

## Supplementary Figure Legends

### Supplementary Figure 1: Bacterial microbiota beta diversity in HS, CD and UC

**(A,B)** Beta diversity. Principal Coordinate Analysis of Bray Curtis distance with each sample colored according to the disease phenotype. PC1, PC2, and PC3 represent the top three principal coordinates that captured most of the diversity. The fraction of diversity captured by the coordinate is shown as a percentage. Groups were compared using Permanova method. \* =  $p < 0.05$ ; \*\* =  $p < 0.01$ ; \*\*\* =  $p < 0.001$ .

### Supplementary Figure 2: Bacterial microbiota alpha diversity in HS, CD and UC

**(A)** OTUs number and Chao1 index **(B, C, D)** describing the alpha diversity of the bacterial microbiota in the various groups studied (Kruskal-Wallis test with Dunn's Multiple Comparison Test, \* =  $p < 0.05$ ; \*\* =  $p < 0.01$ ; \*\*\* =  $p < 0.001$ ).

### Supplementary Figure 3: Bacterial microbiota composition in HS, CD and UC

Global composition of bacterial microbiota at the **(A)** phyla, **(B)** family and **(C)** genus levels. HS and patient sub-groups are labeled on the x-axis and expressed as relative OTUs abundance for each group.

### Supplementary Figure 4: Fungal microbiota Beta diversity in HS, CD and UC

**(A, B, C)** Beta diversity. Principal Coordinate Analysis of the Bray-Curtis distance with each sample colored according to the disease phenotype. PC1, PC2, and PC3 represent the top three principal coordinates that captured most of the diversity. The fraction of diversity captured by the coordinate is shown as a percentage. Groups were compared using Permanova method. In all panels : \* =  $p < 0.05$ ; \*\* =  $p < 0.01$ ; \*\*\* =  $p < 0.001$

### Supplementary Figure 5: Fungal microbiota alpha diversity in HS, CD and UC

**(A)** OTUs number and Chao1 index **(B, C, D)** describing the alpha diversity of the fungal microbiota in the various groups studied. **(E, F, G)** ITS2/16S Chao1 index ratio (Kruskal-Wallis test with Dunn's Multiple Comparison Test, \* =  $p < 0.05$ ; \*\* =  $p < 0.01$ ).

### **Supplementary Figure 6: Fungal microbiota composition in HS, CD and UC**

Global composition of fungal microbiota at the **(A)** phyla, **(B)** family and **(C)** genus levels. HS and patient sub-groups are labeled on the x-axis and expressed as relative OTUs abundance for each group.

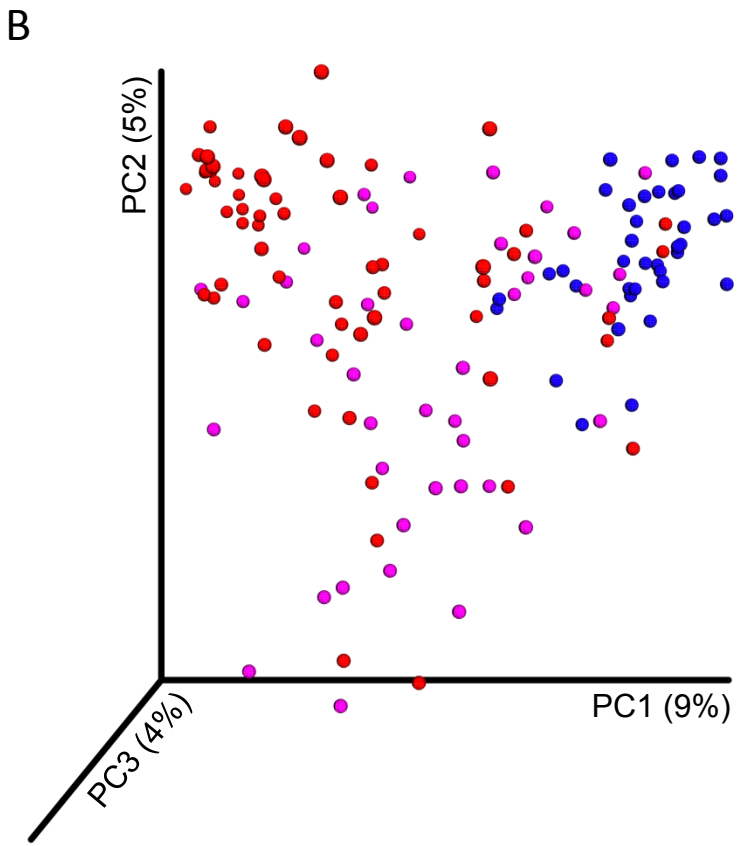
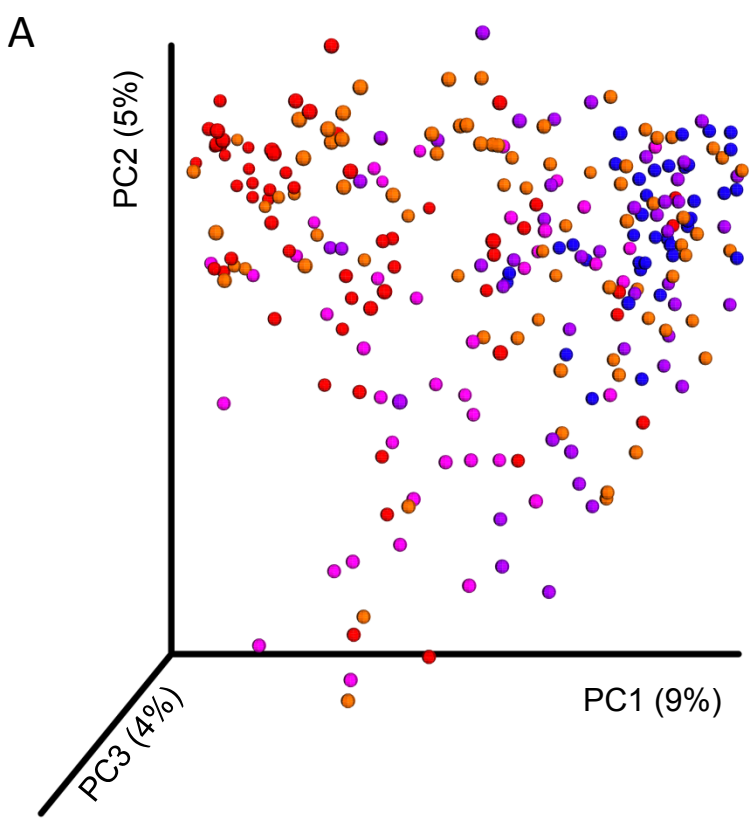
### **Supplementary Figure 7: Bacterial and fungal taxa associated with IBD flare**

Differences in abundance are shown for the **(A)** bacterial and **(B)** fungal taxa using a multivariate statistical approach (see Experimental Procedures). The fold change for each taxon was calculated by dividing the mean abundance in the cases by that of the controls. The number of subjects that have any presence (>0) of the indicated taxon is indicated in brackets and taxon with a mean abundance of >0.5% in at least one of the groups is indicated with "#". **(C)** *S. cerevisiae* levels in the fecal microbiota quantified using qRT-PCR (mean  $\pm$  s.e.m.). In all panels : \* =  $p < 0.05$ ; \*\* =  $p < 0.01$ ; \*\*\* =  $p < 0.001$

### **Supplementary Figure 8: Bacterial and Fungal taxa associated with ileal involvement in CD patients**

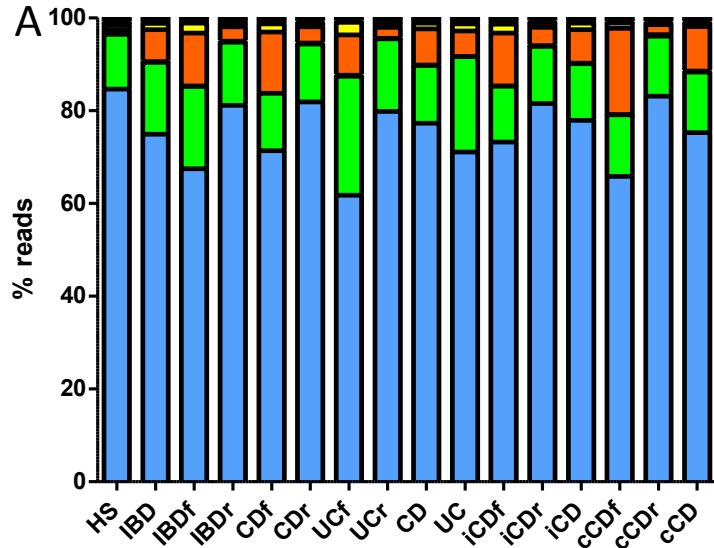
Differences in abundance are shown for the bacterial taxa detected using a multivariate statistical approach (see Experimental Procedures). The fold change for each taxon was calculated by dividing the mean abundance in the cases by that of the controls. The number of subjects that have any presence (>0) of the indicated taxon is indicated in brackets and taxon with a mean abundance of >0.5% in at least one of the groups is indicated with "#". \* =  $p < 0.05$ ; \*\* =  $p < 0.01$ ; \*\*\* =  $p < 0.001$

**Supplementary Figure 9: Relative proportion of *S. cerevisiae* (A, B) and *C. albicans* (C) in the fecal microbiota quantified using qRT-PCR (mean  $\pm$  s.e.m.). In all panels : \* =  $p < 0.05$ ; \*\* =  $p < 0.01$ ; \*\*\* =  $p < 0.001$**

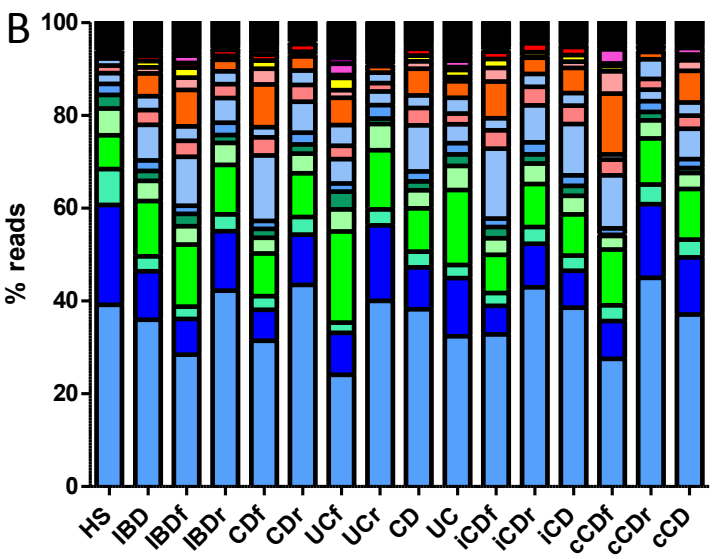




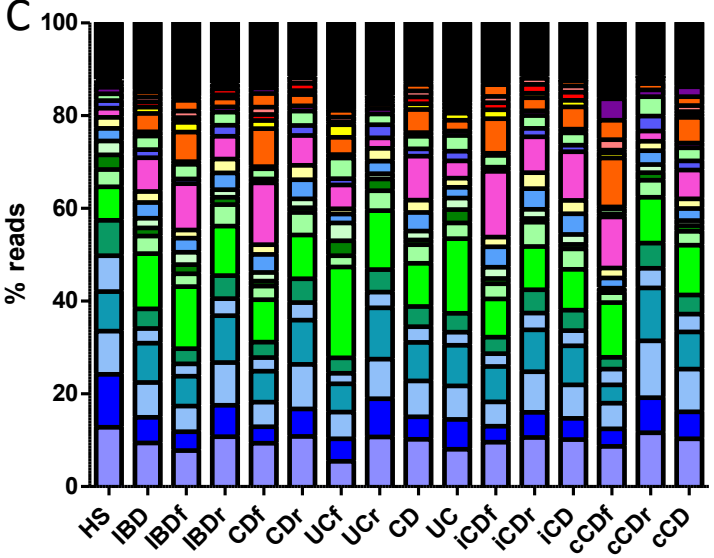
Phyla

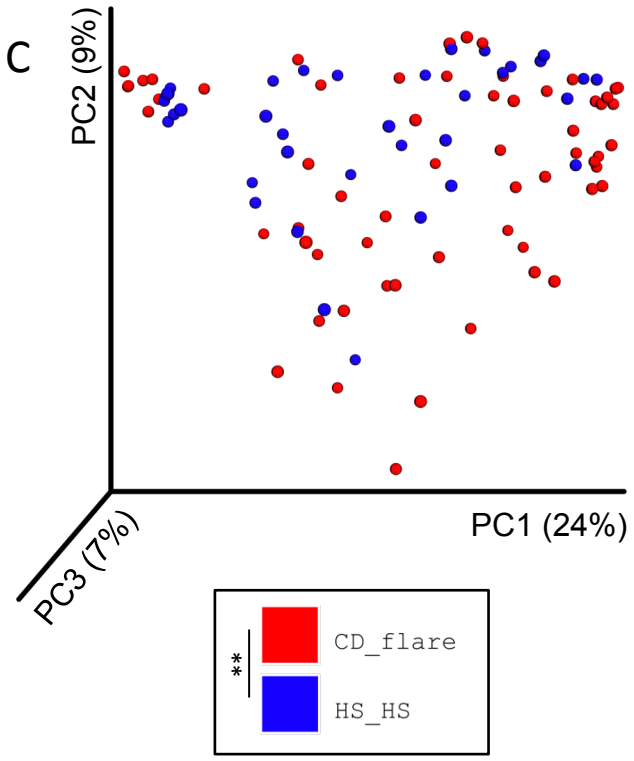
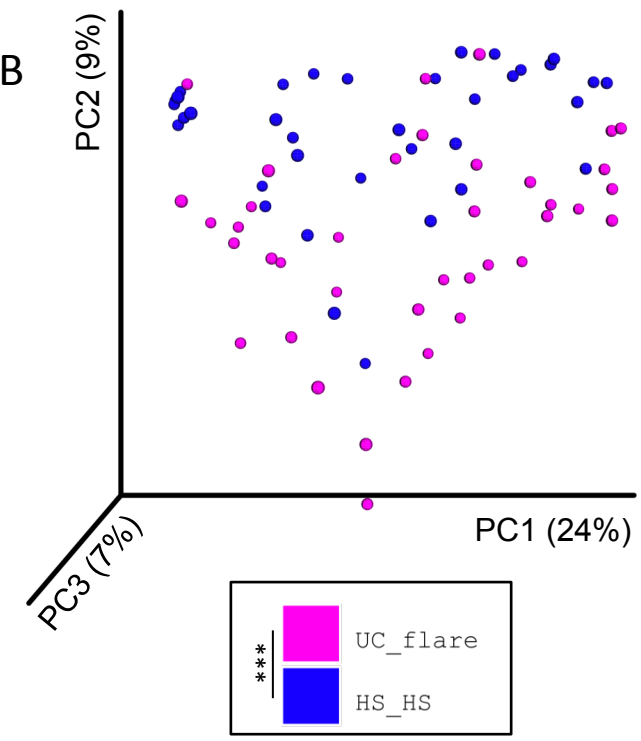
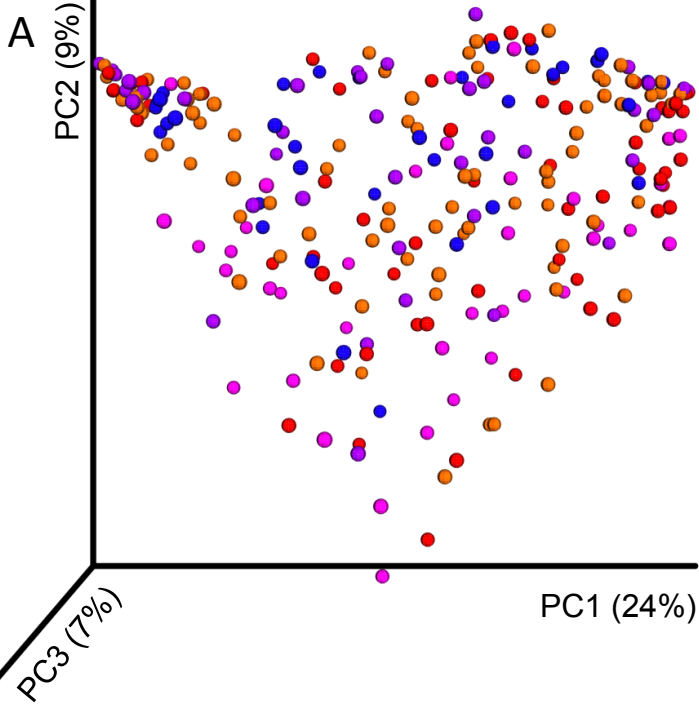


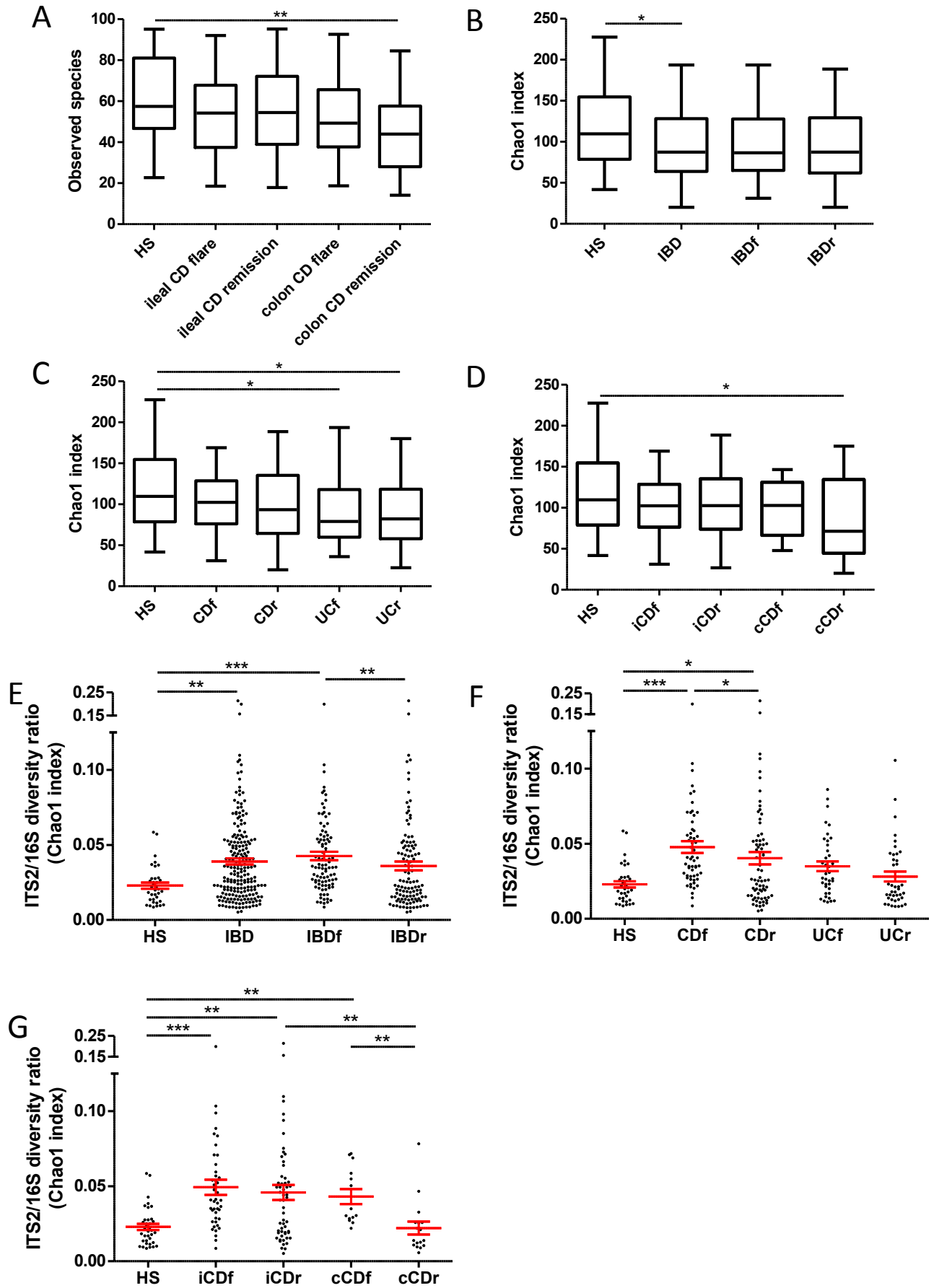
Family



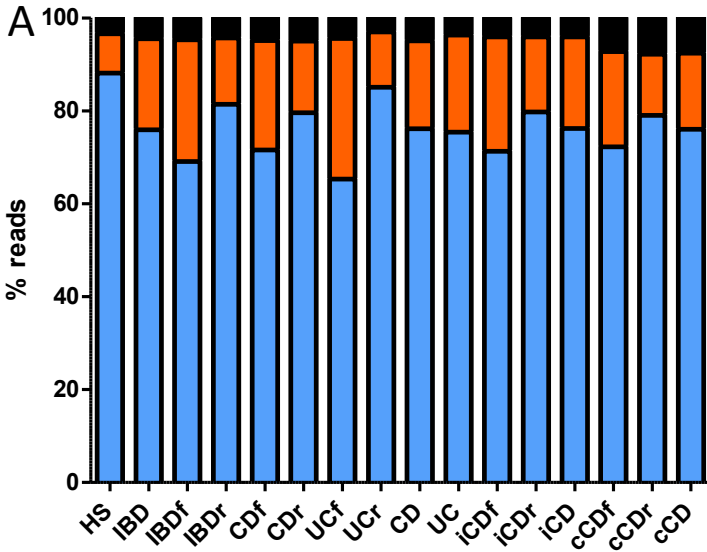
Genus



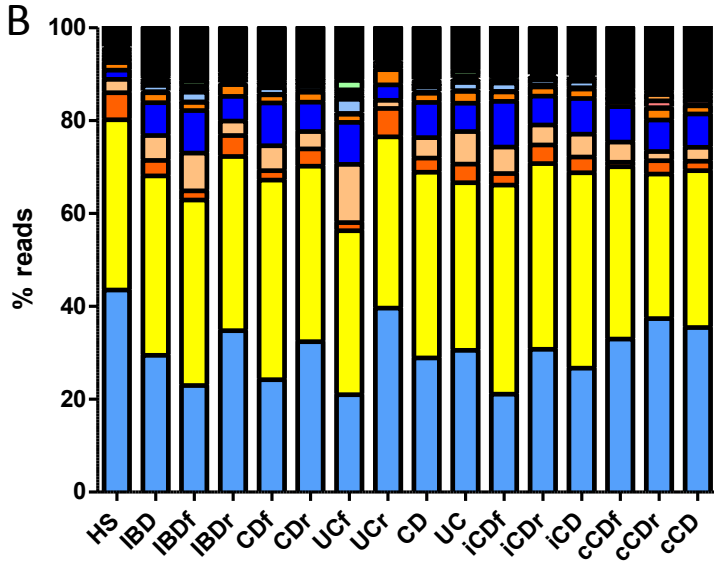




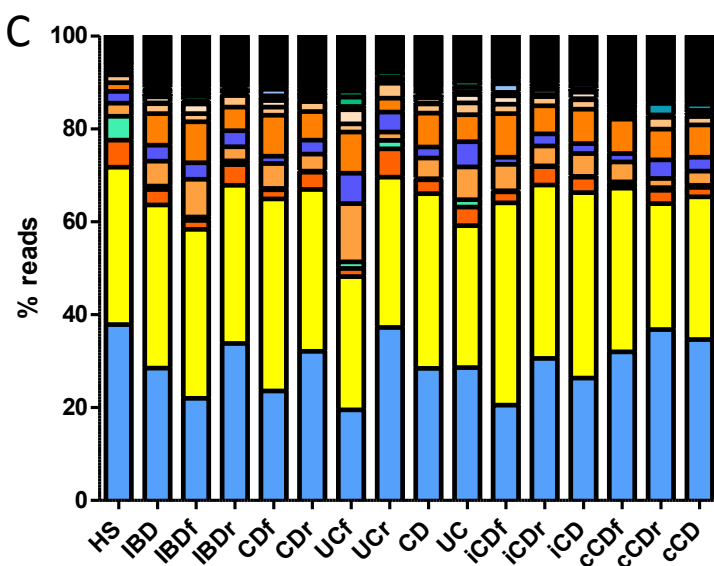
Phyla



Family



Genus





Decreased in flare      Increased in flare

