

**TABLE 1.** Misreading frequency by tRNA<sup>Lys</sup><sub>UUU</sub> at near-cognate and noncognate codons

Codon <sup>a</sup>	Amino acid	Codon position misread	Lysine misreading frequency ( $\times 10^{-4}$ )				
			WT	<i>rpsD</i>	<i>rpsL</i>	Paromomycin (5 $\mu$ g/mL)	Streptomycin (2 $\mu$ g/mL)
<u>U</u> AA	Ter	1	4.1 $\pm$ 0.51	4.0 $\pm$ 0.19	1.4 $\pm$ 0.29	41 $\pm$ 5.0	20 $\pm$ 1.4
<u>U</u> AG			14 $\pm$ 0.66	29 $\pm$ 2.7	1.3 $\pm$ 0.30	85 $\pm$ 2.6	68 $\pm$ 4.1
A <u>U</u> A	Ile	2	3.5 $\pm$ 0.44	3.9 $\pm$ 0.32	3.4 $\pm$ 0.37	9.9 $\pm$ 0.82	23 $\pm$ 0.99
A <u>G</u> A	Arg	2	36 $\pm$ 2.7	51 $\pm$ 5.7	4.3 $\pm$ 0.58	120 $\pm$ 15	95 $\pm$ 4.8
A <u>G</u> G			31 $\pm$ 1.5	49 $\pm$ 6.5	4.1 $\pm$ 0.49	130 $\pm$ 19	53 $\pm$ 2.3
AA <u>U</u>	Asn	3	16 $\pm$ 0.78	140 $\pm$ 7.1	4.9 $\pm$ 0.57	130 $\pm$ 14	120 $\pm$ 8.6
AA <u>C</u>			3.8 $\pm$ 0.52	7.7 $\pm$ 0.37	1.5 $\pm$ 0.20	25 $\pm$ 2.1	16 $\pm$ 1.6
Others <sup>b</sup>	—	—	3.1 $\pm$ 0.74	3.4 $\pm$ 0.56	3.5 $\pm$ 0.45	5.8 $\pm$ 0.58	3.9 $\pm$ 0.53

<sup>a</sup>Mutation from a Lys codon (AAA or AAG) is underlined.<sup>b</sup>Average of all remaining tested codons.