

Multi-omic profiling to assess the effect of iron starvation in *Streptococcus pneumoniae*

TIGR4

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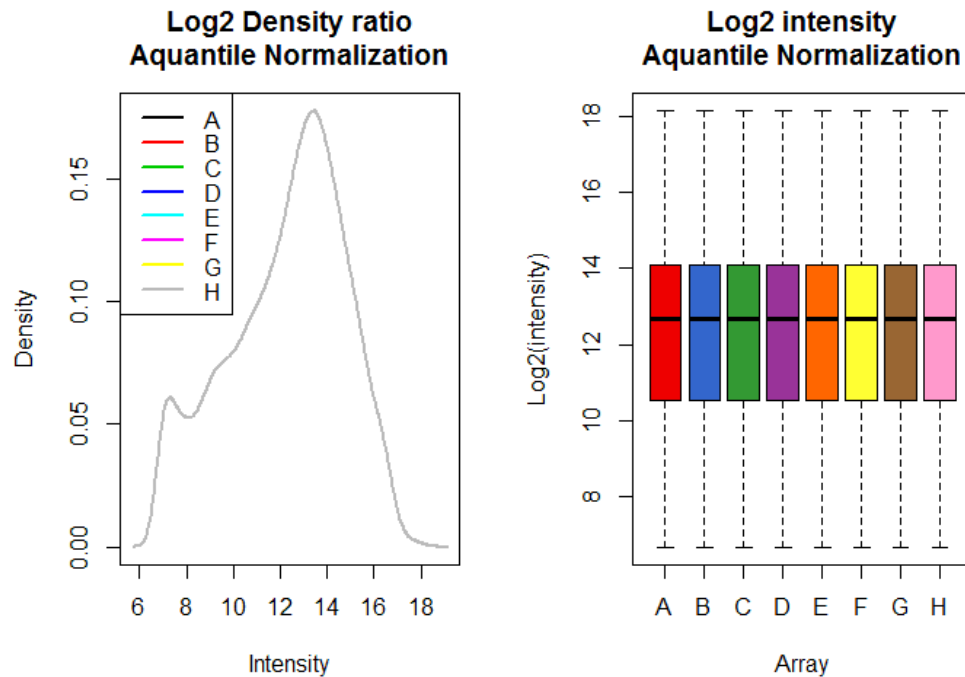


Fig. S1. Normalized data of the DNA microarray. Left panel: Density of intensity signal graph after normalization. Right panel: Intensity graph after normalization. This included two steps: a within and a between normalization with the Limma package as described in Material and Methods.

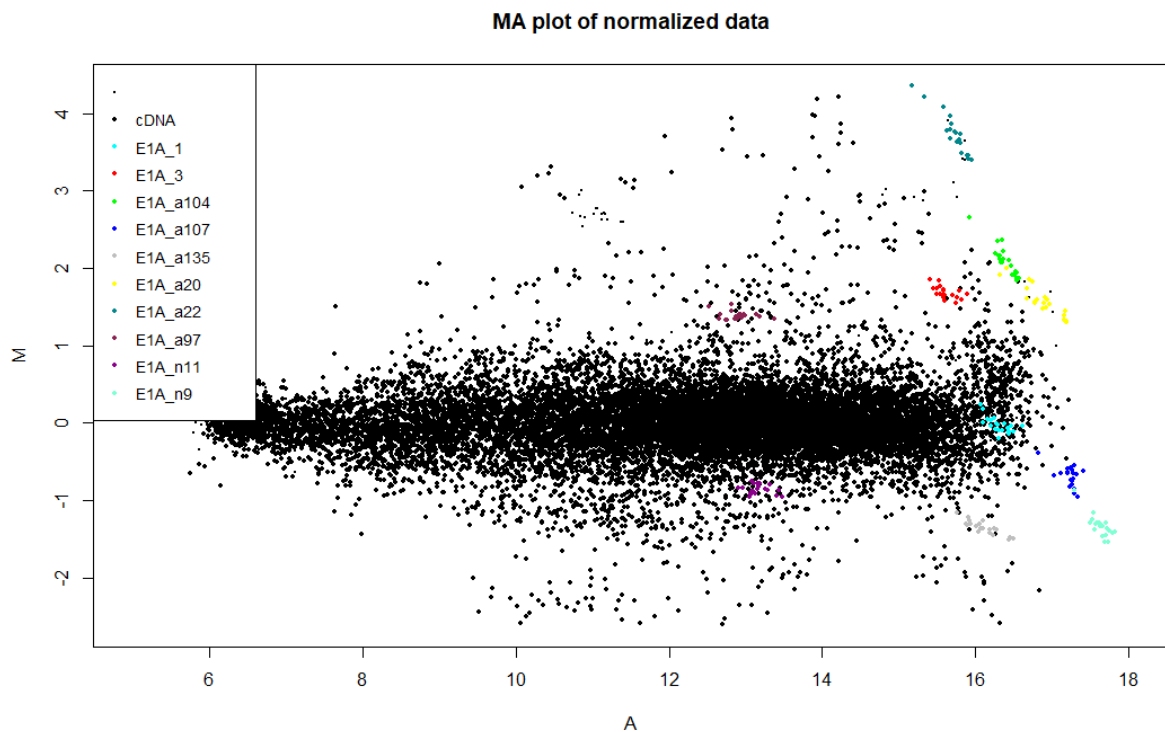


Fig. S2. MA plot of normalized data. Data obtained from microarrays were background subtracted, then normalized according the within-loess and the between-aquantile, and finally was averaged. The black spots correspond to cDNA. The color spots are the Spike-in controls used in the microarray.

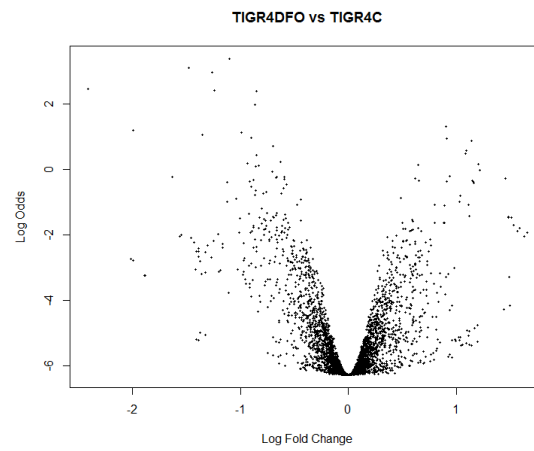


Fig. S3. Volcano plot corresponding to the differentially expressed genes in *Streptococcus pneumoniae* TIGR4 subject to iron starvation after deferoxamine (DFO) treatment.

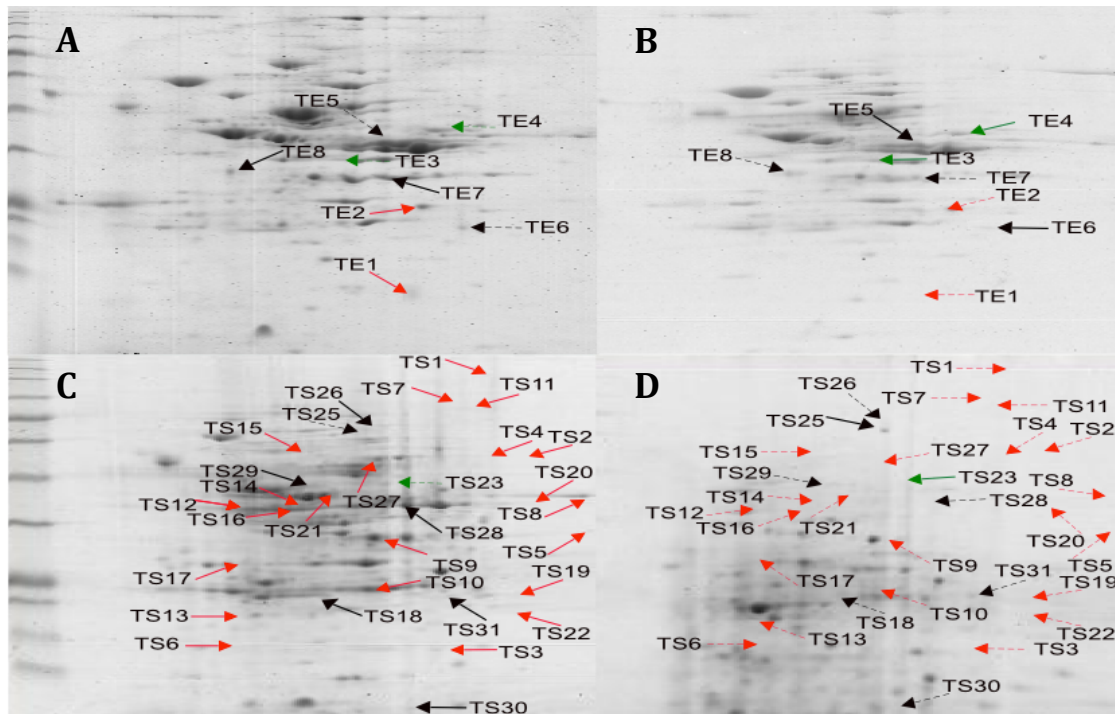


Fig. S4. 2-DE protein profiles of *Streptococcus pneumoniae* TIGR4. A) Control total extract; B) deferoxamine (DFO)-treated total extract; C) control secretome; and D) DFO-treated secretome. Differential proteins are indicated by arrows: Red, spots absent in the DFO-treated samples; Green, spots only present in the DFO-treated samples; and Black, proteins present in both control and treatments, but with increased abundance (>2 fold-change, solid line) or with decreased abundance (<0.5 fold-change, dotted line) in the DFO-treated samples compared to the control.

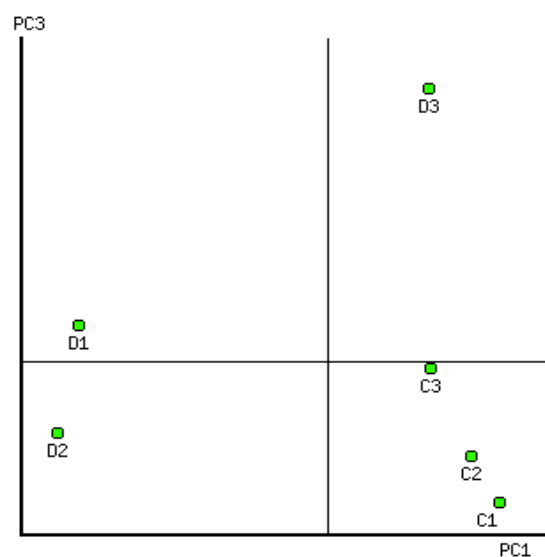


Fig. S5. Principal component analysis plot of differentially abundant metabolites in *Streptococcus pneumoniae* TIGR4. Dots C1-C3 represent the three biological replicates of the control and D1-D3 the three biological replicates of the deferoxamine (DFO) treatment.

Table S1. Microarray validation by RT-qPCR

Locus	Log ₂ FC	
	RT-qPCR	Microarray
SP_0324	-0.39	-0.99
SP_1027	0.28	0.97
SP_0641	0.31	1.03
SP_0176	0.67	1.19
SP_2196	0.25	0.61
SP_1871	0.55	1.51
SP_0981	0.4	0.95
SP_1894	-0.21	-0.65
SP_1591	0.58	0.73
SP_1466	-0.48	-1.45
SP_1857	0.83	1.44
SP_2233	-1.05	-2.05
SP_0427	-0.86	-1.37
SP_0426	-0.61	-1.26
SP_0390	0.23	0.43
SP_2239	1.13	1.64

Supplementary Dataset: Differentially expressed genes in Streptococcus pneumoniae TIGR4 after deferoramine treatment.

No.	Accession (GI)	Locus	Description	Location	Log ₂ FC	p-value	ID	OPERON
1	15899975	SP_0029	Uncharacterized protein	Cytoplasmic	0.46	0.04	38470	
2	15899980	SP_0034	UPF0324 membrane protein SP_0034	Membrane	0.53	0.02	1446351	
3	15900028	SP_0084	Histidine kinase	Membrane	0.32	0.04	38480	
4	15900059	SP_0117	Pneumococcal surface protein A	Membrane	0.8	0.02	1446388	
5	15900111	SP_0174	Uncharacterized protein	Cytoplasmic	1	0.01	1446404	
6	15900112	SP_0175	6,7-dimethyl-8-ribityllumazine synthase	Cytoplasmic	1.13	0	38501	
7	15900113	SP_0176	Riboflavin biosynthesis protein RibBA	Cytoplasmic	1.19	0.01	38501	
8	15900114	SP_0177	Riboflavin synthase, alpha subunit	Cytoplasmic	1.13	0.01	38501	
9	15900115	SP_0178	Riboflavin biosynthesis protein RibD	Cytoplasmic	1.13	0.01	38501	
10	15900138	SP_0202	Anaerobic ribonucleoside-triphosphate reductase	Cytoplasmic	0.61	0.01	38508	
11	15900139	SP_0203	Uncharacterized protein	Cytoplasmic	0.43	0.03	38508	
12	15900140	SP_0204	Acetyltransferase, GNAT family	Cytoplasmic	0.66	0	38509	
13	15900141	SP_0205	Anaerobic ribonucleoside-triphosphate reductase-activating protein	Cytoplasmic	0.64	0.01	38509	
14	15900142	SP_0206	Uncharacterized protein	Cytoplasmic	0.61	0.01	38509	
15	15900143	SP_0207	Conserved domain protein	Cytoplasmic	0.52	0.01	38509	
16	15900215	SP_0281	Aminopeptidase C	Cytoplasmic	0.92	0.01	1446426	
17	15900298	SP_0375	6-phosphogluconate dehydrogenase, decarboxylating	Cytoplasmic	0.41	0.02	38538	
18	15900308	SP_0385	Uncharacterized protein	Membrane	0.44	0.05	38541	
19	15900309	SP_0386	Putative sensor histidine kinase	Membrane	0.6	0.02	38541	
20	15900312	SP_0390	Choline binding protein G	Cytoplasmic	0.43	0.03	38542	
21	15900429	SP_0515	Heat-inducible transcription repressor HrcA	Cytoplasmic	0.84	0.04	38567	
22	15900430	SP_0516	Protein GrpE	Cytoplasmic	0.8	0.04	38567	
23	15900432	SP_0518	Uncharacterized protein	Cytoplasmic	1.05	0.02	38568	
24	15900507	SP_0599	Transmembrane protein Vexp1	Membrane	0.79	0.01	38588	
25	15900508	SP_0600	ABC transporter, ATP-binding protein Vexp2	Cytoplasmic	0.8	0.01	38588	
26	15900509	SP_0601	Transmembrane protein Vexp3	Membrane	0.8	0.01	38588	
27	15900511	SP_0603	DNA-binding response regulator VncR	Cytoplasmic	0.66	0.01	38589	
28	15900512	SP_0604	Histidine kinase	Membrane	0.53	0.02	38589	
29	15900513	SP_0605	Fructose-bisphosphate aldolase	Cytoplasmic	0.58	0.02	1446528	
30	15900524	SP_0616	Beta-lactam resistance factor	Cytoplasmic	0.49	0.02	38592	
31	15900525	SP_0617	Conserved domain protein	Membrane	0.56	0.02	38593	
32	15900530	SP_0622	Nitroreductase family protein	Cytoplasmic	0.89	0.02	38594	
33	15900531	SP_0623	Dipeptidase	Cytoplasmic	0.52	0.02	38594	
34	15900532	SP_0624	Uncharacterized protein	Cytoplasmic	0.43	0.02	38594	
35	15900534	SP_0627	Uncharacterized protein	Cytoplasmic	0.59	0.03	38595	
36	15900535	SP_0628	HIT family protein	Cytoplasmic	0.71	0.01	38595	
37	15900547	SP_0641	Serine protease, subtilase family	Cell Wall	1.03	0.01	1446538	
38	15900561	SP_0660	Peptide methionine sulfoxide reductase MsrA/MsrB 2 [Includes: Peptide methionine sulfoxide reductase MsrA	Cytoplasmic	0.46	0.04	1446542	
39	15900562	SP_0661	DNA-binding response regulator	Cytoplasmic	0.6	0.02	38600	
40	15900563	SP_0662	Putative sensor histidine kinase	Membrane	0.5	0.02	38600	
41	15900677	SP_0784	Glutathione reductase	Cytoplasmic	0.75	0.03	1446583	
42	15900691	SP_0798	Transcriptional regulatory protein CiaR	Cytoplasmic	0.71	0.03	38630	
43	15900751	SP_0868	Uncharacterized protein	Cytoplasmic	0.44	0.03	38642	
44	15900752	SP_0869	Cysteine desulfurase	Cytoplasmic	0.4	0.04	38642	
45	15900782	SP_0901	Uncharacterized protein	Cytoplasmic	0.62	0.02	38651	
46	15900786	SP_0905	Uncharacterized protein	Membrane	0.52	0.03	38652	
47	15900858	SP_0981	Foldase protein PrsA	Lipoprotein	0.95	0.01	38668	
48	15900868	SP_0993	Exonuclease	Cytoplasmic	0.3	0.04	38671	
49	15900872	SP_0999	Cytochrome c-type biogenesis protein CcdA	Membrane	0.6	0.01	38672	
50	15900873	SP_1000	Thioredoxin family protein	Lipoprotein	0.47	0.03	38672	
51	15900898	SP_1027	Uncharacterized protein	Secretory	0.97	0.03	38676	
52	15900963	SP_1095	Ribose-phosphate pyrophosphokinase 2	Cytoplasmic	0.41	0.03	38687	
53	15901082	SP_1220	L-lactate dehydrogenase	Cytoplasmic	0.64	0.04	1446720	
54	15901144	SP_1284	LemA protein	Membrane	0.36	0.03	38728	
55	15901192	SP_1338	Uncharacterized protein	Membrane	0.72	0.02	1446757	
56	15901194	SP_1340	Uncharacterized protein	Membrane	0.66	0.02	38738	
57	15901195	SP_1341	ABC transporter, ATP-binding protein	Cytoplasmic	0.75	0.02	38738	
58	15901196	SP_1342	Drug efflux ABC transporter, ATP-binding/permease protein	Membrane	0.82	0.02	38738	
59	15901197	SP_1343	Prolyl oligopeptidase family protein	Cytoplasmic	0.95	0.01	38738	
60	15901198	SP_1344	Uncharacterized protein	Cytoplasmic	0.88	0.02	38738	
61	15901324	SP_1474	Glycine-tRNA ligase beta subunit	Cytoplasmic	0.42	0.04	38768	
62	15901351	SP_1504	TPR domain protein	Cytoplasmic	0.29	0.04	38775	
63	15901356	SP_1509	ATP synthase gamma chain	Cytoplasmic	0.47	0.03	38776	
64	15901357	SP_1510	ATP synthase subunit alpha	Cytoplasmic	0.36	0.04	38776	
65	15901358	SP_1511	ATP synthase subunit delta	Cytoplasmic	0.49	0.02	38776	
66	15901359	SP_1512	ATP synthase subunit b	Membrane	0.48	0.03	38776	
67	15901360	SP_1513	ATP synthase subunit a	Membrane	0.36	0.03	38776	
68	15901409	SP_1566	UPF0042 nucleotide-binding protein SP_1566	Cytoplasmic	0.34	0.04	38789	
69	15901412	SP_1569	ATP-dependent Clp protease ATP-binding subunit ClpX	Cytoplasmic	0.46	0.02	38789	
70	15901430	SP_1588	Oxidoreductase, pyridine nucleotide-disulfide, class I	Cytoplasmic	0.89	0.02	1446822	
71	15901433	SP_1591	Proline dipeptidase	Cytoplasmic	0.73	0.02	38795	
72	15901434	SP_1592	Conserved domain protein	Membrane	0.67	0.02	38795	
73	15901484	SP_1648	Manganese ABC transporter, ATP-binding protein	Cytoplasmic	0.67	0.02	38805	
74	118090037	SP_1649	Putative manganese ABC transporter, permease protein	Membrane	0.72	0.01	38805	
75	15901485	SP_1650	Manganese ABC transporter substrate-binding lipoprotein	Lipoprotein	0.7	0.03	38805	
76	255964977	SP_1651	Probable thiol peroxidase	Cytoplasmic	0.53	0.03	1447025	
77	15901497	SP_1662	YimH protein	Cytoplasmic	0.42	0.01	38808	
78	15901500	SP_1665	YimE protein	Cytoplasmic	0.31	0.04	38808	
79	15901504	SP_1669	MutT/nudix family protein	Cytoplasmic	0.49	0.03	38809	
80	15901505	SP_1670	UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase	Cytoplasmic	0.47	0.02	38809	
81	15901530	SP_1696	Uncharacterized protein	Cytoplasmic	0.86	0.05	1446861	
82	15901549	SP_1715	ABC transporter, ATP-binding protein	Membrane	0.95	0.01	38820	
83	15901603	SP_1774	Putative transcriptional regulator	Cytoplasmic	0.57	0.03	38833	
84	15901604	SP_1775	Conserved domain protein	Cytoplasmic	0.67	0.02	38833	
85	15901630	SP_1801	Uncharacterized protein	Membrane	0.73	0.01	1446883	
86	15901631	SP_1802	Uncharacterized protein	Membrane	0.65	0.02	38839	
87	15901632	SP_1803	Uncharacterized protein	Membrane	0.59	0.04	38839	
88	15901633	SP_1804	Putative general stress protein 24	Cytoplasmic	0.67	0.03	38839	
89	15901637	SP_1808	Putative type IV prepilin peptidase	Membrane	0.73	0.02	1446886	
90	15901679	SP_1851	Uncharacterized protein	Cytoplasmic	0.41	0.05	1446897	
91	15901684	SP_1856	Transcriptional regulator, MerR family	Cytoplasmic	0.58	0.04	38853	
92	15901685	SP_1857	Cation efflux system protein	Membrane	1.44	0	1446899	
93	15901688	SP_1860	Choline transporter	Membrane	0.53	0.04	38854	
94	15901689	SP_1861	Choline transporter	Cytoplasmic	0.57	0.03	38854	
95	15901690	SP_1862	Uncharacterized protein	Cytoplasmic	0.4	0.04	38854	
96	15901691	SP_1863	Transcriptional regulator, MarR family	Cytoplasmic	0.49	0.02	38854	
97	15901697	SP_1869	Iron-compound ABC transporter, permease protein	Membrane	1.5	0.01	38857	
98	15901698	SP_1870	Iron-compound ABC transporter, permease protein	Membrane	1.49	0.01	38857	
99	15901699	SP_1871	Iron-compound ABC transporter, ATP-binding protein	Cytoplasmic	1.51	0.02	38857	

100	15901700 SP_1872	Iron-compound ABC transporter, iron-compound-binding protein	Lipoprotein	1,01	0,04	1446903
101	15901732 SP_1906	60 kDa chaperonin	Cytoplasmic	0,81	0,02	38862
102	15901733 SP_1907	10 kDa chaperonin	Cytoplasmic	0,75	0,03	38862
103	15901764 SP_1940	Protein RecA	Cytoplasmic	0,4	0,05	38871
104	15901824 SP_2001	Putative sensor histidine kinase	Membrane	0,39	0,02	38884
105	15901825 SP_2002	Uncharacterized protein	Membrane	0,45	0,02	38884
106	15901835 SP_2012	Glyceraldehyde-3-phosphate dehydrogenase	Cytoplasmic	0,77	0,03	1446953
107	15901888 SP_2069	Glutamate-tRNA ligase	Cytoplasmic	0,34	0,02	38895
108	15901889 SP_2070	Glucose-6-phosphate isomerase	Cytoplasmic	0,64	0,02	38896
109	15901890 SP_2071	Uncharacterized protein	Cytoplasmic	0,74	0,02	38896
110	15901984 SP_2174	D-alanine-poly(phosphoribitol) ligase subunit 2	Cytoplasmic	0,66	0,02	38917
111	15901985 SP_2175	DltB protein	Membrane	0,64	0,02	38917
112	15901986 SP_2176	D-alanine-poly(phosphoribitol) ligase subunit 1	Membrane	0,69	0,03	38917
113	15901993 SP_2186	Glycerol kinase	Cytoplasmic	1,78	0,02	38918
114	15901994 SP_2187	Conserved domain protein	Cytoplasmic	0,7	0,03	1447010
115	15902003 SP_2196	ABC transporter, ATP-binding protein	Cytoplasmic	0,61	0,01	38922
116	15902004 SP_2197	Putative ABC transporter, substrate-binding protein	Lipoprotein	0,58	0,03	38922
117	15902042 SP_2239	Serine protease	Membrane	1,64	0,01	38930
118	15902043 SP_2240	SpspJ protein	Cytoplasmic	1,49	0,02	38930
119	330689322 nanA	Sialidase A	Unknown	-0,82	0,01	
120	15899952 SP_0003	Uncharacterized protein	Cytoplasmic	-0,81	0,01	38465
121	15899953 SP_0004	Ribosome-binding ATPase YchF	Cytoplasmic	-0,49	0,02	38466
122	15899966 SP_0018	Uncharacterized protein	Cytoplasmic	-0,64	0,02	1446345
123	15899968 SP_0020	tRNA-specific adenosine deaminase	Cytoplasmic	-0,87	0	1446347
124	15899969 SP_0021	Putative deoxyuridine 5'triphosphate nucleotidohydrolase	Cytoplasmic	-0,54	0,02	38468
125	15899970 SP_0022	Uncharacterized protein	Cytoplasmic	-0,49	0,02	38468
126	15899971 SP_0024	Uncharacterized protein	Cytoplasmic	-0,59	0,02	38469
127	15899972 SP_0025	Uncharacterized protein	Membrane	-0,67	0,03	38469
128	15899973 SP_0026	Uncharacterized protein	Membrane	-0,88	0,02	38469
129	15899987 SP_0042	Transport/processing ATP-binding protein ComA	Membrane	-0,60	0,02	38472
130	15899988 SP_0043	Transport protein ComB	Membrane	-0,78	0,01	38472
131	15899989 SP_0044	Phosphoribosylaminoimidazole-succinocarboxamide synthase	Cytoplasmic	-0,88	0,02	1446354
132	15899995 SP_0050	Bifunctional purine biosynthesis protein PurH [Includes: Phosphoribosylaminoimidazolecarboxamide formyltransferase	Cytoplasmic	-0,54	0,01	38475
133	15899996 SP_0051	Phosphoribosylamine-glycine ligase	Cytoplasmic	-0,73	0,01	1446355
134	15899998 SP_0053	N5-carboxyaminoimidazole ribonucleotide mutase	Cytoplasmic	-0,52	0,02	38476
135	15899999 SP_0054	N5-carboxyaminoimidazole ribonucleotide synthase	Cytoplasmic	-0,68	0,02	38476
136	15900000 SP_0055	Uncharacterized protein	Cytoplasmic	-0,49	0,05	38476
137	15900020 SP_0075	Phosphorylase, Pnp/Udp family	Cytoplasmic	-0,56	0,02	1446367
138	15900044 SP_0101	Putative transporter	Membrane	-0,61	0,05	1446380
139	15900060 SP_0118	tRNA-specific 2-thiouridylase MnmA	Cytoplasmic	-0,72	0	1446389
140	15900061 SP_0119	MutT/nudix family protein	Cytoplasmic	-0,81	0,01	38486
141	15900062 SP_0120	tRNA uridine 5-carboxymethylaminomethyl modification enzyme MnmG	Cytoplasmic	-0,71	0,02	38486
142	15900084 SP_0146	Uncharacterized protein	Membrane	-0,28	0,03	38494
143	15900089 SP_0151	Methionine import ATP-binding protein MetN	Cytoplasmic	-0,31	0,05	38495
144	15900090 SP_0152	Putative ABC transporter, permease protein	Membrane	-0,46	0,02	38495
145	15900101 SP_0163	Putative transcriptional regulator PlcR	Cytoplasmic	-0,45	0,03	1446401
146	15900102 SP_0164	Uncharacterized protein	Membrane	-0,97	0	38498
147	15900103 SP_0165	Flavoprotein	Cytoplasmic	-0,58	0,02	38498
148	15900156 SP_0220	50S ribosomal protein L24	Cytoplasmic	-0,45	0,03	38510
149	15900157 SP_0221	50S ribosomal protein L5	Cytoplasmic	-0,39	0,04	38510
150	15900158 SP_0222	30S ribosomal protein S14	Cytoplasmic	-0,37	0,05	38510
151	15900161 SP_0225	50S ribosomal protein L6	Cytoplasmic	-0,40	0,03	38511
152	15900176 SP_0240	Phosphoglycerate mutase family protein	Cytoplasmic	-0,35	0,04	1446413
153	15900201 SP_0267	Putative oxidoreductase	Cytoplasmic	-0,64	0,01	1446420
154	15900221 SP_0287	Xanthine/uracil permease family protein	Membrane	-1,03	0,01	1446429
155	15900222 SP_0288	Uncharacterized protein	Membrane	-0,98	0	1446430
156	15900246 SP_0313	Glutathione peroxidase	Cytoplasmic	-0,36	0,03	1446444
157	15900250 SP_0318	Carbohydrate kinase, PfkB family	Cytoplasmic	-0,73	0,02	38528
158	15900253 SP_0321	PTS system, IIA component	Cytoplasmic	-1,23	0,01	38529
159	15900254 SP_0322	Glucuronyl hydrolase	Cytoplasmic	-0,84	0,01	38529
160	15900255 SP_0323	PTS system, IIB component	Cytoplasmic	-0,68	0,03	38529
161	15900256 SP_0324	PTS system, IIC component	Membrane	-0,99	0,02	38529
162	15900257 SP_0325	PTS system, IID component	Membrane	-0,88	0,01	38529
163	15900258 SP_0326	Preprotein translocase, YajC subunit	Membrane	-0,85	0,01	38529
164	15900269 SP_0338	Putative ATP-dependent Clp protease, ATP-binding subunit	Cytoplasmic	-1,13	0,05	1446450
165	15900281 SP_0352	Capsular polysaccharide biosynthesis protein Cps4G	Cytoplasmic	-0,67	0,02	38533
166	15900283 SP_0354	Putative membrane protein	Membrane	-0,53	0,02	38533
167	15900290 SP_0366	Oligopeptide-binding protein AliA	Lipoprotein	-0,62	0,02	1446456
168	15900327 SP_0408	Sodium:alanine symporter family protein	Membrane	-0,58	0,01	1446466
169	15900331 SP_0412	Uncharacterized protein	Cytoplasmic	-0,64	0,01	38546
170	15900332 SP_0413	Aspartokinase	Cytoplasmic	-0,59	0,01	38546
171	15900334 SP_0415	Enoyl-CoA hydratase/isomerase family protein	Cytoplasmic	-0,54	0,03	1446471
172	15900335 SP_0416	Transcriptional regulator, MarR family	Cytoplasmic	-0,55	0,01	38547
173	15900336 SP_0417	3-oxoacyl-[acyl-carrier-protein] synthase 3	Cytoplasmic	-0,64	0,01	38547
174	15900338 SP_0419	enoyl-(acyl-carrier-protein) reductase	Cytoplasmic	-1,07	0,01	38548
175	15900339 SP_0420	Malonyl CoA-acyl carrier protein transacylase	Cytoplasmic	-1,22	0,01	38548
176	15900340 SP_0421	3-oxoacyl-[acyl-carrier-protein] reductase	Cytoplasmic	-1,22	0,01	38548
177	15900341 SP_0422	3-oxoacyl-[acyl-carrier-protein] synthase 2	Cytoplasmic	-1,33	0,01	38548
178	15900342 SP_0423	Acetyl-CoA carboxylase, bitoin carboxyl carrier protein	Cytoplasmic	-1,33	0,01	38548
179	15900343 SP_0424	3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ	Cytoplasmic	-1,41	0,01	38548
180	15900344 SP_0425	Acetyl-CoA carboxylase, biotin carboxylase	Cytoplasmic	-1,41	0,01	38548
181	15900345 SP_0426	Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta	Cytoplasmic	-1,52	0,01	38548
182	15900346 SP_0427	Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha	Cytoplasmic	-1,62	0,01	38548
183	15900347 SP_0428	Uncharacterized protein	Cytoplasmic	-1,27	0,02	38548
184	15900348 SP_0429	Uncharacterized protein	Cytoplasmic	-0,86	0,04	38548
185	15900349 SP_0430	Uncharacterized protein	Membrane	-1,10	0,01	38548
186	15900350 SP_0431	Conserved domain protein	Membrane	-1,04	0,01	38548
187	15900368 SP_0451	Uncharacterized protein	Cytoplasmic	-0,41	0,03	1446479
188	15900380 SP_0464	Cell wall surface anchor family protein	Cell Wall	-0,53	0,02	38554
189	15900384 SP_0468	Putative sortase	Membrane	-0,62	0,01	38555
190	15900390 SP_0475	Uncharacterized protein	Cytoplasmic	-0,57	0,02	38557
191	15900391 SP_0476	PTS system, lactose-specific IIA component	Cytoplasmic	-0,88	0,02	38558
192	15900397 SP_0482	UPF0397 protein SP_0482	Membrane	-0,32	0,04	38560
193	15900410 SP_0496	Na/Pi cotransporter II-related protein	Membrane	-0,45	0,01	1446495
194	15900420 SP_0506	Integrase/recombinase, phage integrase family	Cytoplasmic	-0,37	0,04	1446501
195	15900440 SP_0526	Response regulator BlpR	Cytoplasmic	-0,38	0,02	38571
196	15900441 SP_0527	Putative sensor histidine kinase BlpH	Membrane	-0,44	0,02	38571
197	15900444 SP_0531	Bacteriocin BlpI	Secretory	-0,59	0,04	1446509
198	15900445 SP_0532	Bacteriocin BlpJ	Secretory	-0,6	0,02	1446510
199	15900447 SP_0534	Uncharacterized protein	Membrane	-0,54	0,03	1446512
200	15900457 SP_0544	Immunity protein BlpX	Membrane	-0,42	0,02	38576
201	15900460 SP_0547	Conserved domain protein	Membrane	-0,48	0,01	1446515

202	15900462 SP_0549	Uncharacterized protein	Cytoplasmic	-0.47	0,04	38577
203	15900514 SP_0606	Putative oxidoreductase	Membrane	-1.34	0	1446529
204	15900552 SP_0650	Uncharacterized protein	Membrane	-0.38	0,03	1446540
205	15900581 SP_0680	Pseudouridine synthase	Cytoplasmic	-0.75	0,04	1446550
206	15900600 SP_0701	Orotidine 5'-phosphate decarboxylase	Cytoplasmic	-0.85	0,01	38610
207	15900601 SP_0702	Orotate phosphoribosyltransferase	Cytoplasmic	-0.94	0	38610
208	15900626 SP_0729	Cation-transporting ATPase, E1-E2 family	Membrane	-0.43	0,03	1446559
209	15900632 SP_0737	Sodium-dependent transporter	Membrane	-0.73	0,02	38617
210	15900633 SP_0738	Uncharacterized protein	Cytoplasmic	-0.72	0,01	38617
211	15900637 SP_0742	DegV domain-containing protein SP_0742	Cytoplasmic	-1.23	0	38618
212	15900644 SP_0749	Branched-chain amino acid ABC transporter, amino acid-binding protein	Lipoprotein	-0.45	0,02	1446570
213	15900645 SP_0750	Branched-chain amino acid ABC transporter, permease protein	Membrane	-0.46	0,02	38620
214	15900646 SP_0751	Branched-chain amino acid ABC transporter, permease protein	Membrane	-0.44	0,01	38620
215	15900647 SP_0752	Branched-chain amino acid ABC transporter, ATP-binding protein	Cytoplasmic	-0.41	0,03	38620
216	15900648 SP_0753	Branched-chain amino acid ABC transporter, ATP-binding protein	Cytoplasmic	-0.43	0,02	38620
217	15900662 SP_0768	Probable dual-specificity RNA methyltransferase RlmN	Cytoplasmic	-0.39	0,03	38624
218	15900664 SP_0770	ABC transporter, ATP-binding protein	Cytoplasmic	-0.42	0,02	38624
219	15900678 SP_0785	Uncharacterized protein	Membrane	-0.53	0,02	38627
220	15900679 SP_0786	ABC transporter, ATP-binding protein	Cytoplasmic	-0.56	0,02	38627
221	15900680 SP_0787	Uncharacterized protein	Membrane	-0.50	0,02	38627
222	15900683 SP_0790	Conserved domain protein	Membrane	-0.58	0,02	38628
223	15900693 SP_0800	Uncharacterized protein	Membrane	-0.72	0	1446587
224	15900736 SP_0851	Glycerol-3-phosphate acyltransferase	Membrane	-0.64	0,01	1446606
225	15900756 SP_0873	Membrane protein	Membrane	-0.44	0,03	1446612
226	15900772 SP_0889	Uncharacterized protein	Cytoplasmic	-0.49	0,03	38647
227	15900796 SP_0916	Lysine decarboxylase	Cytoplasmic	-0.61	0,03	1446622
228	15900798 SP_0918	Polyamine aminopropyltransferase	Cytoplasmic	-0.64	0,01	38655
229	15900799 SP_0919	Uncharacterized protein	Cytoplasmic	-0.47	0,04	38655
230	15900800 SP_0920	Carboxynorspermidine decarboxylase	Cytoplasmic	-0.47	0,01	38655
231	15900801 SP_0921	Putative agmatine deiminase	Cytoplasmic	-0.57	0,02	38655
232	15900802 SP_0922	Carbon-nitrogen hydrolase family protein	Cytoplasmic	-0.82	0,03	38655
233	15900818 SP_0938	Ribosomal RNA small subunit methyltransferase I	Cytoplasmic	-0.50	0,01	38658
234	15900819 SP_0939	Uncharacterized protein	Cytoplasmic	-0.44	0,04	1446626
235	15900840 SP_0963	dihydroorotate dehydrogenase electron transfer subunit	Cytoplasmic	-0.76	0,01	38665
236	15900841 SP_0964	Dihydroorotate dehydrogenase 1B	Cytoplasmic	-0.83	0	38665
237	15900876 SP_1003	Uncharacterized protein	Membrane	-0.52	0,05	38673
238	15900878 SP_1006	Uncharacterized protein	Membrane	-0.49	0,03	1446639
239	15900885 SP_1013	Aspartate-semialdehyde dehydrogenase	Cytoplasmic	-0.38	0,05	38674
240	15900886 SP_1014	4-hydroxy-tetrahydrodipicolinate synthase	Cytoplasmic	-0.44	0,02	38674
241	15900910 SP_1039	Uncharacterized protein	Cytoplasmic	-0.50	0,02	1446653
242	15900928 SP_1058	Uncharacterized protein	Membrane	-1.41	0	1446664
243	15900929 SP_1059	Uncharacterized protein	Cytoplasmic	-1.09	0	1446665
244	15900930 SP_1060	Uncharacterized protein	Cytoplasmic	-0.54	0,02	38680
245	15900938 SP_1069	Uncharacterized protein	Secretory	-0.69	0,01	38682
246	15900939 SP_1070	Uncharacterized protein	Membrane	-0.62	0,01	38682
247	15900940 SP_1071	ABC transporter, ATP-binding protein	Cytoplasmic	-0.62	0,03	38682
248	15900948 SP_1079	GTPase OgbE	Cytoplasmic	-0.50	0,03	38684
249	15900949 SP_1080	Uncharacterized protein	Cytoplasmic	-0.48	0,04	38684
250	15900986 SP_1119	Glyceraldehyde-3-phosphate dehydrogenase, NADP-dependent	Cytoplasmic	-0.52	0,02	1446679
251	15901005 SP_1139	Uncharacterized protein	Cytoplasmic	-0.45	0,05	1446688
252	15901008 SP_1142	Uncharacterized protein	Cytoplasmic	-0.57	0,01	38696
253	15901091 SP_1229	Formate-tetrahydrofolate ligase	Cytoplasmic	-0.63	0,01	1446723
254	15901135 SP_1275	Carbamoyl-phosphate synthase large chain	Cytoplasmic	-0.69	0,02	1446736
255	15901136 SP_1276	Carbamoyl-phosphate synthase small chain	Cytoplasmic	-0.75	0,03	38726
256	15901137 SP_1277	Aspartate carbamoyltransferase	Cytoplasmic	-0.81	0,03	38726
257	15901138 SP_1278	Bifunctional protein PyrR [Includes: Pyrimidine operon regulatory protein; Uracil phosphoribosyltransferase	Cytoplasmic	-0.79	0,04	38726
258	15901154 SP_1294	Putative fluoride ion transporter CrcB 1	Membrane	-0.53	0,03	38731
259	15901155 SP_1295	Putative fluoride ion transporter CrcB 2	Membrane	-0.46	0,02	38731
260	15901245 SP_1391	Uncharacterized protein	Membrane	-0.42	0,05	38749
261	15901247 SP_1393	Uncharacterized protein	Cytoplasmic	-0.45	0,03	1446767
262	15901248 SP_1394	Amino acid ABC transporter, amino acid-binding protein	Lipoprotein	-0.46	0,02	1446768
263	15901256 SP_1402	NOL1/NOP2/sun family protein	Cytoplasmic	-0.51	0,04	38751
264	15901258 SP_1404	UPF0223 protein SP_1404	Cytoplasmic	-0.42	0,03	38751
265	15901259 SP_1405	Regulatory protein Spx	Cytoplasmic	-0.72	0,01	38751
266	15901280 SP_1427	Peptidase, U32 family	Cytoplasmic	-0.95	0,01	1446775
267	15901281 SP_1428	Uncharacterized protein	Cytoplasmic	-0.85	0,01	38757
268	15901282 SP_1429	Peptidase, U32 family	Cytoplasmic	-0.79	0,01	38757
269	15901285 SP_1433	Transcriptional regulator, AraC family	Cytoplasmic	-0.57	0,02	1446778
270	15901309 SP_1459	Uncharacterized protein	Membrane	-0.60	0,03	1446786
271	15901310 SP_1460	Amino acid ABC transporter, ATP-binding protein	Cytoplasmic	-0.97	0,01	38763
272	15901311 SP_1461	Amino acid ABC transporter, permease protein	Membrane	-0.86	0,02	38763
273	15901312 SP_1462	Uncharacterized protein	Cytoplasmic	-0.94	0,01	38764
274	15901313 SP_1463	Methylated-DNA-protein-cysteine S-methyltransferase	Cytoplasmic	-1.08	0,02	38764
275	15901314 SP_1464	Acetyltransferase, GNAT family	Cytoplasmic	-1.01	0,02	38764
276	15901315 SP_1465	Uncharacterized protein	Cytoplasmic	-2.10	0,01	38765
277	15901316 SP_1466	Hemolysin	Membrane	-2.13	0,01	38765
278	15901368 SP_1522	Conserved domain protein	Cytoplasmic	-0.38	0,02	38778
279	15901369 SP_1523	Snf2 family protein	Cytoplasmic	-0.41	0,02	38778
280	15901429 SP_1587	Oxalate:formate antiporter	Membrane	-0.90	0	1446821
281	15901440 SP_1600	Putative membrane protein	Membrane	-0.59	0,02	1446825
282	15901441 SP_1601	Uncharacterized protein	Membrane	-0.49	0,04	38797
283	15901450 SP_1610	SAM-dependent methyltransferase	Cytoplasmic	-0.38	0,02	38800
284	15901459 SP_1623	Probable cation-transporting ATPase exp7	Membrane	-0.50	0,04	1446830
285	15901470 SP_1634	Uncharacterized protein	Cytoplasmic	-0.36	0,04	1446839
286	15901480 SP_1644	D-aminoacyl-tRNA deacylase	Cytoplasmic	-0.38	0,04	38804
287	15901521 SP_1686	Uncharacterized oxidoreductase SP_1686	Cytoplasmic	-1.08	0	38815
288	15901522 SP_1687	Sialidase B	Membrane	-0.85	0,01	38815
289	15901523 SP_1688	ABC transporter, permease protein	Membrane	-0.95	0,01	38815
290	15901524 SP_1689	ABC transporter, permease protein	Membrane	-0.84	0,01	38815
291	15901557 SP_1724	Sucrose-6-phosphate hydrolase	Cytoplasmic	-0.49	0,03	38822
292	15901558 SP_1725	Sucrose operon repressor	Cytoplasmic	-0.54	0,03	38822
293	15901569 SP_1737	DNA-directed RNA polymerase subunit omega	Cytoplasmic	-0.54	0,04	38827
294	15901638 SP_1809	Transcriptional regulator	Cytoplasmic	-0.57	0,01	38840
295	15901639 SP_1810	Uncharacterized protein	Cytoplasmic	-0.72	0,01	38840
296	15901650 SP_1821	Sugar-binding transcriptional regulator, LacI family	Cytoplasmic	-0.52	0,02	1446888
297	15901721 SP_1894	Sucrose phosphorylase	Cytoplasmic	-0.65	0,02	1446911
298	15901725 SP_1898	Alpha-galactosidase	Cytoplasmic	-0.54	0,05	1446912
299	15901744 SP_1920	Transcriptional regulator, MarR family	Cytoplasmic	-0.56	0,03	38867
300	15901746 SP_1922	Probable transcriptional regulatory protein SP_1922	Cytoplasmic	-0.84	0,01	38867
301	15901747 SP_1923	Pneumolysin	Cytoplasmic	-1.37	0,02	38868
302	15901748 SP_1924	Uncharacterized protein	Cytoplasmic	-1.29	0,02	38868
303	15901749 SP_1925	Uncharacterized protein	Cytoplasmic	-1.19	0,02	38868

304	15901750 SP_1926	Uncharacterized protein	Membrane	-1.04	0,02	38868
305	15901766 SP_1942	Putative transcriptional regulator	Secretory	-0.29	0,05	38872
306	15901770 SP_1946	Putative transcriptional regulator PlcR	Cytoplasmic	-0.58	0,02	1446927
307	15901772 SP_1948	Conserved domain protein	Cytoplasmic	-0.76	0,04	38873
308	15901773 SP_1949	Uncharacterized protein	Cytoplasmic	-0.75	0,03	38873
309	15901774 SP_1950	Putative bacteriocin formation protein	Cytoplasmic	-0.51	0,03	1446929
310	15901775 SP_1951	Uncharacterized protein	Cytoplasmic	-0.61	0,04	38874
311	15901776 SP_1952	Uncharacterized protein	Membrane	-0.71	0,03	38874
312	15901777 SP_1953	Toxin secretion ABC transporter, ATP-binding/permease protein	Membrane	-0.70	0,01	38874
313	118090034 SP_1954	Serine protease, subtilase family	Secretory	-0.54	0,02	38874
314	15901782 SP_1959	Nucleoside diphosphate kinase	Cytoplasmic	-0.46	0,02	1446931
315	15901785 SP_1962	Uncharacterized protein	Cytoplasmic	-1.42	0	1446932
316	15901834 SP_2011	Pseudouridine synthase	Cytoplasmic	-0.43	0,03	1446952
317	15901849 SP_2028	Phosphotyrosine protein phosphatase	Membrane	-0.48	0,03	38887
318	15901862 SP_2041	Membrane protein insertase YidC 2	Membrane	-0.39	0,05	38890
319	15901874 SP_2054	Uncharacterized protein	Cytoplasmic	-0.67	0,02	1446967
320	15901880 SP_2060	Pyroldone-carboxylate peptidase 2	Cytoplasmic	-0.37	0,04	1446973
321	118090038 SP_2063	LysM domain protein	Membrane	-0.77	0,04	1446338
322	15901886 SP_2067	Uncharacterized protein	Cytoplasmic	-0.59	0,01	1446975
323	15901894 SP_2077	Arginine repressor	Cytoplasmic	-0.60	0,01	1446978
324	15901900 SP_2084	Phosphate-binding protein PstS 2	Lipoprotein	-1.06	0,01	1446982
325	15901901 SP_2085	Phosphate ABC transporter, permease protein	Membrane	-0.78	0,02	38898
326	15901902 SP_2086	Phosphate ABC transporter, permease protein	Membrane	-0.74	0,02	38898
327	15901903 SP_2087	Phosphate import ATP-binding protein PstB 3	Cytoplasmic	-0.87	0,01	38898
328	15901904 SP_2088	Phosphate-specific transport system accessory protein PhoU homolog	Cytoplasmic	-0.93	0,01	38898
329	15901930 SP_2115	Uncharacterized protein	Membrane	-0.51	0,02	38906
330	15901932 SP_2117	Uncharacterized protein	Membrane	-0.48	0,02	38906
331	15901933 SP_2118	Uncharacterized protein	Membrane	-0.45	0,03	38907
332	15901934 SP_2119	Putative transcriptional regulator	Cytoplasmic	-0.60	0,02	38907
333	15901947 SP_2133	Conserved domain protein	Cytoplasmic	-0.58	0,01	38909
334	15902021 SP_2217	Putative rod shape-determining protein MreD	Membrane	-0.31	0,05	38926
335	15902036 SP_2233	Uncharacterized protein	Cytoplasmic	-1.84	0	1447021
336	15902038 SP_2235	Response regulator ComE	Cytoplasmic	-0.98	0	38929
337	15902039 SP_2236	Putative sensor histidine kinase ComD	Membrane	-0.64	0,01	38929
338	15902041 SP_2238	Ribosomal RNA large subunit methyltransferase H	Cytoplasmic	-0.42	0,01	1447023

Log2 fold changes (FC) are the ratio between deferroxamine treatment and control. Positive values indicate up-regulation, and negative values indicate down-regulation