TABLE 2. Kinetic parameters for tyrosylation of wild-type tRNA^{Tyr} molecules or variants by $\text{TyrRS}_{\text{apm}}$ and methionylation of wild-type tRNA^{Met} molecules or variants by $\text{MetRS}_{\text{apm}}$[a]

tRNA	K_m (μM)	k_{cat} (10^{-3} s^{-1})	k_{cat}/K_m (*n*-fold)	*L* value
Tyrosine				
Wild-type molecules				
Yeast (native)	0.5	126	252	0.3
Yeast (transcript)	1.7	142	83.5	1
P. falciparum	4	18.3	4.6	18
Mutated molecules				
Yeast C_1-G_{72}→A_1-U_{72}	NM[b]	NM	NM	NM
Yeast C_1-G_{72}→G_1-C_{72}	NM	NM	NM	NM
Yeast C_1-G_{72}→A_{73}→G_{73}	NM	NM	NM	NM
Yeast G_{34}→A_{34}	1.3	7.5	5.8	14.4
Yeast G_{34}→C_{34}	1.4	9.3	6.6	12.6
Yeast G_{34}→U_{34}	1.3	8.3	6.4	13
Yeast U_{35}→A_{35}	16	2.5	0.16	522
Yeast U_{35}→C_{35}	33.3	10	0.3	278
Yeast U_{35}→G_{35}	9.3	1.1	0.12	696
Yeast A_{36}→G_{36}	20	7.3	0.36	232
Yeast A_{36}→U_{36}	15.4	14.9	0.96	87
Methionine				
Wild-type molecules				
Yeast (native)	0.13	6.6	252	0.3
Yeast (transcript)	0.74	17.4	83.5	1
E. coli (native)	0.47	47	252	0.3
Mutated molecules				
Yeast C_{34}→G_{34}	NM	NM	NM	NM
Yeast A_{35}→C_{35}	NM	NM	NM	NM
Yeast U_{36}→C_{36}	NM	NM	NM	NM

[a] *L* values correspond to losses of efficiency relative to yeast tRNA^{Tyr} transcript or yeast tRNA^{Met} transcript. Values of >1 correspond to gains in efficiency. Experimental errors for k_{cat} and K_m varied at most by 20%. Results represent averages of at least two independent experiments.

[b] NM, not measurable (loss of $>10^5$).