

Figure 1. The top 8 most informative several SL-independent features used in our MNMC prediction approach. Different from Figure 2, here we show the ratio of the frequencies of each feature in the SL and non-SL sets. The Kolmogorov-Smirnov (KS) test to capture the difference of the distributions of a feature in the SL and non-SL classes. The D-statistics and p-values of the KS test are shown here.

Table 1: Description of 152 SL-independent and 15 SL-dependent features and their discriminative power (measured by KS test and pvalue) for separating the SL interactions from the non-SL ones

| Official Feature Name | Internal Feature Name | Description | Nature of values | KS statistic | KS pvalue | Category |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| Bayesian Network | bayesian_network | value 1 if there is a link in the Bayesian network (Zhu et al., Nature Genetics 2009), 0 otherwise | binary | 0.003773115 |  | SL-independent feature |
| BN SemanSim | bn_cocausality_semsi m | Semantic similarity between nodes in the Bayesian network using Lin's measure (Lin et al., ICML 1998) | real-valued | 0.031544094 | $0.01101$ | SL-independent feature |
| BN Edge Betweenness | bn_edge_betweennes <br> s | Betweenness of edge between two genes in the Bayesian network | real-valued | 0.013106287 | $0.76028$ | SL-independent feature |
| BN Edge Betweenness sqrooted | bn_edge_betweennes <br> s_sqrooted | Square root of betweenness of edges between two genes in Bayesian network (to avoid scale problems) | real-valued | 0.013106287 | $0.76028$ | SL-independent feature |
| BN Edge Degree | bn_edge_degree | Degree of vertex corresponding to an edge in the Bayesian network in its edge graph version | real-valued | 0.003415334 |  | SL-independent feature |
| BN (Undirected) Shortestpath | bn_shortestpath_undi rected | Shortest path over Bayesian network treated as an undirected graph | real-valued | 0.023797362 | $0.10355$ | SL-independent feature |
| Causality Test Network | causality_test_networ <br> k | Value is 1 if there is an undirected link between nodes in causality test network (Schadt et al., Nature Genetics 2005), 0 otherwise | binary | 0.005622043 |  | SL-independent feature |
| Causality Network Shortestpath (undirected) | ctn_shortestpath_undi rected | Shortest path over undirected version of causality network | real-valued | 0.067413792 | $0.05534$ | SL-independent feature |
| Common QTL | common_qtl | Value is 1 if the two genes have a common qtl (Zhu et al., Nature Genetics 2009), else zero. | binary | 3.77E-17 |  | SL-independent feature |
| Common Functions | commonfunctions_cha d | Number of functions shared by two genes among 138 most populated GO BP terms recommended by Myers et al (2006) | real-valued | 0.186161707 |  | SL-independent feature |
| Common TF | commontf | Number of common transcription factors that two genes are regulated by | real-valued | 0.045359829 | $0.12847$ | SL-independent feature |
| Complex <br> Comembership | complex_comembersh ip | Number of complexes two proteins are co-members of | real-valued | 0.115308739 | 0.42069 | SL-independent feature |
| DNA Seq Blast alignmentlength | dna_seq_blast_alignm entlength | Length of BLAST alignment over DNA sequences of two genes | real-valued | 0.009120049 | $0.42465$ | SL-independent feature |
| DNA Seq Blast bitscore | dna_seq_blast_bitscor e | Bit score of BLAST alignment over DNA sequences of two genes | real-valued | 0.009120049 | 0.42465 | SL-independent feature |
| DNA Seq Simil | dna_seq_blast_evalue | E-value of BLAST alignment over DNA sequences of two genes | real-valued | 0.009287368 | 0.40174 | SL-independent feature |


| DNA Seq Blast numgaps | dna_seq_blast_numga ps | Number of gaps included in BLAST alignment over dna sequences of two genes | real-valued | 0.00040028 |  | 1 SL-independent feature |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| DNA Seq Blast nummismatches | dna_seq_blast_nummi smatches | Number of mismatches in BLAST alignment over DNA sequences of two genes | real-valued | 0.008351062 | $0.53855$ | SL-independent feature |
| DNA Seq Blast percentidentity | dna_seq_blast_percen tidentity | Percentage identity in BLAST alignment over DNA sequences of two genes | real-valued | 0.009120049 | $0.42465$ | SL-independent feature |
| Module <br> Comembership (MN Abs) | mn_abs_module | Co-membership in co-expression modules (Zhang \& Horvath, SAGMB 2005) derived from absolute value of correlations over Mnaimneh's expression data set (Mnaimneh et al. Cell 2004) | binary | 0.001012591 |  | 1 SL-independent feature |
| MN Abs TOM | mn_abs_tom | Topological overlap (Zhang \& Horvath, SAGMB 2005) measured over the absolute value of correlations over Mnaimneh's expression data set | real-valued | 0.030461558 | 7.05E-08 | SL-independent feature |
| MN Corrl | mn_corr | Pairwise correlations of genes over Mnaimneh's expression data set | real-valued | 0.047197933 |  | SL-independent feature |
| Module <br> Comembership (MN Neg) | mn_neg_module | Co-membership in co-expression modules derived only from negative correlations over Mnaimneh's expression data set | binary | 0.00304585 |  | 1 SL-independent feature |
| MN Neg TOM | mn_neg_tom | Topological overlap over negative correlations over Mnaimneh's expression data set | real-valued | 0.044054877 | $5.55 \mathrm{E}-16$ | SL-independent feature |
| KO-Signature | oneko_otheraffected | Value is 1 if one gene being knocked out changes the expression of the other gene, 0 otherwise (Hughes et al. Cell 2000) | binary | 0.013816833 | $0.80678$ | SL-independent feature |
| Phyloprofiles Misim | phyloprofiles_misim | Mutual information between the phylogenetic profiles of two proteins | real-valued | 0.067342651 |  | 0 SL-independent feature |
| PPI Clique Comembership | ppi_clique_comember ship | Number of cliques in the PPI network (Zhu et al., Nature Genetics 2009) two proteins are co-members of | real-valued | 0.083961527 |  | 0 SL-independent feature |
| PPI Community Comembership | ppi_community_come mbership | Number of communities derived from PPI network that two proteins are co-members of | real-valued | 0.225759947 |  | 0 SL-independent feature |
| PPI Edge Betweenness | $\begin{aligned} & \text { ppi_edge_betweennes } \\ & \text { s } \end{aligned}$ | Betweenness of the edge between two proteins in the PPI network | real-valued | 0.044418223 | $2.13 \mathrm{E}-14$ | 4 SL-independent feature |
| PPI Edge Betweenness Sqrooted | ppi_edge_betweennes s_sqrooted | Square root of betweenness of the edge between two proteins in PPI network (to avoid scale problems) | real-valued | 0.044418223 | $2.13 \mathrm{E}-14$ | 4 SL-independent feature |
| PPI Edge Degree | ppi_edge_degree | Degree of vertex corresponding to an edge in the PPI network in its edge graph version | real-valued | 0.04443815 | $2.08 \mathrm{E}-14$ | SL-independent feature |


| PPI Module Comembership | ppi_module_comemb ership | Co-membership in module discovered from PPI network (Zhang \& Horvath, SAGMB 2005) | binary | 0.045673668 | $3.33 \mathrm{E}-15$ | SL-independent feature |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| PPI | ppi_network | Value is 1 if there is an edge between two proteins in the PPI network, 0 otherwise | binary | 0.044398296 | $2.20 \mathrm{E}-14$ | 4 SL-independent feature |
| PPI Shortest Path | ppi_shortestpath | Length of shortest path between two proteins in PPI network | real-valued | 0.1400902 |  | 0 SL-independent feature |
| PPI TOM | ppi_tom | Value of topological overlap (Zhang \& Horvath, SAGMB 2005) between two proteins computed from PPI network | real-valued | 0.099168921 |  | 0 SL-independent feature |
| Protein Seq Blast Alignmentlength | protein_seq_blast_alig nmentlength | Length of BLAST alignment over amino acid sequences of two proteins | real-valued | 0.027204966 | $2.25 \mathrm{E}-06$ | SL-independent feature |
| Protein Seq Blast Bitscore | protein_seq_blast_bits core | Bit score of BLAST alignment over amino acid sequences of two proteins | real-valued | 0.027149193 | $2.38 \mathrm{E}-06$ | SL-independent feature |
| Protein Seq Blast Simil | protein_seq_blast_eva lue | E-value of BLAST alignment over amino acid sequences of two proteins | real-valued | 0.027181064 | $2.30 \mathrm{E}-06$ | SL-independent feature |
| Protein Seq Blast Numgaps | protein_seq_blast_nu mgaps | Number of gaps included in BLAST alignment over amino acid sequences of two proteins | real-valued | 0.023544959 | 7.00E-05 | SL-independent feature |
| Protein Seq Blast Nummismatches | protein_seq_blast_nu mmismatches | Number of mismatches in BLAST alignment over amino acid sequences | real-valued | 0.026848923 | $3.21 \mathrm{E}-06$ | SL-independent feature |
| Protein Seq Blast Percentidentity | protein_seq_blast_per centidentity | Percentage identity in BLAST alignment over amino acid sequences | real-valued | 0.027149193 | $2.38 \mathrm{E}-06$ | SL-independent feature |
| Module <br> Comembership (Brem <br> Abs) | brem_abs_module | Value is 1 if two genes are comembers of a co-expression module defined by absolute value of correlations over Brem's data set (Zhu et al., Nature Genetics 2009), 0 otherwise | binary | 0.057280817 |  | 0 SL-independent feature |
| Brem Abs TOM | brem_abs_tom | Topological overlap measured over the absolute value of correlations over Brem's expression data set | real-valued | 0.049681888 |  | 0 SL-independent feature |
| Brem Correl | brem_corr | Pairwise correlation of genes computed over Brem's gene expression data set | real-valued | 0.090469465 |  | 0 SL-independent feature |
| Brem Neg Module Commembership | brem_neg_module | Co-membership in coexpression modules discovered using negative correlations from Brem's expression data set | binary | 0.078155158 |  | 0 SL-independent feature |
| Brem Neg TOM | brem_neg_tom | Topological overlap over negative correlations computed from Brem's expression data set | real-valued | 0.090581254 |  | 0 SL-independent feature |


| Module <br> Comembership (Rosetta Abs) | rosetta_abs_module | Value is 1 if two genes are comembers of a co-expression module defined by absolute value of correlations over Hughes et al's Rosetta microarray compendium (Hughes et al. Cell 2000), 0 otherwise | binary | 0.013910463 | $0.05673$ | 3 SL-independent feature |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| Rosetta Abs TOM | rosetta_abs_tom | Topological overlap measured over the absolute value of correlations over Hughes et al's Rosetta microarray compendium | real-valued | 0.006263813 | $0.86298$ | 8 SL-independent feature |
| Rosetta Corrl | rosetta_corr | Pairwise correlation of genes computed over Hughes et al's Rosetta microarray compendium | real-valued | 0.021969856 | $0.00028$ | 8 SL-independent feature |
| Module <br> Comembership (Rosetta Neg) | rosetta_neg_module | Value is 1 if two genes are comembers of a co-expression module discovered using negative correlations computed from Hughes et al's Rosetta microarray compendium, 0 otherwise | binary | 0.009819535 | $0.33725$ | SL-independent feature |
| Rosetta Neg TOM | rosetta_neg_tom | Topological overlap over negative correlations computed from Hughes et al (2000)'s Rosetta expression compendium | real-valued | 0.019434071 | $0.00191$ | SL-independent feature |
| Same Mutant | same_mutant_phenot ype | Number of mutant phenotypes shared by two genes | real-valued | 0.026814789 | $3.41 \mathrm{E}-06$ | SL-independent feature |
| SemanSim BP | semsim_bp | Similarity of two genes using their annotations to GO BP terms and semantic similarity between the terms (Tao et al. Bioinformatics 2007) | real-valued | 0.230677446 |  | 0 SL-independent feature |
| SemanSim CC | semsim_cc | Similarity of two genes using their annotations to GO CC terms and semantic similarity between the terms | real-valued | 0.182661826 |  | SL-independent feature |
| SemanSim MF | semsim_mf | Similarity of two genes using their annotations to GO MF terms and semantic similarity between the terms | real-valued | 0.076373486 |  | 0 SL-independent feature |
| Module <br> Comembership <br> (Spellman Abs) | spellman_abs_module | Value is 1 if two genes are comembers of a module derived from absolute value of correlations computed from Spellman's expression data set (Spellman et al. Mol Biol Cell 2007) | binary | 0.027265957 | $2.45 \mathrm{E}-06$ | 6 SL-independent feature |
| Spellman Abs TOM | spellman_abs_tom | Topological overlap over absolute value of correlations from Spellman's expression data set | real-valued | 0.064747704 |  | 0 SL-independent feature |
| Spellman Corrl | spellman_corr | Pairwise correlations of genes over Spellman's expression data set | real-valued | 0.059435461 |  | 0 SL-independent feature |


| Module <br> Comembership <br> (Spellman Neg) | spellman_neg_module | Co-membership in modules derived binary from negative correlations from Spellman's data | 0.030391715 | $9.05 \mathrm{E}-08$ | SL-independent feature |
| :---: | :---: | :---: | :---: | :---: | :---: |
| Spellman Neg TOM | spellman_neg_tom | Topological overlap over negative real-valued correlations over Spellman's expression data set | 0.061712989 |  | 0 SL-independent feature |
| TF Activity | tfactivity | ```1 if one of the proteins is a binary transcription factor for the other, else 0 (Reference?)``` | 0.066955929 | $0.27201$ | SL-independent feature |
| Pathway Comembership | within_pathways | Co-membership in the same KEGG binary pathway | 0.438803136 |  | SL-independent feature |
| O(BN, DNA Seq Simil) | bn_cocausality_semsi m_dna_seq_blast_eva lue | Overlay between semantic similarity real-valued between nodes in Bayesian network and E-value of BLAST alignment over DNA sequences of genes | 0.033506277 | $2.82 \mathrm{E}-07$ | SL-independent overlay feature |
| O(BN, MN Abs TOM) | bn_cocausality_semsi m_mn_abs_tom | Overlay between semantic similarity real-valued between nodes in Bayesian network <br> and topological overlap over <br> absolute value of correlations <br> computed from Mnaimneh's <br> expression data set | 0.040759334 | $1.57 \mathrm{E}-05$ | SL-independent overlay feature |
| BN_MN Corrl | bn_cocausality_semsi m_mn_corr | Overlay between semantic similarity real-valued between nodes in Bayesian network and pairwise correlations computed from Mnaimneh's expression data set | 0.045082241 | $1.43 \mathrm{E}-09$ | SL-independent overlay feature |
| O(BN, MN Neg TOM) | bn_cocausality_semsi m_mn_neg_tom | Overlay between semantic similarity real-valued over nodes in Bayesian network and topological overlap over negative correlations computed from Mnaimneh's expression data set | 0.071865925 | $2.92 \mathrm{E}-05$ | SL-independent overlay feature |
| $\mathrm{O}(\mathrm{BN}, \mathrm{PPI})$ | bn_cocausality_semsi <br> m_ppi_network | Overlay between semantic similarity real-valued over nodes in Bayesian network and PPI network | 0.083488599 |  | 0 SL-independent overlay feature |
| O(BN, Protein Seq <br> Simil) | bn_cocausality_semsi m_protein_seq_blast_ evalue | Overlay between semantic similarity real-valued between nodes in Bayesian network and E-value of BLAST alignment over amino acid sequences of proteins | 0.04139262 | $1.20 \mathrm{E}-10$ | SL-independent overlay feature |
| O(BN, Brem Abs TOM) | bn_cocausality_semsi <br> m_brem_abs_tom | Overlay between semantic similarity real-valued between nodes in Bayesian network and topological overlap measured over the absolute value of correlations computed from Brem's expression data set | 0.072567791 |  | 0 SL-independent overlay feature |
| O(BN, Brem Corrl) | bn_cocausality_semsi <br> m_brem_corr | Overlay between semantic similarity real-valued between nodes in Bayesian network and pairwise correlations between genes computed from Brem's expression data set | 0.046601724 | $2.05 \mathrm{E}-13$ | 3 SL-independent overlay feature |


| O(BN, Brem Neg TOM) | bn_cocausality_semsi m_brem_neg_tom | Overlay between semantic similarity real-valued between nodes in Bayesian network and topological overlap measured over negative correlations computed from Brem's expression data set | 0.084354265 |  | 0 SL-independent overlay feature |
| :---: | :---: | :---: | :---: | :---: | :---: |
| O(BN, Same Mutant) | bn_cocausality_semsi m_same_mutant_phe notype | Overlay between semantic similarity real-valued between nodes in Bayesian network and number of mutant phenotypes shared by two genes | 0.038003287 | $4.92 \mathrm{E}-06$ | 6 SL-independent overlay feature |
| O(BN, SemanSim BP) | bn_cocausality_semsi m_semsim_bp | Overlay between semantic similarity real-valued between nodes in Bayesian network and GO BP-based similarity network | 0.027468419 | 4.03E-05 | 5 SL-independent overlay feature |
| O(BN, SemanSim MF) | bn_cocausality_semsi m_semsim_mf | Overlay between semantic similarity real-valued between nodes in Bayesian network and GO MF-based annotation similarities between genes | 0.055350485 |  | 0 SL-independent overlay feature |
| O(DNA Seq Simil, MN Abs TOM) | dna_seq_blast_evalue _mn_abs_tom | Overlay between E-value of BLAST real-valued alignment over DNA sequences of genes and topological overlap over absolute value of correlations computed from Mnaimneh's expression data set | 0.005748227 | 0.99068 | 8 SL-independent overlay feature |
| O(DNA Seq Simil, MN Corrl) | dna_seq_blast_evalue _mn_corr | Overlay between E-value of BLAST real-valued alignment over DNA sequences of genes and pairwise correlations between genes computed from Mnaimneh's expression data set | 0.015058817 | $0.05696$ | 6 SL-independent overlay feature |
| O(DNA Seq Simil, PPI) | dna_seq_blast_evalue _ppi_network | Overlay between E-value of BLAST real-valued alignment over DNA sequences of genes and PPI network | 0.023231347 | $0.0001$ | 1 SL-independent overlay feature |
| O(DNA Seq Simil, Protein Seq Simil) | ```dna_seq_blast_evalue _protein_seq_blast_ev alue``` | Overlay between E-values of BLAST real-valued alignments over DNA sequences of genes and amino acid sequence of proteins | 0.029438767 | $2.79 \mathrm{E}-07$ | 7 SL-independent overlay feature |
| O(DNA Seq Simil, Brem Abs TOM) | dna_seq_blast_evalue _brem_abs_tom | Overlay between E-value of BLAST real-valued alignment over DNA sequences of genes and topological overlap over absolute value of correlations between genes computed from Brem's expression data set | 0.042048381 | $3.27 \mathrm{E}-13$ | 3 SL-independent overlay feature |
| O(DNA Seq Simil, Brem Corrl) | dna_seq_blast_evalue _brem_corr | Overlay between E-value of BLAST real-valued alignment over DNA sequences of genes and correlations between genes computed from Brem's expression data | 0.01906552 | 0.00257 | 7 SL-independent overlay feature |


| O(DNA Seq Simil, SemanSim BP) | dna_seq_blast_evalue _semsim_bp | Overlay between E-value of BLAST alignment over DNA sequences of genes and GO BP-based annotation similarities between genes | real-valued | 0.042519114 | $6.11 \mathrm{E}-15$ | SL-independent overlay feature |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| O(DNA Seq Simil, SemanSim MF) | dna_seq_blast_evalue _semsim_mf | Overlay between E-value of BLAST alignment over DNA sequences of genes and GO MF-based annotation similarities between genes | real-valued | 0.020677145 | 0.00074 | SL-independent overlay feature |
| O(MN Abs TOM, MN Corrl) | $\begin{aligned} & \text { mn_abs_tom_mn_cor } \\ & \text { r } \end{aligned}$ | Overlay between topological overlap over absolute value of correlations computed from Mnaimneh's expression data set and pairwise correlations between genes over Mnaimneh's expression data set | real-valued | 0.031074038 | $0.00275$ | SL-independent overlay feature |
| O(MN Abs TOM, Protein Seq Simil) | mn_abs_tom_protein _seq_blast_evalue | Overlay between topological overlap measured over the absolute value of the correlations computed from Mnaimneh's expression data set and E-value of BLAST alignment over amino acid sequences of proteins | real-valued | 0.009833422 | 0.65455 | SL-independent overlay feature |
| O(MN Abs TOM, Brem Abs TOM) | ```mn_abs_tom_brem_a bs_tom``` | Overlay between topological overlap over absolute value of correlations computed from Mnaimneh's and Brem's expression data sets | real-valued | 0.073671194 |  | 0 SL-independent overlay feature |
| O(MN Abs TOM, Brem Corrl) | $\begin{aligned} & \text { mn_abs_tom_brem_c } \\ & \text { orr } \end{aligned}$ | Overlay between topological overlap over absolute value of correlations computed from Mnaimneh's expression data set and pairwise correlations between genes computed from Brem's expression data set | real-valued | 0.036933483 | $4.07 \mathrm{E}-07$ | SL-independent overlay feature |
| O(MN Abs TOM, SemanSim BP) | $\begin{aligned} & \text { mn_abs_tom_semsim } \\ & \text { _bp } \end{aligned}$ | Overlay between topological overlap measured over the absolute value of the correlations computed from Mnaimneh's expression data set and GO BP-based annotation similarities between genes | real-valued | 0.017973033 | $0.04317$ | SL-independent overlay feature |
| O(MN Abs TOM, SemanSim MF) | mn_abs_tom_semsim _mf | Overlay between topological overlap measured over the absolute value of correlations over Mnaimneh's expression data set and GO MF-based similarity network | real-valued | 0.026803814 | 0.00039 | 9 SL-independent overlay feature |
| O(MN Corrl, Protein Seq Simil) | mn_corr_protein_seq _blast_evalue | Overlay between correlations between genes computed from Mnaimneh's expression data set and E-value of BLAST alignment over amino acid sequences of proteins | real-valued | 0.027525876 | $2.12 \mathrm{E}-05$ | SL-independent overlay feature |


| O(Brem Abs TOM, MN Corrl) | ```brem_abs_tom_mn_c orr``` | Overlay between topological overlap measured over the absolute value of correlations computed from Brem's gene expression data set and pairwise correlations between genes computed from Mnaimneh's expression data set | real-valued | 0.070735606 |  | SL-independent overlay feature |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| O(Brem Abs TOM, <br> Protein Seq Simil) | brem_abs_tom_protei n_seq_blast_evalue | Overlay between topological overlap over absolute value of correlation computed from Brem's expression data set and E-value of BLAST alignment over amino acid sequences of proteins | real-valued | 0.049884225 |  | 0 SL-independent overlay feature |
| O(Brem Abs TOM, Brem Corrl) | brem_abs_tom_brem _corr | Overlay between topological overlap measured over the negative correlations computed from Brem's expression data set and pairwise correlations computed from Brem's expression data set | real-valued | 0.048180526 | $2.22 \mathrm{E}-$ | SL-independent overlay feature |
| O(Brem Corrl, MN Corrl) | brem_corr_mn_corr | Overlay between pairwise correlations between genes computed from Brem's and Mnaimneh's expression data sets | real-valued | 0.056061276 |  | 0 SL-independent overlay feature |
| O(Brem Corrl, Protein Seq Simil) | brem_corr_protein_se q_blast_evalue | Overlay between pairwise correlations between genes computed from Brem's expression data set and E-value of BLAST alignment over amino acid sequences of proteins | real-valued | 0.053322909 |  | 0 SL-independent overlay feature |
| O(Brem Neg TOM, DNA Seq Simil) | brem_neg_tom_dna_s eq_blast_evalue | Overlay between topological overlap over negative correlations computed from Brem's expression data set and E-value of BLAST alignment over DNA sequences of genes | real-valued | 0.039811385 | $2.41 \mathrm{E}-$ | SL-independent overlay feature |
| O(Brem Neg TOM, MN Abs TOM) | brem_neg_tom_mn_a bs_tom | Overlay between topological overlap measured over the negative correlations computed from Brem's expression data set and topological overlap measured over the absolute value of the correlations computed from Mnaimneh's expression data set | real-valued | 0.099627888 |  | 0 SL-independent overlay feature |
| O(Brem Neg TOM, MN Corrl) | brem_neg_tom_mn_c orr | Overlay between topological overlap over negative correlations computed from Brem's expression data set and correlations between genes computed from Mnaimneh's expression data set | real-valued | 0.077880457 |  | 0 SL-independent overlay feature |


| O(Brem Neg TOM, MN Neg TOM) | brem_neg_tom_mn_n eg_tom | Overlay between topological overlap measured over the negative of correlations over brem's expression data set and topological overlap measured over the negative correlations computed from Mnaimneh's expression data set | real-valued | 0.146256768 |  | SL-independent overlay feature |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| O(Brem Neg TOM, PPI) | brem_neg_tom_ppi_n etwork | Overlay between topological overlap over negative correlations computed from Brem's expression data set and PPI network | real-valued | 0.06636798 |  | 0 SL-independent overlay feature |
| O(Brem Neg TOM, Protein Seq Simil) | brem_neg_tom_protei n_seq_blast_evalue | Overlay between topological overlap over negative correlations computed from Brem's expression data and E-value of BLAST alignment over amino acid sequences of proteins | real-valued | 0.06177282 |  | SL-independent overlay feature |
| O(Brem Neg TOM, Brem Abs TOM) | brem_neg_tom_brem _abs_tom | Overlay between topological overlap measured over negative correlations and absolute value of all correlations computed from Brem's gene expression data set | real-valued | 0.092052147 |  | SL-independent overlay feature |
| O(Brem Neg TOM, Brem Corrl) | brem_neg_tom_brem _corr | Overlay between topological overlap over negative correlations computed from Brem's expression data set and correlations between genes computed from Brem's expression data set | real-valued | 0.067768057 |  | SL-independent overlay feature |
| O(Brem Neg TOM, Same Mutant) | brem_neg_tom_same _mutant_phenotype | Overlay between topological overlap over negative correlations computed from Brem's expression data set and number of common mutant phenotypes of genes | real-valued | 0.049584765 | $2.59 \mathrm{E}-10$ | SL-independent overlay feature |
| O(Brem Neg TOM, SemanSim BP) | brem_neg_tom_semsi m_bp | Overlay between topological overlap measured over the negative correlations computed from Brem's expression data set and GO BPbased annotation similarities between genes | real-valued | 0.051382212 |  | SL-independent overlay feature |
| O(Brem Neg TOM, SemanSim MF) | brem_neg_tom_semsi m_mf | Overlay between topological overlap measured over the negative correlations computed from Brem's gene expression data set and GO MF-based annotation similarities between genes | real-valued | 0.055210647 |  | SL-independent overlay feature |
| O(Same Mutant, DNA Seq Simil) | same_mutant_phenot ype_dna_seq_blast_ev alue | Overlay between number of common mutant phenotypes of genes and E-value of BLAST alignment over DNA sequences of genes | real-valued | 0.019848173 | $0.00835$ | 5 SL-independent overlay feature |


| O(Same Mutant, MN Abs TOM) | same_mutant_phenot ype_mn_abs_tom | Overlay between number of common mutant phenotypes of genes and topological overlap over absolute value of correlations computed from Mnaimneh's expression data set | real-valued | 0.038054823 | 7.90E-05 | SL-independent overlay feature |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| O(Same Mutant, MN Corrl) | same_mutant_phenot ype_mn_corr | Overlay between number of common mutant phenotypes of genes and pairwise correlations between genes computed from Mnaimneh's expression data set | real-valued | 0.061030243 |  | 0 SL-independent overlay feature |
| O(PPI, Same Mutant <br> Phenotype) | same_mutant_phenot ype_ppi_network | Overlay between number of common mutant phenotypes of genes and PPI network | real-valued | 0.098738496 |  | 0 SL-independent overlay feature |
| O(Same Mutant, Protein Seq Simil) | same_mutant_phenot ype_protein_seq_blast _evalue | Overlay between number of common mutant phenotypes of genes and E-value of BLAST <br> alignment over amino acid sequences of proteins | real-valued | 0.058405267 |  | 0 SL-independent overlay feature |
| O(Same Mutant, Brem Abs TOM) | same_mutant_phenot ype_brem_abs_tom | Overlay between number of common mutant phenotypes of genes and topological overlap over absolute values of correlations computed from Brem's expression data set | real-valued | 0.02904602 | $0.00013$ | SL-independent overlay feature |
| O(Same Mutant, Brem Corrl) | same_mutant_phenot ype_brem_corr | Overlay between number of common mutant phenotypes of genes and pairwise correlations between genes computed from Brem's expression data set | real-valued | 0.018140671 | $0.0228$ | SL-independent overlay feature |
| O(Same Mutant, SemanSim BP) | same_mutant_phenot ype_semsim_bp | Overlay between number of common mutant phenotypes of genes and GO BP-based annotation similarities between genes | real-valued | 0.038263379 | $2.10 \mathrm{E}-09$ | SL-independent overlay feature |
| O(Same Mutant, SemanSim MF) | same_mutant_phenot ype_semsim_mf | Overlay between number of common mutant phenotypes of genes and GO MF-based annotation similarities between genes | real-valued | 0.024476516 | $0.00042$ | 2 SL-independent overlay feature |
| O(MN Neg TOM, DNA Seq Simil) | mn_neg_tom_dna_se q_blast_evalue | Overlay between topological overlap over negative correlations computed from Mnaimneh's expression data and E -value of BLAST alignment over DNA sequences of genes | real-valued | 0.002104359 |  | 1 SL-independent overlay feature |
| O(MN Neg TOM, MN Abs TOM) | mn_neg_tom_mn_abs _tom | Overlay between topological overlap measured over the negative correlations and the absolute value of correlations computed from Mnaimneh's gene expression data set | real-valued | 0.070476064 | 0.00153 | 3 SL-independent overlay feature |


| O(MN Neg TOM, MN Corrl) | $\begin{aligned} & \text { mn_neg_tom_mn_cor } \\ & \text { r } \end{aligned}$ | Overlay between topological overlap measured over the negative correlations computed from Mnaimneh's expression data set and pairwise correlations computed from Mnaimneh's gene expression data set | real-valued | 0.041075282 | $0.03905$ | SL-independent overlay feature |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| O(MN Neg TOM, PPI) | mn_neg_tom_ppi_net work | Overlay between topological overlap over negative correlations computed from Mnaimneh's expression data set and PPI network | real-valued | 0.005657273 |  | 1 SL-independent overlay feature |
| O(MN Neg TOM, Protein Seq Simil) | mn_neg_tom_protein _seq_blast_evalue | Overlay between topological overlap over negative correlations computed from Mnaimneh's expression data set and E-value of BLAST alignment over amino acid sequences of proteins | real-valued | 0.005396102 |  | 1 SL-independent overlay feature |
| O(Brem Abs TOM, MN Neg TOM) | $\begin{aligned} & \text { mn_neg_tom_brem_a } \\ & \text { bs_tom } \end{aligned}$ | Overlay between topological overlap over negative correlations computed from Mnaimneh's expression data set and pairwise correlations computed from Brem's expression data set | real-valued | 0.116181926 | $2.22 \mathrm{E}-16$ | SL-independent overlay feature |
| O(MN Neg TOM, Brem Corrl) | $\begin{aligned} & \text { mn_neg_tom_brem_c } \\ & \text { orr } \end{aligned}$ | Overlay between topological overlap over negative correlations computed from Mnaimneh's expression data set and pairwise correlations computed from Brem's expression data set | real-valued | 0.042318609 | $0.00316$ | SL-independent overlay feature |
| O(MN Neg TOM< Same Mutant) | mn_neg_tom_same_ mutant_phenotype | Overlay between topological overlap over negative correlations computed from Mnaimneh's expression data set and number of mutant phenotypes shared by genes | real-valued | 0.040529238 | $0.072$ | SL-independent overlay feature |
| O(MN Neg TOM, SemanSim BP) | $\begin{aligned} & \text { mn_neg_tom_semsim } \\ & \text { _bp } \end{aligned}$ | Overlay between topological overlap over negative correlations computed from Mnaimneh's expression data set and GO BPbased annotation similarities between genes | real-valued | 0.012472343 | $0.9265$ | SL-independent overlay feature |
| O(MN Neg TOM, SemanSim MF) | ```mn_neg_tom_semsim _mf``` | Overlay between topological overlap measured over the negative correlations computed from Mnaimneh's expression data set and GO MF-based annotation similarities between genes | real-valued | 0.043351885 |  | 5 SL-independent overlay feature |
| O(SemanSim BP, MN Corrl) | semsim_bp_mn_corr | Overlay between GO BP-based annotation similarities between genes and pairwise correlations computed from Mnaimneh's expression data set | real-valued | 0.052965552 |  | 0 SL-independent overlay feature |


| O(SemanSim BP, Protein Seq Simil) | semsim_bp_protein_s eq_blast_evalue | Overlay between GO BP-based annotation similarities between genes and E-value of BLAST alignment over amino acid sequences of proteins | real-valued | 0.13479471 |  | 0 SL-independent overlay feature |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| O(SemanSim BP, Brem Abs TOM) | $\begin{aligned} & \text { semsim_bp_brem_abs } \\ & \text { _tom } \end{aligned}$ | Overlay between GO BP-based annotation similarities between genes and topological overlap measured over the absolute value of correlations computed from Brem's gene expression data set | real-valued | 0.027322915 | $6.07 \mathrm{E}-06$ | SL-independent overlay feature |
| O(SemanSim BP, Brem Corrl) | $\begin{aligned} & \text { semsim_bp_brem_cor } \\ & \text { r } \end{aligned}$ | Overlay between GO BP-based annotation similarities between genes and pairwise correlations computed from Brem's expression data set | real-valued | 0.032669623 | $5.51 \mathrm{E}-09$ | SL-independent overlay feature |
| O(SemanSim CC, BN) | semsim_cc_bn_cocaus ality_semsim | Overlay between GO CC-based annotation similarities between genes and semantic similarity between nodes in Bayesian network | real-valued | 0.028285293 | $2.10 \mathrm{E}-05$ | SL-independent overlay feature |
| O(SemanSim CC, DNA Seq Simil) | semsim_cc_dna_seq_ blast_evalue | Overlay between GO CC-based annotation similarities between genes and E-value of BLAST alignment over DNA sequences of genes | real-valued | 0.03235424 | $7.88 \mathrm{E}-09$ | SL-independent overlay feature |
| O(SemanSim CC, MN Abs TOM) | $\begin{aligned} & \text { semsim_cc_mn_abs_t } \\ & \text { om } \end{aligned}$ | Overlay between GO CC-based annotation similarities between genes and topological overlap over absolute value of correlations computed from Mnaimneh's expression data | real-valued | 0.028348524 | $0.00014$ | SL-independent overlay feature |
| $\begin{aligned} & \text { O(SemanSim CC, MN } \\ & \text { Corrl) } \end{aligned}$ | semsim_cc_mn_corr | Overlay between GO CC-based annotation similarities between genes and pairwise correlations between Mnaimneh's expression data set | real-valued | 0.043933768 | $9.06 \mathrm{E}-14$ | SL-independent overlay feature |
| O(SemanSim CC, MN Neg TOM) | $\begin{aligned} & \text { semsim_cc_mn_neg_t } \\ & \text { om } \end{aligned}$ | Overlay between GO CC-based annotation similarities between genes and topological overlap measured over the negative correlations computed from Mnaimneh's expression data set | real-valued | 0.043727296 | $0.00132$ | SL-independent overlay feature |
| O(PPI, SemanSim CC) | ```semsim_cc_ppi_netwo rk``` | Overlay between GO CC-based annotation similarities between genes and PPI network | real-valued | 0.176806131 |  | 0 SL-independent overlay feature |
| O(SemanSim CC, Protein Seq Simil) | semsim_cc_protein_se q_blast_evalue | Overlay between GO CC-based annotation similarities between genes and E-value of BLAST alignment over amino acid sequences of proteins | real-valued | 0.127923716 |  | 0 SL-independent overlay feature |


| O(SemanSim CC, Brem Abs TOM) | semsim_cc_brem_abs _tom | Overlay between GO CC-based annotation similarities between genes and topological overlap over absolute value of correlations computed from Brem's expression data set | real-valued | 0.028920246 | $1.32 \mathrm{E}-\mathrm{C}$ | SL-independent overlay feature |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| O(SemanSim CC, Brem Corrl) | semsim_cc_brem_corr | Overlay between GO CC-based annotation similarities between genes and pairwise correlations computed from brem's expression data set | real-valued | 0.028709683 | 4.90E-07 | SL-independent overlay feature |
| O(SemanSim CC, Brem Neg TOM) | semsim_cc_brem_neg _tom | Overlay between GO CC-based annotation similarities between genes and topological overlap over negative correlations computed from Brem's expression data set | real-valued | 0.072506963 |  | SL-independent overlay feature |
| O(SemanSim CC, <br> Same Mutant) | semsim_cc_same_mut ant_phenotype | Overlay between GO CC-based similarity network and number of same mutant phenotypes | real-valued | 0.025819366 | $0.00016$ | SL-independent overlay feature |
| O(SemanSim CC, SemanSim BP) | $\begin{aligned} & \text { semsim_cc_semsim_b } \\ & \text { p } \end{aligned}$ | Overlay between GO CC-based GO BP-based annotation similarities between genes | real-valued | 0.091608888 |  | SL-independent overlay feature |
| O(SemanSim MF, MN Corrl) | semsim_mf_mn_corr | Overlay between GO MF-based annotation similarities between genes and correlations computed from Mnaimneh's expression data set | real-valued | 0.022137984 | $0.00082$ | SL-independent overlay feature |
| O(SemanSim MF, <br> Protein Seq Simil) | semsim_mf_protein_s eq_blast_evalue | Overlay between GO MF-based annotation similarities between genes and E-value of BLAST alignment over amino acid sequences of proteins | real-valued | 0.071513298 |  | SL-independent overlay feature |
| O(SemanSim MF, Brem Abs TOM) | $\begin{aligned} & \text { semsim_mf_brem_abs } \\ & \text { _tom } \end{aligned}$ | Overlay between GO MF-based annotation similarities between genes and correlations computed from Brem's expression data set | real-valued | 0.024805619 | 5.67E-05 | SL-independent overlay feature |
| O(SemanSim MF, Brem Corrl) | $\begin{aligned} & \text { semsim_mf_brem_cor } \\ & \text { r } \end{aligned}$ | Overlay between GO MF-based annotation similarities between genes and correlation computed from Brem's expression data set | real-valued | 0.023577441 | $6.96 \mathrm{E}-05$ | SL-independent overlay feature |
| O(SemanSim MF, SemanSim BP) | ```semsim_mf_semsim_ bp``` | Overlay between GO MF-based and GO BP-based annotation similarities between genes | real-valued | 0.072151332 |  | SL-independent overlay feature |
| O(PPI, MN Abs TOM) | ppi_network_mn_abs _tom | Overlay between PPI network and topological overlap over absolute value of correlations computed from Mnaimneh's expression data set | real-valued | 0.030784057 | 4.59E-05 | SL-independent overlay feature |
| O(PPI, MN Corrl) | ppi_network_mn_corr | Overlay between PPI network and pairwise correlations computed from Mnaimneh's expression data set | real-valued | 0.041908933 | $3.56 \mathrm{E}-12$ | SL-independent overlay feature |


| O(PPI, Proetin Seq <br> Simil) | ppi_network_protein_ <br> seq_blast_evalue | Overlay between PPI network and E- real-valued <br> value of BLAST alignment over <br> amino acid sequences of proteins | 0.075858782 |
| :--- | :--- | :--- | :--- | | 0 SL-independent |
| :---: |
| overlay feature |


| O(SL, Brem Neg TOM) | SL_brem_neg_tom | Overlay between known SL network real-valued and topological overlap measured over the negative correlations computed from Brem's expression data set | 0.093487927 | 0 SL-dependent feature |
| :---: | :---: | :---: | :---: | :---: |
| O(SL, Same Mutant Phenotype) | SL_same_mutant_phe notype | Overlay between known SL network real-valued and number of shared mutant phenotypes of two genes | 0.197997551 | 0 SL-dependent feature |
| O(SL, SemanSim BP) | SL_semsim_bp | Overlay between known SL network real-valued and GO BP-based annotation similarities between genes | 0.386388856 | 0 SL-dependent feature |
| O(SL, SemanSim CC) | SL_semsim_cc | Overlay between known SL network real-valued and GO CC-based annotation similarities between genes | 0.33896039 | 0 SL-dependent feature |
| O(SL, SemanSim MF) | SL_semsim_mf | Overlay between known SL network real-valued and GO MF-based annotation similarities between genes | 0.247916137 | 0 SL-dependent feature |
| $\mathrm{O}(\mathrm{SL}, \mathrm{SL})$ | SL_SL | Overlay between known SL network binary and itself | 0.310965687 | 0 SL-dependent feature |

Table 2 - Thresholds for sparsifying networks

| Network | Threshold |
| :--- | ---: |
| bn_cocausality_semsim | 0 |
| dna_seq_blast_evalue | 0 |
| mn_abs_tom | 0.1 |
| mn_corr | $\pm 0.5$ |
| mn_neg_tom | 0.1 |
| ppi_network | 0 |
| protein_seq_blast_evalue | 0 |
| brem_abs_tom | 0.1 |
| brem_corr | $\pm 0.5$ |
| brem_neg_tom | 0.1 |
| same_mutant_phenotype | 1 |
| semsim_bp | 0.5 |
| semsim_cc | 0.7 |
| semsim_mf | 0.5 |

Table 3-8 known (highlighted rows) and 467 predicted TF SL interactions

| ORF.x | GeneSymbol.x | ORF.y | GeneSymbol.y | Classification Score |
| :---: | :---: | :---: | :---: | :---: |
| YDL056W | MBP1 | YER111C | SWI4 | NA |
| YER111C | SWI4 | YGR044C | RME1 | NA |
| YER111C | SWI4 | YLR403W | SFP1 | NA |
| YER111C | SWI4 | YLR182W | SWI6 | NA |
| YGR044C | RME1 | YLR182W | SWI6 | NA |
| YIL131C | FKH1 | YNL068C | FKH2 | NA |
| YNL199C | GCR2 | YPL075W | GCR1 | NA |
| YOR358W | HAP5 | YPL075W | GCR1 | NA |
| YKR034W | DAL80 | YJL110C | GZF3 | 5.66E-01 |
| YOR113W | AZF1 | YDR043C | NRG1 | $4.99 \mathrm{E}-01$ |
| YOR358W | HAP5 | YBL021C | HAP3 | $4.91 \mathrm{E}-01$ |
| YLR131C | ACE2 | YDR146C | SWI5 | $4.66 \mathrm{E}-01$ |
| YML027W | YOX1 | YDR451C | YHP1 | $4.48 \mathrm{E}-01$ |
| YHR206W | SKN7 | YGL073W | HSF1 | $4.38 \mathrm{E}-01$ |
| YJL110C | GZF3 | YER040W | GLN3 | $4.32 \mathrm{E}-01$ |
| YPL248C | GAL4 | YML051W | GAL80 | $4.31 \mathrm{E}-01$ |
| YNL068C | FKH2 | YBR049C | REB1 | $4.23 \mathrm{E}-01$ |
| YPL038W | MET31 | YDR253C | MET32 | $4.22 \mathrm{E}-01$ |
| YNL314W | DAL82 | YIR023W | DAL81 | $4.19 \mathrm{E}-01$ |
| YOR113W | AZF1 | YDR216W | ADR1 | $4.12 \mathrm{E}-01$ |
| YLR098C | CHA4 | YBL005W | PDR3 | $4.06 \mathrm{E}-01$ |
| YOR113W | AZF1 | YKL062W | MSN4 | $4.03 \mathrm{E}-01$ |
| YMR037C | MSN2 | YKL062W | MSN4 | $3.91 \mathrm{E}-01$ |
| YGL237C | HAP2 | YBL021C | HAP3 | $3.91 \mathrm{E}-01$ |
| YPL089C | RLM1 | YBR182C | SMP1 | 3.90E-01 |
| YOR358W | HAP5 | YGL237C | HAP2 | 3.89E-01 |
| YPL202C | AFT2 | YGL071W | RCS1 | 3.84E-01 |
| YPL089C | RLM1 | YMR043W | MCM1 | 3.80E-01 |
| YOR113W | AZF1 | YMR037C | MSN2 | $3.74 \mathrm{E}-01$ |
| YGL035C | MIG1 | YDR146C | SWI5 | $3.70 \mathrm{E}-01$ |
| YPR104C | FHL1 | YIL131C | FKH1 | $3.69 \mathrm{E}-01$ |
| YFL021W | GAT1 | YER040W | GLN3 | $3.67 \mathrm{E}-01$ |
| YKR034W | DAL80 | YFL021W | GAT1 | 3.66E-01 |
| YOR113W | AZF1 | YGL035C | MIG1 | $3.64 \mathrm{E}-01$ |
| YGL013C | PDR1 | YBR049C | REB1 | 3.63E-01 |
| YJL110C | GZF3 | YDR463W | STP1 | $3.62 \mathrm{E}-01$ |
| YNL068C | FKH2 | YGL013C | PDR1 | $3.57 \mathrm{E}-01$ |
| YGL013C | PDR1 | YDR421W | ARO80 | 3.53E-01 |
| YLR131C | ACE2 | YDR216W | ADR1 | $3.53 \mathrm{E}-01$ |
| YKL062W | MSN4 | YGL035C | MIG1 | $3.49 \mathrm{E}-01$ |
| YHR206W | SKN7 | YDL056W | MBP1 | $3.47 \mathrm{E}-01$ |
| YOR113W | AZF1 | YDR146C | SWI5 | $3.46 \mathrm{E}-01$ |
| YER111C | SWI4 | YDR146C | SWI5 | $3.45 \mathrm{E}-01$ |
| YPR104C | FHL1 | YNL068C | FKH2 | $3.43 \mathrm{E}-01$ |
| YOR113W | AZF1 | YGL071W | RCS1 | $3.42 \mathrm{E}-01$ |
| YMR070W | MOT3 | YMR037C | MSN2 | $3.37 \mathrm{E}-01$ |
| YPL038W | MET31 | YIR017C | MET28 | $3.37 \mathrm{E}-01$ |
| YDR216W | ADR1 | YDR043C | NRG1 | $3.36 \mathrm{E}-01$ |
| YDR463W | STP1 | YDR123C | INO2 | $3.35 \mathrm{E}-01$ |


| YNL103W | MET4 | YDR463W | STP1 | $3.34 \mathrm{E}-01$ |
| :---: | :---: | :---: | :---: | :---: |
| YOR113W | AZF1 | YER169W | RPH1 | $3.33 \mathrm{E}-01$ |
| YGL035C | MIG1 | YDR043C | NRG1 | $3.33 \mathrm{E}-01$ |
| YJL110C | GZF3 | YIL131C | FKH1 | $3.33 \mathrm{E}-01$ |
| YPL038W | MET31 | YNL103W | MET4 | $3.31 \mathrm{E}-01$ |
| YML051W | GAL80 | YDR463W | STP1 | $3.30 \mathrm{E}-01$ |
| YNL103W | MET4 | YDR253C | MET32 | 3.29E-01 |
| YGL035C | MIG1 | YER161C | SPT2 | $3.26 \mathrm{E}-01$ |
| YPR199C | ARR1 | YPL089C | RLM1 | $3.25 \mathrm{E}-01$ |
| YER040W | GLN3 | YEL009C | GCN4 | 3.23E-01 |
| YOR113W | AZF1 | YJL056C | ZAP1 | 3.23E-01 |
| YJL089W | SIP4 | YFL031W | HAC1 | 3.23E-01 |
| YLR131C | ACE2 | YDR259C | YAP6 | 3.23E-01 |
| YPL038W | MET31 | YGL013C | PDR1 | $3.21 \mathrm{E}-01$ |
| YIL131C | FKH1 | YDR310C | SUM1 | 3.16E-01 |
| YDR146C | SWI5 | YBR049C | REB1 | 3.15E-01 |
| YLR131C | ACE2 | YBR049C | REB1 | 3.14E-01 |
| YPR199C | ARR1 | YIL131C | FKH1 | 3.13E-01 |
| YPL038W | MET31 | YKL015W | PUT3 | 3.13E-01 |
| YDR463W | STP1 | YDR259C | YAP6 | 3.12E-01 |
| YPR199C | ARR1 | YJL110C | GZF3 | 3.11E-01 |
| YNL167C | SKO1 | YBR049C | REB1 | $3.08 \mathrm{E}-01$ |
| YOR113W | AZF1 | YGL013C | PDR1 | $3.07 \mathrm{E}-01$ |
| YJL110C | GZF3 | YHL009C | YAP3 | 3.07E-01 |
| YNL103W | MET4 | YLR451W | LEU3 | $3.06 \mathrm{E}-01$ |
| YGL013C | PDR1 | YBL005W | PDR3 | $3.05 \mathrm{E}-01$ |
| YHR206W | SKN7 | YER161C | SPT2 | $3.05 \mathrm{E}-01$ |
| YLR131C | ACE2 | YIL131C | FKH1 | $3.03 \mathrm{E}-01$ |
| YNL167C | SKO1 | YIL131C | FKH1 | 3.03E-01 |
| YKL015W | PUT3 | YGL013C | PDR1 | $3.03 \mathrm{E}-01$ |
| YGL131C | SNT2 | YDL048C | STP4 | 3.02E-01 |
| YJL110C | GZF3 | YIR018W | YAP5 | 3.01E-01 |
| YPL038W | MET31 | YLR098C | CHA4 | $3.01 \mathrm{E}-01$ |
| YPL038W | MET31 | YBR049C | REB1 | $3.00 \mathrm{E}-01$ |
| YJL089W | SIP4 | YEL009C | GCN4 | 2.99E-01 |
| YOR113W | AZF1 | YLR176C | RFX1 | $2.99 \mathrm{E}-01$ |
| YGL162W | SUT1 | YER040W | GLN3 | 2.98E-01 |
| YGL035C | MIG1 | YBR049C | REB1 | $2.97 \mathrm{E}-01$ |
| YIL036W | CST6 | YBR049C | REB1 | $2.96 \mathrm{E}-01$ |
| YPL038W | MET31 | YJL110C | GZF3 | 2.96E-01 |
| YMR037C | MSN2 | YGL035C | MIG1 | $2.95 \mathrm{E}-01$ |
| YOR113W | AZF1 | YNL103W | MET4 | $2.95 \mathrm{E}-01$ |
| YMR021C | MAC1 | YBL005W | PDR3 | $2.94 \mathrm{E}-01$ |
| YOR358W | HAP5 | YKL109W | HAP4 | 2.94E-01 |
| YLR131C | ACE2 | YGL035C | MIG1 | $2.93 \mathrm{E}-01$ |
| YML007W | YAP1 | YER040W | GLN3 | 2.93E-01 |
| YOR113W | AZF1 | YIR018W | YAP5 | $2.91 \mathrm{E}-01$ |
| YJL110C | GZF3 | YGL071W | RCS1 | $2.91 \mathrm{E}-01$ |
| YOR113W | AZF1 | YOR028C | CIN5 | $2.91 \mathrm{E}-01$ |
| YNL167C | SKO1 | YNL068C | FKH2 | $2.90 \mathrm{E}-01$ |
| YPL038W | MET31 | YKR034W | DAL80 | 2.89E-01 |
| YER161C | SPT2 | YBR049C | REB1 | 2.89E-01 |


| YPR199C | ARR1 | YDR123C | INO2 | $2.87 \mathrm{E}-01$ |
| :---: | :---: | :---: | :---: | :---: |
| YOR162C | YRR1 | YML051W | GAL80 | $2.86 \mathrm{E}-01$ |
| YNL309W | STB1 | YLR182W | SWI6 | $2.86 \mathrm{E}-01$ |
| YOL108C | INO4 | YBR049C | REB1 | $2.86 \mathrm{E}-01$ |
| YML007W | YAP1 | YDR463W | STP1 | $2.85 \mathrm{E}-01$ |
| YML051W | GAL80 | YLR256W | HAP1 | $2.85 \mathrm{E}-01$ |
| YKR034W | DAL80 | YER040W | GLN3 | $2.84 \mathrm{E}-01$ |
| YIL131C | FKH1 | YDR423C | CAD1 | $2.84 \mathrm{E}-01$ |
| YDR477W | SNF1 | YDR043C | NRG1 | $2.83 \mathrm{E}-01$ |
| YPL089C | RLM1 | YOL108C | INO4 | $2.83 \mathrm{E}-01$ |
| YPR104C | FHL1 | YMR043W | MCM1 | $2.83 \mathrm{E}-01$ |
| YLR182W | SWI6 | YIL131C | FKH1 | $2.83 \mathrm{E}-01$ |
| YOR372C | NDD1 | YIL131C | FKH1 | $2.82 \mathrm{E}-01$ |
| YJL089W | SIP4 | YDR477W | SNF1 | 2.82E-01 |
| YOR028C | CIN5 | YJL110C | GZF3 | $2.82 \mathrm{E}-01$ |
| YGL035C | MIG1 | YDR310C | SUM1 | $2.80 \mathrm{E}-01$ |
| YOR113W | AZF1 | YIR017C | MET28 | $2.80 \mathrm{E}-01$ |
| YNL068C | FKH2 | YLR131C | ACE2 | $2.78 \mathrm{E}-01$ |
| YJL089W | SIP4 | YDR463W | STP1 | $2.78 \mathrm{E}-01$ |
| YMR042W | ARG80 | YDR463W | STP1 | $2.78 \mathrm{E}-01$ |
| YPR199C | ARR1 | YOL108C | INO4 | $2.77 \mathrm{E}-01$ |
| YOR162C | YRR1 | YHR178W | STB5 | $2.77 \mathrm{E}-01$ |
| YKL062W | MSN4 | YDR043C | NRG1 | $2.77 \mathrm{E}-01$ |
| YOL108C | INO4 | YIL131C | FKH1 | $2.77 \mathrm{E}-01$ |
| YPR065W | ROX1 | YOR372C | NDD1 | $2.77 \mathrm{E}-01$ |
| YLR176C | RFX1 | YIR018W | YAP5 | $2.77 \mathrm{E}-01$ |
| YNL199C | GCR2 | YDR259C | YAP6 | $2.76 \mathrm{E}-01$ |
| YKL015W | PUT3 | YDR463W | STP1 | $2.76 \mathrm{E}-01$ |
| YLR451W | LEU3 | YBR049C | REB1 | $2.76 \mathrm{E}-01$ |
| YJL056C | ZAP1 | YDR463W | STP1 | $2.76 \mathrm{E}-01$ |
| YLR098C | CHA4 | YKR034W | DAL80 | $2.75 \mathrm{E}-01$ |
| YNL167C | SKO1 | YGL035C | MIG1 | $2.75 \mathrm{E}-01$ |
| YMR037C | MSN2 | YDR451C | YHP1 | $2.74 \mathrm{E}-01$ |
| YML007W | YAP1 | YDR423C | CAD1 | $2.74 \mathrm{E}-01$ |
| YDR421W | ARO80 | YBL005W | PDR3 | $2.74 \mathrm{E}-01$ |
| YBR240C | THI2 | YBR049C | REB1 | $2.74 \mathrm{E}-01$ |
| YGL162W | SUT1 | YBL005W | PDR3 | $2.73 \mathrm{E}-01$ |
| YNL314W | DAL82 | YLR098C | CHA4 | $2.73 \mathrm{E}-01$ |
| YMR037C | MSN2 | YDR146C | SWI5 | $2.73 \mathrm{E}-01$ |
| YLR176C | RFX1 | YKL020C | SPT23 | $2.73 \mathrm{E}-01$ |
| YEL009C | GCN4 | YBL005W | PDR3 | $2.72 \mathrm{E}-01$ |
| YOR113W | AZF1 | YML007W | YAP1 | $2.72 \mathrm{E}-01$ |
| YLR098C | CHA4 | YDR421W | ARO80 | $2.71 \mathrm{E}-01$ |
| YMR043W | MCM1 | YDR451C | YHP1 | $2.70 \mathrm{E}-01$ |
| YPL089C | RLM1 | YDR423C | CAD1 | $2.69 \mathrm{E}-01$ |
| YLR098C | CHA4 | YIR018W | YAP5 | $2.69 \mathrm{E}-01$ |
| YIR017C | MET28 | YGL162W | SUT1 | $2.69 \mathrm{E}-01$ |
| YMR042W | ARG80 | YBL005W | PDR3 | $2.69 \mathrm{E}-01$ |
| YLR098C | CHA4 | YDR259C | YAP6 | $2.69 \mathrm{E}-01$ |
| YIR018W | YAP5 | YIL131C | FKH1 | $2.68 \mathrm{E}-01$ |
| YML007W | YAP1 | YEL009C | GCN4 | $2.68 \mathrm{E}-01$ |
| YIL131C | FKH1 | YBR049C | REB1 | 2.68E-01 |


| YJL056C | ZAP1 | YIL131C | FKH1 | $2.67 \mathrm{E}-01$ |
| :---: | :---: | :---: | :---: | :---: |
| YIR017C | MET28 | YDR463W | STP1 | $2.67 \mathrm{E}-01$ |
| YER111C | SWI4 | YDR451C | YHP1 | $2.67 \mathrm{E}-01$ |
| YNL199C | GCR2 | YDR421W | ARO80 | $2.67 \mathrm{E}-01$ |
| YNL314W | DAL82 | YNL199C | GCR2 | $2.67 \mathrm{E}-01$ |
| YNL199C | GCR2 | YNL068C | FKH2 | $2.66 \mathrm{E}-01$ |
| YLR098C | CHA4 | YKL015W | PUT3 | $2.66 \mathrm{E}-01$ |
| YIL131C | FKH1 | YGL071W | RCS1 | $2.65 \mathrm{E}-01$ |
| YML051W | GAL80 | YLR131C | ACE2 | $2.64 \mathrm{E}-01$ |
| YNL314W | DAL82 | YJL110C | GZF3 | $2.64 \mathrm{E}-01$ |
| YLR098C | CHA4 | YIL131C | FKH1 | $2.64 \mathrm{E}-01$ |
| YNL103W | MET4 | YJL110C | GZF3 | $2.63 \mathrm{E}-01$ |
| YLR451W | LEU3 | YBL005W | PDR3 | $2.63 \mathrm{E}-01$ |
| YKL038W | RGT1 | YJL089W | SIP4 | $2.63 \mathrm{E}-01$ |
| YDR463W | STP1 | YDR421W | ARO80 | $2.63 \mathrm{E}-01$ |
| YPL038W | MET31 | YEL009C | GCN4 | $2.63 \mathrm{E}-01$ |
| YLR098C | CHA4 | YGL013C | PDR1 | 2.63E-01 |
| YGR044C | RME1 | YBR049C | REB1 | $2.63 \mathrm{E}-01$ |
| YIR018W | YAP5 | YIR017C | MET28 | $2.62 \mathrm{E}-01$ |
| YIL131C | FKH1 | YDR463W | STP1 | $2.62 \mathrm{E}-01$ |
| YPR104C | FHL1 | YKL112W | ABF1 | $2.62 \mathrm{E}-01$ |
| YOR113W | AZF1 | YHL027W | RIM101 | 2.61E-01 |
| YOR113W | AZF1 | YBR049C | REB1 | $2.61 \mathrm{E}-01$ |
| YOR372C | NDD1 | YNL068C | FKH2 | $2.61 \mathrm{E}-01$ |
| YMR019W | STB4 | YCR106W | RDS1 | $2.61 \mathrm{E}-01$ |
| YPR199C | ARR1 | YDR423C | CAD1 | 2.60E-01 |
| YJL056C | ZAP1 | YGL162W | SUT1 | 2.60E-01 |
| YLR176C | RFX1 | YGR044C | RME1 | $2.59 \mathrm{E}-01$ |
| YPL038W | MET31 | YOR113W | AZF1 | $2.59 \mathrm{E}-01$ |
| YJL110C | GZF3 | YJL056C | ZAP1 | $2.58 \mathrm{E}-01$ |
| YKL015W | PUT3 | YBL005W | PDR3 | $2.58 \mathrm{E}-01$ |
| YHL009C | YAP3 | YDR123C | INO2 | $2.57 \mathrm{E}-01$ |
| YLR131C | ACE2 | YFL021W | GAT1 | $2.56 \mathrm{E}-01$ |
| YHR206W | SKN7 | YBR049C | REB1 | $2.56 \mathrm{E}-01$ |
| YIR017C | MET28 | YBL005W | PDR3 | $2.56 \mathrm{E}-01$ |
| YPL038W | MET31 | YJL089W | SIP4 | $2.54 \mathrm{E}-01$ |
| YIL131C | FKH1 | YDR123C | INO2 | $2.54 \mathrm{E}-01$ |
| YOR113W | AZF1 | YLR131C | ACE2 | $2.54 \mathrm{E}-01$ |
| YMR037C | MSN2 | YDR216W | ADR1 | 2.53E-01 |
| YJL110C | GZF3 | YDR253C | MET32 | $2.53 \mathrm{E}-01$ |
| YLR098C | CHA4 | YGL162W | SUT1 | 2.53E-01 |
| YML007W | YAP1 | YHL009C | YAP3 | 2.53E-01 |
| YNL314W | DAL82 | YKR034W | DAL80 | 2.53E-01 |
| YFL031W | HAC1 | YDR463W | STP1 | $2.53 \mathrm{E}-01$ |
| YLR176C | RFX1 | YBR049C | REB1 | 2.53E-01 |
| YGR044C | RME1 | YDR043C | NRG1 | 2.52E-01 |
| YNL167C | SKO1 | YDR451C | YHP1 | 2.52E-01 |
| YLR131C | ACE2 | YDR423C | CAD1 | $2.52 \mathrm{E}-01$ |
| YDR123C | INO2 | YBR182C | SMP1 | 2.52E-01 |
| YDR463W | STP1 | YBR083W | TEC1 | 2.52E-01 |
| YDR259C | YAP6 | YBL005W | PDR3 | $2.51 \mathrm{E}-01$ |
| YDR123C | INO2 | YBR240C | THI2 | $2.51 \mathrm{E}-01$ |


| YOR028C | CIN5 | YKL038W | RGT1 | $2.51 \mathrm{E}-01$ |
| :---: | :---: | :---: | :---: | :---: |
| YOR113W | AZF1 | YGR044C | RME1 | $2.51 \mathrm{E}-01$ |
| YOR113W | AZF1 | YJL110C | GZF3 | $2.51 \mathrm{E}-01$ |
| YJL110C | GZF3 | YJL089W | SIP4 | $2.49 \mathrm{E}-01$ |
| YMR037C | MSN2 | YDR043C | NRG1 | $2.49 \mathrm{E}-01$ |
| YEL009C | GCN4 | YDR463W | STP1 | $2.49 \mathrm{E}-01$ |
| YNL199C | GCR2 | YLR182W | SWI6 | $2.49 \mathrm{E}-01$ |
| YIR017C | MET28 | YBR240C | THI2 | $2.49 \mathrm{E}-01$ |
| YNL199C | GCR2 | YBR240C | THI2 | $2.49 \mathrm{E}-01$ |
| YML027W | YOX1 | YIL131C | FKH1 | $2.48 \mathrm{E}-01$ |
| YPL038W | MET31 | YER161C | SPT2 | $2.48 \mathrm{E}-01$ |
| YJL110C | GZF3 | YDR123C | INO2 | $2.48 \mathrm{E}-01$ |
| YPL038W | MET31 | YGL035C | MIG1 | $2.48 \mathrm{E}-01$ |
| YIR018W | YAP5 | YDR421W | ARO80 | $2.47 \mathrm{E}-01$ |
| YBR083W | TEC1 | YBL005W | PDR3 | $2.46 \mathrm{E}-01$ |
| YGL013C | PDR1 | YDR123C | INO2 | $2.46 \mathrm{E}-01$ |
| YOR113W | AZF1 | YIL131C | FKH1 | $2.46 \mathrm{E}-01$ |
| YMR037C | MSN2 | YHR206W | SKN7 | $2.46 \mathrm{E}-01$ |
| YLR182W | SWI6 | YDL056W | MBP1 | $2.46 \mathrm{E}-01$ |
| YML007W | YAP1 | YIR018W | YAP5 | $2.46 \mathrm{E}-01$ |
| YGL162W | SUT1 | YEL009C | GCN4 | $2.45 \mathrm{E}-01$ |
| YPL248C | GAL4 | YDR477W | SNF1 | $2.45 \mathrm{E}-01$ |
| YLR182W | SWI6 | YGL181W | GTS1 | $2.45 \mathrm{E}-01$ |
| YOR372C | NDD1 | YBR049C | REB1 | $2.44 \mathrm{E}-01$ |
| YKL043W | PHD1 | YJL110C | GZF3 | $2.43 \mathrm{E}-01$ |
| YJL089W | SIP4 | YGL162W | SUT1 | $2.43 \mathrm{E}-01$ |
| YOR113W | AZF1 | YNL199C | GCR2 | $2.43 \mathrm{E}-01$ |
| YLR013W | GAT3 | YER040W | GLN3 | $2.43 \mathrm{E}-01$ |
| YIL131C | FKH1 | YBL005W | PDR3 | $2.43 \mathrm{E}-01$ |
| YDR123C | INO2 | YBR049C | REB1 | $2.43 \mathrm{E}-01$ |
| YLR131C | ACE2 | YDR463W | STP1 | $2.43 \mathrm{E}-01$ |
| YML007W | YAP1 | YLR131C | ACE2 | $2.43 \mathrm{E}-01$ |
| YLR451W | LEU3 | YJL089W | SIP4 | $2.42 \mathrm{E}-01$ |
| YJL110C | GZF3 | YGL035C | MIG1 | $2.42 \mathrm{E}-01$ |
| YNL103W | MET4 | YKL015W | PUT3 | $2.41 \mathrm{E}-01$ |
| YNL167C | SKO1 | YBL005W | PDR3 | $2.41 \mathrm{E}-01$ |
| YLR176C | RFX1 | YBR240C | THI2 | $2.41 \mathrm{E}-01$ |
| YNL199C | GCR2 | YKL062W | MSN4 | $2.40 \mathrm{E}-01$ |
| YNL199C | GCR2 | YIL131C | FKH1 | $2.40 \mathrm{E}-01$ |
| YGL162W | SUT1 | YDR463W | STP1 | $2.40 \mathrm{E}-01$ |
| YNL068C | FKH2 | YDR451C | YHP1 | $2.40 \mathrm{E}-01$ |
| YPL248C | GAL4 | YHL009C | YAP3 | $2.39 \mathrm{E}-01$ |
| YLR098C | CHA4 | YDR123C | INO2 | $2.39 \mathrm{E}-01$ |
| YPL248C | GAL4 | YBR240C | THI2 | $2.39 \mathrm{E}-01$ |
| YOR113W | AZF1 | YKL020C | SPT23 | $2.39 \mathrm{E}-01$ |
| YOR028C | CIN5 | YLR098C | CHA4 | $2.39 \mathrm{E}-01$ |
| YDR123C | INO2 | YBL103C | RTG3 | $2.39 \mathrm{E}-01$ |
| YDR421W | ARO80 | YDR259C | YAP6 | $2.38 \mathrm{E}-01$ |
| YLR098C | CHA4 | YGR044C | RME1 | $2.38 \mathrm{E}-01$ |
| YGR044C | RME1 | YGL035C | MIG1 | $2.38 \mathrm{E}-01$ |
| YNL199C | GCR2 | YGL013C | PDR1 | $2.38 \mathrm{E}-01$ |
| YIL131C | FKH1 | YBR182C | SMP1 | 2.38E-01 |


| YPL202C | AFT2 | YDR123C | INO2 | $2.38 \mathrm{E}-01$ |
| :---: | :---: | :---: | :---: | :---: |
| YOR113W | AZF1 | YDR463W | STP1 | $2.38 \mathrm{E}-01$ |
| YLR182W | SWI6 | YLR131C | ACE2 | $2.38 \mathrm{E}-01$ |
| YLR013W | GAT3 | YJL110C | GZF3 | $2.38 \mathrm{E}-01$ |
| YOR028C | CIN5 | YDR259C | YAP6 | $2.38 \mathrm{E}-01$ |
| YLR013W | GAT3 | YKR034W | DAL80 | $2.37 \mathrm{E}-01$ |
| YLR098C | CHA4 | YHR178W | STB5 | $2.37 \mathrm{E}-01$ |
| YGL013C | PDR1 | YDR043C | NRG1 | $2.37 \mathrm{E}-01$ |
| YOR113W | AZF1 | YER161C | SPT2 | $2.37 \mathrm{E}-01$ |
| YPL089C | RLM1 | YLR131C | ACE2 | $2.36 \mathrm{E}-01$ |
| YGL035C | MIG1 | YDR477W | SNF1 | $2.36 \mathrm{E}-01$ |
| YGL071W | RCS1 | YDR463W | STP1 | $2.36 \mathrm{E}-01$ |
| YPL038W | MET31 | YIR023W | DAL81 | $2.36 \mathrm{E}-01$ |
| YOR344C | TYE7 | YDR463W | STP1 | $2.36 \mathrm{E}-01$ |
| YML051W | GAL80 | YJL110C | GZF3 | $2.35 \mathrm{E}-01$ |
| YDR423C | CAD1 | YDR421W | ARO80 | $2.35 \mathrm{E}-01$ |
| YLR131C | ACE2 | YJL110C | GZF3 | $2.35 \mathrm{E}-01$ |
| YOR113W | AZF1 | YLR182W | SWI6 | $2.35 \mathrm{E}-01$ |
| YOL108C | INO4 | YDR123C | INO2 | $2.35 \mathrm{E}-01$ |
| YIL131C | FKH1 | YDR259C | YAP6 | $2.34 \mathrm{E}-01$ |
| YNL199C | GCR2 | YKL015W | PUT3 | $2.34 \mathrm{E}-01$ |
| YPR104C | FHL1 | YBR240C | THI2 | $2.33 \mathrm{E}-01$ |
| YER169W | RPH1 | YDR216W | ADR1 | $2.33 \mathrm{E}-01$ |
| YPL089C | RLM1 | YGL071W | RCS1 | $2.33 \mathrm{E}-01$ |
| YPL089C | RLM1 | YDR463W | STP1 | $2.33 \mathrm{E}-01$ |
| YKL043W | PHD1 | YIL131C | FKH1 | $2.32 \mathrm{E}-01$ |
| YOR372C | NDD1 | YNL199C | GCR2 | $2.32 \mathrm{E}-01$ |
| YML007W | YAP1 | YGL162W | SUT1 | $2.32 \mathrm{E}-01$ |
| YPL089C | RLM1 | YLR182W | SWI6 | $2.32 \mathrm{E}-01$ |
| YLR256W | HAP1 | YBR240C | THI2 | $2.32 \mathrm{E}-01$ |
| YIR023W | DAL81 | YDR123C | INO2 | $2.32 \mathrm{E}-01$ |
| YOR372C | NDD1 | YJL110C | GZF3 | $2.32 \mathrm{E}-01$ |
| YPL038W | MET31 | YDR146C | SWI5 | 2.32E-01 |
| YDR463W | STP1 | YBL005W | PDR3 | $2.31 \mathrm{E}-01$ |
| YKL015W | PUT3 | YDR421W | ARO80 | $2.31 \mathrm{E}-01$ |
| YKL109W | HAP4 | YBL021C | HAP3 | $2.31 \mathrm{E}-01$ |
| YPL089C | RLM1 | YML051W | GAL80 | $2.31 \mathrm{E}-01$ |
| YPR104C | FHL1 | YBR049C | REB1 | $2.31 \mathrm{E}-01$ |
| YPL089C | RLM1 | YGL073W | HSF1 | $2.30 \mathrm{E}-01$ |
| YNL103W | MET4 | YLR098C | CHA4 | $2.30 \mathrm{E}-01$ |
| YOR162C | YRR1 | YJL089W | SIP4 | $2.30 \mathrm{E}-01$ |
| YPR104C | FHL1 | YNL139C | RLR1 | $2.30 \mathrm{E}-01$ |
| YPL038W | MET31 | YDR123C | INO2 | $2.30 \mathrm{E}-01$ |
| YPL248C | GAL4 | YOR358W | HAP5 | $2.30 \mathrm{E}-01$ |
| YMR042W | ARG80 | YDR421W | ARO80 | $2.29 \mathrm{E}-01$ |
| YJL110C | GZF3 | YDR451C | YHP1 | $2.29 \mathrm{E}-01$ |
| YJL056C | ZAP1 | YDR123C | INO2 | $2.29 \mathrm{E}-01$ |
| YNL167C | SKO1 | YDR463W | STP1 | $2.29 \mathrm{E}-01$ |
| YPR065W | ROX1 | YLR098C | CHA4 | $2.29 \mathrm{E}-01$ |
| YLR176C | RFX1 | YLR098C | CHA4 | $2.28 \mathrm{E}-01$ |
| YKR034W | DAL80 | YKL043W | PHD1 | $2.28 \mathrm{E}-01$ |
| YLR098C | CHA4 | YBR049C | REB1 | $2.28 \mathrm{E}-01$ |


| YBL103C | RTG3 | YBL005W | PDR3 | $2.28 \mathrm{E}-01$ |
| :---: | :---: | :---: | :---: | :---: |
| YHR206W | SKN7 | YDR043C | NRG1 | $2.28 \mathrm{E}-01$ |
| YNL216W | RAP1 | YKL112W | ABF1 | $2.27 \mathrm{E}-01$ |
| YPR104C | FHL1 | YOL108C | INO4 | $2.26 \mathrm{E}-01$ |
| YLR131C | ACE2 | YEL009C | GCN4 | $2.26 \mathrm{E}-01$ |
| YKL062W | MSN4 | YDL106C | PHO2 | $2.26 \mathrm{E}-01$ |
| YDR259C | YAP6 | YBR049C | REB1 | $2.26 \mathrm{E}-01$ |
| YJL089W | SIP4 | YFL021W | GAT1 | $2.25 \mathrm{E}-01$ |
| YKR034W | DAL80 | YDR463W | STP1 | $2.25 \mathrm{E}-01$ |
| YNL314W | DAL82 | YBR240C | THI2 | $2.25 \mathrm{E}-01$ |
| YHLO20C | OPI1 | YBR049C | REB1 | $2.25 \mathrm{E}-01$ |
| YPL089C | RLM1 | YJR060W | CBF1 | $2.25 \mathrm{E}-01$ |
| YNL167C | SKO1 | YER161C | SPT2 | $2.25 \mathrm{E}-01$ |
| YIL131C | FKH1 | YDR421W | ARO80 | $2.24 \mathrm{E}-01$ |
| YJL056C | ZAP1 | YDR043C | NRG1 | 2.23E-01 |
| YPL089C | RLM1 | YGL013C | PDR1 | $2.23 \mathrm{E}-01$ |
| YNL167C | SKO1 | YMR037C | MSN2 | $2.23 \mathrm{E}-01$ |
| YOR162C | YRR1 | YBR182C | SMP1 | 2.23E-01 |
| YLR098C | CHA4 | YBR240C | THI2 | $2.23 \mathrm{E}-01$ |
| YOR113W | AZF1 | YOL108C | INO4 | 2.22E-01 |
| YMR042W | ARG80 | YJL089W | SIP4 | $2.22 \mathrm{E}-01$ |
| YNL199C | GCR2 | YDR310C | SUM1 | $2.22 \mathrm{E}-01$ |
| YOR028C | CIN5 | YMR042W | ARG80 | $2.22 \mathrm{E}-01$ |
| YKL020C | SPT23 | YGL071W | RCS1 | $2.22 \mathrm{E}-01$ |
| YLR176C | RFX1 | YLR131C | ACE2 | $2.22 \mathrm{E}-01$ |
| YDR259C | YAP6 | YDR146C | SWI5 | $2.21 \mathrm{E}-01$ |
| YDR423C | CAD1 | YDR146C | SWI5 | $2.21 \mathrm{E}-01$ |
| YIR017C | MET28 | YFL021W | GAT1 | $2.21 \mathrm{E}-01$ |
| YLR013W | GAT3 | YDL056W | MBP1 | $2.20 \mathrm{E}-01$ |
| YMR037C | MSN2 | YJL056C | ZAP1 | $2.20 \mathrm{E}-01$ |
| YNL199C | GCR2 | YLR098C | CHA4 | 2.20E-01 |
| YKL015W | PUT3 | YJL110C | GZF3 | $2.20 \mathrm{E}-01$ |
| YOR372C | NDD1 | YML027W | YOX1 | $2.20 \mathrm{E}-01$ |
| YOR344C | TYE7 | YKL043W | PHD1 | $2.20 \mathrm{E}-01$ |
| YOR113W | AZF1 | YLR098C | CHA4 | $2.20 \mathrm{E}-01$ |
| YML027W | YOX1 | YJL110C | GZF3 | $2.20 \mathrm{E}-01$ |
| YNL216W | RAP1 | YFL021W | GAT1 | $2.20 \mathrm{E}-01$ |
| YPR199C | ARR1 | YPL202C | AFT2 | $2.20 \mathrm{E}-01$ |
| YGL035C | MIG1 | YER169W | RPH1 | 2.19E-01 |
| YOR344C | TYE7 | YJL110C | GZF3 | 2.19E-01 |
| YHR178W | STB5 | YDR123C | INO2 | $2.19 \mathrm{E}-01$ |
| YKL020C | SPT23 | YDR146C | SWI5 | 2.19E-01 |
| YML051W | GAL80 | YBL005W | PDR3 | $2.19 \mathrm{E}-01$ |
| YKL020C | SPT23 | YBR049C | REB1 | 2.19E-01 |
| YLR176C | RFX1 | YJL110C | GZF3 | 2.19E-01 |
| YPL089C | RLM1 | YJL089W | SIP4 | 2.19E-01 |
| YIL131C | FKH1 | YER161C | SPT2 | 2.19E-01 |
| YLR176C | RFX1 | YHL027W | RIM101 | $2.18 \mathrm{E}-01$ |
| YML051W | GAL80 | YIL131C | FKH1 | $2.18 \mathrm{E}-01$ |
| YNL103W | MET4 | YIR018W | YAP5 | $2.18 \mathrm{E}-01$ |
| YNL199C | GCR2 | YER161C | SPT2 | $2.18 \mathrm{E}-01$ |
| YLR098C | CHA4 | YDL056W | MBP1 | 2.18E-01 |


| YNL068C | FKH2 | YIL036W | CST6 | $2.18 \mathrm{E}-01$ |
| :---: | :---: | :---: | :---: | :---: |
| YPL089C | RLM1 | YDR216W | ADR1 | $2.18 \mathrm{E}-01$ |
| YOR372C | NDD1 | YDR463W | STP1 | $2.17 \mathrm{E}-01$ |
| YPL038W | MET31 | YNL314W | DAL82 | $2.17 \mathrm{E}-01$ |
| YJR060W | CBF1 | YIR017C | MET28 | $2.17 \mathrm{E}-01$ |
| YKL032C | IXR1 | YGL035C | MIG1 | $2.17 \mathrm{E}-01$ |
| YLR013W | GAT3 | YHR206W | SKN7 | $2.17 \mathrm{E}-01$ |
| YPL248C | GAL4 | YDR216W | ADR1 | $2.16 \mathrm{E}-01$ |
| YPL089C | RLM1 | YDR259C | YAP6 | $2.16 \mathrm{E}-01$ |
| YDR043C | NRG1 | YBR049C | REB1 | $2.16 \mathrm{E}-01$ |
| YJL110C | GZF3 | YIR017C | MET28 | $2.16 \mathrm{E}-01$ |
| YIL131C | FKH1 | YHL020C | OPI1 | $2.16 \mathrm{E}-01$ |
| YIL036W | CST6 | YDR146C | SWI5 | $2.16 \mathrm{E}-01$ |
| YPR104C | FHL1 | YDR146C | SWI5 | $2.14 \mathrm{E}-01$ |
| YPL075W | GCR1 | YLR131C | ACE2 | $2.14 \mathrm{E}-01$ |
| YNL199C | GCR2 | YGL071W | RCS1 | $2.14 \mathrm{E}-01$ |
| YIL131C | FKH1 | YGL035C | MIG1 | $2.13 \mathrm{E}-01$ |
| YIR017C | MET28 | YBR049C | REB1 | $2.13 \mathrm{E}-01$ |
| YOR113W | AZF1 | YDL056W | MBP1 | $2.13 \mathrm{E}-01$ |
| YML051W | GAL80 | YIR018W | YAP5 | 2.13E-01 |
| YHR084W | STE12 | YBL005W | PDR3 | $2.13 \mathrm{E}-01$ |
| YML051W | GAL80 | YDR423C | CAD1 | 2.13E-01 |
| YJL110C | GZF3 | YBR049C | REB1 | 2.13E-01 |
| YKL043W | PHD1 | YBR182C | SMP1 | $2.13 \mathrm{E}-01$ |
| YPL089C | RLM1 | YDR123C | INO2 | $2.12 \mathrm{E}-01$ |
| YJL110C | GZF3 | YBR240C | THI2 | 2.12E-01 |
| YDR463W | STP1 | YBR240C | THI2 | 2.12E-01 |
| YPL075W | GCR1 | YIL131C | FKH1 | $2.12 \mathrm{E}-01$ |
| YKL112W | ABF1 | YKL032C | IXR1 | $2.12 \mathrm{E}-01$ |
| YKL020C | SPT23 | YIR018W | YAP5 | 2.12E-01 |
| YJL110C | GZF3 | YDR423C | CAD1 | $2.11 \mathrm{E}-01$ |
| YOR113W | AZF1 | YEL009C | GCN4 | $2.11 \mathrm{E}-01$ |
| YGL013C | PDR1 | YBR240C | THI2 | $2.10 \mathrm{E}-01$ |
| YIR018W | YAP5 | YIL036W | CST6 | $2.10 \mathrm{E}-01$ |
| YKL043W | PHD1 | YHL009C | YAP3 | $2.10 \mathrm{E}-01$ |
| YOR113W | AZF1 | YNL068C | FKH2 | $2.10 \mathrm{E}-01$ |
| YMR037C | MSN2 | YDR463W | STP1 | $2.10 \mathrm{E}-01$ |
| YLR131C | ACE2 | YLR098C | CHA4 | $2.10 \mathrm{E}-01$ |
| YPL089C | RLM1 | YHL009C | YAP3 | $2.10 \mathrm{E}-01$ |
| YMR042W | ARG80 | YKL043W | PHD1 | 2.10E-01 |
| YPL089C | RLM1 | YNL199C | GCR2 | $2.10 \mathrm{E}-01$ |
| YLR182W | SWI6 | YHLO20C | OPI1 | $2.10 \mathrm{E}-01$ |
| YOL108C | INO4 | YDR451C | YHP1 | $2.09 \mathrm{E}-01$ |
| YDR520C | YDR520C | YDL048C | STP4 | $2.09 \mathrm{E}-01$ |
| YLR451W | LEU3 | YFL021W | GAT1 | $2.09 \mathrm{E}-01$ |
| YPR104C | FHL1 | YHR178W | STB5 | $2.09 \mathrm{E}-01$ |
| YIR023W | DAL81 | YDR146C | SWI5 | $2.09 \mathrm{E}-01$ |
| YNL103W | MET4 | YLR013W | GAT3 | $2.09 \mathrm{E}-01$ |
| YLR098C | CHA4 | YIR023W | DAL81 | $2.09 \mathrm{E}-01$ |
| YPL089C | RLM1 | YLR451W | LEU3 | $2.08 \mathrm{E}-01$ |
| YOL108C | INO4 | YDR423C | CAD1 | $2.08 \mathrm{E}-01$ |
| YNL314W | DAL82 | YIL036W | CST6 | $2.08 \mathrm{E}-01$ |


| YLR256W | HAP1 | YIL131C | FKH1 | $2.08 \mathrm{E}-01$ |
| :---: | :---: | :---: | :---: | :---: |
| YNL068C | FKH2 | YDL056W | MBP1 | 2.08E-01 |
| YNL314W | DAL82 | YKL015W | PUT3 | $2.08 \mathrm{E}-01$ |
| YNL314W | DAL82 | YNL167C | SKO1 | $2.08 \mathrm{E}-01$ |
| YMR070W | MOT3 | YLR013W | GAT3 | $2.07 \mathrm{E}-01$ |
| YGL071W | RCS1 | YDR043C | NRG1 | $2.07 \mathrm{E}-01$ |
| YPL089C | RLM1 | YBR240C | THI2 | $2.07 \mathrm{E}-01$ |
| YIL131C | FKH1 | YHR084W | STE12 | $2.07 \mathrm{E}-01$ |
| YNL068C | FKH2 | YDR421W | ARO80 | $2.07 \mathrm{E}-01$ |
| YKL015W | PUT3 | YJL089W | SIP4 | $2.07 \mathrm{E}-01$ |
| YOL108C | INO4 | YMR043W | MCM1 | $2.07 \mathrm{E}-01$ |
| YOR372C | NDD1 | YmL051W | GAL80 | $2.07 \mathrm{E}-01$ |
| YDR421W | ARO80 | YDR146C | SWI5 | $2.06 \mathrm{E}-01$ |
| YOR372C | NDD1 | YNL103W | MET4 | $2.06 \mathrm{E}-01$ |
| YMR021C | MAC1 | YDR463W | STP1 | $2.06 \mathrm{E}-01$ |
| YPL248C | GAL4 | YDR463W | STP1 | $2.06 \mathrm{E}-01$ |
| YLR098C | CHA4 | YKL038W | RGT1 | $2.06 \mathrm{E}-01$ |
| YPL089C | RLM1 | YHR084W | STE12 | $2.06 \mathrm{E}-01$ |
| YOR372C | NDD1 | YDR146C | SWI5 | $2.06 \mathrm{E}-01$ |
| YOL108C | INO4 | YHL009C | YAP3 | $2.06 \mathrm{E}-01$ |
| YOR113W | AZF1 | YGL073W | HSF1 | $2.06 \mathrm{E}-01$ |
| YML051W | GAL80 | YKL015W | PUT3 | $2.06 \mathrm{E}-01$ |
| YPL038W | MET31 | YNL199C | GCR2 | $2.06 \mathrm{E}-01$ |
| YDR423C | CAD1 | YDR123C | INO2 | 2.05E-01 |
| YJL089W | SIP4 | YDR421W | ARO80 | $2.05 \mathrm{E}-01$ |
| YKL062W | MSN4 | YHR206W | SKN7 | $2.05 \mathrm{E}-01$ |
| YPR199C | ARR1 | YBR240C | THI2 | $2.05 \mathrm{E}-01$ |
| YLR098C | CHA4 | YJL110C | GZF3 | $2.05 \mathrm{E}-01$ |
| YPR104C | FHL1 | YOR372C | NDD1 | $2.04 \mathrm{E}-01$ |
| YPL038W | MET31 | YLR451W | LEU3 | $2.04 \mathrm{E}-01$ |
| YJL089W | SIP4 | YIL131C | FKH1 | $2.04 \mathrm{E}-01$ |
| YNL167C | SKO1 | YLR098C | CHA4 | $2.04 \mathrm{E}-01$ |
| YLR098C | CHA4 | YGL071W | RCS1 | $2.04 \mathrm{E}-01$ |
| YGL071W | RCS1 | YBR049C | REB1 | 2.03E-01 |
| YMR043W | MCM1 | YIL131C | FKH1 | $2.03 \mathrm{E}-01$ |
| YKL062W | MSN4 | YHL027W | RIM101 | $2.03 \mathrm{E}-01$ |
| YMR037C | MSN2 | YIL131C | FKH1 | 2.03E-01 |
| YOL028C | YAP7 | YBR049C | REB1 | 2.03E-01 |
| YMR070W | MOT3 | YLR403W | SFP1 | 2.03E-01 |
| YER161C | SPT2 | YDR259C | YAP6 | 2.03E-01 |
| YGL013C | PDR1 | YDR463W | STP1 | $2.02 \mathrm{E}-01$ |
| YJL089W | SIP4 | YGL035C | MIG1 | $2.02 \mathrm{E}-01$ |
| YDR146C | SWI5 | YBR083W | TEC1 | $2.02 \mathrm{E}-01$ |
| YHLO20C | OPI1 | YBL005W | PDR3 | 2.02E-01 |
| YPR065W | ROX1 | YLR131C | ACE2 | $2.02 \mathrm{E}-01$ |
| YPL089C | RLM1 | YDR451C | YHP1 | 2.02E-01 |
| YMR016C | SOK2 | YHR206W | SKN7 | $2.02 \mathrm{E}-01$ |
| YLR256W | HAP1 | YJL089W | SIP4 | $2.02 \mathrm{E}-01$ |
| YOR372C | NDD1 | YBR182C | SMP1 | $2.01 \mathrm{E}-01$ |
| YMR042W | ARG80 | YIR018W | YAP5 | $2.01 \mathrm{E}-01$ |
| YGL073W | HSF1 | YDR451C | YHP1 | $2.01 \mathrm{E}-01$ |
| YKL112W | ABF1 | YIL131C | FKH1 | $2.01 \mathrm{E}-01$ |


| YLR182W | SWI6 | YKL112W | ABF1 | $2.01 \mathrm{E}-01$ |
| :--- | :--- | :--- | :--- | :--- |
| YPL038W | MET31 | YMR037C | MSN2 | $2.01 \mathrm{E}-01$ |
| YMR037C | MSN2 | YLR182W | SWI6 | $2.01 \mathrm{E}-01$ |
| YKL020C | SPT23 | YIL131C | FKH1 | $2.01 \mathrm{E}-01$ |
| YNL314W | DAL82 | YGL013C | PDR1 | $2.01 E-01$ |
| YNL199C | GCR2 | YBR049C | REB1 | $2.01 E-01$ |
| YML027W | YOX1 | YGL162W | SUT1 | $2.01 E-01$ |
| YNL068C | FKH2 | YKL112W | ABF1 | $2.00 E-01$ |
| YPL202C | AFT2 | YJL089W | SIP4 | $2.00 \mathrm{E}-01$ |
| YIR018W | YAP5 | YDR123C | INO2 | $2.00 \mathrm{E}-01$ |

Table 4 - the number of SL interactions for each TF in the TF SL network

| TF | \# of TF SL interactions |
| :---: | :---: |
| FKH1 | 38 |
| AZF1 | 34 |
| GZF3 | 33 |
| STP1 | 31 |
| REB1 | 30 |
| CHA4 | 29 |
| RLM1 | 23 |
| ACE2 | 21 |
| MET31 | 21 |
| GCR2 | 20 |
| INO2 | 20 |
| PDR3 | 19 |
| SIP4 | 19 |
| MIG1 | 18 |
| SWI5 | 16 |
| MSN2 | 15 |
| PDR1 | 15 |
| THI2 | 15 |
| ARO80 | 14 |
| FKH2 | 14 |
| YAP5 | 14 |
| GAL80 | 13 |
| NDD1 | 13 |
| SWI6 | 13 |
| NRG1 | 12 |
| PUT3 | 12 |
| YAP6 | 12 |
| CAD1 | 11 |
| DAL82 | 11 |
| FHL1 | 11 |
| INO4 | 11 |
| MET28 | 11 |
| MET4 | 11 |
| RCS1 | 11 |
| SKO1 | 11 |
| RFX1 | 10 |
| SUT1 | 10 |
| YHP1 | 10 |
| DAL80 | 9 |
| GCN4 | 9 |
| SKN7 | 9 |
| SPT2 | 9 |
| YAP1 | 9 |
| ARR1 | 8 |
| MSN4 | 8 |
| RME1 | 8 |
| ZAP1 | 8 |
| ADR1 | 7 |
| ARG80 | 7 |


| GAL4 | 7 |
| :---: | :---: |
| GAT1 | 7 |
| GAT3 | 7 |
| GLN3 | 7 |
| LEU3 | 7 |
| MBP1 | 7 |
| PHD1 | 7 |
| SPT23 | 7 |
| YAP3 | 7 |
| ABF1 | 6 |
| CIN5 | 6 |
| SMP1 | 6 |
| SWI4 | 6 |
| CST6 | 5 |
| DAL81 | 5 |
| HAP5 | 5 |
| MCM1 | 5 |
| YOX1 | 5 |
| AFT2 | 4 |
| GCR1 | 4 |
| HAP1 | 4 |
| HSF1 | 4 |
| OPI1 | 4 |
| SNF1 | 4 |
| STB5 | 4 |
| YRR1 | 4 |
| HAP3 | 3 |
| MET32 | 3 |
| MOT3 | 3 |
| RGT1 | 3 |
| RIM101 | 3 |
| ROX1 | 3 |
| RPH1 | 3 |
| STE12 | 3 |
| SUM1 | 3 |
| TEC1 | 3 |
| TYE7 | 3 |
| CBF1 | 2 |
| HAC1 | 2 |
| HAP2 | 2 |
| HAP4 | 2 |
| IXR1 | 2 |
| MAC1 | 2 |
| RAP1 | 2 |
| RTG3 | 2 |
| SFP1 | 2 |
| STP4 | 2 |
| GTS1 | 1 |
| PHO2 | 1 |
| RDS1 | 1 |
| RLR1 | 1 |
| SNT2 | 1 |

SOK2 1
STB1
STB4
YAP7
YDR520C

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