

In silico analyses I

1. Anaerococcus vaginalis vs. Anaerococcus tetradius

ROI 1

CLUSTAL O(1.2.4) multiple sequence alignment

```
Anaerococcus_tetradius_smMIPCopri      TGATGATTTGACGTCATCCCCACCTTCCTCCGGTTTATCACCGGCAGTATATCTAGAGTC      60
Anaerococcus_vaginalis_smMIPCopri      TGATGATTTGACGTCGTCGCCACCTTCCTCCGGTTTATCACCGGCAGTATCGTAGAGTC      60
*****

Anaerococcus_tetradius_smMIPCopri      CCCAACTTAATGATGGTAACTAAATATAGGGGTTGCGCTCGTTATGGGACTTAACCCAAC      120
Anaerococcus_vaginalis_smMIPCopri      CCCAACTTAATGATGGTAACTAAAGATAGGGGTTGCGCTCGTTATGGGACTTAACCCAAC      120
*****

Anaerococcus_tetradius_smMIPCopri      ATCTCACGACACGAGCTGACGACAACCA      148
Anaerococcus_vaginalis_smMIPCopri      ATCTCACGACACGAGCTGACGACAACCA      148
*****
```

5 SNPs on 148 nt = (148-5: 143)/148 * 100 = **96.62% similarity**

ROI 2

CLUSTAL O(1.2.4) multiple sequence alignment

```
Anaerococcus_tetradius_smMIPsSattelless  CTTCATGCACTCGAGTTGCAGAGTCAATCCGAAGTGGGACAGGCTTTTGTAGTTTGTCT 60
Anaerococcus_vaginalis_smMIPsSattelless  CTTCATGTACTCGAGTTGCAGAGTACAATCCGAAGTGGGACAGACTTTGTAGTTTGTCT 60
*****

Anaerococcus_tetradius_smMIPsSattelless  TAACTTCGCAGTCTCGCTTCCCTGTGTACCTGCCATTGTAGCACGTGTGTAGCCCAAGTC 120
Anaerococcus_vaginalis_smMIPsSattelless  TCAGATCGCTCTTTCGCTGCCCTCTGTATCTGCCATTGTAGCACGTGTGTAGCCCAAGTC 120
* * * * *

Anaerococcus_tetradius_smMIPsSattelless  ATAAAGGGCATGATGATTTGACGTCATCCC      150
Anaerococcus_vaginalis_smMIPsSattelless  ATAAAGGGCATGATGATTTGACGTCGTC      150
*****
```

15 SNPs on 150 nt = (150-15: 135)/150 * 100 = **90.00% similarity**

ROI 3

CLUSTAL O(1.2.4) multiple sequence alignment

```
Anaerococcus_tetradius_smMIPCacnes      GACGACAACCATGCACCACCTGTATTACAGTCTCCGAAGAAGTAAGGAACTATCTCTAA 60
Anaerococcus_vaginalis_smMIPCacnes      GACGACAACCATGCACCACCTGTAATACAGTAGACCGAAGTCATAGAAAATTATCTCTAA 60
*****

Anaerococcus_tetradius_smMIPCacnes      TTCCTCCGTAATATGTCAAGACTTGGTAAGGTTCTTCGCGTTGCGTCGAATTAACCAC 120
Anaerococcus_vaginalis_smMIPCacnes      TTCCTCCGTAATATGTCAAGACTTGGTAAGGTTCTTCGCGTTGCGTCGAATTAACCAC 120
*****

Anaerococcus_tetradius_smMIPCacnes      ATGCTCCGCTGCTTGTGCGGGTCCCGTCAATT      153
Anaerococcus_vaginalis_smMIPCacnes      ATGCTCCGCTGCTTGTGCGGGTCCCGTCAATT      153
*****
```

12 SNPs on 153 nt = (153-12: 141)/153 * 100 = **92.16% similarity**

ROI 4

CLUSTAL O(1.2.4) multiple sequence alignment

```
Anaerococcus_tetradium_smMIPBangulatum      TTCCGATACGGCTACCTTGTACGACTTCACCCAGTTACTGACCTACCTTCGACTGCT      60
Anaerococcus_vaginalis_smMIPBangulatum      TTCCGATACGGCTACCTTGTACGACTTCACCCAGTTACTGACCTACCTTCGACTGCT      60
*****

Anaerococcus_tetradium_smMIPBangulatum      GCTTCCTAA-TGGTTAGCTCACAGGCTTCGGGTATTGCCAACTCCATGGTGTGACGGGC      119
Anaerococcus_vaginalis_smMIPBangulatum      GCGTCCTAAAAGGTTTCGCTCACAGGCTTCGGGTATTGCCAACTCCATGGTGTGACGGGC      120
** ***** **

Anaerococcus_tetradium_smMIPBangulatum      GGTGTGTACAAGACCCGGGAACGCATT 146
Anaerococcus_vaginalis_smMIPBangulatum      GGTGTGTACAAGACCCGGGAACGCATT 147
*****
```

5 SNPs on 146 nt = (146-5: 141)/146 * 100 = **96.58% similarity**

ROI 5

CLUSTAL O(1.2.4) multiple sequence alignment

```
Anaerococcus_tetradium_smMIPFpraustnizii    CGTCAATTCCTTTGAGTTTCACACTTGCCTGCGTACTCCAGGGGAGTGTTTATTGCG      60
Anaerococcus_vaginalis_smMIPFpraustnizii    CGTCAATTCCTTTGAGTTTCACACTTGCCTGCGTACTCCAGGGGAGTGTTTATTGCG      60
*****

Anaerococcus_tetradium_smMIPFpraustnizii    TTAGCTGCGGCACCCAGATTATTCCAGACACCTAACACTCATCGTTTACGGCGTGGACTA      120
Anaerococcus_vaginalis_smMIPFpraustnizii    TTAGCTGCGGCTCCAGATTATTCCAAGAACCTAACACTCATCGTTTACAGCGTGGACTA      120
*****

Anaerococcus_tetradium_smMIPFpraustnizii    CCAGGGTATCTAATCCTGTTTGCTA 145
Anaerococcus_vaginalis_smMIPFpraustnizii    CCAGGGTATCTAATCCTGTTTGCTA 145
*****
```

6 SNPs on 145 nt = (145-6: 139)/145 * 100 = **95.86% similarity**

2. Anaerococcus tetradium vs. Peptostreptococcus anaerobius

ROI 1

CLUSTAL O(1.2.4) multiple sequence alignment

```
Anaerococcus_tetradium_smMIPCopri           TGATGATTTGACGTCATCCCCACCTTCCTCCGGTTTATCACCGGCAGTATATCTAGAGTC      60
Peptostreptococcus_anaerobius_smMIPCopri    TGATGATTTGACGTCATCCCCACCTTCCTCCAGGTTATCCCTGGCAGTCTCTAGAGTG      60
*****

Anaerococcus_tetradium_smMIPCopri           CCCAACTTAATGATGGTAACTAAATATAGGGGTTGCGCTCGTTATGGGACTTAACCCAAC      120
Peptostreptococcus_anaerobius_smMIPCopri    CCCAACTGAATGCTGGCAACTAAAGACAAGGTTGCGCTCGTTGCGGGACTTAACCCAAC      120
*****

Anaerococcus_tetradium_smMIPCopri           ATCTCACGACACGAGCTGACGACAACCA 148
Peptostreptococcus_anaerobius_smMIPCopri    ATCTCACGACACGAGCTGACGACAACCA 148
*****
```

14 SNPs on 148 nt = (148-14: 134)/148 * 100 = **90.54% similarity**

ROI 2

CLUSTAL O(1.2.4) multiple sequence alignment

```
Anaerococcus_tetradium_smMIPcacnes      GACGACAACCATGCACCACCTGTATTACAGTCTCCGAAGAAGTAAGGAATATCTCTAA      60
Peptostreptococcus_anaerobius_smMIPcacnes GACGACAACCATGCACCACCTGTACCTCAGC----CCGGAAGGGAAGGTGTGATTAAC      56
***** * * * * *
Anaerococcus_tetradium_smMIPcacnes      TTCCCTCCGTAATATGTCAAGACTTGGTAAGGTTCTTCGCGTTGCGTCGAATTAACCAC      120
Peptostreptococcus_anaerobius_smMIPcacnes ACCGGTCTAAGGGATGTCAAGCTTAGGTAAGGTTCTTCGCGTTGCTTCAATTAACCAC      116
* ** * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
Anaerococcus_tetradium_smMIPcacnes      ATGCTCCGCTGCTTGTGCGGGTCCCGTCAATT      153
Peptostreptococcus_anaerobius_smMIPcacnes ATGCTCCGCTACTTGTGCGGGTCCCGTCAATT      149
***** * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
```

42 SNPs on 149 nt = (149-42: 107)/149 * 100 = **71.81% similarity**

ROI 3

CLUSTAL O(1.2.4) multiple sequence alignment

```
Anaerococcus_tetradium_smMIPpraustinizii CGTCAATTCCTTTGAGTTTCACACTTGCCTGCGTACTCCCGAGGCGGAGTGTATTATGCG      60
Peptostreptococcus_anaerobius_smMIPpraustinizii CGTCAATTCCTTTGAGTTTCACACTTGCCTGCGTACTCCCGAGGCGGAGTACTTAATGCG      60
***** * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
Anaerococcus_tetradium_smMIPpraustinizii      TTAGCTGCGGCACCCAGAT---TATTCCAGACACCTAACACTCATCGTTTACGGCGTGG      116
Peptostreptococcus_anaerobius_smMIPpraustinizii TTAGCTGCGGCACCCAGGGGGTAACCCCGACACTAGTACTCATCGTTTACAGCGTGG      120
***** * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
Anaerococcus_tetradium_smMIPpraustinizii      ACTACCAGGGTATCTAATCCTGTTTGCTA      145
Peptostreptococcus_anaerobius_smMIPpraustinizii ACTACCAGGGTATCTAATCCTGTTTGCTA      149
***** * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
```

17 SNPs on 145 nt = (145-17: 128)/145 * 100 = **88.28% similarity**

ROI 4

CLUSTAL O(1.2.4) multiple sequence alignment

```
Anaerococcus_tetradium_smMIPBangulatum      TTCCGATACGGCTACCTTGTACGACTTCACCCAGTTACTGACCTACCTTCGACTGCT      60
Peptostreptococcus_anaerobius_smMIPBangulatum TTCCGATACGGCTACCTTGTACGACTTCACCCAGTTATCGACGCCACCTTCGACGACT      60
***** * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
Anaerococcus_tetradium_smMIPBangulatum      GCTTCCTAATGGTTAGCTCACAGGCTTCGGGTATTGCCAACTTCCATGGTGTGACGGGCG      120
Peptostreptococcus_anaerobius_smMIPBangulatum TCCTCCTTGCGGTTGGATAATCGGCTTCGGGTGTTCCGACTCCCATGGTGTGACGGGCG      120
* **** * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
Anaerococcus_tetradium_smMIPBangulatum      GTGTGTACAAGACCCGGGAACGCATT      146
Peptostreptococcus_anaerobius_smMIPBangulatum GTGTGTACAAGACCCGGGAACGCATT      146
***** * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
```

20 SNPs on 146 nt = (146-20: 126)/146 * 100 = **86.30% similarity**

3. Peptostreptococcus anaerobius vs Gardnerella vaginalis

ROI 1

CLUSTAL O(1.2.4) multiple sequence alignment

```

Gardnerella_vaginalis_smMIPPcopri      TGATGATCTGACGTCATCCCCACCTTCTCCGAGTTAACCCGCGGTCCCCGTGAGTT      60
Peptostreptococcus_anaerobius_smMIPPcopri  TGATGATTTGACGTCATCCCCACCTTCTCCAGGTTATCCCTGGCAGTCTCTAGAGTG      60
*****
Gardnerella_vaginalis_smMIPPcopri      CCCGGCATAACCCGCTGGCAACACAGGGCGAGGGTTGCGCTCGTTGCGGGACTTAACCCA      120
Peptostreptococcus_anaerobius_smMIPPcopri  CCCAAC--TGAATGCTGGCAACTAAAGACAAGGGTTGCGCTCGTTGCGGGACTTAACCCA      118
*** *
Gardnerella_vaginalis_smMIPPcopri      ACATCTCACGACACGAGCTGACGACGACCA      150
Peptostreptococcus_anaerobius_smMIPPcopri  ACATCTCACGACACGAGCTGACGACAACCA      148
*****

```

25 SNPs on 148 nt = (148-25: 123)/148 * 100 = **83.10% similarity**

ROI 2

CLUSTAL O(1.2.4) multiple sequence alignment

```

Gardnerella_vaginalis_smMIPCacnes      -----AATTGACGGGGGCCCGCACAAGCGGCGGAG----CATGCGGATTAATTCGA      47
Peptostreptococcus_anaerobius_smMIPCacnes  GACGACAACCATGCACCACCTGTCACTCAGCCCCGAAGGGAAGGTGTGATTAACACCG      60
** ** * * * * *
Gardnerella_vaginalis_smMIPCacnes      TGC--AACGCGAAGAACCTTACCTGGGCTTGACATGTGCCTGTCGACTGCAGAGATGTGG      105
Peptostreptococcus_anaerobius_smMIPCacnes  GTCTAAGGGATGTCAAGCTTAGGTAAGTTCTTCGCGTTGCTTCAATTAACACCATGC      120
* * * * * * * * *
Gardnerella_vaginalis_smMIPCacnes      TTTCCCTTCGGGGCAGGTTACAGGTGGTGCATGGTCGTCGTC      148
Peptostreptococcus_anaerobius_smMIPCacnes  TCCGCTACTTGTGCGGGTCCCCGTC AATT-----      149
* * * * * * *

```

95 SNPs on 148 nt = (148-95: 53)/148 * 100 = **35.81% similarity**

4. Gardnerella vaginalis vs Prevotella buccalis

ROI 1

CLUSTAL O(1.2.4) multiple sequence alignment

```

Gardnerella_vaginalis_smMIPPcopri      -TGATGATCTGACGTCATCCCCACCTTCTCCGAGTTA-----ACCCCGCGGTCCC--      51
Prevotella_buccalis_smMIPPcopri      TGTTTGTGTCGTCAGCTCGTGGCGTGAGGTGTCGGCTTAAGTGCATAACGAGCGCAACCCC      60
* * * * * * * * *
Gardnerella_vaginalis_smMIPPcopri      --CCGTGAGTTCCCGGCATAACCCGCTGGCAACACAGGGCGAGGGTTGCGCTCGTTGCGG      109
Prevotella_buccalis_smMIPPcopri      TTTTTTCAGTTGCCATCAGGTAATGCTGGGCACTCTGGA-----GA      101
* * * * * * * * *
Gardnerella_vaginalis_smMIPPcopri      GACTTAACC--CAACATCTCACGACACGAGCTGACGACGACCA-----      150
Prevotella_buccalis_smMIPPcopri      TACTGCCACCGCAAGGTGTGA-GGAAGGTGGGGATGACGTCAAATCAGCA      150
*** * * * * * * * *

```

87 SNPs on 150 nt = (150-87: 63)/150 * 100 = **42.00% similarity**

ROI 2

CLUSTAL O(1.2.4) multiple sequence alignment

```
Gardnerella_vaginalis_smMIPBangulatum    AATGCGTTCCCGGGCCTTGTACACACCGCCCGTCAAGTCATGAAAGTGGGCAGCACCCGA 60
Prevotella_buccalis_smMIPBangulatum      AATACGTTCCCGGGCCTTGTACACACCGCCCGTCAAGCCATGAAAGCCGGGGTGCCTGA 60
*** **

Gardnerella_vaginalis_smMIPBangulatum    AGCCGGTGGCCTAACCTTTTGGGATGGAGCCGTCTAAGGTGAGGCTCGTGATTGGGACT 120
Prevotella_buccalis_smMIPBangulatum      AGTCCGTAACC-----GTCAAGGAGCGGCCTAGGGCAAAGTGGTGATTGGGGCT 110
** * ** * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *

Gardnerella_vaginalis_smMIPBangulatum    AAGTCGTAACAAGGTAGCCGTACCGGAA 148
Prevotella_buccalis_smMIPBangulatum      AAGTCGTAACAAGGTAGCCGTACCGGAA 138
*****
```

35 SNPs on 138 nt = (138-35: 103)/138 * 100 = **74.63% similarity**

In silico analyses II

1. Comparison of V3-V4 variable regions

CLUSTAL O(1.2.4) multiple sequence alignment

Bifidobacterium_longum	TGGGAATATTGCACAATGGGCGCAAGCCTGATGCAGCGACGCCGCGTGAGGGATGGAGG	60
Gardnerella_vaginalis	TGGGAATATTGCACAATGGGGGAAACCTGACGACGCGACGNCGCGTGCGGGATGAAGG ***** * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *	60
Bifidobacterium_longum	CCTTCGGGTTGTAACCTCTTTTATCGGGGAGCAAGC--GTGAGTGAGTTTACCCGTTG	117
Gardnerella_vaginalis	CCTTCGGGTTGTAACCGCTTTTGATTGGGAGCAAGCCTTTGGGTGAGTGACCTTTCG ***** * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *	120
Bifidobacterium_longum	AATAAGCACC GGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAT	177
Gardnerella_vaginalis	AATAAGCACC GGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAT ***** * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *	180
Bifidobacterium_longum	CCGGAATTATTGGGCGTAAAGGGCTCGTAGGCGGTTTCGTCGCGTCCGGTGTGAAAGTCCA	237
Gardnerella_vaginalis	CCGGAATTATTGGGCGTAAAGAGCTTAGGCGGTTTCGTCGCGTCCGGTGTGAAAGCCCA ***** * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *	240
Bifidobacterium_longum	TCGCTTAACGGTGGATCCGCGCCGGTACGGGCGGGCTTGAGTGCAGTAGGGGAGACTGG	297
Gardnerella_vaginalis	TCGCTTAACGGTGGNTTGCGCCGGTACGGGCGGGCTAGAGTGCAGTAGGGGAGACTGG ***** * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *	300
Bifidobacterium_longum	AATCCCGGTGTAACGGTGGAAATGTGTAGATATCGGGAAGAACACCAATGGCGAAGGCAG	357
Gardnerella_vaginalis	AATTCGCGTGAACGGTGGAAATGTGTAGATATCGGGAAGAACACCAATGGCGAAGGCAG **** * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *	360
Bifidobacterium_longum	GTCTCTGGGCCGTTACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACA	407
Gardnerella_vaginalis	GTCTCTGGCGTGTACTGACGCTGAGAAGCGAAAGCGTGGGGAGCGAACA	410
	***** * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *	

37 SNPs on 410 nt = $(410-37: 373)/410 * 100 = 90.97\%$ similarity

2. Comparison of the five ROIs from V5 - V9 variable regions

ROI from VR V7

CLUSTAL O(1.2.4) multiple sequence alignment

Bifidobacterium_longum_ROI_VR7_Prevotella_copri_NZ_GG703855_1_rna43_0029	TGATGATCTGACGTCATCCCACCTTCTCCGAGTTAACCCGCGGTTCCCGTGAGTT	60
Gardnerella_vaginalis_ROI_VR7_Prevotella_copri_NZ_GG703855_1_rna43_0029	TGATGATCTGACGTCATCCCACCTTCTCCGAGTTAACCCGCGGTTCCCGTGAGTT ***** * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *	60
Bifidobacterium_longum_ROI_VR7_Prevotella_copri_NZ_GG703855_1_rna43_0029	CCCGGCATAATCCGCTGGCAACACGGGCGAGGGTTGCGCTGTTGCGGGACTTAACCCA	120
Gardnerella_vaginalis_ROI_VR7_Prevotella_copri_NZ_GG703855_1_rna43_0029	CCCGGCATAACCCGCTGGCAACACAGGGCGAGGGTTGCGCTGTTGCGGGACTTAACCCA ***** * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *	120
Bifidobacterium_longum_ROI_VR7_Prevotella_copri_NZ_GG703855_1_rna43_0029	ACATCTCACGACACGAGCTGACGACACCA	150
Gardnerella_vaginalis_ROI_VR7_Prevotella_copri_NZ_GG703855_1_rna43_0029	ACATCTCACGACACGAGCTGACGACACCA ***** * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *	150

2 SNPs on 150 nt = $(150-2: 148)/150 * 100 = 98.66\%$ similarity

ROI from VR V8

CLUSTAL O(1.2.4) multiple sequence alignment

```

Bifidobacterium_longum_ROI_VR8_Shuttleworthia_satelles_DSM_14600_NZ_G6665866_1_rna19_0005      CTTCACGCAGTCGAGTTGCAGACTGCGATCCGAAGTGAAGCCGGTTTTCAGGGATCCGCT      60
Gardnerella_vaginalis_ROI_VR8_Shuttleworthia_satelles_DSM_14600_NZ_G6665866_1_rna19_0005      CTTCACGTAGTCGAGTTGCAGACTACGATCCGAAGTGAAGCCAGTTTAAAGGGATTAGCA      60
*****

Bifidobacterium_longum_ROI_VR8_Shuttleworthia_satelles_DSM_14600_NZ_G6665866_1_rna19_0005      CCGCGTCGCCCGTCGCATCCCGTTGTACCGCCATTTAGTAGCATGCGTGAAGCCCTGGAC      120
Gardnerella_vaginalis_ROI_VR8_Shuttleworthia_satelles_DSM_14600_NZ_G6665866_1_rna19_0005      CCATGTCACCATGAAGCAACCGTTGTACTGGCCATTTAGTAGCATGCGTGAAGCCCTGGAC      120
*****

Bifidobacterium_longum_ROI_VR8_Shuttleworthia_satelles_DSM_14600_NZ_G6665866_1_rna19_0005      GTAAGGGGCATGATGATCTGACGTCATCCC      150
Gardnerella_vaginalis_ROI_VR8_Shuttleworthia_satelles_DSM_14600_NZ_G6665866_1_rna19_0005      GTAAGGGGCATGATGATCTGACGTCATCCC      150
*****

```

15 SNPs on 150 nt = (150-15: 135)/150 * 100 = **90.0% similarity**

ROI from VR V5

CLUSTAL O(1.2.4) multiple sequence alignment

```

Bifidobacterium_longum_ROI_VR5_Mageeibacillus_indolicus_NC_013895_2_rna7_0011      AGTTTTAGCCTTGCGCCGCTACTCCCAGGCGGGATGCTTAACGCGTTAGCTCCGACACG      60
Gardnerella_vaginalis_ROI_VR5_Mageeibacillus_indolicus_NC_013895_2_rna7_0011      -GCGAAAGCGTGG-----GGAGCGAACAGGATTAGATACCTCGGTAGTCCACGCCG      60
*   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *

Bifidobacterium_longum_ROI_VR5_Mageeibacillus_indolicus_NC_013895_2_rna7_0011      GAACCCGTGGAAAGCGGCCACATCCAGCATCCACCGTTTACGGCGTGGACTACCAAGGGT      120
Gardnerella_vaginalis_ROI_VR5_Mageeibacillus_indolicus_NC_013895_2_rna7_0011      TAAACGGTGGACGCTGGATGTGGGGCCATTCCACGGGTTCTGTGTGCGAGCTAACCGCT      110
* * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *

Bifidobacterium_longum_ROI_VR5_Mageeibacillus_indolicus_NC_013895_2_rna7_0011      ATCTAATCCT-----GTTGCTCCCCACGCTTTCGC-      151
Gardnerella_vaginalis_ROI_VR5_Mageeibacillus_indolicus_NC_013895_2_rna7_0011      TAAGCGTCCCGCTGGGGAGTACGGCCGAAGGCTAAAAC      151
* * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *

```

91 SNPs on 151 nt = (151-91: 59)/151 * 100 = **39.0% similarity**

ROI from VR V6

CLUSTAL O(1.2.4) multiple sequence alignment

```

Bifidobacterium_longum_ROI_VR6_Cutibacterium_acnes_J139_NZ_ADFS01000001_1_rna32_0028      ----GACGACGACCATGCACCAC-----TGTGAACCCGCCCGAAGGGGAAG      43
Gardnerella_vaginalis_ROI_VR6_Cutibacterium_acnes_J139_NZ_ADFS01000001_1_rna32_0028      AATTGACGGGGG-CGCAACAAGCGCGGAGCATGCGGATTAATTCGATGCAACGCGAAG      59
*****

Bifidobacterium_longum_ROI_VR6_Cutibacterium_acnes_J139_NZ_ADFS01000001_1_rna32_0028      CCGTATCTCTACGACCTCGGGAACATGTCAAGCGCCAGGTAAGTTCTTCGCGTTCATC      103
Gardnerella_vaginalis_ROI_VR6_Cutibacterium_acnes_J139_NZ_ADFS01000001_1_rna32_0028      AACCTTACCTGGGCTTGACATGTGCTGACGACTGCAGAGATGTGTTTCCTTTCGGGGC      119
* * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *

Bifidobacterium_longum_ROI_VR6_Cutibacterium_acnes_J139_NZ_ADFS01000001_1_rna32_0028      GAATTAATCCGATGCTCCGCCGCTTGTGCG-GGCCCCCGTCAATT      148
Gardnerella_vaginalis_ROI_VR6_Cutibacterium_acnes_J139_NZ_ADFS01000001_1_rna32_0028      AGGTT-----CACAGGTGTGATGGTGTGCTGTC----      148
**   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *

```

84 SNPs on 148 nt = (148-84: 64)/148 * 100 = **43.2% similarity**

ROI from VR V9

CLUSTAL O(1.2.4) multiple sequence alignment

```

Bifidobacterium_longum_ROI_VR9_Bifidobacterium_angulatum_JCM_7096_GCF_0010251551_ASM102515v1_NZ_AP012322_1_rna0_0019      TTCCGGTACGGTACCTTGTACGACTAGTCCCAATCAGGACCTCACCTTAGACGGCT      60
Gardnerella_vaginalis_ROI_VR9_Bifidobacterium_angulatum_JCM_7096_GCF_0010251551_ASM102515v1_NZ_AP012322_1_rna0_0019      -----AATGCGTCCCGGCTGTACACCCCGCTCAAGTCATGAAGGTGGG      50
* * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *

Bifidobacterium_longum_ROI_VR9_Bifidobacterium_angulatum_JCM_7096_GCF_0010251551_ASM102515v1_NZ_AP012322_1_rna0_0019      CCATCCCAAGGGGTTAGGC-CACCGGCTCGGGTCTGCCCATTTTCATGACTT----      115
Gardnerella_vaginalis_ROI_VR9_Bifidobacterium_angulatum_JCM_7096_GCF_0010251551_ASM102515v1_NZ_AP012322_1_rna0_0019      CAGCACCCGAAGCCGGTGGCTAACCTTTTGGGATGGAGCCGCTTAAGGTGAGGCTCGT      110
*   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *   *

Bifidobacterium_longum_ROI_VR9_Bifidobacterium_angulatum_JCM_7096_GCF_0010251551_ASM102515v1_NZ_AP012322_1_rna0_0019      GACGGGCGGT----GTGTACAAGGCCGGGAACGCATT      149
Gardnerella_vaginalis_ROI_VR9_Bifidobacterium_angulatum_JCM_7096_GCF_0010251551_ASM102515v1_NZ_AP012322_1_rna0_0019      GATTGGGACTAAGTCTAACAAGGTAGCGCTACCGGAA-      148
** * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *

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88 SNPs on 148 nt = (148-88: 60)/148 * 100 = **40.5% similarity**