supplementary Table 1. Sequence homology between *vanG-*1, *vanG*-2, previously described *vanG* elements, and homologous elements from *Roseburia intestinalis.*

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Sequential orf designationsA within GBS *vanG* elements (No. bp) | functional domain homology  | % sequence identity/overlapin bp between GBS1 and GBS2orfs | Best matching enterococcal*vanG* element(s) % identity/overlap in bpE | No. of sequential homologous orfs within *Roseburia intestinalis* XB6B4 *vanG*-like element/ % identity/overlap in bp A | No. of sequential homologous orfs within *Roseburia intestinalis* M50/1 *vanG*-like element/ % identity/overlap in bp A |
| *vanG*-1 | *vanG*-2 | to GBS1 | to GBS2 | to GBS1 | to GBS2 | to GBS1 | to GBS2 |
| 1 (347) B | 1 (347) B | unknown | 86/347 | DQ212987/100/347 | AY271781/94/347DQ212987/85/347 | 1/97/347 | 1/85.9/347 | 1/86.7/347 | 1 /94.5/347 |
| - | A (885) | unknown | no matchC | no matchC | AY271781/99/885 | no matchC | no matchC | no matchC | no matchC |
| - | B (1701) | Topoisomerase-Primase/DNA replication and RecF repair  | no matchC | no matchC | AY271781/99/1681 | no matchC | no matchC | no matchC | no matchC |
| - | C (1500) | UvrD-helicase | no matchC | no matchC | AY271781/99/1500 | no matchC | no matchC | no matchC | no matchC |
| 2 (180) | 2 (180) | unknown | 78/180 | DQ212987/83/180  | FJ872410/80/180 | 2/99/180 | 2/78.9/180 | 2/78.9/180 | 2/97.2/180 |
| 3 (828) | 3 (828) | ParA (plasmid partitioning) | 87/828 | FJ872410/77/828 | FJ872410/76/828 | 3/97/828) | 3/87.1/828 | 3/86.4/828 | 3/97.9/828 |
| 4 (936) | 4 (948) | ParB (plasmid partitioning) | 81/948 | FJ872410/83/948 | FJ872410/83/948 | 4/97/936 | 4/81.5/948 | 4/82.2/948 | 4/92.0/948 |
| a (162) | - | unknown | no matchC | no matchC | no matchC | a/96/162 | no matchC | no matchC | no matchC |
| 5 (4146) | 5 (4143) | pilus-associated adhesin (*rrgA*-like), C-terminal wall association motif | 81/4146 | FJ872410/74/3671 | FJ872410/76/3614 | 5/96/4146 | 5/81.1/4146 | 5/81/4146 | 5/98/4143 |
| 6 (303) | 6 (303) | unknown | 80/301 | FJ872410/73/303 | FJ872410/76/301 | 6/99/303 |  6/80.4/301 | 6/80/301 | 6/97/303 |
| 7 (273) | 7 (273) | unknown | 85/273 | FJ872410/78/273 | FJ872410/75/273 | 7/97/273 | 7/85.0/273 | 7/84/273 | 7/99/273 |
| 8 (612) | 8 (603) | unknown | 82/591 | FJ872410/73/585 | FJ872410/76/603 | 8/98/572 | 8/81.0/609 | 8/81/612 | 8/96/603 |
| 9 (699) | 9 (696) | unknown | 81/698 | FJ872410/78/701 | FJ872410/77/699 | no matchC | no matchC | 9/81/698 | 9/97/696 |
| 10 (210) | 10 (207) | unknown | 87/200 | FJ872410/85/209 | FJ872410/84/207 | 10/94/210  | 10/85.2/203 | 10/87/200 | 10/97/207 |
| 11 (8076) | 11 (7764) | DNA/RNA helicase; methylase | 80/8088 | FJ872410/79/8197 | FJ872410/76/8192 |  11/92/8273 | 11/77.1/8271 | 11/80/8085 | 11/98/7764 |
| 12 (330) | 12 (348) | unknown | 71/318 | FJ872410/79/329 | AY271782/96/348 | 12/88/330 | 12/66.9/350 | 12/71/318 | 12/98/348 |
| b (795) | - | unknown | no matchC | no matchC | no matchC | no matchC | no matchC | no matchC | no matchC |
| - | D (1245) | DNA binding transcriptional regulator | no matchC | no matchC | no matchC | no matchC | no matchC | no matchC | no matchC |
| 13 (984) | 13 (993) | Topoisomerase-primase DNA cleavage domain | 80/994 | FJ872410/82/986 | AY271782/93/992 | 13/96/984 | 13/79.0/993 |  13/80/984 | 13/93 (993) |
| 14 (303) | 14 (300) | unknown | 70/246 | FJ872410/73/302 | AY271782/98.3/300 | 14/97/303 | 14/69.0/332 | 14/80/301 | 14/97 (300) |
| 15 (153) | 15 (153) | unknown  | 99/153  | AY271782/100/153 | AY271782/99/153 | 15/79/153 | 15/78.4/153 | 15/99/153 | 15/98 (153) |
| 16 (330) | 16 (330) | transcriptional repressor (copG family), plasmid mobilization (MobC)/relaxase | 99/330 | AY271782/100/330 | AY271782/99/330 | 16/83/330  | 16/83.9/330 | 16/96/330 | 16/97 (330) |
| 17 (1413) | 17 (1413) | relaxase mobilization nuclease domain | 97/1413 | AY271782/99.9/1413 | AY271782/97/1413 | 17/82/1413  | 17/82.2/1413 | 17/96/1413 | 17/96 (1413) |
| 18 (813) | 18 (813) | unknown | 97/813 | AY271782/99.9/813 | AY271782/97/813 | 18/85/813 | 18/86.2/816 | 18/97/813  | 18/98 (831) |
| 19 (864) | 19 (864) | unknown | >99 (864) | AY271782/99.8/864 | AY271782/99.4/864 | 19/84/864  | 19/83.7/864 | 19/97/864 | 19/97 (864) |
| 20 (198) | 20 (198) | unknown | 100 (198) | AY271782/100/198 | AY271782/100/198 | 20/86/198 | 20/86.4/198 | 20/99/198 | 20/99 (198) |
| 21 (1791) | 21 (1791) | VirD4 family; ATP-binding conjugation, type IV secretion) | 100 (1791) | AY271782/99.2/1792 | AY271782/99.2/1792 | 21/86/1794 | 21/86.1/1794 | 21/97/1791 | 21/97 (1791) |
| 22 (357) | 22 (357) | unknown | >99 (357) | AY271782/100/357 | AY271782/99.7/357 | 22/82/363 | 22/82.1/363 | 22/98/357 | 22/99 (357) |
| 23 (837) | 23 (837) | unknown | 100 (837) | AY271782/99.8/837 | AY271782/99.8/837 | 23/84/837 | 23/83.8/837 | 23/97/837 | 23/97 (837) |
| 24 (453) | 24 (453) | unknown type IV secretion | 100 (453) | AY271782/100/453 | AY271782/100/453 | 24/82/452 | 24/82.1/452 | 24/98/433 | 24/98 (433) |
| 25 (2334) | 25 (2334) | type IV secretion, conjugative transfer ATPase  | >99 (2334) | AY271782/100/2334 | AY271782/99.8/2334 | 25/86/2334  | 25/86.5/2334 | 25/97/2334  | 25/97 (2334) |
| 26 (405) | 26 (405) | unknown | 100 (405) | AY271782/100/405 | AY271782/100/405 | 26/84/405 | 26/83.7/405 | 26/98/405 | 26/98 (405) |
| 27 (774) | 27 (774) | type IV secretory pathway, RecA-like ATPase | 94/769 | AY271782/100/774 | AY271782/94/769 | 27/79/772 | 27/78.6/777 | 27/90/769 | 27/96 (774) |
| 28 (1794) | 28 (1776) | peptidoglycan hydrolase | 78/1793 | AY271782/100/1794DQ212986/100/1428B  | AY271782/78/1793 | 28/77/1793 | 28/80.6/1776 | 28/80/1793 | 28/93 (1776) |
| c-c (342) | - | Transposon-related DNA-binding protein | no matchC | AY271782/100/342DQ212986/100/342 | no matchC | c-c/66/335 | no matchC | no matchC | no matchC |
| 29 (228) | 29/30 (762) | VanU transcriptional regulator | 87/30D | AY271782/100/228Q212986/100/228 | FJ872410/65/766 | no matchC | no matchC | no matchC | no matchC |
| 30 (708) | 29/30 (762) | VanR DNA-binding response regulator | 67/714 | AY271782/100/708Q212986/100/708 | FJ872410/65/766 | no matchC | no matchC | no matchC | no matchC |
| 31 (1107) | 31 (1125) | VanS sensor kinase | 57/1115 | AY271782/100/1107Q212986/100/1107 | AY271782/57/1115Q212986/57/1115 | no matchC | no matchC | no matchC | no matchC |
| 32 (840) | 32 (756) | VanY D-ala, D-ala carboxypeptidase  | 78/551 | Q212986/100/840AY271782/99.9/840 | AY271782/78/551Q212986/78/551 | 32/60/587 | 32/60/554 | no matchC | no matchC |
| 33 (846) | 33 (846) | VanW, unknown | 90/846 | Q212986/100/846AY271782/99.9/840 | AY271782/90/846 | no matchC | no matchC | no matchC | no matchC |
| 34 (1050) | 34 (1050) | VanG: D-Ala-D-Ser ligase | 91/1050 | AY271782/100/1050 | FJ872410/92/1050AY271782/91/1050 | no matchC | no matchC | no matchC | no matchC |
| 35 (762) | 35 (762) | VanXY: bi-functional D,D-2 dipeptidase/D,D-carboxypeptidase  | 96/762 | AY271782/100/762 | FJ872410/>99/762AY271782/96/762 | no matchC | no matchC | no matchC | no matchC |
| 36 (2139) | 36 (2139) | vanT: serine racemase | >99/2139 | AY271782/100/2139Q212986/100/2139 | AY271782/>99/2139Q212986/>99/2139 | no matchC | no matchC | no matchC | no matchC |
| 37c (360) | 37-c (360) | transposon-related DNA-binding  | >99/360 | AY271782/100/360Q212986/100/360 | AY271782/>99/360Q212986/>99/360 | no matchC | no matchC | 37c C /92/360 | no matchC |
| 38 (276) | 38 (276) | unknown | >99/276 | AY271782/100/276Q212986/100/276 | AY271782/>99/276Q212986/>99/276 | no matchC | no matchC | no match | no match |
| 39 (429) | 39 (429) | sigma24-like, potential DNA-binding transcriptional activator | 95/429 | AY271782/100/429Q212986/100/429 | AY271782/95/429Q212986/95/429 | no matchC | no matchC | 37/94/429 | 37/98/429 |
| 40c (286) | 40-c (286) | unknown | 100/286 | AY271782/100/279Q212986/100/279 | AY271782/100/279Q212986/100/279 | 40c/80/283 | 40c/79.5/283 | 93/280 | 93/280 |
| 41 (204) | 41 (204) | unknown | 100/204 | AY271782/100/204Q212986/100/204 | AY271782/100/204Q212986/100/204 | 41/87/215 | 41/87/215 | 41/98/204 | 41/98/204 |
| 42 (372) | 42 (372) | PemK-like, cell toxin/plasmid maintenance, autoregulates through promoter binding | >99/372 | AY271782/100/372Q212986/100/372 | AY271782/>99/372Q212986/>99/372 | 42/76/366 | 42/76/366 | 42/97/372 | 42/97/372 |
| 43 (153) | 43 (153) | unknown | 100/153 | AY271782/100/153Q212986/100/153 | AY271782/100/153Q212986/100/153 | 43/71/153/ | 43/71/153/ | 43/99/153 | 43/99/153 |
| 44 (1643)F | 44 (1643) F | serine3 recombinase/integrase | 100/1643 | AY271782/100/1643Q212986/100/1643 | AY271782/100/1643Q212986/100/1643 | 44/82/1643 | 44/82/1643 | 44/98/1643 | 44/98/1643 |

A orf number followed by c indicates orf present on reverse DNA strand.

B fused in frame to 5’ segment of chromosomal RNA methytransferase gene in GBS1-NY, GBS2-NM, and *S. anginosus* strain Sa.

CLacks homologous orf within entire element

DFirst 30 bp only, which shows predicted amino acid sequence identity over predicted amino acids 1-10 with GBS-NM orf29/30.

EExcept for FJ872410, these GenBank accessions depict partial *vanG* element sequences so it is likely that there are additional homologous orfs from the indicated *vanG* elements with homology to *vanG-*1 and *vanG-*2. The general order of open reading frames and the corresponding *vanG-*1, *vanG*-2, and *Roseburia intestinalis* strain putative insertion elements is the same.

FFused in frame to 3’ 11 codon segment of chromosomal RNA methyltransferase gene of GBS1-NY and GBS2-NM. Although a counterpart *S. anginosus* *rumA* gene (from strain F0211) that shared sequence identity to the strain Sa *rumA* 5’ segment (bases 1-1328 fused to *vanG-*1), the Sa segment corresponding to F0211 *rumA* bases 1329-1362 were not present on the Sa genome (see Fig 3).