# Tree + Panphlan

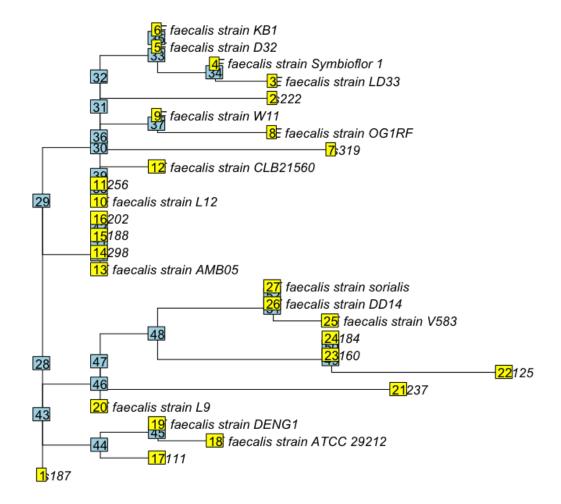
Chunyu Zhao

December 29, 2018

## E. faecalis

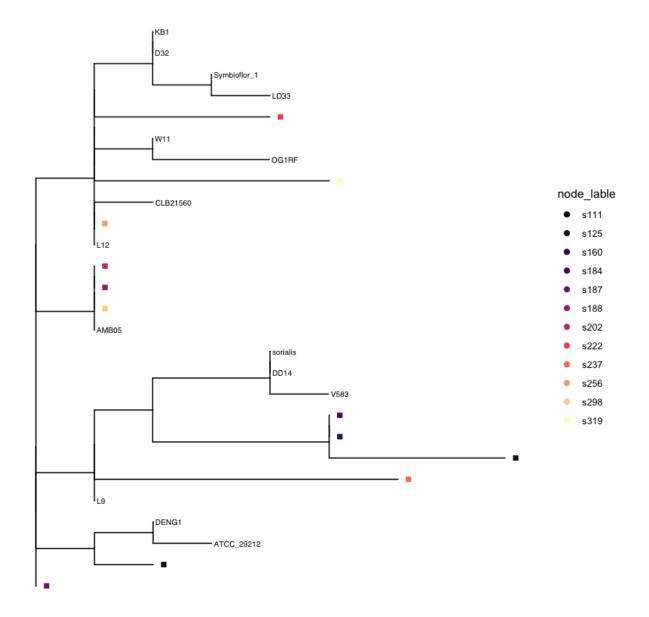
## Phylogenetic Tree

- We read the external genomes list from the anvio pangenome analysis results.
- Read in the tree from  ${\bf panphlan}$
- write to 20180720\_efaecalis\_tree\_tip\_order.txt.



### Tree time

• generate 20180702\_efaecalis\_tree\_v1.pdf => KB18 supple files

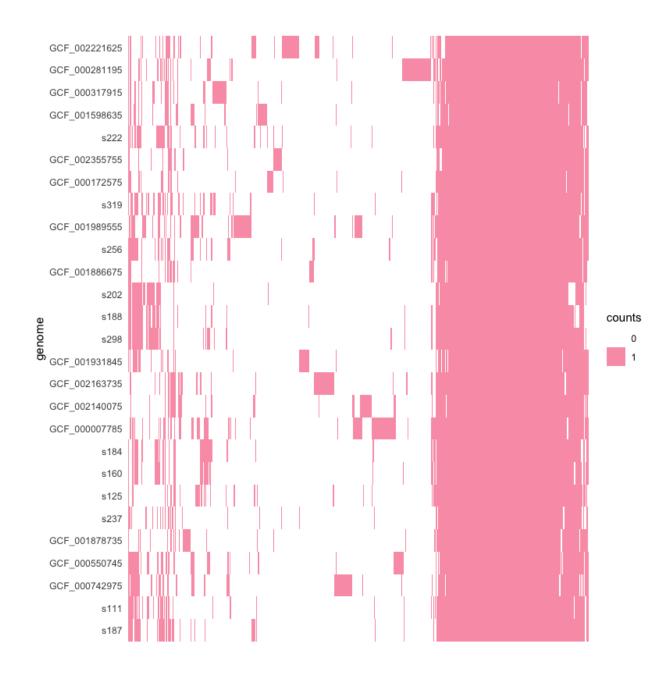


## Panphlan

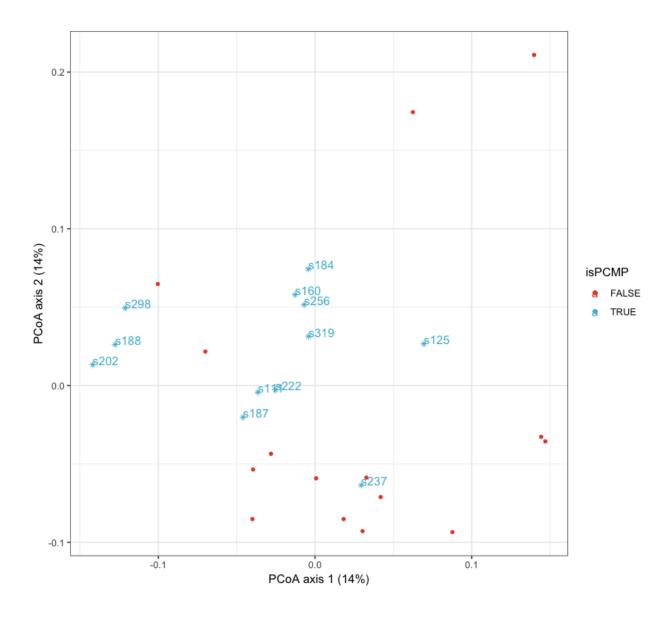
- visualize pangenome results
- read in result\_gene\_presence\_absence.csv
- read in 20180720\_efaecalis\_tree\_tip\_order.txt

### Heatmap

- 20180720\_Fig2A\_efaecalis\_pan\_heatmap.pdf



### PCoA plot based on Jacard Distance

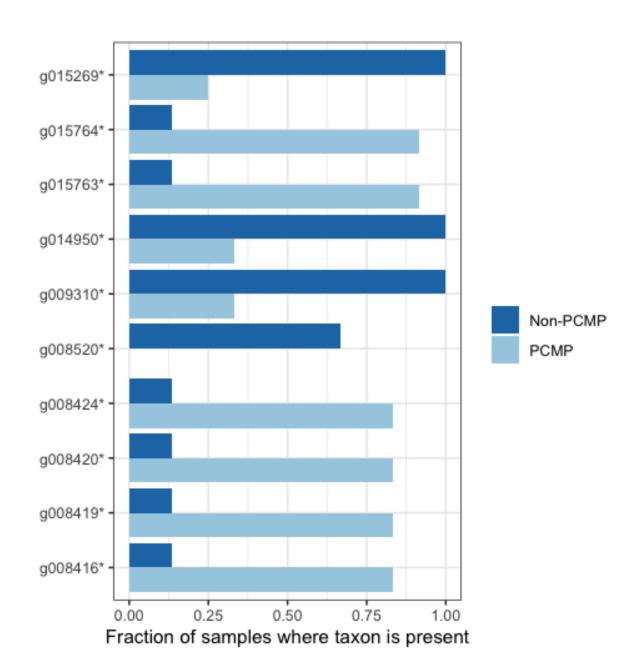


### Fisher's exact test

 $\bullet \ \ 20180720\_efaecalis\_fisher.pdf$ 

Gene	estimate	p.value	conf.low	conf.high	$fdr\_corrected$	isSig
g015269	$\operatorname{Inf}$	4.694 e - 05	5.39	$\operatorname{Inf}$	0.04025	*
g015763	0.01868	6.88e-05	0.0003119	0.2228	0.04025	*
g015764	0.01868	6.88e-05	0.0003119	0.2228	0.04025	*
g009310	$\operatorname{Inf}$	0.000223	3.896	$\operatorname{Inf}$	0.04774	*
g014950	$\operatorname{Inf}$	0.000223	3.896	$\operatorname{Inf}$	0.04774	*
g008520	$\operatorname{Inf}$	0.0003638	3.378	$\operatorname{Inf}$	0.04774	*
g008416	0.03788	0.0004352	0.002246	0.3381	0.04774	*
g008419	0.03788	0.0004352	0.002246	0.3381	0.04774	*

Gene	estimate	p.value	conf.low	conf.high	$fdr\_corrected$	isSig
g008420	0.03788	0.0004352	0.002246	0.3381	0.04774	*
g008424	0.03788	0.0004352	0.002246	0.3381	0.04774	*



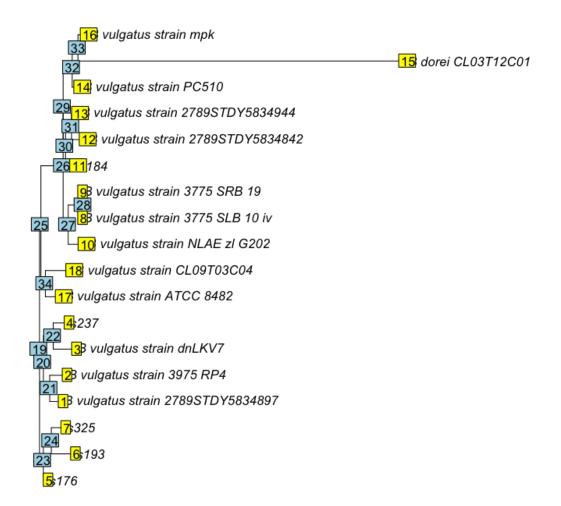
## B. vulgatus

## Phylogenetic Tree

- ## [1] "B\_vulgatus\_strain\_2789STDY5834897"
- ## [2] "B\_vulgatus\_strain\_3975\_RP4"

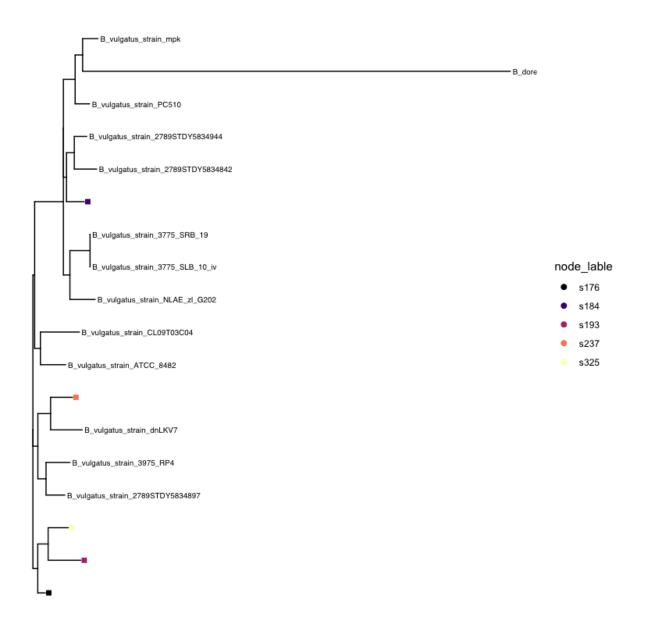
```
[3] "B_vulgatus_strain_dnLKV7"
##
##
    [4] "s237"
    [5] "s176"
##
    [6] "s193"
##
    [7] "s325"
##
##
    [8] "B_vulgatus_strain_3775_SLB_10_iv"
   [9] "B vulgatus strain 3775 SRB 19"
##
## [10] "B_vulgatus_strain_NLAE_zl_G202"
##
   [11] "s184"
##
  [12] "B_vulgatus_strain_2789STDY5834842"
  [13] "B_vulgatus_strain_2789STDY5834944"
   [14] "B_vulgatus_strain_PC510"
   [15] "B_dorei_CL03T12C01"
##
  [16] "B_vulgatus_strain_mpk"
  [17] "B_vulgatus_strain_ATCC_8482"
  [18] "B_vulgatus_strain_CL09T03C04"
    [1] "B_vulgatus_strain_2789STDY5834897"
##
##
    [2] "B_vulgatus_strain_3975_RP4"
    [3] "B_vulgatus_strain_dnLKV7"
##
##
    [4] "s237"
    [5] "s176"
##
    [6] "s193"
##
    [7] "s325"
##
##
    [8] "B_vulgatus_strain_3775_SLB_10_iv"
   [9] "B vulgatus strain 3775 SRB 19"
## [10] "B_vulgatus_strain_NLAE_zl_G202"
  [11] "s184"
##
##
  [12] "B_vulgatus_strain_2789STDY5834842"
  [13] "B_vulgatus_strain_2789STDY5834944"
  [14] "B_vulgatus_strain_PC510"
   [15] "B_dorei_CL03T12C01"
##
## [16] "B_vulgatus_strain_mpk"
```

## [17] "B\_vulgatus\_strain\_ATCC\_8482"
## [18] "B\_vulgatus\_strain\_CL09T03C04"



#### tree time

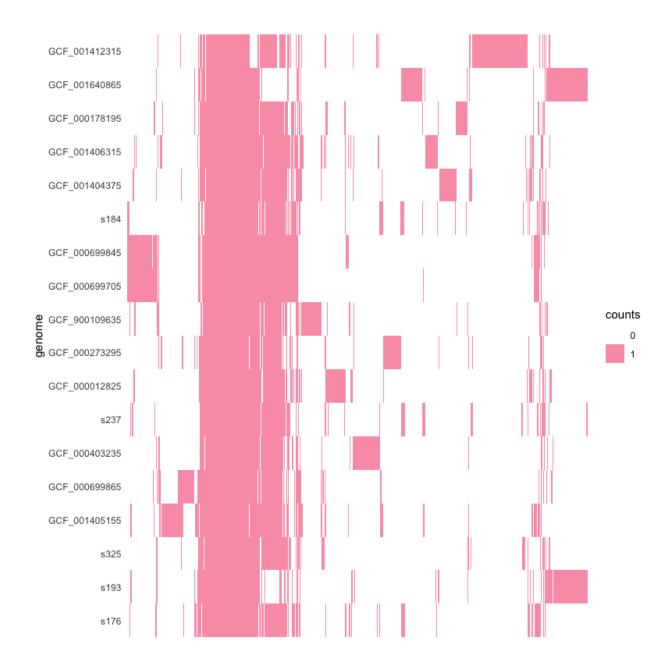
 $\bullet \ 20180702\_bvulgatus\_tree\_v1.pdf \\$ 



## Panphlan

### Heatmap

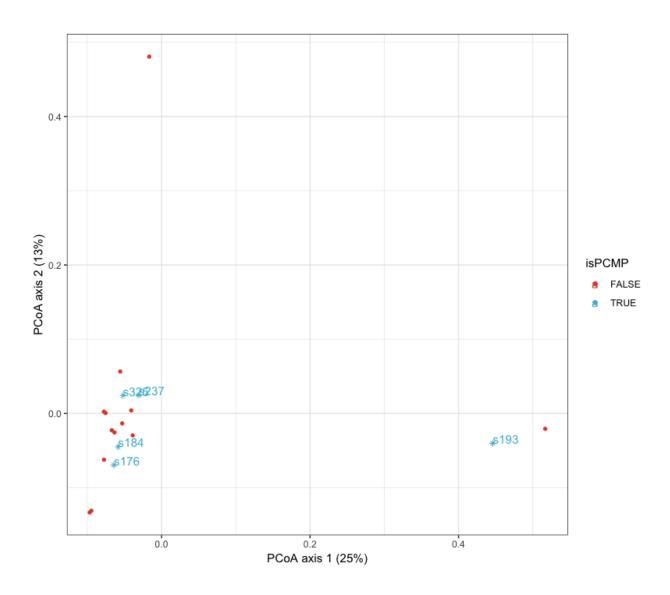
- 20180720\_Fig2A\_bvulgatus\_pan\_heatmap.pdf



### PCoA plot based on Jacard Distance

- 20180720\_bvulgatus\_pcoa.pdf

## character(0)



### Fisher's exact test

- 20180720\_bvulgatus\_fisher.pdf

Gene	estimate	p.value	conf.low	conf.high	$fdr\_corrected$	isSig
g010625	$\operatorname{Inf}$	0.0001167	6.654	$\operatorname{Inf}$	0.3316	
g000612	$\operatorname{Inf}$	0.0007003	3.651	$\operatorname{Inf}$	0.3316	
g004007	$\operatorname{Inf}$	0.0007003	3.651	$\operatorname{Inf}$	0.3316	
g007580	0	0.0007003	0	0.2739	0.3316	
g007582	0	0.0007003	0	0.2739	0.3316	
g007583	0	0.0007003	0	0.2739	0.3316	
g007586	0	0.0007003	0	0.2739	0.3316	
g010862	$\operatorname{Inf}$	0.001634	2.977	$\operatorname{Inf}$	0.6771	

Gene	estimate	p.value	conf.low	conf.high	$fdr\_corrected$	isSig
g005909	0	0.002451	0	0.4163	0.7386	
g004420	$\operatorname{Inf}$	0.002451	2.402	$\operatorname{Inf}$	0.7386	

