Supplementary Table S1. Genes upregulated under iron limitation

Rv no.	Genes	B	Fold change	Putative function
✪Rv0010c		4.54	3.45	CONSERVED MEMBRANE PROTEIN
Rv0127		1.04	2.49	CONSERVED HYPOTHETICAL PROTEIN
Rv0136		1.99	2.76	PROBABLE CYTOCHROME P450 138 CYP138
☆Rv0145		2.76	3.94	CONSERVED HYPOTHETICAL PROTEIN
Rv0146		0.38	2.47	CONSERVED HYPOTHETICAL PROTEIN
Rv0149		2.30	2.82	POSSIBLE QUINONE OXIDOREDUCTASE
Rv0158		3.21	3.97	TRANSCRIPTIONAL REGULATORY PROTEIN
Rv0175		2.10	2.41	CONSERVED MEMBRANE PROTEIN
Rv0186	bglS	5.02	5.50	BETA-GLUCOSIDASE BGLS
Rv0188		6.05	5.35	CONSERVED TRANSMEMBRANE PROTEIN
Rv0191		0.17	2.77	CONSERVED MEMBRANE PROTEIN
Rv0204c		0.10	1.81	CONSERVED TRANSMEMBRANE PROTEIN
Rv0207c		0.25	1.92	CONSERVED HYPOTHETICAL PROTEIN
Rv0208c		2.17	2.29	METHLYTRANSFERASE
Rv0222	echA1	3.56	2.98	ENOYL-CoA HYDRATASE ECHA1
Rv0237	lpqI	1.08	1.86	CONSERVED LIPOPROTEIN LPQI
Rv0241c		0.38	1.99	CONSERVED HYPOTHETICAL PROTEIN
Rv0242c	fabG4	4.82	3.37	3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE FABG4
Rv0243	fadA2	1.35	1.95	ACETYL-CoA ACYLTRANSFERASE FADA2
Rv0244c	fadE5	7.19	21.52	ACYL-CoA DEHYDROGENASE FADE5
Rv0251c	hsp	6.48	9.09	HEAT SHOCK PROTEIN HSP
Rv0281		3.77	2.85	CONSERVED HYPOTHETICAL PROTEIN
☆Rv0282		4.95	6.17	CONSERVED HYPOTHETICAL PROTEIN
☆Rv0283		5.39	5.17	CONSERVED MEMBRANE PROTEIN

☆Rv0284		1.40	3.74	CONSERVED MEMBRANE PROTEIN
☆Rv0286		0.36	3.11	PPE
☆Rv0289		0.58	2.31	CONSERVED HYPOTHETICAL PROTEIN
☆Rv0290		9.44	10.61	CONSERVED TRANSMEMBRANE PROTEIN
☆Rv0291		4.42	3.54	MEMBRANE-ANCHORED MYCOSIN MYCP3
☆Rv0292		1.60	2.64	CONSERVED TRANSMEMBRANE PROTEIN
Rv0305c		6.23	2.33	PPE
Rv0342		1.01	2.26	ISONIAZID INDUCTIBLE GENE PROTEIN INIA
Rv0350	dnaK	5.99	3.80	CHAPERONE PROTEIN DNAK
Rv0834c	PEPGRS	1.35	1.71	PEPGRS
Rv0391	metZ	3.21	2.07	O-SUCCINYLHOMOSERINE SULFHYDRYLASE METZ
Rv0415		0.03	2.70	THIAMINE BIOSYNTHESIS OXIDOREDUCTASE THIO
☆Rv0423c	thiC	0.08	2.45	THIAMINE BIOSYNTHESIS PROTEIN THIC
Rv0434		2.05	2.16	CONSERVED HYPOTHETICAL PROTEIN
☆Rv0450c	mmpL4	1.05	2.97	TRANSMEMBRANE TRANSPORT PROTEIN
☆Rv0465c		4.52	2.60	TRANSCRIPTIONAL REGULATORY PROTEIN
☆Rv0467	aceA	5.28	7.19	ISOCITRATE LYASE ICL
☆Rv0468	fadB2	0.32	3.77	3-HYDROXYBUTYRYL-CoA DEHYDROGENASE FADB2
Rv0473		2.54	1.93	CONSERVED TRANSMEMBRANE PROTEIN
Rv0475		2.69	2.64	IRON-REGULATED HEPARIN BINDING HEMAGGLUTININ HBHA
Rv0485		2.74	2.53	TRANSCRIPTIONAL REGULATORY PROTEIN
Rv0486		7.12	2.14	GLYCOSYLTRANSFERASE MSHA
Rv0512	hemB	1.37	6.52	DELTA-AMINOLEVULINIC ACID DEHYDRATASE HEMB
Rv0525		0.67	1.83	CONSERVED HYPOTHETICAL PROTEIN
Rv0527	ccsA	0.32	1.81	CYTOCHROME C-TYPE BIOGENESIS PROTEIN CCDA
Rv0529	ccsB	0.00	2.08	CYTOCHROME C-TYPE BIOGENESIS PROTEIN CCSA

Rv0541c		8.76	3.25	CONSERVED INTEGRAL MEMBRANE PROTEIN
Rv0560c		0.50	9.29	BENZOQUINONE METHYLTRANSFERASE
Rv0563	htpX	1.46	1.98	PROTEASE TRANSMEMBRANE HEAT SHOCK PROTEIN HTPX
Rv0663	atsD	0.88	2.29	ARYLSULFATASE ATSD
Rv0672	fadE8	5.18	2.32	ACYL-CoA DEHYDROGENASE FADE8
☆Rv0676c	mmpL5	0.12	3.61	TRANSMEMBRANE TRANSPORT PROTEIN MMPL5
☆Rv0677c	mmpS5	2.38	2.63	CONSERVED MEMBRANE PROTEIN MMPS5
Rv0678		3.87	2.37	CONSERVED HYPOTHETICAL PROTEIN
☆Rv0691c		1.43	3.59	TRANSCRIPTIONAL REGULATORY PROTEIN
Rv0712		2.32	2.68	CONSERVED HYPOTHETICAL PROTEIN
Rv0752c	fadE9	3.90	2.81	ACYL-CoA DEHYDROGENASE FADE9
Rv0753c	mmsA	2.96	4.06	METHYLMALONATE-SEMIALDEHYDE DEHYDROGENASE
Rv0790c		0.14	2.68	HYPOTHETICAL PROTEIN
Rv0803	purL	2.20	1.75	PHOSPHORIBOSYLFORMYLGLYCINAMIDINE SYNTHASE II
Rv0818		5.98	32.54	TRANSCRIPTIONAL REGULATORY PROTEIN
Rv0823c		0.44	3.75	TRANSCRIPTIONAL REGULATORY PROTEIN
Rv0847	lpqS	1.90	2.60	PROBABLE LIPOPROTEIN LPQS
Rv0859	fadA	6.50	4.49	ACYL-CoA THIOLASE FADA
☆Rv0878c	PPE	4.81	0.43	PPE
Rv0873	fadE10	1.14	2.76	ACYL-CoA DEHYDROGENASE FADE10
Rv0877		3.91	1.89	CONSERVED HYPOTHETICAL PROTEIN
☆Rv0885		3.22	4.70	CONSERVED HYPOTHETICAL PROTEIN
Rv0886	fprB	2.13	4.63	NADPH:ADRENODOXIN OXIDOREDUCTASE FPRB
Rv0905	echA6	0.11	2.22	ENOYL-CoA HYDRATASE ECHA6
Rv0906		5.28	1.85	CONSERVED HYPOTHETICAL PROTEIN
Rv0939		0.54	3.09	2-HYDROXYHEPTA-2,4-DIENE-1,7-DIOATE ISOMERASE

Rv0951	sucC	5.25	1.85	SUCCINYL-CoA SYNTHETASE (BETA CHAIN) SUCC
Rv0971c	echA7	5.57	3.50	ENOYL-CoA HYDRATASE ECHA7
Rv0972c	fadE12	1.18	5.97	ACYL-CoA DEHYDROGENASE FADE12
Rv0973c	accA2	2.56	2.45	ACETYL-/PROPIONYL-COENZYME A CARBOXYLASE
Rv0974c	accD2	2.22	7.81	ACETYL-/PROPIONYL-CoA CARBOXYLASE
Rv0976c		1.15	4.89	CONSERVED HYPOTHETICAL PROTEIN
Rv0982		0.76	3.36	TWO COMPONENT SENSOR KINASE MPRB
Rv0983		5.36	2.32	SERINE PROTEASE PEPD
Rv0984	moaB2	1.73	3.19	PTERIN-4-ALPHA-CARBINOLAMINE DEHYDRATASE MOAB2
Rv0996		2.15	2.21	CONSERVED TRANSMEMBRANE PROTEIN
Rv0997		1.19	2.12	HYPOTHETICAL PROTEIN
Rv1044		2.59	2.19	CONSERVED HYPOTHETICAL PROTEIN
Rv1057		1.57	7.18	CONSERVED HYPOTHETICAL PROTEIN
Rv1073		1.14	2.39	CONSERVED HYPOTHETICAL PROTEIN
Rv1095	phoH2	0.50	1.92	PHOH-LIKE PROTEIN PHOH2 (PHOSPHATE STARVATION-
Rv1130		1.23	2.31	CONSERVED HYPOTHETICAL PROTEIN
Rv1144		3.48	1.97	SHORT-CHAIN TYPE DEHYDROGENASE/REDUCTASE
Rv1148c		3.04	2.69	CONSERVED HYPOTHETICAL PROTEIN
Rv1162	narH	2.72	2.40	RESPIRATORY NITRATE REDUCTASE
Rv1165		10.98	2.06	GTP-BINDING TRANSLATION ELONGATION FACTOR TYPA
☆Rv1168c	PPE	1.49	137.92	PPE
Rv1170		4.26	1.89	N-ACETYL-1-D-MYO-INOSITYL-2-AMINO-2-DEOXY-ALPHA-D-GLUCOPYRANOSIDE DEACETYLASE MSHB
Rv1192		0.00	3.19	HYPOTHETICAL PROTEIN
☆Rv1195	PE	3.43	2.24	PE
Rv1265		1.00	2.41	HYPOTHETICAL PROTEIN
Rv1295	thrC	0.45	2.48	THREONINE SYNTHASE THRC

Rv1301		6.52	1.92	CONSERVED HYPOTHETICAL PROTEIN
Rv1311	atpC	2.09	4.82	ATP SYNTHASE EPSILON CHAIN ATPC
Rv1323	fadA4	2.33	2.05	ACETYL-CoA ACETYLTRANSFERASE FADA4
Rv1324		1.75	2.60	THIOREDOXIN
Rv1338	murI	2.93	2.47	GLUTAMATE RACEMASE MURI
Rv1340	rphA	0.40	3.70	GLUTAMATE RACEMASE MURI
☆Rv1342c	pks14	1.74	1.96	CONSERVED MEMBRANE PROTEIN
☆Rv1344		7.08	2.23	ACYL CARRIER PROTEIN (ACP)
☆Rv1345	fadD33	5.62	4.35	POLYKETIDE SYNTHASE FADD33
☆Rv1346	fadE14	0.51	4.60	ACYL-CoA DEHYDROGENASE FADE14
☆Rv1349		3.17	5.56	DRUGS-TRANSPORT TRANSMEMBRANE ATP-BINDING ABC TRANSPORTER
Rv1410c		1.29	2.76	AMINOGLYCOSIDE/TETRACYCLINE-TRANSPORT MEMBRANE PROTEIN
Rv1411c	lprG	0.18	2.14	CONSERVED LIPOPROTEIN LPRG
Rv1448c	tal	6.28	1.80	PROBABLE TRANSALDOLASE TAL
☆Rv1461		2.68	7.24	CONSERVED HYPOTHETICAL PROTEIN
☆Rv1462		5.02	3.11	CONSERVED HYPOTHETICAL PROTEIN
☆Rv1463		5.89	3.02	CONSERVED ATP-BINDING PROTEIN ABC TRANSPORTER
☆Rv1464		3.31	4.93	CYSTEINE DESULFURASE CSD
☆Rv1465		2.70	7.48	NITROGEN FIXATION RELATED PROTEIN
☆Rv1466		0.54	2.77	CONSERVED HYPOTHETICAL PROTEIN
Rv1472	echA12	2.86	1.81	ENOYL-CoA HYDRATASE ECHA12
Rv1480		2.77	2.09	CONSERVED HYPOTHETICAL PROTEIN
☆Rv1535		1.66	2.14	HYPOTHETICAL PROTEIN
Rv1566c		1.41	2.14	POSSIBLE INVASION PROTEIN
Rv1567c		2.64	2.44	HYPOTHETICAL MEMBRANE PROTEIN
Rv1592c		0.84	2.36	CONSERVED HYPOTHETICAL PROTEIN

Rv1593c		3.95	2.35	CONSERVED HYPOTHETICAL PROTEIN
Rv1595	nadB	0.13	2.87	L-ASPARTATE OXIDASE NADB
Rv1596	nadC	6.37	2.21	NICOTINATE-NUCLEOTIDE PYROPHOSPHATASE NADC
Rv1599	hisD	0.46	3.09	HISTIDINOL DEHYDROGENASE HISD (HDH)
Rv1607	chaA	4.00	1.92	IONIC TRANSPORTER INTEGRAL MEMBRANE PROTEIN CHAA
Rv1616		0.18	2.49	CONSERVED MEMBRANE PROTEIN
Rv1617	pykA	5.71	1.65	PYRUVATE KINASE PYKA
☆Rv1623c	appC	3.45	8.85	INTEGRAL MEMBRANE CYTOCHROME D UBIQUINOL OXIDASE (SUBUNIT I) CYDA
Rv1644	tsnR	1.46	2.49	23S RRNA METHYLTRANSFERASE TSNR
Rv1647		1.06	2.30	CONSERVED HYPOTHETICAL PROTEIN
Rv1675c		2.55	2.07	TRANSCRIPTIONAL REGULATORY PROTEIN
Rv1685c		0.90	3.03	CONSERVED HYPOTHETICAL PROTEIN
Rv1695		1.90	2.22	INORGANIC POLYPHOSPHATE/ATP-NAD KINASE PPNK
Rv1717		3.49	5.23	CONSERVED HYPOTHETICAL PROTEIN
Rv1731	gabD1	1.51	3.13	SUCCINATE-SEMIALDEHYDE DEHYDROGENASE
Rv1754c		0.60	2.58	CONSERVED HYPOTHETICAL PROTEIN
Rv1769		0.17	1.96	CONSERVED HYPOTHETICAL PROTEIN
Rv1771		2.17	1.88	PROBABLE OXIDOREDUCTASE
Rv1774		0.88	2.67	OXIDOREDUCTASE
Rv1775		4.08	1.99	CONSERVED HYPOTHETICAL PROTEIN
Rv1782		2.59	3.53	CONSERVED MEMBRANE PROTEIN
Rv1783		0.91	2.44	CONSERVED MEMBRANE PROTEIN
Rv1810		0.39	2.01	CONSERVED HYPOTHETICAL PROTEIN
Rv1811	mgtC	0.29	1.95	POSSIBLE Mg2+ TRANSPORT P-TYPE ATPASE C MGTC
Rv1819c		3.56	2.12	DRUGS-TRANSPORT TRANSMEMBRANE ATP-BINDING ABC TRANSPORTER
Rv1820	ilvG	1.84	2.56	ACETOLACTATE SYNTHASE ILVG

Rv1827		1.23	2.08	CONSERVED HYPOTHETICAL PROTEIN
Rv1828		0.85	2.06	CONSERVED HYPOTHETICAL PROTEIN
Rv1832	gcvB	4.60	2.07	GLYCINE DEHYDROGENASE GCVB
Rv1837c	glcB	4.61	3.09	MALATE SYNTHASE G GLCB
Rv1843c	guaB1	0.90	3.17	INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE GUAB1
Rv1853	ureD	3.82	2.00	UREASE ACCESSORY PROTEIN URED
Rv1854c	ndh	6.67	2.50	NADH DEHYDROGENASE NDH
Rv1856c		3.15	7.91	OXIDOREDUCTASE
Rv1857	modA	2.84	3.58	MOLYBDATE-BINDING LIPOPROTEIN MODA
Rv1954c		5.73	2.93	HYPOTHETICAL PROTEIN
Rv1992c	ctpG	2.70	4.09	METAL CATION TRANSPORTER P-TYPE ATPASE G CTPG
Rv2005c		4.16	2.76	CONSERVED HYPOTHETICAL PROTEIN
Rv2115c		1.76	3.84	ATPASE
Rv2136c		0.25	2.03	CONSERVED TRANSMEMBRANE PROTEIN
Rv2150c	ftsZ	0.23	1.99	CELL DIVISION PROTEIN FTSZ
Rv2153c	murG	5.00	5.74	UPD-N-ACETYLGLUCOSAMINE-N-ACETYLMURAMYL-PYROPHOSPHORYL-UNDECAPRENOL-N-ACETYLGLUCOSAMINE TRANSFERASE MURG
Rv2156c	murX	1.55	3.13	PHOSPHO-N-ACETYLMURAMOYL-PENTAPPEPTIDETRANSFERASE MURX
Rv2163c	pbpB	1.65	3.15	PENICILLIN-BINDING MEMBRANE PROTEIN PBPB
Rv2164c		1.36	2.16	CONSERVED PROLINE RICH MEMBRANE PROTEIN
Rv2169c		0.95	2.15	CONSERVED TRANSMEMBRANE PROTEIN
Rv2178c	aroG	3.53	2.08	3-DEOXY-D-ARABINO-HEPTULOSONATE 7-PHOSPHATE SYNTHASE AROG
Rv2181		4.76	7.75	CONSERVED INTEGRAL MEMBRANE PROTEIN
☆Rv2182c		0.55	3.97	1-ACYLGLYCEROL-3-PHOSPHATE O-ACYLTRANSFERASE
Rv2195	qcrA	3.71	2.11	RIESKE IRON-SULFUR PROTEIN QCRA
Rv2210c	ilvE	1.72	2.45	BRANCHED-CHAIN AMINO ACID TRANSAMINASE ILVE
Rv2256c		4.54	2.17	CONSERVED HYPOTHETICAL PROTEIN

Rv2261c		0.69	5.21	CONSERVED HYPOTHETICAL PROTEIN
Rv2319c		2.79	2.60	HYPOTHETICAL PROTEIN
Rv2325c		1.75	3.10	CONSERVED HYPOTHETICAL PROTEIN
Rv2329c	narK1	2.49	1.99	NITRITE EXTRUSION PROTEIN 1 NARK1
Rv2366c		3.72	2.09	CONSERVED TRANSMEMBRANE PROTEIN
Rv2373c	dnaJ2	0.50	2.53	CHAPERONE PROTEIN DNAJ2
☆Rv2379c	mbtF	3.29	5.15	PEPTIDE SYNTHETASE MBTF
☆Rv2380c	mbtE	0.10	5.03	PEPTIDE SYNTHETASE MBTE
☆Rv2381c	mbtD	4.31	4.38	POLYKETIDE SYNTHETASE MBT
☆Rv2383c	mbtB	2.55	8.35	PHENYLOXAZOLINE SYNTHASE MBTB
☆Rv2384	mbtA	3.63	4.49	BIFUNCTIONAL ENZYME MBTA: SALICYL-AMP LIGASE
☆Rv2385	mbtJ	1.56	3.94	ACETYL HYDROLASE MBTJ
☆Rv2386c	mbtI	3.40	8.98	ISOCHORISMATE SYNTHASE MBTI
☆Rv2391	nirA	5.01	3.04	FERREDOXIN-DEPENDENT NITRITE REDUCTASE NIRA
☆Rv2429	ahpD	1.91	4.14	ALKYL HYDROPEROXIDE REDUCTASE D PROTEIN AHPD
Rv2451		0.38	3.04	PROLINE AND SERINE RICH PROTEIN
Rv2462c	tig	0.22	1.89	TRIGGER FACTOR (TF) PROTEIN TIG
Rv2495c	pdhC	2.55	2.29	PROBABLE TRIGGER FACTOR (TF) PROTEIN TIG
Rv2496c	pdhB	2.76	2.55	PYRUVATE DEHYDROGENASE E1 COMPONENT (BETA SUBUNIT) PDHB
Rv2498c	citE	1.52	3.88	CITRATE (PRO-3S)-LYASE
Rv2501c	accA1	3.9	3.02	ACETYL-/PROPIONYL-COENZYME A CARBOXYLASE
Rv2504c	scoA	0.40	2.75	SUCCINYL-COA:3-KETOACID-COENZYME A TRANSFERASE
Rv2552c	aroE	5.44	1.93	SHIKIMATE 5-DEHYDROGENASE AROE
☆Rv2590	fadD9	7.13	4.25	FATTY-ACID-CoA LIGASE FADD9
☆Rv2620c		4.56	5.53	FATTY-ACID-CoA LIGASE FADD9
☆Rv2621c		2.99	2.89	TRANSCRIPTIONAL REGULATORY PROTEIN

Rv2622		4.91	2.54	METHYLTRANSFERASE
Rv2641		0.25	7.26	CADMIUM INDUCIBLE PROTEIN CADI
Rv2643	arsC	0.17	2.43	ARSENIC-TRANSPORT INTEGRAL MEMBRANE PROTEIN ARSC
Rv2651c		1.18	2.28	phiRv2 PROPHAGE PROTEASE
Rv2675c		0.83	2.16	CONSERVED HYPOTHETICAL PROTEIN
Rv2682c	dxs	0.13	2.39	1-DEOXY-D-XYLULOSE 5-PHOSPHATE SYNTHASE DXS1
Rv2707		0.61	1.97	CONSERVED TRANSMEMBRANE ALANINE AND LEUCINE RICH PROTEIN
☆Rv2710	sigB	0.40	4.91	RNA POLYMERASE SIGMA FACTOR SIGB
Rv2714		3.00	1.81	RNA POLYMERASE SIGMA FACTOR SIGB
Rv2724c	fadE20	2.74	3.58	ACYL-CoA DEHYDROGENASE FADE20
Rv2726c	dapF	4.99	2.39	DIAMINOPIMELATE EPIMERASE DAPF (DAP EPIMERASE)
Rv2729c		1.15	4.84	CONSERVED INTEGRAL MEMBRANE ALANINE, VALINE, LEUCINE RICH PROTEIN
Rv2743c		2.69	2.64	CONSERVED TRANSMEMBRANE ALANINE RICH PROTEIN
☆Rv2744c	35kd_ag	0.94	2.93	CONSERVED 35 KDA ALANINE RICH PROTEIN
Rv2745c		0.063	2.20	TRANSCRIPTIONAL REGULATORY PROTEIN
Rv2753c	dapA	3.36	2.02	DIHYDRODIPICOLINATE SYNTHASE DAPA
Rv2782c	pepR	0.00	3.08	ZINC PROTEASE PEPR
Rv2783c	gpsI	0.10	1.87	BIFUNCTIONAL PROTEIN POLYRIBONUCLEOTIDE NUCLEOTIDYLTRANSFERASE GPSI
Rv2786c	ribF	0.18	2.04	BIFUNCTIONAL FAD SYNTHETASE/RIBOFLAVIN BIOSYNTHESIS PROTEIN RIBF
☆Rv2787		2.42	1.76	CONSERVED HYPOTHETICAL ALANINE RICH PROTEIN
Rv2793c	truB	2.79	2.53	TRNA PSEUDOURIDINE SYNTHASE B TRUB
Rv2836c	dinF	2.08	4.18	DNA-DAMAGE-INDUCIBLE PROTEIN F DINF
Rv2837c		1.59	3.61	CONSERVED HYPOTHETICAL PROTEIN
Rv2838c	rbfA	4.12	2.18	RIBOSOME-BINDING FACTOR A RBF
Rv2839c	infB	5.84	3.32	TRANSLATION INITIATION FACTOR IF-2 INFB
Rv2842c		2.98	3.12	CONSERVED HYPOTHETICAL PROTEIN

Rv2850c		3.89	2.55	MAGNESIUM CHELATASE
Rv2852c		5.71	3.19	MALATE:QUINONE OXIDOREDUCTASE MQO
Rv2867c		1.79	3.50	CONSERVED HYPOTHETICAL PROTEIN
Rv2899c	fdhD	1.76	2.39	POSSIBLE FDHD PROTEIN HOMOLOG
Rv2900c	fdhF	1.02	2.18	FORMATE DEHYDROGENASE H FDHF
Rv2920c	amt	0.02	2.23	AMMONIUM-TRANSPORT INTEGRAL MEMBRANE PROTEIN AMT
Rv2925c	rnc	4.66	1.90	RIBONUCLEASE III RNC (RNASE III
☆Rv2930	fadD26	2.82	4.15	FATTY-ACID-CoA LIGASE FADD26
Rv2933	ppsC	0.36	2.75	PHENOLPTHIOCEROL SYNTHESIS TYPE-I POLYKETIDE SYNTHASE PPSC
Rv2934	ppsD	3.41	4.30	PHENOLPTHIOCEROL SYNTHESIS TYPE-I POLYKETIDE SYNTHASE PPSD
Rv2950c	fadD29	1.11	2.44	FATTY-ACID-CoA LIGASE FADD29 (FATTY-ACID-CoA SYNTHETASE
Rv2977c	thiL	1.08	2.17	THIAMINE-MONOPHOSPHATE KINASE THIL
Rv2978c		1.89	1.96	PROBABLE TRANSPOSASE
☆Rv2988c	leuC	0.79	4.48	3-ISOPROPYLMALATE DEHYDRATASE (LARGE SUBUNIT) LEUC
Rv3001c	ilvC	2.03	2.12	KETOL-ACID REDUCTOISOMERASE ILVC
☆Rv3010c	pfkA	0.89	2.26	PROBABLE 6-PHOSPHOFRUCTOKINASE PFKA
Rv3029c	fixA	3.40	2.06	ELECTRON TRANSFER FLAVOPROTEIN (BETA-SUBUNIT) FIXA
Rv3037c		0.41	2.26	CONSERVED HYPOTHETICAL PROTEIN
Rv3042c	serB2	2.14	2.03	PHOSPHOSERINE PHOSPHATASE SERB2
☆Rv3049c		5.57	3.89	MONOOXYGENASE
Rv3097c	PE	2.38	2.25	PE-PGRS FAMILY PROTEIN, PROBABLY TRIACYLGLYCEROL LIPASE
Rv3139	fadE24	0.93	5.24	ACYL-CoA DEHYDROGENASE FADE24
☆Rv3140	fadE23	1.53	5.82	ACYL-CoA DEHYDROGENASE FADE23
Rv3236c	kefB	0.84	3.98	CONSERVED INTEGRAL MEMBRANE TRANSPORT PROTEIN
✪Rv3246c	mtrA	1.86	1.96	TWO COMPONENT SENSORYTRANSCRIPTIONAL REGULATOR
Rv3248c	sahH	1.56	2.43	ADENOSYLHOMOCYSTEINASE SAHH

Rv3256c		2.04	3.41	CONSERVED HYPOTHETICAL PROTEIN
Rv3259		2.24	2.18	CONSERVED HYPOTHETICAL PROTEIN
Rv3264c	rmlA2	5.00	2.58	D-ALPHA-D-MANNOSE-1-PHOSPHATE GUANYLYLTRANSFERASE MANB
Rv3266c	rmlD	2.35	1.91	dTDP-6-DEOXY-L-LYXO-4-HEXULOSE REDUCTASE RMLD
Rv3270	ctpC	2.13	6.68	METAL CATION-TRANSPORTING P-TYPE ATPASE C CTPC
Rv3273		1.33	1.98	TRANSMEMBRANE CARBONIC ANHYDRASE
Rv3274c	fadE25	0.19	2.33	ACYL-CoA DEHYDROGENASE FADE25
Rv3279c	birA	0.18	4.57	BIFUNCTIONAL PROTEIN BIRA: BIOTIN OPERON REPRESSOR + BIOTIN
Rv3290c	lat	0.22	3.74	L-LYSINE-EPSILON AMINOTRANSFERASE LAT
Rv3335c		0.59	2.26	CONSERVED INTEGRAL MEMBRANE PROTEIN
Rv3375	amiD	1.43	1.94	PROBABLE AMIDASE AMID
Rv3383c	idsB	3.55	2.88	POLYPRENYL SYNTHETASE IDSB
☆Rv3402c		4.39	3.90	CONSERVED HYPOTHETICAL PROTEIN
Rv3409c	choD	1.77	2.41	CHOLESTEROL OXIDASE PRECURSOR CHOD
Rv3414c	sigD	2.30	2.86	PROBABLE ALTERNATIVE RNA POLYMERASE SIGMA-D FACTOR SIGD
Rv3419c	gcp	1.13	2.98	O-SIALOGLYCOPROTEIN ENDOPEPTIDASE GCP
Rv3457c	rpoA	1.96	2.26	PROBABLE DNA-DIRECTED RNA POLYMERASE (ALPHA CHAIN) RPOA
Rv3482c		1.90	1.85	CONSERVED MEMBRANE PROTEIN
Rv3520c		3.92	1.94	SHORT-CHAIN TYPE DEHYDROGENASE/REDUCTASE
Rv3562	fadE31	2.22	2.09	ACYL-CoA DEHYDROGENASE FADE31
Rv3568c		3.44	2.36	BIPHENYL-2,3-DIOL 1,2-DIOXYGENASE BPHC
Rv3581c	ispF	0.78	2.87	2C-METHYL-D-ERYTHRITOL 2,4-CYCLODIPHOSPHATE SYNTHASE ISPF
Rv3582c	ispD	6.07	3.64	PROBABLE 4-DIPHOSPHOCYTIDYL-2C-METHYL-D-ERYTHRITOL SYNTHASE ISPD
Rv3592		1.88	1.98	CONSERVED HYPOTHETICAL PROTEIN
Rv3600c		1.49	3.41	CONSERVED HYPOTHETICAL PROTEIN
Rv3602c	panC	0.09	2.42	PANTOATE--BETA-ALANINE LIGASE PANC

Rv3603c		0.39	3.10	CONSERVED HYPOTHETICAL ALANINE AND LEUCINE RICH PROTEIN
Rv3608c	folP	4.22	1.81	DIHYDROPTEROATE SYNTHASE 1 FOLP
Rv3627c		1.03	1.89	CONSERVED HYPOTHETICAL PROTEIN
Rv3645		1.47	3.43	CONSERVED TRANSMEMBRANE PROTEIN
Rv3671c		0.14	1.89	MEMBRANE-ASSOCIATED SERINE PROTEASE
Rv3672c		9.44	2.69	CONSERVED HYPOTHETICAL PROTEIN
Rv3710	leuA	2.44	1.92	2-ISOPROPYLMALATE SYNTHASE LEUA
Rv3743c		1.42	8.69	CATION TRANSPORTER P-TYPE ATPASE CTPJ
Rv3745c		3.32	6.06	CONSERVED HYPOTHETICAL PROTEIN
Rv3756c	proZ	2.30	2.24	OSMOPROTECTANT TRANSPORT INTEGRAL MEMBRANE PROTEIN ABC TRANSPORTER PROZ
Rv3765c	tcrx	1.03	2.83	TWO COMPONENT TRANSCRIPTIONAL REGULATORY PROTEIN TCRX
Rv3767c		2.97	2.10	CONSERVED HYPOTHETICAL PROTEIN
Rv3798		3.80	1.98	TRANSPOSASE
Rv3802c		3.07	2.42	CONSERVED MEMBRANE PROTEIN
Rv3804c	fbpA	3.42	2.53	SECRETED ANTIGEN 85-A FBPA
Rv3806c		8.93	2.26	CONSERVED INTEGRAL MEMBRANE PROTEIN
Rv3825c	pks2	1.35	3.02	POLYKETIDE SYNTHASE PKS2
Rv3827c		2.52	12.85	TRANSPOSASE
Rv3837c		5.01	2.36	PHOSPHOGLYCERATE MUTASE
Rv3838c	pheA	1.77	2.32	PREPHENATE DEHYDRATASE PHEA
☆Rv3839		1.65	5.74	CONSERVED HYPOTHETICAL PROTEIN
✪Rv3842c	glpQ1	2.67	2.16	GLYCEROPHOSPHORYL DIESTER PHOSPHODIESTERASE GLPQ1
Rv3858c	gltD	4.99	1.94	NADH-DEPENDENT GLUTAMATE SYNTHASE (SMALL SUBUNIT) GLTD
Rv3859c	gltB	0.83	2.85	PROBABLE FERREDOXIN-DEPENDENT GLUTAMATE SYNTHASE GLTB
Rv3870		3.12	3.04	CONSERVED TRANSMEMBRANE PROTEIN
Rv3871		2.22	2.23	CONSERVED HYPOTHETICAL PROTEIN

Rv3879c	0.08	2.58	ALANINE AND PROLINE RICH PROTEIN
Rv3884c	0.75	2.37	CBXX/CFQX FAMILY PROTEIN
Rv3885c	0.14	1.83	CONSERVED MEMBRANE PROTEIN
Rv3888c	1.25	2.27	CONSERVED MEMBRANE PROTEIN
Rv3889c	4.93	1.72	HYPOTHETICAL PROTEIN
Rv3892c	1.26	2.32	PPE
Rv3905c	4.54	9.88	ESAT-6 LIKE PROTEIN ESXF

✪Genes found to be repressed in *M. tuberculosis* (H37Rv) under low-iron conditions by Rodriguez *et al*. (2002).
☆Genes found to be upregulated in *M. tuberculosis* (H37Rv) under low-iron conditions by Rodriguez *et al*. (2002).