Oligonucleotide sequences (5' → 3') used in this study.

Primers for pCDF-1b linearization:

pCDF-1b-fwd GGTATATCTCCTTATTAAAGTTAAACAAAATTATTTCTACAGGGG

pCDF-1b-rev TTAACCTAGGCTGCTGCCACCG

Primers for *Pt*NTT2 cloning:

PtNTT2-fwd GTTTAACTTTAATAAGGAGATATACCATGAGACCATTTCCGAC

PtNTT2-rev GCAGCAGCCTAGGTTAACTACTTTTCTTTGTTGGTCTTTG

Primers for *Tp*NTT2 cloning:

TpNTT2-fwd GTTTAACTTTAATAAGGAGATATACCATGAAAAAATCTTGTACAATCC

TpNTT2-rev GCAGCAGCCTAGGTTAACTACTTCTGGTGCTCTTTTG

Primers for pUC19 linearization:

pUC19-lin-fwd TGGGGTGCCTAATGAGTGAGC

pUC19-lin-rev CTATGACCATGATTACGCCAAGCTTG

Unnatural fragment with d**NaM:**

TK-1-d**NaM** CTGTTTCCTGTGTGAAATTGTTATCCGCTCACA **NaM** TTCCACACAACATACGAGCCGGAAGCAT AAAGTGTAAAGCC

Natural fragment with dT:

TK-1-dT CTGTTTCCTGTGTGAAATTGTTATCCGCTCACA **T** TTCCACACAACATACGAGCCGGAAGCATAA AGTGTAAAGCC

Primers for unnatural fragment cloning:

pUC19-fusion-fwd CAAGCTTGGCGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGC

pUC19-fusion-rev GCTCACTCATTAGGCACCCCAGGCTTTACACTTTATGCTTCCGGC

Primers for pINF analysis by gel shift and Sanger sequencing:

pUC19-seq-fwd GCAGGCATGCAAGCTTGGCGTAATCATGG

pUC19-seq2-fwd GCTGCAAGGCGATTAAGTTGGGTAACGCC

pUC19-seq-rev CTGGCACGACAGGTTTCCCGACTGG

Example of calculation of plasmid amplification after 19 h:

Known (or measured) parameters:

Number of colonies after transformation (10 µl of culture plated)	1750 ± 200
Dilution for growth experiment, fold	33.3
Volume of culture purified for plasmid extraction, µl	100
Elution volume, µl	30
pINF fraction (mass) in total plasmid mixture, %	43
Total plasmid concentration, ng μl^{-1}	2.97
Biotin shift, %	74.2

Calculation of plasmid concentration before growth:

$$\frac{175\ molecules\ \mu l^{-1}}{33.3} = 5.3\ molecules\ \mu l^{-1}$$

Calculation of plasmid amount in 100 µl of media after growth (19 h):

pINF amount: 2.97 ng μl^{-1} × 43% × 30 µl = 38 ng

Number of pINF molecules:

$$\frac{38 \times 10^{-9} g}{2686\ bp \times 660\ g\ mol^{-1}\ bp^{-1}} \times 6.02 \times 10^{23}\ molecules\ mol^{-1} = 1.3 \times 10^{10}\ molecules$$

Plasmid concentration: $\frac{1.3 \times 10^{10} molecules}{100 \mu l} = 1.3 \times 10^{8}\ molecules\ \mu l^{-1}$

Calculation of amplification (A), the number of doubling (n), retention (F), and fidelity (f)

$$A = \frac{1.3 \times 10^{8} molecules\ \mu l^{-1}}{5.3\ molecules\ \mu l^{-1}} = 2.4 \times 10^{7}$$

$$n = \log_2(2.4 \times 10^{7}) = 24.5$$

$$F = \frac{0.742 - 0.020}{0.772} = 93.5\%$$ (see biotin shift calibration and Extended Data Fig. 6).

$$f = 0.935^{\frac{1}{24.5}} = 99.7\%$$

Since plasmid recovery during purification is below 100%, our calculations underestimate the amplification level (A) and thus the number of doubling (n).

The fidelity (retention per doubling) is related to retention of the UBP (F) as $f^n = F$ and, since $n = \log_2(A)$, fidelity was calculated as $f = F^{\frac{1}{n}}$.

Sequence of the pACS plasmid with the *Pt*NTT2 gene sequence capitalized.

```
>pACS_PtNTT2
ggggaattgtgagcggataacaattcccctgtagaaataattttgtttaactttaataaggagatataccATGAGACCATTTCCGACGATTGCCTTGATT
TCGGTTTTTCTTTCGGCGGCGACTCGCATTTCGGCAACTTCCTCTCATCAAGCAAGTGCACTTCCTCTCAAAAAGGGAACGCATGTCCCGGACTCTCCGA
AGTTGTCAAAGCTATATATCATGGCCAAAACCAAGAGTGTATCCTCGTCCTTCGACCCCCCTCGGGGAGGCAGTACTGTTGCACCAACTACACCGTTGGC
AACCGGCGGTGCGCTCCGCAAAGTGCGACAAGCCGTCTTTCCCATCTACGGAAACCAAGAAGTCACCAAATTTCTGCTCATCGGATCCATTAAATTCTTT
ATAATCTTGGCACTCACGCTCACGCGTGATACCAAGGACACGTTGATTGTCACGCAATGTGGTGCCGAAGCGATTGCCTTTCTCAAAATATACGGGGTGC
TACCCGCAGCGACCGCATTTATCGCGCTCTATTCCAAAATGTCCAACGCCATGGGCAAAAAAATGCTATTTTATTCCACTTGCATTCCTTTCTTTACCTT
TTTCGGGCTGTTTGATGTTTTCATTTACCCGAACGCGGAGCGACTGCACCCTAGTTTGGAAGCCGTGCAGGCAATTCTCCCGGGCGGTGCCGCATCTGGC
GGCATGGCGGTTCTGGCCAAGATTGCGACACACTGGACATCGGCCTTATTTTACGTCATGGCGGAAATATATTCTTCCGTATCGGTGGGGCTATTGTTTT
GGCAGTTTGCGAACGACGTCGTCAACGTGGATCAGGCCAAGCGCTTTTATCCATTATTTGCTCAAATGAGTGGCCTCGCTCCAGTTTTAGCGGGCCAGTA
TGTGGTACGGTTTGCCAGCAAAGCGGTCAACTTTGAGGCATCCATGCATCGACTCACGGCGGCCGTAACATTTGCTGGTATTATGATTTGCATCTTTTAC
CAACTCAGTTCGTCATATGTGGAGCGAACGGAATCAGCAAAGCCAGCGGCAGATAACGAGCAGTCTATCAAACCGAAAAAGAAGAAACCCAAAATGTCCA
TGGTTGAATCGGGGAAATTTCTCGCGTCAAGTCAGTACCTGCGTCTAATTGCCATGCTGGTGCTGGGATACGGCCTCAGTATTAACTTTACCGAAATCAT
GTGGAAAAGCTTGGTGAAGAAACAATATCCAGACCCGCTAGATTATCAACGATTTATGGGTAACTTCTCGTCAGCGGTTGGTTTGAGCACATGCATTGTT
ATTTTCTTCGGTGTGCACGTGATCCGTTTGTTGGGGTGGAAAGTCGGAGCGTTGGCTACACCTGGGATCATGGCCATTCTAGCGTTACCCTTTTTTGCTT
GCATTTTGTTGGGTTTGGATAGTCCAGCACGATTGGAGATCGCCGTAATCTTTGGAACAATTCAGAGTTTGCTGAGCAAAACCTCCAAGTATGCCCTTTT
CGACCCTACCACACAAATGGCTTATATTCCTCTGGACGACGAATCAAAGGTCAAAGGAAAAGCGGCAATTGATGTTTTGGGATCGCGGATTGGCAAGAGT
GGAGGCTCACTGATCCAGCAGGGCTTGGTCTTTGTTTTTGGAAATATCATTAATGCCGCACCTGTAGTAGGGGTTGTCTACTACAGTGTCCTTGTTGCGT
GGATGAGCGCAGCTGGCCGACTAAGTGGGCTTTTTCAAGCACAAACAGAAATGGATAAGGCCGACAAAATGGAGGCAAAGACCAACAAAGAAAAGTAGtt
aacctaggctgctgccaccgctgagcaataactagcataaccccttggggcctctaaacgggtcttgaggggttttttgctgaaacctcaggcatttgag
aagcacacggtcacactgcttccggtagtcaataaaccggtaaaccagcaatagacataagcggctatttaacgaccctgccctgaaccgacgaccgggt
catcgtggccggatcttgcggcccctcggcttgaacgaattgttagacattatttgccgactaccttggtgatctcgcctttcacgtagtggacaaattc
ttccaactgatctgcgcgcgaggccaagcgatcttcttcttgtccaagataagcctgtctagcttcaagtatgacgggctgatactgggccggcaggcgc
tccattgcccagtcggcagcgacatccttcggcgcgattttgccggttactgcgctgtaccaaatgcgggacaacgtaagcactacatttcgctcatcgc
cagcccagtcgggcggcgagttccatagcgttaaggtttcatttagcgcctcaaatagatcctgttcaggaaccggatcaaagagttcctccgccgctgg
acctaccaaggcaacgctatgttctcttgcttttgtcagcaagatagccagatcaatgtcgatcgtggctggctcgaagatacctgcaagaatgtcattg
cgctgccattctccaaattgcagttcgcgcttagctggataacgccacggaatgatgtcgtcgtgcacaacaatggtgacttctacagcgcggagaatct
cgctctctccaggggaagccgaagtttccaaaaggtcgttgatcaaagctcgccgcgttgtttcatcaagccttacggtcaccgtaaccagcaaatcaat
atcactgtgtggcttcaggccgccatccactgcggagccgtacaaatgtacggccagcaacgtcggttcgagatggcgctcgatgacgccaactacctct
gatagttgagtcgatacttcggcgatcaccgcttccctcatactcttccttttttcaatattattgaagcatttatcagggttattgtctcatgagcggat
acatatttgaatgtatttagaaaaataaacaaatagctagctcactcggtcgctacgctccgggcgtgagactgcggcgggcgctgcggacacatacaaa
gttacccacagattccgtggataagcaggggactaacatgtgaggcaaaacagcagggccgcgccggtggcgtttttccataggctccgccctcctgcca
gagttcacataaacagacgcttttccggtgcatctgtgggagccgtgaggctcaaccatgaatctgacagtacgggcgaaacccgacaggacttaaagat
ccccaccgtttccggcgggtcgctccctcttgcgctctcctgttccgaccctgccgtttaccggatacctgttccgcctttctcccttacgggaagtgtg
gcgctttctcatagctcacacactggtatctcggctcggtgtaggtcgttcgctccaagctgggctgtaagcaagaactccccgttcagcccgactgctg
cgccttatccggtaactgttcacttgagtccaacccggaaaagcacggtaaaacgccactggcagcagccattggtaactgggagttcgcagaggatttg
tttagctaaacacgcggttgctcttgaagtgtgcgccaaagtccggctacactggaaggacagatttggttgctgtgctctgcgaaagccagttaccacg
gttaagcagttccccaactgacttaaccttcgatcaaaccacctccccaggtggtttttcgtttacagggcaaaagattacgcgcagaaaaaaaggatc
tcaagaagatcctttgatcttttctactgaaccgctctagatttcagtgcaatttatctcttcaaatgtagcacctgaagtcagccccatacgatataag
ttgtaattctcatgttagtcatgccccgcgcccaccggaaggagctgactgggttgaaggctctcaagggcatcggtcgagatcccggtgcctaatgagt
gagctaacttacattaattgcgttgcgctcactgcccgctttccagtcgggaaacctgtcgtgccagctgcattaatgaatcggccaacgcgcggggaga
ggcggtttgcgtattgggcgccagggtggtttttcttttcaccagtgagacgggcaacagctgattgcccttcaccgcctggccctgagagagttgcagc
aagcggtccacgctggtttgccccagcaggcgaaaatcctgtttgatggtggttaacggcgggatataacatgagctgtcttcggtatcgtcgtatccca
ctaccgagatgtccgcaccaacgcgcagcccggactcggtaatggcgcgcattgcgcccagcgccatctgatcgttggcaaccagcatcgcagtgggaac
gatgccctcattcagcatttgcatggtttgttgaaaaccggacatggcactccagtcgccttcccgttccgctatcggctgaatttgattgcgagtgaga
tatttatgccagccagccagacgcagacgcgccgagacagaacttaatgggcccgctaacagcgcgatttgctggtgacccaatgcgaccagatgctcca
cgcccagtcgcgtaccgtcttcatgggagaaaataatactgttgatgggtgtctggtcagagacatcaagaaataacgccggaacattagtgcaggcagc
ttccacagcaatggcatcctggtcatccagcggatagttaatgatcagcccactgacgcgttgcgcgagaagattgtgcaccgccgctttacaggcttcg
acgccgcttcgttctaccatcgacaccaccacgctggcacccagttgatcggcgcgagatttaatcgccgcgacaatttgcgacggcgcgtgcagggcca
gactggaggtggcaacgccaatcagcaacgactgtttgcccgccagttgttgtgccacgcggttgggaatgtaattcagctccgccatcgccgcttccac
tttttcccgcgttttcgcagaaacgtggctggcctggttcaccacgcgggaaacggtctgataagagacaccggcatactctgcgacatcgtataacgtt
actggtttcacattcaccaccctgaattgactctcttccgggcgctatcatgccataccgcgaaaggttttgcgccattcgatggtgtccgggatctcga
cgctctcccttatgcgactcctgcattaggaaattaatacgactcactata
```