

## Supplemental material

### Long-distance transmission of pathogenic *Vibrio* species by migratory waterbirds: a potential threat to the public health

Songzhe Fu<sup>1#</sup>, Jingwei Hao<sup>2#</sup>, Qian Yang<sup>3#</sup>, Ruiting Lan<sup>4</sup>, Yi Wang<sup>2</sup>, ShigenYe<sup>2</sup>, Ying Liu<sup>1</sup>, and Ruijun Li<sup>2</sup>

<sup>#</sup> contribute equally to this paper

1. College of Marine Technology and Environment, Dalian Ocean University, Dalian, China
2. College of Fisheries and Life Science, Dalian Ocean University, Dalian, China
3. Yellow Sea Fisheries Research Institute, Chinese Academy of Fishery Sciences
4. School of Biotechnology and Biomolecular Sciences, University of New South Wales, Sydney, New South Wales, Australia

#### \* Correspondence:

Songzhe Fu

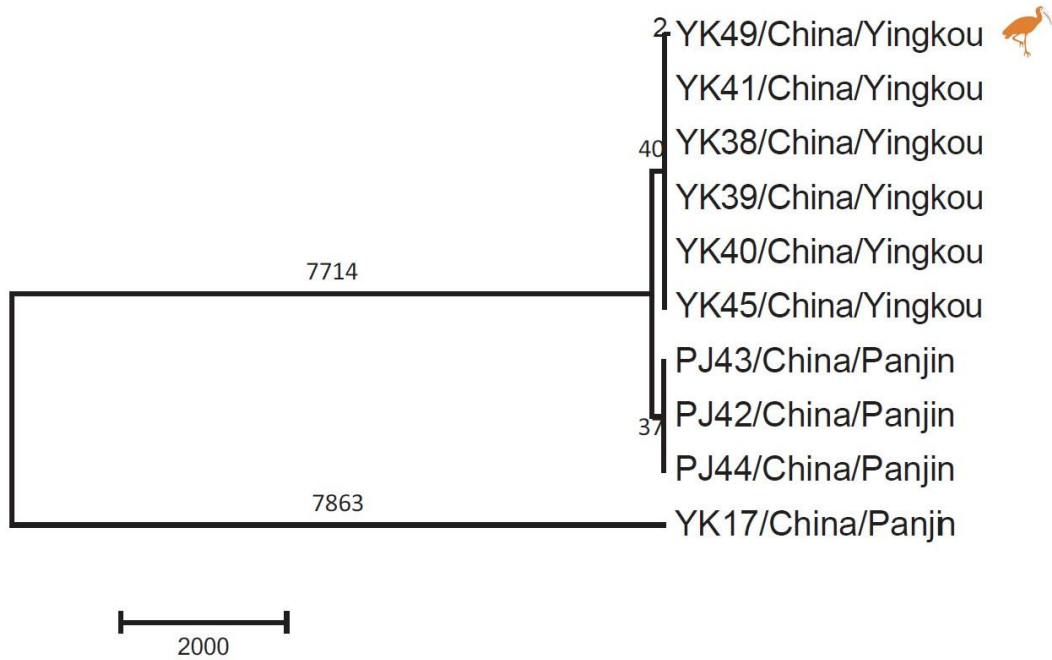
[fusongzhe@hotmail.com](mailto:fusongzhe@hotmail.com)

Ruijun Li

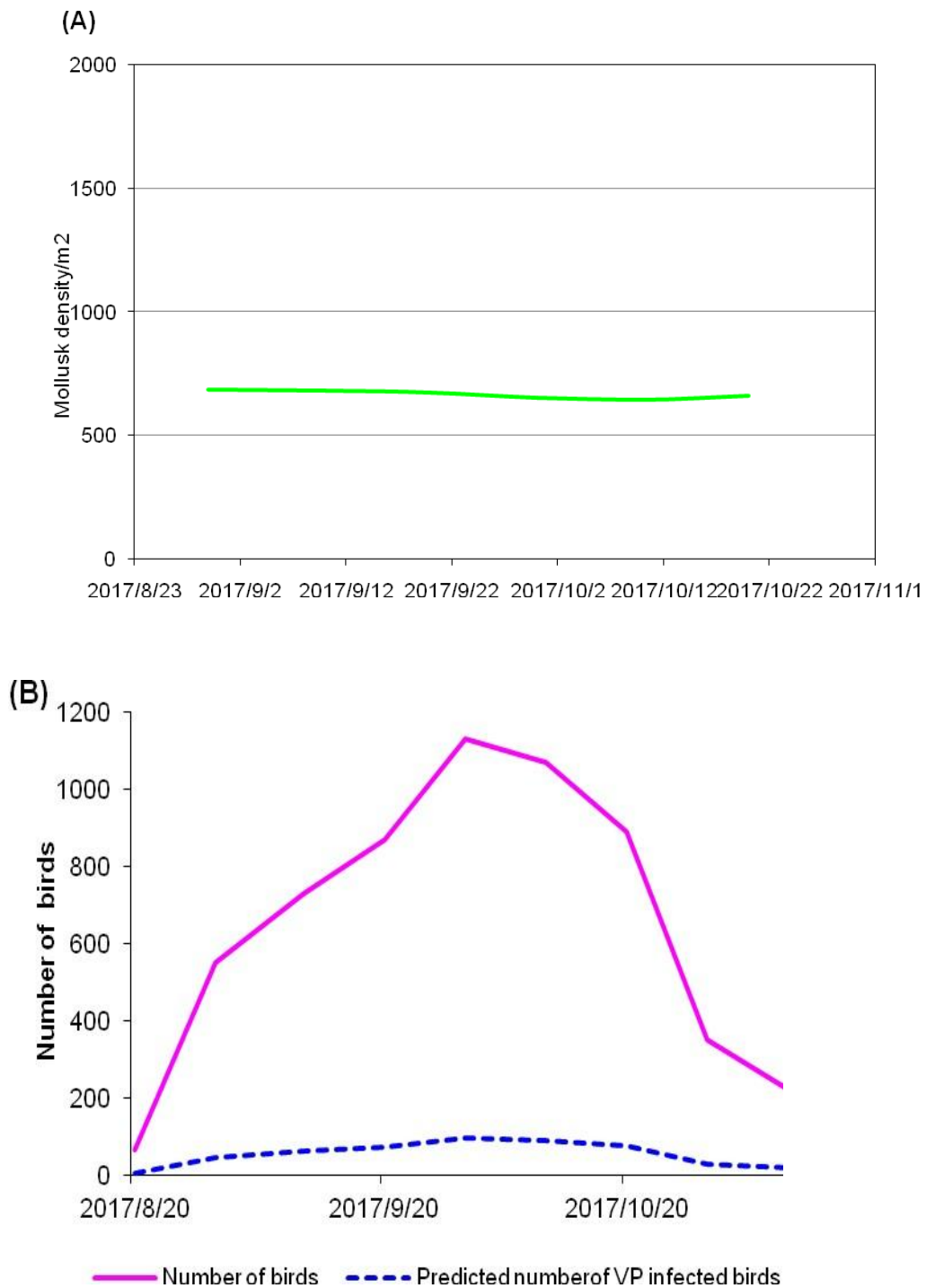
[liruijun@dlou.edu.cn](mailto:liruijun@dlou.edu.cn)

## Supplementary Figure

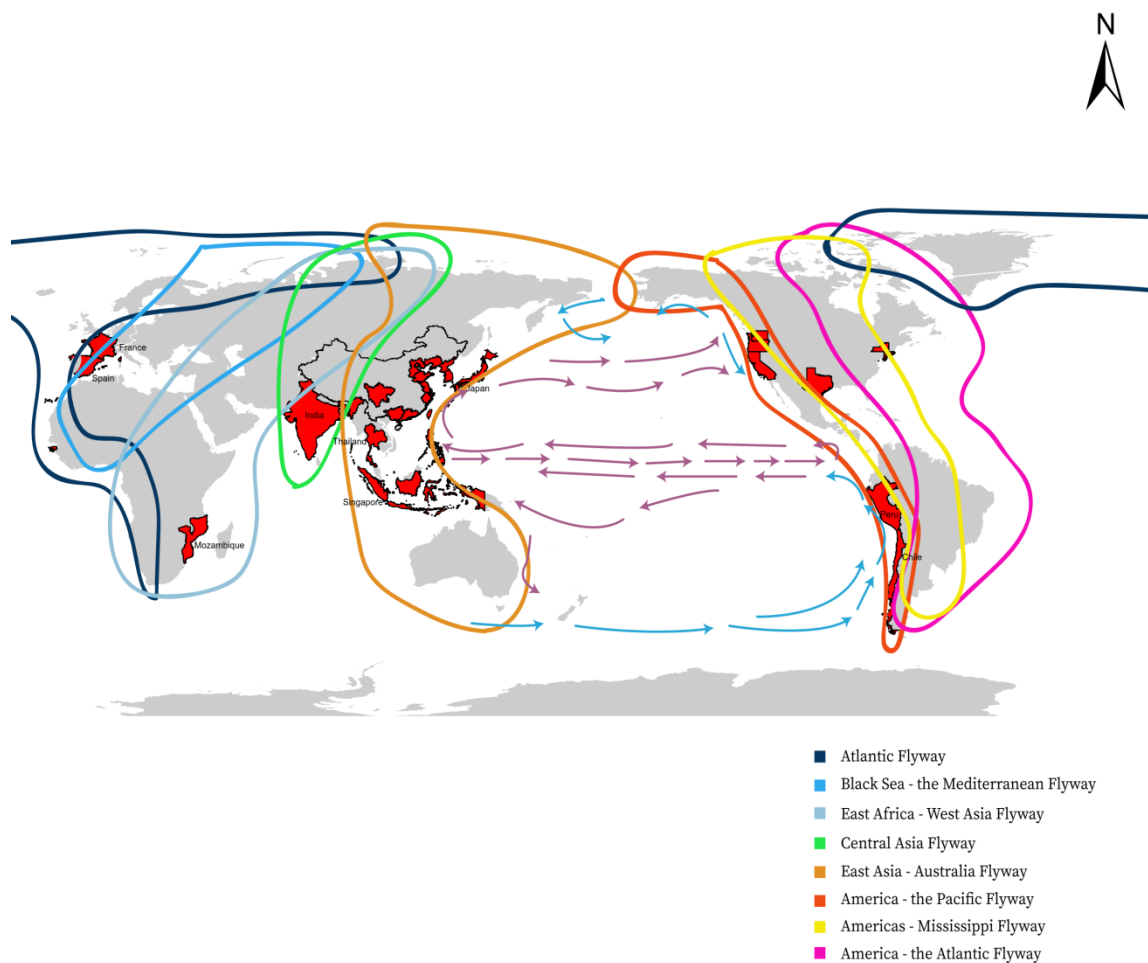
Figure S1 Maximum-parsimony tree of ST1823 *V. parahaemolyticus* genomes. Homoplasy index (HI) is 0.0. The tree was rooted using strain YK17. The number above the branches indicates the number of SNPs.



**Figure S2 Dynamics of mollusk density in the intertidal zone of Yingkou (A) and modeling of the dynamics of *V. parahaemolyticus* (VP)-carrying birds (B). The solid line indicates the observed number of Common Greenshank, while dot line presents the predicted number of VP-carrying Common Greenshank.**



**Figure S3 Distribution of the *V. parahaemolyticus* isolates belonged to ST3 and its correlation with global bird migration routes. The map was generated by the ArcGIS Desktop 10.2 software (<http://desktop.arcgis.com/>). The eight major bird migration routes around the global are labeled in eight colored circles as suggested by Yun et al. (2015)<sup>1</sup>. Blue and purple arrow indicates the direction of warm and cold currents in the Pacific Ocean, respectively. Red regions in the global map indicate the countries or regions with the clinical cases of *V. parahaemolyticus* ST3 isolates between 1996 and 2013 as suggested by Nair et al.(2007)<sup>2</sup> and Velazquez-Roman et al.(2013)<sup>3</sup>.**



## Supplementary text

### Appendix 1

#### Detection of recombination in *V. parahaemolyticus* (VP)

Previous studies suggested that recombination was the major factor driving the evolution of the *V. parahaemolyticus*<sup>4</sup>. To remove the potential impact of recombination, RDP program<sup>5</sup> was employed to identify recombination events to obtain a more accurate phylogenetic reconstruction.

SNP analysis identified 102,306 *V. parahaemolyticus* core genome SNPs. As the accessory genomes have been removed from the core genome of VP, the number of recombination events was relatively lower than the values reported by another study<sup>4</sup>. RDP identified 12 large recombination events in the core genome of VP (Table S5), many of which were also reported previously<sup>4</sup>. Some hotspots of recombination sites, including the genes involved in the ABC transporter substrate-binding protein, secretion protein, DNA binding (peptidases), endonuclease, metalloendopeptidase, and N(6)-L-threonylcarbamoyladenine synthase activities were also identified in this study.

A total of 11,613 recombinant SNPs were removed, which contributed to 11.3% of the variants identified in the dataset. For the ST3 strains, a total of 613 recombinant SNPs were removed, which contributed to 0.0468% of the variants identified in the core genome of *V. parahaemolyticus*. Only non-recombinant core genome SNPs were used to infer the genomic relationship of *V. parahaemolyticus*. Maximum parsimony (MP) method was used to infer the phylogenetic relationship of ST3 clones by using non-recombinant core genome SNPs. Only one MP tree was generated.

## Appendix 2

### Modeling the dynamics of VP-carrying birds by a predator-prey model

We chose the intertidal zone near the Yingkou City for sampling and modeling, which has a square with approximate  $1.5 \times 10^6 \text{ m}^2$

If the prevalence is extremely low ( $<0.1\%$ ), a reasonable approach might be to assume that there is only one positive sample in each positive pool.

Let  $k$  be the pool size,  $x$  the number of positive pools, and  $m$  the number of pools tested. The prevalence of VP-infected mollusk was denoted as  $\Pi$ .

As suggested by Cowling et al. (1999)<sup>5</sup>, the maximum-likelihood estimator (MLE) of

VP prevalence in mollusk ( $\Pi$ ) can be written as

$$\hat{\pi}_{MLE} = 1 - \left(1 - \frac{x}{m}\right)^{1/k} \quad (1)$$

Note that  $x$  (the number of positive pools) has a binomial distribution with parameters:  $n$  and  $P$ .

The variance of MLE can be estimated by Eq. (2)

$$\text{Var}(\hat{\pi}_{MLE}) = \frac{(x/m)(1-x/m)^{2/k-1}}{k^2 m} \quad (2)$$

In our case, the number of pools tested was 138. As all of samples came from six times of samplings (each time consists of 25 sampling points) and average number of mollusk in each sampling point was 660 individuals, the size of the pools was  $6 \times 25 \times 660 = 99,000$ . Because six *V. parahaemolyticus* strains were isolated from mollusks, the number of positive pools was six.

When we input these parameters into equation 1, the prevalence of *V. parahaemolyticus*-infected mollusks was calculated to be  $4.5 \times 10^{-7}$  (95% confidence interval:  $1.64-9.77 \times 10^{-7}$ ).

The number of infected of VP-carrying birds can be estimated by the following equations:

$$\beta(t) = P \times s \times H \times B(t) \quad (3)$$

$P$  denotes the prevalence of VP in the mollusk, while  $s$  indicates the daily predation rate.  $B(t)$  is the total number of birds in the investigated region in certain date. If we assume  $P$  and  $s$  are the constant values, then  $s \times H$  is the number of mollusks can be caught by one bird daily, where  $P \times s \times H$  indicates the number of VP infected mollusks that caught by a bird per day. The predation rate  $s$  can be calculated as :

$$S = \frac{\text{the number of mollusks predated per day}}{\text{total number of mollusks presented in the places bird stopover}} \quad (4)$$

Based on our in-field observation, we found that Common Greenshank typically stopover at around 180-500  $\text{m}^2$  sediment for predation daily (average 200  $\text{m}^2$ ). The average density of mollusks was around 660 individual/  $\text{m}^2$ . Each individual usually consumes 20-30 mollusks per day. Therefore, the predation rate  $s$  can be calculated as

$$s = \frac{25}{(200 \times 660)} = 1.9 \times 10^{-4}$$

As the square of the investigated area in Yingkou is  $1.5 \times 10^6 \text{ m}^2$ ,

the total number of mollusk can be calculated as

$$H = \text{density of mollusks} \times \text{square of investigated area} = 660 \times 1.5 \times 10^6 = 9.9 \times 10^8$$

Therefore, we can calculate the number of infected of VP-carrying birds by Eq. (4):

$$\beta(t) = P \times s \times H \times B(t) = 4.45 \times 10^{-7} \times 1.9 \times 10^{-4} \times 9.9 \times 10^8 \times B(t) = 0.084 \times B(t)$$

Thus, we can obtain the dynamics of VP infected birds. As we do not know the chance of VP to pass the digestive tract, the predicted number of VP infected birds might be overestimated.

## Supplementary table

**Table S1 Information of the water, sediment and bird feces sampled in the bird migration season**

| Sample type |           |                     | Sampling site <sup>a</sup> |         |          |         |
|-------------|-----------|---------------------|----------------------------|---------|----------|---------|
|             |           |                     | Anshan                     | Yingkou | Shanghai | Panjing |
| Water       |           |                     | 66                         | 5       | 0        | 8       |
| Sediment    |           |                     | /                          | 34      | 0        | 20      |
| Mollusk     |           |                     | /                          | 138     | 0        | 32      |
| Crab        |           |                     | /                          | 5       | 0        | 25      |
| bird feces  | Sandpiper | Common Greenshank   | /                          | 41      | 25       | 21      |
|             |           | Black-billed Godwit | /                          | 24      | 0        | 12      |
|             |           | Eurasian Curlew     | /                          | 10      | 0        | 0       |
|             | Gull      | Black-billed Gull   | /                          | 8       | 0        | 12      |
|             |           | Red-billed Gull     | /                          | 1       | 0        | 8       |
|             | Goose     | Bean Goose          | /                          | 5       | 0        | 3       |
|             |           | White-front Goose   | /                          | 6       | 0        | 4       |

a: the numbers in the table indicates the number of individual samples



Table S2 Environmental variables of three sampling sites in the sampling period

| Sampling site |             |         | pH  | Temp( °C) <sup>a</sup> | DOC(mg L <sup>-1</sup> ) <sup>b</sup> | Total phosphorus( $\mu\text{g L}^{-1}$ ) | Nitrite(mg L <sup>-1</sup> ) |
|---------------|-------------|---------|-----|------------------------|---------------------------------------|--|------------------------------|
| Anshan        | groundwater | Average | 8.2 | 17.5                   | 11.2                                  | 45                                       | 0.31                         |
|               |             | Min     | 8   | 13.7                   | 10.6                                  | 36                                       | 0.45                         |
|               |             | Max     | 8.4 | 21.3                   | 23.1                                  | 79                                       | 0.21                         |
| Yingkou       | seawater    | Average | 8.3 | 18.3                   | 22.3                                  | 67                                       | 0.45                         |
|               |             | Min     | 7.9 | 12.3                   | 11.2                                  | 58                                       | 0.24                         |
|               |             | Max     | 8.7 | 22.7                   | 28.7                                  | 87                                       | 0.76                         |
| Panjin        | seawater    | Average | 8.6 | 18.2                   | 11.9                                  | 23                                       | 0.24                         |
|               |             | Min     | 8.1 | 11.8                   | 10.9                                  | 18                                       | 0.15                         |
|               |             | Max     | 8.9 | 22.6                   | 15.2                                  | 39                                       | 0.48                         |

a. Water Temperature

b. Dissolved organic carbon

**Table S3 General features of genomes sequenced in this study**

| <b>Species</b>            | <b>Strain Name</b> | <b>N50<sup>a</sup></b> | <b>Contig Number</b> | <b>Total Length (bp)</b> | <b>GC content(%)</b> | <b>Accession</b> |
|---------------------------|--------------------|------------------------|----------------------|--------------------------|----------------------|------------------|
| <i>V.mimicus</i>          | VM14               | 175236                 | 60                   | 4148181                  | 46.7                 | SAMN10233604     |
| <i>V.mimicus</i>          | VM34               | 673223                 | 51                   | 4165063                  | 46.7                 | SAMN10233608     |
| <i>V.mimicus</i>          | VM61               | 175640                 | 58                   | 4154324                  | 46.7                 | SAMN10233642     |
| <i>V.parahaemolyticus</i> | YK38               | 539419                 | 56                   | 5381751                  | 45.1                 | SAMN10233644     |
| <i>V.parahaemolyticus</i> | YK39               | 539460                 | 57                   | 5375477                  | 45.1                 | SAMN10239529     |
| <i>V.parahaemolyticus</i> | YK40               | 539459                 | 56                   | 5374470                  | 45.1                 | SAMN10239530     |
| <i>V.parahaemolyticus</i> | YK13               | 317677                 | 65                   | 5128954                  | 45.2                 | SAMN10239531     |
| <i>V.parahaemolyticus</i> | YK17               | 430667                 | 48                   | 5149308                  | 45.3                 | SAMN10239532     |
| <i>V.parahaemolyticus</i> | YK41               | 539271                 | 12                   | 5114506                  | 45.2                 | SAMN10239612     |
| <i>V.parahaemolyticus</i> | YK32               | 980059                 | 24                   | 5059557                  | 45.3                 | SAMN10240008     |
| <i>V.parahaemolyticus</i> | YK34               | 532654                 | 35                   | 5217375                  | 45.2                 | SAMN10240007     |
| <i>V.parahaemolyticus</i> | YK45               | 539460                 | 59                   | 5375779                  | 45.1                 | SAMN10240009     |
| <i>V.mimicus</i>          | VM20               | 521068                 | 53                   | 4172938                  | 46.7                 | SAMN10240010     |
| <i>V.parahaemolyticus</i> | YK33               | 557374                 | 13                   | 4952683                  | 45.4                 | SAMN10240051     |
| <i>V.scophthalmi</i>      | YK47               | 151923                 | 52                   | 4699994                  | 44.6                 | SAMN10240052     |
| <i>V.parahaemolyticus</i> | YK51               | 185265                 | 87                   | 5127397                  | 44.6                 | SAMN11475395     |
| <i>V.parahaemolyticus</i> | YK49               | 214972                 | 14                   | 3924830                  | 44.7                 | SAMN10240056     |
| <i>V.mimicus</i>          | VM27               | 175640                 | 67                   | 4166494                  | 46.7                 | SAMN10240057     |
| <i>V.mimicus</i>          | VM37               | 662907                 | 48                   | 4169986                  | 46.7                 | SAMN10240079     |
| <i>V.mimicus</i>          | VM41               | 672907                 | 53                   | 4170794                  | 46.7                 | SAMN10240080     |
| <i>V.parahaemolyticus</i> | PJ42               | 653087                 | 58                   | 5568010                  | 45.1                 | SAMN10240082     |
| <i>V.parahaemolyticus</i> | PJ43               | 539460                 | 56                   | 5575081                  | 45.1                 | SAMN10240083     |
| <i>V.parahaemolyticus</i> | PJ44               | 539418                 | 61                   | 5572779                  | 45.1                 | SAMN10240085     |
| <i>V.parahaemolyticus</i> | PJ37               | 557374                 | 38                   | 5117397                  | 45.3                 | SAMN10240148     |
| <i>V.parahaemolyticus</i> | PJ18               | 177983                 | 108                  | 5380834                  | 45.3                 | SAMN10240086     |
| <i>V.parahaemolyticus</i> | PJ35               | 425693                 | 44                   | 5093812                  | 45.3                 | SAMN10240147     |
| <i>V.parahaemolyticus</i> | SH50               | 675840                 | 35                   | 5120439                  | 45.3                 | SAMN11475416     |

a: a median value of contig lengths for de novo assemblies

**Table S4 General information of four STs in the pubmlst data**

| Strain         | collection_date | country          | isolation_source | serotype  |
|----------------|-----------------|------------------|------------------|-----------|
| <b>ST415</b>   |                 |                  |                  |           |
| LN_Vp274       | 2016            | China: Dalian    | environmental    |           |
| 962            | 2015            | Philippines      | environmental    |           |
| GZ96           | 2014            | China: Guangzhou | environmental    |           |
| GZ97           | 2014            | China: Guangzhou | environmental    |           |
| 642B3          | 2013            | China            | environmental    | O12       |
| VP13-009       | 2013            | China            | clinical         | O3:KUT    |
| E74            | 2013            | Thailand         | environmental    |           |
| E76            | 2013            | Thailand         | environmental    |           |
| 2012-163       | 2012            | China: Zhejiang  | environmental    |           |
| 3/24           | 2012            | Ecuador          | environmental    |           |
| 2012-170       | 2012            | China: Zhejiang  | environmental    |           |
| I-172          | 2012            | Ecuador          | environmental    |           |
| CR053-18       | 2012            | USA              | environmental    |           |
| SH11VP246      | 2011            | China: Shanghai  | environmental    | O10       |
| 907            | 2011            | Ecuador          | environmental    |           |
| S6-b           | 2011            | China            | environmental    |           |
| IT_CR_Vp274    | 2011            | Venetian         | environmental    |           |
| 2011-00142-02  | 2011            | Canada           | environmental    |           |
| Vp061          | 2011            | China            | environmental    | O2:Kunk   |
| IT_CR_Vp79     | 2011            | Venetian         | environmental    |           |
| XM-VP185       | 2010            | China            | environmental    |           |
| IB3884         | 2004            | Mozambique       | clinical         | O3:K58    |
| IB3885         | 2004            | Mozambique       | clinical         | O3:K58    |
| IB3891         | 2004            | Mozambique       | clinical         | O3:K58    |
| IB3886         | 2004            | Mozambique       | clinical         | O3:K58    |
| VP142          | 2003            | Thailand         | environmental    | Ounk:Kunk |
| VP168          | 1996            | Thailand         | clinical         | O3:Kunk   |
| <b>ST1823</b>  |                 |                  |                  |           |
| PH-1096        | 2015            | Philippines      | environmental    |           |
| PH-1042        | 2015            | Philippines      | environmental    |           |
| 2014W310       | 2014            | China: Zhejiang  | environmental    |           |
| 2014W298       | 2014            | China: Zhejiang  | environmental    |           |
| VP1043B1       | 2013            | China            | environmental    | O4        |
| ningbo2012-044 | 2012            | China: Zhejiang  | environmental    | O5:KUT    |
| 41-4-i         | 2011            | Madurankuliya    | environmental    |           |
| 23-3-ii        | 2011            | Puttalam         | environmental    |           |
| VP06157        | 2006            | China            | clinical         | O8:K22    |
| VP130A         | 2003            | Thailand         | environmental    | O1:Kunk   |
| VP130B         | 2003            | Thailand         | environmental    | O1:Kunk   |
| VP12           | 1999            | Thailand         | environmental    | O1KUT     |
| <b>ST236</b>   |                 |                  |                  |           |
| YK32           | 2017            | China: Liaoning  | environmental    |           |
| VP26           | 1999            | Thailand         | environmental    |           |
| <b>ST1498</b>  |                 |                  |                  |           |
| YK34           | 2017            | China: Liaoning  | environmental    |           |
| III-132        | 2012            | Ecuador          | environmental    |           |
| VN-4016        | 2010            | Netherland       | environmental    |           |

**Table S5 General features of *V. parahaemolyticus* used in this study**

| Strain             | Country     | province(or city) | Year | isolation source | ST      |
|--------------------|-------------|-------------------|------|------------------|---------|
| S160               | China       | Shandong          | 2006 | environment      | ST329   |
| S132               | China       | Liaoning          | 2005 | human            | ST332   |
| VIP-0434           | China       | Hongkong          | 2008 | human            | ST332   |
| S157               | China       | Shandong          | 2006 | environment      | ST1009  |
| S159               | China       | Shandong          | 2006 | environment      | ST1009  |
| S022               | Japan       | /                 | 1984 | human            | ST8     |
| S034               | India       | /                 | 1999 | human            | ST8     |
| GIXMxtfL71-2011.05 | China       | Shenzhen          | 2011 | human            | ST8     |
| S060               | China       | Taiwan            | 1992 | human            | ST272   |
| GIXMxtf283-2012    | China       | Shenzhen          | 2012 | human            | Unknown |
| S162               | Thailand    | /                 | 2007 | environment      | ST595   |
| GIXMxtfL61-2011.05 | China       | Shenzhen          | 2011 | human            | ST3     |
| GIXMxtfL65-2011.05 | China       | Shenzhen          | 2011 | human            | ST3     |
| VIP-0407           | China       | Hongkong          | 2008 | mollusk          | ST3     |
| GIXMxtf40-2013.07  | China       | Jinan             | 2013 | human            | ST396   |
| GIXMxtf41-2013.07  | China       | Jinan             | 2013 | human            | ST396   |
| S056               | China       | Taiwan            | 1994 | human            | ST69    |
| S055               | China       | Taiwan            | 1994 | human            | ST69    |
| S057               | China       | Taiwan            | 1994 | human            | ST69    |
| S134               | China       | Liaoning          | 2005 | human            | ST527   |
| HZ-7               | China       | Zhejiang          | 2014 | human            | ST150   |
| PB1937             | China       | Fujian            | 2012 | human            | ST150   |
| S173               | China       | Shanghai          | 2005 | environment      | ST289   |
| S171               | China       | Shanghai          | 2007 | environment      | ST288   |
| S145               | China       | Inner Mongolia    | 2006 | human            | Unkonwn |
| ATCC17082          | Japan       | /                 | 2005 | human            | ST1     |
| FORC22             | South Korea | /                 | 2017 | human            | ST233   |
| GIXMxtf381-2013.06 | China       | /                 | 2013 | human            | Unkonwn |
| FORC14             | South Korea | /                 | 2015 | human            | ST1629  |
| S031               | Japan       | /                 | 1984 | human            | ST189   |
| 100156             | China       | Guangdong         | 2013 | human            | Unknown |
| 100143             | China       | Guangdong         | 2013 | human            | Unknown |
| 100136             | China       | Guangdong         | 2008 | human            | Unknown |
| NA9                | Malaysia    | /                 | 2017 | Shrimp           | ST1911  |
| NA7                | Malaysia    | /                 | 2017 | Shrimp           | ST1911  |
| NA4                | Malaysia    | /                 | 2017 | Shrimp           | ST1911  |
| GIXMxtfL88-2011.05 | China       | Shenzhen          | 2011 | human            | Unknown |
| GIXMxtfL83-2011.05 | China       | Shenzhen          | 2011 | human            | Unknown |
| FORC8              | South Korea | /                 | 2014 | human            | ST984   |
| FORC18             | South Korea | /                 | 2014 | human            | ST984   |
| S154               | China       | Shandong          | 2005 | human            | ST419   |
| S156               | China       | Shandong          | 2005 | human            | ST419   |
| S166               | China       | Shandong          | 2005 | human            | ST419   |
| S144               | China       | Shandong          | 2005 | human            | ST419   |
| S158               | China       | Shandong          | 2005 | human            | ST419   |
| S153               | China       | Shandong          | 2005 | human            | ST419   |
| S151               | China       | Shandong          | 2005 | human            | ST419   |

**Table S6. List of core genes of *V. parahaemolyticus* in strain RIMD 2210633 and recombination sites identified**

| <b>locus</b> | <b>associated with recombination</b> | <b>gene product</b>   |
|--------------|--------------------------------------|---|
| VP0001       | NO                                   | flavodoxin  |
| VP0003       | NO                                   | inner membrane protein translocase component YidC           |
| VP0004       | NO                                   | ribonuclease P  |
| VP0005       | NO                                   | 50S ribosomal protein L34                                   |
| VP0006       | YES                                  | amino acid ABC transporter ATP-binding protein              |
| VP0007       | YES                                  | amino acid ABC transporter permease                         |
| VP0012       | YES                                  | DNA polymerase III subunit beta                             |
| VP0015       | YES                                  | hypothetical protein  |
| VP0016       | YES                                  | hypothetical protein  |
| VP0018       | YES                                  | 16 kDa heat shock protein A                                 |
| VP0019       | NO                                   | valine--pyruvate transaminase                               |
| VP0022       | NO                                   | glycyl-tRNA synthetase subunit alpha                        |
| VP0025       | YES                                  | sulfur transfer protein SirA                                |
| VP0026       | YES                                  | hypothetical protein  |
| VP0032       | YES                                  | potassium uptake protein TrkH                               |
| VP0034       | YES                                  | DNA-binding transcriptional regulator IlvY                  |
| VP0035       | NO                                   | ketol-acid reductoisomerase                                 |
| VP0036       | NO                                   | hypothetical protein  |
| VP0038       | NO                                   | multidrug resistance protein                                |
| VP0040       | NO                                   | TetR family transcriptional regulator                       |
| VP0041       | NO                                   | ATP-dependent DNA helicase Rep                              |
| VP0042       | NO                                   | cytochrome c5   |
| VP0044       | NO                                   | hypothetical protein  |
| VP0045       | NO                                   | hypothetical protein  |
| VP0047       | YES                                  | peptide ABC transporter ATP-binding protein                 |
| VP0048       | YES                                  | peptide ABC transporter periplasmic peptide-binding protein |
| VP0050       | YES                                  | peptide ABC transporter permease                            |
| VP0055       | NO                                   | RNA polymerase ECF-type sigma factor                        |
| VP0056       | NO                                   | hypothetical protein  |
| VP0061       | NO                                   | multidrug transmembrane resistance signal peptide protein   |
| VP0069       | NO                                   | hypothetical protein  |
| VP0070       | NO                                   | oligopeptidase A  |
| VP0072       | NO                                   | DNA-binding transcriptional regulator AsnC                  |
| VP0073       | NO                                   | hypothetical protein  |
| VP0074       | NO                                   | hypothetical protein  |
| VP0075       | NO                                   | MadN protein  |
| VP0076       | NO                                   | universal stress protein A                                  |
| VP0077       | NO                                   | ferritin  |
| VP0078       | NO                                   | universal stress protein UspB                               |
| VP0079       | NO                                   | hypothetical protein  |
| VP0082       | NO                                   | transmembrane protein                                       |
| VP0083       | NO                                   | hypothetical protein  |
| VP0086       | NO                                   | hypothetical protein  |
| VP0087       | NO                                   | hypothetical protein  |
| VP0089       | NO                                   | hypothetical protein  |
| VP0093       | NO                                   | hypothetical protein  |
| VP0094       | NO                                   | hypothetical protein  |
| VP0095       | NO                                   | ubiquinone/menaquinone biosynthesis methyltransferase       |
| VP0096       | NO                                   | hypothetical protein  |

|        |    |  |
|--------|----|--|
| VP0097 | NO | ubiquinone biosynthesis protein UbiB             |
| VP0098 | NO | twin arginine translocase protein A              |
| VP0100 | NO | hypothetical protein                             |
| VP0103 | NO | hypothetical protein                             |
| VP0104 | NO | delta-aminolevulinic acid dehydratase            |
| VP0105 | NO | hypothetical protein                             |
| VP0107 | NO | DNA polymerase I                                 |
| VP0109 | NO | ribosome biogenesis GTP-binding protein YsxC     |
| VP0110 | NO | cytochrome c4                                    |
| VP0113 | NO | hypothetical protein                             |
| VP0114 | NO | hypothetical protein                             |
| VP0115 | NO | coproporphyrinogen III oxidase                   |
| VP0116 | NO | adenosine deaminase                              |
| VP0117 | NO | GGDEF family protein                             |
| VP0119 | NO | nitrogen regulation protein NR(II)               |
| VP0120 | NO | hypothetical protein                             |
| VP0121 | NO | glutamine synthetase                             |
| VP0122 | NO | BipA protein                                     |
| VP0123 | NO | hypothetical protein                             |
| VP0124 | NO | hypothetical protein                             |
| VP0130 | NO | Hsp33-like chaperonin                            |
| VP0131 | NO | hypothetical protein                             |
| VP0132 | NO | general secretion pathway protein C              |
| VP0134 | NO | general secretion pathway protein E              |
| VP0135 | NO | general secretion pathway protein F              |
| VP0136 | NO | general secretion pathway protein G              |
| VP0137 | NO | general secretion pathway protein H              |
| VP0141 | NO | general secretion pathway protein L              |
| VP0142 | NO | general secretion pathway protein M              |
| VP0143 | NO | general secretion pathway protein N              |
| VP0144 | NO | CysQ protein                                     |
| VP0145 | NO | ADP-ribose diphosphatase NudE                    |
| VP0146 | NO | DNA uptake protein                               |
| VP0147 | NO | ComF-like protein                                |
| VP0148 | NO | BioH protein                                     |
| VP0149 | NO | hypothetical protein                             |
| VP0150 | NO | hypothetical protein                             |
| VP0151 | NO | hypothetical protein                             |
| VP0152 | NO | transcription elongation factor GreB             |
| VP0155 | NO | osmolarity sensor protein                        |
| VP0156 | NO | xanthine/uracil permease family protein          |
| VP0157 | NO | ATP-dependent DNA helicase RecG                  |
| VP0158 | NO | tRNA guanosine-2'-O-methyltransferase            |
| VP0160 | NO | DNA-directed RNA polymerase subunit omega        |
| VP0161 | NO | guanylate kinase                                 |
| VP0164 | NO | TonB system transport protein ExbD2              |
| VP0165 | NO | TonB system transport protein ExbB2              |
| VP0166 | NO | TolR   |
| VP0167 | NO | hypothetical protein                             |
| VP0170 | NO | transmembrane ABC transporter protein            |
| VP0172 | NO | binding protein component of ABC transporter     |
| VP0173 | NO | oligopeptide ABC transporter ATP-binding protein |

|        |    |  |
|--------|----|--|
| VP0174 | NO | oligopeptide ABC transporter ATP-binding protein                                 |
| VP0175 | NO | hypothetical protein   |
| VP0177 | NO | ribonuclease PH  |
| VP0178 | NO | orotate phosphoribosyltransferase  |
| VP0179 | NO | lipid A biosynthesis lauroyl acyltransferase                                     |
| VP0180 | NO | nucleoid occlusion protein   |
| VP0181 | NO | bifunctional phosphopantothencysteine decarboxylase/phosphopantothenate synthase |
| VP0185 | NO | 50S ribosomal protein L28  |
| VP0186 | NO | 50S ribosomal protein L33  |
| VP0239 | NO | triosephosphate isomerase  |
| VP0240 | NO | 5-carboxymethyl-2-hydroxyruconate delta isomerase                                |
| VP0241 | NO | hypothetical protein   |
| VP0242 | NO | hypothetical protein   |
| VP0243 | NO | hypothetical protein   |
| VP0244 | NO | fructose 1,6-bisphosphatase II   |
| VP0246 | NO | hypothetical protein   |
| VP0251 | NO | cell division protein FtsN   |
| VP0253 | NO | primosome assembly protein PriA  |
| VP0254 | NO | hypothetical protein   |
| VP0255 | NO | 50S ribosomal protein L31  |
| VP0256 | NO | 30S ribosomal protein S10  |
| VP0257 | NO | 50S ribosomal protein L3   |
| VP0258 | NO | 50S ribosomal protein L4   |
| VP0259 | NO | 50S ribosomal protein L23  |
| VP0260 | NO | 50S ribosomal protein L2   |
| VP0261 | NO | 30S ribosomal protein S19  |
| VP0262 | NO | 50S ribosomal protein L22  |
| VP0263 | NO | 30S ribosomal protein S3   |
| VP0264 | NO | 50S ribosomal protein L16  |
| VP0265 | NO | 50S ribosomal protein L29  |
| VP0266 | NO | 30S ribosomal protein S17  |
| VP0267 | NO | 50S ribosomal protein L14  |
| VP0268 | NO | 50S ribosomal protein L24  |
| VP0269 | NO | 50S ribosomal protein L5   |
| VP0270 | NO | 30S ribosomal protein S14  |
| VP0271 | NO | 30S ribosomal protein S8   |
| VP0272 | NO | 50S ribosomal protein L6   |
| VP0273 | NO | 50S ribosomal protein L18  |
| VP0274 | NO | 30S ribosomal protein S5   |
| VP0275 | NO | 50S ribosomal protein L30  |
| VP0276 | NO | 50S ribosomal protein L15  |
| VP0277 | NO | preprotein translocase subunit SecY  |
| VP0278 | NO | 50S ribosomal protein L36  |
| VP0279 | NO | 30S ribosomal protein S13  |
| VP0280 | NO | 30S ribosomal protein S11  |
| VP0281 | NO | 30S ribosomal protein S4   |
| VP0282 | NO | DNA-directed RNA polymerase subunit alpha  |
| VP0283 | NO | 50S ribosomal protein L17  |
| VP0284 | NO | hypothetical protein   |
| VP0285 | NO | FKBP-type peptidylprolyl isomerase   |
| VP0286 | NO | hypothetical protein   |
| VP0287 | NO | ElaA protein   |

|        |     |   |
|--------|-----|---|
| VP0288 | NO  | ATP-dependent RNA helicase DbpA   |
| VP0290 | NO  | bifunctional 2',3'-cyclic nucleotide 2'-phosphodiesterase/3'-nucleotidase periplasmic protein |
| VP0291 | NO  | uroporphyrin-III C-methyltransferase  |
| VP0292 | NO  | sulfate adenylyltransferase   |
| VP0293 | NO  | sulfate adenylyltransferase   |
| VP0296 | NO  | adenylylsulfate kinase  |
| VP0297 | NO  | hypothetical protein  |
| VP0299 | NO  | hypothetical protein  |
| VP0300 | NO  | hypothetical protein  |
| VP0301 | NO  | ABC transporter ATP-binding protein   |
| VP0303 | NO  | hypothetical protein  |
| VP0305 | NO  | hypothetical protein  |
| VP0306 | NO  | methionine sulfoxide reductase A  |
| VP0307 | NO  | hypothetical protein  |
| VP0308 | NO  | hypothetical protein  |
| VP0309 | NO  | hypothetical protein  |
| VP0310 | NO  | hypothetical protein  |
| VP0311 | NO  | inorganic pyrophosphatase   |
| VP0313 | NO  | fructose-1,6-bisphosphatase   |
| VP0314 | NO  | UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl-meso-diaminopimelate ligase                    |
| VP0316 | NO  | thiamine transporter substrate binding subunit  |
| VP0317 | NO  | thiamine transporter membrane protein   |
| VP0318 | NO  | thiamine ABC transporter ATP-binding protein  |
| VP0320 | NO  | hypothetical protein  |
| VP0323 | NO  | hypothetical protein  |
| VP0324 | NO  | arginine repressor ArgR   |
| VP0325 | NO  | malate dehydrogenase  |
| VP0326 | NO  | hypothetical protein  |
| VP0327 | NO  | octaprenyl-diphosphate synthase   |
| VP0329 | NO  | 50S ribosomal protein L27   |
| VP0330 | NO  | GTPase ObgE   |
| VP0331 | NO  | hypothetical protein  |
| VP0334 | NO  | diadenosine tetraphosphatase  |
| VP0335 | NO  | ApaG protein  |
| VP0336 | NO  | dimethyladenosine transferase   |
| VP0338 | NO  | survival protein SurA   |
| VP0339 | NO  | organic solvent tolerance protein   |
| VP0340 | NO  | Dna-J like membrane chaperone protein   |
| VP0341 | NO  | hypothetical protein  |
| VP0342 | NO  | isopropylmalate isomerase small subunit   |
| VP0344 | NO  | 3-isopropylmalate dehydrogenase   |
| VP0346 | NO  | 2-isopropylmalate synthase  |
| VP0347 | NO  | hypothetical protein  |
| VP0348 | NO  | hypothetical protein  |
| VP0350 | NO  | leucine transcriptional activator   |
| VP0351 | NO  | long-chain-fatty-acid-CoA ligase  |
| VP0352 | NO  | acetolactate synthase 3 catalytic subunit   |
| VP0353 | NO  | acetolactate synthase 3 regulatory subunit  |
| VP0354 | NO  | sensory box/GGDEF family protein  |
| VP0355 | YES | LuxZ  |
| VP0356 | YES | pyruvate kinase   |
| VP0357 | YES | hypothetical protein  |



|        |     |   |
|--------|-----|---|
| VP0358 | YES | DeoR family transcriptional regulator   |
| VP0359 | YES | glucosamine--fructose-6-phosphate aminotransferase  |
| VP0369 | YES | mannitol-1-phosphate 5-dehydrogenase  |
| VP0370 | YES | PTS system mannitol-specific transporter subunit IIABC  |
| VP0374 | YES | hypothetical protein  |
| VP0378 | YES | hypothetical protein  |
| VP0404 | YES | RNA polymerase sigma factor RpoD  |
| VP0406 | YES | hypothetical protein  |
| VP0408 | YES | DNA-binding/iron metalloprotein/AP endonuclease   |
| VP0409 | YES | beta-ketoadipate enol-lactone hydrolase   |
| VP0411 | YES | dihydroneopterin aldolase FolB  |
| VP0412 | NO  | 2-amino-4-hydroxy-6- hydroxymethyldihydropteridine pyrophosphokinase                                  |
| VP0413 | NO  | undecaprenyl pyrophosphate phosphatase  |
| VP0414 | NO  | multifunctional tRNA nucleotidyl transferase/2'3'-cyclic phosphodiesterase/2'nucleotidase/phosphatase |
| VP0415 | NO  | general secretion pathway protein A   |
| VP0419 | NO  | hypothetical protein  |
| VP0420 | NO  | hypothetical protein  |
| VP0424 | NO  | bifunctional heptose 7-phosphate kinase/heptose 1-phosphate adenylyltransferase                       |
| VP0426 | NO  | MutT/nudix family protein   |
| VP0427 | NO  | hypothetical protein  |
| VP0429 | NO  | esterase  |
| VP0430 | NO  | DNA topoisomerase IV subunit B  |
| VP0431 | NO  | DNA topoisomerase IV subunit A  |
| VP0432 | NO  | protease DegS   |
| VP0433 | NO  | protease Do   |
| VP0434 | NO  | cytochrome d ubiquinol oxidase subunit III  |
| VP0436 | NO  | hypothetical protein  |
| VP0438 | NO  | 50S ribosomal protein L13   |
| VP0441 | NO  | ubiquinol-cytochrome c reductase, iron-sulfur subunit   |
| VP0442 | NO  | ubiquinol-cytochrome c reductase, cytochrome b  |
| VP0443 | NO  | ubiquinol-cytochrome c reductase, cytochrome c1   |
| VP0444 | NO  | stringent starvation protein A  |
| VP0449 | NO  | lipoprotein   |
| VP0450 | NO  | hypothetical protein  |
| VP0451 | NO  | hypothetical protein  |
| VP0452 | NO  | S-adenosyl-methyltransferase MraW   |
| VP0453 | NO  | cell division protein FtsL  |
| VP0454 | NO  | penicillin-binding protein 3  |
| VP0455 | NO  | UDP-N-acetylmuramoylalanyl-D-glutamate--2, 6-diaminopimelate ligase                                   |
| VP0456 | NO  | UDP-N-acetylmuramoylalanyl-D-glutamyl-2, 6-diaminopimelate-D-alanyl-D-alanyl ligase                   |
| VP0457 | NO  | phospho-N-acetylmuramoyl-pentapeptide- transferase  |
| VP0458 | NO  | UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase  |
| VP0459 | NO  | cell division protein FtsW  |
| VP0461 | NO  | UDP-N-acetylmuramate--L-alanine ligase  |
| VP0463 | NO  | cell division protein FtsA  |
| VP0464 | NO  | cell division protein FtsZ  |
| VP0465 | NO  | UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase  |
| VP0466 | NO  | hypothetical protein  |
| VP0467 | NO  | preprotein translocase subunit SecA   |
| VP0468 | NO  | mutator MutT protein  |
| VP0469 | NO  | dihydrodipicolinate reductase   |
| VP0470 | NO  | carbamoyl phosphate synthase small subunit  |

|        |    |   |
|--------|----|---|
| VP0475 | NO | LysR family transcriptional regulator                         |
| VP0476 | NO | hypothetical protein  |
| VP0477 | NO | hypothetical protein  |
| VP0478 | NO | adenosylcobinamide-phosphate synthase                         |
| VP0479 | NO | 5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase    |
| VP0481 | NO | glutamate synthase subunit beta                               |
| VP0484 | NO | glutamate synthase, large subunit                             |
| VP0485 | NO | hypothetical protein  |
| VP0486 | NO | sensory box/GGDEF family protein                              |
| VP0487 | NO | aerobic respiration control sensor protein ArcB               |
| VP0488 | NO | DNA polymerase III, beta chain                                |
| VP0492 | NO | ribonuclease activity regulator protein RraA                  |
| VP0493 | NO | hypothetical protein  |
| VP0494 | NO | bifunctional aspartokinase I/homoserine dehydrogenase I       |
| VP0495 | NO | homoserine kinase   |
| VP0496 | NO | threonine synthase  |
| VP0499 | NO | hypothetical protein  |
| VP0500 | NO | uracil-DNA glycosylase  |
| VP0502 | NO | hypothetical protein  |
| VP0503 | NO | sodium/alanine symporter                                      |
| VP0504 | NO | hypothetical protein  |
| VP0505 | NO | ATP-dependent RNA helicase SrmB                               |
| VP0506 | NO | hypothetical protein  |
| VP0507 | NO | branched chain amino acid transport system II carrier protein |
| VP0511 | NO | ssDNA exonuclease RecJ  |
| VP0512 | NO | peptide chain release factor 2                                |
| VP0513 | NO | lysyl-tRNA synthetase   |
| VP0516 | NO | aldo/keto reductase   |
| VP0517 | NO | hypothetical protein  |
| VP0519 | NO | hypothetical protein  |
| VP0520 | NO | dinucleoside polyphosphate hydrolase                          |
| VP0522 | NO | hypothetical protein  |
| VP0523 | NO | prolipoprotein diacylglycerol transferase                     |
| VP0525 | NO | hypothetical protein  |
| VP0527 | NO | transcriptional activator NhaR                                |
| VP0528 | NO | hypothetical protein  |
| VP0529 | NO | transcriptional activator HlyU                                |
| VP0531 | NO | 30S ribosomal protein S20                                     |
| VP0532 | NO | MviN protein  |
| VP0533 | NO | bifunctional riboflavin kinase/FMN adenylyltransferase        |
| VP0534 | NO | isoleucyl-tRNA synthetase                                     |
| VP0536 | NO | FKBP-type peptidylprolyl isomerase                            |
| VP0537 | NO | 4-hydroxy-3-methylbut-2-enyl diphosphate reductase            |
| VP0538 | NO | two-component response-regulatory protein YehT                |
| VP0539 | NO | hypothetical protein  |
| VP0540 | NO | carbon starvation protein A                                   |
| VP0542 | NO | hypothetical protein  |
| VP0543 | NO | N-acetylmuramic acid-6-phosphate etherase                     |
| VP0545 | NO | beta-hexosaminidase   |
| VP0546 | NO | phospho-2-dehydro-3-deoxyheptonate aldolase                   |
| VP0547 | NO | bifunctional chorismate mutase/prephenate dehydrogenase       |
| VP0548 | NO | ToxR-activated protein TagE                                   |

|        |    |   |
|--------|----|---|
| VP0549 | NO | hypothetical protein  |
| VP0551 | NO | ABC transporter ATP-binding protein                             |
| VP0552 | NO | soluble lytic murein transglycosylase                           |
| VP0553 | NO | Trp operon repressor  |
| VP0554 | NO | NTPase  |
| VP0555 | NO | chorismate mutase/prephenate dehydratase                        |
| VP0556 | NO | sigma-54 modulation protein                                     |
| VP0558 | NO | hypothetical protein  |
| VP0560 | NO | hypothetical protein  |
| VP0561 | NO | ClpB protein  |
| VP0563 | NO | hypothetical protein  |
| VP0564 | NO | penicillin-insensitive murein endopeptidase                     |
| VP0565 | NO | hypothetical protein  |
| VP0566 | NO | ferredoxin  |
| VP0569 | NO | DNA-binding response regulator PhoB                             |
| VP0570 | NO | phosphate regulon sensor protein                                |
| VP0571 | NO | phosphate ABC transporter periplasmic phosphate-binding protein |
| VP0573 | NO | polyphosphate kinase  |
| VP0575 | NO | phosphate ABC transporter permease                              |
| VP0576 | NO | phosphate transporter ATP-binding protein                       |
| VP0577 | NO | transcriptional regulator PhoU                                  |
| VP0579 | NO | copper homeostasis protein                                      |
| VP0580 | NO | anti-oxidant AhpCTSA family protein                             |
| VP0581 | NO | LysR family transcriptional regulator                           |
| VP0582 | NO | hypothetical protein  |
| VP0583 | NO | malate synthase   |
| VP0584 | NO | isocitrate lyase  |
| VP0585 | NO | acetoin utilization protein AcuB                                |
| VP0587 | NO | S-adenosylmethionine:tRNA ribosyltransferase-isomerase          |
| VP0588 | NO | queuine tRNA-ribosyltransferase                                 |
| VP0589 | NO | preprotein translocase subunit YajC                             |
| VP0590 | NO | preprotein translocase subunit SecD                             |
| VP0591 | NO | preprotein translocase subunit SecF                             |
| VP0593 | NO | inositol monophosphatase  |
| VP0594 | NO | RNA methyltransferase   |
| VP0596 | NO | cysteine desulfurase  |
| VP0597 | NO | scaffold protein  |
| VP0598 | NO | HesB family protein   |
| VP0599 | NO | co-chaperone HscB   |
| VP0601 | NO | ferredoxin  |
| VP0602 | NO | hypothetical protein  |
| VP0604 | NO | nucleoside diphosphate kinase                                   |
| VP0605 | NO | ribosomal RNA large subunit methyltransferase N                 |
| VP0607 | NO | hypothetical protein  |
| VP0608 | NO | 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase            |
| VP0610 | NO | hypothetical protein  |
| VP0611 | NO | outer membrane protein assembly complex subunit YfgL            |
| VP0613 | NO | hypothetical protein  |
| VP0614 | NO | hypothetical protein  |
| VP0615 | NO | exodeoxyribonuclease VII large subunit                          |
| VP0616 | NO | inosine 5'-monophosphate dehydrogenase                          |
| VP0617 | NO | GMP synthase  |

|        |    |   |
|--------|----|---|
| VP0620 | NO | hypothetical protein                                |
| VP0621 | NO | nonspecific acid phosphatase                        |
| VP0623 | NO | D-amino acid dehydrogenase small subunit            |
| VP0624 | NO | LysR family transcriptional regulator               |
| VP0628 | NO | hypothetical protein                                |
| VP0629 | NO | homocysteine synthase                               |
| VP0630 | NO | hypothetical protein                                |
| VP0632 | NO | Na <sup>+</sup> /H <sup>+</sup> antiporter          |
| VP0636 | NO | outer membrane protein A                            |
| VP0644 | NO | SsrA-binding protein                                |
| VP0645 | NO | hypothetical protein                                |
| VP0647 | NO | small protein A                                     |
| VP0648 | NO | recombination and repair protein                    |
| VP0650 | NO | inorganic polyphosphate/ATP-NAD kinase              |
| VP0651 | NO | heat shock protein GrpE                             |
| VP0652 | NO | hypothetical protein                                |
| VP0653 | NO | molecular chaperone DnaK                            |
| VP0654 | NO | molecular chaperone DnaJ                            |
| VP0662 | NO | hypothetical protein                                |
| VP0664 | NO | hypothetical protein                                |
| VP0665 | NO | transglycosylase                                    |
| VP0669 | NO | hypothetical protein                                |
| VP0670 | NO | hypothetical protein                                |
| VP0671 | NO | aminoacyl-histidine dipeptidase                     |
| VP0672 | NO | hypothetical protein                                |
| VP0673 | NO | xanthine-guanine phosphoribosyltransferase          |
| VP0674 | NO | fermentation/respiration switch protein             |
| VP0676 | NO | gamma-glutamyl kinase                               |
| VP0678 | NO | transcriptional regulator NrdR                      |
| VP0679 | NO | riboflavin-specific deaminase                       |
| VP0680 | NO | riboflavin synthase subunit alpha                   |
| VP0681 | NO | 3,4-dihydroxy-2-butanone 4-phosphate synthase       |
| VP0682 | NO | 6,7-dimethyl-8-ribityllumazine synthase             |
| VP0683 | NO | transcription antitermination protein NusB          |
| VP0684 | NO | thiamine monophosphate kinase                       |
| VP0686 | NO | 1-deoxy-D-xylulose-5-phosphate synthase             |
| VP0687 | NO | geranyltranstransferase                             |
| VP0688 | NO | exodeoxyribonuclease VII small subunit              |
| VP0689 | NO | flagellar motor protein PomA                        |
| VP0690 | NO | flagellar motor protein MotB                        |
| VP0691 | NO | thiamine biosynthesis protein ThiI                  |
| VP0692 | NO | DNA-binding transcriptional activator GcvA          |
| VP0694 | NO | hypothetical protein                                |
| VP0695 | NO | RNA 2'-O-ribose methyltransferase                   |
| VP0697 | NO | exonuclease IX                                      |
| VP0698 | NO | hypothetical protein                                |
| VP0699 | NO | GGDEF family protein                                |
| VP0700 | NO | hypothetical protein                                |
| VP0701 | NO | 7-cyano-7-deazaguanine reductase                    |
| VP0702 | NO | SecY interacting protein Syd                        |
| VP0703 | NO | hypothetical protein                                |
| VP0704 | NO | DL-methionine transporter substrate-binding subunit |

|        |    |  |
|--------|----|--|
| VP0706 | NO | DL-methionine transporter ATP-binding subunit                    |
| VP0707 | NO | hypothetical protein   |
| VP0708 | NO | D,D-heptose 1,7-bisphosphate phosphatase                         |
| VP0709 | NO | trehalose repressor  |
| VP0710 | NO | PTS system trehalose(maltose)-specific transporter subunits IIBC |
| VP0711 | NO | trehalose-6-phosphate hydrolase                                  |
| VP0714 | NO | hypothetical protein   |
| VP0716 | NO | lipoyl synthase  |
| VP0717 | NO | lipoate-protein ligase B   |
| VP0718 | NO | hypothetical protein   |
| VP0719 | NO | D-alanyl-D-alanine carboxypeptidase                              |
| VP0720 | NO | rare lipoprotein A   |
| VP0722 | NO | penicillin-binding protein 2                                     |
| VP0723 | NO | rRNA large subunit methyltransferase                             |
| VP0724 | NO | hypothetical protein   |
| VP0725 | NO | DNA polymerase III subunit delta                                 |
| VP0726 | NO | rare lipoprotein B   |
| VP0727 | NO | leucyl-tRNA synthetase   |
| VP0728 | NO | hypothetical protein   |
| VP0729 | NO | apolipoprotein N-acyltransferase                                 |
| VP0730 | NO | hemolysin  |
| VP0731 | NO | metalloprotease  |
| VP0735 | NO | 2-octaprenyl-3-methyl-6-methoxy-1,4-benzoquinol hydroxylase      |
| VP0737 | NO | GTP-dependent nucleic acid-binding protein EngD                  |
| VP0738 | NO | peptidyl-tRNA hydrolase  |
| VP0739 | NO | ribose-phosphate pyrophosphokinase                               |
| VP0742 | NO | glutamyl-tRNA reductase  |
| VP0743 | NO | peptide chain release factor 1                                   |
| VP0744 | NO | HemK protein   |
| VP0745 | NO | hypothetical protein   |
| VP0746 | NO | hypothetical protein   |
| VP0747 | NO | 2-dehydro-3-deoxyphosphooctonate aldolase                        |
| VP0748 | NO | bifunctional UDP-sugar hydrolase/5'-nucleotidase periplasmic     |
| VP0749 | NO | hypothetical protein   |
| VP0752 | NO | hypothetical protein   |
| VP0753 | NO | hypothetical protein   |
| VP0755 | NO | N,N'-diacetylchitobiase  |
| VP0756 | NO | hypothetical protein   |
| VP0757 | NO | hypothetical protein   |
| VP0759 | NO | hypothetical protein   |
| VP0763 | NO | hypothetical protein   |
| VP0768 | NO | hypothetical protein   |
| VP0770 | NO | polar flagellar FlgN   |
| VP0771 | NO | polar flagellar FlgM   |
| VP0774 | NO | chemotaxis methyltransferase CheR                                |
| VP0781 | NO | flagellar basal body rod protein FlgG                            |
| VP0783 | NO | flagellar basal body P-ring biosynthesis protein FlgA            |
| VP0786 | NO | flagellar hook-associated protein FlgL                           |
| VP0793 | NO | PTS system glucose-specific transporter subunit                  |
| VP0794 | NO | phosphoenolpyruvate-protein phosphotransferase                   |
| VP0795 | NO | phosphocarrier protein HPr                                       |
| VP0796 | NO | hypothetical protein   |

|        |    |   |
|--------|----|---|
| VP0797 | NO | cysteine synthase A   |
| VP0798 | NO | sulfate transport protein CysZ                                    |
| VP0802 | NO | hypothetical protein  |
| VP0804 | NO | hypothetical protein  |
| VP0806 | NO | hypothetical protein  |
| VP0807 | NO | hypothetical protein  |
| VP0808 | NO | short chain dehydrogenase   |
| VP0809 | NO | sugar nucleotide epimerase  |
| VP0810 | NO | PTS system mannose-specific, factor IIC                           |
| VP0812 | NO | hypothetical protein  |
| VP0814 | NO | hypothetical protein  |
| VP0815 | NO | hypothetical protein  |
| VP0816 | NO | phosphodiesterase   |
| VP0817 | NO | selenoprotein W-like protein                                      |
| VP0818 | NO | hypothetical protein  |
| VP0819 | NO | ToxS protein  |
| VP0820 | NO | ToxR protein  |
| VP0821 | NO | heat shock protein 90   |
| VP0822 | NO | adenylate kinase  |
| VP0823 | NO | ferrochelataase   |
| VP0824 | NO | permease  |
| VP0825 | NO | transcriptional activator RfaH                                    |
| VP0826 | NO | asparagine synthetase B   |
| VP0827 | NO | glutathione-regulated potassium-efflux system protein KefB        |
| VP0828 | NO | N-acetylglucosamine repressor                                     |
| VP0829 | NO | N-acetylglucosamine-6-phosphate deacetylase                       |
| VP0831 | NO | PTS system N-acetylglucosamine-specific transporter subunit IIABC |
| VP0832 | NO | glutaminyl-tRNA synthetase  |
| VP0833 | NO | ferric uptake regulator   |
| VP0834 | NO | hypothetical protein  |
| VP0835 | NO | flavodoxin FldA   |
| VP0836 | NO | hypothetical protein  |
| VP0837 | NO | esterase/lipase YbfF  |
| VP0840 | NO | hypothetical protein  |
| VP0841 | NO | hypothetical protein  |
| VP0842 | NO | type II citrate synthase  |
| VP0845 | NO | succinate dehydrogenase flavoprotein subunit                      |
| VP0846 | NO | succinate dehydrogenase iron-sulfur subunit                       |
| VP0847 | NO | 2-oxoglutarate dehydrogenase E1                                   |
| VP0850 | NO | succinyl-CoA synthetase subunit alpha                             |
| VP0853 | NO | zinc ABC transporter periplasmic zinc-binding protein             |
| VP0854 | NO | AraC family transcriptional regulator                             |
| VP0857 | NO | ferrous iron transport protein A                                  |
| VP0861 | NO | arginyl-tRNA synthetase   |
| VP0862 | NO | hypothetical protein  |
| VP0865 | NO | ATP-dependent helicase DinG                                       |
| VP0866 | NO | hypothetical protein  |
| VP0867 | NO | hypothetical protein  |
| VP0868 | NO | outer membrane lipoprotein Slp                                    |
| VP0869 | NO | hypothetical protein  |
| VP0870 | NO | long-chain-fatty-acid--CoA ligase                                 |
| VP0871 | NO | ribonuclease D  |

|        |    |   |
|--------|----|---|
| VP0872 | NO | cell division topological specificity factor MinE   |
| VP0873 | NO | septum site-determining protein MinD  |
| VP0874 | NO | septum formation inhibitor  |
| VP0877 | NO | LysR family transcriptional regulator   |
| VP0878 | NO | NupC family protein   |
| VP0879 | NO | bifunctional 5,10-methylene-tetrahydrofolate dehydrogenase/<br>5,10-methylene-tetrahydrofolate cyclohydrolase |
| VP0881 | NO | 3-oxoacyl-ACP synthase  |
| VP0882 | NO | 3-ketoacyl-ACP reductase  |
| VP0884 | NO | 3-oxoacyl-ACP synthase  |
| VP0885 | NO | lipoprotein   |
| VP0886 | NO | hypothetical protein  |
| VP0888 | NO | hypothetical protein  |
| VP0890 | NO | hypothetical protein  |
| VP0894 | NO | acyl carrier protein  |
| VP0895 | NO | acyl carrier protein  |
| VP0896 | NO | phospholipid biosynthesis acyltransferase   |
| VP0898 | NO | lipoprotein   |
| VP0899 | NO | O-methyltransferase   |
| VP0900 | NO | oxidoreductase  |
| VP0902 | NO | hemolysin   |
| VP0903 | NO | RhIE protein  |
| VP0904 | NO | KtrA protein  |
| VP0907 | NO | hypothetical protein  |
| VP0910 | NO | C4-dicarboxylate-binding periplasmic protein  |
| VP0911 | NO | C4-dicarboxylate transport protein DctQ   |
| VP0912 | NO | C4-dicarboxylate transport protein  |
| VP0913 | NO | hypothetical protein  |
| VP0915 | NO | C4-dicarboxylate transport sensor protein   |
| VP0916 | NO | trigger factor  |
| VP0917 | NO | ATP-dependent Clp protease proteolytic subunit  |
| VP0918 | NO | ATP-dependent protease ATP-binding subunit ClpX   |
| VP0919 | NO | ATP-dependent protease LA   |
| VP0920 | NO | DNA-binding protein HU-beta   |
| VP0921 | NO | peptidyl-prolyl cis-trans isomerase D   |
| VP0922 | NO | hypothetical protein  |
| VP0923 | NO | hypothetical protein  |
| VP0925 | NO | deoxyguanosinetriphosphate triphosphohydrolase-like protein   |
| VP0927 | NO | aminotransferase  |
| VP0928 | NO | menaquinone-specific isochorismate synthase   |
| VP0931 | NO | naphthoate synthase   |
| VP0933 | NO | O-succinylbenzoic acid--CoA ligase  |
| VP0936 | NO | hypothetical protein  |
| VP0937 | NO | hypothetical protein  |
| VP0939 | NO | hypothetical protein  |
| VP0940 | NO | hypothetical protein  |
| VP0941 | NO | multidrug resistance protein  |
| VP0942 | NO | fimbrial protein  |
| VP0947 | NO | AsnC family transcriptional regulator   |
| VP0949 | NO | acyl-CoA thioesterase   |
| VP0950 | NO | lipoprotein-like protein  |
| VP0951 | NO | methylated-DNA-protein-cysteine methyltransferase-like protein  |
| VP0953 | NO | hypothetical protein  |

|        |    |  |
|--------|----|--|
| VP0954 | NO | RNA methyltransferase  |
| VP0955 | NO | ferredoxin   |
| VP0956 | NO | hypothetical protein   |
| VP0958 | NO | inosine monophosphate dehydrogenase-like protein             |
| VP0959 | NO | zinc/cadmium/mercury/lead-transporting ATPase                |
| VP0960 | NO | uridine phosphorylase  |
| VP0962 | NO | hypothetical protein   |
| VP0963 | NO | methyl-accepting chemotaxis protein                          |
| VP0964 | NO | Hit family protein   |
| VP0965 | NO | hypothetical protein   |
| VP0966 | NO | hypothetical protein   |
| VP0967 | NO | hypothetical protein   |
| VP0969 | NO | hypothetical protein   |
| VP0971 | NO | NADH dehydrogenase   |
| VP0973 | NO | ribosomal-protein-serine acetyltransferase                   |
| VP0975 | NO | transcription-repair coupling factor                         |
| VP0976 | NO | hypothetical protein   |
| VP0977 | NO | hypothetical protein   |
| VP0979 | NO | outer membrane-specific lipoprotein transporter subunit LolE |
| VP0980 | NO | hypothetical protein   |
| VP0982 | NO | lipid transporter ATP-binding/permease                       |
| VP0983 | NO | tetraacyldisaccharide 4'-kinase                              |
| VP0984 | NO | 3-deoxy-manno-octulosonate cytidylyltransferase              |
| VP0986 | NO | hypothetical protein   |
| VP0988 | NO | hypothetical protein   |
| VP0990 | NO | hypothetical protein   |
| VP0991 | NO | hypothetical protein   |
| VP0992 | NO | pyruvate formate lyase-activating enzyme 1                   |
| VP0993 | NO | hypothetical protein   |
| VP0994 | NO | formate acetyltransferase                                    |
| VP0995 | NO | hypothetical protein   |
| VP0998 | NO | amino acid ABC transporter ATP-binding protein               |
| VP0999 | NO | amino acid ABC transporter substrate-binding protein         |
| VP1000 | NO | amino acid ABC transporter permease                          |
| VP1003 | NO | exonuclease III  |
| VP1004 | NO | hypothetical protein   |
| VP1005 | NO | primosomal replication protein N"                            |
| VP1006 | NO | hypothetical protein   |
| VP1007 | NO | ATP-dependent DNA helicase DinG                              |
| VP1011 | NO | isocitrate dehydrogenase                                     |
| VP1013 | NO | ATP-dependent Clp protease adaptor protein ClpS              |
| VP1016 | NO | translation initiation factor IF-1                           |
| VP1017 | NO | arginyl-tRNA-protein transferase                             |
| VP1018 | NO | leucyl/phenylalanyl-tRNA--protein transferase                |
| VP1019 | NO | outer membrane protein                                       |
| VP1020 | NO | 3-phosphoshikimate 1-carboxyvinyltransferase                 |
| VP1021 | NO | hypothetical protein   |
| VP1022 | NO | DNA topoisomerase I  |
| VP1025 | NO | beta-ketoadipate enol-lactone hydrolase                      |
| VP1026 | NO | hypothetical protein   |
| VP1027 | NO | hypothetical protein   |
| VP1028 | NO | hypothetical protein   |



|        |    |   |
|--------|----|---|
| VP1030 | NO | LacI family transcription regulator                             |
| VP1031 | NO | chaperone protein TorD  |
| VP1032 | NO | DNA-binding transcriptional regulator TorR                      |
| VP1033 | NO | hypothetical protein  |
| VP1034 | NO | metallothionein SmtA  |
| VP1035 | NO | condesin subunit F  |
| VP1037 | NO | cell division protein MukB                                      |
| VP1038 | NO | hypothetical protein  |
| VP1040 | NO | hypothetical protein  |
| VP1041 | NO | gonadoliberin III-like protein                                  |
| VP1043 | NO | hypothetical protein  |
| VP1044 | NO | hypothetical protein  |
| VP1045 | NO | hypothetical protein  |
| VP1047 | NO | aspartyl-tRNA synthetase  |
| VP1048 | NO | Holliday junction resolvase                                     |
| VP1051 | NO | Holliday junction DNA helicase RuvA                             |
| VP1052 | NO | Holliday junction DNA helicase RuvB                             |
| VP1053 | NO | cytochrome d ubiquinol oxidase subunit I                        |
| VP1054 | NO | cytochrome d ubiquinol oxidase subunit II                       |
| VP1057 | NO | TolQ protein  |
| VP1060 | NO | translocation protein TolB                                      |
| VP1061 | NO | peptidoglycan-associated lipoprotein                            |
| VP1062 | NO | hypothetical protein  |
| VP1063 | NO | quinolinate synthetase  |
| VP1100 | NO | hypothetical protein  |
| VP1101 | NO | transcriptional regulator CysB                                  |
| VP1106 | NO | outer-membrane lipoprotein carrier protein                      |
| VP1107 | NO | recombination factor protein RarA                               |
| VP1112 | NO | adenosylmethionine-8-amino-7-oxononanoate aminotransferase      |
| VP1114 | NO | 8-amino-7-oxononanoate synthase                                 |
| VP1115 | NO | biotin synthesis protein BioC                                   |
| VP1117 | NO | hypothetical protein  |
| VP1119 | NO | transcriptional regulator                                       |
| VP1120 | NO | short chain dehydrogenase                                       |
| VP1121 | NO | hypothetical protein  |
| VP1123 | NO | cyclopropane-fatty-acyl-phospholipid synthase                   |
| VP1125 | NO | hypothetical protein  |
| VP1126 | NO | hypothetical protein  |
| VP1128 | NO | adenylosuccinate lyase  |
| VP1129 | NO | hypothetical protein  |
| VP1130 | NO | tRNA-specific 2-thiouridylase MnmA                              |
| VP1131 | NO | hypothetical protein  |
| VP1133 | NO | DNA-binding protein H-NS  |
| VP1134 | NO | hypothetical protein  |
| VP1135 | NO | hypothetical protein  |
| VP1136 | NO | transcription regulator TxR                                     |
| VP1137 | NO | ATP phosphoribosyltransferase                                   |
| VP1138 | NO | histidinol dehydrogenase  |
| VP1139 | NO | histidinol-phosphate aminotransferase                           |
| VP1140 | NO | imidazole glycerol-phosphate dehydratase/histidinol phosphatase |
| VP1141 | NO | imidazole glycerol phosphate synthase subunit HisH              |
| VP1143 | NO | imidazole glycerol phosphate synthase subunit HisF              |

|        |    |   |
|--------|----|---|
| VP1144 | NO | bifunctional phosphoribosyl-AMP cyclohydrolase/phosphoribosyl-ATP pyrophosphatase protein |
| VP1145 | NO | hypothetical protein  |
| VP1147 | NO | hypothetical protein  |
| VP1148 | NO | UDP-2,3-diacetylglucosamine hydrolase   |
| VP1149 | NO | peptidyl-prolyl cis-trans isomerase B   |
| VP1150 | NO | cysteinyl-tRNA synthetase   |
| VP1151 | NO | thymidine kinase  |
| VP1152 | NO | hypothetical protein  |
| VP1153 | NO | hypothetical protein  |
| VP1156 | NO | DNA-binding protein inhibitor Id-2-like protein   |
| VP1157 | NO | formate transporter I   |
| VP1158 | NO | hypothetical protein  |
| VP1160 | NO | NapE protein  |
| VP1161 | NO | cytochrome c-type protein TorC  |
| VP1162 | NO | trimethylamine-N-oxide reductase  |
| VP1163 | NO | alpha-1,6-galactosidase   |
| VP1164 | NO | hypothetical protein  |
| VP1165 | NO | manganese-dependent inorganic pyrophosphatase   |
| VP1166 | NO | hypothetical protein  |
| VP1167 | NO | peptide ABC transporter ATP-binding protein   |
| VP1168 | NO | peptide ABC transporter ATP-binding protein   |
| VP1170 | NO | peptide ABC transporter permease  |
| VP1171 | NO | peptide ABC transporter periplasmic peptide-binding protein                               |
| VP1172 | NO | psp operon transcriptional activator  |
| VP1173 | NO | phage shock protein A   |
| VP1175 | NO | phage shock protein C   |
| VP1176 | NO | multidrug resistance protein  |
| VP1177 | NO | periplasmic linker protein  |
| VP1179 | NO | DNA-3-methyladenine glycosidase I   |
| VP1181 | NO | lactonizing lipase  |
| VP1182 | NO | cystathionine beta-lyase  |
| VP1183 | NO | cardiolipin synthetase  |
| VP1185 | NO | chemotaxis transducer   |
| VP1186 | NO | pseudouridine synthase  |
| VP1187 | NO | hypothetical protein  |
| VP1188 | NO | ferredoxin oxidoreductase protein   |
| VP1189 | NO | hydroxylamine reductase   |
| VP1190 | NO | anaerobic nitric oxide reductase transcription regulator                                  |
| VP1191 | NO | hypothetical protein  |
| VP1192 | NO | outer membrane lipoprotein Pcp  |
| VP1195 | NO | ABC transporter permease  |
| VP1196 | NO | ABC transporter solute-binding protein  |
| VP1197 | NO | hypothetical protein  |
| VP1200 | NO | thiosulfate sulfurtransferase   |
| VP1203 | NO | heat shock protein HslJ   |
| VP1204 | NO | hypothetical protein  |
| VP1210 | NO | 50S ribosomal protein L25   |
| VP1213 | NO | hypothetical protein  |
| VP1214 | NO | helicase-like protein   |
| VP1215 | NO | ribosomal small subunit pseudouridine synthase A  |
| VP1218 | NO | outer membrane protein  |
| VP1219 | NO | deca-heme c-type cytochrome   |

|        |     |   |
|--------|-----|---|
| VP1221 | NO  | cytochrome subunit of sulfide dehydrogenase         |
| VP1223 | NO  | hypothetical protein                                |
| VP1226 | NO  | hypothetical protein                                |
| VP1227 | NO  | hypothetical protein                                |
| VP1228 | NO  | pH-dependent sodium/proton antiporter               |
| VP1229 | NO  | Na <sup>+</sup> /H <sup>+</sup> -antiporter protein |
| VP1230 | YES | acyl-CoA dehydrogenase                              |
| VP1231 | YES | trans-2-enoyl-CoA reductase                         |
| VP1232 | YES | hypothetical protein                                |
| VP1233 | YES | glutaredoxin  |
| VP1235 | YES | iron-containing alcohol dehydrogenase               |
| VP1236 | YES | DNA-binding transcriptional regulator HexR          |
| VP1237 | YES | glutamate decarboxylase                             |
| VP1238 | NO  | hypothetical protein                                |
| VP1239 | NO  | hypothetical protein                                |
| VP1240 | NO  | hypothetical protein                                |
| VP1241 | NO  | hypothetical protein                                |
| VP1243 | NO  | hypothetical protein                                |
| VP1244 | NO  | response regulator                                  |
| VP1245 | NO  | response regulator                                  |
| VP1247 | NO  | phosphoserine aminotransferase                      |
| VP1251 | NO  | thioredoxin reductase                               |
| VP1253 | NO  | NifS-like protein                                   |
| VP1261 | NO  | hypothetical protein                                |
| VP1265 | NO  | hypothetical protein                                |
| VP1267 | NO  | lipoprotein   |
| VP1274 | NO  | urocanate hydratase                                 |
| VP1276 | NO  | imidazolonepropionase                               |
| VP1280 | NO  | threonyl-tRNA synthetase                            |
| VP1281 | NO  | 50S ribosomal protein L35                           |
| VP1282 | NO  | 50S ribosomal protein L20                           |
| VP1284 | NO  | hypothetical protein                                |
| VP1287 | NO  | hypothetical protein                                |
| VP1290 | NO  | phenylalanyl-tRNA synthetase subunit alpha          |
| VP1293 | NO  | hypothetical protein                                |
| VP1294 | NO  | integration host factor subunit alpha               |
| VP1296 | NO  | thiopurine S-methyltransferase                      |
| VP1297 | NO  | phosphoribosylglycinamide formyltransferase 2       |
| VP1299 | NO  | hypothetical protein                                |
| VP1300 | NO  | hypothetical protein                                |
| VP1302 | NO  | sodium/dicarboxylate symporter                      |
| VP1306 | NO  | adenosylcobinamide kinase                           |
| VP1311 | NO  | vitamin B12-transporter permease                    |
| VP1313 | NO  | hypothetical protein                                |
| VP1315 | NO  | multidrug resistance protein                        |
| VP1316 | NO  | LysR family transcriptional regulator               |
| VP1324 | NO  | SAM-dependent methyltransferase                     |
| VP1327 | NO  | hypothetical protein                                |
| VP1330 | NO  | hydroxyproline-2-epimerase                          |
| VP1331 | NO  | D-amino acid dehydrogenase, small subunit           |
| VP1332 | NO  | binding protein component of ABC transporter        |
| VP1333 | NO  | ornithine cyclodeaminase                            |

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|--------|----|---|
| VP1335 | NO | dihydrodipicolinate synthetase  |
| VP1342 | NO | aminopeptidase  |
| VP1343 | NO | oligopeptide ABC transporter ATP-binding protein                      |
| VP1347 | NO | oligopeptide ABC transporter periplasmic oligopeptide-binding protein |
| VP1348 | NO | M20A family peptidase   |
| VP1350 | NO | oxidoreductase  |
| VP1352 | NO | glutathione S-transferase   |
| VP1354 | NO | hypothetical protein  |
| VP1374 | NO | transporter   |
| VP1377 | NO | hypothetical protein  |
| VP1378 | NO | HD-GYP domain-containing protein                                      |
| VP1379 | NO | homoserine/homoserine lactone efflux protein                          |
| VP1381 | NO | pyruvate formate lyase activating enzyme                              |
| VP1422 | NO | SM-20-like protein  |
| VP1423 | NO | hypothetical protein  |
| VP1426 | NO | tyrosine-specific transport protein                                   |
| VP1427 | NO | hypothetical protein  |
| VP1430 | NO | hypothetical protein  |
| VP1431 | NO | ATP-binding protein of a transport system                             |
| VP1434 | NO | V10 pilin   |
| VP1436 | NO | hypothetical protein  |
| VP1437 | NO | hypothetical protein  |
| VP1438 | NO | molecular chaperone DnaK  |
| VP1442 | NO | hypothetical protein  |
| VP1443 | NO | hypothetical protein  |
| VP1445 | NO | hypothetical protein  |
| VP1447 | NO | anaerobic dimethyl sulfoxide reductase subunit A                      |
| VP1448 | NO | anaerobic dimethyl sulfoxide reductase subunit B                      |
| VP1449 | NO | anaerobic dimethyl sulfoxide reductase subunit C                      |
| VP1450 | NO | component of anaerobic dehydrogenase                                  |
| VP1452 | NO | azoreductase  |
| VP1454 | NO | hypothetical protein  |
| VP1455 | NO | hypothetical protein  |
| VP1457 | NO | hypothetical protein  |
| VP1458 | NO | hypothetical protein  |
| VP1459 | NO | intercellular adhesion protein A                                      |
| VP1460 | NO | hypothetical protein  |
| VP1463 | NO | glycosyltransferase   |
| VP1464 | NO | ExoQ family protein   |
| VP1465 | NO | lipopolysaccharide biosynthesis protein                               |
| VP1469 | NO | LuxO repressor protein  |
| VP1472 | NO | phosphorelay protein  |
| VP1473 | NO | capsular polysaccharide biosynthesis                                  |
| VP1474 | NO | capsule transport protein OtnA  |
| VP1475 | NO | hypothetical protein  |
| VP1476 | NO | anti-sigma F factor antagonist  |
| VP1479 | NO | multidrug efflux protein  |
| VP1481 | NO | hypothetical protein  |
| VP1482 | NO | response regulator  |
| VP1484 | NO | hypothetical protein  |
| VP1485 | NO | lipoprotein NlpC  |
| VP1486 | NO | methyl-accepting chemotaxis protein                                   |

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|--------|----|---|
| VP1494 | NO | N-acetyl-D-glucosamine kinase   |
| VP1495 | NO | hypothetical protein  |
| VP1501 | NO | hypothetical protein  |
| VP1503 | NO | sensor histidine kinase   |
| VP1504 | NO | ABC transporter ATP-binding protein   |
| VP1506 | NO | formate dehydrogenase accessory protein   |
| VP1511 | NO | formate dehydrogenase-specific chaperone  |
| VP1512 | NO | hypothetical protein  |
| VP1513 | NO | formate dehydrogenase large subunit   |
| VP1514 | NO | formate dehydrogenase, iron-sulfur subunit  |
| VP1515 | NO | formate dehydrogenase, cytochrome b556 subunit  |
| VP1524 | NO | NAD-dependent deacetylase   |
| VP1525 | NO | spermidine/putrescine ABC transporter periplasmic spermidine/putrescine-binding protein |
| VP1526 | NO | spermidine/putrescine ABC transporter periplasmic spermidine/putrescine-binding protein |
| VP1527 | NO | spermidine/putrescine ABC transporter membrane protein                                  |
| VP1529 | NO | putrescine/spermidine ABC transporter ATPase protein                                    |
| VP1531 | NO | Bax protein   |
| VP1532 | NO | hypothetical protein  |
| VP1533 | NO | C32 tRNA thiolase   |
| VP1535 | NO | universal stress protein UspE   |
| VP1536 | NO | fumarate/nitrate reduction transcriptional regulator                                    |
| VP1537 | NO | hypothetical protein  |
| VP1538 | NO | FixS-like protein   |
| VP1539 | NO | cation transporter E1-E2 family ATPase  |
| VP1540 | NO | hypothetical protein  |
| VP1541 | NO | cytochrome c oxidase subunit CcoP   |
| VP1542 | NO | cytochrome c oxidase subunit CcoQ   |
| VP1544 | NO | cbb3-type cytochrome c oxidase subunit I  |
| VP1588 | NO | hypothetical protein  |
| VP1593 | NO | ribosome modulation factor  |
| VP1598 | NO | hypothetical protein  |
| VP1599 | NO | hypothetical protein  |
| VP1603 | NO | hypothetical protein  |
| VP1608 | NO | hypothetical protein  |
| VP1609 | NO | ABC transporter ATP-binding protein   |
| VP1611 | NO | hypothetical protein  |
| VP1612 | NO | rRNA (cytosine-C(5)-)-methyltransferase RsmF  |
| VP1613 | NO | hypothetical protein  |
| VP1614 | NO | hypothetical protein  |
| VP1615 | NO | hypothetical protein  |
| VP1616 | NO | phospho-2-dehydro-3-deoxyheptonate aldolase   |
| VP1617 | NO | nucleotide-binding protein  |
| VP1620 | NO | amino acid ABC transporter substrate-binding protein                                    |
| VP1621 | NO | amino acid ABC transporter permease   |
| VP1622 | NO | amino acid ABC transporter permease   |
| VP1625 | NO | hypothetical protein  |
| VP1626 | NO | sulfite reductase, gamma subunit-like protein   |
| VP1627 | NO | acylphosphatase   |
| VP1629 | NO | SAM-dependent methyltransferase   |
| VP1656 | NO | translocator protein PopD   |
| VP1658 | NO | low calcium response locus protein H  |
| VP1662 | NO | low calcium response protein  |

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|--------|-----|--|
| VP1665 | YES | type III secretion protein                         |
| VP1669 | YES | type III secretion protein YscO                    |
| VP1672 | YES | type III secretion system protein                  |
| VP1673 | YES | translocation protein in type III secretion        |
| VP1674 | YES | translocation protein in type III secretion        |
| VP1683 | YES | hypothetical protein                               |
| VP1684 | YES | hypothetical protein                               |
| VP1687 | YES | type III chaperone                                 |
| VP1690 | YES | type III secretion lipoprotein                     |
| VP1691 | YES | type III export protein                            |
| VP1693 | YES | type III secretion protein                         |
| VP1694 | YES | type III export protein YscF                       |
| VP1695 | YES | type III export protein PscD                       |
| VP1696 | YES | type III secretion protein YscC                    |
| VP1698 | NO  | hypothetical protein                               |
| VP1699 | NO  | transcriptional regulator ExsA                     |
| VP1702 | NO  | hypothetical protein                               |
| VP1705 | NO  | hypothetical protein                               |
| VP1706 | NO  | hypothetical protein                               |
| VP1708 | NO  | 6-phosphogluconate dehydrogenase                   |
| VP1709 | NO  | 6-phosphogluconolactonase                          |
| VP1710 | NO  | glucose-6-phosphate 1-dehydrogenase                |
| VP1711 | NO  | response regulator                                 |
| VP1712 | NO  | sensor kinase CitA                                 |
| VP1713 | NO  | hypothetical protein                               |
| VP1717 | NO  | hypothetical protein                               |
| VP1719 | NO  | aspartate kinase                                   |
| VP1720 | NO  | L-ectoine synthase                                 |
| VP1724 | NO  | DNA polymerase III subunit epsilon                 |
| VP1725 | NO  | hypothetical protein                               |
| VP1729 | NO  | thermostable hemolysin delta-VPH                   |
| VP1730 | NO  | long-chain-fatty-acid-CoA ligase                   |
| VP1731 | NO  | hypothetical protein                               |
| VP1732 | NO  | short chain dehydrogenase                          |
| VP1733 | NO  | hypothetical protein                               |
| VP1736 | NO  | hypothetical protein                               |
| VP1737 | NO  | hypothetical protein                               |
| VP1738 | NO  | hypothetical protein                               |
| VP1740 | NO  | hypothetical protein                               |
| VP1741 | NO  | sodium/alanine symporter                           |
| VP1743 | NO  | hypothetical protein                               |
| VP1745 | NO  | lipid A biosynthesis lauroyl acyltransferase       |
| VP1751 | NO  | homoserine O-succinyltransferase                   |
| VP1752 | NO  | fimbrial biogenesis and twitching motility protein |
| VP1753 | NO  | alkylphosphonate ABC transporter                   |
| VP1757 | NO  | hypothetical protein                               |
| VP1758 | NO  | galactoside O-acetyltransferase                    |
| VP1760 | NO  | adenylate cyclase                                  |
| VP1763 | NO  | MarR family transcriptional regulator              |
| VP1764 | NO  | transmembrane protein                              |
| VP1768 | NO  | hypothetical protein                               |
| VP1866 | NO  | hypothetical protein                               |

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|--------|----|--|
| VP1868 | NO | ribosomal-protein-alanine acetyltransferase                        |
| VP1869 | NO | transcriptional regulator TyrR                                     |
| VP1871 | NO | hypothetical protein   |
| VP1872 | NO | hypothetical protein   |
| VP1873 | NO | fumarate hydratase, class I  |
| VP1876 | NO | hypothetical protein   |
| VP1877 | NO | guanylate cyclase-like protein                                     |
| VP1878 | NO | MutT/nudix family protein  |
| VP1879 | NO | serine transporter   |
| VP1880 | NO | L-serine dehydratase 1   |
| VP1881 | NO | hypothetical protein   |
| VP1882 | NO | hypothetical protein   |
| VP1892 | NO | methyl-accepting chemotaxis protein                                |
| VP1893 | NO | asparaginyl-tRNA synthetase  |
| VP1897 | NO | hypothetical protein   |
| VP1900 | NO | aromatic amino acid aminotransferase                               |
| VP1901 | NO | outer membrane protein Ail and OmpX                                |
| VP1903 | NO | DNA polymerase III subunit epsilon                                 |
| VP1904 | NO | methyl-accepting chemotaxis protein                                |
| VP1905 | NO | BCCT family transporter  |
| VP1906 | NO | MarR family transcriptional regulator                              |
| VP1908 | NO | sensor histidine kinase  |
| VP1909 | NO | hypothetical protein   |
| VP1911 | NO | ABC transporter substrate-binding protein                          |
| VP1913 | NO | hypothetical protein   |
| VP1914 | NO | glyoxylase   |
| VP1915 | NO | hypothetical protein   |
| VP1916 | NO | amidase  |
| VP1919 | NO | hypothetical protein   |
| VP1921 | NO | GTP cyclohydrolase II  |
| VP1922 | NO | hypothetical protein   |
| VP1926 | NO | formate dependent nitrate reductase NrfD                           |
| VP1927 | NO | nitrite reductase Fe-S protein NrfC                                |
| VP1928 | NO | cytochrome c nitrite reductase pentaheme subunit                   |
| VP1929 | NO | cytochrome c552  |
| VP1931 | NO | YfrE protein   |
| VP1933 | NO | 3-demethylubiquinone-9 3-methyltransferase                         |
| VP1934 | NO | ribonucleotide-diphosphate reductase subunit alpha                 |
| VP1935 | NO | ribonucleotide-diphosphate reductase subunit beta                  |
| VP1936 | NO | iron-sulfur cluster-binding protein                                |
| VP1939 | NO | hypothetical protein   |
| VP1940 | NO | carboxynorspermidine decarboxylase                                 |
| VP1943 | NO | CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase |
| VP1944 | NO | excinuclease ABC subunit C   |
| VP1947 | NO | hypothetical protein   |
| VP1948 | NO | elongation factor P  |
| VP1949 | NO | dsDNA-mimic protein  |
| VP1951 | NO | pseudouridine synthase   |
| VP1952 | NO | hypothetical protein   |
| VP1953 | NO | translation factor   |
| VP1954 | NO | metal-dependent phosphoesterase YciV                               |
| VP1955 | NO | Trp operon leader peptide  |

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|--------|-----|--|
| VP1956 | NO  | anthranilate synthase component I  |
| VP1957 | NO  | anthranilate synthase component II   |
| VP1958 | NO  | anthranilate phosphoribosyltransferase   |
| VP1959 | NO  | bifunctional indole-3-glycerol phosphate synthase/phosphoribosylanthranilate isomerase |
| VP1960 | NO  | tryptophan synthase subunit beta   |
| VP1961 | NO  | tryptophan synthase subunit alpha  |
| VP1962 | NO  | transcriptional regulator  |
| VP1969 | NO  | hypothetical protein   |
| VP1970 | NO  | intracellular septation protein A  |
| VP1971 | NO  | acyl-CoA hydrolase   |
| VP1978 | NO  | hypothetical protein   |
| VP1982 | NO  | hypothetical protein   |
| VP1983 | NO  | two-component response regulator   |
| VP1987 | NO  | hypothetical protein   |
| VP1988 | NO  | LysR family transcriptional regulator  |
| VP1989 | NO  | secretion protein  |
| VP1991 | NO  | 5-methyltetrahydropteroyltriglutamate-- homocysteine S-methyltransferase               |
| VP1992 | NO  | hypothetical protein   |
| VP1996 | NO  | hypothetical protein   |
| VP1997 | NO  | hypothetical protein   |
| VP1998 | NO  | outer membrane protein TolC  |
| VP2006 | NO  | suppressor for copper-sensitivity B  |
| VP2009 | NO  | tetrathionate reductase complex: response regulator                                    |
| VP2011 | NO  | tetrathionate reductase subunit B  |
| VP2013 | NO  | tetrathionate reductase complex subunit C  |
| VP2014 | NO  | tetrathionate reductase subunit A  |
| VP2015 | NO  | cytochrome c   |
| VP2018 | NO  | paraquat-inducible protein B   |
| VP2019 | NO  | hypothetical protein   |
| VP2020 | NO  | hypothetical protein   |
| VP2021 | NO  | hypothetical protein   |
| VP2022 | NO  | glycosyl transferase family protein  |
| VP2026 | NO  | orotidine 5'-phosphate decarboxylase   |
| VP2027 | NO  | tetratricopeptide repeat protein   |
| VP2028 | NO  | hypothetical protein   |
| VP2029 | NO  | integration host factor subunit beta   |
| VP2031 | NO  | cytidylate kinase  |
| VP2032 | NO  | periplasmic protease   |
| VP2033 | YES | short chain dehydrogenase  |
| VP2034 | YES | hypothetical protein   |
| VP2035 | YES | hypothetical protein   |
| VP2036 | YES | DNA polymerase III alpha chain   |
| VP2037 | YES | chemotaxis protein CheV  |
| VP2038 | YES | ROK family transcriptional regulator   |
| VP2039 | YES | pyruvate kinase II   |
| VP2044 | NO  | hypothetical protein   |
| VP2048 | NO  | DNA polymerase III subunit delta'  |
| VP2049 | NO  | thymidylate kinase   |
| VP2050 | NO  | hypothetical protein   |
| VP2051 | NO  | 4-amino-4-deoxychorismate lyase  |
| VP2052 | NO  | 3-oxoacyl-ACP synthase   |
| VP2053 | NO  | acyl carrier protein   |



|        |    |   |
|--------|----|---|
| VP2054 | NO | 3-ketoacyl-ACP reductase  |
| VP2055 | NO | ACP S-malonyltransferase  |
| VP2056 | NO | 3-oxoacyl-ACP synthase  |
| VP2057 | NO | glycerol-3-phosphate acyltransferase PlsX                             |
| VP2058 | NO | 50S ribosomal protein L32   |
| VP2059 | NO | hypothetical protein  |
| VP2061 | NO | 23S rRNA ribosomal pseudouridine synthase                             |
| VP2063 | NO | sulfate permease  |
| VP2064 | NO | phosphotyrosine protein phosphatase                                   |
| VP2065 | NO | cob(D)yrinic acid a,c-diamide adenosyltransferase                     |
| VP2066 | NO | AsmA protein  |
| VP2068 | NO | Mrp protein   |
| VP2069 | NO | methionyl-tRNA synthetase   |
| VP2071 | NO | fatty acid metabolism regulator                                       |
| VP2072 | NO | sodium/proton antiporter  |
| VP2074 | NO | preprotein translocase SecA subunit-like protein                      |
| VP2078 | NO | ABC transporter ATP-binding protein                                   |
| VP2079 | NO | ABC transporter permease  |
| VP2080 | NO | ABC transporter substrate-binding protein                             |
| VP2081 | NO | hypothetical protein  |
| VP2082 | NO | acetate kinase  |
| VP2083 | NO | phosphate acetyltransferase   |
| VP2084 | NO | hypothetical protein  |
| VP2086 | NO | glutathione S-transferase   |
| VP2087 | NO | oligopeptide ABC transporter ATP-binding protein                      |
| VP2089 | NO | oligopeptide ABC transporter permease                                 |
| VP2090 | NO | oligopeptide transporter permease                                     |
| VP2091 | NO | oligopeptide ABC transporter periplasmic oligopeptide-binding protein |
| VP2092 | NO | molybdenum cofactor biosynthesis protein E                            |
| VP2093 | NO | molybdopterin synthase small subunit                                  |
| VP2094 | NO | molybdenum cofactor biosynthesis protein MoaC                         |
| VP2095 | NO | molybdenum cofactor biosynthesis protein B                            |
| VP2096 | NO | molybdenum cofactor biosynthesis protein A                            |
| VP2097 | NO | hypothetical protein  |
| VP2100 | NO | excinuclease ABC subunit B  |
| VP2102 | NO | Na(+)-translocating NADH-quinone reductase subunit E                  |
| VP2103 | NO | electron transport complex protein RnfB                               |
| VP2105 | NO | electron transport complex protein RnfD                               |
| VP2106 | NO | electron transport complex protein RnfG                               |
| VP2109 | NO | lactoylglutathione lyase  |
| VP2110 | NO | hypothetical protein  |
| VP2111 | NO | sodium-type flagellar protein MotY                                    |
| VP2112 | NO | MotY protein  |
| VP2113 | NO | hypothetical protein  |
| VP2114 | NO | ribonuclease T  |
| VP2115 | NO | hypothetical protein  |
| VP2116 | NO | hypothetical protein  |
| VP2117 | NO | glutaredoxin protein  |
| VP2118 | NO | manganese superoxide dismutase Mn-SOD                                 |
| VP2119 | NO | hypothetical protein  |
| VP2120 | NO | short chain dehydrogenase   |
| VP2121 | NO | bifunctional acetaldehyde-CoA/alcohol dehydrogenase                   |

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|--------|----|--|
| VP2122 | NO | hypothetical protein   |
| VP2123 | NO | potassium channel  |
| VP2124 | NO | aspartate-semialdehyde dehydrogenase                             |
| VP2125 | NO | Na <sup>+</sup> /H <sup>+</sup> antiporter                       |
| VP2126 | NO | hypothetical protein   |
| VP2127 | NO | hypothetical protein   |
| VP2128 | NO | nucleoid-associated protein NdpA                                 |
| VP2129 | NO | hypothetical protein   |
| VP2130 | NO | hypothetical protein   |
| VP2147 | NO | hypothetical protein   |
| VP2149 | NO | DNA topoisomerase III  |
| VP2151 | NO | 2,4-dienoyl-CoA reductase  |
| VP2152 | NO | protease IV  |
| VP2153 | NO | cytoplasmic asparaginase I                                       |
| VP2154 | NO | hypothetical protein   |
| VP2156 | NO | methionine sulfoxide reductase B                                 |
| VP2157 | NO | glyceraldehyde-3-phosphate dehydrogenase                         |
| VP2158 | NO | hypothetical protein   |
| VP2161 | NO | hypothetical protein   |
| VP2162 | NO | hypothetical protein   |
| VP2163 | NO | alkaline phosphatase   |
| VP2165 | NO | hypothetical protein   |
| VP2166 | NO | lactoylglutathione lyase   |
| VP2167 | NO | hypothetical protein   |
| VP2168 | NO | hypothetical protein   |
| VP2170 | NO | transglycosylase associated gene                                 |
| VP2171 | NO | proteinase inhibitor   |
| VP2173 | NO | hypothetical protein   |
| VP2176 | NO | aquaporin Z  |
| VP2177 | NO | recombination protein RecR                                       |
| VP2178 | NO | hypothetical protein   |
| VP2180 | NO | adenine phosphoribosyltransferase                                |
| VP2181 | NO | hypothetical protein   |
| VP2182 | NO | hypothetical protein   |
| VP2184 | NO | LysR family transcriptional regulator                            |
| VP2185 | NO | amidophosphoribosyltransferase                                   |
| VP2186 | NO | bacteriocin production protein                                   |
| VP2189 | NO | acetyl-CoA carboxylase subunit beta                              |
| VP2190 | NO | tRNA pseudouridine synthase A                                    |
| VP2192 | NO | aspartate-semialdehyde dehydrogenase                             |
| VP2193 | NO | erythronate-4-phosphate dehydrogenase                            |
| VP2194 | NO | 3-oxoacyl-ACP synthase   |
| VP2195 | NO | 5-methylaminomethyl-2-thiouridine methyltransferase              |
| VP2197 | NO | hypothetical protein   |
| VP2198 | NO | hypothetical protein   |
| VP2200 | NO | hypothetical protein   |
| VP2201 | NO | hypothetical protein   |
| VP2203 | NO | N5-glutamine S-adenosyl-L-methionine-dependent methyltransferase |
| VP2204 | NO | hypothetical protein   |
| VP2207 | NO | CG2 omega domain-containing protein                              |
| VP2208 | NO | multifunctional fatty acid oxidation complex subunit alpha       |
| VP2209 | NO | 3-ketoacyl-CoA thiolase  |

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|--------|----|---|
| VP2211 | NO | hypothetical protein                              |
| VP2214 | NO | VacJ lipoprotein                                  |
| VP2215 | NO | cytochrome c-type biogenesis protein              |
| VP2216 | NO | cytochrome c-type biogenesis protein              |
| VP2217 | NO | thiol:disulfide interchange protein DsbE          |
| VP2219 | NO | cytochrome c-type biogenesis protein CcmE         |
| VP2220 | NO | heme exporter protein D                           |
| VP2222 | NO | heme exporter protein B                           |
| VP2223 | NO | cytochrome c biogenesis protein CcmA              |
| VP2224 | NO | hypothetical protein                              |
| VP2225 | NO | chemotaxis protein CheW                           |
| VP2230 | NO | chemotaxis protein CheZ                           |
| VP2231 | NO | chemotaxis protein CheY                           |
| VP2233 | NO | flagellar biosynthesis protein FlhG               |
| VP2234 | NO | flagellar biosynthesis regulator FlhF             |
| VP2235 | NO | flagellar biosynthesis protein FlhA               |
| VP2236 | NO | flagellar biosynthesis protein FlhB               |
| VP2237 | NO | flagellar biosynthesis protein FliR               |
| VP2238 | NO | flagellar biosynthesis protein FliQ               |
| VP2239 | NO | flagellar biosynthesis protein FliP               |
| VP2241 | NO | flagellar motor switch protein                    |
| VP2242 | NO | flagellar motor switch protein FliM               |
| VP2243 | NO | flagellar basal body protein FliL                 |
| VP2245 | NO | flagellar biosynthesis chaperone                  |
| VP2250 | NO | flagellar hook-basal body protein FliE            |
| VP2255 | NO | polar flagellar rod protein FlaI                  |
| VP2257 | NO | flagellar protein FlaG                            |
| VP2261 | NO | flagellin   |
| VP2262 | NO | TyrA protein                                      |
| VP2263 | NO | hypothetical protein                              |
| VP2264 | NO | hypothetical protein                              |
| VP2265 | NO | outer membrane lipoprotein                        |
| VP2266 | NO | hypothetical protein                              |
| VP2269 | NO | succinyl-diaminopimelate desuccinylase            |
| VP2270 | NO | D,D-carboxypeptidase-like protein                 |
| VP2271 | NO | hypothetical protein                              |
| VP2272 | NO | lipoprotein                                       |
| VP2273 | NO | dihydrodipicolinate synthase                      |
| VP2274 | NO | glycine cleavage system transcriptional repressor |
| VP2276 | NO | permease PerM                                     |
| VP2277 | NO | hypothetical protein                              |
| VP2278 | NO | hypothetical protein                              |
| VP2279 | NO | arsenate reductase                                |
| VP2280 | NO | Trp repressor-binding protein                     |
| VP2281 | NO | hypothetical protein                              |
| VP2283 | NO | uracil permease                                   |
| VP2284 | NO | uracil phosphoribosyltransferase                  |
| VP2285 | NO | phosphoribosylaminoimidazole synthetase           |
| VP2286 | NO | phosphoribosylglycinamide formyltransferase       |
| VP2287 | NO | amidotransferase                                  |
| VP2288 | NO | phosphoheptose isomerase                          |
| VP2289 | NO | acyl-CoA dehydrogenase                            |

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| VP2290 | NO | sulfate permease   |
| VP2292 | NO | DNA polymerase III subunit epsilon                         |
| VP2293 | NO | ribonuclease H   |
| VP2295 | NO | hydroxyacylglutathione hydrolase GloB                      |
| VP2296 | NO | membrane-bound lytic murein transglycosylase D             |
| VP2297 | NO | hypothetical protein                                       |
| VP2298 | NO | hypothetical protein                                       |
| VP2299 | NO | nitrogen regulatory protein P-II                           |
| VP2300 | NO | cytochrome c554  |
| VP2301 | NO | cell cycle protein MesJ                                    |
| VP2302 | NO | acetyl-CoA carboxylase carboxyltransferase subunit alpha   |
| VP2303 | NO | DNA polymerase III subunit alpha                           |
| VP2304 | NO | ribonuclease HII   |
| VP2305 | NO | lipid-A-disaccharide synthase                              |
| VP2306 | NO | UDP-N-acetylglucosamine acyltransferase                    |
| VP2307 | NO | (3R)-hydroxymyristoyl-ACP dehydratase                      |
| VP2308 | NO | UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase |
| VP2310 | NO | outer membrane protein assembly factor YaeT                |
| VP2311 | NO | membrane-associated Zn-dependent protease                  |
| VP2312 | NO | 1-deoxy-D-xylulose 5-phosphate reductoisomerase            |
| VP2313 | NO | phosphatidate cytidyltransferase                           |
| VP2314 | NO | undecaprenyl diphosphate synthase                          |
| VP2315 | NO | ribosome recycling factor                                  |
| VP2316 | NO | uridylate kinase   |
| VP2317 | NO | elongation factor Ts                                       |
| VP2318 | NO | 30S ribosomal protein S2                                   |
| VP2319 | NO | methionine aminopeptidase                                  |
| VP2320 | NO | PII uridylyl-transferase                                   |
| VP2321 | NO | hypothetical protein                                       |
| VP2322 | NO | tRNA pseudouridine synthase C                              |
| VP2323 | NO | hypothetical protein                                       |
| VP2326 | NO | acetyltransferase-like protein                             |
| VP2327 | NO | hypothetical protein                                       |
| VP2328 | NO | hypothetical protein                                       |
| VP2331 | NO | 50S ribosomal protein L31                                  |
| VP2332 | NO | hypothetical protein                                       |
| VP2333 | NO | prolyl-tRNA synthetase                                     |
| VP2335 | NO | hypothetical protein                                       |
| VP2336 | NO | hypothetical protein                                       |
| VP2338 | NO | chitinase  |
| VP2339 | NO | hypothetical protein                                       |
| VP2340 | NO | ATP-dependent DNA helicase RecQ                            |
| VP2343 | NO | hypothetical protein                                       |
| VP2344 | NO | hypothetical protein                                       |
| VP2345 | NO | thiamin biosynthesis lipoprotein ApbE                      |
| VP2346 | NO | Na(+)-translocating NADH-quinone reductase subunit F       |
| VP2347 | NO | Na(+)-translocating NADH-quinone reductase subunit E       |
| VP2348 | NO | Na(+)-translocating NADH-quinone reductase subunit D       |
| VP2350 | NO | Na(+)-translocating NADH-quinone reductase subunit B       |
| VP2351 | NO | Na(+)-translocating NADH-quinone reductase subunit A       |
| VP2352 | NO | cell division protein BolA                                 |
| VP2353 | NO | methyltransferase  |

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| VP2354 | NO | lipoprotein  |
| VP2355 | NO | peptidyl-prolyl cis-trans isomerase A                                      |
| VP2356 | NO | AmpG protein   |
| VP2357 | NO | transcriptional activator ChrR   |
| VP2358 | NO | RNA polymerase sigma factor  |
| VP2365 | NO | class V aminotransferase   |
| VP2367 | NO | hypothetical protein   |
| VP2368 | NO | HesA/MoeB/ThiF family protein  |
| VP2369 | NO | murein transglycosylase A  |
| VP2370 | NO | hypothetical protein   |
| VP2371 | NO | N-acetylglutamate synthase   |
| VP2372 | NO | hypothetical protein   |
| VP2373 | NO | exodeoxyribonuclease V   |
| VP2375 | NO | exonuclease V subunit gamma  |
| VP2377 | NO | hypothetical protein   |
| VP2379 | NO | DNA damage-inducible gene in SOS regulon, dependent on cyclic AMP and H-NS |
| VP2380 | NO | 2,3,4,5-tetrahydropyridine-2,6-carboxylate N-succinyltransferase           |
| VP2381 | NO | glycerophosphodiester phosphodiesterase                                    |
| VP2386 | NO | glycerol kinase  |
| VP2387 | NO | DeoR family transcriptional regulator                                      |
| VP2388 | NO | glycerol-3-phosphate dehydrogenase   |
| VP2392 | NO | hypothetical protein   |
| VP2404 | NO | cryptic beta-D-galactosidase subunit beta                                  |
| VP2406 | NO | LysR family transcriptional regulator                                      |
| VP2407 | NO | chromate resistance protein-like protein                                   |
| VP2431 | NO | phosphoserine phosphatase  |
| VP2432 | NO | smp protein  |
| VP2433 | NO | purine nucleoside phosphorylase  |
| VP2436 | NO | deoxyribose-phosphate aldolase   |
| VP2440 | NO | peptide chain release factor 3   |
| VP2442 | NO | DNA polymerase III subunit psi   |
| VP2448 | NO | protease   |
| VP2451 | NO | lipoprotein NlpI   |
| VP2458 | NO | hypothetical protein   |
| VP2465 | NO | RNA-binding protein  |
| VP2468 | NO | D-alanyl-D-alanine carboxypeptidase/endopeptidase                          |
| VP2470 | NO | tyrosyl-tRNA synthetase  |
| VP2471 | NO | hypothetical protein   |
| VP2474 | NO | iron-sulfur cluster insertion protein ErpA                                 |
| VP2475 | NO | glutamate-1-semialdehyde aminotransferase                                  |
| VP2476 | NO | permease   |
| VP2477 | NO | 16S rRNA m2G 1207 methyltransferase  |
| VP2478 | NO | sensory box sensor histidine kinase/response regulator                     |
| VP2479 | NO | peptide ABC transporter periplasmic peptide-binding protein                |
| VP2480 | NO | peptide ABC transporter permease   |
| VP2482 | NO | peptide ABC transporter ATP-binding protein                                |
| VP2483 | NO | peptide ABC transporter ATP-binding protein                                |
| VP2485 | NO | N-acetylglucosamine kinase   |
| VP2486 | NO | beta-N-hexosaminidase  |
| VP2487 | NO | N,N'-diacetylchitobiose phosphorylase                                      |
| VP2489 | NO | iron(III) ABC transporter ATP-binding protein                              |
| VP2490 | NO | iron(III) ABC transporter permease   |

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| VP2491 | NO | iron(III) ABC transporter periplasmic iron-compound-binding protein  |
| VP2492 | NO | ammonium transporter   |
| VP2493 | NO | nitrogen regulatory protein P-II                                     |
| VP2494 | NO | hypothetical protein   |
| VP2500 | NO | DnaK suppressor protein  |
| VP2501 | NO | hypothetical protein   |
| VP2502 | NO | glutamyl-Q tRNA(Asp) synthetase                                      |
| VP2505 | NO | 2-amino-4-hydroxy-6- hydroxymethyldihydropteridine pyrophosphokinase |
| VP2506 | NO | 3-methyl-2-oxobutanoate hydroxymethyltransferase                     |
| VP2507 | NO | pantoate--beta-alanine ligase  |
| VP2510 | NO | permease   |
| VP2514 | NO | carbonic anhydrase   |
| VP2515 | NO | hypoxanthine-guanine phosphoribosyltransferase                       |
| VP2516 | NO | OpaR protein   |
| VP2517 | NO | dihydrolipoamide dehydrogenase                                       |
| VP2519 | NO | pyruvate dehydrogenase subunit E1                                    |
| VP2521 | NO | N-acetyl-anhydromuranmyl-L-alanine amidase                           |
| VP2525 | NO | type IV pilin biogenesis protein PilC                                |
| VP2526 | NO | type IV prepilin-like proteins leader peptide processing enzyme      |
| VP2527 | NO | dephospho-CoA kinase   |
| VP2528 | NO | hypothetical protein   |
| VP2530 | NO | 50S ribosomal protein L19  |
| VP2531 | NO | tRNA (guanine-N(1)-)-methyltransferase                               |
| VP2532 | NO | 16S rRNA-processing protein RimM                                     |
| VP2533 | NO | 30S ribosomal protein S16  |
| VP2534 | NO | signal recognition particle protein                                  |
| VP2535 | NO | hypothetical protein   |
| VP2536 | NO | hemolysin  |
| VP2537 | NO | S-ribosylhomocysteinase  |
| VP2538 | NO | hypothetical protein   |
| VP2539 | NO | glutamate--cysteine ligase   |
| VP2540 | NO | insulinase family protease   |
| VP2542 | NO | quinone oxidoreductase   |
| VP2545 | NO | oxaloacetate decarboxylase subunit gamma                             |
| VP2546 | NO | carbon storage regulator   |
| VP2547 | NO | aspartate kinase   |
| VP2548 | NO | alanyl-tRNA synthetase   |
| VP2549 | NO | recombination regulator RecX   |
| VP2551 | NO | CinA-like protein  |
| VP2555 | NO | protein-L-isoaspartate O-methyltransferase                           |
| VP2556 | NO | stationary phase survival protein SurE                               |
| VP2557 | NO | tRNA pseudouridine synthase D  |
| VP2558 | NO | 2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase                |
| VP2559 | NO | 2-C-methyl-D-erythritol 4-phosphate cytidyltransferase               |
| VP2560 | NO | cell division protein FtsB   |
| VP2562 | NO | CTP synthetase   |
| VP2566 | NO | 23S rRNA 5-methyluridine methyltransferase                           |
| VP2568 | NO | 4'-phosphopantetheinyl transferase                                   |
| VP2569 | NO | pyridoxine 5'-phosphate synthase                                     |
| VP2571 | NO | GTP-binding protein Era  |
| VP2573 | NO | signal peptidase I   |
| VP2574 | NO | GTP-binding protein LepA   |

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| VP2575 | NO | sigma-E factor regulatory protein RseC                 |
| VP2576 | NO | periplasmic negative regulator of sigmaE               |
| VP2577 | NO | sigma-E factor negative regulatory protein RseA        |
| VP2578 | NO | RNA polymerase sigma factor RpoE                       |
| VP2579 | NO | hypothetical protein                                   |
| VP2580 | NO | L-aspartate oxidase                                    |
| VP2581 | NO | hypothetical protein                                   |
| VP2583 | NO | hypothetical protein                                   |
| VP2585 | NO | hypothetical protein                                   |
| VP2586 | NO | 2-octaprenyl-6-methoxyphenol hydroxylase               |
| VP2587 | NO | 2-octaprenyl-6-methoxyphenyl hydroxylase               |
| VP2588 | NO | hypothetical protein                                   |
| VP2590 | NO | hypothetical protein                                   |
| VP2592 | NO | ribose-5-phosphate isomerase A                         |
| VP2593 | NO | D-3-phosphoglycerate dehydrogenase                     |
| VP2594 | NO | hypothetical protein                                   |
| VP2596 | NO | LysE/YggA family protein                               |
| VP2598 | NO | hypothetical protein                                   |
| VP2599 | NO | fructose-bisphosphate aldolase                         |
| VP2600 | NO | phosphoglycerate kinase                                |
| VP2601 | NO | erythrose 4-phosphate dehydrogenase                    |
| VP2602 | NO | enterobactin receptor protein                          |
| VP2603 | NO | iron-regulated virulence regulatory protein            |
| VP2606 | NO | S-adenosylmethionine synthetase                        |
| VP2607 | NO | cytochrome c oxidase subunit I                         |
| VP2608 | NO | hypothetical protein                                   |
| VP2612 | NO | hypothetical protein                                   |
| VP2613 | NO | Holliday junction resolvase-like protein               |
| VP2616 | NO | FkuA protein   |
| VP2618 | NO | FkuB protein   |
| VP2619 | NO | hypothetical protein                                   |
| VP2620 | NO | hypothetical protein                                   |
| VP2621 | NO | deoxyribonucleotide triphosphate pyrophosphatase       |
| VP2623 | NO | glutaminase  |
| VP2625 | NO | tRNA (guanine-N(7)-)-methyltransferase                 |
| VP2627 | NO | hypothetical protein                                   |
| VP2628 | NO | membrane-bound lytic murein transglycosylase C         |
| VP2631 | NO | HD-GYP domain-containing protein                       |
| VP2637 | NO | PTS system cellobiose-specific transporter subunit IIB |
| VP2647 | NO | hypothetical protein                                   |
| VP2648 | NO | acetyltransferase                                      |
| VP2654 | NO | aspartate carbamoyltransferase                         |
| VP2655 | NO | aspartate carbamoyltransferase                         |
| VP2656 | NO | hypothetical protein                                   |
| VP2659 | NO | BolA/YrbA family protein                               |
| VP2661 | NO | hypothetical protein                                   |
| VP2671 | NO | sigma-54 modulation protein                            |
| VP2673 | NO | hypothetical protein                                   |
| VP2676 | NO | peptidase PmbA   |
| VP2677 | NO | hypothetical protein                                   |
| VP2679 | NO | ribosomal large subunit pseudouridine synthase A       |
| VP2683 | NO | hypothetical protein                                   |

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|--------|----|---|
| VP2684 | NO | TldD protein  |
| VP2685 | NO | carbon-nitrogen hydrolase                                       |
| VP2702 | NO | MSHA biogenesis protein MshN                                    |
| VP2706 | NO | MSHA biogenesis protein MshJ                                    |
| VP2710 | NO | LuxR family transcriptional regulator                           |
| VP2711 | NO | UTP-glucose-1-phosphate uridylyltransferase                     |
| VP2721 | NO | sulfite reductase subunit beta                                  |
| VP2722 | NO | sulfite reductase (NADPH) flavoprotein subunit alpha            |
| VP2723 | NO | hypothetical protein  |
| VP2724 | NO | hypothetical protein  |
| VP2725 | NO | phage shock protein G   |
| VP2729 | NO | zinc uptake regulation protein                                  |
| VP2730 | NO | hypothetical protein  |
| VP2731 | NO | glucose-6-phosphate isomerase                                   |
| VP2735 | NO | replicative DNA helicase  |
| VP2736 | NO | hypothetical protein  |
| VP2737 | NO | 50S ribosomal protein L9  |
| VP2738 | NO | 30S ribosomal protein S18                                       |
| VP2739 | NO | primosomal replication protein N                                |
| VP2740 | NO | 30S ribosomal protein S6  |
| VP2741 | NO | ribulose-phosphate 3-epimerase                                  |
| VP2744 | NO | 3-dehydroquinase synthase                                       |
| VP2745 | NO | shikimate kinase I  |
| VP2748 | NO | fimbrial assembly protein PilO                                  |
| VP2750 | NO | fimbrial assembly protein PilM                                  |
| VP2751 | NO | penicillin-binding protein 1A                                   |
| VP2752 | NO | DNA-binding transcriptional regulator OxyR                      |
| VP2753 | NO | peroxiredoxin family protein/glutaredoxin                       |
| VP2755 | NO | hypothetical protein  |
| VP2756 | NO | bifunctional argininosuccinate lyase/N-acetylglutamate synthase |
| VP2757 | NO | argininosuccinate synthase                                      |
| VP2758 | NO | acetylglutamate kinase  |
| VP2760 | NO | acetylornithine deacetylase                                     |
| VP2761 | NO | phosphoenolpyruvate carboxylase                                 |
| VP2762 | NO | hypothetical protein  |
| VP2763 | NO | 5,10-methylenetetrahydrofolate reductase                        |
| VP2764 | NO | bifunctional aspartate kinase II/homoserine dehydrogenase II    |
| VP2765 | NO | cystathionine gamma-synthase                                    |
| VP2766 | NO | transcriptional repressor protein MetJ                          |
| VP2767 | NO | malate oxidoreductase   |
| VP2768 | NO | bacterioferritin  |
| VP2769 | NO | bacterioferritin-associated ferredoxin                          |
| VP2772 | NO | 30S ribosomal protein S7  |
| VP2775 | NO | oxidation of intracellular sulfur                               |
| VP2776 | NO | sulfur transfer complex subunit TusD                            |
| VP2777 | NO | hypothetical protein  |
| VP2778 | NO | FKBP-type peptidylprolyl isomerase                              |
| VP2779 | NO | hypothetical protein  |
| VP2780 | NO | hypothetical protein  |
| VP2781 | NO | asparaginase  |
| VP2783 | NO | FKBP-type peptidylprolyl isomerase                              |
| VP2784 | NO | hypothetical protein  |



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|--------|----|--|
| VP2787 | NO | hypothetical protein   |
| VP2788 | NO | ABC transporter ATP-binding protein  |
| VP2789 | NO | hypothetical protein   |
| VP2790 | NO | hydrolase  |
| VP2791 | NO | hypothetical protein   |
| VP2792 | NO | phosphoribulokinase  |
| VP2793 | NO | cAMP-regulatory protein  |
| VP2794 | NO | hypothetical protein   |
| VP2795 | NO | succinylglutamic semialdehyde dehydrogenase  |
| VP2796 | NO | arginine/ornithine succinyltransferase   |
| VP2797 | NO | bifunctional N-succinyldiaminopimelate-aminotransferase/acetylornithine transaminase protein |
| VP2798 | NO | para-aminobenzoate synthase component II   |
| VP2804 | NO | tryptophanyl-tRNA synthetase   |
| VP2805 | NO | phosphoglycolate phosphatase   |
| VP2806 | NO | 23S rRNA (guanosine-2'-O-)-methyltransferase   |
| VP2807 | NO | ribonuclease R   |
| VP2808 | NO | transcriptional repressor NsrR   |
| VP2809 | NO | nitric oxide dioxygenase   |
| VP2811 | NO | sodium-type polar flagellar protein MotX   |
| VP2812 | NO | adenylosuccinate synthetase  |
| VP2813 | NO | hypothetical protein   |
| VP2814 | NO | HflC protein   |
| VP2815 | NO | HflK protein   |
| VP2816 | NO | GTPase HflX  |
| VP2817 | NO | RNA-binding protein Hfq  |
| VP2818 | NO | tRNA delta(2)-isopentenylpyrophosphate transferase   |
| VP2820 | NO | N-acetylmuramoyl-L-alanine amidase   |
| VP2822 | NO | (Fe-S)-binding protein   |
| VP2823 | NO | oligoribonuclease  |
| VP2824 | NO | ribosome-associated GTPase   |
| VP2825 | NO | phosphatidylserine decarboxylase   |
| VP2826 | NO | transporter  |
| VP2827 | NO | methyl-accepting chemotaxis protein  |
| VP2828 | NO | hypothetical protein   |
| VP2829 | NO | phosphoglyceromutase   |
| VP2830 | NO | hypothetical protein   |
| VP2831 | NO | preprotein translocase subunit SecB  |
| VP2832 | NO | NAD(P)H-dependent glycerol-3-phosphate dehydrogenase   |
| VP2833 | NO | serine acetyltransferase   |
| VP2834 | NO | NlpD-like protein  |
| VP2835 | NO | hypothetical protein   |
| VP2836 | NO | TetR family transcriptional regulator  |
| VP2837 | NO | hypothetical protein   |
| VP2838 | NO | lysyl-tRNA synthetase  |
| VP2839 | NO | hypothetical protein   |
| VP2840 | NO | fumarate reductase flavoprotein subunit  |
| VP2841 | NO | fumarate reductase iron-sulfur subunit   |
| VP2842 | NO | fumarate reductase subunit C   |
| VP2843 | NO | fumarate reductase subunit D   |
| VP2845 | NO | elongation factor P  |
| VP2846 | NO | hypothetical protein   |
| VP2849 | NO | hypothetical protein   |

|        |    |   |
|--------|----|---|
| VP2850 | NO | hypothetical protein  |
| VP2852 | NO | co-chaperonin GroES   |
| VP2853 | NO | hypothetical protein  |
| VP2855 | NO | 6-phosphofructokinase   |
| VP2856 | NO | ferrous iron efflux protein F   |
| VP2858 | NO | transcriptional regulator CpxR  |
| VP2859 | NO | two-component sensor protein  |
| VP2861 | NO | rRNA methylase  |
| VP2862 | NO | FxsA protein  |
| VP2863 | NO | aspartate ammonia-lyase   |
| VP2865 | NO | thiol:disulfide interchange protein   |
| VP2866 | NO | LuxR family transcriptional regulator   |
| VP2867 | NO | potassium/proton antiporter   |
| VP2868 | NO | hypothetical protein  |
| VP2870 | NO | hypothetical protein  |
| VP2872 | NO | hypothetical protein  |
| VP2873 | NO | fumarate hydratase  |
| VP2875 | NO | 3-phenylpropionic acid transporter  |
| VP2876 | NO | hypothetical protein  |
| VP2877 | NO | DNA polymerase III subunit epsilon  |
| VP2881 | NO | acetyl-CoA carboxylase biotin carboxylase subunit   |
| VP2883 | NO | ribosomal protein L11 methyltransferase   |
| VP2884 | NO | NifR3/Smm1 family protein   |
| VP2885 | NO | DNA-binding protein Fis   |
| VP2893 | NO | DNA-binding transcriptional activator CadC  |
| VP2895 | NO | hypothetical protein  |
| VP2896 | NO | bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase |
| VP2898 | NO | phosphoribosylamine--glycine ligase   |
| VP2913 | NO | hypothetical protein  |
| VP2916 | NO | uroporphyrinogen decarboxylase  |
| VP2920 | NO | anti-RNA polymerase sigma 70 factor   |
| VP2925 | NO | 50S ribosomal protein L1  |
| VP2926 | NO | 50S ribosomal protein L11   |
| VP2928 | NO | preprotein translocase subunit SecE   |
| VP2929 | NO | hypothetical protein  |
| VP2936 | NO | glutamate racemase  |
| VP2941 | NO | DNA-binding transcriptional repressor FabR  |
| VP2942 | NO | soluble pyridine nucleotide transhydrogenase  |
| VP2949 | NO | chorismate-pyruvate lyase   |
| VP2950 | NO | flagellar basal body protein FlhL   |
| VP2951 | NO | GlpG protein  |
| VP2954 | NO | cell division protein FtsX  |
| VP2957 | NO | hypothetical protein  |
| VP2958 | NO | hypothetical protein  |
| VP2960 | NO | hypothetical protein  |
| VP2961 | NO | hypothetical protein  |
| VP2964 | NO | hypothetical protein  |
| VP2965 | NO | hypothetical protein  |
| VP2970 | NO | glyceraldehyde-3-phosphate dehydrogenase  |
| VP2971 | NO | ArsR family transcriptional regulator   |
| VP2976 | NO | hypothetical protein  |
| VP2978 | NO | hypothetical protein  |

|        |    |  |
|--------|----|--|
| VP2983 | NO | diaminopimelate epimerase  |
| VP2985 | NO | lipoprotein L  |
| VP2986 | NO | frataxin-like protein  |
| VP2989 | NO | uroporphyrinogen-III synthase                                    |
| VP2991 | NO | HemY protein   |
| VP2999 | NO | hypothetical protein   |
| VP3001 | NO | thioredoxin  |
| VP3004 | NO | hypothetical protein   |
| VP3014 | NO | signal peptide protein   |
| VP3015 | NO | hypothetical protein   |
| VP3017 | NO | transmembrane protein  |
| VP3020 | NO | LysR family transcriptional regulator                            |
| VP3031 | NO | carbonic anhydrase   |
| VP3032 | NO | hypothetical protein   |
| VP3033 | NO | shikimate 5-dehydrogenase  |
| VP3034 | NO | coproporphyrinogen III oxidase                                   |
| VP3035 | NO | Sua5/YciO/YrdC family protein                                    |
| VP3038 | NO | DNA topoisomerase I-like protein                                 |
| VP3039 | NO | hypothetical protein   |
| VP3040 | NO | Smf protein  |
| VP3042 | NO | peptide deformylase  |
| VP3043 | NO | methionyl-tRNA formyltransferase                                 |
| VP3044 | NO | Sun protein  |
| VP3046 | NO | potassium uptake protein TrkH                                    |
| VP3048 | NO | hemolysin III  |
| VP3049 | NO | SpoOM-like protein   |
| VP3050 | NO | hypothetical protein   |
| VP3052 | NO | FixG-like protein  |
| VP3054 | NO | thiol:disulfide interchange protein                              |
| VP3056 | NO | periplasmic protein  |
| VP3059 | NO | acetolactate synthase 2 regulatory subunit                       |
| VP3062 | NO | threonine dehydratase  |
| VP3063 | NO | DNA-binding transcriptional regulator                            |
| VP3068 | NO | ATP synthase F0F1 subunit epsilon                                |
| VP3069 | NO | ATP synthase F0F1 subunit beta                                   |
| VP3073 | NO | ATP synthase F0F1 subunit B                                      |
| VP3074 | NO | ATP synthase F0F1 subunit C                                      |
| VP3075 | NO | ATP synthase F0F1 subunit A                                      |
| VP3076 | NO | F0F1 ATP synthase subunit I                                      |
| VP3077 | NO | ParB family protein  |
| VP3078 | NO | ParA family protein  |
| VP3079 | NO | 16S rRNA methyltransferase GidB                                  |
| VP3080 | NO | tRNA uridine 5-carboxymethylaminomethyl modification enzyme GidA |

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**Table S7 Publicly available *V. mimicus* genomes used in this study**

| <b>Strain</b> | <b>Size (Mb)</b> | <b>Location(Country)</b> | <b>Isolation_Source</b>               |
|---------------|------------------|--------------------------|---------------------------------------|
| ATCC 33654    | 4.4387           |                          | /                                     |
| SCCF01        | 4.48402          |                          | /                                     |
| SX-4          | 4.27361          | China                    | diarrheal patient                     |
| VM603         | 4.35071          |                          | /                                     |
| VM573         | 4.36655          |                          | /                                     |
| MB-451        | 4.31345          | Bangladesh: Matlab       | diarrheal patient                     |
| VM223         | 4.34797          | Brazil: Sao Paulo        | /                                     |
| FDAARGOS_113  | 4.43209          | USA: TN                  | Human                                 |
| 532-80        | 4.4325           | USA                      | /                                     |
| CAIM 602      | 4.32029          |                          | /                                     |
| CAIM 1882     | 3.97976          |                          | water from a shrimp washing container |
| CAIM 1883     | 3.98557          |                          | water from a shrimp washing container |

**Table S8 Antibiotic resistance genes identified from the sequenced strains**

| Species                    | Strain Name | Aminoglycoside               | Beta-lactam       | Fluoroquinolone | Streptogramin | Phenicol    | Sulphonamide | Tetracycline   | Trimethoprim  |
|----------------------------|-------------|------------------------------|-------------------|-----------------|---------------|-------------|--------------|----------------|---------------|
| <i>V. mimicus</i>          | VM14        | <i>aph(3'')-Ib/aph(6)-Id</i> | -                 | <i>qnrVC4</i>   | -             | <i>floR</i> | <i>sul2</i>  | <i>tet(59)</i> | <i>dfrA6</i>  |
| <i>V. mimicus</i>          | VM34        | <i>aph(3'')-Ib/aph(6)-Id</i> | -                 | <i>qnrVC4</i>   | -             | <i>floR</i> | <i>sul2</i>  | <i>tet(59)</i> | <i>dfrA6</i>  |
| <i>V. mimicus</i>          | VM61        | <i>aph(3'')-Ib/aph(6)-Id</i> | -                 | <i>qnrVC4</i>   | -             | <i>floR</i> | <i>sul2</i>  | <i>tet(59)</i> | <i>dfrA6</i>  |
| <i>V. parahaemolyticus</i> | YK38        | -                            | <i>blaCARB-47</i> | -               | -             | -           | -            | -              | -             |
| <i>V. parahaemolyticus</i> | YK39        | -                            | <i>blaCARB-47</i> | -               | -             | -           | -            | -              | -             |
| <i>V. parahaemolyticus</i> | YK40        | -                            | <i>blaCARB-47</i> | -               | -             | -           | -            | -              | -             |
| <i>V. parahaemolyticus</i> | YK13        | -                            | <i>blaCARB-48</i> | -               | -             | -           | -            | -              | -             |
| <i>V. parahaemolyticus</i> | YK17        | -                            | <i>blaCARB-47</i> | -               | -             | -           | -            | -              | -             |
| <i>V. parahaemolyticus</i> | YK41        | -                            | <i>blaCARB-47</i> | -               | -             | -           | -            | -              | -             |
| <i>V. mimicus</i>          | VM20        | <i>aph(3'')-Ib/aph(6)-Id</i> | -                 | <i>qnrVC4</i>   | -             | <i>floR</i> | <i>sul2</i>  | <i>tet(59)</i> | <i>dfrA6</i>  |
| <i>V. parahaemolyticus</i> | YK45        | -                            | <i>blaCARB-47</i> | -               | -             | -           | -            | -              | -             |
| <i>V. parahaemolyticus</i> | YK51        | -                            | <i>blaCARB-47</i> | -               | -             | -           | -            | -              | -             |
| <i>V. parahaemolyticus</i> | YK49        | -                            | <i>blaCARB-47</i> | -               | -             | -           | -            | -              | -             |
| <i>V. parahaemolyticus</i> | YK32        | -                            | <i>blaCARB-47</i> | -               | -             | -           | -            | -              | <i>dfrA31</i> |
| <i>V. parahaemolyticus</i> | YK33        | -                            | <i>blaCARB-47</i> | -               | -             | -           | -            | -              | -             |
| <i>V. parahaemolyticus</i> | YK34        | -                            | <i>blaCARB-47</i> | <i>qnrC</i>     | -             | -           | -            | -              | -             |
| <i>V. scophthalmi</i>      | YK47        | -                            | <i>blaOXA-12</i>  | -               | <i>mph(A)</i> | <i>floR</i> | -            | -              | -             |
| <i>V. mimicus</i>          | VM27        | <i>aph(3'')-Ib/aph(6)-Id</i> | -                 | <i>qnrVC4</i>   | -             | <i>floR</i> | <i>sul2</i>  | <i>tet(59)</i> | <i>dfrA6</i>  |
| <i>V. mimicus</i>          | VM37        | <i>aph(3'')-Ib/aph(6)-Id</i> | -                 | <i>qnrVC4</i>   | -             | <i>floR</i> | <i>sul2</i>  | <i>tet(59)</i> | <i>dfrA6</i>  |
| <i>V. mimicus</i>          | VM41        | <i>aph(3'')-Ib/aph(6)-Id</i> | -                 | <i>qnrVC4</i>   | -             | <i>floR</i> | <i>sul2</i>  | <i>tet(59)</i> | <i>dfrA6</i>  |
| <i>V. parahaemolyticus</i> | PJ43        | -                            | <i>blaCARB-47</i> | -               | -             | -           | -            | -              | -             |
| <i>V. parahaemolyticus</i> | PJ42        | -                            | <i>blaCARB-47</i> | -               | -             | -           | -            | -              | -             |
| <i>V. parahaemolyticus</i> | PJ44        | -                            | <i>blaCARB-47</i> | -               | -             | -           | -            | -              | -             |

|                            |      |   |                   |   |   |   |   |   |   |
|----------------------------|------|---|-------------------|---|---|---|---|---|---|
| <i>V. parahaemolyticus</i> | PJ37 | - | <i>blaCARB-47</i> | - | - | - | - | - | - |
| <i>V. parahaemolyticus</i> | PJ18 | - | <i>blaCARB-47</i> | - | - | - | - | - | - |
| <i>V. parahaemolyticus</i> | PJ35 | - | <i>blaCARB-47</i> | - | - | - | - | - | - |
| <i>V. parahaemolyticus</i> | SH50 | - | <i>blaCARB-47</i> | - | - | - | - | - | - |

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