

Table S1

Sequences of *ermEp* and *SF14P* promoters

Promoter	Sequence
<i>ermEp</i>	TCGATC <u>TTGACGGCTGGCGAGAGGTGCGGGGAGGAT</u> CTGACCGACGCGGTCCACACGTGGCAC CGCGATGCTGTTGTGGGCTGGACAATCGTGCCGGTTGGTAGGATCCAGCG
<i>ermEp*</i>	TCGATC <u>TTGACGGCTGGCGAGAGGTGCGGGGAGGAT</u> CTGACCGACGCGGTCCACACGTGGCAC CGCGATGCTGTTGTGGGCACAATCGTGCCGGTTGGTAGGATCCAGCG
<i>ermEp1</i>	GTTGTGGGCTGGACAATCGTGCCGGTTGGTAGGATCCAGCG
<i>ermEp2</i>	TCGATC <u>TTGACGGCTGGCGAGAGGTGCGGGGAGGAT</u> CTGAC
<i>ermEp1*</i>	GTTGTGGGCACAATCGTGCCGGTTGGTAGGATCCAGCG
<i>SF14P</i>	CCTATCCAGGAGATATTATGAGTTACGTAGACCTACGCCTTGACCTTGATGAGGCGGCGTGAGC TACAATCAATACTCGATT

Promoter sequences are given in the 5' to 3' direction. -10 and -35 sequences are underlined.

Synthetic promoters recognized by the major vegetative sigma factor HrdB

Promoter	Sequence
C2-6	CAAAGGAGGTTT <u>GACT</u> GGGTTGATGATAGTTTCTAGGATACGCA
A5-11	TTCAAATATATTGACCGGGAAGAGTCGGGAGCGTAGGTTGGGG
A2-1	GATGATCATATTGACCCGGTAGCTTTCGAAGGATAGGTTGATTG
7-SP	AGCATTGATATTGACAGGGGCTGGTCGGAATTATAGCTTAGCTA
A5-18	AATCAAGACTTTGACCTGGGATCCCCTTGAAGTAGCTTTTGCA
A4-4	GCCTGTATTGTTGACTGCTGTGGGGCATAAACATAGCTTCGAGG
A5-15	GCGGCCGCGATTGACAAGGGAAGTTGTCCAATAGAGTCGGAT
A5-1	TACTATGTGATTGACCAGATTCGTGCTCGCCTTAGAGTCGCGG
A4-19	TTGGGGGAACCTTGACGTAGAGTGATTGTTTTATACGTTGAGCG
A5-10	CACGGGGTCATTGACGAGACCCTGACGGGCGCGTACGGTTTCGT
A1-13	GGCTTGATGTTGACGTGGACGAGTTCGTTGCATACCTTCAGTA
A5-17	CCTACCTGGTTGACTCGCTTACAACAGAACATTACCGTCTAGC
10-SP	TCGCACTCCGTTGACGCAAGCCTGTGGATCCATACATTGCGAC
A5-24	TTGCCCCGCTTTGACGATGGAGTAGGTATGATTACATTGATTG
C4-15	AAAAGTAGAATTGACTCGATAGTGGGGGCCGCTAGGGTGCCGC
A4-15	CAAAGCACAAATTGACCGCTATGACAGGATTGGTTAGGGTGGGGT
A1-4	GAGTGCGAGATTGACGTAATGAGGGTGTGTGCCTAGGTTCTGTA
A2-19	TTATTTAGAGTTGACTGTGTTCTCGTCTCCCATAGCGTGGA
A5-12	CTCCGGAAGTTGACTTCGAGGGGCTCATTTATAGAGTGATAC
A3-12	ACTGTTGTAATTGACGAAAGGGGACTTCAAGCGTAGAGTCAACG
B4-21	ACGCAGTAATTTGACCTTGTTGTACCGGTCGCCTACGTTGTGCT
C3-20	GAATAAAATTTTGACGGAGAGCGCGAGAGCAAGTACGGTCGTTA
A1-12	TGGGATCACATTGACTCAGCTGAATATGGTGCTTACCTTCGGAA
C4-14	CCCTCGCTGGTTGACACAGTTAGTCAGATTGCCTACGATTCGT
C4-1	GGCAACTAGGTTGACGTATTTTTCCGTTAGGCCTAGGGTGAGTG
A5-19	TATGCGTTGCTTGACCAACCTATGTATAGGGATAGGGTTGGTC
D1-1	CGATGTCGCGTTGACAACGCTGAGGTGAGGGGTTAGGGTAGGTG
A1-14	GTGGGTCGTATTGACGATGTATTTGGGGAGTGTTAGGATATGCG
D1-7	AATTGCCCACTTGACGTTGAGAGTGAAGCAATATAGGTTAACCT
C4-18	GGTGATCAGTTTGACGCCCCTGACATCGGGTGGTAGCGTCGCTG
B3-16	TCGGTGGAAGTTGACTGACGAGGGGTCGCTGCTAGCATGAGGA
B4-12	GGCGTAGGGTTTGACTAAAATAATATCCATTATAGAGTCGTCA
D1-10	GTCTGTGTCCTTGACGCCGCGGGGTGTAGAGATAGAGTCTGGC
A1-2	GCAGGTTTCGTTGACAGGATCGAGGGGTATAACTAGAGTGTCGA
D1-11	TACATCGCAGTTGACAAGCCGGCTTTCTGATCATACGGTGTGAC
D1-9	TCCGCTGCAGTTGACCGCCGCACTATCCGGGTACGGTGC
D1-6	TGAGTACTCGTTGACGCTCTTGCTCGTTGGTGGTACGTTAGTGT
B4-8	TCACATGTGTTTGACCCGTGGGTCTGAGTTGCTACCATCAAAG

9 Promoter sequences are given in the 5' to 3' direction. -10 and -35 sequences are underlined. Weak
 10 promoters – from C2-6 to A5-24, medium – from C4-15 to C4-14, strong – from C4-1 to B4-8.

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Table S3

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Synthetic derivatives of *kasOP* promoter

Promoter	Sequence
<i>kasOP</i> ₃₁₄	TGTTCACATTCTGAACGGTCTCTGCTTTGACAACACGCTGTACTGTGTTGTAAAGTCGTGGCC
<i>kasOP</i> ₃₆₁	TGTTCACATTCTGAACGGTCTCTGCTTTGACAACATGCTGTGCGGTGTTGTAAAGTCGTGGCC
<i>kasOP</i> ₃₈₂	TGTTCACATTCTGAACGGTCTCTGCTTTGACATGGAGTCGTGAGCTACTGTAAAGTCGTGGCC
<i>kasOP</i> ₃₁₅₄	TGTTCACATTCTGAACGGTCTCTGCTTTGACAATCGTGCCGTTGGTATGTAAAGTCGTGGCC

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15 Promoter sequences are given in the 5' to 3' direction. -10 and -35 sequences are underlined.

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Second-stage derivatives of the *kasOP** promoter

Promoter	Sequence	Activity
SP1	TGTTACATTCTGAACCGTCTCTGCTTTGACATGGAGAGAAGTTTGTAAAGTCGTGGCC	0,95
SP2	TGTTACATTCTGAACCGTCTCTGCTTTGACAGAGCCCCTACCAGAATTGTAAAGTCGTGGCC	0,97
SP3	TGTTACATTCTGAACCGTCTCTGCTTTGACAATGATTTAAGCGTAAATGTAAAGTCGTG GCC	1,02
SP4	TGTTACATTCTGAACCGTCTCTGCTTTGACAGCCTTGCTGAAAATCTTGTAAAGTCGTG GCC	2,37
SP5	TGTTACATTCTGAACCGTCTCTGCTTTGACATCTTATGATTCTCGACTGTAAAGTCGTG GCC	3,91
SP6	TGTTACATTCTGAACCGTCTCTGCTTTGACATGGTCTAGCCGTTGATTGTAAAGTCGTG GCC	3,99
SP7	TGTTACATTCTGAACCGTCTCTGCTTTGACAATTGGATTACGTATGTGTAAAGTCGTG GCC	4,58
SP8	TGTTACATTCTGAACCGTCTCTGCTTTGACACCCGCGGATTACCTCCTGTAAAGTCGTG GCC	6,12
SP9	TGTTACATTCTGAACCGTCTCTGCTTTGACACGCAAGATCAACCCGCTGTAAAGTCGT GGCC	6,39
SP10	TGTTACATTCTGAACCGTCTCTGCTTTGACATGTTCTTACGGTCACATGTAAAGTCGTG GCC	7,42
SP11	TGTTACATTCTGAACCGTCTCTGCTTTGACAATGGCTTGAATTGGGGTGTAAAGTCGT GGCC	8,66
SP12	TGTTACATTCTGAACCGTCTCTGCTTTGACAGGTCCATACACGCGCTGTAAAGTCGTG GCC	11,26
SP13	TGTTACATTCTGAACCGTCTCTGCTTTGACAAGCCGACCTATAAACATGTAAAGTCGTG GCC	12,54
SP14	TGTTACATTCTGAACCGTCTCTGCTTTGACACGACCCACTTTCGCTGTGTAAAGTCGTG GCC	16,52
SP15	TGTTACATTCTGAACCGTCTCTGCTTTGACACCTACGTGACACATCTTGTAAAGTCGTG GCC	16,89
SP16	TGTTACATTCTGAACCGTCTCTGCTTTGACATACTTGGGTGCGGCACTGTAAAGTCGT GGCC	16,92
SP17	TGTTACATTCTGAACCGTCTCTGCTTTGACAATCGCAGACTTTATGCTGTAAAGTCGTG GCC	17,40
SP18	TGTTACATTCTGAACCGTCTCTGCTTTGACAGGCTCTGCTGTGAACGTGTAAAGTCGT GGCC	20,68
SP19	TGTTACATTCTGAACCGTCTCTGCTTTGACACGACCCACTTTCGCTGTGTAAAGTCGTG GCC	23,44
SP20	TGTTACATTCTGAACCGTCTCTGCTTTGACACATGACGCTCACCCGTTGTAAAGTCGTG GCC	26,51
SP21	TGTTACATTCTGAACCGTCTCTGCTTTGACAATGGGTCCGCCTCGAGTGTAAAGTCGT GGCC	27,30
SP22	TGTTACATTCTGAACCGTCTCTGCTTTGACAAGTCGCAAAACAACCTGTAAAGTCGTG GCC	47,96
SP23	TGTTACATTCTGAACCGTCTCTGCTTTGACAACATGCTGTGCGGTGTTGTAAAGTCCTG CTA	50,75
SP24	TGTTACATTCTGAACCGTCTCTGCTTTGACAACCAAGGCACATCTAATGTAAAGTCGTG GCC	55,91
SP25	TGTTACATTCTGAACCGTCTCTGCTTTGACAGAGGTAGGCACGCTCATGTAAAGTCGT	58,99

	GGCC	
SP26	TGTTACATTCTGAACCGTCTCTGCTTTGACAGCTCACTGGGCATGGGTGTAAAGTCGT GGCC	70,22
SP27	TGTTACATTCTGAACCGTCTCTGCTTTGACAAGGTCCCGTCTTAGGTGTAAAGTCGT GGCC	71,08
SP28	TGTTACATTCTGAACCGTCTCTGCTTTGACAACATGCTGTGCGGTGTTGTAAAGTCAA GGAG	73,51
SP29	TGTTACATTCTGAACCGTCTCTGCTTTGACATCCTACACACGTTTAGTGTAAAGTCGTG GCC	73,63
SP30	TGTTACATTCTGAACCGTCTCTGCTTTGACATCGTGTGGCGCTTGGGTGTAAAGTCGT GGCC	75,14
SP31	TGTTACATTCTGAACCGTCTCTGCTTTGACAACATGCTGTGCGGTGTTGTAAAGTCAGT AAC	84,27
SP32	TGTTACATTCTGAACCGTCTCTGCTTTGACAACATGCTGTGCGGTGTTGTAAAGTCCAG TGT	91,19
SP33	TGTTACATTCTGAACCGTCTCTGCTTTGACAACATGCTGTGCGGTGTTGTAAAGTCGAT GGC	94,27
SP34	TGTTACATTCTGAACCGTCTCTGCTTTGACAACATGCTGTGCGGTGTTGTAAAGTCTTC AAG	94,94
SP35	TGTTACATTCTGAACCGTCTCTGCTTTGACAACATGCTGTGCGGTGTTGTAAAGTCGG GGGG	95,92
SP36	TGTTACATTCTGAACCGTCTCTGCTTTGACAACATGCTGTGCGGTGTTGTAAAGTCTAA CCG	96,30
SP37	TGTTACATTCTGAACCGTCTCTGCTTTGACAACATGCTGTGCGGTGTTGTAAAGTCATC CGT	97,50
SP38	TGTTACATTCTGAACCGTCTCTGCTTTGACAACATGCTGTGCGGTGTTGTAAAGTCGCT GGC	100
SP39	TGTTACATTCTGAACCGTCTCTGCTTTGACAACATGCTGTGCGGTGTTGTAAAGTCCCA TGA	105,15
SP40	TGTTACATTCTGAACCGTCTCTGCTTTGACAACATGCTGTGCGGTGTTGTAAAGTCCCG TAG	116,55
SP41	TGTTACATTCTGAACCGTCTCTGCTTTGACAACATGCTGTGCGGTGTTGTAAAGTCCAG CTG	127,45
SP42	TGTTACATTCTGAACCGTCTCTGCTTTGACAACATGCTGTGCGGTGTTGTAAAGTCGG GTGA	135,95
SP43	TGTTACATTCTGAACCGTCTCTGCTTTGACACGGACAAGCGCTATGGTGTAAAGTCGT GGCC	154,50
SP44	TGTTACATTCTGAACCGTCTCTGCTTTGACAACATGCTGTGCGGTGTTGTAAAGTCTGG TGT	187,45

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20 Promoter sequences are given in the 5' to 3' direction. -10 and -35 sequences are underlined. Relative
21 activity of promoters is shown in % of the *kasOP*₃₆₁ (*kasOP**) promoter's activity.

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ermEp1-based synthetic promoters and their activity (with control promoters used in the study)

Promoter	Sequence	Activity
D4	CCCGTCGGCTGGAAACACTTGATCCAACCTAGGATACTTCC	3,3
C9	TAAAGGGGCTCCCTCAAAAAAGACTTAGTTAGGATGCCAAG	3,6
62	CGCCGCGGCTAAAAAAGAAATAGGCTCAATAGGATGAACCC	3,6
C3	CTGAAATGATGTGGAGCACTTTAGGATAAATGA	3,9
76	AACATAGGCTATACAAAAAACCGCAGTTTAGGATAAATAC	4,0
71	GTGTATGGCTTCAACGTGGAATACCTCCATAGGATAACGAG	4,0
D3	CCACGAGGCTCTGACGATTTCTTAGGATGGCACG	4,2
74	GGCTCAGGCTGAATGGTCTACCAAGCTATTAGGATCAGCAG	4,5
D11	ACGCCGGGCTACAAAAATAATATCAGAACTAGGATGGACTC	4,8
D6	TAACGAGGCTTGGAAACATTATGGACTCCATAGGATACGTAA	4,8
A6	GAGGGAGGCTATGTGATCGGGGAAAGAAATAGGATAGCGGT	4,9
63	CCCCCGGCTTTTACCATTGCGCAAGTTCTAGGATCCCCAA	5,0
C1	ACTTTCGGCTAAAAAGCAATTCATTCAATTAGGATGGAAGA	5,0
A2	AGTGGAGGCTACCTCACAATGGTGGAAATTAGGATGCAACC	5,4
D2	CGCGTAGGCTAAAGATGACATCTTTAACATAGGATGTGCGC	5,5
A1	AGGCCGGGCTGCACTTATTCATCTGTAGATAGGATAACCAA	6,3
64	ACCTAAGGCTAAACCATTATATAGACTCATAGGATAGCGAG	6,5
D1	TTTAGAGGCTCATTGATGGAATCCGAGGATAGGATAAAGTG	6,7
49	TGTTTCGGCTCAGTTCTAGACCTACTCATTAGGATTTTTCA	6,8
114	TCGGGGGGCTCGACACGGCCTCTAACTACTAGGATAACGCT	6,8
B7	TACGCGGGCTGAAACCAGGTTTCTTACAATAGGATATGGAG	6,8
B13	TGCTCGGGCTTTGCGGAATTCTAACTACGTAGGATTAGCTT	7,0
C4	CTTCAGGGCTTTTGTGGCTTAAATCCGTAGGATAAAAAG	7,1
66	GCACCCGGCTAGACATAAACTGAGTGCAATAGGATATTTAA	7,2
A5	TCAAGAGGCTCCCTCATTAGAGTCTTATATAGGATGGGCAT	7,2
69	TTACCAGGCTCCATAAGTCAAGACGCTTGTAGGATAAAAGT	7,7
C2	GTAAAAGGCTAAGACTGAAGGCGAGTAGCTAGGATGCTCTA	8,1
68	CAGCCGGGCTCTTATCTTAACTGGAGCCTAGGATCTCATT	8,0
D7	AAGAAGGGCTAAGTTGATTATGCCAGTAATAGGATAAACTA	8,6
C7	TCAAAGGGCTAGTATGTGACTCCCCATATAGGATACACCT	8,6
B5	ATAAAAGGCTCGTTATAGCAAATAACTATTAGGATCATCCA	8,9
B6	TCAAATGGCTAGGATATAACCTACACGATTAGGATAGCCCC	9,1
D9	CTTAGAGGCTGGTGTCAACTAGATCACCATAGGATTACCA	9,3
D8	ACAGAAGGCTCCCCGTTGCGCCACATATGTAGGATCGACTG	9,5
39	CACGACGGCTAAACCAGAAAGGCCTGGCCTAGGATTAATGT	9,7
A8	TATAGAGGCTGTCAGATCAATGTGAGGGCTAGGATCTTCAA	9,7
B1	CGTCAGGGCTACTCTGGCAACCAAGCGATTAGGATTGAAGG	10,3
65	AGATCTGGCTCCTTTCAAAACGTACTCATAGGATAGGTTT	11,1
70	ACCCGTGGCTACTCAGCGAATAACTCTTGTAGGATACATAA	12,7
67	TAAAGGGGCTGCCGTATGGTTAAGGTGAGTAGGATCGGAAG	13,2
C10	TCTCGCGGCTCTATCGCTTAGGTGGGTAGTAGGATGGCAAG	13,5
82	TCCTGAGGCTAAAATTAGGATTCTTCAAGTAGGATTGTAGC	15,2
B12	CGGGATGGCTTATGAAGGATTGTCTCACTTAGGATAGAGCA	15,3
D10	TAGACTGGCTCGTTGCTAGCGTAACCAAATAGGATACAACG	15,9
102	TCACAGGGCTCAATGCTAAAAGCTAATCATAGGATAGAATC	16,7
A4	AAAAGCGGCTATATCGCTACAGCTTCCAGTAGGATACAAGA	17,5

<i>ermEp1*</i>	GTTGTGGGCACAATCGTGCCGGTTGGTAGGATCCAGCG	21,2
<i>B4</i>	GCTGTAGGCTGTTAATATATTTTCGGTGTGTAGGATACGGGC	21,2
<i>ermEp1</i>	GTTGTGGGCTGGACAATCGTGCCGGTTGGTAGGATCCAGCG	21,5
<i>61</i>	CACGCTGGCTACATTATACCTCGGCATAGTAGGATATCCGC	21,6
<i>81</i>	CAGGTCGGCTGGTTGGCTGACAAAGTGCGTAGGATGACTGT	21,8
<i>C5</i>	TCCGATGGCTGGGGTAAAGACAACCGGGTTAGGATGGTTGT	23,7
<i>A3</i>	TAGCAGGGCTCCAAACTAACGCCTGATGTAGGATCAGATG	30,0
<i>B10</i>	CTAGGGGGCTATGATAAAATGTGAGTCAATAGGATCGGTAA	33,0
<i>57</i>	TTGAACGGCTGGAGGGATACACCTGGTCATAGGATACCATC	33,5
<i>ermEp*</i>	GCTAGCCGCGGTCGATCTTGACGGCTGGCGAGAGGTGCGGGGAGGATCTGACCGA CGCGGTCCACACGTGGCACC GCGATGCTGTTGTGGGCACAATCGTGCCGGTTGGTA GGATCCAGCG	37,6
<i>A9</i>	CCGGGCGGCTTCCTCATGCTTGACTTGACTAGGATAAAGGG	38,0
<i>ermEp</i>	GCTAGCCGCGGTCGATCTTGACGGCTGGCGAGAGGTGCGGGGAGGATCTGACCGA CGCGGTCCACACGTGGCACC GCGATGCTGTTGTGGGCTGGACAATCGTGCCGGTTG GTAGGATCCAGCG	39,4
<i>21</i>	TGTGCGGGCTCTAACACGTCCTAGTATGGTAGGATGAGCAA	62,2

25

26 Promoter sequences are given in the 5' to 3' direction. -10 and -35 sequences are underlined. Relative
27 activity of the promoters is given in units of Gus activity per gram of dry weight. Activity of the reference
28 promoters *ermEp*, *ermEp**, *ermEp1* and *ermEp1** is also shown.

29

31 Promoter regions of glyceraldehyde-3-phosphate dehydrogenase and 30S ribosomal protein S12 from
 32 selected actinobacteria species

Promoter	Sequence
<i>Pgadph(SG)</i>	CTCGGCGGCGAGCGGGGACGTTGGTCCCGCACCCGCCGGGACCCGGGTCCCGGCGGGCGAA ACGGAGGTCCGTGCTCCTACTGGCGAGTACGGATCTCCGGCCGTATCCGGTGGCGTGCGGTGG CCCTCTCGATGTCACCCCCGGGGCCTCGGAGAGGTAGGGTCGGAAGCGGTCGGGGACATCCCT ATACAACCTCGCCGCGTCGAAAACCGGCGTACCTAACGAGGAGATCGGTTC
<i>PrpsL(SG)</i>	AGGGGCGCGCGGCCCGGCCGCGCGCTCCCGTCCGGGGGCGCGTGGCCGGGGCGGTCCCG GCGTGTGCGGCGGACAGCATTTGTTTTGACCCAGCTCCGTGAGGTAGGTACGCTCAAGCCTTG TGCCTGGGGTGTGCTGGGCTCGGGTGCCTGTCCTCAACCGCATCGCGAGTCCGTCAAGTACCA CCGCAATCTGCGCCCTTCCTGCCTTCGGGGCGGGAGTCCGCAGTATTCGACACACCCGACCGCG TGGGTGCGCGATGTTCCAGGTAGTTTACGAACGGCACACAGAAACCGGAGAAGTA
<i>Pgadph(CF)</i>	CACCGGGGCGCCCGTCTGTCGGCGCGCCCGGTGGTCCAGCATGCGAACGCAGGTCCGGGCCGG ACCTTCGTCTTGCCGACGCCCTCGCCGCGGGGTATAGGCTCGGGTCATCCGATCGCAACGACG ACGCAACGCGTGGGCACATCCCGCGGTGGTGGTGGTGGCGCGCGGCCGGAACGCACAGCGGC GTGCGTGACCCGAACACCAACTGTGTGCGCCGCGATGGGATCGGCGCGTGCCGAGGAGGGCAA
<i>Pgapdh(EL)</i>	GCTGCTCCTTCGGTCGGACGTGCGTCTACGGGCACCTTACCGCAGCCGTCCGGTGTGCGACACG GACGGATCGGGCGAACTGGCCGATGCTGGGAGAAGCGCGCTGCTGTACGGCGCGACCCGGGT GCGGAGCCCTCGGCGAGCGGTGTGAACTTCTGTGAATGGCTGTTCCGTTGCTTTTTTATAC GGCTGCCAGATAAGGCTTGACAGCATCTGGGCGGCTACCGCTATGATCGGGGCGTTCTCTGCAATT CTAGTGCGAGTATCTGAAAGGGGATACGC
<i>Pgapdh(KR)</i>	CACGGGCCGGTGAACCCCGCATGAATGTTGGTTCATGTGGGGTTTGCGCCAGCTGTGTGCGAGT TGCCCCCGCCACTGTTCCCGGGGCATGAATCCCGCTAGAATGAACACGGAAGAGCAGGTGGA CCCCGGGTGCTCACCGCACTTCGGGTGTGGGATTATGCCGATTGTTTGTATCCACATCCGGA CGGGCCGGAGTGACCCGCACACCCACTCGCAGAGGAGATTGCA
<i>Pgapdh(TP)</i>	TCCGTTCCCGGCGGGGAGCGGGACACCCGGGGAGTTCGCCCAGAAATGTCCGAAGCTAGGCGA AGAAAGTGTGACGAGCACGAAGTCCCTGCTCCCTGCCGGTGCGAATGTGCCACGCGATAGGGT GTGGTGACAGGCACACCCAGTCGAAGGAGCAGTTAA
<i>PrpsL(AC)</i>	GCGCGGTCTCGCCGGCCGGCGGCGGTGCCCGTTGTTCACTCCGACGGTCCGGGAGTCGCCG GAGCCGTGCGCGAGAAGAGGGCCGGTGCCTTCGTATTGGCGCAGGCGTTCCCCGTGCCGT CGAGCGGTGGGTTGCTCCGTGACGTGCGGTCCCGGTGGCTGGCGTAGCCGCGAACTACGGCA GCGACTGACCGCTGCTGCGGCCGGCTACTCGGCGCGCCGGCGGAGTCCCTGCGCTGAAACGGG ACCCGGTTTTGACCTGCCGGCACGGGCTCGGTAACCTAGTCGCTCGTCCCGGCTTCCCGGGCG CCTTCGCTGTTCTGCGCGCTTGCTTGTTTGC GCGGTGCTCGGCGTGTGGCCGCCGGCAGGCG GCCTCCGGCCGAGCCCGACACGCCCGACCGGTGGAGCGGCGATAGGGTGCAGGGAGCAGGA CATCGGACAGACCGAGCGATCACGTTGAGGATCCACGAAGGGCGCGT
<i>PrpsL(CF)</i>	CCCCCGCGGGCGCTGGAGGCTCGGGCGGGCCCCGGGCGGAGGCGGGCCGCGACACGACGC CCGCGGGACGTGACGAGCGGCACGACTCGACGACTCCGGGCTCCTTGACGCTGTCCGTGCGCG CGGGTAGCGTAGGACACCGTGCCCGCGCCGTGGGGCCCTCGCGCGTGCCTCGGTGACCGCTC CCTGCCGGAGTGGGTGCGGGTGACGGGGTGGTCCCCACCTCCTCTCGGATCGGTCTTCGCGG ACTGCCGCCGTGCGGAGGACCGGGGCGACACGCCCGGGCGCGGGGGTGGTGGCGGACTCCA GACCTCCGGGGTAGTCGTGCGACGGGCGACGATCCGGGCCGAGCCGGCCGTCTGGGTGACG GGTGCCGGTCAGACCAGAGAACACCGACAGACGGAGACGTA
<i>PrpsL(KR)</i>	TCACGCGTGGCTGGGTGCGGGCTCGGTGGTCTGGGGCGTCGGTTTCCCTGAGCTGCCGTGGCT GATACGATGGGCCAGAATTGCTCGATTCCGGGCGAGTTTGAATGAGATGGCAAATCGGACTCCG TCCTGTGGTACGCACCATGTACCTAGATGCCATCTTTCGTATGCTCAGGTGCGGTTTCCGAGGC GTTCCGCCCCGCGACGCACCGGGCACCCCGGGATCAACGTTCCGTATCGGCGGGGGCCGGCACA CACCGCGCACCCGCCCAACAGGAGGCACT
<i>PrpsL(LX)</i>	GGGCAGGGGCGGAGCGGACCGGGAGAGCCGGCGGGACACCACGCTCTCTTCGCAACCTCAGG

	GGGAAGCGCCGGTAGCATGCCCCGCGATCATTTGACCAGCTTTCGCGTGACGATAGTATTTATC GGGTGTGCGCTCTGTGCGCGCTTGTCTATGGTCACTGACCGGCTCGGTCCGGGACTGGGAGG AGCGGGCCGGCACGTACTCATCCGATGGGCTGAGGAGACCGCACGGGAACCCGCCCCACGGC ATATCGGCAGCTCGCCGATACCCACGACCAGAGGCGCCGCGAGGCGCGGTGGGCCGTGGG AAAGCAACAACGTGCACCGTGCAGTCCTAAAAGGAGAAGTTCA
<i>PrpsL(RO)</i>	TGTGCCCTTGCCCGTACCGACAGCTCCGAGCAGTTCCCGACATCGCAGGTCAGCCTTTACCATTG TCCGCCCACTTTGACCTTCCGGCGCGCCGCCGGGTATCGTTGTGGGTCTGTGCCGGCATGCCCCG GGCCGATCTGTGTGCCTAGCGAGGTATTGCCGTGCGCGCGTTCTGTGCAGATTTCTGCATGGAAC GAGCATCCGGCTGCCTGTGTGGGGGTATGCGACACACCCGACCTCGGGTGCAGCTCGAGGTGC GGGTGAGGGGCAGCAGCTCTCTTGCCCCAACTGCTAGATCCCTAATTTCAGAACAGCCAAGGTT GCTTGTCAGAGCAGTCTGTTCAACACGAAGAAAGCCGGTAA
<i>PrpsL(TP)</i>	ACCGGGTCCGCGATCGGCGGAGGCGAACACTTTTGACCACTATGAGTTCATCCAGGTAAGCTTG GTCGCCGTGCCTGGTGAATGCCAGGACGATCGCTCGTGCCCATACTGCAGGCCGGACCTCCGGG ACCACGTACGGACACGCGACACGCCCCGACCTCGGGGTACGTGCGAGGCGGGTAGCTACTTCCC GGAAACGGGACTGACCAGCAGAGACGGCGAAAGCCGGAAGTCCCGGTGGGGCCGCGCTGCGG AAGTCGCACCCTCGATGAGGGACGGCTTGCCCGGAGCTACAACCGCAGCAGTAGAGCCACCGG CCGGACGGCCGATGGCAGCCGAAACGAAGTAAGGAACCTGCGCTTCT
<i>PrpsL(XC)</i>	GCCCTGCAGGCGGAAGTCAGGTAGACACGACTTCCGCTAGTCCTTGCAAGGTCTGCTGACGTGA GGCGGGGCGGTCGTTTTTGACCGCCCCGCTTCGTCATGTAGGCTCGCTCGCTGTGCCTGGCGT GTCTTCAGACGCCCAGGTCCCGGTGCCGTGAGGCCCGGGCCATCGAGCCGGTGGTACGTGGCT GCGGTCCCCTTGTGAGGGCTGCGCGCCGTGTGCTGTCCGGCGCGCACAGCCTTGAATCCACCCG CGGGGGCCGGCCGGTCTCCGTGAGCTCGAGAAGACGACGGAGACGTA

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34 Promoter sequences are given in the 5' to 3' direction.

35

Strong constitutive promoter regions from *Streptomyces albus*

Promoter	Sequence
1 (XNR_3584)	CTCGTGAGGCTAGCTCCGCCGCGGACCCCGCTCGCGCCGGGGCCCGCCGAACGGTGCCGGGC GCGCGGCCACGAGTACGGCAGGTGTACCGTTGTCAACGCCTGACCTGCGGCAATCAAACA TCCGGGTGAAGTGATCTTTCCCTCTACCGGTGCCGAGCTTCTGCGTGCTAGGCTCGCCGCAAGT TGCAGTTTGTTTCCCTTGCAGTACAGAGCCTGCGGAGCATGTGACCGCAGGCTCTCGTCATTT TCAGACTTTTGCACTTGTTTTCACTTGCAAGTTCTGGAGCAGGGCAACCCTTTGGCCCAAGG AGGGCTT
2 (XNR_3799)	GCCCGGCCATATCCGGCCCCGCCAAATCTCGGCCGGCCACCTCGGCCTGGCCAGCCTGGCCCCG GCCAATCTCGGCCCGACCAACTTCAGCCCCGGCCGGCGCTTGAGGCCGATGAGCCGCGGAGCG GCGAGTCTTCCGCCCGGCCGGTCCGGGTGGCCTCAAGCGCCGGCCGGGCTGGTTTTGGTGCG GACACGTCTGACCGTGCCGGTCACCGATGGCCTCAAGCGCCGGCCGGGCTGGGAGTGGTGGC CGAGGCTTCGGGCGTACGTGCCAGCCCGCAAGGGGCTGCGGTGGGGTGGCCTCAAGCGCCG GCCGGGCTGAGGTTGGCTGGCTGGGCCGGGTTCCGGCCGGTGGGTGCGAGGTGGCCTGGCCGG GCTCGCCAGGGTGAGTTGGCCGACGGGCCGAGGCGGCCCGCCCGGGCTCCCCGGGCCGAGT TGGCGCGGCCAGGCCAGGGCTCAGCAGGGTGGGGGAGTGGGGCAGGCGGCCCGGTAGGGG AGTGCGGGAGGGCAGCGCGCGCCGCGCGCATTGGCACTCCGCTTGACCGAGTGCTAATCGCG GTCATAGTCTCAGCTCTGGCACTCCCCGAGGAGAGTGCCAACACAGCGACGGGCAGGTCCG GCACCCGCGACGACGGATCGACCTGGTCGCCACACTCAGATCAGTTAACCCCGTGATCTCCGA AGGGGGAGGTCGGATC
6 (XNR_2393)	GGCGCCGACCGCACCACACTCACGAGGGCCCCGCCCCACCAACAGGGGGCGGGCCCTCTGTGC TGGCCTCAGGCGCCGACCGGGCTCGGTGCCCTCAAGCGCCGGCCGGGCTCCAAGGGTGGCCT CAAGCGCCGGCCGGGCTGAGTTGGGCCGGTCTGGGCCCGCACGCGCGCCTCACTGACGGCCT CAAGCGCCGGCCGGGCTATCTATAGCCCGGCCGGCGCTTGAGGCCGTCTTTGGCGCGCGCCT GTGAGCGGACGGCCCGTCAAAGATCAGCCCGGCCGGCGCTTGAGGCCATCTTCGAGCCCGG CCGGCGTTTGAGGGCACCCACCCCGCCCCGGCAGGGGCGGCCTGACCTCCGCATCCGCCGG CGCGGACAGGGCACCCCAAGTAGACGGGCGCGGGGCCGGAGGCCCTAGCGCCTTGCACTCT CCTACCCCGAGTGCTAATTATTGGCGTTAGCACTCTCCGAGTGAGAGTGACAGAAGGACCGGG TCGGTGAGGCCCCGCTGGCCACGCGGGGCAAGGAACCGCGAGGCAGGCAGGCCGTCCGTCGC GGGCGCCAGCACGGTCCGGAGTATCCACCCTCCCCAGACAGAGTCCGGGGGGACCCCCAGT CCTGGGAGGACCACTTAC
7 (XNR_3752)	TCCAGAGATGTCCGGCGTGCGCGTCCCGTGGGGCGCGTGCGGCCGGCGGATTCTGTCCTCCGG GCGGGTCTGCGACGGTCTGCGGCCGGGACGCATAAGGATCAGCGCATCGGGGCATTGTTCC TCGATTGCGCTTTTGCGGGAGCCCTGGCGTAGACTGACGCGTCGGCTCTCGTGACCCCGTATG TCCGTATGGATGTGCAAGGGACACGGAGCCGGTCAAGGTAGTCGATTGCAAGGGCGAAGC
13 (XNR_3728)	GAGTGCTCCTGCCTCGGGACCGGCGGACAAGCGGCCGGTCTGATCATCGGGGCAGCAACATA TGAATCCGGCACATGTCAGGGAGCTCCGAACGGGTGCGTTACCCCTGATGGGGGAGTACGGG AGCGCCCGTGCGGAAGATCCTCGAAGGGTGTCCCGCCCTCGTTGCGCCGCGTCCGCGTTTGAC GGCGGGAAGGCCGGGGGTAAGCTTCTCGGCTCGATTGGCTCTACGCGGGGCCCGTGTGGCA GACTGTCCGGGTTGCTCGGTTGAGTGCCGATGCCGCGCGCCTCCCGCCGGGAGGACTGGAAG CGAGTCCACAGTACTCGTCGCCTCAACTGCCCCAGGTTGCGCGAAGGCAGCGCTGTGGCGGA CGTACGGGAATCTTCGGGAAGCGTGTGCGGGGTACCAGCCAGGCGCCCGGTGGTCAACCACA CCGCAAGGTGTGGCTTACCGAACC CGTGGCCACGGTGTGGAACGCAGCCCCCAGATGGG ATTCCGCGAGGAAATTTCTGACGGGCGGGGAAGGCGACACACCCGACCGCGTGGGTGCGAGA GAGAGACCGGACCCCGGGTCCAGAGCGTTACGAGAGACAGGACTACCAAGTAGCC
15 (XNR_1700)	TCCGCGCCCGCCGGCCCGACGGTGCCCGGCCCGTACCCCCCGGGTGGTGCGGGGCCGGGC ACCGGCCTTTTGGCGCTGCGGAGTTGACGGAAGTTGGCCGAACCGGATGCGCTCGGCGCCCCG GGGGCTGAAAGATGCTCACAGCCCCCTTCCACGGCGGTCCGGGAGGGGAGGCCGGGCAACC GGTTTTCGGGGGCGGAGTGTCGGTATGCGGACGGCCGCGCCCGATAGATGTGTAACGAGTC

	CGTTTCGCAACCATCTATCTCGGATCGGTTTGTCCGGATTTTGGGAAGATGTGAGTGTGAGGTGT GATCGAACCGAGACCAAAAGGGTGTGGTCGGGCCGAACACCATGGCTAATAGTTGAGCGCGT AGAGCTCGGGTCAATGGGTACGCGCTGTGGGGAGCGCCGACTCACGAGCACACTGGGGCAC TCGATCTTCGCCGTCAGGGGTGTGCGCGGATCGTCCTGTGCCCTCTCTTGCAAGTGAACAAGTG GACTCATGAGGAGGAACCC
23 (XNR_4375)	GCGTGGTCCTGGTTCTTGAGACGTGAGACGTGAGGCGGGCGGGCGGGCGGAGCCGGAC GGGGGCGAGTAGGCGCCTCACCTCGGGTGGGCTCACGCCGCTGGGCGCGCCACCGGGCCG GCACACGACCCCCGGGGTCCGCGGCCCCATCGTCCCATGCGCGGGGACCGGCGACCGGTTT GGGCCGCGCGTGGGGCCGCTGGTAGCCTGGCCCGATGTGTCTCGTAGCCCTCTCAGCGTCGG GACACGACCGGAAACACCCAACCTGAACCTGTAAAGGCTCTTTC
24 (XNR_3720)	CGGCCCCCTCCCCGTGGTTCCCCGTTCGCCGCGCCGCGTGGCCCGTACGGCGGTACGG ACGGGGCGGGACGGGTCAACGTACTGACCCCCGGCCAGGTGGCCCGCCCTTGACCGGAAT GAATCCCCCGCCCCGCTACTCGGCGGGAAAGCTGCGCTCTGTGGCCGAAACACACAGAGG GTGGGAGGGGGCGTGCCGGGGGCGGCGAACGATTCCGGCCAGGGTGCCCTGGCACCACC CGGCGGCCCGGTGTAGCGTCCCCGCGGGACAGAAAGACGATCATGCAGCGGAGGGCGCCG GTCCGCCCCGGGTACGGGGCGTCTGACCAGCCCGTCCGCTGCGCGTGCAATTTGTTTTGACCG AACTCCGTGCGATAGGTACGCTCAGACCTTGTGCTGGGGTGTGCTGGGCTCCCGTGCGTGT CCAACCGCGCGGCGAGCGTCAGGCGTCAGCACCGCAATCTGCGCTTCTCCCGTGTGCTAGCG GGGCTCCGCGGTATTCGACACACCCGACCGCGTGGGTGCGGAGTGTTCAGGTTAGCTTTACC TGTTCCGGCACACAGAAACCGGAGAAGTA
28 (XNR_1131)	TGCCCCGCTCCCTCTTACGTCCCGACGGCGAAACCGGCCGCCAGTCTGCCGTGCCCGGCCCG GTCCCAACCACTCCTCCGGCGGACGCCCCCGAAGGAGCGGACCCGCCCGGACTTCCGGCCG GCGGCGCCCCGACCTCGTAGAACCCCGCCGAGCGCCGCGCTAACCTCGCGCCACGCGT CACCCGGCCCCCTCCCGGCTGCGGCGCGACCGGCTCCCCGCCCTGCTACTCTGTCCGAGGCC GTCTGTGCCACGTCCCGAGCCCCGCGTTCGACACGCGGTCCCGGACGACCGGACGGATCCAT CCGCCTCCCGAGTCACCGAAGCCTCCCCTGAGACGAAGACCAGGGGCGCTCGGAGGCAAGCG AAGACATCACAGAGGAGTACGC
31 (XNR_3170)	CCGGACCTCTCCTACGCTCACCTGCGCGCTTCCGCGCGACAGGCACAATTACCCGTATATGT CCCGACTCGCCACAGTCTCCGCCTTCGGCCGGGTCAATCCCCGACCGACCCGGCCCGGCCA CCCATTTCCGGCCCGGCCGGCGTTTGAGGCCGACCGGTGACGGACACCCGAAGCCCTCGGAG CGCGCTCGGCATCAGCCCGACGACGCTTGAGGCCACCTCGACCGCCGCCGGACGGCTTCATC CGAAGTGCCTCTGAACTGGTAAAACGAGCCGTGCTGGCAGCTCTCTGCACAACCAGGCAGAAC AAAATTGAGCCCGTCCGACTCAACCGATTGACGCGCCGCGTCCCCTCGTGCATCCTTGAGTG AGTTCCAATCAAGTAGTCAGCTGGAGGAATTGAC

38

39 Promoter sequences are given in the 5' to 3' direction.

40

41

Table S8

42

Synthetic promoters based on *actII orf4* promoter of *Streptomyces coelicolor*

Promoter	Sequence
<i>ScoSPL7</i>	CGGGCT <u>GGGGCT</u> CGGGGCCCGCGGTGAGCTGGTAGACG
<i>ScoSPL9</i>	GCGGGAGAACTTAACAGCGGGTAGTTCGTAATTTGCAA
<i>ScoSPL13</i>	TGGGGATGAATTAGTTCCGACCCGAATTCTGTTATTCCG
<i>ScoSPL20</i>	TGAGCTGGTAGACGAAGGCGCCCGAGTCTCCTTCGTTCTC
<i>ScoSPL25</i>	GCTGGTAGACGAAGGCGCCCGAGTCTCCTTCGTTCACTG
<i>ScoSPL50</i>	GAGGTTTGCGAATGTCGCCTTGGTGCCCTTGTTTCGTCA
<i>ScoSPL51</i>	CATATTTTGATTATTCTTTTTCTTTTTCTTCTCTCTG
<i>ScoSPL52</i>	GTGCCTTGCTTTGATTGGCTTTATCGTTGTTGTGGC
<i>ScoSPL110</i>	GGCAAGTGTTTCAAGAGATAAAGGGCTCGGTTATTAGGGA
<i>ScoSPL117</i>	TGCTCGCTGTTTTTTTACGTCTTGGGGATTACTGGAAC
<i>ScoSPL185</i>	TGGCCCCGACCAGGCTCGCTCCCCATTTTACCTCGG

43

44 Promoter sequences are given in the 5' to 3' direction. -10 and -35 sequences are underlined.

45

Constitutive promoter regions from *Streptomyces coelicolor*

Promoter	Sequence
<i>P_{sco4503}</i>	CCTCGCCGAGCGGGAGGGGCGGGGCGCGCCTGATCTCGATCTGCGCGGCGGGCGGGCCAGG GCGTCACCGCCATACTGGAACGAACGTGATTGGGTCTGCCC GGCGGATCAGGTCGCAGGAAAG TCGCGGTGCCTCATCGACGCCGGTGAGCGGGGGCTGGTGCGTGACAGCTGCAAGGCGGAGGAG GGAGTCGACGCGGAGCGTCGGCGAGTGACGACAACGCCGAGATGTGCGCACAGCCCCCGC GTCTGCGGCATGATCCGCCGGGCAGGCCCAAACCCTCAGGTAACCCCCAACACTGCACACGTCC GGCGCGGGAAGATCGTGGAACGCGCACCAAGTCCCCACCTGGGCGCCGTACGATCCCGGGACT GACCGTCGGTAACCCATGTCCGCGGAACCGGCGATGAACGCCTCGGCGCGCGAGGCACGTACG TCATGCAGCAGAGCAGCGACAGCAGAAGCAGTGCTTTGCTGCACGTCCAGGAGCCGCCC
<i>P_{sco4508}</i>	AGGCCGTCGAGGGTGTCTTGCGCCGCGGGTGAACCTCGTCGAAGTTGTCGTCGAAGGCCTTG GAGGACGACTTCGTGACGTAGCCCGACTCGACCAGTTTCGCGATGTACTTGCGGAGGCCGTGCG AGCTTCTCCTGGAGCTTTTCTTCTCCTTCACGACATGCTTGCGGCATCCCGCATGTCCTGATAT GTGATGTCAAGGTCTTTGGGCATGAAGCCGCTTCTCTACAACGCCGAGGGCCAACCCCCGT GGCTCCTCGTGTGCGGATCGAACCGGCGCACCGGTACGCCGGTCTGATGACACGACCGGTGT GATCGTCCGCTCTGAGGCAGCAGCTTACGGGGGAGGCCAGTGGTGTACATCCCTGCGTTGCCA ACGGGAACGTCCGCTACCGCCCTGTTGCCGACCGCGACACCCAGCGGATATCGTCGCCTGGA CTGTGAGCCGTGGTGTGAAGCGGCCGAGGGGCTCGCCTGGGGAGGACAAGC
<i>P_{sco6740}</i>	GCGCGGTACTCGGCGCCGGAGAAGCGGTAGGGGCCGATGCCGGGGTAGGCGTTCAGCTCCAG GTGCGCGTGTTCGGCGGTCTGCCAGGCGAAGTCCCGCCAGACGAAGTCGTCGCCGTCCCGCAG GATCACGGCGGTACCGCGCCCGAGGCCAGGTGCGCGCACTCGGGGCAGCCGTAGATGACGTA CCGGCCGCCGGGCGAGGGGCGCGTCGGCCTCCAGGAGCAGGCAGCGGACCTGCGCGGTGAAGA TGGCGGGCGGTACGTGCGAGGCGAGCGGGGAGACGGCGTCCAGATCGGAGAGCCGGAACAG GAGGGGGCGTCCGTCGACGACGAAGTCCATGAAGTCGCGGTGGACCTGGAAGTCGCCGTGCGC GTGGACTCCGCCGCGCGCGTCGCCGGGGCCAGACCGAAGTTCGCTACTCGGCAGCCATGCG GTGAGTATTCCTCGGCCGGGCTCTTGAGACGCGCGTCCGGCGTTCGGTTAACGTCTGGT
<i>P_{sco3410}</i>	CGCCTGGACCGCCGCTGTTACCTCGACCGCCTACCCGACCGACTACGGCTTCGTCGAGAACAC CCTCGGCGAGGACGGCGACCCGCTGGACGCGCTGGTCATCCTGGACGAGCCGACCTTCCCGGG CTGCCTCATCCGCTGCCGCGCATCGGCATGTTCCGGATGACGGACGAGGCCGGCGGCGACGA CAAGCTGCTGTGCGTGCCGTCGACCGACCCGCGCGTGGAGCACCTGCGTGACATCCACCACGTG TCGGAGTTCGACCGCCTGGAGATCCAGCACTTCTTCGAGGTCTACAAGGACCTGGAGCCCGGCA AGTCCGTCGAGGGGCGCGACTGGGTGGGCCGACCGAGGCCGAGGCCGAGATCGAGCGGTCC TACAAGCGCTTCAAGGACCAGGGCGGCCACTGATCAGGCGCCTCTCCCGTAACGGGCCGACGC ACACGCGTGCGGCCCGTTCGTGTTTGAAGTACCATCTGAGGTCAACAGGAGGGT
<i>P_{sco4658}</i>	GCGCCGGGTAGAGCGGGAAGAACCGGACCGAGTTCTGCTGGACCGTGAACAGGCCGTGCGAA TCCAGCCGGACAGGGCGGGGCTGTAGCCGTGCTCGGCGACCTGGAGGTACCACCAGCCGTCC CAGGTGGCCAGCACGTCCACCAAGTGGGCGCCGCCGCCGAAGCGCGGGTCTTCCCCCGGAAG TCCCCGGCGTGGGTGAGGAGGGAGGCGAAGACCCGAGGCCGACGAGTTTCGTGACGCCGTA GAGCGCCAGCGGGGCGAGGTAGGGCCGGGCCCCGGGCGGGAGGGCGGGGAGCCGGTCCGC CAGGAGCGTGCCGCCCCCTCGCCGCCGGCGGCCGTTCCGGGTGCCGTCCGGCCCGTCCGTCA CCGTGTCGTGCGCAGCCGTGTCCATGGCTGTCATCCCCCTCGGGCCACCTCAAGCGTCAATTGC TGCCATAAGATCGCACAAGAGTCGCACATCTGTACTCAAGGTCATGAGGAGGGAGGCGCG
<i>P_{sco2468}</i>	CGCGCGACGCGGCGGCATCGTCGTCGACGACCACCTGCGCACCTCCGACCCCGACATCTTCG CGGCCGGCGACGTGGCCTCCTTCCACCACGCCCTCTTCGACACCAGCCTGCGCGTGGAGCACTG GGCCAACGCCCTGAACGGCGGTCCGGCCGCCGCCGCGCGATGCTCGGCAGGGGCTCGCCCA CGACCGCGTGCCCTACTTCTTACCGACCAAGTACGACCTGGGCATGGAGTACTCCGGCTGGGCG CCGGCCGGCTCGTACGACCAGGTGGTGATCCGCGGGGACGCGGCGAAGCGCGAGTTATCGCC TTCTGGGTGAAGGAGGGCCGGGTGCTGGCCGGGATGAACGTCAACGTGTGGGACGTACGGA GCCGATCCAGCAGCTGATCCGCTCGAAGACCCGGGTGGACACGGAGGACCTGGCGAACCCGCA CGTATCCCTCGAAAGCCTCGTCGCATAGTTGTCGGTCCGCCCCCGTAGACTTCACGC

<i>Psc02074</i>	GCTGTTCCCAAGGCCCGCGGCACCGCCGCGGTCCCCGGCGACCTCGCGGTACGCCCCGGCGAG GAACCCTGGACCCCGCAGGAGGTGAGGAGGCGCGCGGCGAGCTTCAGTCCGAGGCCGACCG GCTGCGCACCGAGATCGACACCTCCGAGCGGTGCTGCGAGGGCATGATGCGGGACTCCGGCGA CGGCGCGGGCGACGACGAGGCGGACACAGGCAGCAAGAACATCACGCGCGAGCACGAACTGG CGCTGGCCGCCACCGCGCGCGAGGTGCTCAGCCAGACCGAGCGTGCCCTGGACCGCCTGGACG CGGGCACCTACGGCCTGTGCGAGAACTGCGGCAACCCGATCGGCAAGGCGCGGATGCAGGCGT TCCCGCGGGCCACCCTCTGCGTCGAGTGCAAGCAGAAGCAGGAGCGCCGGTACTGAGCCGCAG CCGGGACGGGAAGTGTGCCGTACCCTCGTGCTCAGTCAAGGACCTAGGCTGAGGGACTCAC
<i>Psc05768</i>	CCCGAGGACTCGGGGCCGTAGACCTCCACGACACGGCCACGCGGGATGCCTCCGACGCCGAGG GCCACGTCGAGCGCGGTAGACCCGGTCGGGATGACCTCGATGGGCTCGTTGGTCCGGTCACCC ATGCGCATGACCGCGCCCTTGCCGAATTGCCGTTCAATCTGTGCGAGCGCGGCGTCCAGGGCCT TCTCGCGGTCGGTTCCTGCCATGGGTTCCACCCGGTTTGCTTGATTGATCGCTTCACGTCAAAG ACGCTAATGCCTGCCACTGACAATGGGCCCCGATGCGGGTCCGGCCTGTGGATAACTCGGGTGC ATCTACCCCGAACCCACTCGAATCACCCGTCACGAGCCCCGCCGGAGCCTCCATAAGAATGGAT GTTTCGATTTTCGTGTCAAGCGCACCGGCACTTCCGAGCGTACGTCCCCCGGGCGGCGAGC CAGGTGGTTGGATGCGGATGCGACACCGGGAGAGGTGCGAGAGGGGACGCAC

48

49 Promoter sequences are given in the 5' to 3' direction.

50

51

Table S10

52

Inducible promoters

Promoter	Sequence
<i>PtipA</i>	GAACGTCCGGGCTTGACCTCACGTACGTGAGGAGGCAGCGTGGACGGCG
<i>PnitA</i>	GCGAACTCCCTTATGCGGGTGGCGCAGAATGCCAGGACCCTTGTCATTCCACGTCAATTCATGCG CCTTTTCACCTCGTACTGTCCTGCCAAACACAAGCAAC
<i>tcp830</i>	CTGTTGGCTACTCTATCATTGATAGTGGTAGGATCCCTATCAGTGATAGAGAT
<i>gylP1</i>	GCCGGGCGGGAGATCGATAGCCCACGACGATCAGTAACGATCGTGCTTTCGATAACACAGCTCT TGACGCGCGCGTGACGTGGAACGAGACTCGCGTCCAT
<i>gylP2</i>	AACACAGCTCTTGACGCGCGCGTGACGTGGAACGAGACTCGCGTCCATCGGTCGGCATTGTCGA ACACCTACCGGCAATACGCGTTAGAGTGTCACAGTG
<i>PA3-roIO</i>	TAGCAGGGCTCCAAAATAACGCCTGATGTAGGATCAGATGTGAACCCTTGTTCAATTTATGAATC ATGATTCA
<i>P21-cmt</i>	TGTGCGGGCTCTAACACGTCCTAGTATGGTAGGATGAGCAAAACAAACAGACAATCTGGTCTGT TTGTATTAT

53

54 Promoter sequences are given in the 5' to 3' direction. -10 and -35 sequences are underlined.

55