**Supplementary File 1: Proteomics identify differentially abundant proteins**

|  |  |  |
| --- | --- | --- |
| Uniprot | Gene Name | Fasta headers |
| I - More abundant in WT |  |  |  |
| I – 1. PresentF606WT\_AbsentJ420tgt |   |   |   |
| Q9KTY9 | tgt | Queuine tRNA-ribosyltransferase  |  |  |  |
| Q9KNM6 | VC\_2706 | queuosine precursor transporter  |  |  |  |
| Q9KNH8 | VC\_2761 | Bcr/CflA family efflux transporter  |  |  |  |
| Q9KMV7 | VC\_A0211 | Sensory box sensor histidine kinase  |  |  |  |
| Q9KN55 | VC\_A0110 | Uncharacterized protein  |  |  |  |
| Q9KP41 | VC\_2538 | Thiamine ABC transporter, permease protein,  |  |  |  |
| Q9KTU0 | VC\_0798 | Citrate lyase, beta subunit  |  |  |  |
| Q9KSB8 | VC\_1340 | PrpE protein  |  |  |  |
| Q9KRW0 | VC\_1524 | ABC transporter, permease protein  |  |  |  |
| Q9KMB6 | VC\_A0457 | Uncharacterized protein  |  |  |  |
| Q9KUU0 | VC\_0425 | lacZ  |  |  |  |
| Q9KND5 | VC\_A0030 | Uncharacterized protein  |  |  |  |
| Q9KNP5 | zapB | Cell division protein ZapB  |  |  |  |
| Q9KUS6 | VC\_0439 | ThrE\_2 domain-containing protein |  |  |  |
| Q9KLK9 | VC\_A0734 | Uncharacterized protein  |  |  |  |
| Q9KRP8 | VC\_1588 | Transcriptional regulator, LysR family |  |  |  |
| Q9KRB9 | VC\_1723 | TVP38/TMEM64 family membrane protein  |  |  |  |
| Q9KNT7 | argB | Acetylglutamate kinase  |  |  |  |
| Q9KRX3 | VC\_1510 | Uncharacterized protein  |  |  |  |
| Q9KPM7 | VC\_2340 | HD-GYP domain-containing protein |  |  |  |
| Q9KL36 | VC\_A0913 | Hemin ABC transporter, periplasmic hemin-binding protein HutB  |  |  |  |
| Q9KVY3 | VC\_0005 | Putative membrane protein insertion efficiency factor  |  |  |  |
| Q9KQV1 | VC\_1897 | Hit family protein  |  |  |  |
| Q9KMY2 | VC\_A0184 | cspE Cold shock DNA-binding domain protein  |  |  |  |
| Q9KL45 | VC\_A0903 | Uncharacterized protein glycertae kinase  |  |  |  |
| Q9KRM7 | VC\_1609 | Uncharacterized protein ABC-2 type transport system permease  |  |  |  |
| Q9KSC1 | VC\_1337 | Citrate synthase  |  |  |  |
| Q9KLD9 | VC\_A0807 | ABC transporter, periplasmic substrate-binding protein |  |  |  |
| Q9KT63 | VC\_1042 | Long-chain fatty acid transport protein  |  |  |  |
| Q9KN12 | VC\_A0154 | Uncharacterized protein Na+:H+ antiporter subunit E  |  |  |  |
| Q9KN05 | tnaA | Tryptophanase  |  |  |  |
| Q9KS94 | queE | 7-carboxy-7-deazaguanine synthase  |  |  |  |
| Q9KQI2 | tmk |  Thymidylate kinase  |  |  |  |
| Q9KVP6 | ubiC | Probable chorismate pyruvate-lyase  |  |  |  |
| Q9KMP2 | VC\_A0281 | Integrase  |  |  |  |
| Q9KUW3 | VC\_0396 | Transcriptional regulator, LuxR family  |  |  |  |
| Q9KUK3 | VC\_0515 | Uncharacterized protein  |  |  |  |
| Q9KSC8 | VC\_1330 | Uncharacterized protein  |  |  |  |
| Q9KUQ7 | VC\_0458 | UPF0235 protein yggU  |  |  |  |
| I – 2. MoreF606wt\_ThanJ420tgt  | **log2FC WT/tgt** | **p value** | **Adjusted p value** |
| Q9KTJ4 | gmhB | D-glycero-beta-D-manno-heptose-1,7-bisphosphate 7-phosphatase  | 3,51 | 0,0001 | 0,0005 |
| Q9KTU3 | VC\_0795 | Citrate/sodium symporter | 3,46 | 0,0085 | 0,0068 |
| Q9KSB4 | VC\_1345 | Putative dioxygenase  | 3,35 | 0,0024 | 0,0034 |
| Q9KS61 | cheR2 | Chemotaxis protein methyltransferase  | 2,93 | 0,0053 | 0,0050 |
| Q9KN74 | VC\_A0091 | UPF0251 protein VC\_A0091  | 2,86 | 0,0013 | 0,0025 |
| Q9KR81 | VC\_1762 | EH\_Signature domain-containing protein  | 2,54 | 0,0023 | 0,0034 |
| Q9KM90 | VC\_A0491 | Uncharacterized protein  | 2,26 | 0,0013 | 0,0025 |
| Q9KQ10 | VC\_2197 | Flagellar hook protein FlgE | 2,23 | 0,0036 | 0,0042 |
| Q9KVI7 | murI | Glutamate racemase  | 2,11 | 0,0015 | 0,0028 |
| Q9KV46 | VC\_0312 | NAD(P)H-flavin reductase  | 2,10 | 0,0004 | 0,0014 |
| Q9KL60 | VC\_A0888 | Transcriptional regulator malT , LuxR family  | 2,01 | 0,0038 | 0,0042 |
| Q9KSV5 | VC\_1151 | Uncharacterized protein lysO  | 1,85 | 0,0003 | 0,0012 |
| Q9KUR5 | VC\_0450 | Membrane-bound lytic murein transglycosylase C  | 1,81 | 0,0057 | 0,0052 |
| Q9KVM8 | VC\_0113 | ubiG? Methyltransferase-related protein  | 1,76 | 0,0047 | 0,0046 |
| Q9KPC7 | VC\_2445 | gspA General secretion pathway protein A | 1,75 | 0,0039 | 0,0042 |
| Q9KNL2 | nfuA | Fe/S biogenesis protein NfuA  | 1,68 | 0,0010 | 0,0022 |
| Q9KVI5 | VC\_0161 | Transcriptional activator IlvY  | 1,63 | 0,0128 | 0,0090 |
| Q9KL10 | VC\_A0940 | Transcriptional regulator, DeoR family  | 1,62 | 0,0003 | 0,0012 |
| Q9KR73 | VC\_1770 | Uncharacterized protein  | 1,52 | 0,0112 | 0,0082 |
| Q9KKR5 | VC\_A1037 | Amino acid ABC transporter, ATP-binding protein  | 1,43 | 0,0080 | 0,0065 |
| H9L4R1 | VC\_0412 | MshO Uncharacterized protein  | 1,43 | 0,0094 | 0,0071 |
| Q9KKN4 | VC\_A1068 | LRP Transcriptional regulator, AsnC family  | 1,43 | 0,0061 | 0,0053 |
| P45784 | epsN | Type II secretion system protein N  | 1,38 | 0,0022 | 0,0034 |
| Q9KU51 | VC\_0673 | Probable membrane transporter protein  | 1,37 | 0,0076 | 0,0063 |
| Q9KNR9 | VC\_2662 | Uncharacterized protein  | 1,24 | 0,0008 | 0,0019 |
| Q9KRY1 | rsmF | Ribosomal RNA small subunit methyltransferase F  | 1,18 | 0,0060 | 0,0053 |
| Q9KLX1 | VC\_A0620 | Thiosulfate sulfurtransferase SseA, putative  | 1,10 | 0,0020 | 0,0034 |
| Q9KV88 | VC\_0268 | ygaJ Uncharacterized protein  | 1,09 | 0,0070 | 0,0060 |
| Q9KPI7 | VC\_2380 | Cobalamin biosynthesis protein CbiB, putative  | 1,00 | 0,0042 | 0,0042 |
| I – 3. PresentF606TOB\_AbsentJ420TOB |  |  |  |
| P0C6D1 | irgB | Iron-regulated virulence regulatory protein IrgB  |  |  |  |
| P0C6D6 | tcpN | TCP pilus virulence regulatory protein |  |  |  |
| Q56632 | vibA | Vibriobactin-specific 2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase  |  |  |  |
| Q9KKP3 | VC\_A1059 | Putative pseudouridine methyltransferase  |  |  |  |
| Q9KL40 | hutX | Intracellular heme transport protein HutX  |  |  |  |
| Q9KLG0 | fabV2 | Enoyl-[acyl-carrier-protein] reductase [NADH] 2  |  |  |  |
| Q9KLJ6 | glpB | Anaerobic glycerol-3-phosphate dehydrogenase subunit B  |  |  |  |
| Q9KLR1 | VC\_A0681 | 33-cGAMP-specific phosphodiesterase 1 |  |  |  |
| Q9KMY6 | pepT | Peptidase T  |  |  |  |
| Q9KNL4 | bioH | Pimeloyl-[acyl-carrier protein] methyl ester esterase  |  |  |  |
| Q9KPE3 | coaE | Dephospho-CoA kinase  |  |  |  |
| Q9KRQ1 | VC\_1585 | Catalase  |  |  |  |
| Q9KS61 | cheR2 | Chemotaxis protein methyltransferase 2  |  |  |  |
| Q9KSB4 | VC\_1345 | Putative dioxygenase  |  |  |  |
| Q9KSW7 | hisI | Histidine biosynthesis bifunctional protein HisIE  |  |  |  |
| Q9KTY9 | tgt | Queuine tRNA-ribosyltransferase  |  |  |  |
| Q9KU27 | VC\_0702 | Inosine/xanthosine triphosphatase  |  |  |  |
| H9L4T3 | VC\_2212 | Uncharacterized protein  |  |  |  |
| Q9K2M8 | VC\_A0348 | Uncharacterized protein  |  |  |  |
| Q9KKK0 | VC\_A1105 | DNA-binding response regulator  |  |  |  |
| Q9KKX8 | VC\_A0972 | MFS domain-containing protein  |  |  |  |
| Q9KL71 | VC\_A0876 | D-serine deaminase activator  |  |  |  |
| Q9KLB3 | VC\_A0833 | Transcriptional regulator, LysR family  |  |  |  |
| Q9KLG6 | VC\_A0778 | AHS2 domain-containing protein  |  |  |  |
| Q9KLK5 | VC\_A0738 | Uncharacterized protein  |  |  |  |
| Q9KLK9 | VC\_A0734 | Uncharacterized protein  |  |  |  |
| Q9KLQ1 | VC\_A0691 | Acetoacetyl-CoA reductase  |  |  |  |
| Q9KM02 | VC\_A0587 | PPC domain-containing protein  |  |  |  |
| Q9KM77 | VC\_A0511 | Anaerobic ribonucleoside-triphosphate reductase  |  |  |  |
| Q9KM86 | VC\_A0496 | Glutathione S-transferase, putative  |  |  |  |
| Q9KM98 | VC\_A0483 | Uncharacterized protein  |  |  |  |
| Q9KMX3 | VC\_A0193 | Na+/H+ antiporter, putative  |  |  |  |
| Q9KN01 | VC\_A0165 | GGDEF family protein  |  |  |  |
| Q9KN09 | VC\_A0157 | NADH dehydrogenase, putative  |  |  |  |
| Q9KN25 | VC\_A0141 | C4-dicarboxylate transport sensor protein, putative  |  |  |  |
| Q9KN46 | VC\_A0119 | ImpA\_N domain-containing protein  |  |  |  |
| Q9KN85 | VC\_A0080 | GGDEF family protein  |  |  |  |
| Q9KN89 | VC\_A0076 | Gate domain-containing protein  |  |  |  |
| Q9KN99 | VC\_A0066 | Uncharacterized protein  |  |  |  |
| Q9KNA1 | VC\_A0064 | TonB system receptor, putative  |  |  |  |
| Q9KNA2 | VC\_A0063 | Protease II  |  |  |  |
| Q9KNB4 | VC\_A0051 | Uncharacterized protein  |  |  |  |
| Q9KNE3 | VC\_A0022 | Glutathione S-transfersae-related protein  |  |  |  |
| Q9KNF6 | VC\_A0008 | Methyl-accepting chemotaxis protein  |  |  |  |
| Q9KNM6 | VC\_2706 | Probable queuosine precursor transporter  |  |  |  |
| Q9KNN0 | VC\_2702 | Transcriptional regulator, LuxR family  |  |  |  |
| Q9KPD7 | cpdA | 3,5-cyclic adenosine monophosphate phosphodiesterase CpdA  |  |  |  |
| Q9KPJ7 | VC\_2370 | Sensory box/GGDEF family protein  |  |  |  |
| Q9KPR2 | VC\_2304 | Uncharacterized protein  |  |  |  |
| Q9KPY8 | VC\_2224 | GGDEF family protein |  |  |  |
| Q9KQ04 | VC\_2203 | Flagellar protein, putative  |  |  |  |
| Q9KQ78 | fliP | Flagellar biosynthetic protein FliP  |  |  |  |
| Q9KQN1 | VC\_1967 | Methyl-accepting chemotaxis protein  |  |  |  |
| Q9KQQ9 | VC\_1939 | Uncharacterized protein  |  |  |  |
| Q9KQW7 | VC\_1880 | DUF2062 domain-containing protein  |  |  |  |
| Q9KR48 | VC\_1798 | Eha protein  |  |  |  |
| Q9KRH6 | VC\_1666 | VIBCH ABC transporter, ATP-binding protein, putative  |  |  |  |
| Q9KRJ6 | VC\_1644 | Uncharacterized protein  |  |  |  |
| Q9KRL9 | VC\_1617 | Transcriptional regulator, LysR family |  |  |  |
| Q9KRN2 | VC\_1604 | Transcriptional regulatory protein  |  |  |  |
| Q9KRW9 | VC\_1515 | Chaperone, formate dehydrogenase-specific, putative  |  |  |  |
| Q9KSC1 | VC\_1337 | Citrate synthase |  |  |  |
| Q9KSC6 | VC\_1332 | Uncharacterized protein  |  |  |  |
| Q9KSC9 | VC\_1329 | Opacity protein-related protein  |  |  |  |
| Q9KSE2 | VC\_1315 | Sensor histidine kinase  |  |  |  |
| Q9KSP0 | VC\_1216 | GGDEF family protein  |  |  |  |
| Q9KSV5 | VC\_1151 | Uncharacterized protein  |  |  |  |
| Q9KT20 | VC\_1085 | Sensor histidine kinase  |  |  |  |
| Q9KT74 | VC\_1031 | Inosine monophosphate dehydrogenase-related protein  |  |  |  |
| Q9KTC3 | VC\_0979 | Oxidoreductase, short-chain dehydrogenase/reductase family  |  |  |  |
| Q9KTI4 | VC\_0918 | UDP-N-acetyl-D-mannosaminuronic acid dehydrogenase  |  |  |  |
| Q9KTV0 | VC\_0787 | Transcriptional regulator, LysR family  |  |  |  |
| Q9KU51 | VC\_0673 | Probable membrane transporter protein  |  |  |  |
| Q9KUQ1 | VC\_0464 | Transcriptional regulator, LuxR family  |  |  |  |
| Q9KUW6 | VC\_0393 | Uncharacterized protein  |  |  |  |
| Q9KV54 | VC\_0303 | Sensor histidine kinase |  |  |  |
| Q9KVM2 | VC\_0119 | Uroporphyrinogen-III synthase |  |  |  |
| Q9KVM8 | VC\_0113 | Methyltransferase-related protein  |  |  |  |
| Q9KVP4 | VC\_0097 | Flagellar protein FliL  |  |  |  |
| Q9KVS6 | VC\_0063 | ThiF protein  |  |  |  |
| I – 4. MoreF606TOB\_ThanJ420TOB | **log2 FC WT/tgt** | **p value** | **Adjusted p value** |
|
| Q9KMV8 | VC\_A0210 | 33-cGAMP-specific phosphodiesterase 2  | 5,21 | 0,00000 | 0,00005 |
| Q9KSR2 | VC\_1194 | J domain-containing protein  | 3,68 | 0,00929 | 0,00488 |
| Q9KKY6 | VC\_A0964 | Glycine cleavage operon activator, putative  | 5,30 | 0,00002 | 0,00043 |
| Q9KKL6 | VC\_A1087 | Anti-sigma F factor antagonist, putative  | 3,72 | 0,00060 | 0,00202 |
| Q9KSK7 | VC\_1249 | ACT domain-containing protein  | 2,37 | 0,00973 | 0,00488 |
| Q9KS89 | VC\_1370 | GGDEF family protein  | 3,51 | 0,00007 | 0,00062 |
| Q9KNA0 | VC\_A0065 | P/Homo B domain-containing protein  | 3,48 | 0,00876 | 0,00488 |
| Q9KT21 | VC\_1084 | Sensory box sensor histidine kinase  | 1,77 | 0,00183 | 0,00235 |
| Q9KRA1 | VC\_1741 | Transcriptional regulator, TetR family  | 1,71 | 0,01423 | 0,00606 |
| Q9KU00 | cutC | Copper homeostasis protein CutC  | 1,85 | 0,01810 | 0,00696 |
| Q9KTH7 | VC\_0925 | Polysaccharide biosynthesis protein, putative  | 3,09 | 0,00236 | 0,00256 |
| Q9KSD3 | VC\_1325 | Galactoside ABC transporter, periplasmic D-galactose/D-glucose-binding protein SV=1" | 1,77 | 0,02018 | 0,00745 |
| Q9KUU2 | arcA | ARCA\_VIBCH Arginine deiminase  | 2,78 | 0,00191 | 0,00235 |
| Q9KLB8 | phhA | PH4H\_VIBCH Phenylalanine-4-hydroxylase  | 2,16 | 0,03098 | 0,00967 |
| Q9KPI7 | VC\_2380 | Cobalamin biosynthesis protein CbiB, putative | 1,83 | 0,00973 | 0,00488 |
| Q9KSE3 | VC\_1314 | Transporter, putative  | 2,64 | 0,02472 | 0,00834 |
| Q9KQX3 | VC\_1874 | Uncharacterized protein | 2,66 | 0,00403 | 0,00309 |
| Q9KMJ2 | VC\_A0356 | Uncharacterized protein | 2,60 | 0,00439 | 0,00321 |
| Q9KRW3 | VC\_1521 | Sensor histidine kinase  | 2,69 | 0,00011 | 0,00085 |
| Q9KN34 | rbsK | Ribokinase | 2,49 | 0,00270 | 0,00269 |
| Q9KQX5 | VC\_1872 | AAA\_PrkA domain-containing protein  | 2,94 | 0,00216 | 0,00245 |
| Q9KS12 | rtxA | Multifunctional-autoprocessing repeats-in-toxin  | 3,68 | 0,01920 | 0,00716 |
| Q9KQ01 | VC\_2206 | Uncharacterized protein  | 2,76 | 0,00003 | 0,00043 |
| P45774 | epsH | Type II secretion system protein H  | 2,58 | 0,02202 | 0,00772 |
| Q9KU02 | VC\_0728 | PPK2 domain-containing protein  | 3,08 | 0,01270 | 0,00574 |
| Q9KKL7 | VC\_A1086 | Response regulator  | 2,65 | 0,02350 | 0,00806 |
| Q9KSG5 | VC\_1291 | Uncharacterized protein  | 3,38 | 0,00096 | 0,00223 |
| Q9KSV0 | VC\_1156 | Sensor histidine kinase  | 2,48 | 0,00113 | 0,00224 |
| Q9KN48 | VC\_A0117 | Sigma-54 dependent transcriptional regulator  | 1,56 | 0,00974 | 0,00488 |
| Q9KRG0 | VC\_1682 | Peptide ABC transporter, permease protein | 2,56 | 0,00020 | 0,00109 |
| Q9KRG1 | VC\_1681 | Peptide ABC transporter, permease protein  | 2,86 | 0,00015 | 0,00099 |
| Q9KSD1 | mglA | Galactose/methyl galactoside import ATP-binding protein MglA  | 2,08 | 0,02068 | 0,00754 |
| Q9KLT8 | VC\_A0653 | PTS system, sucrose-specific IIBC component  | 2,43 | 0,00003 | 0,00043 |
| P0C6Q8 | dam | DNA adenine methylase | 2,26 | 0,00448 | 0,00324 |
| P0C6D3 | vibB | Vibriobactin-specific isochorismatase  | 2,32 | 0,00194 | 0,00235 |
| Q9KLF1 | VC\_A0795 | Resolvase, putative  | 2,33 | 0,00078 | 0,00215 |
| Q9KNN7 | VC\_2694 | Superoxide dismutase  | 1,34 | 0,00647 | 0,00419 |
| Q9KNW3 | VC\_2617 | Arginine N-succinyltransferase OS=Vibrio cholerae serotype  | 1,27 | 0,02884 | 0,00915 |
| Q9KUA1 | VC\_0622 | Histidine kinase  | 1,89 | 0,00950 | 0,00488 |
| Q9KQX9 | VC\_1868 | Methyl-accepting chemotaxis protein  | 2,27 | 0,01417 | 0,00606 |
| Q9KS63 | VC\_1397 | Chemotaxis protein CheA | 2,42 | 0,02557 | 0,00852 |
| Q9KR16 | VC\_1831 | Sensor histidine kinase | 2,54 | 0,00188 | 0,00235 |
| Q9KKR5 | VC\_A1037 | Amino acid ABC transporter, ATP-binding protein | 1,56 | 0,02096 | 0,00754 |
| Q9KPK6 | grcA | GRCA\_VIBCH Autonomous glycyl radical cofactor  | 2,66 | 0,00332 | 0,00269 |
| Q9KQX4 | VC\_1873 | UPF0229 protein VC\_1873  | 2,70 | 0,02180 | 0,00770 |
| Q9KTI9 | VC\_0913 | HlyD\_D23 domain-containing protein  | 1,71 | 0,02570 | 0,00852 |
| Q9KTC7 | VC\_0975 | NfeD domain-containing protein  | 2,07 | 0,00048 | 0,00177 |
| Q9KU65 | VC\_0658 | C-di-GMP phosphodiesterase A-related protein  | 2,14 | 0,00930 | 0,00488 |
| Q9KNB6 | VC\_A0049 | GGDEF family protein  | 2,45 | 0,00175 | 0,00235 |
| Q9KNY0 | VC\_2600 | Uncharacterized protein  | 1,81 | 0,00123 | 0,00224 |
| Q9KTF2 | mrdA | Peptidoglycan D,D-transpeptidase MrdA  | 1,65 | 0,01002 | 0,00488 |
| Q9KQY2 | VC\_1865 | Uncharacterized protein  | 1,78 | 0,00316 | 0,00269 |
| Q9KL39 | VC\_A0909 | Oxygen-independent coproporphyrinogen III oxidase, putative | 2,04 | 0,01389 | 0,00602 |
| Q9KVF6 | VC\_0190 | DNA helicase uvrD | 1,94 | 0,01686 | 0,00663 |
| Q9KUM9 | VC\_0486 | Transcriptional regulator, DeoR family  | 1,92 | 0,03066 | 0,00961 |
| Q9KRI2 | VC\_1659 | Uncharacterized protein  | 2,10 | 0,01469 | 0,00612 |
| Q9KNJ0 | VC\_2748 | Nitrogen regulation protein  | 1,87 | 0,00126 | 0,00224 |
| Q9KP22 | VC\_2557 | Uncharacterized protein OS | 1,81 | 0,00291 | 0,00269 |
| Q9KRV1 | VC\_1533 | DTW domain-containing protein  | 1,83 | 0,00205 | 0,00235 |
| Q9KQC8 | VC\_2072 | Peptidase, insulinase family  | 1,58 | 0,00893 | 0,00488 |
| Q9KUM3 | VC\_0492 | Uncharacterized protein  | 2,34 | 0,00243 | 0,00259 |
| Q9KQI3 | VC\_2015 | DNA polymerase III, delta prime subunit  | 1,77 | 0,00063 | 0,00202 |
| Q9KPT7 | crl | Sigma factor-binding protein Crl  | 1,58 | 0,00088 | 0,00219 |
| Q9KS69 | VC\_1390 | Transcriptional regulator, LysR family  | 1,89 | 0,00007 | 0,00062 |
| Q9KSC3 | VC\_1335 | Transcriptional regulator, GntR family  | 1,55 | 0,00321 | 0,00269 |
| Q9KRL1 | VC\_1629 | Uncharacterized protein  | 1,89 | 0,00322 | 0,00269 |
| Q9KLS5 | VC\_A0666 | L-serine dehydratase  | 1,71 | 0,00079 | 0,00215 |
| Q9KM52 | VC\_A0537 | Uncharacterized protein  | 1,27 | 0,01088 | 0,00511 |
| Q9KRI6 | VC\_1655 | Magnesium transporter MgtE  | 1,72 | 0,00363 | 0,00282 |
| Q9KTJ1 | VC\_0911 | Trehalose-6-phosphate hydrolase  | 1,70 | 0,00042 | 0,00166 |
| Q9KPZ9 | VC\_2208 | Uncharacterized protein  | 1,79 | 0,01534 | 0,00629 |
| Q9KM32 | VC\_A0557 | GGDEF family protein | 1,37 | 0,02135 | 0,00762 |
| Q9KSA6 | VC\_1353 | GGDEF family protein  | 1,52 | 0,00156 | 0,00231 |
| Q9KUC2 | VC\_0600 | AB hydrolase-1 domain-containing protein  | 1,72 | 0,00123 | 0,00224 |
| Q9KM15 | VC\_A0574 | N-acetyltransferase domain-containing protein  | 1,39 | 0,01767 | 0,00683 |
| Q9KS83 | VC\_1376 | GGDEF family protein  | 1,51 | 0,00363 | 0,00282 |
| Q9KPT2 | VC\_2280 | Uncharacterized protein  | 1,45 | 0,00471 | 0,00331 |
| Q9KVN8 | VC\_0103 | Uncharacterized protein  | 1,55 | 0,00249 | 0,00262 |
| Q9KT24 | VC\_1081 | Response regulator  | 1,65 | 0,02632 | 0,00861 |
| Q9KRJ1 | VC\_1649 | Trypsin, putative  | 1,54 | 0,00092 | 0,00220 |
| Q9KLP6 | VC\_A0697 | Sensory box/GGDEF family protein  | 1,63 | 0,00022 | 0,00109 |
| Q9KQ23 | ispE | ISPE\_VIBCH 4-diphosphocytidyl-2-C-methyl-D-erythritol kinase ispE  | 1,57 | 0,00119 | 0,00224 |
| H9L4T1 | VC\_A0450 | Uncharacterized protein  | 1,76 | 0,00290 | 0,00269 |
| Q9KU16 | VC\_0714 | Uncharacterized protein  | 1,60 | 0,02409 | 0,00820 |
| Q9KRS6 | katG | KATG\_VIBCH Catalase-peroxidase katG  | 1,39 | 0,01256 | 0,00571 |
| P29485 | tcpP | Toxin coregulated pilus biosynthesis protein P tcpP  | 1,56 | 0,00124 | 0,00224 |
| Q9KU53 | rppH | RPPH\_VIBCH RNA pyrophosphohydrolase rppH  | 2,03 | 0,00467 | 0,00331 |
| Q9KKX3 | VC\_A0977 | ABC transporter, ATP-binding protein  | 1,84 | 0,02092 | 0,00754 |
| Q9KQL5 | VC\_1983 | Peptidase, putative  | 2,47 | 0,02205 | 0,00772 |
| Q9KSG0 | VC\_1296 | Phosphomethylpyrimidine kinase  | 3,54 | 0,00005 | 0,00054 |
| Q9KPJ4 | VC\_2373 | Glutamate synthase, large subunit  | 1,53 | 0,00120 | 0,00224 |
| Q9KS96 | VC\_1363 | Siroheme synthase component enzyme  | 1,31 | 0,00930 | 0,00488 |
| Q9KP89 | VC\_2484 | Long-chain-fatty-acid--CoA ligase, putative  | 1,53 | 0,00535 | 0,00367 |
| Q9KSM2 | VC\_1234 | Exodeoxyribonuclease I  | 1,59 | 0,02087 | 0,00754 |
| Q9KSX5 | VC\_1131 | Na\_H\_antiporter domain-containing protein  | 2,07 | 0,01089 | 0,00511 |
| Q9KTJ2 | VC\_0910 | PTS system, trehalose-specific IIBC component  | 1,33 | 0,00205 | 0,00235 |
| Q9KKZ7 | VC\_A0953 | Peptidyl-prolyl cis-trans isomerase C  | 1,30 | 0,00997 | 0,00488 |
| Q9KUU7 | VC\_0418 | dTTP/UTP pyrophosphatase  | 1,24 | 0,00258 | 0,00267 |
| Q9KV39 | birA | Bifunctional ligase/repressor BirA  | 1,47 | 0,00649 | 0,00419 |
| Q9KS28 | VC\_1433 | Uncharacterized protein  | 1,23 | 0,00965 | 0,00488 |
| Q9KMM4 | VC\_A0307 | HNHc domain-containing protein  | 1,46 | 0,00110 | 0,00224 |
| Q9KUJ8 | VC\_0522 | Beta-ketoadipate enol-lactone hydrolase, putative  | 1,37 | 0,00202 | 0,00235 |
| Q9KVT7 | purE | N5-carboxyaminoimidazole ribonucleotide mutase  | 1,45 | 0,00886 | 0,00488 |
| Q9KRU5 | VC\_1539 | Probable ketoamine kinase VC\_1539  | 1,09 | 0,01619 | 0,00652 |
| Q9KSU7 | serC | Phosphoserine aminotransferase  | 1,41 | 0,00147 | 0,00231 |
| Q9KQU2 | VC\_1906 | Methyltranfer\_dom domain-containing protein  | 2,00 | 0,00065 | 0,00202 |
| Q9KRW4 | VC\_1520 | ABC transporter, ATP-binding protein  | 1,17 | 0,00887 | 0,00488 |
| Q9KU52 | VC\_0672 | Phosphoenolpyruvate-protein phosphotransferase  | 1,41 | 0,00145 | 0,00231 |
| Q9KLI6 | VC\_A0758 | Arginine ABC transporter, permease protein  | 1,24 | 0,01152 | 0,00534 |
| Q9KPQ9 | panE | 2-dehydropantoate 2-reductase  | 1,32 | 0,02013 | 0,00745 |
| Q9KNW7 | VC\_2613 | Phosphoribulokinase  | 1,22 | 0,00346 | 0,00278 |
| Q9KT18 | VC\_1087 | Response regulator  | 1,12 | 0,00908 | 0,00488 |
| Q9KPP6 | recB | RecBCD enzyme subunit RecB  | 1,24 | 0,00085 | 0,00218 |
| Q9KQK1 | VC\_1997 | Uncharacterized protein  | 1,16 | 0,00200 | 0,00235 |
| Q9KUN3 | argP | ARGP\_VIBCH HTH-type transcriptional regulator ArgP  | 1,53 | 0,00885 | 0,00488 |
| Q9KMW8 | VC\_A0198 | Site-specific DNA-methyltransferase, putative  | 1,15 | 0,00300 | 0,00269 |
| Q9KVB8 | VC\_0228 | Uncharacterized protein  | 1,27 | 0,00223 | 0,00248 |
| Q9KVE7 | VC\_0199 | Hemolysin secretion ATP-binding protein, putative  | 1,29 | 0,00999 | 0,00488 |
| Q9KQM5 | menB | 1,4-dihydroxy-2-naphthoyl-CoA synthase menB  | 1,40 | 0,00328 | 0,00269 |
| Q9KR89 | VC\_1753 | Paraquat-inducible protein A  | 1,11 | 0,00739 | 0,00467 |
| Q9KQJ7 | VC\_2001 | Putative glucose-6-phosphate 1-epimerase  | 1,57 | 0,01040 | 0,00501 |
| P57070 | lolB | Outer-membrane lipoprotein LolB  | 1,04 | 0,01285 | 0,00577 |
| Q9KL63 | VC\_A0884 | Uncharacterized protein  | 1,15 | 0,02695 | 0,00863 |
| H9L4P1 | VC\_0259 | Lipopolysaccharide biosynthesis protein RfbV  | 1,21 | 0,00560 | 0,00377 |
| Q9KMU4 | VC\_A0225 | Glutamine amidotransferase type-2 domain-containing protein  | 1,14 | 0,00164 | 0,00235 |
| Q9KKU5 | VC\_A1005 | Transcriptional regulator, MarR family  | 1,14 | 0,02484 | 0,00834 |
| Q9KVK1 | VC\_0142 | DUF4145 domain-containing protein  | 1,20 | 0,01451 | 0,00609 |
| Q9KVB5 | VC\_0231 | Uncharacterized protein  | 1,09 | 0,00932 | 0,00488 |
| Q9KKS4 | VC\_A1026 | Uncharacterized protein  | 1,31 | 0,00883 | 0,00488 |
| Q9KUU0 | VC\_0425 | Uncharacterized protein  | 1,54 | 0,01872 | 0,00702 |
| Q9KTA5 | VC\_0998 | Uncharacterized protein  | 1,15 | 0,00530 | 0,00367 |
| Q9KNC4 | gltS | Sodium/glutamate symporter  | 1,21 | 0,02667 | 0,00862 |
| Q9KRS8 | VC\_1558 | 6-phospho-beta-glucosidase  | 1,37 | 0,00196 | 0,00235 |
| Q9KMT9 | VC\_A0230 | Iron(III) ABC transporter, ATP-binding protein  | 1,08 | 0,01196 | 0,00547 |
| Q9KPZ0 | VC\_2222 | Smr domain-containing protein  | 1,04 | 0,02562 | 0,00852 |
| Q9KQE2 | VC\_2058 | Uncharacterized protein  | 1,05 | 0,00651 | 0,00419 |
| P57066 | lolD | LOLD\_VIBCH Lipoprotein-releasing system ATP-binding protein LolD  | 1,01 | 0,00981 | 0,00488 |
| Q9KLE5 | VC\_A0801 | Q9KLE5\_VIBCH Inosine-guanosine kinase  | 1,00 | 0,02622 | 0,00861 |
| Q9KS35 | VC\_1426 | Spermidine/putrescine ABC transporter, permease protein  | 1,11 | 0,00158 | 0,00231 |
| Q9KSV4 | VC\_1152 | HDOD domain-containing protein  | 1,07 | 0,00926 | 0,00488 |
| Q9KUM2 | VC\_0493 | Q9KUM2\_VIBCH Uncharacterized protein  | 1,76 | 0,01375 | 0,00600 |
| Q9KNA9 | VC\_A0056 | Q9KNA9\_VIBCH Transcriptional regulator, MerR family  | 1,07 | 0,01454 | 0,00609 |
| Q9KQ71 | VC\_2130 | Flagellum-specific ATP synthase FliI  | 1,15 | 0,00357 | 0,00282 |
| Q9KLD8 | VC\_A0808 | NodN-related protein  | 1,27 | 0,00802 | 0,00488 |
| Q9KP78 | VC\_2497 |  HD-GYP domain-containing protein  | 1,09 | 0,00149 | 0,00231 |
| Q60153 | tcpA | TCPA\_VIBCH Toxin coregulated pilin  | 1,01 | 0,02653 | 0,00862 |
| Q9KRU1 | VC\_1543 | Uncharacterized protein  | 1,09 | 0,00268 | 0,00269 |
| Q9KQ38 | VC\_2166 |  Trp repressor-binding protein | 1,46 | 0,01086 | 0,00511 |
| Q9KQN3 | VC\_1965 | TetR\_C\_33 domain-containing protein  | 1,28 | 0,00698 | 0,00445 |
| Q9KN86 | VC\_A0079 | Uncharacterized protein | 1,23 | 0,00556 | 0,00377 |
| Q9KRD3 | VC\_1709 | Zinc protease, insulinase family  | 1,25 | 0,00993 | 0,00488 |
| Q9KKS7 | VC\_A1023 | Uncharacterized protein  | 1,16 | 0,00537 | 0,00367 |
| Q9KVB7 | VC\_0229 | Uncharacterized protein  | 1,66 | 0,01838 | 0,00696 |
| Q9KNR2 | VC\_2669 | 5-carboxymethyl-2-hydroxymuconate delta isomerase, putative  | 1,22 | 0,01524 | 0,00628 |
| Q9KUI6 | mutS | MUTS\_VIBCH DNA mismatch repair protein MutS  | 1,07 | 0,00298 | 0,00269 |
| Q9KVF0 | VC\_0196 | ATP-dependent DNA helicase RecQ | 1,04 | 0,00303 | 0,00269 |
| Q9KTJ3 | VC\_0909 | Trehalose operon repressor  | 1,03 | 0,00981 | 0,00488 |
| Q9KVH1 | VC\_0175 | Deoxycytidylate deaminase-related protein  | 1,28 | 0,01307 | 0,00584 |
| Q9KR77 | VC\_1766 | Uncharacterized protein  | 1,01 | 0,01408 | 0,00606 |
| Q9KTL4 | truC | tRNA pseudouridine synthase C truC  | 1,09 | 0,00416 | 0,00310 |
| Q9KUM4 | VC\_0491 | Uncharacterized protein  | 1,10 | 0,00571 | 0,00379 |
| P52022 | dnaE | DNA polymerase III subunit alpha  | 1,07 | 0,00324 | 0,00269 |
| Q9KP97 | VC\_2476 | UPF0149 protein VC\_2476  | 1,70 | 0,02715 | 0,00865 |
| Q9KS92 | VC\_1367 | GGDEF family protein  | 1,19 | 0,00957 | 0,00488 |
| Q9KU08 | ppx | Exopolyphosphatase ppx  | 1,04 | 0,01694 | 0,00663 |
| Q9KSI6 | VC\_1270 | Glyoxylase II family protein  | 1,32 | 0,01645 | 0,00653 |
| Q9KRA6 | bpt | Aspartate/glutamate leucyltransferase bpt  | 1,04 | 0,01838 | 0,00696 |
| Q9KQF5 | topB | DNA topoisomerase 3 topB  | 1,05 | 0,02938 | 0,00928 |
| Q9KNF3 | malT | HTH-type transcriptional regulator MalT  | 1,10 | 0,00227 | 0,00249 |
| Q9KPE8 | VC\_2420 | Flavodoxin  | 1,39 | 0,00897 | 0,00488 |
| Q9KNT4 | ppc | Phosphoenolpyruvate carboxylase ppc  | 1,05 | 0,00302 | 0,00269 |
| Q9KU29 | VC\_0700 | Soluble lytic murein transglycosylase  | 1,07 | 0,00291 | 0,00269 |
| Q9KQV0 | VC\_1898 | Methyl-accepting chemotaxis protein  | 1,01 | 0,00574 | 0,00379 |
| Q9KPE7 | VC\_2421 | ampD protein | 1,04 | 0,02430 | 0,00824 |
| Q9KU20 | rluD | Ribosomal large subunit pseudouridine synthase D rluD  | 1,03 | 0,00290 | 0,00269 |
| Q9KNQ5 | VC\_2676 | Cell division protein FtsN, putative | 1,20 | 0,01452 | 0,00609 |
| H9L4T5 | VC\_0847 | Integrase, phage family | 1,28 | 0,02687 | 0,00863 |
| Q9KQ28 | VC\_2176 | UPF0162 protein VC\_2176  | 1,04 | 0,00311 | 0,00269 |
| Q9KUC0 | mrcB | PBPB\_VIBCH Penicillin-binding protein 1B  | 1,15 | 0,01050 | 0,00502 |
| Q9KPV6 | uppS | UPPS\_VIBCH Ditrans,polycis-undecaprenyl-diphosphate synthase  | 1,03 | 0,00800 | 0,00488 |
| Q9KVU5 | rsmB | RSMB\_VIBCH Ribosomal RNA small subunit methyltransferase B  | 1,02 | 0,01178 | 0,00542 |
| Q9KMC3 | VC\_A0441 | Uncharacterized protein  | 1,17 | 0,00930 | 0,00488 |
| Q9KVL9 | VC\_0122 | Adenylate cyclase  | 1,23 | 0,02356 | 0,00806 |
| Q9KUW9 | metH | Methionine synthase  | 1,28 | 0,02670 | 0,00862 |
| Q9KL09 | VC\_A0941 | Acyl-CoA thioester hydrolase-related protein  | 1,03 | 0,02584 | 0,00853 |
| Q9KMY4 | VC\_A0182 | Sigma-54 dependent transcriptional regulator  | 1,00 | 0,00859 | 0,00488 |
| Q9KQ13 | flgH | Flagellar L-ring protein  | 1,06 | 0,01335 | 0,00593 |
| Q9KT38 | VC\_1067 | GGDEF domain-containing protein  | 1,04 | 0,02971 | 0,00935 |
| Q9KM78 | VC\_A0510 | Uncharacterized protein  | 1,01 | 0,01640 | 0,00653 |
| P0C6R0 | irgA | IRGA\_VIBCH Iron-regulated outer membrane virulence protein  | 1,03 | 0,02028 | 0,00745 |
| Q9KPD8 | VC\_2432 | Uncharacterized protein  | 1,23 | 0,03115 | 0,00968 |
| Q9KVS4 | thiG | THIG\_VIBCH Thiazole synthase  | 1,50 | 0,03191 | 0,00983 |
| Q9KMG4 | higA-1 | Antitoxin HigA-1  | 1,30 | 0,01712 | 0,00665 |
| Q9KUY5 | VC\_0373 | Uncharacterized protein  | 1,25 | 0,02357 | 0,00806 |
| Q9KMG8 | VC\_A0388 | Uncharacterized protein  | 1,58 | 0,00081 | 0,00215 |

|  |  |  |
| --- | --- | --- |
| Uniprot | Gene Name | Fasta headers |
| II - More abundant in *∆tgt* |
| II – 1. PresentJ420tgt\_AbsentF606wt |
| O34419 | rstR1 | Cryptic phage CTXphi transcriptional repressor RstR  |  |  |  |
| Q9KN37 | rbsA | Ribose import ATP-binding protein RbsA  |  |  |  |
| Q9KT77 | moaE | Molybdopterin synthase catalytic subunit  |  |  |  |
| Q9KVG9 | vspR | Transcriptional regulator VspR  |  |  |  |
| H9L4R3 | VC\_A0444 | RelE protein  |  |  |  |
| Q9KKW7 | VC\_A0983 | L-lactate permease  |  |  |  |
| Q9KL14 | VC\_A0935 | Uncharacterized protein  |  |  |  |
| Q9KLD8 | VC\_A0808 | NodN-related protein  |  |  |  |
| Q9KLF6 | VC\_A0788 | DnaJ-related protein  |  |  |  |
| Q9KLJ2 | VC\_A0752 | Thioredoxin 2  |  |  |  |
| Q9KLV6 | VC\_A0635 | Transcriptional regulator, LysR family  |  |  |  |
| Q9KM02 | VC\_A0587 | PPC domain-containing protein  |  |  |  |
| Q9KM27 | VC\_A0562 | Uncharacterized protein  |  |  |  |
| Q9KMP9 | VC\_A0271 | Uncharacterized protein  |  |  |  |
| Q9KNC6 | VC\_A0039 | Uncharacterized protein  |  |  |  |
| Q9KNE3 | VC\_A0022 | Glutathione S-transfersae-related protein  |  |  |  |
| Q9KNI2 | VC\_2757 | Uncharacterized protein  |  |  |  |
| Q9KNM7 | VC\_2705 | Sodium/solute symporter, putative  |  |  |  |
| Q9KPF0 | VC\_2418 | Thiol:disulfide interchange protein  |  |  |  |
| Q9KQ76 | VC\_2125 | Flagellar motor switch protein FliN  |  |  |  |
| Q9KQG6 | VC\_2032 | Uncharacterized protein  |  |  |  |
| Q9KQS3 | VC\_1925 | C4-dicarboxylate transport sensor protein |  |  |  |
| Q9KR71 | VC\_1772 | WYL domain-containing protein  |  |  |  |
| Q9KRG4 | VC\_1678 | Phage shock protein A  |  |  |  |
| Q9KRH0 | VC\_1672 | DNA-3-methyladenine glycosidase I  |  |  |  |
| Q9KRM1 | VC\_1615 | Uncharacterized protein  |  |  |  |
| Q9KRR5 | VC\_1571 | Quinol oxidase, subunit I  |  |  |  |
| Q9KSM4 | VC\_1232 | Uncharacterized protein  |  |  |  |
| Q9KSN9 | VC\_1217 | N-acetyltransferase domain-containing protein  |  |  |  |
| Q9KTS9 | VC\_0809 | SWIM-type domain-containing protein |  |  |  |
| Q9KTV0 | VC\_0787 | Transcriptional regulator, LysR family |  |  |  |
| Q9KUN2 | VC\_0483 | Uncharacterized protein |  |  |  |
| Q9KUW6 | VC\_0393 | Uncharacterized protein  |  |  |  |
| Q9KVR9 | VC\_0070 | Uncharacterized protein  |  |  |  |
| II – 2. MoreJ420tgt\_ThanF606wt | **log2 wt/tgt** | **p value** | **Adjusted p value** |
| Q9KNX3 | kefG | Glutathione-regulated potassium-efflux system ancillary protein KefG | -7,30 | 0,00001 | 0,00036 |
| Q9KLB8 | phhA | Phenylalanine-4-hydroxylase  | -4,14 | 0,00010 | 0,00068 |
| P09545 | hlyA | Hemolysin  | -3,90 | 0,00039 | 0,00140 |
| Q9KQN1 | VC\_1967 | Methyl-accepting chemotaxis protein  | -3,84 | 0,00567 | 0,00521 |
| Q9KV16 | queG | Epoxyqueuosine reductase  | -3,39 | 0,00416 | 0,00420 |
| H9L4T3 | VC\_2212 | Uncharacterized protein - putative Fe3+-citrate ABC transporter | -3,32 | 0,00017 | 0,00094 |
| Q9KTJ9 | syd | Syd  | -3,29 | 0,00057 | 0,00177 |
| Q9KNW3 | VC\_2617 | Arginine N-succinyltransferase | -2,93 | 0,00002 | 0,00050 |
| Q9KU56 | mutH | DNA mismatch repair protein MutH  | -2,90 | 0,00004 | 0,00050 |
| Q9KTZ6 | VC\_0734 | Malate synthase  | -2,81 | 0,00306 | 0,00389 |
| Q9KKQ7 | mtlA | PTS system mannitol-specific EIICBA component  | -2,80 | 0,00214 | 0,00343 |
| Q9KLB3 | VC\_A0833 | Transcriptional regulator, LysR family | -2,66 | 0,00379 | 0,00420 |
| Q9KTM2 | VC\_0880 | Uncharacterized protein  | -2,50 | 0,00364 | 0,00420 |
| Q9KSQ4 | hutH | Histidine ammonia-lyase  | -2,42 | 0,00105 | 0,00227 |
| Q9KPR5 | VC\_2301 | Transcriptional activator, putative  | -2,39 | 0,00075 | 0,00195 |
| Q9KNF6 | VC\_A0008 | Methyl-accepting chemotaxis protein  | -2,27 | 0,00264 | 0,00357 |
| Q9KRF2 | VC\_1690 | Alpha-1,6-galactosidase, putative  | -2,25 | 0,00022 | 0,00110 |
| Q9KS52 | VC\_1408 | Transcriptional regulator, TetR family  | -2,20 | 0,00047 | 0,00154 |
| Q9KUN3 | argP | HTH-type transcriptional regulator ArgP  | -2,20 | 0,00006 | 0,00050 |
| Q9KU74 | VC\_0649 | Transcriptional regulator, MarR family  | -2,08 | 0,00232 | 0,00343 |
| Q9KRA1 | VC\_1741 | Transcriptional regulator, TetR family  | -2,03 | 0,00074 | 0,00195 |
| Q9KQ71 | VC\_2130 | Flagellum-specific ATP synthase FliI  | -1,89 | 0,00016 | 0,00094 |
| Q9KUU2 | arcA | Arginine deiminase  | -1,88 | 0,00990 | 0,00732 |
| Q9KM69 | VC\_A0519 | Fructose repressor  | -1,80 | 0,00183 | 0,00331 |
| Q9KS51 | VC\_1409 | Multidrug resistance protein, putative  | -1,77 | 0,00895 | 0,00699 |
| Q9KS17 | VC\_1444 | Uncharacterized protein  | -1,73 | 0,01228 | 0,00882 |
| P0C6Q5 | tcpF | Toxin coregulated pilus biosynthesis protein F  | -1,72 | 0,00006 | 0,00050 |
| Q9KVH8 | VC\_0168 | Cytochrome c5  | -1,65 | 0,00187 | 0,00331 |
| Q9KP69 | VC\_2507 | PINc domain-containing protein  | -1,62 | 0,00903 | 0,00699 |
| Q9KM51 | VC\_A0538 | Cytochrome b561, putative  | -1,62 | 0,00417 | 0,00420 |
| Q9KTY1 | VC\_0749 | Iron-sulfur cluster assembly scaffold protein IscU | -1,59 | 0,00072 | 0,00195 |
| Q9KMJ5 | VC\_A0351 | Uncharacterized protein | -1,56 | 0,00615 | 0,00534 |
| Q9KS13 | VC\_1449 | Uncharacterized protein  | -1,54 | 0,01266 | 0,00895 |
| Q9KLM0 | VC\_A0723 | 3-hydroxy-3-methylglutaryl CoA reductase  | -1,53 | 0,00266 | 0,00357 |
| Q9KV51 | VC\_0306 | Thioredoxin  | -1,50 | 0,00255 | 0,00357 |
| Q9KRR1 | VC\_1575 | Uncharacterized protein  | -1,32 | 0,00274 | 0,00358 |
| Q9F854 | hisD | Histidinol dehydrogenase  | -1,28 | 0,00385 | 0,00420 |
| Q9KUS1 | pdxA | 4-hydroxythreonine-4-phosphate dehydrogenase  | -1,25 | 0,00082 | 0,00195 |
| Q9KSI8 | VC\_1268 | Uncharacterized protein  | -1,13 | 0,00714 | 0,00600 |
| Q9KPA8 | VC\_2465 | Sigma-E factor regulatory protein RseB  | -1,08 | 0,00400 | 0,00420 |
| Q9KLG6 | VC\_A0778 | AHS2 domain-containing protein | -1,08 | 0,00343 | 0,00420 |
| Q9KVJ1 | VC\_0153 | Uncharacterized protein  | -1,05 | 0,00936 | 0,00708 |
| II – 3. PresentJ420tgtTOB\_AbsentF606wtTOB |   |   |   |
| Q9KNM4 | gmk | Guanylate kinase  |  |  |  |
| Q9KNC1 | VC\_A0044 | Uncharacterized protein put mb protease  |  |  |  |
| Q9KRS9 | VC\_1557 | Transcriptional regulator, LacI family lipid A biosynthesis acyltransferase |  |  |  |
| Q9KQH2 | VC\_2026 | Uncharacterized protein rRNA accumulation protein YceD  |  |  |  |
| Q9KRR2 | VC\_1574 | Uncharacterized protein put Transmembrane signal peptide protein |  |  |  |
| Q9KT04 | VC\_1101 | Uncharacterized protein putative tryptophan/tyrosine transport system substrate-binding protein or T6SS  |  |  |  |
| Q9KVH8 | VC\_0168 | Cytochrome c5  |  |  |  |
| Q9KR31 | VC\_1816 | Uncharacterized protein 1 HYP TRANSPORTER |  |  |  |
| Q9KQN0 | VC\_1968 | Transcriptional regulator, HTH\_3 family sutR regulator utilization of sulfur |  |  |  |
| Q9KNT7 | argB | Acetylglutamate kinase ornithine and arginine biosynthesis |  |  |  |
| Q9KU61 | VC\_0662 | Branched-chain amino acid transport system carrier protein brnQ transport leucine, valine, and isoleucine |  |  |  |
| Q9KPR5 | VC\_2301 | Transcriptional activator, putative putative anti-ECFsigma factor, ChrR |  |  |  |
| Q9KQ26 | prmC | Release factor glutamine methyltransferase  |  |  |  |
| Q9KM00 | VC\_A0589 | Peptide ABC transporter, permease protein, putative oligopeptide ABC transporter membrane subunit YejE |  |  |  |
| Q9KVR7 | VC\_0072 | Sensory box/GGDEF family protein  |  |  |  |
| II – 4. MoreJ420tgtTOB\_ThanF606wtTOB | **log2 wt/tgt** | **p value** | **Adjusted p value** |
| Q9KSP4 | VC\_1212 | DNA polymerase  | -2,38 | 0,01099 | 0,00512 |
| Q9KR61 | nanK | N-acetylmannosamine kinase  | -4,31 | 0,00003 | 0,00043 |
| Q9KT86 | rnfA/rsxA | Ion-translocating oxidoreductase complex subunit A  | -3,56 | 0,00002 | 0,00043 |
| Q9KRT1 | VC\_1555 | Uncharacterized protein  | -1,48 | 0,00902 | 0,00488 |
| Q9KV51 | VC\_0306 | Thioredoxin trxA | -1,69 | 0,02226 | 0,00776 |
| Q9KM51 | VC\_A0538 | Cytochrome b561, putative  | -2,87 | 0,00756 | 0,00474 |
| Q9KNR9 | VC\_2662 | Uncharacterized protein  | -1,31 | 0,03255 | 0,00995 |
| Q9KR73 | VC\_1770 | Uncharacterized protein  | -1,31 | 0,01849 | 0,00696 |
| P0C6C8 | fur | Ferric uptake regulation protein  | -2,39 | 0,00030 | 0,00141 |
| Q9KMN5 | VC\_A0293 | Uncharacterized protein | -2,14 | 0,00017 | 0,00099 |
| Q9KV88 | VC\_0268 | Uncharacterized protein  | -2,11 | 0,00406 | 0,00309 |
| Q9KNQ9 | rraA | Regulator of ribonuclease activity A  | -2,42 | 0,00310 | 0,00269 |
| Q9KPZ5 | VC\_2217 | Beta-N-acetylhexosaminidase  | -2,91 | 0,00054 | 0,00191 |
| Q9KTN7 | tadA | tRNA-specific adenosine deaminase | -2,04 | 0,00110 | 0,00224 |
| Q9KRP5 | VC\_1591 | Oxidoreductase, short-chain dehydrogenase/reductase family  | -2,14 | 0,00804 | 0,00488 |
| P0C6C4 | flaB | Flagellin B  | -1,88 | 0,00131 | 0,00228 |
| Q9KTZ8 | VC\_0732 | Transcriptional regulator, LysR family oxyR like | -1,96 | 0,00070 | 0,00210 |
| Q9KSV6 | VC\_1150 | Uncharacterized protein  | -1,29 | 0,01007 | 0,00488 |
| Q9KVM9 | VC\_0112 | Cytochrome c4  | -2,60 | 0,01486 | 0,00616 |
| Q9KVK6 | cdgJ | Cyclic di-GMP phosphodiesterase CdgJ  | -3,89 | 0,00017 | 0,00099 |
| Q9KR96 | VC\_1746 | Transcriptional regulator, TetR family  | -1,85 | 0,00299 | 0,00269 |
| P0C6C5 | flaC | Flagellin C OS=Vibrio cholerae serotype  | -1,82 | 0,00042 | 0,00166 |
| Q9KPX7 | VC\_2235 | Methyltransf\_11 domain-containing protein  | -1,53 | 0,00144 | 0,00231 |
| Q9KL76 | VC\_A0871 | Transcriptional regulator, GntR family  | -1,20 | 0,00284 | 0,00269 |
| Q9KQ58 | VC\_2146 | Uncharacterized protein  | -1,38 | 0,00181 | 0,00235 |
| Q9KKP2 | ribB | 3,4-dihydroxy-2-butanone 4-phosphate synthase  | -2,73 | 0,00036 | 0,00157 |
| Q9KNL7 | greB | Transcription elongation factor GreB  | -2,29 | 0,02154 | 0,00765 |
| Q9KV61 | VC\_0296 | Biotin carboxyl carrier protein of acetyl-CoA carboxylase | -1,70 | 0,00429 | 0,00317 |
| Q9KUN2 | VC\_0483 | Uncharacterized protein | -1,46 | 0,00180 | 0,00235 |
| P0C6P9 | tpx | Thiol peroxidase  | -1,42 | 0,01847 | 0,00696 |
| Q9KN91 | VC\_A0074 | GGDEF family protein  | -1,35 | 0,00934 | 0,00488 |
| Q9KV27 | nudC | NADH pyrophosphatase  | -1,38 | 0,00104 | 0,00224 |
| Q9KTF3 | mrdB | Peptidoglycan glycosyltransferase  | -1,35 | 0,00766 | 0,00476 |
| Q9F854 | hisD | Histidinol dehydrogenase  | -1,60 | 0,00994 | 0,00488 |
| Q9KV12 | miaA | tRNA dimethylallyltransferase  | -1,44 | 0,00177 | 0,00235 |
| Q9KT82 | VC\_1023 | Putative gluconeogenesis factor | -1,72 | 0,02103 | 0,00754 |
| Q9KKQ1 | VC\_A1051 | Uncharacterized protein  | -1,32 | 0,00452 | 0,00324 |
| Q9KKZ9 | VC\_A0951 | UPF0145 protein VC\_A0951  | -1,30 | 0,01376 | 0,00600 |
| Q9KLK6 | luxP | Autoinducer 2-binding periplasmic protein LuxP  | -1,19 | 0,00413 | 0,00310 |
| Q9KTX4 | ndk | Nucleoside diphosphate kinase  | -1,10 | 0,01640 | 0,00653 |
| Q9KMJ8 | VC\_A0345 | Uncharacterized protein  | -1,18 | 0,01699 | 0,00663 |
| Q9KU82 | rimP | Ribosome maturation factor RimP  | -1,24 | 0,01367 | 0,00600 |
| Q9KSF3 | VC\_1303 | Para-aminobenzoate synthase, component I | -1,14 | 0,02352 | 0,00806 |
| Q9KS93 | queC | 7-cyano-7-deazaguanine synthase  | -1,01 | 0,01568 | 0,00635 |
| Q9KQM0 | VC\_1978 | 5-deoxynucleotidase  | -1,18 | 0,00153 | 0,00231 |
| Q9KST2 | trpE | Anthranilate synthase component 1  | -1,86 | 0,03127 | 0,00968 |
| Q9KN74 | VC\_A0091 | UPF0251 protein  | -1,10 | 0,01555 | 0,00634 |
| Q9KL95 | VC\_A0851 | HATPase\_c domain-containing protein  | -1,55 | 0,00154 | 0,00231 |
| Q9KNJ9 | VC\_2739 | AsmA domain-containing protein  | -1,16 | 0,03228 | 0,00991 |