

Supplementary Table 1: Oligonucleotides used in the study:

| Oligo Name | Sequence (5' to 3') | Description |
|------------|---|---|
| ORG 210 | GGTACCGCCTTTAAAATCCATTTATTTGGATTCTAAGGG | <i>tcsR</i> upstream (Forward with KpnI) |
| ORG 211 | GAGCTC TACTCATATTATGCACTCCTTTATGG | <i>tcsR</i> upstream (Reverse with SacI) |
| ORG 208 | GAGCTCATATAAGAGAGGATGATTTTATGC | <i>tcdR</i> ORF (Forward with SacI) |
| ORG 209 | GGATCCTTAATGATGATGATGATGATGCAAGTTAAAAT AATTTTC | <i>tcdR</i> -ORF (Reverse with BamHI) |
| ORG 203 | GAGCTCACCATAAAGGAGTGCATAATTATGA | <i>tcsR</i> ORF (Forward with SacI) |
| ORG 204 | GGATCCTTAATGATGATGATGATGATGATTTATTAATTT TTTTAG | <i>tcsR</i> ORF (Reverse with BamHI) |
| ORG 194 | GGAATGGTACCTCACTTCCTCCATGACCTAA | <i>tcsL</i> upstream (Forward with KpnI) |
| ORG 195 | GGAATGAGCTCTAAAATTCCCCCTTATATAACAT | <i>tcsL</i> upstream (Reverse with SacI) |
| ORG 197 | ACGGCTCAACCGTAGTAAGC | 16srRNA (Q-RT PCR-Forward) |
| ORG 198 | TCTACGCATTTACCGCTAC | 16srRNA (Q-RT PCR-Reverse) |
| ORG 192 | GGGATGTTTGAGGGCAATAA | <i>tcsE</i> (Q-PCR RT- Forward) |
| ORG 193 | TTCCTCCATTGATTCCAAAAC | <i>tcsE</i> (Q-PCR RT- Reverse) |
| ORG 190 | CATGGACTAAGGGAATCTGAAA | <i>tcsR</i> (Q-PCR RT- Forward) |
| ORG 191 | TTTTCCAAAGCTCTTAAATGTGTTT | <i>tcsR</i> (Q-PCR RT- Reverse) |
| ORG 186 | CAGCAGCTTCAACTGCAATC | <i>tcsL</i> (Q-PCR RT-Forward) |
| ORG 187 | CTGAAATTCCTGCCAAAGGA | <i>tcsL</i> (Q- PCR RT-Reverse) |
| ORG 310 | TTTAGCTGCAGCATCTGATTT | <i>tcsH</i> (Q-PCR RT- Forward) |
| ORG 311 | TAAATCTGGTTGTATCCCTGGC | <i>tcsH</i> (Q- PCR RT – Reverse) |
| ORG 17 | GGTCGGTACCATGGACCCAAGAGATGCTGGTGCTTCT | <i>erm B</i> (Forward) |
| ORG 18 | GCTAGAGCTCGAACGCGTGCGACTCATAGAATTATTTCT CT | <i>erm B</i> (Reverse) |
| ORG 292 | GGTACCTTAAATAAATTTCAAAGAAATAGTTGC | <i>tcsH</i> upstream ((Forward with KpnI) |
| ORG 293 | GAGCTCAAGACCCTCCTAATATTATTATTTTGGGC | <i>tcsH</i> upstream (Reverse with SacI) |
| ORG 294 | GGTACCGGTATAATGAAAACAGGGCTTATCATTG | <i>tcsE</i> upstream (Forward with KpnI) |
| ORG 295 | GAGCTCAATGCCTCCTAGTTTTGTAATTAATAAAT | <i>tcsE</i> upstream (Reverse with SacI) |

Supplementary Table 2: ATCC 9714 toxin locus

| Locus tag | Length (aa) | Predicted product | Hit description | E-value | % identity | Conserved domains |
|-----------|----------------|--|--|---------|---------------|--|
| H477_0243 | 149 | Leucine Rich repeat family protein | S4 domain protein [<i>Clostridium perfringens</i> D str. JGS1721 ZP_02954940.1] | 93-27 | 49% 71/145 | No putative conserved domains |
| H477_0244 | 126 | Hypothetical protein | No homology found | | | No putative conserved domains |
| H477_0245 | 126 | Hypothetical protein | No homology found | | | No putative conserved domains |
| H477_0246 | 206 | RNA polymerase sigma factor, sigma-70 family | RNA polymerase sigma factor SigV [<i>Clostridium</i> sp. D5] ZP_08131089.1 | 33-24 | 33% 61/187 | Sigma70_r2, r4 superfamily |
| H477_0247 | 216 | EAL domain protein | Cyclic diguanylate phosphodiesterase (EAL) domain protein [<i>Clostridium</i> sp. HGF2] ZP_07832144.1 | 2e-18 | 27% 60/221 | EAL domain, bacterial signalling protein |
| H477_0248 | 252 | RNA polymerase sigma factor, sigma-70 family | RNA polymerase sigma-70 factor [<i>Clostridium perfringens</i> D str. JGS1721] ZP_02953213.1 | 2e-22 | 38% 65/173 | Sigma70_r2 , Sigma 70 region 4 |
| H477_0249 | 59 | Hypothetical protein | No homology found | | | No putative conserved domains |
| H477_0250 | 174 | Hypothetical protein | Sigma-70 family RNA polymerase sigma factor [<i>Stomatobaculum longum</i>] ZP_09521451.1 | 3e-07 | 28% 32/115 | No putative conserved domain |
| H477_0251 | 158 | Bacterial Ig-like domain family protein" | Bacterial group 3 Ig-like protein [<i>Clostridium celatum</i> DSM 1785] ZP_19299437.1 | 8e-08 | 56% 31/55 | Bacterial Ig like domain group III |

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|-----------|-----|--|--|--------|-----|------------------|---|
| H477_0252 | 316 | Actino bacterial surface-anchored domain protein | Bacterial group 3 Ig-like protein [<i>Clostridium celatum</i> DSM 1785] ZP_19299437.1 | 2e-69 | 48% | Big_3 153/325 | Bacterial Ig like domain group III |
| H477_0253 | 296 | Bacterial Ig-like domain family protein | Chitinase B [<i>Clostridium paraputrificum</i>] BAA23796.1 | 7e-16 | 46% | 65/141 | No putative conserved domain |
| H477_0254 | 218 | Hypothetical protein | No homology found | | | | No putative conserved domain |
| H477_0255 | 57 | Transcriptional regulator family protein | Rrf2 family transcriptional regulator [<i>Clostridium difficile</i> 630] YP_001089272.1 | 0.030 | 45% | 21/47 | RrF2 superfamily transcriptional regulator |
| H477_0256 | 93 | Hypothetical protein | Hypothetical protein phiCD27_gp59 [<i>Clostridium</i> phage phiCD27] YP_002290935.1 | 0.63 | 64% | 16/25 | No putative conserved domain |
| H477_0257 | 65 | Antidote-toxin recognition MazE family protein | Hypothetical protein CdifQCD_20326 [<i>Clostridium difficile</i> QCD-37x79] ZP_05399442.1 | 6e-11 | 42% | 25/60 | No putative conserved domain |
| H477_0258 | 46 | Hypothetical protein | No homology found | | | | No putative conserved domain |
| H477_0259 | 278 | ParB-like nuclease domain protein | ParB protein [<i>Clostridium perfringens</i> C str. JGS1495] ZP_02865546.1 | 2e-105 | 69% | 164/237 | ParBc superfamily |
| H477_0260 | 69 | Soj domain protein | Soj protein [<i>Clostridium perfringens</i> str. 13] NP_149993.1 | 4e-15 | 54% | 37/68 | Soj, mind_arch, flhG domain |
| H477_0261 | 146 | CobQ/CobB/MinD /ParA nucleotide binding domain | Chromosome partitioning related protein [<i>Clostridium perfringens</i>] YP_209675.1 | 5e-73 | 76% | 105/139 | Plasmid partitioning protein, ParA, superfamily |

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|-----------|------|---------------------------------------|--|-------|-----|--|
| H477_0262 | 220 | Cell wall hydrolase/autolysin | N-acetylmuramoyl-L-alanine amidase [<i>Clostridium</i> sp. D5] ZP_08128126.1 | 3e-25 | 37% | N-Acetylmuramoyl-L-alanine amidase I, II |
| H477_0263 | 2364 | Cytotoxin L (TcsL) | <i>C. sordellii</i> -cytotoxin L CAA57959.1 | 0.0 | 99% | N terminal Glycosyltransferase domain |
| H477_0264 | 141 | Holin (TcsE) | TcdE protein [<i>Clostridium difficile</i>] CAC79642.1 | 2e-66 | 73% | Phage Holin |
| H477_0265 | 60 | Haemorrhagic toxin (TcsH (Truncated)) | Truncated toxin A [<i>Clostridium difficile</i>] AAC08437.1 | 3e-08 | 93% | TcdA_TcdB |
| H477_0266 | 142 | Haemorrhagic toxin (TcsH (Truncated)) | Truncated toxin A [<i>Clostridium difficile</i>] AAC08437.1 | 1e-66 | 77% | Glycosyltransferase domain |
| H477_0267 | 170 | Sigma factor (TcsR) (<i>tcsR</i>) | TcdR [<i>Clostridium difficile</i>] ABI93806.1 | 2e-15 | 35% | Sigma 70- region 4 |
| H477_0268 | 87 | Hypothetical protein | Conserved hypothetical protein [<i>Beggiatoa</i> sp. PS] ZP_01999532.1 | 0.36 | 34% | No putative conserved domain |
| H477_0269 | 60 | Hypothetical protein | Hypothetical protein LsueK3_08561 [<i>Lactobacillus suebicus</i> KCTC 3549] ZP_09451275.1 | 2.1 | 43% | No putative conserved domain |
| H477_0270 | 407 | Initiator family Replication protein | RepB protein [<i>Clostridium difficile</i> 002-P50-2011] ZP_17071833.1 | 7e-56 | 36% | Rep_3 superfamily, Replication protein |
| H477_0271 | 63 | Hypothetical protein | No homology found | | | No putative conserved domain |

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|-----------|-----|--|---|-------|--------|---|
| H477_0272 | 126 | Hypothetical | No homology found | | | |
| H477_0273 | 370 | Hypothetical protein | Hypothetical protein CBCST_p6CBCSt0005 [<i>Clostridium botulinum</i>] ZP_11680199.1 | 2e-09 | 48% | No putative conserved domain |
| H477_0274 | 135 | Hypothetical protein | No homology found | | | DNA binding helix turn helix motif |
| H477_0275 | 369 | Recombination protein | Recombinase A [<i>Clostridium difficile</i> 630] YP_001087824.1 | 0.0 | 80% | Recombination protein |
| H477_0276 | 48 | Hypothetical protein | No homology found | | | No putative conserved domain |
| H477_0277 | 100 | Hypothetical protein | No homology found | | | No putative conserved domain |
| H477_0278 | 325 | Transcriptional regulator | DNA binding helix-turn-helix protein [<i>Clostridium difficile</i> 050-P50-2011] ZP_17073318.1 | 2e-09 | 49% | DNA binding helix turn helix protein, transcription repressor and regulator protein |
| H477_0279 | 162 | Hypothetical protein | Conserved hypothetical protein [<i>Clostridium perfringens</i> B str ATCC 3626 ZP_02636631.1] | 1e-05 | 29% | No putative conserved domain |
| H477_0280 | 341 | Cysteine rich secretory family Extracellular protein | SCP-like protein [<i>Clostridium difficile</i> 002-P50-2011] >ref ZP_17073080.1 ZP_17069969.1 | 3e-06 | 28% | SCP-like Extracellular protein domain, Cysteine-rich secretory protein |
| H477_0281 | 79 | Hypothetical protein | No homology found | | | Glycoside hydrolase like superfamily |
| H477_0282 | 177 | Hypothetical protein | Conserved hypothetical protein [<i>Clostridium perfringens</i> E str. | 1e-10 | 37% | No putative conserved domain |
| | | | | | 46/125 | |

JGS1987 ZP_02633035.1

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|-----------|------|----------------------------------|--|-------|-----------------|---|
| H477_0283 | 144 | Hypothetical protein | No significant Homology | | | No putative conserved domain |
| H477_0284 | 75 | Regulatory protein | Phage regulatory protein [<i>Clostridium difficile</i> ATCC 43255] <u>ZP_05349371.1</u> | 4e-04 | 38% 24/64 | HTH_XRE superfamily, HipB |
| H477_0285 | 76 | Regulatory protein | Transcriptional Regulator [<i>Clostridium perfringens</i> D str. JGS1721] <u>ZP_02952728.1</u> | 2.3 | 31% 21/68 | No putative conserved domain |
| H477_0286 | 1354 | Collagen adhesion protein | Collagen adhesin [<i>Clostridium perfringens</i> str. 13] <u>NP_150050.1</u> | 0 | 48% 496/1039 | Cna peptidase protein |
| H477_0287 | 107 | Hypothetical protein | No homology found | | | No putative conserved domain |
| H477_0288 | 120 | Hypothetical protein | Hypothetical protein AC3_A0045 [<i>Clostridium perfringens</i> E str. JGS1987] <u>ZP_02632952.1</u> | 2e-06 | 34% 30/89 | No putative conserved domain |
| H477_0289 | 84 | Hypothetical protein | Hypothetical protein Cspa_c57090 [<i>Clostridium saccharoperbutylacetonicum</i> N1-4(HMT)] gb AGF59434.1 | 93-06 | 35% 29/83 | No putative conserved domain |
| H477_0290 | 213 | Dna Topoisomerase family protein | putative DNA topoisomerase [<i>Clostridium difficile</i> QCD-97b34] <u>ZP_05385472.1</u> | 6e-48 | 45% 96/213 | Putative nucleotide, metal binding protein, TOPRIM_TopoIA_TopoII ITOP1Ac superfamily, topoisomerase primase, topoisomerase I, III |
| H477_0291 | 276 | Dna Topoisomerase | DNA topoisomerase type IA [<i>Clostridium difficile</i> 630] | 2e-29 | 33% | TOP1Ac, DNA topoisomerase 1, III |

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|-----------|-----|---|---|--------|---------|---|
| | | family protein | YP_001088916.1 | | 89/266 | |
| H477_0292 | 132 | DNA topoisomerase | DNA topoisomerase [<i>Clostridium difficile</i> QCD-23m63] ZP_05400436.1 | 4e-17 | 40% | PRK08173, DNA topoisomerase III |
| | | | | | 46/114 | |
| H477_0293 | 161 | Hypothetical protein | Conserved hypothetical protein [<i>Clostridium perfringens</i> D str. JGS1721] ZP_02954621.1 | 4e-08 | 26% | No putative conserved domain |
| | | | | | 37/144 | |
| H477_0294 | 54 | Hypothetical protein | No homology found | | | No putative conserved domain |
| H477_0295 | 76 | Putative membrane protein | Conserved hypothetical protein [<i>Clostridium perfringens</i> D str. JGS1721] ZP_02952703.1 | 2E-12 | 50% | No putative conserved domain |
| | | | | | 38/76 | |
| H477_0296 | 94 | Hypothetical protein | No Homology detected | | | No putative conserved domain |
| H477_0297 | 339 | type IV secretory system Conjugative DNA | Type IV secretory pathway, VirD4 component [<i>Clostridium perfringens</i> D str. JGS1721] ZP_02952628.1 | 2e-113 | 51% | Type IV secretory pathway, VirD4 components |
| | | | | | 192/377 | |
| H477_0298 | 210 | type IV secretory system Conjugative DNA | Type IV secretory pathway, VirD4 component [<i>Clostridium perfringens</i> D str. JGS1721] ZP_02952628.1 | 1e-94 | 66% | TraG-D_C superfamily, VirD4, type IV conjugal transfer coupling protein |
| | | | | | 139/210 | |
| H477_0299 | 45 | No homology found | No homology found | | | No putative conserved domain |
| H477_0300 | 163 | Hypothetical protein | Putative membrane protein [<i>Clostridium perfringens</i> C str. JGS1495] ZP_02865646.1 | 4e-30 | 41% | No putative conserved domain |
| | | | | | 60/148 | |
| H477_0301 | 264 | Hypothetical protein | Putative membrane protein [<i>Clostridium perfringens</i> B str. ATCC | 6e-35 | 35% | No putative conserved domain |
| | | | | | 110/312 | |

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|-----------|-----|--|---|--------|----------------|---|
| H477_0301 | 264 | Hypothetical protein | Putative membrane protein [<i>Clostridium perfringens</i> B str. ATCC 3626] ZP_02636580.1 | 6e-35 | 35% 110/312 | No putative conserved domain |
| H477_0302 | 80 | Hypothetical protein | No homology found | | | No putative conserved domain |
| H477_0303 | 97 | Hypothetical protein | Conserved hypothetical protein [<i>Clostridium perfringens</i> B str. ATCC 3626] ZP_02635907.1 | 7e-17 | 46% 41/89 | No putative conserved domain |
| H477_0304 | 47 | Hypothetical protein | No homology found | | | No putative conserved domain |
| H477_0305 | 141 | Hypothetical protein | conserved hypothetical protein [<i>Clostridium perfringens</i> E str. JGS1987] ZP_02633032.1 | 4e-29 | 42% 60/143 | No putative conserved domain |
| H477_0306 | 51 | Hypothetical protein | No homology found | | | No putative conserved domain |
| H477_0307 | 328 | Hypothetical protein | Conserved hypothetical protein [<i>Clostridium perfringens</i> B str. ATCC 3626] ZP_02636571.1 | 7e-100 | 51% 161/313 | ATP-binding cassette domain of multidrug resistance protein-like transporters. AAA domain |
| H477_0308 | 151 | zonular occludens toxin family protein | conserved hypothetical protein [<i>Clostridium perfringens</i> C str. JGS1495] >ref[ZP_16922172.1 ZP_02865588.1 | 9e-57 | 63% 91/148 | Zot superfamily, AAA like domain, conjugal transfer ATP binding protein |
| H477_0309 | 221 | Hypothetical | No homology found | | | No putative conserved |

Supplementary Table 3: VPI 9048 toxin locus genes

| Locus tag | Length (aa) | Predicted product | Hit description | E-value | % identity | Conserved domains |
|-----------|----------------|--|--|---------|----------------|---|
| H476_0259 | 497 | Bacterial Ig-Like domain family protein | <i>Enterococcus faecalis</i> TX0470, collagen binding protein; ZP_07761016.1 | 3e-08 | 24% 107/449 | No putative conserved domain |
| H476_0260 | 137 | Transcriptional regulator | BadM/Rrf2 family transcriptional regulator [<i>Moorella thermoacetica</i> ATCC 39073] YP_430929.1 | 8e-18 | 31% 42/134 | Rrf2 transcriptional regulator |
| H476_0261 | 120 | Hypothetical protein | Hypothetical protein [<i>C. difficile</i> CdifQCD-6_20123] ZP_05332106.1 | 0.031 | 31% 31/101 | GIY-YIG_C term superfamily |
| H476_0262 | 42 | Transposase IS200 like family protein | Transposase [<i>Clostridium</i> sp. M62/1] ZP_06346833.2 | 4e-10 | 59% 24/41 | Y1_Tnp superfamily |
| H476_0263 | 362 | Transposase, IS605 OrfB family | Transposase [<i>Clostridium perfringens</i> C str. JGS1495] ZP_02865789.1 | 0.0 | 73% 267/364 | Putative transposase dna binding domain |
| H476_0264 | 65 | Antidote-toxin recognition MazE family protein | Putative PemI [<i>Clostridium difficile</i> ATCC 43255] ZP_05350752.1 | 9e-06 | 37% 21/57 | No putative conserved domain |
| H476_0265 | 445 | Partitioning protein | Partition protein [<i>Clostridium perfringens</i> E str. JGS1987] | 8e-115 | 62% | ParB nuclease domain |

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|-----------|------|-------------------------------|---|--------|------------------|--|
| | | | <u>ZP_02630615.1</u> | | 191/310 | |
| H476_0266 | 250 | Cell division protein | Sporulation initiation inhibitor protein soj [<i>Clostridium perfringens</i> C str. JGS1495] <u>ZP_02865591.1</u> | 2e-125 | 70% 174/250 | cobQ/CobB/MinD/ParA nucleotide binding domain |
| H476_0267 | 44 | Hypothetical protein | No homology found | | | No putative conserved domain |
| H476_0268 | 220 | Cell wall hydrolase/autolysin | <i>Clostridium cellulovorans</i> 743B - cell wall hydrolase <u>YP_003842332.1</u> | 2e-28 | 36% 81/226 | N-Acetylmuramoyl-L-alanine amidase |
| H476_0269 | 2364 | cytotoxin L (TcsL) | <i>C. sordellii</i> -cytotoxin L <u>CAA57959.1</u> | 0.0 | 96% 2272/2364 | N terminal Glycosyltransferase domain. Toxin B |
| H476_0270 | 141 | Holin (TcsE) | TcdE protein [<i>Clostridium difficile</i>] CAC79642.1 | 1e-67 | 74% 103/141 | Toxin secretion Phage lysis Holin family |
| H476_0271 | 2597 | Hemorrhagic toxin, TcsH | <i>C. difficile</i> Toxin A (TcdA) QCD-66c26] <u>ZP_05270743.1</u> | 0.0 | 78% 2055/2618 | Glycosyltransferase domain |
| H476_0272 | 173 | Sigma factor (TcsR) | TcdR [<i>Clostridium</i>] <i>difficile</i>] <u>ABI93806.1</u> | 1e-14 | 34% 60/174 | RNA polymerase Sigma 70 family- region 4 |
| H476_0273 | 60 | Hypothetical protein | No homology found | | | No putative conserved domain |
| H476_0274 | 407 | Replication protein | RepB protein [<i>Clostridium difficile</i> 002-P50-2011] | 9e-56 | 36% | Initiator Replication family protein |

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|-----------|-----|---------------------------|---|-------|----------------|---|
| H476_0274 | 407 | Replication protein | RepB protein [<i>Clostridium difficile</i> 002-P50-2011] <u>ZP_17071833.1</u> | 9e-56 | 36% 122/340 | Initiator Replication family protein |
| H476_0275 | 128 | Hypothetical protein | conserved hypothetical protein [<i>Clostridium difficile</i> NAP08] <u>ZP_06892370.1</u> | 0.005 | 26% 29/112 | Helix turn helix motif NUMOD1 domain protein |
| H476_0276 | 368 | Hypothetical protein | hypothetical protein CBCST_p6CBCSt0005 [<i>Clostridium botulinum</i>] <u>ZP_11680199.1</u> | 2e-09 | 48% 32/66 | No putative conserved domain |
| H476_0277 | 135 | Hypothetical protein | No homology found | | | |
| H476_0278 | 368 | Recombination protein | Recombinase A [<i>Clostridium difficile</i> 630] <u>ZP_05271345.1</u> | 0.0 | 80% 268/336 | Protein RecA like NTPases superfamily |
| H476_0279 | 48 | Hypothetical protein | Hypothetical protein CD196_1775 [<i>Clostridium difficile</i> CD196] <u>YP_003218309.1</u> | 0.64 | 42% 16/38 | No putative conserved domain |
| H476_0280 | 101 | Hypothetical protein | No homology found | | | |
| H476_0281 | 306 | Transcriptional regulator | SOS-response Transcriptional Lex A repressor [<i>Clostridium perfringens</i> D str. JGS1721] <u>ZP_02952675.1</u> | 2e-22 | 31% | DNA binding helix turn helix protein, transcription repressor and regulator protein |
| H476_0282 | 162 | Hypothetical protein | Conserved hypothetical protein [<i>Clostridium perfringens</i> C str. | 3e-05 | 28% | No putative conserved domain |

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|-----------|------|---------------------------|---|-------|-----------------|---|
| H476_0283 | 331 | Extracellular protein | Putative calcium chelating exported protein [<i>Clostridium difficile</i> QCD-23m63] ZP_05402067.1 | 1.2 | 26% 71/275 | Extracellular protein Cysteine rich secretory family protein |
| H476_0284 | 44 | Hypothetical protein | No homology found | | | No putative conserved domain |
| H476_0285 | 188 | Resolvase | Resolvase domain-containing protein [<i>Clostridium difficile</i> QCD-76w55] ZP_05358063.1 | 2e-93 | 90% 132/146 | Resolvase N terminal domain protein |
| H476_0286 | 387 | Transposase | IS605 family transposase OrfB [<i>Clostridium difficile</i> B11] YP_006197023.1 | 0.0 | 87% 335/387 | Putative Transposase family protein |
| H476_0287 | 75 | Regulatory protein | Putative phage regulator [<i>Clostridium difficile</i> ATCC 43255] ZP_05349371.1 | 4e-04 | 38% 24/64 | Helix turn helix proteins |
| H476_0288 | 76 | Regulatory proteins | Transcriptional regulator [<i>Clostridium cellulolyticum</i>] YP_002507585.1 | 1.2 | 29% 16/56 | Hypothetical protein |
| H476_0289 | 1357 | Collagen adhesion protein | Collagen adhesin [<i>Clostridium perfringens</i> str. 13] NP_150050.1 | 0.0 | 42% 553/1323 | CnaB type peptidase domain |
| H476_0290 | 171 | Hypothetical protein | Conserved hypothetical protein [<i>Clostridium perfringens</i> E str. JGS1987] ZP_02633035.1 | 9e-06 | 36% 48/133 | No putative conserved domain |
| H476_0291 | 160 | Hypothetical protein | No homology found | | | No putative conserved domain |

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|-----------|-----|--|--|--------|-----|--|
| H476_0292 | 216 | Hypothetical protein | No homology found | | | No putative conserved domain |
| H476_0293 | 700 | Topoisomerase | DNA topoisomerase [<i>Clostridium difficile</i> QCD-76w55] ZP_05358121.1 | 2e-105 | 34% | TOPRIM_TopoiA_TopoiI superfamily, TOP1Ac superfamily, DNA topoisomerase family protein |
| H476_0294 | 167 | Hypothetical protein | Hypothetical protein CLL_0015 [<i>Clostridium botulinum</i> B str. Eklund 17B] YP_001893638.1 | 6e-12 | 36% | No putative conserved domain |
| H476_0295 | 54 | Hypothetical protein | Hypothetical protein EFOG_03015 [<i>Enterococcus faecalis</i> X98] ZP_05600032.1 | 0.059 | 48% | No putative conserved domain |
| H476_0296 | 76 | Putative membrane protein | Conserved hypothetical protein [<i>Clostridium perfringens</i> D str. JGS1721] ZP_02952703.1 | 2e-12 | 50% | No putative conserved domain |
| H476_0297 | 925 | Type IV secretory system conjugative DNA | Type IV secretory pathway, VirD4 component [<i>Clostridium perfringens</i> D str. JGS1721] ZP_02952628.1 | 0 | 47% | TraG-D_C superfamily, VirD4 |
| H476_0298 | 682 | Putative membrane protein | Putative membrane protein [<i>Clostridium perfringens</i> C str. JGS1495] ZP_02865646.1 | 2e-90 | 36% | No putative conserved domain |
| H476_0299 | 97 | Hypothetical protein | Conserved hypothetical protein [<i>Clostridium perfringens</i> B str. ATCC 3626] ZP_02635907.1 | 1e-16 | 46% | No putative conserved domain |

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|-----------|-----|---|---|--------|----------------|---|
| H476_0300 | 201 | Hypothetical protein | Hypothetical protein HA1_15800 [<i>Clostridium perfringens</i> F262] <u>ZP_16922174.1</u> | 6e-38 | 44% 88/201 | No putative conserved domain |
| H476_0301 | 59 | Hypothetical protein | Hypothetical protein CdifA_02598 [<i>Clostridium difficile</i> ATCC 43255] <u>ZP_05349623.1</u> | 1e-04 | 58% 22/38 | No putative conserved domain |
| H476_0302 | 635 | Type IV secretion system coupling dna binding | Type IV secretion system VirB4 component [<i>Bacillus thuringiensis</i> MC28] <u>YP_006815694.1</u> | 5e-141 | 45% 223/497 | Conjugal transfer ATP binding cassette domain of MRP, iron sulphur cluster transporters |
| H476_0303 | 54 | Hypothetical protein | Hypothetical protein CdifA_02598 [<i>Clostridium difficile</i> ATCC 43255] <u>ZP_17069585.1</u> | 0.019 | 58% 19/33 | No putative conserved domain |
| H476_0304 | 225 | Hypothetical protein | No putative conserved domain | | | No putative conserved domain |
| H476_0305 | 392 | Cell wall binding protein | Cell wall-binding protein [<i>Clostridium perfringens</i> str. 13] <u>NP_150037.1</u> | 6e-149 | 58% 225/387 | Lysozyme like superfamily, nlpC/P60 family protein |
| H476_0306 | 125 | SS Dna binding protein | Single-strand binding protein [<i>Clostridium difficile</i> QCD-63q42] <u>ZP_05332107.1</u> | 1e-15 | 38% 41/107 | Single stranded DNA binding family protein |
| H476_0307 | 300 | Hypothetical protein | Hypothetical protein PBCN14 [<i>Clostridium perfringens</i>] | 1e-22 | 30% | No putative conserved domain |

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| H476_0307 | 300 | Hypothetical protein | Hypothetical protein PBCN14 [<i>Clostridium perfringens</i>] <u>YP_209672.1</u> | 1e-22 | 30% 85/279 | No putative conserved domain |
| H476_0308 | 77 | Hypothetical protein | No homology found | | | No putative conserved domain |
| H476_0309 | 89 | CopG family protein | Toxin-antitoxin system, antitoxin component, ribbon- helix-helix domain protein [<i>Enterococcus faecium</i> R497] <u>ZP_18306856.1</u> | 5e-06 | 38% 28/74 | No putative conserved domain |
| H476_0310 | 142 | Hypothetical protein | Peptidoglycan GlcNAc deacetylase [<i>Streptococcus</i> <i>pneumoniae</i> TIGR4] <u>ZP_22472958.1</u> | 7.2 | 27% 29/106 | No putative conserved domain |
| H476_0311 | 386 | Hypothetical protein | putative conjugative relaxase [<i>Lactococcus garvieae</i>] <u>YP_005352364.1</u> | 2e-63 | 32% 133/420 | TraI, conjugal transfer relaxase |
| H476_0312 | 80 | Hypothetical protein | No homology found | | | No putative conserved domain |
| H476_0313 | 607 | Hypothetical protein | LtrC-like protein [<i>Bacillus</i> <i>thuringiensis</i> MC28] <u>YP_006815671.1</u> | 2e-102 | 50% | Domain of undefined function (DUF)955 superfamily |
| H476_0314 | 60 | Hypothetical protein | No homology found | | | No putative conserved domain |
| H476_0315 | 95 | Hypothetical protein | Hypothetical protein Clole_3081 [<i>Clostridium lentocellum</i> DSM | 2e-15 | 44% | No putative conserved domain |

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|-----------|-----|--------------------------|--|--------|----------------|---------------------------------|
| H476_0316 | 259 | Hypothetical protein | Hypothetical protein Clocel_0429 [<i>Clostridium cellulovorans</i> 743B] <u>YP_003841970.1</u> | 3e-13 | 50% 37/74 | No putative conserved domain |
| H476_0317 | 54 | Hypothetical protein | | | | No putative conserved domain |
| H476_0318 | 187 | Resolvase | Resolvase domain-containing protein [<i>Clostridium difficile</i> QCD-66c26] <u>ZP_05273846.1</u> | 4e-90 | 72% 128/179 | Ser_Recombinase superfamily |
| H476_0319 | 187 | TraB family protein | TraB family protein [<i>Vibrio cholerae</i> HE-40] <u>ZP_17735271.1</u> | 1e-04 | 25% 38/152 | No putative conserved domain |
| H476_0320 | 109 | YcxB like family protein | Primase-like protein [<i>Staphylococcus aureus</i>] <u>ADN53668.1</u> | 3.1 | 29% 23/80 | No putative conserved domain |
| H476_0321 | 418 | Transposase, | transposase, IS605 OrfB family [<i>Clostridium difficile</i> 70-100- 2010] <u>ZP_17077481.1</u> | 6e-116 | 45% 189/419 | IS605 OrfB family |
| H476_0322 | 119 | Hypothetical protein | Permease [<i>Lactobacillus reuteri</i> CF48-3A] <u>ZP_03975395.1</u> | 8.6 | 32% 13/61 | No putative conserved domain |
| H476_0323 | 204 | Hypothetical protein | Hypothetical protein HMPREF9469_00031 [<i>Clostridium citroniae</i> WAL- 17108] <u>ZP_09056994.1</u> | 1e-34 | 38% 78/203 | DUF3267 superfamily |
| H476_0324 | 77 | Hypothetical protein | Hypothetical protein CdifQCD_20341 [<i>Clostridium</i> | 4e-13 | 65% | No putative conserved |

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|-----------|----|------------------------------|---|-------|--------------|-------------------------------------|
| H476_0324 | 77 | Hypothetical protein | Hypothetical protein CdifQCD_20341 [<i>Clostridium difficile</i> QCD-37x79] <u>ZP_05399445.1</u> | 4e-13 | 65% 31/48 | No putative conserved domain |
| H476_0325 | 46 | Peptidase M28 family protein | Putative aminopeptidase [<i>Clostridium</i> sp. JC122] <u>ZP_10929384.1</u> | 2e-05 | 65% 24/37 | Zinc peptidase like superfamily M28 |
| H476_0326 | 42 | Peptidase M28 family protein | Putative aminopeptidase [<i>Clostridium</i> sp. JC122] | .001 | 54% | Zinc peptidase like superfamily M28 |