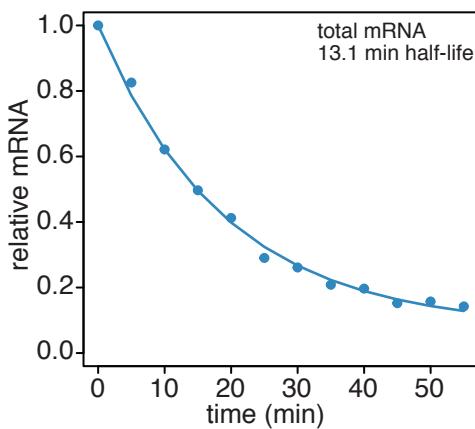
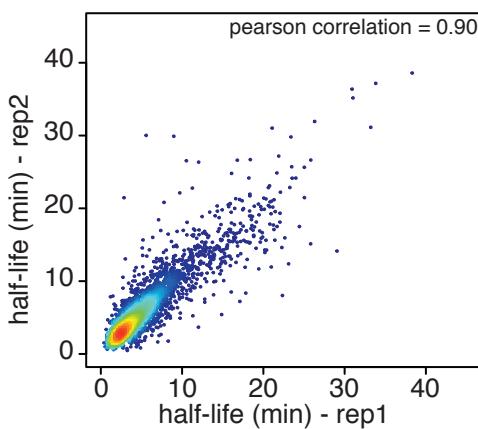
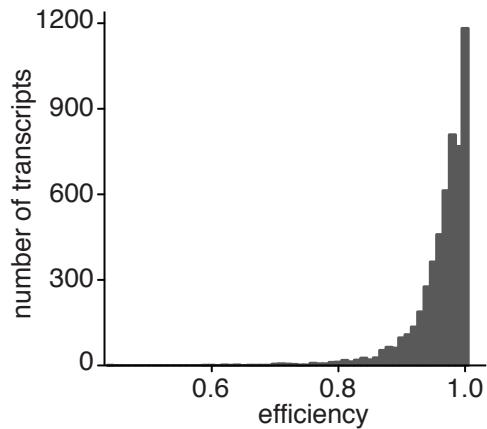
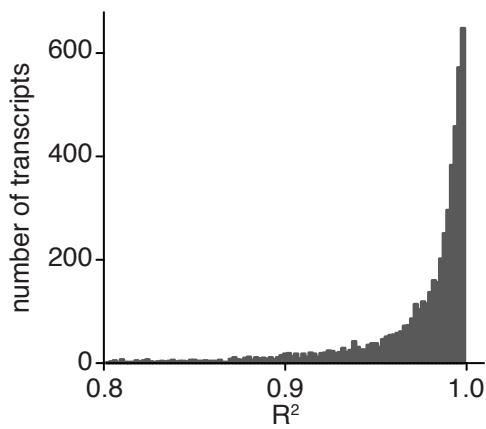
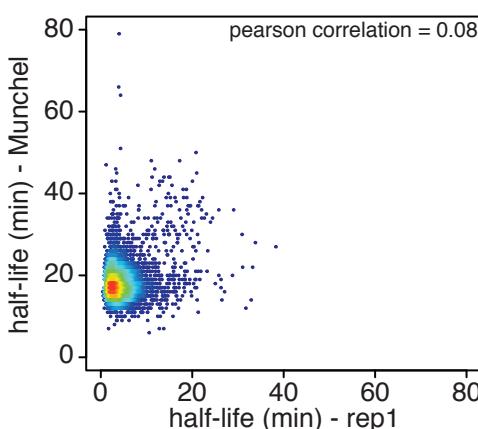


**A****B**

fit transcripts	5378
low abundance (total mRNA FPKM < 2)	653
cufflinks HIDATA (reads exceed maximum cutoff)	27
fit to model failed	197
goodness of fit below threshold ( $R^2 < 0.8$ )	209
total transcripts	6464

**C****D****E****F****G**

GO enrichment for stable mRNA genes		P-value
translation		3.3E-48
regulation of translation		6.1E-29
posttranscriptional regulation of gene expression		1.1E-27
regulation of cellular protein metabolic processes		5.3E-27
monosaccharide catabolic process		8.5E-14
alcohol catabolic process		1.3E-13
glucose catabolic process		2.5E-12
hexose catabolic process		6.6E-12
cellular carbohydrate catabolic process		1.5E-11
oxidation reduction		1.7E-11
carbohydrate catabolic process		2.7E-10
nitrogen compound biosynthesis process		3.4E-10

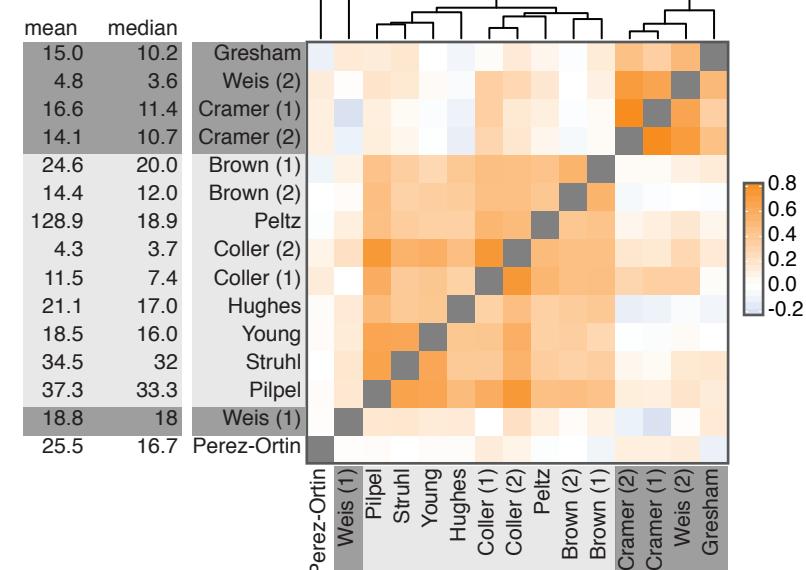
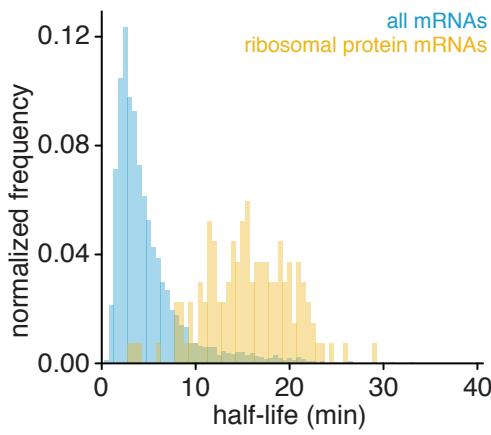
**H**

Figure 1-figure supplement 1