**Table S1.** Primer sequences.

| **oligonucleotides** | **sequence (5′-3′)** [a] | **note** |
|---|---|---|
| *spoVG*-up-F | TTTGGTCTCATGACGGATTGTTGAGGCTGAGTAA | amplification of *spoVG* up fragment |
| *spoVG*-up-R | TTTGGTCTCACTCC CTTGTGTTCACCACCCTTT | |
| *spoVG*-down-F | TTTGGTCTCAATCGGGTTGAGTTTGAAGAAGCG | amplification of *spoVG* down fragment |
| *spoVG*-down-R | TTTGGTCTCACCAACATGACCATTCTCATTACGAAC | |
| *spoVG*-US-F | TCAGGTTCTTCTAAGCGAAT | screening for *spoVG* deletion strains |
| *spoVG*-US-R | TGTCAATGGTTCAGATACGA | |
| *spoVG*-SD-F | TGGAGAATGGTTACAAGAGC | |
| *spoVG*-SD-R | AGCCGATACAATATGACCTTC | |
| *spoVG*-in-F | GAAGTGACTGACGTAAGATTAC | |
| *spoVG*-in-R | ACCTCTTCTAACTCGCCTAA | |
| R*spoVG*-F | CGGGATCCATGGAAGTGACTGACGTAAG | amplification of *spoVG* ORF fragment |
| R*spoVG*-R | CCCAAGCTTTTACGAAGCGCCCGCTTCTT | |
| *spoIIB*-F | ACGCGTCGACATTGATTTTCTTTCTTCCC | amplification of *spoIIB* fragment containing $P_{spoIIB}$ |
| *spoIIB*-R | GCTCTAGATTTTACGACGGCTAACAGCT | |
| *spoIIE*-lacZ-F | ACGACGGCCAGTGCCAAGCTTGTTCATACCCGTGAGGTC | amplification of $P_{spoIIE}$ fragment for LacZ assay |
| *spoIIE*-LacZ-R | ATCAATTCAAGCTGGGGATCCCATTCGCAACTTACTCGT | |

| | | |
|---|---|---|
| pHT304-LacZ-F | CGCCAGGGTTTTCCCAGTCACGAC | verification of pHT304-$P_{spoIIE}$-LacZ |
| pHT304-LacZ-R | GCGCTCAGGTCAAATTCAGACGGC | |
| RT-qPCR-*spoIIM*-F | TGTAATTGGAGCGGTGTT | Primer used to RT-qPCR analysis |
| RT-qPCR-*spoIIM*-R | AATAGCCTCAACGACTTCTT | |
| RT-qPCR-*spoIIQ*-F | TGACATTGCTGCGAAGAA | |
| RT-qPCR-*spoIIQ*-R | ACAACATAACCAAGAAGTGAATC | |
| RT-qPCR-*cotE*-F | GAATAATGAGCCAACAAG | |
| RT-qPCR-*cotE*-R | ACGATAGCCAATACTTAC | |
| Q*gatB*_Yqey_F | CGGCATAACAGCAGTCATCA | internal reference of RT-qPCR |
| Q*gatB*_Yqey_R | AGCTGGTCGTGAAGACCTTG | |

[a] Restriction enzyme sites are underscored

**Table S2.** List of all differentially-expressed proteins identified via iTRAQ analysis

| Accession | Description | Abundance Ratio: ΔspoVG /A16R |
|---|---|---|
| BA_0314 | BA_0314 ABC transporter substrate-binding protein | 2.076 |
| BA_1326 | BA_1326 maoC family protein | 2.011 |
| BA_1450 | BA_1450 proton/glutamate symporter family protein | 1.972 |
| BA_0093 | sigH RNA polymerase factor sigma-70 | 1.9 |
| BA_3642 | BA_3642 oligopeptide ABC transporter substrate-binding protein | 1.745 |
| BA_5529 | murA1 UDP-N-acetylglucosamine 1-carboxyvinyltransferase | 1.716 |
| BA_4807 | BA_4807 HD domain-containing protein | 1.693 |
| BA_1564 | panD aspartate alpha-decarboxylase | 1.669 |
| BA_2775 | acoB TPP-dependent acetoin dehydrogenase E1 beta-subunit | 1.627 |
| BA_4359 | proC-3 pyrroline-5-carboxylate reductase | 1.626 |
| BA_2754 | BA_2754 TetR family transcriptional regulator | 1.614 |
| BA_0510 | pflA pyruvate formate-lyase-activating enzyme | 1.612 |
| BA_4255 | mtnW 2,3-diketo-5-methylthiopentyl-1-phosphate enolase | 1.608 |
| BA_0728 | BA_0728 ABC transporter substrate-binding protein | 1.576 |
| BA_5668 | BA_5668 major facilitator family transporter | 1.567 |
| BA_5626 | BA_5626 4-oxalocrotonate tautomerase | 1.556 |
| BA_4252 | mtnK methylthioribose kinase | 1.529 |
| BA_4481 | metC-2 cystathionine beta-lyase | 1.526 |
| BA_1981 | BA_1981 siderophore biosynthesis protein | 1.523 |
| BA_4293 | BA_4293 sodium-dependent symporter family protein | 1.52 |
| BA_0351 | BA_0351 iron compound ABC transporter substrate-binding protein | 1.491 |
| BA_0509 | pfl formate acetyltransferase | 1.482 |
| BA_1292 | sinR transcriptional regulator SinR | 1.48 |
| BA_4035 | divIVA cell-division initiation protein DivIVA | 1.479 |
| BA_3594 | cspB-2 cold shock protein CspB | 1.478 |

| | | |
|---|---|---|
| BA_5512 | wecC UDP-N-acetyl-D-mannosamine dehydrogenase | 1.475 |
| BA_4489 | BA_4489 5-formyltetrahydrofolate cyclo-ligase | 1.468 |
| BA_0352 | BA_0352 pyridine nucleotide-disulfide oxidoreductase family protein | 1.462 |
| BA_2373 | BA_2373 mbtH-like protein | 1.46 |
| BA_5424 | cspC cold shock protein CspC | 1.449 |
| BA_4576 | BA_4576 acetyltransferase | 1.445 |
| BA_2774 | acoC branched-chain alpha-keto acid dehydrogenase subunit E2 | 1.438 |
| BA_2773 | acoL dihydrolipoamide dehydrogenase | 1.423 |
| BA_1270 | sucA 2-oxoglutarate dehydrogenase E1 component | 1.423 |
| BA_4049 | murG UDPdiphospho-muramoylpentapeptide beta-N- acetylglucosaminyltransferase | 1.415 |
| BA_3988 | acpP acyl carrier protein | 1.414 |
| BA_3206 | BA_3206 M20/M25/M40 family peptidase | 1.411 |
| BA_0174 | BA_0174 ABC transporter ATP-binding protein | 1.41 |
| BA_1240 | BA_1240 acetyltransferase | 1.386 |
| BA_0348 | fucA L-fuculose phosphate aldolase | 1.383 |
| BA_1832 | BA_1832 acetyltransferase | 1.38 |
| BA_4256 | mtnX 2-hydroxy-3-keto-5-methylthiopentenyl-1-phosphate phosphatase | 1.366 |
| BA_3048 | BA_3048 ABC transporter ATP-binding protein | 1.361 |
| BA_2371 | dhbB isochorismatase | 1.352 |
| BA_1194 | BA_1194 oligopeptide ABC transporter ATP-binding protein | 1.344 |
| BA_5663 | thiD-2 pyridoxal kinase | 1.341 |
| BA_4480 | metC-1 cystathionine gamma-synthase | 1.33 |
| BA_3665 | BA_3665 glycerol-3-phosphate acyltransferase PlsY | 1.319 |
| BA_0121 | rplX 50S ribosomal protein L24 | 1.315 |
| BA_0072 | folB dihydroneopterin aldolase | 1.313 |
| BA_4827 | gap-1 glyceraldehyde-3-phosphate dehydrogenase | 1.311 |
| BA_4608 | udk uridine kinase | 1.31 |
| BA_3690 | alkK medium-chain-fatty-acid--CoA ligase | 1.307 |
| BA_1383 | BA_1383 hypothetical protein | 1.303 |
| BA_0499 | glsA-1 glutaminase | 1.3 |
| BA_2776 | acoA TPP-dependent acetoin dehydrogenase E1 | 1.296 |

| | | |
|---|---|---|
| | alpha-subunit | |
| BA_2899 | BA_2899 aspartate aminotransferase | 1.293 |
| BA_5422 | yfiA ribosomal subunit interface protein | 1.292 |
| BA_1421 | leuB 3-isopropylmalate dehydrogenase | 1.287 |
| BA_5581 | spo0F stage 0 sporulation protein F | 1.285 |
| BA_4804 | pheS phenylalanyl-tRNA synthetase subunit alpha | 1.282 |
| BA_5043 | BA_5043 mutT/nudix family protein | 1.277 |
| BA_2691 | BA_2691 endoribonuclease L-PSP | 1.274 |
| BA_0729 | tenI transcriptional regulator TenI | 1.274 |
| BA_0657 | BA_0657 oligopeptide ABC transporter permease | 1.267 |
| BA_4483 | BA_4483 ArsR family transcriptional regulator | 1.266 |
| GBAA_pXO1_0155 | GBAA_pXO1_0155 resolvase | 1.263 |
| BA_4950 | trmB tRNA (guanine-N(7)-)-methyltransferase | 1.263 |
| BA_0502 | BA_0502 penicillin-binding protein | 1.259 |
| BA_5584 | rpoE DNA-directed RNA polymerase subunit delta | 1.257 |
| BA_2370 | dhbE 2,3-dihydroxybenzoate-AMP ligase | 1.257 |
| BA_0766 | BA_0766 nitroreductase | 1.253 |
| BA_4258 | BA_4258 5-methylthio-3-oxo-1-penten-1,2-diol dioxygenase | 1.251 |
| BA_1195 | BA_1195 oligopeptide ABC transporter ATP-binding protein | 1.251 |
| BA_0312 | BA_0312 ABC transporter ATP-binding protein | 1.25 |
| BA_1977 | BA_1977 polysaccharide deacetylase | 1.249 |
| BA_5220 | BA_5220 ABC transporter substrate-binding protein | 1.244 |
| BA_4751 | BA_4751 4-hydroxybenzoyl-CoA thioesterase | 1.241 |
| BA_4062 | rpmF 50S ribosomal protein L32 | 1.239 |
| BA_0855 | BA_0855 amino acid ABC transporter amino acid-binding protein | 1.239 |
| BA_1595 | BA_1595 hypothetical protein | 1.239 |
| BA_1191 | BA_1191 oligopeptide ABC transporter substrate-binding protein | 1.237 |
| BA_2534 | BA_2534 acetyltransferase | 1.236 |
| BA_4448 | yqhJ glycine dehydrogenase subunit 1 | 1.236 |
| BA_2436 | asd-1 aspartate-semialdehyde dehydrogenase | 1.236 |
| BA_5617 | BA_5617 agmatinase | 1.228 |
| BA_0010 | BA_0010 pyridoxal biosynthesis lyase PdxS | 1.228 |

| | | |
|---|---|---|
| BA_5222 | BA_5222 ABC transporter ATP-binding protein | 1.226 |
| BA_4251 | mtnA methylthioribose-1-phosphate isomerase | 1.225 |
| BA_4038 | BA_4038 ylmF protein | 1.225 |
| BA_4766 | BA_4766 iron compound ABC transporter substrate-binding protein | 1.224 |
| GBAA_pXO1_0190 | GBAA_pXO1_0190 hypothetical protein | 1.221 |
| BA_5047 | luxS S-ribosylhomocysteinase 4 | 1.221 |
| BA_1982 | BA_1982 siderophore biosynthesis protein | 1.219 |
| BA_1154 | rocD ornithine--oxo-acid transaminase | 1.219 |
| BA_4818 | rpmI 50S ribosomal protein L35 | 1.218 |
| BA_1983 | BA_1983 acyl-CoA synthetas | 1.218 |
| BA_4449 | gcvT glycine cleavage system aminomethyltransferase T | 1.216 |
| BA_0615 | BA_0615 iron compound ABC transporter substrate-binding protein | 1.214 |
| BA_2258 | BA_2258 lipoprotein | 1.213 |
| BA_2249 | BA_2249 lipoprotein | 1.211 |
| BA_3645 | BA_3645 oligopeptide ABC transporter substrate-binding protein | 1.207 |
| BA_0345 | ahpC alkyl hydroperoxide reductase subunit C | 1.205 |
| BA_0034 | abrB transition state transcriptional regulator AbrB | 1.204 |
| BA_0675 | BA_0675 zinc-containing alcohol dehydrogenase | 1.202 |
| BA_0493 | BA_0493 acetylornithine deacetylase | 1.201 |
| BA_4043 | sigE sporulation sigma factor SigE | 0.209 |
| BA_0061 | spoIIE stage II sporulation protein E | 0.23 |
| BA_3383 | BA_3383 lipoprotein | 0.263 |
| BA_1636 | BA_1636 aminotransferase | 0.279 |
| BA_2287 | racA polar chromosome segregation protein | 0.282 |
| BA_3609 | dhaS aldehyde dehydrogenase | 0.328 |
| BA_4295 | spoIIAB anti-sigma F factor | 0.352 |
| BA_4457 | aroK shikimate kinase | 0.385 |
| BA_2457 | BA_2457 O-methyltransferase | 0.386 |
| BA_4296 | spoIIAA anti-sigma F factor antagonist | 0.389 |
| BA_4240 | BA_4240 acetyl-CoA acetyltransferase | 0.432 |
| BA_4294 | sigF sporulation sigma factor SigF | 0.438 |
| BA_1290 | BA_1290 spore coat-associated protein | 0.44 |

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|---|---|---|
| BA_1288 | BA_1288 spore coat-associated protein | 0.478 |
| BA_1931 | BA_1931 branched-chain amino acid ABC transporter branched chain amino acid-binding protein | 0.495 |
| BA_4346 | cpdB bifunctional 2',3'-cyclic nucleotide 2'-phosphodiesterase/3'-nucleotidase protein | 0.502 |
| BA_4491 | BA_4491 nucleotidyl transferase | 0.521 |
| BA_0372 | BA_0372 PTS system transporter subunit IIBC | 0.535 |
| GBAA_pXO1_0202 | GBAA_pXO1_0202 hypothetical protein | 0.541 |
| BA_2071 | BA_2071 mutT/nudix family protein | 0.558 |
| BA_0368 | BA_0368 amino acid ABC transporter ATP-binding protein | 0.567 |
| BA_2169 | BA_2169 TetR family transcriptional regulator | 0.574 |
| BA_2399 | BA_2399 metallo-beta-lactamase | 0.574 |
| BA_3076 | lysP lysine-specific permease | 0.574 |
| BA_2632 | BA_2632 cytochrome P450 family protein | 0.574 |
| BA_2552 | BA_2552 carboxyl transferase domain-containing protein | 0.579 |
| BA_2109 | BA_2109 DEAD/DEAH box helicase | 0.582 |
| BA_1817 | BA_1817 N-acetylmuramoyl-L-alanine amidase | 0.583 |
| BA_5597 | BA_5597 DNA-binding response regulator | 0.585 |
| BA_0311 | BA_0311 isochorismatase | 0.585 |
| BA_4149 | amiF formamidase | 0.587 |
| BA_2352 | BA_2352 acyl-CoA dehydrogenase | 0.592 |
| BA_1933 | BA_1933 branched-chain amino acid ABC transporter ATP-binding protein | 0.594 |
| BA_3911 | BA_3911 dipeptidase | 0.596 |
| BA_2551 | BA_2551 enoyl-CoA hydratase | 0.596 |
| BA_5606 | BA_5606 aminopeptidase | 0.601 |
| BA_2553 | BA_2553 acetoacetyl-CoA synthase | 0.605 |
| BA_2001 | BA_2001 intracellular serine protease | 0.611 |
| BA_2561 | BA_2561 DNA-binding response regulator | 0.615 |
| BA_3584 | BA_3584 collagenase | 0.615 |
| BA_3737 | BA_3737 N-acetylmuramoyl-L-alanine amidase | 0.618 |
| BA_0898 | BA_0898 N-acetylmuramoyl-L-alanine amidase | 0.619 |
| BA_5568 | BA_5568 sua5/yciO/yrdC/ywlC family protein | 0.619 |
| BA_3330 | BA_3330 beta-lactam antibiotic acylase | 0.621 |

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|---|---|---|
| BA_5248 | BA_5248 acetyl-CoA acetyltransferase | 0.637 |
| GBAA_pXO1_0079 | GBAA_pXO1_0079 surface layer protein | 0.638 |
| BA_2872 | BA_2872 degV family protein | 0.638 |
| BA_4983 | BA_4983 homoserine O-acetyltransferase | 0.639 |
| BA_0902 | BA_0902 ornithine cyclodeaminase | 0.639 |
| BA_1228 | BA_1228 glucose-1-phosphate thymidylyltransferase | 0.64 |
| BA_2379 | BA_2379 DinB family DNA polymerase | 0.64 |
| BA_2550 | mvaB hydroxymethylglutaryl-CoA lyase | 0.64 |
| BA_0477 | BA_0477 prophage LambdaBa04, tape measure protein | 0.644 |
| BA_3368 | BA_3368 ribonuclease activity regulator protein RraA | 0.645 |
| BA_1130 | BA_1130 S-layer protein | 0.645 |
| BA_2548 | BA_2548 acetyl-CoA carboxylase biotin carboxylase subunit | 0.645 |
| BA_0701 | qoxC quinol oxidase subunit III | 0.646 |
| BA_4558 | nadD nicotinic acid mononucleotide adenylyltransferase | 0.65 |
| BA_0876 | BA_0876 long-chain-fatty-acid--CoA ligase | 0.657 |
| BA_0564 | BA_0564 ankyrin repeat-containing protein | 0.659 |
| BA_2183 | BA_2183 neutral metalloprotease | 0.659 |
| BA_4671 | BA_4671 DNA-binding response regulator | 0.66 |
| BA_2814 | BA_2814 uvrD/Rep helicase | 0.66 |
| BA_1132 | aceA isocitrate lyase | 0.662 |
| BA_2227 | BA_2227 acetyltransferase | 0.662 |
| BA_1747 | BA_1747 alpha/beta fold family hydrolase | 0.662 |
| BA_4561 | aroE shikimate 5-dehydrogenase | 0.664 |
| BA_0318 | BA_0318 MarR family transcriptional regulator | 0.666 |
| BA_3578 | BA_3578 methyltransferase | 0.668 |
| BA_1287 | sipW signal peptidase I | 0.67 |
| BA_1296 | ywdH aldehyde dehydrogenase | 0.671 |
| BA_0371 | BA_0371 glycosyl hydrolase | 0.671 |
| BA_5119 | glgP glycogen phosphorylase | 0.671 |
| BA_1217 | BA_1217 bis(5'-nucleosyl)-tetraphosphatase | 0.673 |
| BA_4655 | BA_4655 ArsR family transcriptional regulator | 0.673 |
| BA_1129 | BA_1129 S-layer protein | 0.674 |
| BA_2154 | spoVS-1 stage V sporulation protein S | 0.675 |

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|---|---|---|
| BA_5132 | yugI general stress protein 13 | 0.676 |
| BA_2890 | BA_2890 UbiE/COQ5 family methlytransferase | 0.678 |
| BA_0936 | BA_0936 lipoprotein | 0.681 |
| BA_4345 | nhaC-3 Na+/H+ antiporter NhaC | 0.682 |
| BA_2053 | BA_2053 cytosolic long-chain acyl-CoA thioester hydrolase family protein | 0.683 |
| BA_2064 | csaA chaperone CsaA | 0.683 |
| BA_5317 | BA_5317 methyl-accepting chemotaxis protein | 0.684 |
| BA_0887 | eag S-layer protein | 0.684 |
| BA_4548 | holA DNA polymerase III subunit delta | 0.686 |
| BA_2883 | BA_2883 lipoprotein | 0.686 |
| BA_2720 | BA_2720 HAD superfamily hydrolase | 0.687 |
| BA_5437 | BA_5437 BigG family transcription antiterminator | 0.689 |
| BA_0664 | rbsR ribose operon repressor | 0.691 |
| BA_4823 | dnaB DNA replication protein DnaB | 0.691 |
| BA_1424 | hisZ ATP phosphoribosyltransferase regulatory subunit | 0.691 |
| BA_0992 | sigB RNA polymerase sigma factor SigB | 0.692 |
| BA_5719 | BA_5719 DHH subfamily 1 protein | 0.692 |
| BA_4109 | fosB-2 fosfomycin resistance protein FosB | 0.694 |
| BA_1463 | BA_1463 ribosomal protein L5 domain-containing protein | 0.694 |
| BA_1251 | trpC Indole-3-glycerol phosphate synthase | 0.694 |
| BA_4399 | BA_4399 hemolysin A | 0.695 |
| BA_4348 | BA_4348 MarR family transcriptional regulator | 0.698 |
| BA_5258 | BA_5258 cell wall surface anchor family protein | 0.699 |
| BA_2420 | BA_2420 acetyltransferase | 0.7 |
| BA_4493 | pstB phosphate transporter ATP-binding protein | 0.7 |
| BA_4729 | BA_4729 solute-binding family 5 protein | 0.701 |
| BA_5257 | BA_5257 hypothetical protein | 0.704 |
| BA_0140 | cbiO cobalt transporter ATP-binding protein | 0.706 |
| BA_4369 | BA_4369 ribosomal-protein-alanine acetyltransferase | 0.706 |
| BA_4628 | BA_4628 recombination factor protein RarA | 0.707 |
| BA_3912 | spoVS-2 stage V sporulation protein S | 0.707 |
| BA_2627 | cypA cytochrome P450 | 0.707 |
| BA_2705 | BA_2705 endo/excinuclease amino terminal | 0.709 |

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|---|---|---|
| | domain-containing protein | |
| BA_4402 | ispA geranyltranstransferase | 0.715 |
| BA_1327 | BA_1327 phaP protein | 0.716 |
| BA_3655 | BA_3655 Gfo/Idh/MocA family oxidoreductase | 0.719 |
| BA_1635 | BA_1635 sodium/solute symporter family protein | 0.719 |
| BA_0923 | BA_0923 sensor histidine kinase | 0.72 |
| BA_0697 | BA_0697 acetyltransferase | 0.721 |
| BA_4249 | BA_4249 3-hydroxybutyrate dehydrogenase | 0.721 |
| BA_4237 | BA_4237 lipoprotein | 0.723 |
| BA_2318 | BA_2318 DNA-binding protein | 0.723 |
| BA_0327 | gabD succinate-semialdehyde dehydrogenase | 0.726 |
| BA_0592 | ald-1 alanine dehydrogenase | 0.726 |
| BA_1040 | BA_1040 UvrD/Rep family helicase | 0.727 |
| BA_3919 | BA_3919 ACT domain-containing protein | 0.728 |
| BA_0384 | BA_0384 ABC transporter ATP-binding protein | 0.73 |
| BA_5203 | BA_5203 phosphoglycerate mutase | 0.73 |
| BA_3984 | BA_3984 DNA-binding protein | 0.731 |
| BA_0570 | BA_0570 serine/threonine phosphatase | 0.731 |
| BA_3699 | BA_3699 hypothetical protein | 0.731 |
| BA_2079 | dal-2 alanine racemase | 0.731 |
| BA_2016 | BA_2016 luciferase | 0.733 |
| BA_5651 | BA_5651 lipase/acylhydrolase | 0.734 |
| BA_1142 | addA ATP-dependent nuclease subunit A | 0.734 |
| BA_2608 | BA_2608 homoserine dehydrogenase | 0.742 |
| BA_2296 | BA_2296 CoA-transferase subunit beta | 0.742 |
| BA_2547 | BA_2547 acyl-CoA dehydrogenase | 0.742 |
| BA_4008 | rpoZ DNA-directed RNA polymerase subunit omega | 0.743 |
| BA_0205 | BA_0205 molybdopterin biosynthesis protein | 0.744 |
| BA_0401 | BA_0401 tellurium resistance protein | 0.744 |
| BA_0680 | BA_0680 FAD-binding oxidoreductase | 0.745 |
| BA_4340 | bioD dithiobiotin synthetase | 0.745 |
| BA_1376 | BA_1376 ABC transporter ATP-binding protein | 0.745 |
| BA_4639 | recJ single-stranded-DNA-specific exonuclease RecJ | 0.746 |
| BA_1515 | BA_1515 pyridine nucleotide-disulfide oxidoreductase family protein | 0.747 |
| BA_5177 | phnA alkylphosphonate utilization operon protein | 0.748 |

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|---|---|---|
| | PhnA | |
| BA_1435 | BA_1435 CDP-diacylglycerol--serine O-phosphatidyltransferase | 0.749 |
| BA_1162 | BA_1162 alpha-amylase 1 | 0.751 |
| BA_3236 | BA_3236 D-cysteine desulfhydrase | 0.752 |
| BA_0702 | qoxB quinol oxidase subunit I | 0.753 |
| BA_1941 | BA_1941 MarR family transcriptional regulator | 0.754 |
| BA_2003 | BA_2003 aldo/keto reductase family oxidoreductase | 0.755 |
| BA_0394 | BA_0394 type I phosphodiesterase/nucleotide pyrophosphatase family protein | 0.755 |
| BA_4923 | BA_4923 Gfo/Idh/MocA family oxidoreductase | 0.756 |
| BA_3707 | BA_3707 Oye family NADH-dependent flavin oxidoreductase | 0.757 |
| BA_4874 | fabG 3-ketoacyl-ACP reductase | 0.757 |
| BA_3070 | BA_3070 uridine kinase | 0.757 |
| BA_3657 | parE DNA topoisomerase IV subunit B | 0.757 |
| BA_4858 | BA_4858 thioesterase | 0.757 |
| BA_5496 | BA_5496 ABC transporter ATP-binding protein | 0.76 |
| BA_5122 | glgC glucose-1-phosphate adenylyltransferase | 0.76 |
| BA_0901 | BA_0901 proline racemase | 0.76 |
| BA_0325 | gabT 4-aminobutyrate aminotransferase | 0.76 |
| BA_0400 | BA_0400 tellurium resistance protein | 0.761 |
| BA_4229 | BA_4229 maltosaccharide ABC transporter maltosaccharide-binding protein | 0.762 |
| BA_4006 | priA primosome assembly protein PriA | 0.763 |
| BA_4542 | hemN coproporphyrinogen III oxidase | 0.763 |
| BA_4000 | BA_4000 serine/threonine protein kinase | 0.764 |
| BA_4953 | BA_4953 pullulanase | 0.765 |
| BA_1309 | glcD glycolate oxidase subunit GlcD | 0.765 |
| BA_4389 | BA_4389 sensory box sigma-54 dependent DNA-binding response regulator | 0.766 |
| BA_2072 | BA_2072 amidase | 0.767 |
| BA_3440 | BA_3440 short chain dehydrogenase/reductase family oxidoreductase | 0.767 |
| BA_4394 | spo0A stage 0 sporulation protein A | 0.767 |
| BA_3672 | BA_3672 DNA polymerase III subunit epsilon | 0.768 |

| | | |
|---|---|---|
| BA_4231 | malL oligo-1,6-glucosidase | 0.768 |
| BA_0080 | BA_0080 negative regulator of genetic competence ClpC/MecB89690:92125 | 0.769 |
| BA_3409 | dxr-1 1-deoxy-D-xylulose 5-phosphate reductoisomerase | 0.77 |
| BA_1352 | BA_1352 MarR family transcriptional regulator | 0.77 |
| BA_3703 | BA_3703 phospholipase/carboxylesterase | 0.77 |
| BA_5064 | feoB ferrous iron transport protein B | 0.77 |
| BA_3986 | smC chromosome segregation protein SMC | 0.77 |
| BA_4516 | dnaG DNA primase | 0.771 |
| BA_4846 | accD acetyl-CoA carboxylase subunit beta | 0.773 |
| BA_3463 | BA_3463 aldo/keto reductase family oxidoreductase 3185456:3186466 forward MW:37129 | 0.774 |
| BA_1891 | BA_1891 deoxyribonucleoside regulator DeoR | 0.774 |
| BA_2377 | hup-2 DNA-binding protein HU | 0.775 |
| BA_5075 | BA_5075 bmrU protein | 0.776 |
| BA_3996 | rpmB 50S ribosomal protein L28 | 0.777 |
| BA_1426 | hisD histidinol dehydrogenase | 0.779 |
| GBAA_pXO1_0199 | GBAA_pXO1_0199 hypothetical protein | 0.779 |
| BA_5717 | BA_5717 replicative DNA helicase | 0.781 |
| BA_1503 | fer ferredoxin | 0.781 |
| BA_0774 | BA_0774 pyridine nucleotide-disulfide oxidoreductase, class I | 0.781 |
| BA_0044 | purR pur operon repressor | 0.781 |
| BA_3661 | BA_3661 DNA-binding response regulator | 0.782 |
| BA_1295 | BA_1295 immune inhibitor A metalloprotease | 0.782 |
| BA_2860 | BA_2860 x-prolyl-dipeptidyl aminopeptidase | 0.783 |
| BA_3346 | BA_3346 6-aminohexanoate-dimer hydrolase | 0.783 |
| BA_2057 | BA_2057 oxidoreductase | 0.784 |
| BA_4136 | BA_4136 PDZ domain-containing protein | 0.784 |
| BA_2353 | garR 2-hydroxy-3-oxopropionate reductase | 0.785 |
| BA_0715 | BA_0715 phosphate ABC transporter substrate-binding protein | 0.786 |
| BA_4191 | BA_4191 TrkA family potassium uptake protein | 0.787 |
| BA_3343 | BA_3343 alpha/beta fold family hydrolase | 0.788 |
| BA_5731 | BA_5731 stage 0 sporulation protein J | 0.788 |

| | | |
|---|---|---|
| BA_5121 | glgD glycogen biosynthesis protein GlgD | 0.789 |
| BA_1385 | BA_1385 2-nitropropane dioxygenase | 0.789 |
| BA_3992 | BA_3992 fatty acid biosynthesis transcriptional regulator | 0.79 |
| BA_3991 | plsX glycerol-3-phosphate acyltransferase | 0.79 |
| BA_4547 | rpsT 30S ribosomal protein S20 | 0.79 |
| BA_2768 | BA_2768 thioredoxin reductase | 0.791 |
| BA_1213 | ppnK inorganic polyphosphate/ATP-NAD kinase | 0.791 |
| BA_2952 | BA_2952 acetyltransferase | 0.791 |
| BA_5184 | BA_5184 nucleotidyltransferase domain-containing protein | 0.792 |
| BA_5539 | nuoD NADH dehydrogenase subunit D | 0.792 |
| BA_1948 | BA_1948 lipoprotein | 0.793 |
| BA_0004 | recF recombination protein F | 0.794 |
| BA_3105 | BA_3105 acyl-CoA dehydrogenase, short-chain specificreverse | 0.794 |
| BA_5123 | glgB glycogen branching protein | 0.794 |
| BA_1964 | BA_1964 mutT/nudix family protein | 0.795 |
| BA_5585 | BA_5585 TetR family transcriptional regulator | 0.795 |
| BA_1483 | deoD purine nucleoside phosphorylase | 0.795 |
| BA_3257 | BA_3257 ArsR family transcriptional regulator | 0.796 |
| BA_2919 | ssuD alkanesulfonate monooxygenase | 0.796 |
| BA_4830 | mutM formamidopyrimidine-DNA glycosylase | 0.796 |
| BA_4208 | ppk polyphosphate kinase | 0.796 |
| BA_0202 | modB molybdenum ABC transporter permease | 0.797 |
| BA_0875 | BA_0875 coproporphyrinogen III oxidase | 0.797 |
| BA_4728 | BA_4728 deaminase | 0.797 |
| BA_5249 | BA_5249 3-hydroxyacyl-CoA dehydrogenase | 0.797 |
| BA_3501 | BA_3501 lysozyme | 0.798 |
| BA_3913 | BA_3913 phosphoesterase | 0.799 |
| BA_4318 | lolS lolS protein | 0.799 |
| BA_2932 | BA_2932 glutathionylspermidine synthase | 0.8 |
| BA_3847 | fruB 1-phosphofructokinase | 0.8 |
| BA_0536 | bcP bacterioferritin comigratory protein | 0.8 |
| BA_5246 | BA_5246 acyl-CoA dehydrogenase | 0.8 |
| BA_5065 | BA_5065 FeoA family protein | 0.801 |

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|---|---|---|
| GBAA_pXO1_0037 | GBAA_pXO1_0037 nucleotidyltransferase domain-containing protein | 0.801 |
| BA_2654 | BA_2654 thiJ/pfpI family protein | 0.802 |
| BA_3111 | BA_3111 aminoglycoside phosphotransferase | 0.802 |
| GBAA_pXO1_0206 | GBAA_pXO1_0206 hypothetical protein | 0.802 |
| BA_2549 | BA_2549 acetyl-CoA carboxylase biotin carboxyl carrier protein subunit | 0.803 |
| BA_3610 | fabG 3-oxoacyl-ACP reductase 3319812:3320552 reverse MW:26512 | 0.803 |
| BA_1558 | BA_1558 glycosyl transferase family protein | 0.804 |
| BA_0996 | BA_0996 sensor histidine kinase/response regulator | 0.804 |
| BA_1545 | qcrB cytochrome b6 | 0.804 |
| BA_0079 | BA_0079 ATP:guanido phosphotransferase | 0.804 |
| BA_2650 | BA_2650 penicillin-binding protein | 0.805 |
| BA_4562 | BA_4562 GTP-binding protein Yqe 4146595:4147701 reverse MW:41283 | 0.805 |
| BA_4492 | BA_4492 phosphate transport system regulatory protein PhoU | 0.806 |
| BA_1418 | ilvH acetolactate synthase 3 regulatory subunit | 0.806 |
| BA_1152 | BA_1152 fumarylacetoacetate hydrolase | 0.806 |
| BA_5414 | BA_5414 carboxyl-terminal protease | 0.806 |
| BA_2354 | mmsA-1 methylmalonic acid semialdehyde dehydrogenase | 0.806 |
| BA_1797 | pyrH uridylate kinase | 0.807 |
| BA_3993 | recG ATP-dependent DNA helicase RecG | 0.807 |
| BA_0375 | topB-1 DNA topoisomerase III | 0.808 |
| BA_0046 | BA_0046 endoribonuclease L-PSP | 0.808 |
| BA_3842 | hfq RNA-binding protein Hfq | 0.808 |
| BA_4331 | ribD riboflavin biosynthesis protein RibD | 0.809 |
| BA_4717 | racE-2 glutamate racemase | 0.809 |
| BA_4536 | BA_4536 16S ribosomal RNA methyltransferase RsmE | 0.809 |
| BA_2164 | BA_2164 ABC transporter ATP-binding protein | 0.809 |
| BA_0014 | BA_0014 deoxynucleoside kinase | 0.81 |
| BA_3945 | rpsO 30S ribosomal protein S15 | 0.81 |
| BA_1008 | BA_1008 DNA repair exonuclease | 0.811 |

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|---|---|---|
| BA_2263 | BA_2263 mechanosensitive ion channel family protein | 0.811 |
| BA_5120 | glgA glycogen synthase | 0.811 |
| BA_4360 | sdhA-2 iron-sulfur-dependent L-serine dehydratase subunit alpha | 0.811 |
| BA_5049 | BA_5049 carbonic anhydrase | 0.811 |
| BA_2596 | BA_2596 acetamidase/formamidase | 0.812 |
| BA_2111 | BA_2111 glyoxalase | 0.812 |
| BA_2265 | BA_2265 LuxR family DNA-binding response regulator | 0.813 |
| BA_5590 | BA_5590 ferredoxin, 4Fe-4S | 0.813 |
| BA_0084 | ispD 2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase | 0.814 |
| BA_4308 | BA_4308 purine nucleoside phosphorylase | 0.814 |
| BA_0095 | secE preprotein translocase subunit SecE | 0.815 |
| BA_5195 | fbp-1 fructose 1,6-bisphosphatase II | 0.815 |
| BA_4994 | BA_4994 TrkA domain-containing protein | 0.815 |
| BA_2818 | recQ-2 ATP-dependent DNA helicase RecQ | 0.815 |
| BA_0399 | BA_0399 tellurium resistance protein | 0.815 |
| BA_0599 | BA_0599 neutral protease | 0.816 |
| BA_4013 | BA_4013 fibronectin/fibrinogen-binding protein | 0.817 |
| BA_1629 | cspB-1 cold shock protein CspB | 0.817 |
| BA_2405 | BA_2405 hydrolase | 0.818 |
| BA_0021 | recR recombination protein RecR | 0.818 |
| BA_3514 | BA_3514 metallo-beta-lactamase | 0.818 |
| BA_4024 | pyrK dihydroorotate dehydrogenase electron transfer subunit | 0.818 |
| BA_1836 | BA_1836 polysaccharide deacetylase | 0.819 |
| BA_0056 | BA_0056 S4 domain-containing protein | 0.82 |
| BA_5380 | clpP ATP-dependent Clp protease proteolytic subunit | 0.82 |
| BA_0410 | BA_0410 heavy metal-transporting ATPase | 0.821 |
| BA_4777 | BA_4777 DNA-binding response regulator | 0.821 |
| BA_1758 | BA_1758 GntR family transcriptional regulator | 0.821 |
| BA_0344 | ahpF alkyl hydroperoxide reductase subunit F | 0.821 |
| BA_0965 | BA_0965 dihydroxyacetone kinase | 0.822 |
| BA_0052 | mfd transcription-repair coupling factor | 0.822 |

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|---|---|---|
| BA_5074 | hpt-2 hypoxanthine-guanine phosphoribosyltransferase | 0.823 |
| BA_2850 | BA_2850 mandelate racemase/muconate lactonizing protein | 0.823 |
| BA_3985 | ftsY signal recognition particle-docking protein FtsY | 0.823 |
| BA_5472 | dat-2 D-amino acid aminotransferase | 0.823 |
| BA_3905 | mutS DNA mismatch repair protein MutS | 0.823 |
| BA_4153 | ctaD cytochrome c oxidase subunit I | 0.824 |
| BA_2048 | BA_2048 dedA family protein | 0.825 |
| BA_3095 | BA_3095 LamB/YcsF family protein | 0.825 |
| BA_1537 | aroF-1 chorismate synthase | 0.825 |
| BA_2135 | moeA-1 molybdopterin biosynthesis protein MoeA | 0.826 |
| BA_4650 | ruvB Holliday junction DNA helicase RuvB | 0.826 |
| BA_5639 | BA_5639 D-alanyl-D-alanine carboxypeptidase | 0.827 |
| BA_4336 | bioB biotin synthase | 0.827 |
| BA_5334 | vacB ribonuclease R | 0.827 |
| BA_5079 | BA_5079 aldo/keto reductase family oxidoreductase | 0.828 |
| BA_4400 | dxs 1-deoxy-D-xylulose-5-phosphate synthase | 0.828 |
| BA_1250 | trpD anthranilate phosphoribosyltransferase | 0.828 |
| BA_5714 | yycG sensory box histidine kinase YycG | 0.829 |
| BA_4276 | scpB segregation and condensation protein B | 0.829 |
| BA_4622 | BA_4622 helicase | 0.83 |
| BA_4147 | BA_4147 hypothetical protein | 0.83 |
| BA_1952 | BA_1952 NLP/P60 family protein | 0.83 |
| BA_2673 | BA_2673 chitosanase | 0.83 |
| BA_2360 | BA_2360 exonuclease | 0.83 |
| BA_0830 | BA_0830 AsnC family transcriptional regulato | 0.831 |
| BA_5667 | BA_5667 response regulator | 0.832 |
| BA_4477 | murG UDPdiphospho-muramoylpentapeptide beta-N-acetylglucosaminyltransferase | 0.832 |
| BA_4815 | BA_4815 M42 family peptidase | 0.833 |
| BA_3966 | codY transcriptional repressor | 0.873 |

**Protein extraction and iTRAQ analysis.** Proteomic analysis of *B. anthracis* cells was performed according to methods reported previously. Specifically, protein samples cultured in DSM were collected at $T_1$. Proteomic analysis of *B. anthracis* cells was performed according to methods

reported previously [1]. Protein concentrations were determined using the Bradford method. Solutions containing 100 μg protein were loaded into a 10 KDa ultrafiltration (OD010C35, PALL, Port Washington, NY, USA) tube and digested using trypsin for 12 h at 37°C after an initial reduction step with DTT and alkylation. A16R, Δ*spoVG*, and mix sample were labeled with 113, 114, and 116 mass tags, respectively. Data was analyzed using Proteome Discoverer™ 2.2 software (Thermo, San Jose, CA, USA), and the Ames chromosome amino acids database (NCBI Accession: NC_003997.3) was used. The false-positive rate of peptide identification was controlled below 1%. Protein fold changes of ≥1.2 with at least one unique peptide were considered significantly different.

**Table S3.** List of differentially-expressed proteins related to growth and spore formation.

| Accession | Description | Abundance Ratio | Δ*spoVG*[a] |
|---|---|---|---|
| **Growth metabolic pathway** | | | |
| BA_0701 | qoxC quinol oxidase subunit III | 0.646 | down |
| BA_0702 | qoxB quinol oxidase subunit I | 0.753 | down |
| BA_4240 | acetyl-CoA acetyltransferase | 0.432 | down |
| BA_1288 | spore coat-associated protein | 0.478 | down |
| BA_1290 | BA_1290 spore coat-associated protein | 0.44 | down |
| BA_3966 | codY transcriptional repressor | 0.873 | down |
| **Sporulation Process** | | | |
| BA_0061 | spoIIE stage II sporulation protein E | 0.23 | down |
| BA_4295 | spoIIAB anti-sigma F factor | 0.352 | down |
| BA_4296 | spoIIAA anti-sigma F factor antagonist | 0.389 | down |
| BA_4294 | sigF sporulation sigma factor SigF | 0.438 | down |
| BA_4394 | spo0A stage 0 sporulation protein A | 0.767 | down |
| BA_0093 | sigH RNA polymerase factor sigma-70 | 1.9 | up |
| BA_5581 | spo0F stage 0 sporulation protein F | 1.285 | up |

[a]: up and down denote the upregulated and downregulated proteins of the *spoVG* mutant strain with respect to the wild-type *B. anthracis* A16R strain

**Figure S1**

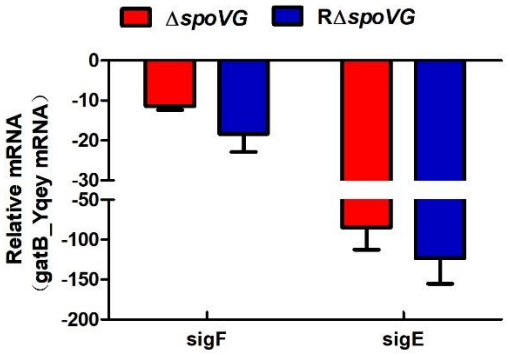



**Figure S1.** Verification of differentially expressed genes using RT-qPCR. Relative expression of *sigF* and *sigE* genes was determined in the Δ*spoVG* and RΔ*spoVG* strains compared with A16R at $T_1$. The mRNAs of both *sigF* and *sigE* were significantly down-regulated in Δ*spoVG* compared with A16R. Values are mean ± SD of triplicate experiments.

**Table S4. Conservation of comC between *B. anthracis* and *B. subtilis*.***

| Query | Sbjct | Range | Identities |
|---|---|---|---|
| comC (*B. anthracis)*<br>240bp | comC (*B. subtilis)*<br>248bp | 9-229 | 39% |

* Sequence alignment results are shown below

Query 11

GMVFGSFFMLIAMRIPLGESIIIPRSHCHYCKYVLKPKELIPIISFCIQRGRCTNCKRKI 70

G++ GSF+ RIPL SII PRS C +C+ L P ELIPI+SF Q+G+C +C +I

Sbjct 9 GLILGSFYYTAGCRIPLHLSIIAPRSSCPFCRRTLTPAELIPILSFLFQKGKCKSCGHRI 68

Query 71 SILYVIFELVTGIICLLTVYMIGVERELIIILSLFSLLLIISVTDYIYMLIPNRILAWFS 130

S +Y ELVT + G+ EL + SLL+I++VTD +MLIPNRIL +F

Sbjct 69 SFMYPAAELVTACLFAAAGIRFGISLELFPAVVFISLLIIVAVTDIHFMLIPNRILIFFL 128

Query 131

CLLILECVFVPLVTWTESIVGSGVIFILLYCMQKIYPEGLGGGDIKLLSLLGFIAGLKGV 190

L + PL +W ++G+ F+ L + I G+GGGDIKL +++GF+ G+K +

Sbjct 129

PFLAAARLISPLDSWYAGLLGAAAGFLFLAVIAAITHGGVGGGDIKLFAVIGFVLGVKML 188

Query 191 FMILFLSSFFSLCFFGAGLVLKRMKMRTQIPFGPFISLGAI 231

F S + A ++ R+ R +PF P I+ G+I

Sbjct 189 AAAFFFSVLIGALYGAAAVLTGRLAKRQPLPFAPAIAAGSI 229

**Figure S2**

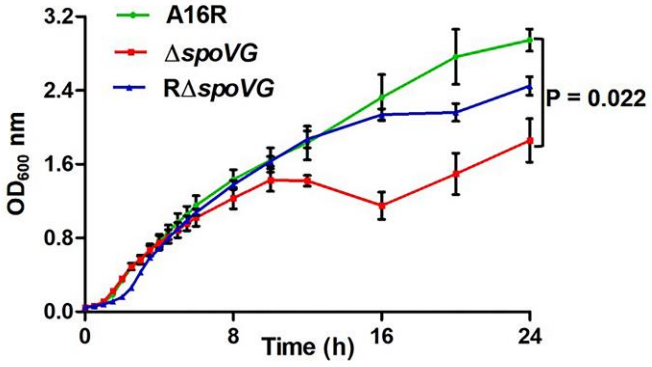



**Figure S2.** Effect of SpoVG on growth. Growth curve assays were performed in DSM (A16R, green; Δ*spoVG*, red; RΔ*spoVG*, blue; repeated measures ANOVA, F = 348, P = 0.000).

**REFERENCES**


*1.* Han, J., P. Gao, S. Zhao, X. Bie, Z. Lu, C. Zhang, and F. Lv. "Itraq-Based Proteomic Analysis of Li-F Type Peptides Produced by *Paenibacillus polymyxa* Jsa-9 Mode of Action against *Bacillus cereus*." Journal of Proteomics 150 (2017): 130-40.