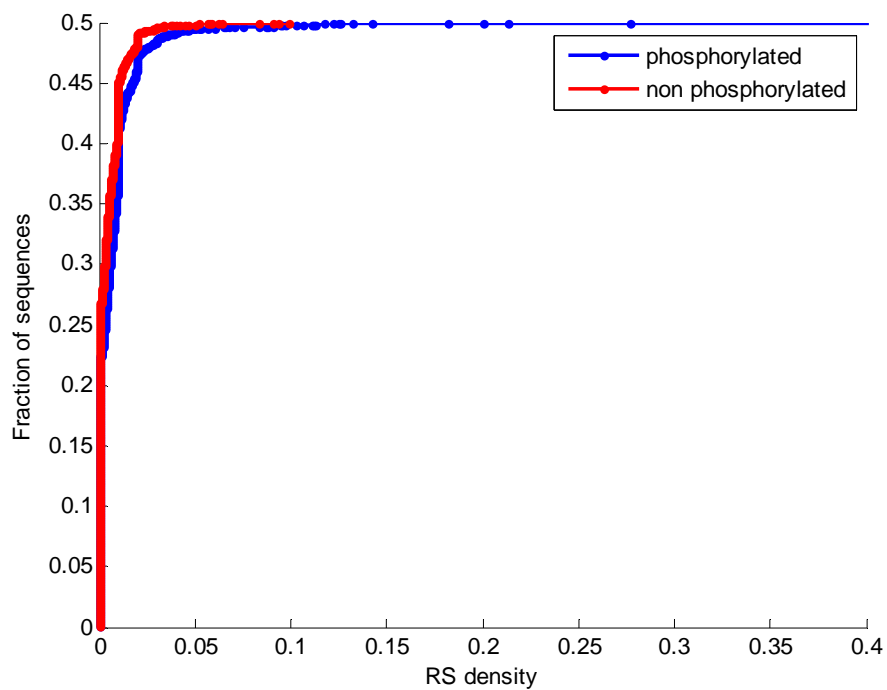


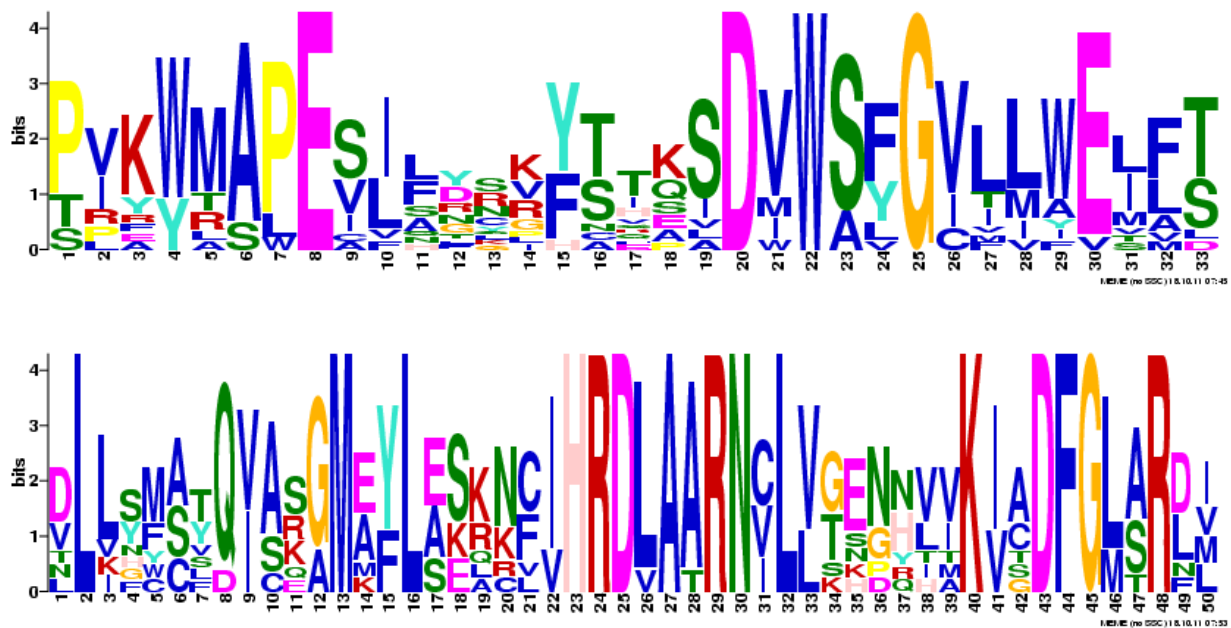
**Figure S1 – Evaluating DRIMUST time complexity and actual performance**

The total complexity of this algorithm is  $\sum_P |C(P)|^2$ . This quantity was evaluated for datasets with actual biological sequences of total size 500,000-1,000,000 characters, testing three lengths of motifs: 7, 10 and 13. Results are shown in blue (left y axis). Additionally, the total running time, on a standard PC, was measured for these datasets – see red graph (right y axis; time is in seconds).



**Figure S2 – RS di-residual density comparison of serine phosphorylated and non-phosphorylated sequences in humans**

We compared RS di-residual density among serine phosphorylated and non-phosphorylated sequences. For each value, the number of sequences having RS density smaller than this value is indicated.



**Figure S3 – MEME’s output for tyrosine phosphorylated sequences**

The motif SDVW appears as part of the upper logo, and the motif HRDLAARN-X<sup>12</sup>-DFGL is present at the lower logo, consistent with DRIMUST predictions.

**Table S1**

The motifs predicted by DRIMUST on the Harbison dataset

<b>TF</b>	<b>motif</b>	<b>N</b>	<b>B</b>	<b>n</b>	<b>b</b>	<b>p-value ≤</b>	<b>corrected p-value ≤</b>
A1 (MATA1)	ATAA-[0, 2, 3, 6, 7, 9]-TATT	5615	1232	1846	520	5.64E-12	7.57E-04
A1 (MATA1)	AATGAA	5615	1589	4822	1451	2.21E-11	2.97E-03
ABF1	TCGT-[6]-TGAT	6057	159	1045	124	3.53E-63	4.74E-55
ABF1	ATCA-[6]-ACGA	6057	151	1043	120	7.23E-63	9.70E-55
ABT1	ATTT-[0, 1, 2, 4, 6, 7, 8, 9, 10]-AAAT	6100	2059	3117	1239	4.49E-21	6.03E-13
ABT1	AATA-[0, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10]-TTTA	6100	2091	3399	1349	1.42E-20	1.91E-12
ACA1	AACA-[1, 4, 6]-TTCG	6041	136	891	51	4.34E-09	5.83E-01
ACA1	TGCT-[2, 4, 5, 6, 8, 10]-AGCA	6041	251	3072	178	8.30E-09	1.00E+00
ACE2	CACA-[4, 6, 7, 9, 10]-CACA	6148	257	160	30	4.68E-10	6.28E-02
ACE2	ACAC-[0, 6, 7, 8, 9]-ACAC	6148	198	390	41	1.13E-09	1.52E-01
ADR1	ACTT-[2, 3, 6, 9, 10]-TGAC	6167	208	2663	135	2.41E-08	1.00E+00
ADR1	AGAT-[0, 1, 3, 4, 5, 10]-CAAC	6167	289	665	68	4.38E-08	1.00E+00
AFT2	TATCCACGA	5921	19	420	17	6.11E-17	8.20E-09
AFT2	AGATACTGTG	5921	16	420	15	1.10E-15	1.48E-07
ARG80	ATTT-[1, 2, 4, 7, 8, 9, 10]-AAAT	6128	1783	2701	975	1.35E-23	1.81E-15
ARG80	AAAT-[0, 1, 3, 5, 6, 7, 8, 9, 10]-AATT	6128	2042	3319	1300	3.81E-23	5.11E-15
ARG81	AATT-[2, 5, 6, 7, 10]-ATAT	6115	1111	2550	601	2.63E-17	3.53E-09
ARG81	TATT-[0, 1, 2, 3, 4, 5, 6, 7, 8, 9]-TAAT	6115	1781	2350	842	1.49E-16	2.00E-08
ARO80	ATTT-[0, 2, 3, 4, 6, 8, 9, 10]-AATA	6104	1737	3031	1000	6.21E-12	8.33E-04
ARO80	TAAT-[2, 3, 4, 6, 7, 8, 9]-TTTA	6104	1330	3441	869	4.87E-11	6.54E-03
ARR1	ATTT-[0, 3, 4, 5, 6, 8, 9, 10]-TTAT	6153	2080	2288	961	3.40E-22	4.56E-14
ARR1	ATAT-[1, 3, 5, 6, 7, 8, 9, 10]-TAAT	6153	1552	2210	722	2.31E-20	3.10E-12
ASH1	GGTC-[9]-GCGG	6156	17	386	15	1.45E-15	1.95E-07
ASH1	CTCCTCGAC	6156	17	386	15	1.45E-15	1.95E-07
ASK10	AAAT-[1, 2, 3, 4, 5, 6, 8, 9]-TCAA	6126	1559	3568	1052	5.48E-15	7.36E-07
ASK10	TGAT-[0, 3, 4, 5, 6, 7, 8, 9]-TCAA	6126	684	3678	511	7.34E-15	9.85E-07
AZF1	AAATCACTTC	6137	6	3	3	3.12E-09	4.19E-01
AZF1	ACAGCTGTA	6137	7	5	3	6.36E-08	1.00E+00
BAS1	TAAT-[2, 3, 4, 5, 6, 7, 8, 9]-TTTA	6096	1455	5034	1293	4.87E-11	6.54E-03
BAS1	ATTT-[1, 5, 7, 9, 10]-TATT	6096	1511	3684	1028	1.93E-09	2.59E-01

BYE1	AATT-[2, 3, 5, 6, 7, 10]-AATT	6127	1184	2792	676	6.80E-16	9.13E-08
BYE1	TATT-[2, 3, 5, 6, 10]-ATGT	6127	645	3699	478	4.98E-12	6.68E-04
CAD1	ATCC-[0, 10]-CCAC	6092	65	677	35	1.35E-15	1.81E-07
CAD1	CCAC-[3, 6]-GCGG	6092	47	639	28	1.04E-14	1.40E-06
CBF1	CACGTG	6090	372	263	119	9.79E-77	1.31E-68
CBF1	CACGTGA	6090	180	233	77	1.37E-62	1.84E-54
CHA4	ATTT-[1, 2, 3, 6, 7, 8, 10]-AAAA	5821	1875	2312	902	3.35E-16	4.50E-08
CHA4	ATTT-[1, 2, 3, 7, 8, 9, 10]-AAAT	5821	1665	1819	655	8.35E-14	1.12E-05
CIN5	TTAC-[1]-TAAT	6135	131	590	54	3.77E-20	5.06E-12
CIN5	ATTA-[1]-GTAA	6135	128	439	46	1.84E-19	2.47E-11
CRZ1	CCTCGACTAA	6103	22	359	17	3.71E-16	4.98E-08
CRZ1	CTCGACTAA	6103	22	359	17	3.71E-16	4.98E-08
CST6	TGAA-[1, 3, 4, 6, 7, 8, 9, 10]-TTAA	6182	977	2385	485	1.18E-11	1.58E-03
CST6	TAAA-[3, 5, 6, 9, 10]-TTAA	6182	912	1472	308	7.91E-11	1.06E-02
CUP9	GAGG-[1, 2, 6, 9]-CGTA	6059	111	3890	102	1.06E-09	1.42E-01
CUP9	CATC-[0, 9]-TACT	6059	155	2043	92	5.14E-09	6.90E-01
DAL80	TTCA-[0, 1, 6, 8]-AATG	5527	360	410	68	3.70E-11	4.97E-03
DAL80	ATTAAA	5527	1584	877	342	5.88E-10	7.89E-02
DAL81	TCCT-[2, 5, 7]-AGGA	5953	211	1174	95	3.54E-15	4.75E-07
DAL81	GGAT-[1, 2]-CCTA	5953	115	1257	60	1.41E-11	1.89E-03
DAL82	GATA-[3, 4, 5, 6, 7, 9]-CTCA	6045	242	937	76	4.40E-08	1.00E+00
DAL82	CAGG-[1, 3, 7]-TATA	6045	127	854	45	1.22E-07	1.00E+00
DAT1	CTGAGCAACG	6126	15	173	12	1.12E-15	1.50E-07
DAT1	CGGCTGAGCA	6126	15	173	12	1.12E-15	1.50E-07
DIG1	CTGTATACCT	6096	62	794	42	1.08E-21	1.45E-13
DIG1	CTGT-[3]-CCTA	6096	70	809	45	1.91E-21	2.56E-13
DOT6	CGGC-[0, 2, 3, 7, 8, 10]-GCCG	6003	80	2385	63	7.09E-11	9.52E-03
DOT6	ACGA-[7, 9]-CGTG	6003	32	1243	24	1.91E-09	2.56E-01
ECM22	CACA-[4, 5, 6]-CGCA	6084	87	3138	78	1.93E-12	2.59E-04
ECM22	GCAG-[0, 1, 2, 3, 4, 5, 8, 10]-CGGC	6084	115	1641	67	1.21E-10	1.62E-02
EDS1	ATTA-[5, 9, 10]-TTCA	6115	418	2215	218	1.74E-09	2.34E-01
EDS1	AAGA-[0, 1, 3, 4, 6, 8, 9]-CTAT	6115	558	735	120	9.45E-09	1.00E+00
FAP7	TAAG-[0, 1, 3, 5, 9]-TTTT	6172	692	4728	594	8.13E-08	1.00E+00
FAP7	TAAA-[3, 4, 5, 6, 9, 10]-TTTA	6172	1239	4840	1052	1.20E-07	1.00E+00

FHL1	ATCC-[2]-ACAT	6076	79	182	40	2.16E-39	2.90E-31
FHL1	ATCC-[1]-TACA	6076	74	182	39	2.73E-39	3.66E-31
FKH1	TGTTTAC	6169	290	593	86	9.19E-21	1.23E-12
FKH1	TTGT-[0]-TTAC	6169	128	308	39	4.59E-19	6.16E-11
FKH2	GTAACA	6164	358	596	88	4.62E-15	6.20E-07
FKH2	TTGTTTAC	6164	129	477	42	1.52E-14	2.04E-06
FZF1	AAAT-[0, 1, 5, 6, 7, 9, 10]-ATTT	6104	1964	2029	790	2.94E-12	3.95E-04
FZF1	TATT-[0, 1, 2, 3, 4, 6, 9]-AAAT	6104	1480	3038	855	1.30E-09	1.74E-01
GAL3	TAAT-[0, 3, 7, 8, 10]-ACTT	6118	533	3123	353	4.92E-11	6.60E-03
GAL3	TGAA-[1, 2, 4, 5, 6, 7]-TCAA	6118	795	1720	313	9.56E-11	1.28E-02
GAL4	CGGA-[10]-CCGT	6157	13	6	4	2.33E-09	3.13E-01
GAL4	ATCA-[1, 10]-GTTA	6157	113	20	9	2.75E-09	3.69E-01
GAL80	AAAT-[0, 1, 2, 3, 4, 5, 6, 7, 9, 10]-TCAA	6156	1805	3138	1060	4.63E-12	6.21E-04
GAL80	TTGA-[0, 2, 5, 6, 8, 9]-ATCA	6156	524	3340	359	1.39E-09	1.87E-01
GAT1	CCAC-[0, 1, 3, 4, 5, 6, 7, 8, 9, 10]-CCAG	6172	175	1947	112	6.31E-17	8.47E-09
GAT1	CGGCGC	6172	220	2291	141	3.07E-14	4.12E-06
GAT3	GCGG-[7, 10]-ACGA	6069	51	54	23	2.49E-34	3.34E-26
GAT3	CACG-[5, 8]-GAGC	6069	51	49	21	3.78E-31	5.07E-23
GCN4	TGACTCA	6176	140	225	46	1.15E-30	1.54E-22
GCN4	ATGACTCA	6176	38	244	22	2.52E-20	3.38E-12
GCR1	CCATTTTGAG	6121	48	206	20	4.86E-16	6.52E-08
GCR1	ATTCCATTTT	6121	66	149	20	1.52E-15	2.04E-07
GCR2	AAAT-[0, 1, 4, 6, 9, 10]-TCAT	6121	946	4678	814	1.27E-12	1.70E-04
GCR2	TAAA-[1, 2, 4, 8, 9, 10]-TTTA	6121	1157	2428	573	3.18E-11	4.27E-03
GLN3	AAAT-[1, 2, 3, 4, 5, 6, 9]-ATTT	6132	1857	4956	1627	4.97E-17	6.67E-09
GLN3	TAAA-[0, 1, 2, 3, 4, 5, 7, 8, 10]-TATT	6132	1805	5028	1598	6.84E-16	9.18E-08
GTS1	ATAA-[0, 2, 5, 7, 10]-AAGT	6142	745	5361	701	5.78E-08	1.00E+00
GTS1	CATA-[2, 3]-GCCA	6142	64	2360	48	1.59E-07	1.00E+00
GZF3	ATGA-[1, 2, 3, 4, 6, 8]-AACA	5935	479	2158	242	1.34E-08	1.00E+00
GZF3	CTGA-[0, 1, 3, 4, 7, 9, 10]-TGAT	5935	320	2389	185	1.78E-08	1.00E+00
HAA1	CAAA-[0, 3, 5, 6, 7, 8, 9]-TTGA	5846	768	5167	733	3.02E-10	4.05E-02
HAA1	ATGAAG	5846	964	4092	766	3.30E-10	4.43E-02
HAC1	AAAT-[0, 3, 4, 5, 7, 8, 9, 10]-TAAA	6178	2179	2195	916	5.51E-12	7.40E-04
HAC1	AAAA-[1, 2, 4, 5, 7, 8, 9, 10]-AAAT	6178	2983	3702	1937	1.34E-11	1.80E-03

HAL9	TGTT-[1]-GAAT	6126	144	2402	108	1.64E-16	2.20E-08
HAL9	AATT-[2, 3, 6, 7, 9, 10]-AATT	6126	1182	2239	566	4.49E-16	6.03E-08
HAP1	TTTATCGG	6119	30	188	18	4.96E-19	6.66E-11
HAP1	TTTA-[0]-TCGG	6119	30	188	18	4.96E-19	6.66E-11
HAP2	AATATT	6072	2327	1138	535	4.82E-08	1.00E+00
HAP2	GTTA-[2, 4, 8]-AGAT	6072	217	533	48	1.88E-07	1.00E+00
HAP3	AAAT-[0, 2, 4, 6, 7, 9, 10]-TTTA	6154	1555	3714	1087	2.01E-16	2.70E-08
HAP3	ATTT-[0, 2, 4, 5, 8, 9]-AATA	6154	1398	2459	695	3.57E-14	4.79E-06
HAP4	CACG-[6, 8]-GAGC	6115	36	242	19	1.89E-16	2.54E-08
HAP4	GACTAAGCA	6115	20	443	17	5.80E-16	7.78E-08
HAP5	TATT-[1, 2, 4, 5, 7, 8, 9, 10]-AATA	6115	1676	1842	638	2.27E-13	3.05E-05
HAP5	ATAT-[0, 1, 2, 3, 6, 8, 10]-TTTA	6115	1596	2813	865	2.27E-11	3.05E-03
HIR1	ATTT-[1, 2, 5, 6, 8, 9]-ATTT	6089	1898	934	407	4.57E-15	6.13E-07
HIR1	AATTTT	6089	2909	2086	1136	8.51E-11	1.14E-02
HIR2	ATAT-[0, 1, 3, 4, 5, 10]-ATAT	6047	1895	3326	1240	1.79E-25	2.40E-17
HIR2	TATA-[0, 1, 2, 5, 9]-TATA	6047	1676	3032	1028	3.24E-24	4.35E-16
HIR3	TTTT-[0, 1, 2, 3, 4, 5, 6, 7, 8, 10]-AAAA	6176	2367	3873	1687	3.11E-25	4.17E-17
HIR3	AAAT-[0, 4, 5, 6, 7, 8, 9, 10]-ATTT	6176	2218	4557	1816	4.12E-25	5.53E-17
HMS1	ATTT-[0, 5, 7, 10]-TTTT	6018	2439	1963	943	2.91E-13	3.91E-05
HMS1	AAAT-[0, 2, 5, 7, 9]-ATTT	6018	1486	4032	1120	8.24E-13	1.11E-04
HMS2	TGTA-[2, 6]-TTTT	6038	524	368	70	4.47E-08	1.00E+00
HMS2	TTAA-[0, 1, 8]-TTAC	6038	281	857	77	6.29E-07	1.00E+00
HOG1	TTTA-[0, 1, 3, 4, 5, 6, 7, 8, 9]-AAAT	6041	1851	3320	1208	5.95E-24	7.99E-16
HOG1	ATTT-[0, 2, 4, 5, 6, 7, 9, 10]-AATT	6041	1792	3511	1224	8.54E-23	1.15E-14
HSF1	AATG-[0, 1, 2, 5]-CATT	6155	354	54	18	1.58E-07	1.00E+00
HSF1	TAAA-[0, 5]-ATCA	6155	267	2028	135	2.40E-07	1.00E+00
IFH1	TCAC-[6, 8, 9]-AATT	6140	273	24	13	8.81E-10	1.18E-01
IFH1	ATTT-[0, 1, 2, 3, 8]-GAAC	6140	437	1688	180	4.27E-08	1.00E+00
IME1	ATCC-[3, 6, 10]-TCGT	4899	85	438	29	5.38E-09	7.22E-01
IME1	CAGC-[0, 8, 9, 10]-ACCG	4899	50	2713	47	6.99E-08	1.00E+00
IME4	CACA-[1, 2]-CACA	5841	144	302	33	1.92E-11	2.58E-03
IME4	ACACACACAC	5841	29	80	10	6.14E-11	8.24E-03
INO2	CATGTG	5974	420	431	83	5.50E-16	7.38E-08
INO2	GCATGTG	5974	110	429	36	1.65E-13	2.21E-05

INO4	CACGTG	6089	368	2954	274	4.64E-23	6.23E-15
INO4	CATGTGAA	6089	50	57	15	4.48E-18	6.01E-10
IXR1	AAAT-[2, 3, 4, 5, 7, 8, 9]-CTCA	5995	570	2059	272	1.69E-09	2.27E-01
IXR1	CATC-[3, 5]-AATC	5995	115	138	18	8.91E-09	1.00E+00
KRE33	AATG-[9]-CAAC	5996	58	476	20	4.16E-07	1.00E+00
KRE33	AGAA-[0, 1, 5, 8]-CTGA	5996	283	1477	113	1.20E-06	1.00E+00
KSS1	TATT-[0, 1, 2, 4, 5, 6, 7]-GCTG	6118	411	2755	256	1.07E-10	1.44E-02
KSS1	ATAT-[0, 1, 2]-CAGC	6118	207	3953	174	4.57E-08	1.00E+00
LEU3	TAAT-[1, 2, 6, 7, 9, 10]-TTAG	6129	566	1400	205	1.34E-11	1.80E-03
LEU3	ACCC-[2, 8]-ACAT	6129	105	589	36	2.64E-10	3.54E-02
MAC1	CCTA-[1, 9]-GACT	6112	30	520	15	1.02E-07	1.00E+00
MAC1	CCTATGACT	6112	9	509	8	1.65E-07	1.00E+00
MAL13	CCTCGACTAA	5514	22	626	19	2.12E-14	2.85E-06
MAL13	CTCGACTAA	5514	22	626	19	2.12E-14	2.85E-06
MAL33	GCTT-[3, 4, 10]-CCAC	6055	86	1268	48	8.71E-11	1.17E-02
MAL33	CACA-[0, 1, 2, 3, 4, 5, 6]-CACA	6055	344	3043	236	3.51E-10	4.71E-02
MBF1	TCAT-[6]-CTGT	3394	33	181	13	1.37E-07	1.00E+00
MBF1	GTAA-[1, 7, 9]-TAAG	3394	92	1632	72	1.65E-07	1.00E+00
MBP1	ACGCGT	6169	326	1067	166	2.97E-44	3.99E-36
MBP1	CGCG-[1, 3, 6, 8, 9, 10]-CGCG	6169	92	434	50	2.76E-32	3.70E-24
MCM1	AAAT-[0, 1, 2, 4, 7, 9, 10]-ATTT	6184	1921	3403	1222	6.73E-17	9.03E-09
MCM1	AATA-[0, 1, 3, 4, 7, 9]-TAAT	6184	1307	2974	759	3.39E-13	4.55E-05
MDS3	ATTT-[1, 2, 4, 5, 7, 8, 9, 10]-AAAT	6180	1985	2001	816	2.11E-20	2.83E-12
MDS3	AAAT-[0, 1, 2, 3, 4, 5, 6, 7, 9]-TCAA	6180	1708	3987	1261	8.70E-19	1.17E-10
MET18	GTATCCAAGA	6091	17	248	12	1.40E-12	1.88E-04
MET18	CGAACAGAAT	6091	16	248	11	2.39E-11	3.21E-03
MET28	ATAA-[0, 3, 4, 6, 7]-TTAT	6026	937	670	169	3.11E-09	4.17E-01
MET28	GGTC-[2, 10]-TTTA	6026	73	342	21	1.96E-08	1.00E+00
MET31	ATCC-[0, 5, 7, 10]-GTAC	6112	112	1121	50	1.02E-08	1.00E+00
MET31	AGTA-[4, 5, 10]-ATTA	6112	340	2316	187	1.17E-08	1.00E+00
MET32	CACGTGA	6070	176	46	14	3.33E-09	4.47E-01
MET32	CACGTG	6070	365	24	13	5.43E-08	1.00E+00
MET4	CACGTG	6079	368	2755	240	6.90E-13	9.26E-05
MET4	CCAC-[0, 2, 4, 6, 10]-GTGG	6079	79	18	9	2.32E-11	3.11E-03



MGA1	TTAA-[0, 2, 4, 5, 6, 7, 9]-AAGT	6114	791	699	155	2.97E-10	3.99E-02
MGA1	TTAA-[1, 2, 5, 7, 9, 10]-TTGA	6114	701	2405	363	6.18E-10	8.29E-02
MIG1	CCTA-[1, 2, 8]-AGCT	6116	62	80	12	8.50E-10	1.14E-01
MIG1	ATAC-[3, 9]-CGGA	6116	30	75	9	1.34E-09	1.80E-01
MIG2	ATTT-[0, 1, 4, 5, 6, 7, 8, 9, 10]-AAAT	6063	2035	1073	473	3.29E-12	4.42E-04
MIG2	ATAT-[4, 5, 7, 8, 10]-TAAT	6063	1098	2318	527	2.20E-10	2.95E-02
MIG3	AAAT-[3, 5, 6, 7, 8, 9, 10]-AATT	6180	1764	2742	959	2.24E-20	3.01E-12
MIG3	AAAT-[0, 1, 2, 3, 4, 6, 8, 9, 10]-AAAA	6180	2935	2818	1514	4.49E-16	6.03E-08
MOT3	ATAT-[0, 2, 4, 5, 6, 9]-TATA	5811	1624	3031	1005	1.80E-17	2.42E-09
MOT3	ATATTATCAT	5811	91	655	41	2.15E-14	2.89E-06
MSN1	GCCT-[4, 5]-CAAC	6088	105	3109	89	3.04E-11	4.08E-03
MSN1	GCGA-[2, 7, 8, 9]-TCGC	6088	58	780	29	3.59E-10	4.82E-02
MSN2	ATAA-[0, 1, 4, 5, 8]-AATA	6171	1432	1328	400	3.79E-08	1.00E+00
MSN2	ATGT-[5, 6, 10]-GTGG	6171	73	21	7	1.80E-07	1.00E+00
MSN4	GCGG-[7, 10]-ACGA	6182	53	169	20	8.63E-17	1.16E-08
MSN4	CGTAGGTCCA	6182	15	166	12	6.02E-16	8.08E-08
MSS11	ATTT-[0, 3, 9, 10]-TCAA	5644	763	3930	612	8.28E-10	1.11E-01
MSS11	ATTA-[0, 1, 4, 5, 8, 9]-TTAT	5644	982	3573	710	3.84E-08	1.00E+00
MTH1	CCAC-[0, 2, 3, 5, 7, 10]-CGGC	5975	77	1765	53	6.85E-11	9.19E-03
MTH1	CCCT-[1, 7, 8, 10]-GGAG	5975	55	730	28	1.38E-10	1.85E-02
NDD1	GTCT-[1, 3, 4]-GCGG	6181	33	798	20	4.81E-09	6.46E-01
NDD1	GTCT-[2, 4, 5, 6, 10]-CGGA	6181	68	521	24	2.97E-08	1.00E+00
NDT80	TAAT-[0, 1, 9]-TATT	6032	621	367	77	1.81E-07	1.00E+00
NDT80	TGCT-[2, 3, 6, 9]-TGAG	6032	134	1800	73	2.17E-07	1.00E+00
NNF2	ATTT-[1, 3, 5, 6, 7, 8, 10]-TAAT	5997	1329	3350	880	3.10E-15	4.16E-07
NNF2	TTAT-[2, 3, 5, 10]-AAAT	5997	834	3444	585	2.39E-13	3.21E-05
NRG1	GGGG-[1, 2]-TGCT	6096	13	34	6	4.10E-10	5.50E-02
NRG1	ATGT-[0, 4, 5, 6]-TGTG	6096	195	113	22	8.95E-10	1.20E-01
OAF1	GTTC-[0, 4, 6, 8]-GAGC	6052	94	767	39	1.70E-10	2.28E-02
OAF1	ACGA-[0, 1, 2, 4, 5, 10]-TCGT	6052	142	431	36	9.59E-10	1.29E-01
OPI1	GCATGTGAA	6181	13	157	8	2.18E-09	2.93E-01
OPI1	CTAG-[1, 3]-ATTC	6181	139	140	20	3.28E-09	4.40E-01
PDC2	TGTTGGAATA	6120	83	404	51	3.52E-38	4.72E-30
PDC2	CATATACGGT	6120	78	404	49	2.50E-37	3.36E-29

PDR1	AGATACTGTG	6136	16	161	13	1.44E-17	1.93E-09
PDR1	TCTCCTCGAC	6136	16	161	13	1.44E-17	1.93E-09
PDR3	TTGA-[4, 5, 6, 10]-TCAA	5957	436	1356	162	5.05E-10	6.78E-02
PDR3	AATG-[0, 4, 6, 8, 9, 10]-ATCA	5957	427	2771	265	6.76E-09	9.07E-01
PHD1	ATTT-[1, 3, 5, 9, 10]-TTTT	6104	2548	3782	1724	1.00E-11	1.34E-03
PHD1	ATTT-[0, 2, 3, 4, 6]-TTTC	6104	1764	3652	1181	3.47E-10	4.66E-02
PHO2	ATAT-[2, 5, 7, 9]-TAGT	6143	504	2077	238	2.77E-08	1.00E+00
PHO2	TTTA-[0, 1, 7, 8, 9]-TAAA	6143	1123	2152	489	4.38E-08	1.00E+00
PHO4	TGACGATAG	5995	9	244	7	5.14E-08	1.00E+00
PHO4	CACC-[0, 2, 3, 5, 9]-GCTT	5995	126	82	14	1.31E-07	1.00E+00
PIP2	TTGACCGAAA	5537	12	608	11	3.35E-09	4.50E-01
PIP2	ACATGAGTGC	5537	10	656	10	5.13E-09	6.89E-01
PPR1	GCAA-[0, 4, 6]-TTGC	6042	162	9	7	4.88E-08	1.00E+00
PPR1	TCTA-[0, 4, 8, 10]-TAAC	6042	208	5008	201	8.14E-08	1.00E+00
PUT3	CGGG-[0, 2, 3, 8]-CCCG	6032	31	1322	24	2.05E-09	2.75E-01
PUT3	CCGG-[1, 3, 6, 10]-TCGA	6032	57	613	25	2.29E-09	3.07E-01
RAP1	CCCA-[1]-ACAT	5984	81	705	54	9.46E-30	1.27E-21
RAP1	ACCC-[2, 7]-ACAT	5984	110	410	49	7.23E-27	9.70E-19
RCO1	AGTC-[0, 6]-AAAC	5566	74	3886	72	9.47E-08	1.00E+00
RCO1	GAGA-[3]-TAAT	5566	56	2885	50	1.19E-07	1.00E+00
RCS1	ATTT-[1, 2, 4, 6, 7, 8, 10]-AAAA	6045	2002	4341	1604	9.73E-22	1.31E-13
RCS1	ATTT-[0, 1, 2, 4, 7, 8, 9, 10]-AAAT	6045	1850	3279	1179	5.95E-20	7.99E-12
RDR1	ATTT-[0, 2, 3, 4, 7, 8, 9, 10]-AAAT	6076	1873	3804	1332	2.73E-17	3.66E-09
RDR1	TTAT-[0, 1, 2, 3, 5, 6, 10]-AAAT	6076	1312	3673	932	2.20E-16	2.95E-08
RDS1	TAAA-[0, 1, 2, 4, 5, 7, 8, 10]-TATT	6080	1631	3129	1035	5.36E-27	7.19E-19
RDS1	AATA-[0, 1, 2, 3, 4, 5, 7, 8, 10]-TTTA	6080	1807	2830	1042	1.55E-26	2.08E-18
REB1	TTACCCG	6174	312	747	171	1.72E-77	2.31E-69
REB1	CGGGTAA	6174	298	611	149	1.58E-72	2.12E-64
RFX1	TATA-[1, 2, 3, 5, 9]-TTTA	5915	1096	2477	567	2.22E-10	2.98E-02
RFX1	TTTT-[1, 2, 3, 5, 8, 10]-AAAA	5915	1993	4560	1645	6.52E-10	8.75E-02
RGM1	CCTCGACTAA	6050	22	315	22	6.27E-28	8.42E-20
RGM1	CTCGACTAA	6050	22	315	22	6.27E-28	8.42E-20
RGT1	GGGG-[4, 5, 6, 7, 9, 10]-CCCC	6113	54	3084	51	1.01E-10	1.36E-02
RGT1	ACAT-[0, 2, 8]-CATC	6113	208	5366	208	2.12E-10	2.85E-02

RIM101	CTAT-[2, 3, 5, 8, 9]-AGTC	6146	139	3371	112	1.64E-08	1.00E+00
RIM101	GTAA-[1, 4, 8, 10]-ACTT	6146	290	2562	173	6.20E-08	1.00E+00
RLM1	TAAT-[0, 3]-ATCA	6122	326	2549	201	1.97E-11	2.64E-03
RLM1	TACG-[2, 3]-GTTA	6122	134	2524	94	9.98E-10	1.34E-01
RLR1	TTTA-[0, 1, 2, 3, 4, 5, 6, 7, 9]-AAAT	6097	1863	3378	1202	1.51E-18	2.03E-10
RLR1	ATAT-[0, 1, 3, 4, 5, 7, 8, 9, 10]-AATT	6097	1651	1958	673	3.24E-15	4.35E-07
RME1	GGGC-[0, 3, 5, 8, 9]-GCCC	6176	55	1365	33	6.81E-08	1.00E+00
RME1	TCTC-[0, 5, 7, 9]-GATA	6176	170	736	50	6.90E-08	1.00E+00
ROX1	TTTC-[0, 9]-TTTT	6110	1572	1730	552	7.08E-09	9.50E-01
ROX1	ACCC-[1, 5, 7, 8, 10]-GGCG	6110	63	1289	36	2.32E-08	1.00E+00
RPH1	GGGG-[1]-TCGA	6137	35	856	23	8.89E-11	1.19E-02
RPH1	ACCG-[1, 5, 8, 9, 10]-CCCC	6137	46	1012	28	5.47E-10	7.34E-02
RPI1	ATTT-[0, 1, 2, 4, 6, 7, 8, 10]-AAAT	6071	1826	1870	705	1.45E-14	1.95E-06
RPI1	AATT-[2, 4, 5, 7, 8, 10]-AATT	6071	1211	2183	554	3.43E-12	4.60E-04
RPN4	AATATT	5984	2282	2723	1218	1.23E-18	1.65E-10
RPN4	TAAT-[0, 5, 8]-ATTA	5984	638	2900	416	1.05E-16	1.41E-08
RTG1	CTCT-[0, 1, 4]-AAAG	6029	170	4418	157	3.08E-08	1.00E+00
RTG1	AAAA-[0, 2, 4, 8]-TGTT	6029	670	861	154	5.58E-08	1.00E+00
RTG3	TGAT-[1, 3, 4, 5, 8]-ATCA	6043	381	1132	132	6.81E-12	9.14E-04
RTG3	AAAT-[0, 3, 4, 7, 8, 9, 10]-AATT	6043	1669	435	187	1.02E-09	1.37E-01
RTS2	TTGA-[1, 2, 6, 8]-TCAA	5934	448	309	57	3.82E-08	1.00E+00
RTS2	ATTG-[0, 9]-GATA	5934	141	2763	102	4.29E-08	1.00E+00
SFL1	TTGA-[1, 5, 10]-TATA	5425	388	501	78	2.50E-09	3.36E-01
SFL1	TTTA-[0, 4, 5]-GATA	5425	301	719	82	6.57E-09	8.82E-01
SFP1	ATGTATGGGT	6145	17	467	11	6.03E-08	1.00E+00
SFP1	ACCCATACAT	6145	20	381	11	9.15E-08	1.00E+00
SIG1	ATCG-[0, 8]-CGAT	5977	65	1043	34	8.79E-09	1.00E+00
SIG1	ATCGCGAT	5977	37	647	19	3.49E-08	1.00E+00
SIP3	AAAT-[1, 2, 3, 4, 5, 6, 7, 9]-TCAA	6053	1527	4320	1214	9.25E-14	1.24E-05
SIP3	TTGA-[1, 5, 7, 8]-TCAA	6053	497	4504	437	4.23E-12	5.68E-04
SIP4	ACAG-[2, 4, 7]-TCGG	6051	51	3701	51	5.76E-10	7.73E-02
SIP4	TTTG-[4, 6, 9]-TGGA	6051	233	2715	149	4.25E-07	1.00E+00
SKN7	GGCC-[0, 1, 2, 3, 6, 8, 9, 10]-GGCC	6156	97	3065	85	2.39E-13	3.21E-05
SKN7	GGGC-[0, 1, 3, 7, 8, 9]-CCCC	6156	36	310	16	1.23E-10	1.65E-02

SKO1	ATCCACGAA	5749	20	875	19	8.49E-14	1.14E-05
SKO1	ATGACGT	5749	113	621	44	3.01E-13	4.04E-05
SMK1	TCAA-[0, 1, 4, 5, 8, 9, 10]-AATG	5983	679	2732	386	2.44E-07	1.00E+00
SMK1	CAGGCTCTA	5983	9	870	9	2.52E-07	1.00E+00
SMP1	GACTAAGCA	6136	20	507	16	2.68E-13	3.60E-05
SMP1	CGACTAAGCA	6136	18	507	15	5.47E-13	7.34E-05
SNF1	CTGA-[0, 5, 7, 8]-TTGA	6166	220	4278	198	2.40E-11	3.22E-03
SNF1	GATTC A	6166	727	4292	589	7.06E-11	9.48E-03
SNT2	TGATAGCGCC	6168	9	36	8	4.72E-17	6.34E-09
SNT2	TCCT-[3, 4, 6, 7, 9]-AGGA	6168	282	1390	129	2.49E-16	3.34E-08
SOK2	TATG-[1, 5]-GTTG	5842	95	118	15	4.19E-08	1.00E+00
SOK2	ATCA-[1, 4, 9]-TGCA	5842	157	172	22	1.08E-07	1.00E+00
SPT10	ATTT-[2, 3, 4, 5, 6, 7, 8, 9, 10]-AAAT	6078	2144	1825	785	2.99E-13	4.01E-05
SPT10	TCAAAT	6078	1442	4566	1190	1.96E-11	2.63E-03
SPT2	TATA-[4, 5, 7]-TATA	6179	1177	1945	498	2.01E-15	2.70E-07
SPT2	ATAT-[3, 5, 6, 8, 9, 10]-ATAA	6179	1494	2983	866	6.79E-15	9.11E-07
SPT23	AAAT-[0, 3, 5, 6, 7, 8, 9]-ATTT	6176	2024	1529	640	9.12E-15	1.22E-06
SPT23	AATT-[2, 3, 5, 6, 7, 10]-AATT	6176	1192	2118	534	4.04E-14	5.42E-06
SRD1	TATT-[1, 5, 10]-AATA	6107	754	1238	236	8.23E-12	1.10E-03
SRD1	TATA-[1, 3, 5, 7, 8]-AATA	6107	1298	1429	404	3.80E-10	5.10E-02
STB1	AGGCCTC	6114	66	3665	62	1.89E-08	1.00E+00
STB1	CTTG-[2, 3, 5, 6, 8, 9]-ATCG	6114	171	408	36	5.37E-08	1.00E+00
STB2	CTCTAGTACT	6052	7	99	5	1.52E-07	1.00E+00
STB2	GGTT-[1, 4, 5, 8, 9]-TCGA	6052	136	3214	106	1.61E-07	1.00E+00
STB4	TCGG-[1, 6, 7, 9]-CCGA	6080	53	23	10	5.76E-14	7.73E-06
STB4	TATT-[0, 2, 4, 5, 8, 9]-AGAC	6080	344	2251	190	4.21E-10	5.65E-02
STB5	CCTA-[0, 6, 9]-TAGC	5969	119	3772	106	1.40E-08	1.00E+00
STB5	AGTA-[0, 3, 8, 9, 10]-ACTA	5969	317	3313	230	3.26E-08	1.00E+00
STB6	AAAT-[2, 3, 4, 5, 8, 9, 10]-TCAA	5976	1286	4116	1006	4.71E-14	6.32E-06
STB6	TTGA-[1, 7, 8]-TCAA	5976	361	3723	286	2.85E-10	3.83E-02
STE12	AACTTCTAGT	6180	90	1784	75	3.54E-25	4.75E-17
STE12	GAACCTTCTAG	6180	87	1784	73	7.09E-25	9.52E-17
STP1	TATT-[2, 3, 4, 5, 6, 9]-TGTA	6123	933	1709	363	1.48E-12	1.99E-04
STP1	ATTA-[1, 3, 4, 5, 7, 8, 9]-TTTA	6123	1278	3967	944	6.39E-12	8.58E-04

STP2	TATA-[1, 3, 8, 10]-AATT	5920	796	1823	344	9.10E-13	1.22E-04
STP2	ATAA-[0, 1, 7, 8, 9, 10]-AATT	5920	1253	1470	416	3.57E-11	4.79E-03
STP4	CGAA-[6]-CCTG	6171	26	971	19	2.66E-09	3.57E-01
STP4	AACGAACAGA	6171	20	207	10	4.01E-09	5.38E-01
SUM1	AATA-[0, 1, 2, 3, 4, 6, 7, 8, 10]-TATT	6081	1928	2114	869	5.44E-27	7.30E-19
SUM1	AATA-[0, 1, 2, 3, 5]-TTAT	6081	1096	1719	455	1.08E-22	1.45E-14
SUT1	CGGCGT	6107	220	1340	98	5.02E-12	6.74E-04
SUT1	CGGAGT	6107	261	1802	134	9.01E-12	1.21E-03
SUT2	GGGGGGCAAG	6071	2	2	2	1.09E-07	1.00E+00
SUT2	CGTACTGTGA	6071	2	2	2	1.09E-07	1.00E+00
SWI4	CGCGAAA	6109	180	134	34	4.28E-21	5.74E-13
SWI4	CGCG-[0, 9, 10]-AAAA	6109	193	82	27	7.38E-19	9.91E-11
SWI5	CACA-[1, 7]-ACAC	6148	133	330	36	1.47E-14	1.97E-06
SWI5	ACAC-[2]-ACAC	6148	93	341	29	4.42E-13	5.93E-05
SWI6	ACGCGT	6158	326	1021	135	1.43E-25	1.92E-17
SWI6	CGCG-[1, 3, 5, 8, 9, 10]-CGCG	6158	89	770	54	2.76E-25	3.70E-17
TBS1	AATA-[5, 6]-TTAG	6178	237	612	58	5.84E-09	7.84E-01
TBS1	CCAACGTTG	6178	10	935	10	6.05E-08	1.00E+00
TEC1	TGTTGGAATA	6170	86	856	51	4.92E-21	6.60E-13
TEC1	TGATAATGTA	6170	92	856	53	4.97E-21	6.67E-13
THI2	TTGA-[0, 1, 3, 4, 5, 8, 9]-ATTG	6072	747	4057	576	2.76E-08	1.00E+00
THI2	TCAT-[0, 1, 2, 3, 7, 8, 9, 10]-AATT	6072	1030	4117	786	3.74E-08	1.00E+00
TOS8	CCTCGACTAA	6003	22	650	20	1.55E-16	2.08E-08
TOS8	CTCGACTAA	6003	22	650	20	1.55E-16	2.08E-08
TYE7	TCACGTG	6178	179	263	60	4.01E-37	5.38E-29
TYE7	CACGTGA	6178	183	270	60	9.16E-36	1.23E-27
UGA3	TATT-[0, 1, 2, 3, 5, 6, 9, 10]-AATA	4799	1231	2672	802	4.43E-12	5.95E-04
UGA3	TAAT-[0, 1, 5, 6, 9]-GTAA	4799	470	909	148	1.82E-09	2.44E-01
UME6	AGCCGCC	5930	126	556	79	7.57E-49	1.02E-40
UME6	TAGC-[0]-CGCC	5930	76	556	61	5.16E-48	6.93E-40
UPC2	TTTA-[1, 3, 5, 6, 7, 8, 9]-AAAT	5994	1569	3215	1018	1.30E-22	1.74E-14
UPC2	AATA-[0, 1, 2, 4, 7, 8, 9, 10]-TTTA	5994	1654	3727	1197	2.46E-21	3.30E-13
USV1	TGCCATAAA	5555	28	1117	20	1.67E-07	1.00E+00
USV1	ACGA-[1]-TCGT	5555	33	1975	28	2.31E-07	1.00E+00

WAR1	ATTT-[1, 3, 4, 5, 7, 9]-AAAA	5991	1776	3925	1307	5.88E-15	7.89E-07
WAR1	ATGA-[0, 2, 3, 4, 5, 7, 8, 9]-TTAT	5991	831	4580	719	4.98E-12	6.68E-04
WTM1	AAAT-[3, 6, 7, 9]-AATT	6111	1095	751	229	1.36E-16	1.83E-08
WTM1	AAAT-[2, 3, 4, 5, 7, 8, 9]-TCAA	6111	1334	3643	936	1.92E-16	2.58E-08
WTM2	TGAG-[2, 6, 8]-CAGT	6089	90	2367	66	2.24E-09	3.01E-01
WTM2	TTAA-[4, 5, 8, 10]-TTAA	6089	622	1719	247	2.91E-08	1.00E+00
XBP1	CACG-[0, 2, 3, 5, 6, 7, 8, 10]-CGGC	6037	83	2866	75	7.44E-15	9.99E-07
XBP1	CCTCGACTAA	6037	22	907	20	1.08E-13	1.45E-05
YAP1	TTAA-[0, 1, 2, 3, 4, 6, 7, 9]-AATA	6178	1511	2876	846	2.69E-14	3.61E-06
YAP1	ATTA-[1, 2, 3, 6, 8, 10]-TAAT	6178	960	1045	252	8.08E-13	1.08E-04
YAP3	GACT-[8, 9, 10]-TAGT	5938	85	2370	62	4.44E-08	1.00E+00
YAP3	TATG-[6]-GTAT	5938	57	3778	55	1.79E-07	1.00E+00
YAP5	GCGG-[7]-ACGA	5844	32	53	21	5.20E-36	6.98E-28
YAP5	TCCA-[9, 10]-ATCC	5844	77	45	24	3.42E-33	4.59E-25
YAP6	TTTC-[0, 6, 9, 10]-TTTT	6130	2182	1243	562	6.37E-12	8.55E-04
YAP6	CCTA-[10]-CTTC	6130	43	11	7	6.96E-12	9.34E-04
YAP7	ATTG-[0, 2, 3, 4, 5, 6, 7, 8]-AATG	5971	696	4085	558	8.81E-11	1.18E-02
YAP7	AATA-[0, 1, 5, 6, 8, 10]-TTAA	5971	1124	827	234	5.12E-10	6.87E-02
YBL054W	AAAT-[0, 3, 5, 6, 7, 8, 9]-TGTA	6164	966	3855	704	1.12E-10	1.50E-02
YBL054W	TGAT-[0, 1, 2, 3, 6, 7, 8]-TTTG	6164	754	2100	340	1.03E-08	1.00E+00
YBR239c	TTTA-[0, 1, 3, 4, 5, 6, 7, 8, 9]-AAAT	6143	1884	3640	1283	3.62E-18	4.86E-10
YBR239c	TTTA-[0, 1, 2, 4, 5, 7, 8, 9, 10]-AATT	6143	1671	3760	1177	4.65E-17	6.24E-09
YBR267W	AAGA-[2, 3, 4, 6]-TGAT	5757	412	1801	200	9.85E-12	1.32E-03
YBR267W	ATGAAG	5757	943	4223	780	1.09E-10	1.46E-02
YDR026c	CCGGGTAAA	6064	35	88	18	1.70E-23	2.28E-15
YDR026c	CCGG-[0, 8, 10]-GTAA	6064	136	236	37	5.79E-20	7.77E-12
YDR049W	ATTT-[1, 4, 7, 8, 9, 10]-AAAT	6042	1566	2177	705	1.48E-14	1.99E-06
YDR049W	TTTA-[0, 1, 2, 3, 4, 6, 7, 8, 9, 10]-AATT	6042	1836	2255	825	1.07E-12	1.44E-04
YDR266c	TTGA-[1, 2, 5, 6, 7, 8, 9]-TCAA	6092	808	3422	556	1.74E-12	2.34E-04
YDR266c	ATTT-[1, 2, 4, 7, 8, 9, 10]-AAAT	6092	1768	1577	568	2.46E-09	3.30E-01
YDR520C	CTCCGGCGG	6073	4	26	4	1.06E-09	1.42E-01
YDR520C	TCTCCGGCGG	6073	3	14	3	2.93E-08	1.00E+00
YER051w	ATTT-[1, 4, 7, 8, 9, 10]-AAAT	6135	1596	1390	494	2.45E-16	3.29E-08
YER051w	TTAA-[0, 1, 3, 4, 5, 8, 10]-TCAT	6135	752	2018	345	1.26E-12	1.69E-04

YER130C	ATTT-[1, 4, 7, 8, 9, 10]-AAAT	6059	1576	1881	629	2.73E-15	3.66E-07
YER130C	AATT-[2, 3, 4, 7, 8, 9, 10]-TAAA	6059	1499	2632	786	6.52E-13	8.75E-05
YER184C	TTCA-[1, 2, 6]-TGAA	5740	345	43	19	2.84E-10	3.81E-02
YER184C	ATTC-[2, 4, 9, 10]-CGAG	5740	136	240	24	1.65E-07	1.00E+00
YFL044C	ATTT-[3, 4, 6, 7, 9, 10]-TTAT	6156	1669	3511	1092	3.24E-13	4.35E-05
YFL044C	TTCAAT	6156	1698	3128	1002	1.86E-12	2.50E-04
YFL052w	TTGA-[1, 3, 4, 5, 6, 7, 8, 9, 10]-TCAA	5966	980	3413	683	1.20E-15	1.61E-07
YFL052w	AAAT-[1, 2, 3, 4, 5, 7, 8]-TCAA	5966	1327	3081	819	5.21E-14	6.99E-06
YGR067C	ATTT-[0, 1, 2, 3, 5, 6, 7, 8, 10]-TAAT	5913	1569	3969	1180	6.52E-13	8.75E-05
YGR067C	ATTT-[0, 1, 2, 4, 6, 8, 9, 10]-AAAT	5913	1770	4994	1594	1.10E-12	1.48E-04
YHP1	TGAA-[1, 2, 3, 4, 5, 6, 7, 9, 10]-AATT	5963	1505	3621	1038	1.87E-11	2.51E-03
YHP1	AAAT-[0, 2, 3, 5, 6, 7, 8, 10]-TCAA	5963	1421	3540	956	2.00E-09	2.68E-01
YJL206C	TGCAACGCTA	6055	3	5	3	8.11E-10	1.09E-01
YJL206C	GTATTGCAAC	6055	3	5	3	8.11E-10	1.09E-01
YKL222C	CTAA-[0, 1, 4, 7, 8, 9, 10]-ATTT	6071	838	4486	711	2.14E-13	2.87E-05
YKL222C	TAAA-[5, 6, 7, 9]-ATTT	6071	1011	4168	796	4.74E-12	6.36E-04
YKR064W	ATTT-[1, 2, 4, 5, 6, 7, 8, 9, 10]-AAAT	6145	2160	3821	1509	4.39E-17	5.89E-09
YKR064W	AATT-[1, 2, 3, 5, 6, 7, 8, 9, 10]-TGAA	6145	1418	3336	905	1.24E-13	1.66E-05
YLR278C	ATTT-[0, 2, 3, 5, 6, 7]-TCAA	5985	1147	4330	938	1.81E-13	2.43E-05
YLR278C	TTTA-[1, 2, 3, 4, 5, 7, 8, 10]-AATT	5985	1554	4173	1209	2.24E-13	3.01E-05
YML081W	ATCGTCTAT	6174	49	1405	38	2.43E-14	3.26E-06
YML081W	ATTATCATAT	6174	90	1282	54	3.18E-14	4.27E-06
YNR063W	AAAT-[2, 3, 4, 6, 7, 8, 9, 10]-ATTT	6022	2059	3761	1431	3.12E-13	4.19E-05
YNR063W	AATT-[2, 3, 4, 7, 8, 9, 10]-AATT	6022	1350	2804	757	1.63E-12	2.19E-04
YOX1	AAAT-[0, 1, 2, 3, 4, 6, 9, 10]-TTTT	6179	2299	4977	2016	6.09E-26	8.17E-18
YOX1	AAAT-[0, 1, 2, 3, 4, 5, 6, 7, 9]-ATTT	6179	2318	3270	1427	5.79E-23	7.77E-15
YPR022C	ATTT-[0, 6, 7, 9, 10]-AAAT	5977	1236	2661	673	2.94E-12	3.95E-04
YPR022C	TATT-[0, 2, 3, 5, 6, 8, 10]-AATA	5977	1423	2925	819	7.90E-11	1.06E-02
YPR196W	GGTC-[7, 8]-AGCG	6132	38	197	14	1.47E-10	1.97E-02
YPR196W	AAGTATCCAA	6132	17	197	10	2.54E-10	3.41E-02
YRR1	CAAC-[3, 7, 10]-TGAG	6030	100	2544	74	7.86E-09	1.00E+00
YRR1	TCCA-[2, 8, 10]-TCCA	6030	173	1906	95	1.87E-08	1.00E+00
ZAP1	CAGA-[2, 6]-CCTG	6084	48	106	14	1.40E-12	1.88E-04
ZAP1	AATATT	6084	2332	1390	654	6.18E-11	8.29E-03

ZMS1	GCGG-[2, 3, 6, 8]-GCAG	5996	59	2976	53	3.03E-09	4.07E-01
ZMS1	CTTCGACCC	5996	4	9	3	3.74E-08	1.00E+00



**Table S2**

Comparison between the predictions of DRIMUST and those of other applications on the Harbison dataset

<b>TFs for which Harbison and DRIMUST predict similar motifs</b>	<b>TFs for which DRIMUST and Harbison predict different motifs</b>	<b>TFs for which DRIMUST identifies motifs that Harbison does not</b>
<b>22</b>	<b>80</b>	<b>101</b>
ABF1	ACE2	A1 (MATA1)
CBF1	ADR1	ABT1
CIN5	AFT2	ACA1
FKH2	ARR1	ARG80
GAL4	ASH1	ARG81
GCN4	AZF1	ARO80
INO4	BAS1	ASK10
MBP1	CAD1	BYE1
MET4	DAL80	CHA4
PUT3	DAL81	CRZ1
RAP1	DAL82	CST6
REB1	DIG1	CUP9
RLM1	FHL1	DAT1
SFP1	FKH1	DOT6
SKN7	GAL80	ECM22
STB4	GAT1	EDS1
SUT1	GCR1	FAP7
SWI4	GLN3	FZF1
TYE7	GZF3	GAL3
UME6	HAC1	GAT3
YAP1	HAP1	GCR2
YOX1	HAP2	GTS1
	HAP3	HAA1
	HAP4	HAL9
	HAP5	HIR1
	HSF1	HIR2
	IME1	HIR3
	INO2	HMS1

LEU3	HMS2
MAC1	HOG1
MCM1	IFH1
MET31	IME4
MET32	IXR1
MOT3	KRE33
MSN2	KSS1
MSN4	MAL13
NDD1	MAL33
NRG1	MBF1
OPI1	MDS3
PDR1	MET18
PDR3	MET28
PHD1	MGA1
PHO2	MIG1
PHO4	MIG2
RCS1	MIG3
RDS1	MSN1
RFX1	MSS11
RGT1	MTH1
RIM101	NDT80
RLR1	NNF2
ROX1	OAF1
RPH1	PDC2
RPN4	PIP2
RTG3	PPR1
SIG1	RCO1
SIP4	RDR1
SKO1	RGM1
SMP1	RME1
SNT2	RPI1
SOK2	RTG1
SPT2	RTS2
SPT23	SFL1
STB1	SIP3

STB5  
STE12  
STP1  
SUM1  
SWI5  
SWI6  
TEC1  
THI2  
UGA3  
XBP1  
YAP3  
YAP5  
YAP6  
YAP7  
YDR026c  
YHP1  
ZAP1

SMK1  
SNF1  
SPT10  
SRD1  
STB2  
STB6  
STP2  
STP4  
SUT2  
TBS1  
TOS8  
UPC2  
USV1  
WAR1  
WTM1  
WTM2  
YBL054W  
YBR239c  
YBR267W  
YDR049W  
YDR266c  
YDR520C  
YER051w  
YER130C  
YER184C  
YFL044C  
YFL052w  
YGR067C  
YJL206C  
YKL222C  
YKR064W  
YLR278C  
YML081W  
YNR063W  
YPR022C

YPR196W

YRR1

ZMS1

\* We marked in red the TFs at the second and third columns for which our predictions are similar to those reported in:  
Eden E, Lipson D, Yogev S, Yakhini Z (2007) Discovering Motifs in Ranked Lists of DNA Sequences. PLoS Comput Biol 3: e39.

Details for Table S2:

TF	first half	second half	gap lengths	p-value ≤	Harbison's motif	Annotated motif as define by Harbison et al.	Agreement indication (with any of the previous two columns)	Agreement with Eden et al. (in case DRIMUST and others don't agree) (DRIMUST closest prediction is indicated in parenthesis)
A1 (MATA1)	ATAA	TATT	[0, 2, 3, 6, 7, 9]	5.64E-12			Only DRIMUST	
A1 (MATA1)	AATGAA			2.21E-11			Only DRIMUST	
ABF1	TCGT	TGAT	[6]	3.53E-63	rTCAYtntnnnAcg	rTCAYTnnnnACGw	Agree	
ABF1	ATCA	ACGA	[6]	7.23E-63	rTCAYtntnnnAcg	rTCAYTnnnnACGw	Agree	
ABT1	ATTT	AAAT	[0, 1, 2, 4, 6, 7, 8, 9, 10]	4.49E-21			Only DRIMUST	
ABT1	AATA	TTTA	[0, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10]	1.42E-20			Only DRIMUST	
ACA1	AACA	TTTC	[1, 4, 6]	4.34E-09			Only DRIMUST	
ACA1	TGCT	AGCA	[2, 4, 5, 6, 8, 10]	8.30E-09			Only DRIMUST	
ACE2	CACA	CACA	[4, 6, 7, 9, 10]	4.68E-10	tGCTGGT	GCTGGT	Disagree	
ACE2	ACAC	ACAC	[0, 6, 7, 8, 9]	1.13E-09	tGCTGGT	GCTGGT	Disagree	CACACA (ACACACAC)
ADR1	ACTT	TGAC	[2, 3, 6, 9, 10]	2.41E-08		GGrGk	Disagree	
ADR1	AGAT	CAAC	[0, 1, 3, 4, 5, 10]	4.38E-08		GGrGk	Disagree	
AFT2	TATCCACGA			6.11E-17	rCACCC	AAAGTGACCCATT	Disagree	
AFT2	AGATACTGTG			1.10E-15	rCACCC	AAAGTGACCCATT	Disagree	
ARG80	ATTT	AAAT	[1, 2, 4, 7, 8, 9, 10]	1.35E-23			Only DRIMUST	
ARG80	AAAT	AATT	[0, 1, 3, 5, 6, 7, 8, 9, 10]	3.81E-23			Only DRIMUST	
ARG81	AATT	ATAT	[2, 5, 6, 7, 10]	2.63E-17			Only DRIMUST	
ARG81	TATT	TAAT	[0, 1, 2, 3, 4, 5, 6, 7, 8, 9]	1.49E-16			Only DRIMUST	AWTWGA (TATTTAAT)
ARO80	ATTT	AAATA	[0, 2, 3, 4, 6, 8, 9, 10]	6.21E-12			Only DRIMUST	
ARO80	TAAT	TTTA	[2, 3, 4, 6, 7, 8, 9]	4.87E-11			Only DRIMUST	
ARR1	ATTT	TTAT	[0, 3, 4, 5, 6, 8, 9, 10]	3.40E-22		TTACTAA	Disagree	
ARR1	ATAT	TAAT	[1, 3, 5, 6, 7, 8, 9, 10]	2.31E-20		TTACTAA	Disagree	
ASH1	GGTC	GCGG	[9]	1.45E-15		yTGACT	Disagree	
ASH1	CTCCTCGAC			1.45E-15		yTGACT	Disagree	CCWCGW (CTCCTCGAC)
ASK10	AAAT	TCAA	[1, 2, 3, 4, 5, 6, 8, 9]	5.48E-15			Only DRIMUST	
ASK10	TGAT	TCAA	[0, 3, 4, 5, 6, 7, 8, 9]	7.34E-15			Only DRIMUST	
AZF1	AAATCACTTC			3.12E-09	YwTTkckkTyycgykky	TTTTTCTT	Disagree	
AZF1	ACAGCTGTA			6.36E-08	YwTTkckkTyycgykky	TTTTTCTT	Disagree	
BAS1	TAAT	TTTA	[2, 3, 4, 5, 6, 7, 8, 9]	4.87E-11	TGACTC	TGACTC	Disagree	
BAS1	ATTT	TATT	[1, 5, 7, 9, 10]	1.93E-09	TGACTC	TGACTC	Disagree	
BYE1	AATT	AATT	[2, 3, 5, 6, 7, 10]	6.80E-16			Only DRIMUST	
BYE1	TATT	ATGT	[2, 3, 5, 6, 10]	4.98E-12			Only DRIMUST	
CAD1	ATCC	CCAC	[0, 10]	1.35E-15	mTTAsTmAkC	TTACTAA	Disagree	
CAD1	CCAC	GCGG	[3, 6]	1.04E-14	mTTAsTmAkC	TTACTAA	Disagree	
CBF1	CACGTG			9.79E-77	tCACGTG	rTCACrTGA	Agree	
CBF1	CACGTGA			1.37E-62	tCACGTG	rTCACrTGA	Agree	
CHA4	ATTT	AAAA	[1, 2, 3, 6, 7, 8, 10]	3.35E-16			Only DRIMUST	
CHA4	ATTT	AAAT	[1, 2, 3, 7, 8, 9, 10]	8.35E-14			Only DRIMUST	
CIN5	TTAC	TAAT	[1]	3.77E-20	TTAcrTAA	TTACTAA	Agree	
CIN5	ATTA	GTAA	[1]	1.84E-19	TTAcrTAA	TTACTAA	Agree	
CRZ1	CCTCGACTAA			3.71E-16			Only DRIMUST	
CRZ1	CTCGACTAA			3.71E-16			Only DRIMUST	
CST6	TGAA	TTAA	[1, 3, 4, 6, 7, 8, 9, 10]	1.18E-11			Only DRIMUST	
CST6	TAAA	TTAA	[3, 5, 6, 9, 10]	7.91E-11			Only DRIMUST	
CUP9	GAGG	CGTA	[1, 2, 6, 9]	1.06E-09			Only DRIMUST	
CUP9	CATC	TACT	[0, 9]	5.14E-09			Only DRIMUST	
DAL80	TTCA	AATG	[0, 1, 6, 8]	3.70E-11		GATAA	Disagree	
DAL80	ATTAAA			5.88E-10		GATAA	Disagree	
DAL81	TCCT	AGGA	[2, 5, 7]	3.54E-15		AAAAGCCGCGGGCGGGATT	Disagree	
DAL81	GGAT	CCTA	[1, 2]	1.41E-11		AAAAGCCGCGGGCGGGATT	Disagree	
DAL82	GATA	CTCA	[3, 4, 5, 6, 7, 9]	4.40E-08	GATAAG		Disagree	
DAL82	CAGG	TATA	[1, 3, 7]	1.22E-07	GATAAG		Disagree	
DAT1	CTGAGCAACG			1.12E-15			Only DRIMUST	
DAT1	CGGCTGAGCA			1.12E-15			Only DRIMUST	
DIG1	CTGTATACCT			1.08E-21	TgAAAcA		Disagree	
DIG1	CTGT	CCTA	[3]	1.91E-21	TgAAAcA		Disagree	
DOT6	CGGC	GCCG	[0, 2, 3, 7, 8, 10]	7.09E-11			Only DRIMUST	CGSGSC (CGGCGCCG)
DOT6	ACGA	CGTG	[7, 9]	1.91E-09			Only DRIMUST	

ECM22	CACA	CGCA	[4, 5, 6]	1.93E-12		Only DRIMUST	
ECM22	GCAG	CGGC	[0, 1, 2, 3, 4, 5, 8, 10]	1.21E-10		Only DRIMUST	
EDS1	ATTA	TTCA	[5, 9, 10]	1.74E-09		Only DRIMUST	
EDS1	AAGA	CTAT	[0, 1, 3, 4, 6, 8, 9]	9.45E-09		Only DRIMUST	
FAP7	TAAG	TTTT	[0, 1, 3, 5, 9]	8.13E-08		Only DRIMUST	
FAP7	TAAA	TTTA	[3, 4, 5, 6, 9, 10]	1.20E-07		Only DRIMUST	
FHL1	ATCC	ACAT	[2]	2.16E-39	TGTayGGrtg	Disagree	
FHL1	ATCC	TACA	[1]	2.73E-39	TGTayGGrtg	Disagree	WNMAYCCRTACAYHH (ATCCNTACA)
FKH1	TGTTTAC			9.19E-21	gtAAAcAA	Disagree	
FKH1	TTGT	TTAC	[0]	4.59E-19	gtAAAcAA	Disagree	
FKH2	GTAACAA			4.62E-15	GTAACAA	Agree	
FKH2	TTGTTTAC			1.52E-14	GTAACAA	Agree	
FZF1	AAAT	ATTT	[0, 1, 5, 6, 7, 9, 10]	2.94E-12		Only DRIMUST	
FZF1	TATT	AAAT	[0, 1, 2, 3, 4, 6, 9]	1.30E-09		Only DRIMUST	
GAL3	TAAT	ACTT	[0, 3, 7, 8, 10]	4.92E-11		Only DRIMUST	
GAL3	TGAA	TCAA	[1, 2, 4, 5, 6, 7]	9.56E-11		Only DRIMUST	
GAL4	CGGA	CCGT	[10]	2.33E-09	CGGnnnnnnnnnnnCg	Agree	
GAL4	ATCA	GTTA	[1, 10]	2.75E-09	CGGnnnnnnnnnnnCg	Agree	
GAL80	AAAT	TCAA	[0, 1, 2, 3, 4, 5, 6, 7, 9, 10]	4.63E-12		Disagree	
GAL80	TTGA	ATCA	[0, 2, 5, 6, 8, 9]	1.39E-09		Disagree	
GAT1	CCAC	CCAG	[0, 1, 3, 4, 5, 6, 7, 8, 9, 10]	6.31E-17	aGATAAG	Disagree	CCRCYC (CCACCCAG)
GAT1	CGGCGC			3.07E-14	aGATAAG	Disagree	
GAT3	GCGG	ACGA	[7, 10]	2.49E-34		Only DRIMUST	
GAT3	CACG	GAGC	[5, 8]	3.78E-31		Only DRIMUST	
GCN4	TGACTCA			1.15E-30	TGAsTCa	Agree	
GCN4	ATGACTCA			2.52E-20	TGAsTCa	Agree	
GCR1	CCATTTTGAG			4.86E-16		Disagree	
GCR1	ATTCCATTTT			1.52E-15		Disagree	
GCR2	AAAT	TCAT	[0, 1, 4, 6, 9, 10]	1.27E-12		Only DRIMUST	
GCR2	TAAA	TTTA	[1, 2, 4, 8, 9, 10]	3.18E-11		Only DRIMUST	
GLN3	AAAT	ATTT	[1, 2, 3, 4, 5, 6, 9]	4.97E-17	GATAAGa	Disagree	
GLN3	TAAA	TATT	[0, 1, 2, 3, 4, 5, 7, 8, 10]	6.84E-16	GATAAGa	Disagree	DHDATAWAGGDH (TAAATATT)
GTS1	ATAA	AAGT	[0, 2, 5, 7, 10]	5.78E-08		Only DRIMUST	
GTS1	CATA	GCCA	[2, 3]	1.59E-07		Only DRIMUST	
GZF3	ATGA	AACA	[1, 2, 3, 4, 6, 8]	1.34E-08		Disagree	
GZF3	CTGA	TGAT	[0, 1, 3, 4, 7, 9, 10]	1.78E-08		Disagree	
HAA1	CAAA	TTGA	[0, 3, 5, 6, 7, 8, 9]	3.02E-10		Only DRIMUST	
HAA1	ATGAAG			3.30E-10		Only DRIMUST	
HAC1	AAAT	TAAA	[0, 3, 4, 5, 7, 8, 9, 10]	5.51E-12		Disagree	
HAC1	AAAA	AAAT	[1, 2, 4, 5, 7, 8, 9, 10]	1.34E-11		Disagree	
HAL9	TGTT	GAAT	[1]	1.64E-16		Only DRIMUST	
HAL9	AATT	AATT	[2, 3, 6, 7, 9, 10]	4.49E-16		Only DRIMUST	
HAP1	TTTATCGG			4.96E-19	GGnnaTAnCGs	Disagree	
HAP1	TTTA	TCGG	[0]	4.96E-19	GGnnaTAnCGs	Disagree	
HAP2	AATATT			4.82E-08		Disagree	
HAP2	GTTA	AGAT	[2, 4, 8]	1.88E-07		Disagree	
HAP3	AAAT	TTTA	[0, 2, 4, 6, 7, 9, 10]	2.01E-16		Disagree	AAWCTW (AAATTTTA)
HAP3	ATTT	AATA	[0, 2, 4, 5, 8, 9]	3.57E-14		Disagree	
HAP4	CACG	GAGC	[6, 8]	1.89E-16	gnCcAAtcA	Disagree	
HAP4	GACTAAGCA			5.80E-16	gnCcAAtcA	Disagree	
HAP5	TATT	AATA	[1, 2, 4, 5, 7, 8, 9, 10]	2.27E-13		Disagree	
HAP5	ATAT	TTTA	[0, 1, 2, 3, 6, 8, 10]	2.27E-11		Disagree	
HIR1	ATTT	ATTT	[1, 2, 5, 6, 8, 9]	4.57E-15		Only DRIMUST	ATWTR (ATTTNATTT)
HIR1	AATTTT			8.51E-11		Only DRIMUST	
HIR2	ATAT	ATAT	[0, 1, 3, 4, 5, 10]	1.79E-25		Only DRIMUST	
HIR2	TATA	TATA	[0, 1, 2, 5, 9]	3.24E-24		Only DRIMUST	
HIR3	TTTT	AAAA	[0, 1, 2, 3, 4, 5, 6, 7, 8, 10]	3.11E-25		Only DRIMUST	
HIR3	AAAT	ATTT	[0, 4, 5, 6, 7, 8, 9, 10]	4.12E-25		Only DRIMUST	ATTTWR (TTTTAAAA)
HMS1	ATTT	TTTT	[0, 5, 7, 10]	2.91E-13		Only DRIMUST	
HMS1	AAAT	ATTT	[0, 2, 5, 7, 9]	8.24E-13		Only DRIMUST	
HMS2	TGTA	TTTT	[2, 6]	4.47E-08		Only DRIMUST	
HMS2	TTAA	TTAC	[0, 1, 8]	6.29E-07		Only DRIMUST	AAWYTC (TTAATTAC)

HOG1	TTTA	AAAT	[0, 1, 3, 4, 5, 6, 7, 8, 9]	5.95E-24		Only DRIMUST	NDDNDWAWTAADNND (TTTAAAT)
HOG1	ATTT	AATT	[0, 2, 4, 5, 6, 7, 9, 10]	8.54E-23		Only DRIMUST	
HSF1	AATG	CATT	[0, 1, 2, 5]	1.58E-07	TTCynnnnnnTTC	Disagree	
HSF1	TAAA	ATCA	[0, 5]	2.40E-07	TTCynnnnnnTTC	Disagree	
IFH1	TCAC	AATT	[6, 8, 9]	8.81E-10		Only DRIMUST	
IFH1	ATTT	GAAC	[0, 1, 2, 3, 8]	4.27E-08		Only DRIMUST	
IME1	ATCC	TCGT	[3, 6, 10]	5.38E-09	AAkGAAAnkWA	Disagree	
IME1	CAGC	ACCG	[0, 8, 9, 10]	6.99E-08	AAkGAAAnkWA	Disagree	
IME4	CACA	CACA	[1, 2]	1.92E-11		Only DRIMUST	
IME4	ACACACACAC			6.14E-11		Only DRIMUST	ACACACACACA (ACACACAC)
INO2	CATGTG			5.50E-16	CaCaTGc	Disagree	NHNGCAHRTGADNW (CATGTG)
INO2	GCATGTG			1.65E-13	CaCaTGc	Disagree	
INO4	CACGTG			4.64E-23	CATGTGaa	Agree	
INO4	CATGTGAA			4.48E-18	CATGTGaa	Agree	
IXR1	AAAT	CTCA	[2, 3, 4, 5, 7, 8, 9]	1.69E-09		Only DRIMUST	DNCAGVWNDNNWNHNHNHVVCCANNW (AAATNNNNNNNNCTCA)
IXR1	CATC	AATC	[3, 5]	8.91E-09		Only DRIMUST	
KRE33	AATG	CAAC	[9]	4.16E-07		Only DRIMUST	
KRE33	AGAA	CTGA	[0, 1, 5, 8]	1.20E-06		Only DRIMUST	
KSS1	TATT	GCTG	[0, 1, 2, 4, 5, 6, 7]	1.07E-10		Only DRIMUST	
KSS1	ATAT	CAGC	[0, 1, 2]	4.57E-08		Only DRIMUST	
LEU3	TAAT	TTAG	[1, 2, 6, 7, 9, 10]	1.34E-11	cCGgtacCGG	Disagree	
LEU3	ACCC	ACAT	[2, 8]	2.64E-10	cCGgtacCGG	Disagree	
MAC1	CCTA	GACT	[1, 9]	1.02E-07		Disagree	
MAC1	CCTATGACT			1.65E-07		Disagree	
MAL13	CCTCGACTAA			2.12E-14		Only DRIMUST	
MAL13	CTCGACTAA			2.12E-14		Only DRIMUST	
MAL33	GCTT	CCAC	[3, 4, 10]	8.71E-11		Only DRIMUST	
MAL33	CACA	CACA	[0, 1, 2, 3, 4, 5, 6]	3.51E-10		Only DRIMUST	ACACACACACA (CACACACA)
MBF1	TCAT	CTGT	[6]	1.37E-07		Only DRIMUST	
MBF1	GTAA	TAAG	[1, 7, 9]	1.65E-07		Only DRIMUST	
MBP1	ACGCGT			2.97E-44	ACGCGT	Agree	
MBP1	CGCG	CGCG	[1, 3, 6, 8, 9, 10]	2.76E-32	ACGCGT	Agree	
MCM1	AAAT	ATTT	[0, 1, 2, 4, 7, 9, 10]	6.73E-17	CCnrAtnngg	Disagree	
MCM1	AATA	TAAT	[0, 1, 3, 4, 7, 9]	3.39E-13	CCnrAtnngg	Disagree	
MDS3	ATTT	AAAT	[1, 2, 4, 5, 7, 8, 9, 10]	2.11E-20		Only DRIMUST	
MDS3	AAAT	TCAA	[0, 1, 2, 3, 4, 5, 6, 7, 9]	8.70E-19		Only DRIMUST	
MET18	GTATCCAAGA			1.40E-12		Only DRIMUST	
MET18	CGAACAGAAT			2.39E-11		Only DRIMUST	
MET28	ATAA	TTAT	[0, 3, 4, 6, 7]	3.11E-09		Only DRIMUST	
MET28	GGTC	TTTA	[2, 10]	1.96E-08		Only DRIMUST	
MET31	ATCC	GTAC	[0, 5, 7, 10]	1.02E-08		Disagree	
MET31	AGTA	ATTA	[4, 5, 10]	1.17E-08	AAACTGTGG	Disagree	
MET32	CACGTGA			3.33E-09	AAACTGTGG	Disagree	CACGTG (CACGTGA)
MET32	CACGTG			5.43E-08	AAACTGTGG	Disagree	
MET4	CACGTG			6.90E-13	RMmAwsTGKSgyGsc	Agree	
MET4	CCAC	GTGG	[0, 2, 4, 6, 10]	2.32E-11	RMmAwsTGKSgyGsc	Agree	
MGA1	TTAA	AAGT	[0, 2, 4, 5, 6, 7, 9]	2.97E-10		Only DRIMUST	
MGA1	TTAA	TTGA	[1, 2, 5, 7, 9, 10]	6.18E-10		Only DRIMUST	
MIG1	CCTA	AGCT	[1, 2, 8]	8.50E-10		Only DRIMUST	
MIG1	ATAC	CGGA	[3, 9]	1.34E-09		Only DRIMUST	
MIG2	ATTT	AAAT	[0, 1, 4, 5, 6, 7, 8, 9, 10]	3.29E-12		Only DRIMUST	
MIG2	ATAT	TAAT	[4, 5, 7, 8, 10]	2.20E-10		Only DRIMUST	
MIG3	AAAT	AATT	[3, 5, 6, 7, 8, 9, 10]	2.24E-20		Only DRIMUST	
MIG3	AAAT	AAAA	[0, 1, 2, 3, 4, 6, 8, 9, 10]	4.49E-16		Only DRIMUST	
MOT3	ATAT	TATA	[0, 2, 4, 5, 6, 9]	1.80E-17		Disagree	
MOT3	ATATTATCAT			2.15E-14	yAGGyA	Disagree	
MSN1	GCCT	CAAC	[4, 5]	3.04E-11		Only DRIMUST	
MSN1	GCGA	TCGC	[2, 7, 8, 9]	3.59E-10		Only DRIMUST	
MSN2	ATAA	ATAA	[0, 1, 4, 5, 8]	3.79E-08	mAGGGGsgg	Disagree	
MSN2	ATGT	GTGG	[5, 6, 10]	1.80E-07	mAGGGGsgg	Disagree	
MSN4	GCGG	ACGA	[7, 10]	8.63E-17		Disagree	
MSN4	CGTAGGTCCA			6.02E-16	mAGGGG	Disagree	

MSS11	ATTT	TCAA	[0, 3, 9, 10]	8.28E-10		Only DRIMUST
MSS11	ATTA	TTAT	[0, 1, 4, 5, 8, 9]	3.84E-08		Only DRIMUST
MTH1	CCAC	CGGC	[0, 2, 3, 5, 7, 10]	6.85E-11		Only DRIMUST
MTH1	CCCT	GGAG	[1, 7, 8, 10]	1.38E-10		Only DRIMUST
NDD1	GTCT	GCGG	[1, 3, 4]	4.81E-09	CcNrAwnnGG	Disagree
NDD1	GTCT	CGGA	[2, 4, 5, 6, 10]	2.97E-08	CcNrAwnnGG	Disagree
NDT80	TAAT	TATT	[0, 1, 9]	1.81E-07		Only DRIMUST
NDT80	TGCT	TGAG	[2, 3, 6, 9]	2.17E-07		Only DRIMUST
NNF2	ATTT	TAAT	[1, 3, 5, 6, 7, 8, 10]	3.10E-15		Only DRIMUST
NNF2	TTAT	AAAT	[2, 3, 5, 10]	2.39E-13		Only DRIMUST
NRG1	GGGG	TGCT	[1, 2]	4.10E-10	GGaCCCT	Disagree
NRG1	ATGT	TGTG	[0, 4, 5, 6]	8.95E-10	GGaCCCT	Disagree
OAF1	GTTC	GAGC	[0, 4, 6, 8]	1.70E-10		Only DRIMUST
OAF1	ACGA	TCGT	[0, 1, 2, 4, 5, 10]	9.59E-10		Only DRIMUST
OPI1	GCATGTGAA			2.18E-09	TCGAAyC	Disagree
OPI1	CTAG	ATTC	[1, 3]	3.28E-09	TCGAAyC	Disagree
PDC2	TGTTGGAATA			3.52E-38		Only DRIMUST
PDC2	CATATACGGT			2.50E-37		Only DRIMUST
PDR1	AGATACTGTG			1.44E-17	ccGCCgRAwr	Disagree
PDR1	TCTCCTCGAC			1.44E-17	ccGCCgRAwr	Disagree
PDR3	TTGA	TCAA	[4, 5, 6, 10]	5.05E-10	TCCGCGGA	Disagree
PDR3	ATAG	ATCA	[0, 4, 6, 8, 9, 10]	6.76E-09	TCCGCGGA	Disagree
PHD1	ATTT	TTTT	[1, 3, 5, 9, 10]	1.00E-11	scnGCngg	Disagree
PHD1	ATTT	TTTC	[0, 2, 3, 4, 6]	3.47E-10	scnGCngg	Disagree
PHO2	ATAT	TAGT	[2, 5, 7, 9]	2.77E-08	SGTGCgsygyG	Disagree
PHO2	TTTA	TAAA	[0, 1, 7, 8, 9]	4.38E-08	SGTGCgsygyG	Disagree
PHO4	TGACGATAG			5.14E-08	CACGTGs	Disagree
PHO4	CACC	GCTT	[0, 2, 3, 5, 9]	1.31E-07	CACGTGs	Disagree
PIP2	TTGACCGAAA			3.35E-09		Only DRIMUST
PIP2	ACATGAGTGC			5.13E-09		Only DRIMUST
PPR1	GCAA	TTGC	[0, 4, 6]	4.88E-08		Only DRIMUST
PPR1	TCTA	TAAC	[0, 4, 8, 10]	8.14E-08		Only DRIMUST
PUT3	CGGG	CCCG	[0, 2, 3, 8]	2.05E-09	CGGnnnnnnnnnCCG	Agree
PUT3	CCGG	TCGA	[1, 3, 6, 10]	2.29E-09	CGGnnnnnnnnnCCG	Agree
RAP1	CCCA	ACAT	[1]	9.46E-30	cayCCrtrCa	Agree
RAP1	ACCC	ACAT	[2, 7]	7.23E-27	cayCCrtrCa	Agree
RCO1	AGTC	AAAC	[0, 6]	9.47E-08		Only DRIMUST
RCO1	GAGA	TAAT	[3]	1.19E-07		Only DRIMUST
RCS1	ATTT	AAAA	[1, 2, 4, 6, 7, 8, 10]	9.73E-22	ggGTGcant	Disagree
RCS1	ATTT	AAAT	[0, 1, 2, 4, 7, 8, 9, 10]	5.95E-20	ggGTGcant	Disagree
RDR1	ATTT	AAAT	[0, 2, 3, 4, 7, 8, 9, 10]	2.73E-17		Only DRIMUST
RDR1	TTAT	AAAT	[0, 1, 2, 3, 5, 6, 10]	2.20E-16		Only DRIMUST
RDS1	TAAA	TATT	[0, 1, 2, 4, 5, 7, 8, 10]	5.36E-27	kCGGCCGa	Disagree
RDS1	AATA	TTTA	[0, 1, 2, 3, 4, 5, 7, 8, 10]	1.55E-26	kCGGCCGa	Disagree
REB1	TTACCCG			1.72E-77	TTACCCG	Agree
REB1	CGGGTAA			1.58E-72	TTACCCG	Agree
RFX1	TATA	TTTA	[1, 2, 3, 5, 9]	2.22E-10	TtgccATggCAAC	Disagree
RFX1	TTTT	AAAA	[1, 2, 3, 5, 8, 10]	6.52E-10	TtgccATggCAAC	Disagree
RGM1	CCTCGACTAA			6.27E-28		Only DRIMUST
RGM1	CTCGACTAA			6.27E-28		Only DRIMUST
RGT1	GGGG	CCCC	[4, 5, 6, 7, 9, 10]	1.01E-10	CGGAnnA	Disagree
RGT1	ACAT	CATC	[0, 2, 8]	2.12E-10	CGGAnnA	Disagree
RIM101	CTAT	AGTC	[2, 3, 5, 8, 9]	1.64E-08	TGCCAAG	Disagree
RIM101	GTAA	ACTT	[1, 4, 8, 10]	6.20E-08	TGCCAAG	Disagree
RLM1	TAAT	ATCA	[0, 3]	1.97E-11	CTAwwwTAG	Agree
RLM1	TACG	GTTA	[2, 3]	9.98E-10	CTAwwwTAG	Agree
RLR1	TTTA	AAAT	[0, 1, 2, 3, 4, 5, 6, 7, 9]	1.51E-18	ATTTTCnnCwTt	Disagree
RLR1	ATAT	AATT	[0, 1, 3, 4, 5, 7, 8, 9, 10]	3.24E-15	ATTTTCnnCwTt	Disagree
RME1	GGGC	GCCC	[0, 3, 5, 8, 9]	6.81E-08		Only DRIMUST
RME1	TCTC	GATA	[0, 5, 7, 9]	6.90E-08		Only DRIMUST
ROX1	TTTT	TTTT	[0, 9]	7.08E-09	ysyATTGTT	Disagree
ROX1	ACCC	GGCG	[1, 5, 7, 8, 10]	2.32E-08	ysyATTGTT	Disagree



RPH1	GGGG	TCGA	[1]	8.89E-11	CCCCTTAAGG	Disagree	
RPH1	ACCG	CCCC	[1, 5, 8, 9, 10]	5.47E-10	CCCCTTAAGG	Disagree	
RP1	ATTT	AAAT	[0, 1, 2, 4, 6, 7, 8, 10]	1.45E-14		Only DRIMUST	
RP1	AATT	AATT	[2, 4, 5, 7, 8, 10]	3.43E-12		Only DRIMUST	
RPN4	AATATT			1.23E-18	GGTGGCAAA	Disagree	
RPN4	TAAT	ATTA	[0, 5, 8]	1.05E-16	GGTGGCAAA	Disagree	
RTG1	CTCT	AAAG	[0, 1, 4]	3.08E-08		Only DRIMUST	
RTG1	AAAA	TGTT	[0, 2, 4, 8]	5.58E-08		Only DRIMUST	
RTG3	TGAT	ATCA	[1, 3, 4, 5, 8]	6.81E-12	GGTCAC	Disagree	
RTG3	AAAT	AATT	[0, 3, 4, 7, 8, 9, 10]	1.02E-09	GGTCAC	Disagree	
RTS2	TTGA	TCAA	[1, 2, 6, 8]	3.82E-08		Only DRIMUST	
RTS2	ATTG	GATA	[0, 9]	4.29E-08		Only DRIMUST	
SFL1	TTGA	TATA	[1, 5, 10]	2.50E-09		Only DRIMUST	
SFL1	TTTA	GATA	[0, 4, 5]	6.57E-09		Only DRIMUST	
SFP1	ATGTATGGGT			6.03E-08	ayCcrTACay	Agree	
SFP1	ACCATACAT			9.15E-08	ayCcrTACay	Agree	
SIG1	ATCG	CGAT	[0, 8]	8.79E-09	ArGmAwCrAmAA	Disagree	
SIG1	ATCGCGAT			3.49E-08	ArGmAwCrAmAA	Disagree	
SIP3	AAAT	TCAA	[1, 2, 3, 4, 5, 6, 7, 9]	9.25E-14		Only DRIMUST	
SIP3	TTGA	TCAA	[1, 5, 7, 8]	4.23E-12		Only DRIMUST	
SIP4	ACAG	TCGG	[2, 4, 7]	5.76E-10	CGGnynAATGGrr	Disagree	
SIP4	TTTG	TGGA	[4, 6, 9]	4.25E-07	CGGnynAATGGrr	Disagree	
SKN7	GGCC	GGCC	[0, 1, 2, 3, 6, 8, 9, 10]	2.39E-13	GnCnnGsCs	Agree	
SKN7	GGGC	CCCC	[0, 1, 3, 7, 8, 9]	1.23E-10	GnCnnGsCs	Agree	
SKO1	ATCCACGAA			8.49E-14	ACGTCA	Disagree	
SKO1	ATGACGT			3.01E-13	ACGTCA	Disagree	
SMK1	TCAA	AATG	[0, 1, 4, 5, 8, 9, 10]	2.44E-07		Only DRIMUST	
SMK1	CAGGCTCTA			2.52E-07		Only DRIMUST	
SMP1	GACTAAGCA			2.68E-13		Disagree	
SMP1	CGACTAAGCA			5.47E-13	ACTACTAwwwwTAG	Disagree	
SNF1	CTGA	TTGA	[0, 5, 7, 8]	2.40E-11	ACTACTAwwwwTAG	Disagree	
SNF1	GATTCA			7.06E-11		Only DRIMUST	
SNT2	TGATAGCGCC			4.72E-17	yGGCGCTAyca	Disagree	
SNT2	TCCT	AGGA	[3, 4, 6, 7, 9]	2.49E-16	yGGCGCTAyca	Disagree	
SOK2	TATG	GTTG	[1, 5]	4.19E-08	tGCagnna	Disagree	
SOK2	ATCA	TGCA	[1, 4, 9]	1.08E-07	tGCagnna	Disagree	
SPT10	ATTT	AAAT	[2, 3, 4, 5, 6, 7, 8, 9, 10]	2.99E-13		Only DRIMUST	
SPT10	TCAAAAT			1.96E-11		Only DRIMUST	
SPT2	TATA	TATA	[4, 5, 7]	2.01E-15	yMtGTmTytAw	Disagree	
SPT2	ATAT	ATAA	[3, 5, 6, 8, 9, 10]	6.79E-15	yMtGTmTytAw	Disagree	
SPT23	AAAT	ATTT	[0, 3, 5, 6, 7, 8, 9]	9.12E-15	rAAATsaA	Disagree	ATSTTY (AAATATTT)
SPT23	AATT	AATT	[2, 3, 5, 6, 7, 10]	4.04E-14	rAAATsaA	Disagree	
SRD1	TATT	AATA	[1, 5, 10]	8.23E-12		Only DRIMUST	
SRD1	TATA	AATA	[1, 3, 5, 7, 8]	3.80E-10		Only DRIMUST	
STB1	AGGCCTC			1.89E-08	rracGCsAa	Disagree	
STB1	CTTG	ATCG	[2, 3, 5, 6, 8, 9]	5.37E-08	rracGCsAa	Disagree	
STB2	CTCTAGTACT			1.52E-07		Only DRIMUST	
STB2	GGTT	TCGA	[1, 4, 5, 8, 9]	1.61E-07		Only DRIMUST	
STB4	TCGG	CCGA	[1, 6, 7, 9]	5.76E-14	TCGgnnCGA	Agree	
STB4	TATT	AGAC	[0, 2, 4, 5, 8, 9]	4.21E-10	TCGgnnCGA	Agree	
STB5	CCTA	TAGC	[0, 6, 9]	1.40E-08	CGGnstTAta	Disagree	
STB5	AGTA	ACTA	[0, 3, 8, 9, 10]	3.26E-08	CGGnstTAta	Disagree	
STB6	AAAT	TCAA	[2, 3, 4, 5, 8, 9, 10]	4.71E-14		Only DRIMUST	
STB6	TTGA	TCAA	[1, 7, 8]	2.85E-10		Only DRIMUST	
STE12	AACTTCTAGT			3.54E-25	tgAAAC	Disagree	
STE12	GAACTTCTAG			7.09E-25	tgAAAC	Disagree	
STP1	TATT	TGTA	[2, 3, 4, 5, 6, 9]	1.48E-12	rCGGcnnrCGGC	Disagree	
STP1	ATTA	TTTA	[1, 3, 4, 5, 7, 8, 9]	6.39E-12	rCGGcnnrCGGC	Disagree	
STP2	TATA	AATT	[1, 3, 8, 10]	9.10E-13		Only DRIMUST	
STP2	ATAA	AATT	[0, 1, 7, 8, 9, 10]	3.57E-11		Only DRIMUST	GWARAA (ATAAAATT)
STP4	CGAA	CCTG	[6]	2.66E-09		Only DRIMUST	
STP4	AACGAACAGA			4.01E-09		Only DRIMUST	

SUM1	AATA	TATT	[0, 1, 2, 3, 4, 6, 7, 8, 10]	5.44E-27	gyGwCAswaaw	AGyGwCACAAAk	Disagree	AWTTWA (AATATATT)
SUM1	AATA	TTAT	[0, 1, 2, 3, 5]	1.08E-22	gyGwCAswaaw	AGyGwCACAAAk	Disagree	
SUT1	CGGCGT			5.02E-12	gcsGsgnnsG	CGCG	Agree	
SUT1	CGGAGT			9.01E-12	gcsGsgnnsG	CGCG	Agree	
SUT2	GGGGGGCAAG			1.09E-07			Only DRIMUST	
SUT2	CGTACTGTGA			1.09E-07			Only DRIMUST	
SWI4	CGCGAAA			4.28E-21	CgCsAAA	CnCGAAA	Agree	
SWI4	CGCG	AAAA	[0, 9, 10]	7.38E-19	CgCsAAA	CnCGAAA	Agree	
SWI5	CACA	ACAC	[1, 7]	1.47E-14		kGCTGr	Disagree	
SWI5	ACAC	ACAC	[2]	4.42E-13		kGCTGr	Disagree	
SWI6	ACGCGT			1.43E-25	CGCgaaa	CnCGAAA	Disagree	
SWI6	CGCG	CGCG	[1, 3, 5, 8, 9, 10]	2.76E-25	CGCgaaa	CnCGAAA	Disagree	
TBS1	AATA	TTAG	[5, 6]	5.84E-09			Only DRIMUST	
TBS1	CCAACGTTG			6.05E-08			Only DRIMUST	ACATTS (CCAACGTTG)
TEC1	TGTTGGAATA			4.92E-21	CATTcy	CATTcy	Disagree	
TEC1	TGATAATGTA			4.97E-21	CATTcy	CATTcy	Disagree	
THI2	TTGA	ATTG	[0, 1, 3, 4, 5, 8, 9]	2.76E-08	gmAAcyntwAgA		Disagree	
THI2	TCAT	AATT	[0, 1, 2, 3, 7, 8, 9, 10]	3.74E-08	gmAAcyntwAgA		Disagree	
TOS8	CCTCGACTAA			1.55E-16			Only DRIMUST	
TOS8	CTCGACTAA			1.55E-16			Only DRIMUST	
TYE7	TCACGTG			4.01E-37	tCACGTGa	CAnnTG	Agree	
TYE7	CACGTGA			9.16E-36	tCACGTGa	CAnnTG	Agree	
UGA3	TATT	AATA	[0, 1, 2, 3, 5, 6, 9, 10]	4.43E-12		CCGnnnnCGG	Disagree	WTWAAA (TATTAATA)
UGA3	TAAT	GTAA	[0, 1, 5, 6, 9]	1.82E-09		CCGnnnnCGG	Disagree	
UME6	AGCCGCC			7.57E-49	taGCCGCCsa	wGCCGCCGw	Agree	
UME6	TAGC	CGCC	[0]	5.16E-48	taGCCGCCsa	wGCCGCCGw	Agree	
UPC2	TTTT	AAAT	[1, 3, 5, 6, 7, 8, 9]	1.30E-22			Only DRIMUST	
UPC2	AATA	TTTA	[0, 1, 2, 4, 7, 8, 9, 10]	2.46E-21			Only DRIMUST	
USV1	TGCCATAAA			1.67E-07			Only DRIMUST	
USV1	ACGA	TCGT	[1]	2.31E-07			Only DRIMUST	
WAR1	ATTT	AAAA	[1, 3, 4, 5, 7, 9]	5.88E-15			Only DRIMUST	
WAR1	ATGA	TTAT	[0, 2, 3, 4, 5, 7, 8, 9]	4.98E-12			Only DRIMUST	
WTM1	AAAT	AATT	[3, 6, 7, 9]	1.36E-16			Only DRIMUST	
WTM1	AAAT	TCAA	[2, 3, 4, 5, 7, 8, 9]	1.92E-16			Only DRIMUST	
WTM2	TGAG	CAGT	[2, 6, 8]	2.24E-09			Only DRIMUST	
WTM2	TTAA	TTAA	[4, 5, 8, 10]	2.91E-08			Only DRIMUST	
XBP1	CACG	CGGC	[0, 2, 3, 5, 6, 7, 8, 10]	7.44E-15		CTTCGAG	Disagree	
XBP1	CCTCGACTAA			1.08E-13		CTTCGAG	Disagree	
YAP1	TTAA	AATA	[0, 1, 2, 3, 4, 6, 7, 9]	2.69E-14	TtAGTmAGc	TTAsTmA	Agree	
YAP1	ATTA	TAAT	[1, 2, 3, 6, 8, 10]	8.08E-13	TtAGTmAGc	TTAsTmA	Agree	
YAP3	GACT	TAGT	[8, 9, 10]	4.44E-08		TTACTAA	Disagree	
YAP3	TATG	GTAT	[6]	1.79E-07		TTACTAA	Disagree	
YAP5	GCGG	ACGA	[7]	5.20E-36		TTACTAA	Disagree	
YAP5	TCCA	ATCC	[9, 10]	3.42E-33		TTACTAA	Disagree	
YAP6	TTTT	TTTT	[0, 6, 9, 10]	6.37E-12		TTACTAA	Disagree	
YAP6	CCTA	CTTC	[10]	6.96E-12		TTACTAA	Disagree	
YAP7	ATTG	AATG	[0, 2, 3, 4, 5, 6, 7, 8]	8.81E-11	mTkAsTmA	TTACTAA	Disagree	
YAP7	AATA	TTAA	[0, 1, 5, 6, 8, 10]	5.12E-10	mTkAsTmA	TTACTAA	Disagree	
YBL054W	AAAT	TGTA	[0, 3, 5, 6, 7, 8, 9]	1.12E-10			Only DRIMUST	
YBL054W	TGAT	TTTG	[0, 1, 2, 3, 6, 7, 8]	1.03E-08			Only DRIMUST	
YBR239c	TTTT	AAAT	[0, 1, 3, 4, 5, 6, 7, 8, 9]	3.62E-18			Only DRIMUST	
YBR239c	TTTT	AATT	[0, 1, 2, 4, 5, 7, 8, 9, 10]	4.65E-17			Only DRIMUST	
YBR267W	AAGA	TGAT	[2, 3, 4, 6]	9.85E-12			Only DRIMUST	
YBR267W	ATGAAG			1.09E-10			Only DRIMUST	
YDR026c	CCGGGTAAA			1.70E-23	tTACCCGGm		Disagree	DNKCCGGGTAAADW (CCGGGTAAA)
YDR026c	CCGG	GTAA	[0, 8, 10]	5.79E-20	tTACCCGGm		Disagree	
YDR049W	ATTT	AAAT	[1, 4, 7, 8, 9, 10]	1.48E-14			Only DRIMUST	
YDR049W	TTTT	AATT	[0, 1, 2, 3, 4, 6, 7, 8, 9, 10]	1.07E-12			Only DRIMUST	
YDR266c	TTGA	TCAA	[1, 2, 5, 6, 7, 8, 9]	1.74E-12			Only DRIMUST	
YDR266c	ATTT	AAAT	[1, 2, 4, 7, 8, 9, 10]	2.46E-09			Only DRIMUST	
YDR520C	CTCCGGCGG			1.06E-09			Only DRIMUST	
YDR520C	TCTCCGGCGG			2.93E-08			Only DRIMUST	

YER051w	ATTT	AAAT	[1, 4, 7, 8, 9, 10]	2.45E-16		Only DRIMUST
YER051w	TTAA	TCAT	[0, 1, 3, 4, 5, 8, 10]	1.26E-12		Only DRIMUST
YER130C	ATTT	AAAT	[1, 4, 7, 8, 9, 10]	2.73E-15		Only DRIMUST
YER130C	AATT	TAAA	[2, 3, 4, 7, 8, 9, 10]	6.52E-13		Only DRIMUST
YER184C	TTCA	TGAA	[1, 2, 6]	2.84E-10		Only DRIMUST
YER184C	ATTC	CGAG	[2, 4, 9, 10]	1.65E-07		Only DRIMUST
YFLO44C	ATTT	TTAT	[3, 4, 6, 7, 9, 10]	3.24E-13		Only DRIMUST
YFLO44C	TTCAAT			1.86E-12		Only DRIMUST
YFLO52w	TTGA	TCAA	[1, 3, 4, 5, 6, 7, 8, 9, 10]	1.20E-15		Only DRIMUST
YFLO52w	AAAT	TCAA	[1, 2, 3, 4, 5, 7, 8]	5.21E-14		Only DRIMUST
YGR067C	ATTT	TAAT	[0, 1, 2, 3, 5, 6, 7, 8, 10]	6.52E-13		Only DRIMUST
YGR067C	ATTT	AAAT	[0, 1, 2, 4, 6, 8, 9, 10]	1.10E-12		Only DRIMUST
YHP1	TGAA	AATT	[1, 2, 3, 4, 5, 6, 7, 9, 10]	1.87E-11	TAATTG	Disagree
YHP1	AAAT	TCAA	[0, 2, 3, 5, 6, 7, 8, 10]	2.00E-09	TAATTG	Disagree
YJL206C	TGCAACGCTA			8.11E-10		Only DRIMUST
YJL206C	GTATTGCAAC			8.11E-10		Only DRIMUST
YKL222C	CTAA	ATTT	[0, 1, 4, 7, 8, 9, 10]	2.14E-13		Only DRIMUST
YKL222C	TAAA	ATTT	[5, 6, 7, 9]	4.74E-12		Only DRIMUST
YKR064W	ATTT	AAAT	[1, 2, 4, 5, 6, 7, 8, 9, 10]	4.39E-17		Only DRIMUST
YKR064W	AATT	TGAA	[1, 2, 3, 5, 6, 7, 8, 9, 10]	1.24E-13		Only DRIMUST
YLR278C	ATTT	TCAA	[0, 2, 3, 5, 6, 7]	1.81E-13		Only DRIMUST
YLR278C	TTTA	AATT	[1, 2, 3, 4, 5, 7, 8, 10]	2.24E-13		Only DRIMUST
YML081W	ATCGTCTAT			2.43E-14		Only DRIMUST
YML081W	ATTATCATAT			3.18E-14		Only DRIMUST
YNR063W	AAAT	ATTT	[2, 3, 4, 6, 7, 8, 9, 10]	3.12E-13		Only DRIMUST
YNR063W	AATT	AATT	[2, 3, 4, 7, 8, 9, 10]	1.63E-12		Only DRIMUST
YOX1	AAAT	TTTT	[0, 1, 2, 3, 4, 6, 9, 10]	6.09E-26	YAATA	Agree
YOX1	AAAT	ATTT	[0, 1, 2, 3, 4, 5, 6, 7, 9]	5.79E-23	YAATA	Agree
YPR022C	ATTT	AAAT	[0, 6, 7, 9, 10]	2.94E-12		Only DRIMUST
YPR022C	TATT	AATA	[0, 2, 3, 5, 6, 8, 10]	7.90E-11		Only DRIMUST
YPR196W	GGTC	AGCG	[7, 8]	1.47E-10		Only DRIMUST
YPR196W	AAGTATCCAA			2.54E-10		Only DRIMUST
YRR1	CAAC	TGAG	[3, 7, 10]	7.86E-09		Only DRIMUST
YRR1	TCCA	TCCA	[2, 8, 10]	1.87E-08		Only DRIMUST
ZAP1	CAGA	CCTG	[2, 6]	1.40E-12	ACCCTmAAGGTyrT	Disagree
ZAP1	AATATT			6.18E-11	ACCCTmAAGGTyrT	Disagree
ZMS1	GCGG	GCAG	[2, 3, 6, 8]	3.03E-09		Only DRIMUST
ZMS1	CTTCGACCC			3.74E-08		Only DRIMUST