Table 4: Yeast genes identified under iron overload conditions, ranked by fitness score and showing the homologous genes in humans, if any, obtained by SGD Best Hits BLASTP.

Systematic	Standard	Alias	Fitness	Human Best Hit <sup>b</sup>	Ln (E-value) <sup>c</sup>	Ensembl Gene ID	HGNC Gene
Name	Gene Name		Score <sup>a</sup>	Ensembl Peptide ID			Name <sup>d</sup>
YPL057C	SUR1	LPE15 CSG1 BCL21	-3.69	·			
YBR036C	CSG2	CLS2	-2.79				
YLR374C			-2.53				
YPL226W	NEW1		-2.47	ENSP00000292808	1.00E-44	ENSG00000161204	ABCF3
YKL053C-A	MDM35		-2.44	ENSP00000304997	4.00E-05	ENSG00000170855	TRIAP1
YLR220W	CCC1		-2.24				
YPL241C	CIN2		-2.21				
YOL001W	PH080	VAC5 TUP7 AGS3	-2.20				
YOL041C	NOP12		-2.16	ENSP00000345961	1.00E-20	ENSG00000188739	RBM34
				ENSP00000355565	1.00E-20	ENSG00000188739	RBM34
				ENSP00000354765	1.00E-20	ENSG00000188739	RBM34
YML047C	PRM6		-2.05				
YLR131C	ACE2		-1.96	ENSP00000250916	1.00E-11	ENSG00000129911	KLF16
YCR031C	RPS14A	RPL59 CRY1	-1.94	ENSP00000311028	2.00E-32	ENSG00000164587	RPS14
YMR284W	YKU70	NES24 HDF1	-1.91	ENSP00000353192	6.00E-04	ENSG00000196419	XRCC6
YER019W	ISC1		-1.91	ENSP00000258052	2.00E-26	ENSG00000135587	SMPD2
YOR136W	IDH2		-1.86	ENSP00000299518	3.00E-86	ENSG00000166411	IDH3A
YPL205C			-1.85				
YOL006C	TOP1	MAK17 MAK1	-1.81	ENSP00000328835	1.00E-261	ENSG00000184428	TOP1MT
YMR202W	ERG2	END11	-1.73	ENSP00000353935	1.00E-17	ENSG00000147955	OPRS1
YOR085W	OST3		-1.73	ENSP00000354649	1.00E-09	ENSG00000102158	
				ENSP00000304504	1.00E-09	ENSG00000102158	
YDR004W	RAD57		-1.69	ENSP00000340560		ENSG00000182185	RAD51L1
YER090W	TRP2		-1.60				
YGL212W	VAM7	VPS43	-1.59				
YPL195W	APL5	YKS4	-1.58	ENSP00000341579	2.00E-91	ENSG00000065000	AP3D1
YPR032W	SR07	SOP1 SNI1	-1.56	ENSP00000273666	2.00E-10	ENSG00000145087	STXBP5L
YIL069C	RPS24B	RPS24EB	-1.55	ENSP00000350214	4.00E-18	ENSG00000138326	RPS24
				ENSP00000361430	4.00E-18	ENSG00000138326	RPS24
				ENSP00000361435	4.00E-18	ENSG00000138326	RPS24
				ENSP00000336696	4.00E-18	ENSG00000138326	RPS24
				ENSP00000354074	4.00E-18	ENSG00000138326	RPS24

YNL170W			-1.55				
YIR009W	MSL1	YIB9 YIB9w	-1.48	ENSP00000243563	2.00E-08	ENSG00000077312	SNRPA
YNR004W		,	-1.47				
YDL118W			-1.47				
YCR028C	FEN2		-1.42				
YPR087W	VPS69		-1.41				
YOL064C	MET22	HAL2	-1.39				
YJL024C	APS3	YKS7	-1.38	ENSP00000325369	2.00E-28	ENSG00000177879	AP3S1
YHR200W	RPN10	SUN1 MCB1	-1.33	ENSP00000357878	3.00E-48	ENSG00000159352	PSMD4
				ENSP00000357876	7	ENSG00000159352	
YPL213W	LEA1		-1.30	ENSP00000254193	2.00E-04	ENSG00000131876	SNRPA1
YPL178W	CBC2	CBP20 SAE1 MUD13	-1.30	ENSP00000326806	9.00E-34	ENSG00000114503	NCBP2
YGL127C	SOH1	MED31	-1.29	ENSP00000225728	6.00E-09	ENSG00000108590	MED31
				ENSP00000370484	6.00E-09	ENSG00000108590	MED31
YMR289W			-1.26				
YDR083W	RRP8		-1.26	ENSP00000254605	1.00E-34	ENSG00000132275	KIAA0409
YPL214C	THI6		-1.26				
YMR262W			-1.22				
YOR014W	RTS1	SCS1	-1.21	ENSP00000329009	1.00E-140	ENSG00000078304	PPP2R5C
YER028C	MIG3		-1.21	ENSP00000309570	1.00E-09	ENSG00000118263	KLF7
YGL025C	PGD1	MED3 HRS1	-1.18				
YOL012C	HTZ1	H2A.F/Z H2AZ HTA3	-1.13	ENSP00000340708	2.00E-28	ENSG00000105968	H2AFV
YPR164W	MMS1	SLM6 RTT108	-1.06				
YOR061W	CKA2	YOR29-12	-1.04	ENSP00000217244	2.00E-93	ENSG00000101266	CSNK2A1
				ENSP00000371400	2.00E-93	ENSG00000101266	CSNK2A1
				ENSP00000341595	2.00E-93	ENSG00000101266	CSNK2A1
				ENSP00000339247	2.00E-93	ENSG00000101266	CSNK2A1
YDR363W	ESC2		-0.96				
YMR251W-A	HOR7		-0.91				
YOL128C	YGK3		-0.91	ENSP00000264235	9.00E-54	ENSG00000082701	GSK3B
YER114C	BOI2	BEB1	-0.88	ENSP00000347883	5.00E-03	ENSG00000166689	PLEKHA7
YDR176W	NGG1	SWI7 ADA3	-0.85				
YMR310C			-0.84	ENSP00000354812	3.00E-06	ENSG00000198917	C9orf114
				ENSP00000354931	3.00E-06	ENSG00000198917	C9orf114
YLR337C	VRP1	YLR337W MDP2 END5	-0.82				
YMR276W	DSK2		-0.81	ENSP00000345195	3.00E-09	ENSG00000188021	UBQLN2
				ENSP00000364060	3.00E-09	ENSG00000188021	UBQLN2
YMR190C	SGS1		-0.79	ENSP00000318727	1.00E-109	ENSG00000004700	RECQL

YOR036W	PEP12	VPT13 VPS6 VPL6	-0.78	ENSP00000236419	1.00E-04	ENSG00000117758	STX12
				ENSP00000363054	1.00E-04	ENSG00000117758	STX12
YPL140C	MKK2	SSP33 LPI6	-0.71	ENSP00000178640	1.00E-50	ENSG00000137764	MAP2K5
YPL263C	KEL3	·	-0.53	ENSP00000270583	8.00E-37	ENSG00000104731	KLHDC4
YMR244W			-0.53				
YER017C	AFG3	YTA10	0.15	ENSP00000269143	1.00E-261	ENSG00000141385	AFG3L2
YGL064C	MRH4		0.46	ENSP00000362687	4.00E-18	ENSG00000107625	DDX50
				ENSP00000277804	4.00E-18	ENSG00000107625	DDX50
YDR528W	HLR1		0.53				
YLR315W	NKP2		0.87				
YLR233C	EST1		0.94				
YLR206W	ENT2		0.99	ENSP00000370895	8.00E-25	ENSG00000176177	ENTHD1
YGL136C	MRM2		1.05	ENSP00000327660	3.00E-24	ENSG00000122687	FTSJ2
YGR034W	RPL26B		1.15	ENSP00000370506	2.00E-24	ENSG00000197947	
YPR066W	UBA3		1.29	ENSP00000354340	3.00E-66	ENSG00000144744	UBE1C
YHR051W	COX6		1.65	ENSP00000317780	8.00E-12	ENSG00000178741	COX5A
YJL056C	ZAP1	ZRG10	2.02	ENSP00000295208	7.00E-29	ENSG00000144026	ZNF514
YHR167W	THP2		2.21				
YGL071W	RCS1	AFT1	3.09				
YHR073W	OSH3		3.34	ENSP00000315331	2.00E-57	ENSG00000070882	OSBPL3

<sup>&</sup>lt;sup>a</sup>The fitness score is a measure of the relative growth of a particular deletion mutant in the treatment and control media.

<sup>&</sup>lt;sup>b</sup> Information for homologous genes in humans was obtained from SGD's model organism BLASTP best hits, which contains the results of NCBI BLASTP analysis using the protein sequence of each *S. cerevisiae* ORF as the query sequence against the predicted protein sequences in humans. Blank fields indicate absence of a significant hit in the human database.

<sup>&</sup>lt;sup>c</sup>The expect threshold (E-value) represents the number of hits expected to be found by chance.

<sup>&</sup>lt;sup>d</sup>Gene name as indicated by the HUGO Gene Nomenclature Committee (HGNC).