**SUPPLEMENTAL MATERIAL**

**Table S1. Bacterial strains and plasmids**

| Bacterial strain or plasmid | Description | Reference |
|-----------------------------|-------------|-----------|
| **Escherichia coli** | | |
| DH5α | Strain for cloning purposes | (1) |
| S17-1 | Strain for plasmid mobilization | (2) |
| BL21(DE3) | Strain for protein expression | Novagen |
| **Chromobacterium violaceum** | | |
| ATCC 12472 | Wild type (Sequenced genome) | (3) |
| ΔclpV(CV_3965) | WT strain with CV_3965 gene deleted | This work |
| Δhcp (CV_3977) | WT strain with CV_3977 gene deleted | This work |
| ΔvipA (CV_3979) | WT strain with CV_3979 gene deleted | This work |
| ΔvgrG1 (CV_3986) | WT strain with CV_3986 gene deleted | This work |
| ΔvgrG2 (CV_3975) | WT strain with CV_3975 gene deleted | This work |
| ΔvgrG3 (CV_1432) | WT strain with CV_1432 gene deleted | This work |
| ΔvgrG4 (CV_1233) | WT strain with CV_1233 gene deleted | This work |
| ΔvgrG5 (CV_0023) | WT strain with CV_0023 gene deleted | This work |
| ΔvgrG6 (CV_0016) | WT strain with CV_0016 gene deleted | This work |
| ΔvgrG1-2 | WT strain with CV_3986 and CV_3975 genes deleted | This work |
| ΔvgrG1-3 | WT strain with CV_3986, CV_3975 and CV_1432 genes deleted | This work |
| ΔvgrG1-4 | WT strain with CV_3986, CV_3975, CV_1432 and CV_1233 genes deleted | This work |
| ΔvgrG1-5 | WT strain with CV_3986, CV_3975, CV_1432, CV_1233 and CV_0023 genes deleted | This work |
| ΔvgrG1-6 | WT strain with CV_3986, CV_3975, CV_1432, CV_1233, CV_0023 and CV_0016 genes deleted | This work |
| ΔcviR | WT strain with CV_4090 gene deleted | (4) |
| ΔcviI | WT strain with CV_4091 gene deleted | (5) |
| WT(pSEVA) | WT strain containing the empty vector pSEVA | This work |
| ΔvgrG3(pSEVA) | ΔvgrG3 strain containing the empty vector pSEVA | This work |
| ΔvgrG3(vgrG3) | In trans complementation of vgrG3 with pSEVA vector in ΔvgrG3 | This work |
| WT(pMR20) | WT strain containing the empty vector pMR20 | This work |
| Δhcp(hcp) | In trans complementation of hcp with pMR20 vector in Δhcp | This work |
| ΔvipA(vipA) | In trans complementation of vipA with pMR20 vector in ΔvipA | This work |
| Strain | Description | Reference |
|--------|-------------|-----------|
| ΔvgrG1-6(vgrG1) | In trans complementation of vgrG1 with pMR20 vector in the sextuple mutant (ΔvgrG1-6) | This work |
| ΔvgrG1-6(vgrG2) | In trans complementation of vgrG2 with pMR20 vector in the sextuple mutant (ΔvgrG1-6) | This work |
| ΔvgrG1-6(vgrG3) | In trans complementation of vgrG3 with pMR20 vector in the sextuple mutant (ΔvgrG1-6) | This work |
| ΔvgrG1-6(vgrG4) | In trans complementation of vgrG4 with pMR20 vector in the sextuple mutant (ΔvgrG1-6) | This work |
| ΔvgrG1-6(vgrG5) | In trans complementation of vgrG5 with pMR20 vector in the sextuple mutant (ΔvgrG1-6) | This work |
| ΔvgrG1-6(vgrG6) | In trans complementation of vgrG6 with pMR20 vector in the sextuple mutant (ΔvgrG1-6) | This work |
| WT(pCV_3981) | WT strain containing the promoter of CV_3981 with lacZ fusion | This work |
| ΔcviR(pCV_3981) | ΔcviR strain containing the promoter of CV_3981 with lacZ fusion | This work |
| WT(pCV_3982) | WT strain containing the promoter of CV_3982 with lacZ fusion | This work |
| ΔcviR(pCV_3982) | ΔcviR strain containing the promoter of CV_3982 with lacZ fusion | This work |
| WT(pvgrG1) | WT strain containing the promoter of vgrG1 with lacZ fusion | This work |
| WT(pvgrG2) | WT strain containing the promoter of vgrG2 with lacZ fusion | This work |
| WT(pvgrG3) | WT strain containing the promoter of vgrG3 with lacZ fusion | This work |
| WT(pvgrG4) | WT strain containing the promoter of vgrG4 with lacZ fusion | This work |
| WT(pvgrG5) | WT strain containing the promoter of vgrG5 with lacZ fusion | This work |
| WT(pvgrG6) | WT strain containing the promoter of vgrG6 with lacZ fusion | This work |
| ΔcviR(pvgrG3) | ΔcviR strain containing the promoter of vgrG3 with lacZ fusion | This work |
| ΔcviR(pvgrG4) | ΔcviR strain containing the promoter of vgrG4 with lacZ fusion | This work |
| WT(vipA_sfGFP) | WT with vipA_sfGFP cloned into pJN105 vector for L-arabinose induction | This work |
| ΔclpV(vipA_sfGFP) | ΔclpV with vipA_sfGFP cloned into pJN105 vector for L-arabinose induction | This work |
| Δhcp(vipA_sfGFP) | Δhcp with vipA_sfGFP cloned into pJN105 vector for L-arabinose induction | This work |
| ΔvgrG3(vipA.sfGFP) | ΔvgrG3 with vipA_sfGFP cloned into pJN105 vector for L-arabinose induction | This work |
| ΔvgrG1-3(vipA.sfGFP) | ΔvgrG1-3 with vipA_sfGFP cloned into pJN105 vector for L-arabinose induction | This work |
| **ΔvgrG1-6(vipA_sfGFP)** | **ΔvgrG1-6 with vipA_sfGFP cloned into pJN105 vector for L-arabinose induction** | This work |
|-------------------------|-----------------------------------------------------------------------------|-----------|
| **ΔcviR(vipA_sfGFP)**  | **ΔcviR with vipA_sfGFP under L-arabinose induction**                        | This work |
| **ΔcviI(vipA_sfGFP)**  | **ΔcviI with vipA_sfGFP under L-arabinose induction**                        | This work |
| **ΔvgrG3(vgrG3-HA)**   | **ΔvgrG3 in trans complemented with pMR20 expressing vgrG3 gene fused to hemagglutinin tag at C-terminal portion** | This work |

### Plasmids

| **pNPTS138** | Suicide vector containing oriT, Km\(^r\), sacB | D. Alley |
|--------------|-----------------------------------------------|----------|
| **pJN105**  | Broad-host-range vector, araC-PBAD cassette; Gm\(^r\) | (6)      |
| **pMR20**   | Broad-host-range low-copy vector containing oriT, Tet\(^R\) | (7)      |
| **pET-15b** | His-tagged protein expression vector; Amp\(^R\) | Novagen  |
| **pGEM-T easy** | Cloning plasmid; Amp\(^R\) | Promega  |
| **pRKlacZ290** | Vector containing promoterless E. coli lacZ, Tet\(^R\) | (8)      |
| **pSEVA221** | Broad-host-range vector, Km\(^R\), oriRK2, oriT. | (9)      |

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### Table S2. Primers used in this work

| Name            | Sequence 5’ - 3’* | Description                  |
|-----------------|-------------------|------------------------------|
| **Construction of mutant strains** |                   |                              |
| CV_3965 del1    | GATCATAGCTAAGGCGGTTGATCCGCGGCTGGGAAGCAAGGCGGCTGGGAAG | 767 pb, HindIII/EcoRI. CV_3965 deletion |
| CV_3965 del2    | GATCATAGCTAAGGCGGTTGATCCGCGGCTGGGAAGCAAGGCGGCTGGGAAG | 652 pb, EcoRI/Sall. CV_3965 deletion |
| CV_3965 del3    | GATCATAGCTAAGGCGGTTGATCCGCGGCTGGGAAGCAAGGCGGCTGGGAAG | 635 pb, HindIII/PstI. CV_3977 deletion |
| CV_3977 del1    | GATCATAGCTAAGGCGGTTGATCCGCGGCTGGGAAGCAAGGCGGCTGGGAAG | 687 pb, PstI/PstI. CV_3979 deletion |
| CV_3977 del2    | GATCATAGCTAAGGCGGTTGATCCGCGGCTGGGAAGCAAGGCGGCTGGGAAG | 607 pb, BamHI/EcoRI. CV_3979 deletion |
| CV_3979 del1    | GATCATAGCTAAGGCGGTTGATCCGCGGCTGGGAAGCAAGGCGGCTGGGAAG | 547 pb, BamHI/EcoRI. CV_3979 deletion |
| CV_3979 del2    | GATCATAGCTAAGGCGGTTGATCCGCGGCTGGGAAGCAAGGCGGCTGGGAAG | 606 pb, HindIII/BamHI. CV_3986 deletion |
| CV_3975 del1    | GATCATAGCTAAGGCGGTTGATCCGCGGCTGGGAAGCAAGGCGGCTGGGAAG | 665 pb, BamHI/EcoRI. CV_3986 deletion |
| CV_3975 del2    | GATCATAGCTAAGGCGGTTGATCCGCGGCTGGGAAGCAAGGCGGCTGGGAAG | 509 pb, HindIII/BamHI. CV_3975 deletion |
| CV_3977 del1    | GATCATAGCTAAGGCGGTTGATCCGCGGCTGGGAAGCAAGGCGGCTGGGAAG | 660 pb, BamHI/EcoRI. CV_3975 deletion |
| CV_3977 del2    | GATCATAGCTAAGGCGGTTGATCCGCGGCTGGGAAGCAAGGCGGCTGGGAAG | 626 pb, HindIII/BamHI. CV_1432 deletion |
| CV_1233 del1    | GATCATAGCTAAGGCGGTTGATCCGCGGCTGGGAAGCAAGGCGGCTGGGAAG | 603 pb, BamHI/EcoRI. CV_1432 deletion |
| CV_1233 del2    | GATCATAGCTAAGGCGGTTGATCCGCGGCTGGGAAGCAAGGCGGCTGGGAAG | 611 pb, HindIII/BamHI. CV_1233 deletion |
| CV_3979 del1    | GATCATAGCTAAGGCGGTTGATCCGCGGCTGGGAAGCAAGGCGGCTGGGAAG | 583 pb, BamHI/EcoRI. CV_1233 deletion |
| CV_3979 del2    | GATCATAGCTAAGGCGGTTGATCCGCGGCTGGGAAGCAAGGCGGCTGGGAAG | 593 pb, HindIII/BamHI. CV_0023 deletion |
| CV_3979 del3    | GATCATAGCTAAGGCGGTTGATCCGCGGCTGGGAAGCAAGGCGGCTGGGAAG | 657 pb, BamHI/EcoRI. CV_0023 deletion |
| CV_0016 del1    | GATCATAGCTAAGGCGGTTGATCCGCGGCTGGGAAGCAAGGCGGCTGGGAAG | 592 pb, Apal/BamHI. CV_0016 deletion |
| CV_0016 del2    | GATCATAGCTAAGGCGGTTGATCCGCGGCTGGGAAGCAAGGCGGCTGGGAAG | 632 pb, BamHI/Sall. CV_0016 deletion |
| **Construction of complemented strains** |                   |                              |
| CV_3977 Comp Fw | GATCATAGCTAAGGCGGTTGATCCGCGGCTGGGAAGCAAGGCGGCTGGGAAG | 852 pb, PstI/Sall. Product with hcp gene and its promoter region |
| CV_3977 Comp Rv | GATCATAGCTAAGGCGGTTGATCCGCGGCTGGGAAGCAAGGCGGCTGGGAAG | 699 pb, EcoRI/Sall. Product with vipA gene and its promoter region |
| CV_3979 Over Fw | GATCATAGCTAAGGCGGTTGATCCGCGGCTGGGAAGCAAGGCGGCTGGGAAG | 526 pb, PstI/EcoRI. vipA full gene plus 3 Gly x 3 Ala linker |
| CV_3979_sfgfp Rv | GATCATAGCTAAGGCGGTTGATCCGCGGCTGGGAAGCAAGGCGGCTGGGAAG | 714 pb, PstI/Sall. Product with super folder GFP for cloning with vipA into pJN105 |
| sGFP, Fw       | GATCATAGCTAAGGCGGTTGATCCGCGGCTGGGAAGCAAGGCGGCTGGGAAG | 498 pb, NdelI/BamHI. Product with hcp gene for heterologous expression |
| sGFP, Rv       | GATCATAGCTAAGGCGGTTGATCCGCGGCTGGGAAGCAAGGCGGCTGGGAAG | 2861 pb, KpnI/BamHI. CV_3986 complementation |
| CV_3975 Comp Fw | GATCATAGCTAAGGCGGTTGATCCGCGGCTGGGAAGCAAGGCGGCTGGGAAG | 3019 pb, KpnI/BamHI. CV_3975 complementation |
| CV_3975 Comp Rv | GATCATAGCTAAGGCGGTTGATCCGCGGCTGGGAAGCAAGGCGGCTGGGAAG | 3554 pb, KpnI/BamHI. CV_1432 complementation |
Table S3. Bacteria strains used as prey in interbacterial competition assay

| Bacteria                     | Strain         | Abbreviation * |
|------------------------------|----------------|----------------|
| Burkholderia cepacia         | ATCC 17759     | Bc             |
| Escherichia coli             | ATCC 25922     | Ec             |
| Pseudomonas aeruginosa       | ATCC 27853     | Pa             |
| Staphylococcus aureus        | ATCC 29313     | Sa             |
| Salmonella typhimurium       | ATCC 14028     | St             |
| Stenotrophomonas maltophilia | ATCC 13637     | Sma            |
| Enterobacte cloacae          | ATCC 13047     | Ecl            |
| Shigella flexneri            | ATCC 12022     | Sf             |
| Enterococcus faecium         | NCTC 13047     | Ef             |
| Klebsiella pneumonia         | ATCC 13883     | Kp             |
| Klebsiella pneumoniae        | ATCC BAA-1705  | Kpn            |
| Enterococcus faecalis        | ATCC 4083      | Efa            |
| Shigella sonnei              | ATCC 25931     | Ss             |
| Pseudomonas aeruginosa       | PAO1           | Pao            |

*Abbreviation referring to Figure 2A
Table S4. Proteins identified in coimmunoprecipitation assay of WT(pMR20) and ΔvgrG3(vgrG3-HA)

**WT(pMR20)**

| Accession* | Description | mW (Da) | Peptides | Coverage (%) | Products | Amount (fmol) |
|------------|-------------|---------|----------|--------------|----------|--------------|
| Q7M7F1     | Elongation factor Tu | 43045   | 92       | 86,3636      | 974      | 32,4532      |
| Q7NQF7     | DNA-directed RNA polymerase subunit beta' | 155194  | 86       | 63,8252      | 640      | 2,0263       |
| Q7NQF0     | Elongation factor G | 76958   | 60       | 79,7994      | 442      | 1,4946       |
| Q7NQG4     | 50S ribosomal protein L5 | 20292   | 14       | 46,3887      | 70       | 0,3518       |
| Q7NQG5     | 30S ribosomal protein S14 | 11589   | 7        | 38,6139      | 18       | 0,4214       |
| Q7NQG8     | 50S ribosomal protein L18 | 12765   | 9        | 64,1026      | 52       | 0,5157       |
| Q7NQG9     | 30S ribosomal protein S5 | 18207   | 14       | 47,6744      | 81       | 0,1538       |
| Q7NQM5     | Aspartate ammonia-lyase | 50287   | 24       | 76,8737      | 218      | 0,9865       |
| Q7NQX1     | 60 kDa chaperonin 2 | 57382   | 40       | 69,7802      | 347      | 1,5874       |
| Q7NR97     | Nudix hydrolase domain-containing protein | 23223   | 10       | 66,8269      | 105      | 0,1679       |
| Q7NUY8     | Trigger factor | 48546   | 34       | 81,3793      | 262      | 1,2455       |
| Q7NV09     | Uncharacterized protein | 6615    | 3        | 68,3333      | 38       | 0,0807       |
| Q7NV22     | Probable transmembrane protein | 13147   | 4        | 71,7742      | 53       | 0,0143       |
| Q7NVZ4     | 30S ribosomal protein S2 | 27112   | 18       | 69,1358      | 111      | 1,3853       |
| Q7NWY4     | Phosphonate metabolism protein PhnH | 20435   | 6        | 54,2105      | 66       | 0,0398       |
| Q7NX50     | Probable transcriptional regulator_ MerR family | 15218   | 9        | 58,4615      | 100      | 0,0483       |
| Q7NZ92     | Uncharacterized protein | 10198   | 4        | 43,8202      | 40       | 0,5778       |
| Q7P095     | ATP synthase subunit beta | 50024   | 40       | 81,0753      | 434      | 2,0939       |
| Q7P097     | ATP synthase subunit alpha | 54676   | 36       | 69,0661      | 327      | 2,4705       |
| Q7P0N9     | Acetyltransferase component | 56484   | 19       | 49,0975      | 210      | 1,8117       |
| Q7P0P0     | Pyruvate dehydrogenase E1 component | 99230   | 67       | 81,2852      | 584      | 2,3749       |

**ΔvgrG3(vgrG3-HA)**

| Accession | Description | mW (Da) | Peptides | Coverage (%) | Products | Amount (fmol) |
|-----------|-------------|---------|----------|--------------|----------|--------------|
| Q7M7F1    | Elongation factor Tu | 43045   | 54       | 72,2222      | 714      | 45,6856      |
| Q7NQF0    | Elongation factor G | 76958   | 39       | 55,5874      | 313      | 2,9557       |
| Q7NQF9    | 50S ribosomal protein L16 | 15401   | 4        | 30,4348      | 49       | 5,6009       |
| Q7NQG2    | 50S ribosomal protein L14 | 13409   | 15       | 51,6393      | 89       | 3,7829       |
| Q7NQG4    | 50S ribosomal protein L5 | 20292   | 16       | 65,3631      | 108      | 0,739        |
| Q7NQG5    | 30S ribosomal protein S14 | 11589   | 5        | 45,5446      | 56       | 4,4619       |
| Q7NQG8    | 50S ribosomal protein L18 | 12765   | 7        | 52,9915      | 88       | 9,9647       |
| Q7NQG9    | 30S ribosomal protein S5 | 18207   | 18       | 59,8837      | 149      | 3,5319       |
| Q7NQH0    | 50S ribosomal protein L30 | 6780    | 5        | 37,7049      | 33       | 1,1832       |
| Q7NQX1    | 60 kDa chaperonin | 57382   | 18       | 46,1538      | 164      | 2,9832       |
| Q7NQZ9    | VgrG1 (CV_3986) | 93995   | 27       | 41,7431      | 314      | 0,2691       |
| Q7NR08    | Hcp (CV_3977) | 17881   | 8        | 53,3333      | 81       | 0,9134       |
| Q7NR10    | VgrG2 (CV_3975) | 94022   | 20       | 35,8945      | 255      | 1,3435       |
| Q7NRL5    | 30S ribosomal protein S21 | 8490    | 2        | 28,5714      | 19       | 1,6007       |
| Accession | Protein Description                                | PPI | TIF-1 | TIF-2 | TIF-3 |
|-----------|-----------------------------------------------------|-----|-------|-------|-------|
| Q7NRT4    | 30S ribosomal protein S9                           | 14356 | 4     | 36,1538 | 44    | 2,1704 |
| Q7NRV5    | 30S ribosomal protein S16                         | 9536  | 7     | 59,0361 | 84    | 8,6455 |
| Q7NU57    | Uncharacterized protein (CV_2846)                 | 7517  | 2     | 45,4545 | 58    | 77,9891 |
| Q7NUY8    | Trigger factor                                     | 48546 | 15    | 42,7586 | 187   | 2,7161 |
| Q7NY43    | VgrG3 (CV_1432)                                    | 107856 | 29    | 42,1782 | 363   | 2,6193 |
| Q7P095    | ATP synthase subunit beta                          | 50024 | 27    | 51,1828 | 324   | 3,949  |
| Q7P097    | ATP synthase subunit alpha                         | 54676 | 18    | 33,8521 | 217   | 4,4851 |
| Q7P0N9    | Acetyltransferase component                       | 56484 | 12    | 32,3105 | 147   | 1,1308 |
| Q7P238    | VgrG5 (CV_0023)                                    | 94125 | 17    | 29,9771 | 247   | 1,2663 |

*Accessions highlighted in bold indicate proteins identified in both assays and are probably contaminant proteins with affinity to the magnetic beads.

**Fig S1** Growth curves of the indicated strains grown in LB medium. (A) Mutants for T6SS core components. (B) Single mutant strains for each vgrG. (C) Sequential vgrG mutants. None of these strains showed any growth delay compared to the WT strain.
A

|       | VgrG1 (CV_3986) | VgrG2 (CV_3975) | VgrG3 (CV_1432) | VgrG4 (CV_1233) | VgrG5 (CV_0023) | VgrG6 (CV_0016) |
|-------|----------------|----------------|----------------|----------------|----------------|----------------|
| VgrG1 | 100            | 93.43          | 93.46          | 76.46          | 84.36          | 81.68          |
| VgrG2 | 93.43          | 100            | 92.20          | 76.23          | 84.27          | 83.20          |
| VgrG3 | 93.46          | 92.20          | 100            | 71.06          | 83.55          | 81.80          |
| VgrG4 | 76.46          | 76.23          | 71.06          | 100            | 82.50          | 80.18          |
| VgrG5 | 84.36          | 84.27          | 83.55          | 82.50          | 100            | 93            |
| VgrG6 | 81.68          | 83.20          | 81.80          | 80.18          | 93             | 100            |

B

C

VgrG1 MDLTSLLSSFASAFQDQRLLTLELGSGQVAAEQLLPQSLNGEEGVSQAYRYQLTCLSPD 60
VgrG2 MDLSSLLSSFASAFQDQRLLTLELGSGQVAAEQLLPQSLNGEEGVSQAYRYQLTCLSPD 60
VgrG3 MDLDLLSSFASAFQDQRLLTLELGSGQVAAEQLLPQSLNGEEGVSQAYRYQLTCLSPD 60
VgrG4 MDLNALLSSFASAFQDQRLLTLELGSGQVAAEQLLPQSLNGEEGVSQAYRYTVTCLSPD 60
VgrG5 MDLNALSSFASAFQDQRLLTLELGSGQVAAEQLLPQSLNGEEGVSQAYRYTVTCLSPD 60
VgrG6 MDLSSSSSSFAFQDQRLLTLELGSGQVAAEQLLPQSLNGEEGVSQAYRYTVTCLSPD 60

VgrG1 GAIELKTLLGQAARIGIADAQGQETIRCGVVSQARLMGSDGGFAQYGLTIEPPIALLRHR 120
VgrG2 GAIELKTLLGQAARIGIADAQGQETIRCGVVSQARLMGSDGGFAQYGLTIEPPIALLRHR 120
VgrG3 GAIELKTLLGQAARIGIADAQGQETIRCGVVSQARLMGSDGGFAQYGLTIEPPIALLRHR 120
VgrG4 GNIELKTLLGQAARIGIADAQGQETIRCGVVSQARLMGSDGGFAQYGLTIEPPIALLRHR 120
VgrG5 GHIELKTLLGQAARIGIADAQGQETIRCGVVSQARLMGSDGGFAQYGLTIEPPIALLRHR 120
VgrG6 GHIELKTLLGQAARIGIADAQGQETIRCGVVSQARLMGSDGGFAQYGLTIEPPIALLRHR 120

VgrG1 KTSRVFQDLSVPDVQQIVHEHQAANPVFARAQSIEFKVGPAQPRSYCLQYREDDFSIV 180
VgrG2 KTSRVFQDLSVPDVQQIVHEHQAANPVFARAQTSVEFKVGPAQPRSYCLQYREDDFSIV 180
VgrG3 KTSRVFQDLSVPDVQQIVHEHQAANPVFARAQSIEFKVGPAQPRSYCLQYREDDFSIV 180
VgrG4 KTSRVFQDLSVPDVQQIVHEHQAANPVFARAQTSVEFKVGPAQPRSYCLQYREDDFSIV 180
VgrG5 KTSRVFQDLSVPDVQQIVHEHQAANPVFARAQTSVEFKVGPAQPRSYCLQYREDDFSIV 180
VgrG6 KTSRVFQDLSVPDVQQIVHEHQAANPVFARAQTSVEFKVGPAQPRSYCLQYREDDFSIV 180

VgrG1 RLLHEEGYAWRFHVD----------GDSQPVLVFDDAYSLLPPAEVERVRHRSDAT 229
VgrG2 RLLHEEGYAWRFHVD----------GDAQPVKLAVFDAYSLPPLPPEVERVRHRSDAT 229
VgrG3 RLLHEEGYAWRFHVD----------GDSQPVLVFDDAYSLLPPAEVERVRHRSDAT 229
VgrG4 RLLHEEGYAWRFHVD----------GDSQPVLVFDDAYSLLPPAEVERVRHRSDAT 229
VgrG5 RLLHEEGYAWRFHVD----------GDSQPVLVFDDAYSLLPPAEVERVRHRSDAT 229
VgrG6 RLLHEEGYAWRFHVD----------GDSQPVLVFDDAYSLLPPAEVERVRHRSDAT 229

VgrG1 EEEDGLTDWQARQIVPGNVALATFDYQPVSTQHGDSSQIDQGPGQALQSSLQDYDPQ 289
VgrG2  EEEGLTDSAAARQIVPNGVALATFDYQPSTQHTGDSQIDQPGGQALQSSLQDYDPQ  289
VgrG3  EEEGLTDSAAARQIVPNGVALATFDYQPSTQHTGDSQIDQPGGQALQSSLQDYDPQ  289
VgrG4  EEEGLTDSAAARQIVPNGVALATFDYQPSTQHTGDSQIDQPGGQALQSSLQDYDPQ  289
VgrG5  EEEGLTDSAAARQIVPNGVALATFDYQPSTQHTGDSQIDQPGGQALQSSLQDYDPQ  300
VgrG6  EEEGLTDSAAARQIVPNGVALATFDYQPSTQHTGDSQIDQPGGQALQSSLQDYDPQ  300

VgrG1  GLYYAGDAEQLSHYARLRQQAHDLQAKTFEGAGSIRGLTAGQWFRLDDHPAHEADSHEQR  349
VgrG2  GLYYAGDAEQLSHYARLRQQAHDLQAKTFEGAGSIRGLTAGQWFRLDDHPAHEADSHEQR  349
VgrG3  GLYYAGDAEQLSHYARLRQQAHDLQAKTFEGAGSIRGLTAGQWFRLDDHPAHEADSHEQR  349
VgrG4  GLYYAGDAEQLSHYARLRQQAHDLQAKTFEGAGSIRGLTAGQWFRLDDHPAHEADSHEQR  349
VgrG5  GLYYAGDAEQLSHYARLRQQAHDLQAKTFEGAGSIRGLTAGQWFRLDDHPAHEADSHEQR  349
VgrG6  GLYYAGDAEQLSHYARLRQQAHDLQAKTFEGAGSIRGLTAGQWFRLDDHPAHEADSHEQR  349

VgrG1  EFVVTGQTLQVRNNLPDLQSILPTGDKADAPFRTRIQAQRGIPITLAQYTGTEHAKPKS  409
VgrG2  EFVVTGQTLQVRNNLPDLQSILPTGDKADAPFRTRIQAQRGIPITLAQYTGTEHAKPKS  409
VgrG3  EFVVTGQTLQVRNNLPDLQSILPTGDKADAPFRTRIQAQRGIPITLAQYTGTEHAKPKS  409
VgrG4  EFVVTGQSFQARNNLPTDLAQHIGAEQDAAPFTTSIQAQRRGIPLTPAYAGTAHAKPTS  408
VgrG5  EFVVTGQSFQARNNLPTDLAQHIGAEQDAAPFTTSIQAQRRGIPLTPAYAGTAHAKPTS  408
VgrG6  EFVVTGQSFQARNNLPTDLAQHIGAEQDAAPFTTSIQAQRRGIPLTPAYAGTAHAKPTS  408

VgrG1  RGVQTATVVGPAGEEVHTDGRIKVQFHWQRPDEHPTIGAALDDKSSCWLRVAMSAGA  469
VgrG2  RGVQTATVVGPAGEEVHTDGRIKVQFHWQRPDEHPTIGAALDDKSSCWLRVAMSAGA  469
VgrG3  RGVQTATVVGPAGEEVHTDGRIKVQFHWQRPDEHPTIGAALDDKSSCWLRVAMSAGA  469
VgrG4  RGVQTATVVGPAGEEVHTDGRIKVQFHWQRPDEHPTIGAALDDKSSCWLRVAMSAGA  469
VgrG5  RGVQTATVVGPAGEEVHTDGRIKVQFHWQRPDEHPTIGAALDDKSSCWLRVAMSAGA  469
VgrG6  RGVQTATVVGPAGEEVHTDGRIKVQFHWQRPDEHPTIGAALDDKSSCWLRVAMSAGA  469

VgrG1  GWGHQFIPRIGQEVLVDFIEGDIDRPVITGVLYNGSHPTPDFSGAGSLPANKTLSGIKSK  529
VgrG2  GWGHQFIPRIGQEVLVDFIEGDIDRPVITGVLYNGSHPTPDFSGAGSLPANKTLSGIKSK  529
VgrG3  GWGHQFIPRIGQEVLVDFIEGDIDRPVITGVLYNGSHPTPDFSGAGSLPANKTLSGIKSK  529
VgrG4  GWGHQFIPRIGQEVLVDFIEGDIDRPVITGVLYNGSHPTPDFSGAGSLPANKTLSGIKSK  529
VgrG5  GWGHQFIPRIGQEVLVDFIEGDIDRPVITGVLYNGSHPTPDFSGAGSLPANKTLSGIKSK  529
VgrG6  GWGHQFIPRIGQEVLVDFIEGDIDRPVITGVLYNGSHPTPDFSGAGSLPANKTLSGIKSK  529

VgrG1  EHQGGAYNELLFDDTPGEVRAKLSSELGKTQLNQGFLTHPRSNGKAQPRGDGFELRTDHH  588
VgrG2  EHQGGAYNELLFDDTPGEVRAKLSSELGKTQLNQGFLTHPRSNGKAQPRGDGFELRTDHH  588
VgrG3  EHQGGAYNELLFDDTPGEVRAKLSSELGKTQLNQGFLTHPRSNGKAQPRGDGFELRTDHH  588
VgrG4  EHQGGAYNELLFDDTPGEVRAKLSSELGKTQLNQGFLTHPRSNGKAQPRGDGFELRTDHH  588
VgrG5  EHQGGAYNELLFDDTPGEVRAKLSSELGKTQLNQGFLTHPRSNGKAQPRGDGFELRTDHH  588
VgrG6  EHQGGAYNELLFDDTPGEVRAKLSSELGKTQLNQGFLTHPRSNGKAQPRGDGFELRTDHH  588

VgrG1  GAIRAAHGLLLTTEAQNGASGKQLAREHAQSQLDAALSLSQALAETASGQLADTMETGPD  648
VgrG2  GAIRAAHGLLLTTEAQNGASGKQLAREHAQSQLDAALSLSQALAETASGQLADTMETGPD  648
VgrG3  GAIRAAHGLLLTTEAQNGASGKQLAREHAQSQLDAALSLSQALAETASGQLADTMETGPD  648
VgrG4  GAIRAAHGLLLTTEAQNGASGKQLAREHAQSQLDAALSLSQALAETASGQLADTMETGPD  648
VgrG5  GAIRAAHGLLLTTEAQNGASGKQLAREHAQSQLDAALSLSQALAETASGQLADTMETGPD  648
VgrG6  GAIRAAHGLLLTTEAQNGASGKQLAREHAQSQLDAALSLSQALAETASGQLADTMETGPD  648

VgrG1  EIQPDNACKGKTDFDGLHQAHDALKANEAGSTDKDGKTADQAGQQPQLVLSAPAGA  709
VgrG2  EIQPDNACKGKTDFDGLHQAHDALKANEAGSTDKDGKTADQAGQQPQLVLSAPAGA  709
VgrG3  EIQPDNACKGKTDFDGLHQAHDALKANEAGSTDKDGKTADQAGQQPQLVLSAPAGA  709
VgrG4  EIQPDNACKGKTDFDGLHQAHDALKANEAGSTDKDGKTADQAGQQPQLVLSAPAGA  709
VgrG5  EIQPDNACKGKTDFDGLHQAHDALKANEAGSTDKDGKTADQAGQQPQLVLSAPAGA  709
VgrG6  EIQPDNACKGKTDFDGLHQAHDALKANEAGSTDKDGKTADQAGQQPQLVLSAPAGA  709

VgrG1  LTEQSQTVSAGQNLNLVQARQNDANTHTGRWLNHVGQHISLFLVAGVKDVKVALKIAAGKV  769
VgrG2  LTEQSQTVSAGQNLNLVQARQNDANTHTGRWLNHVGQHISLFLVAGVKDVKVALKIAAGKV  769
VgrG3  LTEQSQTVSAGQNLNLVQARQNDANTHTGRWLNHVGQHISLFLVAGVKDVKVALKIAAGKV  769
VgrG4  LTEQSQTVSAGQNLNLVQARQNDANTHTGRWLNHVGQHISLFLVAGVKDVKVALKIAAGKV  769
VgrG5  LTEQSQTVSAGQNLNLVQARQNDANTHTGRWLNHVGQHISLFLVAGVKDVKVALKIAAGKV  769
VgrG6  LTEQSQTVSAGQNLNLVQARQNDANTHTGRWLNHVGQHISLFLVAGVKDVKVALKIAAGKV  769
The six VgrG proteins of *C. violaceum* show high sequence identity and similar domain organization. (A) Identity percentages shared among the six VgrG proteins of *C. violaceum*. The values were obtained with the Clustal Omega tool for multiple alignment. (B) Modular domains of VgrG proteins from analysis in the Pfam database. Green, red, and blue indicate the typical VgrG domains. All VgrGs have an additional C-terminal domain, DUF2345 (yellow). VgrG3 contains another additional region at C-terminus with low complexity (light blue). VgrG1, VgrG2, VgrG4, and VgrG5 have putative signal sequences at their N-termini (orange). (C) Multiple sequence alignment of VgrGs using the Clustal Omega tool.