

SUPPORTING INFORMATION

***In Vivo* Structure-Activity Relationships and Optimization of an Unnatural Base Pair For Replication in a Semi-Synthetic Organism**

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Methods

***In vivo* UBP replication**

Assembly of UBP-containing plasmids

Inserts for Golden Gate assembly bearing the UBP were generated by PCR of chemically synthesized oligonucleotides bearing dNaM (**O1** for context 1, **O2** for context 2, **O3** for context 3, **O4** for context 4; 0.025 ng per 50 μ L reaction) using the primers **P1/P2** for context 1 or **P3/P4** for contexts 2–4 and conditions described previously,¹ under the following thermocycling protocol (times denoted as mm:ss): [96 °C 0:30 | 25 \times [96 °C 0:30 | 47 °C 0:30 | 68 °C 4:00]].

Golden Gate assembly reactions were prepared by combining destination plasmid pUCX2 (1 μ g),² PCR insert (3:1 insert:plasmid molar ratio), T4 DNA ligase (533 U), BsaI-HF (53.3 U), and ATP (1 mM) in 1 \times NEB CutSmart buffer (final volume 80 μ L). The reactions were thermocycled under the following conditions: [37 °C 20:00 | 40 \times [37 °C 5:00 | 16 °C 10:00 | 22 °C 5:00] | 37 °C 20:00 | 50 °C 15:00 | 70 °C 30:00]. Following thermocycling, T5 exonuclease (13.3 U) and additional BsaI-HF (26.6 U) were added, and the reactions were incubated at 37 °C for an additional hour. Assembled plasmids were purified on a Zymo-Spin I column, and quantified fluorometrically using a Qubit fluorometer (ThermoFisher). Refer to Table S1 for list of sequences.

Transformation and replication of UBP-containing plasmids

The *E. coli* SSO was made electrocompetent as described previously,² and an aliquot (50 μ L) was transformed with 2 ng pINF plasmid. Upon electroporation, cells were immediately diluted with media supplemented with chloramphenicol (950 μ L). An aliquot of diluted cells (10 μ L) was immediately diluted 10-fold with the same media, and further supplemented with dNaMTP (125 μ M) and dTPT3TP (25 μ M) for plasmid recovery. Transformed cells were incubated at 37 °C for 1 h before pelleting each sample by centrifugation. Recovery media was removed, and cells were resuspended in an equivalent volume of fresh media lacking unnatural triphosphate and supplemented with ampicillin for pINF selection. An aliquot of these cells (10 μ L) was used to inoculate cultures of fresh media supplemented with ampicillin for pINF selection, as well as fresh unnatural triphosphates at specified concentrations (final volume of 100 μ L). Samples were then further incubated at 37 °C, monitoring for growth, and harvesting by pelleting (9,000 r.c.f., 10 min) at an OD₆₀₀ of ~0.7.

Analysis of pINF plasmids by biotin shift PCR

Plasmids were isolated for analysis using commercial miniprep kits (ZR Plasmid Miniprep Classic, Zymo Research), and analyzed for UBP retention by biotin shift PCR, as described previously.^{1,2} PCR conditions were as follows: plasmid miniprep (0.5 μ L, diluted 5-fold for samples grown to saturation), dNTPs (400 μ M), 1 \times SYBR Green, MgSO₄ (2.2 mM), primers (**P5/P6** for context 1, **P7/P8** for contexts 2–4; 1 μ M each), d5SICSTP and dMMO2^{BIO}TP (65 μ M each), OneTaq DNA polymerase (0.018 U/ μ L), and DeepVent DNA polymerase (0.007 U/ μ L) in 1 \times OneTaq standard reaction buffer (final volume 15 μ L). Thermocycling conditions were as follows: [20 \times [95 °C 0:15 | 52 °C 0:15 | 68 °C 4:00]]. An aliquot (1 μ L) of each reaction was mixed with a solution of streptavidin (2.5 μ L, 2 μ g/ μ L, Promega), and incubated at room temperature for 10 min. Streptavidin-bound amplicon was then resolved from unbound amplicon on a 6% polyacrylamide (29:1 acrylamide:bis-acrylamide) TBE gel, at 120 V for 25 min. Gels were then stained with 1 \times SYBR Gold (Thermo Fisher) and imaged using a Molecular Imager Gel Doc XR+ equipped with a 520DF30 filter (Bio-Rad).

UBP retention was measured by densitometric analysis of the gels (Quantity One 1-D Analysis Software, Bio-Rad) from the biotin shift assay and calculation of a percent raw shift, which equals the intensity of the streptavidin-shifted band divided by the sum of the intensities of the shifted and unshifted bands. Reported UBP retentions are percent raw shift for a given sample normalized to the percent raw shift of the input pINF plasmid used.

Table S1. Oligonucleotides and plasmids used in this study.

	<i>Sequence (5'→3')</i>
O1	CTGTTTCCTGTGTGAAATTGTTATCCGCTCACA-dNaM-TTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCC
O2	CTCGAGTACAACCTTTAACTCACACAATGTA-dNaM-AGATCACGGCAGACAAAACAAAAGAATGGAATC
O3	CTCGAGTACAACCTTTAACTCACACAATGTAC-dNaM-CATCACGGCAGACAAAACAAAAGAATGGAATC
O4	CTCGAGTACAACCTTTAACTCACACAATGTAC-dNaM-GATCACGGCAGACAAAACAAAAGAATGGAATC
P1	ATGGGTCTCCAGTGGCTGTTTCTGTGTGAAATTGTTATCCGC
P2	ATGGGTCTCTTCGTTGGCTTTACACTTTATGCTTCCGGC
P3	ATGGGTCTCCAGTGGCTCGAGTACAACCTTTAACTCACAC
P4	ATGGGTCTCTTCGTTGATTCCATTCTTTTGTGTTGTCTGC
P5	CTGTTTCCTGTGTGAAATTGTTATCC
P6	GGCTTTACACTTTATGCTTCCG
P7	CTCGAGTACAACCTTTAACTCACAC
P8	GATTCCATTCTTTTGTGTTGTCTGC

pUCX2 (3174 bp)

AACGCCAGCAACGCGGCCTTTTTACGGTTCCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCTGCGTTATCCC
 CTGATTCTGTGGATAACCGTATTACCGCCTTTGAGTGAGCTGATACCGCTCGCCGACGCCGAACGACCGAGCGCAGCA
 GTCAGTGAGCGAGGAAGCGGAAGAGCGCCCAATACGCAAACCGCCTCTCCCGCGCGTTGGCCGATTCAATTAATGCAAGC
 TGGCAGCAGAGGTTTCCCGACTGGAAAGCGGGCAGTGAGCGCAACGCAATTAATGTAAGTTAGCTCACTCATTAGGCAC
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 GTGCACGAGTGGGTTACATCGAAGTGGATCTCAACAGCGGTAAGATCCTTGAGAGTTTTCGCCCCGAAGAACGTTTTCC
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 TCATTAAGTGGATCTATCAACAGGAGTCCAAGCGAGCTCTCAGTCTGCTCCTCGGCCACGAAGTGCACGCAGTTGCCGG
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 TCACGACGGGTCTCCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGGATCCTTTTTTTCTGCGC
 GTAATCTGCTGCTTGCAAACAAAAAACCCGCTACCAGCGGTGGTTTTGTTTGGCGGATCAAGAGCTACCAACTCTTT
 TTCCGAAGTAACTGGCTTCAGCAGAGCGCAGATACCAATACTGTTCTTCTAGTGTAGCCGTAGTTAGGCCACCACTT
 CAAGAAGTGTAGCACCGCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCTG
 TGCTTACCAGGTTGGACTCAAGCAGATAGTTACCGGATAAGGCGCAGCGGTGGGCTGAACGGGGGTTCTGTGCACAC
 AGCCAGCTTGGAGCGAACGACCTACACCGAAGTACAGGATACCTACAGCGTGTGAGCTATGAGAAAGCGCCACGCTTCCCGA
 AGGGAGAAAGCGGACAGGTATCCGGTAAGCGGCAGGGTCCGAAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGAAAC
 GCCTGGTATCTTTATAGTCTGTCGGGTTTTCGCCACCTCTGACTTGAGCGTGCATTTTTTGTGTGCTCGTCAGGGGGCG
 GAGCCTATGGAAA

Table S2. Nucleotides used in this study.

dXTPs				dYTPs				
		Ref.		Ref.			Ref.	
1	dDMN	3	39	dTOK587	4	1	dICS	3
2	d4OMe	5	40	dTOK576	4	2	d4MICS	6
3	dIQ	7	41	dTOK581	4	3	d5MICS	6
4	d2MN	3	42	dTOK580	4	4	dNICS	8
5	d3OMe	5	43	dPhMO	9	5	dSICS	8
6	dQL	7	44	dPyMO1	9	6	d4SICS	10
7	d2Np	3	45	dPyMO2	9	7	d5SICS	10
8	dDM4	11	46	dPMO3	9	8	dSNICS	8
9	dBEN	11	47	dPMO2	9	9	dONICS	8
10	dMM1	11	48	dFuMO1	9	10	d7OFP	12
11	dDM2	11	49	dFuMO2	9	11	d7OTP	12
12	dDM	3	50	dTpMO1	9	12	d4OTP	12
13	d3FB	14	51	dTpMO2	9	13	dTPT3	13
14	dMMO1	5	52	dFIMO	9	14	dFTPT1	13
15	dDM5	11	53	dMIMO	9	15	dTPT1	13
16	d2Py	7	54	dFEMO	9	16	dTPT3 ^{PA}	13
17	d3MPy	7	55	dIMO	9			
18	d4MPy	7	56	dMEMO	9			
19	d5MPy	7	57	dEMO	9			
20	d34DMPy	7	58	dMMO2	5			
21	d35DMPy	7	59	dDMO	5			
22	dEPy	7	60	d5FM	15			
23	d45DMPy	7	61	d2OMe	5			
24	dBp	16	62	dNaM	15			
25	dBTP	16	63	dAPy	7			
26	dIN	16	64	dMAPy	7			
27	dBzT	16	65	dDMAPy	7			
28	dBf	16	66	dFDMO	9			
29	dTp	17	67	dZMO	9			
30	dMTp	17	68	dTfMO	9			
31	dAM	18	69	dVMO	9			
32	dADM	18	70	dCIMO	9			
33	dMAN	18	71	dCNMO	9			
34	dMMAN	18	72	dMMO2 ^A	19			
35	dDMMAN	18	73	dMMO2 ^{PA}	19			
36	dTOK588	4	74	dMMO2 ^{BIO}	2			
37	dTOK582	4	75	dMMO2 ^{SSBIO}	19			
38	dTOK586	4						

Table S3. UBP retention data for Figure 4a. An asterisk indicates no cell growth was observed.

name	125 μ M				10 μ M			
	Trial 1	Trial 2	Trial 3	avg \pm sd	Trial 1	Trial 2	Trial 3	avg \pm sd
dMMO2	103	110	107	107 \pm 4	86	80	82	83 \pm 3
dDMO	100	104	102	102 \pm 2	4	12	12	10 \pm 5
dCIMO	103	95	99	99 \pm 4	88	75	81	81 \pm 7
dCNMO	99	96	98	98 \pm 1	78	95	85	86 \pm 9
d5FM	100	95	98	98 \pm 3	89	107	73	90 \pm 17
dNaM	105	90	97	97 \pm 7	44	44	36	41 \pm 5
dFDMO	96	94	95	95 \pm 1	22	40	27	30 \pm 9
dFIMO	100	88	94	94 \pm 6	72	43	62	59 \pm 15
dN3MO	93	95	94	94 \pm 1	6	31	26	21 \pm 13
dIMO	98	89	94	94 \pm 5	58	67	44	56 \pm 11
dMIMO	103	84	93	93 \pm 9	6	5	1	4 \pm 3
dFEMO	96	83	90	90 \pm 6	66	49	26	47 \pm 20
dMMO2 ^A	93	86	89	89 \pm 4	33	58	44	45 \pm 13
d2OMe	99	68	84	84 \pm 16	13	30	24	22 \pm 8
dCF3MO	85	70	77	77 \pm 7	1	12	3	5 \pm 6
dMEMO	*	86	75	54 \pm 47	7	2	1	3 \pm 3
dVMO	*	79	69	50 \pm 43	17	31	11	20 \pm 10
dDM5	85	9	23	39 \pm 40	*	13	2	5 \pm 7
d2MN	77	6	21	34 \pm 38	4	10	2	5 \pm 4
d45DMPy	82	5	15	34 \pm 42	2	0	8	3 \pm 4
dEMO	55	9	32	32 \pm 23	5	6	5	6 \pm 1
dDM	62	4	17	28 \pm 30	1	12	4	6 \pm 5
dTOK581	65	*	16	27 \pm 34	5	15	5	8 \pm 6
dTOK587	45	5	13	21 \pm 21	5	2	3	3 \pm 1
dPyMO2	45	5	13	21 \pm 21	4	9	0	5 \pm 5
d35DMPy	48	*	12	20 \pm 25	1	8	3	4 \pm 4
d5MPy	45	*	11	19 \pm 24	2	6	0	3 \pm 3
dPyMO1	27	9	18	18 \pm 9	3	0	14	6 \pm 7
dPMO2	36	5	10	17 \pm 16	4	5	1	4 \pm 2
dMMO1	29	6	9	15 \pm 13	0	3	5	3 \pm 2
dBTP	21	8	15	15 \pm 6	2	2	0	1 \pm 1
dDM2	29	6	9	14 \pm 12	4	7	4	5 \pm 2
dMMO2 ^{SSBIO}	25	3	14	14 \pm 11	1	10	4	5 \pm 5
dMMO2 ^{PA}	23	5	14	14 \pm 9	8	5	6	6 \pm 1
dDMMAN	26	4	7	12 \pm 11	4	0	2	2 \pm 2
dQL	19	6	12	12 \pm 6	1	4	0	2 \pm 2
dMM1	24	5	7	12 \pm 10	1	3	0	1 \pm 2
d4MPy	26	0	7	11 \pm 14	3	0	0	1 \pm 2
dBzT	19	6	6	11 \pm 7	4	6	1	4 \pm 2

d3OMe	20	4	6	10 ± 9	0	5	5	3 ± 3
dPhMO	6	14	10	10 ± 4	4	13	10	9 ± 5
d2Py	13	7	10	10 ± 3	1	3	5	3 ± 2
d3MPy	23	0	6	10 ± 12	1	6	0	2 ± 3
d4OMe	14	5	10	10 ± 5	0	7	5	4 ± 4
dPMO3	16	3	10	10 ± 6	1	10	0	4 ± 5
dBPy	20	3	6	10 ± 9	3	5	7	5 ± 2
dMAN	11	7	9	9 ± 2	2	1	7	3 ± 4
dDMN	9	10	9	9 ± 1	0	7	10	6 ± 5
dIQ	15	3	9	9 ± 6	1	3	5	3 ± 2
d2NP	14	4	9	9 ± 5	3	14	2	6 ± 7
dFuMO2	19	1	5	9 ± 9	5	1	2	3 ± 2
dEPy	11	5	8	8 ± 3	3	5	4	4 ± 1
dDM4	11	4	8	8 ± 4	1	9	3	4 ± 4
dMMAN	11	4	8	8 ± 3	2	9	12	8 ± 5
dMTp	15	0	8	8 ± 8	1	7	0	2 ± 4
d3FB	10	4	7	7 ± 3	1	9	2	4 ± 4
dIN	14	0	7	7 ± 7	3	2	4	3 ± 1
dBEN	10	4	7	7 ± 3	4	6	0	3 ± 3
dMAP	6	8	7	7 ± 1	2	1	0	1 ± 1
dTp	13	0	6	6 ± 6	0	6	2	3 ± 3
dDMAP	8	5	6	6 ± 1	0	6	7	4 ± 4
d34DMPy	12	0	6	6 ± 6	1	9	2	4 ± 4
dBf	12	0	6	6 ± 6	3	2	0	2 ± 2
dTOK588	6	5	6	6 ± 1	4	3	4	3 ± 1
dAM	8	4	6	6 ± 2	5	16	4	8 ± 7
dTOK586	7	4	6	6 ± 1	3	9	1	4 ± 4
dTOK576	6	5	6	6 ± 1	2	3	5	3 ± 1
dAP	6	4	5	5 ± 1	5	1	2	3 ± 2
dTOK580	4	7	5	5 ± 2	1	28	0	10 ± 16
dFuMO1	11	0	5	5 ± 5	4	1	2	3 ± 1
dTpMO1	7	3	5	5 ± 2	3	0	3	2 ± 2
dMMO2 ^{BIO}	7	2	4	4 ± 2	4	10	2	5 ± 5
dTpMO2	7	2	4	4 ± 3	1	1	0	1 ± 1
dTOK582	4	4	4	4 ± 0	3	0	5	3 ± 2
dADM	0	6	3	3 ± 3	2	8	1	4 ± 4

Table S4. UBP retention data for Figure 4b. An asterisk indicates no cell growth was observed.

name	125 μ M				25 μ M			
	Trial 1	Trial 2	Trial 3	avg \pm sd	Trial 1	Trial 2	Trial 3	avg \pm sd
dTPT3 ^{PA}	98	69	94	87 \pm 16	70	93	93	85 \pm 13
dTPT3	92	71	89	84 \pm 12	87	97	87	90 \pm 6
dSICS	96	54	96	82 \pm 24	91	97	98	95 \pm 4
dFPT1	80	88	78	82 \pm 5	73	82	85	80 \pm 6
d4SICS	59	90	90	80 \pm 18	84	90	92	89 \pm 4
dTPT1	79	69	79	76 \pm 6	80	96	90	89 \pm 8
d5SICS	59	82	86	76 \pm 14	68	89	93	83 \pm 13
dNICS	81	62	79	74 \pm 10	76	88	85	83 \pm 6
dSNICS	65	71	41	59 \pm 16	71	86	89	82 \pm 10
dICS	*	*	*	*	71	86	86	81 \pm 8
d4MICS	*	*	*	*	66	80	94	80 \pm 14
d5MICS	*	*	*	*	59	74	80	71 \pm 11
dONICS	*	*	*	*	*	*	*	*
d7OFP	*	*	*	*	*	*	*	*
d7OTP	*	*	*	*	*	*	*	*
d4OTP	*	*	*	*	*	*	*	*

Table S5. UBP retention data for Figure 4c.

dTPT3 analog	dNaM analog	Trial 1	Trial 2	Trial 3	avg \pm sd
dSICS	d5FM	88	52	63	68 \pm 18
	dMMO2	39	9	9	19 \pm 18
	dCNMO	65	82	89	79 \pm 12
	dCIMO	66	50	66	61 \pm 10
dTPT3	d5FM	100	78	83	87 \pm 12
	dMMO2	90	93	80	88 \pm 7
	dCNMO	97	94	94	95 \pm 2
	dCIMO	98	95	96	96 \pm 2
dTPT1	d5FM	0	0	0	0 \pm 0
	dMMO2	0	0	0	0 \pm 0
	dCNMO	0	0	0	0 \pm 0
	dCIMO	0	0	0	0 \pm 0
d4SICS	d5FM	0	0	0	0 \pm 0
	dMMO2	2	3	0	2 \pm 1
	dCNMO	9	5	4	6 \pm 3
	dCIMO	0	5	6	4 \pm 3
dTPT3 ^{PA}	d5FM	0	0	0	0 \pm 0
	dMMO2	0	4	3	3 \pm 2
	dCNMO	5	2	0	2 \pm 2
	dCIMO	2	5	6	4 \pm 2
d5SICS	d5FM	0	0	0	0 \pm 0
	dMMO2	0	0	0	0 \pm 0
	dCNMO	6	5	5	5 \pm 1
	dCIMO	12	0	9	7 \pm 6
dNICS	d5FM	0	0	0	0 \pm 0
	dMMO2	2	1	4	3 \pm 2
	dCNMO	0	7	2	3 \pm 4
	dCIMO	3	0	4	2 \pm 2
dSNICS	d5FM	0	0	5	2 \pm 3
	dMMO2	0	0	0	0 \pm 0
	dCNMO	1	5	0	2 \pm 3
	dCIMO	6	11	2	6 \pm 4
dICS	d5FM	4	3	5	4 \pm 1
	dMMO2	5	2	0	2 \pm 2
	dCNMO	1	0	0	0 \pm 1
	dCIMO	6	3	4	4 \pm 1
dFPT1	d5FM	0	4	0	0 \pm 0
	dMMO2	1	4	4	3 \pm 2
	dCNMO	4	0	4	3 \pm 2
	dCIMO	0	5	0	0 \pm 0
d4MICS	d5FM	1	4	6	4 \pm 3

	dMMO2	4	4	1	3 ± 2
	dCNMO	0	0	0	0 ± 0
	dCIMO	3	5	3	4 ± 1
d5MICS	d5FM	1	3	6	4 ± 3
	dMMO2	2	2	3	2 ± 0
	dCNMO	0	0	0	0 ± 0
	dCIMO	1	2	2	2 ± 1

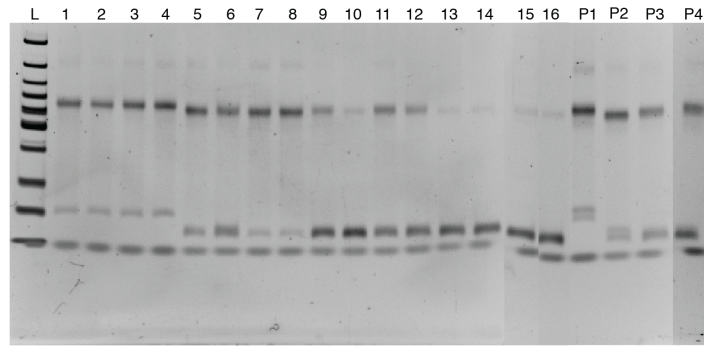


Figure S1. Representative 6% native PAGE gel of a single trial from Figure 6. Lane “L” is low molecular weight DNA ladder. Each grouping of four lanes from lane 1 to 16 represents, from left to right, dNaMTP at 125 μ M, dNaMTP at 25 μ M, dCNMOTP at 125 μ M, and dCNMOTP at 25 μ M. Lanes 1–4 show replication under these conditions in context 1. Lanes 5–8 show replication under these conditions in context 2. Lanes 9–12 show replication under these conditions in context 3. Lanes 13–16 show replication under these conditions in context 4. Lane P1 shows PCR products directly from *in vitro* constructed plasmids of context 1. Lane P2 shows PCR products directly from *in vitro* constructed plasmids of context 2. Lane P3 shows PCR products directly from *in vitro* constructed plasmids of context 3. Lane P4 shows PCR products directly from *in vitro* constructed plasmids of context 4.

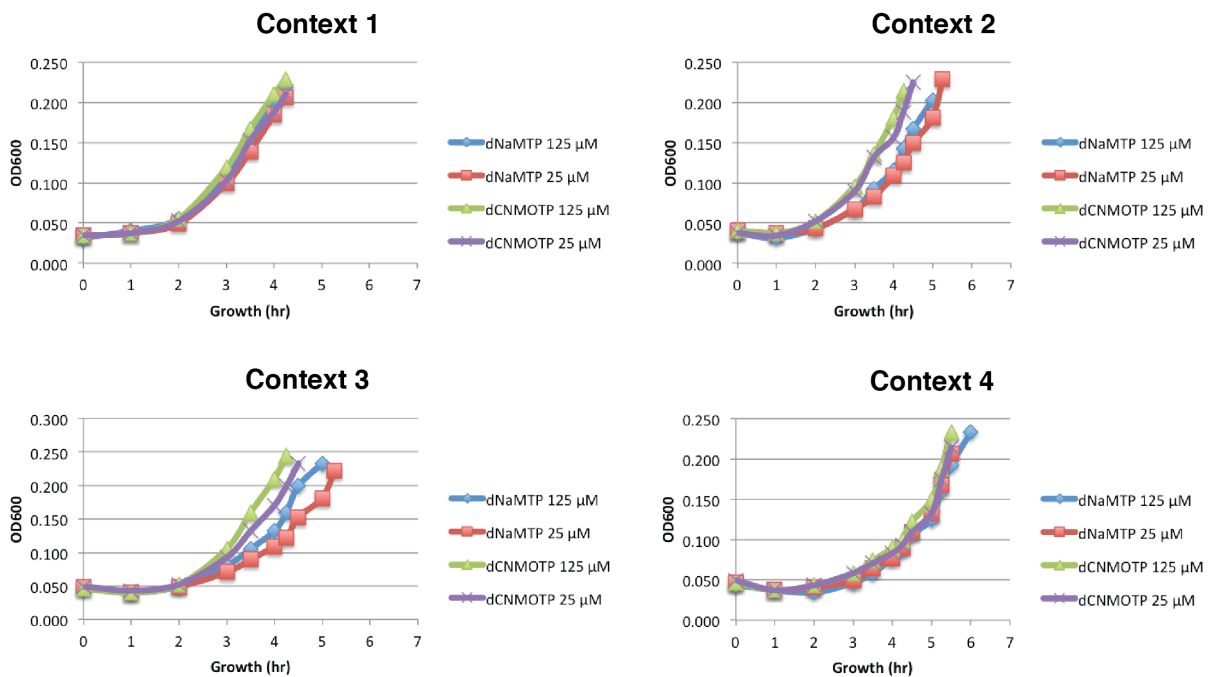


Figure S2. Growth curves of a single trial for the data presented in Figure 6.

References

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