF, PNG & TXT format)】
|   |   |   |-- Unigenes.blast.m8.filter.anno.xls        【Annotation results of filtered blast.m8 result】
|   |   |   |-- Unigenes.blast.m8.filter.xls            【Blast.m8 result after filtered】
|   |   |   |-- Unigenes.level1.bar.png                 【Bar plot for relative abundance at level 1 of eggNOG (PNG & SVG format)】
|   |   |   |-- Unigenes.level1.bar.tree.png(svg)       【Cluster result of annotation at level 1 of eggNOG (PNG & SVG format)】
|   |   |-- eggNOG_MAT                                  【eggNOG annotation abundance】
|   |   |   |-- Absolute                                【Absolute abundance of eggNOG annotation at each level】
|   |   |   `-- Relative                                【Relative abundance of eggNOG annotation at each level】
|   |   |-- GeneNums                                    【Statistics for numbers of eggNOG annotation at each level】
|   |   |-- GeneNums.BetweenSamples                     【Statistics for annotated numbers in different samples at each level】
|   |   |-- GeneNums.BetweenSamples.heatmap            【Heatmap analysis of annotated genes at each level】
|   |   |-- heatmap                                     【Cluster heatmap of annotated genes at each level】
|   |   |-- NOG.Tax                                     【Ortholog group analysis result】
|   |   |-- MetaStats                                   【Metastat analysis at each level】
|   |   `-- PCA                                         【PCA analysis at each level】
|   `-- KEGG                                            【Results based on KEGG database】
|   |   |-- KEGG_Anno                                   【Annotation results based on KEGG database】
|   |   |   |-- kegg.unigenes.num.pdf(png,txt)         【Statistical results for annotated genes at level 1(PDF, PNG & TXT format)】
|   |   |   |-- Unigenes.blast.m8.filter.anno.xls      【Annotation results of filtered blast.m8 result】
|   |   |   |-- Unigenes.blast.m8.filter.xls           【Blast.m8 result after filtered】
|   |   |   |-- Unigenes.level1.bar.png(svg)           【Bar plot for relative abundance at level 1 of KEGG (PNG & SVG format)】
|   |   |   `-- Unigenes.level1.bar.tree.png(svg)      【Cluster result of annotation at level 1 of KEGG(PNG & SVG format)】
|   |   |-- GeneNums                                    【Statistics for numbers of KEGG annotation at each level】
|   |   |-- GeneNums.BetweenSamples                     【Statistics for numbers of KEGG annotation at each level】
|   |   |-- KEGG_MAT                                    【KEGG annotation abundance】
|   |   |   |-- Absolute                                【Absolute abundance of KEGG annotation at each level】
|   |   |   `-- Relative                                【Relative abundance of KEGG annotation at each level】
|   |   |-- MetaStats                                   【Metastat analysis at each level】
|   |   |-- pathwaymaps                                 【Pathway analysis】
|   |   |-- pathwaymaps.report                          【Pathway analysis report】
|   |   |-- PCA                                         【PCA analysis at each level】
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