

TABLE S2. *B. pertussis* genes with decreased transcript abundance under conditions of iron limitation^a

Locus tag	Description	Fold change	FC category ^b	MultiFun heading ^c
BP0038	<i>gloA</i> lactoylglutathione lyase	0.5	3.3.05	Central intermediary metabolism
BP0091	<i>bplC</i> , <i>wlbC</i> lipopolysaccharide biosynthesis protein	0.7	4.1.4	Cell envelope
BP0174	<i>bfr</i> bacterioferritin	0.4	1.6.3	Adaptation
BP0258	conserved hypothetical protein	0.5	0.0.2	Conserved in organism other than <i>E. coli</i>
BP0275	<i>petC</i> cytochrome C1 precursor	0.5	3.5.3	Energy metabolism, carbon
BP0276	<i>petB</i> , <i>cytB</i> cytochrome B	0.4	3.5.3	Energy metabolism, carbon
BP0399	putative glycosyl transferase	0.2	4.1.4	Cell envelope
BP0546	bacterioferritin	0.6	1.6.3	Adaptation
BP0547	putative lysine decarboxylase	0.5	3.4.2	Degradation of small molecules
BP0842	<i>nuoB</i> NADH-ubiquinone oxidoreductase, 20 kDa subunit	0.4	3.5.0	Energy metabolism, carbon
BP0843	<i>nuoC</i> respiratory-chain NADH dehydrogenase, 30 kDa subunit	0.4	3.5.0	Energy metabolism, carbon
BP0844	<i>nuoD</i> respiratory-chain NADH dehydrogenase, 49 kDa subunit	0.4	3.5.0	Energy metabolism, carbon
BP0845	<i>nuoE</i> respiratory-chain NADH dehydrogenase I, 24 kDa subunit	0.4	3.5.0	Energy metabolism, carbon
BP0846	<i>nuoF</i> respiratory-chain NADH dehydrogenase, 51 kDa subunit	0.5	3.5.0	Energy metabolism, carbon
BP0849	<i>nuoI</i> NADH-ubiquinone oxidoreductase, chain I	0.6	3.5.0	Energy metabolism, carbon
BP0989	<i>prlC</i> , <i>opdA</i> oligopeptidase A	0.3	2.1.4	Macromolecule degradation
BP1040	PhoH-like protein	0.5	7.0.0	Some information, but not classifiable
BP1041	conserved hypothetical protein	0.3	0.0.2	Conserved in organism other than <i>E. coli</i>
BP1070	<i>pstC</i> , <i>phoW</i> phosphate transport system permease protein	0.7	3.3.13	Central intermediary metabolism
BP1261	conserved hypothetical protein (pseudogene)	0.5	0.0.2	Conserved in organism other than <i>E. coli</i>
BP1262	<i>rho</i> , <i>nitA</i> , <i>psuA</i> , <i>rnsC</i> , <i>tsu</i> , <i>sbaA</i> transcription termination factor Rho	0.5	2.2.11	Macromolecule synthesis, modification
BP1470	putative iron-sulfur binding protein	0.6	3.5.3	Energy metabolism, carbon
BP1538	<i>ilvG</i> putative acetolactate synthase large subunit	0.5	3.1.21	Amino acid biosynthesis
BP1612	<i>recG</i> ATP-dependent DNA helicase	0.4	2.2.03	Macromolecule synthesis, modification
BP1629	<i>wbpO</i> capsular polysaccharide biosynthesis protein	0.5	4.1.4	Cell envelope
BP1629	<i>wbpO</i> capsular polysaccharide biosynthesis protein	0.6	4.1.4	Cell envelope
BP1630	capsular polysaccharide biosynthesis protein, UDP-N-acetylglucosamine C4 epimerase	0.6	4.1.4	Cell envelope

BP1777	<i>lon, capR, deg, muc, lopA</i> ATP-dependent protease La	0.4	2.1.4	Macromolecule degradation
BP1908	<i>cysS</i> cysteinyl-tRNA synthetase	0.7	2.2.01	Macromolecule synthesis, modification
BP2049	putative sulfate transporter	0.4	1.5.4	Transport/binding proteins
BP2328	putative transferase	0.5	2.2.05	Macromolecule synthesis, modification
BP2362	<i>sdhD</i> succinate dehydrogenase hydrophobic membrane anchor protein	0.5	3.5.8	Energy metabolism, carbon
BP2401	putative coenzyme A transferase subunit	0.6	7.0.0	Some information, but not classifiable
BP2491	putative cytochrome	0.6	3.5.3	Energy metabolism, carbon
BP2574	<i>pheS</i> phenylalanyl-tRNA synthetase alpha chain	0.4	2.2.11	Macromolecule synthesis, modification
BP2752	putative exported protein	0.7	4.1.0	Periplasmic/exported/lipoproteins
BP2790	putative exported protein	0.5	4.1.0	Periplasmic/exported/lipoproteins
BP2792	hypothetical protein	0.5	0.0.0	Unknown proteins, no known homologs
BP2889	putative c' cytochrome	0.6	3.5.3	Energy metabolism, carbon
BP2980	putative lipoprotein	0.5	4.1.0	Periplasmic/exported/lipoproteins
BP3036	putative hydrolase	0.7	7.0.0	Some information, but not classifiable
BP3038	putative membrane protein	0.6	4.1.1	Cell envelope
BP3060	putative transglycosylase	0.5	4.1.2	Cell envelope
BP3086	<i>hslV, htpO</i> ATP-dependent protease heat shock protein	0.4	1.3.1	Folding and ushering proteins
BP3219	putative exported protein	0.6	4.1.0	Periplasmic/exported/lipoproteins
BP3282	<i>atpB, uncB, papD</i> ATP synthase A chain	0.4	3.5.9	Energy metabolism, carbon
BP3291	hemE uroporphyrinogen decarboxylase	0.6	3.2.06	Biosynthesis of cofactors, carriers
BP3325	putative pterin-4-alpha-carbinolamine dehydratase	0.5	7.0.0	Some information, but not classifiable
BP3426	putative amidase	0.7	3.3.00	Central intermediary metabolism
BP3431	putative branched-chain amino acid transport ATP-binding ABC transporter	0.6	1.5.1	Transport/binding proteins
BP3573	putative branched-chain amino acid transport permease	0.5	1.5.1	Transport/binding proteins
BP3596	periplasmic binding protein	0.6	4.1.0	Periplasmic/exported/lipoproteins
BP3609	<i>rpsG</i> 30S ribosomal protein S7	0.5	4.2.2	Ribosome constituents
BP3614	<i>rplD</i> 50S ribosomal protein L4	0.3	4.2.2	Ribosome constituents
BP3617	<i>rpsS</i> 30S ribosomal protein S19	0.4	4.2.2	Ribosome constituents
BP3622	<i>rpsQ</i> 30S ribosomal protein S17	0.5	4.2.2	Ribosome constituents
BP3644	histidine triad protein (pseudogene)	0.6	7.0.0	Some information, but not classifiable
BP3647	putative membrane protein	0.7	4.1.1	Cell envelope
BP3652	putative cytochrome c assembly protein	0.5	3.5.3	Energy metabolism, carbon

BP3744	putative bifunctional protein	0.4	7.0.0	Some information, but not classifiable
BP3754	glutamate synthase [NADPH] small chain precursor	0.5	3.1.07	Amino acid biosynthesis
BP3852	<i>kata</i> catalase	0.5	1.4.2	Protection responses

1 ^a Genes with significant differences in transcript abundance between the two nutritional growth conditions,
2 based on SAM analysis (false discovery rate = 0.56%). Genes are listed in chromosomal order.

3 ^b Functional classification as assigned by Parkhill and coworkers (66).

4 ^c Descriptive multifunctional classification (78).