Tables S11. Prediction of CRE1 binding sites on genes up regulated in a *Δcre1* mutant induced with sophorose.

Protein ID	**Site 1***	**Site 2**	**Distance**	**Description**	**log2 FC (Δcre1/wt)**	**p-val**
47710	-802	-793	9	MFS permease	5.469366622	4.09589E-19
122208	-563	-545	18	Zn2Cys6 transcriptional regulator	5.191488284	4.56595E-43
50618	-1150	-1139	11	MFS permease	3.902106195	0.00012398
30465	-158	-152	6	unknown protein, WD-repeats	3.725897747	1.02183E-23
67035	-958	-950	8	unknown protein	3.33305303	1.7282E-18
102437	-1321	-1312	9	unique protein, secreted	3.28066688	7.45471E-16
58282	-1373	-1364	9	esterase family 9	2.874624778	1.93535E-05
45624	-750	-742	8	unknown protein	2.568530973	1.56194E-11
104081	-657	-651	6	coenzyme F420-dependent N5,N10-methylene tetrahydromethanopterin reductase	2.528127187	0.010505112
122240	-337	-328	9	Carnitine o-acyltransferase	2.477747967	1.5277E-05
47930	-619	-613	6	Mitochondrial oxoglutarate/malate carrier proteins	2.206416088	0.030496393
121298	-1175	-1145	30	formate dehydrogenase	2.062016661	4.69598E-06
52438	-1459	-1445	14	unknown protein	2.043845388	0.010394571
41035	-1398	-1389	9	G-protein coupled receptor protein, contains Molluscan rhodopsine C-terminal tail, possibly involved in signal transduction	1.983074388	0.015155077
21873	-889	-883	6	dihydrounknown protein-acid dehydratase	1.927417882	1.11511E-05
79345	-1160	-1151	9	unknown protein, Mpv17/PMP22 family	1.854222421	0.011982586
68122	-772	-755	17	MFS permease	1.782944386	0.029145175
119823	-678	-669	9	SAM-dependent methyltransferases	1.768952938	0.015155077
122376	-1095	-1086	9	unknown protein	1.641915423	1.5277E-05
122886	-1345	-1332	13	Tubulin beta chain 2	1.573645136	3.08517E-05
122886	-1332	-1305	27	Tubulin beta chain 2	1.573645136	3.08517E-05
120826	-1135	-1119	16	unknown protein	1.568740312	0.00228747
120826	-1119	-1094	25	unknown protein	1.568740312	0.00228747

107187	-1093	-1077	16	unknown protein	1.557728986	0.000267422
123227	-1379	-1369	10	unknown protein	1.517397555	0.002920578
45912	-1240	-1228	12	60s ribosomal protein L36 based on homology to the corresponding protein in other fungi.	1.511037344	0.000532228
76136	-166	-140	26	unknown protein	1.502298385	0.003329457
81676	-463	-457	6	salicylate hydroxylase	1.40398715	0.000248049
34112	-1179	-1166	13	ribosomal protein L22.	1.379697699	2.40481E-05
121074	-194	-188	6	homeobox transcriptional regulator	1.357140841	0.014697572
47221	-30	-21	9	Nucleoside diphosphate kinase	1.319151266	0.000188665
123771	-48	-36	12	GCD, Glutaryl-CoA dehydrogenase	1.245877242	0.001931575
75890	-1466	-1441	25	C1 tetrahydrofolate synthase, putative	1.160734188	0.000773167
79329	-306	-276	30	MFS permease	1.15937328	0.006300146
79329	-276	-264	12	MFS permease	1.15937328	0.006300146
80231	-545	-528	17	glucokinase	1.146707514	0.006227884
80231	-133	-127	6	glucokinase	1.146707514	0.006227884
121915	-894	-884	10	Translationally-controlled tumor protein homolog	1.126868825	0.001284327
121820	-279	-270	9	Methionine_syntMethionine synthasevitamin-B independent	1.105413674	0.002007961

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

References

1. Castro, L.D., Antonieto, A.C., Pedersoli, W.R., Rocha, R.S., Persinoti, G.F. and Silva, R.N. (2014) Expression pattern of cellulolytic and xylanolytic genes regulated by transcriptional factors XYR1 and CRE1 are affected by carbon source in Trichoderma reesei. *Gene expression patterns : GEP*.