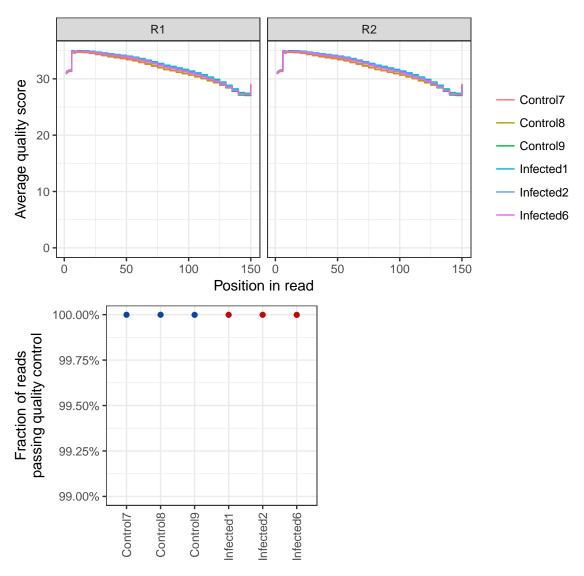
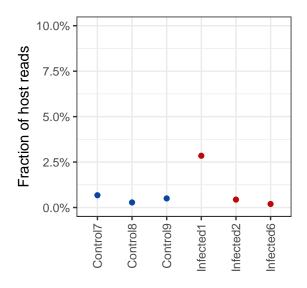
Metagenomics Workshop Report

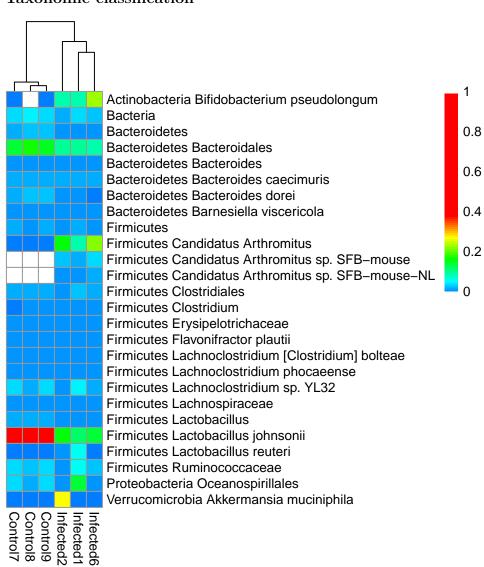
November 8, 2017

Quality Control

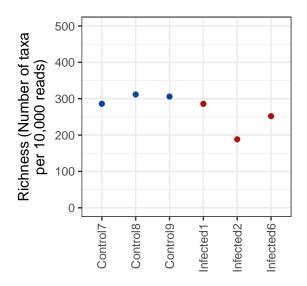




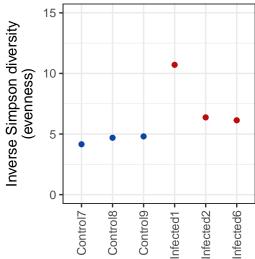
Taxonomic classification



Alpha diversity analysis

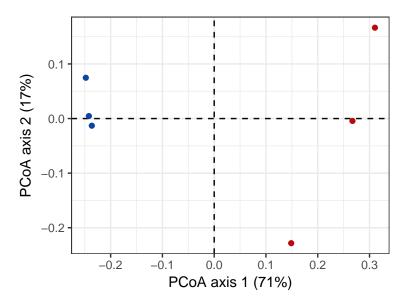


```
##
## Wilcoxon rank sum test
##
## data: Richness10k by study_group
## W = 9, p-value = 0.1
## alternative hypothesis: true location shift is not equal to 0
```



```
##
## Wilcoxon rank sum test
##
## data: InvSimpson by study_group
## W = 0, p-value = 0.1
## alternative hypothesis: true location shift is not equal to 0
```

Beta diversity analysis

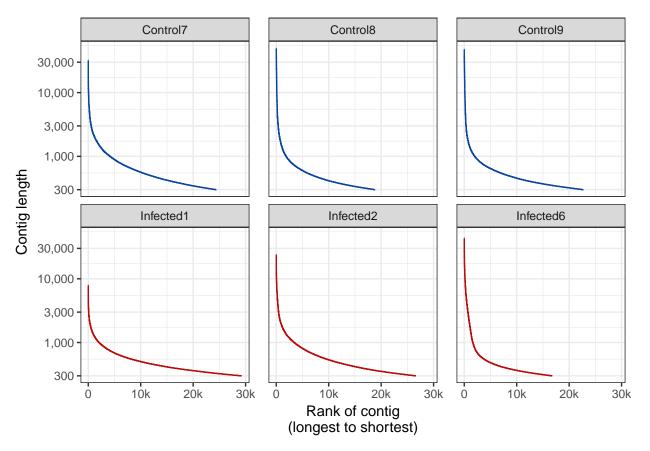


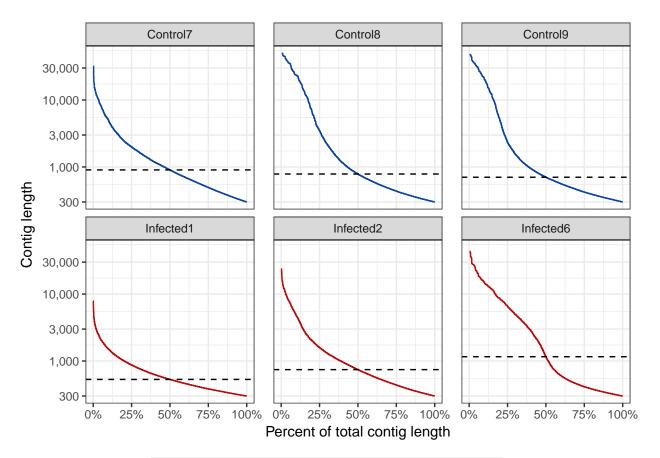
Test for difference in group centroids.

```
##
## Call:
## adonis(formula = bc ~ study_group, data = s)
## Permutation: free
## Number of permutations: 719
## Terms added sequentially (first to last)
##
               Df SumsOfSqs MeanSqs F.Model
                                                   R2 Pr(>F)
## study_group
                    0.35463 0.35463 8.9694 0.69158
                    0.15815 0.03954
## Residuals
                                              0.30842
                4
## Total
                5
                    0.51278
                                              1.00000
Test for difference in group dispersion.
```

```
## Permutation test for homogeneity of multivariate dispersions
## Permutation: free
## Number of permutations: 719
##
## Response: Distances
                 Sum Sq Mean Sq
                                      F N.Perm
             1 0.038298 0.038298 20.842
                                          719 0.001389 **
## Groups
## Residuals 4 0.007350 0.001838
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
```

Metagenomic assembly results





SampleID	Group	Total length	Longest contig	N50
Control7	Control	18,649,294	32,165	903
Control8	Control	13,834,766	49,778	784
Control9	Control	$15,\!691,\!027$	47,804	702
Infected1	Infected	15,689,336	7,934	531
Infected2	Infected	18,108,370	23,955	744
Infected6	Infected	$13,\!191,\!667$	43,455	$1,\!159$

Antibiotic resistance gene database (CARD) results

SampleID	contig	length	card
Control7	cap3-contigs.fa2216	1440	gb M18896 + 0-1920 ARO:3000190 tetO
Control7	cap3-contigs.fa8723	620	gb M18896 + 0-1920 ARO:3000190 tetO
Control8	cap3-contigs.fa16754	319	gb AP006618.1 + 4835199-4838688 ARO:3000501 Nocardia
Control8	cap3-contigs.fa18519	302	gb M18896 + 0-1920 ARO:3000190 tetO
Control9	cap3-contigs.fa20770	314	gb M18896 + 0-1920 ARO:3000190 tetO
Control9	cap3-contigs.fa11725	418	gb M18896 + 0-1920 ARO:3000190 tetO
Control9	cap3-contigs.fa15461	364	gb M18896 + 0-1920 ARO:3000190 tetO
Control9	cap3-contigs.fa14893	371	gb AJ295238 + 0-1920 ARO:3000196 tet32
Control9	cap3-contigs.fa3510	759	gb M18896 + 0-1920 ARO:3000190 tetO
Control9	cap3-contigs.fa10893	434	gb M18896 + 0-1920 ARO:3000190 tetO
Infected1	cap3-contigs.fa25711	320	gb AJ295238 + 0-1920 ARO:3000196 tet32
Infected1	cap3-contigs.fa14717	419	gb FN594949 + 25244-27167 ARO:3000556 tet44
Infected2	cap3-contigs.fa664	2348	gb Z21523 + 0-1974 ARO:3000191 tetQ
Infected2	cap3-contigs.fa25220	309	$gb NC_007779 + 2586250-2589364 ARO:3000491 acrD$
Infected2	cap3-contigs.fa22531	330	gb X98831.1 + 361-1555 ARO:3003359 Streptomyces
Infected2	cap3-contigs.fa5696	751	gb Z21523 + 0-1974 ARO:3000191 tetQ
Infected6	cap3-contigs.fa6461	433	${\rm gb NC_014638 \text{-} 1610636\text{-}1613960 ARO\text{:}3003730 Bifidobacteria}$
Infected6	cap3-contigs.fa44	16589	gb AP006618.1 + 4835199-4838688 ARO:3000501 Nocardia
Infected6	cap3-contigs.fa10680	356	${\rm gb NC_014638 16106361613960 ARO:3003730 Bifidobacteria}$
Infected6	cap3-contigs.fa11957	342	gb M18896 + 0-1920 ARO:3000190 tetO