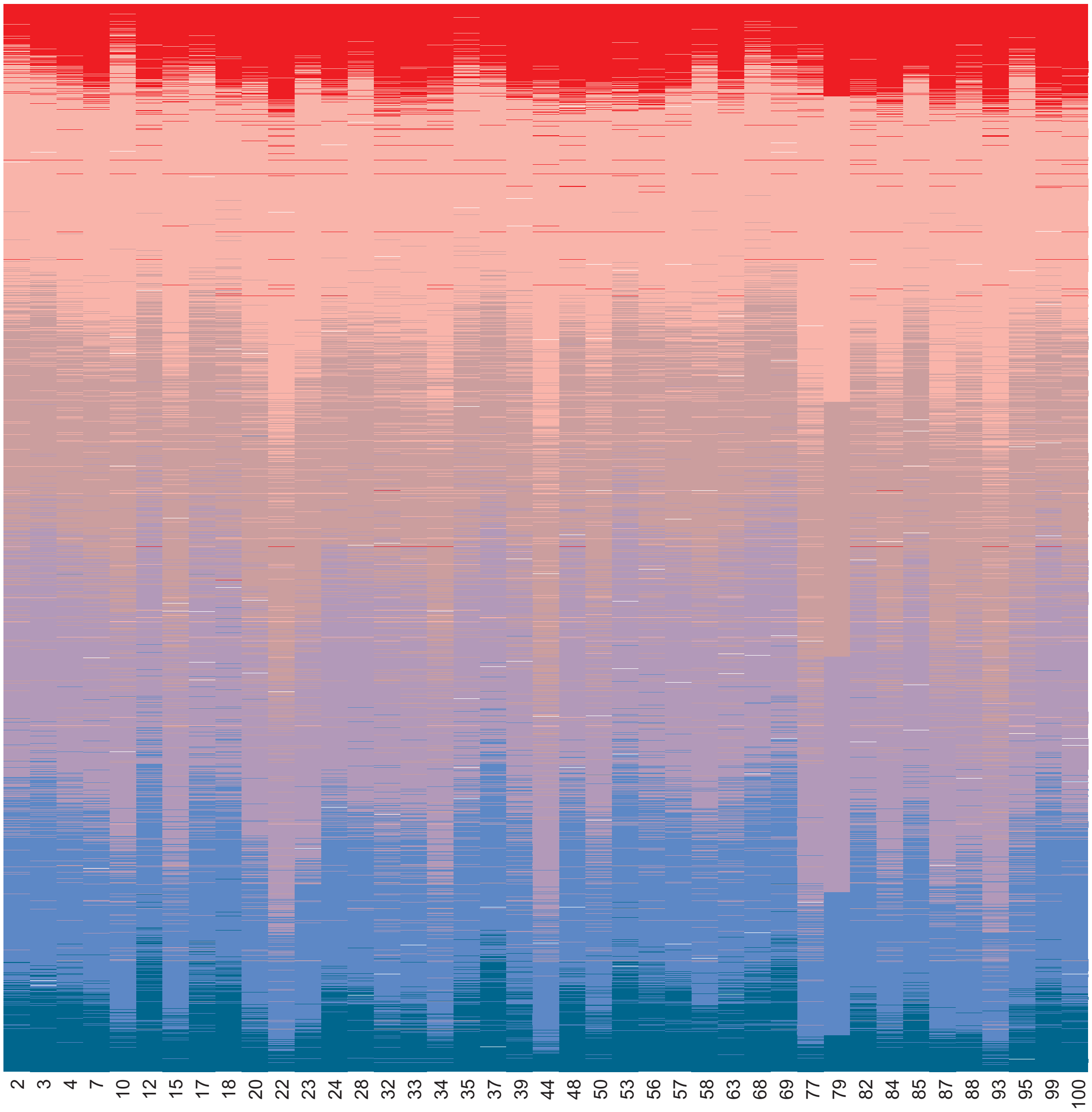

Figure S1. Mean $\log_2$ transcript abundance in each MA line. Expression ranged from not expressed (red; $\log_2$ ratio to background < 1) up to highly expressed features (deep blue; $\log_2$ ratio to background >6; maximum expression 364 times background) ($\log_2$ ratio of: orange = 1-3; grey = 3-4; lilac = 4-5; blue = 5-6). Note, this heat map illustrates only which genes are expressed versus not expressed (interpreted as greater or less than 1 fold $\log_2$ signal intensity above the mean signal intensity of the 20,000 random probes on each array), not whether genes were up versus down regulated among MA lines. Genes were ordered by their expression in MA line 79, which had the least genes expressed (10,602 genes had signal intensity >1 fold above the mean of the random probes). This was done to aid visualization of the relative numbers of unexpressed genes. Between 231 and 1,002 genes in a MA line (on average, 5.6% per line) had expression levels that were not distinguishable from the background signal. We nevertheless included these genes in the analyses because low (no) expression in most lines, but increased expression in one line could reflect a mutation in that line.