



Figure S1. Levels of +1 frameshifting in the constructs with various A- or G- ending test codons decoded by tRNAs lacking the ncm^5 group, the mcm^5 group, the esterified methyl group of mcm^5 or the s^2 group at wobble position. Levels of +1 frameshifting were analyzed by using wild type (blue) and mutant strains (*elp3Δ*: red, *trm9Δ*: yellow, *tuc1Δ*: grey). Each frameshifting value is the mean of three biological replicates and the value of the each biological replicate is the median of three technical replicates. Slippery codons (XXX) are underlined and test codons (NNN) are in bold. Error bars were determined by standard deviation.

Table S1. Plasmids used for luciferase assay system.

Plasmids	Fragments inserted between two luciferase genes ^a	tRNA assayed	Source
ABY1830	GGA.UCC.CCC.GGC.GAG.CUC	In-frame control	(40)
ABY1843	GGA.UCC.CUA.GGC.CCC.CAA.UAG.C.GAG.CUC	tRNA ^{Gln} _{mcm⁵s²UUG}	This study
ABY1846	GGA.UCC.CUA.GGC.CCC.CAG.UAG.C.GAG.CUC		This study
ABY1844	GGA.UCC.CUA.GGC.CCC.AAA.UAG.C.GAG.CUC	tRNA ^{Lys} _{mcm⁵s²UUU}	This study
ABY1847	GGA.UCC.CUA.GGC.CCC.AAG.UAG.C.GAG.CUC		This study
ABY2049	GGA.UCC.CUA.GGC.GGG.GAA.UAG.C.GAG.CUC	tRNA ^{Glu} _{mcm⁵s²UUC}	This study
ABY1845	GGA.UCC.CUA.GGC.GGG.GAG.UAG.C.GAG.CUC		This study
ABY1838	GGA.UCC.CUA.GGC.CCC.AGA.UAG.C.GAG.CUC	tRNA ^{Arg} _{mcm⁵UCU}	This study
ABY1839	GGA.UCC.CUA.GGC.CCC.AGG.UAG.C.GAG.CUC		This study
ABY1840	GGA.UCC.CUA.GGC.CCC.GGA.UAG.C.GAG.CUC	tRNA ^{Gly} _{mcm⁵UCC}	This study
ABY1842	GGA.UCC.CUA.GGC.CCC.GGG.UAG.C.GAG.CUC		This study
ABY1837	GGA.UCC.CUA.GGC.GGG.GUA.UAG.C.GAG.CUC	tRNA ^{Val} _{nem⁵UAC}	This study
ABY2007	GGA.UCC.CUA.GGC.GGG.GUG.UAG.C.GAG.CUC		This study
ABY2008	GGA.UCC.CUA.GGC.UUU.UCA.UAG.C.GAG.CUC	tRNA ^{Ser} _{nem⁵UGA}	This study
ABY2009	GGA.UCC.CUA.GGC.UUU.UCG.UAG.C.GAG.CUC		This study
ABY1835	GGA.UCC.CUA.GGC.GGG.GCA.UAG.C.GAG.CUC	tRNA ^{Ala} _{nem⁵UGC}	This study
ABY1836	GGA.UCC.CUA.GGC.GGG.GCG.UAG.C.GAG.CUC		This study
ABY2006	GGA.UCC.CUA.GGC.UUU.UUA.UAG.C.GAG.CUC	tRNA ^{Leu} _{nem⁵UAA}	This study
ABY1833	GGA.UCC.CUA.GGC.UUU.CCA.UAG.C.GAG.CUC	tRNA ^{Pro} _{nem⁵UGG}	This study
ABY1832	GGA.UCC.CUA.GGC.UUU.CCC.UAG.C.GAG.CUC		This study
ABY1834	GGA.UCC.CUA.GGC.UUU.CCG.UAG.C.GAG.CUC		This study
ABY1831	GGA.UCC.CUA.GGC.UUU.CCU.UAG.C.GAG.CUC		This study
ABY2048	GGA.UCC.CUA.GGC.CCC.ACA.UAG.C.GAG.CUC	tRNA ^{Thr} _{nem⁵UGU}	This study
ABY2012	GGA.UCC.CUA.GGC.UUU.ACA.UAG.C.GAG.CUC		This study
ABY2011	GGA.UCC.CUA.GGC.CCC.ACG.UAG.C.GAG.CUC		This study
ABY2013	GGA.UCC.CUA.GGC.UUU.ACG.UAG.C.GAG.CUC		This study
ABY2014	GGA.UCC.CUA.GGC.UUU.UAC.UAG.C.GAG.CUC	tRNA ^{Tyr} _{GUA}	This study

^a Restriction sites *Bam*HI-*Sac*I are marked with dotted line. Slippery codons are in bold and test codons are in bold and underlined.

Table S2. Oligonucleotides used to alter the Ty1 sequence of plasmids pMB38-9merWT and pMB38-9merFF.

Plasmids	Template ^a	Oligonucleotides used for PCR directed mutagenesis (5' to 3') ^b	tRNA assayed	Source
ABY2138	pMB38-9merWT Test Construct	CCGCTGACA(CTT)(AGA)CCATGAGGTACCCG'	tRNA _{mcm⁵} ^{Arg} UCU	This study
ABY2139		CTCGACGGATCCGCTGACA(CTT)(AAA)CCATGAGGTACC	tRNA _{mcm⁵} ^{Lys} s ² UUU	This study
ABY2140 ^c		GGCTCGACGGATCCGCTGACA(AAA)(AGG)CATGAGG	tRNA _{mcm⁵} ^{Lys} s ² UUU	This study
ABY2141 ^c		GATGGCTCGACGGATCCGCTGACA(AAA)(CGT)CCATGAGGTACCCGA'	tRNA _{mcm⁵} ^{Lys} s ² UUU	This study
ABY2142 ^c		GGATGGCTCGACGGATCCGCTGACA(AAA)(ATT)CCATGAGGTACCCGAT	tRNA _{mcm⁵} ^{Lys} s ² UUU	This study
ABY2143	pMB38-9merFF In-frame Control Construct	CCGCTGACA(CTT)(AGA)CCACGTGAGGTACC	tRNA _{mcm⁵} ^{Arg} UCU	This study
ABY2144		CGACGGATCCGCTGACA(CTT)(AAA)CCACGTGAGGT	tRNA _{mcm⁵} ^{Lys} s ² UUU	This study
ABY2145 ^c		GGCTCGACGGATCCGCTGACA(AAA)(AGG)CCACGTGA	tRNA _{mcm⁵} ^{Lys} s ² UUU	This study
ABY2146 ^c		GGATGGCTCGACGGATCCGCTGACA(AAA)(CGT)CCACGTGAGGTAC	tRNA _{mcm⁵} ^{Lys} s ² UUU	This study
ABY2147 ^c		TTGGATGGCTCGACGGATCCGCTGACA(AAA)(ATT)CCACGTGAGGTACC	tRNA _{mcm⁵} ^{Lys} s ² UUU	This study

^a pMB38-9merWT (test construct) and pMB38-9merFF (in-frame control construct) plasmids carrying the Ty1 sequence (CTT-AGG-C) were used as templates for the PCR mutagenesis (41).

^b Alterations of the Ty1 sequence are labelled in bold.

^c Constructs to test the P-site induced frameshifting.