

NCBI Genome ID NC011761	Gene	Function	Median (8 Microarrays)	One Sample t-Test (Adv)	Fe induced
<i>rus</i> operon					
AFE_3153	<i>cyc2</i>	cytochrome c	2.516	0.000014	*
AFE_3152	<i>cyc1</i>	cytochrome c552	2.838	0	*
AFE_3151	<i>cup</i>	conserved hypothetical protein	3.12	0	*
AFE_3150	<i>coxB</i>	cytochrome c oxidase, aa3-type, subunit II	2.941	0.000399	*
AFE_3149	<i>coxA</i>	cytochrome c oxidase, aa3-type, subunit I	2.499	0.000002	*
AFE_3148	<i>coxC</i>	cytochrome c oxidase, aa3-type, subunit III	1.662	0.022353	*
AFE_3146	<i>rus</i>	rusticyanin	1.595	0.002216	*
AFE_3146	<i>rus</i>	rusticyanin	2.106	0.000016	*
AFE_3146	<i>rus</i>	rusticyanin	1.887	0	*
Cytochrome c oxidase complex biogenesis operon					
AFE_3144	<i>ctaA</i>	heme a synthase	2.429	0.000011	*
AFE_3143	<i>ctaB</i>	heme o synthase, protoheme IX farnesyltransferase	0.381	0.1811	
AFE_3142	<i>ctaT</i>	major facilitator family transporter	0.842	0.003286	*
AFE_3141	<i>ctaR</i>	iron responsive regulator of the Rrf2 family	ND	ND	
AFE_3139	<i>ctaU</i>	hypothetical protein	1.792	0.000219	*
AFE_3138	<i>ctaS</i>	oxidoreductase, 2OG-Fe(II) oxygenase family	1.413	0.000036	*
<i>regBA</i> operon					
AFE_3137	<i>regA</i>	DNA-binding response regulator	0.667	0.024382	
AFE_3136	<i>regB</i>	sensor histidine kinase	2.012	0.000024	*
<i>petI</i> operon					
AFE_3111	<i>petC1</i>	ubiquinol--cytochrome c reductase, cytochrome c1 subunit	3.749	0.000043	*
AFE_3110	<i>petB1</i>	ubiquinol--cytochrome c reductase, cytochrome b subunit	4.411	0.000011	*
AFE_3109	<i>petA1</i>	ubiquinol--cytochrome c reductase, iron-sulfur subunit	3.675	0.000042	*
AFE_3108	<i>sdrA1</i>	oxidoreductase, short-chain dehydrogenase/reductase family	3.945	0.001167	*
AFE_3107	<i>cycA1</i>	cytochrome c4	3.731	0.000001	*
NADH complex operon					
AFE_2630	<i>nuoA</i>	NADH-quinone oxidoreductase, A subunit	-0.05	0.799856	
AFE_2629	<i>nuoB</i>	NADH-quinone oxidoreductase, B subunit	0.279	0.127471	
AFE_2628	<i>nuoC</i>	NADH-quinone oxidoreductase, C subunit	0.033	0.69215	
AFE_2627	<i>nuoD</i>	NADH-quinone oxidoreductase, D subunit	-0.517	0.640804	
AFE_2626	<i>nuoE</i>	NADH-quinone oxidoreductase, E subunit	-1.091	0.053432	
AFE_2625	<i>nuoF</i>	NADH-quinone oxidoreductase, F subunit	0.402	0.005774	
AFE_2624	<i>nuoG</i>	NADH-quinone oxidoreductase, G subunit	-0.197	0.23897	
AFE_2623	<i>nuoH</i>	NADH-quinone oxidoreductase, H subunit	-0.749	0.000019	
AFE_2622	<i>nuoI</i>	NADH-quinone oxidoreductase, I subunit	1.446	0.001601	*

AFE_2621	<i>nuoJ</i>	NADH-quinone oxidoreductase, J subunit	-0.108	0.209363	
AFE_2620	<i>nuoK</i>	NADH-quinone oxidoreductase, K subunit	0.878	0.026311	*
AFE_2619	<i>nuoL</i>	NADH-quinone oxidoreductase, L subunit	-0.948	0.000005	
AFE_2618	<i>nuoM</i>	NADH-quinone oxidoreductase, M subunit	-0.838	0.000026	
AFE_2617	<i>nuoN</i>	NADH-quinone oxidoreductase, N subunit	-0.357	0.19121	
ATP synthetase complex operon					
AFE_3209	<i>atpB</i>	ATP synthase F0, A subunit	1.754	0.000004	*
AFE_3208	<i>atpE</i>	ATP synthase F0, C subunit	1.444	0.000053	*
AFE_3207	<i>atpF</i>	ATP synthase F0, B subunit	0.427	0.011886	
AFE_3206	<i>atpH</i>	ATP synthase F1, delta subunit	0.423	0.022868	
AFE_3205	<i>atpA</i>	ATP synthase F1, alpha subunit	-0.191	0.988306	
AFE_3204	<i>atpG</i>	ATP synthase F1, gamma subunit	-0.478	0.228767	
AFE_3203	<i>atpD</i>	ATP synthase F1, beta subunit	0.031	0.747753	
AFE_3202	<i>atpC</i>	ATP synthase F1, epsilon subunit	-0.638	0.009246	