

Enhanced expression of pullulanase in *Bacillus subtilis* by new strong promoters mined from transcriptome data, both alone and in combination

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Table S1 primers used in this study

Name	Description	Primers	Restriction sites
F1	amplify <i>amyE</i> -up arm	ggatccGACTCCGAAGTAAGTCTTC	<i>Bam</i> HI
R1	amplify <i>amyE</i> -up arm	cgtcgacgCGCCCGATCAGACCAGTTTTTAA	<i>Sgr</i> DI
F2	amplify <i>amyE</i> -down arm	ccatggCAAGTGAACGATGGTAAACT	<i>Nco</i> I
R2	amplify <i>amyE</i> -down arm	agatctTCAATGGGGAAGAGAACCG	<i>Bgl</i> II
F3	amplify mRNA stab	gaattcAGGGATGCCTAAAAACGAAG	<i>Eco</i> RI
R3	amplify mRNA stab	acgcgtCACTTTTCATAATACATAAT	<i>Mlu</i> I
F4	amplify <i>pulA</i>	gtcgacGCAGCAGCTAAACCCGCTG	<i>Sal</i> I
R4	amplify <i>pulA</i>	cgtcgacgTTAACTTTTACCGTGGT	<i>Sgr</i> DI
F5	amplify signal peptide <i>amyE</i>	acgcgtATGTTTGCAAAACGATTCA	<i>Mlu</i> I
R5	amplify signal peptide <i>amyE</i>	gtcgagAGCACTCGCAGCCGCCGGT	<i>Sal</i> I
F6	amplify promoter <i>amyE</i> to form pCBS4	cccggtTAGAGTGATTGTGATAAT	<i>Sma</i> I
R6	amplify promoter <i>amyE</i> to form pCBS4	gaattcTCTTGACACTCCTTCTTTG	<i>Eco</i> RI
F7	amplify promoter <i>hag</i> to form pCBS5	cccggtGGATTTTTTATTTTTGTAT	<i>Sma</i> I
R7	amplify promoter <i>hag</i> to form pCBS5	gaattcTGTTTTGTTCCTCCCTGAAT	<i>Eco</i> RI
F8	amplify promoter <i>tufA</i> to form pCBS6	cccggtTGATTTTGCCGCTTAACTC	<i>Sma</i> I
R8	amplify promoter <i>tufA</i> to form pCBS6	gaattcTCTAAAATCCTCCTTAAG	<i>Eco</i> RI
F9	amplify promoter <i>csuD</i> to form pCBS7	cccggtGGCGTACTTGAGAGCATACGA	<i>Sma</i> I
R9	amplify promoter <i>csuD</i> to form pCBS7	gaattcATTGCTTAATTCCTCCTAG	<i>Eco</i> RI
F10	amplify promoter <i>yqeY</i> to form pCBS8	cccggtAACGAATCGCTTGAAGATGCTC	<i>Sma</i> I
R10	amplify promoter <i>yqeY</i> to form pCBS8	gaattcAAATCCACCCTCTTTAGAAATTGC	<i>Eco</i> RI
F11	amplify promoter <i>sodA</i> to form pCBS9	cccggtGAAATGCTGGCGGCAGGTTTAATG	<i>Sma</i> I
R11	amplify promoter <i>sodA</i> to form pCBS9	gaattcGATAATTCCTCCTTAGTATAT	<i>Eco</i> RI
F12	amplify promoter <i>fusA</i> to form pCBS10	cccggtCTGGTGCTGCTGTTAAGAAAC	<i>Sma</i> I
R12	amplify promoter <i>fusA</i> to form pCBS10	gaattcTGGGTAAATTCCTCCTTCCT	<i>Eco</i> RI
F13	amplify promoter <i>gapA</i> to form pCBS11	cccggtATCGAGGCTTACTTTAAAAAAGC	<i>Sma</i> I
R13	amplify promoter <i>gapA</i> to form pCBS11	gaattcGATTGTTTCCTCCTTTAAAT	<i>Eco</i> RI
F14	amplify promoter <i>ahpF</i> to form pCBS12	cccggtTGACAAAAAATATATATTAATT	<i>Sma</i> I
R14	amplify promoter <i>ahpF</i> to form pCBS12	gaattcAATGTATATTCCTCCTAAAAATG	<i>Eco</i> RI
F15	amplify promoter <i>glnA</i> to form pCBS13	cccggtATTTTTTAAAAATTCTCTGGATTG	<i>Sma</i> I
R15	amplify promoter <i>glnA</i> to form pCBS13	gaattcCTCAATTCCTCCTTTTCTTAAC	<i>Eco</i> RI
F16	amplify promoter <i>mdh</i> to form pCBS14	cccggtGACTGAAGTGAAATGTTC	<i>Sma</i> I
R16	amplify promoter <i>mdh</i> to form pCBS14	gaattcGTCTCTCTTCTCCTTTATG	<i>Eco</i> RI
F17	amplify <i>sodA</i> promoter to form pCBS15,16,17,18,27, 40	ggtaccGAAATGCTGGCGGCAGGTTTAATG	<i>Kpn</i> I
R17	amplify <i>sodA</i> promoter to form pCBS15,16,17,18,27, 40	cccggtGATAATTCCTCCTTAGTATAT	<i>Sma</i> I
F18	amplify <i>hag</i> promoter to form pCBS19,20,21,25,30,31,32,41	ggtaccGGATTTTTTTATTTTGTAT	<i>Kpn</i> I
R18	amplify <i>hag</i> promoter to form pCBS19,20,21,25,30,31,32,41	cccggtTGTTTTGTTCCTCCCTGAAT	<i>Sma</i> I
F19	amplify <i>tufA</i> promoter to form pCBS22,23,26,33,34,36,37,42	ggtaccTTGATTTTGCCGCTTAACTC	<i>Kpn</i> I

R19	amplify tufA promoter to form	cccgggTCTAAAATCCTCCTTAAG	<i>SmaI</i>
	pCBS22,23,26,33,34,36,37,42		
F20	amplify fusA promoter to form	ggtaccCTGGTGCTGCTGTTAAGAAAC	<i>KpnI</i>
	pCBS24,28,35,38,39		
R20	amplify fusA promoter to form	cccgggTGGGTAATTCTCCTTCCT	<i>SmaI</i>
	pCBS24,28,35,38,39		
F21	amplify amyE promoter to form	ggtaccTAGAGTGATTGTGATAAT	<i>KpnI</i>
	pCBS29,43		
R21	amplify amyE promoter to form	cccgggTCTTGACACTCCTTCTTTG	<i>SmaI</i>
	pCBS29,43		
F22	amplify sodA promoter to form	ccatggGAAATGCTGGCGGCAGGTTTAAT	<i>NcoI</i>
	pCBS30-35,40		
R22	amplify sodA promoter to form pCBS30-	ggtaccGATAATTCCTCCTTAGTATAT	<i>KpnI</i>
	35,40		
F23	amplify hag promoter to form pCBS36-	ccatggGGATTTTTTTATTTTGTAT	<i>NcoI</i>
	38,41		
R23	amplify hag promoter to form pCBS36-	ggtaccTGTTTTGTTCCCTCCTGAAT	<i>KpnI</i>
	38,41		
F24	amplify tufA promoter to form	ccatggTTGATTTTGCCGCTTAAGTC	<i>NcoI</i>
	pCBS39,42		
R24	amplify tufA promoter to form	ggtaccTCTAAAATCCTCCTTAAG	<i>KpnI</i>
	pCBS39,42		
F25	amplify amyE promoter to form pCBS43	ccatggTAGAGTGATTGTGATAAT	<i>NcoI</i>
R25	amplify amyE promoter to form pCBS43	ggtaccTCTTGACACTCCTTCTTTG	<i>KpnI</i>

Lowercase letters are restriction site

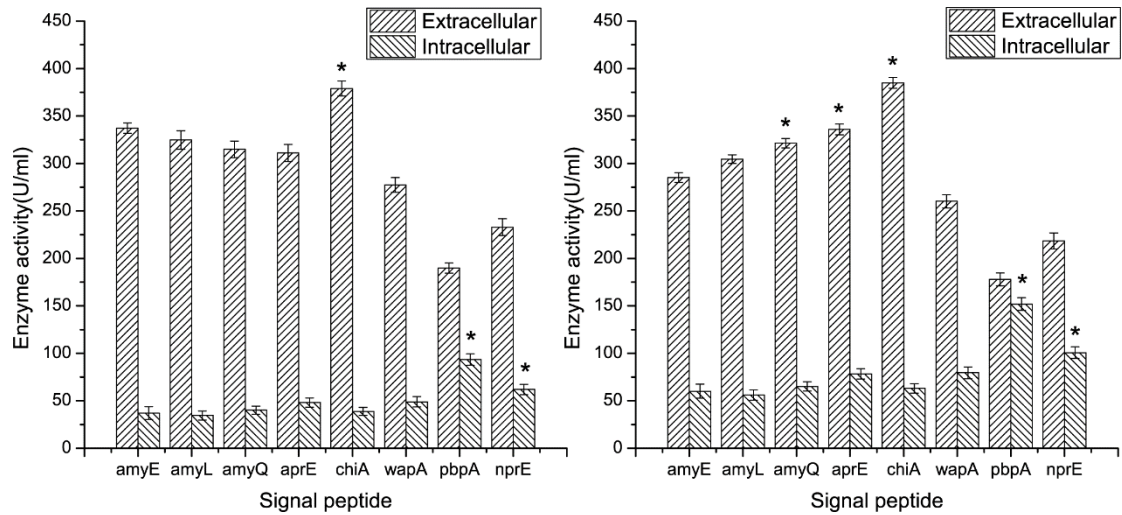


Figure S1 the effect of signal peptide on the extracellular and intracellular enzyme activity.
 (a) the extracellular and intracellular enzyme activity of engineering strain PsodA+fusA+amyE with the different signal peptide. (b) the extracellular and intracellular enzyme activity of engineering strain PsodA+hag+tufA with the different signal peptide. “*” means the effect of the increase was significant ($P<0.05$) compared to control group PamyE.

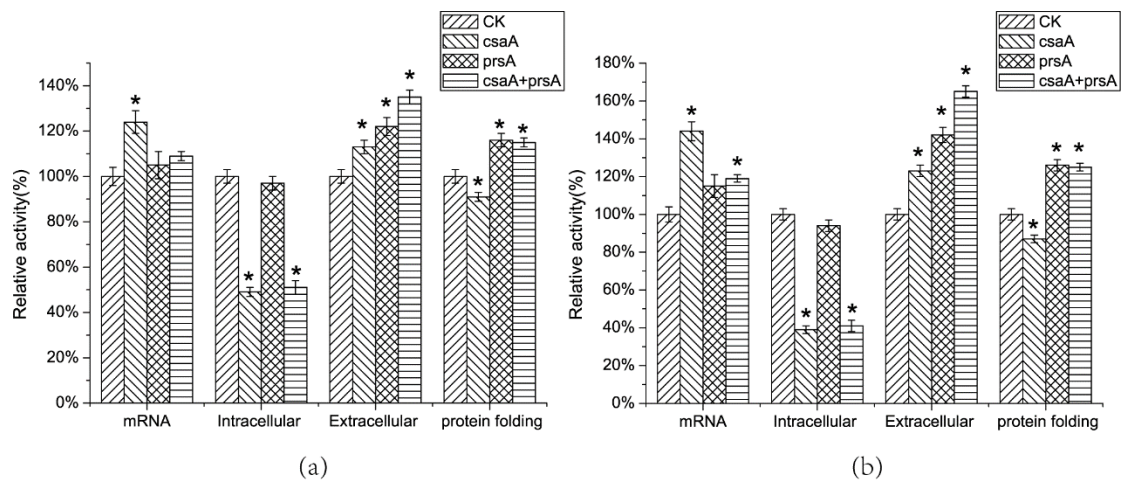


Figure S2 the effect of chaperone on the secretion efficiency and protein folding rate.
 (a) The effect of chaperone on the amount of mRNA, intercellular and extracellular enzyme activity, and extracellular protein folding rate of strain PsodA+fusA+amyE. (b) The effect of chaperone on the amount of mRNA, intercellular and extracellular enzyme activity, and extracellular protein folding rate of strain PsodA+hag+tufA. “*” means the difference was significant ($P<0.05$) compared to control group PamyE.

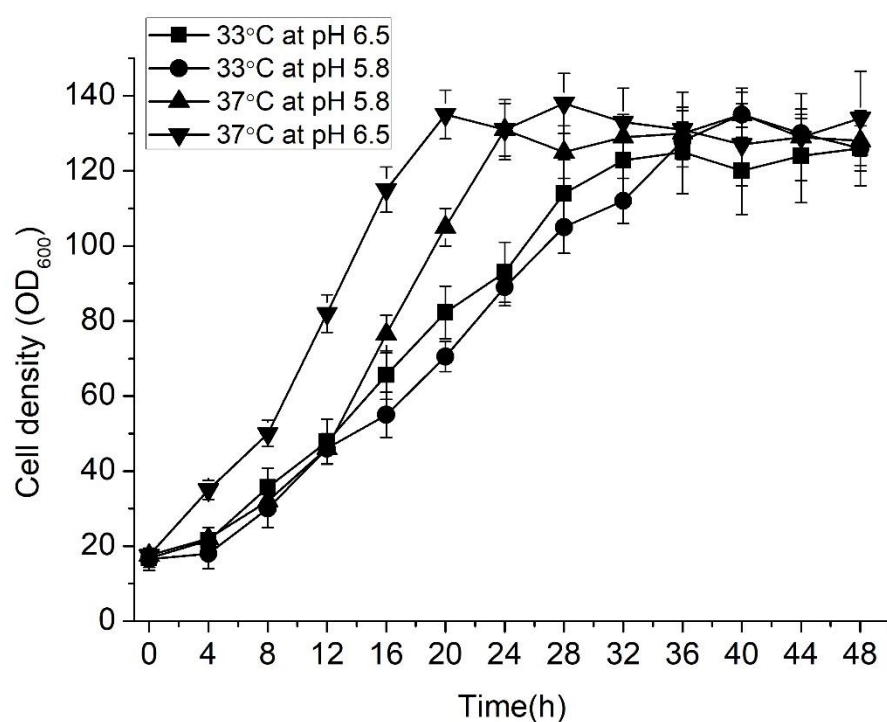


Figure S3 The cell density (OD_{600}) of engineered strains with the promoter PsodA+fusA+amyE in 50-Liter fermenter under different conditions.

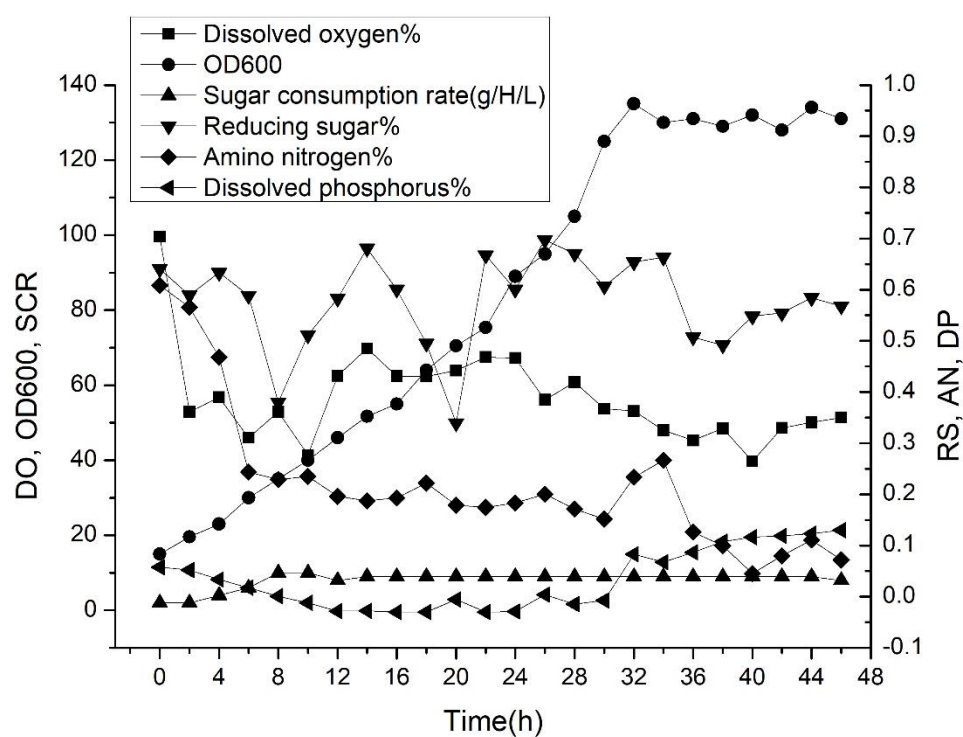


Figure S4 The fermentation related parameters of engineered strains with the promoter PsodA+fusA+amyE in 50-

Liter fermenter. DO is dissolved oxygen, OD600 is the cell density, SCR is sugar consumption rate, RS is reducing sugar in supernatant, AN is free form amino nitrogen, DP is dissolved phosphorus.

The sequence of homology arm, *pulA* and promoters.

amyE-up homology arm

```
AGAATGAAGTAAGAGGGATTTTTGACTCCGAAGTAAGTCTTCAAAAAATCAAATAAGGAGTGTC
AAGAATGTTTGCAAAACGATTCAAACCTCTTTACTGCCGTTATTCGCTGGATTTTTATTGCTGTT
TCATTTGGTTCTGGCAGGACCGGCGGCTGCGAGTGCTGAAACGGCGAACAATCGAATGAGCT
TACAGCACCGTCGATCAAAAGCGGAACCATTCTTCATGCATGGAATTGGTCGTTCAATACGTTA
AAACACAATATGAAGGATATTCATGATGCAGGATATACAGCCATTCAGACATCTCCGATTAACC
AAGTAAAGGAAGGGAATCAAGGAGATAAAAGCATGTGGAAGTGGTACTGGCTGTATCAGCCGA
CATCGTATCAAATTGGCAACCGTTACTTAGGTAAGTGAACAAGAATTTAAAGAAATGTGTGCAGC
CGCTGAAGAATATGGCATAAAGGTCATTGTTGACGCGGTCATCAATCATACCACAGTGATTAT
GCCGCGATTTCCAATGAGGTTAAGAGTATTCCAAACTGGACACATGGAAACACACAAATTAATA
ACTGGTCTGATCGGGCG
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amyE-down homology arm

```
CAAGTGAACGATGGTAAACTGACAGGCACGATCAATGCCAGGTCTGTAGCTGTGCTTTATCCTG
ATGATATTGCAAAAGCGCCTCATGTTTTCTTGAGAATTACAAAACAGGTGTAACACATTCTTTC
AATGATCAACTGACGATTACCTTGCCTGCAGATGCGAATACAACAAAAGCCGTTTATCAAATCA
ATAATGGACCAGAGACGGCGTTTAAGGATGGAGATCAATTCACAATCGGAAAAGGAGATCCAT
TTGGCAAAACATACACCATCATGTTAAAGGAACGAACAGTGATGGTGTAAACGAGGACCGAGA
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TTGGAGCCAGGTAAATGCTTATATCTATAAACATGATGGGAGCCGAGTAATTGAATTGACCGGA
TCTTGGCCTGGAAAACCAATGACTAAAAATGCAGACGGAATTTACACGCTGACGCTGCCTGCG
GACACGGATACAACCAACGCAAAAGTGATTTTTAATAATGGCAGCGCCCAAGTGCCCGGTCAG
AATCAGCCTGGCTTTGATTACGTGCTAAATGGTTTATATAATGACTCGGGCTTAAGCGGTTCTCT
TCCCCATTGA
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Sequence of *pulA*

```
GCAGCAGCTAAACCCGCTGTAAGCAACGCTTATTTAGATGCTTCAAACCAGGTGCTGGTTAAAC
TTAGCCAGCCGTTAACTCTTGGGGAAGGCGCAAGCGGCTTTACGGTTCATGACGACACAGCAA
ATAAGGATATTCCAGTGACATCTGTGAAGGATGCAAGTCTTGGTCAAGATGTAACCGCTGTTTTG
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CAGGTGATACCTCGTAATGTGCTTAATTCATCACAGTACTACTATTCAGGAGATGATCTTGGGAA
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CTGTAGCAACCATCAATTTGCCGAGCGGGAAATGGGCAATCAATGCTACGAGCGGTAAGGTAG
GAGAATCCACCCTTGGTCAAGCAGAGGGAAGTGTCCAAGTACCAGGTATATCTATGATGATCCT
TCATCAAGAGGTAAGCCCAGACCACGGTAAAAAGTAA

mRNA stable sequence

AGGGATGCCTAAAAACGAAGAACATTAATAACATATATTTGCACCGTCTAATGGATTTATGAAA
AATCATTTTATCAGTTTGAAAATTATGTATTATGAAAAGTG

The sequence of PamyE

TAGAGTGATTGTGATAATTTTAAATGTAAGCGTTAACAAAATTCTCCAGTCTTCACATCGGTTTGA
AAGGAGGAAGCGGAAGAATGAAGTAAGAGGGATTTTTGACTCCGAAGTAAGTCTTCAAAAAAT
CAAATAAGGAGTGTCAAGA

The sequence of Phag

GGATTTTTTTATTTTTGTATTAACAAAATCAGAGACAATCCGATATTAATGATGTAGCCGGGAGG
AGGCGCAAAAGACTCAGCCAGTTACAAAATAAGGGCACAAGGACGTGCCTTAACAACATATTC
AGGGAGGAACAAAACA

The sequence of PtufA

TTGATTTTGCCGCTTAACTCAAGTATAACTACTATTGTAAGATGAGGAAGTGAAAGCTTTCTTTCA
CTTCCTATCACTCTATACATTACTAATTAAGGCTCTTAAGGAGGATTTTAGA

The sequence of PcspD

GGCGTACTTGAGAGCATACGAAAATCGTGTGCTCTTTTTATTTATATTCAGCCATCAATAAAAGC
GGTTACATTTTTTTATGGAACCTGCCCTTCTTTTGAAAAATAAGCCGTTTCGCAACTTGACGGGTG
CTCCCAGATGGTGTATAGTTGAACCATCATTTAACAATGAATCAAAGTTAGATGATGACAAAATT
TTTTTTAGCACATGGGTGCTACAGTACTAGGAGGAATTAAGCAAT

The sequence of PyqeY

AACGAATCGCTTGAAGATGCTCTTCGTCGCTTCAAACGCAGTGTATCAAAGACAGGTACTTTGC
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The sequence of PsodA

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The sequence of PfusA

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TCACTATCGCTGGTAGGATTTATAGATTAACAAAACACAATTCCTAATAAGGAAGGAGAAATTA
CCCA

The sequence of PgapA

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AAGTTATTAAGGGATGAATAATCCCTCAATATAAATATCTCTCACTTATTTAAAGGAGGAAACAA
TC

The sequence of PahpF

TTGACAAAAAATATATATTAATTAATAATTCATATATAATTAGAATTATTATTGAAAGCGATTATG
CTTTCTAATACATTTTTAGGAGGAATATACATT

mdh

The sequence of PglA

ATTTTTTAAAAATTTCTCTGGATTTGATGTTAAGAATCCTTACATCGTATTGACACATAATATAAC
ATCACCTATAATGAAACTAAGTTAAGAAAAGGAGGAAATTGAG

The sequence of Pmdh

GACTGAAGTGAAATGTTTCAGAGTTCGGAGAAGAACTGATCAAAAACATGGACTAAGCAAGGAA
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SPamyE

ATGTTTGCAAACGATTCAAACCTCTTTACTGCCGTTATTCGCTGGATTTTTATTGCTGTTTCATT
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SPamyL

ATGATTCAAAAACGAAAGCGTGCCATATCATGGGGTCTGGTGTTTTCTTAACACTACTGTTTGT

CACGCTGCCGGTATCTAAAACTTGGGCTGCA

SPamyQ

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SPaprE

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SPchiA

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SPwapA

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SPpbpA

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CTGAATATTTATTTTAGCTGCCTTTGTTATATTACCTG

SPnprE

GTGGGTTTAGGTAAGAAATTGTCTGTTGCTGTCGCTGCTTCGTTTATGAGTTTATCAATCAGCCTG
CCAGGTGTTCAAGCT