

Table S3: OueS-regulated biofilm genes obtained by comparing expression values of WT and $\Delta ompU$ -pOueS biofilm grown cells to their expression in the *ompU* mutant.

Genes repressed by OueS					
Locus Tag	Function	WT/ $\Delta ompU$		$\Delta ompU$ -pOueS/ $\Delta ompU$	
		FC	FDR <i>p</i> -value	FC	FDR <i>p</i> -value
VC0017	hypothetical protein	-2.7	1.1E-05	-4.1	7.4E-21
VC0063	thiF protein	-3.1	1.0E-04	-3.0	7.6E-05
VC0065	thiG protein	-3.3	1.2E-06	-3.2	3.2E-05
VC0066	thiH protein	-2.5	4.6E-04	-2.6	1.5E-05
VC0091	O-methyltransferase- related protein	-3.7	4.1E-07	-2.7	6.1E-07
VC0107	RyhB sRNA	-8.4	1.6E-16	-3.8	7.0E-08
VC0157	alkaline serine protease	-4.5	2.0E-12	-2.2	4.9E-06
VC0199	hemolysin secretion ATP-binding protein,putative	-3.4	3.1E-05	-3.1	8.9E-06
VC0200	iron(III) compound receptor	-6.5	6.9E-11	-4.6	1.8E-11
VC0202	iron(III) ABC transporter, periplasmiciron-compound-binding protein	-2.5	4.1E-03	-2.9	3.0E-04
VC0284	putative outer membrane receptor	-3.1	1.3E-08	-2.6	6.8E-08
VC0474	iron-regulated virulence regulatory proteinIrgB	-3.3	4.5E-05	-2.1	9.1E-03
VC0475	iron-regulated outer membrane virulence protein,TonB receptor family	-8.2	2.5E-37	-2.4	1.2E-09
VC0608	iron(III) ABC transporter, periplasmiciron-compound-binding protein	-4.8	1.2E-12	-2.9	4.4E-11
VC0771	vibriobactin-specific isochorismatase	-8.0	3.6E-13	-4.1	1.4E-09
VC0773	vibriobactin-specific isochorismate synthase	-5.0	1.5E-05	-2.4	3.2E-04
VC0774	vibriobactin-specific c2,3-dihydro-2,3-dihydroxybenz oate dehydrogenase	-5.8	1.6E-14	-5.3	3.3E-18
VC0775	vibriobactin synthesis protein, putative	-2.7	6.6E-05	-3.2	7.5E-12
VC0777	ferric vibriobactin ABC transporter, permeaseprotein	-3.5	1.1E-05	-2.9	1.1E-05
VC0820	ToxR-activated gene A protein	-4.0	5.9E-09	-2.6	1.6E-04
VC0821	hypothetical protein	-3.6	3.5E-13	-2.4	2.1E-08
VC0823	hypothetical protein	-2.8	9.0E-09	-2.1	9.8E-06
VC0838	TCP pilus virulence regulatory protein	-4.6	2.4E-05	-2.3	4.5E-03
VC0929	RbmB	-5.8	6.0E-27	-2.8	5.0E-11
VC0930	hemolysin-related protein, RbmC	-2.7	6.8E-03	-2.9	1.0E-11
VC0931	RbmD	-3.1	3.1E-04	-2.6	3.3E-05
VC0932	RbmE	-4.8	4.4E-07	-2.8	2.6E-10
VC0940	conserved hypothetical protein	-2.1	3.7E-03	-2.6	7.6E-05
VC0972	porin, putative	-2.3	3.2E-04	-2.4	7.0E-06
VC1029	GGDEF family protein	-2.3	5.5E-03	-2.3	2.0E-05
VC1061	cysteine synthase/cystathionine beta-synthasefamily protein	-3.4	7.6E-09	-3.0	6.5E-12
VC1265	hypothetical protein	-2.4	3.6E-05	-2.1	3.6E-04
VC1268	conserved hypothetical protein	-2.4	1.0E-03	-2.5	1.4E-05
VC1329	opacity protein-related protein	-13.6	2.5E-37	-6.7	4.0E-23
VC1330	hypothetical protein	-4.3	1.9E-12	-2.2	5.4E-05
VC1346	conserved hypothetical protein	-4.9	2.5E-21	-2.0	3.7E-05
VC1456	cholera enterotoxin, B subunit	-6.2	1.1E-09	-4.0	5.7E-09
VC1457	cholera enterotoxin, A subunit	-3.6	2.2E-07	-3.6	1.0E-14
VC1543	hypothetical protein	-2.6	8.0E-08	-2.1	3.0E-05
VC1544	tonB2 protein	-2.8	1.3E-06	-2.6	1.6E-07
VC1545	TonB system transport protein ExbD2	-2.8	1.1E-04	-3.6	3.6E-11
VC1546	TonB system transport protein ExbB2	-3.7	5.5E-09	-2.7	7.0E-08
VC1547	biopolymer transport protein ExbB-relatedprotein	-3.6	2.1E-11	-2.6	2.7E-11
VC1548	hypothetical protein	-3.6	4.3E-06	-2.2	1.8E-03
VC1570	quinol oxidase, subunit II	-3.9	1.9E-07	-3.1	7.4E-04
VC1571	quinol oxidase, subunit I	-3.3	8.0E-08	-2.2	1.0E-04
VC1573	fumarate hydratase, class II	-4.4	2.7E-07	-3.2	7.1E-05
VC1585	catalase	-5.7	2.5E-10	-3.4	9.7E-06
VC1644	hypothetical protein	-2.3	2.4E-05	-2.4	3.5E-08
VC1688	hypothetical protein	-9.3	7.6E-12	-7.1	3.6E-10
VC1888	hemolysin-related protein, Bap1	-4.1	3.5E-12	-2.3	9.0E-07
VC1945	FAD monooxygenase, PheA/TfdB family	-2.6	2.2E-06	-3.4	1.0E-13
VC1947	transcriptional regulator, LysR family	-3.2	4.8E-06	-6.9	1.4E-21
VC1948	hypothetical protein	-52.7	1.1E-06	-38.3	3.3E-11
VC1949	pvcA protein	-6.4	3.5E-13	-8.4	1.1E-38
VC2004	conserved hypothetical protein	-3.4	1.5E-10	-2.2	4.0E-03
VC2069	flagellar biosynthetic protein FlhA	-2.2	7.7E-05	-2.0	6.8E-04
VC2209	nonribosomal peptide synthetase VibF	-4.5	1.5E-13	-4.1	3.0E-21
VC2210	vibriobactin utilization protein ViuB	-7.1	1.2E-28	-3.8	1.9E-14
VC2211	ferric vibriobactin receptor	-5.5	4.5E-11	-3.0	1.2E-04
VC2212	hypothetical protein	-3.1	5.8E-09	-2.3	2.4E-05
VC2539	thiamin ABC transporter, periplasmicthiamin-binding protein	-2.7	2.8E-05	-2.1	6.7E-06
VC2667	hypothetical protein	-6.7	2.8E-12	-4.1	2.8E-10
VC2691	periplasmic protein cpxP, putative	-2.3	8.7E-04	3.1	1.2E-12
VC2694	superoxide dismutase, Mn	-3.5	8.2E-14	-3.0	4.5E-14

VCA0083	multidrug resistance protein D	-4.8	1.4E-05	-5.1	4.6E-07
VCA0084	soxR protein	-2.2	4.2E-03	-2.5	1.3E-04
VCA0094	conserved hypothetical protein	-14.1	2.5E-23	-13.3	3.6E-30
VCA0095	hypothetical protein	-5.8	5.5E-05	-5.0	1.2E-04
VCA0140	spindolin-related protein	-4.7	1.1E-14	-2.5	7.3E-07
VCA0144	immunogenic protein	-3.0	3.1E-03	-3.4	3.2E-05
VCA0146	conserved hypothetical protein	-2.9	1.6E-03	-3.2	8.5E-04
VCA0147	transcriptional regulator, putative	-3.6	1.3E-04	-3.6	5.2E-10
VCA0160	tryptophan-specific transport protein	-5.2	7.8E-13	-7.0	1.2E-21
VCA0161	tryptophanase	-6.0	5.3E-22	-8.2	4.6E-50
VCA0163	conserved hypothetical protein	-2.7	5.5E-05	-2.1	1.2E-04
VCA0221	lactonizing lipase	-5.7	3.0E-15	-5.1	1.0E-18
VCA0222	lipase activator protein, putative	-3.4	6.9E-05	-2.8	8.5E-04
VCA0227	iron(III) ABC transporter, periplasmic iron-compound-binding protein	-4.3	1.1E-13	-2.1	4.2E-05
VCA0231	transcriptional regulator, AraC/XylS family	-7.9	9.6E-20	-3.8	5.5E-10
VCA0232	enterobactin receptor, VctA	-6.9	2.9E-13	-5.8	2.0E-20
VCA0233	hypothetical protein	-4.6	9.3E-08	-3.4	4.8E-05
VCA0280	glycine cleavage system protein GcvT; contains authentic frameshift	-2.1	8.5E-05	-2.1	7.6E-05
VCA0682	transcriptional regulator UhpA	-2.4	2.5E-04	-2.8	3.0E-09
VCA0683	sensor protein UhpB	-2.1	3.6E-03	-3.1	1.6E-05
VCA0885	threonine 3-dehydrogenase	-3.0	2.1E-11	-3.9	3.7E-17
VCA0886	2-amino-3-ketobutyrate coenzyme A ligase	-3.1	2.1E-08	-3.4	9.4E-17
VCA0907	conserved hypothetical protein	-5.9	1.8E-21	-3.7	4.7E-14
VCA0908	conserved hypothetical protein	-7.5	2.6E-28	-4.1	1.1E-17
VCA0909	oxygen-independent coproporphyrinogen III oxidase, putative	-9.8	1.3E-15	-4.6	6.6E-11
VCA0910	tonB1 protein	-9.8	7.3E-20	-4.9	1.3E-16
VCA0911	TonB system transport protein ExbB1	-10.3	1.5E-17	-5.5	6.1E-16
VCA0912	TonB system transport protein ExbD1	-7.3	2.2E-11	-4.2	1.6E-16
VCA0913	hemin ABC transporter, periplasmic hemin-binding protein HutB	-6.6	8.0E-10	-5.5	1.2E-12
VCA0914	hemin ABC transporter, permease protein, putative	-5.6	6.5E-11	-5.1	4.0E-15
VCA0928	hypothetical protein	-2.4	1.2E-03	-2.4	7.9E-06
VCA0946	maltose/maltodextrin ABC transporter, ATP-binding protein	-2.3	3.5E-05	-4.0	4.8E-21
VCA0976	hypothetical protein	-7.5	2.1E-13	-3.8	2.7E-07
VCA0977	ABC transporter, ATP-binding protein	-5.4	1.4E-21	-3.5	3.1E-14
VCA1041	phosphomannomutase, putative	-2.2	2.2E-04	-2.2	1.4E-06
VCr025	5S ribosomal RNA	-4.7	3.0E-04	-5.1	3.1E-05

Genes activated by OueS

Locus Tag	Function	WT/ Δ ompU		Δ ompU -pOueS/ Δ ompU	
		FC	FDR <i>p</i> -value	FC	FDR <i>p</i> -value
VC0176	transcriptional regulator, putative	2.8	7.1E-03	3.3	3.2E-05
VC0177	hypothetical protein	2.6	9.1E-05	3.6	2.3E-12
VC0178	patatin-related protein	2.2	1.7E-04	2.5	5.6E-08
VC0179	hypothetical protein	2.5	9.0E-06	2.2	4.0E-08
VC0180	conserved hypothetical protein	2.3	1.2E-06	2.1	7.4E-05
VC0494	conserved hypothetical protein	2.9	1.7E-04	3.8	1.1E-08
VC0502	type IV pilin, putative	2.7	1.1E-06	3.1	5.7E-11
VC0503	conserved hypothetical protein	3.3	7.9E-12	2.9	1.9E-14
VC0506	hypothetical protein	2.6	5.0E-04	2.3	3.6E-06
VC0507	hypothetical protein	4.8	2.2E-04	4.8	8.7E-04
VC0633	outer membrane protein OmpU	15766.6	0.0E+00	2471.8	0.0E+00
VC0817	transposase, putative	2.1	2.4E-03	2.5	1.4E-07
VC0818	pseudogene; within VPI-I; unknown function	2.2	5.2E-03	2.6	5.8E-04
VC0825	toxin co-regulated pilus biosynthesis protein I	2.1	4.5E-03	3.4	1.4E-10
VC1472	hypothetical protein	4.3	1.5E-04	4.1	1.2E-03
VC1762	hypothetical protein	2.1	1.1E-03	2.1	2.8E-03
VC1763	chemotaxis protein MotB-related protein	2.8	1.1E-05	2.7	2.7E-04
VC1774	conserved hypothetical protein	2.0	3.7E-03	2.3	3.3E-05
VC1793	hypothetical protein	2.9	5.3E-03	3.3	8.8E-04
VCA0346	H-REV 107-related protein	3.1	2.4E-10	2.1	1.4E-05
VCA0367	hypothetical protein	2.1	2.8E-04	2.3	9.9E-07
VCA0386	hypothetical protein	2.7	1.5E-06	2.8	3.0E-09
VCA0420	hypothetical protein	2.5	6.1E-04	2.1	2.4E-05
VCA0443	lipoprotein Blc	2.4	1.0E-04	2.1	1.2E-04
VCA0446	haemagglutinin	3.6	6.6E-11	2.0	7.1E-04
VCA0449	hypothetical protein	4.7	9.7E-06	3.5	1.4E-03
VCA0450	hypothetical protein	2.7	8.3E-03	2.8	9.9E-04
VCA0508	transposase OrfAB, subunit B	2.8	4.6E-07	2.4	6.5E-04
16Sh	16S ribosomal RNA	2.3	2.1E-05	12.2	1.0E-43
tRNA-Gly-8	tRNA biosynthesis	2.1	2.4E-03	3.0	8.4E-08
tRNA-Met-8	tRNA biosynthesis	2.9	1.8E-04	3.1	1.5E-05