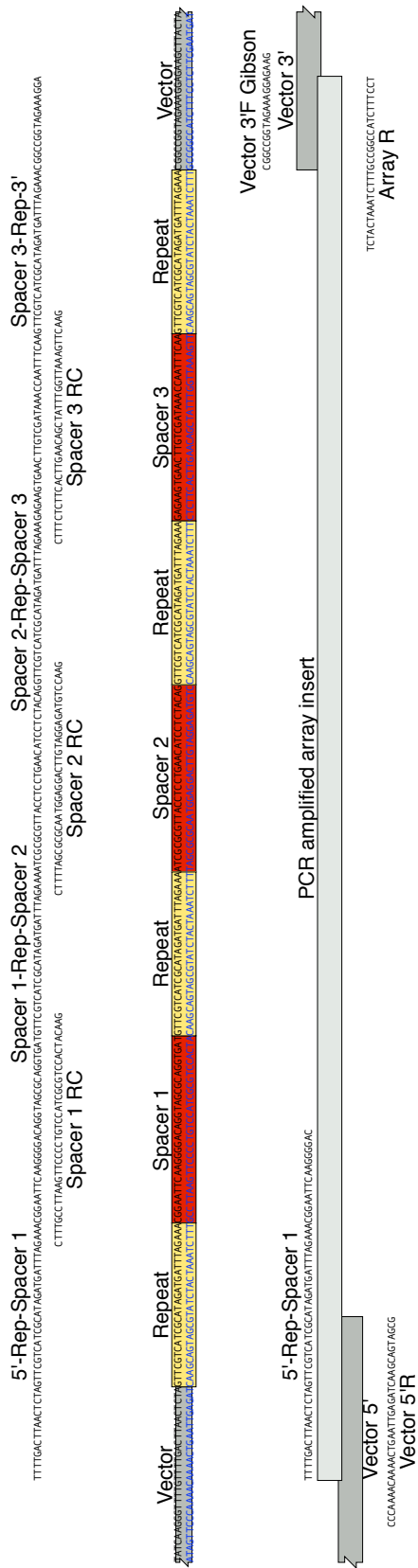


# **One-Day Construction Of Multiplex Arrays to Harness Natural CRISPR-Cas Systems**

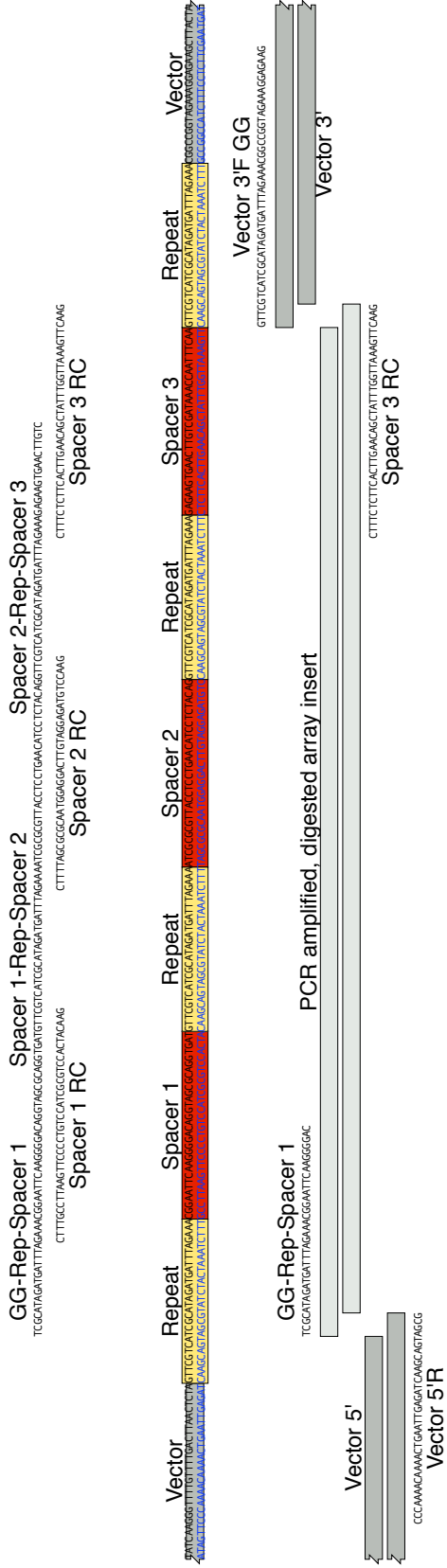
Robert M. Cooper, Jeff Hasty

## **Supporting Information**

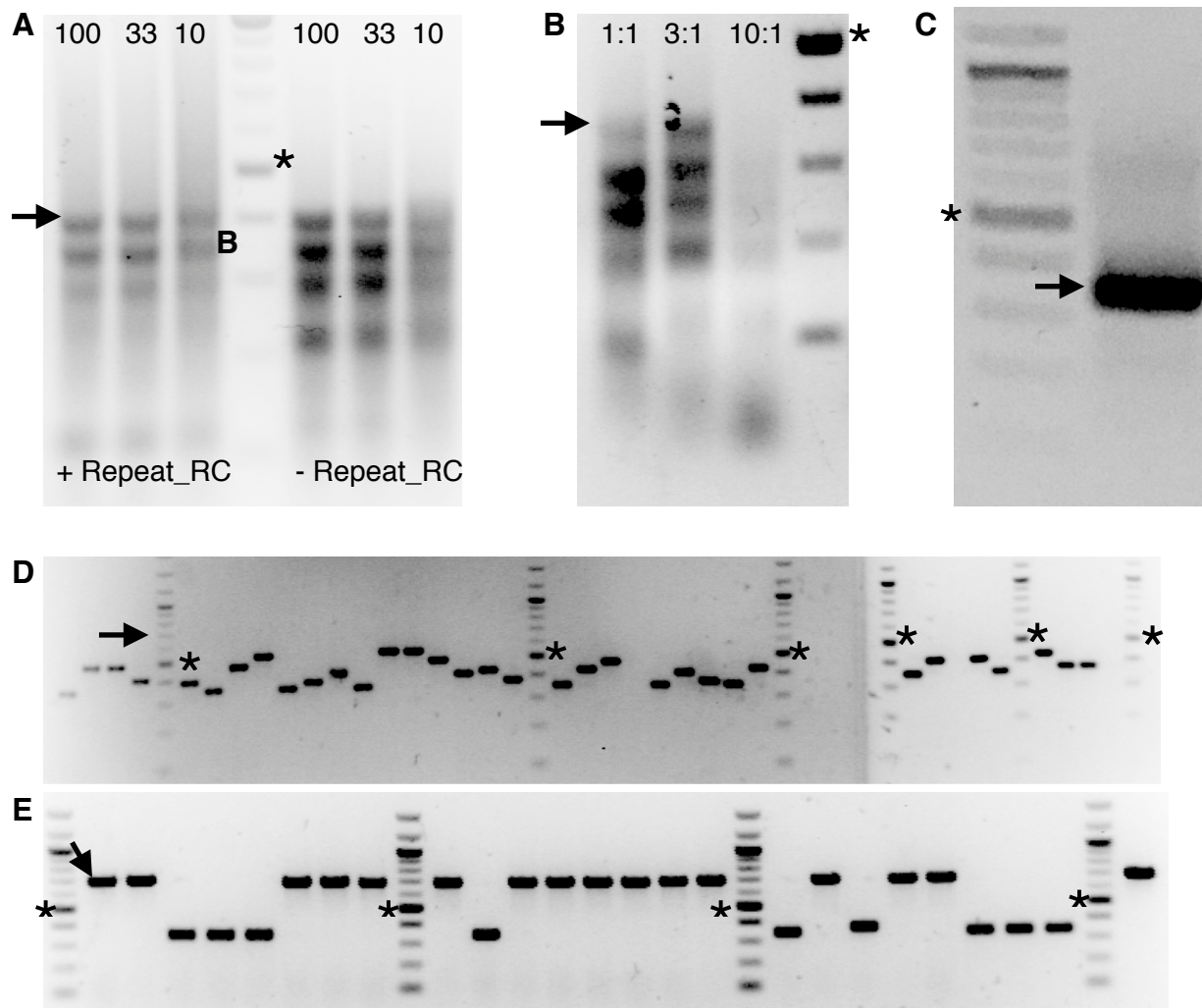
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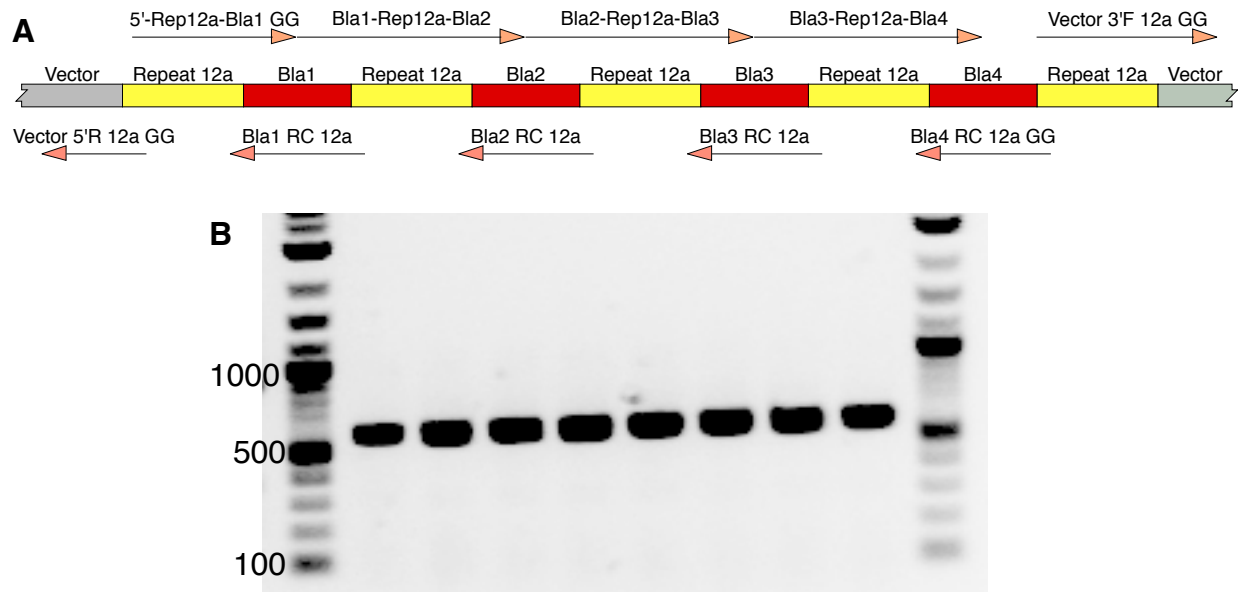
B



**Figure S1: Detailed multiplex natural CRISPR array assembly.** A more detailed version of Figure 2 showing DNA sequences for the 3xBAP CRISPR array. The two array assembly strategies are for insertion into a vector using Gibson assembly or fusion PCR (A) or Golden Gate assembly (B). Note that primers used for Golden Gate assembly (denoted "GG" in B) have an additional BsaI site-containing tail appended to their 5' ends that is not shown, specifically, TTTGGTCTCA.



**Figure S2: Multiplex array assembly optimization.** Protocol optimizations were performed using a 6xIS-CRA array and inserted into pBAV using Golden Gate assembly. A,B: raw ligations, C: PCR amplification, D,E: Colony PCR screening of clones. Asterisks on all gels indicate the 500 bp band of the ladder, and arrows indicate the correctly sized assembly. A) Including the Repeat\_RC oligo increases incorrect, higher-molecular-weight smearing (left 3 vs right 3 lanes), and 100 uM stock oligos (lanes 1 and 5) work better than 33 uM (lanes 2 and 6) or 10 uM (lanes 3 and 7) stock solutions. The center (lane 4) is a 100 bp ladder. B) Annealing and ligation is most efficient using 3 parts bottom oligos to 1 part top oligos. The lanes from left to right are ligations using 1:1, 3:1, and 10:1 ratios of bottom oligos to top oligos, followed by a 100 bp ladder. C) PCR amplification of the resulting ligation improves yield of the correct-sized product. D) Golden Gate assembly directly from ligation products yielded no correct-sized arrays out of 36 tested clones. All of 6 sequenced clones were correct at the 3' end, but truncated at the 5' end of the array. E) As for D, but the ligation product was PCR amplified and gel extracted before inserting into the vector. 16 of 25 colonies were the correct size, and all incorrect clones had 0x arrays (a single repeat only).



**Figure S3: Assembly of a 4-spacer Cas12a array.** A) Design and oligonucleotides for a 4-spacer FnCas12a CRISPR array, to be inserted into the vector using Golden Gate assembly. This is analogous to Figure 2B for *A. baylyi* arrays. All oligos denoted by GG also contain a 5' Golden Gate tail (see Methods and Table S1). B) Screening of 8 clones for the 4-spacer array, of which all had the desired 603 bp product. The primer pair hybridized to the backbone of the vector, outside the inserted CRISPR array. The ladder on the end lanes contains 100 bp increments up to 1 kb.

**Table S1: Oligos/Primers**

Purpose	Name	Sequence
CRISPR <sub>4xKan1</sub> Gibson	kan1 5'-R-T1	TTTTGACTTAACTCTAGTTCGTCATCGCATAGATGATTTAGAA AGGTCGATCAGGGAGGA
	kan1 T1-R-B1	TATCGGGGAAGAACAGGTTTCGTCATCGCATAGATGATTTAGA AATTGCATTCTAAAACCT
	kan1 B1-R-T2	TAAATACAGAAAACAGGTTTCGTCATCGCATAGATGATTTAGAA AGTCGATACTATGTTAT
	kan1 T2-R-B2	ACGCCAACTTTGAAAAGTTCGTCATCGCATAGATGATTTAGA AAAAGCGAGCTCGGTACT
	kan1 B2-R-3'	AAAACAATTCATCCAGGTTTCGTCATCGCATAGATGATTTAGAA ACGGCCGGTAGAAAGGA
	Kan1 T1 RC	GAACCTGTTCTTCCCGATATCCTCCCTGATCGACCTTTC
	Kan1 B1 RC	GAACCTGTTTTCTGTATTTAAGGTTTTAGAATGCAATTC
	Kan1 T2 RC	GAACTTTTCAAAGTTGGCGTATAACATAGTATCGACTTTC
	Kan1 B2 RC	GAACCTGGATGAATTGTTTTAGTACCGAGCTCGCTTTTTTC
	CRISPR <sub>4xKan2</sub> Gibson	kan2 5'-R-T1
kan2 T1-R-B1		GCGCCTTGAGCCTGGCGTTCGTCATCGCATAGATGATTTAGA AAGGCTACCTGCCATTC
kan2 B1-R-T2		GACCACCAAGCGAAACGTTTCGTCATCGCATAGATGATTTAGA ACAACCTTACCAGAGGG
kan2 T2-R-B2		CGCCCCAGCTGGCAATGTTTCGTCATCGCATAGATGATTTAGA AAGGCCGCTTGGGTGGAG
kan2 B2-R-3'		AGGCTATTCGGCTATGGTTCGTCATCGCATAGATGATTTAGAA ACGGCCGGTAGAAAGGA
Kan2 T1 RC		GAACGCCAGGCTCAAGGCGCGCATGCCCGACGGCGATTTC
Kan2 B1 RC		GAACGTTTTCGCTTGGTGGTTCGAATGGGCAGGTAGCCTTTC
Kan2 T2 RC		GAACATTGCCAGCTGGGGCGCCCTCTGGTAAGGTTGTTTC
Kan2 B2 RC		GAACCATAGCCGAATAGCCTCTCCACCCAAGCGGCCTTTC
Array PCR		Array R
	Array R GG	TTTGGTCTCATCCTTTCTACCGGCCGTTTCTAAATCATCT
CRISPR <sub>8xKan</sub> Gibson	Kan1 B2-R- Kan2 T1	AAAACAATTCATCCAGGTTTCGTCATCGCATAGATGATTTAGAA ATCGCCGTCGGGCATGC
Vector Gibson	Vector 5'R	TAGAGTTAAGTCAAACAAAACCC

	Vector 3'F	GAAACGGCCGGTAGAAAGGA
Vector Golden Gate (GG)	Vector 5'R GG	TTTGGTCTCAGCGATGACGAACTAGAGTTAAGTCAAAACAAA ACCC
	Vector 3'F GG	TTTGGTCTCAGTTCGTCATCGCATAGATGATTTAGAAACGGC CGGTAGAAAGGAGAAG
Genomic integrating CRISPR vector	pp 5'F	TGAGCCGACATTTTATTACCCTCT
	pp 3'R	TTACCTGAAAGCCAATCGCTG
CRISPR <sub>3xBAP</sub> GG	GG-R-BAP1	TTTGGTCTCATCGCATAGATGATTTAGAAACGGAATTCAAGG GGAC
	BAP1-R-BAP2	AGGTAGCGCAGGTGATGTTTCGTCATCGCATAGATGATTTAGA AAATCGCGCGTTACCTCC
	BAP2-R-BAP3	TGAACATCCTCTACAGTTCGTCATCGCATAGATGATTTAGAA AGAGAAGTGAACCTGTC
	BAP1 RC	GAACATCACCTGCGCTACCTGTCCCCTTGAATTCCGTTTC
	BAP2 RC	GAACCTGTAGAGGATGTTTCAGGAGGTAACGCGCGATTTTC
	BAP3 RC GG	TTTGGTCTCAGAACTTGAAATTGGTTTATCGACAAGTTCACTT CTCTTC
CRISPR <sub>3xCRA-3xBAP</sub> GG	GG-R-CRA1	TTTGGTCTCATCGCATAGATGATTTAGAAATCTCCGCGCTTG CTTC
	CRA1-R-CRA2	GCATAATGCAGATTGAGTTCGTCATCGCATAGATGATTTAGAA AGTCACTATGACCATGT
	CRA2-R-CRA3	TGCTTTGTATTGTGAAGTTCGTCATCGCATAGATGATTTAGAA ACCCGGATTTTACTGG
	CRA3-R-BAP1	CGAAATGTAGAAGATAGTTCGTCATCGCATAGATGATTTAGAA ACGGAATTCAAGGGGAC
	CRA1 RC	GAACCTCAATCTGCATTATGCGAAGCAAGCGCGGAGATTTTC
	CRA2 RC	GAACCTCACAAATACAAAGCAACATGGTCATAGTACTTTTC
	CRA3 RC	GAACCTATCTTCTACATTTCCGAGTCAAAATCCGGGTTTC
PCR screening of arrays	Array screen F	GGAGTTCTGAGGTCATTAAGGATCTA
	Array screen R	CAAATGTACGGCCAGCAACG
<i>bap</i> deletion donor DNA	BAP 5'F	AGCAGCTGAGAGCCTGAATG
	BAP 5'R	ACATGCCAGCACTTAATCTGA

	BAP 3'F	TCAGATTAAGTGCTGGCATGTGCACCCAATCCCTAACATTAA ACA
	BAP 3'R	GGTTCGGGCACCTCATCATT
CRA $\Phi$ deletion donor DNA	CRA 5'F	ACAGGGCAGCCATTAAGTGA
	CRA 5'R	TCTGAGACTGTAGCCTACGCA
	CRA 3'F	TGCGTAGGCTACAGTCTCAGAACGAAGTTATGTGCCACAAG AAA
	CRA 3'R	TCAGACGCAAGCGTGAAGAT
<i>bap</i> deletion screening	BAP checkF	GCCTCCTAAAATTGGGGGCT
	BAP checkR	CTTGGTTCTGCATTGGGTGC
CRA $\Phi$ deletion screening	CRA checkF	GACTTGCGTAGGCTTGGACT
	CRA checkR	GCATGTCATGGTTTGGTGGG
	CRA circular F	ATGAACGCGATCATTGCAGC
	CRA circular R	TACGGCCAATTGATCACCCA
Cas12a/Cpf1 CRISPR <sub>4xBla</sub> array	GG-R12a-Bla1	TTTGGTCTCATAAGAACTTTAAATAATTTCTACTGTTGTAGATC GGCGTCAATACGGGA
	Bla1-R12a-Bla2	TAATACCGCGCCACATGTCTAAGAACTTTAAATAATTTCTACT GTTGTAGATGGAGCTGAATGAAGCC
	Bla2-R12a-Bla3	ATACCAAACGACGAGCGTCTAAGAACTTTAAATAATTTCTACT GTTGTAGATCTCCCGTATCGTAGTT
	Bla3-R12a-Bla4	ATCTACACGACGGGGAGTCTAAGAACTTTAAATAATTTCTACT GTTGTAGATAGCCGGAAGGGCCGAG
	Vector 3'F 12a GG	TTTGGTCTCAGTCTAAGAACTTTAAATAATTTCTACTGTTGTA GATCGGCCGGTAGAAAGGACA
	Vector 5'R 12a GG	TTTGGTCTCACTTAGACTAGAGTTAAGTCAAACAAAACCC
	Bla1 RC 12a	AGACATGTGGCGCGGTATTATCCCGTATTGACGCCGATCT
	Bla2 RC 12a	AGACGCTCGTCGTTTGGTATGGCTTCATTCAGCTCCATCT
	Bla3 RC 12a	AGACTCCCCGTCGTGTAGATAACTACGATACGGGAGATCT
	Bla4 RC 12a	TTTGGTCTCAAGACCAGGACCACTTCTGCGCTCGGCCCTTC CGGCTATCT



**Table S2: CRISPR spacers**

Name	Sequence
Kan1_T1	GGTCGATCAGGGAGGATATCGGGGAAGAACAG
Kan1_T2	GTCGATACTATGTTATACGCCAACTTTGAAAA
Kan1_B1	TTGCATTCTAAAACCTTAAATACAGAAAACAG
Kan1_B2	AAGCGAGCTCGGTACTAAAACAATTCATCCAG
Kan2_T1	TCGCCGTCTGGGCATGCGCGCCTTGAGCCTGGC
Kan2_T2	CAACCTTACCAGAGGGCGCCCCAGCTGGCAAT
Kan2_B1	GGCTACCTGCCATTGACCACCAAGCGAAAC
Kan2_B2	GGCCGCTTGGGTGGAGAGGCTATTCGGCTATG
CRA1	TCTCCGCGCTTGCTTCGCATAATGCAGATTGA
CRA2	GTCACTATGACCATGTTGCTTTGTATTGTGAA
CRA3	CCCGGATTTTGACTGGCGAAATGTAGAAGATA
BAP1	CGGAATTCAAGGGGACAGGTAGCGCAGGTGAT
BAP2	ATCGCGCGTTACCTCCTGAACATCCTCTACAG
BAP3	GAGAAGTGAACCTTGTGATAAACCAATTTCAA
Random	TAGGGGAAAGCCTACTAGCCGGAGTGTTGCGA

## DNA sequence of sample genomically integrating vector, pp2.1-CRISPR<sub>8xKan</sub>-Spec-pp2.2

LOCUS pp2.1-CR\_4xAPH4x 3872 bp ss-DNA linear SYN 03-Jun-2016

DEFINITION -

ACCESSION -

KEYWORDS -

SOURCE -

FEATURES Location/Qualifiers

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DEFINITION -

ACCESSION -

KEYWORDS -

SOURCE -

FEATURES Location/Qualifiers

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BASE COUNT 899 A 688 C 627 G 948 T 0 OTHER

ORIGIN ?

1 TAGAAAGGAG AAGCTTACTA GTAGCGGCCG CTGCAGGCCT CAGGGCCCCG TCGATGCCGC  
61 CGCTTAATTA ATTAATCCAG AGGCATCAAA TAAAACGAAA GGCTCAGTCG AAAGACTGGG  
121 CCTTTCGTTT TATCTGTTGT TTGTCGGTGA ACGCTCTCCT GAGTAGGACA AATCCGCCGC  
181 CCTAGACCTA GTGTCATTTT ATTTCCCCCG TTCAGCATC AAGAACCTTT GCATAACTTG  
241 CTCTATATCC AACTGATAA TTGCCCTCAA ACCATAATCT AAAGGCGCTA GAGTTTGTG  
301 AAACAATATC TTTTACATCA TTCGTATTTA AAATTCCAAA CTCCGCTCCC CTAAGGCGAA  
361 TAAAAGCCAT TAAATCTTTT GTATTTACCA AATTATAGTC ATCCACTATA TCTAAGAGTA  
421 AATTCTTCAA TTCTCTTTT TGGCTTTCAT CAAGTGTAT ATAGCGGTCA ATATCAAAAT  
481 CATTAAATGTT CAAAATATCT TTTTGTGCGT ATATATGTTT ATTCTTAGCA ATAGCGTCT  
541 TTGATTCATG AGTCAAATAT TCATATGAAC CTTTGATATA ATCAAGTATC TCAACATGAG  
601 CAACTGAACT ATTCCCCAAT TTCGCTTAA TCTTGTTCTT AACGCTTCTT ATTGTTACAG  
661 GATTTTCGTG AATATATATA ACGTGATAGT GTGGTTTTTT ATAGTGCTTT CCATTTTCGTA  
721 TAACATCACT ACTATTCCAT GTATCTTTAT CTTTTTTTTT GTCCATATCG TGTAAGGAC  
781 TGACAGCCAT AGATACGCC AAACCTCTTA ATTTTTCCTT CCAATCATT GGAATTGAGT  
841 CAGGATATAA TAAAATCCA AAATTTCTAG CTTAGTATT TTAATAGCC ATGATATAAT  
901 TACCTTATCA AAAACAAGTA GCGAAAATC GTATCCTTCT AAAAACGCGA GCTTTCGCTT  
961 ATTTTTTTTG TTCTGATTCC TTTCTTGCAT ATCTTCTIAT AGCTAACGCC GCAACCGCAG  
1021 ATTTTGAAAA ACCTTTTTGT TTCGCCATAT CTGTTAATTT TTTATCTTGC TCTTTTGTCA  
1081 GAGAAATCAT AACTCTTTT TTCGATTCTG AAATCACCAT TAAAAAACT CCAATCAAAT  
1141 AATTTTATAA AGTTAGTGTA TCACTTTGA ATCATAAAAA CAACAATAA GCTACTAAA  
1201 TATAGATTTA TAAAAACGT TGGCGAAAAC GTTGGCGATT CGTTGGCGAT TGAAAAACCC  
1261 CTTAAACCCT TGAGCCAGTT GGGATAGAGC GTTTTTGGCA CAAAAATTGG CACTCGGCAC  
1321 TTAATGGGGG GTCGTAGTAC GGAAGCAAAA TTCGCTTCTT TTCCCCCAT TTTTTTCAA  
1381 ATTCAAATT TTTTTCAAAA ATTTCCAGC GCTACCGCTC GGCAAAATTG CAAGCAATTT  
1441 TAAAATCAA ACCCATGAGG GAATTTCAAT CCCTCATACT CCCTTGAGCC TCCTCCAACC  
1501 GAAATAGAAG GCGCTGCGC TTATTATTTC ATTCAGTCAT CGGCTTTCAT AATCTAACAG  
1561 ACAACATCTT CGCTGCAAAG CCACGCTACG CTCAAGGGCT TTTACGCTAC GATAACGCC  
1621 GTTTTAAACG TTATGCCGAT AACTAAACGA AATAAACGCT AAAACGTCTC AGAAACGATT  
1681 TTGAGACGTT TTAATAAAAA ATCGCCTAGT GCTTGGATT CACCAATAA AAAACGCCCG  
1741 GCGGCAACCG AGCGTTCTGA ACAAATCCAG ATGGAGTTCT GAGGTCATTA CTGGATCTAC  
1801 AAGTGATTCA TAACGAAGTA TTTTACTCA TAAAAGCTT ATATAATTGA TATCAAGGGT  
1861 TTTGTTTTGA CTTAACTCTA GTTCGTCATC GCATAGATGA TTAGAAATC TCCGCGCTT  
1921 CTTTCGCATAA TGCAGATTGA GTTCGTCATC GCATAGATGA TTAGAAAGT CACTATGACC  
1981 ATGTTGCTTT GTATTGTGAA GTTCGTCATC GCATAGATGA TTAGAAACC CGGATTTTGA  
2041 CTGGCGAAAT GTAGAAGATA GTTCGTCATC GCATAGATGA TTAGAAACG GCCGGTAGAA  
2101 AGGAGAAGCT TACTAGCTAT TTGTTTATTT TTCTAAATAC ATTCAAATAT GTATCCGCTC  
2161 ATGAGACAAT AACCTGATA AATGCTTCAA TAATATTGAA AAAGGAAGAG TATGAGGGAA  
2221 GCGGTGATCG CCGAAGTATC GACTCAACTA TCAGAGGTAG TTGGCGTCAT CGAGCGCCAT  
2281 CTCGAACCGA CGTTGCTGGC CGTACATTG TACGGCTCCG CAGTGGATGG CGGCCTGAAG  
2341 CCACACAGTG ATATTGATTT GCTGGTTACG GTGACCGTAA GGCTTGATGA AACAACCGG  
2401 CGAGCTTTGA TCAACGACCT TTTGGAAACT TCGGCTTCCC CTGGAGAGAG CGAGATTCTC  
2461 CGCGCTGTAG AAGTCACCAT TGTTGTGCAC GACGACATCA TTCCGTGGCG TTATCCAGCT  
2521 AAGCGCGAAC TGCAATTTGG AGAATGGCAG CGCAATGACA TTCTTGACAG TATCTTCGAG  
2581 CCAGCCACGA TCGACATTGA TCTGGCTATC TTGCTGACAA AAGCAAGAGA ACATAGCGTT  
2641 GCCTTGGTAG GTCCAGCGGC GGAGGAATC TTTGATCCGG TTCCTGAACA GCATCTATTT  
2701 GAGGCGCTAA ATGAAACCTT AACGCTATGG AACTCGCCGC CCGACTGGG TGGCGATGAG

2761 CGAAATGTAG TGCTTACGTT GTCCCGCATT TGGTACAGCG CAGTAACCGG CAAAATCGCG  
2821 CCGAAGGATG TCGCTGCCGA CTGGGCAATG GAGCGCCTGC CGGCCAGTA TCAGCCCGTC  
2881 ATACTTGAAG CTAGACAGGC TTATCTTGGG CAAGAAGAAG ATCGCTGGC CTCGCGCGCA  
2941 GATCAGTTGG AAGAATTGT CCACTACGTG AAAGGCGAGA TCACCAAGGT AGTCGGCAA  
3001 TAATGTCTAA CAATTCGTT CAGCCGAGGG GCCGCAAGAT CCGGCCACGA TGACCCGGTC  
3061 GTCGGTTCAG GGCAGGGTCG TTAAATAGCC GCTTATGTCT ATTGCTGGTT TACCGTTTA  
3121 TTGACTACCG GAAGCAGTGT GACCGTGTGC TTCTCAAATG CC

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