

Supporting Information for

High-resolution mapping of Sigma Factor DNA Binding Sequences using Artificial Promoters, RNA aptamers and Deep Sequencing.

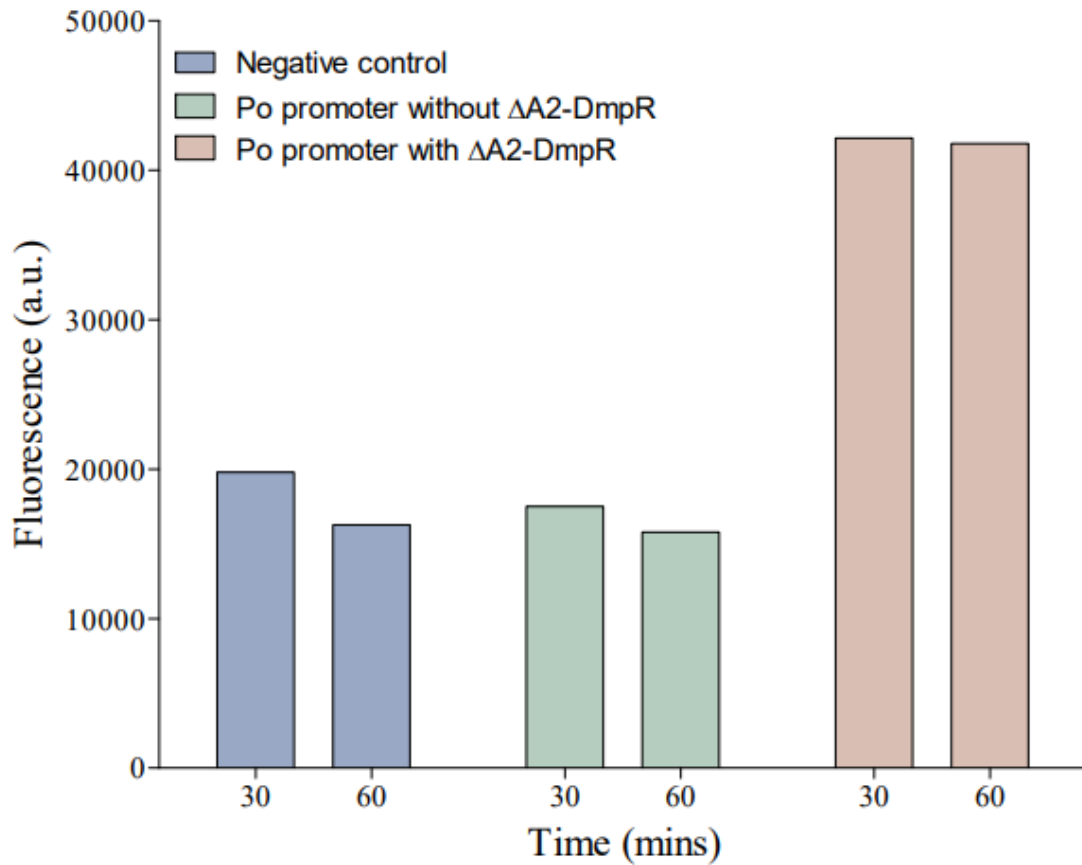
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- Benchling links of plasmid maps

Fig. S1. Importance of $\Delta A2$ -DmpR for *P. putida* σ^{54} -Dependent IVT Reaction

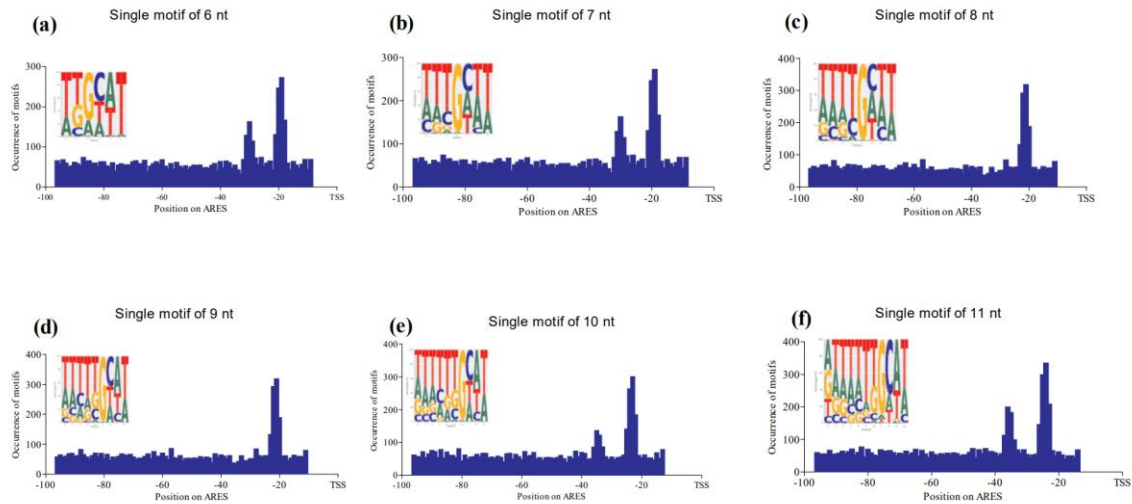


Fluorescence of the Mango aptamer was used to measure RNA synthesis. The results are presented for three experimental groups:

1. **Negative Control:** No template added, showing baseline fluorescence.
2. **Po Promoter without $\Delta A2$ -DmpR:** Template of the Po promoter without $\Delta A2$ -DmpR, showing fluorescence levels similar to the negative control.
3. **Po Promoter with $\Delta A2$ -DmpR:** Template of the Po promoter with $\Delta A2$ -DmpR, showing significantly higher fluorescence levels compared to the negative control.

The data demonstrate that RNA synthesis does not occur in the absence of $\Delta A2$ -DmpR, as indicated by the similar fluorescence levels of the negative control and the Po promoter without $\Delta A2$ -DmpR. In contrast, significant RNA synthesis, indicated by increased fluorescence, is observed in the presence of both the Po promoter template and $\Delta A2$ -DmpR. This highlights the essential role of $\Delta A2$ -DmpR in initiating transcription from the σ^{54} dependent Po promoter.

Fig. S2. Distribution of single motif within a 97 bp Region Upstream of the TSS in the Highest Expressing ARES Subset



This figure illustrates the distribution of a single conserved motif within a 97 bp region upstream of the Transcription Start Site (TSS) across the highest expressing ARES library for motifs ranging from 6 to 11 nucleotides in length. The x-axis represents the position relative to the TSS, and the y-axis indicates the occurrence frequency of each motif.

(a) The 6 bp motif (TTGTCAT) is identified at the -12 position, consistent with previous core promoter analyses.

(b) The 7 bp motif shows a sequence extension, adding a T at the beginning (TTTGCTT).

(c) The 8 bp motif extends further with an additional T (TTTTGCTT).

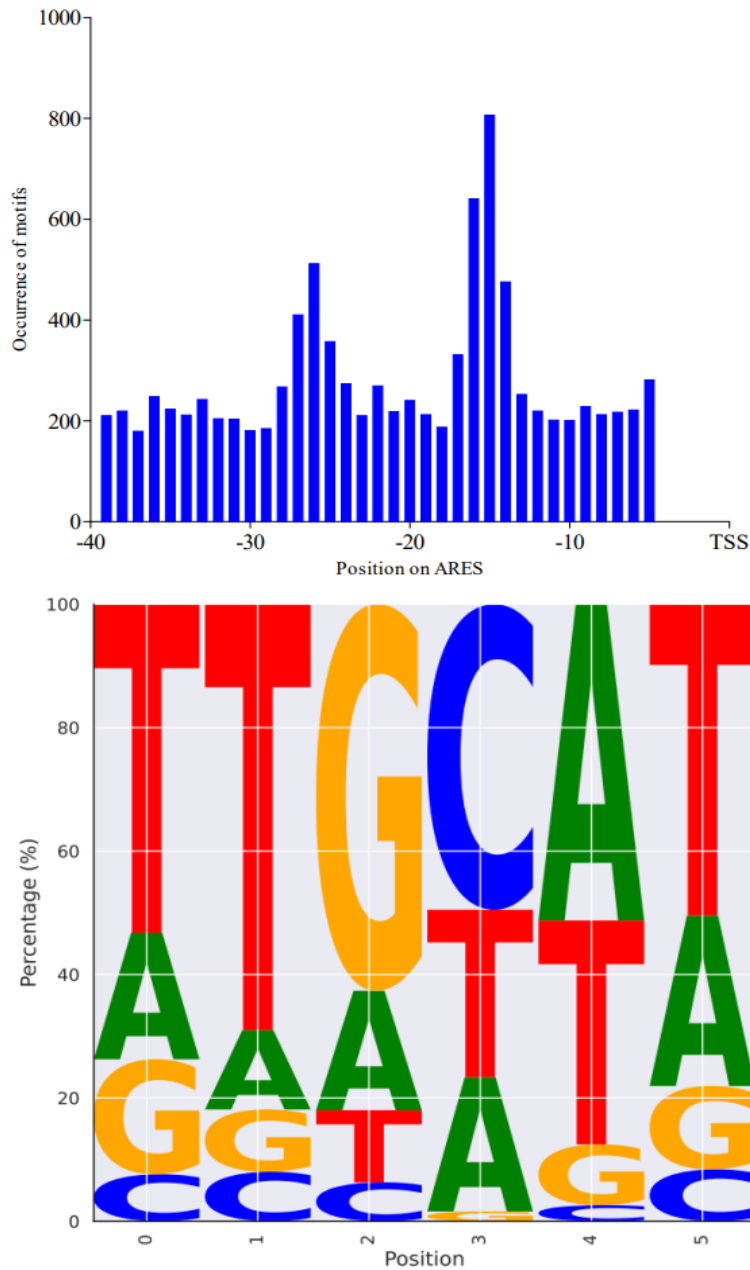
(d) The 9 bp motif continues this pattern (TTTTTGCAT).

(e) The 10 bp motif follows the same trend (TTTTTTGCAT).

(f) The 11 bp motif (ATTTTTTGCAT) displays the final extension in this analysis.

Each motif is consistently located at the same position upstream of the TSS, with the sequence extension demonstrating high conservation across the lengths studied.

Fig. S3. Distribution of single motif within the 40 bp Region Upstream of the TSS in the Highest Expressing ARES Subset



This figure illustrates the distribution of a single conserved motif within a 40 bp region upstream of the TSS among the highest expressing ARES subset. The x-axis represents the position relative to the TSS, and the y-axis indicates the occurrence frequency of the motif. Analysis reaffirmed the presence of the conserved 6 bp motif (TTGCAT) at the -12 position.

Table S1. Primers used in this study

Primer name	Sequence
Cloning of double-stranded 200 nt long ARES to pHH100-dBroccoli backbone	
BBa-Prefix-F	GAATTCGCGGCCGCTTCTAGAG
BBa-Suffix-R	CTGCAGCGGCCGCTACTAGTA
BB1-F	TCGCACGATATACAGGATTTTGCGGATTTGTCCTACTCAGGAG
BB1-R	GTCAGCTTTATGCTTGTAACCGACCGAACAGGCTTATGTC
BB2-F	CGGTTTACAAGCATAAAGCTG
BB2-R	GCAAAATCCTGTATATCGTGC
BB3-F	CGTAATCAAGCCACTTCCTTTT
BB3-R	GTACGCGTACGGTCTCTGGCATCCGACACCCTGCGTCAATG
GG-Col-F	GCGGATTTGTCCTACTCA
GG-Col-R	CTGGATCATCAGAGTATGTG
For validation, 18 ARES, each 200 nt long cloned into the Mango-pSEVA2311 plasmid	
p1-Frag-F	GGCTACGGTCTCCAAGATATCCCGTATAACATTTGTACACTCCGTTATGG
p1-Frag-R	GGCTACGGTCTCTTGGCAACATTTACATTCAGCAGGCACCAGCGCA
p1-BB-F	GGCTACGGTCTCTGCCATGTGTATGTGGGCG
p1-BB-R	GGCTACGGTCTCCTCTTAATTAAAGGCATCAAATAAAACGAAAGG
p2-Frag-F	GGCTACGGTCTCGACGACTGTCTTAAGGTTAAG
p2-Frag-R	GGCTACGGTCTCACCACGAGACATATACAATTAC
p2-BB-F	GGCTACGGTCTCAGTGGATGTAAATGTTGCCATGTG
p2-BB-R	GGCTACGGTCTCGTCGTTAATTAAAGGCATCAAATAAAACG
p3-Frag-F	GGCTACGGTCTCCTTCGTGATAATGAGCTGAG
p3-Frag-R	GGCTACGGTCTCGGGGTAAAATTATATTTAAAGCCG
p3-BB-F	GGCTACGGTCTCGACCCCTGATGTAAATGTTGCCATGTG
p3-BB-R	GGCTACGGTCTCCCGAAATTTAATTAAAGGCATCAAATAAAACG
p4-Frag-F	GGCTACGGTCTCGTAATTGGATTTATTCTACTCTTCC
p4-Frag-R	GGCTACGGTCTCTCGAAAGAATATCACAATGTAG
p4-BB-F	GGCTACGGTCTCTTTCGGGGGTATGTAAATGTTGCCATGTG
p4-BB-R	GGCTACGGTCTCGATTATAACATTAATTAAAGGCATCAAATAAAACG
p5-Frag-F	GGCTACGGTCTCGCCTTTAATTAAAGTTGTCCTGATTATGGTAGTACTAGTAG
p5-Frag-R	GGCTACGGTCTCTTGGCAACATTTACATATGCCCCGCCTCATCATATC
p5-BB-F	GGCTACGGTCTCTGCCATGTGTATGTGGGCG
p5-BB-R	GGCTACGGTCTCGAAGGCATCAAATAAAACGAAAGGC
p6-Frag-F	GGCTACGGTCTCTGAGATTCATTAAATATTATTGGGGAAGAATTGG
p6-Frag-R	GGCTACGGTCTCATGGACACCACCGTATCCGATG
p6-BB-F	GGCTACGGTCTCATCCATGTAAATGTTGCCATGTG
p6-BB-R	GGCTACGGTCTCTTCTCACTTTTAATTAAAGGCATCAAATAAAACG
p7-Frag-F	GGCTACGGTCTCACCTTTAATTAAATAAGCGAGATTCAAGAATTTTATG
p7-Frag-R	GGCTACGGTCTCCTAGTATAATTCCATTCCACAG
p7-BB-F	GGCTACGGTCTCCACTACACGCTGATGTAAATGTTGCCATGTG
p7-BB-R	GGCTACGGTCTCAAAGGCATCAAATAAAACGAAAG
p8-Frag-F	GGCTACGGTCTCCAAGGATTTTGAATAAAGTGGTAAAG
p8-Frag-R	GGCTACGGTCTCACAACATTTACATCCGCTATATGGCTAAATTAG
p8-BB-F	GGCTACGGTCTCAGTTGCCATGTGTATGTGG
p8-BB-R	GGCTACGGTCTCCCTTTAATTAAAGGCATCAAATAAAACG

p9-Frag-F	GGCTACGGTCTCTGAGTTTACTTCGGGTAAC
p9-Frag-R	GGCTACGGTCTCCACATGGCAACATTTACATCTACCTATACCACCTAAGAG
p9-BB-F	GGCTACGGTCTCCTGTGTATGTGGGCGTACG
p9-BB-R	GGCTACGGTCTCTACTCCATTTAATTAAAGGCATCAAATAAAACGAAAG
p10-Frag-F	GGCTACGGTCTCAAAGAGTATGATCCCATTGG
p10-Frag-R	GGCTACGGTCTCGACCATTGATAGGATAGAAAATAAC
p10-BB-F	GGCTACGGTCTCGTGGTTTGAATGTAAATGTTGCCATGTG
p10-BB-R	GGCTACGGTCTCACTTTAATTAAAGGCATCAAATAAAACG
p11-Frag-F	GGCTACGGTCTCTCCTTTAATTAAAATTGTTTTTTGAATGATATGGTTG
p11-Frag-R	GGCTACGGTCTCTTGATCGATTGCCTATTAAC
p11-BB-F	GGCTACGGTCTCTATCAGATCTTGCGATGTAAATGTTGCCATGTG
p11-BB-R	GGCTACGGTCTCTAAGGCATCAAATAAAACGAAAG
p12-Frag-F	GGCTACGGTCTCAACTAGTATACTATTTCAAACATATTTG
p12-Frag-R	GGCTACGGTCTCGCAACATTTACATTCTCATTTTCCATCATC
p12-BB-F	GGCTACGGTCTCGGTTGCCATGTGTATGTGG
p12-BB-R	GGCTACGGTCTCATAGTGTCTTTCTTAATTAAAGGCATCAAATAAAACG
p13-Frag-F	GGCTACGGTCTCACTTAAATAATGTAATACGAGCTCG
p13-Frag-R	GGCTACGGTCTCGTTCCATACCTCAGGTTTGC
p13-BB-F	GGCTACGGTCTCGGGAATGTAAATGTTGCCATGTG
p13-BB-R	GGCTACGGTCTCATAAGTTACAACCTTAATTAAAGGCATCAAATAAAACG
p14-Frag-F	GGCTACGGTCTCTTACGTAGTTTGTGTCCAGTATCC
p14-Frag-R	GGCTACGGTCTCCCAACATTTACATCAAACAGGTGCAGCGGC
p14-BB-F	GGCTACGGTCTCCGTTGCCATGTGTATGTGG
p14-BB-R	GGCTACGGTCTCTCGTAAAATATGAACAATTTAATTAAAGGCATCAAATAAAACG
p15-Frag-F	GGCTACGGTCTCGCCTTTAATTAATGAACCTATATCTTCTGAACCTTTTAAACGTCTTG
p15-Frag-R	GGCTACGGTCTCGTGGCAACATTTACATGTCGGATACCACCGAGCC
p15-BB-F	GGCTACGGTCTCGGCCATGTGTATGTGGGCG
p15-BB-R	GGCTACGGTCTCGAAGGCATCAAATAAAACGAAAGGC
p16-Frag-F	GGCTACGGTCTCGCAAACCTTTAATGTGCCTCG
p16-Frag-R	GGCTACGGTCTCGTCCAACACCGTCTTGGAATG
p16-BB-F	GGCTACGGTCTCGTGGATGTAAATGTTGCCATGTG
p16-BB-R	GGCTACGGTCTCGTTTGCCCCCGCATCTTAATTAAAGGCATCAAATAAAACG
p17-Frag-F	GGCTACGGTCTCAACCCTCTTTTTGGAATCCTG
p17-Frag-R	GGCTACGGTCTCAATCGGAAGCGAGAAAATCGC
p17-BB-F	GGCTACGGTCTCACGATGTAAATGTTGCCATGTG
p17-BB-R	GGCTACGGTCTCAGGGTATTTTAATTAAAGGCATCAAATAAAACG
p18-Frag-F	GGCTACGGTCTCTTCTTTTCGGCGGATTGATAG
p18-Frag-R	GGCTACGGTCTCTCTCCCTTGGCTAATGCGAATATAAAAC
p18-BB-F	GGCTACGGTCTCTGGAGATGTAAATGTTGCCATGTG
p18-BB-R	GGCTACGGTCTCTAAGAAATAGTTAAACCTTAATTAAAGGCATCAAATAAAACG
pO54-Frag-F	GGCTACGGTCTCAGCGGCTTAATTCGCTCG
pO54-Frag-R	GGCTACGGTCTCTCACATGGCAACATTTACATATGTTGACTCCATTATTATTGTAC
pO54-BB-F	GGCTACGGTCTCTTGTGTATGTGGGCGTACG
pO54-BB-R	GGCTACGGTCTCACCGCGCTTGCGCAGATTAATTAAAGGCATCAAATAAAACGAAAG
p-Col-F	GTCTTTCGACTGAGCCTTTCG
p-Col-R	CCACATACCAAACCTTCCTTCG
Construction of Mango-pSEVA2311 plasmid	
Lib1-F	CCTTTAATTAAATGTAAATGTTGCCATGTGTATGTG
Lib2-R	TCCAAGACTAGTACGCGCTACATCCGCTTTAG
Lib3-F	GGATGTAGCGGCTACTAGTCTTGGACTCCTGTTG
Lib4-R	GCAACATTTACATTTAATTAAAGGCATCAAATAAAACGAAAG

Lib7-F	GTCCTACTCAGGAGAGCGTTC
Lib8-R	GCCATGAATGATCCCGAAGG
Sequencing of ARES plasmid library	
SeqDNA forward	ACACTCTTTCCCTACACGACGCTCTTCCGATCTN ₅₋₇ -GACGCAGGGTGTCTGGATG
SeqDNA reverse	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTN ₅₋₇ -TGGTGCTCGAGCTTGTACAG
Sequencing of in vitro transcribed RNA	
SeqRNA forward	AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCGAG
SeqRNA1 reverse	AGACGTGTGCTCTTCCGATCTCCGACCGTCTCAGATGGACC
SeqRNA2 reverse	CAAGCAGAAGACGGCATACGAGATGATCTGGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT

Sequence for validation

Table S2. The sequences and original IDs of the 18 randomly selected ARES, each 200 nt in length, are listed below for the validation experiment.

ID	Original IDs	Sequence
p1	ARES00610543	gatatcccgataacattgtacactccggtatggctgtaataaaattgggatcggttttgcgttctaatttacA gatataggctagagtaactactcgcaaacagtgagatgtgcagtaagggtaaccggcatagaattgg ctcgtgagtagctcgatctaaagagactgggtgctgcgtggctgctgta
P2	ARES00171465	cgactgtcttaaggtaagacaactctattgtgaggtactgggtattggatgcagcatgggtacatttgact acattatggatgggggtctgctacagtgctactgggacaatattgcatcactataatgtGcaaaaaga aaagtccgggccctgtttagaaggatggctatgtaattgtatatgtctcggtg
P3	ARES00389971	atttcgtgataatgagctgagttccttgataaagcagtttgtgaatgaatgaatacatagattataaatgga attgacggctccttataacactccatagattttgggaacgggtgatgcacaacgctgaggttGgaagtaat ggtagattatgatagttaggtggaataaacggcttaaatataattttaccctg
P4	ARES00141878	tgtataattggatttattctactcttctcataaccgggcttgggaacgaatctagcatcaaacttggcGgag agatgtcgtttaggagtagcatatatttctggaaatttcgggattttgttaaggaaattccagtaggtgtgttc gtcaggaatgaaactatagcagctacattgtgatattcttcgggggt
P5	ARES00013532	gttgctctgattatggtagtactagtagagacaacgctacatctataaatcgccaatataggtgtttggga actgtcgaattgtgcgtacatGatcgtctttccgtaactaagacaagtcagcatattgggggtgcagtg aacgattatcgacagaagtgtgtagtctaggtgatatgatgaggcggggcat
P6	ARES00256315	aagtgtgagattcattaaattatttggggaagaattggcttgcgagtggaataaatgactgatattaggataa tctttttgggagcaggttttagcatcagagtttagatGagggcaagcaggtgtgattggagggtgcggaacag tactataactaccatgcgctgcttgggttttagacatcggatacgggtgtgtcc
P7	ARES00413161	taagcgagattcaagaatttttagcttatcgtcgtggctgtcatgtagtaagattgtgcaccgggcttagt ctgtgggagtcggggtagttaaagagttgtGaatgatcaaaggtagtctatgactcagtcctatagatcgg gaatagtggtgtctccacctgtcactgtggaatggaattatactacacgctg
P8	ARES00523631	aggatttgaataaagtgtgaaagtgtgtgctagtgctgaagatggtagtttcgaacgtctgcattgccaa aaataagtttgagcttatttactttcgggtgaatttgggacaataatttactggttcataaattGggggtaagta gttacaatatcagaagtacgttggatgtactaatttagccatatacg
P9	ARES00074902	aattgtcatattttacgtagtttgtgtccagatcccagatacagaccgattagtttgcacgatctgaaggag ggatgggattttgatgcgggtacgcttttgatttaaGggacgaagctggtgcagcgattctgatcaagt atagggagagttaggggtatgtatgtactagccgctgcacgtgtttg
P10	ARES00116280	gatcgggggcacaactttaatgtgcctcgtgaacacgcggtgaacaattgaaatgtgagaggtgaggt tgtttagtgctattgaaatgatttgcattaaactggcggttagtgatGcgtcaaattgtaaaactaagggtg tttcgacaatcgtgtcaggaaagctgcctgttaggcattccaagacgggtgttg
P11	ARES00237232	gaaagacactagtagtatactatttcaaacatatttgggaatgaaattgcttatgccgtgatctacagtgaagg gctggcttcttcggaaagctgtggggacaccagattgatttgcatttcaatacactttaGatggc ggtactaaattataacacttacctgttagctagcggatgatggaatgagga
P12	ARES00287266	agagtatgatccattggttctatagggaatgaacatttgaacatacagtggtatgctgattttgcacggt ctgtgcatgtaggcgtctGtctgtaatgctgtgtgaacaagaatcgtcagtgcggttaatagggggt gttttcgcttccgatcgcgagaatgtattttctatcctatcaatggttga
P13	ARES00086654	tgaacttatcttctgaactttttaacgctctgttggttaccattagattaaaatagctatagaagcggtagatc gtacgttctcctaagagatgtcaaatatgtattcattacagtggtttgatactttgtgaaagttcgaaaaG gtattaagatgggtgttttaggggtgttaaggctcgggtgtatccgac
P14	ARES00422720	gttgtaacttaataatgtaatacagagctcggtagtagtcttagcagtagtttatcactggttggctaaattccat aatgcgaagaacaggggggaacatgatttttccaggaggtcacgccaaagattgtaaGagggctga gagagtcggaaagtgtatacatttaaaggatgtccccgcaaacctgaggtatgga
P15	ARES00952673	ggtttaactatttcttcggcggttagtagtttaacatctcgtgtgttgatggccaaggtgttagaaggatcgt gtcttagggccgtggtgtgtgatgattttggcaggaaagttacaaaaagcaaGgatcttatagtagt cattatgcttaggttttatattcgcattagccaagggag
P16	ARES00173427	aataccctcttttgaatcctgccatgatcggacttcttaggtgggagcttttcaaacgatttttagagtaat gatgacgtacttttgtatGggctcaattgtgttttaggaccttcagccatagatttctcaggctattacagac gagtacacttcattgcataactgtaaagggcgattttctcgttccg

P1 7	ARES00432513	aattgtttttgaatgatatggtgcattcatattacattacatccatatttgtatagcgatttgtaatatggta gtctatgatataaatactGattgatattgccgaaacgaggtaaaaaacatttggtgagccattacatctttg acagatttatcgaagatggttaataggcaatcgatcagatcttgcg
P1 8	ARES00438390	atggagtttactcgggtaacattggtataattgagatttgacacatgaccgcactagacttcactacgtgggt ttaaacgtttactggtattttcagattttgatgaaagttgaatatagggataggGacgctagggctggagtg ccgcagcctgataaagccgatacggggatatctcttaggtggtataggtag
pO ⁵ 4	Pos-Control	atgagctctctgcgcaagcgcggttaatttcgctcgctccgatcattctaaaaattagaaacacattgaaa aacaataccttgaagtctgtttcagaccttggcacagccgttgcttgatgtcctgcgcaacatgtacaataat aatggagtcataacatatgg

Table S3: Annotation of IVT-generated σ^{54} -RNA polymerase binding motifs in the upstream regions of genes in the *P. putida* genome.

Gene	Product	-24 motifs	-12 motifs	p-value
PP_2783	3-oxoacyl-ACP reductase family protein	TGGGCT	TGGCAT	0,00405
PP_4970	cytochrome c	GTGGCT	GTGTTT	0,00353
PP_1666	DUF2066 domain-containing protein	GTGGTT	GTGTAT	0,003
eutC	ethanolamine ammonia-lyase subunit EutC	TTGGCA	TTGCAT	0,000286
PP_1786	glycosyltransferase	ATGGCA	TTGCAT	0,000286
PP_1030	hypothetical protein	TGGGCT	TTGATT	0,000918
PP_1810	hypothetical protein	TTGGCT	TTGTAT	0,00126
PP_1923	hypothetical protein	ATGGCT	TGGCAT	0,00405
PP_0091	lipoprotein	CTGGCA	TGGCTT	0,00462
PP_1622	peptidoglycan DD-metalloendopeptidase family protein	TTGGTT	TTGCAA	0,00329
PP_4204	type II toxin-antitoxin system MqsA family antitoxin	TTGGCA	GTGTAT	0,003
PP_1394	5-guanidino-2-oxopentanoate decarboxylase	ATGGCT	GTGTTT	0,00353
PP_4577	5-oxoprolinase subunit PxpA	TGGGTA	GTGTTT	0,00353
PP_0859	amidohydrolase	CTGGTA	GTGCTT	0,0015
PP_3521	DMT family transporter	GTGGTT	TTGTAT	0,00126
PP_1210	Dps family protein	TCGGCA	TTGAGT	0,00381
PP_1584	DUF2514 domain-containing protein	TGGGCA	GTGCAT	0,00174
PP_3248	Dyp-type peroxidase	TTGATA	TTGCAA	0,00329
motA	flagellar motor stator protein MotA	TTGGTT	TGGCAT	0,00405
purT	formate-dependent phosphoribosylglycinamide formyltransferase	GTGGCT	TGGCAT	0,00405
pgi	glucose-6-phosphate isomerase	TTGATA	TGGCTT	0,00462
PP_4543	GNAT family N-acetyltransferase	TTGTTA	TTGAGT	0,00381
PP_1159	hypothetical protein	TTGGCT	TTGCAT	0,000286
PP_5488	hypothetical protein	ATGGCT	GTGTAT	0,003
PP_0182	hypothetical protein	ATGGCA	TTGCAT	0,000286
PP_2952	LysR family transcriptional regulator	GTGGTT	TGGCAT	0,00405
PP_3132	oligosaccharide flippase family protein	TGGGCA	TAGCAT	0,00381
PP_5043	PhoPQ-activated pathogenicity-related family protein	TTGGCT	TTGCTT	0,000286
edd	phosphogluconate dehydratase	GTGGCA	TTGTTT	0,00208
PP_4924	S8 family serine peptidase	GTGGCA	TTGTTT	0,00208
PP_0146	TerC family protein	CTGGTA	GTGCAT	0,00174
PP_2420	TonB-dependent receptor	ATGGTT	TTGCGT	0,00267
yegQ	tRNA 5-hydroxyuridine modification protein YegQ	ATGGCT	GTGATT	0,00271
dusA	tRNA dihydrouridine(20/20a) synthase DusA	GTGGTA	GTGAAT	0,00248
tssG	type VI secretion system baseplate subunit TssG	TCGGCA	GTGTTT	0,00353

PP_2433	antitoxin Xre/MbcA/ParS toxin-binding domain-containing protein	CTGGCA	TGGCTT	0,00462
cls	cardiolipin synthase	TCGGCA	ATGCAT	0,00491
PP_1188	dicarboxylate/amino acid:cation symporter	TTGGCA	TTGCTA	0,0041
PP_3989	DNA cytosine methyltransferase	ATGGTA	TGGCAT	0,00405
PP_2810	DUF1329 domain-containing protein	CTGGCA	TTGCGT	0,00267
PP_5363	DUF3617 domain-containing protein	GTGGTA	ATGCAT	0,00491
flgA	flagellar basal body P-ring formation chaperone FlgA	TCGGCA	TTGCTT	0,000286
flgB	flagellar basal body rod protein FlgB	TTGGCA	TTGCTA	0,0041
flgF	flagellar basal-body rod protein FlgF	TTGGTT	TTGCTT	0,000286
flgG	flagellar basal-body rod protein FlgG	ATGGCT	TTGCAA	0,00329
fliE	flagellar hook-basal body complex protein FliE	CTGGCA	TTGCTT	0,000286
PP_2836	fumarylacetoacetate hydrolase family protein	GTGGCT	TTGCAA	0,00329
PP_1946	glucose 1-dehydrogenase	TTGGCA	TTGCAA	0,00329
PP_0298	GlxA family transcriptional regulator	TAGGCA	TTGCGT	0,00267
PP_2828	hypothetical protein	TAGGTA	GTGCAT	0,00174
PP_3592	MurR/RpiR family transcriptional regulator	ATGGCT	TTGCAA	0,00329
ntrB	nitrogen regulation protein NR(II)	GTGGTT	TTGCAT	0,000286
PP_0952	RNA polymerase factor sigma-54	AAGGCA	TTGCTT	0,000286
PP_3288	universal stress protein	TCGGTA	TTGAGT	0,00381
urtA	urea ABC transporter substrate-binding protein	TAGGCA	TTGCAA	0,00329
PP_2209	2-aminoethylphosphonate--pyruvate transaminase	ATGGCA	TTGCAA	0,00329
PP_3486	ABC transporter substrate-binding protein	ATGGCT	GTGCTT	0,0015
PP_1141	branched-chain amino acid ABC transporter substrate-binding protein	TGGGCT	TGGCAT	0,00405
bcsB	cellulose biosynthesis cyclic di-GMP-binding regulatory protein BcsB	GTGGTT	TTGCGT	0,00267
ppx	exopolyphosphatase	ATGGCA	TTGCAT	0,000286
PP_3703	hypothetical protein	TGGGCA	GTGTAT	0,003
PP_0052	MBL fold metallo-hydrolase	GTGGCA	TGGCAT	0,00405
PP_3539	MerR family DNA-binding transcriptional regulator	GTGGTT	TTGAGT	0,00381
PP_3060	phage major tail tube protein	GTGGTT	GTGCTT	0,0015
PP_3778	pyrroline-5-carboxylate reductase	TTGACA	TTGCTA	0,0041
PP_1450	HlpA activation/secretion protein HlpB	GTGGCT	TAGCAT	0,00381
PP_5722	type II toxin-antitoxin system PemK/MazF family toxin	CTGGTA	TTGAAT	0,000631
xdhA	xanthine dehydrogenase small subunit	TGGGCA	GTGCAT	0,00174

Plasmid maps

1) N200 ARES

<https://benchling.com/s/seq-wG6faFrPGndrWYAhEMqg?m=slm-wg6jqKmiUQcNzv7zXjAx>

2) pHH100-dBroccoli construct

<https://benchling.com/s/seq-bD8GNHJIVsiaienqUajK?m=slm-NNHWA6VcrijY2MuG6UKe>

3) N200-pHH100-dBroccoli construct

<https://benchling.com/s/seq-VxVk2xeLeUp684jSTSbb?m=slm-LhFMu9GY5rYQlaGJzR3s>

4) Mango-pSEVA2311 construct

<https://benchling.com/s/seq-CfaFXRxx76D39VVFfn3LS?m=slm-Q88cA84fxmZQlkUefZ72>