

## **Project analysis code and data reproducibility**

### **Project analysis code available**

#### **# For SNP calling**

Software: bowtie2, bcftools

Parameter:

```
bowtie2 -p 12 -x /lp082_ref/lp --no-mixed --very-sensitive --n-ceil 0,0.01 -1
ISP_single_genome/hm/H1_1.fq -2 /ISP_single_genome/hm/H1_2.fq | samtools sort -O bam
-@ 24 -o - > h1ref.bam
bcftools mpileup -C 50 -Ou -m 3 -F 0.0002 -f /ISP_single_genome/lp082_ref/ref.fasta
z1ref.bam > z1ref.bcf
bcftools call -c --variants-only -Ob --ploidy 1 z1ref.bcf > z1.bcf
bcftools view -Ov z1.bcf | vcfutils.pl varFilter -d 100 > z1.vcf
# Merge all single *.vcf to the SNP profile:
/ISP_single_genome/callsnp/tabix-0.2.6/bgzip H1.vcf
bcftools index H1.vcf.gz
bcftools merge --merge all -l listvcf -O v > snp.vcf
```

#### **#For isolate single genome assembling**

Software: Spades

Parameter:

```
spades.py -1 H1_1.fq -2 H1_2.fq -o spades_error_corrected_reads -t 24 -m 250
--only-error-correction
spades.py -1 H1_1.00.0_0.cor.fastq.gz -2 H1_2.00.0_0.cor.fastq.gz -o
spades_kmers_set_careful_assembly -t 24 -k 21,33,55,77,89 --careful --only-assembler
```

#### **#Strain mobile element annotation**

```
sed 's/k141/H1_node/g' /ISP_single_genome/assemble_genome/H1/final.contigs.fa >
/ISP_single_genome/assemble_genome/assembled/H1.fasta
cat *.fasta > whole_assembled.fasta
blastall -a 12 -p blastn -i whole_assembled.fasta -d ./ref/ref.fasta -o b1 -W 11 -e 0.00001 -b 1
-m 8
python extracnt_blast.py -i whole_assembled.fasta -b b1 -t 90 -o unreass.fasta
cd-hit-est -i unreass.fasta -o cdhitass.fasta -c 0.9 -M 100000 -aS 0.9 -B 1
awk -v min="500" 'BEGIN {RS = ">" ; ORS = ""} length($2) >= min {print ">"$0}'
cdhitass.fasta > unreass.fasta
bowtie2-build unreass.fasta unress
bowtie2 -p 24 -x ./unreass/unreass --no-mixed --very-sensitive -1
/ISP_single_genome/hm/H1_1.fq -2 /ISP_single_genome/hm/H1_2.fq -S h1ass.sam
soap.coverage -cvg -sam -i h1ass.sam -refsingle ./unreass/unreass500.fasta -o h1ass.txt
-depthsingle h1ass.coverage -plot hiassplot.txt 0 1000
```

#### **#For ANI calculation**

```
average_nucleotide_identity.py -i /ISP_single_genome/aug10/ani/ -o
/ISP_single_genome/aug10/aniout -m ANIm -g
```

#### **#For phylogenetic tree construction**

Software: MEGA-X, iTOL

### **#Shotgun metagenomic sequencing data assembling**

Software: megahit

Parameter:

```
megahit -1 /ISP_metagenome/cleandata/MH1_1.fq -2  
/ISP_metagenome/cleandata/MH1_2.fq -m 1000000000000 -t 12 -o  
/ISP_metagenome/assemble/MH1 --min-contig-len 500
```

### **#For intestinal microbiota evolution analysis**

Software: MDis

Parameter:

```
run_midat.py snps /path/to/outdir --species_id Bacteroides_vulgatus_57955 -1  
/path/to/reads_1.fq.gz -2 /path/to/reads_2.fq.gz
```

### **#For metagenomic data taxonomy annotation**

Software: Bracken

Parameter:

```
kraken2-build --db ${KRAKEN_DB} --threads ${THREADS}  
bracken-build -d ${KRAKEN_DB} -t ${THREADS} -k ${KMER_LEN} -l ${READ_LEN}  
kraken2 --db ${KRAKEN_DB} --threads ${THREADS} --report ${SAMPLE}.kreport  
${SAMPLE}.fq > ${SAMPLE}.kraken  
bracken -d ${KRAKEN_DB} -i ${SAMPLE}.kreport -o ${SAMPLE}.bracken -r ${READ_LEN}  
-l ${LEVEL} -t ${THRESHOLD}
```

### **#For metagenomic data functional annotation**

Software: HUMAnN2

Parameter:

```
humann2 --threads 12 --input examples/demo.fasta --output $OUTPUT_DIR
```

### **#For metagenomic data phage, antibiotic resistant genes and mobile elements annotation**

Software: Bowtie2, R

Parameter:

```
bowtie2 -p 24 -x /ISP_metagenome/mge/mge_ref/mge -D 20 -R 3 -N 1 -L 20 -i S,1,0.50 -1  
/ISP_metagenome/cleandata/MH1_1.fq -2 /ISP_metagenome/cleandata/MH1_2.fq |  
samtools view -bS | samtools sort -T PREFIX -@ 24 -o - >  
/ISP_metagenome/mge/MH1.outputPrefix.bam  
samtools index MH1.outputPrefix.bam  
samtools idxstats MH1.outputPrefix.bam | tee -a MH1.txt  
bowtie2 -p 24 -x /ISP_metagenome/card/card_ref/card -D 20 -R 3 -N 1 -L 20 -i S,1,0.50 -1  
/ISP_metagenome/cleandata/MH1_1.fq -2 /ISP_metagenome/cleandata/MH1_2.fq |  
samtools view -bS | samtools sort -T PREFIX -@ 24 -o - >  
/ISP_metagenome/card/MH1.outputPrefix.bam  
samtools index MH1.outputPrefix.bam  
samtools idxstats MH1.outputPrefix.bam | tee -a MH1.txt
```

```

bowtie2 -p 12 -x /ISP_metagenome/phage/ref_phage/phage -1
/ISP_metagenome/cleandata/MH1_1.fq -2 /ISP_metagenome/cleandata/MH1_2.fq |
samtools view -bS | samtools sort -T PREFIX -@ 24 -o - >
/ISP_metagenome/phage/MH1.outputPrefix.bam
samtools index MH1.outputPrefix.bam
samtools idxstats MH1.outputPrefix.bam | tee -a MH1.txt
R
rm(list=ls())
files <- list.files(pattern = "txt$")
name <- c('gene_name','gene_length')
final_data <- read.table(files[1], header=F, sep="\t")[,1:2]
for (filename in files)
{
  data <- read.table(filename, header=F, sep="\t")[,3]
  name <- c(name,filename)
  final_data <- cbind(final_data, data)
}
name <- gsub(".bowtie2.txt", "", name)
colnames(final_data) <- name
write.table(file='card_bowtie2_unique',final_data, sep="\t", quote=F, row.names=F)

```

## **Data and figures repeatable**

### **#Figure 1**

#(A) Experiment design of the present research.

#(B) The phylogenetic tree was constructed based on the SNPs profile with the iTOL online version, the SNPs sequences were listed in “SNPS22\_tree.fasta” on

Github:[https://github.com/zhjch321123/Host-dependent-co-evolution-of-supplemented-probiotic/tree/master/Figure\\_1B](https://github.com/zhjch321123/Host-dependent-co-evolution-of-supplemented-probiotic/tree/master/Figure_1B)

#(C) Top panel; The curve was drawn by R program, the original code and the raw data were deposited on

[https://github.com/zhjch321123/Host-dependent-co-evolution-of-supplemented-probiotic/tree/master/Figure\\_1C](https://github.com/zhjch321123/Host-dependent-co-evolution-of-supplemented-probiotic/tree/master/Figure_1C)

Bottom panel: The figure was constructed by GraphPad Prism 8, the original code and the raw data were deposited on

[https://github.com/zhjch321123/Host-dependent-co-evolution-of-supplemented-probiotic/tree/master/Figure\\_1C](https://github.com/zhjch321123/Host-dependent-co-evolution-of-supplemented-probiotic/tree/master/Figure_1C)

#(D) The genomic cycle figure with SNPs and GC abundance was constructed with R, the original code and the raw data were deposited on

[https://github.com/zhjch321123/Host-dependent-co-evolution-of-supplemented-probiotic/tree/master/Figure\\_1D](https://github.com/zhjch321123/Host-dependent-co-evolution-of-supplemented-probiotic/tree/master/Figure_1D)

#(E) The simplified phylogenetic tree was constructed based on SNP sequences with the iTOL online version.

[https://github.com/zhjch321123/Host-dependent-co-evolution-of-supplemented-probiotic/tree/master/Figure\\_3](https://github.com/zhjch321123/Host-dependent-co-evolution-of-supplemented-probiotic/tree/master/Figure_3)

#(F) The evolutionary dynamics figures were drawn by Python and R program with the code and dataset “FIG\_3CD.txt” on

[https://github.com/zhjch321123/Host-dependent-co-evolution-of-supplemented-probiotic/tree/master/Figure\\_3](https://github.com/zhjch321123/Host-dependent-co-evolution-of-supplemented-probiotic/tree/master/Figure_3)

### **#Figure 2**

#The FIG\_2A and 2B were constructed based on Table S2 of “Sup\_Tabs.xlsx” deposited in [https://github.com/zhjch321123/Intestinal\\_Selective\\_Pressure\\_project](https://github.com/zhjch321123/Intestinal_Selective_Pressure_project). The genes were annotated with the PROKKA annotation pipeline (<http://kbase.us/>).

# The FIG\_2C was drawn by R program, the original code and the raw data were deposited on

[https://github.com/zhjch321123/Host-dependent-co-evolution-of-supplemented-probiotic/tree/master/Figure\\_2C](https://github.com/zhjch321123/Host-dependent-co-evolution-of-supplemented-probiotic/tree/master/Figure_2C)

### **#Figure 3**

#(A) The distance boxplot was constructed by the R program, the original code and the raw data were deposited on Github:

[https://github.com/zhjch321123/Host-dependent-co-evolution-of-supplemented-probiotic/tree/master/Figure\\_4A](https://github.com/zhjch321123/Host-dependent-co-evolution-of-supplemented-probiotic/tree/master/Figure_4A)

#(B) The 2 curves were constructed by the R program, the original code and the raw data were deposited on Github:

[https://github.com/zhjch321123/Host-dependent-co-evolution-of-supplemented-probiotic/tree/master/Figure\\_4B](https://github.com/zhjch321123/Host-dependent-co-evolution-of-supplemented-probiotic/tree/master/Figure_4B)

#(C) The 2 network figures were constructed by Cytoscape 3.7.1. The correlation strength was calculated by SpiecEasi using R program, the code and raw network file were deposited on Github:

[https://github.com/zhjch321123/Host-dependent-co-evolution-of-supplemented-probiotic/tree/master/Figure\\_4C](https://github.com/zhjch321123/Host-dependent-co-evolution-of-supplemented-probiotic/tree/master/Figure_4C)

#### **#Figure 4**

#(A) The distance boxplot was constructed by the R program, the original code and the raw data were deposited on Github:

[https://github.com/zhjch321123/Host-dependent-co-evolution-of-supplemented-probiotic/tree/master/Figure\\_5A](https://github.com/zhjch321123/Host-dependent-co-evolution-of-supplemented-probiotic/tree/master/Figure_5A)

#(B) The boxplot was constructed by the R program, the raw data was listed in Table S8.

#(C) The 4 figures were constructed by GraphPad Prism 8 with the dataset “META\_SNP\_pro\_pla.pzfx” on Github:

[https://github.com/zhjch321123/Host-dependent-co-evolution-of-supplemented-probiotic/tree/master/Figure\\_5B](https://github.com/zhjch321123/Host-dependent-co-evolution-of-supplemented-probiotic/tree/master/Figure_5B)

#(D) The Heatmap was constructed by the R program, the raw data was listed in Table S8.

#### **#Supplementary figures**

**#Fig\_S1** A-B, The 2 figures were constructed by R, the original code and the raw data were deposited on

[https://github.com/zhjch321123/Host-dependent-co-evolution-of-supplemented-probiotic/tree/master/Supp\\_Figures](https://github.com/zhjch321123/Host-dependent-co-evolution-of-supplemented-probiotic/tree/master/Supp_Figures)

C-G, The phylogenetic tree was constructed based on SNP sequences with the iTOL online version. The raw data were deposited on Github:

[https://github.com/zhjch321123/Host-dependent-co-evolution-of-supplemented-probiotic/tree/master/Supp\\_Figures](https://github.com/zhjch321123/Host-dependent-co-evolution-of-supplemented-probiotic/tree/master/Supp_Figures)

**# Fig\_S2** The SNPs heatmap was constructed with the “FIG\_S2A.txt” by R program, the code and raw network file were deposited on Github:

[https://github.com/zhjch321123/Host-dependent-co-evolution-of-supplemented-probiotic/tree/master/Supp\\_Figures](https://github.com/zhjch321123/Host-dependent-co-evolution-of-supplemented-probiotic/tree/master/Supp_Figures)

**# Fig\_S3** The indigenous microbiome responded to the probiotic invasion. The figures was constructed based on Table S6-S7. The raw data were deposited on Github:

[https://github.com/zhjch321123/Host-dependent-co-evolution-of-supplemented-probiotic/tree/master/Supp\\_Figures](https://github.com/zhjch321123/Host-dependent-co-evolution-of-supplemented-probiotic/tree/master/Supp_Figures)

**# Fig\_S4** The number of SNPs of host intestinal microbiota responded to probiotic consumption in the present study and other published probiotic related study based on the data in “FIG\_S5A.txt” and the correlation between the SNPs and the species alpha diversity was deposited in “FIG\_S5B.txt”, The code and the raw data were deposited on Github:

[https://github.com/zhjch321123/Host-dependent-co-evolution-of-supplemented-probiotic/tree/master/Supp\\_Figures](https://github.com/zhjch321123/Host-dependent-co-evolution-of-supplemented-probiotic/tree/master/Supp_Figures)