Supplementary Information:

Membrane vesicle-mediated release of bacterial RNA

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Legends to Supplementary figures

Supplementary Data Fig. S1.

A) Analyses of RNA extracted from a log-phase (OD = 0.7) culture of *Vibrio cholerae* O1 El Tor strain A1552. Left panel: RNA extracted from whole cells (lane 1) and vesicles (lane 2) using the Total RNA Norgen kit. 1.5 μg RNA were run on a 12 % polyacrylamide denaturing gel stained in GelRed (light red). Right panel: RNA was transferred to a membrane for Northern blot analysis and probed with a probe for gene *vc2478,5* (lane 3; whole cells and lane 4: vesicles)

B) Western blot analysis of using antibodies recognizing RpoS to check for possible lysis of bacteria. Lane 1: whole cell extract from overnight culture; lane 2: supernatant from overnight culture after filtration through 0.22 μm stericup filters; lane 3: supernatant from overnight culture after ultracentrifugation; lane 4: vesicles from overnight culture; lane 5: whole cell extract from a culture at OD_{600} = 3 and lane 6: whole cell extract from A1552 RpoS mutant.

C) Fluorescence microscopy analysis of bacteria after live/dead staining. Staining was performed using the LIVE/DEAD® BacLightTM Bacterial Viability Kit L13152 with bacterial samples from *V. cholerae* O1 El Tor strain A1552 cultures as follows: a) sample from OD_{600} = 0.7 (log-phase); b) sample from OD_{600} = 4.6 (overnight culture); c) sample from OD_{600} = 4.6 (overnight culture) after treatment with isopropanol to obtain a population of only dead bacteria for comparison.

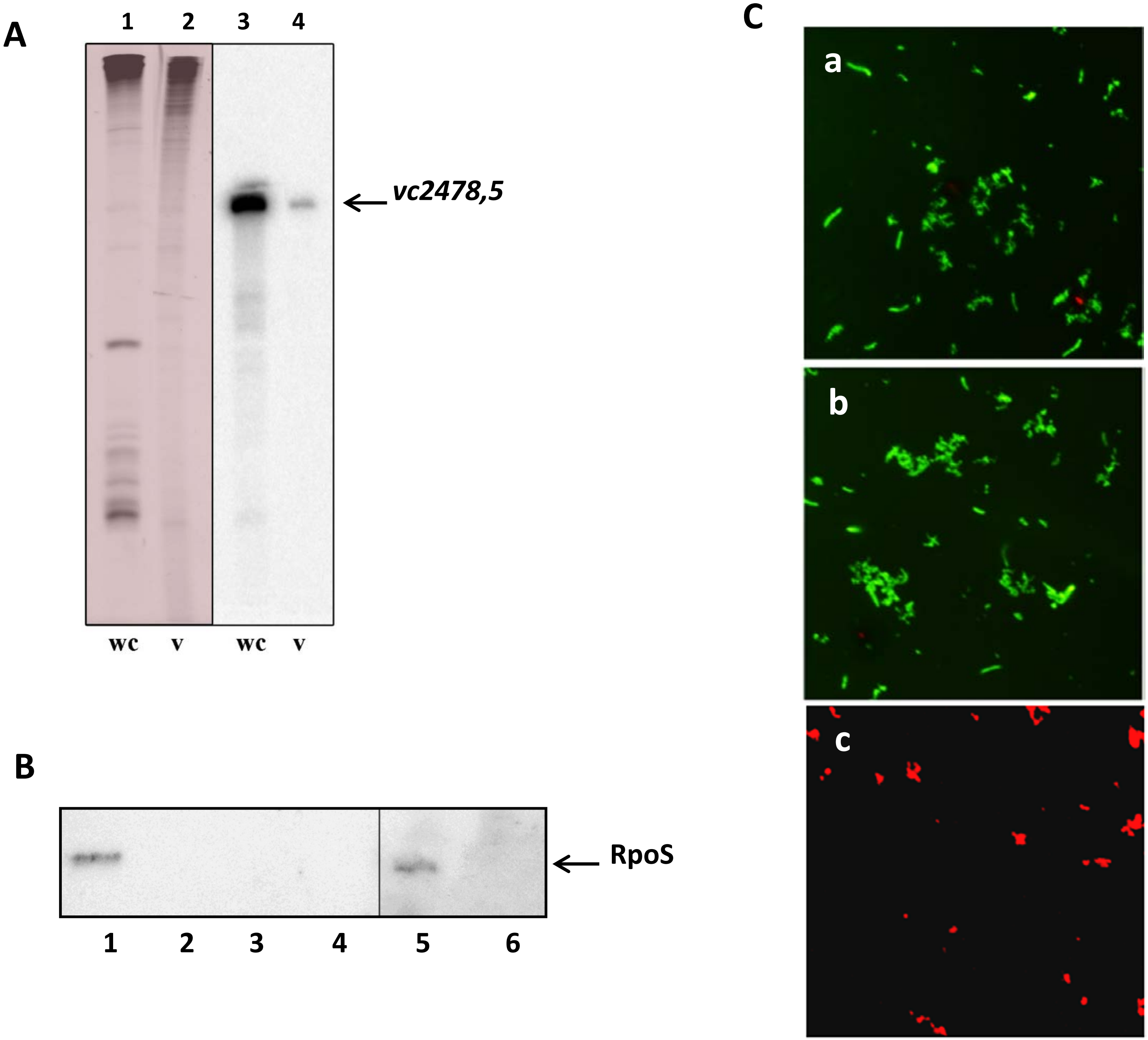
Supplementary Data Fig. S2. Density gradient centrifugation purification of vesicles from an overnight culture of the *V. cholerae* O1 El Tor strain A1552. **A.** Left panel: Photo of the density gradient tube after ultracentrifugation of a vesicle sample. The five visible rings (fractions) are numbered 1 to 5 in increasing density order. Right panel: Western blot analysis of samples from each numbered fraction using antibodies recognizing OmpU (VC 0633, Outer membrane protein U, 37kDa).

B. Analyses of RNA extracted from each of the five density gradient fractions in A. RNA extracts obtained using the Total RNA Norgen kit were separated on a 12 % polyacrylamide denaturing gel. The gel was stained and subsequently blotted for transfer to a membrane. Left panel: Gel stained with GelRed. Right panel: Northern blot membrane probed with probe *vc2478,5*. Lanes: wc, whole cell RNA extract; 1 - 5: samples originating from each of the numbered density gradient fractions described in A.

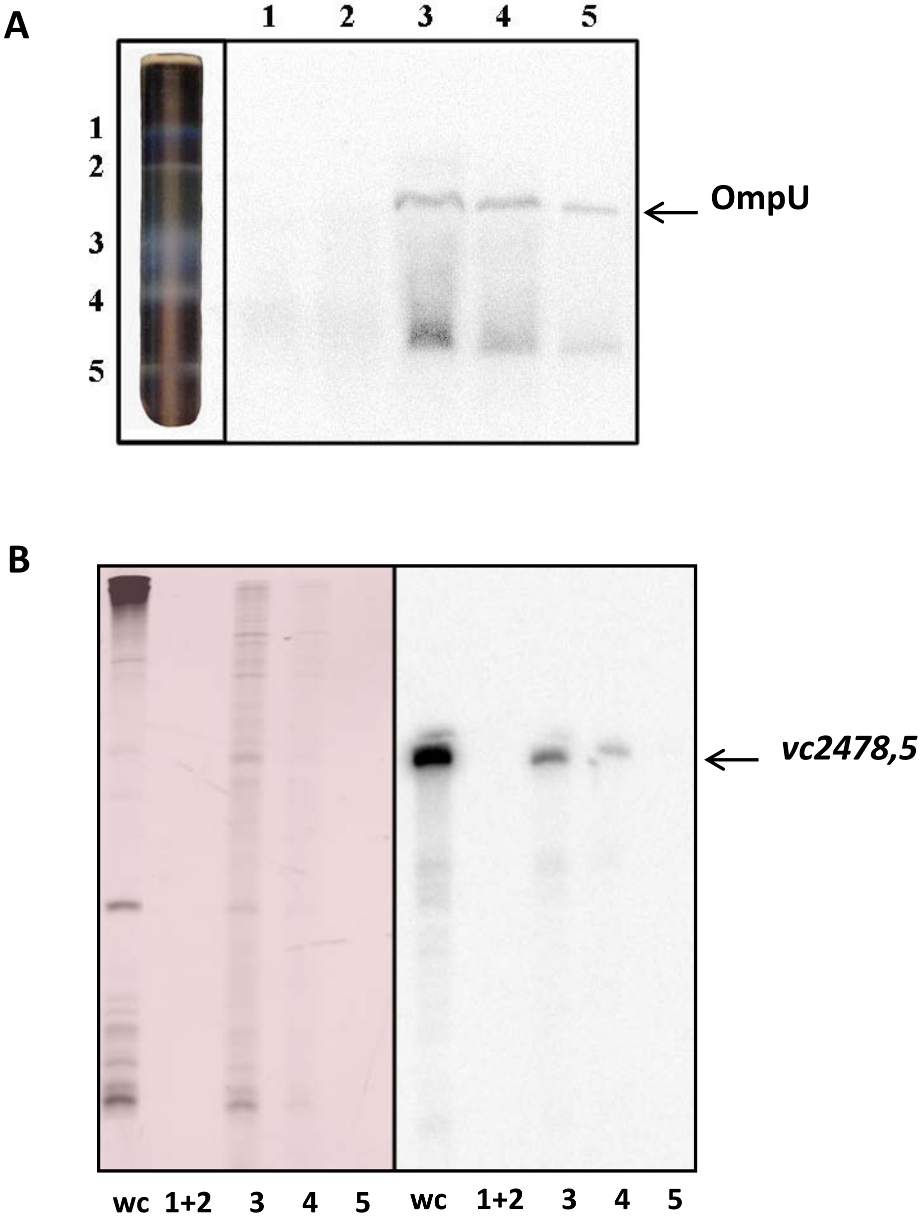
Supplementary Data Fig. S3. Illustrations of vesicle RNA (isolated from *V. cholerae* strain A1552) sequences aligned to chromosomal DNA sequences of *V. cholerae* N16961 strain. Red alignments are in the sense direction, blue alignments are in the anti-sense direction. *: Height indicates the number of sequences aligned. **A.** Typical alignment view **B.** Region *vc2478 – vc2479* **C.** Region *vc0190 – vc0191* **D.** Region *vca0526 – vca0527*.

Supplementary Data Fig. S4. RNA extracted from an overnight culture of *Vibrio cholerae* O1 El Tor A1552 whole cells (wc) and vesicles (v) using the Total RNA Norgen kit. RNA from whole cells (5 μg) and RNA from vesicles (3.5μg) were run on a 12 % polyacrylamide denaturing gel stained in GelRed (panel A). The RNA was transferred to a membrane that was probed with probe *vc2478,5* (panel B) and consecutively re-probed first with probe *vc0190,5* (panel C) and then with probe *vca0526,5* (panel D).

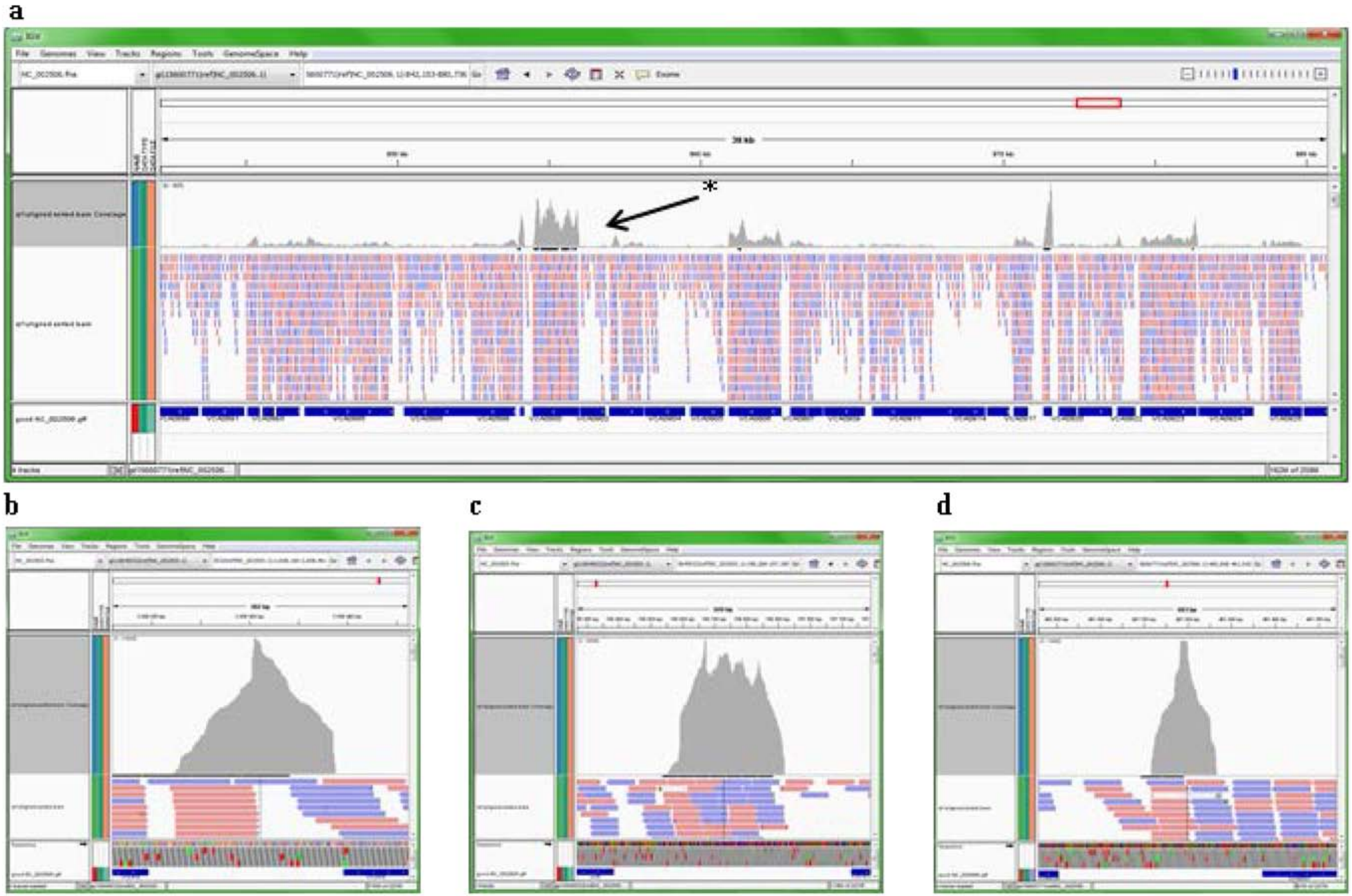
Supplementary Data Fig. 5. DNase I treatment of RNA extracted from bacterial vesicles. PCR analysis for detection of DNA in RNA samples extracted from vesicles released by *Vibrio cholerae* O1 El Tor strain A1552. The analysis was performed before (lanes 2 & 3) and after (lanes 4 & 5) treatment with DNase I. PCR products after amplifications using *ompU* primers (lanes 2 & 4) or *vc2478,5* primers (lanes 3 & 5) were analysed on a 1% agarose gel. Lane 1 shows a GeneRuler^{TM} DNA Ladder (Fermentas).



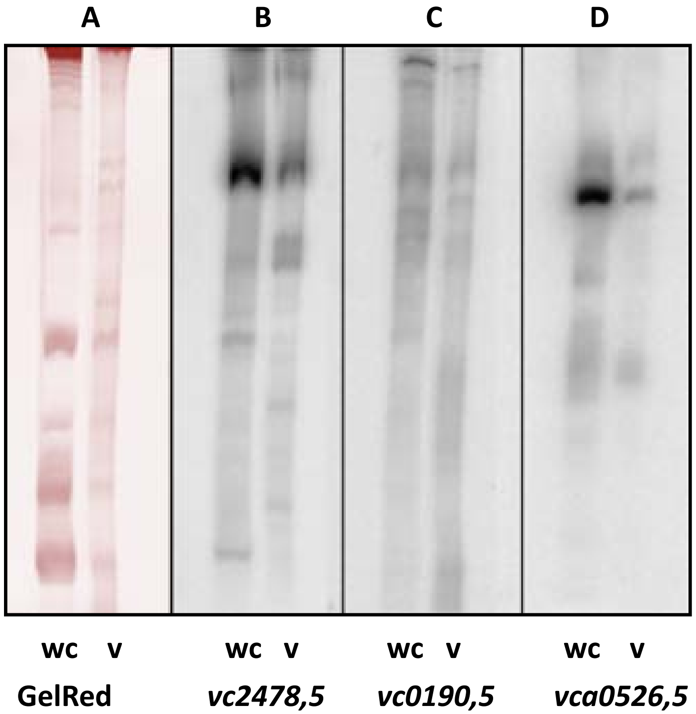
Supplementary Fig. S1



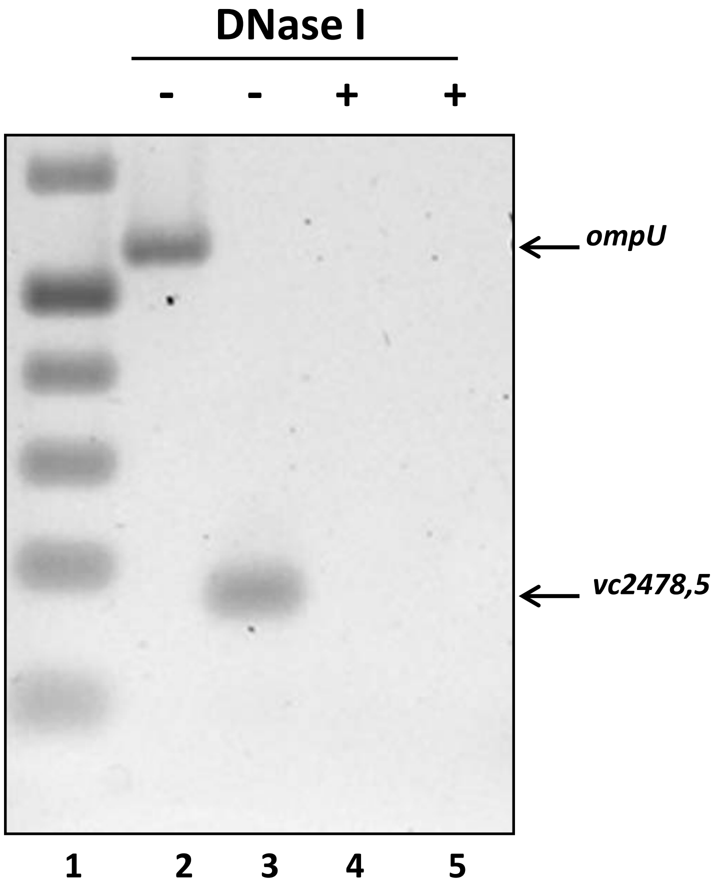
Supplementary Fig. S2



Supplementary Fig. S3



Supplementary Fig. S4



Supplementary Fig. S5

Supplementary Table 1a. Alignment of sequenced vesicle RNA to *V. cholerae* N16961 chromosome I.

Peak	**Start**	**End**	**Region in N16961 chromosome I**
1090000	2658225	2658386	upstream of uncharacterized protein **vc2479** **6S RNA**
120000	196545	196933	intergenic region between **vc0190** and **vc0191** **CsrB**
111000	914315	914654	upstream of phage integrase family **vc0847** **SrsA**
41500	943857	944200	uncharacterized protein **vc0883** **CsrB**
41200	2375908	2376115	uncharacterized protein **vc2221**
37800	2580714	2581110	upstream of uncharacterized protein **vc2410** svch2581.1
23500	1588979	1589272	ribosome modulating factor **vc1484**
17800	69300	69684	multidrug resistant protein **vc0069**
13000	2334461	2334692	downstream of flagellin A **vc2188**
12100	954751	954916	uncharacterized protein **vc0895** **GcvB**
9400	36506	36828	uncharacterized protein **vc0038**
7300	1578748	1578913	intergenic region between **vc1470** and **vc1471** svch1579.1 & 2
7150	1584873	1585042	intergenic region between **vc1478** and **vc1479**
6700	2619094	2619268	uncharacterized protein **vc2440**
6200	381650	382992	elongation factor Tu-B **vc0362**
5600	1719935	1720319	uncharacterized protein **vc1605a**
5480	1992699	1993856	putative porin **vc1854**
5100	1185676	1185924	putative glutaredoxin **vc1116**
5000	335290	336538	elongation factor Tu-A **vc0321**
4300	612554	613240	pseudo **vc0583** svch613.1 & 2
4000	1300189	1300577	integration host factor subunit alfa **vc1222**
3700	674802	675992	outer membrane protein **vc0633**
3280	1471635	1471788	uncharacterized protein **vc1378**
3100	2956240	2956682	ATP synthase F0F1 subunit I **vc2771**
3010	2174106	2174453	acyl carrier protein **vc2020**
2930	2332957	2334180	flagellin C **vc2187**
2580	1318751	1319201	uncharacterized protein **vc1247**
2280	2517106	2517539	autonomous glycyl radical cofactor **vc2361**
2260	2365289	2366647	outer membrane protein **vc2213**
2190	762615	762798	uncharacterized protein **vc0713**
2000	1538123	1539689	cbb-3 type Cytochrome c oxidase, subunit II **vc1442**
1980	1417217	1417374	upstream of uncharacterized protein **vc1333**
1970	222697	222833	coenzyme A biosynthesis bifunctional protein **vc0215**
1940	2063226	2063618	integration host factor subunit beta **vc1914**
1910	2295417	2295764	flagellar capping protein **vc2140**
1880	2754248	2755599	preprotein translocase subunit **vc2576**
1800	1408994	1410076	galactoside ABC transporter, periplasmic D-galactose/D-glucose-binding protein **vc1325**
1780	102446	102657	putative uncharacterized protein **vc0107** **RyhB & Spot_42**
1750	1198128	1198673	DNA binding protein **vc1130**
1690	1211912	1212296	cold shock-like protein **vc1142**
1680	2295764	2296334	flagellar protein **vc2141**
1650	2068862	2069279	DNA-binding protein HU-beta **vc1919**

1650	2909984	2911682	Phosphoenolpyruvate carboxykinase [ATP] **vc2738**
1600	1458356	1458653	uncharacterized protein **vc1368**
1500	86471	87681	cytochrome peroxidase c551 **vc0089**
1490	1670845	1673232	catalase/peroxidase **vc1560**
1480	1794805	1795288	heat shock protein **vc1663**
1470	2163539	2163748	uncharacterized protein **vc2009**
1400	786571	787319	antioxidant ahp CTSA family protein **vc0731**
1390	1536322	1537322	cbb-3 type Cytochrome c oxidase, subunit P **vc1439**
1390	2949663	2950113	ATP synthase F0F1 subunit epsilon **vc2763**
1370	2713024	2713375	RNA polymerase factor sigma-54 **vc2529**
1330	1537495	1538123	cbb-3 type Cytochrome c oxidase, subunit II **vc1441**
1330	2448193	2449428	Na(+)-translocating NADH-quinone reductase subunit **vc2294**
1260	1537322	1537495	cbb-3 type Cytochrome c oxidase, subunit Q **vc1440**
1260	2152257	2153283	glyceraldehyde-3-phosphate dehydrogenase **vc2000**
1250	2249553	2250272	succinate dehydrogenase iron-sulfur subunit **vc2088**
1240	580419	580787	upstream of and the whole carbon storage regulator **vc0548**
1230	1644504	1644628	intergenic region between **vc1531** and **vc1532**
1200	1097620	1099948	zink/cadmium/mercury/lead-transporting ATPase **vc1033**
1190	2449428	2450823	Na(+)-translocating NADH-quinone reductase subunit A **vc2295**
1180	2221154	2221925	flagellar biosynthesis sigma factor **vc2066**
1140	1031609	1031884	phosphocarrier protein HPr **vc0966**
1140	2394692	2394907	downstream of cytochrome c554 **vc2241**
1140	2669986	2670098	upstream of 2-isopropylmalate synthase **vc2490** svch2670.1
1120	1597539	1602466	uncharacterized protein **vc1492**
1100	1029112	1029661	PTS system glucos-specific IIA component **vc0964**
1100	2657848	2658199	uncharacterized protein **vc2478**
1090	1838582	1838921	uncharacterized protein **vc1707**
1070	564258	564667	lipoprotein **vc0533**
1070	2152042	2152257	putative uncharacterized protein **vc1999**
1070	2564959	2565969	cell division protein **vc2397**
1060	2564178	2564959	UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase **vc2396**
1050	2166629	2168114	PTS system glucose-specific transporter subunit IIBC **vc2013**
1020	2297656	2298854	flagellin D **vc2143**
1000	2296334	2297482	flagellin B **vc2142**
1000	462204	463183	malate dehydrogenase **vc0432**
1000	1520426	1520674	intergenic region between **vc1422** and **vc1423** svch1521.1
1000	1111516	1112882	long-chain fatty acid transport protein **vc1043**
1000	756233	756588	sigma-54 modulation protein **vc0706**
980	2253168	2254463	type II citrate synthase **vc2092**
950	2420154	2420290	upstream of uncharacterized protein **vc2264**
950	1310940	1311270	upstream of nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase **vc1237**
930	2654106	2654548	uncharacterized protein **vc2473**
920	2019596	2019906	SpoVR family protein **vc1874**
920	1447024	1447739	uncharacterized membrane protein **vc1358**
910	2394907	2395221	cytochrome c554 **vc2241**
910	1650724	1651517	uncharacterized protein **vc1539** svch1651.1
890	2252361	2252772	succinate dehydrogenase cytochrome b556 subunit **vc2091**

870	1214761	1215323	ATP-dependent Clp protease ATP-binding subunit **vc1144**	
870	1608509	1609145	solute/DNA competence effector, protein ProQ homolog **vc1497**	
870	76886	77365	ferritin **vc0078**	
860	305064	307130	acetyl-CoA synthetase **vc0298**	
850	2071844	2073125	ATP-dependent protease ATP-binding subunit **vc1921**	
830	2864880	2866417	aspartate ammonia-lyase **vc2698**	
830	278425	278694	DNA binding HU-alfa **vc0273**	
820	2444902	2446158	Na(+)-translocating NADH-quinone reductase subunit **vc2290**	
810	1021356	1022017	uncharacterized protein **vc0957**	
810	1814878	1815035	peptide ABC transporter substrate-binding protein **vc1680**	
810	2764786	2765042	upstream of **vc2597**	svch2765.1
800	1832388	1832689	uncharacterized protein **vc1699**	
800	76031	76651	universal stress protein A **vc0076**	
780	139954	140888	RNA polymerase sigma factor-32 **vc0150**	
770	2713375	2713710	sigma-54 modulation protein **vc2530**	
760	435431	435989	MSHA pilin protein **vc0409**	
740	1451138	1452295	amino acid ABC transporter substrate binding protein **vc1362**	
740	1158698	1160377	oligopeptide ABC transporter substrate binding protein **vc1091**	
730	633774	636488	bifunctional aconitate hydratase 2/2 methylisocitrate **vc0604**	
730	2081097	2082120	C4-dicarboxylate-binding periplasmic protein **vc1929**	
720	2834286	2834637	co-chaperonin, 10 kDa chaperonin 1 **vc2665**	
720	1135448	1135547	upstream of ArsR family transcriptional regulator **vc1068**	svch1136.1 & 2
720	2178616	2179044	uncharacterized protein **vc2026**	
700	2955395	2956240	ATP synthase F0F1 subunit A **vc2770**	
700	2447420	2448193	Na(+)-translocating NADH-quinone reductase subunit **vc2293**	
700	383504	384000	bactoferritin **vc0365**	
700	132719	133283	DPS family protein **vc0139**	
700	554239	554693	uncharacterized protein **vc0519**	
700	2014929	2016993	uncharacterized protein **vc1872**	
680	2954571	2955048	ATP synthase F0F1 subunit B **vc2768**	
680	2446782	2447420	Na(+)-translocating NADH-quinone reductase subunit **vc2292**	
670	692148	692445	polyribonucleotide nucleotidyltransferase **vc0647**	
670	2877100	2878819	putative Sodium/solute symporter **vc2705**	
650	2626588	2627926	enolase **vc2447**	
630	2832601	2834286	molecular chaperone **vc2664**	
630	1332776	1332950	DNA gyrase subunit A **vc1258**	
630	2203125	2203796	superoxide dismutase **vc2045**	svch2204.1
620	380939	381650	elongation factor G1 **vc0361**	
620	500283	500485	S-adenosylmethionine synthetase **vc0472**	
610	1319201	1320911	methyl-accepting chemotaxis protein **vc1248**	
600	2950113	2951534	ATP synthase F0F1 subunit beta **vc2764**	
600	2495392	2497494	elongation factor G 2 **vc2342**	
600	2501622	2501760	intergenic region inbetween **vc2344** and **vc2345**	
590	2250272	2252031	succinate dehydrogenase flavoprotein subunit **vc2089**	
590	2450823	2450982	upstream of Na(+)-translocating NADH-quinone reductase subunit **vc2295**	
590	2892438	2892948	uncharacterized protein **vc2717**	
580	2347213	2348056	chemotaxis protein methyltransferase 1 **vc2201**	

560	1374791	1375004	upsteam of phosphomethylpyrimidine kinase **vc1296** **TPP riboswitch**
560	1321079	1321598	uncharacterized protein **vc1249**
550	2344123	2345436	flagellar hook protein **vc2197**
550	2187578	2190491	bifunctional acetaldehyde-CoA/alcohol dehydrogenase **vc2033**
550	1283771	1284105	ds-DNA mimic protein **vc1208**
540	1477000	1477430	uncharacterized protein **vc1384**
540	2041347	2041496	intergenic region inbetween and parts of uncharacterized proteins **vc1893** and **vc1894**
530	1523028	1524280	spermidine/putrescine ABC transporter, periplasmic spermidine/putrescine-binding protein **vc1425**
530	1257042	1257620	uncharacterized protein **vc1183**
520	1651869	1652043	uncharacterized protein **vc1539a**
520	2952435	2954047	ATP synthase F0F1 subunit alfa **vc2766**
520	623301	623784	DnaK suppressor protein **vc0596**
520	2334684	2335901	flagellin A **vc2188**
510	133961	134317	uncharacterized protein **vc0142**
510	2083993	2084133	uncharacterized protein **vc1932**
510	952618	952804	chemotaxis protein **vc0893**
500	2955048	2955395	ATP synthase F0F1 subunit C **vc2769**
500	2334692	2336031	flagellin B **vc2142**
500	317733	318109	thioredoxin **vc0306**
490	1300020	1300189	upstream of **vc1222**
480	2327636	2327793	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase **vc2182**
470	2582987	2584882	pyruvate dehydrogenase **vc2413**
470	2951534	2952435	ATP synthase F0F1 subunit gamma **vc2765**
470	2414371	2415329	elongation factor Ts **vc2259**
470	2006853	2009215	formate acetyltrancferase **vc1866**
470	935777	935909	upstream of IS1004 transposase **vc0870**
460	2782151	2782911	cAMP-regulatory protein **vc2614**
460	107395	108097	cytochrome c4 **vc0112**
450	2783856	2784067	N-succinylglutamate 5-semialdehyde dehydrogenase **vc2616**
450	2954047	2954571	ATP synthase F0F1 subunit delta **vc2767**
450	2856763	2857292	6-phosphofructokinase **vc2689**
450	1976501	1977100	peptidoglycan-associated lipoprotein **vc1835**
440	1385378	1386948	putative fumarate hydratase, class I **vc1304**
440	2393494	2393849	nitrogen regulatory protein P-II **vc2239**
430	1530646	1531594	putative stress protein **vc1433**
415	2055506	2056621	alanine dehydrogenase **vc1905**
410	1050496	1051173	Adenylate kinase **vc0986**
410	77365	77729	universal stress protein B, ppGpp-dependent, membrane associated **vc0079**
400	2348056	2349080	chemotaxis protein **vc2202**
400	803130	803283	HesB family protein **vc0750**
400	1100574	1101161	uridine phosphorylase **vc1034**
390	354674	355141	2,3-bisphosphoglycerate-independent phosphoglycerate mutase **vc0336**
390	2130297	2130520	putative aspartate amino transferase **vc1977**
390	302338	302528	Acetyl-CoA carboxylase, biotin carboxylase **vc0295**
390	2513905	2514095	uncharacterized protein **vc2357**
380	2218550	2219998	chemotaxis protein **vc2063**
380	2610643	2611874	outer membrane channel protein **vc2436**

370	2944713	2945721	3-ketoacyl-CoA thiolase **vc2759**
370	2343586	2343966	flagellar basal-body rod protein **vc2196**
370	1801911	1802093	intergenic region between **vc1669** and **vc1670**
350	564667	565745	RNA polymerase sigma factor-38 **vc0534**
350	348760	349396	anti-RNA polymerase sigma 70 factor **vc0330**
350	96097	97811	methyl accepting chemotaxis protein **vc0098**
340	2581316	2582415	dihydrolipoyl dehydrogenase **vc2412**
340	2446158	2446782	Na(+)-translocating NADH-quinone reductase subunit **vc2291**
330	2524608	2525234	aerobic respiration control protein **vc2368**
330	2345436	2346180	basal-body rod modification protein **vc2198**
330	1407889	1408268	uncharacterized proteins **vc1322** and **vc1323**
330	2143461	2143732	uncharacterized protein **vc1991**
320	2584882	2587569	pyruvate dehydrogenase E1 component **vc2414**
320	792153	792676	putative Acetoin utilization protein **vc0737**
320	1381458	1382755	serine transporter **vc1301**
320	1396268	1396793	methyl-accepting chemotaxis protein **vc1313**
320	2799112	2799302	DamX-related protein **vc2627**
310	2214140	2214592	purine-binding chemotaxis protein **vc2059**
310	1336667	1336810	uncharacterized protein **vc1262**
300	2220725	2221154	chemotaxis protein **vc2065**
300	1021344	1021482	intergenic region between **vc0956** and **vc0957**
290	2263005	2263276	intergenic region between **vc2105** and **vc2106**
280	1114605	1114725	intergenic region between **vc1045** and **vc1046**
280	1061324	1062905	PTS systemN-acetylglucosamine-specific transporter subunit **vc0995**
280	2801124	2801281	fimbrial assembly protein **vc2630**
280	132624	132718	uncharacterized protein **vc0138**
270	665838	666197	essential respiratory protein A, iron-sulfur insertion prot **vc0627**
270	2346618	2347031	flagellar basal body rod protein **vc2200**
270	2221925	2222617	site-determining protein **vc2067**
260	2587569	2588098	pyruvate dehydrogenase complex repressor v**c2415**
260	53506	53590	uncharacterized protein **vc0059**
250	2349799	2350245	negative regulator of flagellin synthesis **vc2204**
250	2288320	2288626	flagellar hook-basal body complex protein **vc2134**
250	2627926	2628183	CTP synthase **vc2448**
250	422634	423163	single-stranded DNA-binding protein **vc0397**
250	2420288	2420723	UPF0325 protein **vc2264**
250	2252772	2252962	upstream of **vc2091**
250	937693	937804	uncharacterized protein **vc0874**
240	2549464	2549770	upstream of RNA-directed DNA polymerase **vc2385** **IGR3**
230	2839602	2840135	regulator of ribonuclease activity A **vc2672**
220	1401314	1402103	outer membrane protein **vc1318**

Peak: the highest number of RNA sequences aligned to a specific nucleotide the region. Grey box: region contains a sRNA. **Start** and **end**: positions in the chromosome. Orange box: cytoplasmic location, Blue box:

inner membrane location, Red box: outer membrane location, Purple box: membrane, Light yellow box: pilus association, Yellow box: flagellar association, and White box: unknown location.

Supplementary Table 1b. Alignment of sequenced vesicle RNA to *V. cholerae* N16961 chromosome II.

Peak	**Start**	**End**	**Region in N16961 chromosome II**
115300	461118	461267	intergenic region between **vca0526** and **vca0527** svch462.1
92300	783813	784124	uncharacterized protein **vca0839** **CsrB**
24200	886914	887278	uncharacterized protein **vca0935**
19400	66495	66837	major outer membrane lipoprotein **vca0059**
8400	61091	61300	uncharacterized protein **vca0052**
7590	1031448	1031574	upstream of LuxR family transcriptional regulator **vca1078**
7500	308592	309077	translation initiation factor IF-3 **vca0288** **LR-PK1**
7000	485524	485763	uncharacterized protein **vca0547** svch486.1
5800	213120	213285	upstream of GMP reductase **vca0197** svch214.1
4650	893294	893459	downstream of maltose transport system permease protein **vca0943** **MicX**
4220	817334	819261	hemagglutinin/protease **vca0865**
3090	819602	820290	outer membrane protein **vca0867**
2700	284969	285940	methyl-accepting chemotaxis protein **vca0268**
2180	627734	628099	uncharacterized protein **vca0689**
2180	893459	893603	maltose transport system permease protein **vca0943** svch894.2
1670	834562	835685	uncharacterized protein **vca0883**
1600	4061	4387	uncharacterized protein **vca0004**
1430	308245	308592	upstream of translation initiation factor IF-3 **vca0288**
1370	487754	488020	uncharacterized protein **vca0551**
1140	203421	203797	cold shock DNA-binding domain-containing protein **vca0184**
1100	39233	40071	upstream of and uncharacterized protein **vca0032**
1020	232124	232329	upstream of uncharacterized protein **vca0213** svch233.1
1010	994761	994875	upstream of PTS system mannitol-specific EIICBA component **vca1045** **MtlS**
950	88629	89022	uncharacterized protein **vca0078**
830	776851	776956	uncharacterized protein **vca0831**
660	629320	630236	acetyl-CoA reductase **vca0691**
630	833061	833490	uncharacterized protein **vca0881**
610	628099	629320	acetyl-CoA acetyltransferase **vca0690**
580	971762	972073	uncharacterized protein **vca1024**
560	532373	532660	hemolysin **vca0594**
550	237171	237395	upstream of hemolysin **vca0219**
530	220268	220397	pseudo **vca0203**
510	684347	685544	uncharacterized protein **vca0738**
500	508610	509011	uncharacterized protein **vca0571**
500	871320	871655	uncharacterized protein **vca0919**
500	929290	929858	uncharacterized protein **vca0981**
490	1003717	1004369	uncharacterized protein **vca1054**
480	546334	546515	uncharacterized protein **vca0609**
450	556852	558082	upstream of and transaldolase **vca0623** svch557.1
430	702687	702937	arginine ABC transporter, permease protein **vca0758**
420	833490	834562	uncharacterized protein **vca0882**
410	678373	678819	uncharacterized protein **vca0732**
400	89052	90407	uncharacterized protein **vca0079**
400	204597	205022	uncharacterized protein **vca0186**
400	760422	760987	agmatinase **vca0814**

390	292709	292829	upstream of IS1004 transposase **vca0275**
390	854501	855376	uncharacterized protein **vca0900**
370	38714	39233	methyl-accepting chemotaxis protein **vca0031**
370	508251	508610	translation initiation factor Sui1 **vca0570**
360	1050275	1050461	chemotaxis protein **vca1095**
360	1052862	1053168	uncharacterized protein **vca1097**
350	1068928	1069971	spermidine/putrescine ABC transporter, periplasmic spermidine/putrescine-binding protein **vca1113**
340	1029148	1029441	uncharacterized protein **vca1075**
330	713202	713355	uncharacterized protein **vca0769**
320	42217	43058	uncharacterized protein **vca0034**
320	760210	760373	intergenic region between **vca0813** and **vca0814**
320	601944	602091	probable anaerobic C4-dicarboxylate transporter **vca0665**
310	787274	787400	downstream of glyceraldehyde 3-phosphate dehydrogenase **vca0844**
310	86599	86766	sulfate permease family protein **vca0077**
300	471351	471626	Sec-independent protein translocase protein **vca0533**
300	1068580	1068928	tRNA(Met) cytidine acetyltransferase **vca1112**
290	295897	296280	glycine cleavage system H protein **vca0277**
290	855376	856001	uncharacterized protein **vca0901**
280	184104	184447	cold shock transcriptional regulator **vca0166**
280	483866	484022	upstream of uncharacterized protein **vca0546** svch484.1
280	750895	751260	uncharacterized protein **vca0806**
280	1049376	1049696	purine-binding chemotaxis protein **vca1093**
270	1026467	1026730	bifunctional proline dehydrogenase/pyrroline-5-carboxylate dehydrogenase **vca1073**
270	637183	637351	upstream of Glucose-1-phosphate adenylyltransferase 2 **vca0699**
260	993053	993422	Ccm2-related protein **vca1042**
260	897542	897683	intergenic region between **vca0945** and **vca0946**
260	969225	969635	uncharacterized protein **vca1021**
250	854000	854194	uncharacterized protein **vca0899**
240	194828	195055	uncharacterized protein **vca0177**
240	531212	532265	uncharacterized protein **vca0593**
240	1021264	1021692	sodium/proline symporter **vca1071**
240	1022765	1023456	uncharacterized protein **vca1072**
230	333994	334479	uncharacterized protein **vca0332**
230	580379	580807	uncharacterized protein **vca0645**
230	876133	876422	methyl-accepting chemotaxis protein **vca0923**
220	860933	861670	methyl-accepting chemotaxis protein **vca0906**
220	832592	833042	uncharacterized protein **vca0880**
210	180156	180453	upstream of tryptophanase **vca0161**

Peak: the highest number of RNA sequences aligned to a specific nucleotide the region. Grey box: region contains a sRNA. **Start** and **end:** positions in the chromosome. Orange box: cytoplasmic location, Red box: outer membrane location, Blue box: inner membrane location, Light blue box: periplasmic location, Purple box: membrane, Green box: secreted protein, and White box: unknown location.

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