

# Generate Panphlan related figures and analysis for the Paper

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## **pangenome**

### **read in pan matrix**

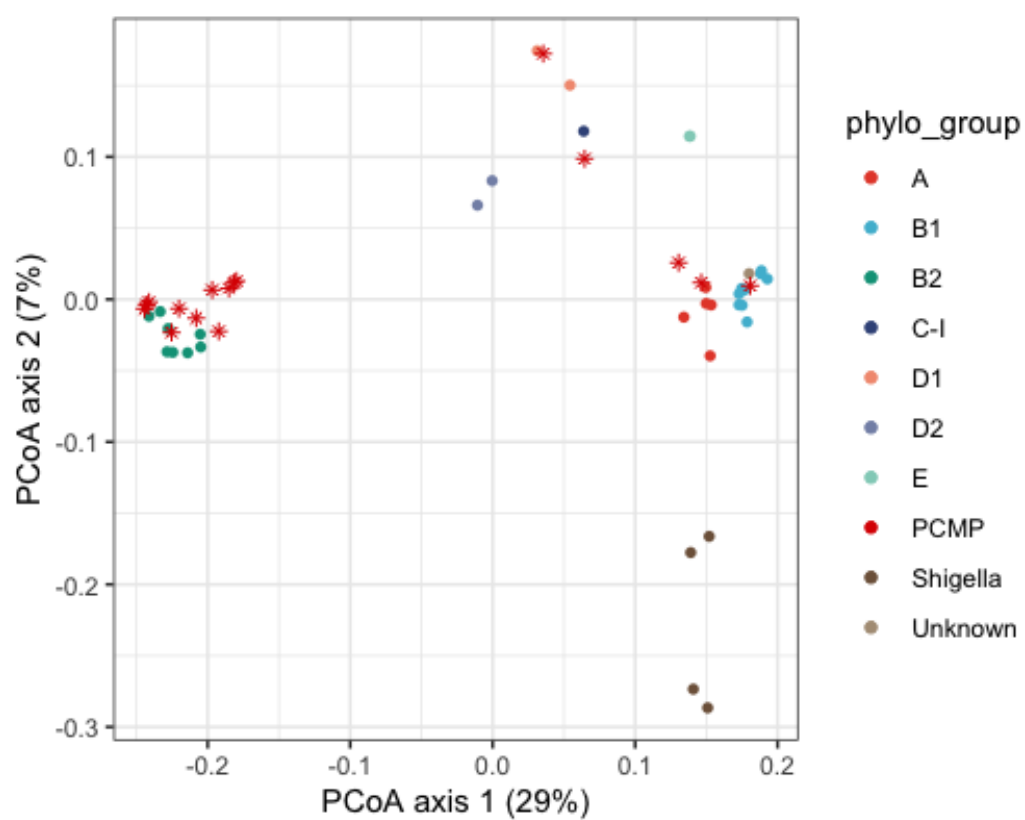
- read in result\_gene\_presence\_absence\_20180721.csv
- read in 20180714\_ecoli\_tree\_tip\_order.txt
- read in 20180604\_tree\_dd.txt
- read in 20171129\_E.coli\_strains\_summary.tsv

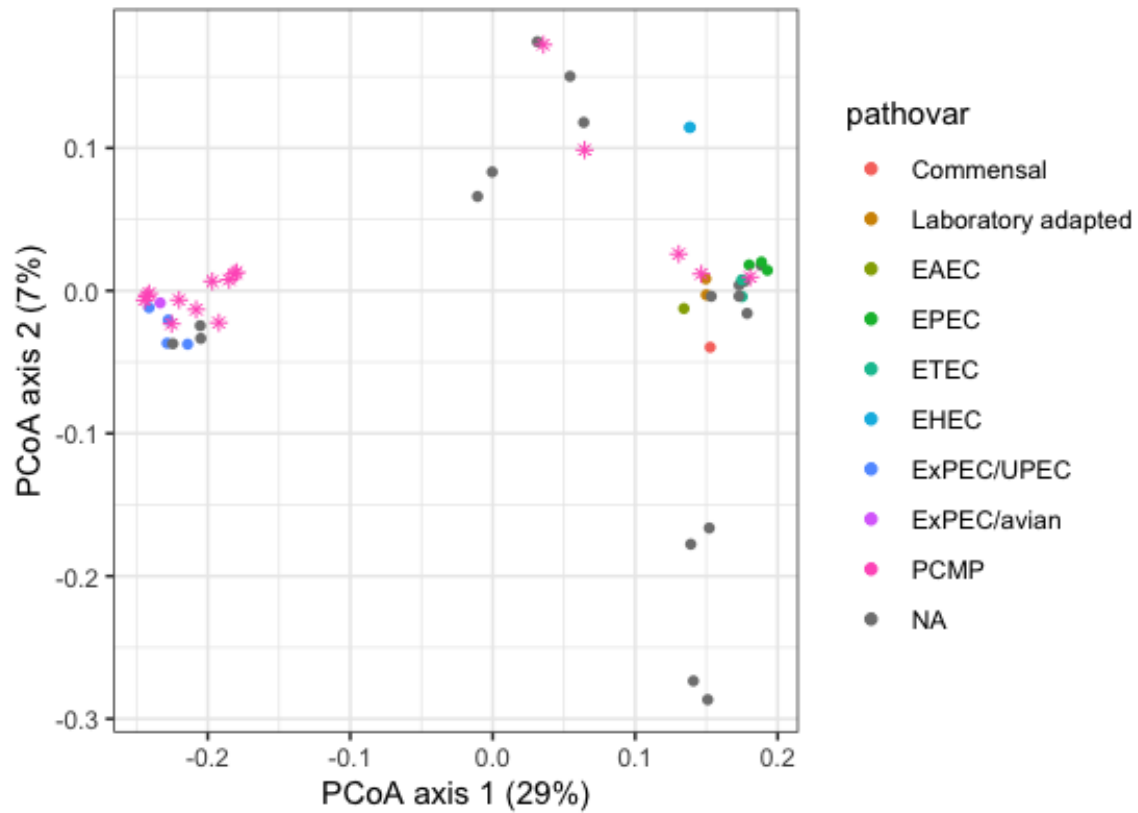
### **heatmap**

**20180714\_Fig2A\_pan\_heatmap.pdf**

**20180604\_pcoa.pdf**

Here, we use Jaccard distance to compare samples based on shared species membership. Plots are described above.





## 20181029 Hierarchical clustering based on Jaccard distance

```
## character(0)
## [1] "the missing strains from the panphaln analysis"
## [1] "s125"
## pdf
## 2
```

## 20180602 Fisher's exact test

- We compare the differential abundance of sparsely-sampled (rare) features using Fisher's exact test. Fisher's exact test models the sampling process according to a hypergeometric distribution (sampling without replacement)
- Plot fraction of samples in each group for which the taxon is present.
- filter out gene clusters show up in only two samples, or not show up in only two samples
- write 20180723\_Fig2D\_gene\_function.txt
- write 20180604\_fisher.pdf

```
## # A tibble: 2 x 2
##   Group      n
##   <chr>   <int>
## 1 non-PCMP 821474
## 2 PCMP    386576
```

Gene	estimate	p.value	conf.low	conf.high	fdr_corrected	isSig
g010729	83.02	1.76e-07	8.878	4206	0.001371	*
g019485	36.01	1.123e-06	5.887	418.2	0.004375	*
g003420	27.62	4.98e-06	4.93	225.4	0.007763	*
g008022	27.62	4.98e-06	4.93	225.4	0.007763	*
g011743	27.62	4.98e-06	4.93	225.4	0.007763	*
g008547	31.31	7.081e-06	4.947	370.3	0.009199	*
g003417	18.56	2.589e-05	3.667	134	0.02008	
g008000	18.56	2.589e-05	3.667	134	0.02008	
g021762	20.98	3.171e-05	3.705	228.2	0.02008	
g003413	24.14	3.824e-05	3.877	279.5	0.02008	

