

Culture independent assessment of human milk microbial community in lactational mastitis

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Supplementary Figure legends:

Supplementary Fig. 1: PCoA of Phylum to species level taxa revealed more pronounced clustering of healthy, SAM and AM samples at Genus and species level.

Supplementary Fig. 2: Dendrogram based on ward linkage clustering of OTU level taxa show different clustering of healthy, SAM and AM samples.

Supplementary Fig. 3: Heatmap representation of most abundant family level taxa in healthy, SAM and AM samples.

Supplementary Fig. 4: Aerotolerant odds ratio at 95% CI revealed depletion of obligate anaerobes during mastitis.

Supplementary Fig. 5: Relative proportion of different metabolic pathways at level 2 between healthy, SAM and AM samples.

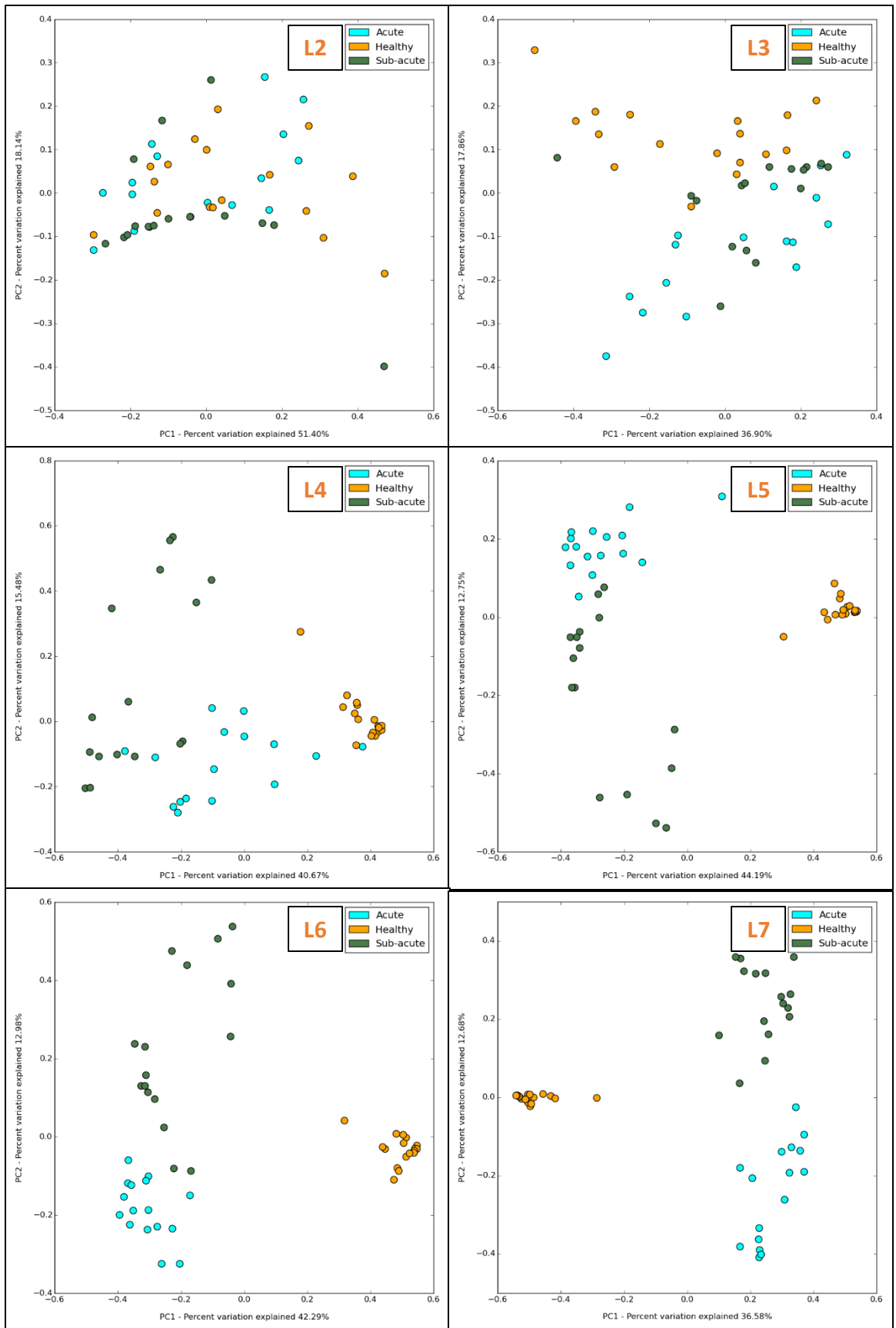
Supplementary Fig. 6: Predicted KEGG functions such as (a) immune system (b) metabolic disease and (c) infectious disease in individual healthy, SAM and AM samples.

Supplementary Table legends:

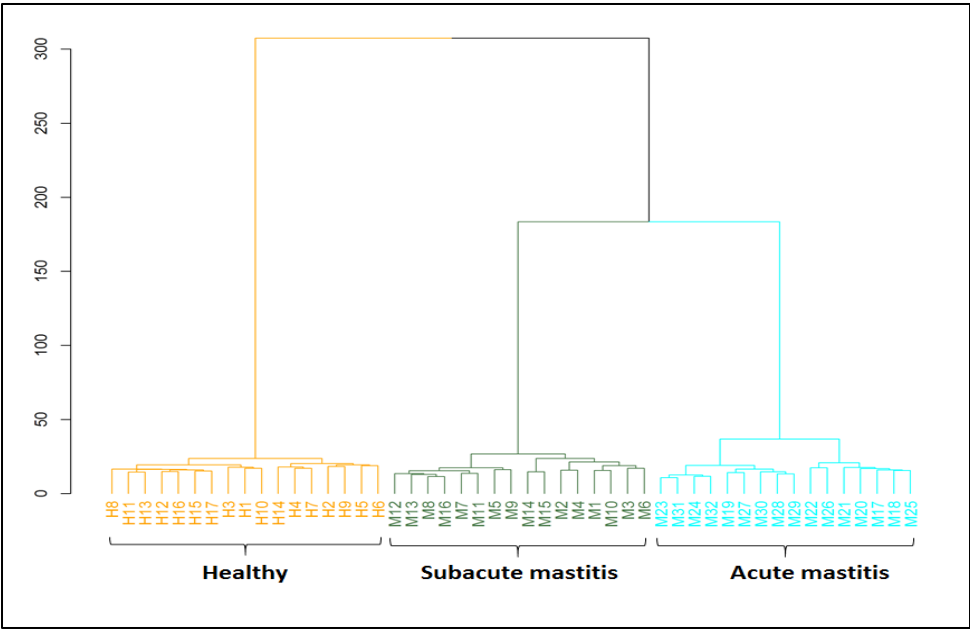
Supplementary Table 1: Characteristic of the participants involved in the study.

Supplementary Table 2: Summary of sequencing and alpha diversity indices.

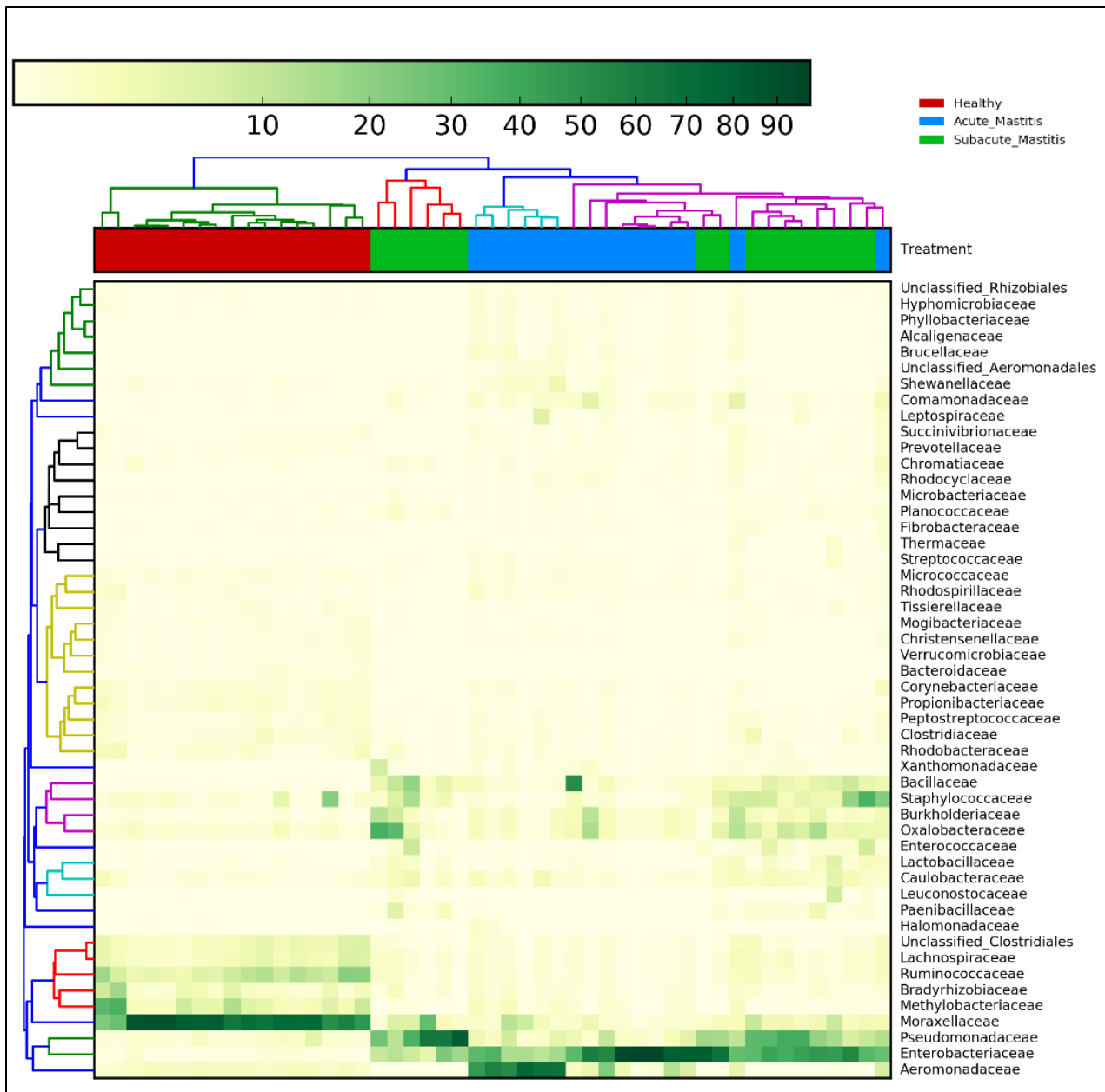
Supplementary Fig. 1



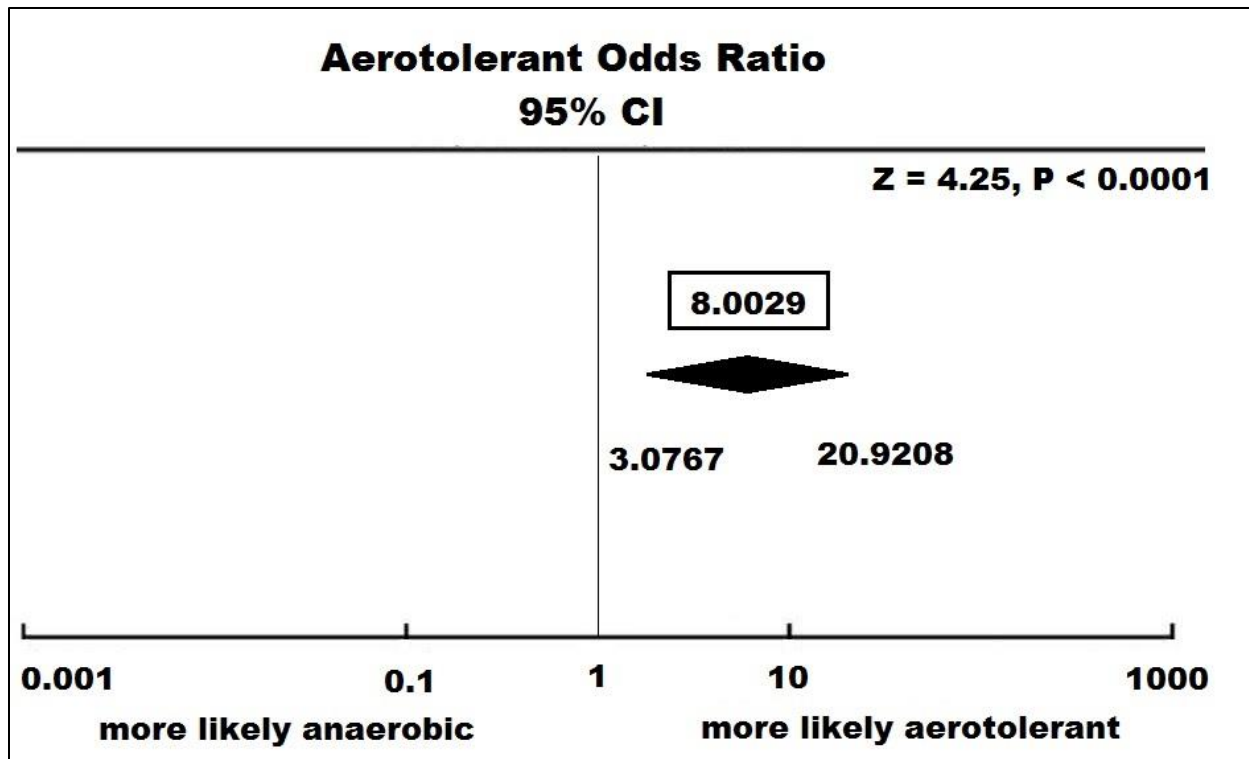
Supplementary Fig. 2



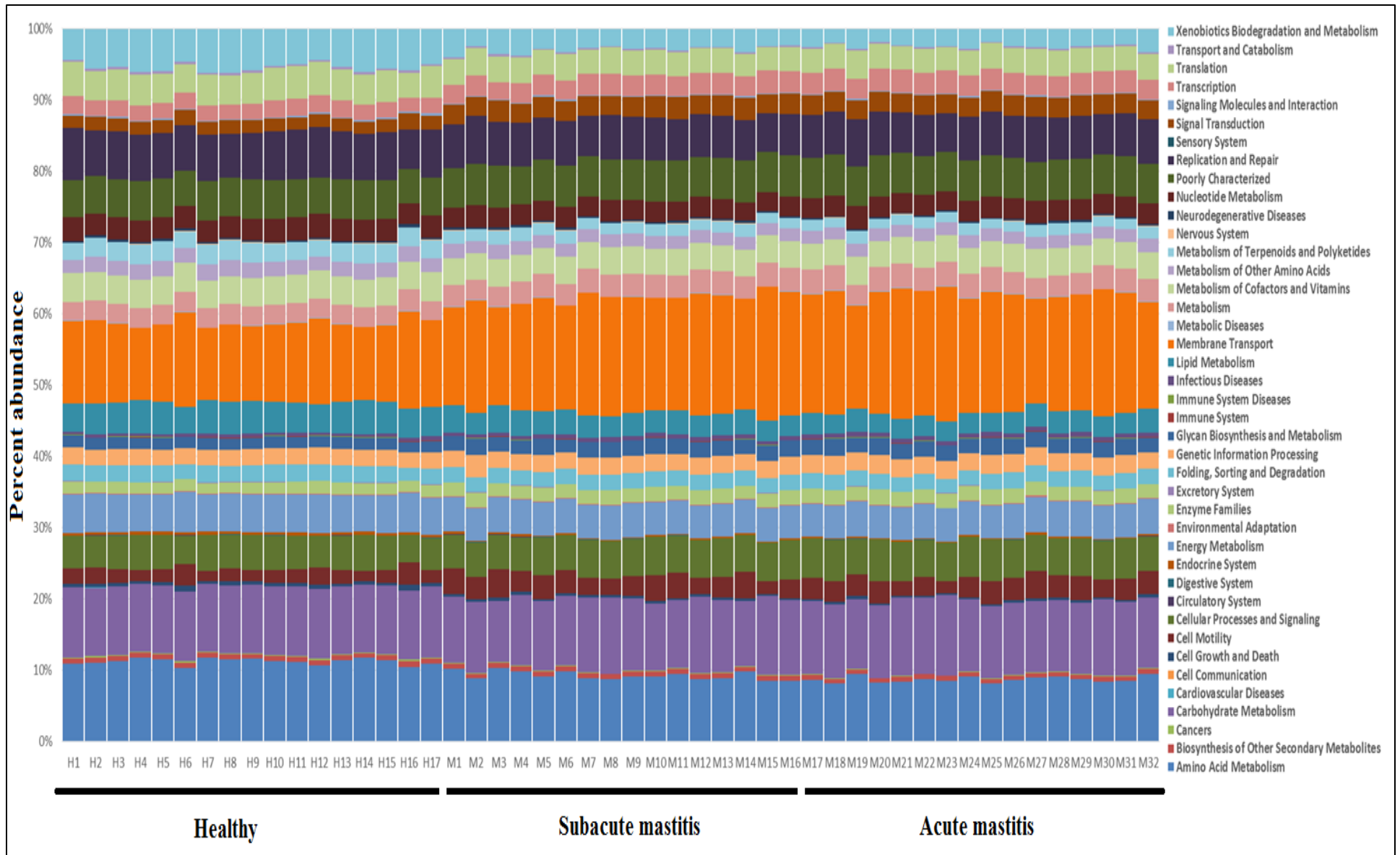
Supplementary Fig. 3



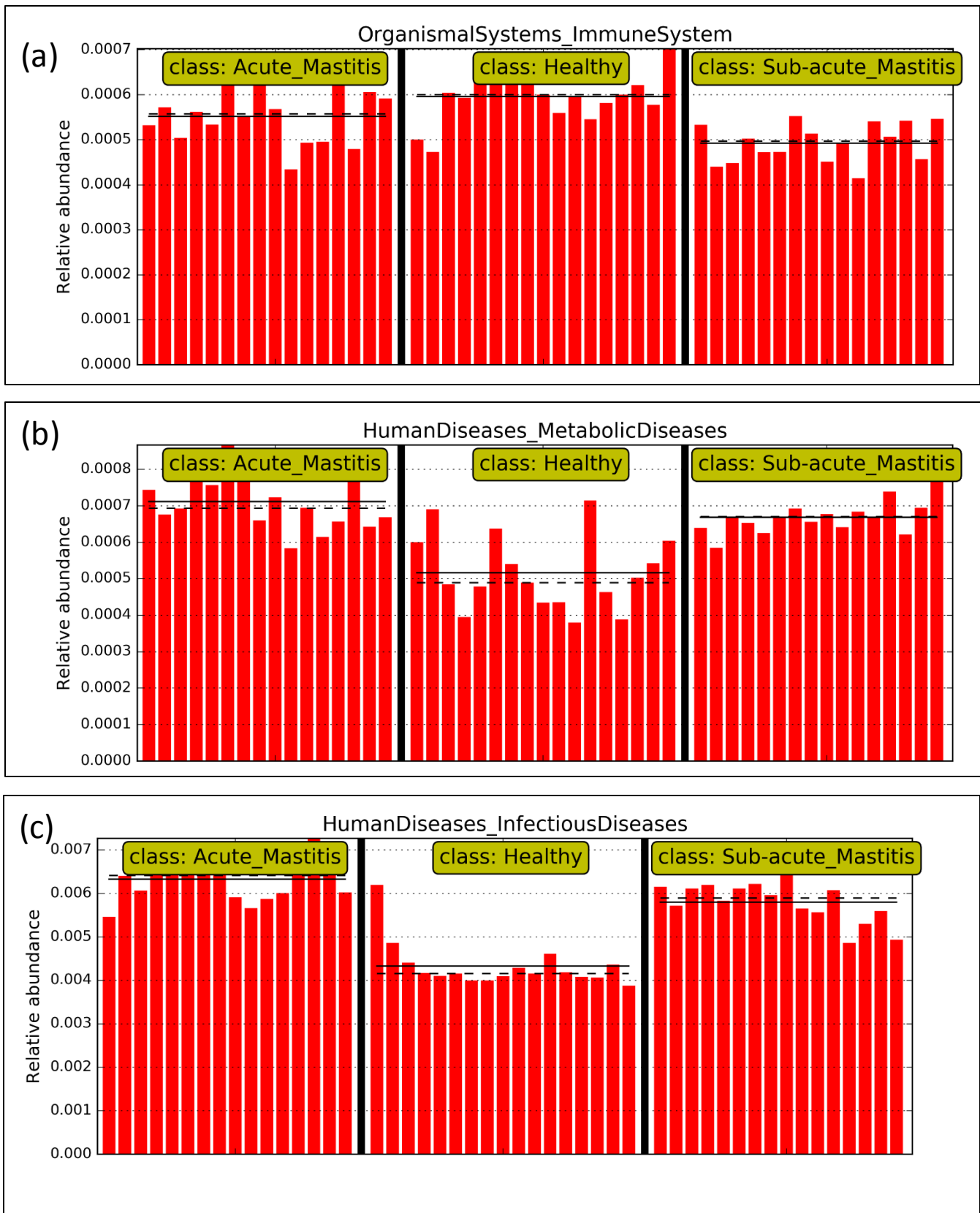
Supplementary Fig. 4



Supplementary Fig. 5:



Supplementary Fig. 6



Supplementary Table 1:

	Healthy	Subacute mastitis	Acute mastitis
Study population, n	18	16	16
Age, years \pm SD	25.29 \pm 1.82	25.93 \pm 2.37	26.12 \pm 1.31
Postpartum period, days \pm SD	20.58 \pm 4.04	24.93 \pm 3.92	24.75 \pm 2.97

Supplementary Table 2:

Sample Group	Raw sequences	Quality Filtered Sequences	Observed OTUs*	Phylogenetic diversity*
Healthy	1066028	839140	506 (297-788)	20.37 (14.29-27.98)
Subacute mastitis	962855	647843	430 (255-603)	12.01 (5.24-19.61)
Acute mastitis	1416549	655902	427 (206-764)	16.38 (7.60-29.13)

*Asterisk indicate calculation of alpha diversity indices after rarefaction to 4718 sequences per sample.