

Supplementary Table 1 List of regulators and environmental conditions examined*

A1	Dat1	Hap3	Met18	Pho4 ¹¹	Sig1 ¹	Swi4	YDR266C
Abf1	Dig1 ^{5,6}	Hap4 ^{2,3}	Met28 ³	Pip2	Sip3	Swi5	YDR520C
Abt1	Dot6	Hap5 ³	Met31 ³	Ppr1	Sip4 ³	Swi6	YER051W
Aca1	Ecm22	Hir1	Met32 ³	Put3 ^{2,3}	Skn7 ^{1,2,7}	Tbs1	YER130C
Ace2	Eds1	Hir2	Met4 ³	Rap1 ³	Sko1	Tec1 ^{5,6}	YER184C
Adr1 ^{3,7}	Fap7	Hir3	Mga1 ¹	Rco1	Smk1	Thi2 ¹²	YFL044C
Aft2 ^{1,2}	Fhl1 ^{1,3,4}	Hms1	Mig1 ⁸	Rcs1 ^{1,2,3}	Smp1	Tos8	YFL052W
Arg80 ³	Fkh1	Hms2	Mig2 ¹	Rdr1	Snf1	Tye7	YGR067C
Arg81 ³	Fkh2 ^{1,2}	Hog1	Mig3	Rds1 ¹	Snt2	Uga3 ^{3,4}	Yhp1
Aro80 ³	Fzf1	Hsf1 ^{1,2,7}	Mot3 ^{1,2,3}	Reb1 ^{1,2}	Sok2 ⁵	Ume6 ¹	YJL206C ^{1,2}
Arr1 ¹	Gal3	lfh1	Msn1	Rfx1	Spt10	Upc2	YKL222C
Ash1 ⁵	Gal4 ^{8,9}	lme1 ¹	Msn2 ^{1,2,4,7,10}	Rgm1	Spt2	Usv1	YKR064W
Ask10	Gal80	lme4 ¹	Msn4 ^{1,2,4,10}	Rgt1 ⁸	Spt23	War1	YLR278C
Azf1	Gat1 ^{3,4,7}	Ino2	Mss11 ⁵	Rim101 ^{1,2}	Srd1	Wtm1	YML081W
Bas1 ³	Gat3	Ino4	Mth1 ⁸	Rlm1 ⁵	Stb1	Wtm2	YNR063W
Bye1	Gcn4 ^{3,4}	lxr1	Ndd1	Rlr1	Stb2	Xbp1 ^{2,7}	Yox1
Cad1 ^{1,3}	Gcr1	Kre33	Ndt80	Rme1	Stb4	Yap1 ^{1,2,7}	YPR022C
Cbf1 ³	Gcr2 ³	Kss1 ^{5,6}	Nnf2	Rox1 ^{1,2}	Stb5	Yap3 ¹	YPR196W
Cha4 ³	Gln3 ^{3,4}	Leu3 ³	Nrg1 ^{1,2}	Rph1 ^{1,2,3}	Stb6	Yap5 ¹	Yrr1
Cin5 ^{1,2}	Gts1	Mac1 ¹	Oaf1	Rpi1	Ste12 ^{5,6}	Yap6 ^{1,2}	Zap1
Crz1	Gzf3 ^{1,4}	Mal13	Opi1	Rpn4 ^{1,2}	Stp1 ³	Yap7 ^{1,2}	Zms1
Cst6	Haa1	Mal33 ^{1,2}	Pdc2	Rtg1 ^{3,4}	Stp2	YBL054W	
Cup9	Hac1	Mbf1	Pdr1 ²	Rtg3 ^{1,2,3,4}	Stp4	YBR239C	
Dal80 ⁴	Hal9	Mbp1 ^{1,2}	Pdr3	Rts2	Sum1	YBR267W	
Dal81 ^{3,4}	Hap1	Mcm1 ^{5,6}	Phd1 ⁵	Sfl1	Sut1	YDR026C	
Dal82 ^{3,4}	Hap2 ⁴	Mds3	Pho2 ^{1,2,3,11}	Sfp1 ^{1,2,3}	Sut2	YDR049W	

¹ Highly hyperoxic

² Mildly hyperoxic

³ Amino acid starved

⁴ Nutrient deprived

⁵ Filamentation

⁶ Mating

⁷ Heat

⁸ Galactose

⁹ Raffinose

¹⁰ Acidic

¹¹ Phosphate deprived

¹² Vitamin deprived

*All regulators were profiled in rich medium. A subset of these were profiled in at least one other environmental condition, as indicated. A complete description of the conditions can be found at the authors' website.

Supplementary Table 2 Similarity of discovered specificities to literature

Regulator	Distance ¹	Discovered	Literature
Abf1	0.143	rTCAYtnnnnAcg	rTCAYTnnnnACGw
Ace2	0.18	tGCTGGT	GCTGGT
Aft2	0.15	rCACCC	ATCTTCAAAAGTGCACCCATTTGCAGGTGC
Azf1	0.203	YwTTkcKkTyckgykky	TTTTTCTT
Bas1	0.045	TGACTC	TGACTC
Cad1	0.089	mTTAsTmAkC	TTACTAA
Cbf1	0.105	tCACGTG	rTCACrTGA
Cin5	0.324	TTAcTAA	TTACTAA
Fkh1	0.123	gtAAAcAA	GGTAAACAA
Fkh2	0.212	GTAAACA	GGTAAACAA
Gal4	0.11	CGGnnnnnnnnnnnCg	CGGnnnnnnnnnnnCCG
Gat1	0.004	aGATAAG	GATAA
Gcn4	0.123	TGAsTCa	ArTGACTCw
Gln3	0.148	GATAAGa	GATAAGATAAG
Hap1	0.191	GGnnaTAnCGs	CGGnnnTAnCGG
Hap4	0.146	gnCcAAtcA	YCNNCCAATNANM
Hsf1	0.198	TTcYnnnnnnTTC	TTCTAGAAAnnTTCT
Ino2	0.236	CAcaTGc	ATTTCACATC
Ino4	0.163	CATGTGaa	CATGTGAAAT
Leu3	0.131	cCGgtacCGG	yGCCGGTACCGGyk
Mbp1	0.073	ACGCGt	ACGCGT
Mcm1	0.181	CCnrAtnngg	wTTCCyAAwnnGGTAA
Msn2	0.308	mAGGGGsgg	mAGGGG
Nrg1	0.042	GGaCCCT	CCCT
Pdr1	0.301	ccGCCgRAwr	CCGCGG
Pho4	0.096	CACGTGs	cacgtkng
Rap1	0.181	cayCCrtrCa	wrmACCCATACAYy
Rcs1	0.184	ggGTGcant	AAmTGGGTGCAkT
Reb1	0.055	TTACCCG	TTACCCGG
Rpn4	0.049	GGTGCCAAA	GGTGCCAAA
Sip4	0.184	CGGnynAATGGrr	yCGAYrrAwGG
Skn7	0.228	GnCnnGsCs	ATTTGGCyGGsCC
Stb5	0.058	CGGnstTAta	CGG
Ste12	0.087	tgAAAC	ATGAAAC
Sum1	0.221	gyGwCAswaaw	AGyGwCACAAAk
Sut1	0.295	gcsGsgnnsG	CGCG
Swi4	0.122	CgCsAAA	CnCGAAA
Swi6	0.214	CGCgaaa	CnCGAAA
Tec1	0.064	CATTCyy	CATTCy
Tye7	0.193	tCACGTGa	CAnnTG
Ume6	0.16	taGCCGCCsa	wGCCGCCGw
Yap1	0.124	TTaGTmAGc	TTAsTmA
Yap7	0.15	mTkAsTmA	TTACTAA
Zap1	0.085	ACCCTmAAGGTyrT	ACCCTAAAGGT

¹Distance from known specificity was computed using the distance metric described in Supplementary Methods.

Supplementary Table 3 Regulator specificities

Regulator	Discovered specificity ¹	Known specificity ^{1,2}	Programs ³
Abf1	rTCAYtnnnnAcg	rTCAYTnnnnACGw	A, C, D, K, M, N
Ace2	tGCTGGT	GCTGGT	K
Adr1		GGrGk	
Aft2	rCACCC	...AAAGTGCACCCATT...	A, C, D, M, N
Arr1		TTACTAA	
Ash1		yTGACTION	
Azf1	YwTTkckKkTyckgykky	TTTTTCTT	N
Bas1	TGACTC	TGACTC	A, K, M, N
Cad1	mTTAsTmAkC	TTACTAA	A, C, D, M, N
Cbf1	tCACGTG	rTCACrTGA	A, C, D, K, M, N
Cin5	TTAcrTAA	TTACTAA	A, C, D
Dal80		GATAA	
Dal81		AAAAGCCGCGGGCGGGATT	
Dal82	GATAAG		D, K
Dig1	TgAAAcA		A, C, D, K, M, N
Fhl1	TGTayGGrtg		A, C, D, K, M, N
Fkh1	gtAAAcAA	GGTAAACAA	A, C, D, K, M, N
Fkh2	GTAAACA	GGTAAACAA	A, C, D, K, M, N
Gal4	CGGnnnnnnnnnnncCg	CGGnnnnnnnnnnnCCG	A, K
Gal80		CGGnnnnnnnnnnnCCG	
Gat1	aGATAAG	GATAA	K
Gcn4	TGAsTCa	ArTGACTIONw	A, C, D, K, M, N
Gcr1		GGCTTCCwC	
Gln3	GATAAGa	GATAAGATAAG	C, D, K
Gzf3		GATAAG	
Hac1		kGmCAGCGTGTC	
Hap1	GGnnaTAnCGs	CGGnnnTAnCGG	C, M
Hap2		CCAAT	
Hap3		CCAAT	
Hap4	gnCcAAtcA	YCNCCCAATNANM	A, C, D, M, N
Hap5		CCAAT	
Hsf1	TTCynnnnnnTTC	TTCTAGAAAnnTTCT	A, C, D, K, M, N
Ime1	AAkGAAAnkwA		A
Ino2	CAcaTGc	ATTTCACATC	C, D, M, N
Ino4	CATGTGaa	CATGTGAAAT	A, C, D, K, M, N
Leu3	cCGgtacCGG	yGCCGGTACCGGyk	A, D, K, M
Mac1		GAGCAAA	
Mbp1	ACGCGt	ACGCGT	A, C, D, K, M, N
Mcm1	CCnrAtnngg	wTTCCyAAwnnGGTAA	A, C, D, M, N
Met31		AAACTGTGG	
Met32		AAACTGTGG	
Met4	RMmAwsTGKSgyGsc		C
Mot3		yAGGyA	
Msn2	mAGGGGsgg	mAGGGG	M
Msn4		mAGGGG	

Regulator	Discovered specificity ¹	Known specificity ^{1,2}	Programs ³
Ndd1	CCnrAwnnGG		A, D
Nrg1	GGaCCCT	CCCT	A, C, D, M, N
Opi1		TCGAAyC	
Pdr1	ccGCCgRAwr	CCGCGG	M
Pdr3		TCCGCGGA	
Phd1	scnGCngg		A, D, N
Pho2	SGTGCGsygyG		N
Pho4	CACGTGs	cacgtkng	D, K, N
Put3		CGGnnnnnnnnnnCCG	
Rap1	cayCCrtrCa	wrmACCCATACAy	A, C, D, M, N
Rcs1	ggGTGcant	AAmTGGGTGCAkT	C, D, M, N
Rds1	kCGGCCGa		D, N
Reb1	TTACCCG	TTACCCGG	A, C, D, K, M, N
Rfx1	TTgccATggCAAC		D
Rgt1		CGGAnnA	
Rim101		TGCCAAG	
Rlm1		CTAwwwTAG	
Rlr1	ATTTTCnnCwTt		N
Rox1		ysyATTGTT	
Rph1		CCCCTTAAGG	
Rpn4	GGTGGCAAA	GGTGGCAAA	A, C, D, K, M, N
Rtg3		GGTCAC	
Sfp1	ayCrtACay		A, C, D, M, N
Sig1	ArGmAwCrAmAA		M
Sip4	CGGnynAATGGrr	yCGGAyrrAwGG	D
Skn7	GnCnnGsCs	ATTTGGCyGGsCC	A, C, D, M, N
Sko1		ACGTCA	
Smp1		ACTACTAwwwTAG	
Snt2	yGGCGCTAyca		A, C, D, M, N
Sok2	tGCagnna		A
Spt2	ymtGTmTytAw		M
Spt23	rAAATsaA		C
Stb1	rracGCsAa		C, D, K, M, N
Stb4	TCGgnnCGA		K
Stb5	CGGnstTata	CGG	D, N
Ste12	tgAAAC	ATGAAAC	A, C, D, K, M, N
Stp1		rCGGCnnnrCGGC	
Sum1	gyGwCAswaaw	AGyGwCACAAAk	A, C, D, M, N
Sut1	gcsGsgnnsG	CGCG	A, D, M
Swi4	CgCsAAA	CnCGAAA	A, C, D, K, M, N
Swi5		kGCTGr	
Swi6	CGCgaaa	CnCGAAA	A, C, D, M, N
Tec1	CATTCyy	CATTCy	C
Thi2	gmAAcyntwAgA		C, D
Tye7	tCACGTGa	CAnnTG	A, C, D, M
Uga3		CCGnnnnCGG	
Ume6	taGCCGCCsa	wGCCGCCGw	A, C, D, K, M, N

Regulator	Discovered specificity ¹	Known specificity ^{1,2}	Programs ³
Xbp1		CTTCGAG	
Yap1	TTaGTmAGc	TTAsTmA	A, C, D, M
Yap3		TTACTAA	
Yap5		TTACTAA	
Yap6		TTACTAA	
Yap7	mTkAsTmA	TTACTAA	A, C, D, M, N
YDR026C	tTACCCGGm		C, D, M, N
Yhp1		TAATTG	
Yox1		YAATA	
Zap1	ACCCTmAAGGTyrT	ACCCTAAAGGT	N

¹Text representation of the probability matrices. Lowercase letters indicate a weaker preference (less information content at that position of the probability matrix). Ambiguity Codes: S = C or G, W = A or T, R = A or G, Y = C or T, K = G or T, M = A or C, n = A, C, G or T.

²Known specificities are taken from the YPD, SCPD, and TRANSFAC databases.

³Program Codes: A = AlignACE, C = CONVERGE, D = MDscan, K = Kellis et al., M = MEME, N = MEME_c.

Supplementary Table 4 Overrepresented MIPS categories among single-regulator architecture binding targets

Regulator	<i>P</i> value ¹	Enriched MIPS category ²
Bas1	6.10e-09	nucleotide metabolism*
Fhl1	1.73e-15	ribosome biogenesis
Gal4	2.18e-04	C-compound and carbohydrate metabolism*
Gat1	4.92e-05	nitrogen and sulfur metabolism*
Gat1	2.63e-02	mRNA transcription*
Gat1	4.38e-02	amino acid metabolism
Gcn4	8.72e-12	amino acid metabolism*
Gzf3	2.21e-02	transport mechanism
Hap3	6.03e-03	lipid, fatty-acid and isoprenoid metabolism
Hap3	1.61e-02	allantoin and allantoate transporters
Hap3	2.50e-02	other energy generation activities
Hap4	3.33e-10	respiration
Hap4	1.78e-05	mitochondrial transport
Hap4	1.03e-02	transport mechanism
Hap4	2.12e-02	assembly of protein complexes
Hsf1	6.58e-06	stress response*
Ino4	5.31e-03	lipid, fatty-acid and isoprenoid metabolism*
Mbp1	1.04e-04	DNA processing
Met32	1.13e-04	amino acid metabolism*
Met32	1.21e-03	nitrogen and sulfur metabolism*
Met32	4.64e-02	amino-acid transporters
Mot3	3.89e-02	DNA processing
Msn2	4.40e-02	metabolism of energy reserves (glycogen, trehalose)
Put3	3.45e-02	other transport facilitators
Reb1	2.09e-05	vesicular transport (Golgi network, etc.)
Rfx1	3.57e-02	other protein-synthesis activities
Rox1	3.43e-02	cell death
Rpn4	2.49e-13	proteolytic degradation*
Rtg3	8.50e-03	other transcription activities
Sig1	2.97e-02	cell cycle
Sip4	2.69e-03	glyoxylate cycle
Sip4	1.57e-02	glycolysis and gluconeogenesis
Stb4	4.02e-02	allantoin and allantoate transporters
Stb5	2.42e-02	electron transport and membrane-associated energy conservation
Ste12	5.56e-03	cell differentiation*
Sut1	5.37e-03	glyoxylate cycle
Swi6	7.96e-03	nitrogen and sulfur metabolism
Thi2	1.15e-02	mRNA transcription*
Thi2	2.45e-02	metabolism of vitamins, cofactors, and prosthetic groups

¹*P* values represent the probability, based on the hypergeometric distribution, of finding the observed number of genes (or more) with the specified MIPS Level 2 category under the null hypothesis that the genes were selected at random. The values have been corrected for testing multiple categories using Bonferroni correction.

²An asterisk (*) indicates that the category is also associated with the regulator itself.

Supplementary Table 5 Regulators with a preference for repetitive motifs

Regulator	<i>P</i> value ¹	Non-repetitive	Repetitive
Dig1	1.43e-08	O: 25 E: 45	O: 38 E: 17
Mbp1	2.99e-08	O: 34 E: 56	O: 44 E: 21
Swi6	7.36e-06	O: 34 E: 50	O: 37 E: 20
Sok2	1.34e-05	O: 13 E: 24	O: 21 E: 9
Bas1	2.84e-04	O: 6 E: 12	O: 12 E: 5
Ste12	5.57e-04	O: 48 E: 62	O: 39 E: 24
Swi4	7.29e-04	O: 27 E: 38	O: 26 E: 14
Phd1	7.89e-03	O: 15 E: 21	O: 15 E: 8
Aft2	9.73e-03	O: 22 E: 29	O: 19 E: 11
Swi5	1.05e-02	O: 11 E: 16	O: 12 E: 6
Sfp1	3.03e-02	O: 7 E: 10	O: 8 E: 4
Ino2	4.77e-02	O: 11 E: 15	O: 10 E: 5

¹*P* values represent the one-tailed probability, based on the chi-square distribution, of finding the observed number of non-repetitive and repetitive motif architecture promoters under the null hypothesis that the distribution for each regulator is the same as the average distribution for all regulators. O = observed number of occurrences; E = expected number of occurrences.

Supplementary Table 6 Co-occurring regulator pairs¹

Ace2, Fkh2	Dig1, Swi4	Mbp1, Stb1	Rlm1, Sko1
Ace2, Swi5	Dig1, Swi6	Mbp1, Swi4	Rox1, Sut1
Aft2, Rcs1	Dig1, Tec1	Mbp1, Swi6	Sip4, Stp1
Arr1, Yap3	Fhl1, Rap1	Mcm1, Ndd1	Skn7, Sok2
Azf1, Gzf3	Fhl1, Sfp1	Mcm1, Ste12	Skn7, Sut1
Bas1, Met4	Fkh1, Fkh2	Mcm1, Swi4	Skn7, Swi6
Cad1, Yap1	Fkh2, Mcm1	Mcm1, Swi6	Skn7, Xbp1
Cad1, Yap7	Fkh2, Ndd1	Mcm1, Tec1	Sko1, Sok2
Cbf1, Met31	Fkh2, Swi6	Met31, Met32	Sok2, Sut1
Cbf1, Met32	Gat1, Spt23	Met31, Met4	Sok2, Swi6
Cbf1, Met4	Gcn4, Gln3	Met32, Met4	Spt23, Yox1
Cbf1, Pho4	Gcn4, Leu3	Mot3, Rox1	Stb1, Swi4
Cbf1, Tye7	Gcr1, Tye7	Mot3, Skn7	Stb1, Swi6
Cin5, Phd1	Gln3, Hap2	Msn2, Msn4	Stb1, Tec1
Cin5, Skn7	Gzf3, Pdr1	Msn4, Nrg1	Ste12, Swi4
Cin5, Sok2	Hap2, Hap3	Nrg1, Rlm1	Ste12, Swi6
Cin5, Sut1	Hap2, Hap4	Nrg1, Skn7	Ste12, Tec1
Cin5, Xbp1	Hap2, Hap5	Phd1, Rox1	Swi4, Swi6
Cin5, Yap6	Hap3, Hap5	Phd1, Skn7	Swi4, Tec1
Dal82, Gat1	Hap4, Hap5	Phd1, Sok2	Swi6, Tec1
Dal82, Gln3	Hsf1, Msn4	Phd1, Sut1	Yap1, Yap7
Dal82, Hap2	Ino2, Ino4	Phd1, Swi6	Yap6, Yap7
Dig1, Mcm1	Ino4, Sko1	Rap1, Sfp1	
Dig1, Ste12	Mac1, Rcs1	Rim101, Yox1	

¹Shown are co-occurring regulator pairs ($P \leq 0.005$). P values represent the probability, based on the hypergeometric distribution, of finding the observed number of intergenic regions (or more) bound by both regulators under the null hypothesis that binding for the two regulators is independent.

Supplementary Table 7 Behaviour classifications of regulators¹

Condition invariant ²	Condition enabled ³	Condition expanded ⁴	Condition altered ⁵
Fhl1	Adr1	Bas1	Adr1
Gal4	Arr1	Cad1	Aft2
Gcn4	Ash1	Cbf1	Cad1
Hsf1	Dal81	Cin5	Cin5
Leu3	Fhl1	Dal82	Dal80
Put3	Gat1	Fkh2	Dal82
Ste12	Hap4	Gal4	Dig1
Ume1	Hsf1	Gcn4	Fkh2
Yap7	Mot3	Gln3	Gat1
	Msn2	Hap2	Gln3
	Pdr1	Mac1	Gzf3
	Phd1	Mbp1	Hap4
	Pho2	Mcm1	Hap5
	Put3	Met31	Mbp1
	Rap1	Met32	Mot3
	Rgt1	Met4	Msn2
	Rim101	Nrg1	Msn4
	Rim1	Rcs1	Phd1
	Rph1	Rds1	Pho4
	Rpn4	Reb1	Reb1
	Rtg3	Rox1	Rox1
	Sfp1	Rpn4	Rtg3
	Sig1	Rtg3	Skn7
	Sip4	Skn7	Ste12
	Sok2	Ste12	Tec1
	Stp1		Ume6
	Thi2		Yap1
	Uga3		Yap6
	Xbp1		
	Yap1		
	Yap7		

¹ The binding of each regulator was compared in pairwise fashion for every environmental condition in which that regulator was profiled. Some regulators fall into multiple categories depending on exactly which conditions are compared.

² The ratio of the overlap of bound probes for a regulator ($P \leq 0.001$) was greater than 0.66 and the ratio of the number of bound probes was between 0.66 and 1.5.

³ Regulator bound to no probes in one environment.

⁴ The ratio of the overlap of bound probes for a regulator was greater than 0.66 and the ratio of the number of bound probes was less than 0.66 or greater than 1.5.

⁵ Regulator bound at least one probe in both environments and the ratio of the overlap of bound probes was less than 0.66.

**Supplementary Table 8. Motif score significance cutoffs
($P \leq 0.001$)**

Number of sequences	Enrichment Score ¹				
	Converge	AlignACE	MDscan	MEME	MEME_c
10	12.70	20.32	11.78	13.54	n/a
20	11.96	21.14	12.95	12.89	9.81
30	11.43	20.43	13.30	12.57	n/a
40	11.34	20.62	14.04	11.64	7.53
50	10.74	19.94	12.23	12.81	7.43
60	10.50	19.71	10.95	12.37	n/a
70	10.34	18.30	13.25	11.34	n/a
80	10.20	19.40	12.84	11.93	n/a
100	9.36	20.31	11.56	10.58	2.91
120	n/a	18.59	13.14	10.94	n/a
140	8.14	18.52	11.26	10.87	n/a
160	n/a	20.04	11.38	9.77	n/a

Number of sequences	ROC a.u.c. ¹				
	Converge	AlignACE	MDscan	MEME	MEME_c
10	n/a	n/a	n/a	n/a	n/a
20	0.812	0.842	0.857	0.925	n/a
30	0.758	0.773	0.793	0.831	0.785
40	0.720	0.713	0.758	0.764	0.737
50	0.687	0.674	0.719	0.737	0.711
60	0.670	0.662	0.688	0.706	0.654
70	0.663	0.641	0.686	0.684	0.664
80	0.643	0.626	0.670	0.675	0.648
100	0.634	0.615	0.664	0.633	0.606
120	0.624	0.604	0.629	0.624	0.602
140	0.608	n/a	0.634	n/a	0.590
160	0.594	0.580	0.613	0.593	0.588

¹Motif score significance $P \leq 0.001$ thresholds for "Enrichment" and "ROC a.u.c." specificity metrics obtained from calculations on randomized selections of intergenic regions as described in Methods. Entries containing "n/a" denote that the empirical distribution was not normal. The threshold for the CC4 metric (4.95) is not dependent on the number of sequences.