

Supplemental Material

Table S1. Genes upregulated by CHP stress.

Open reading frame ^a	Gene	Predicted function	Fold-change (CHP/control)
Antioxidant enzymes			
CV_0209	<i>ohrA</i>	organic hydroperoxide resistance protein	61.45
CV_0300		probable cytochrome-c peroxidase	3.19
CV_1107	<i>gpx</i>	glutathione peroxidase	9.18
CV_2036	<i>garA</i>	probable peroxiredoxin/glutaredoxin family protein	75.25
CV_2504	<i>sodB1</i>	superoxide dismutase, Fe-Mn family	2.40
CV_2815	<i>bcp</i>	bacterioferritin comigratory protein; peroxiredoxin Q/BCP	2.00
CV_3549	<i>katE</i>	catalase	72.90
Reducing systems			
CV_1106	<i>trxC</i>	thioredoxin 2	19.54
CV_1164	<i>gst1</i>	glutathione S-transferase family protein	2.26
CV_2037	<i>garB</i>	probable dihydrolipoamide dehydrogenase	85.30
CV_2424	<i>gstA</i>	glutathione S-transferase	7.79
CV_2813	<i>trxB</i>	thioredoxin reductase (NADPH)	3.26
CV_4275	<i>gshB</i>	glutathione synthetase protein	2.43
CV_4276	<i>gshA</i>	glutamate-cysteine ligase	2.72
Glyoxalases/Oxidoreductases			
CV_0197		hypothetical protein (Glyoxalase//Dioxygenase superfamily)	3.85
CV_0969	<i>hpd</i>	4-hydroxyphenylpyruvate dioxygenase	3.14
CV_1319		conserved hypothetical protein (Glyoxalase//Dioxygenase superfamily)	3.52
CV_2043		probable quinone oxidoreductase; NADPH2:quinone reductase	4.23
CV_2341		conserved hypothetical protein (Glyoxalase//Dioxygenase superfamily)	4.47
CV_2565		probable oxidoreductase	7.63
CV_3486		conserved hypothetical protein (Glyoxalase/Dioxygenase superfamily)	11.84
CV_3500	<i>nfsA</i>	oxygen-insensitive NADPH nitroreductase; FMN reductase [NAD(P)H]	15.66
CV_3501	<i>nemA1</i>	NADH-dependent oxidoreductase; N-ethylmaleimide reductase	21.25
Degradation of aromatic compounds			
CV_0993	<i>pcaK</i>	MFS transporter, AAHS family, 4-hydroxybenzoate transporter	2.58
CV_3287		probable tautomerase	5.44
CV_3288	<i>pcaC</i>	4-carboxymuconolactone decarboxylase	7.63
CV_3550		conserved hypothetical protein (aromatic ring-opening dioxygenase)	15.36
DNA damage/repair			
CV_0578		guanine deaminase	2.54
CV_1363		trans-acting regulatory HvrA protein; DNA-binding protein H-NS	3.12
CV_2111		probable methyltransferase; DNA adenine methylase	3.56
CV_2332	<i>umuD</i>	SOS mutagenesis; DNA polymerase V	4.10
CV_2814		conserved hypothetical protein (Smr domain)	2.59
CV_3229		deoxyribodipyrimidine photolyase-related protein	2.26
CV_3481	<i>phrB</i>	deoxyribodipyrimidine photo-lyase	4.79
CV_4253	<i>dps</i>	DNA-binding stress protein; starvation-inducible DNA-binding protein	4.45
Heat shock response (sigma RpoH)			
CV_0401	<i>hslV</i>	heat shock protein; ATP-dependent HslUV protease	7.26
CV_0402	<i>hslU</i>	heat shock protein hslU; ATP-dependent HslUV protease	6.34
CV_1177		probable small heat shock protein; HSP20 family protein	8.86
CV_1318	<i>hptG</i>	probable chaperone heat shock protein hptG	3.27
CV_1642	<i>grpE</i>	heat shock protein GrpE	5.43
CV_1643	<i>dnaK</i>	heat shock protein DnaK; chaperone protein	4.07
CV_1944	<i>clpB</i>	ATP-dependent Clp protease subunit; heat-shock protein	23.09
CV_2555	<i>lon</i>	endopeptidase La; ATP-dependent Lon protease	4.98
CV_3232	<i>groES</i>	GroES; chaperonin 10kD subunit	3.93

CV_3233	<i>groEL</i>	chaperonin 60kD subunit	2.25
CV_3668		ATP-dependent Clp protease adaptor protein ClpS	8.87
CV_3669	<i>clpA</i>	ATP-dependent Clp protease, ATP-binding subunit	7.00
CV_4014	<i>groEL1</i>	chaperonin 60kD subunit	5.46
CV_4015	<i>groES1</i>	chaperonin 10kD subunit	4.96
CV_4206	<i>rpoH</i>	RNA polymerase sigma-32 factor	3.23
Iron uptake systems (Fur regulon)			
CV_0077		probable TonB-dependent receptor	3.00
CV_0398	<i>exbD2</i>	biopolymer transport exbD transmembrane protein	11.23
CV_0399		probable exbB-like biopolymer transport	13.78
CV_0400		periplasmic protein TonB	8.60
CV_0793		probable nitrogen fixation protein VnfA	2.11
CV_0794		probable high-affinity iron permease	2.69
CV_0795		hypothetical protein (Cupredoxin-like domain)	3.24
CV_0796		periplasmic iron binding protein	7.96
CV_1481	<i>aroF</i>	2-dehydro-3-deoxy-phosphoheptonate aldolase	40.54
CV_1482	<i>entA</i>	2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase	60.68
CV_1483	<i>entB</i>	bifunctional isochorismate lyase/aryl carrier protein	56.75
CV_1484	<i>entE</i>	2,3-dihydroxybenzoate-AMP ligase	44.76
CV_1485	<i>entC</i>	isochorismate synthase EntC / MenF	26.54
CV_1486	<i>entF</i>	enterobactin synthetase component F	41.81
CV_1487		probable iron transport system ATP-binding protein	9.68
CV_1488	<i>ecD</i>	ferric citrate transport system permease protein	9.18
CV_1489		probable periplasmic substrate-binding transport protein	9.54
CV_1490		conserved hypothetical protein	9.03
CV_1491		outer membrane receptor for ferrienterochelin and colicins	21.04
CV_1971		conserved hypothetical protein	2.04
CV_1972	<i>exbB1</i>	biopolymer transport protein	2.77
CV_1973	<i>exbD5</i>	biopolymer transport exbD transmembrane protein	2.60
CV_1974	<i>exbD3</i>	biopolymer transport exbD transmembrane protein	2.64
CV_1982		probable tonB dependent receptor	5.35
CV_1983		periplasmic protein TonB	2.48
CV_1986	<i>exbD4</i>	biopolymer transport exbD transmembrane protein	2.49
CV_2230	<i>fepA</i>	enterobactin-iron outermembrane receptor protein	21.68
CV_2231	<i>fes</i>	enterochelin esterase	18.86
CV_2232		probable MbtH-like protein	46.87
CV_2233	<i>cbsF</i>	synthetase CbsF	4.57
CV_2234	<i>fepC</i>	enterobactin-iron transport system ATP-binding protein	11.10
CV_2235	<i>fepG</i>	enterobactin-iron transport system permease protein	10.78
CV_2236	<i>fepD</i>	enterobactin-iron transport system permease protein	4.16
CV_2237		MFS transporter, ENTS family, enterobactin (siderophore) exporter	9.70
CV_2239	<i>fepB</i>	ferrienterobactin-binding periplasmic protein precursor	20.84
CV_2251	<i>thiA</i>	ferrichrome-iron outermembrane receptor protein	17.79
CV_2387	<i>ribE</i>	riboflavin synthase, alpha chain	5.41
CV_2388		conserved hypothetical protein	4.58
CV_2389	<i>ribAB</i>	riboflavin biosynthesis bifunctional protein	3.62
CV_3895		hypothetical protein (Hemin uptake protein hemP)	22.72
CV_3896		TonB-dependent receptor; hemoglobin/transferrin/lactoferrin receptor	35.35
CV_3897		probable hemin degrading factor	36.73
CV_3898		probable permease of ABC transporter; iron complex transport system	15.55
CV_3899	<i>fecE</i>	ferric citrate transport system ATP-binding protein	7.76
CV_4254		periplasmic protein TonB	2.81
Nitrogen starvation response (NtrC regulon)			
CV_0118	<i>gltK</i>	glutamate/aspartate transport system permease protein	2.47
CV_3589	<i>glnA</i>	glutamine synthetase	6.57
CV_3591	<i>ntrB</i>	two-component sensor NtrB; nitrogen regulation histidine kinase GlnL	2.73
CV_3592	<i>glnG</i>	NtrC family, nitrogen regulation response regulator GlnG	3.27
CV_4002	<i>glnK</i>	nitrogen regulatory protein P-II-2; nitrogen regulatory protein P-II 2	39.44

CV_4003	<i>amtB</i>	ammonium transporter, Amt family	32.43
CV_4038	<i>gltB</i>	glutamate synthase (NADPH/NADH) large chain	2.31
Efflux systems			
CV_0921	<i>chrB</i>	chromate resistance signal peptide protein	3.90
CV_0922	<i>chrA</i>	chromate ion transporter protein	3.83
CV_1154	<i>zntA</i>	lead,cadmium,zinc and mercury exporting ATPase	2.32
CV_1179		probable multidrug resistance protein	3.87
CV_1180	<i>estX</i>	esterase/lipase	2.80
CV_1181		hypothetical protein	2.91
CV_2240		probable multidrug efflux protein; membrane fusion protein	18.91
CV_2241	<i>acrB</i>	acriflavin resistance protein B; multidrug efflux pump	25.62
CV_2242	<i>ibeB</i>	outer membrane drug efflux lipoprotein	16.16
CV_3923		probable transport/efflux transmembrane protein	2.40
CV_3924		probable transmembrane drug efflux protein	3.15
Signal transduction/Regulatory function			
CV_0208		hypothetical protein (GGDEF domain)	9.21
CV_0210	<i>ohrR</i>	MarR family transcriptional regulator	23.08
CV_0239		conserved hypothetical protein (Protoglobin; GGDEF domain)	2.53
CV_0657		conserved hypothetical protein (EAL domain)	2.60
CV_1095		Rrf2 family transcriptional regulator, iron-sulfur cluster assembly	2.44
CV_1827	<i>cbl</i>	LysR family transcriptional regulator, cys transcriptional activator	2.09
CV_1919		conserved hypothetical protein (Response regulator receiver domain)	3.19
CV_3480		probable transcriptional regulator, AraC family	2.80
CV_3533	<i>hfq</i>	host factor-I protein	3.04
CV_3631		probable transcriptional regulator AraC family	2.56
CV_3713		probable transcriptional regulator (AraC family)	2.75
CV_3860		hypothetical protein (Helix-turn-helix domain)	4.60
CV_3922		probable transcription regulator, TetR family	2.22
CV_4096		GntR family transcriptional regulator / MocR family aminotransferase	2.49
Fatty acid modification			
CV_1644	<i>desD</i>	linoleoyl-CoA desaturase	2.21
CV_3226	<i>cfa</i>	cyclopropane-fatty-acyl-phospholipid synthase	3.19
Transport and metabolism of peptides and amino acids			
CV_0057	<i>lasB</i>	class 4 metalloprotease; pseudolysin	2.28
CV_0315		probable peptidase	3.22
CV_0405		probable amino acid ABC transporter; substrate-binding protein	3.38
CV_0586	<i>ilvI</i>	acetolactate synthase isozyme III, large subunit	3.38
CV_0587	<i>ilvH</i>	acetolactate synthase isozyme III, small subunit	3.92
CV_0588	<i>ilvC</i>	ketol-acid reductoisomerase	3.70
CV_0852	<i>argT</i>	subunit of the lysine/arginine/ornithine transporter (ABC superfamily)	2.21
CV_0853	<i>hisQ1</i>	histidine transport system permease protein	2.47
CV_0854	<i>hisM1</i>	histidine transport system membrane protein M	2.77
CV_0876	<i>prtC</i>	oligopeptidase A	6.48
CV_1097		probable binding protein component of ABC dipeptide transporter	3.57
CV_1098	<i>dppB</i>	dipeptide transport system permease protein	2.45
CV_1292	<i>ctaQ</i>	carboxypeptidase Taq	3.50
CV_1934	<i>metY</i>	O-acetylhomoserine (thiol)-lyase	2.08
CV_1992		probable lysine decarboxylase	2.55
CV_1994	<i>argG</i>	argininosuccinate synthase	2.54
CV_2094	<i>ilvE</i>	branched-chain-amino-acid transaminase	2.26
CV_2481		probable amino acid ABC transporter; substrate-binding protein	3.04
CV_3085	<i>aotJ</i>	arginine/ornithine transport, substrate-binding protein (ABC superfamily)	2.21
CV_3093	<i>ilvA</i>	threonine dehydratase	2.82
CV_3180	<i>phhA</i>	phenylalanine 4-monooxygenase	2.98
CV_3506		probable protease precursor; peptidyl-Lys metalloendopeptidase	4.42
CV_4329		probable oligopeptide ABC transporter system, substrate-binding protein	4.48
Miscellaneous			

CV_0362		probable thermolabile hemolysin, lecithin dependent	2.30
CV_0372		probable resistance protein; phosphinothricin acetyltransferase	3.23
CV_0762	<i>cstA2</i>	carbon starvation protein	3.55
CV_0917		probable C4-dicarboxylate transporter large subunit	2.34
CV_0918	<i>dctQ</i>	C4-dicarboxylate transport system, permease small subunit	3.08
CV_0919		probable C4-dicarboxylate-binding periplasmic protein	3.59
CV_1094	<i>nifS</i>	pyridoxal-phosphate-dependent aminotransferase;cysteine desulfurase	2.01
CV_1167		probable ABC transporter protein	2.67
CV_1184	<i>eutC</i>	ethanolamine ammonia-lyase light chain	2.00
CV_1185	<i>eutB</i>	ethanolamine ammonia-lyase heavy chain	2.82
CV_1186		probable ethanolamin permease	4.23
CV_1299		probable MFS transporter	3.21
CV_1758		probable acetyl-coenzyme A synthetase	2.16
CV_1880	<i>cynS</i>	cyanate lyase	2.83
CV_1881	<i>cynT</i>	carbonate dehydratase; carbonic anhydrase	2.72
CV_1920		probable pirin-like protein	3.40
CV_2005	<i>ribA</i>	GTP cyclohydrolase II	2.45
CV_2054	<i>acnA2</i>	aconitate hydratase	2.27
CV_2056	<i>prpC</i>	citrate synthase 2; 2-methylcitrate synthase	3.30
CV_2336		probable ThiJ/Pfpl family protein	2.88
CV_2495	<i>fliC2</i>	flagellin	2.94
CV_2816		PhoH-like ATPase	2.56
CV_3210	<i>dgt</i>	dGTPase	2.92
CV_3211	<i>gpmB</i>	phosphoglycerate mutase 2	2.50
CV_3278		probable cytochrome b561	2.26
CV_3298	<i>lamB</i>	maltoporin precursor	2.34
CV_3402	<i>trmU</i>	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase	2.41
CV_3424	<i>ompC</i>	porin signal peptide protein	2.11
CV_3511		probable signal peptide protein	2.30
CV_3653	<i>ugpC</i>	sn-glycerol-3-phosphate transport, ATP-binding protein	2.21
CV_3654		probable ABC transporter family protein	2.45
CV_3655	<i>ugpA</i>	sn-glycerol-3-phosphate transport system, permease protein	2.46
CV_3694		iron-sulfur cluster insertion protein	3.13
CV_3711		translation initiation factor 1	2.80
CV_3797	<i>hflB</i>	cell division protein FtsH	2.36
CV_4156		methyl-accepting chemotaxis protein	2.38
CV_4252		protein FxsA	3.91
CV_4264	<i>fmt</i>	methionyl-tRNA formyltransferase	2.35
CV_4265	<i>def</i>	polypeptide deformylase	2.57
CV_4281	<i>secA</i>	preprotein translocase secA subunit	2.73
CV_4335	<i>moaC</i>	molybdenum cofactor biosynthesis protein C	3.71
CV_4337	<i>lpxC</i>	UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase	3.32
CV_4376	<i>bioC</i>	biotin synthesis protein; malonyl-CoA O-methyltransferase	2.05
CV_4377	<i>bioH</i>	BioH protein; pimeloyl-[acyl-carrier protein] methyl ester esterase	2.26
		Hypothetical/Conserved hypothetical protein	
CV_0301		hypothetical protein	5.27
CV_0317		hypothetical protein	2.83
CV_0330		conserved hypothetical protein (DUF4243 domain)	12.65
CV_0397		conserved hypothetical protein (Transglutaminase-like superfamily)	2.75
CV_0636		hypothetical protein	2.86
CV_0637		hypothetical protein	2.66
CV_0658		conserved hypothetical protein (Tim44-like domain)	2.59
CV_0686		conserved hypothetical protein	2.77
CV_0801		conserved hypothetical protein (MFS domain)	2.67
CV_1165		conserved hypothetical protein; Ala-tRNA(Pro) deacylase	10.99
CV_1166		conserved hypothetical protein	12.03
CV_1210		conserved hypothetical protein	2.76
CV_1211		hypothetical protein	2.64

CV_1441	conserved hypothetical protein	6.41
CV_1617	conserved hypothetical protein	9.54
CV_2038	conserved hypothetical protein (Shigella flexneri OspC protein motif)	4.64
CV_2053	conserved hypothetical protein (PrpF protein motif)	2.03
CV_2055	conserved hypothetical protein (Glycolipid_bind)	2.65
CV_2080	conserved hypothetical protein	2.17
CV_2250	conserved hypothetical protein (PepSY-associated TM helix motif)	15.45
CV_2331	hypothetical protein	4.21
CV_2486	conserved hypothetical protein	2.28
CV_2563	hypothetical protein	3.86
CV_2564	hypothetical protein	2.90
CV_2695	hypothetical protein	3.46
CV_2696	conserved hypothetical protein (Putative modulator of DNA gyrase)	2.20
CV_2861	conserved hypothetical protein (SnoaL-like domain)	14.23
CV_2900	hypothetical protein	2.71
CV_2902	conserved hypothetical protein	15.18
CV_2970	conserved hypothetical protein	23.97
CV_3225	conserved hypothetical protein	2.62
CV_3228	conserved hypothetical protein (SnoaL-like domain)	2.26
CV_3276	conserved hypothetical protein (YceI-like domain)	2.44
CV_3277	conserved hypothetical protein	2.61
CV_3580	conserved hypothetical protein	2.26
CV_3632	hypothetical protein	7.64
CV_3634	conserved hypothetical protein	2.73
CV_3712	hypothetical protein	2.58
CV_3714	conserved hypothetical protein (SnoaL-like domain)	2.30
CV_3861	conserved hypothetical protein	6.40
CV_3862	conserved hypothetical protein	16.20
CV_3962	hypothetical protein	4.99
CV_4106	hypothetical protein	2.50
CV_4107	conserved hypothetical protein	3.22
CV_4308	conserved hypothetical protein (extracellular solute-binding proteins)	2.33
CV_4336	hypothetical protein	3.39
VBIBhrVio67196_0754 ^b	Hypothetical small protein yjiX	3.43
VBIBhrVio67196_1151 ^b	hypothetical protein	2.62
VBIBhrVio67196_1164 ^b	hypothetical protein	3.36
VBIChrVio67196_1450 ^b	hypothetical protein	16.49
VBIChrVio67196_1608 ^b	hypothetical protein	2.05
VBIChrVio67196_1918 ^b	hypothetical protein	2.75
VBIChrVio67196_1943 ^b	hypothetical protein	2.28
VBIChrVio67196_3145 ^b	Putative lipoprotein precursor	2.63
VBIChrVio67196_3148 ^b	hypothetical protein	2.18
VBIChrVio67196_3323 ^b	Bacterioferritin-associated ferredoxin	5.03
VBIChrVio67196_3428 ^b	hypothetical protein	69.44
VBIChrVio67196_3790 ^b	hypothetical protein	11.59
VBIChrVio67196_3826 ^b	Periplasmic hemin-binding protein	10.80

^aORF nomenclature as described from the former *C. violaceum* genome annotation.

^bNew ORFs annotated by PATRIC (Pathosystems Integration Resource Center).

Table S2. Genes downregulated by CHP stress.

Open reading frame ^a	Gene	Predicted function	Fold-change (CHP/control)
Electron transport chain			
CV_0665		ATP synthase protein I	0.35
CV_0666	<i>atpB</i>	ATP synthase F0, A subunit; F-type H ⁺ -transporting ATPase subunit a	0.30
CV_0667	<i>atpE</i>	ATP synthase F0, C subunit; F-type H ⁺ -transporting ATPase subunit c	0.36
CV_0668	<i>atpF</i>	ATP synthase F0, B subunit; F-type H ⁺ -transporting ATPase subunit b	0.24
CV_0669	<i>atpH</i>	ATP synthase F1, delta subunit; F-type H ⁺ -transporting ATPase subunit delta	0.32
CV_0670	<i>atpA</i>	ATP synthase F1, alpha subunit; F-type H ⁺ -transporting ATPase subunit alpha	0.36
CV_0671	<i>atpG</i>	F-type H ⁺ -transporting two-sector ATPase, gamma subunit	0.41
CV_0672	<i>atpD</i>	F-type H ⁺ -transporting two-sector ATPase, beta subunit	0.47
CV_0673	<i>atpC</i>	F-type H ⁺ -transporting two-sector ATPase, epsilon subunit	0.47
CV_0944	<i>nuoD</i>	NADH-ubiquinone oxidoreductase, chain D; NADH-quinone oxidoreductase subunit D	0.36
CV_0945	<i>nuoE</i>	NADH-ubiquinone oxidoreductase, chain E; NADH-quinone oxidoreductase subunit E	0.30
CV_0946	<i>nuoF</i>	NADH-ubiquinone oxidoreductase, chain F; NADH-quinone oxidoreductase subunit F	0.30
CV_0947	<i>nuoG</i>	NADH-ubiquinone oxidoreductase, chain G; NADH-quinone oxidoreductase subunit G	0.35
CV_0948	<i>nuoH</i>	NADH-ubiquinone oxidoreductase, chain H; NADH-quinone oxidoreductase subunit H	0.37
CV_0949	<i>nuoI</i>	NADH-ubiquinone oxidoreductase, chain I; NADH-quinone oxidoreductase subunit I	0.33
CV_0950	<i>nuoJ</i>	NADH-ubiquinone oxidoreductase, chain J; NADH-quinone oxidoreductase subunit J	0.41
CV_0951	<i>nuoK</i>	NADH-ubiquinone oxidoreductase, chain K; NADH-quinone oxidoreductase subunit K	0.42
CV_1171		probable cytochrome-c oxidase, subunit III; cytochrome c oxidase cbb3-type subunit III	0.30
CV_1172		cytochrome c oxidase cbb3-type subunit IV	0.26
CV_1173		probable cytochrome-c oxidase, subunit II; cytochrome c oxidase cbb3-type subunit II	0.21
CV_1174		probable cytochrome-c oxidase, subunit I; cytochrome c oxidase cbb3-type subunit I	0.24
CV_3368	<i>frdB</i>	fumarate reductase, subunit B; fumarate reductase iron-sulfur subunit	0.47
CV_3369	<i>frdA</i>	fumarate reductase flavoprotein subunit	0.47
CV_3370	<i>dcuB</i>	anaerobic C4-dicarboxylate membrane transporter protein	0.49
CV_3992	<i>cyoE</i>	farnesyl-diphosphate farnesyltransferase; protoheme IX farnesyltransferase	0.26
CV_3993	<i>cyoD</i>	cytochrome o ubiquinol oxidase subunit IV	0.32
CV_3994	<i>cyoC</i>	cytochrome o ubiquinol oxidase, subunit III	0.22
CV_3995	<i>cyoB</i>	cytochrome o ubiquinol oxidase, subunit I	0.21
CV_3996	<i>cyoA</i>	cytochrome o ubiquinol oxidase, subunit II	0.26
CV_4007	<i>petB</i>	ubiquinol-cytochrome c reductase	0.50
CV_4008	<i>petA</i>	ubiquinol-cytochrome c reductase	0.49
Nucleotide biosynthesis			
CV_0369	<i>pyrB</i>	aspartate carbamoyltransferase catalytic chain	0.46
CV_0370	<i>pyrI</i>	aspartate carbamoyltransferase; aspartate carbamoyltransferase regulatory subunit	0.36
CV_0546	<i>purH</i>	phosphoribosylaminoimidazolecarboxamide formyltransferase / IMP cyclohydrolase	0.41
CV_0547	<i>purD</i>	phosphoribosylamine-glycine ligase	0.49
CV_1812	<i>pyrD</i>	dihydroorotate oxidase	0.40
CV_2198	<i>pyrH</i>	uridylylase kinase	0.39
CV_2284	<i>nrdB</i>	ribonucleoside-diphosphate reductase system	0.46
CV_2285		hypothetical protein	0.45
CV_2286		hypothetical protein	0.46
CV_2287	<i>nrdA</i>	ribonucleoside-diphosphate reductase system; alpha chain	0.39
CV_2922		probable GMP reductase	0.23
CV_3528	<i>purA2</i>	adenylosuccinate synthetase	0.32
CV_3834	<i>purB</i>	adenylosuccinate lyase	0.36
CV_3900	<i>hpT</i>	hypoxanthine phosphoribosyltransferase	0.29
CV_4058	<i>prsA</i>	ribose-phosphate diphosphokinase	0.27
CV_4248	<i>pyrE</i>	orotate phosphoribosyltransferase	0.32
Fatty acids metabolism			
CV_2446	<i>fabH</i>	probable 3-oxoacyl-[acyl-carrier-protein] synthase III	0.41
CV_3183	<i>fadL</i>	long-chain fatty acid transport protein precursor	0.35

CV_3412	<i>fabF</i>	3-oxoacyl-[acyl-carrier-protein] synthase II	0.42
CV_4318	<i>luxE</i>	long-chain-fatty-acid--luciferin-component ligase, Acyl-protein synthase	0.44
CV_4319	<i>luxC</i>	conserved hypothetical protein (Acyl-CoA reductase, LuxC, domain)	0.27
Signal transduction/Regulatory function			
CV_0563	<i>phoR</i>	two-component system, OmpR family, phosphate sensor histidine kinase PhoR	0.39
CV_1029		probable transcriptional regulator, GntR family	0.45
CV_3106		probable two-component sensor histidine kinase	0.34
CV_3107		two-component system, OmpR family, response regulator	0.46
CV_3378	<i>oxyR</i>	hydrogen peroxide-inducible genes activator; LysR family transcriptional regulator	0.44
CV_4220		two-component system, NtrC family, response regulator GlrR	0.46
Transport			
CV_0925	<i>potF2</i>	polyamine ABC transporter system, substrate-binding protein	0.44
CV_0938	<i>pstS</i>	ABC transporter phosphate-binding protein	0.35
CV_1105	<i>gltS</i>	sodium/glutamate symport carrier protein; glutamate:Na ⁺ symporter, ESS family	0.40
CV_1151		probable murein hydrolase exporter; holin-like protein	0.42
CV_1278		multidrug resistance signal peptide protein; spermidine export protein MdtI	0.34
CV_1279		multidrug resistance signal peptide protein; spermidine export protein MdtJ	0.47
CV_2040		sodium-dependent nucleoside transporter; concentrative nucleoside transporter	0.47
CV_2348	<i>mglA</i>	sugar ABC transporter, ATP-binding protein; simple sugar transport system	0.18
CV_2349		probable ABC transporter, permease protein; simple sugar transport system	0.21
CV_2350		probable sugar ABC transporter, permease protein	0.27
CV_2380		probable sodium-dependent transporter; neurotransmitter:Na ⁺ symporter, NSS family	0.38
CV_2704		probable ABC transporter, ATP-binding protein; macrolide transport system	0.49
CV_3100	<i>mgtA</i>	Mg ²⁺ -importing ATPase	0.26
CV_3432		probable amino acid permease; basic amino acid/polyamine antiporter, APA family	0.40
CV_3478		probable manganese transport transmembrane protein	0.25
CV_3731		MFS transporter, CP family, cyanate transporter	0.44
CV_3783	<i>arcD</i>	arginine/ornithine antiporter / lysine permease	0.47
CV_4070		ATP-binding cassette, subfamily B, multidrug efflux pump	0.44
Metabolism of tRNA, rRNA and ribosomal proteins			
CV_0544		NifR3; tRNA-dihydrouridine synthase B	0.44
CV_1353	<i>pheT</i>	phenylalanyl-tRNA synthetase beta chain	0.46
CV_1373		probable oxidoreductase; ribosomal protein S12 methylthiotransferase	0.21
CV_1932		probable RNA methyltransferase; 23S rRNA (uracil1939-C5)-methyltransferase	0.49
CV_2410	<i>typA</i>	GTP-binding protein TypA	0.31
CV_3674	<i>rimM</i>	16S rRNA processing protein	0.45
CV_3675	<i>rpsP</i>	30S ribosomal protein S16	0.44
CV_3786		S-adenosylmethionine-dependent methyltransferase	0.40
CV_4056	<i>pth</i>	aminoacyl-tRNA hydrolase	0.32
CV_4057	<i>rplY</i>	50S ribosomal protein L25	0.41
Miscellaneous			
CV_0190		glyceraldehyde 3-phosphate dehydrogenase	0.41
CV_0191	<i>tktA</i>	transketolase 1	0.43
CV_0224		probable carboxycyclohexadienyl dehydratase; cyclohexadienyl dehydratase	0.39
CV_0266		probable collagenase; putative protease	0.46
CV_1137	<i>adhE</i>	acetaldehyde dehydrogenase; alcohol dehydrogenase	0.47
CV_1170		probable iron-sulfur 4Fe-4S ferredoxin transmembrane protein	0.38
CV_1327	<i>upk</i>	undecaprenol kinase; undecaprenyl-diphosphatase	0.46
CV_1516	<i>hrpA</i>	ATP-dependent helicase hrpA; ATP-dependent helicase HrpA	0.34
CV_1529		probable transmembrane protein	0.50
CV_1530	<i>pta</i>	phosphate acetyltransferase	0.42
CV_1531	<i>ackA</i>	acetate kinase	0.41
CV_1532		probable dioxygenase, alpha subunit	0.29
CV_1538	<i>putA</i>	proline dehydrogenase; DNA-binding domain of proline dehydrogenase	0.41
CV_1650	<i>kbl</i>	glycine C-acetyltransferase	0.45
CV_1660	<i>gloA</i>	lactoylglutathione lyase	0.42
CV_1917	<i>shlB</i>	hemolysin activator protein; hemolysin activation/secretion protein	0.35
CV_1925	<i>folD</i>	methylenetetrahydrofolate dehydrogenase (NADP+)	0.46

CV_1955		probable protease	0.40
CV_2217		probable FAD-dependent dehydrogenases	0.45
CV_2347		probable membrane lipoprotein; basic membrane protein A and related proteins	0.22
CV_2449		probable coenzyme F390 synthetase	0.47
CV_2467		probable membrane lipoprotein; basic membrane protein A and related proteins	0.25
CV_2503		probable Transmembrane protein	0.44
CV_2540	<i>narI</i>	nitrate reductase gamma subunit	0.27
CV_2541	<i>narJ</i>	nitrate reductase delta subunit	0.28
CV_2542	<i>narH</i>	nitrate reductase beta subunit	0.28
CV_2543	<i>narG</i>	respiratory nitrate reductase alpha chain	0.20
CV_2637	<i>dsbG</i>	thiol:disulfide interchange protein DsbG	0.45
CV_2703		probable outer membrane protein	0.46
CV_2841	<i>rhIE2</i>	ATP-dependent RNA helicase	0.41
CV_2853	<i>dbpA</i>	ATP-dependent RNA helicase dbpA; ATP-independent RNA helicase DbpA	0.41
CV_2876	<i>speA</i>	arginine decarboxylase	0.39
CV_2892	<i>rhIE1</i>	ATP-dependent RNA helicase	0.39
CV_2904		carboxylate-amine ligase	0.43
CV_3193	<i>dsbH</i>	protein-disulfide reductase; disulfide bond formation protein DsbB	0.37
CV_3209	<i>osmB</i>	osmotically inducible lipoprotein	0.48
CV_3399	<i>bfr</i>	bacterioferritin	0.27
CV_3476	<i>fumA</i>	fumarate hydratase	0.47
CV_3529		ATP phosphoribosyltransferase regulatory subunit	0.42
CV_3530	<i>hflC</i>	membrane protease subunit HflC	0.43
CV_3584	<i>hemK</i>	HemK protein; release factor glutamine methyltransferase	0.50
CV_3639	<i>priB</i>	primosomal replication protein N	0.47
CV_3644	<i>suhB</i>	myo-inositol-1(or 4)-monophosphatase	0.40
CV_3648	<i>hemN</i>	oxygen-independent coproporphyrinogen III oxidase	0.30
CV_3791		probable FkbP-type peptidyl-prolyl cis-trans isomerase	0.50
CV_3901	<i>galU</i>	UTP-glucose-1-phosphate uridylyltransferase	0.36
CV_3926	<i>goaG</i>	4-aminobutyrate transaminase	0.47
CV_3927	<i>gabD</i>	succinate-semialdehyde dehydrogenase [NAD(P)]	0.44
CV_4004	<i>sspB</i>	stringent starvation protein B	0.46
CV_4084		probable protease	0.33
Hypothetical/Conserved hypothetical protein			
CV_0223		conserved hypothetical protein	0.42
CV_0272		conserved hypothetical protein (Gly-zipper_Omp domain)	0.37
CV_0929		hypothetical protein	0.41
CV_1169		conserved hypothetical protein (FixH domain, symbiotic nitrogen fixation)	0.42
CV_1661		conserved hypothetical protein (Citrate transporter domain)	0.49
CV_1936		conserved hypothetical protein (LysE type translocator motif)	0.49
CV_1953		hypothetical protein	0.37
CV_1963		conserved hypothetical protein (PhoPQ-activated pathogenicity-related protein motif)	0.36
CV_2047		conserved hypothetical protein	0.43
CV_2300		conserved hypothetical protein (Thioesterase superfamily domain)	0.48
CV_2409		hypothetical protein	0.48
CV_2812		hypothetical protein	0.40
CV_2851		conserved hypothetical protein (FAD binding domain)	0.45
CV_2890		hypothetical protein	0.40
CV_3069		conserved hypothetical protein (Cytochrom_C_2 domain)	0.37
CV_3077		conserved hypothetical protein (Homoserine dehydrogenase, NAD binding domain)	0.31
CV_3098		hypothetical protein	0.36
CV_3099		hypothetical protein	0.29
CV_3123		conserved hypothetical protein	0.43
CV_3147		conserved hypothetical protein	0.46
CV_3509		conserved hypothetical protein (Radical SAM superfamily domain)	0.41
CV_3566		hypothetical protein	0.43
CV_3583		conserved hypothetical protein (PAP2 superfamily domain)	0.47
CV_3788		conserved hypothetical protein	0.38

CV_4054	conserved hypothetical protein (Chain length determinant protein domain)	0.36
CV_4055	conserved hypothetical protein (Ferrous iron transport protein B domain)	0.32
CV_4108	conserved hypothetical protein	0.42
CV_4219	hypothetical protein	0.42
CV_4249	conserved hypothetical protein	0.43
CV_4304	conserved hypothetical protein (YfaZ_precursor domain)	0.48
CV_4320	conserved hypothetical protein (AMP-binding enzyme domain)	0.33
CV_4321	conserved hypothetical protein (Acetyltransferase, GNAT, family domain)	0.48
VBIChrVio67196_1489^b	hypothetical protein	0.46
VBIChrVio67196_2283^b	hypothetical protein	0.29
VBIChrVio67196_3403^b	hypothetical protein	0.31
VBIChrVio67196_3489^b	hypothetical protein	0.31
VBIChrVio67196_3711^b	hypothetical protein	0.44
VBIChrVio67196_4098^b	hypothetical protein	0.40
VBIChrVio67196_4105^b	hypothetical protein	0.37

^aORF nomenclature as described from the former *C. violaceum* genome annotation.

^bNew ORFs annotated by PATRIC (Pathosystems Integration Resource Center).

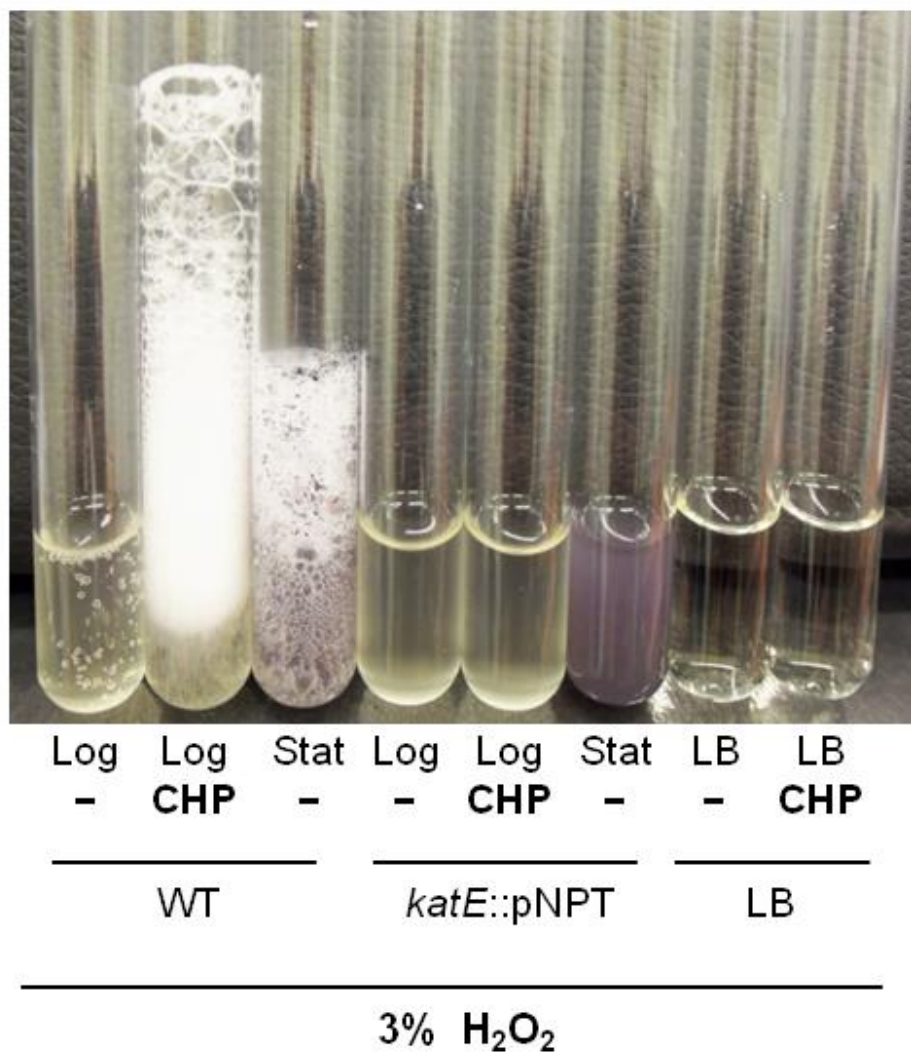


Figure S1. Effect of CHP in catalase activity. Catalase tests with *C. violaceum* wild-type and *katE* mutant strain were performed before and 10 minutes after addition of 100 μ M CHP in cultures of logarithmic phase (Log) or stationary phase (Stat) without CHP. After addition of 3% H₂O₂ in the cultures, the catalase activity was visualized by immediate production of oxygen bubbles. LB medium and LB with 100 μ M CHP were used as controls.

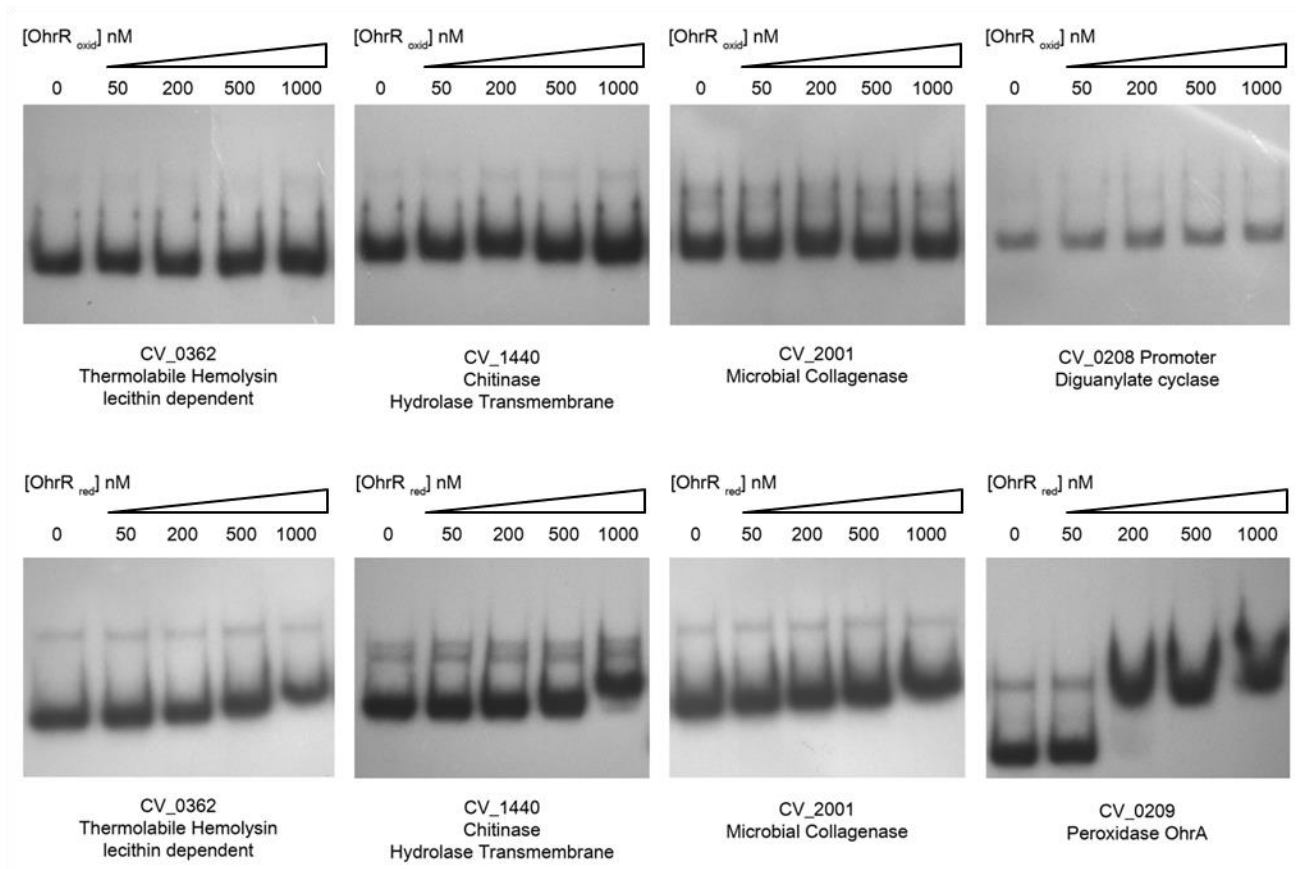


Figure S2. OhrR interaction with promoter region of genes belonging to the OhrR regulon. DNA probes corresponding to promoter region of the indicated genes were incubated with various concentrations of the purified OhrR protein previously oxidized (100 μ M CHP for 1 h) or reduced (10 mM DTT for 1 h). After incubation at 25 $^{\circ}$ C for 25 minutes, the samples were separated on polyacrylamide non-denaturing gel. As a positive control was used the promoter region of *ohrA* (CV_0209). OhrR bound only to the promoter of *ohrA*.

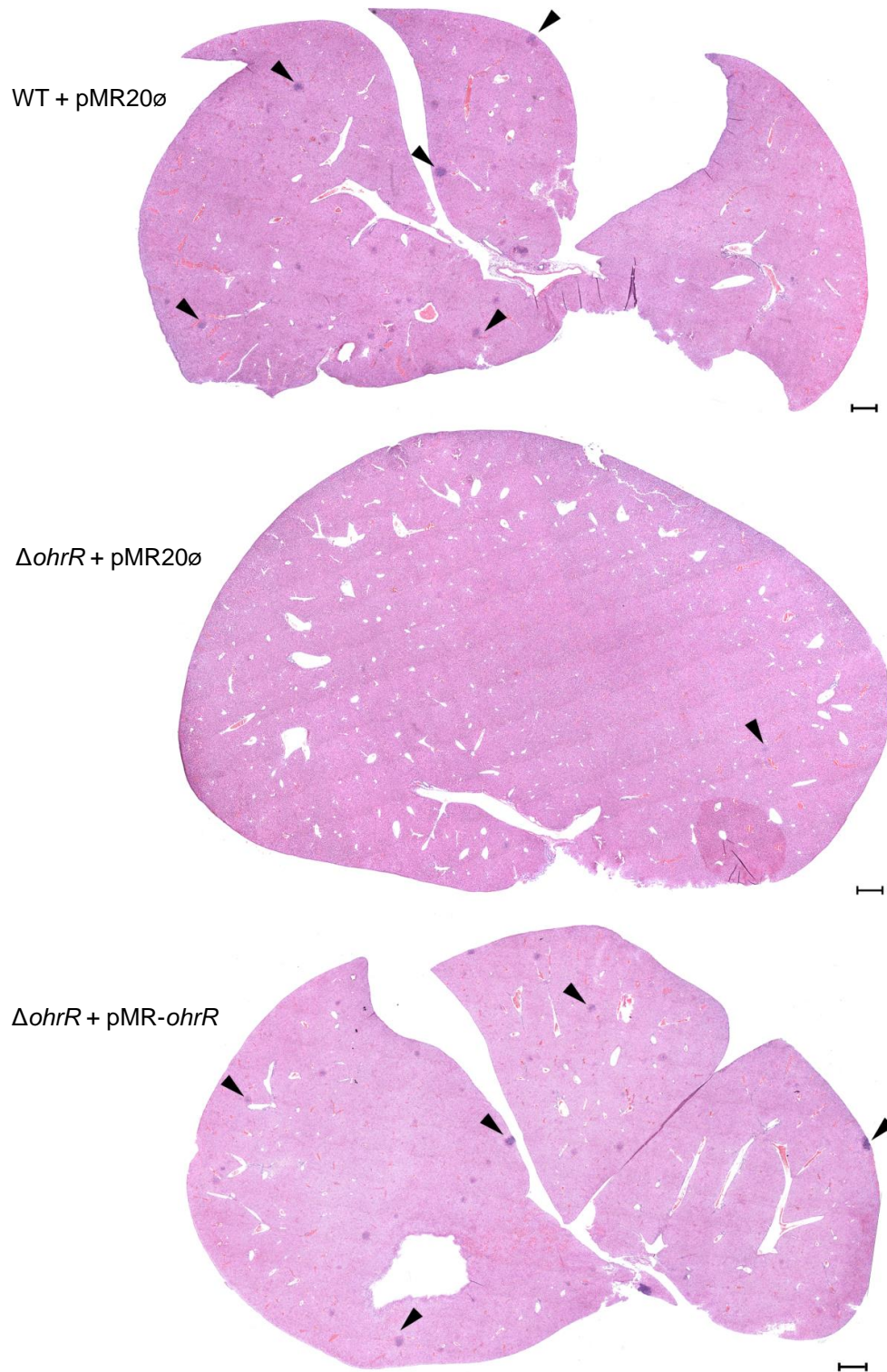


Figure S3. Histopathological analysis in livers of mice infected with *C. violaceum*. BALBc mice were infected with the indicated *C. violaceum* strains and the liver samples were stained with hematoxylin and eosin. The multiple microscopic lesion foci, indicated by arrows, were counted for each strain: 20 for wild type; 5 for Δ ohrR mutant; 23 for complement strain. Bar, 500 μ m.