Expanding the Dynamic Range of a Transcription Factor-Based Biosensor in *Saccharomyces cerevisiae*

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1 **Expanding the dynamic range of a transcription factor-based biosensor in**
2 ***Saccharomyces cerevisiae***

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21 **SUPPORTING INFORMATION**
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Table S1. Main biosensor parameters summarizing the quantifiable data across multiple modified promoters.

Promoters	BS	Relative basal activity ^a	“Leakiness” ^b	Maximum dynamic range ^c
P _{CCW12}	1	63	75	1.8
	2	95	2.2	95
	3	83	132	1.4
	4	64	95	1.5
	1,2,3	48	1.2	72
P _{TDH3}	1	48	74	1.3
	2	44	5.6	15
	3	63	76	1.6
	4	45	63	1.4
	2,3	35	2.4	25
P _{TPH1}	1	70	15	2.3
	2	27	13	1.0
	3	47	13	1.8
	4	12	2.5	2.4
	1,3	29	4.6	4.8
P _{ADH2}	1	61	7.7	4.4
	2	32	2.1	8.6
	3	69	18	2.1
	4	45	30	0.82
	1,3	57	3.0	6.8
	1,2,3	21	1.5	5.0
P _{TEF1}	1,3,4 ^d	90	60	1.4
	1,3,4 ^e	90	15	5.4

^a**Retained strength of modified promoter compared to the native promoter** (median fluorescence intensity of cells expressing GFP from modified promoter divided by median fluorescence intensity of cells expressing GFP from native promoter, %)

^b**GFP expression in cells expressing FapR compared to the negative control (No GFP)** (fold-change of median fluorescence intensity of cells expressing GFP from modified promoters (with FapR) divided by median fluorescence intensity of the negative control) (the closer to 1 the value the lower the “leakiness”)

^c**Maximum dynamic range of the sensor constructs** (fold-change of median fluorescence intensity of cells expressing GFP from modified promoters without and with FapR, respectively)

^d**Data calculated for FapR construct**

^e**Data calculated for FapR-Mig1 fusion construct**

50 **Table S2. Oligonucleotide primers used in this study**

Primer	Sequence (5'-3')
pSensor-F	ATGCGAATCCCCGGGTTAATT
pSensor-R	GAGCTCCAGCTTTTGTTCCT
pCCW12-F	CAATTAACCCCTACTAAAGGGAACAAAAGCTGGAGCTCCGACACGCAAAAAGAAAACCT
pCCW12-R	TCTCCTTTACTGTTAATTAACCCGGGGATTTCGCATTATTGATATAGTGTTTAAGCGAATG
pADH1-F	CAATTAACCCCTACTAAAGGGAACAAAAGCTGGAGCTCagggggatcgaagaaatgatg
pADH1-R	TCTCCTTTACTGTTAATTAACCCGGGGATTTCGCATtgatatagatagttgattgatg
pADH2-F	ATTAACCCCTACTAAAGGGAACAAAAGCTGGAGCTCcttaactgatagtttgatcaagg
pADH2-R	TCTCCTTTACTGTTAATTAACCCGGGGATTTCGCATtggtattacgatagtttaaatg
pHXT7-F	CAATTAACCCCTACTAAAGGGAACAAAAGCTGGAGCTCACTTCTCGTAGGAACAATTTTC
pHXT7-R	CTCCTTTACTGTTAATTAACCCGGGGATTTCGCATTTTTTGATTAATAATTAATAAACTTT
pMDH2-F	TAACCCCTACTAAAGGGAACAAAAGCTGGAGCTCgtacacgtatatagacattttacg
pMDH2-R	CTCCTTTACTGTTAATTAACCCGGGGATTTCGCATgttactataactttatgatattga
pPDC1-F	CAATTAACCCCTACTAAAGGGAACAAAAGCTGGAGCTCagggtagcctccccataacat
pPDC1-R	CTCCTTTACTGTTAATTAACCCGGGGATTTCGCATtttgattgattgactgtgtatttt
pPGK1-F	CAATTAACCCCTACTAAAGGGAACAAAAGCTGGAGCTCGGAAGTACCTTCAAAGAATGG
pPGK1-R	CTCCTTTACTGTTAATTAACCCGGGGATTTCGCATTTGTTTATATTGTTGTAAAAAGTA
pPYK1-F	CAATTAACCCCTACTAAAGGGAACAAAAGCTGGAGCTCgaaagttttccggcaagctaaatgg
pPYK1-R	TTCTCCTTTACTGTTAATTAACCCGGGGATTTCGCATtgatgatgttttattgttttgattg
pREV1-F	caattaaccctcactaaagggaacaaaagctggagctccctagactcaggttgctaac
pREV1-R	cttctcctttactgttaattaaccgggattcgcattgtttacctgcactcgtgga
pTDH3-F	ATTAACCCCTACTAAAGGGAACAAAAGCTGGAGCTCTCGAGTTATCATTATCAATACTG
pTDH3-R	TCTCCTTTACTGTTAATTAACCCGGGGATTTCGCATTTTGTGTTTATGTGTGTTTATTC
pTPI1-F	TTAACCCCTACTAAAGGGAACAAAAGCTGGAGCTCgttttaagattacggatattaac
pTPI1-R	TCTCCTTTACTGTTAATTAACCCGGGGATTTCGCATttttagtttatgtatgtttttg
pADH2-BS1-F	aAATTATATACTACTATTAGTACCTAGTCTTAATTtccatataaataagagtgccagta
pADH2-BS1-R	gaAATTAAGACTAGGTACTAATAGTAGTATATAATTtagcatgctatagctttaccaaa
pADH2-BS2-F	ccAATTATATACTACTATTAGTACCTAGTCTTAATTtagtagcagctttttcacactc
pADH2-BS2-R	tAATTAAGACTAGGTACTAATAGTAGTATATAATTggcactctatttatgtgatagg
pADH2-BS3-F	aAATTATATACTACTATTAGTACCTAGTCTTAATTgaatatcaagctacaaaagcatac
pADH2-BS3-R	cAATTAAGACTAGGTACTAATAGTAGTATATAATTtattaccaagaagaacaagaagt
pADH2-BS4-F	tAATTATATACTACTATTAGTACCTAGTCTTAATTcaactatcaactattaactatatcg
pADH2-BS4-R	tgAATTAAGACTAGGTACTAATAGTAGTATATAATTattgtatgctttttgtagctgat
pCCW12-BS1-F	TCAATTATATACTACTATTAGTACCTAGTCTTAATTCGTTCAAGTATATAAAGTCGGCA
pCCW12-BS1-R	CGAATTAAGACTAGGTACTAATAGTAGTATATAATTGAGGCAAAGGATGCAAAATTTTC
pCCW12-BS2-F	AAATTATATACTACTATTAGTACCTAGTCTTAATTTGCTTGATAATCTTTCTTCCATCC
pCCW12-BS2-R	GCAAATTAAGACTAGGTACTAATAGTAGTATATAATTTGCCGACTTTATATACTTGAACG

pCCW12-BS3-F CAATTATATACTACTATTAGTACCTAGTCTTAATTCTAACATACCAAGAAATTAATCTTC

pCCW12-BS3-R GAATTAAGACTAGGTACTAATAGTAGTATATAATTGAAAGAATAAAGGAGAATAAGAATAA

pCCW12-BS4-F AAAATTATATACTACTATTAGTACCTAGTCTTAATTTTAATCTTCTGTCATTCGCTTAAAC

pCCW12-BS4-R AAAATTAAGACTAGGTACTAATAGTAGTATATAATTTTTCTTGGTATGTTAGGAAAGAATA

pMDH2-BS1-F gaAATTATATACTACTATTAGTACCTAGTCTTAATTttatcgatatgagataaagattgct

pMDH2-BS1-R aAATTAAGACTAGGTACTAATAGTAGTATATAATTtctttatctttatatctacgcacg

pMDH2-BS2-F ccAATTATATACTACTATTAGTACCTAGTCTTAATTcctctgtataaatcgtagcagca

pMDH2-BS2-R ggAATTAAGACTAGGTACTAATAGTAGTATATAATTggagaaaatatatacagggaagaaag

pMDH2-BS3-F gtAATTATATACTACTATTAGTACCTAGTCTTAATTccagaatatagtctgcagact

pMDH2-BS3-R ggAATTAAGACTAGGTACTAATAGTAGTATATAATTactactctgactgtacgatttat

pMDH2-BS4-F atAATTATATACTACTATTAGTACCTAGTCTTAATTcataaagttatagtaacATGCGAA

pMDH2-BS4-R gAATTAAGACTAGGTACTAATAGTAGTATATAATTatattgtattgaacttttgaatagt

pTDH3-BS1-F GAATTATATACTACTATTAGTACCTAGTCTTAATTACTAATAAGTATATAAAGACGGTAG

pTDH3-BS1-R GTAATTAAGACTAGGTACTAATAGTAGTATATAATTCAAGTAGGGGAATAATTCAGGG

pTDH3-BS2-F GGAATTATATACTACTATTAGTACCTAGTCTTAATTTAGGTATTGATTGTAATTCTGTAAAT

pTDH3-BS2-R AAATTAAGACTAGGTACTAATAGTAGTATATAATCCGCTTTTATATACTTATTAGTCAAG

pTDH3-BS3-F AAAATTATATACTACTATTAGTACCTAGTCTTAATTACACCAAGAACTTAGTTTCGAATAA

pTDH3-BS3-R GTAATTAAGACTAGGTACTAATAGTAGTATATAATTTTTAAACTAAAAAAGACTAACTA

pTDH3-BS4-F AGAATTATATACTACTATTAGTACCTAGTCTTAATTTTTCGAATAAACACACATAAACAAAC

pTDH3-BS4-R AAATTAAGACTAGGTACTAATAGTAGTATATAATTCTAAGTTCTTGGTGTTTTAAACTAA

pTPI1-BS1-F caaAATTATATACTACTATTAGTACCTAGTCTTAATTcatttactatttcccttctttag

pTPI1-BS1-R tgAATTAAGACTAGGTACTAATAGTAGTATATAATTtgcaagttcactaaactcctaaa

pTPI1-BS2-F ttAATTATATACTACTATTAGTACCTAGTCTTAATTcaattttttgtttgtattctttct

pTPI1-BS2-R gAATTAAGACTAGGTACTAATAGTAGTATATAATTaaaaagattgattagaattaaaaag

pTPI1-BS3-F aaAATTATATACTACTATTAGTACCTAGTCTTAATTtctataactacaaaaacatacat

pTPI1-BS3-R gaAATTAAGACTAGGTACTAATAGTAGTATATAATTttaagcaagaaaagaatacaacaa

pTPI1-BS4-F aaAATTATATACTACTATTAGTACCTAGTCTTAATTaaacacatacataaactaaaaATGC

pTPI1-BS4-R ttAATTAAGACTAGGTACTAATAGTAGTATATAATTttagttatagatttaagcaagaaa

pTEF1_up1-F CAATTATATACTACTATTAGTACCTAGTCTTAATTCAAAATGTTTCTACTCCTTTTTTAC

pTEF1_up1-R TGAATTAAGACTAGGTACTAATAGTAGTATATAATTGAGCTCCAGCTTTTGTTCCCTT

pTEF1_up2-F CCAAATTATATACTACTATTAGTACCTAGTCTTAATTCCTCAAAACACCCAAGCACAGCA

pTEF1_up2-R AGAATTAAGACTAGGTACTAATAGTAGTATATAATTTGGTACGGCGATGCGCGGAGTC

pTEF1_up3-F TAATTATATACTACTATTAGTACCTAGTCTTAATTCCTCTAGGGTGTCGTTAATT

pTEF1_up3-R AGAATTAAGACTAGGTACTAATAGTAGTATATAATTAAGAGGGGAAATTTAGTAGTCT

pTEF1_up4-F AAATTATATACTACTATTAGTACCTAGTCTTAATTGGTTTGAAAAAGAAAAAGAGACC

pTEF1_up4-R CCAATTAAGACTAGGTACTAATAGTAGTATATAATTTTAGTACGGGTAATTAACGACAC

pTEF1_up5-F GGAATTATATACTACTATTAGTACCTAGTCTTAATTCATAAAAAATTTTATCACGTTTC

pTEF1_up5-R TGAATTAAGACTAGGTACTAATAGTAGTATATAATTCCTTTTTTCGACGAAGAAAAAGAA

pTEF1_up6-F AAATTATATACTACTATTAGTACCTAGTCTTAATTTTGATATTTAAGTTAATAAACGGTC

pTEF1_up6-R	CAAAATTAAGACTAGGTACTAATAGTAGTATATAATTTGGGAGGTCATCGAAAGAGAAA
HR_UP-F	CGAGATCTTTGTGTTTCGG
HR_UP-R	TCTCGTATGTCGGCTCTC
HR_DW-F	CCACTTTTCAATGAAACG
HR_DW-R	GAGGTGGTTATTGATCACC
pTEF1-F	CAAGAAGTAGGCGAGAGCCGACATACGAGACAGCTATGACCATGATTACG
pFapR-R1	TCATAAGAAATTCGCTTATGAATGTTTTGAACGATACATGTC
pMig1-F	CGCTTTGACATGTATCGTTCAAAACATTCAggatctggttctggttctCAAAGCCCATATCCAATGACAC
pMig1-R	CTTATTTAATAATAAAAAATCATAAATCATAAGAAATTCGCTCAGTCCATGTGTGGGAAG
tADH1-F	GCGAATTTCTTATGATTTATG
tADH1-R	CTAGCATATCAATATCCGTTTCATTGAAAAGTGGATAAGAGCGACCTCATGCTATAC
pFapR-R2	CGTTAGACACTTGTGTGTCATTGGATATGGGCTTTGagaaccagaaccagatccTGAATGTTTTGAACGATACATGTC
pRox1-F	CGCTTTGACATGTATCGTTCAAAACATTCAggatctggttctggttctAATCCTAAATCCTCTACACCTAAG
pRox1-R	CTTATTTAATAATAAAAAATCATAAATCATAAGAAATTCGCTCATTTCGGAGAAACTAGGC
pFapR-R3	GGGTCTTGGAATCTTAGGTGTAGAGGATTTAGGATTagaaccagaaccagatccTGAATGTTTTGAACGATACATGTC
pCPCR_F	CACAGTTATATAGTTATATACACATAGACA
pCPCR_R	ATTATCTATGCTTTTGTCTTAAAGAGAAG

52 **Table S3. Plasmids used in this study**

Plasmids	Backbone; Description	References
p416TEF	CEN6, <i>TEF1</i> promoter, <i>URA3</i> marker	Ref ¹
pFDA7	p416TEF; P _{TEF1} _BS_A_B_C-GFP-T _{CYC1}	Ref ²
p416TEF-GFP	p416TEF; P _{TEF1} -GFP	Ref ²
pX&Y01	p416TEF; P _{ADH1} -GFP	This study
pX&Y02	p416TEF; P _{ADH2} -GFP	This study
pX&Y03	p416TEF; P _{CCW12} -GFP	This study
pX&Y04	p416TEF; P _{HXT7} -GFP	This study
pX&Y05	p416TEF; P _{MDH2} -GFP	This study
pX&Y06	p416TEF; P _{PDC1} -GFP	This study
pX&Y07	p416TEF; P _{PGK1} -GFP	This study
pX&Y08	p416TEF; P _{PYK1} -GFP	This study
pX&Y09	p416TEF; P _{REV1} -GFP	This study
pX&Y10	p416TEF; P _{TDH3} -GFP	This study
pX&Y11	p416TEF; P _{TPH1} -GFP	This study
pX&Y12	pX&Y02; P _{ADH2} _BS_1-GFP	This study
pX&Y13	pX&Y02; P _{ADH2} _BS_2-GFP	This study
pX&Y14	pX&Y02; P _{ADH2} _BS_3-GFP	This study
pX&Y15	pX&Y02; P _{ADH2} _BS_4-GFP	This study
pX&Y16	pX&Y02; P _{ADH2} _BS_1_3-GFP	This study
pX&Y17	pX&Y02; P _{ADH2} _BS_1_2_3-GFP	This study
pX&Y18	pX&Y03; P _{CCW12} _BS_1-GFP	This study
pX&Y19	pX&Y03; P _{CCW12} _BS_2-GFP	This study
pX&Y20	pX&Y03; P _{CCW12} _BS_3-GFP	This study
pX&Y21	pX&Y03; P _{CCW12} _BS_4-GFP	This study
pX&Y22	pX&Y03; P _{CCW12} _BS_1_2_3-GFP	This study
pX&Y23	pX&Y05; P _{MDH2} _BS_1-GFP	This study
pX&Y24	pX&Y05; P _{MDH2} _BS_2-GFP	This study
pX&Y25	pX&Y05; P _{MDH2} _BS_3-GFP	This study
pX&Y26	pX&Y05; P _{MDH2} _BS_4-GFP	This study
pX&Y27	pX&Y10; P _{TDH3} _BS_1-GFP	This study
pX&Y28	pX&Y10; P _{TDH3} _BS_2-GFP	This study
pX&Y29	pX&Y10; P _{TDH3} _BS_3-GFP	This study
pX&Y30	pX&Y10; P _{TDH3} _BS_4-GFP	This study
pX&Y31	pX&Y10; P _{TDH3} _BS_2_3-GFP	This study
pX&Y32	pX&Y11; P _{TPH1} _BS_1-GFP	This study
pX&Y32	pX&Y11; P _{TPH1} _BS_2-GFP	This study
pX&Y33	pX&Y11; P _{TPH1} _BS_3-GFP	This study
pX&Y34	pX&Y11; P _{TPH1} _BS_4-GFP	This study
pX&Y35	pX&Y11; P _{TPH1} _BS_1_3-GFP	This study
pX&Y36	p416TEF; P _{TEF1} _BS_up_1-GFP	This study
pX&Y37	p416TEF; P _{TEF1} _BS_up_2-GFP	This study
pX&Y38	p416TEF; P _{TEF1} _BS_up_3-GFP	This study
pX&Y39	p416TEF; P _{TEF1} _BS_up_4-GFP	This study
pX&Y40	p416TEF; P _{TEF1} _BS_up_5-GFP	This study
pX&Y41	p416TEF; P _{TEF1} _BS_up_6-GFP	This study
pX&Y42	p416TEF; P _{TEF1} _BS_up_1-3-4_GFP	This study
pQC005	2 μ m ampR <i>KIURA3</i> gRNA- <i>CAN1</i> .Y	Lab collection

54 **Table S4. Strains used in this study**

Strains	Genotype	Plasmid	References
IMX581	<i>MATa ura3-52 can1Δ::cas9-natNT2 TRP1 LEU2 HIS3</i>	-	Ref ³
Y&X01	IMX581; P _{TEF1} -NLS- <i>fapR</i> -T _{ADHI}	-	This study
Y&X02	IMX581; P _{TEF1} -NLS- <i>fapR</i> - <i>MIG1</i> -T _{ADHI}	-	This study
Y&X03	IMX581; P _{TEF1} -NLS- <i>fapR</i> - <i>ROX1</i> -T _{ADHI}	-	This study
Y&X04	IMX581	p416TEF	This study
Y&X05	IMX581	p416TEF-GFP	This study
Y&X06	IMX581	pX&Y01	This study
Y&X07	IMX581	pX&Y02	This study
Y&X08	IMX581	pX&Y03	This study
Y&X09	IMX581	pX&Y04	This study
Y&X10	IMX581	pX&Y05	This study
Y&X11	IMX581	pX&Y06	This study
Y&X12	IMX581	pX&Y07	This study
Y&X13	IMX581	pX&Y08	This study
Y&X14	IMX581	pX&Y09	This study
Y&X15	IMX581	pX&Y10	This study
Y&X16	IMX581	pX&Y11	This study
Y&X17	Y&X02	pX&Y12	This study
Y&X18	Y&X02	pX&Y13	This study
Y&X19	Y&X02	pX&Y14	This study
Y&X20	Y&X02	pX&Y15	This study
Y&X21	Y&X02	pX&Y16	This study
Y&X22	Y&X02	pX&Y17	This study
Y&X23	Y&X02	pX&Y18	This study
Y&X24	Y&X02	pX&Y19	This study
Y&X25	Y&X02	pX&Y20	This study
Y&X26	Y&X02	pX&Y21	This study
Y&X27	Y&X02	pX&Y22	This study
Y&X28	Y&X02	pX&Y23	This study
Y&X29	Y&X02	pX&Y24	This study
Y&X30	Y&X02	pX&Y25	This study
Y&X31	Y&X02	pX&Y26	This study
Y&X32	Y&X02	pX&Y27	This study
Y&X33	Y&X02	pX&Y28	This study
Y&X34	Y&X02	pX&Y29	This study
Y&X35	Y&X02	pX&Y30	This study
Y&X36	Y&X02	pX&Y31	This study
Y&X37	Y&X02	pX&Y32	This study
Y&X38	Y&X02	pX&Y33	This study
Y&X39	Y&X02	pX&Y34	This study
Y&X40	Y&X02	pX&Y35	This study
Y&X41	IMX581	pX&Y36	This study
Y&X42	IMX581	pX&Y37	This study
Y&X43	IMX581	pX&Y38	This study
Y&X44	IMX581	pX&Y39	This study
Y&X45	IMX581	pX&Y40	This study
Y&X46	IMX581	pX&Y41	This study

Strains	Genotype	Plasmid	References
Y&X47	Y&X02	pX&Y36	This study
Y&X48	Y&X02	pX&Y37	This study
Y&X49	Y&X02	pX&Y38	This study
Y&X50	Y&X02	pX&Y39	This study
Y&X51	Y&X02	pX&Y40	This study
Y&X52	Y&X02	pX&Y41	This study
Y&X53	Y&X03	pX&Y36	This study
Y&X54	Y&X03	pX&Y37	This study
Y&X55	Y&X03	pX&Y38	This study
Y&X56	Y&X03	pX&Y39	This study
Y&X57	Y&X03	pX&Y40	This study
Y&X58	Y&X03	pX&Y41	This study
Y&X59	Y&X01	pX&Y42	This study
Y&X60	Y&X01	pFDA7	This study
Y&X61	Y&X02	pX&Y42	This study
Y&X62	Y&X02	pFDA7	This study

55

56 Sequences of promoters with different BSs for FapR

57 P_{TDH3} (BS1, 2, 3, 4)

58 TCGAGTTTATCATTATCAATACTGCCATTTCAAAGAATACGTAAATAATTAATAGTAGTGATTTTCCTAACTTTATTAGTCAA
59 AAAATTAGCCTTTTAAATTCTGCTGTAACCCGTACATGCCCAAAATAGGGGGCGGGTTACACAGAATATATAACATCGTAGGT
60 GTCTGGGTGAACAGTTTATTCCTGGCATCCACTAAATATAATGGAGCCCGCTTTTAAAGCTGGCATCCAGAAAAAAGAA
61 TCCCAGCACCAAAATATTGTTTTCTTACCAACCATCAGTTTCATAGGTCCATTCTCTAGCGCAACTACAGAGAACAGGGGCA
62 CAAACAGGCAAAAAACGGGCACAACCTCAATGGAGTGATGCAACCTGGCTGGAGTAAATGATGACACAAGGCAATTGACCC
63 ACGCATGTATCTATCTCATTTCCTTACACCTTCTATTACCTTCTGCTCTCTGATTGGAAGAGCTGAAAAAAGGTTGAA
64 ACCAGTCCCTGAAATATTCCCTACTTGAATTATATACTACTATTAGTACCTAGTCTTAATTACTAATAAGTATATAAGAC
65 GGAATTATATACTACTATTAGTACCTAGTCTTAATTAGGTATTGATTGTAATTCTGTAAATCTATTTCTTAACTTCTTAAAT
66 TCTACTTTTATAGTTAGTCTTTTCTTGTATTTTAAATATTATATACTACTATTAGTACCTAGTCTTAATTACACCAAGAACTTAG
67 AATTATATACTACTATTAGTACCTAGTCTTAATTITTCGAATAAACACACATAAACAAACAAA

68

69 P_{CCW12} (BS1, 2, 3, 4)

70 CGACACGCAAAAGAAAACCTTCGAGGTTGCGCACTTCGCCACCCATGAACCACACGGTTAGTCCAAAAGGGGCAGTTCAG
71 ATTCCAGATGCGGGAATTAGCTTGCTGCCACCTCACCTACTAACGCTGCGGTGTGCGGATACTTCATGCTATTTATAGACG
72 CGCGTGTGCGGAATCAGCACGCGCAAGAACCAATGGGAAAAATCGGAATGGGTCCAGAACTGCTTTGAGTGCTGGCTATTGG
73 CGTCTGATTTCCGTTTGGGAATCCTTTGCCGCGCGCCCTCTCAAACTCCGCACAAGTCCAGAAAGCGGGAAAGAAATA
74 AAACGCCACCAAAAAAATAAAGCCAATCCTCGAAGCGTGGGTGGTAGGCCCTGGATTATCCCGTACAAGTATTCTCA
75 GGAGTAAAAAACCGTTTGTGTTGGAATCCCCATTCGCGGCCACCTACGCCGCTATCTTGCAACAACATCTGCGATAAC
76 TCAGCAAATTTGCATATTGCTGTTGCAGTATTGCGATAATGGGAGTCTTACTTCCAACATAACGGCAGAAAGAAATGTGAG
77 AAAATTTTGATCCTTTGCCTCAATTATATACTACTATTAGTACCTAGTCTTAATTCGTTCAAGTATATAAGTTCGGCAATTA
78 TATACTACTATTAGTACCTAGTCTTAATTGCTTGATAATCTTTCTTCCATCCTACATTGTTCTAATTATTCTATTCTCTTAA
79 TTCTTTCAATTATATACTACTATTAGTACCTAGTCTTAATTCTAACATACCAAGAAAAATTATATACTACTATTAGTACCTAGT
80 CTTAATTITAATCTTCTGTCACTCGCTTAAACACTATATCAATA

81

82 P_{TPII} (BS1, 2, 3, 4)

83 TGTTTAAAGATTACGGATATTTAACTTACTTAGAATAATGCCATTTTGTGAGTTATAATAATCCTACGTTAGTGTGAGCGGG
84 ATTTAAACTGTGAGGACCTTAATACATTACAGACTTCTGCGGTATCACCTACTTATCCCTTCGAGATTATATCTAGGAAC
85 CCATCAGGTTGGTGAAGATTACCGTTCTAAGACTTTTCAGCTTCCTCTATTGATGTTACACCTGGACACCCCTTTCTGGCA
86 TCCAGTTTTTAATCTTCAGTGGCATGTGAGATTCTCCGAAATTAATTAAGCAATCACACAATTCTCTCGGATACCACCTCGG
87 TTGAAACTGACAGGTGGTTGTGACGCATGCTAATGCAAAGGAGCTATATACCTTTGGCTCGGCTGCTGTAACAGGGAATA
88 TAAAGGGCAGCATAATTTAGGAGTTTGTGAACTTGCAAAATTATATACTACTATTAGTACCTAGTCTTAATTCATTTACTAT
89 TTCCCTTCTTACGTAAATATTTTCTTTTAAATCTAAATCAATCTTTTAAATTATATACTACTATTAGTACCTAGTCTTAATTC
90 AATTTTGTGTTGATTCTTTCTTGTCTTAAATATTATATACTACTATTAGTACCTAGTCTTAATTTCTATAACTACAAAATTAT
91 ATACTACTATTAGTACCTAGTCTTAATTAACACATACATAAACTAAAA

92

$$P_{ADH2} (BS1, 2, 3, 4)$$

CTTAAC TGATAG TTTGAT CAAAGGGG CAAAACGT AGGGGCAA CAAACGGA AAAATCG TTTCTCAA ATTTTCTG ATGCCAAG
AACTCTA ACCAGTCTT ATCTAAAA ATTGCCTT ATGATCCG TCTCTCCG GTTACAGC CTGTGTA ACTGATTA ATCCTGC TTTTCT
AATCACC ATTCTA ATGTTTAA TTAAGGG ATTTTGTCT TCATTAAC GGCCTTTC GCCTATA AAAATGTT ATGACG TTTTGCC CGC
AGGCGGG AAAACCAT CCACCTT CACGAG ACTGATCT CCTCTGCC GGAACACCG GGCATCTCCA ACTTATA AGTTGG AGAAATAA
GAGAAT TTTAGATT GAGAGA ATGAAAAAAAA AAAAAAAAAA AGGCAG AGGAGAGC ATAAAAA TGGGGT TCACTTTT TGGT
AAAGCT ATAAGCAT GCCTAA AATTATATA CTACTATT AGTACCT AGTCTTAA TTTCACA TATAA TAGAGT GCCAATTATATA CT
ACTATTAGTACCTAGTCTTAA TTAGTAGCGACT TTTTTCAC ACTCGAAAT ACTTCTACTGCTCTCT GTTGT TTTTATCACT
TCTGTG TTTCTTCT GTGTAATAA AATTATATA CTACTACTATT AGTACCTAGTCTTAA TTGAATATCA AAGCTACAAA AAGCATACAAT
AATTATATA CTACTATTAGTACCTAGTCTTAA TTCAACTATCA ACTATTA AACTATATCGTAATACACA

$$P_{MDH2} (BS1, 2, 3, 4)$$

GTACACGTATATATAGACATTTACGTAATGGAGAAACTGAGGTTTTGTGTTTCACCTTTTTTCTTTCTTTTTCACCTATTGCTCG
AACC GCCTGCGATGAGCTAAGAAAAAAGTGAAAGAAATCATAGAAAGCAAAAATGAGATTATATAGCCCAGAGCCCTCT
CTGTGGCGCCTGTCCCAAGGCGGACCAACAACAACACTTGCCCAAACCTAAGAAAAATCCCTCATACCTTTCCGTTTGTATCTC
CTACTTTCTTACTTCCCTTTTTTCTTCTTTATTTGCTTGGTTACCAATTGAAGTCCATTTTTACTACAGCAATAGCTAGTCATT
CGCTACTTCCGTTGTCTACTTTTTTCAAATTTCTCATCTATATAGCAAGTACGGAAGAACGTAAGTCACTTCCCGGCATCTCGG
CCTTCCCGCGCAAAATGGACTACATCATCTACGATAGCGCCCTTTAATCCGCAATTACTTTGCCATTTCGGCCGTAGCGGTTCT
AAAGCCGCCGTGCCTTGCCCCCAATACTCCCTAATGATCCGGGAAGTTCGGTTTTTTTTCTTTGTTTAGTGGCATTTTGTGT
TGCCCAAGGTTGGGAAGGTCCGATTGACTTTAAGGAACACGGAAGGTATCTAAGGTTTCTAAAAACAATATACACGCGCG
TGCGTAGATATATAAAGATAAAGAAATTATATACTACTATTAGTACCTAGTCTTAATTTTTATCGATATGAGATAAAGATTGC
TGCATGATTTCTCTTCTGATTCTTTTTTCCCTGTATATATTTCTCCAAATTATATACTACTATTAGTACCTAGTCTTAATTTCTTCT
GTATAAATCGTACAGTCAGAAGTAGTAAATTATATACTACTATTAGTACCTAGTCTTAATTCAGAATATAGTGTGCAGACTA
TACAAAAGTTCAATACAATATAATTATATACTACTATTAGTACCTAGTCTTAATTCATAAAAAGTTATAGTAAC

P_{TEF1} (unmodified)

CAAAATGTTTCTACTCCTTTTAACTCTTCCAGATTTTCTCGACTCCGCGCATCGCCGTACCACTTCAAAAGACCCCAAGCACAGCATACTAAATTTCCCTCTTTCTTCTCTAGGGTGTCTGTTAATTACCCGTAATAAGGTTTGAAAAAGAAAAAGAGACCGCTCGTGTCTTTTTCTCTGTCGAAAAAGGCATAAAAAATTTTATCACGTTTCTTTTTCTTGAAATTTTTTTTTTTGATTTTTTCTCTTTTCATGACCTCCCATGTATATTTAAGTATAAATACCGGTCTCAATTTCTCAAGTTTCAGTTTCATTTTCTTGTTCTATCAACTTTTTTACTCTTGCTCATTAGAAAGAAAGCATGAATCTAATCTAAGTTTAATTACAAA

P_{TEF1} (BSs UP 1, 2, 3 4, 5, 6)

AATTATATACTACTATTAGTACCTAGTCTTAATTCAAATGTTTCTACTCCTTTTTACTCTTCCAGATTTTCTCGGACTCCGCG
CATCGCCGTACCAAATTATATACTACTATTAGTACCTAGTCTTAATTCTTCAAAACACCCAAGCACAGCATACTAAATTTCCC
CTCTTTAATTATATACTACTATTAGTACCTAGTCTTAATTTCTCCTCTAGGGTGTCGTTAATTACCCGTAATAAAATTATATA
CTACTATTAGTACCTAGTCTTAATTGGTTTGGAAAAGAAAAAGAGACCGCCTCGTTTCTTTTCTTCGTCGAAAAAGGAATT
ATATACTACTATTAGTACCTAGTCTTAATTCATAAAAAATTTTTATCACGTTTCTTTTTCTTGAAAATTTTTTTTTTGATTTTTT
CTCTTTTCGATGACCTCCCAATTATATACTACTATTAGTACCTAGTCTTAATTTTGATATTTAAGTTAATAAACGGTCTTCAAT
TCTCAAGTTTTCAGTTTCAATTTTTCTTGTTCTATTACAACTTTTTTACTTCTTGCTCATTAGAAAGAAAGCATAGCAATCTAAT
CTAAGTTTAAATACAA

$$P_{TEF1} \text{ (BSs A B C)}^2$$

CAAAATGTTTCTACTCCTTTTIACTCTTCCAGATTTTCTCGGACTCCGCGCATCGCCGTACCACTTCAAAACACCCCAAGCACA
GCATACTAAATTTCCCTCTTTCTTCTCTAGGGTGTCGTTAATTACCCGTAATAAGGTTTGAAAAAGAAAAAGAGACCGC
CTCGTTTCTTTTCTTCGTCGAAAAAGGCAATAAAAAATTTTATCACGTTTCTTTTCTTGAAAATTTTTTTTTTGATTTTTTC
TCTTTCGATGACCTCCCATTGATATTTAAGTTAATAAACGGTCTTCAATTTCTCAAGTTTCAGTTTCATTTTCTTGTTCAATTAT
TATACTACTATTAGTACCTAGTCTTAATTATTACAACTTTTTACTTCTTGCTCATTAGAAATTATATACTACTATTAGTACC
TAGTCTTAATTAGAAAGCAAATTATATACTACTATTAGTACCTAGTCTTAATTAGCAATCTAATCTAAGTTTAATTACAA
A

Grey regions: integrated binding sites (FapR)

NNNNNNNN: TATA box⁴⁻⁸

X: TSS⁹

ACACCCAAGCAC: UAS in P_{TEF1}¹⁰

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