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Supp Table 3. Accession numbers of the selected genomes from IslandViewer. For each genome, there are at least 20 kb of DNA segments were predicted as GIs by at least two of the three methods: IslandPick, SIGI-HMM and IslandPath-DIMOB, and at least 40% of the total DNA were predicted as GIs by any of three methods.

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Mer		At Least Expected Mer Count								
Length	1	2	3	4	5	6	7	8	9	10
2	47	76	100	124	147	169	190	211	231	252
3	192	302	398	495	584	674	757	840	924	1007
4	768	1206	1590	1974	2333	2691	3024	3357	3689	4022
5	3070	4816	6353	7889	9322	10756	12087	13418	14750	16081
6	12274	19256	25400	31544	37279	43013	48338	53663	58987	64312
7	49086	77010	101587	126163	149100	172038	193337	214636	235936	257235
8	196333	308026	406330	504634	596385	688135	773332	858529	943725	1028922
9	785320	1232085	1625301	2018517	2385518	2752520	3093307	3434094	3774882	4115669
10	3141261	4928316	6501180	8074044	9542051	11010057	12373206	13736355	15099503	16462652

Supp Table 1. Window sizes for mer length from 2 to 10, with expected counts at least from 1 to 10.

Method	Predicted GI			At Nucleotide Level (%)		
	Total Length	Total Number	Average Length	Accuracy	Precision	Recall
Centroid	5573339	320	17417	82.37	61.35	27.63
INDeGenIUS	3641371	277	13146	82.43	67.94	19.99
SigHunt	5813441	758	4670	80.54	51.00	23.95
Zisland	4156542	653	6365	83.78	75.90	25.49
MTGIpick	15843860	522	30352	86.15	72.79	47.19

Supp Table 2. Comparison of the window-based methods (Centroid, INDeGenIUS, SigHunt, Zisland Explorer and the proposed MTGIpick) on classification of GIs/non-GI datasets. The precision, recall and overall accuracy of each method are calculated based on the number of overlapping nucleotides in both published GIs and predicted GIs.

Genome Name	Accession
<i>Anaeromyxobacter</i> sp. K	NC_011145.1
<i>Burkholderia Cenocepacia</i> MC0-3 Chr. 3	NC_010512.1
<i>Burkholderia Cenocepacia</i> MC0-3 Chr. 2	NC_010515.1
<i>Burkholderia multivorans</i> ATCC 17616 Chr. 1	NC_010084.1
<i>Burkholderia Pseudomallei</i> 1710b Chr. 2	NC_007435.1
<i>Burkholderia Pseudomallei</i> 1710b Chr. 1	NC_007434.1
<i>Burkholderia Vietnamiensis</i> G4 Chr. 1	NC_009256.1
<i>Escherichia coli</i> 536	NC_008253.1
<i>Pseudomonas Aeruginosa</i> PA7	NC_009656.1
<i>Pseudomonas putida</i> KT2440	NC_002947.4
<i>Pseudomonas putida</i> GB-1	NC_010322.1
<i>Pseudomonas syringae</i> Pv. <i>phaseolicola</i> 1448A	NC_005773.3
<i>Rhizobium etli</i> CFN 42	NC_007761.1
<i>Rhodobacter Sphaeroides</i> 17025	NC_009428.1
<i>Rhodopseudomonas Palustris</i> BisB5	NC_007958.1
<i>Rhodopseudomonas Palustris</i> HaA2	NC_007778.1
<i>Shewanella baltica</i> OS185	NC_009665.1
<i>Shewanella</i> sp. ANA-3 Chr. 1	NC_008577.1
<i>Sinorhizobium meliloti</i> 1021	NC_003047.1
<i>Vibrio parahaemolyticus</i> RIMD 2210633 Chr. 1	NC_004603.1

Supp Table 3. Accession numbers of the selected genomes from IslandViewer. For each genome, there are at least 20 kb of DNA segments were predicted as GIs by at least two of the three methods: IslandPick, SIGI-HMM and IslandPath-DIMOB, and at least 40% of the total DNA were predicted as GIs by any of three methods.

	Genome Name	TPR	TNR	ACC	OACC	MCC	F1
MTGlpick	<i>Bartonella tribocorum</i> CIP 105476	0.288	0.943	0.615	0.722	0.319	0.411
	<i>Bordetella petrii</i> DSM 12804	0.838	0.982	0.910	0.953	0.848	0.876
	<i>Burkholderia cenocepacia</i> J2315 Chr. 1	0.827	0.973	0.900	0.959	0.768	0.790
	<i>Burkholderia cenocepacia</i> J2315 Chr. 2	0.934	0.979	0.956	0.976	0.804	0.808
	<i>Burkholderia cenocepacia</i> J2315 Chr. 3	0.882	0.930	0.906	0.927	0.611	0.612
	<i>Clavibacter michiganensis</i> NCPPB 382	0.947	1.000	0.974	0.998	0.972	0.973
	<i>Corynebacterium diphtheriae</i> NCTC 13129	0.139	0.997	0.568	0.911	0.315	0.238
	<i>Cronobacter sakazakii</i> ATCC BAA-894	0.784	0.972	0.878	0.957	0.726	0.749
	<i>Escherichia coli</i> CFT073	0.625	0.983	0.804	0.924	0.700	0.730
	<i>Proteus mirabilis</i> HI4320	0.647	0.975	0.811	0.939	0.669	0.700
	<i>Salmonella typhi</i> CT18	0.647	0.992	0.820	0.968	0.730	0.738
	<i>Streptococcus equi</i> 4047	0.870	0.972	0.921	0.959	0.818	0.841
	<i>Vibrio cholerae</i> O1 biovar El Tor str. N16961 Chr. 1	0.783	0.996	0.889	0.985	0.833	0.838
	<i>Vibrio cholerae</i> O1 biovar El Tor str. N16961 Chr. 2	0.990	0.999	0.994	0.997	0.990	0.992
Islandpick	<i>Bartonella tribocorum</i> CIP 105476	0.000	1.000	0.500	0.640	0.000	0.000
	<i>Bordetella petrii</i> DSM 12804	0.000	1.000	0.500	0.799	0.000	0.000
	<i>Burkholderia cenocepacia</i> J2315 Chr. 1	0.389	0.992	0.691	0.933	0.543	0.531
	<i>Burkholderia cenocepacia</i> J2315 Chr. 2	0.251	1.000	0.626	0.954	0.490	0.402
	<i>Burkholderia cenocepacia</i> J2315 Chr. 3	0.000	0.958	0.479	0.890	-0.056	0.000
	<i>Clavibacter michiganensis</i> NCPPB 382	0.000	1.000	0.500	0.967	0.000	0.000
	<i>Corynebacterium diphtheriae</i> NCTC 13129	0.043	1.000	0.521	0.902	0.197	0.082
	<i>Cronobacter sakazakii</i> ATCC BAA-894	0.086	0.997	0.542	0.918	0.235	0.155

	<i>Escherichia coli</i> CFT073	0.162	0.993	0.577	0.852	0.321	0.270
	<i>Proteus mirabilis</i> HI4320	0.268	1.000	0.634	0.914	0.494	0.422
	<i>Salmonella typhi</i> CT18	0.079	0.998	0.539	0.924	0.236	0.144
	<i>Streptococcus equi</i> 4047	0.063	0.996	0.529	0.863	0.185	0.116
	<i>Vibrio cholerae</i> O1 biovar El Tor str. N16961 Chr. 1	0.000	1.000	0.500	0.951	0.000	0.000
	<i>Vibrio cholerae</i> O1 biovar El Tor str. N16961 Chr. 2	0.000	1.000	0.500	0.802	0.000	0.000
IslandPath-DIM OB	<i>Bartonella tribocorum</i> CIP 105476	0.161	1.000	0.581	0.698	0.331	0.277
	<i>Bordetella petrii</i> DSM 12804	0.425	0.987	0.706	0.874	0.562	0.576
	<i>Burkholderia cenocepacia</i> J2315 Chr. 1	0.608	0.976	0.792	0.940	0.637	0.666
	<i>Burkholderia cenocepacia</i> J2315 Chr. 2	0.608	0.973	0.791	0.951	0.577	0.603
	<i>Burkholderia cenocepacia</i> J2315 Chr. 3	0.389	0.921	0.655	0.883	0.266	0.323
	<i>Clavibacter michiganensis</i> NCPPB 382	0.194	0.989	0.592	0.963	0.254	0.257
	<i>Corynebacterium diphtheriae</i> NCTC 13129	0.185	0.974	0.579	0.893	0.237	0.261
	<i>Cronobacter sakazakii</i> ATCC BAA-894	0.445	0.985	0.715	0.938	0.544	0.556
	<i>Escherichia coli</i> CFT073	0.450	0.991	0.720	0.899	0.597	0.602
	<i>Proteus mirabilis</i> HI4320	0.154	0.987	0.571	0.890	0.269	0.246
	<i>Salmonella typhi</i> CT18	0.420	0.928	0.674	0.887	0.316	0.375
	<i>Streptococcus equi</i> 4047	0.413	0.988	0.700	0.906	0.551	0.555
	<i>Vibrio cholerae</i> O1 biovar El Tor str. N16961 Chr. 1	0.600	0.974	0.787	0.956	0.550	0.573
	<i>Vibrio cholerae</i> O1 biovar El Tor str. N16961 Chr. 2	0.542	0.967	0.754	0.882	0.594	0.646
SIGI-HMM	<i>Bartonella tribocorum</i> CIP 105476	0.000	1.000	0.500	0.640	0.000	0.000
	<i>Bordetella petrii</i> DSM 12804	0.510	0.968	0.739	0.876	0.573	0.623
	<i>Burkholderia cenocepacia</i> J2315 Chr. 1	0.457	0.985	0.721	0.933	0.561	0.573
	<i>Burkholderia cenocepacia</i> J2315 Chr. 2	0.655	0.980	0.818	0.960	0.648	0.669

	<i>Burkholderia cenocepacia</i> J2315 Chr. 3	0.259	0.937	0.598	0.888	0.190	0.250
	<i>Clavibacter michiganensis</i> NCPPB 382	0.694	0.997	0.845	0.987	0.776	0.777
	<i>Corynebacterium diphtheriae</i> NCTC 13129	0.133	0.956	0.544	0.871	0.120	0.175
	<i>Cronobacter sakazakii</i> ATCC BAA-894	0.334	0.987	0.661	0.930	0.456	0.454
	<i>Escherichia coli</i> CFT073	0.257	0.958	0.608	0.839	0.300	0.352
	<i>Proteus mirabilis</i> HI4320	0.263	0.995	0.629	0.910	0.452	0.405
	<i>Salmonella typhi</i> CT18	0.321	0.962	0.642	0.910	0.323	0.367
	<i>Streptococcus equi</i> 4047	0.000	1.000	0.500	0.857	0.000	0.000
	<i>Vibrio cholerae</i> O1 biovar El Tor str. N16961 Chr. 1	0.576	0.987	0.781	0.966	0.614	0.629
	<i>Vibrio cholerae</i> O1 biovar El Tor str. N16961 Chr. 2	1.000	0.969	0.985	0.975	0.928	0.941
Islander	<i>Bartonella tribocorum</i> CIP 105476	0.416	0.999	0.708	0.789	0.558	0.587
	<i>Bordetella petrii</i> DSM 12804	0.141	0.983	0.562	0.814	0.250	0.234
	<i>Burkholderia cenocepacia</i> J2315 Chr. 1	0.153	0.969	0.561	0.889	0.178	0.213
	<i>Burkholderia cenocepacia</i> J2315 Chr. 2	0.439	1.000	0.719	0.966	0.651	0.610
	<i>Burkholderia cenocepacia</i> J2315 Chr. 3	0.000	1.000	0.500	0.928	0.000	0.000
	<i>Clavibacter michiganensis</i> NCPPB 382	0.000	1.000	0.500	0.967	0.000	0.000
	<i>Corynebacterium diphtheriae</i> NCTC 13129	0.189	1.000	0.594	0.916	0.410	0.317
	<i>Cronobacter sakazakii</i> ATCC BAA-894	0.364	0.985	0.674	0.931	0.473	0.479
	<i>Escherichia coli</i> CFT073	0.664	0.939	0.802	0.893	0.613	0.678
	<i>Proteus mirabilis</i> HI4320	0.242	0.998	0.620	0.910	0.455	0.386
	<i>Salmonella typhi</i> CT18	0.482	0.955	0.718	0.916	0.437	0.482
	<i>Streptococcus equi</i> 4047	0.224	1.000	0.612	0.889	0.445	0.366
	<i>Vibrio cholerae</i> O1 biovar El Tor str. N16961 Chr. 1	0.000	1.000	0.500	0.951	0.000	0.000
	<i>Vibrio cholerae</i> O1 biovar El Tor str. N16961 Chr. 2	0.000	1.000	0.500	0.802	0.000	0.000

	<i>Bartonella tribocorum</i> CIP 105476	0.338	0.988	0.663	0.754	0.466	0.498
	<i>Bordetella petrii</i> DSM 12804	0.291	0.980	0.635	0.841	0.413	0.424
	<i>Burkholderia cenocepacia</i> J2315 Chr. 1	0.628	0.982	0.805	0.948	0.679	0.702
	<i>Burkholderia cenocepacia</i> J2315 Chr. 2	0.930	0.962	0.946	0.960	0.739	0.741
	<i>Burkholderia cenocepacia</i> J2315 Chr. 3	1.000	0.917	0.958	0.923	0.665	0.651
	<i>Clavibacter michiganensis</i> NCPPB 382	0.786	0.962	0.874	0.956	0.548	0.538
Zisland	<i>Corynebacterium diphtheriae</i> NCTC 13129	0.305	0.983	0.644	0.913	0.414	0.419
Explorer	<i>Cronobacter sakazakii</i> ATCC BAA-894	0.523	0.969	0.746	0.930	0.529	0.566
	<i>Escherichia coli</i> CFT073	0.459	0.965	0.712	0.880	0.516	0.564
	<i>Proteus mirabilis</i> HI4320	0.521	0.955	0.738	0.905	0.510	0.561
	<i>Salmonella typhi</i> CT18	0.614	0.954	0.784	0.926	0.535	0.574
	<i>Streptococcus equi</i> 4047	0.374	0.984	0.679	0.897	0.499	0.508
	<i>Vibrio cholerae</i> O1 biovar El Tor str. N16961 Chr. 1	0.472	0.998	0.735	0.972	0.654	0.628
	<i>Vibrio cholerae</i> O1 biovar El Tor str. N16961 Chr. 2	1.000	0.994	0.997	0.995	0.984	0.987

Supp Table 4. The sensitivity (TPR), specificity (TNR), overall accuracy (OACC), accuracy (ACC), F1 and Matthews correlation coefficient (MCC) of the IslandPick, Islander, SIGI-HMM, IslandPath-DIMOB, Zisland Explorer and MTGIpick on the L-data set.

Method	Predicted GI			Nucleotides in both RGIs and PGIs*	PGIs/RGIs** (>50%)
	Length	Number	Average length		
IslandPick	106793	6	17799	106587	1
IslandPath-DIMOB	291264	13	22405	233096	5
Sigi-HMM	241154	31	7779	137308	4
Alien Hunter	980086	86	11396	449085	18
Centroid	174000	12	14500	68483	3
INDeGenIUS	120000	12	10000	61214	3
SigHunt	258000	34	7588	102160	6
MTGIpick	582232	18	32346	456619	14

* Total number of the overlapping nucleotides in both really GIs (RGIs) and predicted GIs (PGIs) Data.

** Number of the really GIs (RGI) which are covered by more than 50% of the predicted GIs (PGI).

Supp Table 5. Total length, average length and number of genomic islands predicted by MTGIpick, SIGI-HMM, Alien_Hunter, Centroid, IslandPath-DIMOB, INDeGenIUS, SigHunt and IslandPick in *S. enterica* Typhi CT18, and total number of the overlapping nucleotides in both known GIs and predicted GIs Data as well as the number of the known GIs which are covered by more than 50% of the results of the prediction method.

Method		Method	Precision	FDR	F1-score
comparative genomics		IslandPick	16.67	83.33	7.41
Sequence composition	HMM-based methods	IslandPath-DIMOB	38.46	61.54	29.41
		Sigi-HMM	12.90	87.10	15.38
		Alien Hunter	20.93	79.07	33.64
	Window-based methods	Centroid	25.00	75.00	18.18
		INDeGenIUS	25.00	75.00	18.18
		SigHunt	17.65	82.35	21.82
		MTGIpick	77.78	22.22	71.79

Supp Table 6. Precision, false discovery rate (FDR) and F1-score of the proposed method MTGIpick, SIGI-HMM, Alien_Hunter, Centroid, IslandPath-DIMOB, INDeGenIUS, SigHunt and IslandPick on detection of genomic islands in *S. enterica* Typhi CT18, and the precision, false positive rate and F1-score are calculated based on the number of the known GIs which are covered by more than 50% of the results of the prediction method.

Method	SPI-6			SPI-16			SopD2Islet			Prophage10			SPI-5			Bacteriophage			SPI-2		
	Start	End	Size	Start	End	Size	Start	End	Size	Start	End	Size	Start	End	Size	Start	End	Size	Start	End	Size
	302172	361067	58896	605515	609992	4478	964573	965531	959	1008747	1051266	42520	1085156	1092735	7580	1538899	1572919	34021	1625084	1664823	39740
IslandPick	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1538899	1547653	8755	0	0	0
IslandPath	0	0	0	0	0	0	0	0	0	1010087	1018788	8702	0	0	0	1539263	1572916	33654	0	0	0
Sigi-HMM	319019	327694	8676	605515	609992	4478	0	0	0	1008747	1017160	8414	0	0	0	0	0	0	1625241	1629735	4495
	335381	343609	8229	605515	609992	4478	964573	965531	959	1010087	1018788	8702	0	0	0	1539263	1572916	33654	1633059	1650502	17444
	348682	353100	4419																Total size		21939
	355919	360757	4839																1625084	1652500	27417
	Total size		26163																		
Alien_Hunter	302500	307500	5001	605515	609992	4478	964573	965531	959	1012500	1017500	5001	1085156	1092500	7345	1540000	1572500	32501	1625084	1652500	27417
	320000	361067	41068	605515	609992	4478	964573	965531	959	1047500	1051266	3767	1085156	1092500	7345	1540000	1572500	32501	1625084	1652500	27417
	Total size		46069							Total size		8768									
Centroid	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
INDeGenIUS	350001	360000	10000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1640001	1650000	10000
SigHunt	321001	326000	5000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	330001	340000	10000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	Total size		15000																		
Zisland Explorer	335381	361067	25687	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MTGIpick	309216	360850	51635	0	0	0	0	0	0	1028448	1051266	22819	0	0	0	1539015	1569444	30430	1625084	1650824	25741

Method	NovellIsland			Bacteriophage			SPI-17			SPI-CS54			SPI-9			Bacteriophage27			SPI-1		
	Start	End	Size	Start	End	Size	Start	End	Size	Start	End	Size	Start	End	Size	Start	End	Size	Start	End	Size
	1776200	1791815	15616	1887450	1933558	46109	2460793	2465914	5122	2597945	2615052	17108	2743495	2759190	15696	2759733	2782364	22632	2859262	2899034	39773
IslandPick	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2759733	2768828	9096	0	0	0
IslandPath	1778007	1791815	13809	1912212	1920788	8577	0	0	0	0	0	0	0	0	0	2760478	2768771	8294	0	0	0
				1921745	1933558	11814															
				Total size		20391															
Sigi-HMM	1777746	1791815	14070	1912585	1921726	9142	0	0	0	0	0	0	0	0	0	0	0	0	2862665	2867017	4353
Alien_Hunter	1776200	1791815	15616	1887450	1892500	5051	2460793	2465914	5122	2600000	2612500	12501	0	0	0	2762500	2767500	5001	2862500	2880000	17501
				1910000	1933558	23559										2777500	2782364	4865	2890000	2899034	9035
				Total size		28610										Total size		9866	Total size		26536
Centroid	1776200	1791815	15616	0	0	0	0	0	0	0	0	0	2744001	2756000	12000	0	0	0	2864001	2874000	10000
INDeGenIUS	1780001	1790000	10000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
SigHunt	1785001	1791815	6815	0	0	0	2462001	2465914	3914	2601001	2606000	5000	2745001	2756000	11000	0	0	0	0	0	0
										2607001	2612000	5000									
										Total size		10000									
Zisland Explorer	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2859262	2899034	39773
MTGIpick	1777591	1791815	14225	1887450	1933558	46109	0	0	0	2597945	2614594	16650	0	0	0	0	0	0	2862448	2899034	36587

Method	SPI-15			SPI-8			Bacteriophage			SPI-3			SPI-4			SPI-7			SPI-10		
	Start	End	Size	Start	End	Size	Start	End	Size	Start	End	Size	Start	End	Size	Start	End	Size	Start	End	Size
	3053654	3060017	6364	3132606	3139414	6809	3515397	3549055	33659	3883111	3900458	17348	4321943	4346614	24672	4409511	4543072	133562	4683690	4716539	32850
IslandPick	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4409569	4459514	49946	0	0	0
																4461264	4473872	12609			
																4509638	4518267	8630			
																4519049	4536599	17551			
IslandPath																Total size		88736			
	3053654	3060017	6364	0	0	0	3519664	3548972	29309	0	0	0	0	0	0	4409511	4479514	70004	0	0	0
																4483138	4508108	24971			
Sigi-HMM																4521572	4539169	17598			
																Total size		112573			
	0	0	0	3134156	3139414	5259	0	0	0	0	0	0	4322993	4327581	4589	4435339	4450341	15003	4694767	4705191	10425
																4460652	4467050	6399			
Alien_Hunter																4531179	4538252	7074			
																Total size		28476			
	3053654	3060017	6364	3132606	3139414	6809	3515397	3520000	4604	3892500	3900000	7501	4321943	4346614	24672	4409511	4410000	490	4683690	4707500	23811
							3522500	3537500	15001							4412500	4475000	62501	4710000	4716539	6540
							3542500	3547500	5001							4485000	4507500	22501	Total size		30351
Centroid							Total size		24606							4510000	4537500	27501			
																Total size		112993			
	0	0	0	3132606	3139414	6809	0	0	0	0	0	0	4321943	4332000	10058				4692001	4706000	14000
INDeGenIUS	3053654	3060000	6347	3132606	3139414	6809	0	0	0	0	0	0	4321943	4330000	8058	4520001	4530000	10000	0	0	0
SigHunt	3055001	3060017	5017	3134001	3139414	5414	3531001	3537000	6000	0	0	0	4322001	4340000	18000	4486001	4493000	7000	4685001	4690000	5000
																			4696001	4705000	9000

Zisland Explorer	0			0			0			0			0			4321943			4409511			4484754			75244			Total size			14000																														
	0			0			0			0			0			4321943			4496059			4541343			45285			4685181			4702925			17745																											
	0			0			0			0			0			24672			45285			4716539			6354																																				
MTGIpick	3053654			3060017			6364			3133694			3139414			5721			3518147			3548528			30382			0			0			0			4321947			4346614			24668			4409511			4536667			127157			Total size			24099			
	3053654			3060017			6364			3133694			3139414			5721			3518147			3548528			30382			0			0			0			4321947			4346614			24668			4409511			4536667			127157			4684759			4702889			18131
	3053654			3060017			6364			3133694			3139414			5721			3518147			3548528			30382			0			0			0			4321947			4346614			24668			4409511			4536667			127157									

Supp Table 7. The start and end positions of 21 known genomic islands, and those of the overlap between the 21 known genomic islands and the predicted genomic islands from SIGI-HMM, Alien_Hunter, Centroid, IslandPath-DIMOB, INDeGenIUS, SigHunt, IslandPick, Zisland Explorer and MTGIpick.