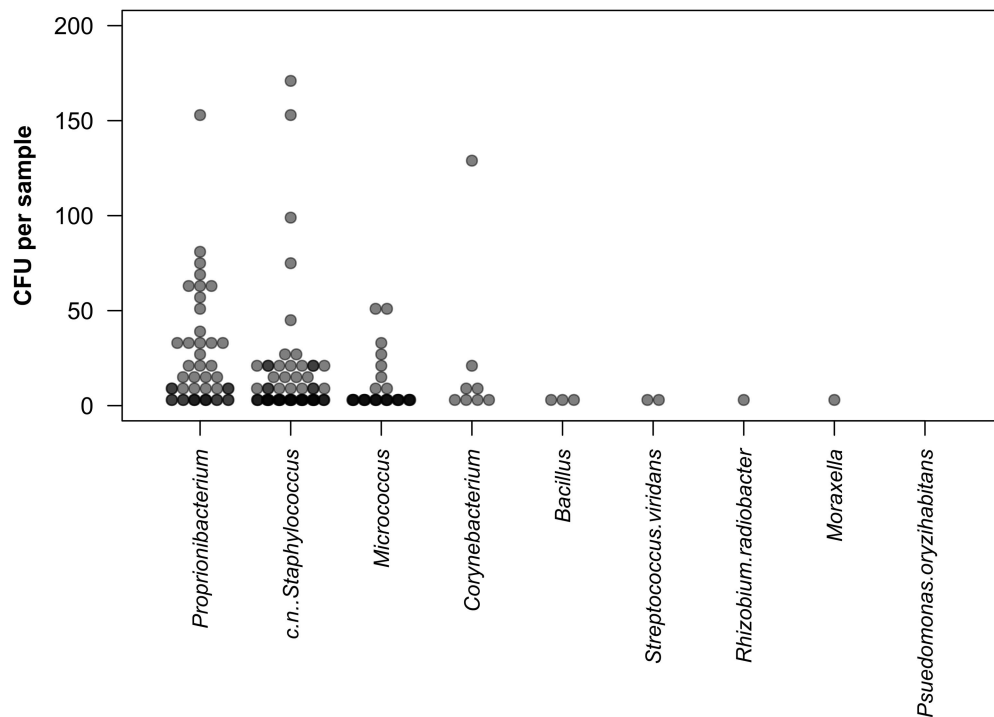**Supplementary Information**

Temporal Stability and Composition of the Ocular Surface Microbiome

Jerome Ozkan, Shaun Nielsen, Cristina Diez-Vives, Minas Coroneo,
Torsten Thomas, Mark Willcox

Supplementary Figure 1: Colony forming units per swab of bacterial taxa isolated from the ocular surface from 43 subjects sampled monthly for three months (n = 132)
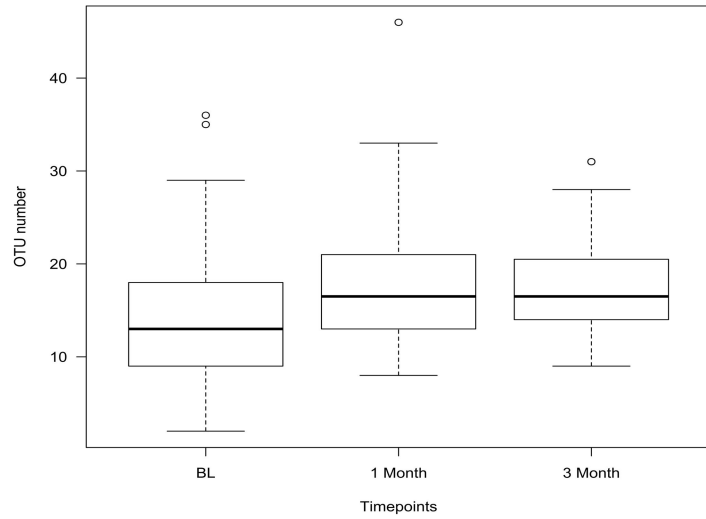

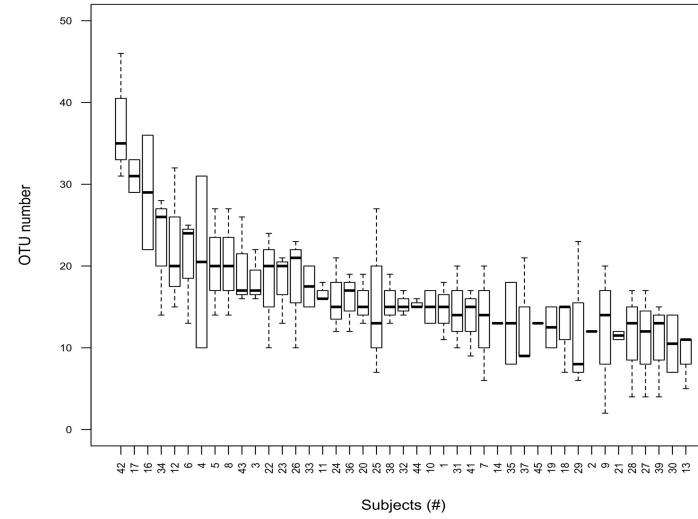**Supplementary Figure 2:** OTU rarefaction
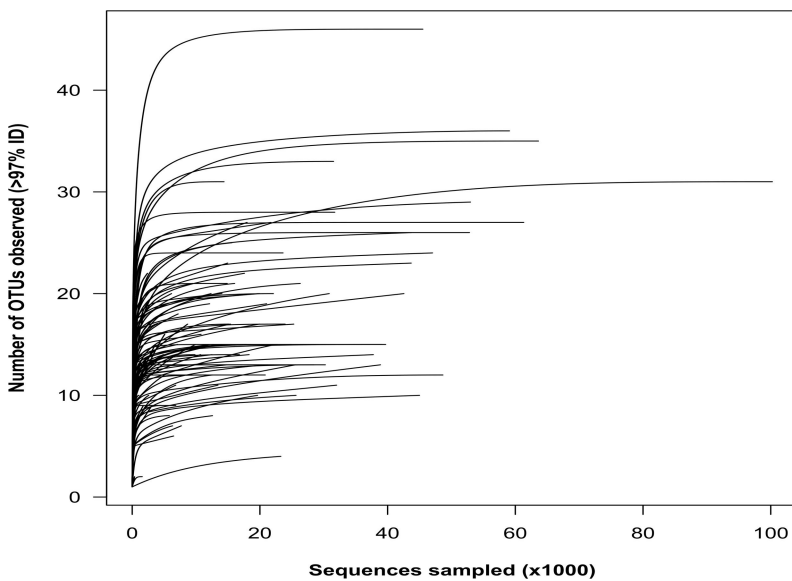
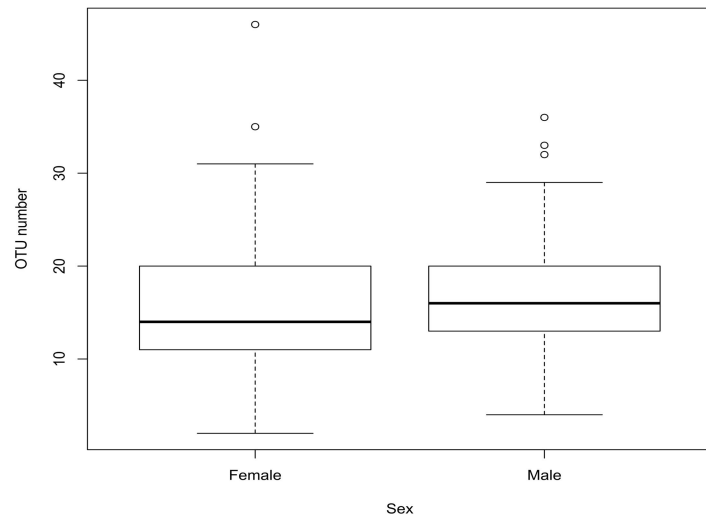**Supplementary Figure 3:** Microbial richness at OTU level for **(a)** time, **(b)** individuals, **(c)** sex, and **(d)** age
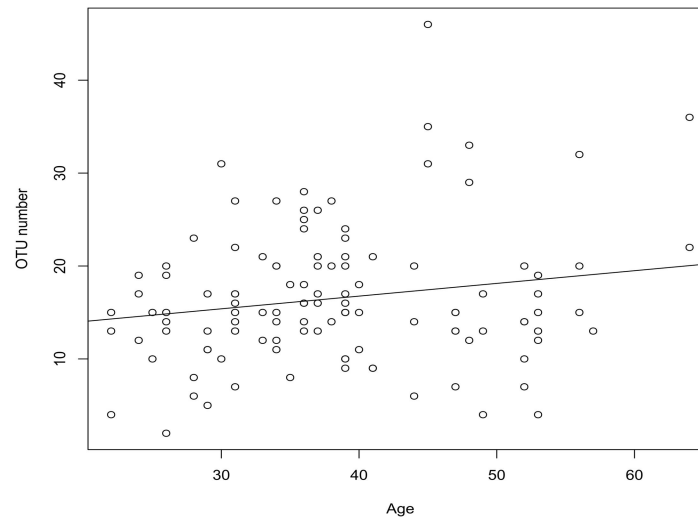
Supplementary Figure 4: Shannon diversity index at OTU level for, **(a)** time, **(b)** individuals, **(c)** sex and **(d)** age
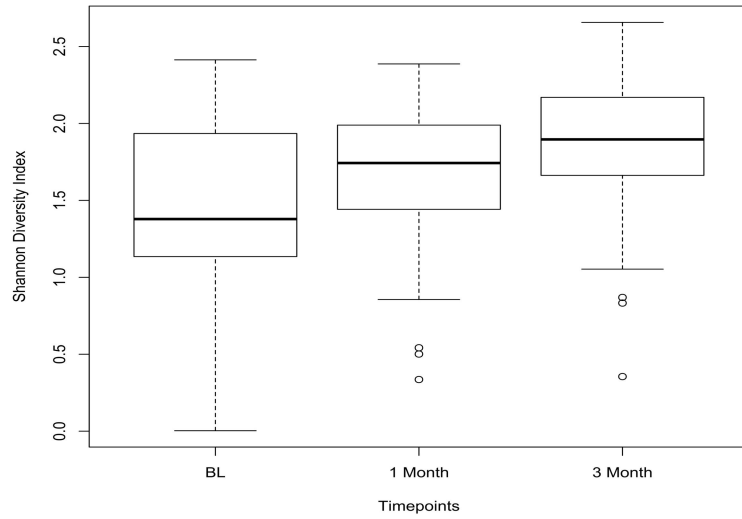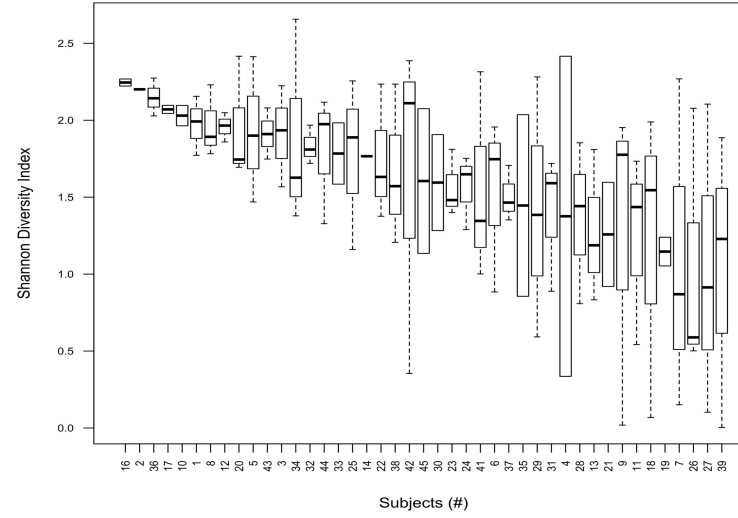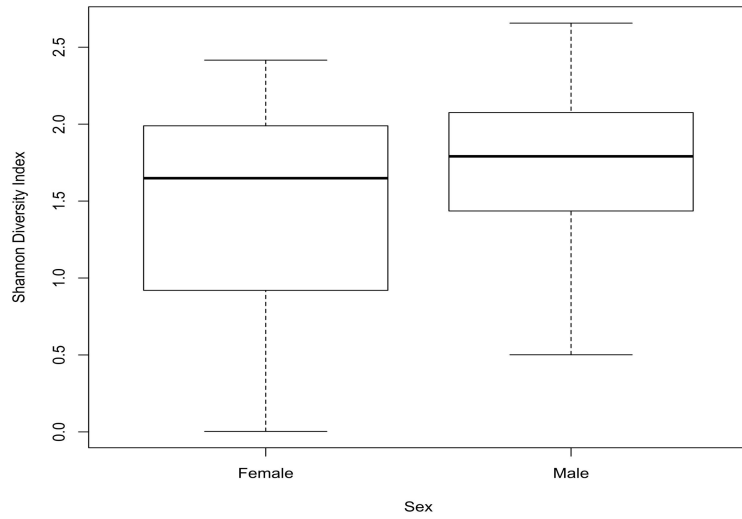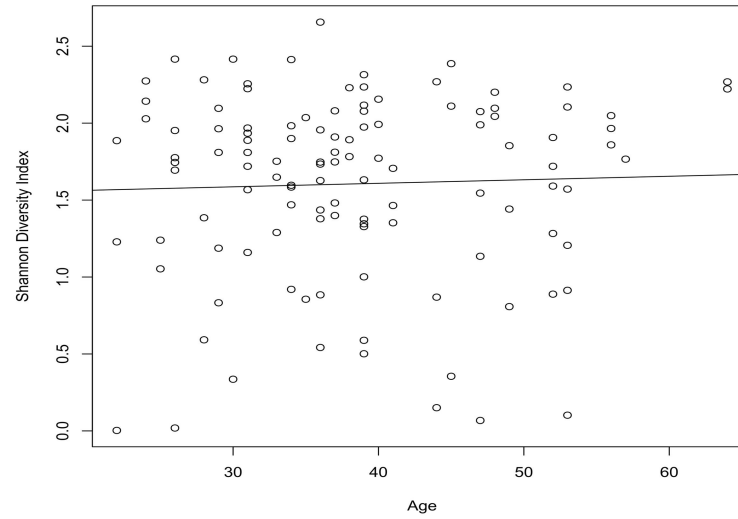
Supplementary Figure 5: Relative abundance at the level of, **(a)** phylum, **(b)** genus

(a) Phylum

(b) Genus
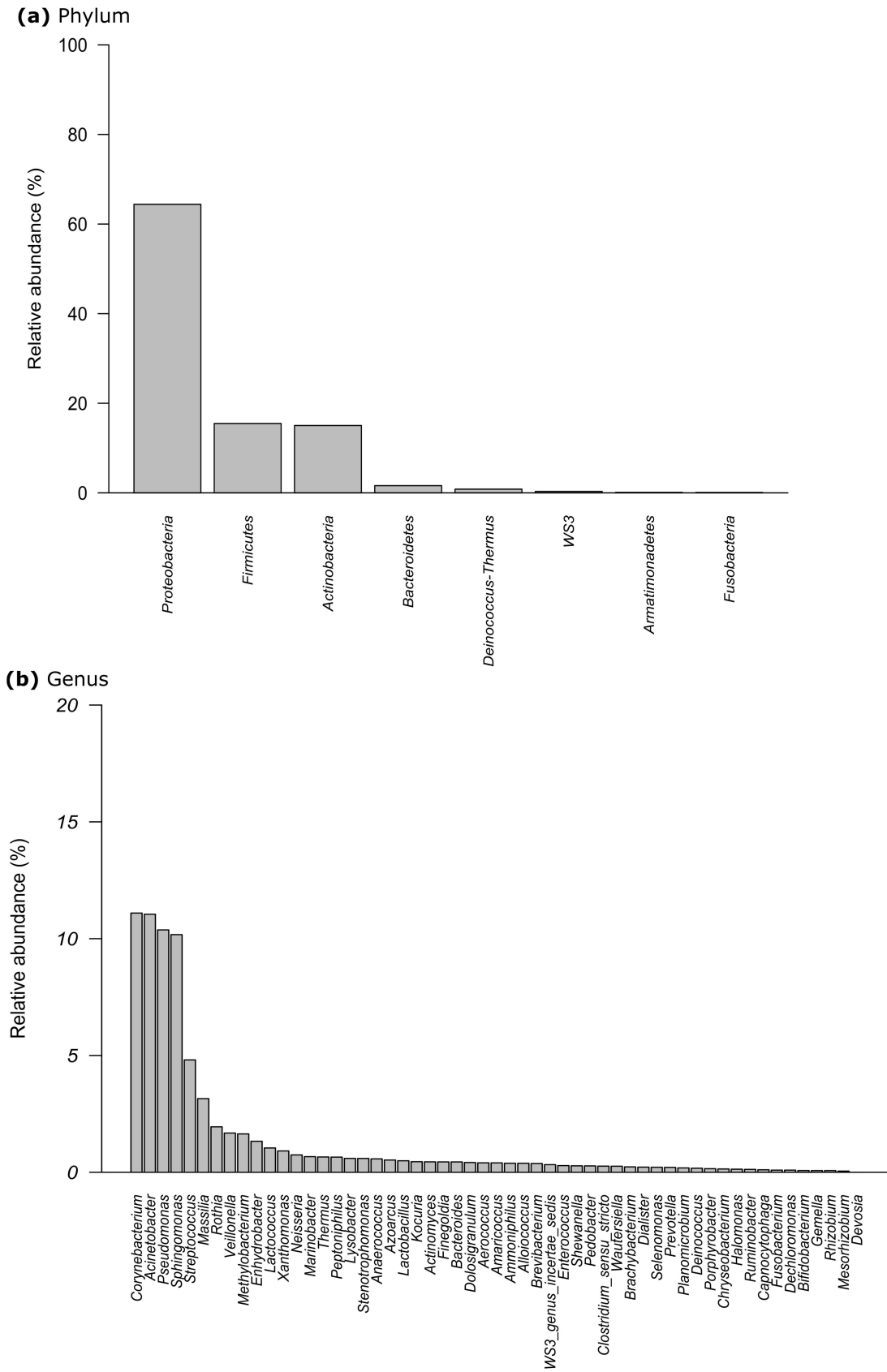
Supplementary Figure 6: Sequence counts (Log10) per sample. Samples with < 10,000 sequences (indicated by dashed line) were removed.
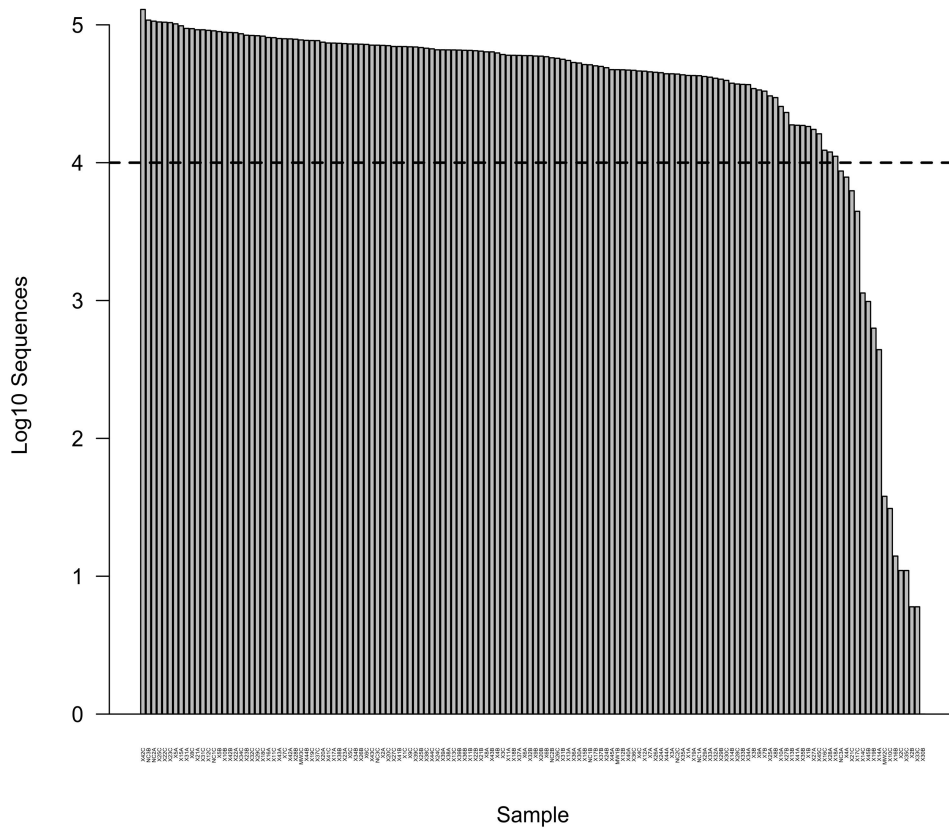
Supplementary Figure 7: OTU relative abundance. OTUs present at less than 0.0001% relative abundance (indicated by dashed line) were removed.
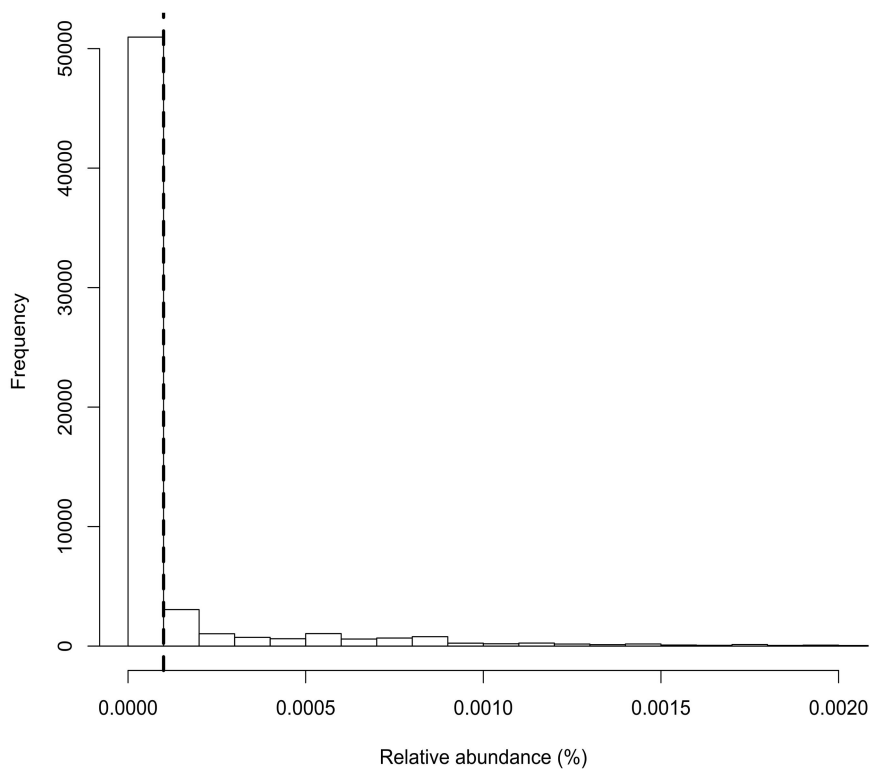
Supplementary Figure 8: Linear regression filter to determine OTUs present on ocular surface samples, **(a)** Initial linear regression filter, **(b)** Linear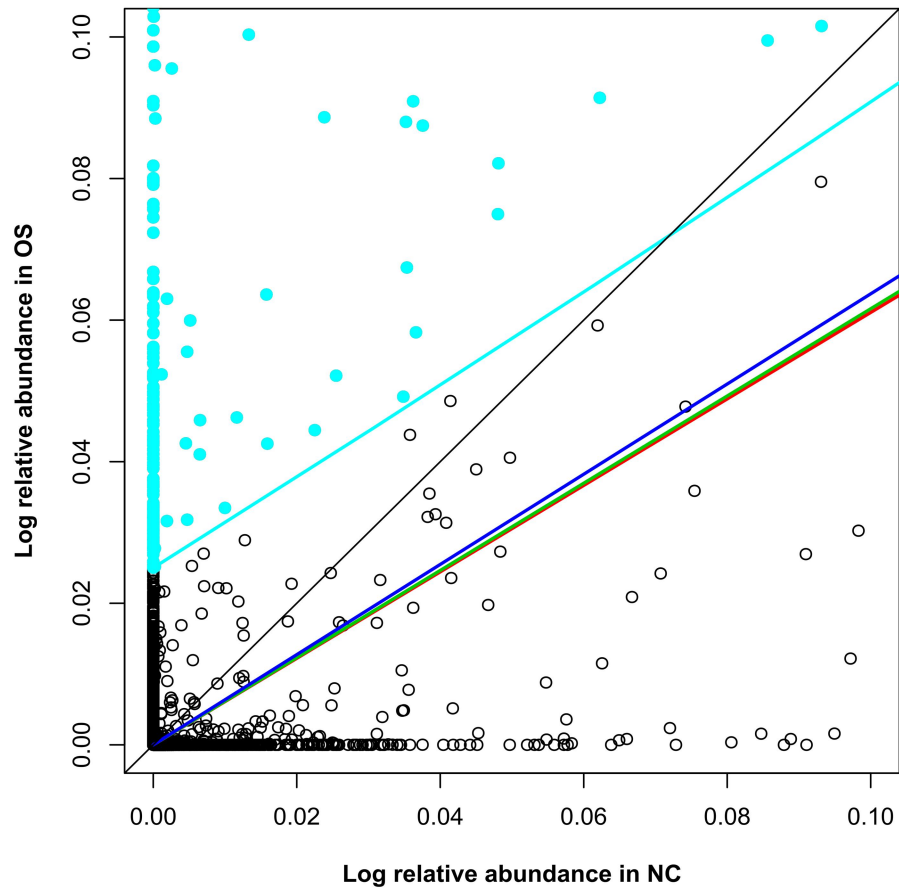 regression filter repeated (OS = ocular samples, NC = negative control samples, Black = 1:1 line, Red = regression line, Green = standard error [SE] line, Blue = SE multiplied by a factor of five, Aqua = exponent of 5x SE; Black circles = OTUs; Green points = retained OTUs after initial filter; Aqua points = final retained OS OTUs)

(a) Initial linear regresssion filter

(b) Final linear regresssion filter

Supplementary Figure 9: Linear regression filter to determine OTUs present in ocular surface samples and retained for downstream statistical analysis (OS = ocular samples, NFW = nuclease free water; Black = 1:1 line, Red = regression line, Green = standard error line, Blue = standard error by a factor of five, Aqua = exponent of 5x error bar; Black circles = OTUs, Aqua points = final retained OS OTUs)