Table S1. Unknown and unclassified genes regulated by changes of iron conditions

ORF (Assembly6)	ORF & Allele (Assembly19)[a]	Gene name	Description	Fold changes[b] Wt (L-Fe vs. H-Fe)
6.864	19.9673		no good homologies	2.3
6.3980	19.4244		no good homologies	2.4
6.8823	19.6808/19.14100		no good homologies	2.4
6.888	19.1681/19.9250		no good homologies	2.4
6.4069	19.4667/19.12137		no good homologies	2.5
6.5987	19.2048/19.9596		no good homologies	2.5
6.1745	19.8770		no good homologies	2.5
6.2459	19.871/19.8490		no good homologies	2.5
6.6118	19.2904/19.10422		no good homologies	2.6
6.937	19.157/19.7796		no good homologies	2.6
6.1382	19.2377		no good homologies	2.6
6.1531	19.1082/19.8683		no good homologies	2.7
6.523	19.712/19.8331		no good homologies	2.7
6.1953	19.3520		no good homologies	2.7
6.2687	19.241/19.7871		no good homologies	2.7
6.334	19.381		no good homologies	2.7
6.7041	19.1879/19.9435		no good homologies	2.7
6.7265	19.4452/19.11932		no good homologies	2.7
6.7765	19.3028/19.10546		no good homologies	2.7
6.8381	19.7300		no good homologies	2.7
6.2152	19.8683/19.1082		no good homologies	2.8
6.8245	19.3245/19.10755		no good homologies	2.8
6.5265	19.6549/19.13902		no good homologies	2.9
6.2206	19.12986/19.5540		no good homologies	2.9
6.4880	19.1318/19.8898		no good homologies	2.9
6.3731	19.3090/19.10602		no good homologies	2.9
6.5206	19.11756/19.4280		no good homologies	2.9
6.477	19.1573/19.9146		no good homologies	3.0
6.6227	19.6114/19.13533		no good homologies	3.0
6.1006	19.2548		no good homologies	3.0
6.3871	19.9913		no good homologies	3.0
6.6877	19.6728/19.14020		no good homologies	3.1
6.1879	19.3196		no good homologies	3.1
6.9047	19.5990/19.13411		no good homologies	3.1
6.4255	19.9755/19.2210		no good homologies	3.2
6.622	19.1020		no good homologies	3.2
6.8692	19.5456/19.12911		no good homologies	3.2
6.9123	19.5914/19.13335		no good homologies	3.3
6.3847	19.836/19.8456		no good homologies	3.3
6.5206	19.11756/19.4280		no good homologies	3.3
6.5733	19.1266/19.8852		no good homologies	3.4
6.687	19.4860/19.12323		no good homologies	3.4
6.468	19.5063/19.12529		no good homologies	3.5
6.4965	19.2470/19.10007		no good homologies	3.5

Table S1. Continued

ORF (Assembly6)	ORF & Allele (Assembly19)[a]	Gene name	Description	Fold changes[b] Wt (L-Fe vs. H-Fe)
6.7644	19.6516/19.13869		no good homologies	3.5
6.8385	19.7304		no good homologies	3.5
6.5758	19.3571/19.11055		no good homologies	3.6
6.6409	19.1551/19.9125		no good homologies	3.6
6.520	19.233		no good homologies	3.7
6.5472	19.11227/19.3742		no good homologies	3.7
6.8436	19.7117		no good homologies	3.7
6.747	19.1101		no good homologies	3.7
6.5651	19.3975/19.11458		no good homologies	3.8
6.3082	19.8803/19.1215		no good homologies	3.9
6.4295	19.298/19.7930		no good homologies	4.0
6.2259	19.1487/19.9064		no good homologies	4.0
6.9056	19.5981/19.13402		no good homologies	4.1
6.6757	19.545/19.8180		no good homologies	4.1
6.5230	19.4149/19.11625		no good homologies	4.3
6.4712	19.4661/19.12131		no good homologies	4.4
6.4350	19.5502		no good homologies	4.5
6.6988	19.6839/19.14129		no good homologies	4.5
6.1076	19.6491/19.13844		no good homologies	4.6
6.7828	19.6426/19.13784		no good homologies	4.7
6.3276	19.2854/19.10373		no good homologies	4.8
6.1470	19.4794/19.12258		no good homologies	4.8
6.2469	19.9702/19.2155		no good homologies	4.8
6.4257	19.2212/19.9757		no good homologies	4.8
6.1618	19.12370/19.4905		no good homologies	4.9
6.1630	19.3073/19.10585		similar to *S. cerevisiae* YLR466W	5.1
6.2006	19.8652/19.1050		no good homologies	5.2
6.6098	19.3427/19.10931		no good homologies	5.2
6.912	19.1293		no good homologies	5.2
6.7051	19.1869/19.9425		no good homologies	5.4
6.1847	19.11818		no good homologies	5.5
6.112	19.12338/19.4874		no good homologies	5.6
6.3975	19.4249/19.11724		no good homologies	5.6
6.7226	19.342/19.7975		no good homologies	5.6
6.8427	19.7126		no good homologies	5.6
6.7028	19.1892/19.9448		no good homologies	5.8
6.1265	19.1906/19.9462		no good homologies	5.9
6.2337	19.9212		no good homologies	5.9
6.4454	19.5512/19.12958		no good homologies	5.9
6.7808	19.6446/19.13804		no good homologies	5.9
6.952	19.7863/19.233		no good homologies	5.9
6.5230	19.4149/19.11625		no good homologies	6.4
6.8384	19.7303		no good homologies	6.5
6.3063	19.3790		no good homologies	7.1

Table S1. Continued

ORF (Assembly6)	ORF & Allele (Assembly19)[a]	Gene name	Description	Fold changes[b] Wt (L-Fe vs. H-Fe)
6.2837	19.4968/19.12433		no good homologies	7.2
6.8908	19.7560		no good homologies	7.2
6.3944	19.5290/19.12748		no good homologies	7.5
6.2392	19.2240		no good homologies	7.5
6.5200	19.4286/19.11762		no good homologies	7.6
6.7681	19.5261/19.12726		no good homologies	7.6
6.1279	19.1928/19.9484		no good homologies	7.7
6.5971	19.2032/19.9580		no good homologies	7.7
6.8745	19.7493		no good homologies	8.0
6.6767	19.6658		no good homologies	8.1
6.4289	19.3543/19.11027		no good homologies	8.4
6.6693	19.4547/19.12022		no good homologies	8.7
6.7720	19.6974		no good homologies	8.7
6.1891	19.9777/19.2235		no good homologies	9.7
6.4918	19.8673/19.1071		no good homologies	9.7
6.8111	19.7211		no good homologies	10.9
6.8177	19.7277		no good homologies	11.9
6.5724	19.1257		no good homologies	12.1
6.2392	19.2240		no good homologies	13.0
6.1190	19.7889		no good homologies	13.2
6.694	19.257/19.7889		no good homologies	15.5
6.9033	19.6004/19.13425		no good homologies	21.9
6.6984	19.6835		no good homologies	25.5
6.2940	19.1205/19.8796		no good homologies	27.4
6.3480	19.134		no good homologies	52.0
6.2466	19.3610/19.11093		sim to hypothetical plant protein	6.8
6.3752	19.8462/19.842		sim to hypothetical protein	2.5
6.6551	19.658/19.8274		sim to hypothetical protein	2.9
6.6018	19.725/19.8344		sim to hypothetical protein	3.5
6.44	19.12418/19.4953		Similar to *S. cerevisiae* YCL047C	3.5
6.7968	19.7042		sim to Hypothetical protein	3.5
6.4195	19.11979/19.4503		sim to hypothetical protein	3.6
6.3939	19.5295/19.12754		sim to hypothetical protein	3.8
6.6458	19.3447/19.10951		sim to hypothetical protein	4.0
6.6466	19.3439/19.10943		sim to hypothetical protein	4.5
6.6035	19.6276/19.13655		sim to hypothetical protein	5.2
6.3350	19.2653/19.10176		sim to hypothetical protein	6.4
6.1471	19.12259/19.4795		sim to hypothetical protein	25.1
6.3353	19.2650/19.10173		sim to hypothetical protein, PFC0960c	3.4
6.6440	19.1632/19.9200		sim to hypothetical protein.	4.3
6.3119	19.1708/19.9275		sim to unknown protein	3.0
6.344	19.1509/19.9084		sim to unknown protein	3.5
6.409	19.715/19.8334		sim to unknown protein	3.6
6.7135	19.6871/19.14160		sim to unknown protein	3.7

Table S1. Continued

ORF (Assembly6)	ORF & Allele (Assembly19)[a]	Gene name	Description	Fold changes[b] Wt (L-Fe vs. H-Fe)
6.4704	19.4653/19.12123		sim to unknown protein	21.9
6.154	19.9011/19.1437		sim to unknown (protein for MGC:13000)	9.5
6.3956	19.3763/19.11247		sim to unknown protein	2.7
6.3583	19.10265/19.2751		sim to unknown protein	3.8
6.979	19.1350/19.8930		sim to unnamed protein product	4.5
6.4438	19.5596/19.13041		sim to WD-repeat protein	2.7
6.777	19.2011/19.9562		sim to wsv320	3.7
6.3110	19.4276/19.11752		sim to XMAP4	3.4
6.3794	19.13148/19.5725		sim to YBR1006	3.2
6.3313	19.5036/19.12503		sim to Ydr425wp; CAI: 0.15	3.7
6.8960	19.7612		similar to *S. cerevisiae* YHR109W	2.3
6.6297	19.5079/19.12545	*CDR4*	ABC transporter	2.4
6.6213	19.6601		Low complexity orf	4.6
6.1102	19.1090/19.8691		Q-rich orf	4.1
6.3501	19.5190/19.12657		questionable orf	4.8
6.2885	19.4486		questionable orf	6.0
6.4135	19.746/19.8365		sim to BcDNA.GH08385	2.6
6.3219	19.1032/19.8634		sim to bZIP protein similar to ATF-2 (CRE-BP1, a cAMP response element)	3.1
6.5361	19.2127/19.9674		sim to C terminus of orf19.9674	3.7
6.5601	19.9493/19.1938		sim to CG11274 gene product	2.5
6.3419	19.5203/19.12670		sim to CG15040 gene product	5.3
6.171	19.13044/19.5601		sim to conserved hypothetical protein	3.2
6.1900	19.2826/19.10344		no good homologies	3.4
6.2032	19.4465/19.11945		sim to mkpA	5.5
6.246	19.385/19.8015		P-subunit of Glycine cleavage system	2.6
6.6496	19.427/19.8057		sim to ORF YBR275c	3.7
6.3363	19.6498/19.13851		sim to *S. cerevisiae* YDL115c	2.9
6.6387	19.1418/19.8994		sim to *S. cerevisiae* YGL233w	3.0
6.4805	19.276/19.7908		sim to *S. cerevisiae* YGR177c	2.3
6.3260	19.4326/19.11801		sim to *S.cerevisiae* YOR308c	2.6
6.5923	9.29/19.7700		no good homologies	4.2
6.2716	19.8257/19.643		sim to protein of unknown function	4.6
6.6057	19.4163/19.11639		sim to Rhf1	2.6
6.1899	19.10343		sim to SgcA	3.3
6.6096	19.3429/19.10933		sim to TipC	3.1
6.236	19.4145/19.11621		N term Fungal Zn2Cys6 Cluster domain	4.6
6.2094	19.8043/19.413		Sim to transcription factor KIYAP1	2.5
6.1795	19.8298/19.681		Similar to fungal AP1-like transcription factor	10.7
6.3344	19.4647/19.12116		Transcriptional activator of respiratory genes	77.4
6.3950	19.912/19.8530		no good homologies	3.7
6.3448	19.5205/19.12672		weak sim to A.thal orf At5g51150	3.1

Table S1. Continued

ORF (Assembly6)	ORF & Allele (Assembly19)[a]	Gene name	Description	Fold changes[b] Wt (L-Fe vs. H-Fe)
6.950	19.7818		similar to *S. cerevisiae* YAL011W	4.1
6.3233	19.1732/19.9300		similar to *S.cerevisiae* YBL004w	2.3
6.2579	19.10876/19.3369		similar to *S. cerevisiae* YBL049W	3.4
6.6956	19.5180/19.12647		similar to *S. cerevisiae* YBL064c	2.6
6.7914	19.4615/19.12085		similar to *S. cerevisiae* YBR095C	2.5
6.5332	19.1588/19.9161		similar to *S. cerevisiae* YBR269C	3.6
6.1702	19.14/19.7687		similar to *S. cerevisiae* YBR287W	2.8
6.7349	19.12326/19.4862		similar to *S. cerevisiae* YDR084C	2.8
6.1319	19.2226		similar to *S. cerevisiae* YDR093W	3.3
6.2773	19.1307/19.8887		similar to *S. cerevisiae* YDR438W	2.6
6.1991	19.7882/19.251		similar to *S. cerevisiae* YDR533C	4.1
6.4230	19.4894/19.12359		similar to *S. cerevisiae* YER010C	2.5
6.1621	19.12367/19.4901		similar to *S. cerevisiae* YER175C	9.2
6.764	19.8267/19.652		similar to *S. cerevisiae* YER041W	3.8
6.344	19.1509/19.9084		similar to *S. cerevisiae* YFR022W	3.5
6.2086	19.4735/19.12197		similar to *S. cerevisiae* YGL159W	3.1
6.1085	19.1597/19.9165		similar to *S. cerevisiae* YGR106C	2.9
6.2463	19.3607/19.11090		similar to *S. cerevisiae* YGR110W	7.6
6.4532	19.6220/19.13601		similar to *S. cerevisiae* YGR134W	2.7
6.794	19.11467/19.3984		similar to *S. cerevisiae* YGR237C	4.4
6.1520	19.5067/19.12533		similar to *S. cerevisiae* YHR081W	3.5
6.1262	19.1862/19.9418		similar to *S. cerevisiae* YHR087W	4.1
6.179	19.4760/19.12224		similar to *S. cerevisiae* YIL110W	2.4
6.1766	19.12155/19.4686		similar to *S. cerevisiae* YIL151C	2.7
6.7722	19.6976		similar to *S. cerevisiae* YJL163C	2.8
6.1037	19.9785/19.2244		similar to *S. cerevisiae* YJR096W	3.1
6.4283	19.3537/19.11021		similar to *S. cerevisiae* YKL086W	11.9
6.8121	19.7221		similar to *S. cerevisiae* YKR029C	3.6
6.3581	19.9748/19.2202		similar to *S. cerevisiae* YKR043	7.5
6.8457	19.7096		similar to *S. cerevisiae* YLR001C	2.7
6.2441	19.12692/19.5227		similar to *S. cerevise* YLR021W	5.4
6.557	19.5754/19.13177		similar to *S. cerevisiae* YLR023C	2.6
6.356	19.1557		similar to *S. cerevisiae* YLR137W	4.4
6.7668	19.5274/19.12739		similar to *S. cerevisiae* YLR187W	2.3
6.5742	19.1667/19.9236		similar to *S. cerevisiae* YLR247C	3.0
6.5916	19.22/19.7693		similar to *S. cerevisiae* YLR251w	2.3
6.2655	19.7693/19.22		similar to *S. cerevisiae* YLR251W	2.9
6.8391	19.7310		similar to *S. cerevisiae* YML128C	5.2
6.3559	19.9994/19.2458		similar to *S.cerevisiae* YMR140W	5.2
6.5491	19.2703/19.10218		similar to *S. cerevisiae* YMR171C	3.0
6.3813	19.2564/19.10096		similar to *S. cerevisiae* YMR269W	3.4
6.438	19.4730/19.12192		similar to *S. cerevisiae* YNL050C	3.2
6.437	19.4731/19.12193		similar to *S. cerevisiae* YNL051C	3.4
6.2223	19.11087/19.3604		similar to *S. cerevisiae* YNL215W	4.6

Table S1. Continued

ORF (Assembly6)	ORF & Allele (Assembly19)[a]	Gene name	Description	Fold changes[b] Wt (L-Fe vs. H-Fe)
6.4244	19.1281/19.8868		similar to *S. cerevisiae* YNL245C	2.5
6.7854-1	19.13758/19.6400		similar to *S. cerevisiae* YOL032W	2.8
6.7854-2	19.13758/19.6400		similar to *S. cerevisiae* YOL032W	3.3
6.1835	19.11208/19.3724		similar to *S. cerevisiae* YOR004W	2.6
6.8665	19.5429/19.12884		similar to *S. cerevisiae* YOR080W	2.4
6.331	19.8936/19.1356		similar to *S. cerevisiae* YOR251C	2.5
6.1001	19.1356/19.8936		similar to *S. cerevisiae* YOR251C	2.1
6.1343	19.1341/19.8921		similar to *S. cerevisiae* YOR267C	3.5
6.8604	19.7444		similar to *S. cerevisiae* YOR352W	3.5
6.4688	19.10246/19.2732		similar to *S. cerevisiae* YPL120W	3.7
6.7361	19.4850/19.12313		similar to *S. cerevisiae* YPL260W	2.8
6.2676	19.1240/19.8825		similar to *S. cerevisiae* YPR117W	3.9
6.4335	19.3396/19.10899		similar to *S. cerevisiae* HCH1; high copy Hsp90 supressor	-2.1
6.6949	19.3096/19.10608		no good homologies	-29.3
6.4418	19.4052/19.11534		no good homologies	-11.3
6.5180	19.9951		no good homologies	-11.1
6.2070	19.378/19.8011		no good homologies	-7.0
6.5407	19.6186		no good homologies	-5.6
6.1028	19.9185		no good homologies	-5.0
6.1246	19.2452/19.9988		no good homologies	-4.9
6.6407	19.1549/19.9123		no good homologies	-4.9
6.819	19.1179		no good homologies	-4.8
6.1979	19.1953/19.9508		no good homologies	-4.4
6.7151	19.6887/19.14176		no good homologies	-4.2
6.6048	19.4942/19.12408		no good homologies	-3.8
6.5314	19.3716/19.11201		no good homologies	-3.7
6.2290	19.3773		no good homologies	-3.6
6.214	19.9351/19.1785		no good homologies	-3.4
6.818	19.1178/19.8768		no good homologies	-3.1
6.805	19.11599/19.4117		no good homologies	-2.9
6.8565	19.7405		no good homologies	-2.9
6.6381	19.1412/19.8988		no good homologies	-2.9
6.3105	19.8888/19.1308		no good homologies	-2.8
6.6228	19.6113/19.13532		no good homologies	-2.6
6.9054	19.5983/19.13404		no good homologies	-2.6
6.8318	19.5329/19.12789		no good homologies	-2.5
6.8172	19.7272		no good homologies	-2.5
6.4301	19.292/19.7924		no good homologies	-2.5
6.7184	19.6920		no good homologies	-2.3
6.8937	19.7589		no good homologies	-2.2
6.279	19.11989/19.4514		no good homologies	-2.1
6.5580	19.2328/19.9864		no good homologies	-2.1
6.2045	19.3587		no good homologies	-2.1

Table S1. Continued

ORF (Assembly6)	ORF & Allele (Assembly19)[a]	Gene name	Description	Fold changes[b] Wt (L-Fe vs. H-Fe)
6.6455	19.1617/19.9184		similar to *S. cerevisiae* YDR282C	-2.1
6.4110	19.2586/19.10117		no good homologies	-2.0
6.5406	19.6185		PCP1, phyogenetically conserved protein	-2.7
6.5632	19.326/19.7958		PCP3, phylogenetically conserved protein	-2.3
6.6447	19.1625/19.9193		sim to CG3214 gene product	-5.3
6.7278	19.899/19.8518		sim to CG3792 gene product	-2.0
6.5878	19.10653/19.3141		sim to hypothetical protein	-2.1
6.3509	19.3962/19.11444		sim to Hypothetical protein C33G8.2	-5.8
6.7096	19.1477/19.9052		similar to *S. cerevisiae* YGL010W	-3.4
6.206	19.12836/19.5381		similar to *S. cerevisiae* YGL014w	-2.4
6.6471	19.3434/19.10938		similar to *S. cerevisiae* YGR067C	-2.5
6.2176	19.1140/19.8733		similar to *S. cerevisiae* YGR235C	-2.7
6.4002	19.2938/19.10455		similar to *S. cerevisiae* YLR077W	-4.1
6.2902	19.166		sim to orf, len: 964, CAI: 0.15, possible regulatory protein	-2.1
6.4979	19.3480/19.10984		no good homologies	-2.2
6.7922	19.4623/19.12093		sim to ORFveg132; similar to *C. elegans* ORF F59B10.1 encoded by EMBL Accession Number Z49132	-2.3
6.253	19.4358/19.11836		sim to putative protein	-4.1
6.4994	19.4517/19.11992		sim to unique hypothetical	-2.1
6.3013	19.8830/19.1246		sim to unknown	-2.8
6.3235	19.1730/19.9298		similar to *S. cerevisiae* YDL002C	-2.0
6.3417	19.5201/19.12668		similar to *S. cerevisiae* YER050C; mitochondrial ribosome small subunit component	-2.1
6.8872	19.6759/19.14051		sim to *S. cerevisiae* YER132C	-2.3
6.7660	19.5282/19.12747		weak similarity to *S. cerevisiae* YHR131C	-2.5
6.6729	19.517/19.8148		Transcriptional activator of CYC1	-2.5
6.4515	19.5646/19.13091		sim to Ypl034wp	-3.5
6.1200	no match	*DPH5*	Diphthamide biosynthesis	-11.5
6.6785-1	19.6676	*DPH5*	Diphthamide biosynthesis	-2.4
6.6785-2	19.6676	*DPH5*	Diphthamide biosynthesis	-6.0
6.6663	19.2953/19.10470	*TOM20*	Outer membrane translocase	-2.2
6.2476	19.2163/19.9709		similar to *S. cerevisiae* YBR074W	-2.1
6.8359	19.5370/19.12830		similar to *S. cerevisiae* YBR075W	-2.9
6.6575	19.2777/19.10293		similar to *S. cerevisiae* YBR162C	-4.9
6.31	19.4496/19.11972		similar to *S. cerevisiae* YBR187W	-2.7
6.8221	19.972/19.8587		similar to *S. cerevisiae* YBR228W	-2.5
6.3754	19.4907/19.12373		similar to *S. cerevisiae* YCR061W	-4.9
6.8160	19.7260		similar to *S. cerevisiae* YDL124W	-2.0
6.2478	19.1982/19.9538		similar to *S. cerevisiae* YDR031W	-4.3
6.8884	19.6747/19.14039		similar to *S. cerevisiae* YDR051C	-6.3
6.8169	19.7269		similar to *S. cerevisiae* YDR071C	-2.1
6.1633	19.3076/19.10588		similar to *S. cerevisiae* YDR100W	-3.5

Table S1. Continued

ORF (Assembly6)	ORF & Allele (Assembly19)[a]	Gene name	Description	Fold changes[b] Wt (L-Fe vs. H-Fe)
6.2917	19.3799/19.11280		similar to *S. cerevisiae* YDR233C	-3.9
6.1264	19.1864/19.9420		similar to *S. cerevisiae* YDR333C	-3.4
6.5521	19.6328		similar to *S. cerevisiae* YDR511W	-2.5
6.1146	19.1372/19.8952		similar to *S. cerevisiae* YEL001C	-3.5
6.6133	19.2889/19.10407		similar to *S. cerevisiae* YEL044W	-3.3
6.8584	19.7424	*NSA2*	similar to *S. cerevisiae* YER126C	-3.0
6.6678	19.12007/19.4532		similar to *S. cerevisiae* YER156C	-4.6
6.7	19.42		similar to *S. cerevisiae* YER163C	-3.4
6.6326	19.4381/19.11859		similar to *S. cerevisiae* YFL004W	-2.3
6.637	19.10100/19.2568		similar to *S. cerevisiae* YFL010C	-2.5
6.8163	19.7263		similar to *S. cerevisiae* YFR006W	-2.3
6.4061	19.3915/19.11397		similar to *S. cerevisiae* YFR044C	-2.3
6.3382	19.5054/19.12521		similar to *S. cerevisiae* YFR047C	-3.2
6.3566	19.2275/19.9815		similar to *S. cerevisiae* YGL068W	-2.7
6.3266	19.2864/19.10382		similar to *S. cerevisiae* YGL101W	-3.0
6.7531	19.3836/19.11317		similar to *S. cerevisiae* YGR001C	-2.7
6.383	19.13978/19.6686		similar to *S. cerevisiae* YGR145W	-4.7
6.7365	19.4846/19.12309		similar to *S. cerevisiae* YGR210C	-2.1
6.7819	19.6435/19.13793		similar to *S. cerevisiae* YGR243W	-5.0
6.8031	19.7131		similar to *S. cerevisiae* YHL021C	-3.7
6.1829	19.11214/19.3730		similar to *S. cerevisiae* YIL027C	-2.0
6.3450	19.5207/19.12674		similar to *S. cerevisiae* YIL103W	-5.2
6.156	19.163/19.7797		similar to *S. cerevisiae* YIL145C	-2.5
6.8054	19.7154		similar to *S. cerevisiae* YJL069C	-2.0
6.6980	19.5156/19.12623		similar to *S. cerevisiae* YJL097W	-3.2
6.8122	19.7222		similar to *S. cerevisiae* YJL104W	-2.4
6.7788	19.3051/19.10569		similar to *S. cerevisiae* YJR116W	-3.0
6.3719	19.2790/19.10306		similar to *S. cerevisiae* YKL018W	-4.1
6.117	19.2115/19.9663		similar to *S. cerevisiae* YKL027W	-3.0
6.4123	19.5553/19.12999		similar to *S. cerevisiae* YKL069W	-2.5
6.589	19.4396/19.11874		similar to *S. cerevisiae* YKR016W	-3.2
6.1502	19.11012/19.3528		similar to *S. cerevisiae* YKR074W	-2.8
6.6558	19.665/19.8282		similar to *S. cerevisiae* YLR186W	-2.1
6.4867	19.2998/19.10515		similar to *S. cerevisiae* YLR435W	-2.2
6.159	19.93/19.7739		similar to *S. cerevisiae* YMR002W	-5.3
6.252	19.4357/19.11835		similar to *S. cerevisiae* YMR115W	-2.2
6.7030	19.1890/19.9446		similar to *S. cerevisiae* YMR210w	-3.1
6.1778	19.3288/19.10798		similar to *S. cerevisiae* YNL123W	-3.4
6.5889	19.2257/19.9797		similar to *S. cerevisiae* YNR021W	-2.6
6.2043	19.3585/19.11069		similar to *S. cerevisiae* YNR046W	-2.1
6.6934	19.3111/19.10623		similar to *S. cerevisiae* YOL154W	-2.1
6.4855	19.5783/19.13205		similar to *S. cerevisiae* YOR021C	-2.2
6.5264	19.6550/19.13903		similar to *S. cerevisiae* YOR228C	-4.4
6.1483	19.10685/19.3175		similar to *S. cerevisiae* YOR356W	-3.9

Table S1. Continued

ORF (Assembly6)	ORF & Allele (Assembly19)[a]	Gene name	Description	Fold changes[b] Wt (L-Fe vs. H-Fe)
6.4409	19.11525/19.4043		similar to *S. cerevisiae* YPR115W	-4.0
6.6573	19.680/19.8297		similar to *S. cerevisiae* YPL063W	-2.8
6.7606	19.6062/19.13483		similar to *S. cerevisiae* YPL098C	-4.1
6.7082	19.489/19.8119		similar to *S. cerevisiae* YPL170W	-2.8
6.2205	19.12987/19.5541		similar to *S. cerevisiae* YPL184C	-2.5
6.247	19.384/19.8014		similar to *S. cerevisiae* YPL247C	-3.4
6.1848	19.11817/19.4342		similar to *S. cerevisiae* YPR009W	-2.9
6.7663	19.5279/19.12744		similar to *S. cerevisiae* YPR100W	-3.5

[a] Identifical or the most closely matched sequences in the assembly 19 of *C. albicans* genome project.

[b] Fold changes are derived from the average of four individual comparisons as described in experimental procedures. The positive and negative (shaded) values represent the transcripts having a higher expression level at the low- and high-iron conditions, respectively.