

TABLE 3. The effect of mutations in conserved decoding center nucleotides on canonical translation and *trans*-translation

Ribosomes	Peptidyl transfer rate (sec ⁻¹)		GTP hydrolysis rate (sec ⁻¹)	
	Phe-tRNA ^{Phe}	Ala-tmRNA	Phe-tRNA ^{Phe}	Ala-tmRNA
Wild type	1.45 ± 0.02	0.29 ± 0.04	3.4 ± 0.1	4.2 ± 0.5
A1492G	0.0008 ± 0.00005	0.16 ± 0.01	0.28 ± 0.009	4.0 ± 0.6
A1493G	0.0005 ± 0.00006	0.23 ± 0.01	0.22 ± 0.003	3.5 ± 0.7
G530A	0.002 ± 0.0002	0.17 ± 0.06	0.26 ± 0.01	4.6 ± 1.0

Tagged ribosomes containing 16S mutations were isolated and used to form initiation complexes. As shown in Figure 5A, these were reacted with complexes containing EF-Tu, GTP, and either Phe-tRNA^{Phe} or Ala-tmRNA and SmpB to determine the relative rate of peptidyl transfer (*left*) or GTP hydrolysis (*right*). Representative primary data are shown in Figure 5B,C. Standard error is reported.