

































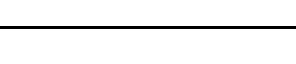


Cluster	Function	Representative motifs	Selected k-mer correlations	
C1	Chromatin remodeling	Rsc3: 	Rsc3/Rsc30: 0.956	
C2	Carbohydrate metabolism, response to stress	Mig1: Ygr067c: Nrg1: Rph1: Yer130c: 	Mig1/Mig2: 0.870 Mig2/Mig3: 0.823 Mig1/Yml081w: 0.718 Mig1/Ygr067c: 0.636 Nrg1/Usv1: 0.475 Rph1/Yer130c: 0.425 Mig1/Yer130c: 0.263 Mig1/Rph1: 0.248 Nrg1/Yer130c: 0.236 Mig1/Nrg1: 0.185	Usv1/Yml081w: 0.167 Nrg1/Ygr067c: 0.158 Mig1/Usv1: 0.143 Mig2/Rph1: 0.0924 Mig3/Nrg1: 0.078
C3	Stress response, drug response	Sip4: Rds1: Ecm22: Hal9: Tbs1: Yrr1: Oaf1: Ynr063w: Rds2: Cep3: Ybr239c: Ume6: Stp2: Rgt1: 	Hal9/Rdr1: 0.834 Gsm1/Ecm22: 0.83 Rdr1/Cha4: 0.82 Hal9/Asg1: 0.82 Asg1/Aro80: 0.812 Gsm1/Put3: 0.809 Hal9/Yll054c: 0.803 Put3/Rds2: 0.774 Hal9/Ykl222c: 0.764 Yll054c/Tbs1: 0.764 Leu3/Gsm1: 0.757 Rds1/Cha4: 0.721 Hal9/Ybr239c: 0.667 Cep3/Aro80: 0.623 Sip4/Ecm22: 0.592 Ynr063w/Ybr239c: 0.532 Oaf1/Rds2: 0.518 Yrr1/Ynr063w: 0.495 Stp4/Stp2: 0.3906 Ume6/Stp2: 0.3808 Tbs1/Oaf1: 0.275 Rds1/Ynr063w: 0.181 Rds1/Yrr1: 0.035 Ume6/Ynr063w: 0.0324 Stp4/Rds2: 0.0288 Stp4/Rgt1: 0.0212 Stp2/Put3: 0.0198	Ume6/Ybr239c: 0.0126 Ume6/Oaf1: 0.012 Stp2/Rds2: 0.011 Stp2/Oaf1: 0.0088 Ume6/Yrr1: -0.0259 Stp2/Ybr239c: -0.0378 Stp2/Ynr063w: -0.082 Stp2/Yrr1: -0.1402

Figure S12. Motifs and 8-mer binding profile correlations for potential co-regulatory TFs from CRACR-predicted condition specificities. Representative motifs and k-mer correlations shown.

Cluster	Function	Representative motifs	Selected k-mer correlations
C4	Cell cycle, sporulation	Yox1:  Nhp6a:  Smp1: 	Smp1/Yox1: 0.511 Pho2/Nhp6a: 0.330 Smp1/Pho2: 0.507 Pho2/Nhp6b: 0.572 Smp1/Nhp6a: 0.352 Nhp6a/Nhp6b: 0.945 Smp1/Nhp6b: 0.390 Yox1/Nhp6a: 0.632 Yox1/Pho2: 0.826 Yox1/Nhp6b: 0.651
C5	Cell Cycle, Mating	Fkh1: 	Fkh1/Fkh2: 0.8612
C6		Sut2:  Ydr520c:  Srd1: 	Sut2/Ydr520c: 0.3447 Srd1/Ydr520c: 0.2755 Sut2/Srd1: 0.2053
C7	Cell fate/cell cycle	Mga1:  Mcm1: 	Mga1/Mcm1: 0.1788
C8	Transport (carb. etc)	Lys14:  Sfl1:  Ypr196w: 	Lys14/Sfl1: 0.376 Ypr196w/Lys14: 0.367 Sfl1/Ypr196w: -0.008
C9	AA metabolism	Gcn4:  Bas1: 	Bas1/Gcn4: 0.151
C10	AA and phosphate metabolism	Met32:  Tye7:  Cbf1:  Pho4: 	Met32/Tye7: 0.038 Tye7/Cbf1: 0.6348 Met32/Cbf1: 0.005 Met32/Pho4: 0.090 Cbf1/Pho4: 0.629
C11	Nitrogen and sulfur metabolism	Gln3:  Gat1: 	Gzf3/Gln3: 0.874 Gzf3/Gat1: 0.951 Gln3/Gat1: 0.901

Cluster	Function	Representative motifs	Selected k-mer correlations	
C12	AA metabolism, cell wall, diverse functions	<p>Ypr013c: </p> <p>Tbf1: </p> <p>Gat3: </p> <p>Gat4: </p> <p>Aft1: </p> <p>Skn7: </p>	<p>Gat3/Gat4: 0.636</p> <p>Aft1/Skn7: 0.458</p> <p>Ypr013c/Gat4: 0.285</p> <p>Ypr013c/Aft1: 0.096</p> <p>Gat3/Aft1: 0.033</p> <p>Tbf1/Aft1: 0.031</p> <p>Tbf1/Skn7: 0.012</p> <p>Gat3/Skn7: 0.003</p>	<p>Ypr013c/Skn7: -0.008</p> <p>Ypr013c/Tbf1: -0.005</p> <p>Tbf1/Gat3: -0.0323</p> <p>Gat4/Skn7: -0.0468</p> <p>Tbf1/Gat4: -0.0805</p>
C13	Protein biosynthesis response to stress, drug response	<p>Sum1: </p> <p>Yap6: </p> <p>Sfp1: </p> <p>Rpn4: </p> <p>Rtg3: </p> <p>Yrm1: </p> <p>Pdr1: </p>	<p>Sum1/Sfp1: 0.6448</p> <p>Yrm1/Pdr1: 0.5748</p> <p>Sfp1/Yrm1: 0.5449</p> <p>Yap6/Sfp1: 0.524</p> <p>Yap6/Yrm1: 0.5194</p> <p>Yap6/Pdr1: 0.5108</p> <p>Sfp1/Pdr1: 0.5086</p> <p>Yap6/Rtg3: 0.4994</p> <p>Rtg3/Yrm1: 0.4766</p> <p>Sum1/Yrm1: 0.4739</p> <p>Sum1/Pdr1: 0.4729</p> <p>Sfp1/Rpn4: 0.4581</p> <p>Rpn4/Yrm1: 0.4545</p>	<p>Rtg3/Pdr1: 0.4396</p> <p>Sum1/Yap6: 0.4355</p> <p>Sfp1/Rtg3: 0.4235</p> <p>Sum1/Rtg3: 0.4208</p> <p>Sum1/Rpn4: 0.417</p> <p>Yap6/Rpn4: 0.3644</p> <p>Rpn4/Pdr1: 0.3062</p> <p>Rpn4/Rtg3: 0.3027</p>
C14	rRNA processing, ribosome	<p>Pbf2: </p> <p>Stb3: </p>	<p>Pbf1/Pbf2: 0.928</p> <p>Pbf2/Stb3: -0.040</p> <p>Pbf1/Stb3: -0.048</p>	