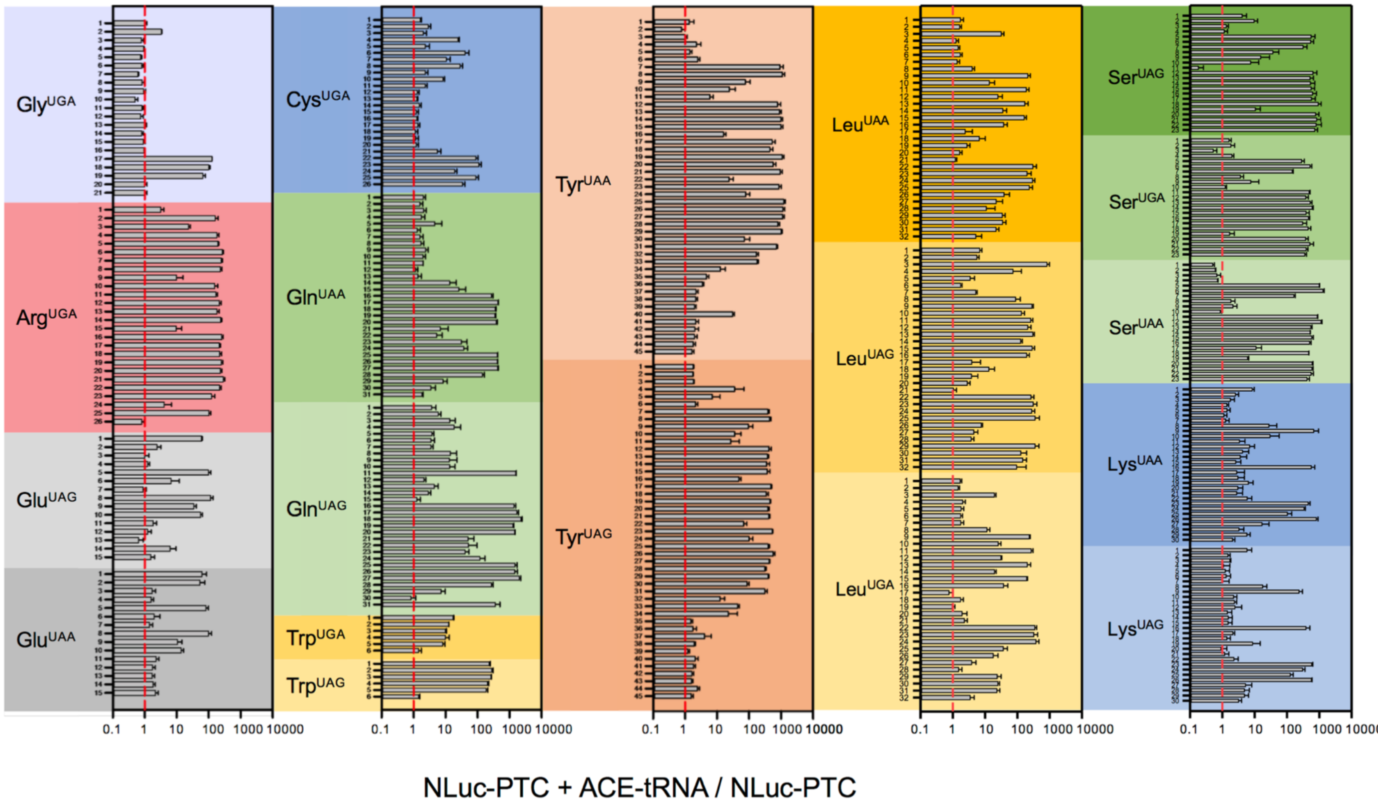
Engineered transfer RNAs for suppression of premature termination codons.

Lueck et al

Amino Acid			Codons					
W	Trp	Tryptophan	TGG					
Y	Tyr	Tyrosine	TAC	TAT				
C	Cys	Cysteine	TGC	TGT				
E	Glu	Glutamic acid	GAA	GAG				
K	Lys	Lysine	AAA	AAG				
Q	Gln	Glutamine	CAA	CAG				
S	Ser	Serine	AGC	AGT	TCA	TCC	TCG	TCT
L	Leu	Leucine	TTA	TTG	CTA	CTC	CTG	CTT
R	Arg	Arginine	AGA	AGG	CGA	CGC	CGG	CGT
G	Gly	Glycine	GGA	GGC	GGG	GGT		
F	Phe	Phenylalanine	TTC	TTT				
D	Asp	Aspartic acid	GAC	GAT				
H	His	Histidine	CAC	CAT				
N	Asn	Asparagine	AAC	AAT				
M	Met	Methionine	ATG					
A	Ala	Alanine	GCA	GCC	GCG	GCT		
P	Pro	Proline	CCA	CCC	CCG	CCT		
T	Thr	Threonine	ACA	ACC	ACG	ACT		
V	Val	Valine	GTA	GTC	GTG	GTT		
I	Ile	Isoleucine	ATA	ATC	ATT			
X	STP	Stop codon	TAA	TAG	TGA			

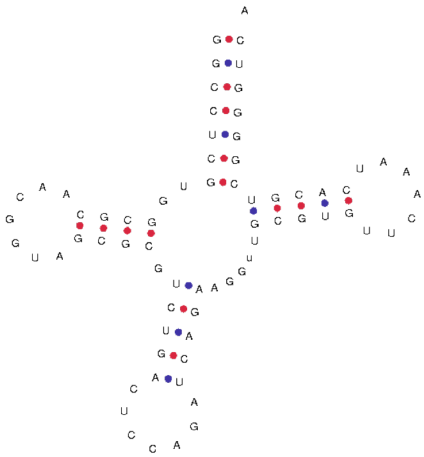
Codon usage for common PTC. Red highlight indicates the most common codons and corresponding amino acid type which can be converted to stop codons by a single nucleotide substitution. Engineered tRNAs have been developed for each type.

Supplementary Fig.1

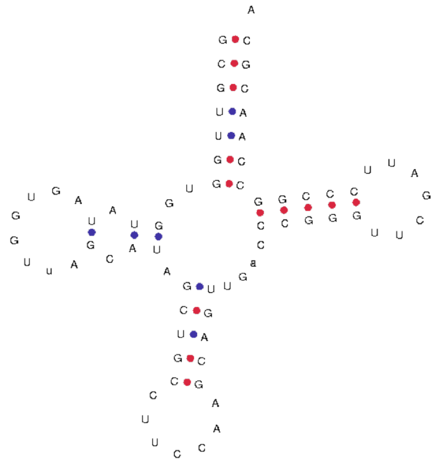


Number referenced ACE-tRNA activity plot.

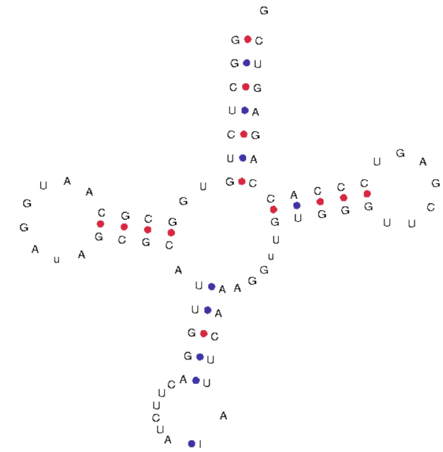
Supplementary Fig.2A



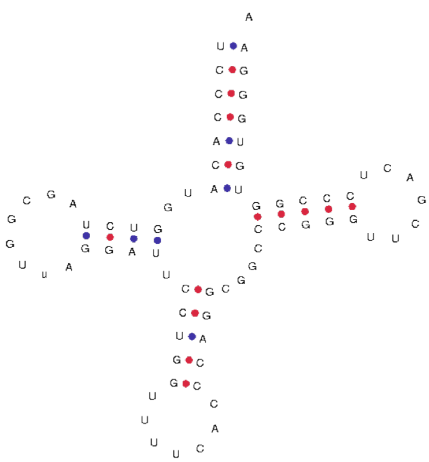
Trp-chr17.trna39
UGA and UAG



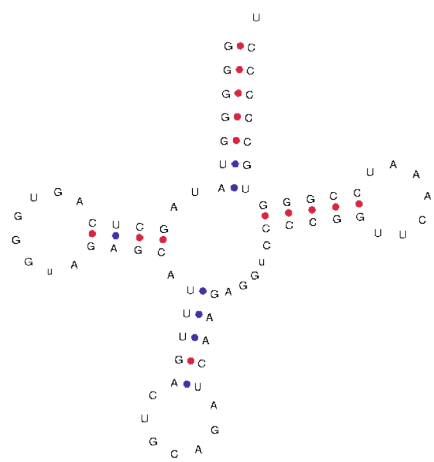
Gly-chr19.trna2
UGA



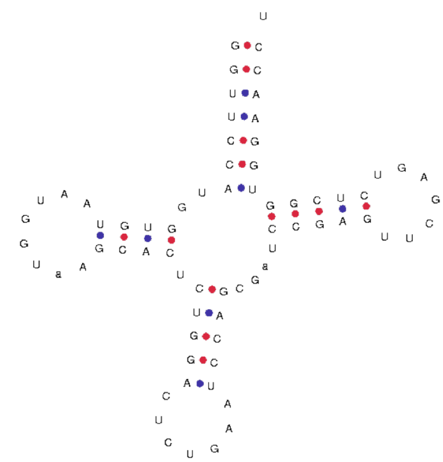
Arg-chr9.trna6
UGA



Glu-chr13.trna2
UAG and UAA

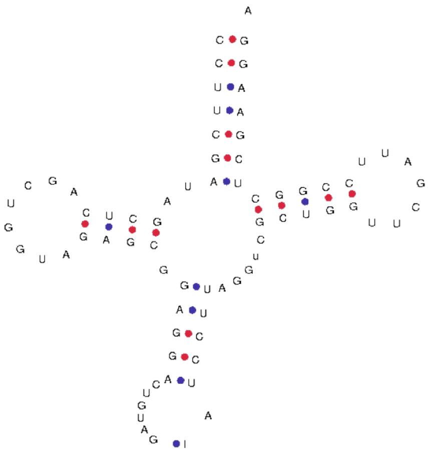


Cys-chr15.trna3
UGA

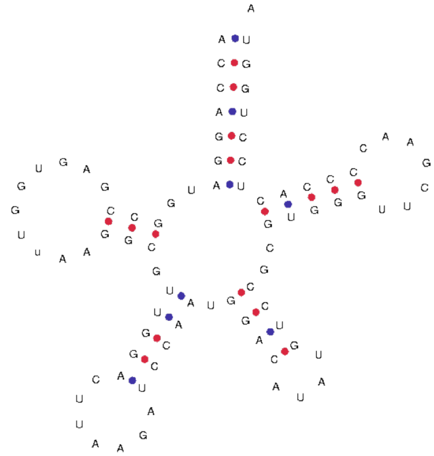


Gln-chr1.trna101
UAA not UAG

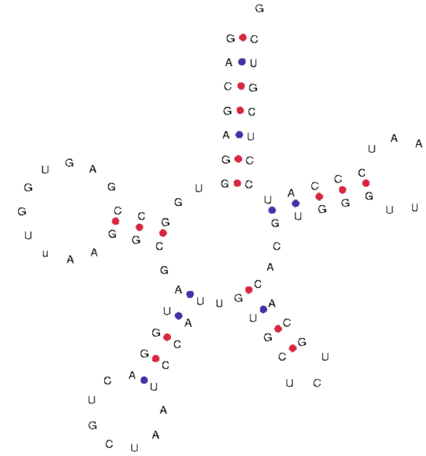
Supplementary Fig. 2B



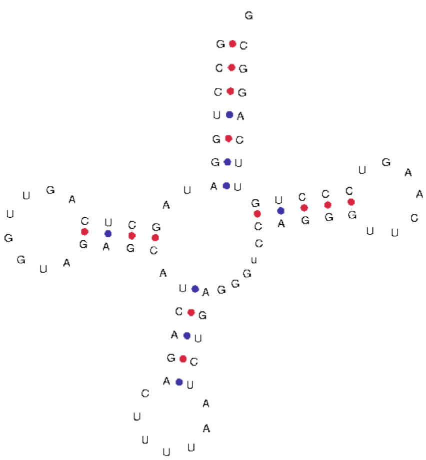
Tyr-chr14.trna17
UAA not UAG



Leu-chr6.trna81
UGA and UAA, not UAG



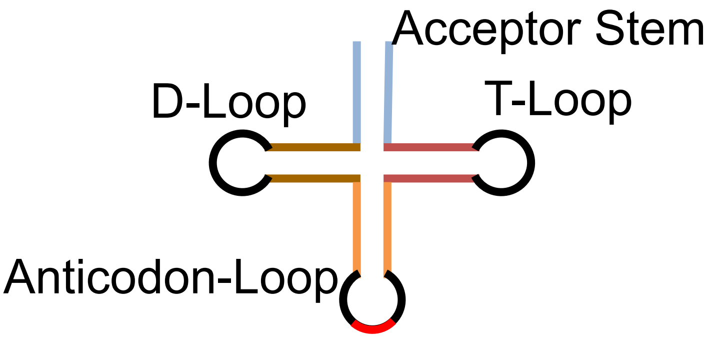
Ser-chr6.trna61



Lys-chr11.trna11
UAG not UAA

Predicted cloverleaf structures for ACE-tRNA examples used in this study. Anticodon type noted for versions that were functional for suppression. Cloverleaf predictions were based off the parent sequence (non-mutated) of each ACE-tRNA using tRNAscan-SE (http://lowelab.ucsc.edu/tRNAscan-SE/).

Supplementary Fig. 2B continued

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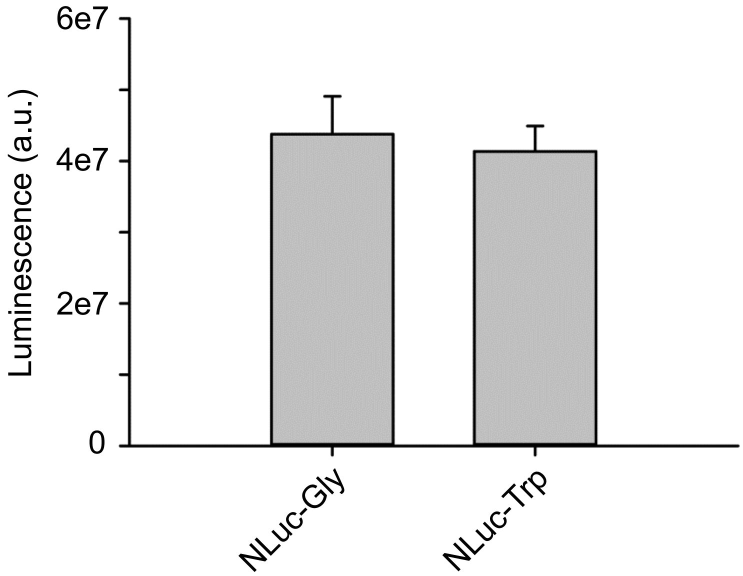
                              >>>>>>>..>>>>.......<<<<.>>>>>.......<<<<<.....>>>>>.......<<<<<<<<<<<<.

1)  Glychr1.trna122           GCAUUGGUGGUUCAGUGGUAGAAUUCUCGCCUUCAACGCGGGAG-ACCCGGGUUCAAUUCCCGGCCAAUGCA
2)  Glychr2.trna25            GCGCCGCUGGUGUAGUGGUAUCAUGCAAGAUUUCAAUUCUUGCG-ACCCGGGUUCGAUUCCCGGGCGGCGCA
3)  Glychr17.trna11           GCAUUGGUGGUUCAAUGGUAGAAUUCUCGCCUUCAACGCAGGAG-ACCCAGGUUCGAUUCCUGGCCAAUGCA
4)  Glychr1.trna120           GCGUUGGUGGUUUAGUGGUAGAAUUCUCGCCUUCAAUGCGGGA-GACCCGGGUUCAAUUCCCGGCCACUGCA
5)  Glychr1.trna2             GCCUUGGUGGUGCAGUGGUAGAAUUCUCGCCUUCAACGUGGGAG-ACCCGGGUUCAAUUCCCGGCCAAUGCA
6)  Glychr1.trna83            GG-----UGGUUCAGUGGU-AGAAUUCUCGCCUUCAACGCGGGAGACCCGGGUUUAAUUCCCGG-----UCA
7)  Glychr2.trna1             G------UGGUCUAGUGGUUAGGAUUCAGCGCUUCAACCGCCGCAGCCCGGGUUCGAUUCCCGGU-----CA
8)  Glychr1.trna2*            GCGUCAGUGGUUUAGUGGUGGAAUUCCUGCCUUCAAUGCACGAG-AUCCGUGUUCAACUCCUGGUUGGUGCA
9)  Glychr1.trna102           GCGUCAGUGGUUUAGUGGUGGAAUUCCUGCCUUCAAUGCACGAGAUCCGUGUUCAACUCCUGGUUGGUGCA
10) Glychr1.trna16            GCGUUGGCAGUUCAGUGGUAGAAUUCUCGCCUUCAACCCGGGAG-ACCUGGAUUCCAUUUCCGGCAAAUGCA
11) Glychr1.trna34            GCAUGGGUGGUUCAGUGGUAGAAUUCUCGCCUUCAACGCGGGAG-GCCCGGGUUCGAUUCCCGGCCCAUGCA
12) Glychr1.trna61            GCAUUGGUGGUUCAGUGGUAGAAUUCUCGCCUUCAACGCGGGAG-GCCCGGGUUCGAUUCCCGGCCAAUGCA
13) Glychr16.trna25           GCAUUGGUGGUUCAGUGGUAGAAUUCUCGCCUUCAACGCGGGAG-GCCCGGGUUUGAUUCCCGGCCAGUGCA
14) Glychr1.trna42            GCAUAGGUGGUUCAGUGGUAGAAUUCUUGCCUUCAACGCAGGAG-GCCCAGGUUUGAUUCCUGGCCCAUGCA
15) Glychr16.trna19           GCAUUGGUGGUUCAGUGGUAGAAUUCUCGCCUUCAAUGCGGGCG-GCCGGGCUUCGAUUCCUGGCCAAUGCA
16) Glychr6.trna80            GCAUGGGUGAUUCAGUGGUAGAAUUUUCACCUUCAAUGCAGGAG-GUCCAGGUUCAUUUCCUGGCCUAUGCA
17) Glychr19.trna2            GCGUUGGUGGUAUAGUGGUUAGCAUAGCUGCCUUCAAAGCAGUUGACCCGGGUUCGAUUCCCGGCCAACGCA
18) Glychr1.trna107           GCGUUGGUGGUAUAGUGGUGAGCAUAGCUGCCUUCAAAGCAGUUGACCCGGGUUCGAUUCCCGGCCAACGCA
19) Glychr17.trna9            GCGUUGGUGGUAUAGUGGUAAGCAUAGCUGCCUUCAAAGCAGUUGACCCGGGUUCGAUUCCCGGCCAACGCA
20) Glychr1.trna75            GCGUUGGUGGUAUAGUGGUGAGCAUAGUUGCCUUCAAAGCAGUUGACCCGGGCUCGAUUCCCGCCCAACGCA
21) Glychr1.trna75-65C-G      GCGUUGGUGGUAUAGUGGUGAGCAUAGUUGCCUUCAAAGCAGUUGACCCGGGCUCGAUUCCCGGCCAACGCA
```

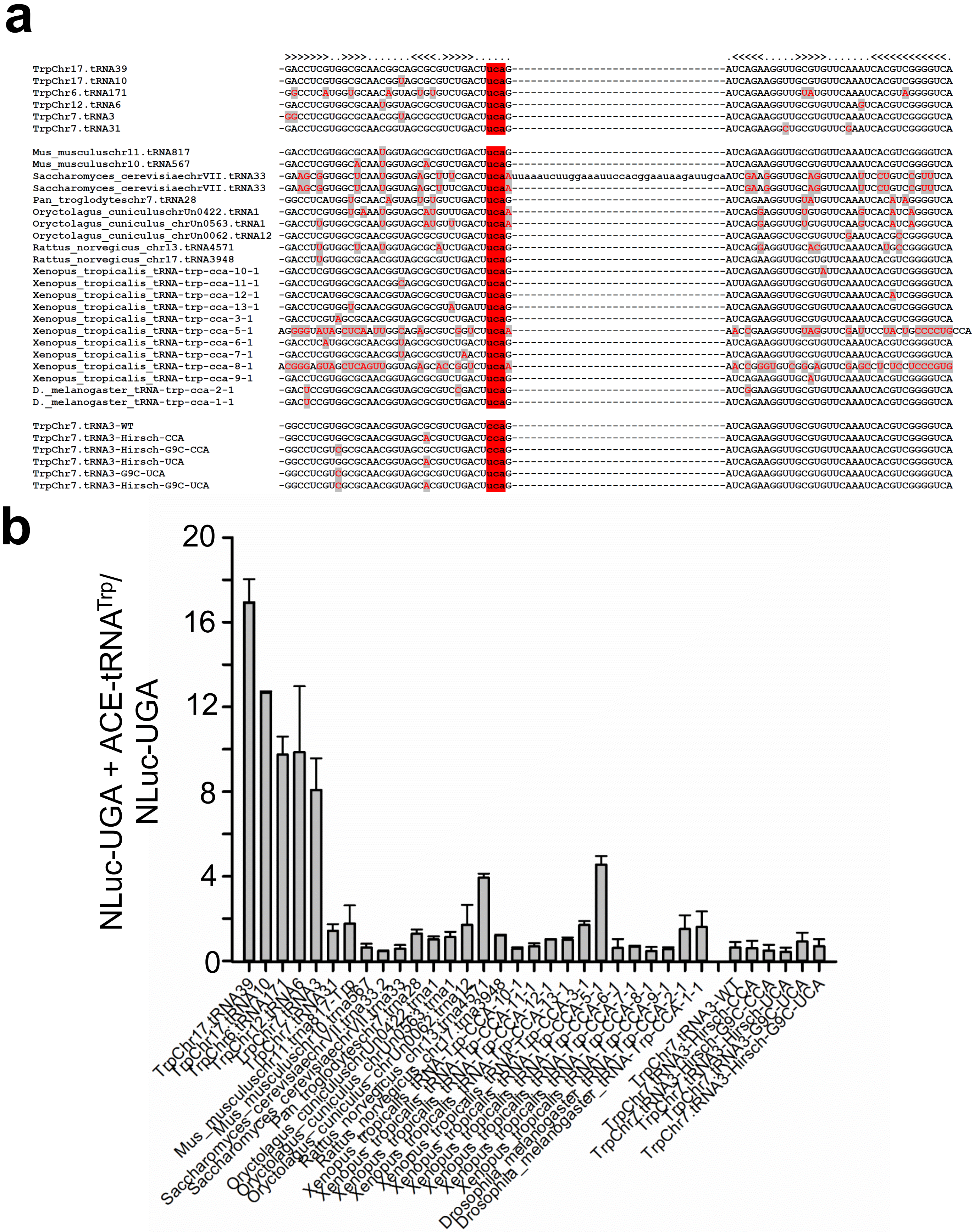
Alignment of Glycine tRNA sequences. 21 $tRNA^{Gly}$ human sequences demonstrate high sequence homology amongst tRNA clades. Color coding indicated in tRNA image.

Supplementary Fig. 3



Side-chain identity at p.162 in Nanoluciferase does not effect activity. Total luminescence activity is indicated for each mutation at site.

Supplementary Fig. 4



Analysis of ACE-tRNA^{Trp} sequences from multiple species and suppressor tRNA mutations.

Supplementary Fig. 5

a

```
MSFNTIIDWNSCTAEQQRQLLMRPAISASESITRTVNDILDNV
KARGDEALREYSAKFDKTTVTALKVSAEEIAAASERLSDELKQ
AMAVAVKNIETFHTAQKLPPVDVETQPGVRCQQVTRPVASVGL
YIPGGSAPLFSTVLMLATPASIAGCKKVVLCSPPPIADEILYA
AQLCGVQDVFNVGGAQAIAALAFGTESVPKVDKIFGPGNAFVT
EAKRQVSQRLDGAAIDMPAGPSEVLVIADSGATPDFVASDLLS
QAEHGPDSQVILLTPAADMARRVAEAVERQLAELPRAETARQA
LNASRLIVTKDLAQCVEISNQYGPEHLIIQTRNARELVDSITS
AGSVFLGDWSPESAGDYASGTNHVLPTYGYTATCSSLGLADFQ
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KEQAHHHHHHHHSGGSAWSHPQFEK
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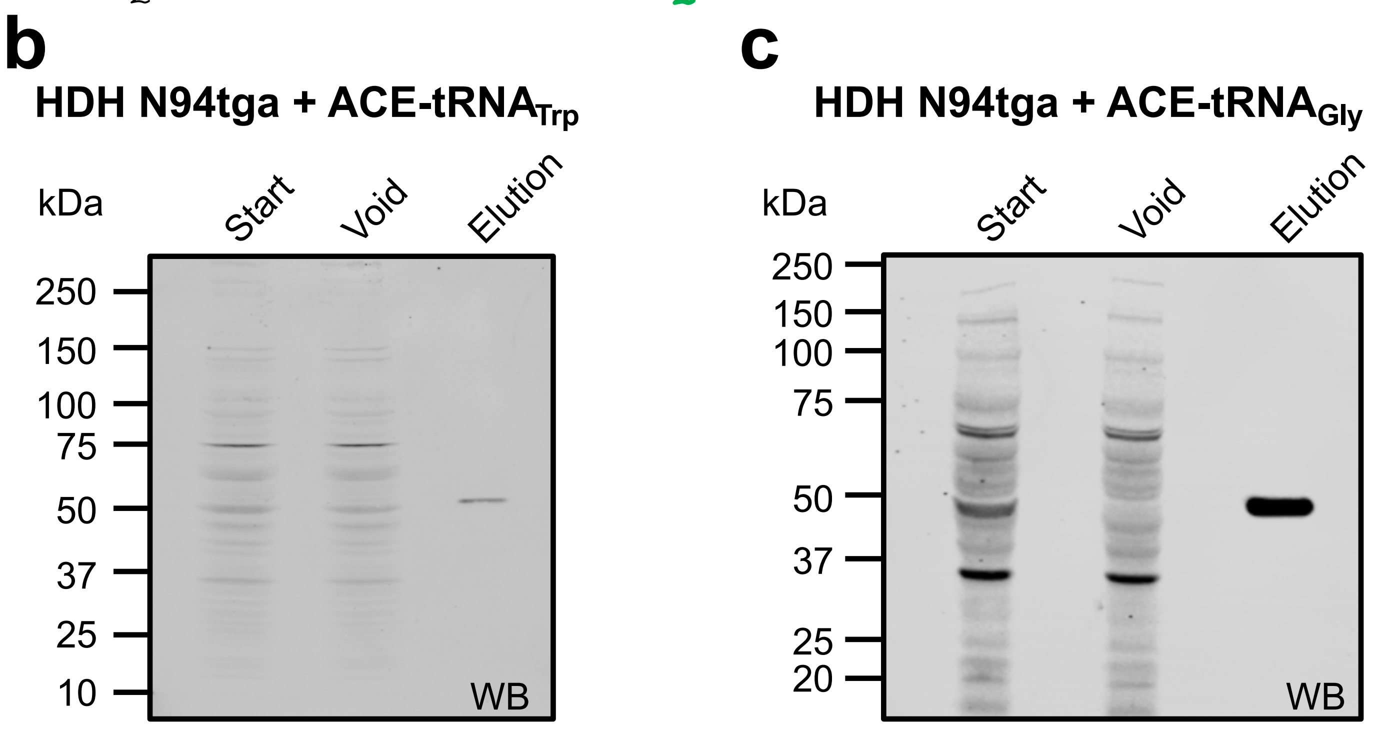
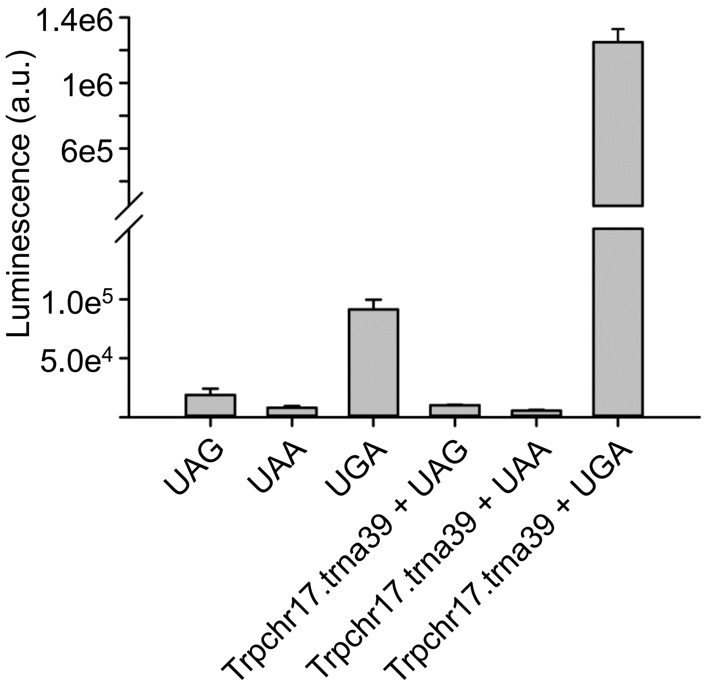


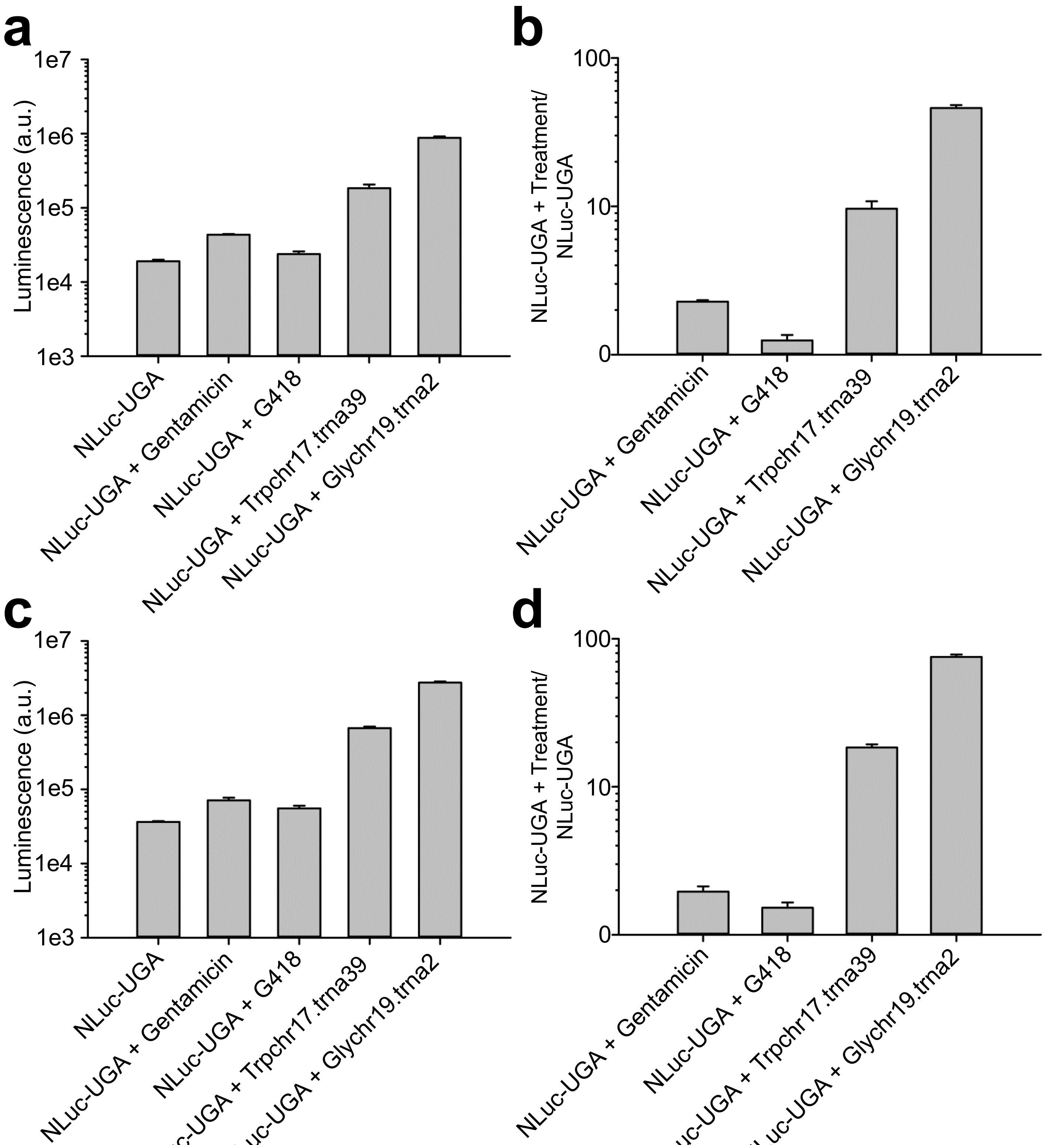
Histidinol dehydrogenase (HDH) His(8)-streptactin expression construct allows for efficient one-step isolation of protein from HEK293 cells. a) Protein sequence of HDH expression construct. Underlined sequence indicates coverage by mass spectrometry. The red asparagine (a.a. position 94) is the residue mutated to a TGA PTC for determining ACE-tRNA fidelity. The dual affinity tag is indicated in green. Silver stain of HDH protein following PTC suppression with **b)** Trpchr17.trna39 and **c)** Glychr19.trna2 .

Supplementary Fig. 6



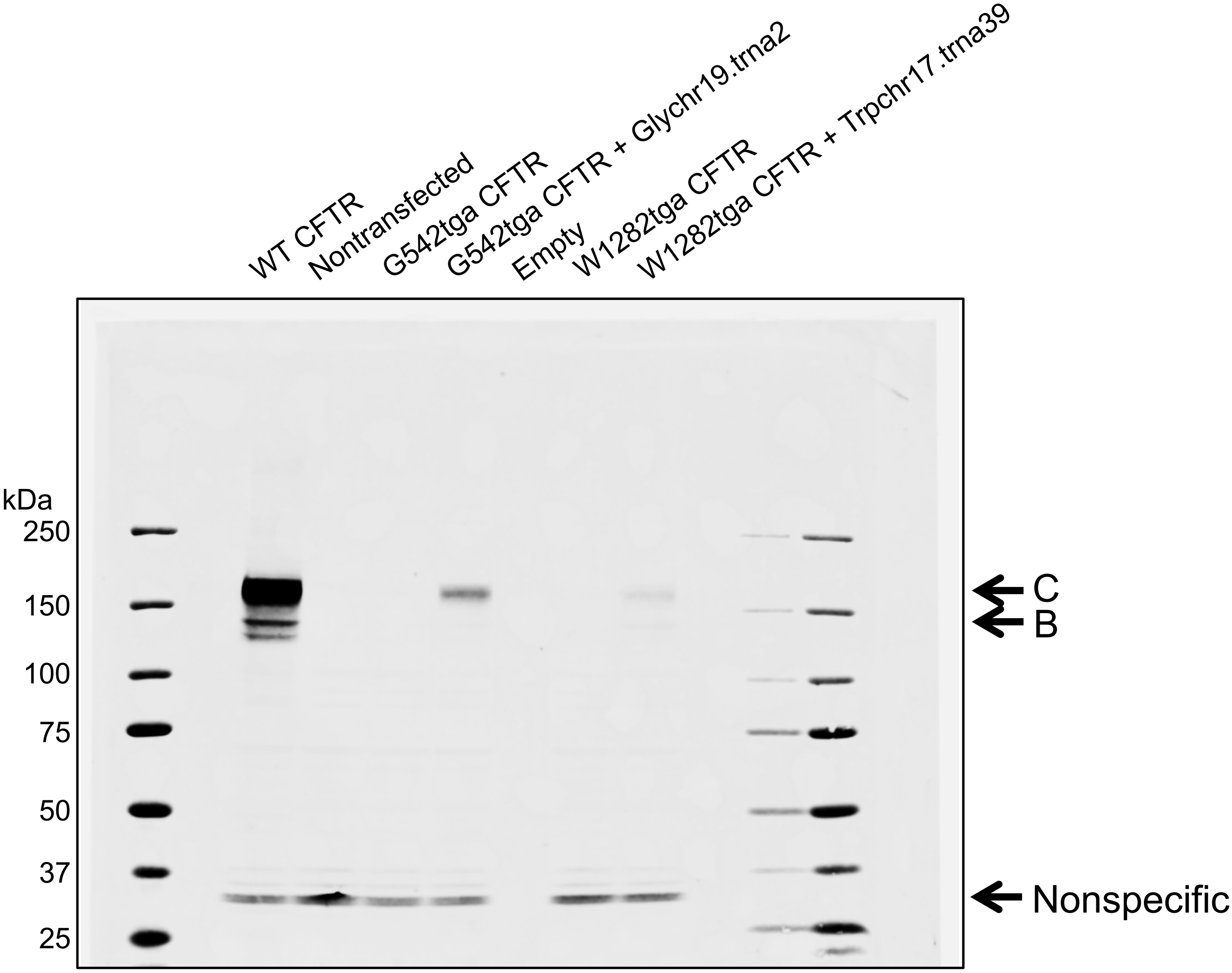
Stop codon specificity is maintained for ACE-tRNA^{Trp}. Suppression activity for tRNA Trp^{TGA} Trpchr17.trna39, the top performing Trp^{TGA} suppressor tRNA, Figure 2. This tRNA was co-expressed with the indicated pNano-STOP plasmid.

Supplementary Fig. 7

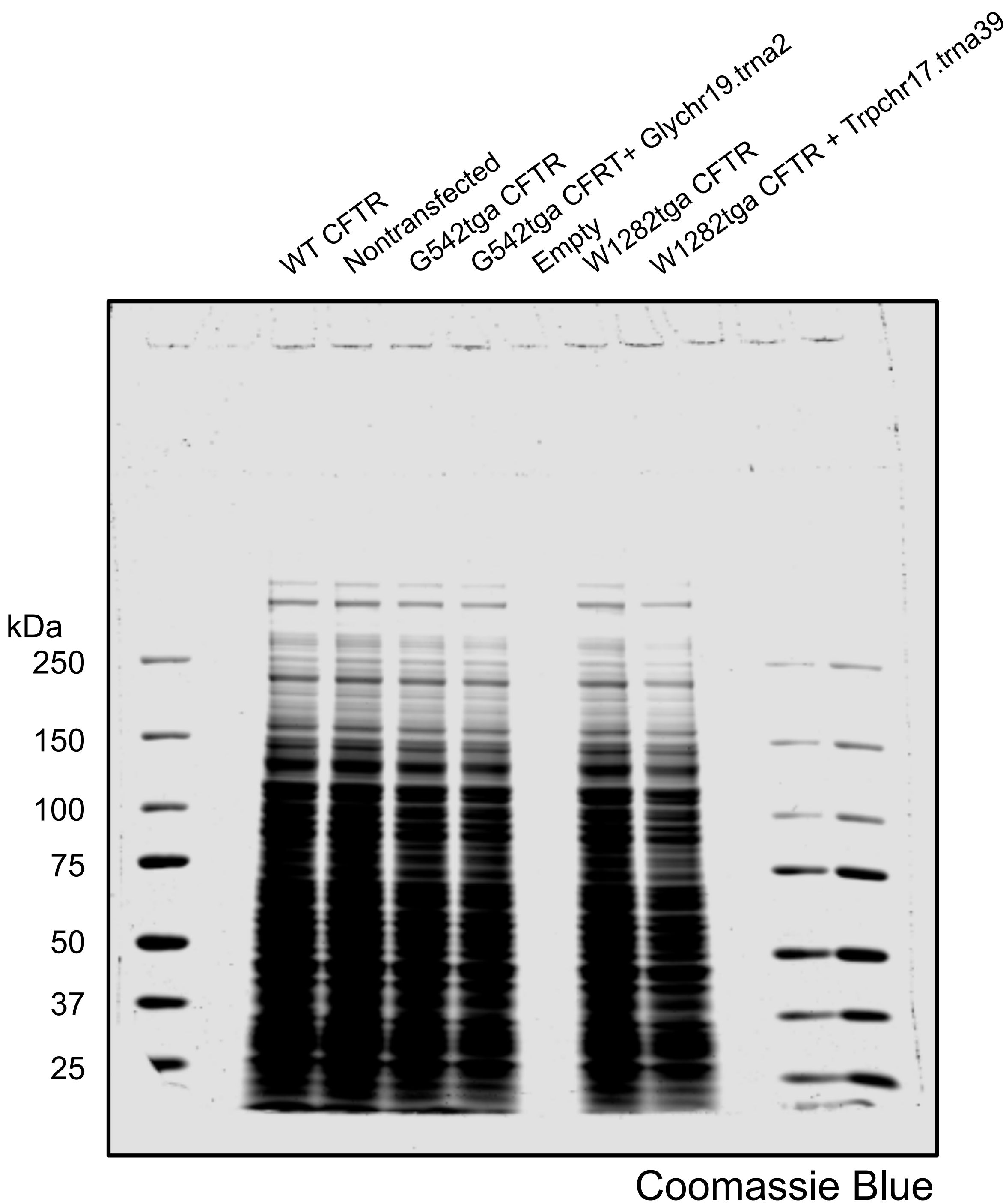


ACE-tRNAs are more efficient than aminoglycoside PTC suppression. a) Raw and **b)** normalized luminescence measured 24hrs following addition of gentamicin (40uM), G418 (150uM) and transfection with Trpchr17.trna39 and Glychr19.trna2 in HEK293 cells stably expressing PTC reporter Nluc-UGA. **c)** Raw and **d)** normalized luminescence measured 24hrs following addition of gentamicin (40uM), G418 (150uM) and co-transfection with Trpchr17.trna39 and Glychr19.trna2 in HEK293 cells.

Supplementary Fig. 8

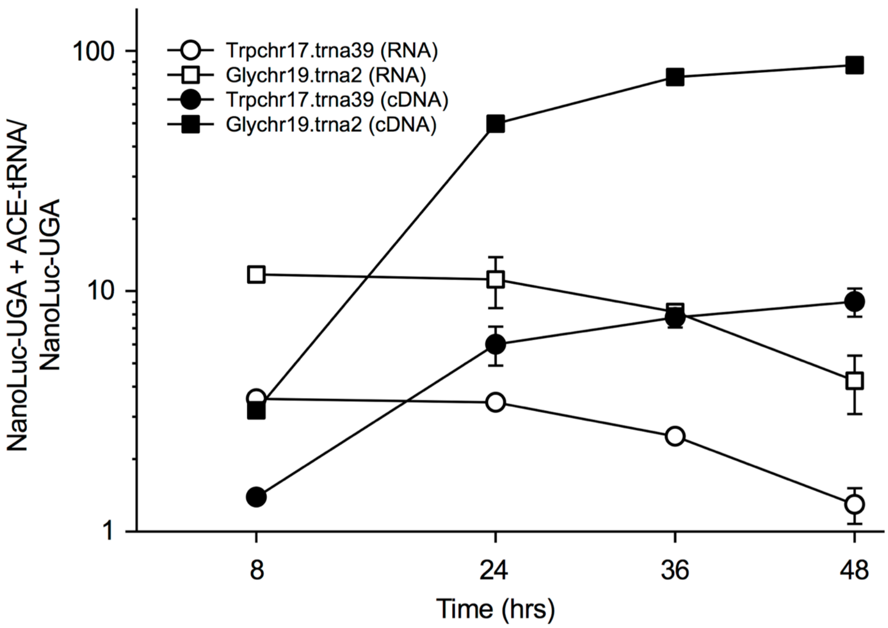


Full-length Western blot figure 5d.



Full-length Coomassie stain of replicate SDS-PAGE gel for figure 5d.

Supplementary Fig. 10



Comparison of time courses of ACE-tRNA activity following delivery as RNA or cDNA. ACE-tRNAs were delivered to HEK293 cells that stably express pNanoLuc-UGA as described in the methods, however only 5μl of the reaction mix was added to the cells to reduce the effect of transfection reagents on cell viability. ACE-tRNA delivered as RNA (open symbols), was more rapid in rescuing expression of the PTC reporter than cDNA constructs (closed circles). However, ACE-tRNA activity continued to rise over the 48 hrs when expressed from cDNA and decreased as a RNA deliverable.

Supplementary Table 1. rRNA depletion oligos

Reference	Sequence (5' to 3')
NR_003285	TCCTCCCGGGGCTACGCCTGTCTGAGCGTCGCT
NR_003286	GGGGGGATGCGTGCATTTATCAGATCA
	TCCCCGCCCCTTGCCTCTCGGCGCCC
	TTGGTGACTCTAGATAACCTCGGGCCGATCGC
	GAGCCGCCTGGATACCGCAGCTAGGAATAATGGA
NR_003287	TCGTGGGGGGCCCAAGTCCTTCTGATCGAGGCCC
	TCCGCCGAGGGCGCACCACCGGCCCGTCTCGCC
	GAGCCTCGGTTGGCCTCGGATAGCCGGTCCCCCGC
	GGGGCCGGGCCACCCCTCCCACGGCGCG
	GCGCCCCGGGCGGGTCGCGCCGTCGGGCCCGG
	CTCGCTTCTGGCGCCAAGCGCCCGGC
	GCGCGCCGCGGCTGGACGAGGCGCCGCCGCC

Supplementary Table 2: Oligo Sequences (5'-3')

	pNanoLuc plasmid for High-throughput cloning and screening mutagenesis primers.
pNanoLuc-For	GCCACCATGGTATTCACACTCGAAGATTTCGTTG
pNanoLuc- TGA-Rev	TTACGCCAGAATGCGTTCGCACAGCCGCCAGCCGGTCACTCATCC
pNanoLuc- TAA-Rev	TTACGCCAGAATGCGTTCGCACAGCCGCCAGCCGGTCACTTATCC
pNanoLuc- TAG-Rev	TTACGCCAGAATGCGTTCGCACAGCCGCCAGCCGGTCACCTATCC
pNanoLuc- WT-Rev	TTACGCCAGAATGCGTTCGCACAGCCGCCAGCCGGTCACTCCACC
	pNanoLuc plasmid for High-throughput cloning and screening Gibson assembly primers.
pNanoLuc-GAFor	ctggctagcgtttaaacttaagcttGCCACCATGGTATTCACAC
pNanoLuc- TGA-GARev	actgtgctggatatctgcagaattcTTACGCCAGAATGCGTTC
pNanoLuc- TAA-GARev	actgtgctggatatctgcagaattcCTACGCCAGAATGCGTTC
pNanoLuc- TAG-GARev	actgtgctggatatctgcagaattcTTACGCCAGAATGCGTTC
pNanoLuc- WT-GARev	actgtgctggatatctgcagaattcTTACGCCAGAATGCGTTC
	Primers for generation of 4 x ACE-tRNA expression Golden Gate puc57 plasmid
tRNA 1F	cacagacgaagactgttcctaatacgactcactatagagcg
tRNA 1R	cacagacgaagactggtattaaattaaccctcactaaagcaaa
tRNA 2F	cacagacgaagacgtatacgactcactatagagcg
tRNA 2R	cacagacgaagacgttcgtattaaattaaccctcactaaagcaaa
tRNA 3F	cacagacgaagacctacgactcactatagagcgc
tRNA 3R	cacagacgaagaccttaaccctcactaaagcaaaaaa
tRNA 4F	cacagacgaagacacgttaatttaatacgactcactatagagcg
tRNA 4R	cacagacgaagacaccctgaattaaccctcactaaagcaaa
	Oligos for Golden Gate MCS in puc57 (EcoRI/HindIII)
GoldenGateMCS-For	aattcttcccgagacgTTCCAAGTCTTCatGAAGACTACAGGcgtctcccagga
GoldenGateMCS-Rev	agcttcctgggagacgCCTGTAGTCTTCatGAAGACTTGGAAcgtctcgggaag
	Primers for amplification SV40 polyA termination signal and Gibson Assembly
SV40 term-For	acagtggcggccgctcgagtTTGTTTATTGCAGCTTATAATG
SV40 term-Rev	tggccgattcattaatgcagctgATAAGATACATTGATGAGTTTGG

Synthesized ccdB Golden Gate cDNA (digested plasmid with PciI and Gibson assembled cDNA)

tcttatcatgtctggatcgaCTAGAGGGCCTTCCTAATACGACTCACTATAGAGCGCTCCGGTTTTTCTG
TGCTGAACCTCAGGGGACGCCGACACACGTACACGTCTAGTCTTCGCGGCCGCATTAGGCACCCCAGGCT
TTACACTTTATGCTTCCGGCTCGTATAATGTGTGGATTTTGAGTTAGGATCCGGCGAGATTTTCAGGAGC
TAAGGAAGCTAAAATGGAGAAAAAAATCACTGGATATACCACCGTTGATATATCCCAATGGCATCGTAAA
GAACATTTTGAGGCATTTCAGTCAGTTGCTCAATGTACCTATAACCAGACCGTTCAGCTGGATATTACGG
CCTTTTTAAAGACCGTAAAGAAAAATAAGCACAAGTTTTATCCGGCCTTTATTCACATTCTTGCCCGCCT
GATGAATGCTCATCCGGAATTCCGTATGGCAATGAAAGACGGTGAGCTGGTGATATGGGATAGTGTTCAC
CCTTGTTACACCGTTTTCCATGAGCAAACTGAAACGTTTTCATCGCTCTGGAGTGAATACCACGACGATT
TCCGGCAGTTTCTACACATATATTCGCAAGATGTGGCGTGTTACGGTGAAAACCTGGCCTATTTCCCTAA
AGGGTTTATTGAGAATATGTTTTTCGTCTCAGCCAATCCCTGGGTGAGTTTCACCAGTTTTGATTTAAAC
GTGGCCAATATGGACAACTTCTTCGCCCCCGTTTTCACCATGGGCAAATATTATACGCAAGGCGACAAGG
TGCTGATGCCGCTGGCGATTCAGGTTCATCATGCCGTCTGTGATGGCTTCCATGTCGGCAGAATGCTTAA
TGAATTACAACAGTACTGCGATGAGTGGCAGGGCGGGGCGTAAAGATCTGGATCCGGCTTACTAAAAGCC
AGATAACAGTATGCGTATTTGCGCGCTGATTTTTGCGGTATAAGAATATATACTGATATGTATACCCGAA
GTATGTCAAAAAGAGGTGTGCTATGAAGCAGCGTATTACAGTGACAGTTGACAGCGACAGCTATCAGTTG
CTCAAGGCATATATGATGTCAATATCTCCGGTCTGGTAAGCACAACCATGCAGAATGAAGCCCGTCGTCT
GCGTGCCGAACGCTGGAAAGCGGAAAATCAGGAAGGGATGGCTGAGGTCGCCCGGTTTATTGAAATGAAC
GGCTCTTTTGCTGACGAGAACAGGGACTGGTGAAATGCAGTTTAAGGTTTACACCTATAAAAGAGAGAGC
CGTTATCGTCTGTTTGTGGATGTACAGAGTGATATTATTGACACGCCCGGGCGACGGATGGTGATCCCCC
TGGCCAGTGCACGTCTGCTGTCAGATAAAGTCTCCCGTGAACTTTACCCGGTGGTGCATATCGGGGATGA
AAGCTGGCGCATGATGACCACCGATATGGCCAGTGTGCCGGTCTCCGTTATCGGGGAAGAAGTGGCTGAT
CTCAGCCACCGCGAAAATGACATCAAAAACGCCATTAACCTGATGTTCTGGGGAATATAAATGTCAGGCT
CCGTTATACACAGCCAGTCTGCAGGGAAgaagaccgGTCCTTTTTTTGCTTTAGTGAGGGTTAATTCAGT
GAGCAAAAGGC

The following mutants gibson assembled into the naturally occurring HindIII-EcoRI sites:

pNanoLuc-TGA
gccaccATGGTaTTCACACTCGAAGATTTCGTTGGGGACTGGCGACAGACAGCCGGCTACAACC
TGGACCAAGTCCTTGAACAGGGAGGTGTGTCCAGTTTGTTTCAGAATCTCGGGGTGTCCGTAAC
TCCGATCCAAAGGATTGTCCTGAGCGGTGAAAATGGGCTGAAGATCGACATCCATGTCATCATC
CCGTATGAAGGTCTGAGCGGCGACCAAATGGGCCAGATCGAAAAAATTTTTAAGGTGGTGTACC
CTGTGGATGATCATCACTTTAAGGTGATCCTGCACTATGGCACACTGGTAATCGACGGGGTTAC
GCCGAACATGATCGACTATTTCGGACGGCCGTATGAAGGCATCGCCGTGTTCGACGGCAAAAAG
ATCACTGTAACAGGGACCCTGTGGAACGGCAACAAAATTATCGACGAGCGCCTGATCAACCCCG
ACGGCTCCCTGCTGTTCCGAGTAACCATCAACGGATGAG**TGA**CCGGCTGGCGGCTGTGCGAACG
CATTCTGGCG*TAA*

pNanoLuc-TAA
gccaccATGGTaTTCACACTCGAAGATTTCGTTGGGGACTGGCGACAGACAGCCGGCTACAACC
TGGACCAAGTCCTTGAACAGGGAGGTGTGTCCAGTTTGTTTCAGAATCTCGGGGTGTCCGTAAC
TCCGATCCAAAGGATTGTCCTGAGCGGTGAAAATGGGCTGAAGATCGACATCCATGTCATCATC
CCGTATGAAGGTCTGAGCGGCGACCAAATGGGCCAGATCGAAAAAATTTTTAAGGTGGTGTACC
CTGTGGATGATCATCACTTTAAGGTGATCCTGCACTATGGCACACTGGTAATCGACGGGGTTAC
GCCGAACATGATCGACTATTTCGGACGGCCGTATGAAGGCATCGCCGTGTTCGACGGCAAAAAG

ATCACTGTAACAGGGACCCTGTGGAACGGCAACAAAATTATCGACGAGCGCCTGATCAACCCCG
ACGGCTCCCTGCTGTTCCGAGTAACCATCAACGGATGAG**TAA**CCGGCTGGCGGCTGTGCGAACG
CATTCTGGCG*TAG*

pNanoLuc-TAG

gccaccATGGTaTTCACACTCGAAGATTTCGTTGGGGACTGGCGACAGACAGCCGGCTACAACC
TGGACCAAGTCCTTGAACAGGGAGGTGTGTCCAGTTTGTTTCAGAATCTCGGGGTGTCCGTAAC
TCCGATCCAAAGGATTGTCCTGAGCGGTGAAAATGGGCTGAAGATCGACATCCATGTCATCATC
CCGTATGAAGGTCTGAGCGGCGACCAAATGGGCCAGATCGAAAAAATTTTTAAGGTGGTGTACC
CTGTGGATGATCATCACTTTAAGGTGATCCTGCACTATGGCACACTGGTAATCGACGGGGTTAC
GCCGAACATGATCGACTATTTCGGACGGCCGTATGAAGGCATCGCCGTGTTCGACGGCAAAAAG
ATCACTGTAACAGGGACCCTGTGGAACGGCAACAAAATTATCGACGAGCGCCTGATCAACCCCG
ACGGCTCCCTGCTGTTCCGAGTAACCATCAACGGATGAG**TAG**CCGGCTGGCGGCTGTGCGAACG
CATTCTGGCG*TAA*

pNanoLuc-WT

gccaccATGGTaTTCACACTCGAAGATTTCGTTGGGGACTGGCGACAGACAGCCGGCTACAACC
TGGACCAAGTCCTTGAACAGGGAGGTGTGTCCAGTTTGTTTCAGAATCTCGGGGTGTCCGTAAC
TCCGATCCAAAGGATTGTCCTGAGCGGTGAAAATGGGCTGAAGATCGACATCCATGTCATCATC
CCGTATGAAGGTCTGAGCGGCGACCAAATGGGCCAGATCGAAAAAATTTTTAAGGTGGTGTACC
CTGTGGATGATCATCACTTTAAGGTGATCCTGCACTATGGCACACTGGTAATCGACGGGGTTAC
GCCGAACATGATCGACTATTTCGGACGGCCGTATGAAGGCATCGCCGTGTTCGACGGCAAAAAG
ATCACTGTAACAGGGACCCTGTGGAACGGCAACAAAATTATCGACGAGCGCCTGATCAACCCCG
ACGGCTCCCTGCTGTTCCGAGTAACCATCAACGGATGAG**TGG**CCGGCTGGCGGCTGTGCGAACG
CATTCTGGCG*TAA*

HDH-TGA-HIS-STREP

ATGTCATTCAATACTATAATCGACTGGAACAGCTGCACTGCTGAGCAGCAAAGACAGCTGTTGATGAGAC
CAGCGATTTCCGCGTCCGAAAGTATCACAAGAACGGTGAATGATATACTTGATAACGTGAAAGCCAGAGG
CGACGAGGCGCTTCGAGAGTACAGCGCTAAATTTGACAAAACTACCGTAACGGCACTTAAAGTCTCTGCT
GAAGAAATCGCAGCCGCCAGCGAGCGGCTTTCTGACGAACTCAAGCAGGCGATGGCCGTTGCTGTAAAA**T**
GATATCGAAACTTTCCACACCGCTCAAAAATTGCCTCCGGTTGATGTAGAAACACAACCCGGAGTCCGCT
GCCAGCAAGTTACCCGGCCTGTAGCCTCAGTCGGATTGTATATTCCGGGTGGATCTGCGCCTCTGTTCAG
CACAGTCCTCATGCTGGCGACGCCCGCATCTATCGCTGGATGTAAGAAAGTCGTATTGTGTTCTCCTCCC
CCTATTGCAGATGAAATATTGTACGCCGCCCAACTGTGTGGTGTCCAAGACGTATTCAATGTGGGAGGCG
CTCAGGCTATAGCTGCTTTGGCATTTGGCACAGAGTCTGTCCCCAAGGTCGACAAGATCTTCGGTCCAGG
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Genbank sequence for pNanoLuc-TGA-pcDNA3.1

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pNanoLuc-TGA-pcDNA3.1

LOCUS       NanLuc_pcDNA3.1_BbsI_le 5025 bp ds-DNA     circular     8-
DEC-2018

DEFINITION  .

FEATURES             Location/Qualifiers

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