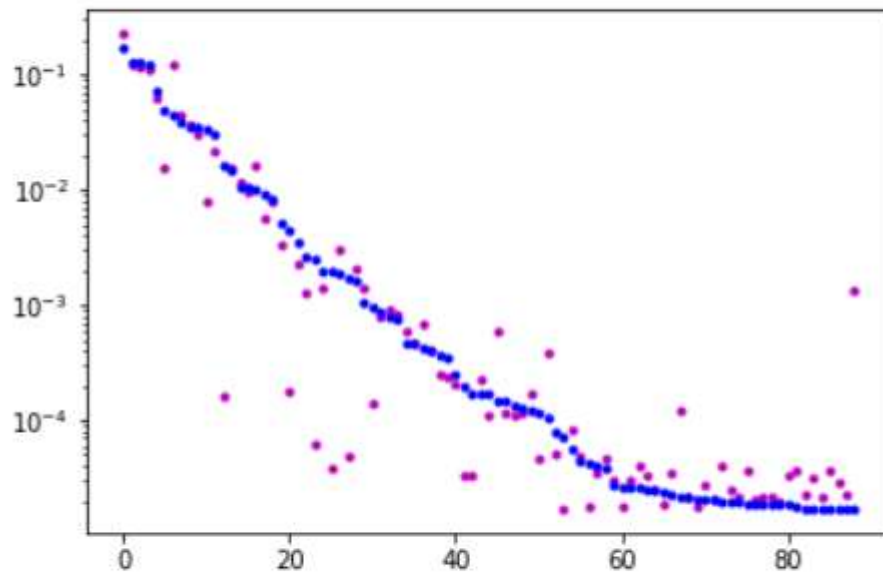


a)

i) At the genus level, there were total 89 OTUs and 506 samples id. The genera from v13 and v35 for tongue samples are positively correlated.

logrank abundance plot

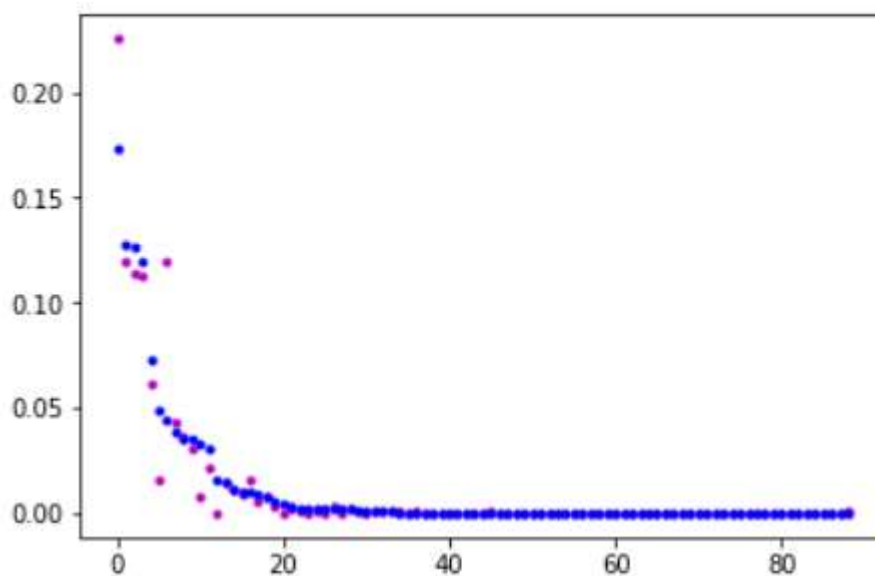


mean relative abundance: $r = 0.95$, $p = 0.00$

log mean relative abundance: $r = 0.91$, $p = 0.00$

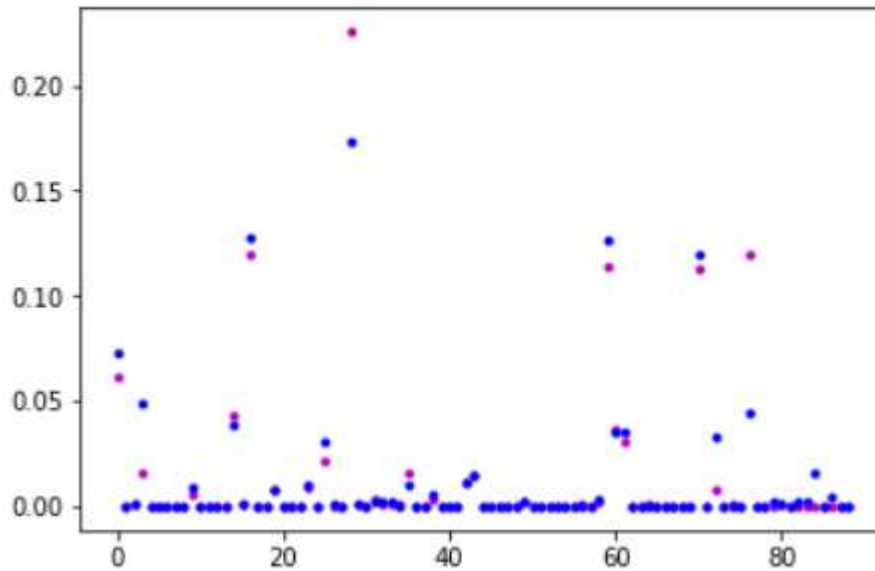
mean log relative abundance: $r = 0.94$, $p = 0.00$

rank abundance plot



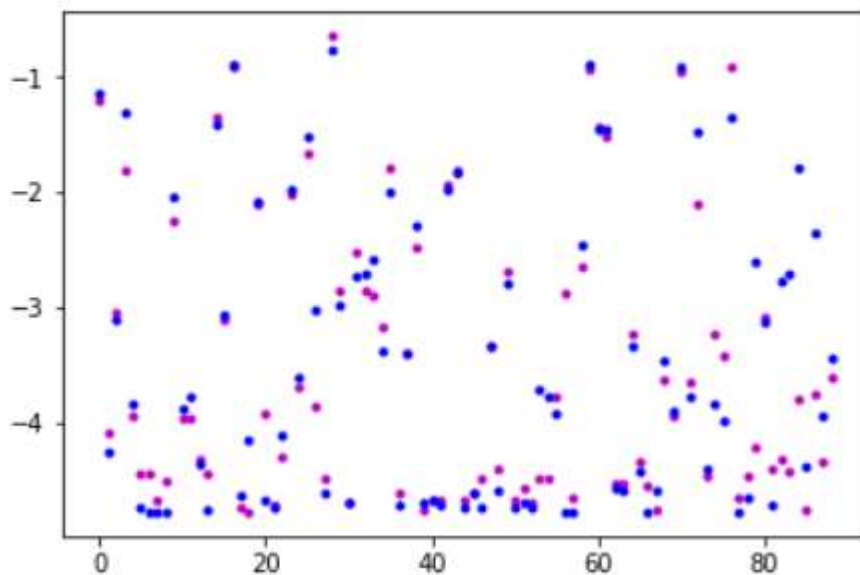
ii)

mean abundance plot



log mean abundance plot

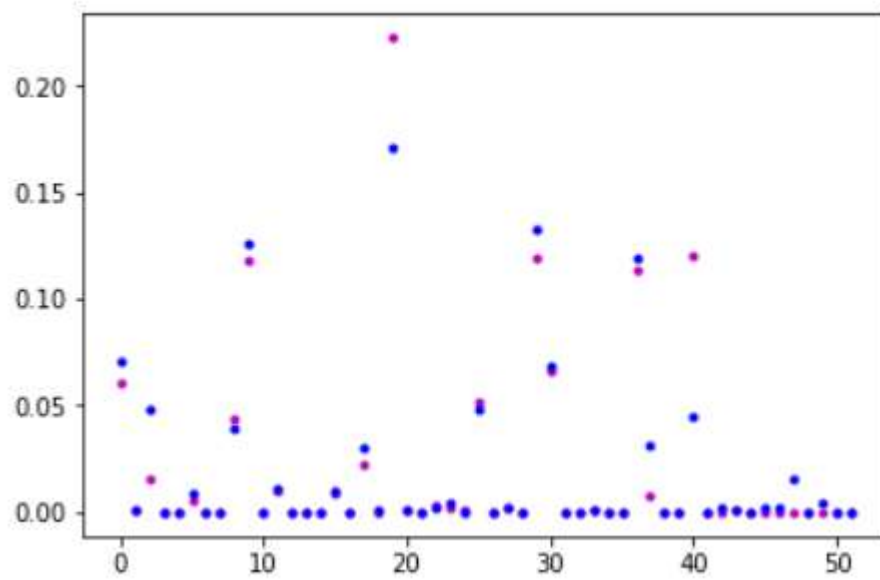
1.7024340432976753e-05



Family level:

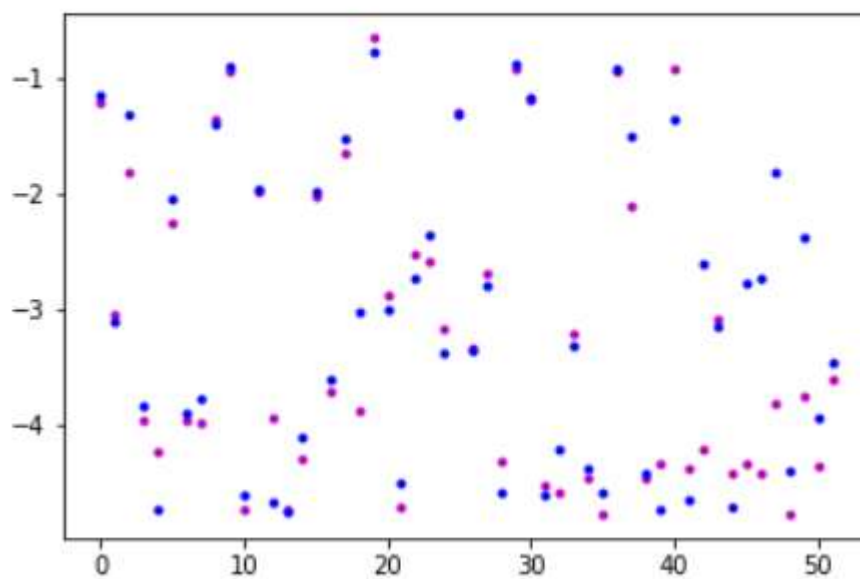
At family level, there are total number of 52 OTUs and 506 sample id. The genera from v13 and v35 for tongue samples are positively correlated.

mean abundance plot

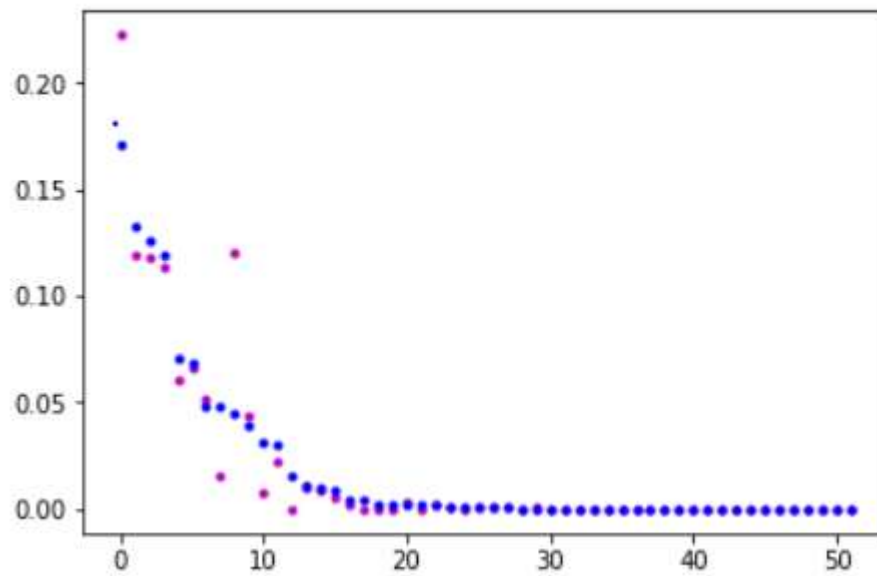


log mean abundance plot

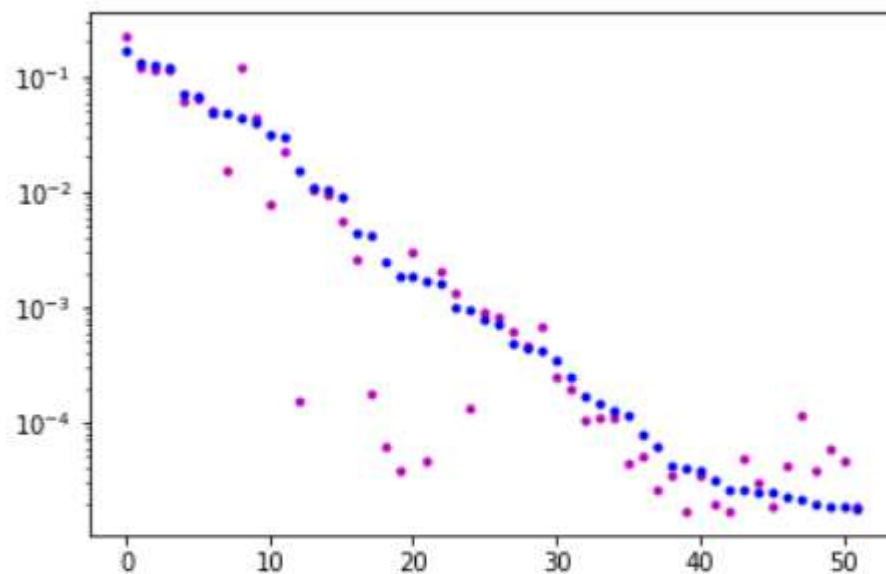
1.672346917461417e-05



rank abundance plot



logrank abundance plot



mean relative abundance: $r = 0.95$, $p = 0.00$

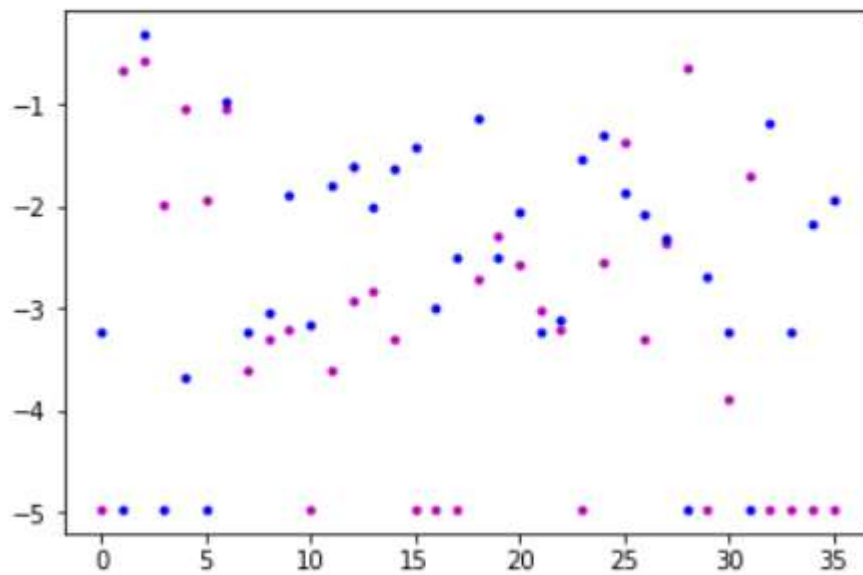
log mean relative abundance: $r = 0.91$, $p = 0.00$

mean log relative abundance: $r = 0.94$, $p = 0.00$

Species level: We cannot do species level analyses as 16S sequencing does not capture species level data at taxonomic level.

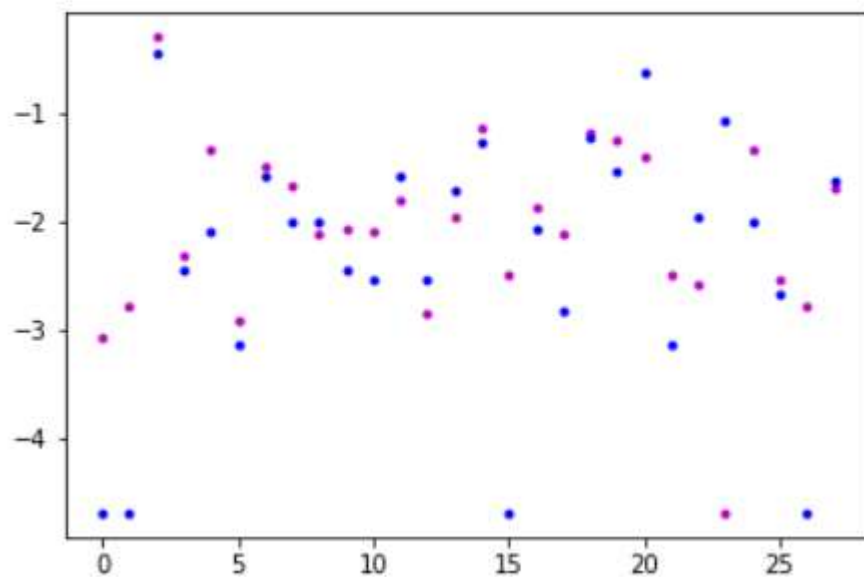
b)

log abundance plot of two people
1.0734220695577501e-05

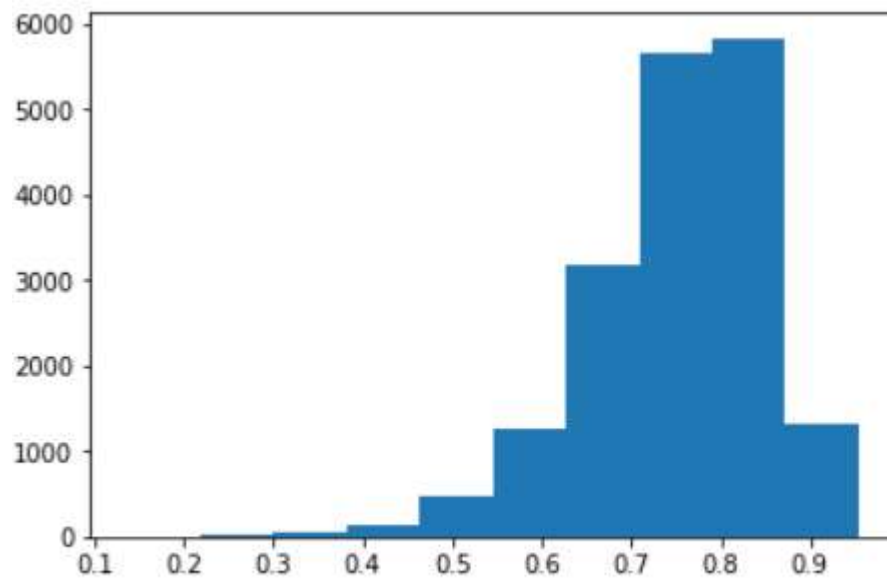


log abundances from the same person sampled at different times.

log abundance plot of two people
1.9966057701906758e-05



Correlation coefficients between log-transformed abundances computed for all pairs of different subjects is given below:

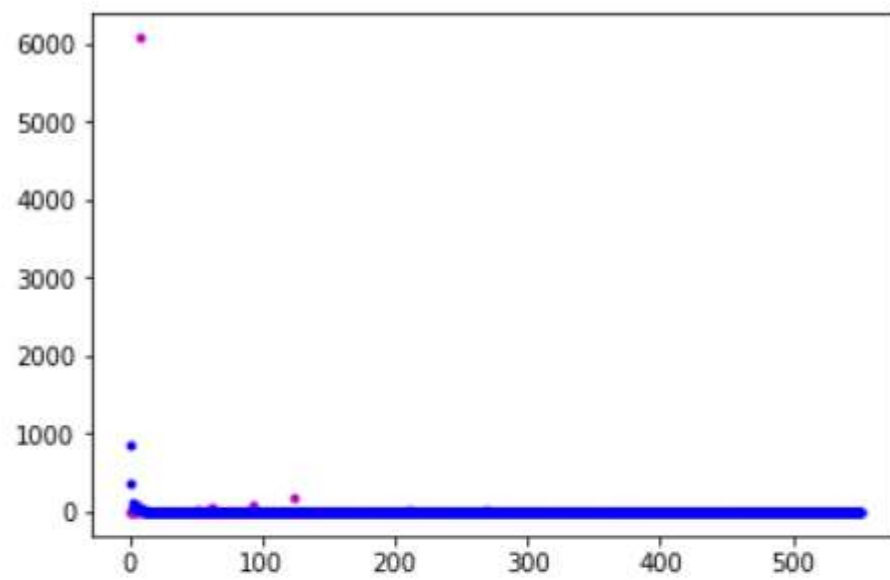


c)

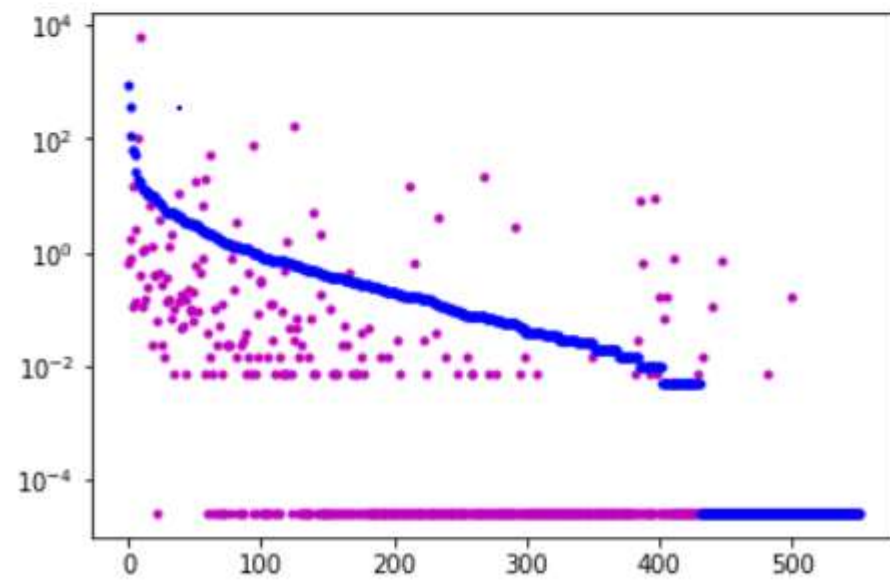
#'Left_Antecubital_fossa' has got most minimum diversity
#'Posterior_fornix' has got maximum diversity

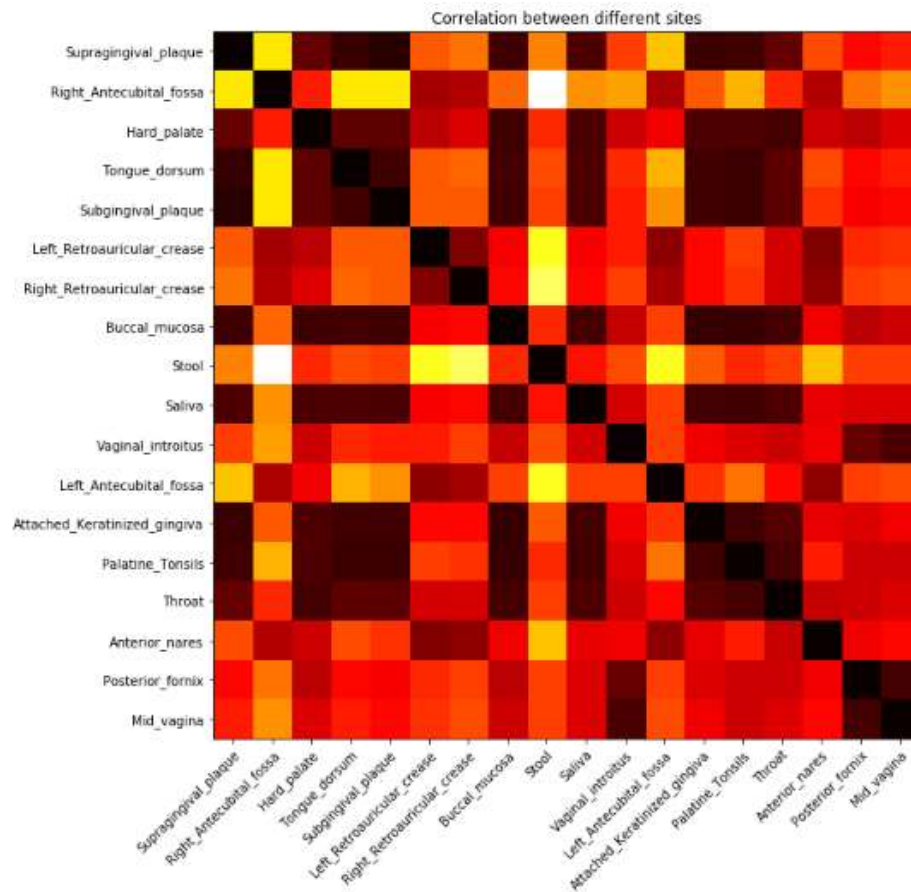
```
{'Anterior_nares': 4768.806691449814,
'Attached_Keratinized_gingiva': 5580.261980830671,
'Buccal_mucosa': 5708.592948717948,
'Hard_palate': 5639.798013245033,
'Left_Antecubital_fossa': 1988.6218905472638,
'Left_Retroauricular_crease': 5760.866666666667,
'Mid_vagina': 6157.067669172932,
'Palatine_Tonsils': 5470.727564102564,
'Posterior_fornix': 6673.0300751879695,
'Right_Antecubital_fossa': 2395.623188405797,
'Right_Retroauricular_crease': 5925.363636363636,
'Saliva': 4803.396551724138,
'Stool': 5761.69592476489,
'Subgingival_plaque': 5309.854368932039,
'Supragingival_plaque': 5511.137380191693,
'Throat': 5162.951140065146,
'Tongue_dorsum': 5892.762658227848,
'Vaginal_introitus': 6580.288}
```

rank abundance plot



logrank abundance plot





The sites related to closely related organ have formed cluster. For example, Hard palate, Tongue dorsum and Subgingival plaque are related to mouth have form clusters. Similarly, Attached Keratinized gingiva, Palatine Tonsils and Throat are closely grouped together.