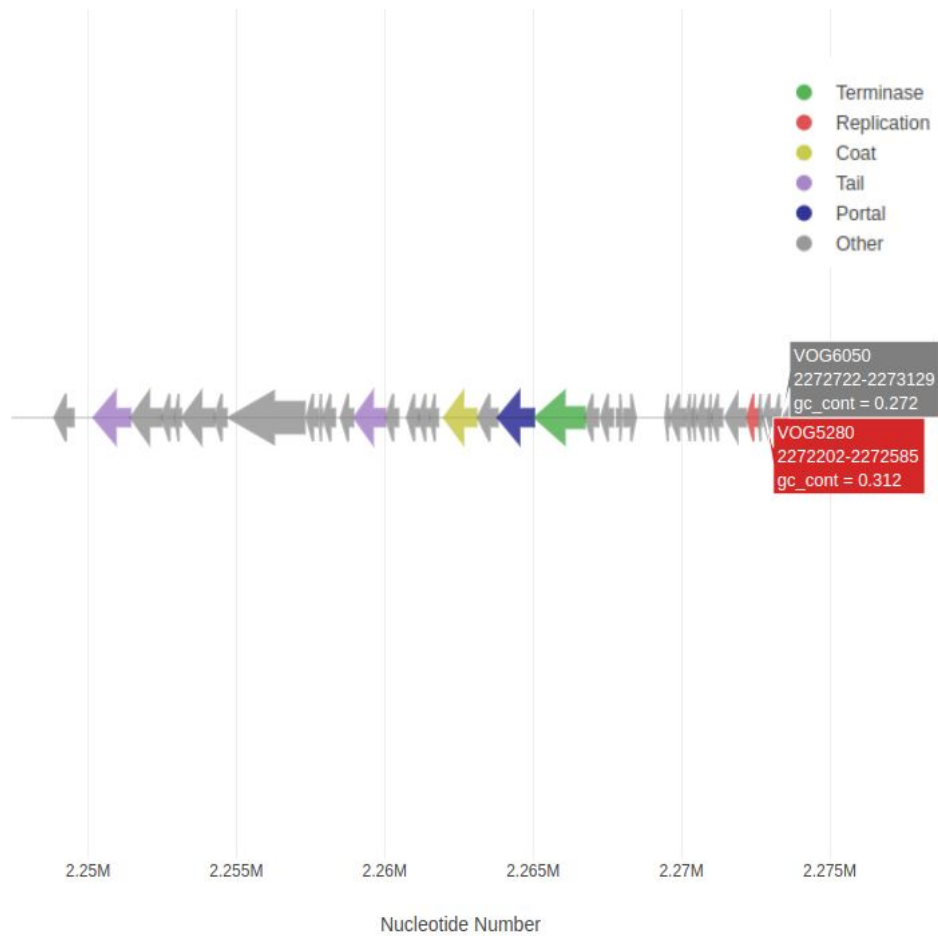


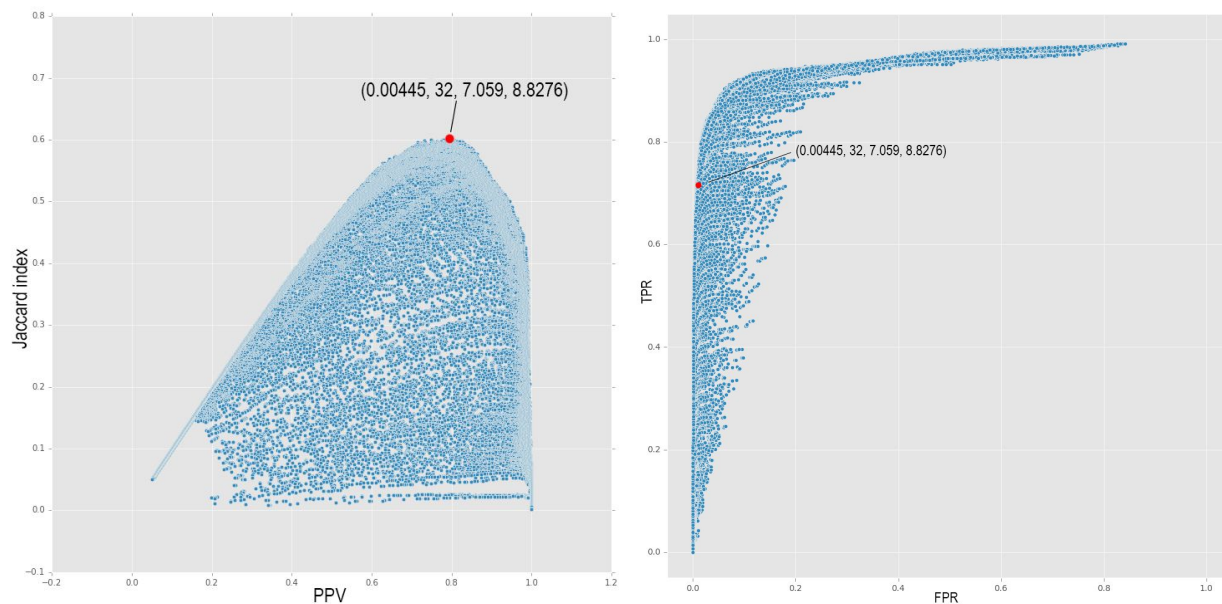
**Supplementary Figure 1.** Example of sliding window algorithm scores. *Staphylococcus aureus* subsp. *aureus* N315 (NC\_003140.1). Threshold min: 45.39, threshold max: 46.00. Top blue curve: total scores with marked predicted and real prophage regions and thresholds. Green curve: gc\_content scores; red curve: phage scores. The bottom plot is a plot of indicators, based on which the phage score was calculated: the tallest black bars stand for the genes are “white phage genes” (+0.7 bonus), medium black bars are genes marked as “neutral phage genes”, the bars placed under the zero line are genes marked as “black phage genes” (-2.2 penalty) and zero bars are genes marked as “non-phage genes”.



**Supplementary Figure 2.** An example of a predicted prophage genome map generated by Phigaro. Genes detected by Prodigal are presented as arrows. The direction of the arrow shows the transcription orientation. Functional categories of genes are annotated in color. The bottom axis shows the genomic coordinate (nucleotide number) along the bacterial chromosome. This is a dynamic webpage HTML interface where the user may zoom in and out of the display and click on the individual genes to view their coordinates, annotations and GC content. The user may also submit the prophage sequences directly to the online NCBI BLAST server via a single click.

## Grid search, step 1

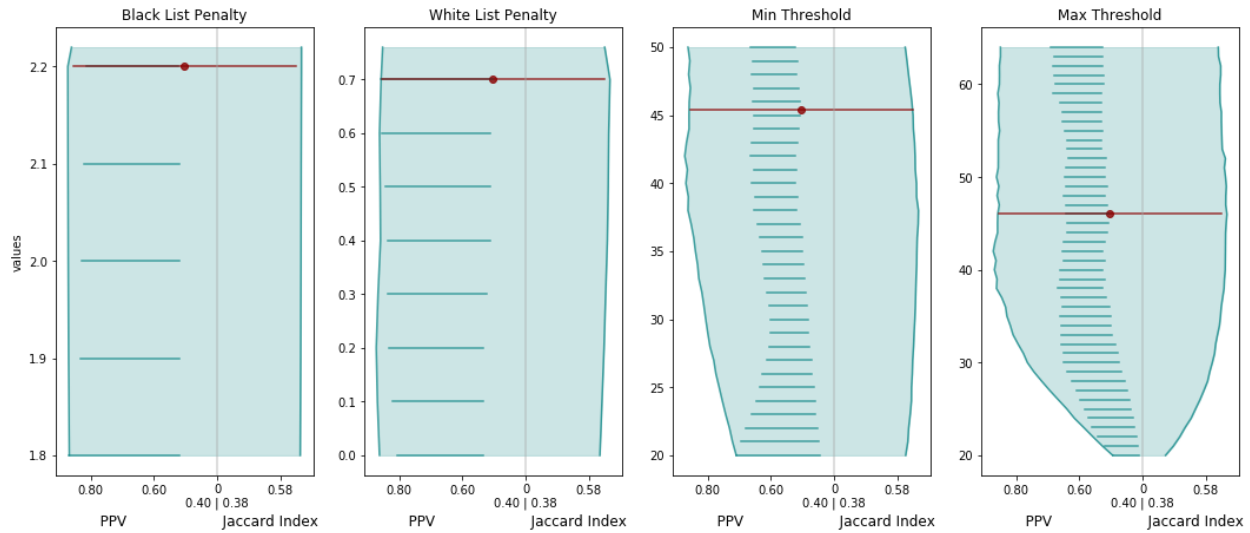
In order to optimize PhigaroFinder performance for the first time, we calculated mean Jaccard index and PPV for each parameter set and chose the optimal set of parameters. During the optimization process, we have determined E-value threshold as 0.00445, window size as 32, min score threshold as 7.058859, and max score threshold as 8.827586. This set of parameters gave the most accurate results with a minimal amount of noise (Supplementary Figure 3). For this set of parameters, mean Jaccard index was: 0.601, TPR (True Positive Rate): 0.72, FPR (False Positive Rate): 0.007, FDR (False Discovery rate): 0.20, PPV (Positive Predictive Value): 0.80.



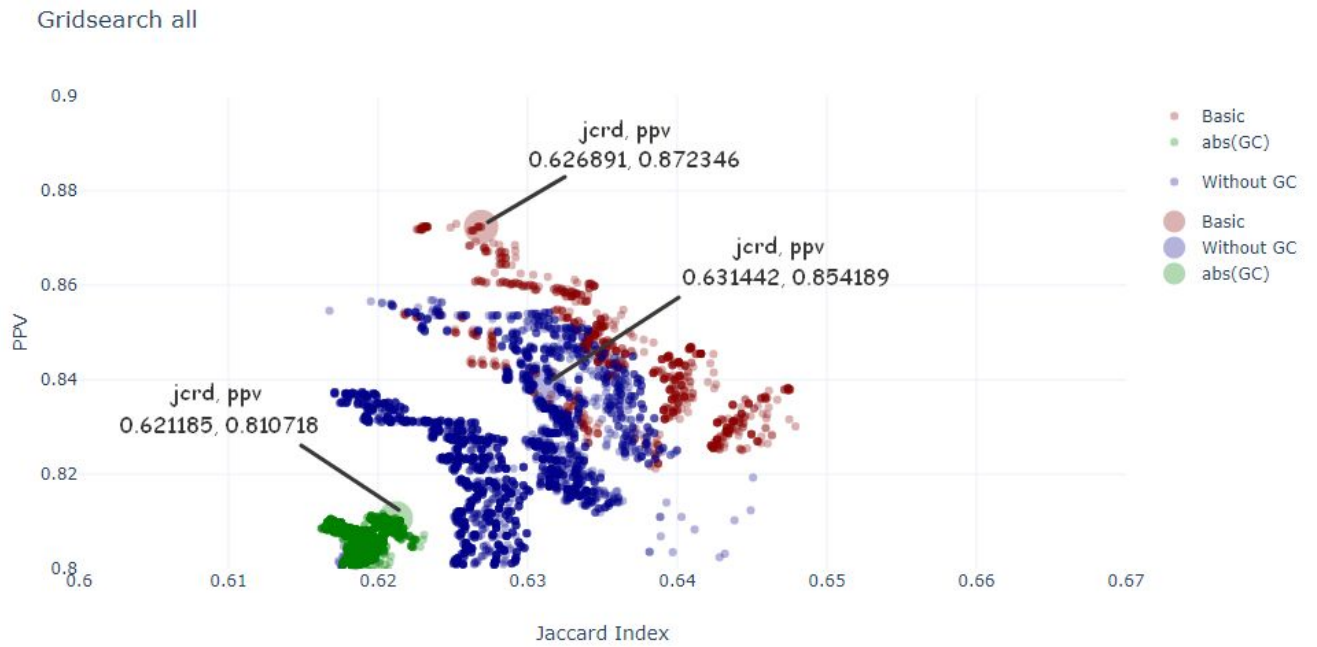
**Supplementary Figure 3.** Grid search results for each set of parameters. Red dot stands for optimal parameters set.

## Grid search, step 2

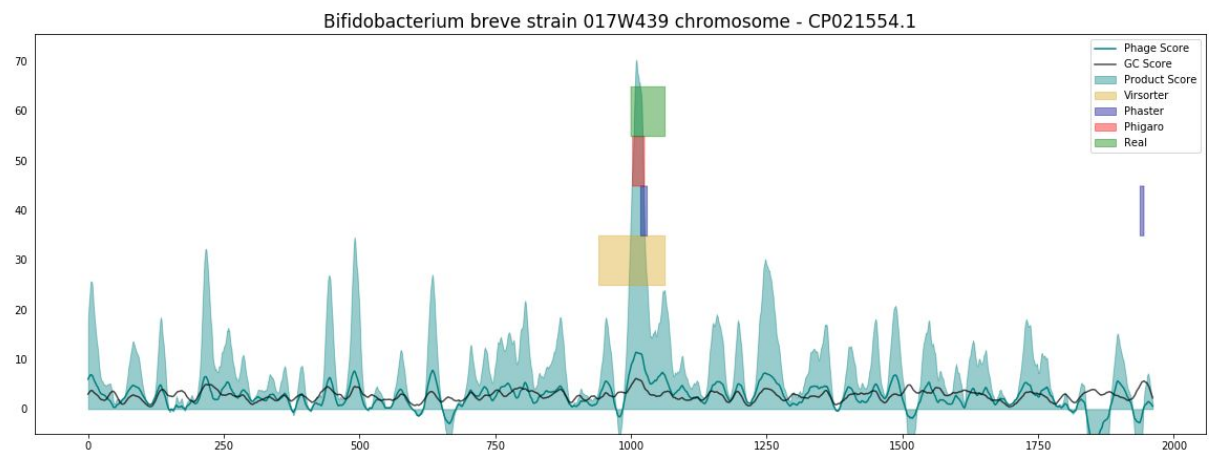
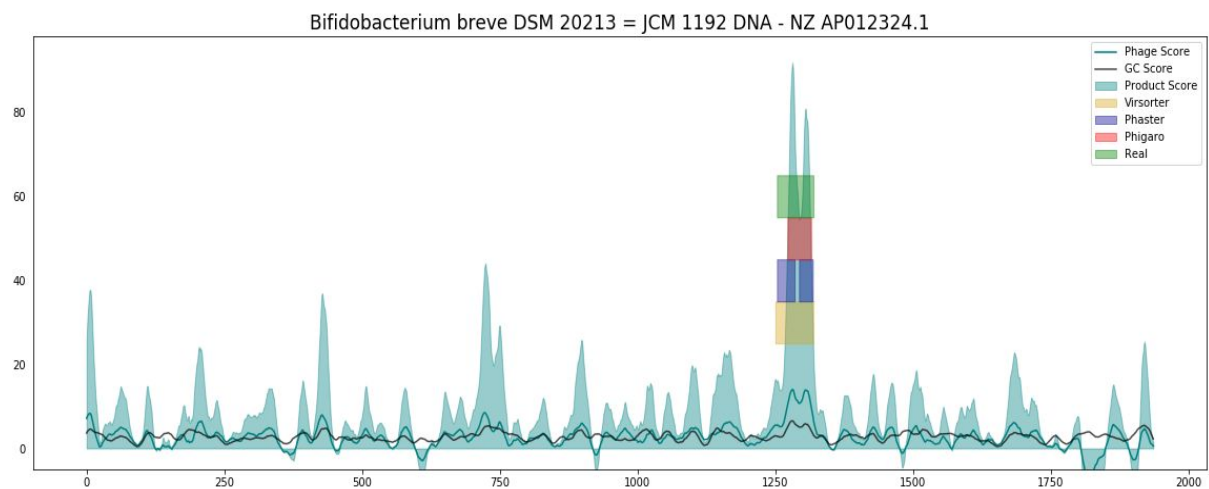
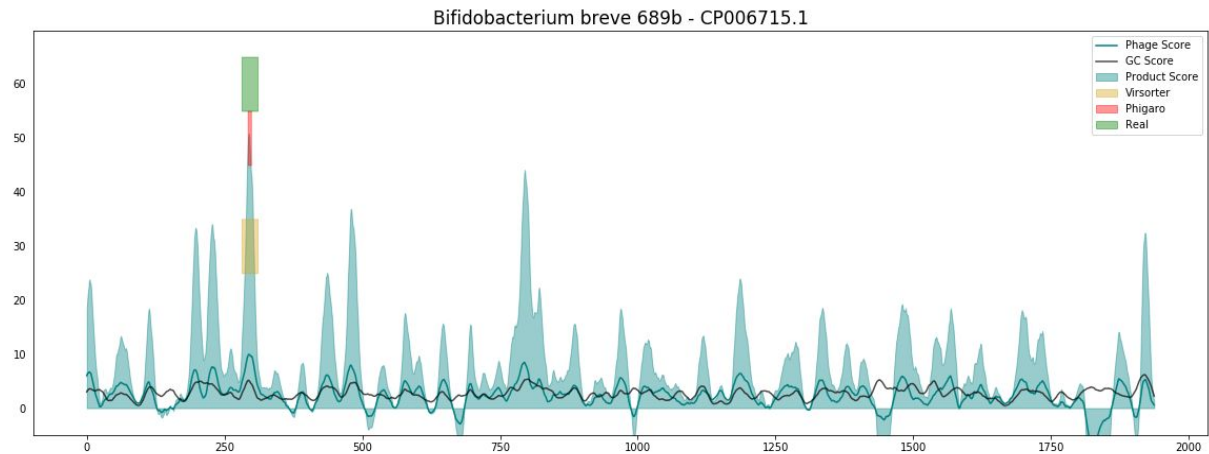
We have used grid search to optimize the four parameters: black and white lists penalties, minimal and maximal score thresholds. We chose the best set of parameters according to Jaccard index and PPV metrics (Supplementary Figure 4A). Considering that it is impossible to find the parameters that would give the highest values for both metrics at the same time, we aimed at maximizing their sum. The highest sum corresponds to the set  $\{-2.2, 0.7, 45.39, 46\}$ , “basic” mode (Supplementary Figure 4B). Grid search results for “abs\_gc” and “without\_gc” modes are shown as Supplementary Figure 5.

**A****B**

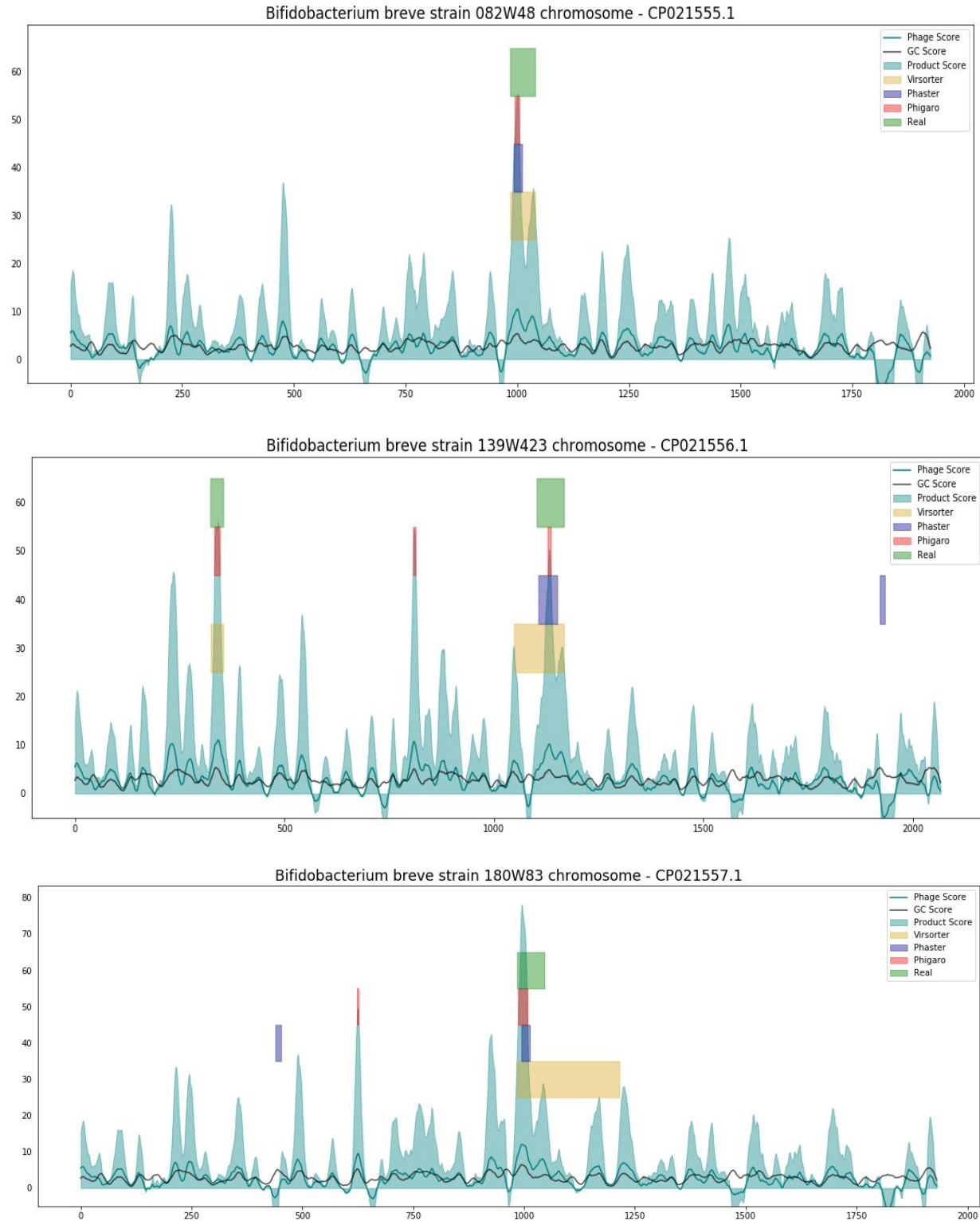
**Supplementary Figure 4.** Grid search results (basic mode). **(A)** Each picture presents the values of Jaccard index and PPV metrics for each of the parameters: black and white lists penalties, minimal and maximal thresholds. The x-axis shows the values of the metrics, the y-axis shows the values of parameters. The range of PPV for different parameter values are depicted on the left side of each picture, and the range values of Jaccard metrics are depicted on the right side. The **0** point is equal to the minimal value for the PPV on the left side and to the minimal value of Jaccard index on the right side. Horizontal segments are the intervals of means between Jaccard index and PPV values. The red line and the red dot present Jaccard index and PPV metrics and their mean for the chosen set of parameters **(B)** The orange line presents the maximal value of the mean between Jaccard index and PPV, where the minimal value of the mean is shifted to zero. The green line presents maximal PPV, where the minimal value is also shifted to zero. The blue line presents the sum of the maximum mean values and PPV. The grey vertical line presents the values for the chosen set of parameters.



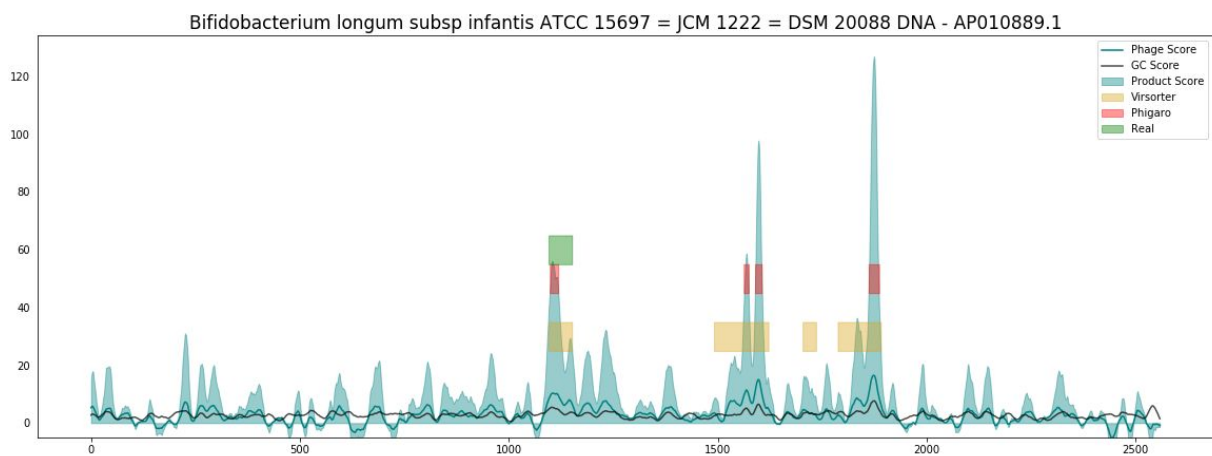
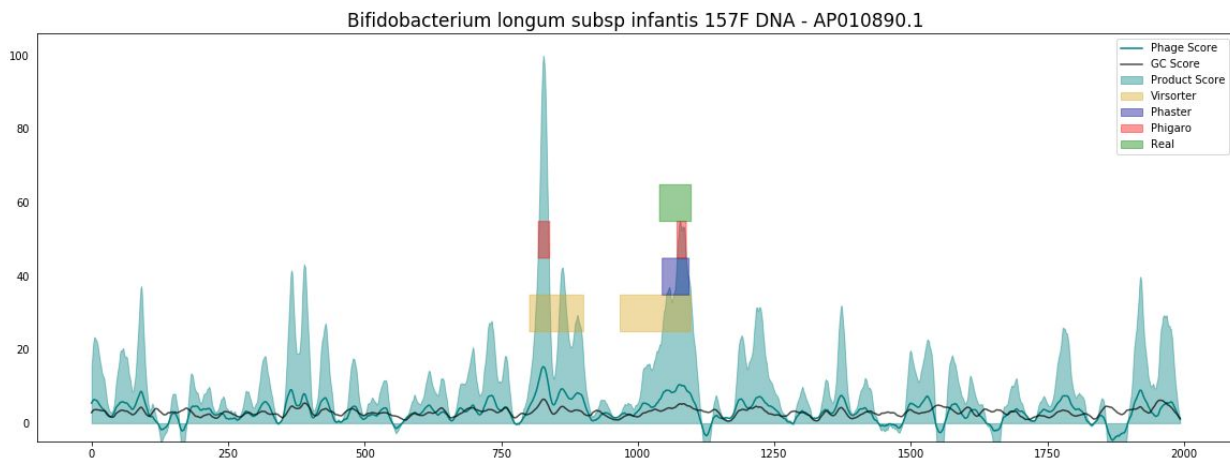
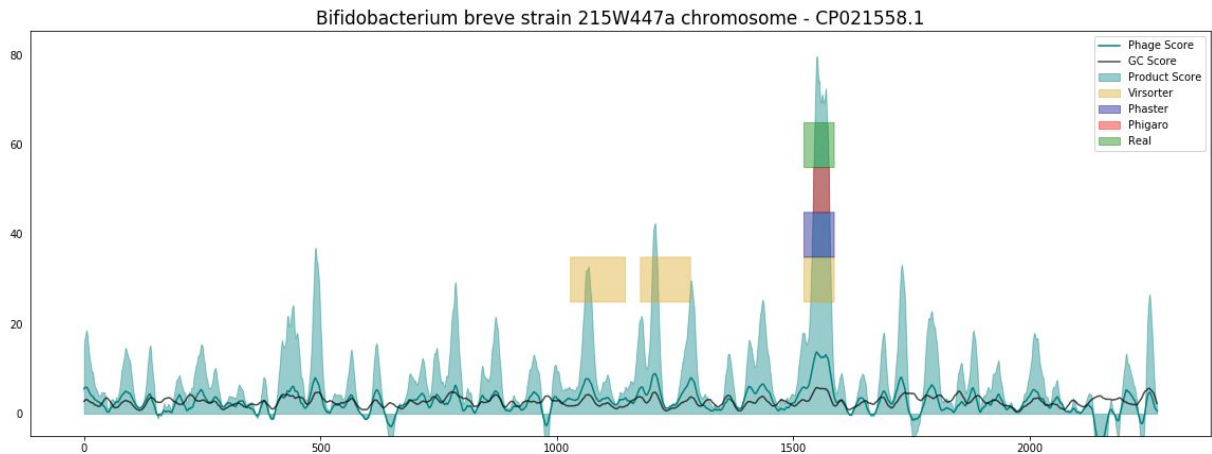
**Supplementary Figure 5.** Grid search results for “basic”, “abs\_gc” and “without\_gc” modes of PhigaroFinder. Red, blue and green circles represent optimal parameter sets chosen for each mode.



**Supplementary Figure 6.1.** Prophage regions predicted by Phigaro in “basic” mode (red areas), Phaster (violet areas) and VirSorter (levels 1&2&4&5) (yellow areas) on the bacterial genomes from validation set as compared to annotated prophages (green areas) along with Phigaro’s Phage Score, GC Score and Product Score plots.

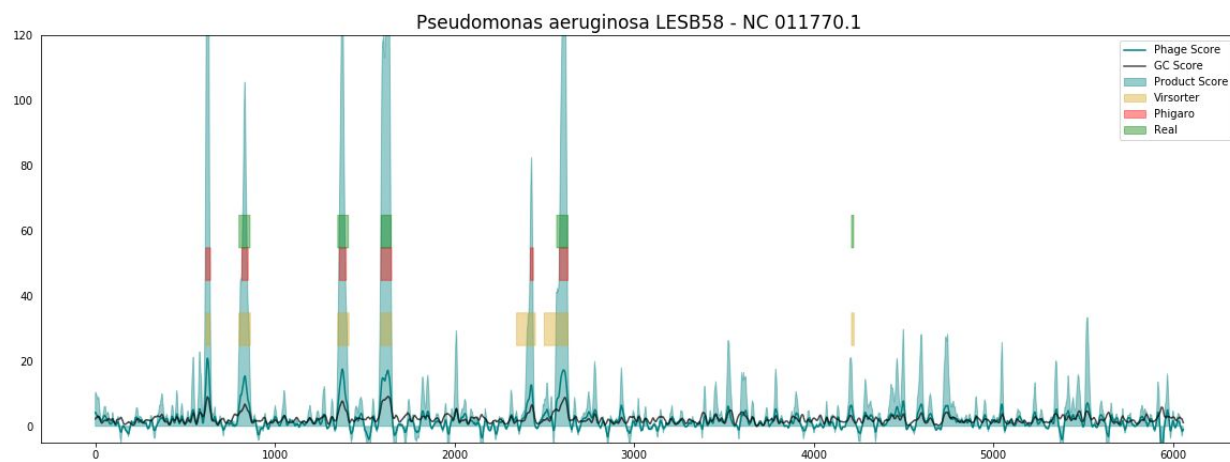
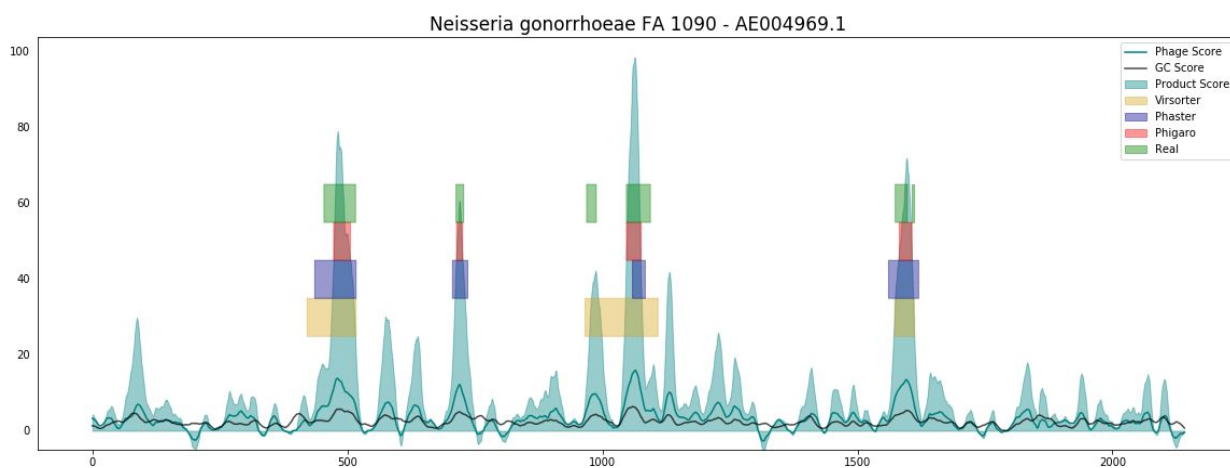
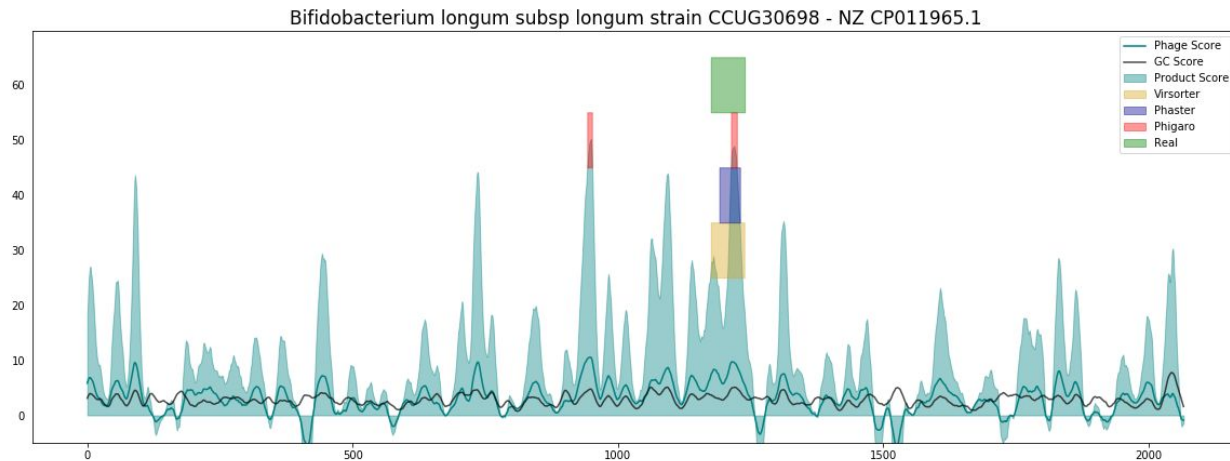


**Supplementary Figure 6.2.** Prophage regions predicted by Phigaro in “basic” mode (red areas), Phaster (violet areas) and VirSorter (levels 1&2&4&5) (yellow areas) on the bacterial genomes from validation set as compared to annotated prophages (green areas) along with Phigaro’s Phage Score, GC Score and Product Score plots.

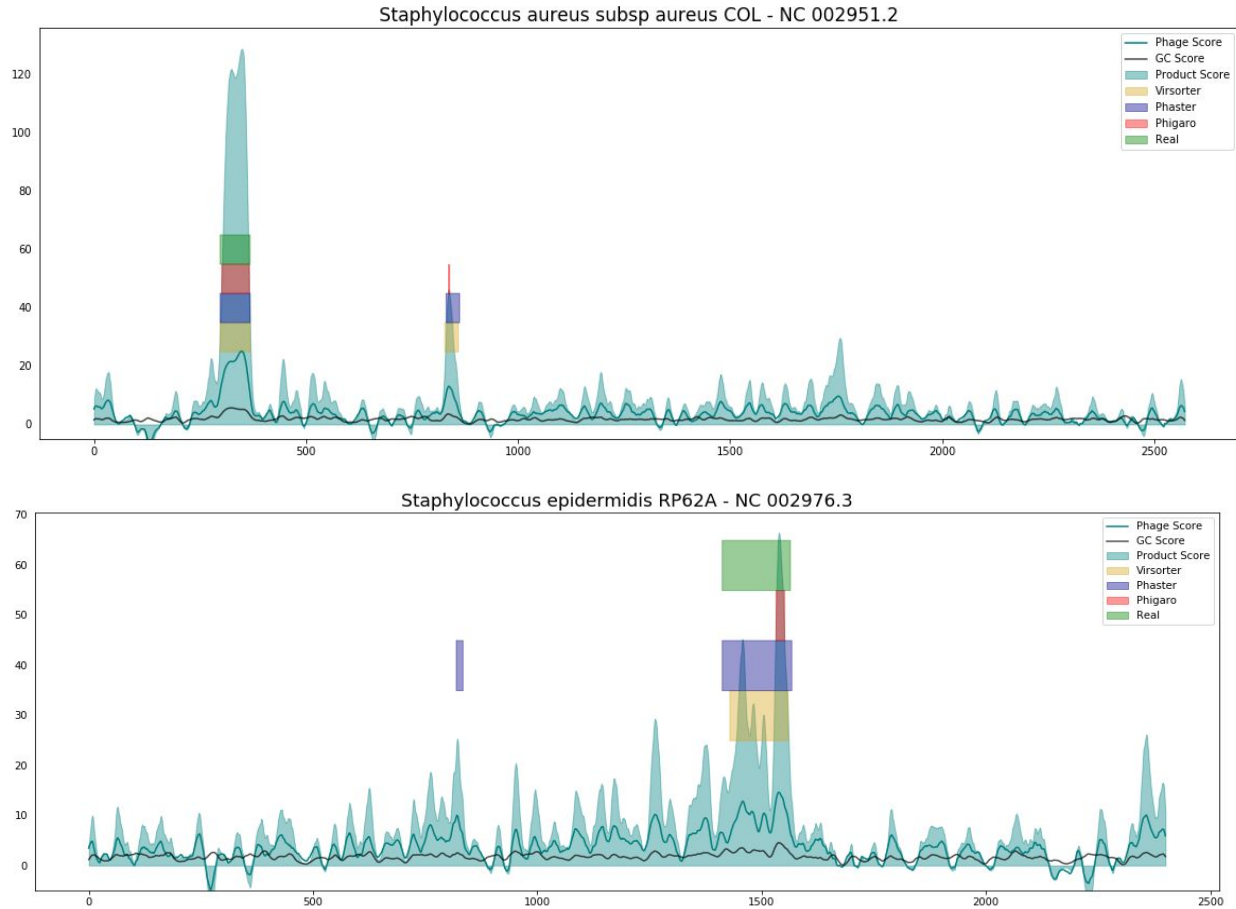


**Supplementary Figure 6.3.** Prophage regions predicted by Phigaro in “basic” mode (red areas), Phaster (violet areas) and VirSorter (levels 1&2&4&5) (yellow areas) on the bacterial genomes from validation set as compared to annotated prophages (green areas) along with Phigaro’s Phage Score, GC Score and Product Score plots.





**Supplementary Figure 6.4.** Prophage regions predicted by Phigaro in “basic” mode (red areas), Phaster (violet areas) and VirSorter (levels 1&2&4&5) (yellow areas) on the bacterial genomes from validation set as compared to annotated prophages (green areas) along with Phigaro’s Phage Score, GC Score and Product Score plots.



**Supplementary Figure 6.5.** Prophage regions predicted by Phigaro in “basic” mode (red areas), Phaster (violet areas) and VirSorter (levels 1&2&4&5) (yellow areas) on the bacterial genomes from validation set as compared to annotated prophages (green areas) along with Phigaro’s Phage Score, GC Score and Product Score plots.

**Supplementary Table 1.** Bacterial strains with annotated prophages used as training set

Bacterial strain	Genbank id
<i>Bacillus anthracis</i> str. Ames	NC_003997.3
<i>Bacillus cereus</i> ATCC 14579	NC_004722.1
<i>Bacillus halodurans</i> C-125	NC_002570.2
<i>Bacillus subtilis</i> subsp. <i>subtilis</i> str. 168	NC_000964.3
<i>Bifidobacterium longum</i> NCC2705	NC_004307.2
<i>Bacillus suis</i> 1330	NC_004310.3
<i>Chromobacterium violaceum</i> ATCC 12472	NC_005085.1
<i>Clostridium acetobutylicum</i> ATCC 824	NC_003030.1

<i>Clostridium perfringens</i> str. 13	NC_003366.1
<i>Clostridium tetani</i> E88	NC_004557.1
<i>Corynebacterium diphtheriae</i> NCTC 13129	NZ_LN831026.1
<i>Enterococcus faecalis</i> V583	NC_004668.1
<i>Escherichia coli</i> CFT073	NC_004431.1
<i>Escherichia coli</i> K12	NC_000913.3
<i>Escherichia coli</i> O157:H7 EDL933	NZ_CP008957.1
<i>Escherichia coli</i> O157:H7 str. Sakai	NC_002695.1
<i>Haemophilus influenzae</i> Rd KW20	NC_000907.1
<i>Lactobacillus johnsonii</i> NCC 533	NC_005362.1
<i>Lactobacillus plantarum</i> WCFS1	NC_004567.2
<i>Lactococcus lactis</i> subsp. <i>lactis</i> II1403	NC_002662.1
<i>Listeria innocua</i> Clip11262	NC_003212.1
<i>Listeria monocytogenes</i> EGD-e	NC_003210.1
<i>Mesorhizobium loti</i> MAFF303099	NC_002678.2
<i>Mycobacterium tuberculosis</i> H37Rv	NC_000962.3
<i>Neisseria meningitidis</i> MC58	NC_003112.2
<i>Neisseria meningitidis</i> Z2491	AL157959.1
<i>Photobacterium luminescens</i> subsp. <i>laumondii</i> TTO1	NC_005126.1
<i>Pseudomonas aeruginosa</i> PAO1	NC_002516.2
<i>Pseudomonas putida</i> KT2440	NC_002947.4
<i>Pseudomonas syringae</i> pv. <i>tomato</i> str. DC3000	NC_004578.1
<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar Typhi Ty2	NC_004631.1
<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar Typhi str. CT18	NC_003198.1
<i>Salmonella typhimurium</i> LT2	NC_003197.2
<i>Shewanella oneidensis</i> MR-1	NC_004347.2
<i>Shigella flexneri</i> 2a str. 2457T	NC_004741.1

<i>Shigella flexneri</i> 2a str. 301	NC_004337.2
<i>Staphylococcus aureus</i> subsp. <i>aureus</i> MW2	NC_003923.1
<i>Staphylococcus aureus</i> subsp. <i>aureus</i> Mu50	NC_002758.2
<i>Staphylococcus aureus</i> subsp. <i>aureus</i> N315	NC_002745.2
<i>Streptococcus agalactiae</i> 2603V	NC_004116.1
<i>Streptococcus pyogenes</i> M1 GAS	NC_002737.2
<i>Streptococcus pyogenes</i> MGAS315	NC_004070.1
<i>Streptococcus pyogenes</i> MGAS8232	NC_003485.1
<i>Streptococcus pyogenes</i> SSI-1	NC_004606.1
<i>Treponema denticola</i> ATCC 35405	NC_002967.9
<i>Wolbachia</i> endosymbiont of <i>Drosophila melanogaster</i>	NC_002978.6
<i>Xanthomonas axonopodis</i> pv. <i>citri</i> str. 306	NC_003919.1
<i>Xanthomonas campestris</i> pv. <i>campestris</i> str. ATCC 33913	NC_003902.1
<i>Xylella fastidiosa</i> 9a5c	NC_002488.3
<i>Xylella fastidiosa</i> Temecula1	NC_004556.1
<i>Yersinia pestis</i> CO92	NC_003143.1
<i>Yersinia pestis</i> KIM	NC_004088.1

**Supplementary Table 2.** Prophages used for performance analysis of Phigaro, Phaster and VirSorter

<i>Temperate phage's name</i>	<i>Prophage starts at</i>	<i>Prophage ends at</i>	<i>Phage GC%</i>	<i>Host strain</i>	<i>Host GC%</i>	<i>Genbank id</i>	<i>PubMed/PMC ID</i>
Bb439phi1	1194717	1234971	61.1	<i>Bifidobacterium breve</i> 017W439	58.7	CP021554.1	PMC5829577
Bb48phi1	1193403	1232804	61.3	<i>Bifidobacterium breve</i> 082W48	58.8	CP021555.1	PMC5829577
Bb423phi1	1302639	1342715	60.9	<i>Bifidobacterium breve</i> 139W423	58.6	CP021556.1	PMC5829577
Bb423phi2	420545	438765	61.4	<i>Bifidobacterium breve</i> 139W423	58.6	CP021556.1	PMC5829577
Bb83phi1	1179127	1219381	61.1	<i>Bifidobacterium breve</i> 180W83	58.8	CP021557.1	PMC5829577
Bb447phi1	1694074	1735438	58.6	<i>Bifidobacterium breve</i> 215W447a	59.3	CP021558.1	PMC5829577

689b-1	372287	390546	61.4	<i>Bifidobacterium breve</i> 689b	58.7	CP006715	PMC4007704
Bb1192phi1	1468985	1509872	59.4	<i>Bifidobacterium breve</i> JCM 1192	58.9	NZ_AP0123 24.1	PMC6109161
Binf-1b	1288185	1330866	61.1	<i>Bifidobacterium longum</i> ATCC 15697	59.8	CP001095.1	PMC2772436
Bl157phi1	1207777	1246936	60.9	<i>Bifidobacterium longum</i> 157F	60.1	AP010890.1	PMC6109161
Bl30698phi 1	1336483	1375860	61.1	<i>Bifidobacterium longum</i> CCUG 30698	60.2	NZ_CP0119 65.1	PMC6109161
NgoΦ1	455173	498100	54.6	<i>Neisseria gonorrhoeae</i> FA1090	52.6	AE004969.1	PMC1931599
NgoΦ2	1044447	1078281	56.3	<i>Neisseria gonorrhoeae</i> FA1090	52.6	AE004969.1	PMC1931599
NgoΦ3	1583028	1599049	53.7	<i>Neisseria gonorrhoeae</i> FA1090	52.6	AE004969.1	PMC1931599
NgoΦ3	1606828	1609808	55.5	<i>Neisseria gonorrhoeae</i> FA1090	52.6	AE004969.1	PMC1931599
NgoΦ4	972837	984008	49.0	<i>Neisseria gonorrhoeae</i> FA1090	52.6	AE004969.1	PMC1931599
NgoΦ5	721256	729870	56.9	<i>Neisseria gonorrhoeae</i> FA1090	52.6	AE004969.1	PMC1931599
LES prophage 2	863875	906018	61.3	<i>Pseudomonas aeruginosa</i> LESB58	66.4	NC_011770. 1	PMC2612960
LES prophage 3	1433756	1476547	61.7	<i>Pseudomonas aeruginosa</i> LESB58	66.4	NC_011770. 1	PMC2612960
LES prophage 4	1684045	1720850	64.4	<i>Pseudomonas aeruginosa</i> LESB58	66.4	NC_011770. 1	PMC2612960
LES prophage 5	2690450	2740350	59.2	<i>Pseudomonas aeruginosa</i> LESB58	66.4	NC_011770. 1	PMC2612960
LES prophage 6	4545190	4552788	60.4	<i>Pseudomonas aeruginosa</i> LESB58	66.4	NC_011770. 1	PMC2612960
φCOL	354674	398267	33.8	<i>Staphylococcus aureus</i> COL	32.8	NC_002951. 2	PMC1065214
φSPβ	1567637	1694334	30.5	<i>Staphylococcus epidermidis</i> RP62A	32.2	NC_002976. 3	PMC1065214

**Supplementary Table 3.** Detailed performance analysis of Phigaro, Phaster and VirSorter. True positives (TP), false positives (FP) and false negatives (FN) are given in base pairs

<i>Genbank id</i>	Phigaro (basic mode)			Phigaro (abs_gc mode)			Phigaro (without_gc mode)			Phaster			Virsorter levels 1&4			Virsorter levels 1&2&4&5			Virsorter levels 1&2&3&4&5&6		
	TP	FP	FN	TP	FP	FN	TP	FP	FN	TP	FP	FN	TP	FP	FN	TP	FP	FN	TP	FP	FN
AP0108 89.1	20843	39836	21838	13522	37593	29159	0	32401	42681	0	0	42681	0	0	42681	42472	222158	209	42472	385296	209
CP0215 57.1	20821	3916	19433	18513	0	21741	11464	0	28790	14529	11377	25725	0	0	40254	40073	161821	181	40073	161821	181
AE0049 69.1	68307	7779	47240	57907	7488	57640	49531	6317	66016	85261	58333	30286	0	0	115547	106933	115160	8614	106933	115160	8614
CP0215 55.1	7623	0	31778	5150	0	34251	0	0	39401	14531	0	24870	0	0	39401	39143	0	258	39143	94180	258
NC_00 2976.3	35013	0	91684	80304	17047	46393	45976	0	80721	126697	14572	0	0	0	126697	109657	0	17040	109657	0	17040
NC_01 1770.1	129329	43849	49908	122952	37621	56285	107573	25165	71664	0	0	179237	0	0	179237	179178	192484	59	179178	231486	59
NC_00 2951.2	38255	1250	5338	43593	26717	0	41332	8583	2261	43357	21208	236	42831	0	762	42831	19035	762	42831	19035	762
NZ_AP 012324.1	22138	0	18749	21470	0	19417	18432	0	22455	36692	29	4195	0	0	40887	40788	1694	99	40788	130289	99
CP0067 15	3882	0	14377	0	0	18259	0	0	18259	0	0	18259	0	0	18259	18047	77	212	18047	39967	212
AP0108 90.1	14996	15890	24163	11673	14822	27486	0	13423	39159	33314	0	5845	0	62127	39159	38951	124497	208	38951	181634	208
CP0215 58.1	19146	0	22218	18132	0	23232	17407	0	23957	41355	10	9	0	0	41364	41167	160114	197	41167	160114	197
NZ_CP 011965.1	9084	5888	30293	0	0	39377	0	0	39377	26713	0	12664	0	0	42681	39377	0	210	39167	213109	210

CP0215 54.1	19851	0	20403	18039	0	22215	4543	0	35711	8307	9286	31947	0	0	40254	40253	65167	1	40253	154680	1
CP0215 56.1	16998	6944	41298	8695	4856	49601	0	0	58296	29595	16200	28701	0	0	58296	57897	58296	399	57897	85330	399

**Supplementary Table 4.** Prophage coordinates predicted by Phigaro, Phaster and Virsorter

Strain	Scaffold	Reported prophage coordinates	Phigaro coordinates (basic mode)	Phigaro coordinates (abs_gc mode)	Phigaro coordinates (without_gc mode)	Phaster coordinates	Virsorter coordinates (levels 1&4)	Virsorter coordinates (levels 1&2&4&5)	Virsorter coordinates (levels 1&2&3&4&5&6)
Bifidobacterium_l ongum_subsp_lo ngum_strain_CC UG30698	NZ_CP011965.1	-	1131754- 1137642	-	-	-	-	-	1083790- 1197047
Bifidobacterium_l ongum_subsp_lo ngum_strain_CC UG30698	NZ_CP011965.1	-	-	-	-	-	-	-	1207396- 1307248
Bifidobacterium_l ongum_subsp_lo ngum_strain_CC UG30698	NZ_CP011965.1	<b>1336483- 1375860</b>	<b>1357945- 1367029</b>	-	-	<b>1343855- 1370568</b>	-	<b>1336484- 1375651</b>	<b>1336484- 1375651</b>
Bifidobacterium_l ongum_subsp_in fantis_157F_DN A	AP010890.1	-	1022555- 1038445	1023107- 1037929	1023795- 1037218	-	1006142- 1068269	1006142- 1068269	1006142- 1068269
Bifidobacterium_l ongum_subsp_in fantis_157F_DN A	AP010890.1	<b>1207777- 1246936</b>	<b>1227033- 1242029</b>	<b>1229124- 1240797</b>	-	<b>1211424- 1244738</b>	-	<b>1145407- 1246728</b>	<b>1145407- 1246728</b>
Bifidobacterium_l ongum_subsp_in fantis_157F_DN A	AP010890.1	-	-	-	-	-	-	-	1322512- 1379649
Bifidobacterium_ breve_DSM_202 13_=JCM_1192 _DNA	NZ_AP012324.1	<b>1468985- 1509872</b>	<b>1485228- 1507366</b>	<b>1485551- 1507021</b>	<b>1486074- 1496358</b>	<b>1468956- 1494343</b>	-	<b>1467291- 1509773</b>	<b>1467291- 1509773</b>



Bifidobacterium_breve_DSM_20213=_JCM_1192_DNA	NZ_AP012324.1	-	-	-	<b>1498873-1507021</b>	<b>1497060-1508394</b>	-	-	1249162-1344877
Bifidobacterium_breve_DSM_20213=_JCM_1192_DNA	NZ_AP012324.1	-	-	-	-	-	-	-	1194046-1226926
Bifidobacterium_breve_strain_082 W48_chromosome	CP021555.1	<b>1193403-1232804</b>	<b>1206672-1214295</b>	<b>1207710-1212860</b>	-	<b>1203320-1217851</b>	-	<b>1193660-1232803</b>	<b>1193660-1232803</b>
Bifidobacterium_breve_strain_082 W48_chromosome	CP021555.1	-	-	-	-	-	-	-	1280471-1374651
Bifidobacterium_breve_strain_180 W83_chromosome	CP021557.1	-	765587-769503	-	-	541903-553280	-	-	-
Bifidobacterium_breve_strain_180 W83_chromosome	CP021557.1	<b>1179127-1219381</b>	<b>1179607-1200428</b>	<b>1181262-1199775</b>	<b>1185692-1185692</b>	<b>1188797-1203326</b>	-	<b>1179308-1381202</b>	<b>1179308-1381202</b>
Bifidobacterium_breve_strain_139 W423_chromosome	CP021556.1	<b>420545-438765</b>	<b>424673-435839</b>	<b>426202-434897</b>	-	-	-	<b>420943-438842</b>	<b>420943-438842</b>
Bifidobacterium_breve_strain_139 W423_chromosome	CP021556.1	-	974188-981132	975240-980096	-	2221080-2237280	-	-	1390378-1415815
Bifidobacterium_breve_strain_139 W423_chromosome	CP021556.1	<b>1302639-1342715</b>	<b>1318685-1324517</b>	-	-	<b>1304994-1334589</b>	-	<b>1242823-1342714</b>	<b>1242823-1342714</b>

me									
Bifidobacterium_breve_strain_017 W439_chromosome	CP021554.1	<b>1194717-1234971</b>	<b>1196166-1216017</b>	<b>1197325-1215364</b>	<b>1203494-1208037</b>	<b>1210608-1218915</b>	-	<b>1129550-1234970</b>	<b>1129550-1234970</b>
Bifidobacterium_breve_strain_017 W439_chromosome	CP021554.1	-	-	-	-	2270509-2279795	-	-	1278706-1368219
Bifidobacterium_breve_strain_215 W447a_chromosome	CP021558.1	<b>1694074-1735438</b>	<b>1710824-1729970</b>	<b>1711359-1729491</b>	<b>1712084-1729491</b>	<b>1694064-1735429</b>	-	<b>1694171-1735338</b>	<b>1694171-1735338</b>
Bifidobacterium_breve_strain_215 W447a_chromosome	CP021558.1	-	-	-	-	-	-	1343074-1436109	1343074-1436109
Bifidobacterium_breve_strain_215 W447a_chromosome	CP021558.1	-	-	-	-	-	-	1233723-1300802	1233723-1300802
Bifidobacterium_breve_689b	CP006715.1	<b>372287-390546</b>	<b>377941-381823</b>	-	-	-	-	<b>372499-390623</b>	<b>372499-390623</b>
Bifidobacterium_breve_689b	CP006715.1	-	-	-	-	-	-	-	967972-982427
Bifidobacterium_breve_689b	CP006715.1	-	-	-	-	-	-	-	1277026-1302461
Bifidobacterium_l ongum_subsp_in fantis_ATCC_15 697_=_JCM_122 2_=_DSM_2008 8_DNA	AP010889.1	<b>1288185-1330866</b>	<b>1290017-1310860</b>	<b>1290722-1304244</b>	-	-	-	<b>-1288393-1330865</b>	<b>1288393-1330865</b>
Bifidobacterium_l	AP010889.1	-	1677204-	1677675-	1680005-	-	-	1622695-	1360973-

ongum_subsp_in fantis_ATCC_15 697=_JCM_122 2=_DSM_2008 8_DNA			1683043	1682789	1681549			1723329	1524111
Bifidobacterium_l ongum_subsp_in fantis_ATCC_15 697=_JCM_122 2=_DSM_2008 8_DNA	AP010889.1	-	1690216- 1704374	1690557- 1703909	1690808- 1703593	-	-	-	1905562- 1995488
Bifidobacterium_l ongum_subsp_in fantis_ATCC_15 697=_JCM_122 2=_DSM_2008 8_DNA	AP010889.1	-	1972553- 1992392	1972663- 1991790	1972962- 1991034	-	-	1805760- 1837358	1622695- 1723329
Bifidobacterium_l ongum_subsp_in fantis_ATCC_15 697=_JCM_122 2=_DSM_2008 8_DNA	AP010889.1	-	-	-	-	-	-	1905562- 1995488	1805760- 1837358
Pseudomonas_a eruginosa_LESB 58	NC_011770.1	-	662125- 683222	662125- 683222	664333- 681338	-	-	664283- 680435	664283- 680435
Pseudomonas_a eruginosa_LESB 58	NC_011770.1	<b>863875- 906018</b>	<b>873594- 898785</b>	<b>874970- 896675</b>	<b>875391- 892443</b>	-	-	<b>862819- 907359</b>	<b>862819- 907359</b>
Pseudomonas_a eruginosa_LESB 58	NC_011770.1	<b>1433756- 1476547</b>	<b>1439735- 1468915</b>	<b>1440268- 1468502</b>	<b>1442097- 1463296</b>	-	-	<b>1433804- 1478274</b>	<b>1433804- 1478274</b>
Pseudomonas_a eruginosa_LESB 58	NC_011770.1	<b>1684045- 1720850</b>	<b>1680357- 1723970</b>	<b>1682289- 1721162</b>	<b>1685013- 1720236</b>	-	-	<b>1682239- 1720879</b>	<b>1682239- 1720879</b>
Pseudomonas_a	NC_011770.1	-	2532782-	2533562-	2537197-	-	-	2465070-	2465070-

eruginosa_LESB 58			2548726	2548018	2545357			2562293	2562293
Pseudomonas_a eruginosa_LESB 58	NC_011770.1	<b>2690450- 2740350</b>	<b>2702162- 2740315</b>	<b>2703591- 2739799</b>	<b>2704701- 2738800</b>	-	-	<b>2617980- 2740365</b>	<b>2617980- 2740365</b>
Pseudomonas_a eruginosa_LESB 58	NC_011770.1	<b>4545190- 4552788</b>	-	-	-	-	-	<b>4545201- 4553453</b>	<b>4545201- 4553453</b>
Pseudomonas_a eruginosa_LESB 58	NC_011770.1	-	-	-	-	-	-	-	4931543- 4970545
Neisseria_gonorr hoeae_FA_1090	AE004969.1	<b>455173- 498100</b>	<b>465272- 490462</b>	<b>465633- 484924</b>	<b>465633- 480222</b>	<b>441337- 500418</b>	-	<b>424640- 499873</b>	<b>424640- 499873</b>
Neisseria_gonorr hoeae_FA_1090	AE004969.1	<b>1044447- 1078281</b>	<b>1045279- 1069680</b>	<b>1045279- 1069319</b>	<b>1046644- 1069680</b>	<b>1058674- 1073393</b>	-	<b>968860- 1088321</b>	<b>968860- 1088321</b>
Neisseria_gonorr hoeae_FA_1090	AE004969.1	<b>1583028- 1599049</b>	<b>1588677- 1607367</b>	<b>1589736- 1606537</b>	<b>1589736- 1605366</b>	<b>1573729- 1616725</b>	-	<b>1582978- 1610377</b>	<b>1582978- 1610377</b>
Neisseria_gonorr hoeae_FA_1090	AE004969.1	1606828- 1609808	-	-	-	-	-	-	-
Neisseria_gonorr hoeae_FA_1090	AE004969.1	972837- 984008	-	-	-	-	-	-	-
Neisseria_gonorr hoeae_FA_1090	AE004969.1	<b>721256- 729870</b>	<b>721459- 729264</b>	<b>722896- 728159</b>	<b>725260- 727853</b>	<b>711590- 738388</b>	-	-	-
Staphylococcus_ aureus_subsp_a ureus_COL	NC_002951.2	<b>354674- 398267</b>	<b>357357- 395612</b>	<b>352760- 399477</b>	<b>356184- 397516</b>	<b>354767- 398124</b>	<b>354735- 397566</b>	<b>354735- 397566</b>	<b>354735- 397566</b>
Staphylococcus_ aureus_subsp_a ureus_COL	NC_002951.2	-	906350- 907600	900796- 912998	903491- 912074	900796- 922004	-	899821- 918856	899821- 918856
Staphylococcus_ aureus_subsp_a ureus_COL	NC_002951.2	-	-	1909269- 1920660	-	-	-	-	-
Staphylococcus_ ureus_COL	NC_002976.3	-	-	1396901-	-	891998-	-	-	-

epidermidis_RP6 2A				1404837		903017			
Staphylococcus_ epidermidis_RP6 2A	NC_002976.3	-	-	1523242- 1532353	-	-	-	-	-
Staphylococcus_ epidermidis_RP6 2A	NC_002976.3	<b>1567637- 1694334</b>	<b>1646837- 1681850</b>	<b>1586894- 1608315</b>	<b>1594097- 1601618</b>	<b>1567637- 1697887</b>	-	<b>1580868- 1690525</b>	<b>1580868- 1690525</b>
Staphylococcus_ epidermidis_RP6 2A	NC_002976.3	-	-	<b>1617188- 1627431</b>	<b>1646643- 1685098</b>	-	-	-	-
Staphylococcus_ epidermidis_RP6 2A	NC_002976.3	-	-	<b>1642111- 1690751</b>	-	-	-	-	-