

Table S4. Differentially expressed proteins in the VBNC *Escherichia coli* O157:H7 cells induced by high pressure CO₂.

| Protein and functional category | Accession number ^a | Gene | Fold change ^b |
|---|-------------------------------|--------------|--------------------------|
| Carbohydrate transport and metabolism | | | |
| Pyruvate dehydrogenase subunit E1 | NP_285810.1 | <i>aceE</i> | 1.51 |
| Aconitate hydratase 2 | NP_285814.1 | <i>acnB</i> | 0.72 |
| Type II citrate synthase | NP_286436.1 | <i>gltA</i> | 1.85 |
| D-lactate dehydrogenase | NP_287766.1 | <i>ldhA</i> | 1.53 |
| Glucose-6-phosphate dehydrogenase | NP_288289.1 | <i>zwf</i> | 1.62 |
| 6-phosphogluconate dehydrogenase | NP_288534.1 | <i>gnd</i> | 1.33 |
| β-D-glucoside glucohydrolase | NP_288709.1 | <i>bglX</i> | 0.56 |
| D-lactate dehydrogenase | NP_288710.1 | <i>dld</i> | 0.21 |
| Phosphoenolpyruvate-protein phosphotransferase | NP_288978.1 | <i>ptsI</i> | 0.61 |
| Maltose ABC transporter ATP-binding protein | NP_290669.1 | <i>malK</i> | 2.40 |
| Amino acid transport and metabolism | | | |
| Threonine synthase | NP_285696.1 | <i>thrC</i> | 2.23 |
| Lysine-, arginine-, ornithine-binding periplasmic protein | NP_288884.1 | <i>argT</i> | 2.22 |
| D-3-phosphoglycerate dehydrogenase | NP_289481.1 | <i>serA</i> | 1.49 |
| Nucleotide metabolism | | | |
| Carbamoyl phosphate synthase large subunit | NP_285727.1 | <i>carB</i> | 0.59 |
| Adenylate kinase | NP_286215.1 | <i>adk</i> | 1.34 |
| Ribonucleoside-diphosphate reductase subunit α | NP_288808.1 | <i>nrdA</i> | 2.14 |
| Inosine 5'-monophosphate dehydrogenase | NP_289062.1 | <i>guaB</i> | 0.41 |
| Phosphoribosylformylglycinamide synthase | NP_289113.1 | <i>purL</i> | 0.60 |
| Ribokinase | NP_290391.1 | <i>rbsK</i> | 0.64 |
| Adenylosuccinate synthetase | NP_290807.1 | <i>purA</i> | 1.60 |
| DNA replication | | | |
| DNA polymerase III subunit α | NP_285878.1 | <i>dnaE</i> | 0.36 |
| Replication initiation regulator SeqA | NP_286402.1 | <i>seqA</i> | 1.76 |
| Transcription and translation | | | |
| Isoleucyl-tRNA synthetase | NP_285720.1 | <i>ileS</i> | 1.48 |
| Glutamyl-tRNA synthetase | NP_286394.1 | <i>glnS</i> | 2.12 |
| 30S ribosomal protein S1 | NP_286786.1 | <i>rpsA</i> | 0.79 |
| DNA topoisomerase I | NP_287925.1 | <i>topA</i> | 1.88 |
| Transcription elongation factor GreA | NP_289755.2 | <i>greA</i> | 1.64 |
| 30S ribosomal protein S4 | NP_289857.1 | <i>rpsD</i> | 1.39 |
| 30S ribosomal protein S5 | NP_289864.1 | <i>rpsE</i> | 0.75 |
| 50S ribosomal protein L24 | NP_289870.1 | <i>rplX</i> | 1.55 |
| Glycyl-tRNA synthetase subunit α | NP_290144.1 | <i>glyQ</i> | 0.33 |
| Fic family protein | NP_290168.1 | <i>z5009</i> | 0.25 |

| | | | | |
|---|-------------|--------------|--|------|
| Cell division | | | | |
| DamX protein | NP_289927.1 | <i>damX</i> | | 1.85 |
| Stress response | | | | |
| Heat shock protein 90 | NP_286214.1 | <i>htpG</i> | | 1.51 |
| Glucan biosynthesis protein D | NP_287736.1 | <i>mdoD</i> | | 0.56 |
| Molecular chaperone GroEL | NP_290776.1 | <i>groEL</i> | | 1.24 |
| Electron transfer chain | | | | |
| Glutamate-1-semialdehyde aminotransferase | NP_285850.1 | <i>hemL</i> | | 1.99 |
| Membrane biosynthesis and transport | | | | |
| Outer membrane protein F | NP_286804.1 | <i>ompF</i> | | 1.71 |
| UTP-glucose-1-phosphate uridylyltransferase | NP_287481.1 | <i>galU</i> | | 2.10 |
| <i>sn</i> -glycerol-3-phosphate dehydrogenase subunit A | NP_288817.1 | <i>glpA</i> | | 0.43 |
| Undecaprenyl phosphate 4-deoxy-4-formamido-L-arabinose transferase | NP_288830.1 | <i>z3512</i> | | 0.27 |
| Aminoglycoside/multidrug efflux system | NP_289022.1 | <i>acrD</i> | | 0.22 |
| D-arabinose 5-phosphate isomerase | NP_289257.2 | <i>gutQ</i> | | 0.33 |
| NAD(P)H-dependent <i>sn</i> -glycerol-3-phosphate dehydrogenase | NP_290191.1 | <i>gpsA</i> | | 1.59 |
| Pathogenicity | | | | |
| Outer membrane protein A | NP_286832.1 | <i>ompA</i> | | 0.79 |
| Keto-hydroxyglutarate-aldolase | NP_288287.1 | <i>eda</i> | | 0.67 |
| RNA degradation | | | | |
| Exoribonuclease R | NP_290809.2 | <i>vacB</i> | | 0.44 |
| Protein degradation | | | | |
| Isoaspartyl dipeptidase | NP_290945.1 | <i>iadA</i> | | 0.60 |
| Coenzyme metabolism | | | | |
| Thiamine biosynthesis protein ThiI | NP_286165.1 | <i>yajK</i> | | 0.38 |
| Lipoyl synthase | NP_286354.1 | <i>lipA</i> | | 0.68 |
| Function prediction only | | | | |
| Phage inhibition, colicin resistance and tellurite resistance protein | NP_286707.1 | <i>terA</i> | | 0.31 |
| Outer membrane protein assembly complex subunit YfiO | NP_289150.1 | <i>z3889</i> | | 0.47 |
| ABC transporter ATP-binding protein | NP_289900.1 | <i>yheS</i> | | 0.28 |
| Function unknown | | | | |
| Hypothetical protein | NP_285859.1 | <i>yaeH</i> | | 2.26 |
| Hypothetical protein | NP_288049.1 | <i>ydgA</i> | | 0.48 |
| Hypothetical protein | NP_289066.1 | <i>z3776</i> | | 2.34 |

^aAccession number was from the NCBI database.

^bChanged expression levels in VBNC cells compared to those in the exponential-phase cells.