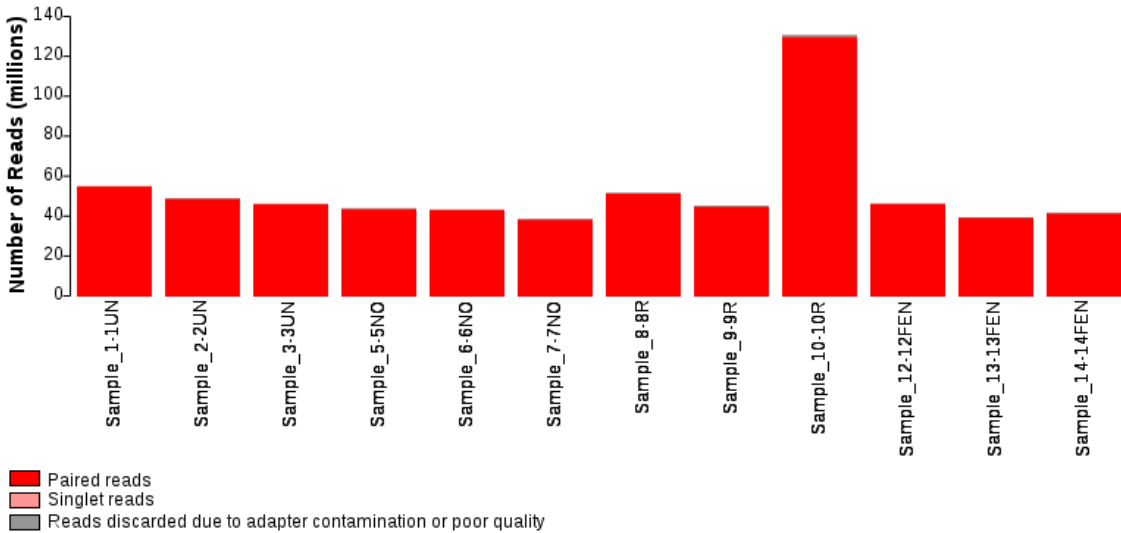
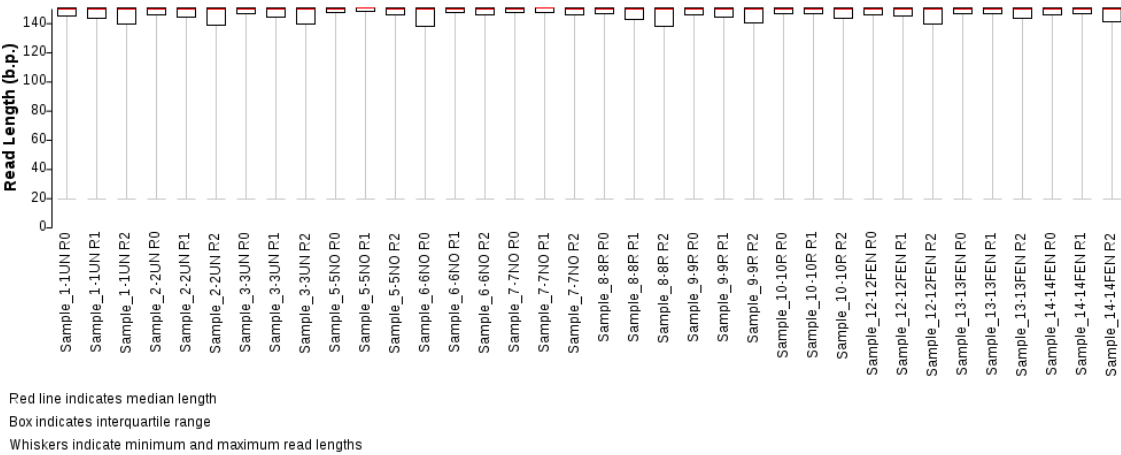


Aedes aegypti transcriptome: resistance to fenitrothion

12 samples divided in 4 groups (3 identical replicates per group). 6 fenitrothion-resistant samples from Angola (3 have been exposed to fenitrothion, 3 unexposed). 6 susceptible samples from laboratory strains (3 from New Orleans, 3 from Rockefeller). Sample classification:

Sample name	Sample group	Phenotype	Exposure	Location
s01_RUN	ResUnex	Res	Unex	Angola
s02_RUN	ResUnex	Res	Unex	Angola
s03_RUN	ResUnex	Res	Unex	Angola
s05_SNO	SusNewO	Sus	Unex	NewOrl
s06_SNO	SusNewO	Sus	Unex	NewOrl
s07_SNO	SusNewO	Sus	Unex	NewOrl
s08_SRO	SusRock	Sus	Unex	Rockef
s09_SRO	SusRock	Sus	Unex	Rockef
s10_SRO	SusRock	Sus	Unex	Rockef
s12_RFE	ResFeex	Res	Feex	Angola
s13_RFE	ResFeex	Res	Feex	Angola
s14_RFE	ResFeex	Res	Feex	Angola



PCA analysis – Using the matrix of normalized transcript counts from *Deseq*, calculating Euclidean distances between samples. Good within-replicate clustering.

PC1 separates susceptible from resistant samples and is by far the most important. PC2 separates exposed from non-exposed. Oddly, RFE seems to be closer to susceptible samples than RUN, along PC1. PC3 highlights differences between SRO and SNO and it is not very relevant (not the focus of this analysis, although it can help contextualize the overlap differences in SRO/SNO-RUN comparisons),

