Tables S8. Prediction of XYR1 binding sites on genes down regulated in a *Δxyr1* mutant induced with sophorose.

Protein ID	**Site 1***	**Site 2**	**Distance**	**Description**	**log2 FC (Δxyr1/wt)**	**p-val**
123261	-939	-920	19	unknown protein	-2.99670971	1.28E-33
123261	-742	-732	10	unknown protein	-2.99670971	1.28E-33
123261	-681	-663	18	unknown protein	-2.99670971	1.28E-33
44278	-860	-847	13	Rab geranyl transferase escort protein	-2.120576253	3.95E-17
123084	-68	-43	25	chloroperoxidase	-1.85817748	0.003089378
119860	-1391	-1379	12	unknown protein	-1.797021174	7.57E-13
120943	-296	-270	26	NAD-dependent glutamate dehydrogenase	-1.788918503	1.01E-10
121121	-83	-56	27	Zn2Cys6 transcriptional regulator	-1.772560265	5.13E-11
21960	-1147	-1130	17	phospholipase C	-1.682812431	9.23E-10
81756	-309	-281	28	unknown protein	-1.59792776	6.06E-12
109317	-150	-126	24	unknown protein	-1.585583444	6.11E-10
79960	-907	-882	25	GH47 α-1,2-mannosidase	-1.442723348	1.2E-09
56780	-91	-72	19	DNA polymerase X family	-1.418313101	3.64E-08
122043	-224	-206	18	unknown protein	-1.379370847	4.21E-09
58381	-1364	-1337	27	unknown protein	-1.372650179	1.16E-08
58381	-1337	-1318	19	unknown protein	-1.372650179	1.16E-08
122724	-1106	-1078	28	unknown protein, only in neurospora and Chaetomium	-1.351846176	0.000000751
123865	-1491	-1479	12	Peptidase S8 and S53, subtilisin, kexin, sedolisin	-1.337624888	0.00000273
122076	-785	-773	12	aspartyl protease	-1.283009181	0.000000238
122076	-773	-746	27	aspartyl protease	-1.283009181	0.000000238
103063	-1332	-1312	20	unknown protein	-1.20931519	0.00000494
75394	-1321	-1310	11	unknown protein	-1.198644528	0.010961175
121065	-848	-835	13	unknown protein	-1.183685907	0.00000701
121839	-1277	-1261	16	HSP70	-1.156469003	0.0000016

36391	-89	-77	12	C2H2 transcriptional regulator	-1.127299804	0.00000192
104219	-455	-426	29	unknown protein	-1.118833451	0.022674252
120224	-142	-125	17	C2H2 transcriptional regulator	-1.116675465	0.0000031
65921	-226	-197	29	Acetyl/propionyl-CoA carboxylase alpha subunit	-1.088095997	0.0000587
65921	-197	-177	20	Acetyl/propionyl-CoA carboxylase alpha subunit	-1.088095997	0.0000587
121107	-1258	-1246	12	Zn2Cys6 transcriptional regulator	-1.085030781	0.00000534
121107	-94	-74	20	Zn2Cys6 transcriptional regulator	-1.085030781	0.00000534
111103	-223	-208	15	unknown protein	-1.079135101	0.00000389
53596	-338	-328	10	unknown protein	-1.078876955	0.0000233
68291	-1167	-1137	30	pyruvate formate lyase activating enzyme (radical SAM superfamily)	-1.067242861	0.000045
47603	-972	-960	12	succinyl-CoA:3-ketoacid-coenzyme A transferase subunit A	-1.055195306	0.0000152
57322	-165	-155	10	ARO Transcriptional regulators containing a DNA-binding HTH domain and an aminotransferase domain (MocR family)	-1.043339166	0.0000907

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