



Fig. S1. Length distribution of *V. parahaemolyticus* unique transcripts.

Table S1. Growth of bacteria affected by neutralizer.

Group	Design	Colony count (CFU/ml)
1	ozone water + <i>bacterial suspension</i>	$7.02 \pm 0.32 \times 10^4$
2	(ozone water + <i>bacterial suspension</i>) + neutralizer	$8.23 \pm 0.14 \times 10^5$
3	(neutralizer + ozone water)+ <i>bacterial suspension</i>	$2.07 \pm 0.26 \times 10^6$
4	neutralizer + <i>bacterial suspension</i>	$2.24 \pm 0.26 \times 10^6$
5	normal saline + <i>bacterial suspension</i>	$2.34 \pm 0.43 \times 10^6$
6	normal saline + neutralizer	0

Table S2. IDs and primer sequences of genes for qPCR.

Gene ID	Forward primer sequence (5'-3')	Reversed primer sequence (5'-3')
16s	GTTGGTGAGGTAAGGGCTCA	GCTGATCATCCTCTCAGACCA
VP1911	ACACGCTTACTTCACTTCTATG	CGACTTAATTTCTTTTTGGAAC
VP2004	CAAGAAGGTTCTAGCCAATACAC	CTAACATGTAAGAAATGCCTAATC
VP2010	CGCTATCAAATCGTGAAATGG	GGCTGTTGGTTTAAGACTCG
VP2266	TCGTACAATTCAAGATGTAATAAG	ATATCTCTCTCCGATCTAAAAC
VP2269	GGATAAAGGCAATGATTACTTC	GAATGTCCAATGTAGATCGTAG
VP2300	AGAGTAATGATCGGTGCAGTG	CTTTGTTTTGTGAAGCTTTGATTG
VP2421	CCTGCGTCAGACAAACTAAG	GCCAAATACATCGGACAACG
VP2422	GGTCGCTGTCACGTGCAAACG	CCGATAGACGCTTCCCACAG
VP2502	AGATTTCAATTATTAACGTCGAG	CAAGTAGCTAACTTCAGTTGTC
VP2517	TAATCTTCGACAAAGAACTCATG	GATTGAACCTTCAAATACTTCAG
VP2714	GAAACTGGGTTTTGAATTTGTAG	TCAGTTAAAGACTCTTCCAGAGC
VP2937	ATCGTTAATGCGTTACAAAGTAG	GATCAACATAGCTTGAATACCAC
VP3025	CTACTCAGACAAACCATCAAATTC	GTCTTTGGTTATAGACATGGTC
VPA0061	GCAAGAGTCTGTGAATGTGC	CGCAGAATGGTCGTAAAGAC
VPA0084	CACACATCAGAACAGCTATTAC	GAATCACATTTCGTACAGACAC
VPA0152	CAGATCATCCTTGTCTATTAGC	TCGTTTTGATAAACAGAAAGAAC
VPA0170	CTAGAAACCAAACAGCTTGGTC	CTTCTAGCACCAGATCCAGC
VPA0335	GAGTGAAAGTCTCTGCCCTG	GCTCTTTGTTAGGAGCTTGG
VPA0376	AGTTTGCATATCAAGCAGTTG	TGATAAGCAGTAAACGTGAAAC
VPA0593	GTGTCAGACAAAAAGAAAGTATGC	GATGATCTTGGCTAAAGTAAACGTAAG
VPA0637	GTATTGATTCTGTATTTGGTGAC	ACCGAAGTACTTGTGTAGATTG
VPA1052	GTTTTGCTAATACATCCATTTC	TAAGGAAAGACTCAAGTTCTGG
VPA1070	CCGCTTGTAGTAATCAACAAGC	CTTATTCAATTTCGTTATCGCACC
VPA1388	TCTAGCCAAATGAATAAATCCTG	AAGTGCTAGCTCCTTTGATATG
VPA1635	ATTGAGTACTACTGTCGTCAAATC	GAAATCGTAGAATTGTTTACCAG
VPA1642	TTACAAAGGGAATAACTTCTACC	TCTTTAATATCCACAACCGTATC
VPA1690	TTGATAACTTAAATGATCCCAAC	AGAATCATATTGTTTTTGAAG
VPA1717	GTTCAGGTGTTTCATTCATATTC	CTAGCTTACTCGACATGAACTC

Table S3. Summary of transcriptome sequencing dataset.

	Control	0.1 mg/l	1 mg/l
No. of reads	16,505,110	17,348,408	22,299,186
No. of clean reads	5,695,016	5,632,096	3,737,032
No. of mapped reads	5,565,170	5,512,696	3,463,481

Table S4. Log-transformed expression ratios from RNA-seq and qPCR.

Concentration of aqueous ozone (mg/L)	Gene ID	RNA-seq	qPCR
0.1	VP1911	-3.05652	-3.275
0.1	VPA1388	-2.53545	-2.638
0.1	VP3025	-1.60169	-1.493
0.1	VP2004	-1.26658	-1.158
0.1	VPA0637	-1.11581	-1.494
0.1	VPA1052	-0.5013	-0.1549
0.1	VPA0376	3.44252	1.93
0.1	VPA1717	1.77251	1.687
0.1	VP2714	1.66639	1.956
0.1	VPA1690	1.35203	1.568
0.1	VPA1635	1.0889	1.73
0.1	VP2300	0.507421	0.198
1	VPA1642	5.37205	4.289
1	VPA0152	4.53734	4.636
1	VP2502	3.82387	3.841
1	VP2266	2.95338	3.834
1	VPA0593	-4.70976	-6.534
1	VPA0061	-4.48137	-5.329
1	VP2937	-3.61704	-3.164
1	VP2517	-2.99392	-2.949
1	VP2269	-0.28771	-0.637

Table S5. IDs and annotation of differentially genes with expression levels more than 2-fold.

Gene ID	Gene description	Log ₂ (fold change)	p-value
0.1 mg/l			
VPA0376	putative transcriptional regulator, LysR family	3.443 up	0.00075
VP2857	inhibitor of the cpx response; periplasmic adaptor cpxP protein	2.938 up	0.00005
VP1733	hypothetical protein	1.974 up	0.03625
VP1732	oxidoreductase, short-chain dehydrogenase/reductase family	1.945 up	0.0163
VPA1731	putative C4-dicarboxylate transport sensor protein	1.861 up	0.0007
VPA1734	hypothetical protein	1.851 up	0.0114
VP2859	sensory histidine kinase in two-component regulatory system with CpxR	1.797 up	0.00845
VPA1717	transcriptional regulator, AsnC family	1.773 up	0.03745
VPA1700	mannonate dehydratase	1.710 up	0.0034
VP2714	aminotransferase, class V	1.666 up	0.00235
VPA1287	putative transporter	1.614 up	0.0031
VPA1719	hypothetical protein	1.614 up	0.00265
VP2197	conserved hypothetical protein	1.558 up	0.0458
VPA0857	hypothetical protein	1.558 up	0.00435
VPA1692	hypothetical protein	1.548 up	0.0035
VPA0413	conserved hypothetical protein	1.479 up	0.0399
VPA0140	conserved hypothetical protein	1.477 up	0.00795
VPA1720	putative acetyltransferase	1.471 up	0.0101
VP3064	multidrug resistance protein	1.464 up	0.0299
VP3052	FixG-related protein	1.463 up	0.0074
VPA1739	oligopeptide ABC transporter, periplasmic oligopeptide-binding protein	1.432 up	0.0486
VPA1713	putative transcriptional regulator	1.403 up	0.0085
VPA1703	putative small integral C4-dicarboxylate membrane transport protein	1.389 up	0.01225
VPA0569	putative permease	1.370 up	0.01395
VPA1693	hypothetical protein	1.363 up	0.032
VPA1690	RNA polymerase sigma-70 factor, ECF subfamily	1.352 up	0.01305
VPA1147	putative phenylacetate-CoA ligase	1.222 up	0.04185
VPA0594	hypothetical protein	1.221 up	0.01695
VPA1695	6-phospho-beta-glucosidase	1.221 up	0.03505
VPA0061	hypothetical membrane protein	1.210 up	0.02195
VPA1689	putative transcriptional regulator	1.139 up	0.03585
VPA1635	ornithine decarboxylase, inducible	1.089 up	0.03745
VP2762	conserved hypothetical protein	1.061 down	0.04755
VPA0995	hypothetical protein	1.076 down	0.0338
VPA1017	transcriptional regulator, AraC/XylS family	1.100 down	0.03185
VPA0637	arginine ABC transporter, periplasmic arginine-binding protein	1.116 down	0.0454
VP2421	AAA family ATPase	1.125 down	0.03235
VP2338	chitinase	1.154 down	0.03865
VP2004	hypothetical protein	1.267 down	0.0315
VP1996	conserved hypothetical protein	1.325 down	0.03505
VPA0614	hypothetical protein	1.345 down	0.0373

Table S5. IDs and annotation of differentially genes with expression levels more than 2-fold.

VP2251	FlaM	1.352 down	0.02915
VPA0171	hypothetical protein	1.397 down	0.0077
VP2419	putative pilus assembly transmembrane protein	1.419 down	0.00865
VP2414	hypothetical protein	1.478 down	0.02465
VPA1039	hypothetical protein	1.487 down	0.0365
VP2427	putative transcriptional regulator, LysR family	1.515 down	0.04925
VP2420	putative pilus assembly protein	1.555 down	0.0042
VPA0600	putative arylsulfatase AtsD	1.579 down	0.0257
VP2409	hypothetical protein	1.590 down	0.00395
VP3025	ThiF protein	1.602 down	0.039
VPA0429	conserved hypothetical protein	1.674 down	0.04165
VPA0084	putative transporter protein	1.685 down	0.0031
VP1964	putative long-chain-fatty-acid-CoA ligase	1.695 down	0.03045
VP2417	hypothetical protein	1.725 down	0.00125
VP1919	hypothetical protein	1.741 down	0.0432
VPA0935	hypothetical protein	1.841 down	0.0125
VP2412	putative pilus assembly protein	1.843 down	0.00065
VP2010	putative tetrathionate reductase complex: sensory histidine kinase	1.907 down	0.0279
VP2398	galactokinase	1.934 down	0.00745
VP2413	putative pilus assembly protein	1.936 down	0.00175
VP2422	prepilin peptidase	1.951 down	0.00005
VPA1125	putative acyl-CoA dehydrogenase	1.961 down	0.0243
VP2749	putative fimbrial assembly protein PilN	2.021 down	0.03485
VPA0335	SoxR protein	2.051 down	0.02075
VP2410	putative tight adherence TadC-related transmembrane protein	2.054 down	0.00155
VP2001	conserved hypothetical protein	2.121 down	0.02915
VP1980	putative Fe-S oxidoreductase family 2	2.242 down	0.00025
VP2159	putative methyl-accepting chemotaxis transmembrane protein	2.251 down	0.00085
VPA0244	hypothetical protein	2.326 down	0.01865
VP2525	type IV pilin biogenesis protein PilC	2.369 down	0.03305
VPA1388	hypothetical protein	2.535 down	0.01325
VP2411	putative tight adherence TadB-related transmembrane protein	2.623 down	0.0056
VP2418	hypothetical protein	2.733 down	0.0244
VP1911	extracellular solute-binding protein, family 7	3.057 down	0.00675
1 mg/l			
VPA1642	putative CymC protein	5.372 up	0.00505
VPA0436	putative resolvase	5.372 up	0.0028
VPA0152	biopolymer transport protein ExbB-related protein	4.537 up	0.00035
VPA1031	hypothetical protein	4.537 up	0.012
VPA1321	cytotoxic necrotizing factor	3.885 up	0.0243
VP2422	prepilin peptidase	3.885 up	0.00855
VP2502	glutamyl-tRNA synthetase-related protein	3.824 up	0.0143
VPA0593	putative transcriptional regulator	3.824 up	0.00755
VPA1013	hypothetical protein	3.632 up	0.0195

Table S5. IDs and annotation of differentially genes with expression levels more than 2-fold.

VP2392	methionyl-tRNA synthetase-related protein	3.593 up	0.01715
VPA0254	L-serine dehydratase 1	3.521 up	0.01865
VP2083	phosphate acetyltransferase	3.432 up	0.00885
VPA0536	cytochrome c oxidase, subunit II	3.432 up	0.02355
VPr026	5S ribosomal RNA	3.287 up	0.04885
VPA0001	conserved hypothetical protein	3.278 up	0.04875
VP1981	putative methyl-accepting chemotaxis protein	3.217 up	0.02495
VPA0020	conserved hypothetical protein	3.212 up	0.03135
VPA0806	transcriptional regulator, TetR family	3.163 up	0.0135
VPA0039	conserved hypothetical protein	3.156 up	0.0289
VP2389	putative membrane transport protein	3.058 up	0.03575
VPA1413	hypothetical protein	3.049 up	0.0164
VPA1378	thermostable direct hemolysin S	2.972 up	0.0369
VP2266	hypothetical protein	2.953 up	0.0431
VPA0811	PTS system, fructose-specific IIBC component	2.916 up	0.03845
VPA0259	hypothetical protein	2.77 up	0.0279
VP2010	sensory histidine kinase	2.751 up	0.0497
VPA0819	amino acid ABC transporter, permease protein	2.701 up	0.0337
VPA0122	hypothetical protein	2.472 up	0.04335
VPA1363	putative chaperone	2.447 down	0.04225
VPA1543	flagellar biosynthetic protein	2.565 down	0.0341
VPA0314	hypothetical protein	2.760 down	0.0206
VPA0631	putative protoheme IX farnesyltransferase	2.917 down	0.0202
VPA1017	transcriptional regulator, AraC/XylS family	2.994 down	0.04085
VP2517	dihydrolipoamide dehydrogenase (E3 component of 2-oxoglutarate dehydrogenase complex)	3.02 down	0.01885
VPA0550	hypothetical protein	3.182 down	0.03375
VPA1019	conserved hypothetical protein	3.228 down	0.01175
VP2068	Mrp protein	3.283 down	0.0289
VPA0162	putative adhesion protein	3.312down	0.02425
VP2534	signal recognition particle protein	3.362 down	0.0063
VP2421	hypothetical protein	3.598 down	0.0283
VPA0084	putative transporter protein	3.617 down	0.02155
VPA0171	hypothetical protein	3.710 down	0.02045
VPA0830	putative AraC-family transcriptional regulatory protein	3.798 down	0.0198
VP2937	hypothetical protein	4.033 down	0.0179
VPA1152	putative long-chain-fatty-acid-CoA ligase	4.167 down	0.04125
VPA0061	hypothetical membrane protein	4.481 down	0.016
VPA1736	toxin secretion ATP-binding protein	4.710 down	0.0139