Tables S9. Prediction of XYR1 binding sites on genes up regulated in a *Δxyr1* mutant induced with sophorose.

Protein ID	**Site 1***	**Site 2**	**Distance**	**Description**	**log2 FC (Δxyr1/wt)**	**p-val**
52315	-211	-201	10	copper transporter Ctr	9.504438019	2.73E-35
111094	-116	-93	23	CBM 13	6.543550884	2.49E-75
82321	-980	-956	24	Aquaporin	4.449578196	8.05E-29
82321	-878	-861	17	Aquaporin	4.449578196	8.05E-29
82321	-543	-526	17	Aquaporin	4.449578196	8.05E-29
58717	-431	-403	28	ß-lactamase class C	3.919694582	0.000000482
123777	-91	-73	18	unique protein	2.661861668	2.36E-10
2316	-560	-547	13	unknown protein with caleosin domain	2.28910924	0.000472964
2316	-547	-519	28	unknown protein with caleosin domain	2.28910924	0.000472964
82327	-161	-151	10	PDR-type ABC transporters	2.021735018	0.011071885
106039	-1022	-994	28	Ribosomal protein S28 based on homology to the corresponding protein of Neurospora crassa.	1.956909629	0.003884709
106039	-517	-489	28	Ribosomal protein S28 based on homology to the corresponding protein of Neurospora crassa.	1.956909629	0.003884709
79238	-1149	-1129	20	unknown protein	1.766548107	2.06E-10
2451	-1437	-1414	23	Secretion related small GTPase Rab6/Ypt6/Ryh1	1.73915014	1.04E-12
78233	-712	-684	28	40s ribosomal protein S21 based on homolgoy to the corresponding protein in Giberella zeae.	1.646507965	0.000419782
34306	-887	-857	30	mitochondrial cytochrome c oxidase assembly factor, putative	1.590507454	5.83E-08
120983	-939	-922	17	uracil phosphoribosyl transferase	1.563816786	0.0000831
54768	-1135	-1124	11	unknown protein	1.557910829	0.00419456
105263	-1264	-1254	10	Zn2Cys6 transcriptional regulator	1.528914054	2.13E-08
68107	-1497	-1475	22	Ribosomal protein S30 by homology with the corresponding protein of Ashbya gossypii.	1.513847592	0.001069802
123176	-754	-731	23	60S ribosomal protein L12 (L11 family).	1.439191543	0.010242256
81930	-166	-139	27	HAM1-like protein, probably related to DNA-repair	1.411901826	0.000000243
120621	-661	-649	12	ribosomal protein L37 of the large (60S) ribosomal subunit. Belongs to the same family as	1.404554321	2.43E-09

				yeast Rpl33Ap and has similarity to rat L35a.		
105003	-1390	-1365	25	unknown protein	1.40290366	3.52E-08
123773	-863	-851	12	Ubiquitin-conjugating enzyme	1.382287706	3.96E-09
103147	-1478	-1459	19	unknown protein	1.339385207	1.18E-08
53947	-1259	-1248	11	HFBs	1.33236182	6.5E-09
119989	-380	-354	26	HFB2	1.327482056	0.001596848
121903	-74	-53	21	iron-sulfur cluster assembly accessory protein, putative	1.316702511	0.000000156
80206	-705	-688	17	unknown protein	1.27696843	0.00000183
21170	-599	-582	17	Ribosomal protein S12	1.261659674	0.0000679
71559	-1435	-1415	20	Translation initiation factor eIF-5A gene based on homologyToThe corresponding genes in several filamentous fungi.	1.230204974	0.000000141
71559	-672	-645	27	Translation initiation factor eIF-5A gene based on homologyToThe corresponding genes in several filamentous fungi.	1.230204974	0.000000141
103487	-140	-123	17	glutathione S transferase	1.198183712	0.009117042
79324	-953	-937	16	nucleoside-diphosphate-sugar epimerase, putative (check!)	1.196939533	0.002519593
40775	-1386	-1362	24	RTA1 protein, 7 TNM, responds to xenobiotic stimulus	1.170915772	0.00000239
74580	-543	-514	29	unknown protein, 3 TM domains	1.153726051	0.000000704
64874	-892	-865	27	MFS toxin efflux pump	1.122511743	0.002675252
49308	-741	-711	30	unknown protein	1.106942966	0.001806411
123202	-44	-22	22	60s ribosomal protein rla2	1.100430395	0.035956414
80709	-672	-642	30	pre-mRNA-splicing factor CWC21, putative	1.09788588	0.000504897
75447	-1346	-1324	22	unknown protein	1.095846806	0.000012
121003	-1393	-1377	16	Ribosomal protein S18, S13 family	1.080354899	0.000103867
49649	-1334	-1324	10	unknown protein	1.080293983	0.006004053
72643	-1338	-1324	14	arginosuccinate synthetase	1.07930415	0.049072183
74807	-661	-633	28	GH76 GPI-anchored α-1,6-mannanase	1.067670775	0.00000811
74807	-601	-580	21	GH76 GPI-anchored α-1,6-mannanase	1.067670775	0.00000811
120184	-658	-646	12	v-SNARE Ykt6; trafficking to and within Golgi, endocytic trafficking to vacuole, vacuolar fusion	1.061753909	0.0000164
60768	-1129	-1112	17	unknown protein	1.061479399	0.0000555

81541	-1157	-1129	28	unknown protein	1.060246101	0.00000798
121449	-638	-627	11	IGPDImidazoleglycerol-phosphate dehydratase	1.057590989	0.0000797
121620	-252	-240	12	NMT1 thiamine biosynthesis protein	1.043177408	0.0000188
80115	-1402	-1372	30	unknown protein	1.034816624	0.027880534
63813	-319	-290	29	cytochrome b5, putative	1.032997124	0.00022569
123659	-859	-842	17	cell wall protein, istantly related to S. cerevisiae Pir3p.	1.023034243	0.001376401
21396	-83	-63	20	sugar isomerase	1.020934128	0.003012859

*Positions of Sites 1 and 2 are relative to the gene start codon.