Table S1 | Changes in the translation system

Step	Natural	Artificial
tRNA/synthetase recognition		
tRNA sequence (anticodon)		Yeast $tRNA^{Met}$ C34→G accepts Ile (REF. 1)
		E. coli $tRNA^{Arg}$ C35→G accepts Thr (REF. 2)
		Numerous suppressor tRNAs[3]
tRNA sequence (elsewhere)	Leu UAG → Thr UAG in yeast mt?[4]	Single-base insertion in yeast $tRNA^{Leu}$ variable arm confers Ser acceptance[5]
Base modification		Lack of thiolation at U34 of *E. coli* $tRNA^{Glu}$ decreases GluRS specificity 520-fold[6]
		Lack of A34→I in yeast $tRNA^{Ile,IAU}$ decreases IleRS acceptance and lack of U34, U36→ψ in $tRNA^{Ile,UAU}$ decreases isoleucylation 40-fold[1]
		Lack of C34→Lys in *E. coli* $tRNA^{Ile}$ causes charging with Met instead of Ile (REF. 7)
Synthetase (tRNA recognition site)	*E. coli* SerRS recognizes only two of three yeast mitochondrial $tRNA^{Ser}$ (not AGY)[62]	*E. coli* GlnRS→$tRNA^{Tyr,amber}$ D235N,G (REF. 11)
	Thermus thermophilus has an AspRS that aminoacylates $tRNA^{Asp}$ and $tRNA^{Asn}$ as well as one that only aminoacylates $tRNA^{Asp}$ (REF. 9)	*E. coli* LeuRS insertion mutant discriminates threefold against GUG isoacceptor[12]
	Yeast GlyRS aminoacylates only certain prokaryotic isoacceptors[10]	
Synthetase (amino-acid recognition site)		Human GlnRS→Glx by C456R and Q481I (REF. 13)
		E. coli GlnRS→Glx by F90L and Y240E (REF. 14)
tRNA/mRNA pairing		
tRNA sequence (anticodon)	CUG Leu→Ser in Candida caused by IGA→CAG at anticodon[15]	*E. coli* $tRNA^{Arg}$ C35→G pairs with Thr, not Arg codons[2]
	Trp C34→U to recognize UGA in Mycoplasma and mt, Gln G36→U to recognize UAR Gln (REF. 16)	Numerous suppressor tRNAs[3]
tRNA sequence (elsewhere)		Disruption of 27–43 base pair in *E. coli* $tRNA^{Trp}$ increases G•U wobble in first position of codon[17]
		G24→A in *E. coli* $tRNA^{Gln}$ increases G•U wobble at first position[18]
Base modification (see also Table 1)	C35→U35 in marsupial mitochondrial $tRNA^{Asp}$ changes pairing from GGY to (canonical) GAYY (REF. 19)	U34→methoxyuridine in *E. coli* $tRNA^{1Ser}$ increases pairing with UCU and UCG at expense of UGA (REF. 20)
		Lack of U34→s2U in *E. coli* $tRNA^{Lys}$ prevents binding at ribosome[21]
		Lack of U34→cmo^5U in *E. coli* $tRNA^{1Ser}$ reads UCA but not (as modified transcript does) U (REF. 22)
		Lack of C34→Lys in *E. coli* $tRNA^{Ile}$ causes pairing with AUG instead of AUA (REF. 7)
		Numerous modified nucleotides in *S. typhimurium* tRNAs affect rate of tRNA selection[74]
Ribosome		rRNA mutations (both subunits) in *E. coli* caused UGA suppression by blocking interaction with RF2 (REF. 24)
Release factors	RF2 not found in *Mycoplasma* genomes, mitochondria; NIKSR → NIKDR in eRF1 in *Tetrahymena* removes UAR recognition?	Mutants in RF1 and RF2 confer altered stop codon specificity[25,26]

(cmo^5U, uridine-5-oxyacetic acid; mt, mitochondria; RF, release factor; RS, tRNA synthetase.)

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