Table S1: Summary of microarray gene expression profile of *P.gingivalis* under single NO stress.

Gene ID[a]	Common Name	Function	Fold-Change	*p* value
PG1181	Hypothetical protein (probable transcriptional regulator tetR family)	Unknown	76.18	2.29E-07
PG0612	Hypothetical protein	Unknown	29.10	0.00089
PG1019	Hypothetical protein	Unknown	24.24	2.10E-06
PG1178	Hypothetical protein	Unknown	12.18	1.28E-06
PG1179	Conserved hypothetical protein	Unknown	11.95	0.000134
PG1236	Hypothetical protein	Unknown	11.94	2.52E-05
PG0914	Hypothetical protein	Unknown	11.34	7.57E-05
PG1858	fldA Flavodoxin A	Energy metabolism; Electron transport	11.28	0.00023
PG0411	PG57 (possible outer membrane protein)	Cell envelope	9.43	0.000176
PG0999	Hypothetical protein	Unknown	9.19	0.001852
PG1492	Hypothetical protein	Unknown	9.16	0.005424
PG0409	Conserved hypothetical protein	Unknown	8.90	2.41E-05
PG0613	Possible outer membrane-associated protein P23	Cell envelope	8.03	0.000382
PG1180	Conserved hypothetical protein (probable membrane transport protein)	Unknown	7.89	0.000379
PG0408	ileS Isoleucyl-tRNA synthetase	Translation; Aminoacyl-tRNA synthetases	7.80	0.000559
PG1237	Possible transcriptional regulator	Regulatory functions	7.74	6.20E-08
PG1030	Hypothetical protein	Unknown	7.37	0.001316
PG0410	Conserved hypothetical protein	Unknown	6.93	0.000281
PG0245	UspA Universal stress protein	Cellular processes; Adaptations to atypical conditions	6.84	0.000107
PG1493	Conserved hypothetical protein	Unknown	6.74	0.001988
PG1491	Hypothetical protein	Unknown	6.53	7.56E-05
PG0521	GroES protein 10 kDa chaperonin/heat shock protein (protein cpn10)	Protein fate; Protein folding and stabilization	6.37	0.001182
PG0614	Hypothetical protein	Unknown	6.31	0.000224
PG0997	Hypothetical protein	Unknown	6.03	0.002304
PG0611	Possible lipoprotein	Unassigned	5.74	8.70E-05
PG0495	Conserved hypothetical protein	Unknown	5.71	0.000293
PG1551	hmuY protein tonB-dependent receptor	Transport and binding; Cations	5.63	1.26E-05
PG1000	Hypothetical protein	Unknown	5.43	0.000193
PG0004	Probable phosphoribosyltransferase transcriptional regulator	Regulatory functions	5.40	3.59E-06
PG1326	Outer membrane receptor; putative hemagglutinin	Cell envelope	5.36	0.000413
PG0090	dps DNA-binding stress protein	Cellular processes; Adaptations to atypical conditions	5.23	0.002799
PG1001	Conserved hypothetical protein	Unknown	5.03	0.002784

PG1870	Methyltransferase	Uncategorized	4.83	0.000327
PG1798	Immunoreactive 46 kDa antigen PG99	Uncategorized	4.80	0.001417
PG0045	htpG heat shock protein; HSP90 family	Cellular processes; Chaperones	4.79	0.000586
PG0319	Conserved hypothetical protein	Unknown	4.69	6.21E-05
PG1829	fadD long-chain-fatty-acid-CoA ligase (probable polyketide synthetase)	Fatty acid and phospholipid metabolism	4.48	9.11E-05
PG0778	gcp (possible glycoprotein endopeptidase)	Protein fate; Degradation of proteins, peptides and glycopeptides	4.38	0.000186
PG0466	Conserved hypothetical protein	Unknown	4.37	0.000191
PG1837	hagA HbR hemagglutinin/adhesin precursor hagA	Cellular processes; Pathogenesis	4.37	7.27E-05
PG0861	Superfamily II helicase	Transcription	4.36	0.000703
PG2215	manC Mannose-1-phosphate guanylyltransferase	Purines, pyrimidines, nucleosides and nucleotides; Sugar-nucleotide Biosynthesis and conversions	4.30	2.88E-05
PG0777	etfB electron transfer flavoprotein beta subunit	Energy metabolism; Electron transport	4.29	5.52E-06
PG1765	acpP acyl carrier protein	Fatty acid and phospholipid metabolism; Biosynthesis	4.22	0.000234
PG1210	Xaa-Pro aminopeptidase	Amino acid biosynthesis	4.06	0.000988
PG1320	ISPg1 fragment (IS1126-related transposase fragment)	Transposon functions	4.04	2.09E-05
PG2049	Hypothetical protein	Unknown	4.03	0.018452
PG0246	UstA stationary-phase-upregulated protein	Cellular processes; Adaptations to atypical conditions	4.00	5.36E-05
PG0460	ISPg1 transposase (IS1106-related transposase)	Transposon functions	3.96	0.000153
PG2031	Hypothetical protein	Unknown	3.90	0.001538
PG0549	ISPg1 transposase (IS1106-related transposase)	Transposon functions	3.84	0.000144
PG0184	ISPg1 transposase (IS1106-related transposase)	Transposon functions	3.80	0.00105
PG1002	Hypothetical protein	Unknown	3.79	0.007273
PG2048	Hypothetical protein	Unknown	3.74	0.000359
PG1682	Glycosyl transferase, group 1 family protein	Unassigned	3.73	0.000734
PG1652	Probable integral outer membrane protein P64	Cell envelope	3.60	0.000256
PG0386	Recombinase/integrase	DNA metabolism; DNA replication, restriction, modification, recombination, and repair	3.60	5.67E-05
PG1857	Hypothetical protein	Unknown	3.52	0.000116
PG1172	Conserved hypothetical protein (containing ferredoxin-like domain)	Unknown	3.45	0.000101
PG0776	etfA electron transfer flavoprotein	Energy metabolism; Electron	3.42	0.000273

	alpha subunit	transport		
PG1176	ABC transporter protein (NBD and MSD domains)	Transport and binding	3.37	0.001575
PG1212	Hypothetical protein	Unknown	3.33	0.000182
PG1239	fabG 3-oxyacyl [acyl-carrier protein] reductase	Fatty acid and phospholipid metabolism	3.32	3.81E-06
PG1862	Hypothetical protein	Unknown	3.31	0.075455
PG1240	Conserved hypothetical protein (probable transcription regulator)	Unknown	3.29	0.000252
PG0686	Conserved hypothetical protein	Unknown	3.29	0.034171
PG2172	Hypothetical protein	Unknown	3.27	0.000331
PG1209	Conserved hypothetical protein	Unknown	3.26	0.002942
PG1681	Agl malQ glycogen debranching enzyme/4-alpha-glucanotransferase	Energy metabolism; Biosynthesis and degradation of polysaccharides	3.25	0.000123
PG1171	Conserved hypothetical protein	Unknown	3.23	1.25E-06
PG2190	ftsE cell-division ATP-binding protein	Cellular processes; Cell division	3.19	0.000576
PG0898	Conserved hypothetical protein	Unknown	3.14	0.001674
PG1683	amyA alpha-amylase	Energy metabolism; Sugars	3.14	0.000921
PG0860	Hypothetical protein (possible transcription regulator Lambda repressor-like)	Transcription	3.13	0.00085
PG1770	Hypothetical protein	Unknown	3.09	0.000117
PG2023	fmt methionyl-tRNA formyltransferase	Translation, Amino Acid Metabolism, Methionine metabolism, biosynthetic process	3.078	1.09E-05
PG1025	Hypothetical protein	DNA metabolic process	3.07	0.002919
PG1003	Conserved hypothetical protein	Unknown	3.02	0.00799
PG2050	Hypothetical protein	Unknown	3.02	0.002325
PG1291	Hypothetical protein (phospholipase D family related)	Metabolic process	3.00	0.001128
PG2042	Hypothetical protein (AhpC-TSA, Thioredoxin-related)	Unknown	2.99	0.006439
PG1764	fabF 3-oxoacyl-acyl-carrier-protein synthase	Fatty acid and phospholipid metabolism	2.99	5.09E-05
PG1732	xerD integrase/recombinase (XerD-related)	DNA metabolism; DNA replication, recombination and repair	2.98	3.14E-05
PG0823	Conserved hypothetical protein (possible transcriptional regulator)	Unknown	2.98	0.074261
PG0933	fusA translation elongation factor G protein	Translation; Translation factors	2.98	9.12E-05
PG1127	asnC transcriptional regulatory protein	Transcription	2.98	0.002257
PG1372	Hypothetical protein	Unknown	2.94	0.000208
PG1684	Hypothetical protein	Unknown	2.93	0.001614
PG0618	ahpC ahpF alkyl hydroperoxide reductase subunit C (alkyl hydroperoxide reductase subunit F)	Cellular processes; Detoxification	2.91	0.040574

PG0340	Hypothetical protein	Unknown	2.91	0.002307
PG1213	ribonuclease H-related protein	Transcription; Degradation of RNA	2.85	0.000565
PG0293	Conserved hypothetical protein	Unknown	2.84	0.001489
PG0339	Hypothetical protein	Unknown	2.83097	0.000636
PG1219	Conserved hypothetical protein	Unknown	2.82	0.00091
PG0520	groEL 60 kD chaperonin (protein cpn60; GroEL protein; heat shock protein 60)	Cellular processes; Chaperones	2.79	0.003218
PG0161	Pg-II fim c (Pg-II fimbriae c)	Cell envelope; Surface structures	2.77	0.012964
PG1175	ABC transporter, ATP-binding protein	Transport and binding	2.77	3.24E-05
PG1696	Conserved hypothetical protein	Unknown	2.71	0.000964
PG0468	manA mannose-6-phosphate isomerase	Energy metabolism; Sugars	2.70	0.000254
PG1208	dnaK (DnaK protein; Hsp70)	Regulatory functions	2.65	0.000213
PG1330	mscL large conductance mechanosensitive channel protein	Transport and binding	2.62	0.001839
PG0350	Conserved hypothetical protein	Unknown	2.60	0.002158
PG0775	acads mmgC yqiN acyl-CoA dehydrogenase (coenzyme A dehydrogenase)	Uncategorized	2.57	4.34E-06
PG0638	lpxK tetraacyldisaccharide 4'-kinase	Cell envelope; Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides	2.55	2.31E-05
PG1819	Conserved hypothetical protein	Unknown	2.51	0.001309
PG1626	Possible outer membrane-associated protein P58	Cell envelope	2.51	0.00014
PG0862	Probable type II DNA modification enzyme (methyltransferase)	DNA metabolism; Restriction/modification	2.50	3.02E-06
PG0706	Hypothetical protein	Unknown	2.50	0.006705
PG1015	Hypothetical protein	Unknown	2.49	0.034398
PG1625	Hypothetical protein	Unknown	2.49	0.004952
PG1020	Conserved hypothetical protein; possible outer membrane receptor protein	Receptor activity; transporter activity	2.48	0.004015
PG0422	Hypothetical protein	Unknown	2.47	0.000495
PG1623	cprC nosR (probable membrane-bound regulatory protein NosR)	Regulatory functions	2.45	0.000266
PG0347	galE NAD-dependent epimerase/dehydratase	Cell envelope; Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides	2.45	2.60E-05
PG0465	fur ferric uptake regulation protein	Regulatory functions	2.45	0.000986
PG1651	Conserved hypothetical protein (possible TPR-repeat protein)	Unknown	2.45	0.000508
PG1777	Conserved hypothetical protein	Unknown	2.44	0.018283
PG1369	gpsA NAD(P)H-dependent glycerol-3-phosphate dehydrogenase (NAD(P)H-	Fatty acid and phospholipid metabolism	2.43	0.003342

	dependent dihydroxyacetone-phosphate reductase)			
PG0058	nadD yqeJ nicotinate-nucleotide adenylyltransferase	Nicotinate and nicotinamide metabolism	2.42	0.012686
PG1211	Conserved hypothetical protein (possible carbonic anhydrase)	Unknown	2.42	0.000582
PG0344	Conserved hypothetical protein	Unknown	2.42	0.014029
PG0012	hisC histidinol-phosphate aminotransferase	Amino acid biosynthesis; Histidine family	2.41	0.003724
PG0998	Hypothetical protein	Unknown	2.41	0.002473
PG1602	tla tlr tonB-linked receptor Tlr	Receptor activity; transporter activity	2.41	0.013588
PG1775	grpE (GrpE-related chaperonin; HSP-70 cofactor)	Cellular processes; Chaperones	2.40	0.00064
PG2189	lysC aspartokinase-I	Amino acid biosynthesis; Aspartate family	2.39	0.000111
PG1063	Conserved hypothetical protein (possible transcriptional regulator)	Unknown	2.39	0.001038
PG1362	Conserved hypothetical protein (possible oxidoreductase)	Unknown	2.38	0.000741
PG0920	Glycosyltransferase (possible polyprenol phosphate mannosyl transferase 1)	Uncategorized	2.38	0.004919
PG2208	Conserved hypothetical protein	Unknown	2.38	0.07226
PG1793	glgB 1,4-alpha-glucan branching enzyme	Energy metabolism; Biosynthesis and degradation of polysaccharides	2.35	0.000618
PG0060	Hypothetical protein	Unknown	2.35	0.003634
PG0560	Unknown	Unknown	2.34	3.06E-06
PG1080	hbd 3-hydroxybutyryl-CoA dehydrogenase; BHBD)	Fatty acid and phospholipid metabolism	2.33	0.011712
PG1697	Restriction endonuclease	DNA metabolism; Restriction/modification	2.32	0.000448
PG1792	napA Na+/H+-exchanging protein (Na+/H+ antiporter)	Transport and binding; Cations	2.32	9.72E-05
PG0020	Possible transcriptional regulator, MarR family	Regulatory functions	2.32	0.002387
PG1085	Hypothetical protein	Unknown	2.32	0.028468
PG0278	Hypothetical protein	Unknown	2.31	0.00023
PG0438	Conserved hypothetical protein	Unknown	2.31	0.000137
PG1151	Conserved hypothetical protein (probable alcohol dehydrogenase)	Unknown	2.29	0.002559
PG1371	udp udp2 uridine phosphorylase	Purines, pyrimidines, nucleosides and nucleotides; Salvage of nucleosides and nucleotides	2.27	0.002429
PG1759	ABC transporter (SBP domain); adhesin	Transport and binding	2.26	0.007114
PG2010	mrsA phosphomannomutase/ phosphoglucomutase	Energy metabolism; Sugars	2.25	0.003112

PG0705	glr murI glutamate racemase	Cell envelope; Biosynthesis of murein sacculus and peptidoglycan	2.24	0.000236
PG2060	thyA thymidylate synthase	Purines, pyrimidines, nucleosides and nucleotides; 2'-Deoxyribonucleotide metabolism	2.24	0.001035
PG1778	Conserved hypothetical protein	Unknown	2.24	0.000436
PG1820	nrfA cytochrome c nitrite reductase large subunit	Energy metabolism; Electron transport	2.23	0.000481
PG2006	Conserved hypothetical protein	Unknown	2.23	0.128591
PG0558	pnp yqkO purine nucleoside phosphorylase	Purines, pyrimidines, nucleosides and nucleotides; Salvage of nucleosides and nucleotides	2.23	0.001942
PG1341	Probable outer membrane lipoprotein P15	Cell envelope	2.22	0.005083
PG2024	hagE rgpA arginine-specific cysteine proteinase; gingipain R1	Protein fate; Degradation of proteins, peptides and glycopeptides	2.22	0.000994
PG1552	hmuR tonB-dependent receptor HmuR (or HemR)	Transport and binding; Cations	2.21	0.000217
PG0249	oadA probable oxaloacetate decarboxylase alpha subunit	Transport and binding; Cations	2.20	0.007731
PG2030	Hypothetical protein	Unknown	2.19	0.000266
PG1863	Hypothetical protein	Unknown	2.19	0.075952
PG0471	Conserved hypothetical protein	Unknown	2.19	0.000701
PG0356	Conserved hypothetical protein	Unknown	2.18	0.000123
PG0056	Conserved hypothetical protein	Unknown	2.18	0.036954
PG1877	nhaA Na+/H+-exchanging protein (Na+/H+ antiporter)	Transport and binding; Cations	2.18	0.011702
PG1230	Hypothetical protein	Unknown	2.18	0.003043
PG2213	Possible nitrite reductase-related protein	Uncategorized	2.17	0.085316
PG0104	Top3 topB DNA topoisomerase III	DNA metabolism; DNA replication, recombination and repair	2.16	0.000659
PG1316	Conserved hypothetical protein	Unknown	2.15	0.007793
PG0174	noxA noxC NADH oxidase/peroxidase	Energy metabolism	2.15	0.015847
PG1058	pal peptidoglycan-associated lipoprotein	Cell envelope; Biosynthesis of murein sacculus and peptidoglycan	2.15	5.83E-05
PG1334	Conserved hypothetical protein (possible secreted protein; possible protease; stomatin-like protein)	Unknown	2.14	0.00054
PG1368	pgi glucose-6-phosphate isomerase	Energy metabolism; Glycolysis/gluconeogenesis	2.13	0.003417
PG1653	Conserved hypothetical protein	Unknown	2.13	1.35E-05
PG0669	cbiK ihtB fetB heme-binding	Cell envelope	2.13	0.000538

	protein/peripheral outer membrane chelatase			
PG0351	Hypothetical protein	Unknown	2.12	0.048539
PG1361	Ptp-A prolyl tripeptidyl peptidase	Protein fate; Degradation of proteins, peptides and glycopeptides	2.11	0.00315
PG0403	Hypothetical protein	Unknown	2.10	0.000721
PG1881	Conserved hypothetical protein	Unknown	2.08	0.003563
PG0923	rbfA ribosome binding factor A	Translation; Translation factors	2.078	0.001049
PG1355	Conserved hypothetical protein (probable 1-acylglycerol-3-phosphate O-acyltransferase)	Unknown	2.04	0.000547
PG1356	Conserved hypothetical protein	Unknown	2.03	0.003276
PG0660	NADPH-oxidoreductase	Energy metabolism	2.02	0.000332
PG1808	relA GTP pyrophosphokinase, (p)ppGpp synthetase	Regulatory functions	2.02	0.002524
PG0257	ycf24 ABC transporter subunit	Transport and binding	-2.00	0.219046
PG0199	Conserved hypothetical protein	Unknown	-2.01	0.00161299
PG1566	gltX gluS glutamyl-tRNA synthetase (glutamate--tRNA ligase)	Translation; Aminoacyl-tRNA synthetases	-2.01	0.00448847
PG0889	pepP probable Xaa-Pro dipeptidase	Protein fate; Degradation of proteins, peptides and glycopeptides	-2.02	0.0300502
PG1278	serC yhaF phosphoserine aminotransferase (PSAT) (vegetative protein 234)	Amino acid biosynthesis; Serine family	-2.02	0.00125546
PG0952	gcpE ispG 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate synthase	Cell envelope	-2.03	0.0017864
PG1805	atpD H+-transporting ATP synthase subunit D	Energy metabolism; ATP-proton motive force	-2.03	0.0017022
PG1596	ileS isoleucyl-tRNA synthetase (isoleucine--tRNA ligase; mupirocin resistance protein)	Translation; Aminoacyl-tRNA synthetases	-2.04	0.000413148
PG1430	Hypothetical protein	Unknown	-2.04	0.00501883
PG0432	fmu nol1 proliferating-cell nucleolar protein/rRNA methylase	Protein fate; Protein modification and repair	-2.04	0.0398006
PG0302	Hypothetical protein	Unknown	-2.05	0.00935446
PG1728	Conserved hypothetical protein (possible deaminase)	Unknown	-2.06	0.00263916
PG1039	Conserved hypothetical protein	Unknown	-2.07	0.000539893
PG1706	Hypothetical protein	Unknown	-2.07	0.0182339
PG0114	Hypothetical protein	Unknown	-2.07	0.0109611
PG0243	Hypothetical protein	Unknown	-2.08	0.00137145
PG2150	Conserved hypothetical protein, with LysM repeats	Unknown	-2.08	0.00063887
PG0791	adk adenylate kinase	Purines, pyrimidines, nucleosides and nucleotides; Purine ribonucleotide biosynthesis	-2.09	0.00638964

PG1564	dTDP-4-dehydrorhamnose 3,5-epimerase	Nucleotide sugars metabolism; Polyketide sugar unit biosynthesis; Streptomycin biosynthesis	-2.09	0.000354666
PG2112	Hypothetical protein	Unknown	-2.10	0.00247654
PG0555	Conserved hypothetical protein	Unknown	-2.11	0.000297158
PG1274	efp efp1 elongation factor P	Translation; Translation factors	-2.13	0.227553
PG1379	Probable thiamine biosynthesis protein/ABC related SBP	Biosynthesis of cofactors, prosthetic groups and carriers; Thiamine	-2.14	0.0202777
PG1739	ppx probable exopolyphosphatase	Central intermediary metabolism; Phosphorus compounds	-2.14	0.00216975
PG0415	Conserved hypothetical protein (possible peptidyl-prolyl isomerase)	Unknown	-2.14	0.00239185
PG1297	rpsA rs1 30S ribosomal protein S1	Translation; Ribosomal proteins	-2.15	0.000142668
PG0568	efp efp1 elongation factor P	Translation; Translation factors	-2.16	0.210948
PG2141	fabH 3-oxyacyl-[acyl-carrier protein] synthase (KAS III)	Fatty acid and phospholipid metabolism	-2.16	0.00229179
PG1357	hmuY tonB-dependent receptor	Transport and binding; Cations	-2.16	0.0119302
PG0908	Conserved hypothetical protein	Unknown	-2.17	0.0339745
PG0888	thrS threonyl-tRNA synthetase	Translation; Aminoacyl-tRNA synthetases	-2.17	0.0937983
PG1583	batB bacteroides aerotolerance operon protein	Cellular processes; Adaptations to atypical conditions	-2.17	0.00540243
PG0166	pth spoVC peptidyl-tRNA hydrolase (stage V sporulation protein C)	Translation; Translation factors	-2.18	0.000150659
PG1866	Hypothetical protein	Unknown	-2.18	0.00472218
PG0451	Conserved hypothetical protein (possible hemolysin-related protein)	Unknown	-2.18	0.00770824
PG0890	ppb alkaline phosphatase	Central intermediary metabolism	-2.19	0.0230628
PG1987	Possible CRISPR-associated protein, TM1793 family	Mobile and extrachromosomal element functions; Other	-2.19	0.135613
PG0806	Conserved hypothetical protein (possible meso-diaminopimelate D-dehydrogenase)	Unknown	-2.20	0.000120879
PG1942	rs12 30S ribosomal protein S12	Translation; Ribosomal proteins	-2.22	0.00193104
PG0189	Hypothetical protein	Unknown	-2.23	0.000549932
PG0990	rl35 50S ribosomal protein L35	Translation; Ribosomal proteins	-2.23	0.0172872
PG0886	Hypothetical protein	Unknown	-2.23	0.0828754
PG0308	Na+-translocating NADH-quinone oxidoreductase	Energy metabolism; Electron transport	-2.23	0.036167

PG0259	Conserved hypothetical protein (possible ABC transporter related membrane protein)	Unknown	-2.24	0.017125
PG2177	nqr6 Na+-translocating NADH-quinone reductase (possible phenolhydroxylase component)	Biosynthesis of cofactors, prosthetic groups and carriers; Menaquinone and ubiquinone	-2.25	0.00172093
PG1123	purB adenylosuccinate lyase	Amino acid biosynthesis; Aspartate family	-2.26	0.0210509
PG1134	trxB NADPH thioredoxin reductase	Purines, pyrimidines, nucleosides and nucleotides; 2'-Deoxyribonucleotide metabolism	-2.26	0.0163313
PG0727	sov gingipains secretion	Unknown	-2.27	0.110241
PG2033	gltD glutamate synthase beta subunit (glutamate synthase small subunit)	Amino acid biosynthesis; Glutamate family	-2.28	0.000884514
PG0046	cdsA phosphatidate cytidylytransferase (CDP diglyceride synthetase/ pyrophosphorylase/synthase; CTP:phosphatidate cytidylyltransferase; CDP-DAG synthase/CDP-DG synthetase)	Fatty acid and phospholipid metabolism	-2.29	0.0153647
PG1256	rng cafE probable cytoplasmic axial filament protein/ribonuclease G	Cellular processes; Cell division	-2.30	0.00223062
PG0796	leuS leucyl-tRNA synthetase	Translation; Aminoacyl-tRNA synthetases	-2.30	0.00147635
PG0565	Hypothetical protein	Unknown	-2.31	0.192126
PG0034	trxA thioredoxin	Energy metabolism; Electron transport	-2.31	0.0177046
PG2216	Conserved hypothetical protein	Unknown	-2.31	0.00189753
PG0047	ftsH ATPase/cell division protein/ATP-dependent zinc metallopeptidase	Cellular processes; Cell division	-2.33	0.0333893
PG2016	Conserved hypothetical protein	Unknown	-2.34	0.039762
PG0273	Hypothetical protein	Unknown	-2.35	0.00756591
PG1257	yacM ygbP ispD probable 4-diphosphocytidyl-2c-methyl-D-erythritol synthase (MEP cytidylyltransferase MCT)	Uncategorized	-2.35	0.0147797
PG0592	rl31 50S ribosomal protein L31	Translation; Ribosomal proteins	-2.37	0.00629189
PG0304	rnfC electron transfer protein	Energy metabolism; Electron transport	-2.38	0.00211701
PG0434	Conserved hypothetical protein	Unknown	-2.39	0.0942855
PG1137	PorS protein	Uncategorized	-2.39	0.00357371
PG0783	Conserved hypothetical protein (possible PHP hydrolase)	Unknown	-2.43	0.000232109
PG1382	Conserved hypothetical protein	Unknown	-2.46	0.0159675
PG0910	Hypothetical protein	Unknown	-2.48	0.00400277

PG0256	Possible CvpA family protein	Unassigned	-2.48	0.00528324
PG1358	Acetyltransferase	Uncategorized	-2.49	0.0528641
PG1060	prc tsp probable tail-specific protease	Protein fate; Degradation of proteins, peptides and glycopeptides	-2.49	0.00412581
PG2088	msrA peptide methionine sulfoxide reductase	Protein fate; Protein modification and repair	-2.52	0.000715319
PG1115	ffh signal recognition particle GTPase protein (SRP)	Protein fate; Protein and peptide secretion and trafficking	-2.52	0.000132477
PG0375	rl13 50S ribosomal protein L13	Translation; Ribosomal proteins	-2.54	0.00252982
PG0956	Conserved hypothetical protein (possible membrane protein)	Unknown	-2.57	0.000896432
PG1941	rs7 30S ribosomal protein S7	Translation; Ribosomal proteins	-2.57	4.86E-05
PG1940	fusA elongation factor G protein	Translation; Translation factors	-2.58	0.000960146
PG1136	Conserved hypothetical protein	Unknown	-2.61	0.000548983
PG1582	batA bacteroides aerotolerance operon protein, batA	Cellular processes; Adaptations to atypical conditions	-2.62	0.0481606
PG0198	Conserved hypothetical protein (possible cytochrome)	Unknown	-2.66	0.00387575
PG1124	Conserved hypothetical protein	Unknown	-2.68	0.00448418
PG1939	rs10 30S ribosomal protein S10	Translation; Ribosomal proteins	-2.69	0.000742838
PG0307	Na+-translocating NADH-quinone reductase	Energy metabolism; Electron transport	-2.70	0.00891258
PG0191	Probable outer membrane protein (Omp85 analog)	Cell envelope	-2.71	0.00355811
PG0203	Conserved hypothetical protein	Unknown	-2.71	0.0492759
PG0950	gcsH gcvT yusH glycine cleavage H protein (glycine decarboxylase component)	Amino acid biosynthesis; Serine family	-2.72	0.0635994
PG2121	ansA L-asparaginase I	Transport and binding; Amino acids, peptides and amines	-2.73	0.000710673
PG0656	rl34 50S ribosomal protein L34	Translation; Ribosomal proteins	-2.73	0.019653
PG0976	purC phosphoribosylaminoimidazole-succinocarboxamide synthase	Purines, pyrimidines, nucleosides and nucleotides; Purine ribonucleotide biosynthesis	-2.74	0.00413635
PG0196	Probable zinc protease/ 106 kDa immunoreactive protein	Protein fate; Degradation of proteins, peptides and glycopeptides	-2.75	0.000232942
PG1440	Hypothetical protein	Unknown	-2.75	0.0734984
PG0954	Conserved hypothetical protein	Unknown	-2.76	0.00192231
PG2085	trpS tryptophanyl-tRNA synthetase	Translation; Aminoacyl-tRNA synthetases	-2.76	0.00172133

PG1234	Hypothetical protein	Unknown	-2.78	0.0197403
PG0253	Conserved hypothetical protein	Unknown	-2.79	0.000420263
PG1695	Hypothetical protein	Unknown	-2.84	0.026891
PG0519	Conserved hypothetical protein (possible membrane protein)	Unknown	-2.85	0.034238
PG0752	upp uracil phosphoribosyltransferase	Purines, pyrimidines, nucleosides and nucleotides; Salvage of nucleosides and nucleotides	-2.89	0.000233162
PG1130	Hypothetical protein	Unknown	-2.90	0.02242
PG1707	Hypothetical protein	Unknown	-2.92	0.00136067
PG1301	Hypothetical protein	Unknown	-2.93	0.00503025
PG1375	crp possible cAMP receptor protein (catabolite gene activator; cAMP-regulatory protein)	Regulatory functions	-2.94	0.00506127
PG0750	wcfJ glycosyltransferase	Uncategorized	-2.94	0.000696555
PG0715	corA possible magnesium and cobalt transport protein	Transport and binding; Cations	-2.95	0.000675176
PG0651	Conserved hypothetical protein	Unknown	-2.97	7.50E-05
PG0037	rl19 50S ribosomal protein L19	Translation; Ribosomal proteins	-2.98	0.000296324
PG0597	rl9 rpL9 50S ribosomal protein L9	Translation; Ribosomal proteins	-3.00	0.00117897
PG0992	thrS threonyl-tRNA synthetase	Translation; Aminoacyl-tRNA synthetases	-3.01	0.000230163
PG0110	Conserved hypothetical protein (possible transferase)	Unknown	-3.01	0.000242252
PG0120	weeA UDP-N-acetylglucosamine 2-epimerase (UDP-GlcNAc 2-epimerase)	Cell envelope; Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides	-3.02	0.00309362
PG1842	Hypothetical protein	Unknown	-3.03	0.0292585
PG0754	top1 topA DNA topoisomerase I	DNA metabolism; DNA replication, recombination and repair	-3.03	3.81E-05
PG0167	ctc rplY 50S ribosomal protein L25/general stress protein	Translation; Ribosomal proteins	-3.04	0.000237394
PG0709	mip fkbP-type peptidyl-prolyl cis-trans isomerase (MIP-like protein)	Protein fate; Protein folding and stabilization	-3.045	0.00196868
PG1401	tnaA tryptophanase (tyrosine phenol-lyase; beta-tyrosinase)	Energy metabolism; Amino acids and amines	-3.05	0.000132057
PG0953	dut deoxyuridine 5'-triphosphate nucleotidohydrolase (dUTPase)	Purines, pyrimidines, nucleosides and nucleotides; Pyrimidine ribonucleotide biosynthesis	-3.06	0.00317982
PG2143	yphC probable GTP binding protein	Uncategorized	-3.06	0.0011839
PG0708	fkbP-type peptidyl-prolyl cis-trans isomerase	Protein fate; Protein folding and stabilization	-3.07	0.00229339
PG0436	Capsular polysaccharide transport protein	Transport and binding proteins; Carbohydrates,	-3.12	0.00338764

		organic alcohols, and acids		
PG0286	Conserved hypothetical protein	Unknown	-3.14	0.00100015
PG0856	Conserved hypothetical protein	Unknown	-3.21	0.0112079
PG1513	gpm pgm phosphoglycerate mutase	Energy metabolism; Glycolysis/gluconeogenesis	-3.22	0.012119
PG1141	wcgR probable glycosyltransferase	Uncategorized	-3.26	0.0110025
PG0188	lipoprotein	Unassigned	-3.27	0.000370592
PG0234	immunoreactive 23kD antigen PG66	Uncategorized	-3.30	0.000893454
PG1723	Hypothetical protein	Unknown	-3.31	0.00192383
PG2140	rl32 50S ribosomal protein L32	Translation; Ribosomal proteins	-3.33	0.0149921
PG0086	DEAD BOX-related helicase	Transcription; Transcription factors	-3.37	0.000735946
PG1936	rl23 50S ribosomal protein L23	Translation; Ribosomal proteins	-3.37	0.00533939
PG1803	vatA atpA ATP synthase subunit A (V-type ATPase subunit A)	Energy metabolism; ATP-proton motive force	-3.41	0.00057516
PG1258	hup ihfA histone-like DNA binding protein, IHFA, IHFB, or DBH	DNA metabolism; DNA replication, recombination and repair	-3.44	0.000827139
PG1828	Putative lipoprotein	Cell envelope	-3.49	0.00184914
PG1895	Hypothetical protein	Unknown	-3.49	0.0427234
PG1960	rl28 50S ribosomal protein L28	Translation; Ribosomal proteins	-3.51	0.00172982
PG2125	transcription regulator	Regulatory functions	-3.54	0.000463365
PG0106	probable glycosyltransferase	Uncategorized	-3.54	0.00529746
PG1598	lspA possible lipoprotein signal peptidase	Protein fate; Protein and peptide secretion and trafficking	-3.56	0.00779254
PG2117	rs16 30S ribosomal protein S16	Translation; Ribosomal proteins	-3.59	0.000649532
PG2192	Conserved hypothetical protein (possible membrane protein related to metalloendopeptidases)	Unknown	-3.62	3.38E-05
PG1121	asnS asparaginyl-tRNA synthetase (asparagine--tRNA ligase)	Translation; Aminoacyl-tRNA synthetases	-3.62	0.00175848
PG0807	Hypothetical protein with conserved nusB domain	Unknown	-3.64	0.00223053
PG0457	Hypothetical protein	Unknown	-3.65	0.00457209
PG0275	trxA thioredoxin	Energy metabolism; Electron transport	-3.67	0.0432035
PG0955	Hypothetical protein	Unknown	-3.72	0.0021198
PG0452	Possible peptidyl-prolyl isomerase	Protein fate; Protein folding and stabilization	-3.76	0.000163616
PG0118	Glycosyltransferase	Uncategorized	-3.92	0.00775525
PG1501	Hypothetical protein	Unknown	-3.94	4.58E-05
PG0596	rpsR 30S ribsomal protein S18	Translation; Ribosomal proteins	-3.96	0.0029703
PG0315	rl27 50S ribosomal protein L27	Translation; Ribosomal proteins	-4.021	0.000912602

PG2091	folQ dihydroneopterin aldolase protein	Biosynthesis of cofactors, prosthetic groups and carriers; Folic acid	-4.08	0.0741892
PG0240	Conserved hypothetical protein (possible phosphatase or hydrolase)	Unknown	-4.13	0.00357654
PG0935	ipk isopentenyl monophosphate kinase	Uncategorized	-4.14	0.0887651
PG1959	rl33 50S ribosomal protein L33	Translation; Ribosomal proteins	-4.16	2.43E-05
PG1599	Conserved hypothetical protein	Unknown	-4.18	0.00326242
PG0456	Conserved hypothetical protein(possible ATPase component)	Unknown	-4.24	0.00825189
PG1786	Probable integral outer membrane protein P30	Cell envelope	-4.25	9.81E-07
PG1758	rs15 30S ribosomal protein S15	Translation; Ribosomal proteins	-4.29	0.001882
PG0991	infC translation initiation factor 3 (IF-3)	Translation; Translation factors	-4.34	0.00055
PG2034	hydG hydrogenase gamma subunit	Energy metabolism	-4.42	0.000181
PG0382	Conserved hypothetical protein	Unknown	-4.43	0.005119
PG0113	Possible aminoglycoside N3-acetyltransferase (AAC3)	Cellular processes; Toxin production and resistance	-4.44	0.003216
PG1114	panD aspartate 1-decarboxylase protein	Biosynthesis of cofactors, prosthetic groups and carriers	-4.48	0.053042
PG0595	rps6 rpsF 30S ribosomal protein S6	Translation; Ribosomal proteins	-4.52	0.00037
PG0505	Hypothetical protein	Unknown	-4.53	0.006274
PG0111	Possible CAPK protein	Uncategorized	-4.60	0.002125
PG0989	rl20 50S ribosomal protein L20	Translation; Ribosomal proteins	-4.90	0.008714
PG1893	Conserved hypothetical protein (with TPR repeat)	Unknown	-4.90	0.006025
PG0109	Conserved hypothetical protein	Unknown	-4.96	0.005243
PG1427	Thiol protease (PrtT related)	Protein fate; Degradation of proteins, peptides and glycopeptides	-5.09	0.00026
PG0274	Hypothetical protein	Unknown	-5.10	0.010379
PG1544	Conserved hypothetical protein	Unknown	-5.14	0.000492
PG2139	Hypothetical protein	Unknown	-5.19	2.48E-06
PG0710	fkbP-type peptidyl-prolyl cis-trans isomerase (MIP-like protein)	Protein fate; Protein folding and stabilization	-5.24	0.001207
PG0314	rl21 50S ribosomal protein L21	Translation; Ribosomal proteins	-5.26	0.00075
PG1974	Hypothetical protein	Hypothetical	-5.27	0.000705
PG1235	Conserved hypothetical protein (possible nucleoside diphosphate-sugar epimerase)	Unknown	-5.31	0.000123
PG0108	wecC UDP-N-acetyl-D-mannosaminuronic acid dehydrogenase	Cell envelope; Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides	-5.35	1.34E-05

PG1801	atpE ATP synthase subunit E	Energy metabolism; ATP-proton motive force	-5.36	0.000231
PG0650	Conserved hypothetical protein	Unknown	-5.37	0.000252
PG0762	tig trigger factor (peptidyl prolyl cis-trans isomerase)	Protein fate; Protein folding and stabilization	-5.38	0.000321
PG0385	rs21 30S ribosomal protein S21	Translation; Ribosomal proteins	-5.48	0.001181
PG0202	hemD uroporphyrinogen-III synthase	Biosynthesis of cofactors, prosthetic groups, and carriers; Heme, porphyrin, and cobalamin NG0359 Cellular processes; Protein and peptide secretion	-5.51	2.56E-05
PG1429	Hypothetical protein	Unknown	-5.58	0.008899
PG2044	Conserved hypothetical protein	Unknown	-5.58	0.000146
PG1138	PorR protein	Uncategorized	-5.77	3.90E-05
PG1139	Hypothetical protein	Unknown	-5.92	0.000931
PG1788	Conserved hypothetical protein (putative cysteine peptidase)	Unknown	-6.20	0.000468
PG0712	Hypothetical protein (possible PAS/PAC domain)	Unknown	-6.31	0.00093
PG0556	Hypothetical protein	Unknown	-6.35	0.008845
PG0616	Hypothetical protein (putative thioredoxin)	Unknown	-6.61	0.000153
PG0201	Ribonuclease P protein component	Unknown	-7.11	0.000173
PG0563	Hypothetical protein	Unknown	-7.31	0.192008
PG1135	epsC glycosyltransferase	Uncategorized	-7.49	0.000505
PG0994	Hypothetical protein	Unknown	-7.57	0.001942
PG0803	nagB glucosamine-6-phosphate isomerase (glucosamine-6-phosphate deaminase)	Energy metabolism; Sugars	-7.81	0.099067
PG1547	prtT trypsin-like proteinase	Protein fate; Degradation of proteins, peptides and glycopeptides	-7.83	0.006372
PG0617	Hypothetical protein	Unknown	-8.04	0.000534
PG1894	Hypothetical protein	Unknown	-8.28	0.00063
PG1140	wbbL probable rhamnosyltransferase	Cell envelope	-8.54	0.002035
PG1428	ribE riboflavin synthase beta subunit	Biosynthesis of cofactors, prosthetic groups and carriers; Riboflavin, FMN and FAD	-8.70	2.40E-05
PG1841	Conserved hypothetical protein	Unknown	-9.73	0.006899
PG0195	Rubrerythrin	Energy metabolism; Electron transport	-12.53	0.000142
PG1222	Hypothetical protein	Unknown	-20.33	0.005532
PG0627	RNA binding protein	Transcription	-22.63	1.05E-05

[a] Differentially expressed genes were determined using fold-change (≥2) plus *p* (≤ 0.05) with FDR = 0.05.