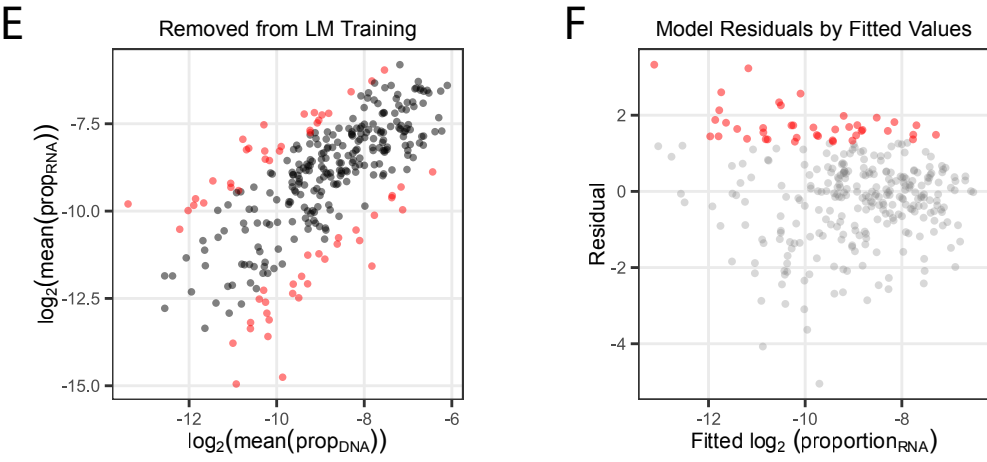
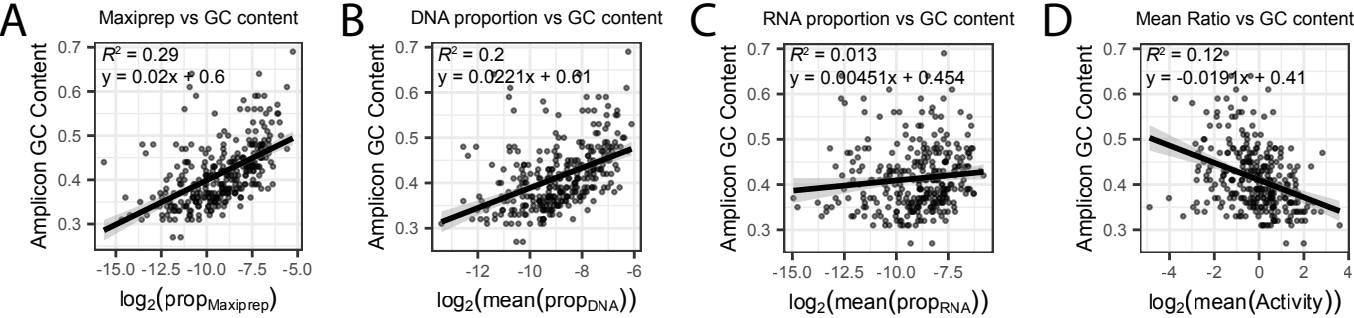


Figure 2–figure supplement 2



G Linear Model Parameters (without GC as a coefficient)

Call:
lm(formula = log2(RNA_prop_mean) ~ log2(DNA_prop_mean), data = data.for.lm)

Residuals:

Min	1Q	Median	3Q	Max
-1.89246	-0.54850	0.06002	0.61099	1.62332

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)	
(Intercept)	-0.78093	0.33900	-2.304	0.0221	*
log2(DNA_prop_mean)	0.92453	0.03837	24.094	<2e-16	***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.8307 on 246 degrees of freedom
Multiple R-squared: 0.7024, Adjusted R-squared: 0.7012
F-statistic: 580.5 on 1 and 246 DF, p-value: <2.2e-16

H Linear Model Parameters (with GC as a coefficient)

Call:
lm(formula = log2(RNA_prop_mean) ~ log2(DNA_prop_mean) + GC, data = data.for.lm)

Residuals:

Min	1Q	Median	3Q	Max
-1.88097	-0.48373	-0.00093	0.51671	1.81914

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)	
(Intercept)	1.93109	0.56097	3.442	0.000678	***
log2(DNA_prop_mean)	1.0486	0.03944	25.838	<2e-16	***
GC	-4.6829	0.77173	-5.869	1.42e-08	***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.7794 on 245 degrees of freedom
Multiple R-squared: 0.7391, Adjusted R-squared: 0.7369
F-statistic: 346.9 on 2 and 245 DF, p-value: <2.2e-16