Kallisto Commands, Brief Description of All Other SI

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1 Kallisto Commands

The Kallisto Commands were written in an automated fashion using a Python script. The shell script can be found at the following url: `https://github.com/WormLabCaltech/Angeles_Leighton_2016/blob/master/input/kallisto_commands.sh`.

The resulting TPM files were analysed using Sleuth via a customized R script, `aging_rna_seq_analysis.R`. This script can be found here: `https://github.com/WormLabCaltech/Angeles_Leighton_2016/blob/master/rdocs/aging_rna_seq_analysis.R`.

The results from Sleuth were analyzed using Python in a Jupyter notebook. All Python code can be found in the `src` directory of our Github repository.

2 Supplementary Files 2, 3, 4

Supplementary Files 2, 3, and 4 contain the output of Sleuth after differential expression analysis. The files contain the columns detailed in Table 1. Supplementary File 2 contains what can be loosely interpreted as the fold-change of each gene between young and old adult worms. Supplementary File 3 contains what can be loosely interpreted as the fold-change of each gene between wild-type and *fog-2* worms. Supplementary File 4 contains the genes that changed differently as wild-type worms aged and *fog-2* worms aged. For Supplementary File 4, the 'b' column should be interpreted as the change in the aging log-fold

Column Name	Description
target_id	Gene identifier, usually unique to each isoform in *C. elegans*
pval	P-value indicating significance of differential expression. NOT FDR Corrected. NOT used to identify D.E. genes
qval	P-value after correcting for multiple hypothesis testing. This column is used to establish statistical significance
b	The slope of the regression along a specified axis. **Loosely** interpreted as natural log of the fold-change.
se_b	Standard error of b.
mean_obs	Mean of the logarithm of the observed counts.
var_obs	Variance of the logarithm of the observed counts.
tech_var	Technical variance of the logarithm of the observed counts.
sigma_sq	Biological variance of the logarithm of the observed counts.
smooth_sigma_sq	Smoothed biological variance of the logarithm of the observed counts.
ens_gene	WormBase Identifier (not isoform specific).
ext_gene	Human-readable Gene Name

Table 1: List of columns in file SI1–3.

change. That is, an aging *fog-2* animal would have a log-fold change in a given gene X equal to $b_{\mathrm{age}} + b_{\mathrm{interaction}}$, whereas an aging wild-type animal would have a log-fold change equal to b_{age}.