

**Supporting Texts for  
"On Statistical Significance of Combinatorial Regulations"  
by Terada, A., Okada-Hatakeyama, M., Tsuda, K., Sese, J.**

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## Supporting Text 1: Mann-Whitney $U$ Test

### Decrease of the minimum $p$ -value with respect to the number of genes in the Mann-Whitney $U$ Test

In this paper, we used Fisher's exact test as the statistical test. LAMP can be applicable to any statistical test as long as it satisfies the following two properties: the existence of a non-zero minimum  $p$ -value and decrease of the minimum value to the number of target genes. Here, we prove that the Mann-Whitney  $U$  test satisfies these properties to show that it can be used in LAMP.

Suppose that we have  $N$  genes and that we know their expression ranks under a specific condition. Given a binding motif combination, the set of genes whose regulatory regions contain all the motifs is defined as  $J$ .  $N$  genes are classified into  $x = |J|$  targeted and  $N - x$  untargeted genes. Mann-Whitney  $U$  is defined as the probability that the ranks achieves more biased than  $J$ .

The  $p$ -value is achieved at the smallest value when expression levels of genes in  $J$  are larger than the others, or they are smaller than the others. The probability to appear the case is described as

$$1 / \binom{N}{x}.$$

This is the minimum  $p$ -value of Mann-Whitney  $U$ .

This value decreases with increase of  $x$  for  $1 \leq x \leq N/2$ , and takes the minimum value when  $x = \lfloor N/2 \rfloor$ , which is non-zero value. Therefore, Mann-Whitney  $U$  can be used in LAMP.

## **Supporting Text 2: Comparison of LAMP with Bonferroni correction with four thresholds**

**Summary of the numbers of significant combinations detected by LAMP and Bonferroni correction with four different thresholds**

We compared LAMP and Bonferroni correction on one yeast and two human datasets with four thresholds that is used to divide the gene expressions in up-regulated and unregulated. Tables in Section A show the summary of the results. Figures in Section B show the number of samples in which at least one significant combination was found. Figures in Section C show the number of significant combinations. The combinations found by the combinations are in Table S1.

### **A. Statistics of the number of significant combinations**

The rows are:

- # of detected samples: The number of samples in which at least one motif combination is significant over all conditions (173 for yeast, 27 for EGF and 28 for HRG).
- # of significant combinations: The sum of the numbers of statistically significant motif combinations over all conditions.
- Maximum arity: The largest arity over all conditions.
- Avg. # of up-regulate genes: The average number of up-regulated genes over all conditions.
- Average, minimum and maximum of  $m'$ : The average, minimum and maximum value of  $m'$  over all conditions.

A. Yeast (The details are in Table S1A)

Threshold (log2 ratio)	0.5	1	1.5	2
Avg. # of up-regulated genes	990.86	363.62	171.36	95.29
# of detected samples	LAMP	157	135	113
	Bonferroni (<=2)	134	111	95
	Bonferroni (<=3)	103	95	71
# of significant combinations	LAMP	513	449	326
	Bonferroni (<=2)	308	264	192
	Bonferroni (<=3)	187	176	108
Stats of LAMP	Maximum arity	3	3	4
	Avg. of $m'$	243.30	366.43	446.30
	Min. of $m'$	132	183	233
	Max of $m'$	554	556	702

B. EGF induced sample (The details are in Table S1B)

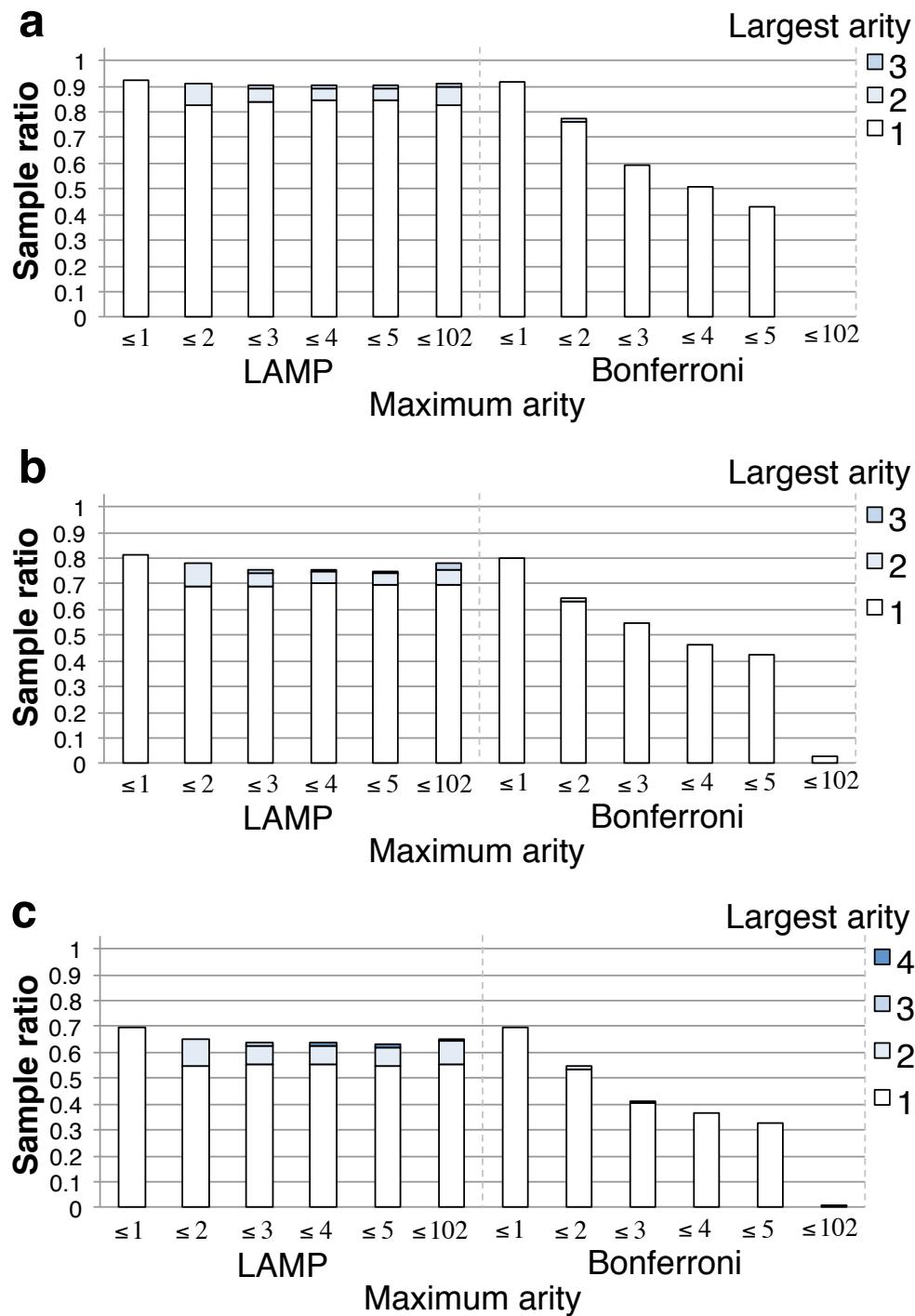
Threshold (log2 ratio)	0.5	1	1.5	2
Avg. # of up-regulated genes	2359.81	1226.67	777.04	491.26
# of detected samples	LAMP	17	20	16
	Bonferroni (<=2)	21	23	22
	Bonferroni (<=3)	8	14	13
# of significant combinations	LAMP	46	43	23
	Bonferroni (<=2)	78	70	41
	Bonferroni (<=3)	20	19	14
Stats of LAMP	Maximum arity	5	8	7
	Avg. of $m'$	1,742,870	3,669,596	5,180,881
	Min. of $m'$	1,459,869	2,700,718	3,750,336
	Max of $m'$	2,700,718	3,750,336	5,238,103

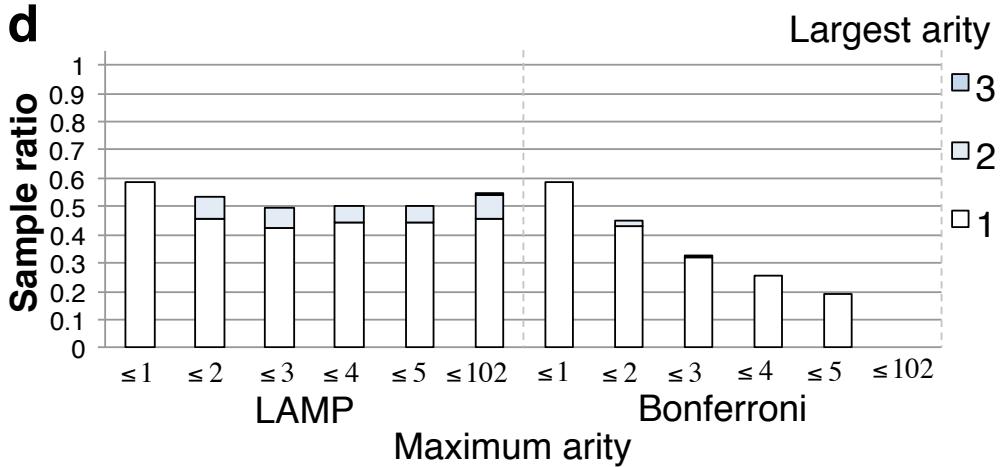
C. HRG induced sample (The details are in Table S1C)

Threshold (log2 ratio)	0.5	1	1.5	2
Avg. # of up-regulated genes	4189.54	2337.36	1277.00	758.68
# of detected samples	LAMP	18	12	10
	Bonferroni (<=2)	25	21	12
	Bonferroni (<=3)	5	6	4
# of significant combinations	LAMP	26	23	16
	Bonferroni (<=2)	40	43	26
	Bonferroni (<=3)	5	7	7
Stats of LAMP	Maximum arity	6	5	5
	Avg. of $m'$	579,531	1,790,220	3,800,657
	Min. of $m'$	359,149	1,174,198	2,874,627
	Max of $m'$	1,174,108	2,874,627	5,542,428
				7,635,557

**B. Comparisons of the numbers of samples in which at least one motif combination is significant between LAMP and Bonferroni correction.**

**B-1. Yeast**



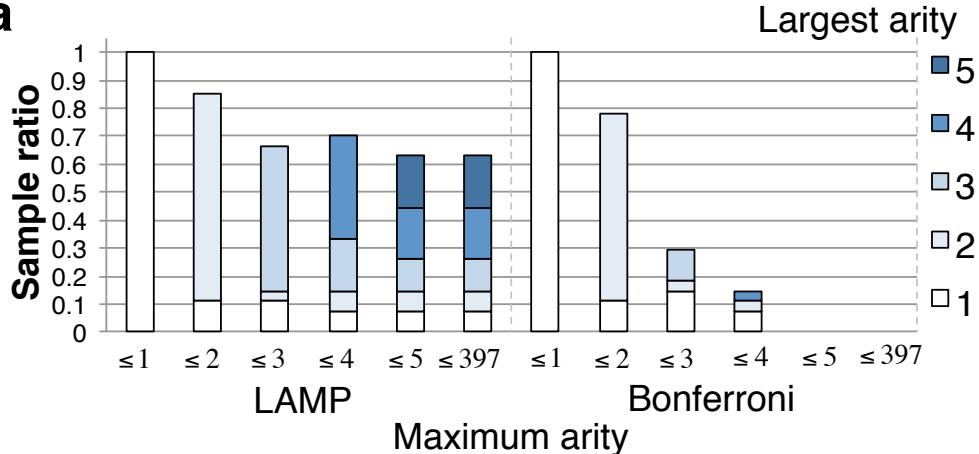


Sample ratios in which at least one motif combination is significant over 173 yeast stress environments. We varied the arity limit and computed the number of samples in which at least one sample was deemed significant for the specified arity limit. The number of motifs we used was 102. The significant level  $\alpha$  was set to 0.05. We also used the Bonferroni correction to compute the motif combinations under three different expression thresholds, which correspond to the data shown in Supporting Table S1. For any threshold, the LAMP found at least one motif combination from at least half the samples even when the arity limit was removed. However, the number of samples detected using the Bonferroni correction decreased with the increasing arity limit, and the Bonferroni correction found significant combinations from only a few samples when the arity limit was removed. The colors indicate the largest arity. The LAMP discovered at most four-motif combinations, whereas the Bonferroni correction found at most two-motif combinations.

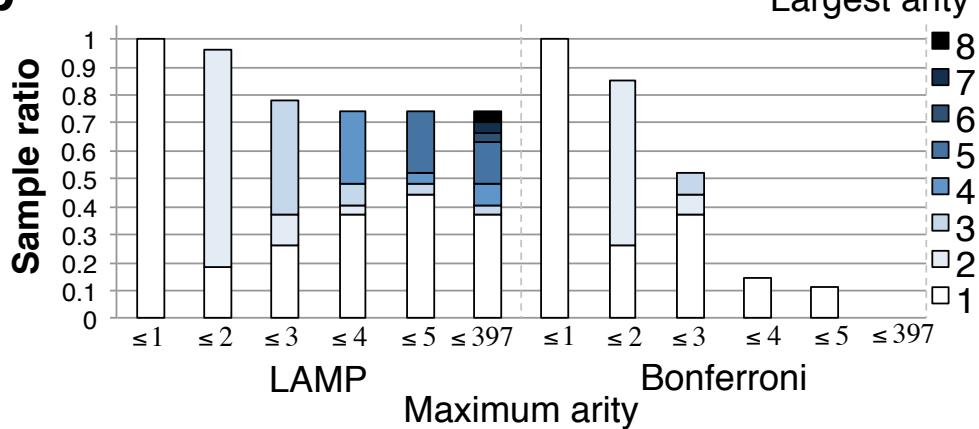
(a) Expression threshold = 0.5. (b) Expression threshold = 1.0. (c) Expression threshold = 1.5. (d) Expression threshold = 2.0.

## B-2. Human MCF-7

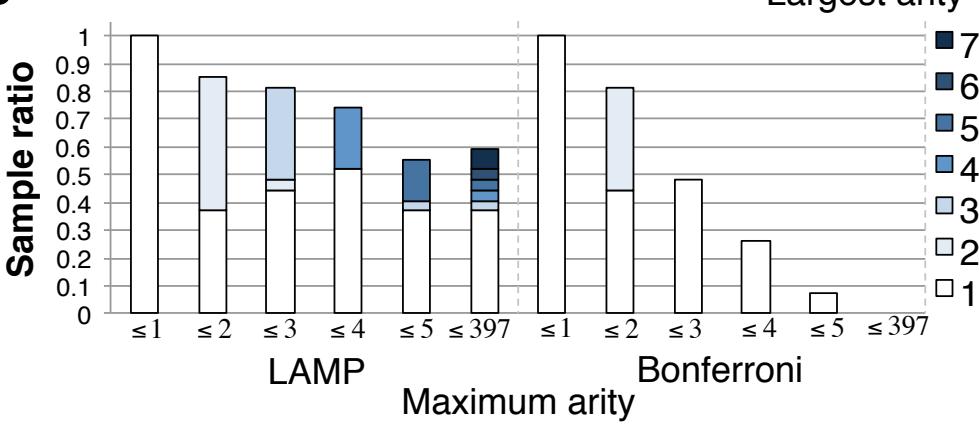
**a**

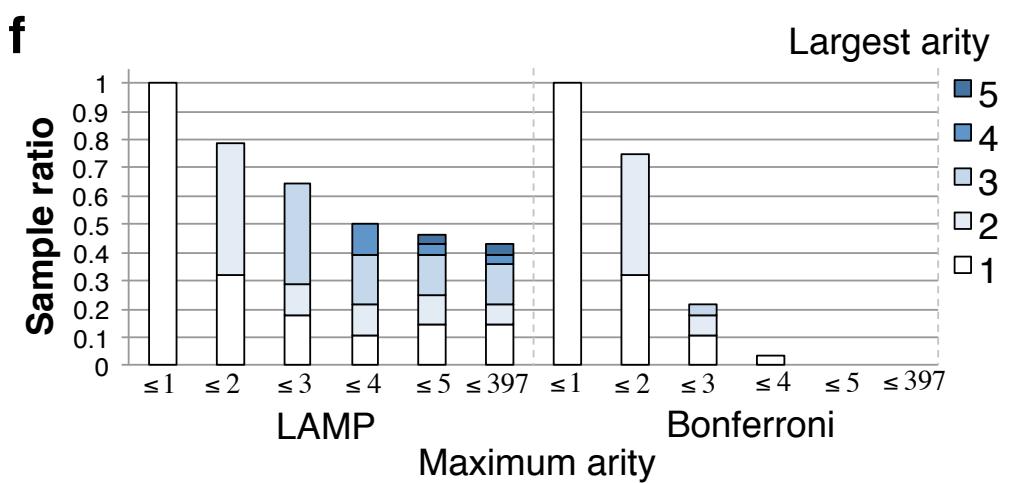
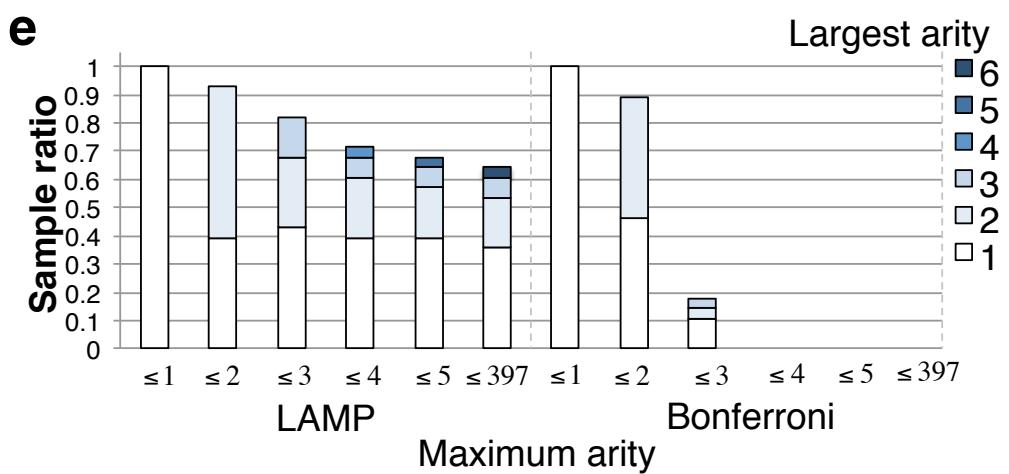
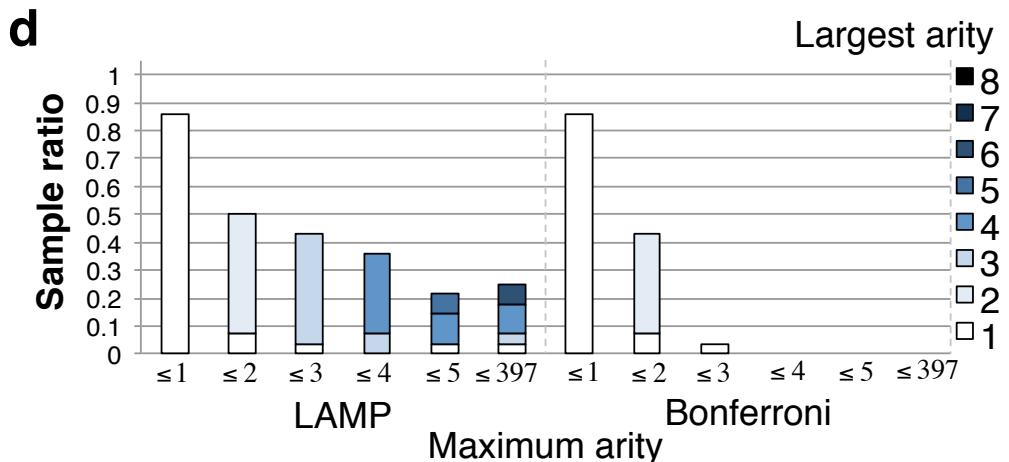


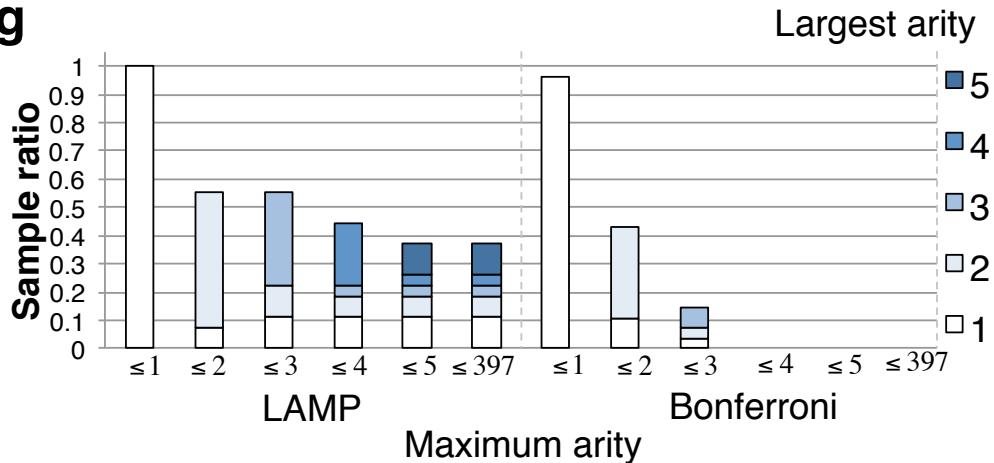
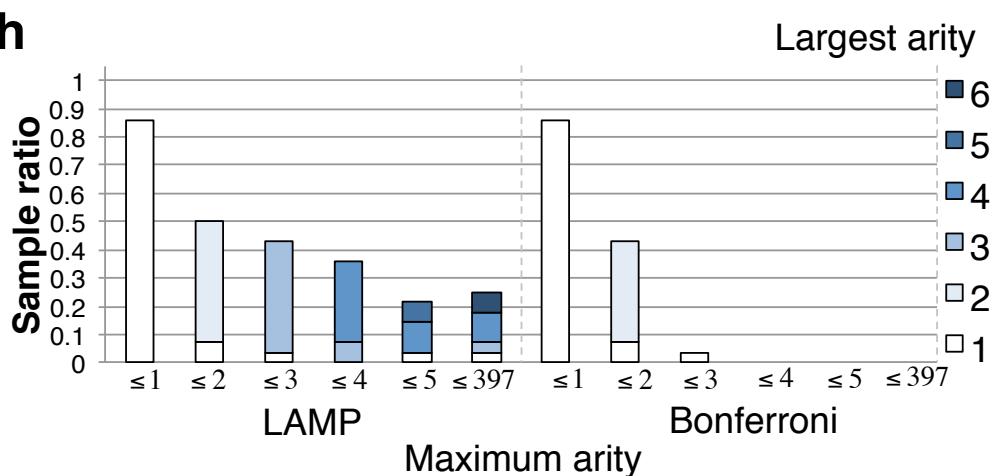
**b**



**c**





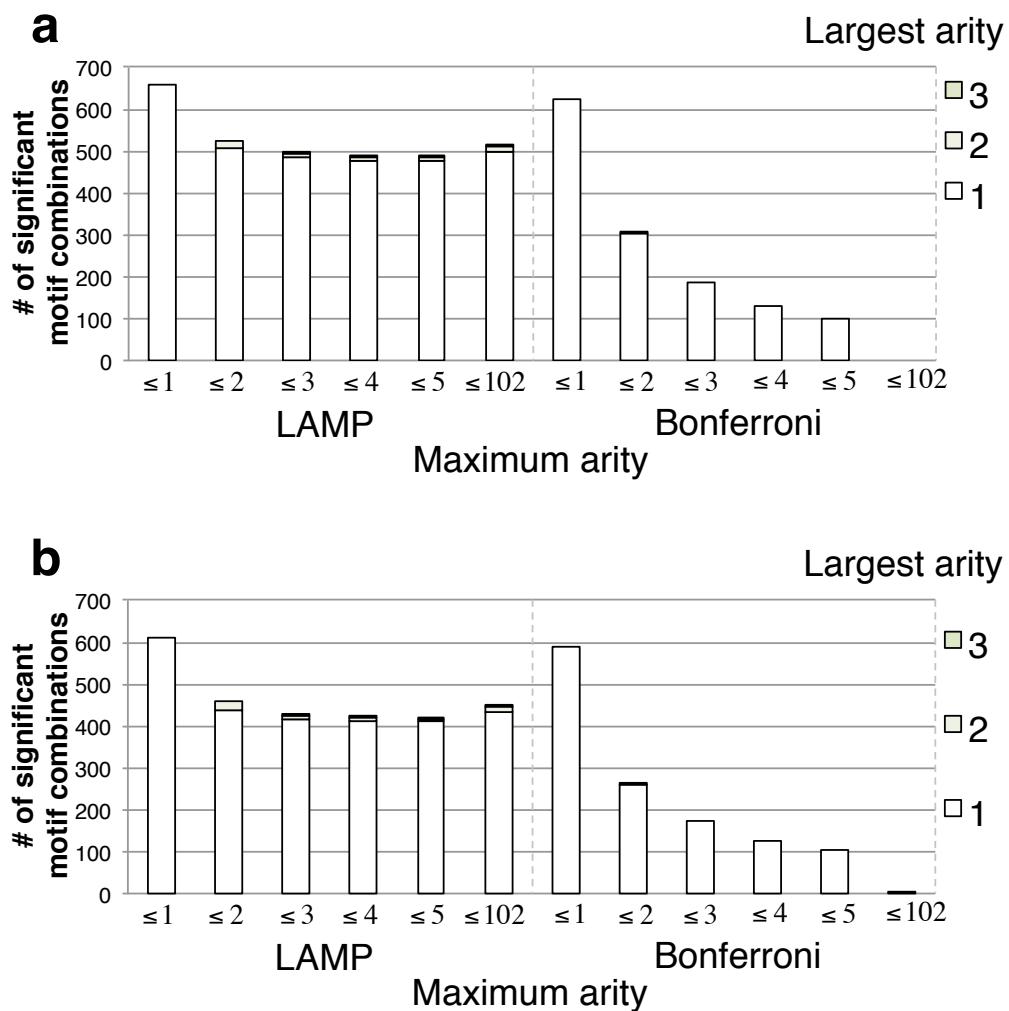
**g****h**

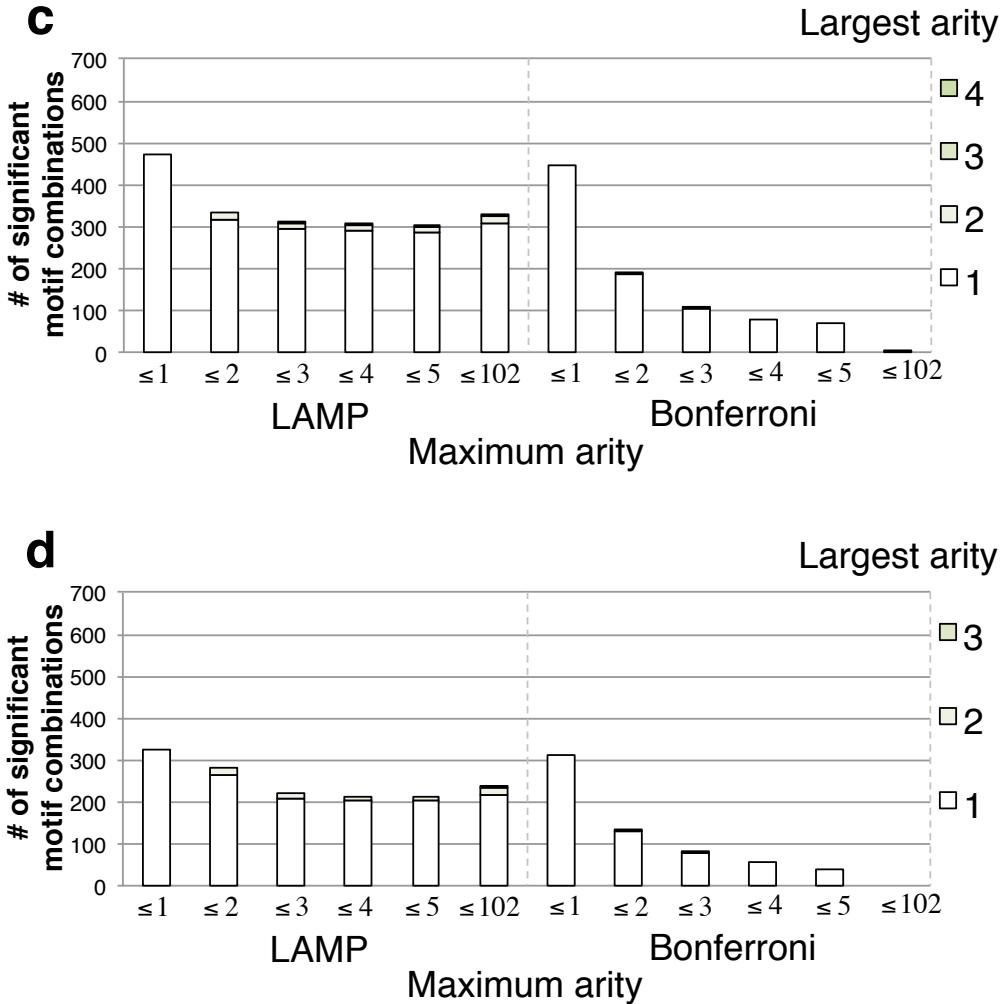
Sample ratios in which at least one motif combination was deemed significant in 27 HRG- and 28 HRG-induced MCF-7 cell samples. We varied the arity limit and computed the number of samples in which at least one sample deemed significant for the specified arity limit. The number of motifs was 397. The significance level  $\alpha$  was set to 0.05. We computed the combinations under three different thresholds for performing Fisher's exact test. The colors indicate the largest arity.

- (a) EGF, expression threshold = 0.5. (b) EGF, expression threshold = 1.0.
- (c) EGF, expression threshold = 1.5. (d) EGF, expression threshold = 2.0.
- (e) HRG, expression threshold = 0.5. (f) HRG, expression threshold = 1.0.
- (g) HRG, expression threshold = 1.5. (h) HRG, expression threshold = 2.0.

**C. Comparison of the numbers of significant combinations between LAMP and Bonferroni correction.**

**C-1. Yeast**

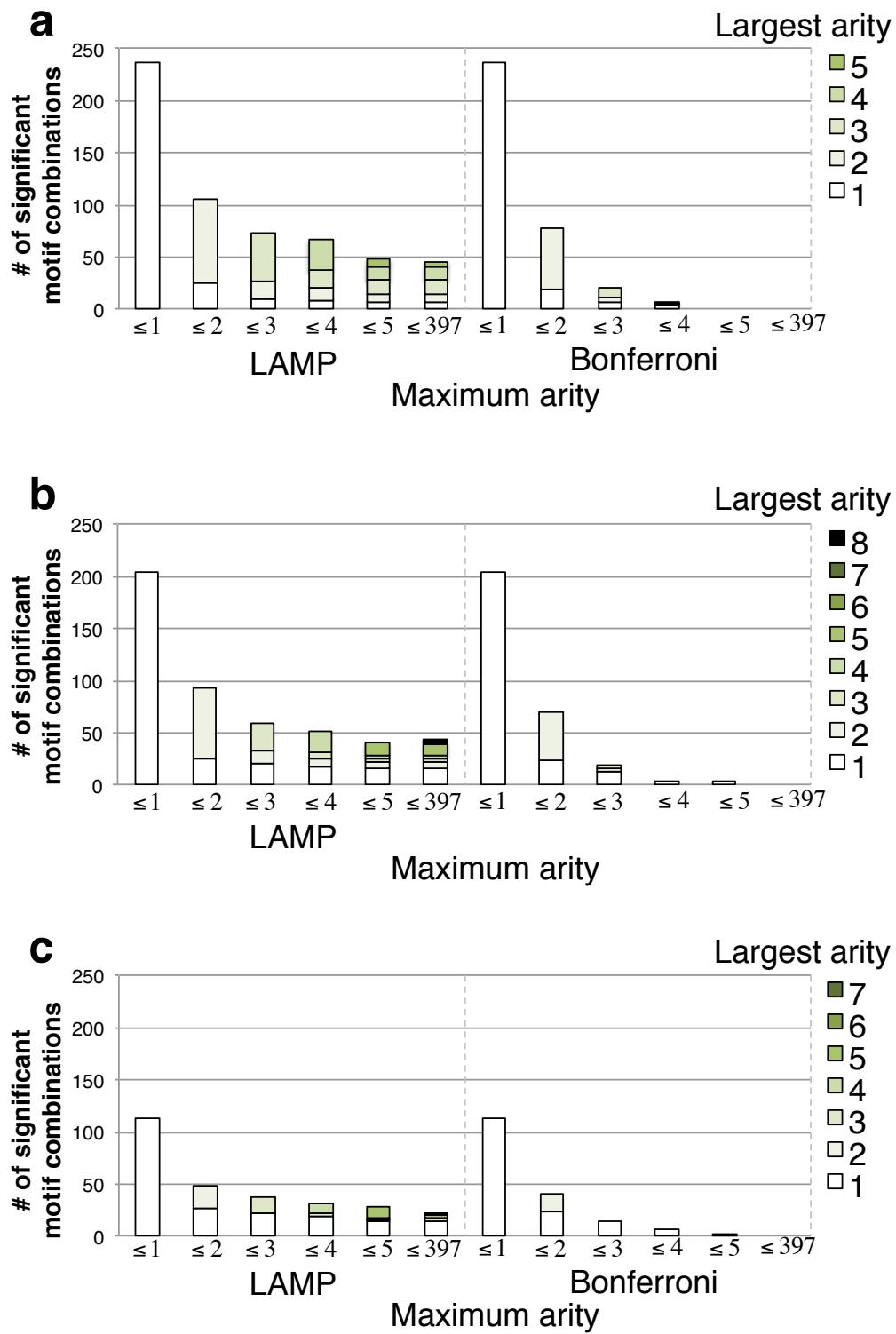


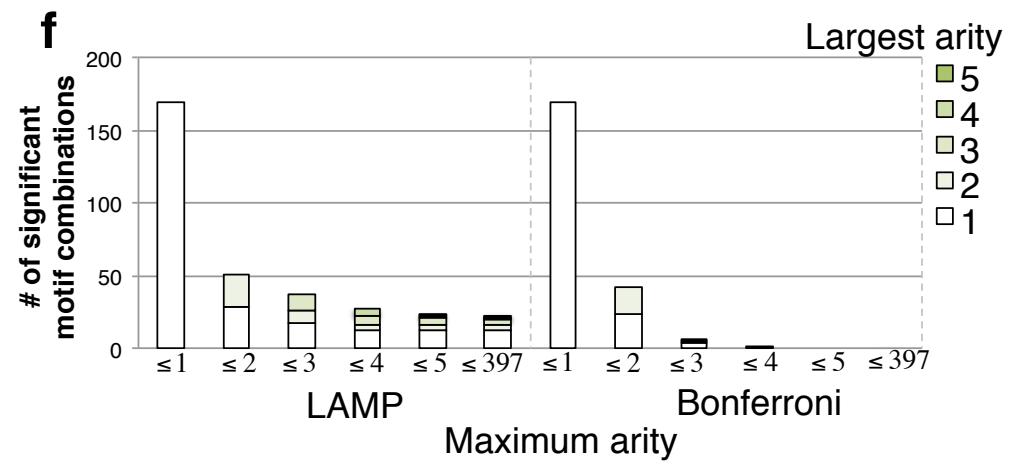
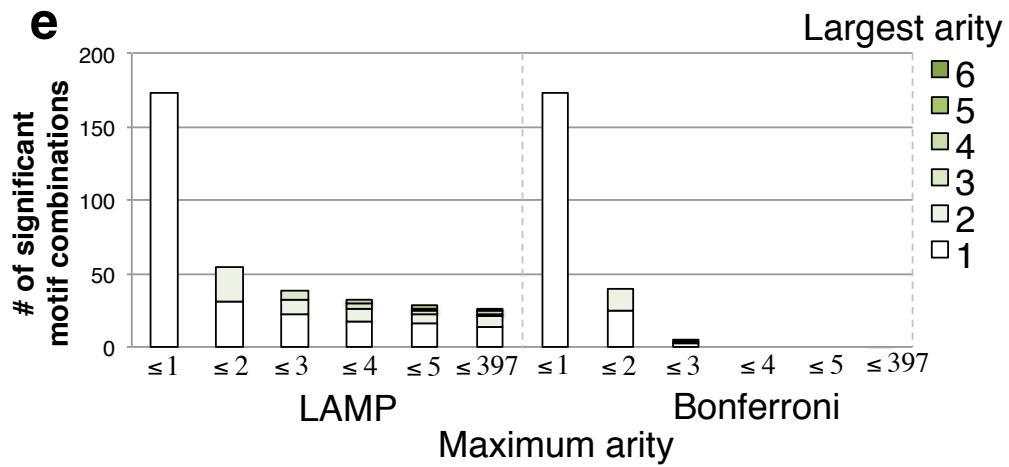
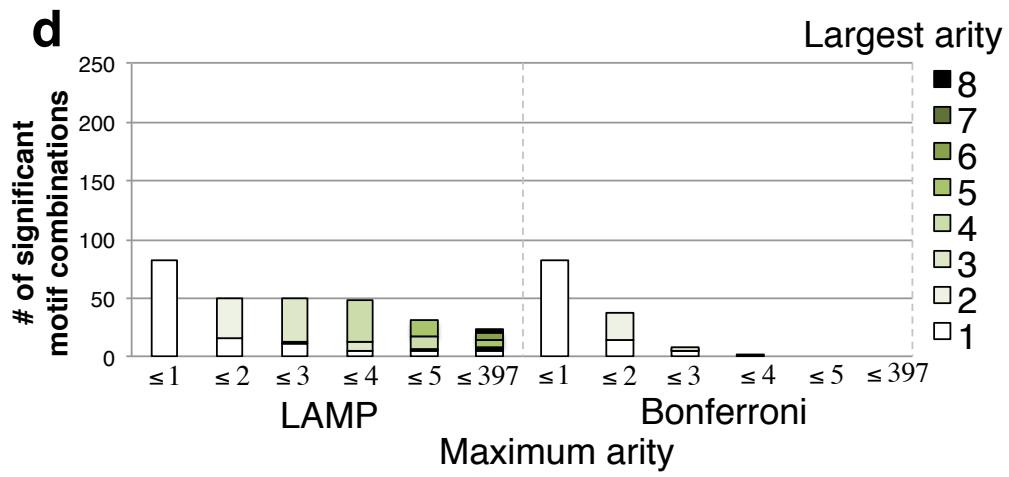


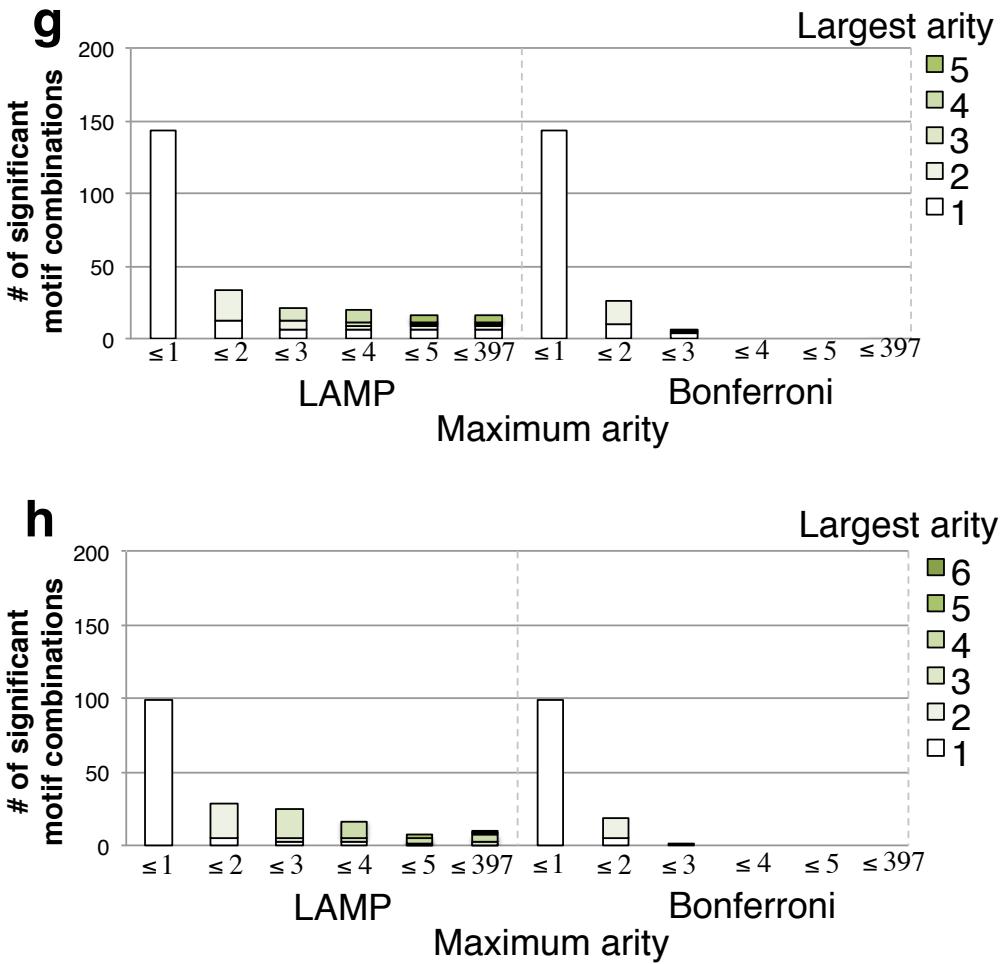
The number of statistically significant motif combinations in the 173 yeast stress environments. Each bar indicates the number of statistically significant motif combinations for a specific arity limit. Within the bar, the colors indicate the largest arity. We computed these combinations under three different expression thresholds for Fisher's exact test. The LAMP found more than 200 motif combinations even when the arity limit was removed, whereas the Bonferroni correction found 9 combinations under any threshold.

(a) Expression threshold = 0.5. (b) Expression threshold = 1.0. (c) Expression threshold = 1.5. (d) Expression threshold = 2.0.

## C-2. Human MCF-7







The number of statistically significant motif combinations in 27 EGF and 28 HRG induced MCF-7 cell samples. Each bar indicates the number of statistically significant motif combinations for the specified arity limit. Within the bar, the colors indicate the largest arity. We computed the combinations under three different thresholds for performing Fisher's exact test. Whereas the Bonferroni correction detected only a few combinations when up to 5-motif combinations were considered, the LAMP found more than 16 combinations, including one 8-motif combination.

- (a) EGF, expression threshold = 0.5. (b) EGF, expression threshold = 1.0.
- (c) EGF, expression threshold = 1.5. (d) EGF, expression threshold = 2.0.
- (e) HRG, expression threshold = 0.5. (f) HRG, expression threshold = 1.0.
- (g) HRG, expression threshold = 1.5. (h) HRG, expression threshold = 2.0.

## Supporting Text 3: Details of the TFs that bind to the motifs in Fig. 4

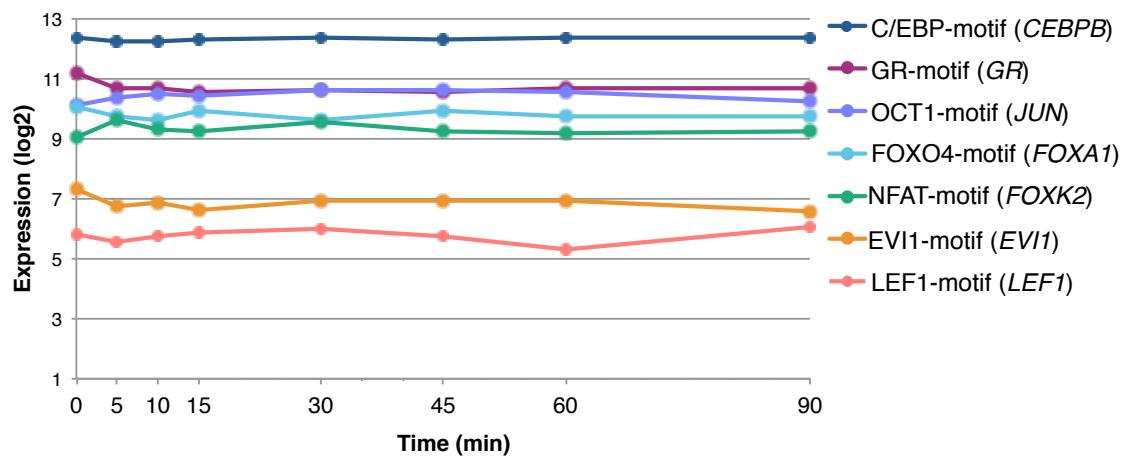
TFs that bind to the motifs in Fig. 4 and their expression levels.

### A. The eight-motif combination

#### A-1. The list of TFs that can bind to the motif

Motif	TFs that bind to the motif
CTTTAAR	-
C/EBP	<i>C/EBP, CEBPB</i>
EVI1	<i>EVI1</i>
FOXO4	<i>FOXA1, FOXA2, FOXO1, FOXO4, HMGA1</i>
GR	<i>GR</i>
LEF1	<i>LEF1</i>
NFAT	<i>ELOF1, FOXK2, NFATC1, NFATC2, NFATC3, NFATC4</i>
OCT1	<i>GATA1, JUN, NFYA, NFYB, NFYC, OCT1, OCT2, SP1</i>

#### A-2. The expression levels of TFs that bind to the motifs.



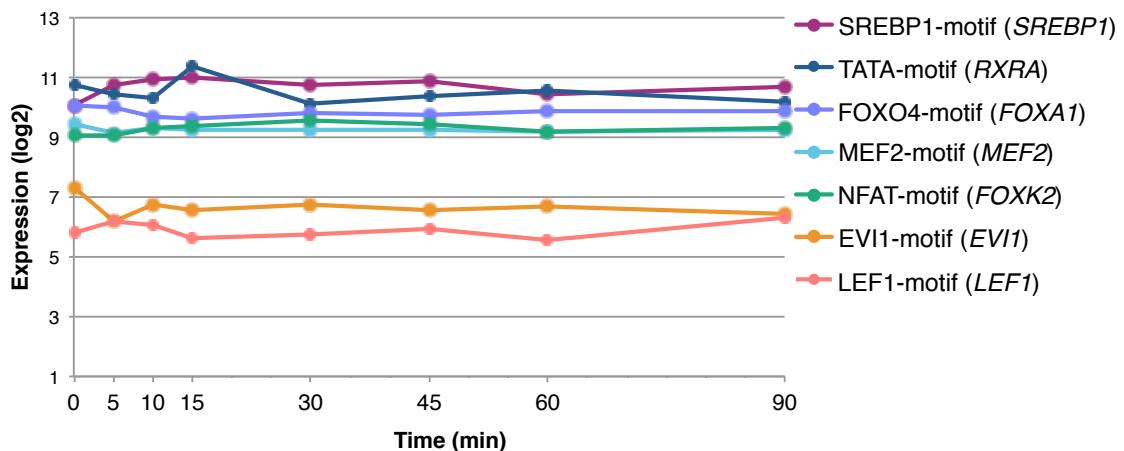
Expression levels of TFs that bind to the motifs in the eight-motif combination. Each line corresponds to one motif and shows the expression levels of a TF that can bind to the motif. When single motif is recognized by multiple TFs, we selected the TF whose expression level under control (0 min) among TFs that can bind to the motif is the highest one. The name on each line is the motif name, and the TF name is in parentheses. For example, since *CEBPB* can bind to the C/EBP-motif and the expression of *CEPB* is higher than that of *C/EBP* at 0 min, the expression levels of *CEPB* are described in the figure as a blue line. When the TF has multiple probes in Affimetrix chip, the probe that has the highest expression level at 0 min is used. The motif "CTTTAAR" is not shown because no TF bound to the motif is identified yet.

## B. The seven-motif combination

### B-1. The list of TFs that can bind to the motifs.

Motif	TFs that bind to the motif
EVI1	<i>EVI1</i>
FOXO4	<i>FOXA1, FOXA2, FOXO1, FOXO4, HMGA1</i>
LEF1	<i>LEF1</i>
MEF2	<i>MEF2, MEF2D</i>
NFAT	<i>ELOF1, FOXK2, NFATC1, NFATC2, NFATC3, NFATC4</i>
SREBP1	<i>SREBP1</i>
TATA	<i>GTF2B, HINFP, RXRA, TBP, THR, TMF1</i>

### B-2. The expression levels of the TFs that bind to the motifs.



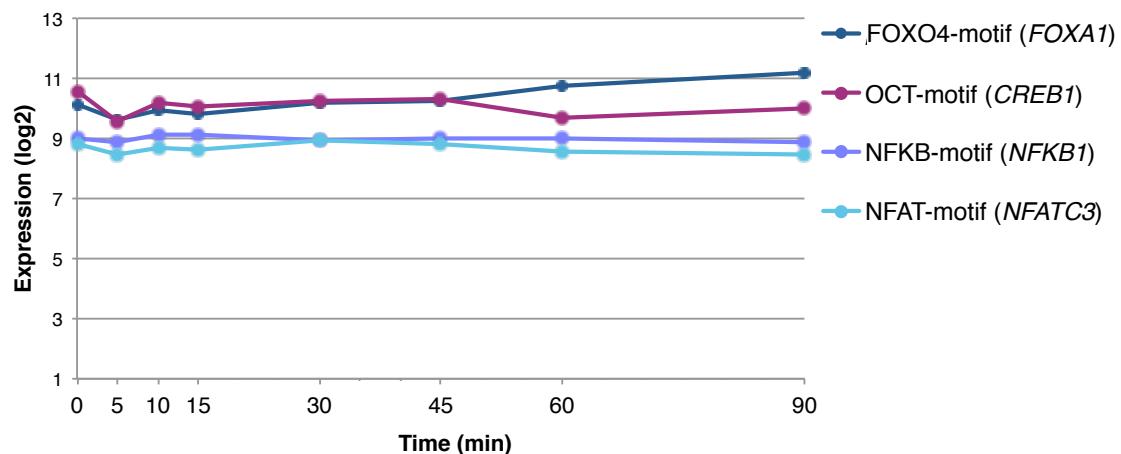
Expression levels of the TFs that bind to the motifs in seven-motif combination. Each line indicates the expression levels of the TF that binds to the motif. If multiple TFs can be bound to the motif, the expression levels of the TF whose expression level at control sample is the highest are shown. The name of the TF is in parentheses.

## C. The five-motif combination

### C-1. The list of TFs that can bind to the motifs

Motif	TFs that bind to the motif
AACTTT	-
FOXO4	<i>FOXA1, FOXA2, FOXO1, FOXO4, HMGA1</i>
NFKB	<i>NFKB1, NFKB2, REL, RELA</i>
OCT	<i>CREB1, GATA1, JUN, NFYA, NFYB, NFYC, POU5F1, POU5F1B, SP1</i>
NFAT	<i>ELOF1, FOXK2, NFATC1, NFATC2, NFATC3, NFATC4</i>

### C-2. The expression levels of the TFs that bind to the motifs.



Expression levels of the TFs that bind to the motifs in the five-motif combination. Each line indicates the expression levels of the TF that binds to the motif. If multiple TFs can be bound to the motif, the expression levels of the TF whose expression level at control sample is the highest are shown. The name of the TF is in parentheses. The motif "AACTTT" is not shown because no TF bound to the motif is identified yet.

#### Supporting Text 4: Monotonicity of the minimum $p$ -value

Our algorithm takes advantage of the fact that the minimum  $p$ -value decreases to its occurrence frequency. In this section, we show the detail of the minimum  $p$ -value.

Suppose that we have  $N$  genes. Only one expression level is available for each of the  $N$  genes. Given a motif combination, the genes are partitioned in two ways. In one way, the genes are classified into  $x$  targeted and  $N - x$  untargeted genes, depending on whether they are targeted by all of the members of the motif combination or not. In the other way, they are classified into  $n_u$  up-regulated genes and  $N - n_u$  unregulated genes. Let  $n$  be the number of genes that are targeted and upregulated.

Using One-sided Fisher's exact test, the  $p$ -value of the motif combination is computed as

$$p = \sum_{n_x=n}^B P(n_x), P(n_x) = \binom{n_u}{n_x} \binom{N-n_u}{x-n_x} / \binom{N}{x},$$

where  $B = \min\{n_u, x\}$ . If we regard that  $n$  is a variable, the minimum value of  $p$  is achieved at  $n = B$ , and described as

$$f'(x) = \binom{n_u}{x} / \binom{N}{x} \text{ (for } x \leq n_u\text{)}, \binom{N-n_u}{x-n_u} / \binom{N}{x} \text{ (for } x > n_u\text{)}.$$

In the most case,  $x \leq n_u$ , and the following Property 1 confirms the monotonicity of the minimum  $p$ -value, which is required to use the function in LAMP. On the other hand, when  $x > n_u$ , the property is not satisfied. Therefore, we define a function which is smaller than the minimum  $p$ -value to satisfy the monotonicity.

**Property 1.** For  $1 \leq x < N/2$  and  $x \leq n_u$ ,  $f'(x) \leq f'(x-1)$  holds.

*Proof.* Between  $x$  and  $x-1$ , the following equation holds:

$$\begin{aligned} \binom{n_u}{x} &= \frac{n_u(n_u-1)\cdots(n_u-x+2)(n_u-x+1)}{x!} \\ &= \frac{n_u-x+1}{x} \frac{n_u(n_u-1)\cdots(n_u-x+2)}{(x-1)!} \\ &= \frac{n_u-x+1}{x} \binom{n_u}{x-1}. \end{aligned}$$

Similarly,

$$\binom{N}{x} = \frac{N-x+1}{x} \binom{N}{x-1}.$$

Based on these equations,

$$\begin{aligned}
f'(x) &= \binom{n_u}{x} / \binom{N}{x} \\
&= \left\{ \frac{n_u - x + 1}{x} \binom{n_u}{x-1} \right\} / \left\{ \frac{N - x + 1}{x} \binom{N}{x-1} \right\} \\
&= \left\{ \frac{n_u - x + 1}{x} / \frac{N - x + 1}{x} \right\} \left\{ \binom{n_u}{x-1} / \binom{N}{x-1} \right\} \\
&= \frac{n_u - x + 1}{N - x + 1} f'(x-1)
\end{aligned}$$

From  $n_u \leq N$ ,  $(n_u - x + 1)/(N - x + 1) \leq 1$ . Hence,  $f'(x) \leq f'(x-1)$ .  $\square$

For  $x > n_u$ , the similar calculation of Property 1 shows that  $f'(x)$  increases to  $x$  monotonically. LAMP requires a monotonically decreasing function to  $x$ , and hence  $f'(x)$  cannot be used as the minimum  $p$ -value directly. Instead of the function, we use

$$f'(x) = 1 / \binom{N}{n_u}$$

as the minimum value since it is smaller than  $f'(x)$  and constant, which means that  $f'$  is a monotonically decreasing function.

By combining these two formulas, the minimum  $p$ -value  $f(x)$  that satisfies the monotonicity is defined as

$$f(x) = \binom{n_u}{x} / \binom{N}{x} \text{ (for } x \leq n_u\text{), } 1 / \binom{N}{n_u} \text{ (for } x > n_u\text{).}$$

## Supporting Text 5: Frequent itemset mining algorithm

### Overview of the frequent itemset mining algorithms

We here provide an overview of frequent itemset mining algorithms. The frequent itemset mining problem is to list all patterns that appear frequently in a data. One typical application of this problem is to find sets of items (itemsets) that customers are likely to purchase on a given trip to the store. The itemset that satisfies the condition is called a frequent itemset. In this study we used the algorithm to list up sets of motifs that share more than  $\lambda$  target genes.

We here introduce how the frequent itemset mining algorithm efficiently lists up the frequent itemsets. For the listing, the following property is used. Given  $k$ -motif combination  $T$  that targets  $x$  genes. Let  $t$  be a motif which is not in  $T$  and let us generate  $T'$  by adding  $t$  to  $T$ . The number of target genes of  $T'$  is smaller or equal to that of  $T$ . From this property, if  $x$  becomes less than  $\lambda$ , the number of target genes of any  $T'$  is less than  $\lambda$ , and hence it guarantees that  $T'$  contains no motif combinations that target  $\lambda$  or more genes.

The frequent itemset mining algorithm generates the motif combinations from lower-arity combinations. It generates all single motifs first, and motifs that target  $\lambda$  or more genes are selected. Let  $\mathbf{L}_1$  be the set of the selected motifs. In LAMP, all motifs in the  $\mathbf{L}_1$  are testable because their bounds of the minimum  $p$ -value are less than the candidate  $p$ -value. Then, the algorithm generates 2-motif combinations by combining two motifs in  $\mathbf{L}_1$  and selects 2-motifs that target  $\lambda$  or more genes. Since the number of target genes of a 2-motif combination is smaller or equal to both single motifs in the 2-motif, we generate the 2-motif only from the motifs in  $\mathbf{L}_1$ . 2-motif combinations that target  $\lambda$  or more genes are stored in  $\mathbf{L}_2$ .

Let  $\mathbf{L}_k$  be the list of  $k$ -motif combinations that target  $\lambda$  or more genes. From the list,  $\mathbf{L}_{k+1}$  can be generated. The itemset mining algorithm repeats this process until  $\mathbf{L}_k$  contains no motif combinations. By combining all  $\mathbf{L}_k$ , all itemsets that target  $\lambda$  or more genes are listed without the generation of entire combinations.

Based on this idea, the first algorithm to efficiently list up the frequent itemsets called *Apriori* was introduced by Agrawal and Shrikant [31]. Han *et al.* [32] introduced more efficient algorithm under large memory environment to list up frequent itemsets, called FP-tree. It generates a tree of items in frequent itemsets, and then lists up the frequent items using the tree. Uno *et al.* [33] proposed a memory efficient algorithm, called LCM. We used the Uno's implementation to find frequent sets of motifs.

## Supporting Figures

Supporting Fig. S1.

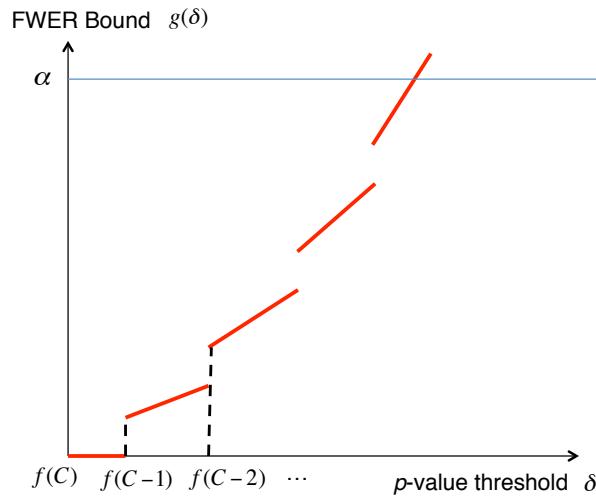


Illustration of the relationship between  $\delta$  and  $g(\delta)$ . The red lines form a piece-wise linear function. The gaps are located at  $f(\lambda)$ , where  $\lambda = C, C - 1, \dots, 1$ .  $\alpha$  is the significance level. The crossing point of the two lines indicates the optimal correction.

Supporting Fig. S2.

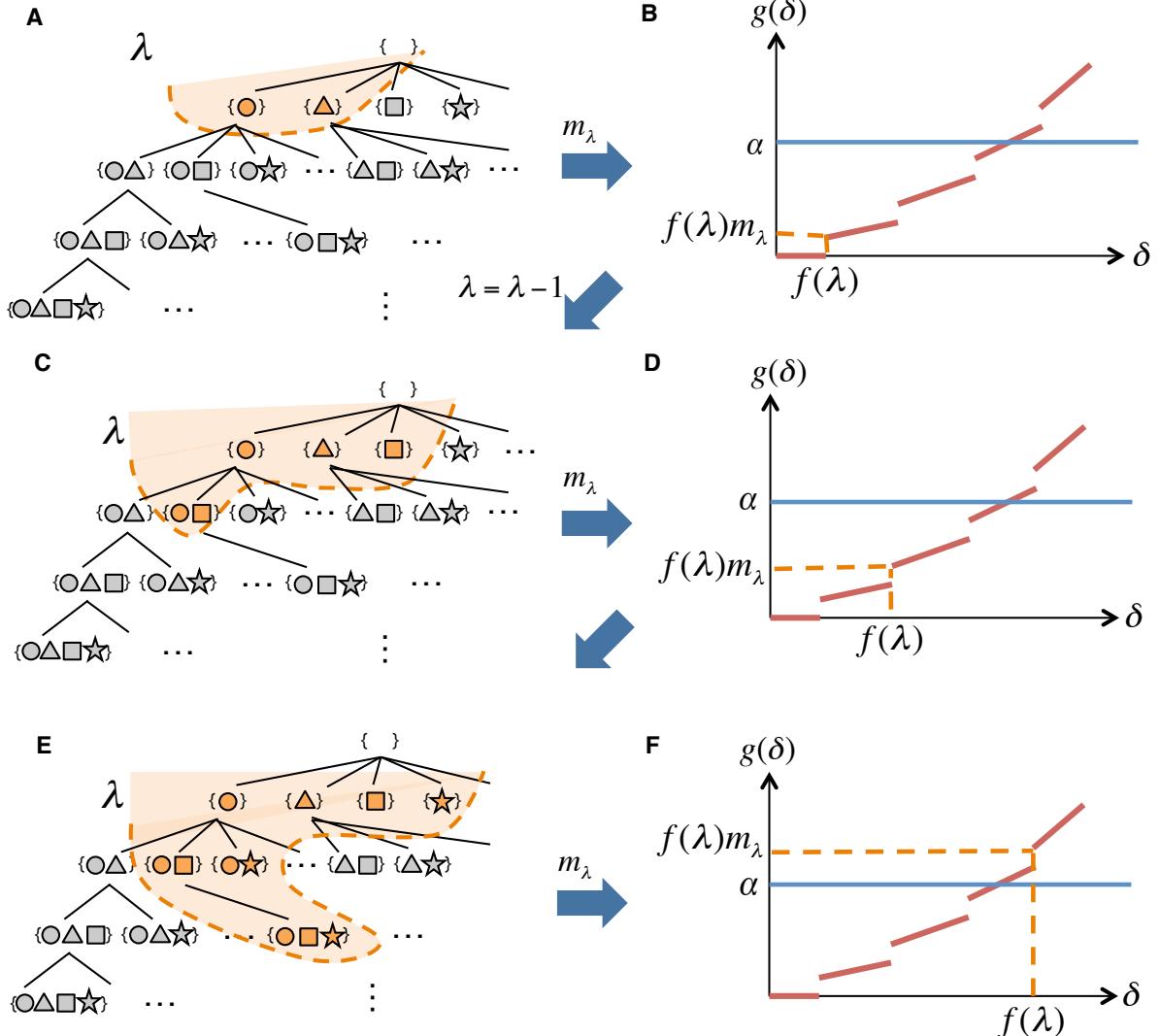


Illustration of the algorithm of the LAMP. (a) Starting from the largest  $\lambda$ , the frequent itemset mining algorithm listed up motif combinations that target  $\lambda$  or more genes. The number of the combinations is  $m_\lambda$ . (b) From  $m_\lambda$  and  $f(\lambda)$ , the FWER bound  $f(\lambda)m_\lambda$  can be calculated. Because the FWER bound is smaller than  $\alpha$  in this figure,  $m_\lambda$  is not sufficiently large to be a corrected significance level. (c) By decreasing  $\lambda$ ,  $m_\lambda$  becomes large. The motif combinations that target  $\lambda$  or more genes were listed up using a frequent itemset mining algorithm.  $m_\lambda$  is computed from the result. (d) If  $f(\lambda)m_\lambda$  is still smaller than  $\alpha$ , we change  $\lambda$  for a smaller value and repeat the process. (e)(f)  $f(\lambda)m_\lambda$  exceeds  $\alpha$ , which indicates that  $f(\lambda)$  is too large to control a FWER less than  $\alpha$ . From the results,  $f(\lambda + 1)$  is the largest value, and  $m_{\lambda+1}$  is the optimal Bonferroni factor.

## Supporting Table

### Supporting Table S1.

#### List of significant motif combinations.

These tables include the statistically significant motif combinations detected by LAMP and the Bonferroni correction. Both results have the possibility to contain significant combinations that do not have higher-arity effect since motif combinations including a very significant motif may become significant even if there is no synergetic effect. To select the significant combinations caused by higher-arity effect, the combinations whose subsets had smaller *p*-value than the original one were removed.

**Supporting Table S1A.** The significant motif combinations in yeast. The yeast gene expression data consist of 173 different stress environments. We computed the combinatorial regulations for each environment. In total 173 experiments were performed. The gene expressions are classified into two groups with three different thresholds: 0.5, 1.0, 1.5 and 2.0. The number of motifs is 102.

**Supporting Table S1B.** The significant motif combinations in EGF-induced cells. This table contains the significant motif combinations from human breast cancer cells that were induced by EGF. The gene expression profiles were obtained from cells treated with four different doses (0.1, 0.5, 1 and 10 nM) of EGF for seven different time points (5, 10, 15, 30, 45, 60 (except 10 nM) and 90 min). The dataset contains 27 samples. We computed the combinatorial regulations for each sample. A gene was considered up-regulated if its log-fold change expressions, as compared to the control condition, was higher than 0.5, 1.0, 1.5 or 2.0. The number of motifs is 397.

**Supporting Table S1C.** The significant motif combinations in HRG-induced cells. This table includes all of the statistically significant motif combinations that were induced by HRG. The gene expression profiles were obtained from cells treated with four different doses (0.1, 0.5, 1 and 10 nM) of HRG for seven different time points (5, 10, 15, 30, 45, 60 and 90 min). Thus, this dataset contains 28 samples. We computed the combinatorial regulations for each sample. A gene was considered up-regulated if its log-fold change expressions, as compared to the control condition, was higher than 0.5, 1.0, 1.5 or 2.0. The number of motifs is 397.

The columns in these tables are:

- Sample: Sample name.
- Motif Combination: Significant motif combinations. “-” indicates that no significant result can be found from the sample.
- Arity: Arity of the motif combination
- # of target genes: The number of genes targeted by the motif combination.

- For each threshold:
  - LAMP ( $m'$ ): The optimized Bonferroni factor used in the LAMP
  - Adjusted  $p$ -value: The adjusted  $p$ -value used by the LAMP. The red numbers indicate that these are significant (adjusted  $p$ -value  $< 0.05$ ). “-” indicates that the combination cannot be found by this condition. The LAMP does not need to limit the maximum arity.
  - Bonferroni ( $\leq S$ ):  $p$ -value adjusted by the Bonferroni correction. The arity limit was varied from 2 to 5. “-” indicates that the combination cannot be found by this condition. For example, if the  $p$ -value of a 3-motif combination cannot be found when the arity limit is 2, then the cell is “-”.

## Supporting Table S1

#### A. Yeast

Environment	Motif Combination	Arity	# of target genes	Adjusted p-value (exp > 0.5)					Adjusted p-value (exp > 1.0)					Adjusted p-value (exp > 1.5)					Adjusted p-value (exp > 2.0)									
				LAMP		Bonferroni			LAMP		Bonferroni			LAMP		Bonferroni			LAMP		Bonferroni							
				m'	Arity limit 2 m=5253	3 176953	4 4426528	5 87718198	m'	Arity limit 2 m=5253	3 176953	4 4426528	5 87718198	m'	Arity limit 2 m=5253	2 176953	3 4426528	4 87718198	m'	Arity limit 2 m=5253	3 176953	4 4426528	5 87718198					
Heat Shock 0 minutes hs-1	HSF1	1	67	221	2.17E-23	5.16E-22	1.74E-20	4.35E-19	8.61E-18	283	1.67E-28	3.11E-27	1.05E-25	2.62E-24	5.19E-23	383	1.67E-25	2.29E-24	7.72E-23	1.93E-21	3.83E-20	383	5.53E-25	7.59E-24	2.56E-22	6.39E-21	1.27E-19	
	MSN2	1	20		2.48E-05	0.00059	0.0199	0.497	>1		0.0326	0.605	>1	>1	>1		0.000269	0.00369	0.124	>1	>1		0.0172	0.236	>1	>1		
	MSN4	1	23		2.63E-05	0.000624	0.021	0.526	>1		0.00114	0.0212	0.714	>1	>1								4.23E-06	5.80E-05	0.00195	0.0489	0.968	
	CIN5	1	46		0.00215	0.0511	>1	>1	>1																			
	PHD1, GCN4	2	5		0.00897	0.213	>1	>1	>1																			
	SKN7	1	65		0.0122	0.289	>1	>1	>1		0.00159	0.0295	0.993	>1	>1		0.000884	0.0121	0.408	>1	>1		0.00262	0.0359	>1	>1	>1	
	NRG1	1	48		0.0171	0.406	>1	>1	>1		0.00101	0.0187	0.629	>1	>1													
	PHD1	1	31		-	-	-	-	-		0.000296	0.00549	0.185	>1	>1		0.0321	0.44	>1	>1	>1							
	SOK2	1	35		-	-	-	-	-		0.00827	0.154	>1	>1	>1													
	SNT2	1	17		-	-	-	-	-		0.0096	0.178	>1	>1	>1													
	MOT3	1	9		-	-	-	-	-		0.024	0.445	>1	>1	>1													
Heat Shock 10 minutes hs-1	HSF1	1	65	222	2.14E-17	5.05E-16	1.70E-14	4.26E-13	8.44E-12	283	1.81E-18	3.36E-17	1.13E-15	2.83E-14	5.61E-13	283	5.30E-21	9.83E-20	3.31E-18	8.28E-17	1.64E-15	378	4.85E-20	6.74E-19	2.27E-17	5.68E-16	1.13E-14	
	MSN2	1	20		5.80E-07	1.37E-05	0.000462	0.0116	0.229		3.14E-06	5.83E-05	0.00196	0.0491	0.973		9.46E-06	0.000176	0.00592	0.148	>1		0.0215	0.299	>1	>1	>1	
	MSN4	1	23		0.00016	0.00378	0.127	>1	>1		2.64E-05	0.00049	0.0165	0.413	>1		5.03E-05	0.000933	0.0314	0.786	>1		1.98E-05	0.000276	0.00929	0.232	>1	
	HAP4	1	25		0.000741	0.0175	0.591	>1	>1																			
	AFT2	1	50		0.00392	0.0928	>1	>1	>1																			
	NRG1	1	47		0.0169	0.399	>1	>1	>1		0.00788	0.146	>1	>1	>1		0.0129	0.239	>1	>1	>1							
Heat Shock 15 minutes hs-1	HSF1	1	61	183	1.07E-10	3.08E-09	1.04E-07	2.60E-06	5.14E-05	221	7.73E-16	1.84E-14	6.19E-13	1.55E-11	3.07E-10	290	6.33E-10	1.15E-08	3.88E-07	9.66E-06	0.000191	379	1.14E-10	1.58E-09	5.33E-08	1.33E-06	2.64E-05	
	MSN4	1	22		0.000627	0.018	0.606	>1	>1		2.70E-05	0.000642	0.0216	0.541	>1		9.23E-05	0.00167	0.0563	>1	>1		1.84E-06	2.56E-05	0.000861	0.0215	0.427	
	MSN2	1	20		0.000687	0.0197	0.664	>1	>1		2.76E-07	6.55E-06	0.000221	0.00552	0.109		8.85E-08	1.60E-06	5.40E-05	0.00135	0.0268		4.85E-07	6.72E-06	0.00227	0.00567	0.112	
	HAP4	1	27		0.00108	0.031	>1	>1	>1																			
	AFT2	1	54		0.0116	0.334	>1	>1	>1		0.00495	0.118	>1	>1	>1		0.0053	0.096	>1	>1	>1							
	RPN4	1	57		0.0374	>1	>1	>1									0.00115	0.0208	0.702	>1	>1							
Heat Shock 20 minutes hs-1	SNT2	1	18		-	-	-	-	-								0.0255	0.461	>1	>1	>1							
	UME6	1	82		-	-	-	-	-								0.0298	0.423	>1	>1	>1							
	HSF1	1	65	176	1.24E-10	3.69E-09	1.24E-07	3.11E-06	6.16E-05	209	3.45E-12	8.68E-11	2.92E-09	7.31E-08	1.45E-06	276	1.37E-07	2.60E-06	8.76E-05	0.00219	0.0434	370	5.12E-09	7.27E-08	2.45E-06	6.13E-05	0.00121	
	MSN2	1	19		0.00129	0.0384	>1	>1	>1		3.92E-07	9.86E-06	0.000332	0.00831	0.165		6.31E-05	0.0012	0.0404	>1	>1		1.67E-06	2.37E-05	0.000799	0.02	0.396	
	AFT2	1	50		0.0112	0.334	>1	>1	>1																			
	RPN4	1	62		0.0142	0.424	>1	>1	>1																			
Heat Shock 30 minutes hs-1	UME6	1	71		0.0152	0.453	>1	>1	>1		0.0306	0.769	>1	>1	>1													
	MSN4	1	22		0.0167	0.497	>1	>1	>1		0.000737	0.0185	0.624	>1	>1		0.00036	0.00685	0.231	>1	>1		0.000159	0.00225	0.0759	>1	>1	
	NRG1	1	47		0.0332	0.991	>1	>1	>1		0.0309	0.777	>1	>1	>1													
	RLM1	1	7		-	-	-	-	-		0.00579	0.145	>1	>1	>1													
	SNT2	1	18		-	-	-	-	-		0.0315	0.792	>1	>1	>1													
	SKO1	1	6		-	-	-	-	-		0.0389	0.979	>1	>1	>1													
Heat Shock 40 minutes hs-1	HSF1	1	65	180	1.89E-08	5.52E-07	1.86E-05	0.000465	0.00922	278	3.09E-09	5.83E-08	1.96E-06	4.91E-05	0.000974	278	5.63E-08	1.06E-06	3.58E-05	0.000896	0.0178	372	1.40E-06	1.97E-05	0.000665	0.0166	0.33	
	MSN2	1	18		0.00041	0.012	0.403	>1	>1		1.69E-06	3.19E-05	0.01018	0.0269	0.534		0.000313	0.00592	0.199	>1	>1		0.000228	0.00322	0.109	>1	>1	
	UME6	1	72		0.0024	0.0699	>1	>1	>1		0.000159	0.0301	0.102	>1	>1													
	MSN4	1	22		0.00284	0.0829	>1	>1	>1		0.00477	0.0901	>1	>1	>1		0.000237	0.00447	0.151	>1	>1		0.00141	0.02	0.673	>1	>1	
	NRG1	1	48		0.0455	>1	>1	>1			0.0162	0.305	>1	>1	>1		0.0247	0.466	>1	>1	>1		0.0314	0.444	>1	>1	>1	
	SNT2	1	17		-	-	-	-	-								0.0386	0.729	>1	>1	>1		0.0246	0.347	>1	>1	>1	
Heat Shock 60 minutes hs-1	HSF1	1	63	292	1.56E-14	2.81E-13	9.45E-12	2.36E-10	4.69E-09	386	5.51E-17	7.50E-16	2.53E-14	6.32E-13	1.25E-11		386	9.27E-16	1.26E-14	4.25E-13	1.06E-11	2.11E-10	533	2.95E-10	2.91E-09	9.80E-08	2.45E-06	4.86E-05
	MSN4	1	22		0.000468	0.00842	0.284	>1	>1		0.0025	0.0341	>1	>1	>1		0.000141	0.00192	0.0647	>1	>1		0.000174	0.0236	0.797	>1	>1	
	MSN2	1	19		0.000587	0.0106	0.356	>1	>1								0.000174	0.00192	0.0647	>1	>1							
	BAS1	1	22		0.000468	0.00842	0.284	>1	>1		0.0025	0.0341	>1	>1	>1													
	HSF1	1	58	201	2.04E-10	5.33E-09	1.79E-07	4.49E-06	8.90E-05	340	2.40E-15	3.71E-14	1.25E-12	3.13E-11	6.20E-10		340	7.60E-14	1.17E-12	3.95E-11	9.89E-10	1.96E-08	468	2.58E-09	2.89E-08	9.74E-07	2.44E-05	0.000483
	MSN4	1	22		0.00578	0.151	>1	>1	>1		0.0301	0.465	>1	>1	>1													
Heat Shock 80 minutes hs-2	FHL1	1	86	239	3.84E-26	8.44E-25	2.84E-23	7.11E-22	1.41E-20	405	1.04E-14	1.35E-13	4.54E-12	1.14E-10	2.25E-09		556	-	-	-	-	-	703	-	-	-	-	-
	SFP1	1	20		3.27E-05																							

37C to 25C shock - 45 min	FHL1	1	88	239	3.43E-18	7.54E-17	2.54E-15	6.35E-14	1.26E-12	404	-	-	-	-	-	404	-	-	-	-	-	554	-	-	-	-	-
37C to 25C shock - 60 min	FHL1	1	88	195	2.33E-24	6.28E-23	2.12E-21	5.30E-20	1.05E-18	305	2.30E-40	3.95E-39	1.33E-37	3.33E-36	6.60E-35	405	2.27E-30	2.95E-29	9.93E-28	2.48E-26	4.92E-25	555	-	-	-	-	-
	SFP1	1	20		2.84E-06	7.64E-05	0.00257	0.0644	>1		5.19E-11	8.94E-10	3.01E-08	7.53E-07	1.49E-05		-	-	-	-	-		0.00504	0.0477	>1	>1	>1
37C to 25C shock - 90 min	RAP1	1	79							405	1.39E-49	1.80E-48	6.07E-47	1.52E-45	3.01E-44	556	0.00586	0.0553	>1	>1	>1	556	-	-	-	-	-
	FHL1	1	88	240	9.58E-26	2.10E-24	7.08E-23	1.77E-21	3.50E-20		6.10E-12	7.91E-11	2.66E-09	6.66E-08	1.32E-06		0.00284	0.0269	0.905	>1	>1		-	-	-	-	-
heat shock 17 to 37, 20 minutes	HSF1	1	68	170	8.03E-09	2.48E-07	8.35E-06	0.000209	0.00414	238	1.38E-14	3.04E-13	1.02E-11	2.56E-10	5.07E-09	306	1.51E-11	2.59E-10	8.72E-09	2.18E-07	4.32E-06	306	1.59E-08	2.73E-07	9.19E-06	0.00023	0.00455
	MSN2	1	21	0.000813	0.0251	0.846	>1	>1		9.96E-08	2.20E-06	7.41E-05	0.00185	0.0367		1.04E-08	1.78E-07	5.99E-06	0.00015	0.00297		1.66E-07	2.85E-06	9.58E-05	0.0024	0.0475	
	HAP4	1	27	0.00723	0.223	>1	>1	>1		0.00106	0.0234	0.789	>1	>1		0.000161	0.00276	0.0931	>1	>1		0.00154	0.0264	0.89	>1	>1	
	MSN4	1	23	0.0371	>1	>1	>1	>1		0.0148	0.327	>1	>1	>1		0.000113	0.00248	0.0836	>1	>1		0.00171	0.0294	0.99	>1	>1	
	AFT2	1	58	-	-	-	-	-		0.0251	0.555	>1	>1	>1		0.0339	0.748	>1	>1	>1		-	-	-	-	-	
	NRG1	1	56	-	-	-	-	-		0.0388	0.852	>1	>1	>1		0.0117	0.202	>1	>1	>1		0.0191	0.328	>1	>1	>1	
	UME6	1	92	-	-	-	-	-		0.0277	0.621	>1	>1	>1		0.00839	0.145	>1	>1	>1		0.0067	0.0878	>1	>1	>1	
	SNT2	1	18	-	-	-	-	-		0.0272	-	-	-	-		-	-	-	-	-		0.0372	0.488	>1	>1	>1	
heat shock 21 to 37, 20 minutes	HSF1	1	70	170	1.23E-13	3.80E-12	1.28E-10	3.20E-09	6.34E-08	239	4.78E-19	1.05E-17	3.54E-16	8.84E-15	1.75E-13	304	1.62E-22	2.81E-21	9.46E-20	2.37E-18	4.69E-17	401	2.43E-17	3.18E-16	1.07E-14	2.68E-13	5.31E-12
	MSN2	1	21	8.98E-06	0.000277	0.00934	0.234	>1		1.22E-08	2.69E-07	9.05E-06	0.000226	0.00449		1.26E-11	2.17E-10	7.31E-09	1.83E-07	3.62E-06		4.70E-07	6.16E-06	0.000208	0.00519	0.103	
	HAP4	1	27	0.000907	0.028	0.944	>1	>1		0.0162	0.356	>1	>1	>1		0.000443	0.00765	0.258	>1	>1		-	-	-	-	-	
	MSN4	1	25	0.000966	0.0299	>1	>1	>1		0.000113	0.00248	0.0836	>1	>1		0.00172	0.333	>1	>1	>1		0.00818	0.107	>1	>1	>1	
	SNT2	1	18	-	-	-	-	-		0.0192	0.374	>1	>1	>1		0.000911	0.0119	0.4	>1	>1		0.0159	0.208	>1	>1	>1	
	SKO1	1	6	-	-	-	-	-		0.00839	0.145	>1	>1	>1		0.00977	0.128	>1	>1	>1		-	-	-	-	-	
heat shock 25 to 37, 20 minutes	HSF1	1	69	167	7.76E-11	2.44E-09	0.22E-08	2.06E-06	4.08E-05	234	3.80E-18	8.52E-17	2.87E-15	7.18E-14	1.42E-12	303	4.41E-24	7.64E-23	2.57E-21	6.44E-20	1.28E-18	403	3.47E-17	4.52E-16	1.52E-14	3.81E-13	7.55E-12
	MSN2	1	21	3.47E-05	0.00109	0.0368	0.921	>1		2.85E-07	6.39E-06	0.000215	0.00539	0.107		7.37E-11	6.46E-10	2.18E-08	5.45E-07	1.08E-05		2.88E-08	3.76E-07	1.27E-05	0.000317	0.00628	
	RPN4	1	64	0.00066	0.0208	0.699	>1	>1		0.000521	0.0117	0.394	>1	>1		0.000532	0.00923	0.311	>1	>1		5.85E-05	0.000763	0.0257	0.643	>1	
	MSN4	1	24	0.008	0.252	>1	>1	>1		0.00567	0.127	>1	>1	>1		0.0277	0.621	>1	>1	>1		0.00919	0.145	>1	>1	>1	
	AFT2	1	57	-	-	-	-	-		0.0249	0.432	>1	>1	>1		0.0164	0.283	>1	>1	>1		0.0272	0.468	>1	>1	>1	
	SNT2	1	18	-	-	-	-	-		0.0249	0.432	>1	>1	>1		0.0117	0.202	>1	>1	>1		0.00705	0.0924	0.311	>1	>1	
	SKO1	1	6	-	-	-	-	-		0.0192	0.34	>1	>1	>1		0.00411	0.712	>1	>1	>1		0.0159	0.208	>1	>1	>1	
	PHD1, SUT1, SOK2, SKN7	4	7	-	-	-	-	-		0.0164	0.283	>1	>1	>1		0.0272	0.468	>1	>1	>1		-	-	-	-	-	
heat shock 29 to 37, 20 minutes	HSF1	1	69	192	1.69E-12	4.62E-11	1.56E-09	3.89E-08	7.71E-07	303	5.01E-18	8.69E-17	2.93E-15	7.33E-14	1.45E-12	303	3.26E-17	5.66E-16	1.91E-14	4.77E-13	9.45E-12	401	2.94E-14	3.85E-13	1.30E-11	3.24E-10	6.43E-09
	MSN2	1	21	1.78E-06	4.87E-05	0.00164	0.041	0.812		7.63E-08	1.32E-06	4.46E-05	0.00112	0.0221		7.01E-08	1.21E-06	4.09E-05	0.00102	0.0203		0.00235	0.0307	>1	>1	>1	
	RPN4	1	63	2.75E-06	7.54E-05	0.00254	0.0635	>1		0.000152	0.00264	0.0889	>1	>1		8.53E-06	0.000148	0.00498	0.125	>1		0.00049	0.00642	0.216	>1	>1	
	MSN4	1	24	0.00417	0.114	>1	>1	>1		0.00395	0.0866	>1	>1	>1		0.0249	0.432	>1	>1	>1		-	-	-	-	-	
	AFT2	1	57	0.00491	0.134	>1	>1	>1		0.00395	0.0686	>1	>1	>1		0.0249	0.432	>1	>1	>1		0.00919	0.145	>1	>1	>1	
	HAP4	1	27	0.0333	0.911	>1	>1	>1		0.0215	0.374	>1	>1	>1		0.00968	0.0168	0.565	>1	>1		0.0159	0.208	>1	>1	>1	
	SNT2	1	18	-	-	-	-	-		0.0411	0.712	>1	>1	>1		0.00776	0.134	>1	>1	>1		0.0164	0.283	>1	>1	>1	
	MOT3	1	12	-	-	-	-	-		0.0419	0.724	>1	>1	>1		0.0468	0.811	>1	>1	>1		0.00977	0.128	>1	>1	>1	
heat shock 33 to 37, 20 minutes	HSF1	1	69	193	1.09E-13	2.96E-12	9.96E-11	2.49E-09	4.94E-08	304	2.37E-11	4.09E-10	1.38E-08	3.45E-07	6.83E-06	402	1.34E-08	1.75E-07	5.89E-06	0.000147	0.00292	402	8.26E-08	1.08E-06	3.63E-05	0.000909	0.018
	MSN2	1	21	2.37E-05	0.000645	0.0217	0.543	>1		0.000221	0.00383	0.129	>1	>1		0.00108	0.0141	0.476	>1	>1		0.0212	0.158	>1	>1	>1	
	RPN4	1	64	0.00026	0.0709	0.239	>1	>1		0.0128	0.221	>1	>1	>1		0.004	0.0523	>1	>1	>1		0.0298	0.389	>1	>1	>1	
	MSN4	1	25	0.000683	0.0186	0.627	>1	>1		0.0299	0.516	>1	>1	>1		0.0419	0.724	>1	>1	>1		-	-	-	-	-	
	MOT3	1	5	-	-	-	-	-		0.0419	0.531	>1	>1	>1		0.00375	0.049	>1	>1	>1		0.00317	0.0414	>1	>1	>1	
heat shock 33C vs. 30C - 30 minutes	HSF1	1	70	237	4.88E-15	1.07E-13	3.60E-12	9.00E-11	1.78E-09	405	1.26E-13	1.63E-12	5.49E-11	1.37E-09	2.72E-08	405	1.92E-12	2.49E-11	8.40E-10	2.10E-08	4.17E-07	556	7.51E-05	0.00071	0.0239	0.598	>1
	MSN4	1	25	1.11E-05	0.000242	0.00815	0.204	>1		1.37E-06	1.77E-05	0.000596	0.0149	0.296		0.000725	0.00941	0.317	>1	>1		3.11E-05	0.000293	0.0988	0.247	>1	
	SKN7	1	21	0.000534	0.0117	0.394	>1	>1		8.56E-05	0.00111	0.0374	0.936	>1		0.00583	0.0756	>1	>1	>1		0.0162	0.153	>1	>1	>1	
	MOT3	1	13	0.0023	0.0503	>1	>1	>1		0.0118	0.153	>1	>1	>1		0.0178	0.23	>1	>1	>1		-	-	-	-	-	
heat shock 33C + 1M + sorbitol - 15 minutes	RPN4	1	64	237	6.47E-07	1.43E-05	0.000483	0.0121	0.239	402	9.50E-08	1.24E-06	4.18E-05	0.0010													

		YAP7, AFT2	2	5	0.0401	0.881	>1	>1	>1	-	-	-	-	-	-	-	-	0.000101	0.00135	0.0455	>1	>1																	
		MSN2	1	21	-	-	-	-	-	-	-	-	-	-	-	-	0.00503	0.0672	>1	>1	>1																		
		MSN4	1	25	-	-	-	-	-	-	-	-	-	-	-	-	0.0125	0.167	>1	>1	>1																		
constant 0.32	mM H2O2 (20 min) redo	YAP7	1	60	192	1.83E-09	5.00E-08	1.68E-06	4.21E-05	0.000834	296	2.03E-11	3.61E-10	1.22E-08	3.04E-07	6.03E-06	393	9.96E-11	1.33E-09	4.48E-08	1.12E-06	2.22E-05	393	0.000147	0.00197	0.0662	>1	>1											
		RPN4	1	63	0.00156	0.0426	>1	>1	>1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-															
		MSN4	1	24	0.00175	0.0478	>1	>1	>1	-	-	-	-	1.23E-05	0.000217	0.00732	0.183	>1	-	-	-	-	-	-	-														
		GCN4	1	121	0.0105	0.288	>1	>1	>1	-	-	-	-	0.0021	0.0373	>1	>1	>1	0.00144	0.0192	0.647	>1	>1	0.00764	0.102	>1	>1	>1											
		YAP1	1	17	-	-	-	-	-	-	-	-	-	-	-	-	0.0193	0.258	>1	>1	>1	0.0108	0.0144	0.485	>1	>1	-	-	-	-									
constant 0.32	mM H2O2 (30 min) redo	YAP7	1	63	193	2.02E-08	5.50E-07	1.85E-05	0.000463	0.00918	294	3.12E-08	5.58E-07	1.88E-05	0.00047	0.00931	392	0.000125	0.00168	0.0565	>1	>1	392	0.00521	0.0699	>1	>1	>1	-	-	-	-							
		RPN4	1	62	5.37E-08	1.46E-06	4.93E-05	0.00123	0.0244	0.000111	0.000303	0.102	>1	>1	4.43E-05	0.000792	0.0267	0.667	>1	-	-	-	-	-	-	-	-	-	-	-									
		MSN2	1	21	0.000585	0.0159	0.536	>1	>1	-	-	-	-	0.022	0.393	>1	>1	>1	0.0411	0.55	>1	>1	>1	0.000543	0.00727	0.245	>1	>1	-	-	-	-							
		HSF1	1	66	0.000655	0.0178	0.6	>1	>1	-	-	-	-	0.000532	0.0095	0.32	>1	>1	1.41E-05	0.000189	0.00635	0.159	>1	9.59E-07	1.29E-05	0.000433	0.0108	0.215	0.013	0.175	>1	>1	>1						
constant 0.32	mM H2O2 (40 min) rescan	RPN4	1	56	176	0.00956	0.285	>1	>1	>1	-	-	-	-	289	-	-	-	-	-	-	-	-	-	377	-	-	-	-	-	-	-	-						
constant 0.32	mM H2O2 (50 min) redo	RPN4	1	64	235	9.28E-07	2.08E-05	0.000699	0.0175	0.347	0.0025	0.00841	0.21	>1	0.0212	0.281	>1	>1	>1	0.0156	0.207	>1	>1	>1	542	-	-	-	-	-	-	-	-						
		MSN4	1	22	1.12E-05	0.00025	0.00841	-	-	-	0.00023	0.00515	0.173	>1	>1	0.00292	0.0388	>1	>1	>1	4.88E-05	0.000648	0.0218	0.546	>1	0.0253	0.245	>1	>1	>1	0.00109	0.0106	0.356	>1	>1	-	-		
		YAP7	1	63	0.00023	0.00515	0.173	>1	>1	-	5.38E-06	7.14E-05	0.0024	0.0601	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-							
		MSN2	1	21	0.000475	0.0106	0.358	>1	>1	-	0.000659	0.00875	0.295	>1	>1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-							
		GCN4	1	124	-	-	-	-	-	-	0.0385	0.511	>1	>1	>1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-								
		YAP1	1	17	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-								
constant 0.32	mM H2O2 (60 min) redo	YAP7	1	60	293	0.0009	0.0161	0.544	>1	>1	395	0.016	0.213	>1	>1	0.00415	0.00552	0.186	>1	>1	539	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-			
		MSN2	1	21	0.0024	0.0429	>1	>1	>1	STB5	1	15	0.0373	0.668	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-								
		GCN4	1	124	-	-	-	-	-	0.0439	0.584	>1	>1	>1	-	-	0.0119	0.158	>1	>1	>1	-	-	-	-	-	-	-	-	-	-	-							
		MSN4	1	22	-	-	-	-	-	-	-	-	-	-	-	-	0.0165	0.162	>1	>1	>1	-	-	-	-	-	-	-	-	-	-	-							
constant 0.32	mM H2O2 (80 min) redo	MSN2	1	19	295	0.00101	0.018	0.608	>1	>1	390	0.0077	0.104	>1	>1	0.00325	0.0318	>1	>1	>1	537	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
		STB5	1	14	0.00848	0.151	>1	>1	>1	YAP7	1	64	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-						
		MSN4	1	25	-	-	-	-	-	0.0322	0.433	>1	>1	>1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-							
		YAP1	1	17	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-							
constant 0.32	mM H2O2 (100 min) redo	BAS1	1	23	292	4.93E-10	8.87E-09	2.99E-07	7.48E-06	0.000148	392	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-					
		MSN4	1	25	0.000125	0.00225	0.0758	>1	>1	MSN2	1	21	0.000172	0.0031	0.104	>1	>1	0.00185	0.0248	0.834	>1	>1	536	-	-	-	-	-	-	-	-	-	-	0.0238	0.234	>1	>1	>1	
		YAP7	1	63	-	-	-	-	-	0.00704	0.0944	>1	>1	>1	-	-	0.00704	0.0944	>1	>1	>1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-			
constant 0.32	mM H2O2 (120 min) redo	MSN2	1	19	288	0.0025	0.0456	>1	>1	>1	383	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-						
		GCN4	1	25	0.0031	0.0565	>1	>1	>1	YAP7	1	62	0.0253	0.461	>1	>1	>1	0.00119	0.0163	0.548	>1	>1	527	-	-	-	-	-	-	-	-	-	-	0.0101	0.101	>1	>1	>1	
		YAP1	1	16	-	-	-	-	-	0.00152	0.0194	>1	>1	>1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-						
		MSN2, MSN4	2	6	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-						
constant 0.32	mM H2O2 (160 min) redo	YAP7	1	63	294	0.00052	0.00929	0.313	>1	>1	391	0.0298	0.401	>1	>1	0.000416	0.00558	0.188	>1	>1	535	-	-	-	-	-	-	-	-	-	-	0.000599	0.00588	0.198	>1	>1	-	-	
		MSN4	1	25	0.00151	0.027	0.91	>1	>1	MSN2	1	20	0.00726	0.13	>1	>1	>1	0.000416	0.00558	0.188	>1	>1	535	-	-	-	-	-	-	-	-	-	-	0.0307	0.302	>1	>1	>1	
		GCN4	1	14	0.00726	0.13	>1	>1	>1	YAP1	1	51	0.0138	0.247	>1	>1	>1	0.000231	0.00307	0.103	>1	>1	535	-	-	-	-	-	-	-	-	-	-	0.00391	0.0384	>1	>1	>1	
		MSN2	1	19	0.0168	0.3	>1	>1	>1	YAP1	1	17	-	-	-	-	-	0.00663	0.088	0.088	>1	>1	535	-	-	-	-	-	-	-	-	-	-	0.0481	0.48	>1	>1	>1	
1 mM Menadiione (10 min) redo	YAP7	1	62	232	2.71E-09	6.13E-08	2.06E-06	5.16E-05	0.00102	401	4.64E-07	8.46E-06	0.000285	0.00713	0.141	391	2.43E-07	3.18E-06	0.000107	0.00268	0.0531	550	0.00018	0.0172	0.579	>1	>1	-	-	-	-	-	-	-	-	-			
		RPN4	1	63	1.66E-05	0.000375	0.0126	0.316	>1	0.000341	0.0255	-	-	-	-	0.000329	0.00431	0.145	>1	>1	401	0.0033	0.0432	>1	>1	>1	-	-	-	-	-	-	-	-	-	-	-		
		MSN2	1	21	0.00841	0.19	>1	>1	>1	GCN4	1	122	0.00156	0.0349	>1	>1	>1	0.00152	0.0199	0.67	>1	>1	401	0.00825	0.108	>1	>1	>1	-	-	-	-	-	-	-	-	-	-	-
		GCN4	1	125	0.0141	0.319	>1	>1	>1	YAP1	1	17	-	-	-	-	0.015	0.196	>1	>1	>1	401	0.00825	0.108	>1	>1	>1	-	-	-	-	-	-	-	-	-	-	-	
		MSN4	1	25	-	-	-	-	-	YAP1	1	17	-	-	-	-	0.014	0.183	>1	>1	>1	401	0.00113	0.015	0.504	>1	>1	-	-	-	-	-	-	-	-	-	-	-	
1 mM Menadiione (40 min) redo	YAP7	1	62	235	2.29E-06	5.12E-05	0.00172	0.0431	0.854	395	5.87E-09	7.80E-08	2.63E-06	6.58E-05	0.0013	395	4.77E-06	6.34E-05	0.00214	0.0534	>1	546	0.0																

redo	MSN2	1	20	-	-	-	-	-	-	0.0076	0.102	> 1	> 1	> 1	-	-	-	-	-	-	-	-	-	-					
2.5mM DTT 0.05 min	FHL1	1	81	268	1.96E-12	3.84E-11	1.29E-09	3.24E-08	6.41E-07	358	-	-	-	-	490	-	-	-	-	-	-	-	-	644	-	-			
2.5mM DTT 0.15 min	-	-	-	258	-	-	-	-	-	492	-	-	-	-	492	-	-	-	-	-	-	-	-	492	-	-			
2.5mM DTT 0.30 min	YAP7	1	54	252	0.0154	0.322	> 1	> 1	> 1	327	0.000306	0.00492	0.166	> 1	> 1	472	0.000273	0.00304	0.103	> 1	> 1	472	-	-	-	-			
	YAP1	1	16	-	-	-	-	-	-	0.00356	0.0572	> 1	> 1	> 1	-	0.000863	0.00961	0.324	> 1	> 1	-	-	-	-	-	0.00427	0.0475	> 1	> 1
	HAP1, YAP1	2	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.00427	0.0475	> 1	> 1	
2.5mM DTT 0.45 min	HSF1	1	67	274	0.0183	0.351	> 1	> 1	> 1	356	-	-	-	-	356	-	-	-	-	-	-	-	-	505	-	-			
	YAP7	1	57	-	-	-	-	-	-	0.0246	0.362	> 1	> 1	> 1	-	0.0201	0.296	> 1	> 1	> 1	-	-	-	-	-	0.00938	0.0975	> 1	> 1
	YAP1	1	16	-	-	-	-	-	-	0.0371	0.548	> 1	> 1	> 1	-	0.0114	0.169	> 1	> 1	> 1	-	-	-	-	-	0.00092	0.00957	0.322	> 1
2.5mM DTT 0.60 min	HSF1	1	59	218	3.68E-05	0.000887	0.0299	0.747	> 1	354	-	-	-	-	354	-	-	-	-	-	-	-	-	487	-	-			
	MSN2	1	18	-	0.0241	0.581	> 1	> 1	> 1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
	STE12	1	97	-	0.0464	> 1	> 1	> 1	> 1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
	YAP7	1	58	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
	YAP1	1	16	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
2.5mM DTT 0.90 min	STE12	1	104	230	0.0021	0.048	> 1	> 1	> 1	380	0.000453	0.00626	0.211	> 1	> 1	380	-	-	-	-	-	-	-	-	536	-	-		
2.5mM DTT 1.20 min	STE12	1	103	229	0.000562	0.0129	0.434	> 1	> 1	288	2.32E-05	0.000424	0.0143	0.357	> 1	385	-	-	-	-	-	-	-	527	-	-			
2.5mM DTT 1.80 min	STE12	1	95	216	0.00202	0.0492	> 1	> 1	> 1	280	0.0272	0.51	> 1	> 1	> 1	372	-	-	-	-	-	-	-	372	-	-			
dtt 0.00 min	FHL1	1	85	235	1.76E-23	3.94E-22	1.33E-20	3.32E-19	6.58E-18	403	3.06E-31	3.99E-30	1.35E-28	3.37E-27	6.67E-26	553	-	-	-	-	-	-	-	553	-	-			
	SFP1	1	20	-	9.18E-06	0.000205	0.00691	0.173	> 1	-	6.69E-13	8.72E-12	2.94E-10	7.35E-09	1.46E-07	-	-	-	-	-	-	-	-	-	-	-	-		
dtt 0.15 min	FHL1	1	86	233	5.48E-21	1.24E-19	4.16E-18	1.04E-16	2.06E-15	398	2.59E-07	3.42E-06	0.000115	0.00288	0.0571	549	-	-	-	-	-	-	-	-	-	-	-	-	-
	SFP1	1	20	-	3.18E-05	0.000717	0.0241	0.604	> 1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-			
dtt 0.30 min	FHL1	1	87	301	2.00E-20	3.50E-19	1.18E-17	2.95E-16	5.84E-15	553	-	-	-	-	-	701	-	-	-	-	-	-	-	701	-	-			
	YAP1	1	17	-	1.12E-08	1.95E-07	5.68E-06	0.000165	0.00326	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-			
	SFP1	1	20	-	2.82E-07	4.93E-06	0.000166	0.00415	0.0823	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-			
	CAD1, YAP7	2	12	-	0.000437	0.00762	0.257	> 1	> 1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-			
dtt 0.60 min	YAP7	1	65	303	0.00167	0.029	0.978	> 1	> 1	553	0.0428	0.406	> 1	> 1	> 1	553	-	-	-	-	-	-	-	553	-	-			
	YAP1	1	17	-	-	-	-	-	-	0.017	0.161	> 1	> 1	> 1	-	-	-	-	-	-	-	-	-	-	-	-	-		
dtt 1.20 min	STE12	1	104	236	5.98E-07	1.33E-05	0.000449	0.0112	0.222	401	-	-	-	-	-	548	-	-	-	-	-	-	-	694	-	-			
	RPN4	1	63	-	0.00855	0.19	> 1	> 1	> 1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-			
	TYE7	1	34	-	0.0161	0.357	> 1	> 1	> 1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-			
	STE12, DIG1	2	58	-	-	-	-	-	-	0.000624	0.00818	0.275	> 1	> 1	-	-	-	-	-	-	-	-	-	-	-	-			
dtt 2.40 min	SKN7	1	73	195	0.00177	0.0476	> 1	> 1	> 1	301	-	-	-	-	-	399	-	-	-	-	-	-	-	550	-	-			
	HSF1	1	70	-	0.0444	> 1	> 1	> 1	> 1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-			
	HAP4	1	26	-	0.0454	> 1	> 1	> 1	> 1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-			
	MSN2	1	21	-	-	-	-	-	-	0.0147	0.256	> 1	> 1	> 1	-	0.00196	0.0258	0.869	> 1	> 1	-	-	-	-	-	-	-	-	
	RLM1	1	9	-	-	-	-	-	-	0.0492	0.858	> 1	> 1	> 1	-	-	-	-	-	-	-	-	-	-	-	-	-		
dtt 4.80 min	SW16	1	88	303	7.06E-11	1.22E-09	4.12E-08	1.03E-06	2.04E-05	398	0.000379	0.00501	0.169	> 1	> 1	548	-	-	-	-	-	-	-	548	-	-			
	SW14	1	66	-	1.55E-09	2.70E-08	9.08E-07	2.27E-05	0.00045	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-			
	TEC1	1	34	-	7.35E-05	0.00127	0.0429	> 1	> 1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-			
	NRG1	1	54	-	0.00822	0.142	> 1	> 1	> 1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-			
	SKN7	1	73	-	0.0287	0.498	> 1	> 1	> 1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-			
	SOK2	1	41	-	0.0301	0.522	> 1	> 1	> 1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-			
	RLM1	1	9	-	-	-	-	-	-	0.00273	0.036	> 1	> 1	> 1	-	-	-	-	-	-	-	-	-	-	-	-			
1.5 mM diamide (5 min)	HSF1	1	70	299	1.17E-20	2.05E-19	6.90E-18	1.73E-16	3.42E-15	399	3.87E-13	5.09E-12	1.72E-10	4.29E-09	8.50E-08	548	0.00503	0.0482	> 1	> 1	> 1	548	-	-					
	YAP7	1	64	-	5.87E-15	1.03E-13	3.47E-12	8.68E-11	1.72E-09	-	6.83E-08	8.99E-07	3.03E-05	0.000758	0.015	-	0.000192	0.00184	0.0621	> 1	> 1	-	-	-	-	-	-		
	MSN4	1	25	-	1.52E-08	2.66E-07	8.97E-06	0.000224	0.00445	-	0.000502	0.00661	0.223	> 1	> 1	-	0.00324	0.0311	0.0367	0.352	> 1	> 1	-	-	-	-	-	-	
	MSN2	1	21	-	1.91E-06	3.35E-05	0.00113	0.0283	0.56	-	5.31E-06	6.99E-05	0.00235	0.0589	> 1	-	-	-	-	-	-	-	-	-	-	-	-	-	
	YAP1	1	17	-	1.53E-05	0.000268	0.00903	0.226	> 1	-	2.38E-05	0.000314	0.0106	0.264	> 1	-	-	-	-	-	-	-	-	-	-	-	-	-	
	SKN7, NRG1	2	8	-	0.00601	0.106	> 1	> 1	> 1	-	0.00706	0.0929	> 1	> 1	> 1	-	-	-	-	-	-	-	-	-	-	-	-		
	STB5	1	15	-	0.00822	0.144	> 1	> 1	> 1	-	0.000204	0.00353	0.119	> 1	> 1	-	0.00445	0.0589	0.0445	0.0192	0.0252	0.848	> 1	> 1	-	-	-	-	
1.5 mM diamide (10 min)	HSF1	1	70	195	3.34E-12	9.01E-11	3.03E-09	7.59E-08	1.50E-06	304	3.59E-22	6.21E-21	2.09E-19	5.23E-18	1.04E-16	401	1.11E-12	1.45E-11	4.89E-10	1.22E-08	2.42E-07	401	1.09E-09	1.43E-08	4.81E-07	1.20E-05	0.000239		
	YAP7	1	64	-	5.97E-11	1.61E-09	5.41E-08	1.35E-06	2.68E-05	-	2.66E-07	3.42E-06	0.000268	0.000226	0.000127	-	0.000262	0.00343	0.116	> 1	> 1	-	-	-	-	-	-		
	HAP4	1	27	-	1.18E-08	3.18E-07	1.07E-05	0.000268	0.00531	-</																			





diauxic shift timecourse 18.5 h	HAP4 RPN4 HSF1 MSN2 MOT3 MSN4	1 26 1 64 1 69 1 20 1 13 1 24	171 3.84E-05 0.00118 0.0397 0.994 >1 0.00648 0.199 >1 >1 >1 -	305 8.52E-07 1.47E-05 0.000494 0.0124 0.245 0.000722 0.0124 0.419 >1 >1 >1 0.00235 0.0405 >1 >1 >1 0.0323 0.557 >1 >1 >1 - - - - -	403 0.005 0.0651 >1 >1 >1 -	403 - - - - - 0.000418 0.00545 0.184 >1 >1 - - - - - - - - - - - - - - - 0.0404 0.526 >1 >1 >1
diauxic shift timecourse 20.5 h	HAP4 HSF1 SOK2 HAP3 MSN2 UME6 SKN7 HAP1	1 26 1 69 1 41 1 13 1 20 1 92 1 72 1 44	238 3.32E-08 7.33E-07 2.47E-05 0.000617 0.0122 1.19E-05 0.000262 0.00883 0.221 >1 0.0011 0.0243 0.818 >1 >1 0.00616 0.136 >1 >1 >1 0.0165 0.365 >1 >1 >1 - - - - - - - - - - - - - - -	304 4.87E-13 8.41E-12 2.83E-10 7.09E-09 1.40E-07 0.0014 0.0242 0.816 >1 >1 - - - - - - - - - - - - - - - 0.00114 0.0198 0.666 >1 >1 0.00617 0.107 >1 >1 >1 0.0414 0.715 >1 >1 >1 - - - - -	400 1.23E-08 1.61E-07 5.42E-06 0.000136 0.00269 - - - - - - - - - - - - - - - 0.027 0.355 >1 >1 >1 - - - - - - - - - - 0.0103 0.135 >1 >1 >1 - - - - -	400 0.00021 0.00276 0.0929 >1 >1 - 0.00521 0.0684 >1 >1 >1 0.000802 0.0105 0.355 >1 >1
YPD 2 h ypd-2	BAS1	1 24	235 0.0487 >1 >1 >1 >1 8.00E-05 0.00178 0.06 >1 >1 0.0167 0.372 >1 >1 >1	401 - - - - - - - - - - - - - - -	550 - - - - - - - - - - - - - - -	550 - - - - - - - - - - - - - - -
YPD 4 h ypd-2	HAP4 BAS1 MSN2	1 26 1 24 1 20	236 4.39E-07 9.76E-06 0.000329 0.00823 0.163 8.00E-05 0.00178 0.06 >1 >1 0.0167 0.372 >1 >1 >1	402 5.44E-08 7.11E-07 2.39E-05 0.000599 0.0119 0.00129 0.0169 0.57 >1 >1 - - - - -	552 0.000624 0.00594 0.2 >1 >1 0.00965 0.0918 >1 >1 >1 - - - - -	552 - - - - - - - - - - - - - - -
YPD 6 h ypd-2	HAP4 MSN2 HSF1 MSN4	1 25 1 19 1 70 1 24	132 0.000404 0.0161 0.541 >1 >1 0.00636 0.253 >1 >1 >1 - - - - - - - - - -	193 1.66E-05 0.000452 0.0152 0.381 >1 0.0127 0.346 >1 >1 >1 0.0426 >1 >1 >1 - - - - -	233 7.36E-08 1.66E-06 5.59E-05 0.0014 0.0277 0.00563 0.127 >1 >1 >1 0.0148 0.334 >1 >1 >1 0.000369 0.00833 0.28 >1 >1 - - - - -	301 0.000195 0.00339 0.114 >1 >1 0.00594 0.104 >1 >1 >1 0.00813 0.142 >1 >1 >1
YPD 8 h ypd-2	HAP4 AFT2 HAP2 MSN2 SKN7 HAP3 YAP7 SUT1 MSN4 HAP1 CIN5	1 25 1 56 1 19 1 19 1 73 1 13 1 64 1 15 1 24 1 42 1 51	150 2.49E-05 0.000871 0.0294 0.734 >1 0.0195 0.682 >1 >1 >1 0.0438 >1 >1 >1 >1 0.0438 >1 >1 >1 >1 - - - - - - - - - -	236 2.03E-07 4.51E-06 0.000152 0.0038 0.0754 0.00013 0.029 0.0977 >1 >1 0.000751 0.0167 0.563 >1 >1 0.000751 0.0167 0.563 >1 >1 0.0198 0.0441 >1 >1 >1 0.0216 0.048 >1 >1 >1 0.00988 0.222 >1 >1 >1 0.0156 0.347 >1 >1 >1 0.0268 0.598 >1 >1 >1 - - - - - - - - - -	304 4.57E-10 7.89E-09 2.66E-07 6.65E-06 0.000132 0.0026 0.449 >1 >1 >1 0.00329 0.0569 >1 >1 >1 0.00329 0.0569 >1 >1 >1 0.0318 0.549 >1 >1 >1 - - - - - - - - - -	304 2.66E-12 4.60E-11 1.55E-09 3.87E-08 7.68E-07 0.00565 0.0976 >1 >1 >1 0.00565 0.0976 >1 >1 >1 -
YPD 10 h ypd-2	HAP4 SOK2 SKO1 MSN2 SKN7 UME6 MSN4 NRG1	1 26 1 39 1 6 1 20 1 73 1 94 1 25 1 54	168 2.96E-06 9.25E-05 0.00312 0.0779 >1 0.000126 0.00393 0.132 >1 >1 - - - - - - - - - -	233 2.86E-10 6.44E-09 2.17E-07 5.43E-06 0.000108 0.00513 0.116 >1 >1 >1 0.0252 0.568 >1 >1 >1 0.0371 0.837 >1 >1 >1 0.0473 >1 >1 >1 >1 0.0484 >1 >1 >1 >1 - - - - - - - - - - - - - - -	304 8.75E-11 1.51E-09 5.09E-08 1.27E-06 2.52E-05 0.0128 0.22 >1 >1 >1 0.00167 0.0289 0.972 >1 >1 >1 0.00228 0.0394 >1 >1 >1 0.00859 0.148 >1 >1 >1 - - - - - - - - - -	304 1.21E-12 2.09E-11 7.04E-10 1.76E-08 3.49E-07 0.00405 0.07 >1 >1 >1 0.0162 0.28 >1 >1 >1 0.00318 0.0549 >1 >1 >1 0.0409 0.706 >1 >1 >1
YPD 12 h ypd-2	HAP4 HSF1 CIN5 MSN4 SUT1 SKN7 MSN2 HAP2 SOK2 HAP3	1 26 1 70 1 51 1 24 1 15 1 73 1 20 1 19 1 39 1 13	169 2.53E-05 0.000787 0.0265 0.663 >1 - - - - - - - - - -	235 5.39E-09 1.21E-07 4.06E-06 0.000102 0.00201 0.00768 0.172 >1 >1 >1 0.0258 0.576 >1 >1 >1 0.0464 >1 >1 >1 >1 0.0495 >1 >1 >1 >1 -	303 6.81E-09 1.18E-07 3.98E-06 9.95E-05 0.00197 0.00311 0.0539 >1 >1 >1 0.0152 0.263 >1 >1 >1 0.0299 0.518 >1 >1 >1 0.0394 0.683 >1 >1 >1 - - - - - - - - - -	303 5.45E-07 9.44E-06 0.000318 0.00796 0.158 0.00358 0.0621 >1 >1 >1 0.00584 0.0101 0.341 >1 >1 - - - - - - - - - -
YPD 1 d ypd-2	HAP4 SUT1 MSN2 HSF1 AFT2 SOK2 HAP3	1 26 1 15 1 20 1 70 1 56 1 39 1 13	168 0.000202 0.00632 0.213 >1 >1 0.0168 0.524 >1 >1 >1 0.048 >1 >1 >1 >1 -	233 0.000252 0.00568 0.191 >1 >1 0.0109 0.245 >1 >1 >1 0.00112 0.0252 0.849 >1 >1 0.0297 0.669 >1 >1 >1 0.0377 0.849 >1 >1 >1 0.0476 >1 >1 >1 >1 - - - - - - - - - -	302 0.00122 0.0213 0.718 >1 >1 0.00329 0.0572 >1 >1 >1 -	302 - - - - - 0.00702 0.122 >1 >1 >1 - - - - - - - - - -
YPD 2 d ypd-2	HAP4 MSN2 GLN3 SUT1 HSF1 SOK2	1 26 1 21 1 32 1 15 1 70 1 39	169 0.000322 0.01 0.337 >1 >1 0.000575 0.0179 0.602 >1 >1 0.00212 0.0659 >1 >1 >1 0.0224 0.696 >1 >1 >1 0.0475 >1 >1 >1 >1 - - - - - - - - - -	237 5.36E-05 0.00119 0.04 >1 >1 0.00364 0.0807 >1 >1 >1 -	302 0.0185 0.321 >1 >1 >1 0.00145 0.0252 0.848 >1 >1 - - - - - - - - - -	302 - - - - - 0.00122 0.0213 0.716 >1 >1 - - - - -
YPD 3 d ypd-2	MSN4 SUT1, SKN7 MSN2 SOK2 PHD1, GCN4 HAP4 HAP3 UME6 PHD1	1 24 2 11 1 20 1 39 2 5 1 26 1 13 1 94 1 34	148 0.00522 0.195 >1 >1 >1 0.0191 0.679 >1 >1 >1 0.0245 0.869 >1 >1 >1 0.0411 >1 >1 >1 >1 -	195 - - - - - 0.048 >1 >1 >1 >1 - - - - - - - - - -	235 0.0485 >1 >1 >1 >1 0.00566 0.127 >1 >1 >1 0.0141 0.316 >1 >1 >1 0.0229 0.511 >1 >1 >1 0.0269 0.6 >1 >1 >1 - - - - - - - - - -	303 - - - - - 0.00583 0.101 >1 >1 >1 0.0103 0.179 >1 >1 >1 - - - - -
YPD 5 d ypd-2	SOK2 HAP4 UME6 THI2 MSN4 MSN2	1 39 1 26 1 92 1 8 1 25 1 20	149 0.00683 0.241 >1 >1 >1 0.011 0.387 >1 >1 >1 0.0276 0.972 >1 >1 >1 0.0313 >1 >1 >1 >1 - - - - - - - - - -	195 0.0141 0.38 >1 >1 >1 0.012 0.324 >1 >1 >1 0.0478 >1 >1 >1 >1 - - - - - - - - - - - - - - -	235 - - - - - 0.0164 0.367 >1 >1 >1 0.0477 >1 >1 >1 >1 - - - - -	301 - - - - - 0.00831 0.145 >1 >1 >1 0.0323 0.563 >1 >1 >1 0.0401 0.696 >1 >1 >1
YPD stationary phase 2 h ypd-1	MSN2 HSF1 SKN7 HAP1, YAP1	1 21 1 70 1 71 2 3	402 5.99E-06 7.83E-05 0.00264 0.066 >1 6.60E-05 0.000863 0.0291 0.727 >1 0.0128 0.168 >1 >1 >1 0.0468 0.611 >1 >1 >1 - - - - -	553 -	702 -	702 -
YPD stationary phase 4 h ypd-1	FHL1 SW16 STE12 GCR1 HSF1 MOT3	1 87 1 87 1 106 1 4 1 70 1 13	299 0.00174 0.0306 >1 >1 >1 0.00174 0.0306 >1 >1 >1 0.0157 0.276 >1 >1 >1 0.0197 0.346 >1 >1 >1 0.0345 0.607 >1 >1 >1 - - - - -	547 - - - - - - - - - -	328 0.00117 0.0187 0.63 >1 >1 0.000281 0.00594 0.2 >1 >1 0.0341 0.328 >1 >1 >1 - - - - -	474 - - - - - - - - - -
YPD stationary	HAP4 MSN2	1 24 1 17	159 0.000457 0.0151 0.508 >1 >1 >1 0.00356 0.118 >1 >1 >1 - - - - -	248 9.66E-06 0.000205 0.00689 0.172 >1 0.000281 0.00594 0.2 >1 >1 0.0341 0.328 >1 >1 >1 - - - - -	328 0.00117 0.0187 0.63 >1 >1 0.000281 0.00594 0.2 >1 >1 0.0341 0.328 >1 >1 >1 - - - - -	474 - - - - -

phase 8 h YPD-1	BAS1 NRG1	1 1	21 48	0.0129 0.0271	0.426 0.895	> 1 > 1	> 1 > 1	> 1 > 1	0.000246 0.0052	0.175 -	> 1 -	> 1 -	1.48E-08 2.37E-07	8.00E-06 2.27E-06	0.0002 4.51E-05	0.00396 -	7.59E-11 2.87E-13	8.42E-10 5.07E-12	2.83E-08 1.71E-10	7.09E-07 4.27E-09	1.41E-05 8.46E-08						
YPD stationary phase 12 h	HAP4 MSN2 MSN4	1 1 1	27 21 25	142 0.0152	9.25E-05 0.563	0.00342 > 1	0.115 > 1	> 1 > 1	191 0.0357	2.90E-08 0.98	7.97E-07 > 1	2.68E-05 > 1	0.000671 0.0133	0.000295 0.00868	2.27E-06 0.153	4.51E-05 > 1	297 297	1.53E-10 0.00053	2.70E-09 0.153	9.09E-08 > 1	2.27E-06 > 1	4.51E-05 > 1					
YPD stationary phase 1 d YPD-1	SKN7 GLN3 MSN2 UME6 SKO1 MSN4 HAP1	1 1 1 1 1 1 1	27 33 21 93 6 25 45	191 0.000659 0.018	3.71E-06 0.494	0.000102 > 1	0.00344 > 1	0.086 > 1	230 0.0223	2.42E-09 0.509	5.54E-08 > 1	1.87E-06 > 1	4.67E-05 0.385	0.000925 0.197	1.50E-06 0.197	299 299	5.10E-12 0.0316	8.96E-11 0.555	3.02E-09 > 1	7.55E-08 > 1	1.50E-06 > 1						
YPD stationary phase 2 d YPD-1	SKN7 HSF1 SOK2 MSN4 MSN2 SUT1 UME6	1 1 1 1 1 1 1	72 70 41 25 21 15 91	161 0.00106 0.0108 0.0211	1.62E-06 0.354 0.688	5.27E-05 > 1	0.000178 > 1	0.0444 > 1	228 0.000988	5.55E-08 0.0228	1.28E-06 0.767	4.31E-05 > 1	0.00108 0.127	0.0214 0.00741	0.0214 0.132	295 295	2.91E-06 0.00175	5.18E-05 0.0437	0.000295 0.865	0.0437 0.865	391 391	0.0242 0.325	> 1 > 1	> 1 > 1	> 1 > 1		
YPD stationary phase 3 d YPD-1	HAP4 MSN2 HSF1 SUT1 SOK2 SKN7 MSN4	1 1 1 1 1 1 1	27 21 70 15 40 72 24	164 0.000703 0.0102	0.000163 0.0225	0.00522 0.759	0.176 > 1	> 1 > 1	226 5.46E-05	6.30E-06 0.00127	0.000147 0.0428	0.00494 > 1	0.123 > 1	0.000295 0.00103	0.000295 0.0184	0.000295 0.618	295 295	1.88E-06 0.00113	3.35E-05 0.0282	0.000295 0.56	0.000295 0.56	295 295	0.00757 0.0079	0.135 0.141	> 1 > 1	> 1 > 1	> 1 > 1
YPD stationary phase 5 d YPD-1	GAL4 HAP4 SUT1 HAP3 UME6 PHD1	1 1 1 1 1 1	13 27 15 92 33	163 0.0308 0.0255 0.0303	0.00148 0.0476	0.0476 0.818	> 1 > 1	> 1 > 1	183 0.0168	0.0251 0.255	0.000645 0.72	0.0217 > 1	0.544 > 1	0.000295 0.00177	0.000295 0.316	0.000295 > 1	293 293	0.0293 0.0267	0.525 0.479	> 1 > 1	> 1 > 1	293 293	0.0102 0.00611	0.182 0.11	> 1 > 1	> 1 > 1	> 1 > 1
YPD stationary phase 7 d YPD-1	GAL4 SOK2 HAP4 PHD1 UME6	1 1 1 1 1	14 40 26 32 93	163 0.00153 0.0109	0.00039 0.0126	0.424 0.352	> 1 > 1	> 1 > 1	231 0.00192	- 0.00192	0.000645 0.0436	0.0217 > 1	0.544 > 1	0.000295 0.000295	0.000295 0.404	0.000295 > 1	290 290	- 0.0078	- 0.141	- > 1	- > 1	290 290	- 0.00088	- 0.0159	- 0.537	- > 1	- > 1
YPD stationary SOK2	UME6	1 1	80 35	173 -	- -	- -	- -	- -	204 -	0.0373 -	0.96 -	> 1 -	> 1 -	254 -	0.00196 0.0405	0.0405 > 1	> 1 -> 1	> 1 -> 1	345 345	0.0119 0.0341	0.182 0.519	> 1 -> 1	> 1 -> 1	> 1 -> 1			
YPD stationary phase 22 d	YAP7 MSN4 UME6	1 1 1	62 24 92	164 0.0271 0.0467	0.00361 0.116	0.116 0.868	> 1 > 1	> 1 > 1	229 0.00029	0.0467 0.0665	- > 1	- > 1	- > 1	297 0.000242	- 0.0429	- > 1	- -> 1	297 297	- 0.00303	- 0.0536	- > 1	- -> 1	- -> 1				
YPD stationary phase 28 d	YAP7 UME6 SUT1	1 1 1	62 90 15	162 -	0.018 -	0.583 -	> 1 -	> 1 -	228 0.000638	0.05511 0.0147	0.118 0.495	> 1 > 1	> 1 > 1	292 0.000867	0.0156 0.525	0.025 > 1	> 1 -> 1	292 292	0.000673 0.0313	0.0121 0.562	0.408 > 1	> 1 -> 1	> 1 -> 1				
DBYy286 37degree heat - 20 min	HSF1 RPN4 MSN2 MSN4 NRG1 UME6	1 1 1 1 1 1	68 64 21 24 57 93	234 9.53E-10 4.12E-06	1.02E-13 2.14E-08	2.28E-12 7.21E-07	7.69E-11 1.80E-05	1.92E-09 0.000357	303 0.000183	2.39E-18 0.00317	4.15E-17 0.107	1.40E-15 > 1	3.49E-14 > 1	6.93E-13 > 1	401 0.00691	1.01E-15 0.0906	1.32E-14 > 1	4.44E-13 -> 1	1.11E-11 -> 1	2.20E-10 -> 1	401 401	6.63E-13 0.0099	8.68E-12 0.13	2.92E-10 -> 1	7.31E-09 -> 1	1.45E-07 -> 1	
DBYymsn2-4/ 37degree heat - 20 min	HSF1 RPN4 MOT3 RLM1 AFT2, GCN4 UME6	1 1 1 1 2 1	70 63 13 9 3 94	233 7.63E-14	2.22E-14 1.72E-12	5.00E-13 5.80E-11	1.68E-11 1.45E-09	4.21E-10 2.87E-08	398 1.93E-09	6.38E-25 2.55E-08	8.43E-24 8.59E-07	2.84E-22 7.10E-21	7.10E-21 1.41E-19	6.93E-13 1.44E-19	398 6.31E-06	6.52E-25 8.33E-05	8.60E-24 0.00281	2.90E-22 0.0702	7.25E-21 > 1	1.44E-19 -> 1	548 548	2.98E-23 0.00281	2.86E-22 0.0536	9.62E-21 -> 1	2.41E-19 -> 1	4.77E-18 -> 1	
DBYymsn2/4/ 37degrees (real strain) + 37degrees	RPN4 HSF1, PHO2	1 1 2	64 70 4	240 1.49E-08	1.33E-11 3.26E-07	2.91E-10 1.10E-05	9.80E-09 0.000275	2.45E-07 0.00545	405 1.29E-13	2.61E-05 1.67E-12	0.000338 5.64E-11	0.0114 1.41E-09	0.285 2.79E-08	> 1 -> 1	556 4.57E-12	- 4.32E-11	1.32E-14 1.46E-09	4.44E-13 3.64E-08	1.11E-11 7.21E-07	2.20E-10 -> 1	556 556	- 1.11E-07	- 1.05E-06	- 3.54E-05	0.000885 0.0213	0.0175 > 1	
DBYyap1- 37degree heat - 20 min (redo)	HSF1 RPN4 MSN2 MSN4 MOT3 SKN7 UME6 AFT2	1 1 1 1 1 1 1 1	69 64 21 24 12 72 93 57	234 7.39E-08	2.02E-13 4.51E-05	4.53E-12 0.00152	1.53E-08 0.0395	3.82E-09 0.038	401 4.16E-07	1.08E-17 5.45E-06	1.47E-15 0.000183	1.19E-13 0.00459	2.35E-12 0.091	401 0.000248	1.54E-15 0.0105	7.18E-14 0.138	2.42E-12 -> 1	6.05E-11 -> 1	1.20E-09 -> 1	401 401	1.21E-12 0.00544	1.59E-11 0.0713	5.34E-10 -> 1	1.34E-08 -> 1	2.65E-07 -> 1		
DBYyap1 + 37degree heat (repeat)	HSF1 RPN4 MSN2 MSN4 MOT3 SKN7 UME6 AFT2	1 1 1 1 1 1 1 1	64 69 21 24 12 72 93 57	240 5.98E-09	2.02E-13 4.51E-05	6.99E-10 0.000152	1.53E-08 0.0395	3.82E-09 0.038	405 4.37E-06	1.08E-17 5.45E-06	1.47E-15 0.000183	1.19E-13 0.00459	2.35E-12 0.091	405 0.000248	1.54E-15 0.0105	7.18E-14 0.138	2.42E-12 -> 1	6.05E-11 -> 1	1.20E-09 -> 1	405 405	1.11E-07 0.00544	1.59E-11 0.0713	5.34E-10 -> 1	1.34E-08 -> 1	2.65E-07 -> 1		
DBYy286 + 0.3 mM H2O2 (20 min)	RPN4 YAP7 MSN4 RC51 MSN2 YAP1	1 1 1 1 1 1	64 70 25 27 21 17	193 0.000115	1.33E-09 0.0167	3.63E-08 0.456	1.22E-06 0.105	3.06E-05 > 1	304 0.00136	1.65E-11 0.123	2.85E-10 1.70E-10	9.59E-09 4.24E-09	2.40E-07 0.0637	403 0.000662	1.65E-11 0.123	2.85E-10 1.71E-07	9.59E-09 4.28E-06	2.40E-07 8.49E-05	4.75E-06 -> 1	554 554	4.52E-11 0.00361	4.28E-10 0.0342	1.44E-08 -> 1	3.60E-07 -> 1	7.14E-06 -> 1		
DBYymsn2ms n4 (good strain) + 0.32 mM H2O2	RPN4 YAP7 GCN4 HSF1 MSN4, NRG1 YAP1	1 1 1 1 2 1	65 65 126 69 5 17	237 0.00226 0.0017 0.000488 0.00669 0.0448 0.0469	1.37E-12 0.0217 5.79E-07 1.95E-05	3.04E-11 0.4842 5.79E-07 9.74E-10	1.02E-09 > 1	2.56E-08 > 1	299 4.57E-13	6.05E-16 8.04E-12	1.06E-14 2.71E-10	3.58E-13 6.77E-09	8.96E-12 1.34E-07	402 0.00945	3.00E-10 0.123	3.89E-09 1.71E-07	1.31E-07 4.28E-06	3.28E-06 8.49E-05	6.50E-05 -> 1	555 555	4.52E-11 0.00975	4.28E-10 0.127	1.44E-08 -> 1	3.60E-07 -> 1	7.14E-06 -> 1		
DBYymsn2ms n4 (good strain) + 0.32 mM H2O2	RPN4 YAP7 GCN4 HSF1 MSN4, NRG1 YAP1	1 1 1 1 2 1	65 65 126 69 5 17	237 0.00226 0.0017 0.000488 0.00669 0.0448 0.0469	1.37E-12 0.0217 5.79E-07 1.95E-05	3.04E-11 0.4842 5.79E-07 9.74E-10	1.02E-09 > 1	2.56E-08 > 1	299 4.57E-13	6.05E-16 8.04E-12	1.06E-14 2.71E-10	3.58E-13 6.77E-09	8.96E-12 1.34E-07	402 0.00945	3.00E-10 0.123	3.89E-09 1.71E-07	1.31E-07 4.28E-06	3.28E-06 8.49E-05	6.50E-05 -> 1	556 556	4.52E-11 0.00975	4.28E-10 0.127	1.44E-08 -> 1	3.60E-07 -> 1	7.14E-06 -> 1		
DBYyap1- 0.32 mM H2O2 (20 min)	RPN4 YAP7 GCN4 HSF1 MSN4, NRG1 YAP1	1 1 1 1 2 1	64 65 126 69 5 17	240 0.000269 0.0167	6.46E-13 0.366	1.41E-11 > 1	4.76E-10 > 1	1.19E-08 > 1	405 3.49E-10	1.68E-06 4.52E-09	2.18E-05 1.52E-07	4.00E-06 3.81E-06	8.08E-07 7.55E-05	405 0.00541	8.73E-11 0.0702	1.13E-09 0.0744	3.82E-08 > 1	9.54E-07 0.00943	1.89E-05 0.236	4.86E-05 -> 1	556 556	1.83E-09 0.00454	1.73E-08 0.04429	5.84E-07 0.145	1.46E-05 -> 1	0.000289 -> 1	

DBY yap1 + 0.3 mM H2O2 (20 min)	RPN4 GCN4 HAP4 HSF1 MSN2 MSN4	1 64 1 128 1 27 1 70 1 21 1 25	193 2.21E-08 6.97E-06 0.00308 0.0154 - -	6.02E-07 0.00019 0.00639 0.418 - -	2.03E-05 0.00639 >1 >1 >1 -	0.000507 0.16 >1 >1 >1 -	0.01 - - - - -	304 4.40E-13 0.0102 0.176 >1 >1 -	7.60E-12 - - - - -	2.56E-10 - - - - -	6.40E-09 - - - - -	1.27E-07 - - - - -	403 - - - - - -	- - - - - -	- - - - - -	- - - - - -	403 - - - - - -						
DBY yap1 + 0.32 mM H2O2 (20 min)	RPN4 HSF1 MSN4 MSN2	1 64 1 70 1 25 1 21	196 0.000191 0.000208 0.00559 0.00176	0.00511 0.188 0.0471 0.0471	0.172 >1 >1 - -	>1 >1 >1 - -	- - - - -	304 5.11E-06 0.000325 0.000325 0.0232	8.83E-05 0.00561 0.189 0.401	0.00297 0.0434 >1 >1	0.0744 0.121	>1 - - - -	402 1.96E-05 0.00332 0.00923	0.000256 0.0434 0.121	0.00861 >1 >1	0.215 - - - -	402 0.000478 0.000786 0.00624 0.0103	>1 0.21 0.346 >1	>1 - - - -	>1 - - - -	402 0.000478 0.000786 0.00624 0.0103		
Msn2 overexpress on (repeat)	MSN4	1 25	405 -	-	-	-	-	405 0.0138	0.179	>1	>1	>1	556 0.0135	0.127	>1	>1	>1	556 -	-	-	-	-	-
Msn4 overexpression	MSN2 HSF1 MSN4	1 21 1 70 1 25	306 0.00224	0.0385	>1	>1	>1	405 0.00112	0.0146	0.491	>1	>1	405 0.00321	0.0417	>1	>1	>1	556 -	-	-	-	-	-
Yap1 overexpression	YAP7 HSF1 YAP1	1 65 1 69 1 17	239 5.16E-07 0.000765	1.14E-05 0.0168	0.000382 0.566	>1	>1	403 8.57E-08	1.12E-06	3.76E-05	0.000941	0.0186	554 0.000755	0.00716	0.241	>1	>1	554 -	-	-	-	-	-
ethanol vs. reference pool car-1	HAP4 SOK2 MOT3 SUT1 SKN7 SKO1 UME6 CBF1, PHO2 ABF1, CBF1	1 26 1 38 1 13 1 16 1 73 1 5 1 92 2 4 2 12	194 8.21E-07 0.00403	2.22E-05 0.109	0.000749 >1	0.0187	0.371	304 0.000925	0.016	0.538	>1	>1	401 -	-	-	-	-	550 -	-	-	-	-	-
galactose vs. reference pool car-1	HAP4 GAL4 MSN4 MSN2	1 25 1 14 1 24 1 21	299 0.0004	0.00702	0.236	>1	>1	400 2.04E-07	2.67E-06	9.01E-05	0.00225	0.0447	547 7.03E-08	6.75E-07	2.27E-05	0.000569	0.0113	547 1.40E-05	0.000135	0.00453	0.113	>1	-
glucose vs. reference pool car-1	ABF1	1 202	195 0.00211	0.0568	>1	>1	>1	306 -	-	-	-	-	402 -	-	-	-	-	555 -	-	-	-	-	-
mannose vs. reference pool car-1	-	-	233 -	-	-	-	-	394 -	-	-	-	-	547 -	-	-	-	-	547 -	-	-	-	-	-
raffinose vs. reference pool car-1	HAP4	1 26	235 0.000106	0.00237	0.0797	>1	>1	401 -	-	-	-	-	550 -	-	-	-	-	550 -	-	-	-	-	-
sucrose vs. reference pool car-1	-	-	235 -	-	-	-	-	402 -	-	-	-	-	549 -	-	-	-	-	549 -	-	-	-	-	-
YP ethanol vs reference pool car-2	HAP4 AFT2 RCS1 SUT1 SKN7 SOK2 CIN5 UME6 MSN2 MOT3 CBF1, PHO2	1 27 1 58 1 27 1 15 1 73 1 41 1 52 1 94 1 21 1 13 2 4	191 2.80E-06 0.000149	7.69E-05 0.00409	0.00259 0.138	0.0648 >1	>1	300 1.88E-07	3.29E-06	0.000111	0.00277	0.0549	395 0.00412	0.0548	>1	>1	>1	548 -	-	-	-	-	-
YP fructose vs reference	FHL1 SFP1	1 87 1 20	305 4.62E-24 0.000492	7.96E-23 0.00847	2.68E-21 0.285	6.71E-20 >1	1.33E-18 >1	555 0.00211	0.02	0.672	>1	>1	555 -	-	-	-	-	-	-	-	-	-	-
YP galactose vs reference	GAL4 HAP4	1 14 1 27	300 3.72E-09 0.000156	6.52E-08 0.00273	2.20E-06 0.0919	5.49E-05 >1	0.00109 >1	395 2.08E-12	2.77E-11	9.33E-10	2.33E-08	4.62E-07	548 1.25E-06	1.19E-05	0.000402	0.0101	0.199	548 2.01E-06	1.92E-05	0.000648	0.0162	0.321	-
YP glucose vs reference pool car-2	FHL1	1 88	237 7.91E-06	0.000175	0.00591	0.148	>1	402 4.38E-05	0.000572	0.0193	0.482	>1	555 -	-	-	-	-	555 -	-	-	-	-	-
YP mannose vs reference pool car-2	-	-	234 -	-	-	-	-	400 -	-	-	-	-	553 -	-	-	-	-	553 -	-	-	-	-	-
YP raffinose vs reference pool car-2	HAP4 HAP1, HAP2, HAP3, HAP5	1 27 1 45 4 2	230 7.82E-08	1.79E-06	6.01E-05	0.0015	0.0298	394 7.51E-15 0.0125	1.00E-13 0.166	3.37E-12 >1	8.44E-11 >1	1.67E-09 >1	548 0.00143	0.0137	0.461	>1	>1	548 -	-	-	-	-	-
YP sucrose vs reference pool car-2	HAP1 RCS1 SFP1	1 27 1 20 1 20	299 2.71E-13 4.61E-07	4.77E-12 8.10E-06	1.61E-10 0.000273	4.02E-09 0.00683	0.135 -	547 -	-	-	-	-	547 -	-	-	-	-	-	-	-	-	-	-
17 deg growth ct-1	FHL1 PHO4 CBF1, PHO2	1 88 1 24 2 4	237 0.0119	0.264	>1	>1	>1	401 -	-	-	-	-	553 -	-	-	-	-	553 -	-	-	-	-	-
21 deg growth ct-1	RCS1	1 27	306 0.00509	0.0874	>1	>1	>1	402 0.0175	0.229	>1	>1	>1	555 -	-	-	-	-	555 -	-	-	-	-	-
25 deg growth ct-1	SOK2, CIN5, SKN7	3 5	306 0.0327	-	>1	>1	>1	555 -	-	-	-	-	555 -	-	-	-	-	555 -	-	-	-	-	-
29 deg growth ct-1	FHL1 SFP1	1 88 1 20	405 6.89E-12 0.0178	8.94E-11 0.231	3.01E-09 >1	7.53E-08 >1	1.49E-06 >1	556 -	-	-	-	-	556 -	-	-	-	-	556 -	-	-	-	-	-
37 deg growth ct-1	MSN2 HAP4 MSN4 YAP7	1 21 1 26 1 25 1 65	306 0.0153	0.263	>1	>1	>1	402 0.019	0.248	>1	>1	>1	555 -	-	-	-	-	555 -	-	-	-	-	-
steady state	HSF1 FKH2, MBP1	1 69 2 12	302 1.99E-05 0.013	0.000346 0.226	0.0117 >1	0.292 >1	401 -	-	-	-	-	552 -	-	-	-	-	552 -	-	-	-	-	-	
15 dec C ct-2	steady state	1 88 1 20	239 9.00E-06 0.00852	0.000198 0.187	0.00666 >1	0.167 >1	404 -	-	-	-	-	552 -	-	-	-	-	552 -	-	-	-	-	-	
17 dec C ct-2	steady state	1 87 1 20	306 3.71E-22 3.97E-05	3.63E-21 0.000681	1.22E-19 0.023	3.05E-18 0.574	6.05E-17 >1	555 2.89E-07	2.73E-06	9.20E-05	0.0023	0.0456	555 -	-	-	-	-	702 -	-	-	-	-	-
21 dec C ct-2	steady state	1 87 1 20	405 2.09E-16 8.47E-05	2.71E-15 0.0111	9.12E-14 0.292	2.28E-12 >1	4.52E-11 >1	554 -	-	-	-	-	554 -	-	-	-	-	554 -	-	-	-	-	-
25 dec C ct-2	steady state	1 20	405 2.09E-16 8.47E-05	2.71E-15 0.0111	9.12E-14 0.292	2.28E-12 >1	4.52E-11 >1	554 -	-	-	-	-	554 -	-	-	-	-	554 -	-	-	-	-	-

steady state 29 dec C ct-2	<i>FHL1</i>	1	87	405	8.68E-12	1.13E-10	3.79E-09	9.49E-08	1.88E-06	554	-	-	-	-	-	554	-	-	-	-	-	-	702	-	-	-	-	-	-
steady state 33 dec C ct-2	<i>GCN4</i>	1	127	306	0.0134	0.229	> 1	> 1	> 1	405	-	-	-	-	-	555	-	-	-	-	-	-	555	-	-	-	-	-	-
33 dec C ct-2	<i>BAS1</i>	1	24		0.0158	0.272	> 1	> 1	> 1		-	-	-	-	-		-	-	-	-	-	-		-	-	-	-	-	-
steady state 36 dec C ct-2	<i>HSF1</i>	1	70	302	0.00923	0.161	> 1	> 1	> 1	401	-	-	-	-	-	548	-	-	-	-	-	-	548	-	-	-	-	-	-
36 dec C ct-2	<i>SKO1</i>	1	6		0.00972	0.169	> 1	> 1	> 1		-	-	-	-	-		-	-	-	-	-	-		-	-	-	-	-	-
steady state 36 dec C ct-2	<i>HSF1</i>	1	60	274	0.000304	0.00583	0.197	> 1	> 1	372	-	-	-	-	-	514	-	-	-	-	-	-	514	-	-	-	-	-	-
36 dec C ct-2	<i>MSN2</i>	1	19		0.046	0.882	> 1	> 1	> 1		-	-	-	-	-		-	-	-	-	-	-		-	-	-	-	-	-

### B. EGF (human breast cancer cell)

Condition	Motif Combination	Arity	# of target genes	Adjusted p-value (exp > 0.5)					Adjusted p-value (exp > 1.0)					Adjusted p-value (exp > 1.5)					Adjusted p-value (exp > 2.0)									
				LAMP		Bonferroni			LAMP		Bonferroni			LAMP		Bonferroni			LAMP		Bonferroni							
				m'	Arity limit 2	3	4	5	m'	Arity limit 2	3	4	5	m'	Arity limit 2	3	4	5	m'	Arity limit 2	3	4	5					
0.1nM 5min	TATA	1	957	1459869	0.00389	2.10E-04	0.0278	>1	>1	3750336	0.000511	1.08E-05	0.00142	0.14	>1	5238103	2.26E-06	3.41E-08	4.51E-06	0.000445	0.0351	7247034	0.000123	1.34E-06	0.000176	0.0174	>1	
	MEIS1, LMO2COM, AR	3	14		0.03		0.214	>1	>1																			
	GATA6	1	160		0.49	0.0265	>1	>1	>1																			
	CTGYNNTCTYAA, TGACATY	2	12		-	-	-	-	-	1.03	0.0217	>1	>1	>1														
	MEF2, AACTTT	2	198		-	-	-	-	-																			
	RSRFC4, IK1	2	26		-	-	-	-	-																			
0.1nM 10min	TATA	1	957	1459869	-	-	-	-	-	3750336	-	-	-	-	-	5238103	0.175	0.00264	0.349	>1	>1	7247034	-	-	-	-	-	
0.1nM 15min	TATA	1	957	1459869	-	-	-	-	-	3750336	1.1	0.0232	>1	>1	>1	5238103	-	-	-	-	-	7247034	-	-	-	-	-	
0.1nM 30min	CTGCAGY, LEF1, VDR, MAZ	4	28	1459869	0.0177	-	-	>1	>1	3750336	-	-	-	-	-	5238103	-	-	-	-	-	7247034	-	-	-	-	-	
	TATA	1	957	0.877	0.0475	>1	>1	>1		0.000437	9.21E-06	0.00122	0.12	>1		0.0041	6.19E-05	0.00816	0.806	>1		0.284	0.00309	0.409	>1	>1		
	AACTTT, CART1	2	71	-	-	-	-	-	0.000791	1.67E-05	0.0022	0.217	>1		0.326	0.00492	0.649	>1	>1		-	-	-	-	-	-		
	CP2, CTGCAGY, LEF1, MAZ, STAT5A	5	9	-	-	-	-	-	0.00157	-	-	-	>1		-	-	-	-	-	-	-	-	-	-	-	-		
	CP2, CTGCAGY, AACTTT, CTTTAAR	5	18	-	-	-	-	-	0.0127	-	-	-	>1		-	-	-	-	-	-	-	-	-	-	-	-		
	OCT, NFAT, AAAYRNCTG, CART1	2	115	-	-	-	-	-	0.0144	-	-	-	>1		-	-	-	-	-	-	-	-	-	-	-	-		
	AAAYRNCTG, NKX61	2	18	-	-	-	-	-	0.0804	0.00169	0.223	>1	>1		1	0.0151	>1	>1	>1		-	-	-	-	-	-		
	MEF2, GATA6	2	38	-	-	-	-	-	-	-	-	-	-	-	1.81	0.0272	>1	>1	>1		3.13	0.0341	>1	>1	>1			
0.1nM 45min	-	-	-	1969633	-	-	-	-	3750336	-	-	-	-	-	5238103	-	-	-	-	-	7247034	-	-	-	-	-	-	
0.1nM 60min	NFAT, AACTTT	2	425	1969633	0.423	0.017	>1	>1	>1	3750336	-	-	-	-	-	5238103	-	-	-	-	-	7247034	-	-	-	-	-	-
	TATA	1	957	0.619	0.0248	>1	>1	>1		0.395	0.00832	>1	>1	>1		0.109	0.00165	0.218	>1	>1		-	-	-	-	-	-	
0.1nM 90min	SRF, FREAC3	2	16	1969633	0.954	0.0383	>1	>1	>1	3750336	-	-	-	-	-	5238103	-	-	-	-	-	7247034	-	-	-	-	-	-
0.5nM 5min	AACTTT, CART1	2	71	1459869	-	-	-	-	3750336	0.421	0.00887	>1	>1	>1		5238103	-	-	-	-	-	7247034	-	-	-	-	-	-
	E12, AACTTT	2	401	-	-	-	-	-	1.7	0.0358	>1	>1	>1		0.0603	0.000909	0.12	>1	>1		0.348	0.00379	0.501	>1	>1			
	TATA	1	957	-	-	-	-	-	-	-	-	-	-	-	0.0603	0.000909	0.12	>1	>1		0.0398	-	-	-	-	-	-	
0.5nM 10min	NFAT, AACTTT	2	425	1459869	0.409	0.0221	>1	>1	>1	3750336	0.0802	0.00169	0.223	>1	>1	5238103	-	-	-	-	-	7247034	-	-	-	-	-	-
	TATA	1	957	-	-	-	-	-	0.00066	1.39E-05	0.00184	0.181	>1		0.0595	0.000898	0.119	>1	>1		1.83	0.02	>1	>1	>1			
0.5nM 15min	WWTAGGC, NF1	2	27	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.125	0.00136	0.18	>1	>1			
	GATA6, CREB GR, EVI1, CTTTAAR, LEF1, OCT1, NFAT, FOXO4, CEBP	1	957	0.194	0.00776	>1	>1	>1	3750336	0.00139	2.93E-05	0.00387	0.382	>1	5238103	0.00112	1.69E-05	0.00224	0.221	>1	7247034	0.134	0.00146	0.192	>1	>1		
	GATA6, FOX4, FOX2, E12, TGACATY, OCT1, AP1	2	63	-	-	-	-	-	0.904	0.019	>1	>1	>1		0.0198	-	-	-	>1		-	-	-	-	-	-		
	GATA6, PIT1	2	11	-	-	-	-	-	-	-	-	-	-	-	2.84	0.0428	>1	>1	>1		-	-	-	-	-	-	-	
0.5nM 30min	NFAT, AACTTT	2	425	1459869	0.042	0.00227	0.3	>1	>1	2700718	-	-	-	-	-	5238103	-	-	-	-	-	7247034	-	-	-	-	-	-
	TATA	1	957	0.155	0.00838	>1	>1	>1		0.00211	6.18E-05	0.00816	0.805	>1	-	-	-	-	-	-	-	-	-	-	-	-		
	NFAT, AREB6	2	288	0.156	0.00847	>1	>1	>1		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
0.5nM 45min	E12	1	1491	0.65	0.0352	>1	>1	>1		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
	FOXO4, SRF YY1, SRF, AACTTT	2	100	1969633	0.000403	1.62E-05	0.00213	0.211	>1	3750336	0.0223	0.00047	0.062	>1	>1	5238103	-	-	-	-	-	7247034	-	-	-	-	-	-
	HFH8, E4F1, CREB	3	23	0.00534	-	0.0283	>1	>1		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
	SRF, HNF3	2	54	0.0455	0.00183	0.241	>1	>1		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
	SRF, FREAC3	2	65	0.08	0.00321	0.424	>1	>1		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
	NFAT, AACTTT	2	425	0.278	0.0112	>1	>1	>1		0.00138	2.90E-05	0.00383	0.378	>1		-	-	-	-	-	-	-	-	-	-	-		
	SRF, ATF, AACTTT	3	16	-	-	-	-	-	0.00113	-	0.00314	0.31	>1		-	-	-	-	-	-	-	-	-	-	-	-		
	YY1, SRF, NFKB, AACTTT	4	9	-	-	-	-	-	0.00127	-	-	0.348	>1		-	-	-	-	-	-	-	-	-	-	-	-		
	TATA	1	957	-	-	-	-	-	0.00405	8.53E-05	0.0113	>1	>1		0.000145	2.19E-06	0.000289	0.0286	>1		-	-	-	-	-	-		
	GATA6	1	160	-	-	-	-	-	0.0504	0.00106	0.14	>1	>1		-	-	-	-	-	-	-	-	-	-	-	-		
	NFAT, CART1	2	62	-	-	-	-	-	0.744	0.0157	>1	>1	>1		-	-	-	-	-	-	-	-	-	-	-	-		
	NF1, E2F	2	57	-	-	-	-	-	0.836	0.0176	>1	>1	>1		-	-	-	-	-	-	-	-	-	-	-	-		
0.5nM 60min	CTGCAGY, LEF1, CREB, AREB6, AACTTT	5	15	1969633	0.000776	-	-	-	-	3750336	-	-	-	-	-	5238103	-	-	-	-	-	7247034	-	-	-	-	-	-
	E12, NFAT, CREB, MYOD, AACTTT	4	35	0.008	-	-	>1	>1		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
	E12, NFAT, CREB, AACTTT	4	21	0.0142	-	0.0753	>1	>1		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
	TATA	1	957	0.0214	-	-	>1	>1		-	0.0429	0.000904	0.119	>1	>1	0.159	0.0024	0.317	>1	>1		0.57	0.00621	0.82	>1	>1		

0.5nM 90min	LEF1, CTGCAGY, TATA, VDR, MAZ MYC, TATA, CREB, CREBP1, FOXO4 E12, AACTT, LEF1, TATA, OCT1, NFAT, CREB	5 9	1969633	- - - - -	3750336	0.0457	- - - - -	>1	5238103	- - - - -	0.00345	- - - - -	>1	7247034	- - - - -						
1.0nM 5min	TATA AACTT, CART1 NFAT, CART1	1 957 2 71 2 62	1459869	- - - - -	3750336	0.0181	0.00038	0.0502	>1 >1	5238103	0.000195	2.94E-06	0.000388	0.0384	>1	7247034	0.026	0.000283	0.0374	>1	>1
1.0nM 10min	YY1, LEF1, NF1, NFAT CRX, AACTT E12, AACTT NFAT, AACTT AREB6, AACTT TATA FOXO4, TAAYNRNTCC	4 26 2 69 2 401 2 425 2 274 1 957 2 71 2 44	1459869	0.015 0.0268 0.00145 0.0577 0.00312 0.0613 0.00332 0.0262 - - - - -	3750336	0.216 0.00455 0.601 - - - - -	2.01 0.0424 - - - - -	>1 >1	5238103	- - - - -	0.0522 0.000787 0.104 - - - - -	1.7 0.0257 - - - - -	>1 >1	7247034	- - - - -						
1.0nM 15min	NFAT, AACTT TATA FOXO3, HNF3 HFH8, GATA6 CTGYNCTYAA, AACTT	2 425 1 957 2 51 2 10 2 19	1459869	0.00601 0.282 0.0153 0.595 0.0322 - - - - -	3750336	0.0149 - - - - -	0.000313 0.0413 - - - - -	>1 >1	5238103	- - - - -	0.0245 0.00037 0.0488 2.25 0.0339 - - - - -	>1 >1	7247034	0.101 0.0011 0.145 3.67 0.04 - - - - -	>1	>1					
1.0nM 30min	NFAT, AREB6, AACTT TATA ATF6, CTTAACR ATF6, SP1 LEF1, CDPCR3HD, OCT1, MSX1, AACTT YNGTNNNATT, AACTT NFAT, AACTT OCT, NFAT LEF1, NFAT SREBP1, MSX1	3 138 1 957 2 16 2 40 5 8 2 100 2 425 2 115 2 497 2 27	1459869	0.0206 0.0757 0.00409 0.217 0.0117 0.723 0.0391 - - - - -	3750336	0.0319 - - - - -	0.000672 0.0887 - - - - -	>1 >1	5238103	- - - - -	0.00233 3.52E-05 0.00465 0.459 >1	- - - - -	7247034	- - - - -	0.0087 - - - - -	>1					
1.0nM 45min	HFH4, NFAT, E4F1, AACTT CTGCAGY, LEF1, AREB6, AACTT YY1, NF1, NFAT, AACTT TATA, OCT1, CREB, NFAT, AACTT YY1, CHX10, NFAT, AACTT SRF, HNF3 AACTT, CART1 MEIS1, LEF1, NFAT, NKX62 TATA, OCT1, NFAT, AACTT MEIS1, NFAT, AACTT NFAT, CART1 IRF7, PPAR MEF2, CIZ IK3, AACTT HFH4, CREB AACTT, PPAR TATA, NFAT, AACTT, LEF1, CHX10, LHX3, STAT5A, STAT5B	4 11 4 51 4 23 5 15 4 17 2 54 2 71 4 23 4 74 3 97 2 62 2 8 2 32 2 57 2 23 2 55 1 957 7 6	1459869	0.0173 0.0175 0.0251 0.0445 0.045 0.0918 0.00497 0.656 0.708 0.0383 - - - - -	3750336	- - - - -	- - - - -	>1 >1	5238103	- - - - -	0.00895 0.0105 - - - - -	- - - - -	7247034	- - - - -	4.29 0.0468 - - - - -	>1	>1				
1.0nM 60min	MAZ E12, CREB, ATF4, CTGCAGY, LEF1, PAX4, AREB6, AACTT MEIS1, NFAT, FREAC2 NFAT, STAT5A, AACTT LEF1, NFAT LEF1, TATA, NFAT, NFKB, AACTT EV1, MEF2, LEF1, TATA, SREBP1, NFAT, FOXO4 PTF1BETA, LEF1, NFAT, CREB, AACTT MEF2, LEF1, POU6F1, FOXO4, AR	4 15 5 29 3 64 3 106 2 497 5 20 7 10 5 8 5 8	1969633	0.0007 0.0304 0.0312 0.0486 1.13 0.0453 - - - - -	3750336	0.366 - - - - -	- - - - -	>1	5238103	- - - - -	0.00725 0.0207 - - - - -	- - - - -	7247034	- - - - -	0.0184 - - - - -	- - - - -					





## C. HRG (human breast cancer cell)

condition	Motif Combination	Arity	# of target genes	Adjusted p-value (exp > 0.5)					Adjusted p-value (exp > 1.0)					Adjusted p-value (exp > 1.5)					Adjusted p-value (exp > 2.0)						
				LAMP		Bonferroni			LAMP		Bonferroni			LAMP		Bonferroni			LAMP		Bonferroni				
				m'	Arity limit 2	3	4	5	m'	Arity limit 2	3	4	5	m'	Arity limit 2	3	4	5	m'	Arity limit 2	3	4	5		
0.1nM 5min	-	-	-	1174108	-	-	-	-	2874627	-	-	-	-	5542428	-	-	-	-	7635557	-	-	-	-		
0.1nM 10min	MAZ, E12, SP1	3	227	552135	0.00197	-	0.0372	>1	>1	2099869	-	-	-	-	3982295	-	0.262	0.00519	0.686	>1	>1	-	-	5542428	
	E12, YATTNATC	2	83	-	-	-	-	-	-	-	-	-	-	2.17	0.043	>1	>1	>1	-	-	-	-	-	-	
0.1nM 15min	MAZ, E12, SP1	1	1474	552135	0.111	0.0159	>1	>1	>1	1557482	-	-	-	-	3982295	-	-	-	-	5542428	-	-	-	-	
	MAZ, E12	2	478	-	-	-	-	-	-	0.0645	0.00327	0.432	>1	>1	-	-	-	-	-	-	-	-	-	-	
	MAZ, AP4	2	388	-	-	-	-	-	-	0.0857	0.00435	0.574	>1	>1	-	-	-	-	-	-	-	-	-	-	
	ZIC1, E47	2	19	-	-	-	-	-	-	0.293	0.0149	>1	>1	>1	-	-	-	-	-	-	-	-	-	-	
	AP4	1	1016	-	-	-	-	-	-	-	-	-	-	0.00372	7.37E-05	0.00973	0.961	>1	0.835	0.0119	>1	>1	>1	-	-
	LEF1, CTGCAGY, E12, PAX4, MAZ	5	38	-	-	-	-	-	-	-	-	-	-	0.006	-	-	-	-	-	-	-	-	-	-	-
	E12	3	28	-	-	-	-	-	-	-	-	-	-	0.0161	-	0.0422	>1	>1	-	-	-	-	-	-	-
	E12, MAZ, NFAT, FOXO4	4	87	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.0356	-	-	>1	>1	-	
0.1nM 30min	MAZ, E12	2	478	699536	0.108	0.0122	>1	>1	>1	2099869	0.00328	0.000123	0.0163	>1	>1	3982295	-	-	-	-	5542428	-	-	-	-
	ELK1, MYOD, ATF	3	11	-	-	-	-	-	-	0.0115	-	0.0569	>1	>1	-	-	-	-	-	-	-	-	-	-	
0.1nM 45min	SP1	1	1915	699536	0.0193	0.00218	0.288	>1	>1	2099869	-	-	-	-	3982295	-	-	-	-	5542428	-	-	-	-	
	MAZ, E12	2	478	-	0.127	0.0143	>1	>1	>1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
0.1nM 60min	SP1	1	1915	699536	0.0193	0.00218	0.288	>1	>1	1557482	-	-	-	-	3982295	0.00692	0.000137	0.0181	>1	5542428	-	-	-	-	
	MAZ, E12	2	478	552135	0.00616	0.000882	0.116	>1	>1	-	0.0913	0.00463	0.612	>1	>1	-	-	-	-	-	-	-	-	-	
	PAX4	1	1182	-	0.329	0.0471	>1	>1	>1	-	0.0117	-	0.0786	>1	>1	-	-	-	-	-	-	-	-	-	
	ELK1, MYOD, ATF	3	11	-	-	-	-	-	-	0.0317	0.00161	0.212	>1	>1	-	-	-	-	-	-	-	-	-	-	
	MAZ	1	1474	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
	E12, PAX4	2	428	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
	AP4	1	1016	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
	RFX1	1	296	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
	TATA, NFKB	2	75	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.705	0.01	>1	>1	>1	
0.1nM 90min	E12, PAX4	2	428	552135	0.0224	0.0032	0.422	>1	>1	1557482	-	-	-	-	3982295	0.242	0.00481	0.635	>1	5542428	-	-	-	-	
	MAZ	1	1474	-	0.0774	0.0111	>1	>1	>1	-	0.536	0.0272	>1	>1	-	-	-	-	-	-	-	-	-	-	
0.5nM 5min	MAZ	1	1474	699536	0.0432	0.00488	0.644	>1	>1	2099869	-	-	-	-	3982295	-	-	-	-	5542428	-	-	-	-	
	AP4	1	1016	-	-	-	-	-	-	-	0.0467	0.00176	0.232	>1	>1	-	-	-	-	-	-	-	-	-	
0.5nM 10min	MAZ	1	1474	552135	0.0425	0.00608	0.802	>1	>1	1557482	-	-	-	-	3982295	-	-	-	-	5542428	-	-	-	-	
	SP1	1	1915	-	0.0532	0.00761	>1	>1	>1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
	MAZ, E12	2	478	-	-	-	-	-	-	-	0.519	0.0263	>1	>1	>1	-	-	-	-	-	-	-	-	-	
0.5nM 15min	-	-	-	552135	-	-	-	-	-	2099869	-	-	-	-	3982295	-	-	-	-	5542428	-	-	-	-	
0.5nM 30min	MAZ	1	1474	699536	0.000982	0.000111	0.0146	>1	>1	2099869	0.000921	3.47E-05	0.00457	0.452	>1	3982295	-	-	-	-	5542428	-	-	-	-
	ELK1, MYOD, ATF	3	11	-	-	-	-	-	-	-	0.00919	-	0.0457	>1	>1	-	-	-	-	-	-	-	-	-	
	OCT, USF OCT1, NFKB, AACTTT	5	8	-	-	-	-	-	-	-	-	-	-	-	0.0184	-	-	-	-	5542428	-	-	-	-	
	SRF, PAX3	2	12	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.145	0.00207	0.273	>1	>1	-	
0.5nM 45min	PAX4	1	1182	699536	0.00359	0.000406	0.0536	>1	>1	2099869	-	-	-	-	3982295	-	-	-	-	5542428	-	-	-	-	
	MAZ	1	1474	-	0.0838	0.00947	>1	>1	>1	-	0.0203	0.000764	0.101	>1	>1	-	-	-	-	-	-	-	-	-	
	ETS2	1	757	-	0.118	0.0133	>1	>1	>1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
	SP1	1	1915	-	0.142	0.0161	>1	>1	>1	-	-	0.00133	4.99E-05	0.00658	0.65	>1	-	-	-	-	-	-	-	-	
	AP4	1	1016	-	-	-	-	-	-	-	-	-	-	-	0.0262	0.00052	0.0687	>1	>1	-	-	-	-	-	-
	SRF, PAX3	2	12	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1.51	0.0215	>1	>1	>1	-	
0.5nM 60min	SP1	1	1915	699536	0.00278	0.000314	0.0414	>1	>1	2099869	-	-	-	-	3982295	-	-	-	-	5542428	-	-	-	-	
	MAZ	1	1474	-	0.066	0.00745	0.984	>1	>1	-	0.349	0.0131	>1	>1	>1	-	-	-	-	-	-	-	-	-	
	SRF, PAX3	2	12	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3.37	0.048	>1	>1	>1	-
0.5nM 90min	E12	1	1512	552135	3.17E-05	4.54E-06	0.000599	0.0592	>1	1557482	-	-	-	-	3982295	-	-	-	-	5542428	-	-	-	-	
	MAZ, E12	2	478	-	-	-	-	-	-	-	0.223	0.0113	>1	>1	>1	-	-	-	-	-	-	-	-	-	
	E12, PAX4	2	428	-	-	-	-	-	-	-	0.591	0.03	>1	>1	>1	-	-	-	-	-	-	-	-	-	
	MAZ, MYOD	2	303	-	-	-	-	-	-	-	-	-	-	-	-	0.0315	0.000624	0.0824	>1	>1	-	-	-	-	
	MAZ, AP4	2	388	-	-	-	-	-	-	-	-	-	-	-	-	1.83	0.0364	>1	>1	>1	-	-	-	-	-
	ETS2, E12	2	232	-	-	-	-	-	-	-	-	-	-	-	-	1.88	0.0374	>1	>1	>1	-	-	-	-	-
	MAZ, SRF, T3R	3	11	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
	YATTNATC, YCATTAAC	2	55	-	-	-	-	-	-	-	-	-	-	-	-	-	0.0265	-	0.0963	>1	>1	-	-	-	-
	TATA, NFAT, YATTNATC, AACTTT	4	26	-	-	-	-	-	-	-	-	-	-	-	-	-	0.154	0.00424	0.559	>1	>1	-	-	-	-
	NFAT, YATTNATC, YCATTAAC	3	26	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.046	-	-	>1	>1	-
	OCT, TATA	2	91	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.895	0.0177	>1	>1	>1	-
1.0nM 30min	MAZ, E12	2	478	442874	0.00187	0.000333	0.0439	>1	>1	1557482	0.000854	4.33E-05	0.00572	0.565	>1	2874627	0.704	0.0193	>1	>1	5542428	-			

	MAZ, AP4	2	388		0.0063	0.00112	0.148	>1	>1	-	-	-	-	-	-	-	-	-	-	-	
	PAK4, AP4	2	301	-	-	-	-	-	-	0.492	0.025	>1	>1	>1	-	-	-	-	-	-	-
	TATA	1	968	-	-	-	-	-	-	-	-	-	-	-	0.0429	0.00118	0.156	>1	>1	0.104	0.00149
	TTANTCA, MAZ, E12	3	81	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.196	>1	>1	
1.0nM 45min	MAZ, CP2, GATA1, FOXO4, E12, MEF2, TATA, TGCTGAY, NFAT, AACTT, HSF1, ETS2, FOXO4, E12, HSF1, ETS2, E12, AACTT, USF, NFKB, AACTT, OCT, OCT1, NFAT, MAZ, CREBP1	1	1474	442874	0.0256	0.00457	0.604	>1	>1	1174108	0.15	0.0101	>1	>1	>1	2874627	0.044	0.00121	0.16	>1	5542428
	CP2, GATA1, FOXO4, E12, MEF2, TATA, TGCTGAY, NFAT, AACTT, HSF1, ETS2, FOXO4, E12, HSF1, ETS2, E12, AACTT, USF, NFKB, AACTT, OCT, OCT1, NFAT, MAZ, CREBP1	4	14	-	-	-	-	-	-	0.0284	-	-	>1	>1	-	-	-	-	-	-	
	AACTT, HSF1, ETS2, FOXO4, E12, HSF1, ETS2, E12, AACTT, USF, NFKB, AACTT, OCT, OCT1, NFAT, MAZ, CREBP1	5	11	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.0117	-	-	
	AACTT, HSF1, ETS2, FOXO4, E12, HSF1, ETS2, E12, AACTT, USF, NFKB, AACTT, OCT, OCT1, NFAT, MAZ, CREBP1	4	14	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.013	-	>1	
	AACTT, HSF1, ETS2, E12, AACTT, USF, NFKB, AACTT, OCT, OCT1, NFAT, MAZ, CREBP1	4	12	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.0437	-	>1	
	AACTT, HSF1, ETS2, E12, AACTT, USF, NFKB, AACTT, OCT, OCT1, NFAT, MAZ, CREBP1	6	7	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.0488	-	-	
	AACTT, HSF1, ETS2, E12, AACTT, USF, NFKB, AACTT, OCT, OCT1, NFAT, MAZ, CREBP1	2	100	-	-	-	-	-	-	-	-	-	-	-	-	-	2	0.0285	>1	>1	
1.0nM 60min	MAZ, AP4	1	1474	552135	0.17	0.0243	>1	>1	>1	2099869	-	-	-	-	-	3982295	-	-	-	-	5542428
	AP4	1	1016	-	-	-	-	-	-	-	0.328	0.0123	>1	>1	>1	-	-	-	-	-	-
	SRF, PAX3	2	12	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.469	0.00668	0.882	>1
1.0nM 90min	MAZ, E12, E12, PAX4	2	478	552135	0.272	0.039	>1	>1	>1	2099869	-	-	-	-	-	3982295	-	-	-	-	5542428
	E12, PAX4	2	428	-	-	-	-	-	-	-	0.0447	0.00168	0.222	>1	>1	-	-	-	-	-	
	E12, CACCCB BINDING FA CTO R	2	73	-	-	-	-	-	-	-	0.118	0.00445	0.587	>1	>1	-	-	-	-	-	
10.0nM 5min	MAZ, E12, AP4, MYOD, E47	2	478	442874	0.0108	0.00193	0.255	>1	>1	1557482	-	-	-	-	-	3982295	-	-	-	-	5542428
	MAZ, E12, AP4, MYOD, E47	1	1016	-	0.0264	0.00471	0.622	>1	>1	-	0.0172	0.000871	0.115	>1	>1	-	-	-	-	-	
	MAZ, E12, PAX4	2	164	-	0.0628	0.0112	>1	>1	>1	-	-	-	-	-	-	-	-	-	-	-	
	MAZ, E12, PAX4	1	1474	-	-	-	-	-	-	-	0.0156	0.000794	0.105	>1	>1	-	-	-	-	-	
	MAZ, E12, PAX4	1	1182	-	-	-	-	-	-	-	0.164	0.00834	>1	>1	>1	-	-	-	-	-	
10.0nM 10min	MAZ, E12	1	1474	552135	0.00951	0.00136	0.18	>1	>1	1557482	-	-	-	-	-	3982295	-	-	-	-	5542428
	MAZ, E12	1	1512	-	0.0325	0.00464	0.613	>1	>1	-	-	-	-	-	-	-	-	-	-	-	
10.0nM 15min	E12, CACCCB BINDING FA CTO R, LEF1, CTCGAGY, TATA, NFKB, AACTT, OCT, USF, OCT1, NFKB, AACTT	2	73	552135	0.0743	0.0106	>1	>1	>1	1557482	0.979	0.0497	>1	>1	>1	3982295	-	-	-	-	5542428
	E12, CACCCB BINDING FA CTO R, LEF1, CTCGAGY, TATA, NFKB, AACTT, OCT, USF, OCT1, NFKB, AACTT	5	8	-	-	-	-	-	-	-	-	-	-	-	-	-	0.0398	-	-	>1	
	E12, CACCCB BINDING FA CTO R, LEF1, CTCGAGY, TATA, NFKB, AACTT, OCT, USF, OCT1, NFKB, AACTT	5	8	-	-	-	-	-	-	-	-	-	-	-	-	-	0.0398	-	-	>1	
10.0nM 30min	FOXO4, FOXO1, FREAC2, NFKB, STAT5A, IK2, TATA, NFAT, WCTTNNNNNAAA, STAT5A, IK2, LEF1, NFAT, FREAC2, TCACATTKW, FOXO4, FREAC2, STAT5A	6	20	552135	0.0079	-	-	-	-	1557482	-	-	-	-	-	3982295	-	-	-	-	5542428
	FOXO4, FOXO1, FREAC2, NFKB, STAT5A, IK2, LEF1, NFAT, FREAC2, TCACATTKW, FOXO4, FREAC2, STAT5A	4	15	-	0.0453	-	-	>1	>1	-	-	-	-	-	-	-	-	-	-	-	
	FOXO4, FOXO1, FREAC2, NFKB, STAT5A, IK2, LEF1, NFAT, FREAC2, TCACATTKW, FOXO4, FREAC2, STAT5A	4	15	-	0.0453	-	-	>1	>1	-	-	-	-	-	-	-	-	-	-	-	
	FOXO4, FOXO1, FREAC2, NFKB, STAT5A, IK2, LEF1, NFAT, FREAC2, TCACATTKW, FOXO4, FREAC2, STAT5A	1	1474	-	0.0472	0.00676	0.892	>1	>1	0.0296	0.0015	0.198	>1	>1	-	-	-	-	-	-	
	FOXO4, FOXO1, FREAC2, NFKB, STAT5A, IK2, LEF1, NFAT, FREAC2, TCACATTKW, FOXO4, FREAC2, STAT5A	4	14	-	-	-	-	-	-	0.00557	-	-	>1	>1	-	-	-	-	-	-	
	FOXO4, FOXO1, FREAC2, NFKB, STAT5A, IK2, LEF1, NFAT, FREAC2, TCACATTKW, FOXO4, FREAC2, STAT5A	5	11	-	-	-	-	-	-	0.014	-	-	>1	>1	-	-	-	-	-	-	
	FOXO4, FOXO1, FREAC2, NFKB, STAT5A, IK2, LEF1, NFAT, FREAC2, TCACATTKW, FOXO4, FREAC2, STAT5A	1	1016	-	-	-	-	-	-	0.182	0.00921	>1	>1	>1	-	-	-	-	-	-	
	FOXO4, FOXO1, FREAC2, NFKB, STAT5A, IK2, LEF1, NFAT, FREAC2, TCACATTKW, FOXO4, FREAC2, STAT5A	2	74	-	-	-	-	-	-	0.371	0.0188	>1	>1	>1	-	-	-	-	-	-	
10.0nM 45min	PAK4, MAZ, LFA1, E12, FOXO4, NFKB, STAT5A, IK2, LEF1, NFAT, FREAC2, TCACATTKW, FOXO4, FREAC2, STAT5A, AP4, SPI1, STAT5B	1	1182	552135	0.228	0.0326	>1	>1	>1	1557482	0.0176	0.000894	0.118	>1	>1	2874627	-	-	-	-	5542428
	PAK4, MAZ, LFA1, E12, FOXO4, NFKB, STAT5A, IK2, LEF1, NFAT, FREAC2, TCACATTKW, FOXO4, FREAC2, STAT5A, AP4, SPI1, STAT5B	1	1474	-	-	-	-	-	-	7.23E-05	3.67E-06	0.000484	0.0478	>1	-	-	-	-	-	-	
	PAK4, MAZ, LFA1, E12, FOXO4, NFKB, STAT5A, IK2, LEF1, NFAT, FREAC2, TCACATTKW, FOXO4, FREAC2, STAT5A, AP4, SPI1, STAT5B	1	157	-	-	-	-	-	-	0.0284	0.00144	0.19	>1	>1	-	-	-	-	-	-	
	PAK4, MAZ, LFA1, E12, FOXO4, NFKB, STAT5A, IK2, LEF1, NFAT, FREAC2, TCACATTKW, FOXO4, FREAC2, STAT5A, AP4, SPI1, STAT5B	2	393	-	-	-	-	-	-	0.243	0.0123	>1	>1	>1	-	-	-	-	-	-	
	PAK4, MAZ, LFA1, E12, FOXO4, NFKB, STAT5A, IK2, LEF1, NFAT, FREAC2, TCACATTKW, FOXO4, FREAC2, STAT5A, AP4, SPI1, STAT5B	1	334	-	-	-	-	-	-	0.926	0.0469	>1	>1	>1	-	-	-	-	-	-	
	PAK4, MAZ, LFA1, E12, FOXO4, NFKB, STAT5A, IK2, LEF1, NFAT, FREAC2, TCACATTKW, FOXO4, FREAC2, STAT5A, AP4, SPI1, STAT5B	6	7	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.0362	-	-	
10.0nM 60min	MAZ, AP4	1	1474	552135	0.0544	0.00778	>1	>1	>1	1557482	-	-	-	-	-	3982295	-	-	-	-	5542428
	MAZ, AP4	1	1016	-	-	-	-	-	-	0.511	0.0259	>1	>1	>1	-	-	-	-	-	-	
10.0nM 90min	MAZ, HSF1, AP1, PAK4, E12, TATA, STAT5A, MYOD, NFAT, HSF1, LEF1, OCT1, NFKB, AACTT, E12, TATA, NFAT, STAT5A, SRF	1	1474	552135	0.00347	0.000496	0.0655	>1	>1	2099869	0.038	0.00143	0.189	>1	>1	3982295	0.0145	0.000288	0.038	>1	5542428
	MAZ, HSF1, AP1, PAK4, E12, TATA, STAT5A, MYOD, NFAT, HSF1, LEF1, OCT1, NFKB, AACTT, E12, TATA, NFAT, STAT5A, SRF	2	53	-	0.233	0.0334	>1	>1	>1	-	-	-	-	-	-	-	-	-	-	-	
	MAZ, HSF1, AP1, PAK4, E12, TATA, STAT5A, MYOD, NFAT, HSF1, LEF1, OCT1, NFKB, AACTT, E12, TATA, NFAT, STAT5A, SRF	1	1182	-	-	-	-	-	-	0.00022	8.28E-06	0.00109	0.108	>1	0.00792	0.000157	0.0208	>1	>1	-	
	MAZ, HSF1, AP1, PAK4, E12, TATA, STAT5A, MYOD, NFAT, HSF1, LEF1, OCT1, NFKB, AACTT, E12, TATA, NFAT, STAT5A, SRF	3	48	-	-	-	-	-	-	0.0219	-	0.109	>1	>1	-	-	-	-	-	-	
	MAZ, HSF1, AP1, PAK4, E12, TATA, STAT5A, MYOD, NFAT, HSF1, LEF1, OCT1, NFKB, AACTT, E12, TATA, NFAT, STAT5A, SRF	2	229	-	-	-	-	-	-	0.909	0.0342	>1	>1	>1	-	-	-	-	-	-	
	MAZ, HSF1, AP1, PAK4, E12, TATA, STAT5A, MYOD, NFAT, HSF1, LEF1, OCT1, NFKB, AACTT, E12, TATA, NFAT, STAT5A, SRF	4	24	-	-	-	-	-	-	-	-	-	-	-	0.00225	-	-	0.581	>1	-	
	MAZ, HSF1, AP1, PAK4, E12, TATA, STAT5A, MYOD, NFAT, HSF1, LEF1, OCT1, NFKB, AACTT, E12, TATA, NFAT, STAT5A, SRF	1	968	-	-	-	-	-	-	-	-	-	-	-	0.0108	0.000214	0.0282	>1	>1	-	
	MAZ, HSF1, AP1, PAK4, E12, TATA, STAT5A, MYOD, NFAT, HSF1, LEF1, OCT1, NFKB, AACTT, E12, TATA, NFAT, STAT5A, SRF	2	63	-	-	-	-	-	-	-	-	-	-	-	0.0697	0.00138	0.182	>1	>1	-	
	MAZ, HSF1, AP1, PAK4, E12, TATA, STAT5A, MYOD, NFAT, HSF1, LEF1, OCT1, NFKB, AACTT, E12, TATA, NFAT, STAT5A, SRF	2	179	-	-	-	-	-	-	-	-	-	-	-	0.173	0.00343	0.453	>1	>1	-	
	MAZ, HSF1, AP1, PAK4, E12, TATA, STAT5A, MYOD, NFAT, HSF1, LEF1, OCT1, NFKB, AACTT, E12, TATA, NFAT, STAT5A, SRF	1	794	-	-	-	-	-	-	-	-	-	-	-	0.402	0.00797	>1	>1	>1	-	
	MAZ, HSF1, AP1, PAK4, E12, TATA, STAT5A, MYOD, NFAT, HSF1, LEF1, OCT1, NFKB, AACTT, E12, TATA, NFAT, STAT5A, SRF	2	108	-	-	-	-	-	-	-	-	-	-	-	2.32	0.046	>1	>1	>1	0.384	0.00547
	MAZ, HSF1, AP1, PAK4, E12, TATA, STAT5A, MYOD, NFAT, HSF1, LEF1, OCT1, NFKB, AACTT, E12, TATA, NFAT, STAT5A, SRF	4	35	-	-	-	-	-	-	-	-	-	-	-	-	-	0.0249	-	-	>1	
	MAZ, HSF1, AP1, PAK4, E12, TATA, STAT5A, MYOD, NFAT, HSF1, LEF1, OCT1, NFKB, AACTT, E12, TATA, NFAT, STAT5A, SRF	1	291	-	-	-	-	-	-	-	-	-	-	-	-	-	0.0514	0.000732	0.0967	>1	>1