Supplemental Movie Legends and Tables for:

McBride, MJ and Y Zhu. "Gliding motility and Por secretion system genes are widespread among members of the phylum *Bacteroidetes*"

Supplemental Movie Legends.

Movie S1. Gliding motility of *Cellulophaga algicola* and *Maribacter* sp. HTCC2170. Cells of *C. algicola* growing on Cytophaga Agar (DSMZ medium 172) at 15°C were suspended in Cytophaga Broth, introduced into a glass tunnel slide, and incubated for 5 min. Cells on the cover slip were examined using a Photometrics CoolSNAP$_{cf}^{2}$ camera mounted on an Olympus BH-2 phase-contrast microscope with a heated stage at 25°C. Cells of *Maribacter* sp. HTCC2170 growing on Marine Agar at 25°C were suspended in Marine Broth, spotted on a pad of Marine Broth containing 1% agar, covered with an O_2 permeable membrane (Yellow Springs Instrument Co., Yellow Springs, OH) and examined as described above. In both sequences the bar indicates 10 μm, and time is indicated as minutes:seconds.

Movie S2. Gliding motility of *Croceibacter atlanticus*. Cells of *C. atlanticus* growing on Marine Agar at 25°C were suspended in Marine Broth, introduced into a glass tunnel slide, and incubated for 5 min. Cells on the cover slip were examined using a Photometrics CoolSNAP$_{cf}^{2}$ camera mounted on an Olympus BH-2 phase-contrast microscope with a heated stage at 25°C. The images in Fig. 4A came from this movie and correspond to the middle portion of the field. Bar indicates 10 μm, and time is indicated in seconds.

Movie S3. Gliding motility of *Robiginitalea biformata*. Cells of *R. biformata* growing on Marine Agar at 30°C were suspended in Marine Broth. In the first sequence cells were introduced into a glass tunnel slide, incubated for 5 min, and cells on the cover slip were examined using a Photometrics CoolSNAP$_{cf}^{2}$ camera mounted on an Olympus BH-2 phase-contrast microscope with a heated stage at 25°C. In the second sequence cells were spotted on a pad of Marine Broth containing 1% agar, covered with an O_2 permeable membrane, and examined as described above. In both sequences the bar indicates 10 μm, and time is indicated as minutes:seconds. The images in Fig. 4B came from the second part of this movie and correspond to the top middle portion of the field.

Movie S4. Gliding motility of '*Gramella forsetii*'. Cells of '*G. forsetii*' growing on Marine Agar at 25°C were suspended in Cytophaga Salts, which consisted of Cytophaga Agar (DSMZ medium 172) in which yeast extract, tryptone, and agar had been omitted. Cells were spotted on a pad of Cytophaga Salts containing 1% agar, covered with an O_2 permeable membrane and examined using a Photometrics CoolSNAP$_{cf}^{2}$ camera mounted on an Olympus BH-2 phase-contrast microscope with a heated stage at 25°C. The images in Fig. 4C came from this movie and correspond to the top middle portion of the field. Bar indicates 10 μm, and time is indicated as minutes:seconds.

Movie S5. Gliding motility of *Riemerella anatipestifer*. Cells of *R. anatipestifer* growing on TS Agar at 37°C were suspended in TS Broth. In the first sequence cells were introduced into a glass tunnel slide, incubated for 5 min, and cells on the cover slip were examined using a Photometrics CoolSNAP$_{cf}^{2}$ camera mounted on an Olympus BH-2 phase-contrast microscope with a heated stage at 25°C. In the second sequence cells were spotted on a pad of TS containing 1% agar, covered with an O_2 permeable membrane, and examined as described above. In both sequences the bar indicates 10 μm, and time is indicated as minutes:seconds. The images in Fig. 4D came from the second part of this movie and correspond to the lower right portion of the field.

Movie S6. Gliding motility of *Paludibacter propionicigenes*. Cells of *P. propionicigenes* were grown anaerobically on PYG Agar at 25^{o}C. Cells were suspended in PYG Broth and examined for motility in the presence of atmospheric levels of O_2. In the first sequence cells were observed in wet mount, and cells on the cover slip were examined using a Photometrics CoolSNAP$_{cf}^{2}$ camera mounted on an Olympus BH-2 phase-contrast microscope with a heated stage at 25^{o}C. In the second sequence cells were spotted on a pad of PYG containing 1% agar, covered with an O_2 permeable membrane, and examined as described above. In both sequences the bar indicates 10 μm, and time is indicated as minutes:seconds. The images in Fig. 4E came from the second part of this movie and correspond to the lower left portion of the field.

Table S1. Bacterial strains with completed genomes analyzed in this study[a]

Bacterial strain	Class	Reference	Source[b]
Capnocytophaga canimorsus Cc5	*Flavobacteriia*	(*1*)	
Capnocytophaga ochracea DSM 7271^{T}	*Flavobacteriia*	(*2*)	
Cellulophaga algicola DSM 14237^{T}	*Flavobacteriia*	(*3*)	DSMZ
Cellulophaga lytica DSM 7489^{T}	*Flavobacteriia*	(*4*)	
Croceibacter atlanticus HTCC2559^{T}	*Flavobacteriia*	(*5*)	ATCC
Flavobacteriaceae bacterium 3519-10	*Flavobacteriia*	(*6*)	
Flavobacterium johnsoniae ATCC 17061^{T}	*Flavobacteriia*	(*7*)	
Flavobacterium psychrophilum JIP02/86	*Flavobacteriia*	(*8*)	
'*Gramella forsetii*' KT0803	*Flavobacteriia*	(*9*)	Bernhard Fuchs
Maribacter sp. HTCC2170	*Flavobacteriia*	(*10*)	Jang-Cheon Cho
Riemerella anatipestifer DSM 15868^{T}	*Flavobacteriia*	(*11*)	DSMZ
Robiginitalea biformata HTCC2501^{T}	*Flavobacteriia*	(*12*)	ATCC
Weeksella virosa DSM 16922^{T}	*Flavobacteriia*	(*13*)	DSMZ
Zunongwangia profunda SM-A87^{T}	*Flavobacteriia*	(*14*)	DSMZ
Cytophaga hutchinsonii ATCC 33406^{T}	*Cytophagia*	(*15*)	
Dyadobacter fermentans DSM 18053^{T}	*Cytophagia*	(*16*)	ATCC
Leadbetterella byssophila DSM 17132^{T}	*Cytophagia*	(*17*)	DSMZ
Marivirga tractuosa DSM 4126^{T}	*Cytophagia*	(*18*)	
Spirosoma linguale DSM 74^{T}	*Cytophagia*	(*19*)	Michael Marletta
Chitinophaga pinensis DSM 2588^{T}	*Sphingobacteriia*	(*20*)	
Pedobacter heparinus DSM 2366^{T}	*Sphingobacteriia*	(*21*)	
Pedobacter saltans DSM 12145^{T}	*Sphingobacteriia*	(*22*)	
Alistipes shahii WAL8301^{T}	*Bacteroidia*	(*23*)	
Bacteroides fragilis NCTC 9343^{T}	*Bacteroidia*	(*24*)	
Bacteroides helcogenes P 36-108^{T}	*Bacteroidia*	(*25*)	
Bacteroides salanitronis BL78^{T}	*Bacteroidia*	(*26*)	
Bacteroides thetaiotaomicron VPI-5482^{T}	*Bacteroidia*	(*27*)	
Bacteroides vulgatus ATCC 8482^{T}	*Bacteroidia*	(*28*)	
Bacteroides xylanisolvens XB1A^{T}	*Bacteroidia*	(*29*)	
Odoribacter splanchnicus DSM 20712^{T}	*Bacteroidia*	(*30*)	
Paludibacter propionicigenes WB4^{T}	*Bacteroidia*	(*31*)	DSMZ
Parabacteroides distasonis ATCC 8503^{T}	*Bacteroidia*	(*28*)	
Porphyromonas gingivalis ATCC 33277^{T}	*Bacteroidia*	(*32*)	
Prevotella melaninogenica ATCC 25845^{T}	*Bacteroidia*	(*33*)	
Prevotella ruminicola 23	*Bacteroidia*	(*34*)	
Rhodothermus marinus DSM 4252^{T}	*Incertae sedis*	(*35*)	
Salinibacter ruber DSM 13855^{T}	*Incertae sedis*	(*36*)	

[a] Strains within each Class are listed alphabetically.

[b] For strains for which laboratory experiments were conducted, the sources of the strains are indicated.

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14. Q. L. Qin *et al.*, The complete genome of *Zunongwangia profunda* SM-A87 reveals its adaptation to the deep-sea environment and ecological role in sedimentary organic nitrogen degradation. *BMC Genomics* **11**, 247 (2010).
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Table S2. Distribution of *gld* and *spr* orthologs in completed *Bacteroidetes* genomes[a].

									Por Secretion System Genes						
Strains[b]	***gldA***	***gldB***	***gldD***	***gldF***	***gldG***	***gldH***	***gldI***	***gldJ***	***gldK***	***gldL***	***gldM***	***gldN***	***sprA***	***sprE***	***sprT***
Class *Flavobacteriia*															
Capnocytophaga canimorsus Cc5 (Ccan_)	13070	17700	01250	07670	07660	01070	11090	02800/02810 [c]	01610	01620	01630	01640	21890	01790	09030
Capnocytophaga ochracea DSM7271^{T} (Coch_)	1219	1064	1383	1946	1945	1475	1855	0756	0809	0808	0807	0806	1633	2029	1748
Cellulophaga algicola DSM 14237^{T} (Celal_)		2202	1091			1514	2755	0751	0884	0883	0882	0881	2075	1548	2247
Cellulophaga lytica DSM 7489^{T} (Celly_)	1982	2006	1024	3200	3201	1414	0267	2068	0759	0758	0757	0756	1877	1384	0647
Croceibacter atlanticus HTCC2559^{T} (CA2559_)	07370	06580	02655	08366	08361	03460	10703	05475	00725	00730	00735	00740	01210	03020	12253
Flavobacteriaceae bacterium 3519-10 (FIC_)	00573	01789	00461	00812	00811	02552	01350	00569	00488	00489	00490	00491	00396	00009	00515
Flavobacterium johnsoniae ATCC 17061^{T} (Fjoh_)	1516	1793	1540	2722	2721	0890	2369	1557	1853	1854	1855	1856	1653	1051	1466
Flavobacterium psychrophilum JIP02/86 (FP)	0252	2069	1663	1089	1090	0024	1892	1389	1973	1972	1971	1970	2121	2467	0326
'*Gramella forsetii*' KT0803 (orf)	335	2752	3534	1893	1894	3202_a	776	2862	2978	2977	2976	2975	181	3234	383
Maribacter sp. HTCC2170 (FB2170_)		17001	07484			05475	09536	17391	08679	08684	08689	08694	03020	05655	16776
Riemerella anatipestifer DSM 15868^{T} (Riean_)	1635	1624	1556	0098	0099	1186		0093	1644	1645	1646	1647	0835	0909	0053
Robiginitalea biformata HTCC2501^{T} (RB2501_)	03070	02945	08085	13574	13569	06435	01715	09625	09005	09010	09015	09020	03615	06585	02695
Weeksella virosa DSM 16922^{T} (Weevi_)	1318	1288	1161	1486	1485	0886	1603	0213	0551	0550	0549	0548	0823	1752	1787
Zunongwangia profunda SM-A87^{T} (ZPR_)	3620	3822	4488	1833	1832	0091	1687	3927	4150	4149	4148	4147	0590	0057	0935
Class *Cytophagia*															
Cytophaga hutchinsonii ATCC 33406^{T} (CHU_)	1545	3691	3683	1546	1547	0291		3494	0171	0172	0173	0174	0029	0177	2709
Dyadobacter fermentans DSM 18053^{T} (Dfer_)	4207	3615	4560	4470	3719	4014		3694	2915	2916	2917	2918	4465	5028	4024
Leadbetterella byssophila DSM 17132^{T} (Lbys_)	2846	2934	3234	0449	2296	3361		2605	1724	1723	1722	1721	0610	1110	2722
Marivirga tractuosa DSM 4126^{T} (Ftrac_)	1432	2496	1993	1431	1430	3344		2188	2556	2557	2558	2559	3337	2562	2975
Spirosoma linguale DSM 74^{T} (Slin_)	3471	5539	4895	6627	4905	5969		5515	3225	3224	3223	3222	6621	3219	6454

Class *Sphingobacteriia*															
***Chitinophaga pinensis* DSM 2588^T** (Cpin_)	1163	0219	0934	0231	0232	0675		1181	0483	0481	0480	0479	6946	6608	7095
***Pedobacter heparinus* DSM 2366^T** (Phep_)	3248	0409	4156	3237	3236	0077		4062	0383	0384	0385	0386	3831	0389	0978
***Pedobacter saltans* DSM 12145^T** (Pedsa_)	3771	2500	3033	3772	3773	3083		2910	2522	2521	2520	2519	3276	2516	1964
Class *Bacteroidia*															
Alistipes shahii WAL 8301^T (AL1_)															
Bacteroides fragilis NCTC 9343^T (BF)		0895				3911			2489	2813	2814				
Bacteroides helcogenes P 36-108^T (Bache_)						1151									
Bacteroides salanitronis DSM 18170^T (Bacsa_)		1663				1387									
Bacteroides thetaiotaomicron VPI-5482^T (BT)		4189				3818									
Bacteroides vulgatus ATCC 8482^T (BVU_)		1987				1827									
Bacteroides xylanisolvens XB1A^T (BXY_)	09440	32960				48690									
Odoribacter splanchnicus DSM 20712^T (Odosp_)	2849		0203/ 0218 [c]	1042	1042	3291		2175					0141/ 0142	0784	1128
Paludibacter propionicigenes WB4^T (Palpr_)	1936	2885	2874	3026	1453	2407		1925	2503	2504	2505	2506	0997	1699	2881
Parabacteroides distasonis ATCC 8503^T (BDI_)		1780	1991			1879			3324	3323	3322	3321	2659	3149	1856
Porphyromonas gingivalis ATCC 33277^T (PGN_)		1061				1566			1676	1675	1674	1673	0832	1877	0778
Prevotella melaninogenica ATCC25845^T (HMPREF0659_)		A6538				A5420			A5267	A5268	A5269	A5270	A6108	A5453	A5397
Prevotella ruminicola 23 (PRU_)		0632				1703			2175	2174	2173	2172	2040	1900	1922
***Incertae sedis*[d]**															
Rhodothermus marinus DSM 4252^T (Rmar_)	1770			1769	1768								2258	0835	
Salinibacter ruber DSM 13855^T (SRU_)	1251			1250	1249								2553	1028	

[a] Locus tags for orthologs (reciprocal best hits by BLASTP analysis) are listed. The invariant portion of each locus tag (such as 'Fjoh_' for *F. johnsoniae*) is listed after the strain name, in parenthesis. Thus, *F. johnsoniae gldA* corresponds to locus tag Fjoh_1516. All genomes were initially searched using *F. johnsoniae* protein sequences. Maximum E values were set at 1e-50 for GldA, and 1e-5 for the other proteins. In order to confirm weak hits for bacteria distantly related to *F. johnsoniae* (Class *Flavobacteriia*), genomes were also searched with protein sequences from *C. hutchinsonii* (Class *Cytophagia*), *P. heparinus* (Class *Sphingobacteriia*) and *P. gingivalis* (Class *Bacteroidia*).

[b] Species previously known to exhibit gliding motility are in bold.

[c] *C. canimorsus gldJ* and *O. splanchnicus gldD* and *sprA* have apparent frameshift mutations that split the genes. These may be sequencing errors, or may be authentic mutations.

[d] The phylogenetic placement of *R. marinus* and *S. ruber* is uncertain. These species may be deeply rooted members of the phylum *Bacteroidetes*, or they may be members of another phylum.

Table S3. Members of classes *Flavobacteriia*, *Cytophagia*, and *Sphingobacteriia* with incomplete (Draft) genome sequences analyzed in this study[a].

Bacterial strain	Class
Capnocytophaga gingivalis ATCC 33624^T	*Flavobacteriia*
Capnocytophaga ochracea F0287	*Flavobacteriia*
Capnocytophaga sp. oral taxon 329 str. F0087	*Flavobacteriia*
Capnocytophaga sp. oral taxon 338 str. F0234	*Flavobacteriia*
Capnocytophaga sputigena ATCC 33612^T	*Flavobacteriia*
Chryseobacterium gleum F93, ATCC 35910^T	*Flavobacteriia*
Dokdonia donghaensis MED134	*Flavobacteriia*
Flavobacteria MS024-2A	*Flavobacteriia*
Flavobacteria MS024-3C	*Flavobacteriia*
Flavobacteria sp. BAL38	*Flavobacteriia*
Flavobacteria sp. BBFL7	*Flavobacteriia*
Flavobacteriales sp. ALC-1	*Flavobacteriia*
Flavobacterium indicum GPSTA100-9 ^{T}	*Flavobacteriia*
Kordia algicida OT-1^T	*Flavobacteriia*
Krokinobacter sp. 4H-3-7-5	*Flavobacteriia*
Lacinutrix sp. 5H-3-7-4	*Flavobacteriia*
Leeuwenhoekiella blandensis MED217^T	*Flavobacteriia*
Polaribacter irgensii 23-P^T	*Flavobacteriia*
Polaribacter sp. MED152	*Flavobacteriia*
Psychroflexus torquis ATCC 700755^T	*Flavobacteriia*
Ulvibacter sp. SCB49	*Flavobacteriia*
Algoriphagus sp. PR1	*Cytophagia*
Microscilla marina ATCC 23134^T	*Cytophagia*
Mucilaginibacter paludis TPT56, DSM 18603^T	*Sphingobacteriia*
Pedobacter sp. BAL39	*Sphingobacteriia*
Sphingobacterium spiritivorum ATCC 33300	*Sphingobacteriia*
Sphingobacterium spiritivorum ATCC 33861^T	*Sphingobacteriia*

[a] Draft status as of September 2011. Strains within each Class are listed alphabetically. $^{'T'}$ indicates type strain.

Table S4. Protein export and secretion systems predicted for members of the phylum *Bacteroidetes*[a,].

Strains	Sec[b]	Tat[c]	T1SS[d]	T2SS[d]	T3SS[f]	T4SS[g]	T5SS[h]	T6SS[i]	T7SS[j]	ENP[k] (T8SS)	CU[l]	PorSS[m]
Class *Flavobacteriia*												
Capnocytophaga canimorsus Cc5	+	+	-	-	-	-	-	-	-	-	-	+
Capnocytophaga ochracea DSM 7271^{T}	+	+	-	-	-	-	-	-	-	-	-	+
Cellulophaga algicola DSM 14237^{T}	+	+	-	-	-	-	-	-	-	-	-	+
Cellulophaga lytica DSM 7489^{T}	+	+	-	-	-	-	-	-	-	-	-	+
Croceibacter atlanticus HTCC2559^{T}	+	+	-	-	-	-	-	-	-	-	-	+
Flavobacteriaceae bacterium 3519-10	+	+	-	-	-	-	+/-	-	-	+	-	+
Flavobacterium johnsoniae ATCC 17061^{T}	+	+	-	+	-	+/-	-	-	-	+	-	+
Flavobacterium psychrophilum JIP02/86	+	+	-	+	-	-	-	-	-	-	-	+
'*Gramella forsetii*' KT0803	+	+	-	-	-	+/-	-	-	-	-	-	+
Maribacter sp. HTCC2170	+	+	-	-	-	-	-	-	-	-	-	+
Riemerella anatipestifer DSM 15868^{T}	+	+	-	-	-	-	-	-	-	-	-	+
Robiginitalea biformata HTCC2501^{T}	+	+	-	-	-	-	-	-	-	-	-	+
Weeksella virosa DSM 16922^{T}	+	+	-	-	-	-	-	-	-	-	-	+
Zunongwangia profunda SM-A87^{T}	+	+	-	-	-	+/-	-	-	-	-	-	+
Class *Cytophagia*												
Cytophaga hutchinsonii ATCC 33406^{T}	+	+	-	+	-	-	-	-	-	-	-	+
Dyadobacter fermentans DSM 18053^{T}	+	+	-	-	-	-	-	-	-	+/-	-	+
Leadbetterella byssophila DSM 17132^{T}	+	+	-	-	-	+/-	-	-	-	-	-	+
Marivirga tractuosa DSM 4126^{T}	+	+	-	-	-	-	-	-	-	-	-	+
Spirosoma linguale DSM 74^{T}	+	+	-	-	-	+/-	-	-	-	+	-	+
Class *Sphingobacteriia*												
Chitinophaga pinensis DSM 2588^{T}	+	+	-	-	-	-	-	-	-	-	-	+
Pedobacter heparinus DSM 2366^{T}	+	+	-	+	-	-	-	-	-	-	-	+
Pedobacter saltans DSM 12145^{T}	+	+	-	-	-	+/-	-	-	-	-	-	+
Class *Bacteroidia*												
Alistipes shahii WAL 8301^{T}	+/-	+	-	-	-	-	-	-	-	-	-	-
Bacteroides fragilis NCTC 9343^{T}	+	+	+/-	-	-	+/-	-	-	-	-	-	-
Bacteroides helcogenes P 36-108^{T}	+	+	+/-	-	-	-	+/-	-	-	-	-	-
Bacteroides salanitronis BL78^{T}	+	+	+/-	-	-	+/-	-	-	-	-	-	-
Bacteroides thetaiotaomicron VPI-5482^{T}	+/-	+	+/-	-	-	+/-	-	-	-	-	-	-
Bacteroides vulgatus ATCC 8482^{T}	+/-	+/-	+/-	-	-	+/-	-	-	-	-	-	-

Bacteroides xylanisolvens XB1A^T	+/-	-	-	-	-	+/-	-	-	-	-	-	-
Odoribacter splanchnicus DSM 20712^T	+	+	-	+	-	-	-	-	-	-	-	-
Paludibacter propionicigenes WB4^T	+	+	-	-	-	-	-	-	-	-	-	+
Parabacteroides distasonis ATCC 8503^T	+	+	-	-	-	-	-	-	-	-	-	+
Porphyromonas gingivalis ATCC 33277^T	+	-	-	-	-	+/-	-	-	-	-	-	+
Prevotella melaninogenica ATCC 25845^T	+	-	-	-	-	+/-	-	-	-	+/-	-	+
Prevotella ruminicola 23	+	+	-	-	-	-	+/-	-	-	-	-	+
Incertae sedis[3]												
Rhodothermus marinus DSM 4252^T	+	+	+/-	+/-	+	-	-	-	-	-	-	-
Salinibacter ruber DSM 13855^T	+	+	-	+/-	+	-	-	-	-	-	-	-

[a] Secretion and export systems were identified by searching each genome with COGs, PFAMs, or TIGRFAMs corresponding to key components of each system as indicated below using the IMG v 3.5 Function Profile tool.

[b] The following COGs and TIGRFAMs (protein listed in parenthesis) were used to identify genes for key components of the *sec* system: COG0653, Tigr00963 (SecA); COG0690, Tigr00964 (SecE); COG1314, Tigr00810 (SecG); COG0201, Tigr00967 (SecY); COG0706, Tigr 03592 and Tigr03593 (YidC); COG1862, Tigr00739 (YajC). A '+' indicates that genes corresponding to each of these were identified in the genome. *A. shahii* was given a '+/-' because it lacked a homolog to SecY, and *B. thetaiotaomicron*, *B. vulgatus*, and *B. xylanisolvens* were given '+/-' because they lacked homologs to SecE.

[c] The following COGs and TIGRFAMs (protein listed in parenthesis) were used to identify genes for key components of the TAT system: COG0805, Tigr00945 (TatC); COG1826, Tigr01411 (TatA/E). '+' indicates that genes corresponding to *tatA* and *tatC* were identified in the genome, +/- indicates that a gene corresponding to only one was identified, and - indicates that genes corresponding to neither *tatA* nor *tatC* were identified.

[d] T1SSs were identified using the following: Tigr01843 (HlyD); Tigr01846 (HlyB); Tigr01844 (TolC). '-' indicates none of the genes were identified. '+/-' indicates that a gene related to *tolC* gene was identified.

[e] T2SSs were identified using the following COGs: COG1450 (PulD), COG2804 (PulE), COG1459 (PulF), COG2165 (PulG). A '+' indicates that genes corresponding to each of these were identified in the genome. '-' indicates none of the genes were identified. '+/-' indicates that genes corresponding to some of these were present. *R. marinus* and *S. ruber* had genes corresponding to PulD, PulE, and PulF, but these were adjacent to a *pilT* gene, and are thus likely to be associated with Type IV pili rather than Type II secretion.

[f] T3SSs were identified using the following COGs: COG1157 (FliI), COG1766 (FliF), COG1886 (FliN). '+' indicates that genes corresponding to each of these were identified in the genome. '-' indicates none of the genes were identified. Note that the potential T3SS genes of *R. marinus* and *S. ruber* were all clustered with flagellar motility and chemotaxis genes, and are thus likely components of the flagellar apparatus rather than free-standing T3SSs.

[g] T4SSs were identified using the following COGs: COG3838 (VirB2), COG3702 (VirB3), COG3451 (VirB4), COG3704 (VirB6), COG3736 (VirB8), COG3504 (VirB9), COG2948 (VirB10) COG0630 (VirB11), COG3505 (VirD4). '-' indicates none of the genes were identified. '+/-' indicates presence of apparent VirB4 and VirD4 genes, but absence of the other T4SS genes.

[h] T5SSs were identified using the following: COG3468 (adhesin AidA), COG5295 (autotransporter adhesin), COG5571 (autotransporter β-barrel domain), pfam03797 (autotransporter beta domain). '-' indicates that no matches were identified. '+/-' indicates that a match was found to pfam03797.

[i] T6SSs were identified using the following: Tigr03345, Tigr03347, Tigr03350, Tigr03352, Tigr03353, Tigr03354, Tigr03355, Tigr03358, Tigr03362, Tigr03373. '-' indicates that none of the T6SS genes were identified.

[j] T7SSs were identified using the following: Tigr03919, Tigr03920, Tigr03921, Tigr03922, Tigr03923, Tigr03924, Tigr03925, Tigr03926, Tigr03927, Tigr03928, Tigr03931. '-' indicates that none of the T7SS genes were identified.

[k] ENP pathways (T8SSs) were identified using the following: pfam03783 (CsgG), pfam07012 (Curlin associated repeat), pfam10614 (Tafi-CsgF), pfam10627 (CsgE). '+' indicates that genes corresponding to each of these were identified in the genome. '+/-' indicates that a gene corresponding to only CsgG was identified. '-' indicates that genes corresponding to none of the genes were identified.

[l] Chaperone-Usher secretion systems (CU) were identified using pfam00577 (Usher). A '-' indicates that a gene corresponding to the usher gene was not identified.

[m] PorSSs were identified by BLASTP analysis as indicated in Figure 2 and Table S2. A '+' indicates that each of the following core PorSS genes were identified: *gldK*, *gldL*, *gldM*, *gldN*, *sprA*, *sprE*, *sprT*. A '-' indicates that three or fewer of these genes were present.