

## Supplemental Information

### A Genetically Encoded Fluorescent Biosensor for Intracellular Measurement of Malonyl-CoA

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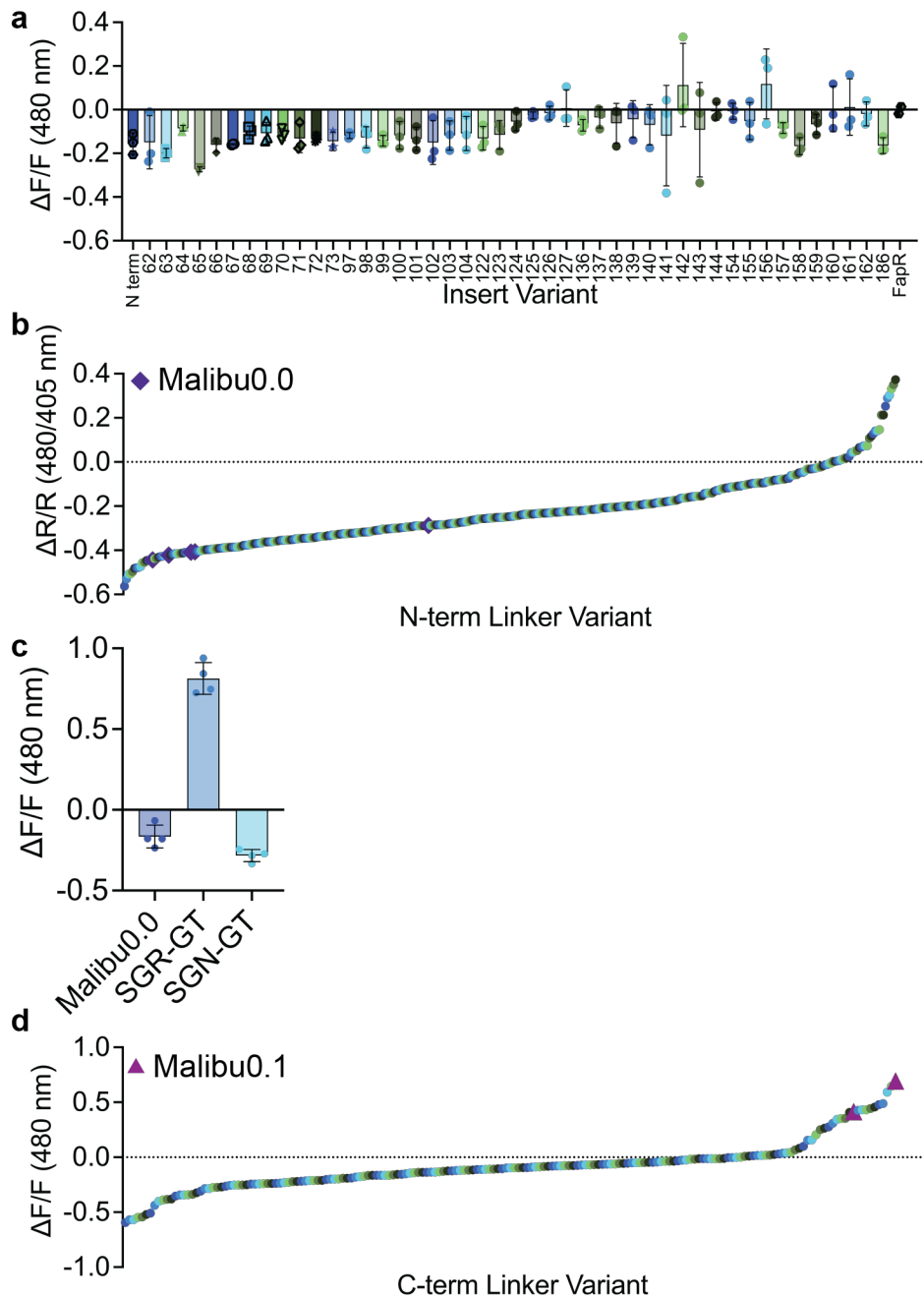
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## Ranzau et al Supplemental Figure 1



### Supplemental Figure 1. Development of Malibu.

**a**, Fluorescence change ( $\Delta F/F$ ) after addition of 500  $\mu\text{M}$  malonyl-CoA of initial Malibu variants in clarified bacterial lysate ( $n = 3$  trials).

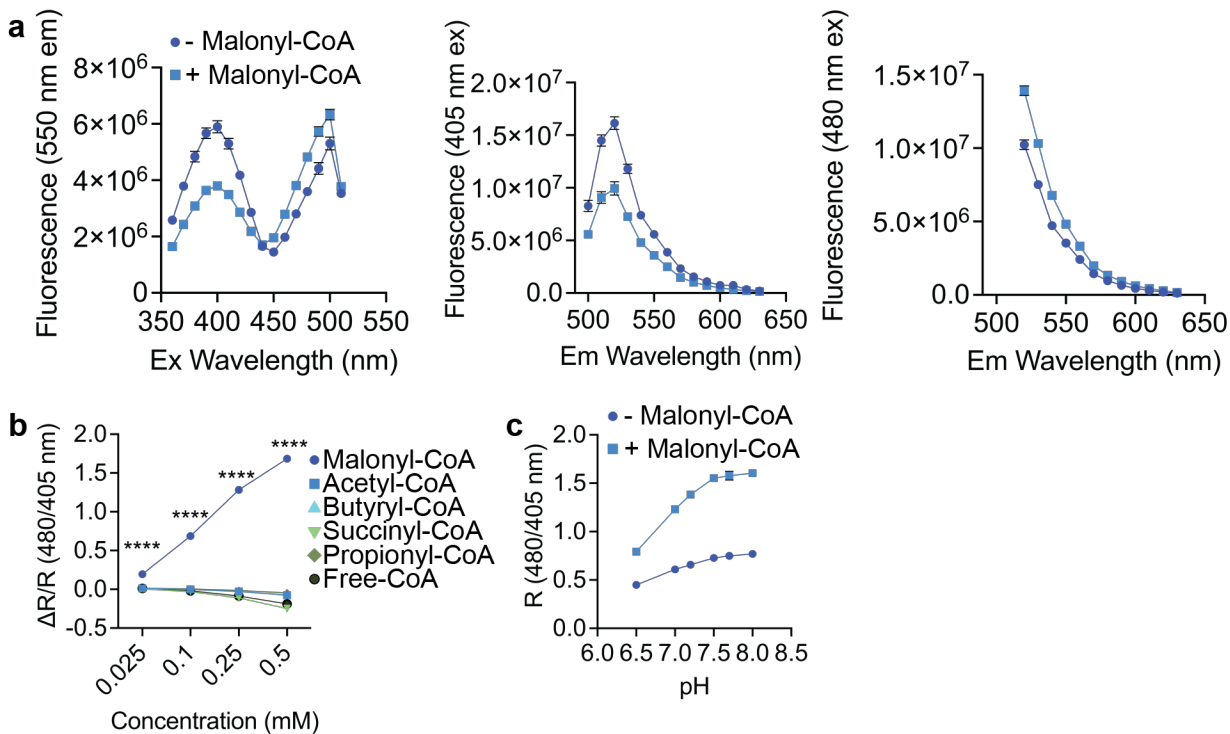
**b**, Ratio change ( $\Delta R/R$ ) of N-terminal linker variants screened in clarified bacterial lysate, treated with 500  $\mu\text{M}$  malonyl-CoA. Performance of Malibu0.0 (purple diamonds) highlighted.

**c**, Fluorescence change ( $\Delta F/F$ ) of top N-terminal linker variants considered. Malibu0.0 has SAG-GT linkers ( $n = 4$  trials).

**d**, Fluorescence change ( $\Delta F/F$ ) of C-terminal linker variants screened in clarified bacterial lysate, treated with 450  $\mu\text{M}$  malonyl-CoA. Performance of Malibu0.1 (pink triangle) highlighted.

For all figures, dot plots show the mean  $\pm$  SD.

## Ranzau et al Supplemental Figure 2



### Supplemental Figure 2. Characterization of Malibu.

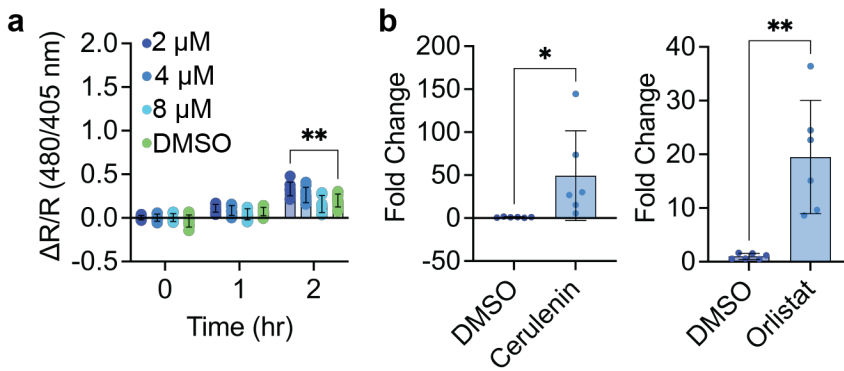
**a**, (left panel) Malibu excitation sweep from 360-510 nm excitation with fluorescence measured at 550 nm emission in the presence of either vehicle (dark blue) or malonyl-CoA (500  $\mu$ M, light blue). (middle panel) Malibu emission sweep from 500-630 nm with excitation at 405 nm in the presence of either vehicle (dark blue) or malonyl-CoA (500  $\mu$ M, light blue). (right panel) Malibu emission sweep from 520-630 nm with excitation at 480 nm in the presence of either vehicle (dark blue) or malonyl-CoA (500  $\mu$ M, light blue). Data represents 4 replicates from 1 protein preparation.

**b**, Selectivity of Malibu towards malonyl-CoA, as measured by ratio change in bacterial lysate. Malibu was incubated with 0.025-0.5 mM of each respective CoA-containing molecule indicated (6 trials;  $p < 0.0001$ , two way ANOVA with Tukey's multiple comparisons test).

**c**, Unnormalized pH dependency of Malibu ratio changes in response to either vehicle (dark blue) or 500  $\mu$ M malonyl-CoA (light blue) between pH 6.5-8, averaged across 8 trials from two independent protein preparations.

For all figures, plots show the mean  $\pm$  SD.

### Ranzau et al Supplemental Figure 3



### Supplemental Figure 3. Malibu reports malonyl-CoA dynamics in cells.

**a**, Ratio change of cpEGFP expressed in BL21 *E. coli* treated with either 2  $\mu$ M cerulenin (dark blue,  $n = 8$  trials), 4  $\mu$ M cerulenin (medium blue,  $n = 8$  trials), 8  $\mu$ M cerulenin (light blue,  $n = 9$  trials), or DMSO (green,  $n = 9$  trials;  $p = 0.0052$ , 2-way ANOVA with Dunnett's multiple comparisons test).

**b**, (left) Fold change of malonyl-CoA in HeLa cells after treatment with either DMSO (dark blue,  $n = 6$  trials) or cerulenin (50  $\mu$ M for 4 hr, light blue,  $n = 6$  trials;  $p = 0.0465$ , unpaired t-test). (right) Fold change of malonyl-CoA in HeLa cells after treatment with either DMSO (dark blue,  $n = 6$  trials) or orlistat (15  $\mu$ M for 12 hr, light blue,  $n = 6$  trials;  $p = 0.0016$ , unpaired t-test).

For all figures, dot plots show the mean  $\pm$  SD.

**Ranzau et al Supplemental Table 1**

Initial Designs	
Primer Number	Sequence 5' to 3'
NT_fwd_bb	GGCACAAGCTGGAGTACAACGGAACGGAGCTTTCCATACCTGAACTGAGAGAAAGAATT AAGAACGTGGC
NT_rev_bb	GCCTTGATATAGACGTTTCCCGCTGACATGGATCCCCATCGATCCTTATCGTCATCGTCCG TACAGATCC
62_fwd_bb	GGCACAAGCTGGAGTACAACGGAACGGAGGACGAAGTGAAGTCCCTGTCACCTTGATGAA GTTATCG
62_rev_bb	GCCTTGATATAGACGTTTCCCGCTGAAAGTGTTTTCTCTGCCACGTTCTTAATTCTTTCTC TCAGTTCAG
63_fwd_bb	GGCACAAGCTGGAGTACAACGGAACGGACGAAGTGAAGTCCCTGTCACCTTGATGAAGTT ATCG
63_rev_bb	GCCTTGATATAGACGTTTCCCGCTGACTCAAGTGTTTTCTCTGCCACGTTCTTAATTCTTT CTCTCAG
64_fwd_bb	GGCACAAGCTGGAGTACAACGGAACGGAAAGTGAAGTCCCTGTCACCTTGATGAAGTTATC GGAG
64_rev_bb	GCCTTGATATAGACGTTTCCCGCTGAGTCCTCAAGTGTTTTCTCTGCCACGTTCTTAATTC TTTCTCTC
65_fwd_bb	CACAAGCTGGAGTACAACGGAACGGTGAAGTCCCTGTCACCTTGATGAAGTTATCGGAGA AATTATTGACC
65_rev_bb	GCCTTGATATAGACGTTTCCCGCTGATTCGTCCTCAAGTGTTTTCTCTGCCACGTTCTTAA TTCTTTCTC
66_fwd_bb	GGCACAAGCTGGAGTACAACGGAACGAAGTCCCTGTCACCTTGATGAAGTTATCGGAGAA ATTATTGACC
66_rev_bb	GCCTTGATATAGACGTTTCCCGCTGACACTTCGTCCTCAAGTGTTTTCTCTGCCACG
67_fwd_bb	TCCCTGTCACCTTGATGAAGTTATCGGAGAAATTATTGACCTTG
67_rev_bb	CTTCACTTCGTCCTCAAGTGTTTTCTCTGCCACG
67_fwd_ins ert	AAAACACTTGAGGACGAAGTGAAGTCAGCGGAAACGTCTATATCAAGGCCGACAAGCA G
67_rev_ins ert	CCGATAACTTCATCAAGTGACAGGGACGTTCCGTTGTA CTCCAGCTTG TGCCCCAGGAT G
68_fwd_bb	GGCACAAGCTGGAGTACAACGGAACGCTGTCACTTGATGAAGTTATCGGAGAAATTATTG ACCTTGAGC
68_rev_bb	GCCTTGATATAGACGTTTCCCGCTGAGGACTTCACTTCGTCCTCAAGTGTTTTCTCTGCC ACG
69_fwd_bb	GGCACAAGCTGGAGTACAACGGAACGTCACCTTGATGAAGTTATCGGAGAAATTATTGACC TTGAGCTGG
69_rev_bb	GCCTTGATATAGACGTTTCCCGCTGACAGGGACTTCACTTCGTCCTCAAGTGTTTTCTCT GCCACG
70_fwd_bb	GGCACAAGCTGGAGTACAACGGAACGCTTGATGAAGTTATCGGAGAAATTATTGACCTTG AGCTGGATG
70_rev_bb	GCCTTGATATAGACGTTTCCCGCTGATGACAGGGACTTCACTTCGTCCTCAAGTGTTTTC TCTGC
71_fwd_bb	GCACAAGCTGGAGTACAACGGAACGGATGAAGTTATCGGAGAAATTATTGACCTTGAGC TGGATGATCAG
71_rev_bb	GCCTTGATATAGACGTTTCCCGCTGAAAGTGACAGGGACTTCACTTCGTCCTCAAGTGTT TTCTCTGC
72_fwd_bb	GGCACAAGCTGGAGTACAACGGAACGGAAGTTATCGGAGAAATTATTGACCTTGAGCTG GATGATCAGGC
72_rev_bb	GCCTTGATATAGACGTTTCCCGCTGAATCAAGTGACAGGGACTTCACTTCGTCCTCAAGT GTTTTCTCTG

73_fwd_bb	GGCACAAGCTGGAGTACAACGGAACGGTTATCGGAGAAATTATTGACCTTGAGCTGGATGATCAGGC
73_rev_bb	GCCTTGATATAGACGTTTCCCGCTGATTCATCAAGTGACAGGGACTTCACTTCGTCTCAAGTG
97_fwd_bb	GGCACAAGCTGGAGTACAACGGAACGGTGTTTCAGCCGGAATCAGATTGCGAGAGGACACC
97_rev_bb	GCCTTGATATAGACGTTTCCCGCTGAGTGCTCCTGTTTTATTTCTAAAATGGATATCGCCTGATCATCC
98_fwd_bb	GGCACAAGCTGGAGTACAACGGAACGTTTCAGCCGGAATCAGATTGCGAGAGGACACC
98_rev_bb	GCCTTGATATAGACGTTTCCCGCTGACACGTGCTCCTGTTTTATTTCTAAAATGGATATCGCCTGATC
99_fwd_bb	AGCCGGAATCAGATTGCGAGAGGACACCAT
99_rev_bb	GAACACGTGCTCCTGTTTTATTTCTAAAATGGATATCGCCTG
99_fwd_insert	GAAATAAACAGGAGCACGTGTTCTCAGCGGAAACGTCTATATCAAGGCCGACAAGCAG
99_rev_insert	TGTCCTCTCGCAATCTGATTCGGGCTCGTTCGGTTGTACTIONCAGCTTGTGCCCCAGGATG
100_fwd_b	GGCACAAGCTGGAGTACAACGGAACGCGGAATCAGATTGCGAGAGGACACCATTATTTGCAC
100_rev_bb	GCCTTGATATAGACGTTTCCCGCTGAGCTGAACACGTGCTCCTGTTTTATTTCTAAAATGGATATCGCC
101_fwd_b	GGCACAAGCTGGAGTACAACGGAACGAATCAGATTGCGAGAGGACACCATTATTTGCACAGGC
101_rev_bb	GCCTTGATATAGACGTTTCCCGCTGACCGGCTGAACACGTGCTCCTGTTTTATTTCTAAATGGATATCG
102_fwd_b	GGCACAAGCTGGAGTACAACGGAACGCAGATTGCGAGAGGACACCATTATTTGCACAGGCG
102_rev_bb	GCCTTGATATAGACGTTTCCCGCTGAATTCCGGCTGAACACGTGCTCCTGTTTTATTTCTAAATGG
103_fwd_b	GGCACAAGCTGGAGTACAACGGAACGATTGCGAGAGGACACCATTATTTGCACAGGCGAAC
103_rev_bb	GCCTTGATATAGACGTTTCCCGCTGACTGATTCCGGCTGAACACGTGCTCCTGTTTTATTCTAAAATGG
104_fwd_b	GGCACAAGCTGGAGTACAACGGAACGGCGAGAGGACACCATTATTTGCACAGGCGAACCTTTGGC
104_rev_bb	GCCTTGATATAGACGTTTCCCGCTGAAATCTGATTCCGGCTGAACACGTGCTCCTG
122_fwd_b	GGCACAAGCTGGAGTACAACGGAACGGATGACGAGCTGGCGCTGACTGCAAGTGC
122_rev_bb	GCCTTGATATAGACGTTTCCCGCTGAAATGACTGCAACGGCCAAAGAGTTTCGCCTGTGC
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123_rev_bb	GCCTTGATATAGACGTTTCCCGCTGAATCAATGACTGCAACGGCCAAAGAGTTTCGCCTGTGC
124_fwd_b	GAGCTGGCGCTGACTGCAAGTGCAGACATC
124_rev_bb	GTCATCAATGACTGCAACGGCCAAAGAGTTTCG
124_fwd_insert	TTGGCCGTTGCAGTCATTGATGACTCAGCGGAAACGTCTATATCAAGGCCGACAAGCAG
124_rev_insert	GATGTCTGCACTTGCAGTCAGCGCCAGCTCCGTTCCGTTGTACTIONCAGCTTGTGCCCAAG
125_fwd_b	GGCACAAGCTGGAGTACAACGGAACGCTGGCGCTGACTGCAAGTGCAGACATCCGC
125_rev_bb	GCCTTGATATAGACGTTTCCCGCTGACTCGTCATCAATGACTGCAACGGCCAAAGAGTTTCG

126_fwd_b b	GGCACAAGCTGGAGTACAACGGAACGGCGCTGACTGCAAGTGCAGACATCCGC
126_rev_bb	GCCTTGATATAGACGTTTCCCGCTGACAGCTCGTCATCAATGACTGCAACGGCCAAAGAGTTTCG
127_fwd_b b	GGCACAAGCTGGAGTACAACGGAACGCTGACTGCAAGTGCAGACATCCGCTTTACAAGACAGGTAAAGC
127_rev_bb	GCCTTGATATAGACGTTTCCCGCTGACGCCAGCTCGTCATCAATGACTGCAACGGC
136_fwd_b b	GGCACAAGCTGGAGTACAACGGAACGACAAGACAGGTAAAGCAGGGTGAACGTGTCGTAGCAAAAAGCG
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139_fwd_b b	GGCACAAGCTGGAGTACAACGGAACGGTAAAGCAGGGTGAACGTGTCGTAGCAAAAAGCG
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144_rev_bb	GCCTTGATATAGACGTTTCCCGCTGATTCACCCTGCTTTACCTGTCTTGTAAGCGGATGTCTGC
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154_rev_bb	GCCTTGATATAGACGTTTCCCGCTGAAGCCGTCACCTTTGCTTTTGGCTACGACACG
155_fwd_b b	GGCACAAGCTGGAGTACAACGGAACGGAAAAGAAAAGGAAGAACGGTTGTCGAAAGTGACAGC
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156_rev_bb	GCCTTGATATAGACGTTTCCCGCTGATTCGACAGCCGTCACCTTTGCTTTTGGCTACGACACG
157_fwd_b b	GGCACAAGCTGGAGTACAACGGAACGGAAAAGGAAGAACGGTTGTCGAAAGTGACAGC

157_rev_bb	GCCTTGATATAGACGTTTCCCGCTGATTTTTTCGACAGCCGTCACCTTTCGCTTTTGCTACG ACACG
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159_fwd_b b	GGCACAAGCTGGAGTACAACGGAACGGGAAGAAGAACGGTTGTCTGAAGTGAACAGCTACGTT GGCG
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160_fwd_b b	GGCACAAGCTGGAGTACAACGGAACGAGAACGGTTGTCTGAAGTGAACAGCTACGTTGG CG
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161_fwd_b b	GGCACAAGCTGGAGTACAACGGAACGACGGTTGTCTGAAGTGAACAGCTACGTTGGCG
161_rev_bb	GCCTTGATATAGACGTTTCCCGCTGATCTTCCTTTTTCTTTTTTCGACAGCCGTCACCTTTCG C
162_fwd_b b	GGCACAAGCTGGAGTACAACGGAACGGTTGTCTGAAGTGAACAGCTACGTTGGCGAAG
162_rev_bb	GCCTTGATATAGACGTTTCCCGCTGACGTTCTTCCTTTTTCTTTTTTCGACAGCCGTCACCT TCGC
186_fwd_b b	GGCACAAGCTGGAGTACAACGGAACGCATTCATAAGAATTCGAAGCTTGATCCGGCTGC TAACAAAGC
186_rev_bb	CTTGATATAGACGTTTCCCGCTGATTTTGAACGATACATGTCAAAGCGTCCAGAAAAAAC AATTTCTTCG
fwd_insert	TCAGCGGGAAACGTCTATATCAAGGCCGACAAGC
rev_insert	CGTTCCGTTGTA CTCCAGCTTGTGCCCCAGG
Further developments	
Primer Number	Sequence 5' to 3'
1	AATGCGTCTCTCGAATCANNKNNKAACGTCTATATCAAGGC
2	TAATCGTCTCATCACCGTTCCGTTGTA CT
3	AATGCGTCTCTGTGAAGTCCCTGTCACTTGATG
4	TAATCGTCTCATTCGTCCTCAAGTGTTTTCTC
5	AATGCGTCTCTGTGAAGTCCCTGTCACTTGATG
6	TAATCGTCTCATACCAGAACCCCGCATATGTATATCTC
7	AATGCGTCTCTGGTATGGCTAGCATGACTGG
8	TAATCGTCTCATCACMNNMNNGTTGTA CTCCAGCTTGTGC
9	GAATTCTGAAGCTTGATCCGGCTGCTAACAAAGCCCGAAAGGAAG
10	GGCCACCGCGTTGCCGCTGCCGGTGCTCTGCAGTGAATGTTTTGAACGATACATG
11	GCAACGCGGTGGGCCAGGATACCCAGGAACGCGCCACCATGGTGAGCAAGGGCGAGG CAG
12	GCCGGATCAAGCTTCTGAATTCTTACTTGTACAGCTCGTCCATGCCGCC
13	GAATTCTGCAGATATCCATCACACTGGCGGCCGCTCG
14	GATCCTTATCGTCATCGTCGTACAGATCCCGACCCATTTGC
15	GTACGACGATGACGATAAGGATCCCATGGAGCTTTCCATACCTGAACTGAGAGAAAGAAT
16	CACCGGCGGCATGGACGAGCTGTACAAGTAAGAATTCTGCAGATATCCATCACACTGGC G
17	GGCGGCATGGACGAGCTGTACAAGTAAGAATTCTGCAG



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19	CAGATTGCGAGAGTACACCATTTATTTGCACAGGCGAACTC
20	GTGTA CTCTCGCAATCTGATTCCGGCTGAACACGTG
21	CGTGGACTGCAAGTGCAGACATCCGCTTTACAAGACAGG
22	CACTTGCAGTCCACGCCAGCTCGTCATCAATGACTGC
23	GATTGCGGCAGGACACCATTTATTTGCACAGGCGAAC
24	GTCCTGCCGCAATCTGATTCCGGCTGAACACGTG
25	TACCGTCTCCCCATGATGATGATGATGATGAGAACCCATATGTATATCTCCTTCTTAAAG TTAAACAAAATTATTC
26	TACCGTCTCCTGGGGGCGGAGAGAATTTGTA CTTTCAGGGAGGCGGAGGATCCATGGA GCTTCCATACCTG
27	TACCGTCTCCCAGGGTGAACGTGTCGTAGC
28	TACCGTCTCCCCTGCTTTACCTGTCTTGTAAGCG