

Duarte_FigS7

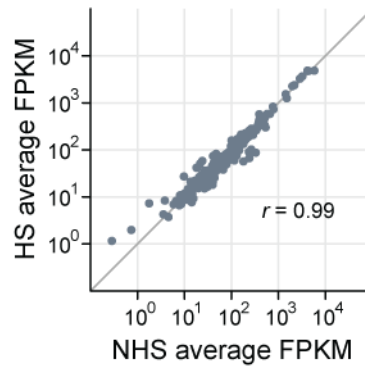


Figure S7: mRNA levels of 335 genes used for normalization are not affected by HS. Correlation plot between the RNA-seq FPKM for the NHS and HS conditions for the 335 HS-unaffected genes that were used to normalize our datasets. The FPKM values are the average of two biological replicates. The Pearson's correlation coefficient is shown in the plot. The gray line represents a 1:1 fit.