SUPPLEMENTAL MATERIAL

Mittra et al., http://www.jem.org/cgi/content/full/jem.20121368/DC1

Table S1. Primers used for qPCR reactions

Gene	Forward primer	Reverse primer
UbH LmxM.08_29.2300	5′-AACGTGAACAACTGGATGTGCGTC-3′	5′-ATGGTACCAAGCTTGACACATGCC-3′
LIT1 LmxM.30.3070	5′-TATGTGTTCTCCGTGGCGAAGTCT-3′	5′-CACAGCAATCAGGGCAAGCAAGAA-3′
LFR1 LmxM.29.1610	5′-GCAACGTGCTTTGTCAACCTGAGA-3′	5′-ATCTCGGCATTCAGCCTCACATCT-3′
CPB LmxM.08.1070	5′-TCAAGGTGAACGAGTGCCACAAGA-3′	5′-AAGTACGGCGAGCACTTACCATCA-3′
ATG8 LmxM.19.1630	5′-ACAAGAGCAAGTTCTTGGTACCGC-3′	5′-AGGTCGCTCATGAGAGTGCTGTTT-3′
ATG8A LmxM.19.0870	5′-ACATCTTCGACGCCTTCAAGCA-3′	5′-GGAGCCAAGCAGGTTTGGGTTATT-3′
ATG4.1 LmxM.31.3890	5′-AAAGGAGAGGATATCGCGGCTGTT-3′	5′-ACCTTGTGCGTGAAAGGCAATCAG-3′
APX LmxM.33.0070	5′-TGCGGTGAATGCCACATCAAGTTC-3′	5′-AAGCATCATCAGCTTCGTCGTTGC-3′
Amastin-like 1 LmxM.08.0760	5′-AGGTGTGATGTGCTGAACGACGAT-3′	5′-ACGGGAGCATCAGGAAGATGATGT-3′
Amastin-like 2 LmxM.08.0770	5′-CATCTTCGTGTACGGCTTTGCGTT-3′	5′-TTCGGTAAGTCACCACCATGAGCA-3′
P27 LmxM.28.0980	5′-TTACCGCTTCCGCTATAACGTGCT-3′	5′-ACCACACCGTGTAGATCACGACAA-3′
ribosomal 60S L5 LmxM.34.1900	5′-GTGCTGCAGGACAAGACGAAGTTT-3′	5′-TGCGCAATGATGTCCTTGTTCGTG-3′
eIF-3 subunit LmxM.36.3880	5′-TCAAGACGCCCTTCACCACTTTCT-3′	5′-AGCGGTTAATCACCTCGTTCTCGT-3′

Table S2. SL RNA-seq analysis of *L. amazonensis* promastigotes cultured with or without iron

Gene ID	Product description	Rep 1		Rep 2		Fold change			P-value
		Fe^+	Fe^-	Fe^+	Fe^-	Rep 1	Rep 2	$\log_2$	
LmxM.08_29.0620	ABC transporter, putative	4,451	95,447	17,859	97,488	7.88	4.16	2.60	0.00
LmxM.30.3070	**iron/zinc transporter protein [LIT1]**	75	870	148	1,244	4.26	6.40	2.48	0.00
LmxM.29.1610	**ferric reductase [LFR1]**	47	427	179	1,472	3.34	6.26	2.42	0.00
LmxM.04.0200	surface antigen-like protein	6	77	20	137	4.72	5.22	2.37	0.00
LmxM.30.1190	hypothetical protein, unknown function	68	843	176	964	4.56	4.17	2.23	0.00
LmxM.14.1360	myo-inositol-1-phosphate synthase	761	9,029	2,204	11,416	4.36	3.95	2.15	0.00
LmxM.33.1730	unspecified product	11	93	46	267	3.11	4.42	2.02	0.00
LmxM.25.1700	hypothetical protein, conserved	4	83	44	184	7.62	3.19	1.98	0.00
LmxM.19.0870	ATG8/AUT7/APG8/PAZ2, putative	88	866	290	1,395	3.62	3.66	1.96	0.00
LmxM.23.1680	hypothetical protein, conserved	20	407	645	2,862	7.48	3.38	1.95	0.01
LmxM.08.0760	amastin-like protein, putative	5	41	26	120	3.01	3.52	1.75	0.01
LmxM.28.0980	hypothetical protein, conserved [P27]	9	104	61	166	4.25	2.07	1.45	0.01
LmxM.09.0150	ATG8/AUT7/APG8/PAZ2, putative [ATG8C.1]	20	104	30	306	1.91	7.77	2.14	0.00
LmxM.19.0820	ATG8/AUT7/APG8/PAZ2, putative	509	3,025	1,164	3,771	2.18	2.47	1.31	0.01
LmxM.24.1260	amastin-like surface protein–like protein	16	98	60	189	2.25	2.40	1.29	0.02
LmxM.24.1270	amastin-like surface protein–like protein	107	733	272	643	2.52	1.80	1.22	0.01
LmxM.08.0770	amastin-like protein, putative	5	20	20	67	1.47	2.55	1.12	0.08
LmxM.08.1080	cathepsin L–like protease, putative	198	1,726	867	1,590	3.20	1.40	1.15	0.03
LmxM.08.1070	cathepsin L–like protease, putative	5	34	22	46	2.50	1.59	0.97	0.11
LmxM.29.0270	AUT2/APG4/ATG4 cysteine peptidase, putative	27	126	83	201	1.71	1.84	0.92	0.08
LmxM.36.3880	eukaryotic translation initiation factor 3 subunit, putative	711	642	1,518	595	0.33	0.30	−1.55	0.00
LmxM.34.1230	short chain dehydrogenase, putative	1,955	1,668	2,901	1,240	0.31	0.33	−1.55	0.01
LmxM.34.1430	60S ribosomal protein L2, putative	301	255	528	220	0.31	0.32	−1.56	0.00
LmxM.34.1540	reiske iron-sulfur protein precursor, putative	3,296	2,613	5,840	2,235	0.29	0.29	−1.67	0.00
LmxM.26.0010	brix domain containing–like protein	266	191	534	217	0.26	0.31	−1.71	0.00
LmxM.05.0140	nucleolar RNA helicase II, putative	657	501	1,516	533	0.28	0.27	−1.76	0.00
LmxM.36.2360	tyrosine aminotransferase, putative	1,882	1,576	5,875	1,883	0.31	0.24	−1.77	0.00
LmxM.08_29.0030	ribosomal protein L3–like protein	11	9	62	20	0.30	0.25	−1.86	0.00
LmxM.07.0040	hypothetical protein, conserved	65	37	80	30	0.21	0.29	−1.97	0.00
LmxM.07.0800	flavoprotein subunit–like protein	190	138	517	141	0.27	0.21	−1.98	0.00
LmxM.25.0920	hypothetical protein, conserved	275	115	230	98	0.15	0.32	−2.24	0.00
LmxM.14.0080	hypothetical protein, conserved	36	14	32	12	0.14	0.29	−2.32	0.00
LmxM.32.1140	hypothetical protein, conserved	8,979	5,067	19,944	3,804	0.21	0.15	−2.38	0.00
LmxM.08.0290	iron superoxide dismutase	320	105	564	175	0.12	0.24	−2.48	0.00

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Table S2. SL RNA-seq analysis of *L. amazonensis* promastigotes cultured with or without iron *(Continued)*

Gene ID	Product description	Rep 1		Rep 2		Fold change			P-value
		Fe^+	Fe^-	Fe^+	Fe^-	Rep 1	Rep 2	$\log_2$	
LmxM.30.1200	hypothetical protein, unknown function	1,347	644	3,783	661	0.18	0.13	−2.60	0.00
LmxM.36.4520	hypothetical protein, conserved	66	21	33	14	0.12	0.32	−2.60	0.00
LmxM.02.0460	hypothetical protein, conserved	788	124	1,078	196	0.06	0.14	−3.45	0.00
LmxM.34.3890	calmodulin-like protein, EF hand containing protein	170	24	37	14	0.05	0.29	−3.71	0.00
LmxM.18.0510	aconitase, putative	976	102	309	121	0.04	0.30	−3.81	0.00
LmxM.05.1030	hypothetical protein, conserved	348	21	52	19	0.02	0.28	−4.68	0.00

The Gene ID and product description are from TriTrypDB version 4.0, with additional annotation added in brackets, e.g. [LIT1]. Genes in bold encode proteins discussed throughout the paper. The columns labeled Rep 1 and Rep 2 contain the raw number of reads mapped to each gene for replicate-independent cultures of promastigotes grown in medium with (Fe^+) or without (Fe^-) iron. The fold change columns numbers for Rep 1 and Rep 2 represent the median-normalized ratio of reads from the Fe^+/Fe^- libraries. The $\log_2$ fold change and p-values were calculated by edgeR. The first 11 rows show all genes with threefold or greater up-regulation in both replicates, whereas the bottom 20 rows show those with threefold or greater down-regulation. Genes in the middle were selected from those that showed less consistent up-regulation but were confirmed by qPCR.