### S1 Table - List of features included in our integrated model of noise

| Feature name          | Description                                                                 | References |
|-----------------------|------------------------------------------------------------------------------|------------|
| STRE_elem             | Presence/Absence of the Stress Response Element in the promoter              | [1]        |
| TATAbox               | presence/Absence of the TATAbox sequence in the promoter                    | [2]        |
| ConsensusClustNum     | Number of consensus clusters of transcription start sites                     | [3]        |
| ClosestTSS            | Closest transcription start site to the coding region                        |            |
| SpreadTSS             | Spread of potential transcription start sites                                 |            |
| MedPromShapeScore     | Median promoter shape score                                                  |            |
| tAI_full              | tRNA adaptation index for the full gene                                      | [4]        |
| tAI_f5                | tRNA adaptation index for the first 5 codons                                 |            |
| tAI_f10               | tRNA adaptation index for the first 10 codons                                |            |
| tAI_f15               | tRNA adaptation index for the first 15 codons                                |            |
| tAI_f20               | tRNA adaptation index for the first 20 codons                                |            |
| tAI_f25               | tRNA adaptation index for the first 25 codons                                |            |
| tAI_f30               | tRNA adaptation index for the first 30 codons                                |            |
| tAI_f40               | tRNA adaptation index for the first 40 codons                                |            |
| tAI_f50               | tRNA adaptation index for the first 50 codons                                |            |
| NumPromNucOcc         | Number of sites in the promoter occupied by nucleosomes                      | [5]        |
| AvPromNucOcc          | Average absolute nucleosome occupancy level per nucleosome bound site in the promoter |            |
| LenAvgPromNucOcc      | Average length of nucleosome occupancy in the promoter                       |            |
| NumGeneNucOcc         | Number of sites in the genebody occupied by nucleosomes                      |            |
| AvGeneNucOcc          | Average absolute nucleosome occupancy level per nucleosome bound site in the genebody |            |
| N_PrNO50              | Number of sites upto 50 bp upstream of the start codon occupied by nucleosomes |            |
| N_PrNO100             | Number of sites between 50 bp and 100bp upstream of the start codon occupied by nucleosomes |            |
| N_PrNO150             | Number of sites between 100 bp and 150bp upstream of the start codon occupied by nucleosomes |            |
| N_PrNO200             | Number of sites between 150 bp and 200bp upstream of the start codon occupied by nucleosomes |            |
| N_PrNO300             | Number of sites between 200 bp and 300bp upstream of the start codon occupied by nucleosomes |            |
| N_PrNO400             | Number of sites between 300 bp and 400bp upstream of the start codon occupied by nucleosomes |            |
| N_PrNO500             | Number of sites between 400 bp and 500bp upstream of the start codon occupied by nucleosomes |            |
| N_PrNO600             | Number of sites between 500 bp and 600bp upstream of the start codon occupied by nucleosomes |            |
| N_PrNO700             | Number of sites between 600 bp and 700bp upstream of the start codon occupied by nucleosomes |            |
| N_PrNO800             | Number of sites between 700 bp and 800bp upstream of the start codon occupied by nucleosomes |            |
| N_PrNO900             | Number of sites between 800 bp and 900bp upstream of the start codon occupied by nucleosomes |            |
| N_PrNO1000            | Number of sites between 900 bp and 1000bp upstream of the start codon occupied by nucleosomes |            |
| V_PrNO50              | Level of absolute nucleosome occupancy in the region upto 50bp upstream of the start codon |            |
| V_PrNO100             | Level of absolute nucleosome occupancy in the region between 50bp and 100bp upstream of the start codon |            |
| V_PrNO150             | Level of absolute nucleosome occupancy in the region between 100bp and 150bp upstream of the start codon |            |
| V_PrNO200             | Level of absolute nucleosome occupancy in the region between 150bp and 200bp upstream of the start codon |            |
| V_PrNO300             | Level of absolute nucleosome occupancy in the region between 200bp and 300bp upstream of the start codon |            |
| **V_PrNO400** | Level of absolute nucleosome occupancy in the region between 300bp and 400bp upstream of the start codon |
| **V_PrNO500** | Level of absolute nucleosome occupancy in the region between 400bp and 500bp upstream of the start codon |
| **V_PrNO600** | Level of absolute nucleosome occupancy in the region between 500bp and 600bp upstream of the start codon |
| **V_PrNO700** | Level of absolute nucleosome occupancy in the region between 600bp and 700bp upstream of the start codon |
| **V_PrNO800** | Level of absolute nucleosome occupancy in the region between 700bp and 800bp upstream of the start codon |
| **V_PrNO900** | Level of absolute nucleosome occupancy in the region between 800bp and 900bp upstream of the start codon |
| **V_PrNO1000** | Level of absolute nucleosome occupancy in the region between 900bp and 1000bp upstream of the start codon |
| **NumGb_H3** | Number of sites in the genebody occupied by H3 |
| **Gb_H3** | Level of H3 in the genebody |
| **NumGb_H4** | Number of sites in the genebody occupied by H4 |
| **Gb_H4** | Level of H4 in the genebody |
| **NumGb_H3K9ac_vsH3** | Level of H3K9ac modification in the genebody |
| **Gb_H3K9ac_vsH3** | Level of H3K9ac modification in the genebody |
| **NumGb_H3K14ac_vsH3** | Number of sites in the genebody showing H3K14ac modification |
| **Gb_H3K14ac_vsH3** | Level of H3K14ac modification in the genebody |
| **NumGb_H3K4me1_vsH3** | Number of sites in the genebody showing H3K4me1 modification |
| **Gb_H3K4me1_vsH3** | Level of H3K4me1 modification in the genebody |
| **NumGb_H3K4me2_vsH3** | Number of sites in the genebody showing H3K4me2 modification |
| **Gb_H3K4me2_vsH3** | Level of H3K4me2 modification in the genebody |
| **NumGb_H3K4me3_vsH3** | Number of sites in the genebody showing H3K4me3 modification |
| **Gb_H3K4me3_vsH3** | Level of H3K4me3 modification in the genebody |
| **NumGb_H3K36me3_vsH3** | Number of sites in the genebody showing H3K36me3 modification |
| **Gb_H3K36me3_vsH3** | Level of H3K36me3 modification in the genebody |
| **NumGb_H3K79me3_vsH3** | Number of sites in the genebody showing H3K79me3 modification |
| **Gb_H3K79me3_vsH3** | Level of H3K79me3 modification in the genebody |
| **NumGb_ESA1** | Number of sites in the genebody showing ESA binding |
| **Gb_ESA1** | Level of ESA1 binding in the genebody |
| **NumGb_GCN5** | Number of sites in the genebody showing GCN5 binding |
| **Gb_GCN5** | Level of GCN5 binding in the genebody |
| **NumGb_GCN4.AA** | Number of sites in the genebody showing GCN4 binding |
| **Gb_GCN4.AA** | Level of GCN4 binding in the genebody |
| **NumProm_H3** | Number of sites in the promoter occupied by H3 |
| **Prom_H3** | Level of H3 in the promoter |
| **NumProm_H4** | Number of sites in the promoter occupied by H4 |
| **Prom_H4** | Level of H4 in the promoter |
| **NumProm_H3K9ac_vsH3** | Number of sites in the promoter showing H3K9ac modification |
| **Prom_H3K9ac_vsH3** | Level of H3K9ac modification in the promoter |
| **NumProm_H3K14ac_vsH3** | Number of sites in the promoter showing H3K14ac modification |
| **Prom_H3K14ac_vsH3** | Level of H3K14ac modification in the promoter |
| **NumProm_H4ac_vsH3** | Number of sites in the promoter showing H4ac modification |
| **Prom_H4ac_vsH3** | Level of H4ac modification in the promoter |
| **NumProm_H3K4me1_vsH3** | Number of sites in the promoter showing H3K4me1 modification |
| **Prom_H3K4me1_vsH3** | Level of H3K4me1 modification in the promoter |
| **NumProm_H3K4me2_vsH3** | Number of sites in the promoter showing H3K4me2 modification |
| **Prom_H3K4me2_vsH3** | Level of H3K4me2 modification in the promoter |
| NumProm_H3K4me3_vsH3 | Number of sites in the promoter showing H3K4me3 modification |
|----------------------|-------------------------------------------------------------|
| Prom_H3K4me3_vsH3   | Level of H3K4me3 modification in the promoter               |
| NumProm_H3K36me3_vsH3 | Number of sites in the promoter showing H3K36me3 modification   |
| Prom_H3K36me3_vsH3   | Level of H3K36me3 modification in the promoter               |
| NumProm_H3K79me3_vsH3 | Number of sites in the promoter showing H3K79me3 modification   |
| Prom_H3K79me3_vsH3   | Level of H3K79me3 modification in the promoter               |
| NumProm_ESA1         | Number of sites in the promoter showing ESA1 binding         |
| Prom_ESA1            | Level of ESA1 binding in the promoter                        |
| NumProm_GCN5         | Number of sites in the promoter showing GCN5 binding         |
| Prom_GCN5            | Level of GCN5 binding in the promoter                        |
| NumProm_GCN4.AA      | Number of sites in the promoter showing GCN4 binding         |
| Prom_GCN4.AA         | Level of GCN4 binding in the promoter                        |

| DionScience2007_Gene_G1Lambda | H3 turnover rate in the coding region of G1 arrested yeast |
|-------------------------------|-----------------------------------------------------------|
| DionScience2007_Gene_G1Lambda_Zscore | H3 turnover rate in the coding region of G1 arrested yeast (Z-score calculated) |
| DionScience2007_Prom_G1Lambda | H3 turnover rate in the promoter region of G1 arrested yeast |
| DionScience2007_Prom_G1Lambda_Zscore | H3 turnover rate in the promoter region of G1 arrested yeast (Z-score calculated) |
| DionScience2007_Gene_H3Occ | H3 occupancy in the coding region |
| DionScience2007_Gene_NucOcc | Nucleosome occupancy in the coding region |
| DionScience2007_Prom_H3Occ | H3 occupancy in the promoter region |
| DionScience2007_Prom_NucOcc | Nucleosome occupancy in the promoter region |
| DionScience2007_Gene_PolII_t0 | RNA pol II occupancy in the coding region at t=0 |
| DionScience2007_Gene_PolII_t60 | RNA pol II occupancy in the coding region at t=60 mins |
| DionScience2007_Prom_PolIII_t0 | RNA pol II occupancy in the promoter region at t=0 |
| DionScience2007_Prom_PolIII_t60 | RNA pol II occupancy in the promoter region at t=60 mins |
| Sun2012_mRNA_Synth_rate | mRNA synthesis rate |
| Sun2012_mRNA_Decay_rate | mRNA decay rate |
| mRNA_PARS1 | mRNA secondary structure PARS score of the first codon |
| mRNA_PARS3 | mRNA secondary structure PARS score of the first three codons |
| mRNA_PARS5 | mRNA secondary structure PARS score of the first five codons |
| mRNA_PARS10 | mRNA secondary structure PARS score of the first ten codons |
| mRNA_PARS15 | mRNA secondary structure PARS score of the first fifteen codons |
| mRNA_PARS20 | mRNA secondary structure PARS score of the first twenty codons |
| mRNA_PARS25 | mRNA secondary structure PARS score of the first twenty-five codons |
| mRNA_PARS50 | mRNA secondary structure PARS score of the first fifty codons |
| mRNA_HL_Mins | mRNA half-life in minutes |
| protein_HL_Mins | protein half-life in minutes |
| Phosphorylation | Number of residues in the protein with phosphorylation |
| Methylation | Number of residues in the protein with methylation |
| Acetylation | Number of residues in the protein with acetylation |
| Ubiquitination | Number of residues in the protein with ubiquitination |
| Succinylation | Number of residues in the protein with succinylation |
| Oxidation | Number of residues in the protein showing oxidation |
| Nitration | Number of residues in the protein showing nitration |
| NtAcetylation | Number of residues in the protein with N-terminal acetylation |
| Glycosylation | Number of residues in the protein with glycosylation |
| Ca | Number of calcium binding sites in the protein |
| Disulfide | Number of residues in the protein showing disulfide bond formation |
| Lipidation | Number of residues in the protein with lipidation |
| ActiveSite | Number of residues in the active site of the protein |
| Sumoylation | Number of residues in the protein with SUMOylation |
| Variable                  | Description                                                                 |
|--------------------------|-----------------------------------------------------------------------------|
| whetherTF                | Whether the gene is a TF (Yes/No)                                           |
| Num_RegTF_YeastractYT    | Number of regulatory TFs (from Yeastract data)                               |
| MedExp_TFYT              | Median expression of regulatory TFs (Yeastract data)                         |
| MedDM_SD_TFYT            | Median noise of regulatory TFs (Yeastract data)                               |
| MedPosDM_SD_TFYT         | Median positive noise (DM values) of regulatory TFs (Yeastract data)          |
| MedNegDM_SD_TFYT         | Median negative noise (DM values) of regulatory TFs (Yeastract data)          |
| PercNegDM_TFYT           | Percentage of TFs showing negative noise (DM) values                         |
| PercPosDM_TFYT           | Percentage of TFs showing positive noise (DM) values                         |
| minDM_TFYT               | Minimum noise (DM) value                                                     |
| maxDM_TFYT               | Maximum noise (DM) value                                                     |
| PosCorTF_YT              | Number of TFs showing positive expression correlation with the target gene   |
| NegCorTF_YT              | Number of TFs showing negative expression correlation with the target gene   |
| PercPosCorTF_YT          | Percentage of TFs showing positive expression correlation with the target gene|
| PercNegCorTF_YT          | Percentage of TFs showing negative expression correlation with the target gene|
| Both_PosCorr_NegCorrTF_YT| Whether the gene has positively and negatively correlated TFs (Yes/No)       |
| NoisePosCorTF_YT         | Noise (DM) value of TFs showing positive expression correlation with the target gene |
| NoiseNegCorTF_YT         | Noise (DM) value of TFs showing negative expression correlation with the target gene |
| MeanStrPosCorTF          | Mean regulation strength of positively correlated TFs                        |
| SdStrPosCorTF            | Sd regulation strength of positively correlated TFs                          |
| MeanStrNegCorTF          | Mean regulation strength of negatively correlated TFs                        |
| SdStrNegCorTF            | Sd regulation strength of negatively correlated TFs                          |
| MeanCorPosCorTF          | Mean correlation value of TFs showing positive expression correlation with the target gene |
| SdCorPosCorTF            | Sd correlation value of TFs showing positive expression correlation with the target gene |
| MeanCorNegCorTF          | Mean correlation value of TFs showing negative expression correlation with the target gene |
| SdCorNegCorTF            | Sd correlation value of TFs showing negative expression correlation with the target gene |
| NumPosCor_withinTFs      | Number of TFs showing positive expression correlation with other TFs regulating the same target gene |
| NumNegCor_withinTFs      | Number of TFs showing negative expression correlation with other TFs regulating the same target gene |
| PercPosCor_withinTFs     | Percentage of TFs showing positive expression correlation with other TFs regulating the same target gene |
| PercNegCor_withinTFs     | Percentage of TFs showing negative expression correlation with other TFs regulating the same target gene |
| PosCor.NegCor_withinTFs  | Ratio of the number of TFs showing positive expression correlation with other regulating TFs of a gene to the number of TFs showing negative expression correlation with other TFs of a gene |
| PercPosCorWN_OVsites     | Percentage of TFs showing positive expression correlation with other TFs regulating the same target gene and binding to overlapping binding sites in the promoter |
| PercNegCorWN_OVsites     | Percentage of TFs showing negative expression correlation with other TFs regulating the same target gene and binding to overlapping binding sites in the promoter |
| AvgMut                   | Average number of mutations in the TF binding motifs in the promoter region  |
| Variable                        | Description                                                                 |
|--------------------------------|-----------------------------------------------------------------------------|
| N_TFSites100                   | Number of TF binding sites upto 100bp upstream region of the start codon    |
| N_TFSites200                   | Number of TF binding sites within 100bp and 200bp upstream region of the start codon |
| N_TFSites300                   | Number of TF binding sites within 200bp and 300bp upstream region of the start codon |
| N_TFSites400                   | Number of TF binding sites within 300bp and 400bp upstream region of the start codon |
| N_TFSites500                   | Number of TF binding sites within 400bp and 500bp upstream region of the start codon |
| N_TFSites600                   | Number of TF binding sites within 500bp and 600bp upstream region of the start codon |
| N_TFSites700                   | Number of TF binding sites within 600bp and 700bp upstream region of the start codon |
| N_TFSites800                   | Number of TF binding sites within 700bp and 800bp upstream region of the start codon |
| N_TFSites900                   | Number of TF binding sites within 800bp and 900bp upstream region of the start codon |
| N_TFSites1000                  | Number of TF binding sites within 900bp and 1000bp upstream region of the start codon |
| ExpTF100                       | Mean expression of TFs binding upto 100bp upstream region of the start codon |
| NoiseTF100                     | Expression noise of TFs binding upto 100bp upstream region of the start codon |
| ExpTF200                       | Mean expression of TFs binding between 100bp and 200bp upstream region of the start codon |
| NoiseTF200                     | Expression noise of TFs binding between 100bp and 200bp upstream region of the start codon |
| ExpTF300                       | Mean expression of TFs binding between 200bp and 300bp upstream region of the start codon |
| NoiseTF300                     | Expression noise of TFs binding between 200bp and 300bp upstream region of the start codon |
| ExpTF400                       | Mean expression of TFs binding between 300bp and 400bp upstream region of the start codon |
| NoiseTF400                     | Expression noise of TFs binding between 300bp and 400bp upstream region of the start codon |
| ExpTF500                       | Mean expression of TFs binding between 400bp and 500bp upstream region of the start codon |
| NoiseTF500                     | Expression noise of TFs binding between 400bp and 500bp upstream region of the start codon |
| ExpTF600                       | Mean expression of TFs binding between 500bp and 600bp upstream region of the start codon |
| NoiseTF600                     | Expression noise of TFs binding between 500bp and 600bp upstream region of the start codon |
| ExpTF700                       | Mean expression of TFs binding between 600bp and 700bp upstream region of the start codon |
| NoiseTF700                     | Expression noise of TFs binding between 600bp and 700bp upstream region of the start codon |
| ExpTF800                       | Mean expression of TFs binding between 700bp and 800bp upstream region of the start codon |
| NoiseTF800                     | Expression noise of TFs binding between 700bp and 800bp upstream region of the start codon |
| ExpTF900                       | Mean expression of TFs binding between 800bp and 900bp upstream region of the start codon |
| NoiseTF900                     | Expression noise of TFs binding between 800bp and 900bp upstream region of the start codon |
| ExpTF1000                      | Mean expression of TFs binding between 900bp and 1000bp upstream region of the start codon |
| NoiseTF1000                    | Expression noise of TFs binding between 900bp and 1000bp upstream region of the start codon |
| PercTFsiteNuc                  | Percentage of TF sites showing nucleosome occupancy                        |
| PercTFsiteHistMod              | Percentage of TF sites with histone modifications                           |
| Feature                          | Description                                                                 |
|---------------------------------|-----------------------------------------------------------------------------|
| AvgTFsiteNucOcc                 | Average TF site nucleosome occupancy level                                   |
| AvgTFsiteHist                   | Average TF site histone level                                               |
| AvgTFsiteMod                    | Average TF site histone modifications                                        |
| AvgTFsiteAsoc                   | Average level of associated regulators and modifiers (GCN4, GCN5, ESA1) in TF |
| PercOfPromNuc                   | Percentage of the total promoter nucleosome occupancy level observed in the TF|
| PercOfPromHist                  | Percentage of the total promoter histone level observed in the TF binding sites|
| PercOfPromMod                   | Percentage of the total promoter histone modifications observed in the TF binding sites|
| PercOfPromAsoc                  | Percentage of the total promoter associated regulators and modifiers observed in the TF binding sites|
| TFsiteH3                        | H3 level in TF binding sites                                                |
| TFsiteH4                        | H4 level in TF binding sites                                                |
| TFsiteH3K9ac_vsH3               | Level of H3K9ac modifications in TF binding sites                           |
| TFsiteH3K14ac_vsH3              | Level of H3K14ac modifications in TF binding sites                           |
| TFsiteH4ac_vsH3                 | Level of H4ac modifications in TF binding sites                             |
| TFsiteH3K4me1_vsH3              | Level of H3K4me1 modifications in TF binding sites                          |
| TFsiteH3K4me2_vsH3              | Level of H3K4me2 modifications in TF binding sites                          |
| TFsiteH3K4me3_vsH3              | Level of H3K4me3 modifications in TF binding sites                          |
| TFsiteH3K36me3_vsH3             | Level of H3K36me3 modifications in TF binding sites                          |
| TFsiteH3K79me3_vsH3             | Level of H3K79me3 modifications in TF binding sites                          |
| TFsiteESA1                      | Level of ESA1 in TF binding sites                                           |
| TFsiteGCN5                      | Level of GCN5 in TF binding sites                                           |
| TFsiteGCN4.AA                   | Level of GCN4 in TF binding sites                                           |
| PercOfPromH3                    | Percentage of the total promoter H3 level observed in the TF binding sites    |
| PercOfPromH4                    | Percentage of the total promoter H4 level observed in the TF binding sites    |
| PercOfPromH3K9ac_vsH3           | Percentage of the total promoter H3K9ac level observed in the TF binding sites|
| PercOfPromH3K14ac_vsH3          | Percentage of the total promoter H3K14ac level observed in the TF binding sites|
| PercOfPromH4ac_vsH3             | Percentage of the total promoter H4ac level observed in the TF binding sites  |
| PercOfPromH3K4me1_vsH3          | Percentage of the total promoter H3K4me1 level observed in the TF binding sites|
| PercOfPromH3K4me2_vsH3          | Percentage of the total promoter H3K4me2 level observed in the TF binding sites|
| PercOfPromH3K4me3_vsH3          | Percentage of the total promoter H3K4me3 level observed in the TF binding sites|
| PercOfPromH3K36me3_vsH3         | Percentage of the total promoter H3K36me3 level observed in the TF binding sites|
| PercOfPromH3K79me3_vsH3         | Percentage of the total promoter H3K79me3 level observed in the TF binding sites|
| PercOfPromESA1                  | Percentage of the total promoter ESA1 level observed in the TF binding sites  |
| PercOfPromGCN5                  | Percentage of the total promoter GCN5 level observed in the TF binding sites  |
| PercOfPromGCN4.AA               | Percentage of the total promoter GCN4 level observed in the TF binding sites  |
| NumSites                        | Number of TF binding sites in the promoter region                           |
| NumOverlaps                     | Number of overlaps in TF binding sites in the promoter region                |
| RatOverlap.NumSites             | Ratio of the number of overlaps to the total number of TF binding sites      |
| AvgOverlapLen                   | Average overlap length                                                       |
| AvgfrOverlapLen                 | Average fraction of TF binding site showing overlap                          |
| OV100                           | Percentage of binding site overlaps up to 100bp upstream region of the start codon of all overlaps in the promoter |
| OV200                           | Percentage of binding site overlaps between 100bp and 200bp upstream region of the start codon |
| OV300  | Percentage of binding site overlaps between 200bp and 300bp upstream region of the start codon |
|--------|------------------------------------------------------------------------------------------------|
| OV400  | Percentage of binding site overlaps between 300bp and 400bp upstream region of the start codon |
| OV500  | Percentage of binding site overlaps between 400bp and 500bp upstream region of the start codon |
| OV600  | Percentage of binding site overlaps between 500bp and 600bp upstream region of the start codon |
| OV700  | Percentage of binding site overlaps between 600bp and 700bp upstream region of the start codon |
| OV800  | Percentage of binding site overlaps between 700bp and 800bp upstream region of the start codon |
| OV900  | Percentage of binding site overlaps between 800bp and 900bp upstream region of the start codon |
| OV1000 | Percentage of binding site overlaps between 900bp and 1000bp upstream region of the start codon |
| PercAct2_Overlap  | Percentage of overlapping sites shared by two activators |
| Avg_stract2_ov  | Average strength of regulation of two activators binding to overlapping sites |
| Df_stract2_ov  | Difference in strength of regulation of two activators binding to overlapping sites |
| Avg_corstr_act2_ov  | Average expression correlation of two activators binding to overlapping sites with the target gene |
| Df_corstr_act2_ov  | Difference in expression correlation of two activators binding to overlapping sites with the target gene |
| PercRep2_overlap  | Percentage of overlapping sites shared by two repressors |
| Avg_strep2_ov  | Average strength of regulation of two repressors binding to overlapping sites |
| Df_strep2_ov  | Difference in strength of regulation of two repressors binding to overlapping sites |
| Avg_corstr_rep2_ov  | Average expression correlation of two repressors binding to overlapping sites with the target gene |
| Df_corstr_rep2_ov  | Difference in expression correlation of two repressors binding to overlapping sites with the target gene |
| PercActrep_overlap  | Percentage of overlapping sites shared by one activator and one repressor |
| Avg_stractrep_ov  | Average strength of regulation of activator and repressor binding to overlapping sites |
| Df_stractrep_ov  | Difference in strength of regulation of activator and repressor binding to overlapping sites |
| Avg_corstr_actrep_ov  | Average expression correlation of activator and repressor binding to overlapping sites with the target gene |
| Df_corstr_actrep_ov  | Difference in expression correlation of activator and repressor binding to overlapping sites with the target gene |
| NumCoopTF_Yang2010  | Number of cooperatively binding regulatory TFs from Yang et al., 2010 data [17] |
| PercCoopTF_Yang2010  | Percentage of cooperatively binding regulatory TFs from Yang et al., 2010 data |
| PercOvNocpTF_Yang2010  | Percentage of TFs showing binding site overlaps that are not cooperatively binding TFs as per Yang et al., 2010 data |
| NumCoopTF_Chen2012  | Number of cooperatively binding regulatory TFs from Chen et al., 2012 data [18] |
| PercCoopTF_Chen2012  | Percentage of cooperatively binding regulatory TFs from Chen et al., 2012 data |
| PercOvNocpTF_Chen2012  | Percentage of TFs showing binding site overlaps that are not cooperatively binding TFs as per Chen et al., 2010 data |
| Pugh2004_SAGA_Dominance  | Genes showing SAGA dominance in the promoter (Yes/No) [19] |
| Pugh2004_TFIID_Dominance  | Genes showing TFIID Dominance in the promoter (Yes/No) |
| Pugh2004_SAGA_TFIID  | Genes activated by both SAGA/TFIID complexes (Yes/No) |
| Donczew2020_Coactivator_redundant_motif  | Number of the coactivator redundant motif present in the promoter [20] |
| Dataset | Description |
|---------|-------------|
| Donczew2020_TFIID_dependent_motif | Number of the TFIID redundant motif present in the promoter |
| TBP.NSMB2009_pol_II | Whether the promoter is a polII transcribed promoter (Yes/No) |
| TBP.NSMB2009_pol_III | Whether the promoter is a polIII transcribed promoter (Yes/No) |
| TBP.NSMB2009_0 | Ratio of inducible TBP expression level to constitutively expressed TBP level at time \( t=0 \) |
| TBP.NSMB2009_10 | Ratio of inducible TBP expression level to constitutively expressed TBP level at time \( t=10 \) mins |
| TBP.NSMB2009_20 | Ratio of inducible TBP expression level to constitutively expressed TBP level at time \( t=20 \) mins |
| TBP.NSMB2009_25 | Ratio of inducible TBP expression level to constitutively expressed TBP level at time \( t=25 \) mins |
| TBP.NSMB2009_30 | Ratio of inducible TBP expression level to constitutively expressed TBP level at time \( t=30 \) mins |
| TBP.NSMB2009_40 | Ratio of inducible TBP expression level to constitutively expressed TBP level at time \( t=40 \) mins |
| TBP.NSMB2009_60 | Ratio of inducible TBP expression level to constitutively expressed TBP level at time \( t=60 \) mins |
| TBP.NSMB2009_90 | Ratio of inducible TBP expression level to constitutively expressed TBP level at time \( t=90 \) mins |
| TBP.NSMB2009_TBP_occupancy | Overall TBP occupancy |
| TBP.NSMB2009_TBP_turnover | TBP turnover rate |
| HolstegeMSB2020_Abf1_NormBindingt0_Gene | Normalized binding levels of Abf1 in the coding region before nuclear depletion of Abf1 |
| HolstegeMSB2020_Abf1_EstBindingt0_Gene | Estimate for binding levels of Abf1 in the coding region before nuclear depletion of Abf1 |
| HolstegeMSB2020_Abf1_Offrate_Gene | Abf1 binding offrate in the coding region |
| HolstegeMSB2020_Abf1_MeanRestimeMins_Gene | Mean residence time of Abf1 in mins in the coding region |
| HolstegeMSB2020_Abf1_NormBindingt0_Prom | Normalized binding levels of Abf1 in the promoter region before nuclear depletion of Abf1 |
| HolstegeMSB2020_Abf1_EstBindingt0_Prom | Estimate for binding levels of Abf1 in the promoter region before nuclear depletion of Abf1 |
| HolstegeMSB2020_Abf1_Offrate_Prom | Abf1 binding offrate in the promoter region |
| HolstegeMSB2020_Abf1_MeanRestimeMins_Prom | Mean residence time of Abf1 in mins in the promoter region |
| MolClutch_Nature2012_Rap1Residency_Gene | Residency of Rap1 in the coding region (in mins) |
| MolClutch_Nature2012_Rap1Residency_Prom | Residency of Rap1 in the promoter region (in mins) |
| MolClutch_Nature2012_Rap1Occupancy_Gene | Occupancy of Rap1 in the coding region |
| MolClutch_Nature2012_Rap1Occupancy_Prom | Occupancy of Rap1 in the promoter region |
| GSE44200_2.5MNase_TBPocc_Gene | TBP occupancy in the coding region (results from 2.5min Mnase treatment) |
| GSE44200_2.5MNase_Mot1occ_Gene | Mot1 occupancy in the coding region (results from 2.5min Mnase treatment) |
| GSE44200_2.5MNase_Mot1TBPrat_Gene | Ratio of Mot1 to TBP occupancy in the coding region (results from 2.5min Mnase treatment) |
| GSE44200_2.5MNase_TBPocc_Prom | TBP occupancy in the promoter region (results from 2.5min Mnase treatment) |
| GSE44200_2.5MNase_Mot1occ_Prom | Mot1 occupancy in the promoter region (results from 2.5min Mnase treatment) |
| GSE44200_2.5MNase_Mot1TBPrat_Prom | Ratio of Mot1 to TBP occupancy in the promoter region (results from 2.5min Mnase treatment) |
| GSE44200_10MNase_TBPocc_Gene | TBP occupancy in the coding region (results from 10min Mnase treatment) |
| GSE44200_10MNase_Mot1occ_Gene | Mot1 occupancy in the coding region (results from 10min Mnase treatment) |
| GSE44200_10MNase_Mot1TBPrat_Gene | Ratio of Mot1 to TBP occupancy in the coding region (results from 10min Mnase treatment) |
| GSE44200_10MNase_TBPocc_Prom | TBP occupancy in the promoter region (results from 10min Mnase treatment) |
| GSE44200_10MNase_Mot1occ_Prom | Mot1 occupancy in the promoter region (results from 10min Mnase treatment) |
| GSE44200_10MNase_Mot1TBPrat_Prom | Ratio of Mot1 to TBP occupancy in the promoter region (results from 10min Mnase treatment) |
| GSE59523_NucleosomeAsymmetry_Prom | Nucleosome asymmetry (+1 or -1) in the promoter [25] |
| YenEtAl_Cell2012_Arp5_Nuc | Whether the gene has Arp5 bound nucleosome (Yes/No) [26] |
| YenEtAl_Cell2012_Ino80_Nuc | Whether the gene has Ino80 bound nucleosome (Yes/No) |
| YenEtAl_Cell2012_Ioc3_Nuc | Whether the gene has Ioc3 bound nucleosome (Yes/No) |
| YenEtAl_Cell2012_Ioc4_Nuc | Whether the gene has Ioc4 bound nucleosome (Yes/No) |
| YenEtAl_Cell2012_Isw1_Nuc | Whether the gene has Isw1 bound nucleosome (Yes/No) |
| YenEtAl_Cell2012_Isw2_Nuc | Whether the gene has Isw2 bound nucleosome (Yes/No) |
| YenEtAl_Cell2012_Rsc8_Nuc | Whether the gene has Rsc8 bound nucleosome (Yes/No) |
| YenEtAl_Cell2012_Snf2_Nuc | Whether the gene has Snf2 bound nucleosome (Yes/No) |
| YenEtAl_Cell2012_Ioc4_terminalNuc | Whether the gene has Ioc4 bound terminal nucleosome (Yes/No) |
| YenEtAl_Cell2012_Ioc3_terminalNuc | Whether the gene has Ioc3 bound terminal nucleosome (Yes/No) |
| YenEtAl_Cell2012_Ino80_terminalNuc | Whether the gene has Ino80 bound terminal nucleosome (Yes/No) |
| YenEtAl_Cell2012_Isw1_terminalNuc | Whether the gene has Isw1 bound terminal nucleosome (Yes/No) |
| YenEtAl_Cell2012_Isw2_terminalNuc | Whether the gene has Isw2 bound terminal nucleosome (Yes/No) |
| Intra_Gb_NumInt | Number of intra-chromosomal interactions in the genebody [27] |
| Intra_Prom_NumInt | Number of intra-chromosomal interactions in the promoter |
| Inter_Gb_NumInt | Number of inter-chromosomal interactions in the genebody |
| Inter_Prom_NumInt | Number of inter-chromosomal interactions in the promoter |

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