**Supplementary materials**

**Table S1** Primers used in this study

|  |  |  |  |
| --- | --- | --- | --- |
| Primer | Sequence, 5’→3’ | Production/bp | Reference |
| *vp0610*-F1 *SacI* | CGAGCTCTCGCTACGACGGTCT | 524 | This study |
| *vp0610*-R1 | CCAATGCGGTCCTTATTCCTGTCCTCTTAA |
| *vp0610*-F2 | TTAAGAGGACAGGAATAAGGACCGCATTGG | 631 | This study |
| *vp0610*-R2 *SphI* | ACATGCATGCCGACCATTTGCCGTAC |
| sacB-F | CTTGGTAGCCATCTTCAGTT | 682 | This study |
| sacB-R | ATTACACGCCATGATATGCT |
| toxR-F | ATGCCATAGCATTTTTATCC | 368 | GENEWIZ, USA |
| toxR-R | CTGCGTTCTGATTTAATCTG |
| vp0610-F4 | TTAGGCATCGACAAGCACG | 1309 | This study |
| vp0610-R4 | GCTGACCACGCTCCACAAT | This study |
| q16SrRNA-F | TAAAATATGTAAGGGGTGAC |  | This study |
| q16SrRNA-R | GGATGTAACGCACTGAG |  |
| qtdh-F | TATCCTTGTTTGCCAGCGAG |  | (Ma et al., 2015) |
| qtdh-R | CTACGACGCACTTTTTGGG |  |
| qaphA-F | TGGCGGAATACCCAACAG |  | This study |
| qaphA-R | GTAACCCAGCGGCATTCA |  |
| qopaR-F | AGGGCATCGTTACCCAATC |  | This study |
| qopaR-R | TAAGTCAACATAGTCCGCATC |  |
| qvp0710-F | TGTTCTAAATGATACCGACAAAGC |  | This study |
| qvp0710-R | CAGCGTTCTTGGATTCGTCT |  |
| qmshA-F | CCGGCTGAGCTGCATTAC |  | This study |
| qmshA-R | CACCGTCGATAGAACTGTCTG |  |
| qvp0793-F | AAATCATCGCACCACTATCT |  | This study |
| qvp0793-R | CTGGCTTGATAGCAATACC |  |
| qcyaA-F | ATGGAAGAGTGTTACGACGAG |  | This study |
| qcyaA-R | CCACAAGTTCGAGCCAAAG |  |
| qflaE-F | ACAGTGCGGATAGCCAGTA |  | This study |
| qflaE-R | CTTTGAGTAGCGTCTCGTTT |  |
| qhfq-F | AACGGTATCAAACTACAAGGTC |  | This study |
| qhfq-R | CCGGCACAACTGTAGAAATCG |  |
| qcdgA-F | ATCGCACTTCCATCGTAA |  | This study |
| qcdgA-R | GCGGGTGTTATTTCTCAA |  |
| qcdgC-F | TATGTAAAGAGTCGGGTGAAG |  | This study |
| qcdgC-R | CCGCTTGGAGCAGATAA |  |
| qvp0610-F | TTGTGCTGGCGAGGAAG |  | This study |
| qvp0610-R | TGTCGTTTGCGTAGACTGG |  |

**Table S2** Interaction partners of VP0610

|  |  |  |
| --- | --- | --- |
| prot\_hit\_num | prot\_acc | prot\_desc |
| 1 | tr|A0A0M3EB58|A0A0M3EB58\_VIBPH | (P)ppGpp synthetase OS=Vibrio parahaemolyticus OX=670 GN=AAY51\_04925 PE=3 SV=1 |
| 2 | tr|A0A0M3E5R0|A0A0M3E5R0\_VIBPH | 3,4-dihydroxy-2-butanone 4-phosphate synthase OS=Vibrio parahaemolyticus OX=670 GN=ribB PE=3 SV=1 |
| 3 | tr|A0A072H799|A0A072H799\_VIBPH | 30S ribosomal protein S11 OS=Vibrio parahaemolyticus OX=670 GN=rpsK PE=3 SV=1 |
| 4 | tr|A0A072IE55|A0A072IE55\_VIBPH | 30S ribosomal protein S13 OS=Vibrio parahaemolyticus OX=670 GN=rpsM PE=3 SV=1 |
| 5 | tr|A0A072FYS6|A0A072FYS6\_VIBPH | 30S ribosomal protein S18 OS=Vibrio parahaemolyticus OX=670 GN=rpsR PE=3 SV=1 |
| 6 | tr|A0A072GS55|A0A072GS55\_VIBPH | 30S ribosomal protein S19 OS=Vibrio parahaemolyticus OX=670 GN=rpsS PE=3 SV=1 |
| 7 | tr|A0A0D1E8T7|A0A0D1E8T7\_VIBPH | 30S ribosomal protein S2 OS=Vibrio parahaemolyticus 49 OX=1288779 GN=rpsB PE=3 SV=1 |
| 8 | tr|A0A0D1DWA1|A0A0D1DWA1\_VIBPH | 30S ribosomal protein S21 OS=Vibrio parahaemolyticus VP766 OX=1288782 GN=rpsU PE=3 SV=1 |
| 9 | tr|A0A072JHR7|A0A072JHR7\_VIBPH | 30S ribosomal protein S5 OS=Vibrio parahaemolyticus OX=670 GN=rpsE PE=3 SV=1 |
| 10 | tr|A0A072K176|A0A072K176\_VIBPH | 30S ribosomal protein S7 OS=Vibrio parahaemolyticus OX=670 GN=rpsG PE=3 SV=1 |
| 11 | tr|A0A072G962|A0A072G962\_VIBPH | 30S ribosomal protein S8 OS=Vibrio parahaemolyticus OX=670 GN=rpsH PE=3 SV=1 |
| 12 | tr|A0A0M3E0F2|A0A0M3E0F2\_VIBPH | 3-dehydroquinate synthase OS=Vibrio parahaemolyticus OX=670 GN=aroB PE=3 SV=1 |
| 13 | tr|A0A0M3ECA5|A0A0M3ECA5\_VIBPH | 3-oxoacyl-[acyl-carrier-protein] synthase 3 OS=Vibrio parahaemolyticus OX=670 GN=fabH PE=3 SV=1 |
| 14 | tr|A0A0D1ETC5|A0A0D1ETC5\_VIBPH | 50S ribosomal protein L13 OS=Vibrio parahaemolyticus 49 OX=1288779 GN=rplM PE=3 SV=1 |
| 15 | tr|A0A072K649|A0A072K649\_VIBPH | 50S ribosomal protein L16 OS=Vibrio parahaemolyticus OX=670 GN=rplP PE=3 SV=1 |
| 16 | tr|A0A072JZQ2|A0A072JZQ2\_VIBPH | 50S ribosomal protein L18 OS=Vibrio parahaemolyticus OX=670 GN=rplR PE=3 SV=1 |
| 17 | tr|A0A0D1E320|A0A0D1E320\_VIBPH | 50S ribosomal protein L19 OS=Vibrio parahaemolyticus 49 OX=1288779 GN=rplS PE=3 SV=1 |
| 18 | sp|P0A481|RL20\_VIBPA | 50S ribosomal protein L20 OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) OX=223926 GN=rplT PE=3 SV=1 |
| 19 | tr|A0A072HFB5|A0A072HFB5\_VIBPH | 50S ribosomal protein L22 OS=Vibrio parahaemolyticus OX=670 GN=rplV PE=3 SV=1 |
| 20 | tr|A0A072M095|A0A072M095\_VIBPH | 50S ribosomal protein L25 OS=Vibrio parahaemolyticus OX=670 GN=rplY PE=3 SV=1 |
| 21 | tr|A0A072GSS4|A0A072GSS4\_VIBPH | 50S ribosomal protein L27 OS=Vibrio parahaemolyticus OX=670 GN=rpmA PE=3 SV=1 |
| 22 | tr|A0A0M3E5U4|A0A0M3E5U4\_VIBPH | 50S ribosomal protein L29 OS=Vibrio parahaemolyticus OX=670 GN=rpmC PE=3 SV=1 |
| 23 | tr|A0A072L946|A0A072L946\_VIBPH | 50S ribosomal protein L29 OS=Vibrio parahaemolyticus OX=670 GN=rpmC PE=3 SV=1 |
| 24 | tr|A0A072GAC7|A0A072GAC7\_VIBPH | 50S ribosomal protein L3 OS=Vibrio parahaemolyticus OX=670 GN=rplC PE=3 SV=1 |
| 25 | tr|A0A0M3ECX9|A0A0M3ECX9\_VIBPH | 50S ribosomal protein L32 OS=Vibrio parahaemolyticus OX=670 GN=rpmF PE=3 SV=1 |
| 26 | tr|A0A072IEJ5|A0A072IEJ5\_VIBPH | 50S ribosomal protein L35 OS=Vibrio parahaemolyticus OX=670 GN=rpmI PE=3 SV=1 |
| 27 | tr|A0A072I935|A0A072I935\_VIBPH | 50S ribosomal protein L6 OS=Vibrio parahaemolyticus OX=670 GN=rplF PE=3 SV=1 |
| 28 | tr|A0A0D1E1A1|A0A0D1E1A1\_VIBPH | 50S ribosomal protein L7/L12 OS=Vibrio parahaemolyticus VP766 OX=1288782 GN=rplL PE=3 SV=1 |
| 29 | tr|A0A072K9H8|A0A072K9H8\_VIBPH | 50S ribosomal protein L9 OS=Vibrio parahaemolyticus OX=670 GN=rplI PE=3 SV=1 |
| 30 | tr|A0A0M3E2B1|A0A0M3E2B1\_VIBPH | 6,7-dimethyl-8-ribityllumazine synthase OS=Vibrio parahaemolyticus OX=670 GN=ribH PE=3 SV=1 |
| 31 | tr|A0A0D1G353|A0A0D1G353\_VIBPH | 60 kDa chaperonin (Fragment) OS=Vibrio parahaemolyticus 49 OX=1288779 GN=groEL PE=3 SV=1 |
| 32 | tr|A0A0D1U8B5|A0A0D1U8B5\_VIBPH | 60 kDa chaperonin OS=Vibrio parahaemolyticus OX=670 GN=groL PE=3 SV=1 |
| 33 | tr|A0A0M3E2S5|A0A0M3E2S5\_VIBPH | ABC transporter ATP-binding protein OS=Vibrio parahaemolyticus OX=670 GN=AAY51\_20520 PE=4 SV=1 |
| 34 | tr|A0A072F7H7|A0A072F7H7\_VIBPH | Acetate kinase OS=Vibrio parahaemolyticus OX=670 GN=ackA PE=3 SV=1 |
| 35 | tr|A0A2R9VQ07|A0A2R9VQ07\_VIBPH | Acetoin utilization protein AcuB OS=Vibrio parahaemolyticus OX=670 GN=BS585\_21210 PE=4 SV=1 |
| 36 | tr|A0A0D1CUP7|A0A0D1CUP7\_VIBPH | Acetylornithine aminotransferase OS=Vibrio parahaemolyticus VP766 OX=1288782 GN=argD PE=3 SV=1 |
| 37 | tr|A0A0L8TID9|A0A0L8TID9\_VIBPH | Acetyltransferase component of pyruvate dehydrogenase complex OS=Vibrio parahaemolyticus OX=670 GN=aceF PE=3 SV=1 |
| 38 | tr|A0A0D1GGA6|A0A0D1GGA6\_VIBPH | Acyl-[acyl-carrier-protein]--UDP-N-acetylglucosamine O-acyltransferase OS=Vibrio parahaemolyticus 901128 OX=1288792 GN=lpxA PE=3 SV=1 |
| 39 | tr|A0A0D1E0H9|A0A0D1E0H9\_VIBPH | Alanine dehydrogenase OS=Vibrio parahaemolyticus VP766 OX=1288782 GN=H323\_02465 PE=3 SV=1 |
| 40 | tr|A0A072IK40|A0A072IK40\_VIBPH | Arginase OS=Vibrio parahaemolyticus OX=670 GN=BS585\_08045 PE=4 SV=1 |
| 41 | tr|A0A0M3ED14|A0A0M3ED14\_VIBPH | Arginine decarboxylase OS=Vibrio parahaemolyticus OX=670 GN=AAY51\_03235 PE=4 SV=1 |
| 42 | tr|A0A072IR40|A0A072IR40\_VIBPH | ATP synthase subunit b OS=Vibrio parahaemolyticus OX=670 GN=atpF PE=3 SV=1 |
| 43 | tr|A0A072J6A3|A0A072J6A3\_VIBPH | ATP synthase subunit delta OS=Vibrio parahaemolyticus OX=670 GN=atpH PE=3 SV=1 |
| 44 | tr|A0A072HIP8|A0A072HIP8\_VIBPH | ATP-dependent 6-phosphofructokinase OS=Vibrio parahaemolyticus OX=670 GN=pfkA PE=3 SV=1 |
| 45 | tr|A0A0L8TZU9|A0A0L8TZU9\_VIBPH | ATP-dependent helicase HrpA OS=Vibrio parahaemolyticus OX=670 GN=WR32\_02805 PE=4 SV=1 |
| 46 | tr|A0A0M3E4A9|A0A0M3E4A9\_VIBPH | Bac\_luciferase domain-containing protein OS=Vibrio parahaemolyticus OX=670 GN=AAY51\_16710 PE=4 SV=1 |
| 47 | tr|A0A0M3E800|A0A0M3E800\_VIBPH | Beta-methylgalactoside transporter permease OS=Vibrio parahaemolyticus OX=670 GN=mglC PE=3 SV=1 |
| 48 | tr|A0A0M3E7C7|A0A0M3E7C7\_VIBPH | Carboxy-terminal protease OS=Vibrio parahaemolyticus OX=670 GN=AAY51\_11920 PE=3 SV=1 |
| 49 | tr|A0A0M3EC00|A0A0M3EC00\_VIBPH | Catalase OS=Vibrio parahaemolyticus OX=670 GN=katE PE=3 SV=1 |
| 50 | tr|A0A0M3E5H1|A0A0M3E5H1\_VIBPH | Cell division protein FtsN OS=Vibrio parahaemolyticus OX=670 GN=AAY51\_17760 PE=3 SV=1 |
| 51 | tr|A0A0M3EA43|A0A0M3EA43\_VIBPH | Cell division protein FtsX OS=Vibrio parahaemolyticus OX=670 GN=ftsX PE=3 SV=1 |
| 52 | tr|A0A072FFG4|A0A072FFG4\_VIBPH | Cell division protein FtsZ OS=Vibrio parahaemolyticus OX=670 GN=ftsZ PE=3 SV=1 |
| 53 | tr|A0A0D1F211|A0A0D1F211\_VIBPH | Cell division protein ZapD OS=Vibrio parahaemolyticus 901128 OX=1288792 GN=zapD PE=3 SV=1 |
| 54 | tr|A0A0D1EN21|A0A0D1EN21\_VIBPH | Cell division protein ZipA OS=Vibrio parahaemolyticus VP766 OX=1288782 GN=zipA PE=3 SV=1 |
| 55 | tr|A0A072JVB5|A0A072JVB5\_VIBPH | Chaperone protein ClpB OS=Vibrio parahaemolyticus OX=670 GN=clpB PE=3 SV=1 |
| 56 | tr|A0A072LLG8|A0A072LLG8\_VIBPH | Chromosomal replication initiator protein DnaA OS=Vibrio parahaemolyticus OX=670 GN=dnaA PE=3 SV=1 |
| 57 | tr|A0A0M3E5R8|A0A0M3E5R8\_VIBPH | CinA-like protein OS=Vibrio parahaemolyticus OX=670 GN=AAY51\_14590 PE=3 SV=1 |
| 58 | tr|A0A0M3E6T4|A0A0M3E6T4\_VIBPH | Clp protease ClpP OS=Vibrio parahaemolyticus OX=670 GN=AAY51\_17015 PE=4 SV=1 |
| 59 | tr|A0A0D1DVS2|A0A0D1DVS2\_VIBPH | Cysteine desulfurase IscS OS=Vibrio parahaemolyticus VP766 OX=1288782 GN=iscS PE=3 SV=1 |
| 60 | tr|A0A0D1F4K7|A0A0D1F4K7\_VIBPH | Cysteine desulfurase OS=Vibrio parahaemolyticus VP766 OX=1288782 GN=H323\_03790 PE=3 SV=1 |
| 61 | tr|A0A0M3E2T9|A0A0M3E2T9\_VIBPH | Cys-tRNA(Pro)/Cys-tRNA(Cys) deacylase OS=Vibrio parahaemolyticus OX=670 GN=AAY51\_20605 PE=3 SV=1 |
| 62 | tr|A0A0M3E2V5|A0A0M3E2V5\_VIBPH | DeoR faimly transcriptional regulator OS=Vibrio parahaemolyticus OX=670 GN=AAY51\_17385 PE=4 SV=1 |
| 63 | tr|A0A0M3E9U2|A0A0M3E9U2\_VIBPH | D-galactose transporter GalP OS=Vibrio parahaemolyticus OX=670 GN=AAY51\_05545 PE=3 SV=1 |
| 64 | tr|A0A0M3E8Q5|A0A0M3E8Q5\_VIBPH | Diaminopimelate decarboxylase OS=Vibrio parahaemolyticus OX=670 GN=lysA PE=3 SV=1 |
| 65 | tr|A0A072F5U6|A0A072F5U6\_VIBPH | Dihydroorotate dehydrogenase (quinone) OS=Vibrio parahaemolyticus OX=670 GN=pyrD PE=3 SV=1 |
| 66 | tr|A0A0M3E133|A0A0M3E133\_VIBPH | DNA helicase OS=Vibrio parahaemolyticus OX=670 GN=helD PE=3 SV=1 |
| 67 | tr|A0A0M3E709|A0A0M3E709\_VIBPH | DNA-binding protein OS=Vibrio parahaemolyticus OX=670 GN=AAY51\_15800 PE=3 SV=1 |
| 68 | tr|A0A0D1EY94|A0A0D1EY94\_VIBPH | Elongation factor G OS=Vibrio parahaemolyticus VP766 OX=1288782 GN=fusA PE=3 SV=1 |
| 69 | tr|A0A0M3EEJ6|A0A0M3EEJ6\_VIBPH | Endolytic murein transglycosylase OS=Vibrio parahaemolyticus OX=670 GN=mltG PE=3 SV=1 |
| 70 | tr|A0A0D1DUM5|A0A0D1DUM5\_VIBPH | Esterase FrsA OS=Vibrio parahaemolyticus 49 OX=1288779 GN=frsA PE=3 SV=1 |
| 71 | tr|A0A658H682|A0A658H682\_VIBPH | Flagellar L-ring protein FlgH OS=Vibrio parahaemolyticus OX=670 GN=DET53\_1088 PE=3 SV=1 |
| 72 | tr|A0A249W7T3|A0A249W7T3\_VIBPH | Formate acetyltransferase OS=Vibrio parahaemolyticus OX=670 GN=pflB PE=4 SV=1 |
| 73 | tr|A0A0M3E729|A0A0M3E729\_VIBPH | Fumarate reductase flavoprotein subunit OS=Vibrio parahaemolyticus OX=670 GN=AAY51\_07985 PE=3 SV=1 |
| 74 | tr|A0A072IIM5|A0A072IIM5\_VIBPH | Fumarate reductase flavoprotein subunit OS=Vibrio parahaemolyticus OX=670 GN=frdA PE=3 SV=1 |
| 75 | tr|A0A0D1DR21|A0A0D1DR21\_VIBPH | GlpT protein OS=Vibrio parahaemolyticus 49 OX=1288779 GN=glpT PE=4 SV=1 |
| 76 | tr|A0A0M3ECR3|A0A0M3ECR3\_VIBPH | Glucosyltransferase I RfaG OS=Vibrio parahaemolyticus OX=670 GN=AAY51\_04835 PE=4 SV=1 |
| 77 | tr|A0A0D1EJL0|A0A0D1EJL0\_VIBPH | Glutamate 5-kinase OS=Vibrio parahaemolyticus 901128 OX=1288792 GN=proB PE=3 SV=1 |
| 78 | tr|A0A0M3E329|A0A0M3E329\_VIBPH | Glycerol dehydrogenase OS=Vibrio parahaemolyticus OX=670 GN=gldA PE=4 SV=1 |
| 79 | tr|A0A0L8SJC5|A0A0L8SJC5\_VIBPH | Glycerophosphodiester phosphodiesterase OS=Vibrio parahaemolyticus OX=670 GN=CA163\_03770 PE=4 SV=1 |
| 80 | tr|A0A0D1DM26|A0A0D1DM26\_VIBPH | Glycine--tRNA ligase beta subunit OS=Vibrio parahaemolyticus VP766 OX=1288782 GN=glyS PE=3 SV=1 |
| 81 | tr|A0A072K8V0|A0A072K8V0\_VIBPH | Heat-shock protein HslJ OS=Vibrio parahaemolyticus OX=670 GN=C1S91\_18200 PE=4 SV=1 |
| 82 | tr|A0A0M3EC39|A0A0M3EC39\_VIBPH | HNHc domain-containing protein OS=Vibrio parahaemolyticus OX=670 GN=AAY51\_01465 PE=4 SV=1 |
| 83 | tr|A0A0M3E5M7|A0A0M3E5M7\_VIBPH | Hydrogenase 2 protein HybA OS=Vibrio parahaemolyticus OX=670 GN=AAY51\_15945 PE=4 SV=1 |
| 84 | tr|A0A0M3E450|A0A0M3E450\_VIBPH | Integration host factor subunit beta OS=Vibrio parahaemolyticus OX=670 GN=ihfB PE=3 SV=1 |
| 85 | tr|A0A0M3E6L0|A0A0M3E6L0\_VIBPH | L-aspartate oxidase OS=Vibrio parahaemolyticus OX=670 GN=AAY51\_11295 PE=3 SV=1 |
| 86 | tr|A0A0D1EMB0|A0A0D1EMB0\_VIBPH | Lipoprotein OS=Vibrio parahaemolyticus 49 OX=1288779 GN=metQ PE=3 SV=1 |
| 87 | tr|A0A0M3EAG0|A0A0M3EAG0\_VIBPH | L-lactate dehydrogenase OS=Vibrio parahaemolyticus OX=670 GN=lldD PE=3 SV=1 |
| 88 | tr|A0A0M3E1L7|A0A0M3E1L7\_VIBPH | Macrodomain Ter protein OS=Vibrio parahaemolyticus OX=670 GN=matP PE=3 SV=1 |
| 89 | tr|A0A0M3E7U1|A0A0M3E7U1\_VIBPH | Membrane protein OS=Vibrio parahaemolyticus OX=670 GN=AAY51\_07925 PE=4 SV=1 |
| 90 | tr|A0A0M3E0Q9|A0A0M3E0Q9\_VIBPH | Membrane protein OS=Vibrio parahaemolyticus OX=670 GN=AAY51\_21675 PE=4 SV=1 |
| 91 | tr|A0A072L5U8|A0A072L5U8\_VIBPH | Membrane protein OS=Vibrio parahaemolyticus OX=670 GN=BS585\_06780 PE=4 SV=1 |
| 92 | tr|A0A0L8U375|A0A0L8U375\_VIBPH | Membrane protein OS=Vibrio parahaemolyticus OX=670 GN=CA163\_11830 PE=4 SV=1 |
| 93 | tr|A0A658HGG5|A0A658HGG5\_VIBPH | Methyl-accepting chemotaxis protein OS=Vibrio parahaemolyticus OX=670 GN=DET53\_101697 PE=4 SV=1 |
| 94 | tr|A0A0D1E679|A0A0D1E679\_VIBPH | Methylglyoxal synthase OS=Vibrio parahaemolyticus 49 OX=1288779 GN=mgsA PE=3 SV=1 |
| 95 | tr|A0A0L8S626|A0A0L8S626\_VIBPH | Molybdenum cofactor biosynthesis protein B OS=Vibrio parahaemolyticus OX=670 GN=moaB PE=3 SV=1 |
| 96 | tr|A0A0L8SKN2|A0A0L8SKN2\_VIBPH | Molybdopterin molybdenumtransferase OS=Vibrio parahaemolyticus OX=670 GN=CGJ74\_17960 PE=3 SV=1 |
| 97 | tr|A0A0D1F3A2|A0A0D1F3A2\_VIBPH | Na(+)-translocating NADH-quinone reductase subunit A OS=Vibrio parahaemolyticus VP766 OX=1288782 GN=nqrA PE=3 SV=1 |
| 98 | tr|A0A072IND5|A0A072IND5\_VIBPH | Na(+)-translocating NADH-quinone reductase subunit F OS=Vibrio parahaemolyticus OX=670 GN=nqrF PE=3 SV=1 |
| 99 | tr|A0A0M3E382|A0A0M3E382\_VIBPH | N-acetylmuramoyl-l-alanine amidase I OS=Vibrio parahaemolyticus OX=670 GN=AAY51\_22750 PE=4 SV=1 |
| 100 | tr|A0A0D1EXT2|A0A0D1EXT2\_VIBPH | NAD kinase OS=Vibrio parahaemolyticus VP766 OX=1288782 GN=nadK PE=3 SV=1 |
| 101 | tr|A0A227J159|A0A227J159\_VIBPH | NADH:ubiquinone reductase (Na(+)-transporting) subunit A (Fragment) OS=Vibrio parahaemolyticus OX=670 GN=CA163\_31920 PE=4 SV=1 |
| 102 | tr|A0A072JT35|A0A072JT35\_VIBPH | OmpA family protein OS=Vibrio parahaemolyticus OX=670 GN=C1S91\_00325 PE=3 SV=1 |
| 103 | tr|A0A0M3E760|A0A0M3E760\_VIBPH | Outer membrane protein assembly factor BamB OS=Vibrio parahaemolyticus OX=670 GN=bamB PE=3 SV=1 |
| 104 | tr|A0A0M3E9C1|A0A0M3E9C1\_VIBPH | Peptidase B OS=Vibrio parahaemolyticus OX=670 GN=pepB PE=3 SV=1 |
| 105 | tr|A0A0M3E8P1|A0A0M3E8P1\_VIBPH | Peptide ABC transporter ATP-binding protein OS=Vibrio parahaemolyticus OX=670 GN=AAY51\_06850 PE=3 SV=1 |
| 106 | tr|A0A0M3E5S4|A0A0M3E5S4\_VIBPH | Peptide deformylase OS=Vibrio parahaemolyticus OX=670 GN=def PE=3 SV=1 |
| 107 | tr|A0A072F9P3|A0A072F9P3\_VIBPH | Peptidoglycan-associated protein OS=Vibrio parahaemolyticus OX=670 GN=pal PE=3 SV=1 |
| 108 | tr|A0A072FQT7|A0A072FQT7\_VIBPH | Peptidyl-prolyl cis-trans isomerase OS=Vibrio parahaemolyticus OX=670 GN=BS585\_00775 PE=3 SV=1 |
| 109 | tr|A0A072F2W5|A0A072F2W5\_VIBPH | Peptidyl-prolyl cis-trans isomerase OS=Vibrio parahaemolyticus OX=670 GN=BS585\_14080 PE=3 SV=1 |
| 110 | tr|A0A072I5F9|A0A072I5F9\_VIBPH | Peptidylprolyl isomerase OS=Vibrio parahaemolyticus OX=670 GN=ppiD PE=4 SV=1 |
| 111 | tr|A0A0F5TDH8|A0A0F5TDH8\_VIBPH | Periplasmic serine endoprotease DegP-like OS=Vibrio parahaemolyticus OX=670 GN=BS585\_11985 PE=3 SV=1 |
| 112 | tr|A0A072KT67|A0A072KT67\_VIBPH | Peroxidase OS=Vibrio parahaemolyticus OX=670 GN=BS585\_21230 PE=4 SV=1 |
| 113 | tr|A0A072JE78|A0A072JE78\_VIBPH | PhaC PHA synthase OS=Vibrio parahaemolyticus OX=670 GN=WR32\_24045 PE=4 SV=1 |
| 114 | tr|A0A0M3E9X4|A0A0M3E9X4\_VIBPH | Phosphatidylserine decarboxylase proenzyme OS=Vibrio parahaemolyticus OX=670 GN=psd PE=3 SV=1 |
| 115 | tr|A0A0M3E431|A0A0M3E431\_VIBPH | Phosphoglucomutase OS=Vibrio parahaemolyticus OX=670 GN=AAY51\_19665 PE=3 SV=1 |
| 116 | tr|A0A0M3E0Y0|A0A0M3E0Y0\_VIBPH | Phosphoribosylglycinamide formyltransferase OS=Vibrio parahaemolyticus OX=670 GN=purN PE=3 SV=1 |
| 117 | tr|A0A072JIB2|A0A072JIB2\_VIBPH | Prepilin peptidase OS=Vibrio parahaemolyticus OX=670 GN=C9I78\_10590 PE=4 SV=1 |
| 118 | tr|A0A0M3E3R6|A0A0M3E3R6\_VIBPH | Primosomal protein N~ OS=Vibrio parahaemolyticus OX=670 GN=priA PE=3 SV=1 |
| 119 | tr|A0A0M3E8X2|A0A0M3E8X2\_VIBPH | Protease OS=Vibrio parahaemolyticus OX=670 GN=AAY51\_07585 PE=4 SV=1 |
| 120 | tr|A0A0D1GQZ4|A0A0D1GQZ4\_VIBPH | Protein adenylyltransferase SelO OS=Vibrio parahaemolyticus 901128 OX=1288792 GN=selO PE=3 SV=1 |
| 121 | tr|A0A060IL13|A0A060IL13\_VIBPH | Protein RecA (Fragment) OS=Vibrio parahaemolyticus OX=670 GN=recA PE=3 SV=1 |
| 122 | tr|A0A072IYW7|A0A072IYW7\_VIBPH | Pseudouridine synthase OS=Vibrio parahaemolyticus OX=670 GN=rluD PE=3 SV=1 |
| 123 | tr|A0A072JPZ5|A0A072JPZ5\_VIBPH | Pseudouridine synthase OS=Vibrio parahaemolyticus OX=670 GN=rsuA PE=3 SV=1 |
| 124 | tr|A0A0M3E809|A0A0M3E809\_VIBPH | PTS system trehalose(Maltose)-specific transporter subunits IIBC OS=Vibrio parahaemolyticus OX=670 GN=AAY51\_08385 PE=4 SV=1 |
| 125 | tr|A0A072LSJ8|A0A072LSJ8\_VIBPH | Pyruvate dehydrogenase E1 component OS=Vibrio parahaemolyticus OX=670 GN=aceE PE=4 SV=1 |
| 126 | tr|A0A0M3EAZ6|A0A0M3EAZ6\_VIBPH | Replicative DNA helicase OS=Vibrio parahaemolyticus OX=670 GN=AAY51\_03555 PE=3 SV=1 |
| 127 | tr|A0A0M3EB21|A0A0M3EB21\_VIBPH | Rhodanese domain-containing protein OS=Vibrio parahaemolyticus OX=670 GN=AAY51\_04740 PE=4 SV=1 |
| 128 | tr|A0A0M3E4R3|A0A0M3E4R3\_VIBPH | Riboflavin biosynthesis protein RibD OS=Vibrio parahaemolyticus OX=670 GN=ribD PE=3 SV=1 |
| 129 | tr|A0A0L8S3Z5|A0A0L8S3Z5\_VIBPH | Ribonuclease E OS=Vibrio parahaemolyticus OX=670 GN=rne PE=3 SV=1 |
| 130 | tr|A0A0F5SKN9|A0A0F5SKN9\_VIBPH | Ribonuclease R OS=Vibrio parahaemolyticus OX=670 GN=rnr PE=3 SV=1 |
| 131 | tr|A0A0M3E1A5|A0A0M3E1A5\_VIBPH | Ribosomal protein S12 methylthiotransferase RimO OS=Vibrio parahaemolyticus OX=670 GN=rimO PE=3 SV=1 |
| 132 | tr|A0A0D1E8Q7|A0A0D1E8Q7\_VIBPH | Ribosomal RNA large subunit methyltransferase G OS=Vibrio parahaemolyticus 49 OX=1288779 GN=rlmG PE=3 SV=1 |
| 133 | tr|A0A0M3E6L8|A0A0M3E6L8\_VIBPH | Ribosomal RNA small subunit methyltransferase I OS=Vibrio parahaemolyticus OX=670 GN=rsmI PE=3 SV=1 |
| 134 | tr|A0A0M3E9S3|A0A0M3E9S3\_VIBPH | RNA polymerase-binding transcription factor DksA OS=Vibrio parahaemolyticus OX=670 GN=dksA PE=3 SV=1 |
| 135 | tr|A0A072G9G3|A0A072G9G3\_VIBPH | RNA-binding protein Hfq OS=Vibrio parahaemolyticus OX=670 GN=hfq PE=3 SV=1 |
| 136 | tr|A0A0M3E8H0|A0A0M3E8H0\_VIBPH | Selenate reductase subunit YgfK OS=Vibrio parahaemolyticus OX=670 GN=AAY51\_09365 PE=4 SV=1 |
| 137 | tr|A0A0M3E676|A0A0M3E676\_VIBPH | Soluble pyridine nucleotide transhydrogenase OS=Vibrio parahaemolyticus OX=670 GN=sthA PE=3 SV=1 |
| 138 | tr|A0A072JBM7|A0A072JBM7\_VIBPH | Spermidine N1-acetyltransferase OS=Vibrio parahaemolyticus OX=670 GN=speG PE=4 SV=1 |
| 139 | tr|A0A0M3E1T6|A0A0M3E1T6\_VIBPH | Stationary phase/starvation inducible regulatory protein CspD OS=Vibrio parahaemolyticus OX=670 GN=AAY51\_18650 PE=4 SV=1 |
| 140 | tr|A0A0M3E9X0|A0A0M3E9X0\_VIBPH | Succinate dehydrogenase iron-sulfur subunit OS=Vibrio parahaemolyticus OX=670 GN=AAY51\_07980 PE=3 SV=1 |
| 141 | tr|A0A0M3E500|A0A0M3E500\_VIBPH | Succinate dehydrogenase OS=Vibrio parahaemolyticus OX=670 GN=sdhC PE=4 SV=1 |
| 142 | tr|A0A0D1F5M3|A0A0D1F5M3\_VIBPH | Threonine--tRNA ligase OS=Vibrio parahaemolyticus 901128 OX=1288792 GN=thrS PE=3 SV=1 |
| 143 | tr|A0A0M3E289|A0A0M3E289\_VIBPH | Tol-Pal system protein TolR OS=Vibrio parahaemolyticus OX=670 GN=tolR PE=3 SV=1 |
| 144 | tr|A0A0M3E1B0|A0A0M3E1B0\_VIBPH | Toprim domain-containing protein OS=Vibrio parahaemolyticus OX=670 GN=AAY51\_18670 PE=4 SV=1 |
| 145 | tr|A0A0M3EC18|A0A0M3EC18\_VIBPH | Transcriptional regulator OS=Vibrio parahaemolyticus OX=670 GN=AAY51\_01290 PE=4 SV=1 |
| 146 | tr|A0A0M3E869|A0A0M3E869\_VIBPH | Transcriptional regulator OS=Vibrio parahaemolyticus OX=670 GN=AAY51\_09820 PE=3 SV=1 |
| 147 | tr|A0A0M3E5K0|A0A0M3E5K0\_VIBPH | Transcriptional regulator OS=Vibrio parahaemolyticus OX=670 GN=AAY51\_14140 PE=3 SV=1 |
| 148 | tr|A0A0M3E6K5|A0A0M3E6K5\_VIBPH | Transcriptional regulator OS=Vibrio parahaemolyticus OX=670 GN=AAY51\_14765 PE=3 SV=1 |
| 149 | tr|A0A0M3E5P7|A0A0M3E5P7\_VIBPH | Transcriptional regulator OS=Vibrio parahaemolyticus OX=670 GN=AAY51\_16060 PE=4 SV=1 |
| 150 | tr|A0A0M3EA37|A0A0M3EA37\_VIBPH | Trehalose repressor OS=Vibrio parahaemolyticus OX=670 GN=treR PE=4 SV=1 |
| 151 | tr|A0A072JSV4|A0A072JSV4\_VIBPH | Trigger factor OS=Vibrio parahaemolyticus OX=670 GN=tig PE=3 SV=1 |
| 152 | tr|A0A0D1EP51|A0A0D1EP51\_VIBPH | tRNA (guanine-N(7)-)-methyltransferase OS=Vibrio parahaemolyticus 49 OX=1288779 GN=trmB PE=3 SV=1 |
| 153 | tr|A0A072KML1|A0A072KML1\_VIBPH | tRNA pseudouridine synthase A OS=Vibrio parahaemolyticus OX=670 GN=truA PE=3 SV=1 |
| 154 | tr|A0A072IDS0|A0A072IDS0\_VIBPH | Tryptophan synthase beta chain OS=Vibrio parahaemolyticus OX=670 GN=trpB PE=3 SV=1 |
| 155 | tr|A0A0M3E7Q0|A0A0M3E7Q0\_VIBPH | Tyrosine recombinase XerD OS=Vibrio parahaemolyticus OX=670 GN=xerD PE=3 SV=1 |
| 156 | tr|A0A0M3E5C7|A0A0M3E5C7\_VIBPH | Ubiquinol oxidase subunit 2 OS=Vibrio parahaemolyticus OX=670 GN=AAY51\_20865 PE=3 SV=1 |
| 157 | tr|A0A0D1E4I6|A0A0D1E4I6\_VIBPH | UDP-glucose 6-dehydrogenase OS=Vibrio parahaemolyticus VP766 OX=1288782 GN=H323\_13825 PE=3 SV=1 |
| 158 | tr|A0A0M3EBT5|A0A0M3EBT5\_VIBPH | UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--2,6-diaminopimelate ligase OS=Vibrio parahaemolyticus OX=670 GN=murE PE=3 SV=1 |
| 159 | tr|A0A4Z7AEJ7|A0A4Z7AEJ7\_VIBPH | Uncharacterized protein (Fragment) OS=Vibrio parahaemolyticus OX=670 GN=CGH73\_26505 PE=4 SV=1 |
| 160 | tr|A0A0M3E902|A0A0M3E902\_VIBPH | Uncharacterized protein OS=Vibrio parahaemolyticus OX=670 GN=AAY51\_07185 PE=4 SV=1 |
| 161 | tr|A0A0M3E5V7|A0A0M3E5V7\_VIBPH | Uncharacterized protein OS=Vibrio parahaemolyticus OX=670 GN=AAY51\_16410 PE=4 SV=1 |
| 162 | tr|A0A0M3E4A6|A0A0M3E4A6\_VIBPH | Uncharacterized protein OS=Vibrio parahaemolyticus OX=670 GN=AAY51\_18790 PE=4 SV=1 |
| 163 | tr|A0A660AQ38|A0A660AQ38\_VIBPH | Uncharacterized protein OS=Vibrio parahaemolyticus OX=670 GN=CGI34\_23030 PE=4 SV=1 |
| 164 | tr|A0A658H5G8|A0A658H5G8\_VIBPH | Uncharacterized protein OS=Vibrio parahaemolyticus OX=670 GN=DET53\_11016 PE=4 SV=1 |
| 165 | tr|A0A0M3EAK2|A0A0M3EAK2\_VIBPH | UPF0267 protein AAY51\_09270 OS=Vibrio parahaemolyticus OX=670 GN=AAY51\_09270 PE=3 SV=1 |
| 166 | tr|A0A0D1CY39|A0A0D1CY39\_VIBPH | UPF0283 membrane protein H323\_09255 OS=Vibrio parahaemolyticus VP766 OX=1288782 GN=H323\_09255 PE=3 SV=1 |
| 167 | tr|A0A0M3E5H6|A0A0M3E5H6\_VIBPH | UTP--glucose-1-phosphate uridylyltransferase OS=Vibrio parahaemolyticus OX=670 GN=AAY51\_13710 PE=4 SV=1 |
| 168 | tr|A0A0D1F6J7|A0A0D1F6J7\_VIBPH | Whole genome shotgun sequence (Fragment) OS=Vibrio parahaemolyticus VP766 OX=1288782 GN=H323\_03830 PE=3 SV=1 |
| 169 | tr|A0A0D1EFN6|A0A0D1EFN6\_VIBPH | Whole genome shotgun sequence OS=Vibrio parahaemolyticus 49 OX=1288779 GN=H320\_03890 PE=4 SV=1 |
| 170 | tr|A0A0D1DUM7|A0A0D1DUM7\_VIBPH | Whole genome shotgun sequence OS=Vibrio parahaemolyticus 49 OX=1288779 GN=H320\_05740 PE=4 SV=1 |
| 171 | tr|A0A0D1FJV9|A0A0D1FJV9\_VIBPH | Whole genome shotgun sequence OS=Vibrio parahaemolyticus 49 OX=1288779 GN=H320\_11650 PE=4 SV=1 |
| 172 | tr|A0A0D1E8F0|A0A0D1E8F0\_VIBPH | Whole genome shotgun sequence OS=Vibrio parahaemolyticus 49 OX=1288779 GN=H320\_13575 PE=4 SV=1 |
| 173 | tr|A0A0D1G1Y6|A0A0D1G1Y6\_VIBPH | Whole genome shotgun sequence OS=Vibrio parahaemolyticus 49 OX=1288779 GN=H320\_15610 PE=3 SV=1 |
| 174 | tr|A0A0D1E4D6|A0A0D1E4D6\_VIBPH | Whole genome shotgun sequence OS=Vibrio parahaemolyticus 49 OX=1288779 GN=H320\_18420 PE=3 SV=1 |
| 175 | tr|A0A0D1GIH2|A0A0D1GIH2\_VIBPH | Whole genome shotgun sequence OS=Vibrio parahaemolyticus 901128 OX=1288792 GN=H334\_11850 PE=3 SV=1 |
| 176 | tr|A0A0D1ENE4|A0A0D1ENE4\_VIBPH | Whole genome shotgun sequence OS=Vibrio parahaemolyticus 901128 OX=1288792 GN=H334\_15120 PE=4 SV=1 |
| 177 | tr|A0A0D1DGJ7|A0A0D1DGJ7\_VIBPH | Whole genome shotgun sequence OS=Vibrio parahaemolyticus VP766 OX=1288782 GN=H323\_02305 PE=3 SV=1 |
| 178 | tr|A0A0D1DKU2|A0A0D1DKU2\_VIBPH | Whole genome shotgun sequence OS=Vibrio parahaemolyticus VP766 OX=1288782 GN=H323\_07520 PE=4 SV=1 |
| 179 | tr|A0A0D1FA36|A0A0D1FA36\_VIBPH | Whole genome shotgun sequence OS=Vibrio parahaemolyticus VP766 OX=1288782 GN=H323\_21530 PE=4 SV=1 |
| 180 | tr|A0A072IGX2|A0A072IGX2\_VIBPH | YjbQ family protein OS=Vibrio parahaemolyticus OX=670 GN=BS585\_03965 PE=4 SV=1 |

**Table S3** KEGG pathway analysis

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **term ID** | **term description** | **observed gene count** | | **background gene count** | **false discovery rate** | **matching proteins in your network (labels)** |
| vpa03010 | Ribosome | | 24 | 55 | 7.53E-23 | *rplC,rplF,rplI,rplL,rplM,rplP,rplR,rplS,rplT,rplV,rplY,rpmA,*  *rpmC,rpmF,rpmI,rpsB,rpsE,rpsG,rpsH,rpsK,rpsM,rpsR,rpsS,rpsU* |
| vpa03018 | RNA degradation | | 5 | 21 | 0.0018 | *vp1890,groL1,hfq,pfkA,rne* |
| vpa01100 | Metabolic pathways | | 25 | 663 | 0.0037 | *vp0363,vp0679,vp0681,vp0843,vp2518,vp2519,argD,aroB,atpF,atpH,fabH1,*  *iscS,lldD,lpxA,lysA,nadK,pepB,pfkA,proB,psd,purN,pyrD,ribH,sthA,trpB1* |
| vpa00740 | Riboflavin metabolism | | 3 | 12 | 0.0245 | *vp0679,vp0681,ribH* |
| vpa01110 | Biosynthesis of secondary metabolites | | 13 | 292 | 0.0245 | *vp0679,vp0681,vp0843,vp2518,vp2519,argD,aroB,lysA,*  *pfkA,psd,purN,ribH,trpB1* |
| vpa01130 | Biosynthesis of antibiotics | | 10 | 201 | 0.0296 | *vp0843,vp2518,vp2519,argD,aroB,lysA,pfkA,proB,purN,trpB1* |
| vpa00300 | Lysine biosynthesis | | 3 | 17 | 0.0329 | *argD,lysA,murE* |



**Figure S1. Interaction analysis of partner proteins.** Network nodes represent proteins, splice isoforms or post-translational modifications are collapsed, i.e. each node represents all the proteins produced by a single, protein-coding gene locus. Edges represent protein-protein associations, associations are meant to be specific and meaningful, i.e. proteins jointly contribute to a shared function; this does not necessarily mean they are physically binding each other.

Ma, Y.-J., Sun, X.-H., Xu, X.-Y., Zhao, Y., Pan, Y.-J., Hwang, C.-A., et al. (2015). Investigation of Reference Genes in Vibrio parahaemolyticus for Gene Expression Analysis Using Quantitative RT-PCR. *PloS one* 10(12)**,** e0144362-e0144362. doi: 10.1371/journal.pone.0144362.