

## Supplementary Material

### Supplementary Tables

**Table S1.** Strains for experiment and the description of their characteristics.

Strains	Description of characteristics
BB120 (Bassler <i>et al.</i> , 1997)	<i>Vibrio harveyi</i> standard wild type strain
BB170 (Bassler <i>et al.</i> , 1993)	<i>luxN</i> ::Tn5 (Kn <sup>R</sup> ) (HAI-1 sensor deactivated)
BB886 (Bassler <i>et al.</i> , 1994)	<i>luxQ</i> ::Tn5 (Kn <sup>R</sup> ) (AI-2 sensor deactivated)
JAF375 (Freeman and Bassler, 1999)	<i>luxQ</i> ::Tn5(Kn <sup>R</sup> ), <i>luxN</i> ::Cm <sup>R</sup> (HAI-1, AI-2 sensor deactivated)
JMH597 (Henke and Bassler, 2004a)	<i>luxN</i> ::Tn5(Kn <sup>R</sup> ), <i>cqsS</i> ::Cm <sup>R</sup> (AI-2, CAI-1 sensor deactivated)
BB152 (Bassler <i>et al.</i> , 1994)	<i>luxLM</i> ::Tn5 (Kn <sup>R</sup> ) (HAI-1 synthetase deactivated)
MM30 (Surette <i>et al.</i> , 1999)	<i>luxS</i> ::Tn5(Kn <sup>R</sup> ) (AI-2 synthetase deactivated)
MM77 (Mok <i>et al.</i> , 2003)	<i>luxLM</i> ::Tn5(Kn <sup>R</sup> ), <i>luxS</i> ::Cm <sup>R</sup> (HAI-1, AI-2 synthetase deactivated)
JAF483 (Freeman and Bassler, 1999)	<i>luxO</i> D47A linked to Kn <sup>R</sup> (LuxO point mutant)
BNL258 (Lenz <i>et al.</i> , 2004)	<i>hfq</i> ::Tn5(Kn <sup>R</sup> ) lacZ (RNA chaperone <i>hfq</i> deactivated)

**Table S2.** Standards used for the search of the potential functional proteins involved in MeSH and DMS metabolism by BLASTp.

Protein	<i>e</i> -value cut-offs	Reference or detailed information
DsyB	$\leq e^{-67}$	Curson <i>et al.</i> , 2017
MmtN	$\leq e^{-50}$	Williams <i>et al.</i> , 2019
DmdA	$< e^{-85}$	Curson <i>et al.</i> , 2011b
DddP	$< e^{-86}$	Curson <i>et al.</i> , 2011b
DddL	$< e^{-52}$	Curson <i>et al.</i> , 2011b
DddD	0.0	Curson <i>et al.</i> , 2011b
DddQ	$< e^{-20}$	Curson <i>et al.</i> , 2011b
DddW	$< e^{-49}$	Curson <i>et al.</i> , 2011b
MegL	$< e^{-80}$	Identity > 40%, Coverage > 90%
DmdB	0.0	Identity > 49%, Coverage > 99%
DmdC	$< e^{-43}$	Identity > 33%, Coverage > 70%
DmdD/AcuH	$< e^{-108}$	Identity > 60%, Coverage > 98%
DddK	$< e^{-7}$	Identity > 39%, Coverage > 95%

(Continued)

Protein	<i>e</i> -value cut-offs	Reference or detailed information
DddX	$< e^{-75}$	Identity > 30%, Coverage > 70%
MddA	$< e^{-9}$	Identity > 36%, Coverage > 70%
DmoA	$< e^{-83}$	Identity > 36%, Coverage > 96%
DdhA	$< e^{-80}$	Identity > 36%
DorA	0.0	Identity > 43%, Coverage > 99%
DddY	$< e^{-5}$	-
DdhA	$< e^{-5}$	-
Tmm	$< e^{-5}$	-
MTO	$< e^{-5}$	-

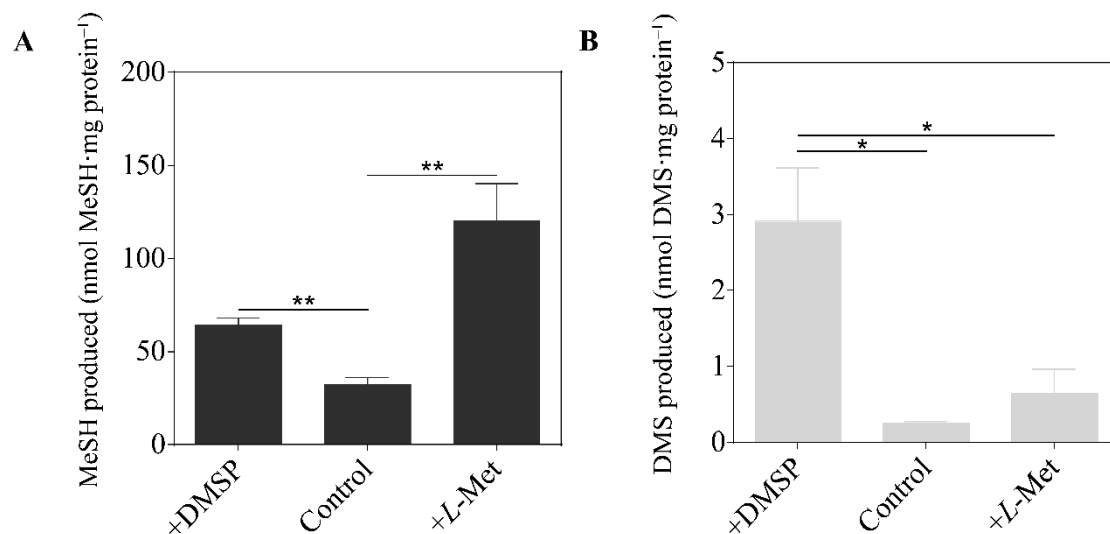
**Table S3.** The comparison results between MegL/DorAs in *Vibrio harveyi* BB120 and the functionally verified MegLs/DorAs.

Query sequence	Subject sequence	Identity	<i>e</i> -value	Coverage
VH2527 (WP_005432739.1)	<i>Brevibacterium linens</i> (AAV54600.1)	44.845%	$4.26 \times e^{-113}$	90.82%
	<i>Clostridium tetani</i> 157.15 (WP_129010005.1)	40.722%	$4.99 \times e^{-93}$	96.98%
	<i>Porphyromonas gingivalis</i> LyG-1 (WP_211600051.1)	40.206%	$8.57 \times e^{-87}$	96.74%
	<i>Micromonospora echinospora</i>	40.110%	$6.13 \times e^{-82}$	99.23%
VH851 (WP_012127641.1)	DorA_ <i>Rhodobacter sphaeroides</i> 2.4.1T (AAB94874.1)	45.000%	0.0	99.76%
	DorA_ <i>Rhodobacter capsulatus</i> 37b4 (AAD13674.1)	44.567%	0.0	99.64%
VH4908 (WP_012129114.1)	DorA_ <i>Rhodobacter sphaeroides</i> 2.4.1T (AAB94874.1)	40.438%	0.0	98.30%

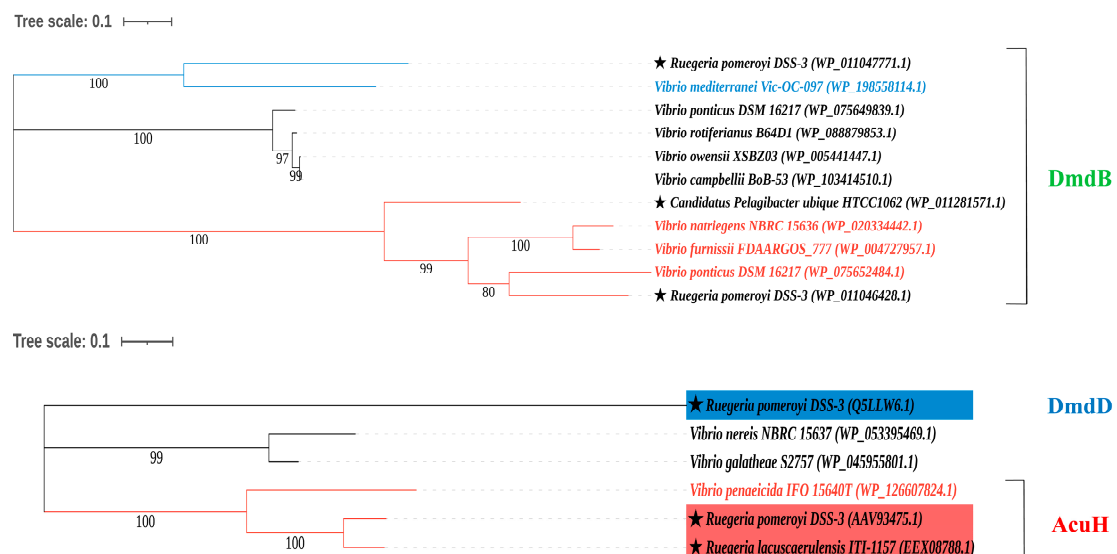
Table S4. Potential functional proteins involved in *L*-Met, DMSP, MeSH and DMS metabolism in typical *Vibrio* strains.

Strains	Numbers of the potential functional proteins																					
	L-Met metabolism	DMSP synthesis		DMSP demethylation					DMSP cleavage							MeSH→DMS	DMS→MeSH	DMS→DMSO		DMSO→DMS	MeSH→HCHO	
	MegL	DsyB	MmtN	DmdA	DmdB	DmdC	DmdD	AcuH	DddD	DddL	DddP	DddQ	DddW	DddY	DddK	DddX	MddA	DmoA	DdhA	Tmm	DorA	MTO
<i>Vibrio aerogenes</i> LMG 19650	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
<i>Vibrio antiquarius</i> EX25	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	
<i>Vibrio aquimaris</i> THAF100	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	
<i>Vibrio artabrorum</i> CECT 7226	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	
<i>Vibrio atlanticus</i> CECT 7223	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	
<i>Vibrio bathopelagicus</i> Sa110	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	
<i>Vibrio campbellii</i> BoB-53	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	
<i>Vibrio chagasii</i> LMG 21353	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	
<i>Vibrio cholerae</i> RFB16	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	
<i>Vibrio coralliirubri</i> DSM 27495	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	
<i>Vibrio cortegadensis</i> CECT 7227	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	
<i>Vibrio diabolicus</i> HS-60-3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	
<i>Vibrio echinoideorum</i> DSM 107264	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	
<i>Vibrio fluvialis</i> ATCC 33809	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	
<i>Vibrio fortis</i> LMG 21557	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	
<i>Vibrio furnissii</i> FDAARGOS_777	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	
<i>Vibrio galathea</i> e S2757	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	
<i>Vibrio gallaecicus</i> CECT 7244	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	
<i>Vibrio gangliei</i> DSM 104291	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
<i>Vibrio gigantis</i> ACE001	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	
<i>Vibrio ishigakensis</i> C1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	
<i>Vibrio japonicus</i> JCM 31412	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	
<i>Vibrio kanaloae</i> R17	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	
<i>Vibrio mangrovi</i> CECT 7927	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
<i>Vibrio marisflavi</i> CECT 7928	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
<i>Vibrio mediterranei</i> Vic-OC-097	1	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	
<i>Vibrio natriegens</i> NBRC 15636	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	
<i>Vibrio neonatus</i> JCM 21521	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
<i>Vibrio nereis</i> NBRC 15637	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	
<i>Vibrio ostreae</i> OG9-811	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	
<i>Vibrio owensii</i> XSBZ03	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	
<i>Vibrio palustris</i> CECT 9027	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
<i>Vibrio parahaemolyticus</i> RIMD 2210633	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	
<i>Vibrio pelagius</i> ATCC 25916	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	
<i>Vibrio penaeicida</i> IFO 15640T	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	
<i>Vibrio pomeroyi</i> LMG 20537	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	
<i>Vibrio ponticus</i> DSM 16217	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	
<i>Vibrio porteresiae</i> DSM 19223	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
<i>Vibrio qinghaiensis</i> Q67	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	
<i>Vibrio rarus</i> LMG 23674	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	
<i>Vibrio rhizosphaerae</i> LMG 23790	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
<i>Vibrio rotiferianus</i> B64D1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	
<i>Vibrio rumoiensis</i> FERM P-14531	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
<i>Vibrio sagamiensis</i> NBRC 104589	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	
<i>Vibrio splendidus</i> 2_C04b	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	
<i>Vibrio tasmaniensis</i> LMG 20012	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	
<i>Vibrio toranzoniae</i> CECT 7225	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	
<i>Vibrio tritonius</i> AM2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	
<i>Vibrio tubiashii</i> ATCC 19109	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	
<i>Vibrio zhugei</i> HBUAS61001	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	
<i>Vibrio ziniensis</i> ZWAL4003	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

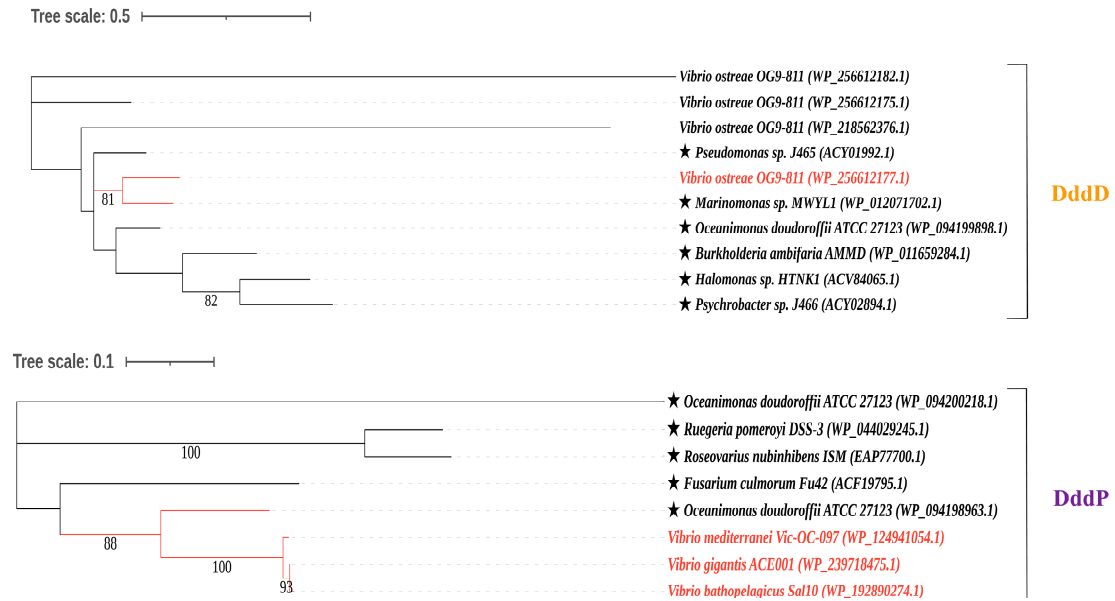
## Supplementary Figures



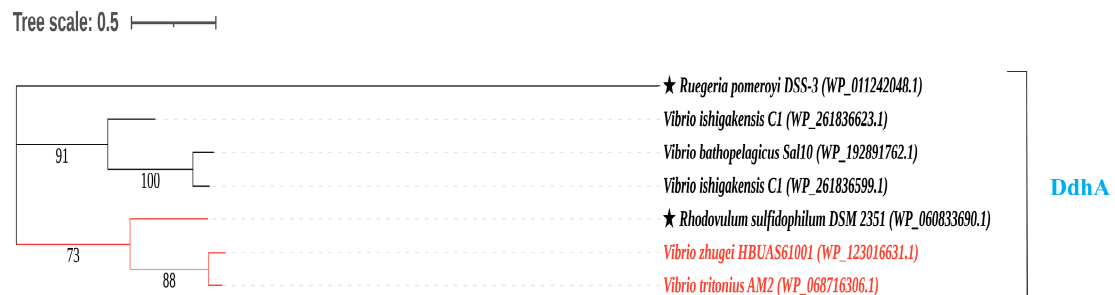
**Figure S1.** Production of sulfur gas by *Vibrio harveyi* BB120 cultured in MA under different treatments. A, Production of MeSH by *V. harveyi* BB120. B, Production of DMS by *V. harveyi* BB120. The data are shown as the mean  $\pm$  standard deviation (SD). The differences between the experimental groups and the control groups were calculated by Student's *t*-test. \*,  $p < 0.05$  in Student's *t*-test. \*\*,  $p < 0.01$  in Student's *t*-test.



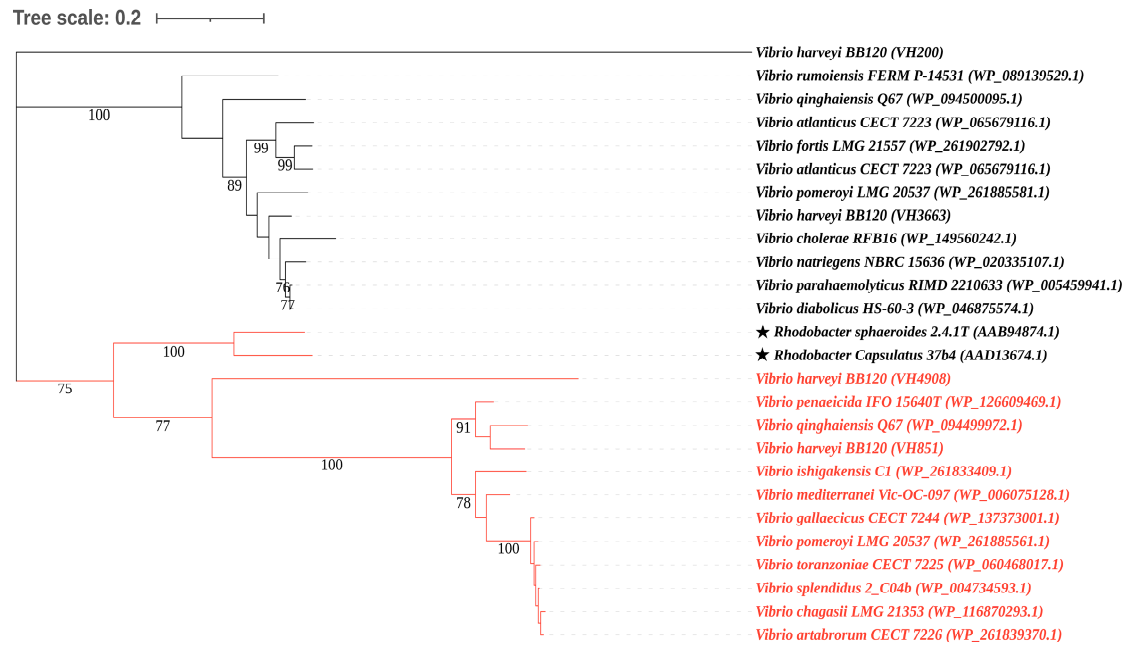
**Figure S2.** Maximum-likelihood phylogenetic tree of Dmd-type proteins (DmdB and DmdD/AcuH) in *Vibrio*. Ratified DmdB and DmdD/AcuH alongside the proteins of the representative vibrios available from NCBI that sharing higher identity with them were used for phylogenetic tree construction. The ratified proteins were marked with a black star and those in red/blue were potential functional proteins. Bootstrap support for nodes was marked.



**Figure S3.** Maximum-likelihood phylogenetic tree of Ddd-type proteins (DddD and DddP) in *Vibrio*. Ratified DddD and DddP alongside the proteins of the representative vibrios available from NCBI that sharing higher identity with them were used for phylogenetic tree construction. Proteins experimentally confirmed to produce DMS were marked with a black star and those in red were potential DMSP lyases. Bootstrap support for nodes was marked.



**Figure S4.** Maximum-likelihood phylogenetic tree of DdhA in *Vibrio*. Ratified DdhA alongside the proteins of the representative vibrios available from NCBI that sharing higher identity with them were used for phylogenetic tree construction. The ratified proteins experimentally confirmed to transform DMS to DMSO were marked with a black star and those in red were potential DdhAs. Bootstrap support for nodes was marked.



**Figure S5.** Maximum-likelihood phylogenetic tree of DorAs in *Vibrio*. Ratified DorAs alongside the proteins of the representative vibrios available from NCBI that sharing higher identity (Top 10) with them were used for phylogenetic tree construction. Proteins experimentally confirmed to transform DMSO to DMS were marked with a black star and those in red were potential DorAs. Bootstrap support for nodes was marked.

## Reference

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