

Figure S1. Protein accumulation measured as S35-methionine incorporation into protein at fast and slow growth rates is determined by growth rate, not ppGpp. Rich and poor media for wt were #4a and #9; for ppGpp⁰ - #4a and #8 with media and growth rates sustained shown in Table I. Labeling was performed under conditions where methionine did not limit growth. The numbers represent the rates of accumulation (slope) normalized to A_{460} at the 20 min time point. The lines are linear regressions for each data set. Incorporation is plotted as a percentage of the highest activity.

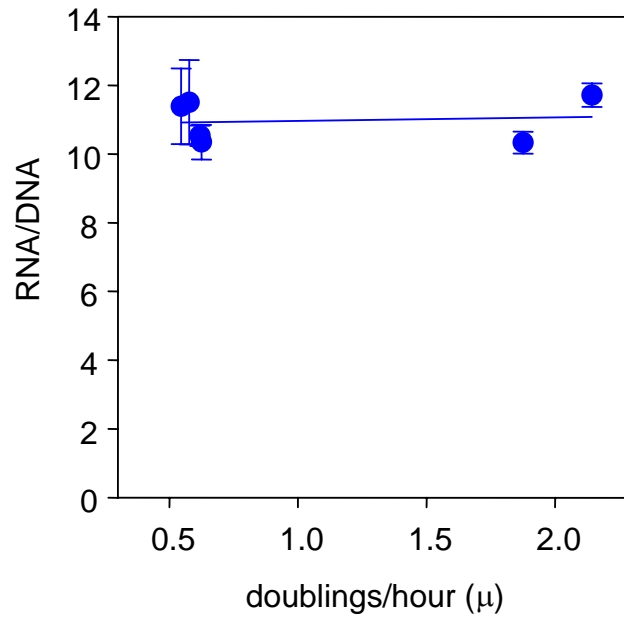


Figure S2. The RNA/DNA ratios during fast and slow growth rates in a *dksA* mutant strain (CF9240). The following media were used: M9 glucose + all AA40+uracil [20 $\mu\text{g/ml}$] ($\mu = 0.62\text{-}0.63$), or M9 glucose+uracil [20 $\mu\text{g/ml}$]+(DGILMQSTV)₄₀ ($\mu = 0.5\text{-}0.58$), M9 glucose + 0.5% yeast extract + uracil [20 $\mu\text{g/ml}$] ($\mu = 1.88\text{-}2.14$). Defined media that would support intermediate growth rates were not found. The solid line represents a linear regression calculated with SigmaPlot software.

Supplementary Table I. Statistical analysis of the polysome profiling data depicted in Figure 2A and D ^a

	Associating conditions				Dissociating conditions			
	wt LB	ppGpp ⁰ LB	wt M9	ppGpp ⁰ MM	wt LB	ppGpp ⁰ LB	wt M9	ppGpp ⁰ MM
Shoulder before 30S (17S)	5.4 ±0.24				10.14 ±1.75			
30S	13.14 ±0.54	13.64 ±0.48	13.75 ±0.82	9.49 ±0.56	29.94 ±1.46	33.34 ±2.37	29.58 ±0.74	36.47 ±0.67
Shoulder before 50S						8.63 ±1.29		
50S	8.78 ±1.41	16.53 ±2.58	4.86 ±0.67	7.27 ±0.17	59.91 ±3.09	58.03 ±3.27	46.48 ±0.62	63.53 ±0.88
Shoulder after 50S							23.94 ±0.64	
70S	33.35 ±3.07	50.43 ±5.38	33.13 ±2.89	66.57 ±1.14				
polysomes	39.32 ±2.21	19.38 ±2.97	48.53 ±2.52	16.98 ±1.26				

^a This data was obtained by calculating area under peaks in the polysome profiles obtained in three independent experiments for each condition. Each profile was also subjected to analysis in triplicate because the base line was set manually. This gave 9 data sets for each experimental condition. Errors are calculated as S.D.