Tables S4. Genome-wide prediction of XYR1 binding sites *in T. reesei*.

Protein ID	**Site 1***	**Site 2**	**Distance**	**Description**	**Functional category**
53947	-1259	-1248	11	SWI-SNF chromatin-remodeling complex protein	Chromatin structure and dynamics
53302	-144	-133	11	Glycolate oxidase	Energy production and conversion
73689	-985	-964	21	FOG: Zn-finger	General function prediction only
53576	-228	-220	8	CREB binding protein/P300 and related TAZ Zn-finger proteins	Transcription
54450	-634	-611	23	mRNA capping enzyme, guanylyltransferase (alpha) subunit	RNA processing and modification
119800	-1179	-1164	15	Cell division control protein/predicted DNA repair exonuclease	Replication, recombination and repair
74258	-1477	-1451	26	Phenylalanyl-tRNA synthetase beta subunit	Translation, ribosomal structure and biogenesis
103113	-1156	-1140	16	Predicted short chain-type dehydrogenase	General function prediction only
53601	-637	-622	15	Synaptobrevin/VAMP-like protein	Intracellular trafficking, secretion, and vesicular transport
62362	-1019	-989	30	Calcium transporting ATPase	Inorganic ion transport and metabolism
108012	-524	-511	13	Prolylcarboxypeptidase (angiotensinase C)	Posttranslational modification, protein turnover, chaperones / General function prediction only
71559	-672	-645	27	Translation initiation factor 5A (eIF-5A)	Translation, ribosomal structure and biogenesis
78560	-424	-416	8	Predicted GTPase	General function prediction only
108087	-1131	-1119	12	Nuclear receptor coregulator SMRT/SMRTER, contains Myb-like domains	Transcription
48951	-993	-978	15	Protein involved in vacuolar polyphosphate accumulation, contains SPX domain	Inorganic ion transport and metabolism
78753	-251	-223	28	Cullins	Cell cycle control, cell division, chromosome partitioning
78939	-911	-891	20	RNA helicase BRR2, DEAD-box superfamily	RNA processing and modification
71689	-142	-127	15	Serine O-acetyltransferase	Amino acid transport and metabolism
4479	-978	-970	8	Small nuclear ribonucleoprotein (snRNP) Sm core protein	RNA processing and modification
49696	-207	-196	11	Molecular chaperone (DnaJ superfamily)	Posttranslational modification, protein turnover, chaperones
122657	-1199	-1174	25	Flavohemoprotein b5+b5R	Energy production and conversion
64752	-102	-92	10	DNA-directed RNA polymerase, subunit RPB10	Transcription
79690	-225	-201	24	Electron transfer flavoprotein ubiquinone oxidoreductase	Energy production and conversion

122778	-1050	-1039	11	Aldo/keto reductase family proteins	General function prediction only
109404	-1113	-1102	11	Splicing coactivator SRm160/300, subunit SRm300	RNA processing and modification
22830	-1338	-1324	14	Glutathione S-transferase	Posttranslational modification, protein turnover, chaperones
4843	-193	-170	23	Carbon-nitrogen hydrolase	Amino acid transport and metabolism
4843	-170	-159	11	Carbon-nitrogen hydrolase	Amino acid transport and metabolism
65921	-226	-197	29	3-Methylcrotonyl-CoA carboxylase, biotin-containing subunit/Propionyl-CoA carboxylase, alpha chain/Acetyl-CoA carboxylase, biotin carboxylase subunit	Amino acid transport and metabolism / Lipid transport and metabolism
65921	-197	-177	20	3-Methylcrotonyl-CoA carboxylase, biotin-containing subunit/Propionyl-CoA carboxylase, alpha chain/Acetyl-CoA carboxylase, biotin carboxylase subunit	Amino acid transport and metabolism / Lipid transport and metabolism
109793	-1194	-1184	10	Uncharacterized conserved protein	Function unknown
66256	-328	-306	22	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	Secondary metabolites biosynthesis, transport and catabolism
66311	-757	-732	25	Predicted transporter (major facilitator superfamily)	General function prediction only
123124	-1362	-1336	26	Serine/threonine protein kinase	General function prediction only
66154	-1119	-1099	20	Nucleolar protein-like/EBNA1-binding protein	RNA processing and modification
55263	-182	-165	17	Ubiquitin-conjugating enzyme-related protein Ft1, involved in programmed cell death	Posttranslational modification, protein turnover, chaperones
55034	-999	-988	11	Sexual differentiation process protein ISP4	Signal transduction mechanisms
123468	-1107	-1088	19	IMP dehydrogenase/GMP reductase	Nucleotide transport and metabolism
51420	-1087	-1074	13	Ribosomal RNA adenine dimethylase	RNA processing and modification
123561	-990	-977	13	Subtilisin-like proprotein convertase	Posttranslational modification, protein turnover, chaperones
81271	-240	-230	10	Sorbitol dehydrogenase	Secondary metabolites biosynthesis, transport and catabolism
51558	-898	-888	10	Ankyrin repeat protein	General function prediction only
81450	-237	-225	12	Mitochondrial import inner membrane translocase, subunit TIM44	Intracellular trafficking, secretion, and vesicular transport
111426	-355	-329	26	Splicing coactivator SRm160/300, subunit SRm300	RNA processing and modification
123884	-206	-177	29	Queuine-tRNA ribosyltransferase	RNA processing and modification
123989	-757	-742	15	Uncharacterized conserved protein (tumor-rejection antigen MAGE in humans)	Function unknown

75139	-607	-579	28	Predicted E3 ubiquitin ligase	Posttranslational modification, protein turnover, chaperones
75204	-136	-111	25	Predicted Zn-finger protein	General function prediction only
75205	-1453	-1428	25	Nucleotide excision repair complex XPC-HR23B, subunit XPC/DPB11	Replication, recombination and repair
104180	-1410	-1384	26	Ankyrin	Cell wall/membrane/envelope biogenesis
104211	-1358	-1342	16	FKBP-type peptidyl-prolyl cis-trans isomerase	Posttranslational modification, protein turnover, chaperones
75428	-1338	-1309	29	Spliceosomal protein snRNP-U1A/U2B	RNA processing and modification
56363	-153	-145	8	Transcriptional regulator	Transcription
23367	-777	-766	11	Glucose dehydrogenase/choline dehydrogenase/mandelonitrile lyase (GMC oxidoreductase family)	General function prediction only
82123	-1336	-1317	19	Predicted transcription factor DATF1, contains PHD and TFS2M domains	Transcription
70025	-681	-658	23	Zinc-binding oxidoreductase	Energy production and conversion / General function prediction only
82321	-980	-956	24	Aquaporin (major intrinsic protein family)	Carbohydrate transport and metabolism
57274	-660	-650	10	WD40 repeat protein	General function prediction only
57600	-511	-494	17	Global transcriptional regulator, cell division control protein	Amino acid transport and metabolism
75985	-934	-915	19	Mitochondrial associated endoribonuclease MAR1 (isochorismatase superfamily)	General function prediction only
105190	-700	-670	30	Nuclear pore complex, Nup214/CAN component	Nuclear structure / Intracellular trafficking, secretion, and vesicular transport
70956	-273	-243	30	Cytochrome P450 CYP3/CYP5/CYP6/CYP9 subfamilies	Secondary metabolites biosynthesis, transport and catabolism
76329	-622	-601	21	Ran-binding protein RANBP1 and related RanBD domain proteins	Intracellular trafficking, secretion, and vesicular transport
58638	-1432	-1420	12	RNA polymerase II transcription factor complex subunit	Transcription
121019	-542	-530	12	Succinate dehydrogenase, flavoprotein subunit	Energy production and conversion
58405	-200	-174	26	U2 snRNP splicing factor, small subunit, and related proteins	RNA processing and modification
58405	-174	-155	19	U2 snRNP splicing factor, small subunit, and related proteins	RNA processing and modification
6108	-161	-146	15	SAM-dependent methyltransferases	Lipid transport and metabolism / General function prediction only
121133	-803	-781	22	Aspartyl protease	Posttranslational modification, protein turnover, chaperones

76887	-1145	-1128	17	Aspartyl protease	Posttranslational modification, protein turnover, chaperones
121262	-217	-200	17	Apoptosis-related protein/predicted DNA-binding protein	Cell cycle control, cell division, chromosome partitioning
77009	-347	-323	24	GTP-binding protein DRG2 (ODN superfamily)	Signal transduction mechanisms
77038	-1349	-1333	16	Synaptobrevin/VAMP-like protein SEC22	Intracellular trafficking, secretion, and vesicular transport
77099	-506	-485	21	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)	General function prediction only
121656	-57	-47	10	Nuclear pore complex, Nup98 component (sc Nup145/Nup100/Nup116)	Nuclear structure / Intracellular trafficking, secretion, and vesicular transport
107082	-800	-783	17	FOG: RRM domain	General function prediction only
22271	-886	-866	20	Zinc-binding oxidoreductase	Energy production and conversion / General function prediction only
107360	-739	-730	9	Prolyl 4-hydroxylase alpha subunit	Amino acid transport and metabolism
62071	-299	-278	21	Dosage compensation regulatory complex/histone acetyltransferase complex, subunit MSL-3/MRG15/EAF3, and related CHROMO domain-containing proteins	Transcription / Chromatin structure and dynamics
121826	-454	-434	20	ATP-citrate lyase	Energy production and conversion
121890	-57	-34	23	Mitochondrial processing peptidase, alpha subunit	Posttranslational modification, protein turnover, chaperones
121903	-74	-53	21	Mitochondrial Fe-S cluster biosynthesis protein ISA2 (contains a HesB-like domain)	Intracellular trafficking, secretion, and vesicular transport / Energy production and conversion
107547	-397	-368	29	Translation initiation factor 4F, ribosome/mRNA-bridging subunit (eIF-4G)	Translation, ribosomal structure and biogenesis
73643	-143	-114	29	beta-1,6-N-acetylglucosaminyltransferase, contains WSC domain	Posttranslational modification, protein turnover, chaperones / Carbohydrate transport and metabolism
53721	-906	-895	11	Predicted alpha-helical protein, potentially involved in replication/repair	Replication, recombination and repair
74080	-1242	-1212	30	Panthothenate synthetase	Coenzyme transport and metabolism
53503	-1034	-1009	25	Predicted transporter (major facilitator superfamily)	General function prediction only
119871	-1301	-1286	15	Ras-related small GTPase, Rho type	General function prediction only
78496	-1333	-1323	10	Flavin-containing monooxygenase	Secondary metabolites biosynthesis, transport and catabolism
78555	-1231	-1223	8	Predicted esterase of the alpha-beta hydrolase superfamily (Neuropathy target esterase), contains cAMP-binding domains	General function prediction only
22678	-523	-504	19	Iron/ascorbate family oxidoreductases	Secondary metabolites biosynthesis, transport and catabolism / General function prediction only

64347	-1072	-1052	20	Projectin/twitchin and related proteins	Cytoskeleton
122656	-1006	-981	25	Splicing coactivator SRm160/300, subunit SRm300	RNA processing and modification
64420	-1315	-1305	10	WD40 repeat protein	Secondary metabolites biosynthesis, transport and catabolism / General function prediction only
64720	-795	-770	25	1-Acyl dihydroxyacetone phosphate reductase and related dehydrogenases	Secondary metabolites biosynthesis, transport and catabolism / General function prediction only
64959	-1145	-1134	11	Predicted phosphatase	General function prediction only
64971	-612	-594	18	Amino acid transporters	Amino acid transport and metabolism
109285	-1015	-994	21	Serine/threonine protein kinase	Signal transduction mechanisms
50077	-988	-974	14	Amino acid transporters	Amino acid transport and metabolism
80058	-21	-9	12	Predicted transporter (major facilitator superfamily)	General function prediction only
65950	-1300	-1276	24	Triglyceride lipase-cholesterol esterase	Lipid transport and metabolism
4990	-1316	-1294	22	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	Secondary metabolites biosynthesis, transport and catabolism
66296	-627	-601	26	Eukaryotic-type DNA primase, large subunit	Replication, recombination and repair
5063	-270	-241	29	SWI-SNF chromatin-remodeling complex protein	Chromatin structure and dynamics
120008	-1332	-1317	15	Glucose dehydrogenase/choline dehydrogenase/mandelonitrile lyase (GMC oxidoreductase family)	General function prediction only
55060	-443	-415	28	Kinesin (SMY1 subfamily)	Cytoskeleton
44928	-718	-707	11	5-formyltetrahydrofolate cyclo-ligase	Coenzyme transport and metabolism
55088	-1346	-1321	25	NADH:ubiquinone oxidoreductase, NDUFS4/18 kDa subunit	Energy production and conversion
110813	-178	-169	9	Amino acid transporters	Amino acid transport and metabolism
67938	-823	-799	24	Reductases with broad range of substrate specificities	General function prediction only
68364	-970	-960	10	NIMA (never in mitosis)-related G2-specific serine/threonine protein kinase	Cell cycle control, cell division, chromosome partitioning
68636	-1332	-1320	12	Mitochondrial/chloroplast ribosomal protein S11	Translation, ribosomal structure and biogenesis
111194	-894	-880	14	Predicted GTPase	General function prediction only
111216	-1352	-1332	20	Histone H3 (Lys9) methyltransferase SUV39H1/Clr4, required for transcriptional silencing	Transcription / Chromatin structure and dynamics
111345	-930	-902	28	beta-1,6-N-acetylglucosaminyltransferase, contains WSC domain	Posttranslational modification, protein turnover, chaperones / Carbohydrate transport and metabolism
68821	-633	-623	10	UDP-glucuronosyl and UDP-glucosyl transferase	Energy production and conversion / Carbohydrate

					transport and metabolism
68813	-1163	-1137	26	Permease of the major facilitator superfamily	Carbohydrate transport and metabolism
82026	-1077	-1049	28	Predicted methyltransferase	General function prediction only
23346	-417	-388	29	Beta-N-acetylhexosaminidase	Carbohydrate transport and metabolism
75380	-710	-685	25	Permease of the major facilitator superfamily	Carbohydrate transport and metabolism
104495	-1079	-1071	8	RNA helicase	RNA processing and modification
104557	-303	-280	23	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	Secondary metabolites biosynthesis, transport and catabolism
72685	-418	-406	12	6-phosphogluconate dehydrogenase	Carbohydrate transport and metabolism
124031	-1160	-1141	19	20S proteasome, regulatory subunit alpha type PSMA4/PRE9	Posttranslational modification, protein turnover, chaperones
82235	-240	-228	12	Maltase glucoamylase and related hydrolases, glycosyl hydrolase family 31	Carbohydrate transport and metabolism
5916	-1073	-1063	10	Histone acetyltransferase (MYST family)	Chromatin structure and dynamics
5916	-1063	-1035	28	Histone acetyltransferase (MYST family)	Chromatin structure and dynamics
82385	-1182	-1156	26	Methionyl-tRNA synthetase	Translation, ribosomal structure and biogenesis
70646	-526	-504	22	Beta, beta-carotene 15,15'-dioxygenase and related enzymes	Secondary metabolites biosynthesis, transport and catabolism
57322	-165	-155	10	Aromatic amino acid aminotransferase and related proteins	Amino acid transport and metabolism
104831	-1064	-1037	27	Splicing coactivator SRm160/300, subunit SRm300	RNA processing and modification
104831	-91	-66	25	Splicing coactivator SRm160/300, subunit SRm300	RNA processing and modification
120789	-1047	-1030	17	Alpha tubulin	Cytoskeleton
120803	-114	-89	25	Predicted divalent cation transporter	Inorganic ion transport and metabolism
120821	-310	-297	13	von Willebrand factor and related coagulation proteins	Defense mechanisms / Extracellular structures
57433	-777	-760	17	Subtilisin kexin isozyme-1/site 1 protease, subtilase superfamily	Posttranslational modification, protein turnover, chaperones
105189	-1282	-1252	30	20S proteasome, regulatory subunit beta type PSMB7/PSMB10/PUP1	Posttranslational modification, protein turnover, chaperones
112520	-827	-800	27	beta-1,6-N-acetylglucosaminyltransferase, contains WSC domain	Posttranslational modification, protein turnover, chaperones / Carbohydrate transport and metabolism
105216	-792	-779	13	Ankyrin	Cell wall/membrane/envelope biogenesis
59056	-1263	-1255	8	Acyl-CoA thioesterase	Lipid transport and metabolism

58851	-1279	-1267	12	Phosphatidylserine-specific receptor PtdSerR, contains JmjC domain	Chromatin structure and dynamics 7 Signal transduction mechanisms
76491	-759	-733	26	Regulator of Rac1, required for phagocytosis and cell migration	Signal transduction mechanisms
76491	-733	-714	19	Regulator of Rac1, required for phagocytosis and cell migration	Signal transduction mechanisms
6103	-43	-21	22	Synaptic vesicle transporter SVOP and related transporters (major facilitator superfamily)	General function prediction only
73110	-759	-737	22	Diamine acetyltransferase	Amino acid transport and metabolism
76710	-538	-525	13	RNA polymerase III, large subunit	Transcription
121230	-170	-145	25	Squalene monooxygenase	Lipid transport and metabolism
106148	-478	-461	17	DNA-binding protein C1D involved in regulation of double-strand break repair	Replication, recombination and repair
77007	-1457	-1433	24	FOG: RRM domain	General function prediction only
77364	-1150	-1125	25	Ubiquitin-specific protease	Posttranslational modification, protein turnover, chaperones
60951	-686	-656	30	Putative Zn-finger protein	General function prediction only
121664	-203	-182	21	Glutamate decarboxylase and related proteins	Amino acid transport and metabolism
77647	-255	-242	13	Threonine aldolase	Amino acid transport and metabolism
60768	-1129	-1112	17	Predicted peptidyl-tRNA hydrolase	Translation, ribosomal structure and biogenesis
22264	-915	-895	20	Apoptosis antagonizing transcription factor/protein transport protein	Transcription / Intracellular trafficking, secretion, and vesicular transport
121901	-1161	-1140	21	Translation initiation factor 3, subunit c (eIF-3c)	Translation, ribosomal structure and biogenesis
61750	-105	-76	29	Sphingolipid hydroxylase	Lipid transport and metabolism
27599	-1152	-1122	30	Mitochondrial Fe2+ transporter MMT1 and related transporters (cation diffusion facilitator superfamily)	Inorganic ion transport and metabolism
60402	-143	-127	16	Mitochondrial GTPase	Translation, ribosomal structure and biogenesis
35202	-190	-167	23	Helicases	Replication, recombination and repair
61948	-1449	-1440	9	Protein disulfide isomerase (prolyl 4-hydroxylase beta subunit)	Posttranslational modification, protein turnover, chaperones
40290	-251	-222	29	Putative translation initiation inhibitor UK114/IBM1	Translation, ribosomal structure and biogenesis
55595	-838	-822	16	Ca2+/H+ antiporter VCX1 and related proteins	Inorganic ion transport and metabolism
21396	-83	-63	20	unknown protein	-
62475	-555	-528	27	unknown protein	-

78499	-1234	-1224	10	unknown protein	-
122178	-777	-761	16	unknown protein	-
108251	-321	-310	11	unknown protein	-
79238	-1149	-1129	20	unknown protein	-
122576	-841	-819	22	unknown protein	-
64172	-99	-79	20	unknown protein	-
65948	-1228	-1204	24	unknown protein	-
80340	-864	-844	20	unknown protein	-
123282	-72	-58	14	unknown protein	-
74576	-661	-648	13	unknown protein	-
55561	-1198	-1183	15	unknown protein	-
45153	-136	-111	25	unknown protein	-
68291	-1167	-1137	30	unknown protein	-
68930	-70	-45	25	unknown protein	-
111514	-582	-564	18	unknown protein	-
72526	-236	-227	9	unknown protein	-
72526	-227	-206	21	unknown protein	-
82032	-609	-580	29	unknown protein	-
104075	-321	-293	28	unknown protein	-
104399	-1491	-1476	15	unknown protein	-
104584	-831	-810	21	unknown protein	-
82227	-659	-643	16	unknown protein	-
82286	-246	-236	10	unknown protein	-
82286	-236	-208	28	unknown protein	-
124119	-888	-877	11	unknown protein	-
124119	-660	-651	9	unknown protein	-
112392	-397	-384	13	unknown protein	-
57527	-1037	-1024	13	unknown protein	-

112603	-56	-39	17	unknown protein	-
58244	-1335	-1327	8	unknown protein	-
121107	-1258	-1246	12	unknown protein	-
121121	-83	-56	27	unknown protein	-
105849	-371	-353	18	unknown protein	-
76820	-622	-596	26	unknown protein	-
73231	-325	-296	29	unknown protein	-
60337	-109	-100	9	unknown protein	-
106755	-521	-496	25	unknown protein	-
74223	-396	-410	14	unknown protein	-
108011	-1026	-1013	13	unknown protein	-
122262	-1265	-1244	21	unknown protein	-
63952	-1010	-999	11	unknown protein	-
64011	-726	-715	11	unknown protein	-
109317	-150	-126	24	unknown protein	-
80181	-290	-266	24	unknown protein	-
109790	-1042	-1013	29	unknown protein	-
109790	-1013	-993	20	unknown protein	-
109846	-871	-863	8	unknown protein	-
110127	-345	-322	23	unknown protein	-
123261	-939	-920	19	unknown protein	-
123261	-681	-663	18	unknown protein	-
110600	-172	-145	27	unknown protein	-
67605	-716	-690	26	unknown protein	-
110731	-999	-979	20	unknown protein	-
111059	-298	-284	14	unknown protein	-
111245	-151	-124	27	unknown protein	-
111442	-976	-961	15	unknown protein	-

69222	-215	-186	29	unknown protein	-
111739	-466	-437	29	unknown protein	-
69493	-820	-804	16	unknown protein	-
45445	-271	-256	15	unknown protein	-
104380	-640	-614	26	unknown protein	-
112122	-1208	-1188	20	unknown protein	-
124175	-1324	-1299	25	unknown protein	-
104838	-1067	-1050	17	unknown protein	-
57730	-1036	-1028	8	unknown protein	-
112518	-931	-921	10	unknown protein	-
105454	-391	-369	22	unknown protein	-
121082	-825	-804	21	unknown protein	-
59244	-1101	-1090	11	unknown protein	-
3488	-642	-618	24	unknown protein	-
60445	-956	-929	27	unknown protein	-
121471	-1149	-1134	15	unknown protein	-
77481	-1168	-1152	16	unknown protein	-
77780	-747	-727	20	unknown protein	-
107490	-1327	-1313	14	unknown protein	-
33650	-167	-141	26	unknown protein	-
69557	-1061	-1033	28	unknown protein	-
63382	-1133	-1125	8	unknown protein	-
26163	-1074	-1058	16	unknown protein	-

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