



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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33 **Table S1. Main biosensor parameters summarizing the quantifiable data across**
 34 **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 _{TPI1}	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

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

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

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

45 ^d**Data calculated for FapR construct**

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

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

Primer	Sequence (5'-3')
pSensor-F	ATGCGAATCCCCGGGTTAATT
pSensor-R	GAGCTCCAGCTTTTGTTCCT
pCCW12-F	CAATTAACCCTCACTAAAGGGAACAAAAGCTGGAGCTCCGACACGCAAAAAGAAAACCT
pCCW12-R	TCTCCTTTACTGTTAATTAACCCGGGGATTTCGCATTATTGATATAGTGTTTAAGCGAATG
pADH1-F	CAATTAACCCTCACTAAAGGGAACAAAAGCTGGAGCTCaggggatcgaagaaatgatg
pADH1-R	TCTCCTTTACTGTTAATTAACCCGGGGATTTCGCATtgtatatgagatagttgattgatg
pADH2-F	ATTAACCCTCACTAAAGGGAACAAAAGCTGGAGCTCcttaactgatagtttgatcaagg
pADH2-R	TCTCCTTTACTGTTAATTAACCCGGGGATTTCGCATtgtgtattacgatagtttaaatg
pHXT7-F	CAATTAACCCTCACTAAAGGGAACAAAAGCTGGAGCTCACTTCTCGTAGGAACAATTTTC
pHXT7-R	CTCCTTTACTGTTAATTAACCCGGGGATTTCGCATTTTTTGATTAATAATTAATAAAAACTTT
pMDH2-F	TAACCCTCACTAAAGGGAACAAAAGCTGGAGCTCgtacacgtatatagacattttacg
pMDH2-R	CTCCTTTACTGTTAATTAACCCGGGGATTTCGCATgtactataactttatgatattgta
pPDC1-F	CAATTAACCCTCACTAAAGGGAACAAAAGCTGGAGCTCagggtagcctcccataacat
pPDC1-R	CTCCTTTACTGTTAATTAACCCGGGGATTTCGCATtttgattgattgactgtgtatttt
pPGK1-F	CAATTAACCCTCACTAAAGGGAACAAAAGCTGGAGCTCGGAAGTACCTTCAAAGAATGG
pPGK1-R	CTCCTTTACTGTTAATTAACCCGGGGATTTCGCATTTGTTTTATATTTGTTGTAATAAAGTA
pPYK1-F	CAATTAACCCTCACTAAAGGGAACAAAAGCTGGAGCTCgaaagttttccgcaagctaaatgg
pPYK1-R	TTCTCCTTTACTGTTAATTAACCCGGGGATTTCGCATtgtgatgatgtttattgttttgattg
pREV1-F	caattaaccctcactaaaggaacaaaagctggagctccctagacttcaggtgtctaac
pREV1-R	cttctccttactgttaattaaccgggattcgcattgtttacctgcactcgtgga
pTDH3-F	ATTAACCCTCACTAAAGGGAACAAAAGCTGGAGCTCTCGAGTTTATCATTATCAATACTG
pTDH3-R	TCTCCTTTACTGTTAATTAACCCGGGGATTTCGCATTTTGTGTTTATGTGTGTTTATTC
pTPI1-F	TTAACCCTCACTAAAGGGAACAAAAGCTGGAGCTCtgtttaagattacggatattaac
pTPI1-R	TCTCCTTTACTGTTAATTAACCCGGGGATTTCGCATttttagttatgtatgttttttg
pADH2-BS1-F	aAATTATATACTACTATTAGTACCTAGTCTTAATTtccatataaatagagtgccagta
pADH2-BS1-R	gaAATTAAGACTAGGTACTAATAGTAGTATATAAATTtaggcatgctatagctttaccaaa
pADH2-BS2-F	ccAATTATATACTACTATTAGTACCTAGTCTTAATTtagtagcactttttcacactc
pADH2-BS2-R	tAATTAAGACTAGGTACTAATAGTAGTATATAAATTggcactctatttatgtgatagg
pADH2-BS3-F	aAATTATATACTACTATTAGTACCTAGTCTTAATTgaatatcaagctacaaaaagcatac
pADH2-BS3-R	cAATTAAGACTAGGTACTAATAGTAGTATATAAATTtattaccaagaagaacaagaagt
pADH2-BS4-F	tAATTATATACTACTATTAGTACCTAGTCTTAATTcaactatcaactattaactatatcg
pADH2-BS4-R	tgAATTAAGACTAGGTACTAATAGTAGTATATAAATTattgtatgcttttttagcttgat
pCCW12-BS1-F	TCAATTATATACTACTATTAGTACCTAGTCTTAATTCGTTCAAGTATATAAAGTCGGCA
pCCW12-BS1-R	CGAATTAAGACTAGGTACTAATAGTAGTATATAAATTGAGGCAAAGGATGCAAAATTTTC
pCCW12-BS2-F	AAATTATATACTACTATTAGTACCTAGTCTTAATTTGCTTGATAATCTTTCTTCCATCC
pCCW12-BS2-R	GCAAATTAAGACTAGGTACTAATAGTAGTATATAAATTTGCCGACTTTATATACTTGAACG

pCCW12-BS3-F CAATTATATACTACTATTAGTACCTAGTCTTAATTCTAACATACCAAGAAATTAATCTTC

pCCW12-BS3-R GAATTAAGACTAGGTACTAATAGTAGTATATAATTGAAAGAATAAAGGAGAATAAGAATAA

pCCW12-BS4-F AAAATTATATACTACTATTAGTACCTAGTCTTAATTTTAATCTTCTGTCATTCGCTTAAAC

pCCW12-BS4-R AAAATTAAGACTAGGTACTAATAGTAGTATATAATTTTTCTTGGTATGTTAGGAAAGAATA

pMDH2-BS1-F gaAATTATATACTACTATTAGTACCTAGTCTTAATTttatcgatagagataaagattgct

pMDH2-BS1-R aAATTAAGACTAGGTACTAATAGTAGTATATAATTctttatctttatatactacgcacg

pMDH2-BS2-F ccAATTATATACTACTATTAGTACCTAGTCTTAATTcctctgtataaatcgtacagca

pMDH2-BS2-R ggAATTAAGACTAGGTACTAATAGTAGTATATAATTggagaaaatatacagggaanaag

pMDH2-BS3-F gtAATTATATACTACTATTAGTACCTAGTCTTAATTccagaatagtgctgcagact

pMDH2-BS3-R ggAATTAAGACTAGGTACTAATAGTAGTATATAATTactactctgactgtacgattat

pMDH2-BS4-F atAATTATATACTACTATTAGTACCTAGTCTTAATTcataaagttatagtaacATGCGAA

pMDH2-BS4-R gAATTAAGACTAGGTACTAATAGTAGTATATAATTatattgtattgaacttttgaatagt

pTDH3-BS1-F GAATTATATACTACTATTAGTACCTAGTCTTAATTACTAATAAGTATATAAAGACGGTAG

pTDH3-BS1-R GTAATTAAGACTAGGTACTAATAGTAGTATATAATTCAAGTAGGGGAATAATTCAGGG

pTDH3-BS2-F GGAATTATATACTACTATTAGTACCTAGTCTTAATTTAGGTATTGATTGTAATTCTGTAAAT

pTDH3-BS2-R AAATTAAGACTAGGTACTAATAGTAGTATATAATTCGCTTTTATATACTTATTAGTCAAG

pTDH3-BS3-F AAAATTATATACTACTATTAGTACCTAGTCTTAATTACACCAAGAAGCTTAGTTTCGAATAA

pTDH3-BS3-R GTAATTAAGACTAGGTACTAATAGTAGTATATAATTTTTAAAAGTAAAAAAGACTAACTA

pTDH3-BS4-F AGAATTATATACTACTATTAGTACCTAGTCTTAATTTTTCGAATAAACACACATAAACAAAC

pTDH3-BS4-R AAATTAAGACTAGGTACTAATAGTAGTATATAATTCTAAGTTCTTGGTGTTTTTAAAAGTAA

pTPI1-BS1-F caaAATTATATACTACTATTAGTACCTAGTCTTAATTcattactatttcccttcttctag

pTPI1-BS1-R tgAATTAAGACTAGGTACTAATAGTAGTATATAATTtgaagtcactaaactcctaaa

pTPI1-BS2-F ttAATTATATACTACTATTAGTACCTAGTCTTAATTcaatttttggttgtattctttct

pTPI1-BS2-R gAATTAAGACTAGGTACTAATAGTAGTATATAATTaaaaagattgattagaftaaaaag

pTPI1-BS3-F aaAATTATATACTACTATTAGTACCTAGTCTTAATTctataactacaaaaacatacat

pTPI1-BS3-R gaAATTAAGACTAGGTACTAATAGTAGTATATAATTttaagcaagaaaagaatacaacaa

pTPI1-BS4-F aaAATTATATACTACTATTAGTACCTAGTCTTAATTaaaacacatacaactaaaaATGC

pTPI1-BS4-R ttAATTAAGACTAGGTACTAATAGTAGTATATAATTttagttatagatttaagcaagaaa

pTEF1_up1-F CAATTATATACTACTATTAGTACCTAGTCTTAATTCAAATGTTTCTACTCCTTTTTTAC

pTEF1_up1-R TGAATTAAGACTAGGTACTAATAGTAGTATATAATTGAGCTCCAGCTTTTGTCCCTT

pTEF1_up2-F CCAAATTATATACTACTATTAGTACCTAGTCTTAATTCTTCAAAAACACCAAGCACAGCA

pTEF1_up2-R AGAATTAAGACTAGGTACTAATAGTAGTATATAATTTGGTACGGCGATGCGCGGAGTC

pTEF1_up3-F TAATTATATACTACTATTAGTACCTAGTCTTAATTCTTCTCTAGGGTGTGCTTAATT

pTEF1_up3-R AGAATTAAGACTAGGTACTAATAGTAGTATATAATTAAGAGGGGAAAATTTAGTAGTCT

pTEF1_up4-F AAATTATATACTACTATTAGTACCTAGTCTTAATTTGGTTTGGAAAAGAAAAAGAGACC

pTEF1_up4-R CCAATTAAGACTAGGTACTAATAGTAGTATATAATTTTTAGTACGGGTAATTAACGACAC

pTEF1_up5-F GGAATTATATACTACTATTAGTACCTAGTCTTAATTCAATAAAAAATTTTTATCACGTTTC

pTEF1_up5-R TGAATTAAGACTAGGTACTAATAGTAGTATATAATTCCTTTTTCGACGAAGAAAAAGAA

pTEF1_up6-F AAATTATATACTACTATTAGTACCTAGTCTTAATTTTTGATATTTAAGTTAATAAACGGTC

pTEF1_up6-R CAAAATTAAGACTAGGTACTAATAGTAGTATATAATTTGGGAGGTCATCGAAAGAGAAA
HR_UP-F CGAGATCTTTGTGTTCCG
HR_UP-R TCTCGTATGTCGGCTCTC
HR_DW-F CCACTTTTCAATGAAACG
HR_DW-R GAGGTGGTTATTGATCACC
pTEF1-F CAAGAAGTAGGCGAGAGCCGACATACGAGACAGCTATGACCATGATTACG
pFapR-1 TCATAAGAAATTCGCTTATGAATGTTTTGAACGATACATGTC
pMig1-F CGCTTTGACATGTATCGTTCAAAACATTCAggatctggttctggttctCAAAGCCCATATCCAATGACAC
pMig1-R CTTATTTAATAATAAAAAATCATAAATCATAAGAAATTCGCTCAGTCCATGTGTGGGAAG
tADH1-F GCGAATTTCTTATGATTTATG
tADH1-R CTAGCATATCAATATCCGTTTCATTGAAAAGTGGATAAGAGCGACCTCATGCTATAC
pFapR-2 CGTTAGACACTTGTGTCATTGGATATGGGCTTTGagaaccagaaccagatccTGAATGTTTTGAACGATACATGTC
pRox1-F CGCTTTGACATGTATCGTTCAAAACATTCAggatctggttctggttctAATCCTAAATCCTCTACACCTAAG
pRox1-R CTTATTTAATAATAAAAAATCATAAATCATAAGAAATTCGCTCATTTCGGAGAAACTAGGC
pFapR-R3 GGGTCTTGAATCTTAGGTGTAGAGGATTTAGGATTagaaccagaaccagatccTGAATGTTTTGAACGATACATGTC
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>CANI.Y</i>	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

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56 Sequences of promoters with different BSs for FapR

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

58 TCGAGTTTATCATTATCAATACTGCCATTTCAAAGAATACGTAATAATTAATAGTAGTGATTTTCCTAACTTTATTAGTCAA
59 AAAATTAGCCTTTTAAATTCTGCTGTAACCCGTACATGCCCAAAATAGGGGGCGGGTTACACAGAATATATAACATCGTAGGT
60 GTCTGGGTGAACAGTTTATTCTGGCATTCCACTAAATATAATGGAGCCCGCTTTTAAAGCTGGCATCCAGAAAAAAAAAGAA
61 TCCCAGCACAAAATATTGTTTTCTTACCAACCATCAGTTTATAGGTCCATTCTTTAGCGCAACTACAGAGAACAGGGGCA
62 CAAAACAGGCAAAAAACGGGCACAACCTCAATGGAGTGATGCAACCTGCCTGGAGTAAATGATGACACAAGGCAATTGACCC
63 ACGCATGTATCTATCTCATTTCCTTACACCTTCTATTACCTTCTGCTGATTGGAAAAAGCTGAAAAAAGGTTGAA
64 ACCAGTCCCTGAAATATTCCCTACTTGAATTATATACTACTATTAGTACCTAGTCTTAATTACTAATAAGTATATAAAGAC
65 GGAATTATATACTACTATTAGTACCTAGTCTTAATTAGGTATTGATTGTAATTCTGTAAATCTATTTCTTAAACTTCTTAAAT
66 TCTACTTTTATAGTTAGTCTTTTTTTAGTTTTAAAATTATATACTACTATTAGTACCTAGTCTTAATTACACCAAGAAGCTTAG
67 AATTATATACTACTATTAGTACCTAGTCTTAATTTTCGAATAAACACACATAAAACAAACAAA

68

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

70 CGACACGCAAAAAGAAAACCTTCGAGGTTGCGCACTTCGCCACCCATGAACCACACGGTTAGTCCAAAAGGGGCAGTTCAG
71 ATTCCAGATGCGGAATTAGCTTGCTGCCACCTCACCTACTAACGCTGCGGTGTGCGGATACTTCATGCTATTTATAGACG
72 CGCGTGTGGAATCAGCACGCGCAAGAACCAATGGGAAAAATCGGAATGGGTCCAGAACTGCTTTGAGTGCTGGCTATTGG
73 CGTCTGATTTCCGTTTTGGGAATCCTTTGCCGCGCGCCCTCTCAAAACTCCGCACAAGTCCAGAAAGCGGGAAAGAAATA
74 AAACGCCACAAAAAATAAAAGCCAATCCTCGAAGCGTGGGTGGTAGGCCCTGGATTATCCCGTACAAGTATTCTCA
75 GGAGTAAAAAACCGTTTGTGTTGGAATTCCTTCCGCGCCACCTACGCCGCTATCTTTGCAACAACATCTGCGATAAC
76 TCAGCAAAATTTGCATATTCGTGTTGCAGTATTGCGATAATGGGAGTCTTACTTCCAACATAACGGCAGAAAGAAATGTGAG
77 AAAATTTGCATCCTTGCCTCAATTATATACTACTATTAGTACCTAGTCTTAATTCGTTCAAGTATATAAGTCCGGCAATTA
78 TATACTACTATTAGTACCTAGTCTTAATTGCTTGATAATCTTTCTTCCATCCTACATGTTCTAATTATTCTATTCTCCTTA
79 TTCTTTCAATTATATACTACTATTAGTACCTAGTCTTAATTTCTAACATACCAAGAAAAAATTATATACTACTATTAGTACCTAGT
80 CTTAATTTAATCTTCTGTCATTCGCTTAAACACTATATCAATA

81

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

83 TGTTTAAAGATTACGGATATTTAACTTACTTAGAATAATGCCATTTTTTTGAGTTATAATAATCCTACGTTAGTGTGAGCGGG
84 ATTTAAACTGTGAGGACCTTAATACATTCAGACACTTCTGCGGTATCACCTACTTATTCCCTTCGAGATTATATCTAGGAAC
85 CCATCAGGTTGGTGAAGATTACCGTTCTAAGACTTTTCAGCTTCTCTATTGATGTTACACCTGGACACCCCTTTCTGGCA
86 TCCAGTTTTAATCTTCAGTGGCATGTGAGATTCTCCGAAATTAATTAAGCAATCACACAATTCTCTCGGATACCACCTCGG
87 TTGAAACTGACAGGTGGTTGTACGCATGCTAATGCAAAGGAGCTATATACCTTTGGCTCGGCTGCTGTAACAGGGAATA
88 TAAAGGGCAGCATAATTTAGGAGTTTGTGAACTTGTGAAAATTAATACTACTATTAGTACCTAGTCTTAATTCATTTACTAT
89 TTCCCTTCTACGTAAATATTTTTCTTTTAAATCTAAATCAATCTTTTTAATTATATACTACTATTAGTACCTAGTCTTAATTC
90 AATTTTTGTTGTATTCTTTCTTGCTTAAAAATTATATACTACTATTAGTACCTAGTCTTAATTTCTATAACTACAAAATTAT
91 ATACTACTATTAGTACCTAGTCTTAATTTAAAACACATACATAAACTAAAA

92

93 P_{ADH2} (BS1, 2, 3, 4)
94 CTAACTGATAGTTTATGATCAAAAGGGGCAAAACGTAGGGGCAAAACAAACGGAAAAATCGTTTCTCAAATTTTCTGATGCCAAG
95 AACTCTAACCGAGTCTTATCTAAAAATTGCCTTATGATCCGTCTCTCCGGTTACAGCCTGTGTAAGTATTAATCCTGCCTTTCT
96 AATCACCATTCTAATGTTTAAATTAAGGGATTTTGTCTTCATTAACGGCTTTCGCTCATAAAAAATGTTATGACGTTTTGCCCGC
97 AGGCGGGAAACCATCCACTTACGAGACTGATCTCTCTGCCGAAACACCGGGCATCTCCAATTATAAGTTGGAGAAATAA
98 GAGAATTCAGATTGAGAGAATGAAAAAAAAAAAAAAAAAAGGCAGAGGAGAGCATAAAAAATGGGGTCACTTTTTGGT
99 AAAGCTATAGCATGCCTAAATTATATACTACTATTAGTACCTAGTCTTAATTCACATATAAATAGAGTGCCAATTATATACT
100 ACTATTAGTACCTAGTCTTAATTAGTAGCGACTTTTTACACTCGAAATACTCTTACTACTGCTCTCTTGTGTTTTATCACT
101 TCTGTTTTCTTCTGGTAAATAAATTATATACTACTATTAGTACCTAGTCTTAATGAATAUCAAGCTACAAAAAGCATACAAT
102 AATTATATACTACTATTAGTACCTAGTCTTAATCAACTATCAACTATTAACATATATCGTAATACACA
103

104 P_{MDH2} (BS1, 2, 3, 4)
105 GTACACGTATATAGACATTTTACGTAATGGAGAAAAGTGGGTTTTGTTTTCACTTTTTTCTTTTCACTATTGCTCG
106 AACCGCTGCGATGAGCTAAGAAAAAAGTGAAGAAATCATAGAAAGCAAAATGAGATTATATAGCCAGAGCCCTCT
107 TCTGGCGCTGTCCAAAGCGGACCAACAACAACACTTGCCCAAACCTAAGAAAAATCCCTCATACTTTTCCGTTGTATCTC
108 TACTTTCTTACTTCTTTTTTCTTTTATTTGCTTGGTTCACCATTGAAGTCCATTTTACTACAGACAATAGCTAGTCATT
109 CGCTATCTCCGTTGTCACTTTTTTCAAATTTCTCATCTATATAGCGAAGTACGGAAAAGATGCACTTGCCGGCATCTCGG
110 CCTTCCCGGCCAAATGGACTCATCTACGATACGGCCCTTTAATCCGCAATTACTTTGCCATTCCGGCCGTAGCCGTTCT
111 AAAGCCCGCTGCCTTGCCCAATACTCCCTAATGATCCGGGAAGTCCGGTTTTTCTTTGTTTAGTGGCATTGTTGTG
112 TGCCAAAGGTTGGGAAGTCCGATTTGACTTTAAGGAACACGGAAGGTATCTAAGTCTTAAAAACAATATACACGCGG
113 TGCGTAGATATATAAAGATAAAGAAATTATATACTACTATTAGTACCTAGTCTTAATTTTATCGATATGAGATAAAGATTG
114 TGCATGATTCTCTCTGATTCTTTTTCCCTGTATATAATTTTCTCCAAATTATATACTACTATTAGTACCTAGTCTTAATTCCTTCT
115 GTATAAATCGTACAGTCAGAAGTAGTAATTATATACTACTATTAGTACCTAGTCTTAATTCAGAAATATAGTGTGCAGACTA
116 TTACAAAAGTTCAATACAATATAAATTATATACTACTATTAGTACCTAGTCTTAATTCATAAAAGTTATAGTAAC
117

118 P_{TEF1} (unmodified)
119 CAAAATGTTTCTACTCTTTTTTACTCTTCCAGATTTTCTCGGACTCCGCGCATCGCCGTACCACTTCAAAAACACCCAAGCAC
120 GCATACTAAATTTCCCTCTTTCTTCTCTAGGGTGTGCTTAATTACCCGTAATAAGGTTTGGAAAAGAAAAAGAGACCCG
121 CTCGTTCTTTTCTTCTCGTAAAGGCAATAAAAAATTTTATCACGTTCTTTTTCTGAAAATTTTTTTTTGATTTTTTCT
122 TCTTTCGATGACCTCCATTGATATTAAGTTAATAACGGTCTCAATTTCTCAAGTTTCAGTTTCATTTTTCTGTTCTATTA
123 CAACTTTTTTACTTCTTGTCTATTAGAAAGAAAGCATAGCAATCTAATCTAAGTTTAAATTACAAA
124

125 P_{TEF1} (BSs_UP_1, 2, 3, 4, 5, 6)
126 AATTATATACTACTATTAGTACCTAGTCTTAATTCAAAATGTTTCTACTCTTTTTTACTCTTCCAGATTTTCTCGGACTCCGCG
127 CATCGCGTACCAAAATTATATACTACTATTAGTACCTAGTCTTAATTCCTCAAACACCCAAGCACAGCATACTAAATTTCC
128 CTCTTAATTATATACTACTATTAGTACCTAGTCTTAATTCCTCTAGGGTGTGCTTAATTACCCGTAATAAATTATATA
129 CTACTATTAGTACCTAGTCTTAATTTGGTTTGGAAAAGAAAAAGAGACCGCTCGTTTCTTTTCTCGTAAAGAAATTT
130 ATATACTACTATTAGTACCTAGTCTTAATTCATAAAAAATTTTATCACGTTTCTTTTTCTGAAAATTTTTTTTTGATTTTTT
131 CTCTTTCGATGACCTCCAAATTATATACTACTATTAGTACCTAGTCTTAATTTGATATTTAAGTTAATAAACGGTCTTCAAT
132 TTCTCAAGTTTCAGTTTCATTTTTCTGTTCTATTACAATTTTTTACTTCTTGCTCATTAGAAAGAAAGCATAGCAATCTAAT
133 CTAAGTTTAAATTACAAA
134

135 P_{TEF1} (BSs_A_B_C)²
136 CAAAATGTTTCTACTCTTTTTTACTCTTCCAGATTTTCTCGGACTCCGCGCATCGCCGTACCACTTCAAAAACACCCAAGCAC
137 GCATACTAAATTTCCCTCTTTCTTCTCTAGGGTGTGCTTAATTACCCGTAATAAGGTTTGGAAAAGAAAAAGAGACCCG
138 CTCGTTCTTTTCTTCTCGTAAAGGCAATAAAAAATTTTATCACGTTTCTTTTTCTGAAAATTTTTTTTTGATTTTTTCT
139 TCTTTCGATGACCTCCATTGATATTAAGTTAATAAACGGTCTCAATTTCTCAAGTTTCAGTTTCATTTTTCTGTTCAATTA
140 TATACTACTATTAGTACCTAGTCTTAATTTATTACAATTTTTTACTTCTTGCTCATTAGAAATTATATACTACTATTAGTACC
141 TAGTCTTAATTAAGAAAGCAAAATTATATACTACTATTAGTACCTAGTCTTAATTTAGCAATCTAATCTAAGTTTAAATTACAA
142 A
143

144 Grey regions: integrated binding sites (FapR)
145 NNNNNNNN: TATA box⁴⁻⁸
146 X: TSS⁹
147 ACACCCAAGCAC: UAS in P_{TEF1}¹⁰
148
149
150
151

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