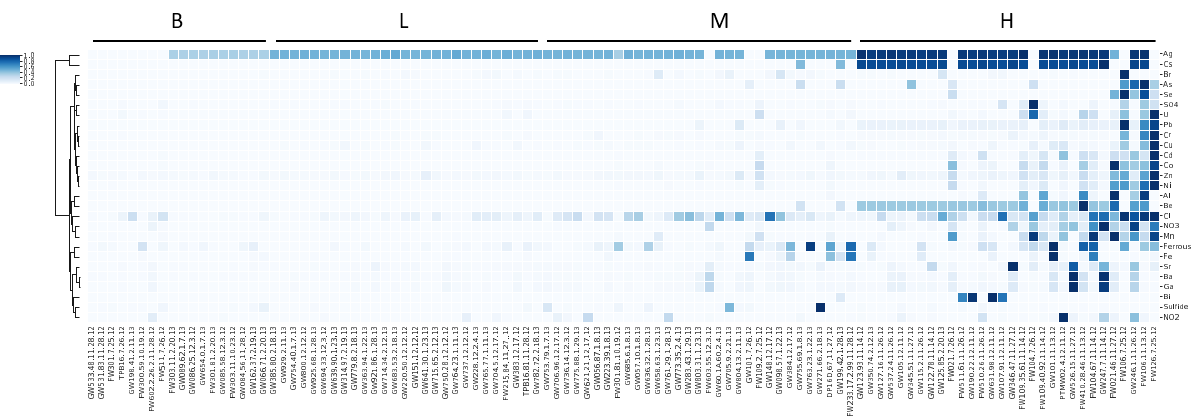
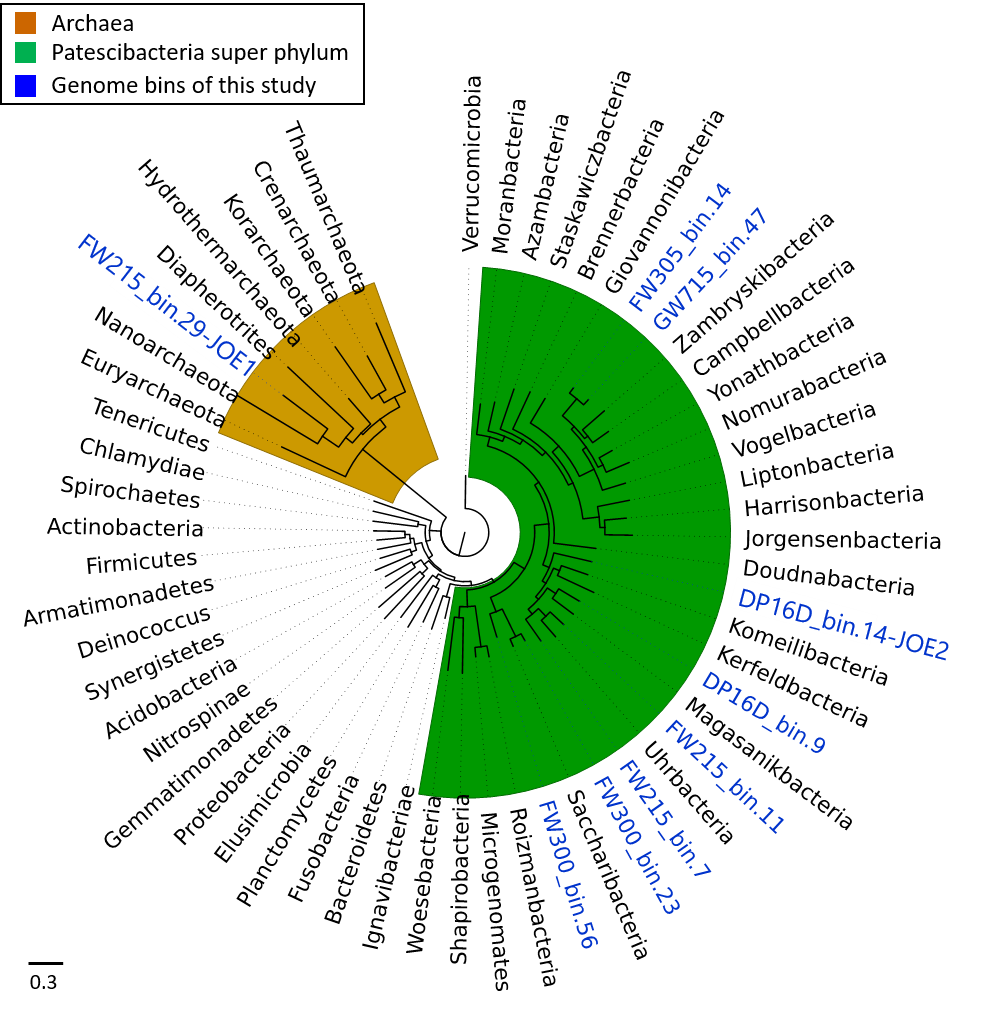
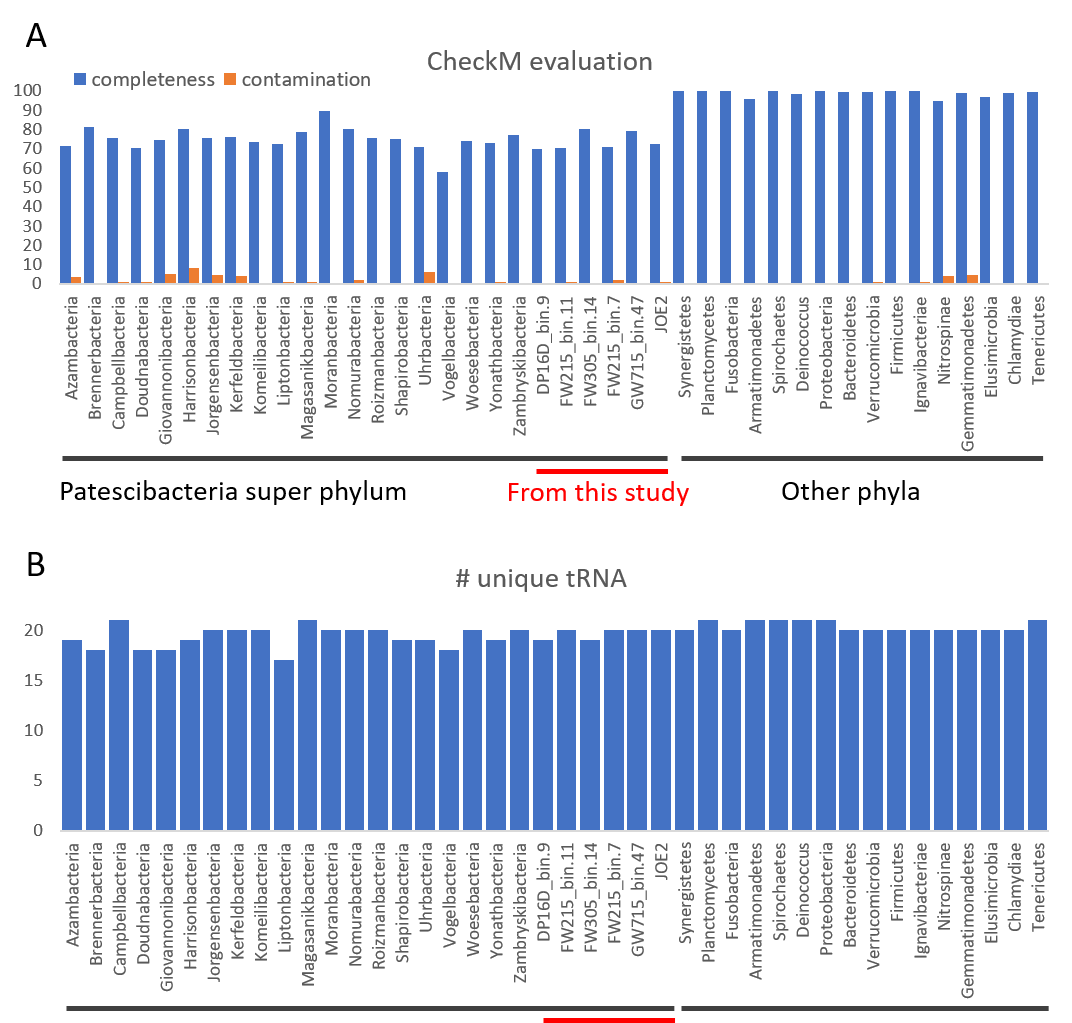
**Supplementary materials**

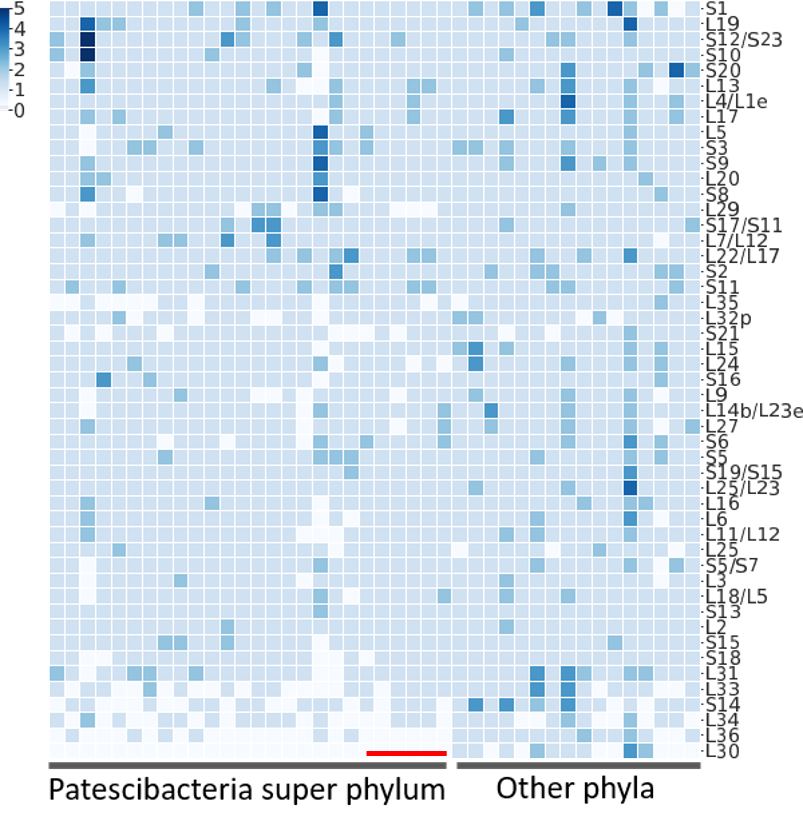
**Figure S1.** Heatmap showing the profile of contaminants in the background (B), low (L), mediate (M) and high (H) contamination wells. The concentrations of each contaminant were scaled linearly [(X-min)/max] to 0-1 for comparison.



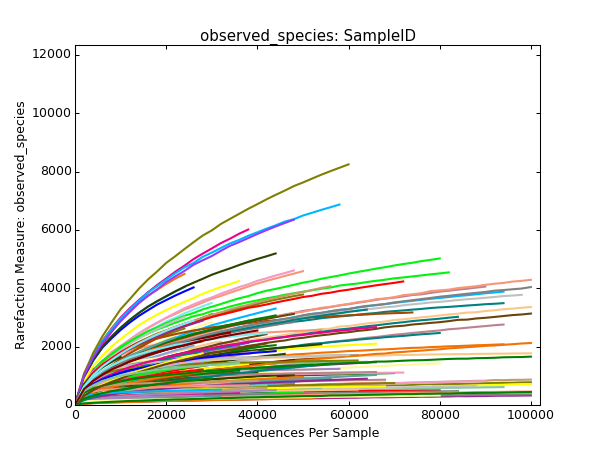
**Figure S2.** Maximum Likelihood (ML) tree of well-established bacterial and archaeal phyla, *Patescibacteria* superphylum and Candidate phyla of this study based on concatenated rp16 genes.



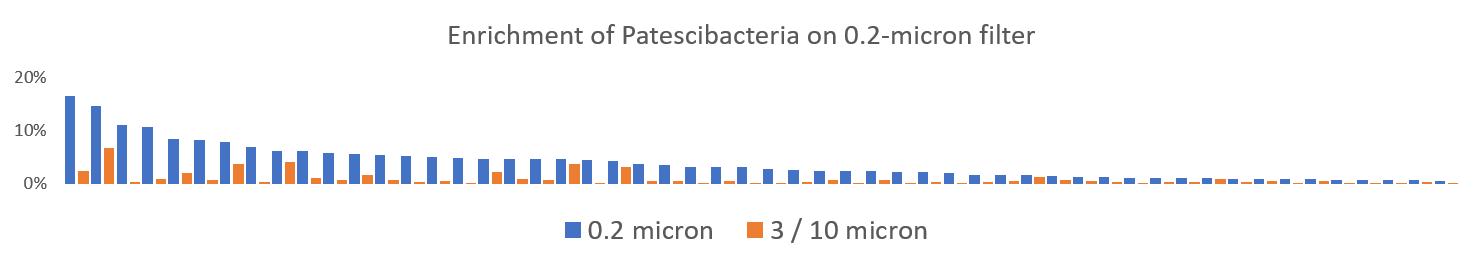
**Figure S3.** Completeness evaluation of genome bins based on CheckM analysis (A) and number of unique tRNA genes (B).



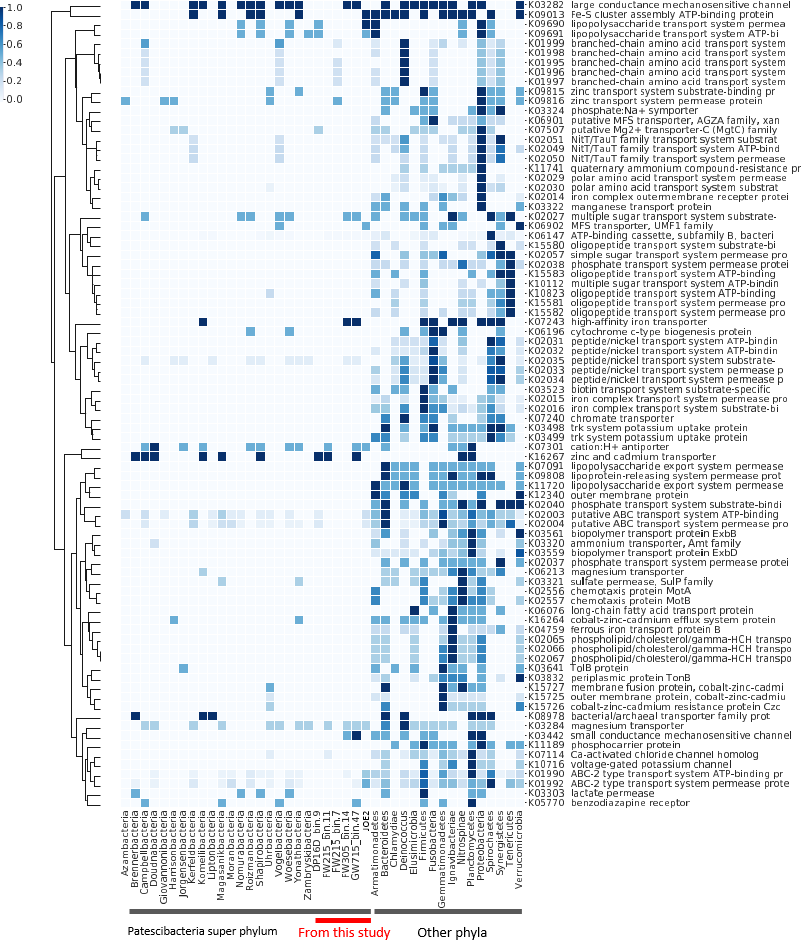
**Figure S4.** Comparison of ribosomal protein genes in the *Patescibacteria* superphylum and the other phyla.



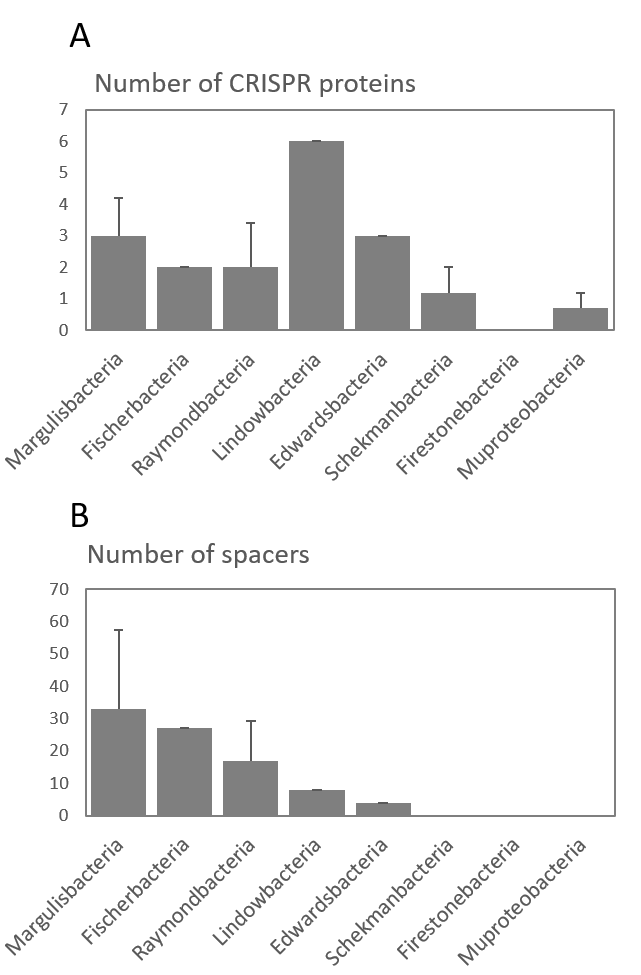
**Figure S5.** The rarefaction curve of the sequences showing the diversity index of observed OTUs and Shannon. The curves were based on calculation of diversity with step size of 2000 and iteration number of 10.



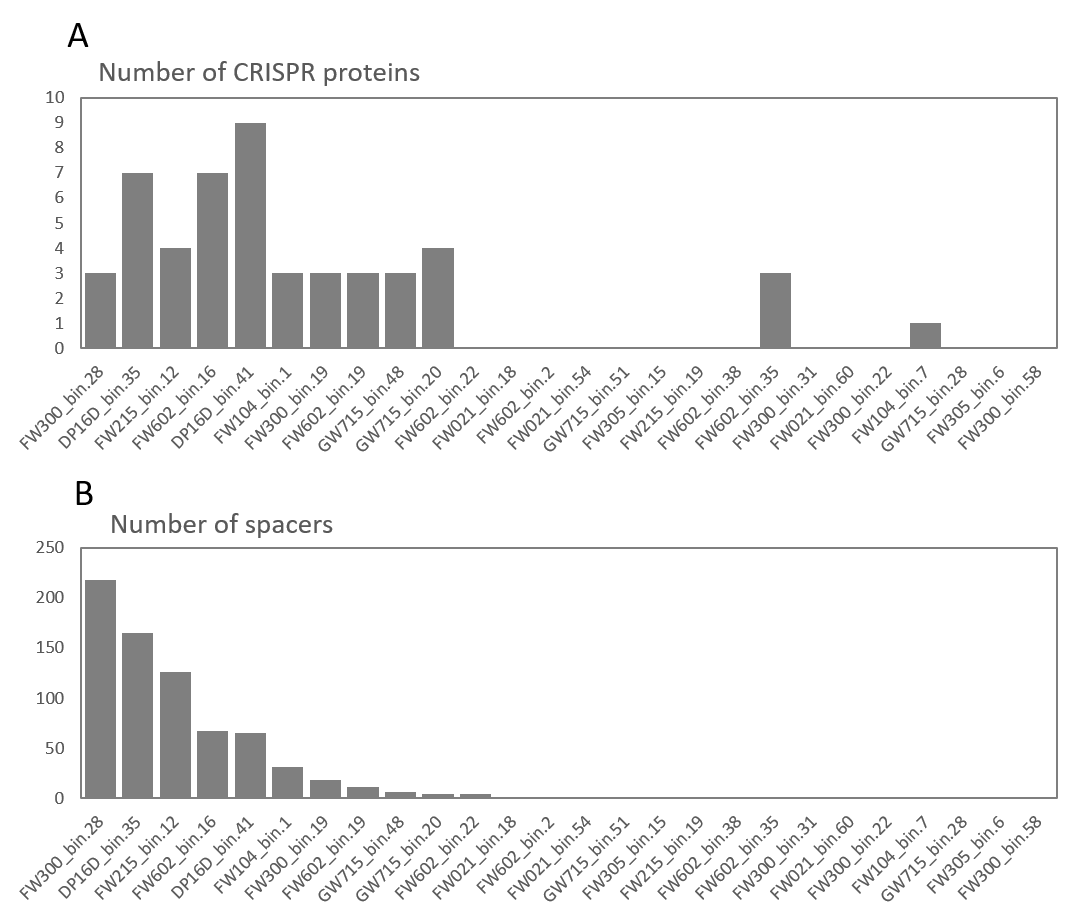
**Figure S6** The enrichment of *Patescibacteria* cells on the 0.2-micron filter in comparison to the 10 or 3 micron filter (showing 108 sample with *Patescibacteria* abundance >0.5% in 0.2-micron filter).



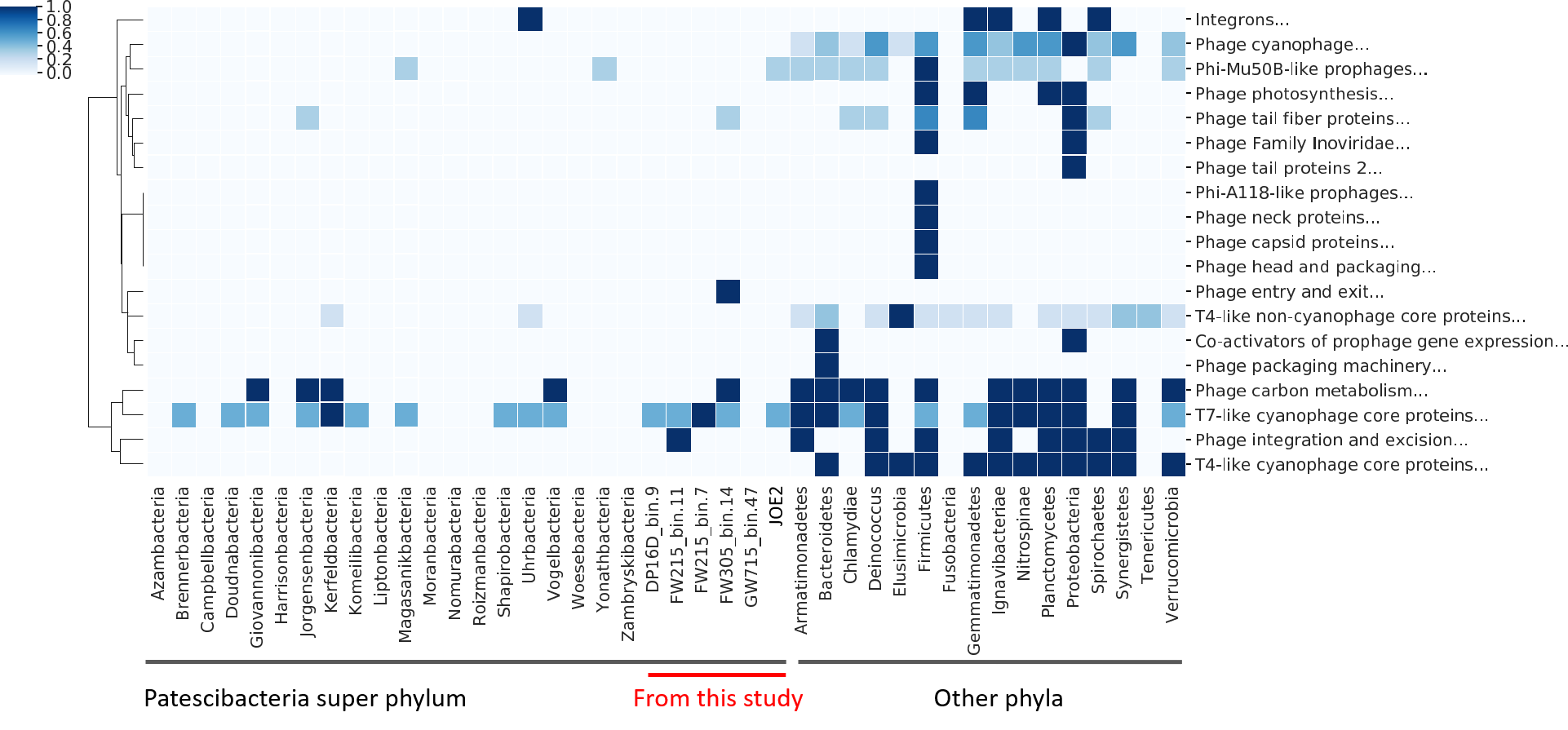
**Figure S7.** Comparison of transporter proteins in the superphylum *Patescibacteria* and other phyla.



**Figure S8.** Number of CRISPR proteins (A) and CRISPR spacers (B) in the non-*Patescibacteria* phyla of Jillian Banfield’s binning.



**Figure S9.** Number of CRISPR proteins (A) and CRISPR spacers (B) in the non-*Patescibacteria* phyla of this study.

**Figure S10.** A heatmap of comparison of phage-associated proteins including phage structure, phage integration and regulation in the *Patescibacteria* superphylum and the other phyla. The color indicates the standardized number of phage proteins in each genome / bin.

**Table S1.** Metadata of the ground water samples. See Figure S1 for the contaminant concentrations and the categorization of wells.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Sample ID | Collection Date | Longitude | Latitude | Depth (m) | Conductivity (S/m) | Dissovled Oxygen (mg/L) | Temperature (°C) | pH |
| DP16D-67-11-27-12 | 11/27/2012 | -84.274678 | 35.9755 | 22.2 | 661 | 0.26 | 17.05 | 6.67 |
| FW021-46-11-27-12 | 11/27/2012 | -84.272033 | 35.977747 | 22.0 | 7967 | 0.27 | 16.41 | 3.43 |
| FW104-67-11-14-12 | 11/14/2012 | -84.273562 | 35.97736 | 44.4 | 13660 | 1.18 | 14.57 | 5.22 |
| FW106-11-13-12 | 11/13/2012 | -84.273484 | 35.977298 | 45.0 | 7864 | 0.18 | 14.84 | 3.55 |
| FW109-35-61-11-14-12 | 11/14/2012 | -84.273577 | 35.977374 | 34.9 | 1531 | 0.19 | 16.89 | 3.68 |
| FW109-40-92-11-14-12 | 11/14/2012 | -84.273577 | 35.977374 | 39.8 | 2726 | 0.29 | 12.42 | 4.08 |
| FW126-7-25-12 | 7/25/2012 | -84.273414 | 35.977358 | 49.6 | 16780 | 0.2 | 33.95 | 3.1 |
| FW215-84-11-27--12 | 11/27/2012 | -84.274722 | 35.975715 | 18.6 | 637.4 | 0.13 | 17.88 | 6.6 |
| FW233-17-2-99-11-28-12 | 11/28/2012 | -84.274723 | 35.975743 | 17.3 | 801.9 | 0.26 | 15.74 | 6.37 |
| FW300-59-10-19-12 | 10/19/2012 | -84.336176 | 35.941092 | 25.0 | 378.9 | 0.28 | 15.54 | 6.59 |
| FW301-7-25-12 | 7/25/2012 | -84.336181 | 35.941069 | 21.9 | 205 | 0.45 | 22.6 | 6.08 |
| FW301-81-10-19-12 | 10/19/2012 | -84.336181 | 35.941069 | 21.9 | 334.4 | 0.78 | 15.77 | 6.68 |
| FW301-81-2-20-13 | 2/20/2013 | -84.336181 | 35.941069 | 21.9 | 44.19 | 3.58 | 12.2 | 5.42 |
| FW303-11-10-23-12 | 10/23/2012 | -84.336279 | 35.941139 | 20.2 | 316.4 | 0.71 | 15.82 | 7.16 |
| FW303-11-2-20-13 | 2/20/2013 | -84.336279 | 35.941139 | 20.2 | 304.5 | 1.75 | 12.86 | 7.28 |
| FW410-28-46-11-13-12 | 11/13/2012 | -84.273957 | 35.977136 | 27.5 | 3355 | 0.34 | 16.02 | 3.69 |
| FW510-26-11-26-12 | 11/26/2012 | -84.272082 | 35.978585 | 25.8 | 1800 | 0.14 | 16.37 | 4.01 |
| FW511-61-11-26-12 | 11/26/2012 | -84.272035 | 35.978501 | 22.3 | 308.9 | 5.97 | 18.95 | 4.96 |
| FW511-7-26-12 | 7/26/2012 | -84.272035 | 35.978501 | 22.3 | 297.4 | 1.32 | 23.23 | 5.01 |
| FW602-2-26-2-11-28-12 | 11/28/2012 | -84.278931 | 35.974046 | 25.9 | 1704 | 0.41 | 16.42 | 6.48 |
| FW603-55-12-3-12 | 12/3/2012 | -84.278791 | 35.973802 | 32.8 | 6913 | 0.54 | 17.85 | 6.08 |
| GW056-87-1-8-13 | 1/8/2013 | -84.300532 | 35.957762 | 18.1 | 784.1 | 0.66 | 12.87 | 6.87 |
| GW057-10-1-8-13 | 1/8/2013 | -84.300523 | 35.957737 | 55.2 | 1003 | 0.71 | 15.08 | 6.72 |
| GW066-71-2-20-13 | 2/20/2013 | -84.281617 | 35.9708 | 22.8 | 69.32 | 0.48 | 11.91 | 6.2 |
| GW084-56-11-28-12 | 11/28/2012 | -84.28314 | 35.973088 | 27.8 | 339.7 | 0.19 | 15.66 | 7.15 |
| GW085-58-12-3-12 | 12/3/2012 | -84.281474 | 35.9725 | 58.8 | 365.1 | 2.5 | 19.2 | 7.29 |
| GW086-25-12-3-12 | 12/3/2012 | -84.281497 | 35.972458 | 29.6 | 275.1 | 0.63 | 20.36 | 6.47 |
| GW089-62-1-7-13 | 1/7/2013 | -84.299049 | 35.965917 | 25.0 | 327.8 | 0.37 | 12.94 | 7.95 |
| GW098-57-1-22-13 | 1/22/2013 | -84.286314 | 35.968022 | 103.4 | 1331 | 0.11 | 16.01 | 6.43 |
| GW101-11-13-12 | 11/13/2012 | -84.274117 | 35.97732 | 16.3 | 1721 | 0.96 | 18.12 | 6.81 |
| GW101-7-26-12 | 7/26/2012 | -84.274117 | 35.97732 | 16.3 | 934.8 | 1.06 | 24.98 | 7.2 |
| GW105-12-11-12 | 12/11/2012 | -84.271679 | 35.979239 | 16.1 | 1674 | 0.39 | 14.72 | 6.43 |
| GW107-91-12-11-12 | 12/11/2012 | -84.269997 | 35.979044 | 12.5 | 2819 | 0.37 | 20.36 | 6.18 |
| GW115-2-11-26-12 | 11/26/2012 | -84.273333 | 35.980507 | 52.0 | 581.6 | 0.41 | 17.45 | 7.03 |
| GW122-78-11-14-12 | 11/14/2012 | -84.273278 | 35.976124 | 142.0 | 1454 | 0 | 16.66 | 6.64 |
| GW123-93-11-14-12 | 11/14/2012 | -84.273314 | 35.976106 | 572.0 | 1631 | 0.02 | 16.61 | 9.99 |
| GW125-85-2-20-13 | 2/20/2013 | -84.271975 | 35.976523 | 552.0 | 2538 | 0.51 | 14.19 | 9.99 |
| GW127-16-11-26-12 | 11/26/2012 | -84.273424 | 35.976405 | 22.8 | 824.9 | 0.12 | 16.97 | 6.55 |
| GW148-12-17-12 | 12/17/2012 | -84.238597 | 35.993332 | 10.6 | 1399 | 1.32 | 16.53 | 6.45 |
| GW151-12-12-12 | 12/12/2012 | -84.236973 | 35.993413 | 96.0 | 432.2 | 0.25 | 15.4 | 7.07 |
| GW162-37-2-19-13 | 2/19/2013 | -84.296806 | 35.968495 | 125.0 | 247.6 | 0.26 | 14.3 | 8.21 |
| GW190-22-12-11-12 | 12/11/2012 | -84.271177 | 35.980705 | 25.9 | 345.4 | 0.92 | 17.91 | 6.69 |
| GW198-41-2-11-13 | 2/11/2013 | -84.244751 | 35.994113 | 26.5 | 468.2 | 3.48 | 16.1 | 6.06 |
| GW199-42-1-28-13 | 1/28/2013 | -84.244432 | 35.993718 | 22.5 | 581.6 | 0.5 | 14.29 | 6.53 |
| GW220-50-12-12-12 | 12/12/2012 | -84.236976 | 35.993381 | 44.7 | 410.7 | 0.52 | 13.09 | 7.49 |
| GW223-39-1-8-13 | 1/8/2013 | -84.239517 | 35.991954 | 90.0 | 466.5 | 0.41 | 16.41 | 6.83 |
| GW228-12-2-4-13 | 2/4/2013 | -84.283453 | 35.96866 | 100.0 | 282.4 | 0.17 | 10.92 | 9.31 |
| GW246-1-11-26-12 | 11/26/2012 | -84.272935 | 35.977144 | 74.6 | 18580 | 0.19 | 17.56 | 4.48 |
| GW247-7-11-14-12 | 11/14/2012 | -84.272726 | 35.9773 | 74.9 | 20620 | 0.09 | 17.5 | 5.88 |
| GW271-66-2-18-13 | 2/18/2013 | -84.27058705 | 35.97989558 | 29.4 | 521.9 | 0.03 | 15.57 | 7.71 |
| GW283-43-1-29-13 | 1/29/2013 | -84.244414 | 35.991366 | 20.0 | 1089 | 0.07 | 18.01 | 6.95 |
| GW314-97-2-19-13 | 2/19/2013 | -84.27177607 | 35.97587976 | 113.0 | 602.7 | 0.23 | 14.69 | 7.37 |
| GW345-51-11-27-12 | 11/27/2012 | -84.276925 | 35.97508 | 26.0 | 183.8 | 1.19 | 15.07 | 5.23 |
| GW346-47-11-27-12 | 11/27/2012 | -84.276916 | 35.975088 | 64.6 | 6931 | 0.26 | 14.79 | 6.58 |
| GW350-74-2-12-13 | 2/12/2013 | -84.268309 | 35.978922 | 43.4 | 545 | 0.02 | 17.98 | 6.67 |
| GW363-94-1-22-13 | 1/22/2013 | -84.287521 | 35.969048 | 75.0 | 424.9 | 0.03 | 15.28 | 9.13 |
| GW383-12-17-12 | 12/17/2012 | -84.239422 | 35.992878 | 23.1 | 521.7 | 4.54 | 17.43 | 7.11 |
| GW384-12-17-12 | 12/17/2012 | -84.239429 | 35.992922 | 55.7 | 802.9 | 0.08 | 16.95 | 6.64 |
| GW385-80-2-18-13 | 2/18/2013 | -84.239425 | 35.992899 | 178.7 | 780.09 | 0.29 | 15.36 | 9.19 |
| GW526-15-11-27-12 | 11/27/2012 | -84.276907 | 35.975102 | 123.0 | 9468 | 0.14 | 14.54 | 7.95 |
| GW531-83-11-28-12 | 11/28/2012 | -84.281558 | 35.973944 | 38.2 | 39.68 | 4.32 | 15.07 | 5.49 |
| GW533-48-11-28-12 | 11/28/2012 | -84.281393 | 35.974108 | 30.1 | 118 | 1.54 | 15.92 | 6.27 |
| GW537-24-11-26-12 | 11/26/2012 | -84.280229 | 35.973362 | 23.0 | 2618 | 0.05 | 15.6 | 6.49 |
| GW60-1A-60-2-4-13 | 2/4/2013 | -84.248782 | 35.987834 | 23.2 | 1076 | 0.23 | 19.23 | 7.38 |
| GW621-21-12-17-12 | 12/17/2012 | -84.2909 | 35.964088 | 40.5 | 356.4 | 0.17 | 14.64 | 7.19 |
| GW631-98-12-11-12 | 12/11/2012 | -84.2704 | 35.97923 | 15.0 | 318.8 | 0.26 | 16.86 | 4.32 |
| GW636-32-1-28-13 | 1/28/2013 | -84.287902 | 35.967252 | 117.0 | 317.9 | 0.2 | 12.17 | 8.87 |
| GW639-90-1-23-13 | 1/23/2013 | -84.291404 | 35.965809 | 125.5 | 845.3 | 0.32 | 12.05 | 9.2 |
| GW641-30-1-23-13 | 1/23/2013 | -84.291542 | 35.965931 | 24.0 | 25.59 | 7.22 | 12.64 | 5.25 |
| GW654-0-1-7-13 | 1/7/2013 | -84.302538 | 35.962761 | 15.3 | 269 | 2.35 | 13.01 | 7.19 |
| GW658-63-1-23-13 | 1/23/2013 | -84.244105 | 35.991761 | 18.8 | 454.3 | 0.03 | 19.06 | 6.4 |
| GW683-53-2-18-13 | 2/18/2013 | -84.299249 | 35.957053 | 196.8 | 393.6 | 5.42 | 13.82 | 7.49 |
| GW685-6-1-8-13 | 1/8/2013 | -84.300271 | 35.957771 | 138.3 | 906.1 | 0.1 | 14.55 | 6.88 |
| GW694-33-12-3-12 | 12/3/2012 | -84.290954 | 35.963467 | 204.5 | 444.6 | 0.15 | 15.11 | 7.3 |
| GW704-5-12-17-12 | 12/12/2012 | -84.290837 | 35.96353 | 256.0 | 529.2 | 0.99 | 13.7 | 7.62 |
| GW705-9-2-21-13 | 2/21/2013 | -84.29107919 | 35.96372889 | 307.0 | 891.7 | 0.33 | 12.37 | 9.19 |
| GW706-96-12-17-12 | 12/17/2012 | -84.291005 | 35.963775 | 182.5 | 710.4 | 0.04 | 14.11 | 7.88 |
| GW714-34-2-12-13 | 2/12/2013 | -84.313845 | 35.949511 | 145.0 | 514.2 | 0.14 | 13.92 | 7.48 |
| GW715-65-2-12-13 | 2/12/2013 | -84.313801 | 35.949545 | 43.1 | 532.9 | 5.47 | 14.59 | 6.65 |
| GW736-14-12-3-12 | 12/3/2012 | -84.280642 | 35.970896 | 102.4 | 916.7 | 0.13 | 15.88 | 6.64 |
| GW737-12-12-12 | 12/12/2012 | -84.280741 | 35.97079 | 89.4 | 937.2 | 0.33 | 13.53 | 6.66 |
| GW750-28-12-12-12 | 12/12/2012 | -84.235312 | 35.994376 | 72.3 | 367.6 | 0.23 | 15.12 | 7.11 |
| GW753-79-1-7-13 | 1/7/2012 | -84.241126 | 35.993391 | 70.3 | 215 | 0.17 | 15.94 | 10.48 |
| GW754-40-1-7-13 | 1/7/2013 | -84.241189 | 35.993378 | 23.9 | 176.6 | 1.29 | 15.91 | 3.13 |
| GW755-69-1-8-13 | 1/8/2013 | -84.242031 | 35.994769 | 59.9 | 386.4 | 1.12 | 14.9 | 9.34 |
| GW761-29-1-28-13 | 1/28/2013 | -84.250491 | 35.989904 | 15.2 | 380.9 | 4.72 | 15.96 | 6.59 |
| GW763-23-1-22-13 | 1/22/2013 | -84.240111 | 35.992222 | 64.8 | 699.5 | 0.13 | 17.11 | 6.65 |
| GW764-23-1-11-13 | 1/11/2013 | -84.257055 | 35.989269 | 31.5 | 197.1 | 0.95 | 19.06 | 8.57 |
| GW765-77-1-11-13 | 1/11/2013 | -84.256997 | 35.989297 | 58.6 | 638.8 | 0.23 | 19.14 | 6.68 |
| GW773-35-2-4-13 | 2/4/2013 | -84.246683 | 35.991147 | 56.2 | 330.1 | 0.24 | 13.43 | 7.46 |
| GW775-88-1-29-13 | 1/29/2013 | -84.245848 | 35.989595 | 58.0 | 583.2 | 0.97 | 19.12 | 7.2 |
| GW779-8-2-18-13 | 2/18/2013 | -84.25334197 | 35.9886503 | 62.0 | 460.9 | 0.2 | 16.74 | 9.55 |
| GW782-72-2-18-13 | 2/18/2013 | -84.255601 | 35.985734 | 34.9 | 556.5 | 2.65 | 17.49 | 7.52 |
| GW800-12-12-12 | 12/12/2012 | -84.28178 | 35.968949 | 29.4 | 379.1 | 8.01 | 13.13 | 6.7 |
| GW803-31-1-23-13 | 1/23/2013 | -84.243755 | 35.991689 | 23.2 | 397.7 | 5.11 | 13.68 | 5.4 |
| GW804-13-2-11-13 | 2/11/2013 | -84.24405271 | 35.99152444 | 23.5 | 603.1 | 6.57 | 15.48 | 4.91 |
| GW921-86-1-28-13 | 1/28/2013 | -84.287507 | 35.970344 | 48.0 | 465.5 | 0.64 | 15.57 | 7.46 |
| GW925-68-1-28-13 | 1/28/2013 | -84.287535 | 35.970325 | 147.0 | 654.7 | 0.35 | 11.97 | 9.79 |
| GW928-54-2-11-13 | 2/11/2013 | -84.264657 | 35.987421 | 43.2 | 241.5 | 0.21 | 16.65 | 6.69 |
| GW929-2-11-13 | 2/11/2013 | -84.264601 | 35.987452 | 28.0 | 34.79 | 3.09 | 16.07 | 5.18 |
| PTMW02-4-12-11-12 | 12/11/2012 | -84.276332 | 35.975573 | 44.7 | 9307 | 0.16 | 14.42 | 4.72 |
| TPB16-7-26-12 | 7/26/2012 | -84.274687 | 35.975643 | 15.3 | 1444 | 0.18 | 26.79 | 7.1 |
| TPB16-81-11-28-12 | 11/28/2012 | -84.274687 | 35.975643 | 15.3 | 843.3 | 0.35 | 18.59 | 6.58 |

**Table S2.** Summary of the raw reads and qualified reads of the metagenomic data.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Sample ID | Raw reads (million) | Raw base (Gbp) | Duplication | | Quality trimming and filtering | | | | | | | | Total base (HQ reads, Gbp) |
| Forward read | | | | Reverse read | | | |
| Deduplicated reads | Duplication rate | No. of HQ reads (million) | No. of bases (Gbp) | No. of HQ bases (Gbp) | Q20 (percentage of HQ bases) | No. of HQ reads (million) | No. of bases (Gbp) | No. of HQ bases (Gbp) | Q20 (percentage of HQ base) |
| DP16D | 218.2 | 32.9 | 213.7 | 2.1% | 99.9 | 15.0 | 14.6 | 97.2% | 99.9 | 15.0 | 14.0 | 93.8% | 30.0 |
| FW021 | 236.4 | 35.7 | 229.6 | 2.9% | 92.1 | 13.9 | 13.5 | 97.4% | 92.1 | 13.8 | 12.7 | 92.3% | 27.7 |
| FW104 | 237.7 | 35.9 | 168.7 | 29.0% | 50.1 | 7.5 | 7.1 | 95.1% | 50.1 | 7.5 | 6.5 | 87.5% | 15.0 |
| FW106 | 180.0 | 27.2 | 159.1 | 11.6% | 62.1 | 9.4 | 8.8 | 94.0% | 62.1 | 9.3 | 8.4 | 90.2% | 18.7 |
| FW106-02 | 300.6 | 45.4 | 289.1 | 3.8% | 133.6 | 20.1 | 19.4 | 96.7% | 133.6 | 20.0 | 18.7 | 93.3% | 40.1 |
| FW106-10 | 549.5 | 83.0 | 531.2 | 3.3% | 242.3 | 36.5 | 34.7 | 95.0% | 242.3 | 36.3 | 33.7 | 92.8% | 72.8 |
| FW215 | 190.5 | 28.8 | 186.8 | 2.0% | 87.6 | 13.2 | 12.8 | 97.2% | 87.6 | 13.1 | 12.2 | 93.2% | 26.3 |
| FW300 | 310.1 | 46.8 | 302.5 | 2.4% | 137.4 | 20.7 | 20.2 | 97.6% | 137.4 | 20.5 | 18.8 | 91.3% | 41.2 |
| FW301 | 190.7 | 28.8 | 187.3 | 1.8% | 84.3 | 12.7 | 12.4 | 97.5% | 84.3 | 12.6 | 11.7 | 92.5% | 25.3 |
| FW301-02 | 373.1 | 56.3 | 345.7 | 7.4% | 169.3 | 25.5 | 25.1 | 98.4% | 169.3 | 25.5 | 24.6 | 96.7% | 51.0 |
| FW301-10 | 341.8 | 51.6 | 315.1 | 7.8% | 154.3 | 23.3 | 22.9 | 98.5% | 154.3 | 23.2 | 22.5 | 96.8% | 46.5 |
| FW305 | 178.9 | 27.0 | 135.6 | 24.2% | 50.5 | 7.6 | 7.4 | 96.9% | 50.5 | 7.6 | 6.8 | 90.3% | 15.2 |
| FW602 | 174.1 | 26.3 | 170.4 | 2.1% | 79.1 | 11.9 | 11.6 | 97.1% | 79.1 | 11.8 | 11.0 | 93.1% | 23.7 |
| GW199 | 229.0 | 34.6 | 124.3 | 45.7% | 41.7 | 6.3 | 6.0 | 95.3% | 41.7 | 6.2 | 5.5 | 89.0% | 12.5 |
| GW715 | 264.1 | 39.9 | 244.2 | 7.5% | 104.3 | 15.7 | 15.3 | 97.6% | 104.3 | 15.6 | 14.3 | 91.8% | 31.3 |
| GW928 | 239.2 | 36.1 | 195.9 | 18.1% | 49.0 | 7.4 | 7.0 | 95.6% | 49.0 | 7.3 | 6.5 | 89.0% | 14.7 |
| Total | 4213.7 | 636.3 | 3799.1 | - | 1637.8 | 246.5 | 238.8 | - | 1637.8 | 245.4 | 228.1 | - | 491.8 |
| Mean | 263.4 | 39.8 | 237.4 | 10.7% | 102.4 | 15.4 | 14.9 | 96.7% | 102.4 | 15.3 | 14.3 | 92.1% | 30.7 |
| SD | 97.1 | 14.7 | 102.3 | 12.5% | 54.0 | 8.1 | 7.9 | 1.3% | 54.0 | 8.1 | 7.8 | 2.6% | 16.2 |

**Table S3.** Metagenomic assembly of the samples plus supplementary sequence. Contigs with length >500 bp were summarized.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Sample ID | Contig number | Total base of contigs | Max sequence length | N50 length | GC content |
| DP16D | 118677 | 1.91E+08 | 273343 | 1952 | 54.77% |
| FW021 | 70823 | 2.09E+08 | 588991 | 8788 | 61.52% |
| FW104 | 13504 | 24809230 | 116275 | 2560 | 57.04% |
| FW106 | 18736 | 44868411 | 560079 | 12032 | 61.69% |
| FW106-02 | 18472 | 57771662 | 430515 | 11148 | 61.89% |
| FW106-10 | 43324 | 1.13E+08 | 430652 | 8514 | 60.03% |
| FW215 | 139593 | 2.01E+08 | 643366 | 1568 | 52.14% |
| FW300 | 175376 | 2.46E+08 | 735234 | 1453 | 55.77% |
| FW301 | 66427 | 86231473 | 199693 | 1279 | 60.14% |
| FW301-02 | 91051 | 1.18E+08 | 251934 | 1273 | 55.55% |
| FW305 | 42729 | 63729503 | 604198 | 1678 | 63.14% |
| FW602 | 133699 | 2.54E+08 | 1783802 | 2652 | 62.62% |
| GW199 | 6604 | 8090154 | 23002 | 1231 | 50.54% |
| GW715 | 135463 | 2.52E+08 | 1047723 | 2740 | 62.33% |
| GW928 | 45056 | 71729291 | 577390 | 1999 | 60.57% |

\* The assembly of the sample FW301-10 failed due to super large data size and high diversity of community.

**Table S4.** The alignment rates of each sample’s reads to its assembly. The alignment rates were calculated by Bowtie2 and Samtools.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Sample ID | # raw reads (million) | # base of raw reads (Gbp) | # base after deduplication, quality trimming and filtering (Gbp) | Percent of high quality reads mapping to assembly |
| DP16D | 218.2 | 32.9 | 30.0 | 19.64% |
| FW021 | 236.4 | 35.7 | 27.7 | 73.13% |
| FW104 | 237.7 | 35.9 | 15.0 | 36.62% |
| FW106 | 180.0 | 27.2 | 18.7 | 73.09% |
| FW106-02 | 300.6 | 45.4 | 40.1 | 65.77% |
| FW106-10 | 549.5 | 83.0 | 72.8 | 63.16% |
| FW215 | 190.5 | 28.8 | 26.3 | 17.36% |
| FW300 | 310.1 | 46.8 | 41.2 | 8.47% |
| FW301 | 190.7 | 28.8 | 25.3 | 3.94% |
| FW301-02 | 373.1 | 56.3 | 51.0 | 3.35% |
| FW305 | 178.9 | 27.0 | 15.2 | 16.91% |
| FW602 | 174.1 | 26.3 | 23.7 | 30.72% |
| GW199 | 229.0 | 34.6 | 12.5 | 11.92% |
| GW715 | 264.1 | 39.9 | 31.3 | 23.74% |
| GW928 | 239.2 | 36.1 | 14.7 | 31.87% |

**Table S5**. Profiles of genome bins generated by MetaBat. Only genome bins with completeness >70% and contamination <10% are listed.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Bin ID | Taxonomic classification (by pplacer of CheckM) | Complet  eness | Contam  ination | Contig number | Total base of contigs | Max sequence length | N50 length |
| DP16D\_bin.48 | k\_\_Bacteria\_(UID3187) | 100 | 5.45 | 120 | 3.23 | 125,024 | 41,819 |
| FW021\_bin.18 | k\_\_Bacteria\_(UID1452) | 100 | 1.85 | 100 | 2.87 | 394,163 | 148,845 |
| FW106-10\_bin.31 | k\_\_Bacteria\_(UID203) | 100 | 8.62 | 333 | 4.06 | 60,718 | 20,711 |
| FW021\_bin.60 | g\_\_Mycobacterium\_(UID1816) | 99.94 | 0.58 | 75 | 6.14 | 384,008 | 140,583 |
| GW715\_bin.37 | c\_\_Alphaproteobacteria\_(UID3422) | 99.89 | 2.73 | 43 | 5.77 | 515,386 | 266,291 |
| FW106\_bin.13 | c\_\_Betaproteobacteria\_(UID3959) | 99.62 | 2.56 | 54 | 5.99 | 560,079 | 200,020 |
| FW301\_bin.9 | o\_\_Burkholderiales\_(UID4000) | 99.53 | 0.35 | 626 | 4.65 | 38,806 | 10,565 |
| FW021\_bin.57 | o\_\_Actinomycetales\_(UID1593) | 99.49 | 1.26 | 41 | 3.95 | 516,796 | 325,858 |
| FW106\_bin.9 | o\_\_Burkholderiales\_(UID4001) | 99.49 | 0.33 | 336 | 4.02 | 123,784 | 17,717 |
| FW106-10\_bin.28 | o\_\_Burkholderiales\_(UID4001) | 99.49 | 0.2 | 165 | 3.09 | 93,290 | 33,103 |
| FW305\_bin.1 | o\_\_Actinomycetales\_(UID1590) | 99.41 | 0 | 13 | 2.68 | 604,198 | 341,920 |
| FW300\_bin.58 | c\_\_Betaproteobacteria\_(UID3888) | 99.36 | 0.88 | 26 | 2.48 | 312,961 | 212,466 |
| FW305\_bin.9 | c\_\_Gammaproteobacteria\_(UID4274) | 99.21 | 1.36 | 157 | 4.60 | 249,922 | 52,387 |
| FW300\_bin.35 | c\_\_Alphaproteobacteria\_(UID3422) | 99.08 | 2.23 | 95 | 4.91 | 318,114 | 97,883 |
| GW715\_bin.44 | o\_\_Burkholderiales\_(UID4000) | 98.81 | 0 | 91 | 8.98 | 634,046 | 178,790 |
| FW021\_bin.31 | p\_\_Bacteroidetes\_(UID2591) | 98.77 | 2.37 | 301 | 4.52 | 114,523 | 25,681 |
| FW021\_bin.74 | k\_\_Bacteria\_(UID1452) | 98.77 | 1.85 | 87 | 3.03 | 196,054 | 59,548 |
| FW602\_bin.22 | k\_\_Bacteria\_(UID1452) | 98.68 | 0.99 | 38 | 4.03 | 346,778 | 186,054 |
| se\_bin.6 | f\_\_Xanthomonadaceae\_(UID4214) | 98.64 | 1.51 | 389 | 3.66 | 63,506 | 15,930 |
| DP16D\_bin.19 | c\_\_Gammaproteobacteria\_(UID4274) | 98.61 | 1.04 | 144 | 4.49 | 214,456 | 50,311 |
| FW021\_bin.21 | c\_\_Betaproteobacteria\_(UID3959) | 98.58 | 1.85 | 86 | 3.41 | 397,732 | 111,098 |
| GW715\_bin.21 | o\_\_Sphingomonadales\_(UID3310) | 98.46 | 4.91 | 295 | 4.27 | 204,652 | 32,436 |
| FW602\_bin.15 | c\_\_Betaproteobacteria\_(UID3971) | 98.42 | 6.68 | 87 | 5.85 | 600,586 | 161,352 |
| GW715\_bin.18 | c\_\_Betaproteobacteria\_(UID3959) | 98.41 | 4.65 | 343 | 3.11 | 85,893 | 25,625 |
| FW106\_bin.8 | o\_\_Burkholderiales\_(UID4000) | 98.36 | 1.87 | 38 | 4.25 | 418,061 | 154,406 |
| DP16D\_bin.35 | k\_\_Bacteria\_(UID3187) | 98.18 | 2.73 | 145 | 3.63 | 273,343 | 56,966 |
| GW715\_bin.29 | c\_\_Alphaproteobacteria\_(UID3422) | 98.05 | 3 | 114 | 3.12 | 188,491 | 55,486 |
| FW602\_bin.18 | o\_\_Rhizobiales\_(UID3642) | 98.02 | 0.79 | 27 | 3.12 | 790,923 | 373,877 |
| FW106-10\_bin.30 | f\_\_Xanthomonadaceae\_(UID4214) | 97.99 | 1.12 | 49 | 3.38 | 365,303 | 124,146 |
| FW301-02\_bin.23 | o\_\_Rhodospirillales\_(UID3754) | 97.99 | 1.45 | 353 | 2.05 | 27,717 | 7,584 |
| FW215\_bin.12 | k\_\_Bacteria\_(UID2570) | 97.98 | 0 | 47 | 4.20 | 643,366 | 175,842 |
| GW715\_bin.31 | o\_\_Rhodospirillales\_(UID3754) | 97.97 | 1.49 | 50 | 6.46 | 924,814 | 338,475 |
| FW021\_bin.58 | f\_\_Xanthomonadaceae\_(UID4214) | 97.82 | 2.5 | 136 | 3.60 | 164,026 | 40,809 |
| FW106-02\_bin.9 | f\_\_Xanthomonadaceae\_(UID4214) | 97.66 | 3.35 | 308 | 3.53 | 69,506 | 17,558 |
| FW106-02\_bin.10 | f\_\_Xanthomonadaceae\_(UID4214) | 97.52 | 1.21 | 456 | 3.60 | 73,209 | 12,337 |
| FW300\_bin.28 | k\_\_Bacteria\_(UID3187) | 97.48 | 3.36 | 45 | 2.88 | 201,346 | 99,979 |
| FW106-02\_bin.3 | f\_\_Xanthomonadaceae\_(UID4214) | 97.47 | 2.67 | 203 | 3.81 | 235,300 | 41,120 |
| FW021\_bin.48 | k\_\_Bacteria\_(UID1452) | 97.38 | 3.94 | 90 | 3.19 | 173,571 | 62,330 |
| FW021\_bin.27 | o\_\_Burkholderiales\_(UID4000) | 97.35 | 1.03 | 122 | 3.14 | 153,140 | 39,867 |
| FW021\_bin.29 | f\_\_Xanthomonadaceae\_(UID4214) | 97.31 | 0.73 | 76 | 3.60 | 168,646 | 65,296 |
| se\_bin.5 | f\_\_Xanthomonadaceae\_(UID4214) | 97.29 | 3.21 | 97 | 3.89 | 230,714 | 76,916 |
| FW106-10\_bin.33 | f\_\_Xanthomonadaceae\_(UID4214) | 97.24 | 3.56 | 139 | 3.08 | 235,696 | 50,340 |
| FW106-02\_bin.7 | c\_\_Gammaproteobacteria\_(UID4202) | 97.21 | 2.83 | 442 | 3.07 | 34,202 | 8,847 |
| FW301-02\_bin.25 | o\_\_Burkholderiales\_(UID4000) | 97 | 3.54 | 453 | 4.91 | 76,807 | 15,656 |
| FW602\_bin.35 | c\_\_Gammaproteobacteria\_(UID4267) | 96.8 | 0.38 | 13 | 3.53 | 1,783,802 | 1,783,802 |
| FW300\_bin.52 | k\_\_Bacteria\_(UID3187) | 96.76 | 3.92 | 250 | 2.67 | 98,754 | 26,967 |
| GW928\_bin.16 | k\_\_Bacteria\_(UID3187) | 96.76 | 3.64 | 23 | 3.26 | 577,390 | 321,837 |
| FW106-10\_bin.21 | c\_\_Betaproteobacteria\_(UID3959) | 96.74 | 2.84 | 61 | 3.24 | 430,652 | 262,923 |
| GW715\_bin.16 | c\_\_Alphaproteobacteria\_(UID3305) | 96.61 | 0.65 | 66 | 6.02 | 363,860 | 176,897 |
| GW715\_bin.19 | f\_\_Rhodocyclaceae\_(UID3972) | 96.56 | 1.04 | 151 | 2.67 | 137,154 | 36,883 |
| FW106\_bin.6 | c\_\_Gammaproteobacteria\_(UID4202) | 96.49 | 1.36 | 139 | 3.78 | 241,417 | 55,622 |
| FW602\_bin.10 | c\_\_Betaproteobacteria\_(UID3959) | 96.45 | 1.18 | 169 | 3.56 | 106,972 | 30,446 |
| GW715\_bin.15 | c\_\_Deltaproteobacteria\_(UID3216) | 96.45 | 3.93 | 197 | 9.40 | 502,942 | 122,654 |
| FW300\_bin.22 | k\_\_Bacteria\_(UID3187) | 96.36 | 8.18 | 416 | 2.35 | 34,885 | 9,381 |
| FW602\_bin.2 | c\_\_Gammaproteobacteria\_(UID4202) | 96.29 | 4.59 | 187 | 3.96 | 135,350 | 35,064 |
| GW715\_bin.6 | k\_\_Bacteria\_(UID203) | 96.24 | 7.21 | 249 | 5.26 | 205,334 | 57,882 |
| FW106-10\_bin.17 | c\_\_Betaproteobacteria\_(UID3959) | 96.21 | 0.54 | 778 | 3.14 | 16,568 | 4,816 |
| GW715\_bin.41 | o\_\_Actinomycetales\_(UID1593) | 96.21 | 1.52 | 20 | 3.77 | 1,047,723 | 344,739 |
| FW602\_bin.16 | k\_\_Bacteria\_(UID1452) | 96.2 | 1.19 | 256 | 5.64 | 123,923 | 39,881 |
| FW104\_bin.7 | p\_\_Proteobacteria\_(UID3880) | 96.14 | 1.95 | 91 | 2.68 | 116,275 | 52,687 |
| FW104\_bin.1 | k\_\_Bacteria\_(UID3187) | 96.08 | 2.56 | 203 | 3.99 | 93,071 | 29,549 |
| FW106-10\_bin.11 | o\_\_Rhizobiales\_(UID3654) | 96.08 | 0.78 | 333 | 5.21 | 75,542 | 25,392 |
| GW715\_bin.48 | p\_\_Bacteroidetes\_(UID2591) | 96.06 | 1.72 | 318 | 2.25 | 165,550 | 37,642 |
| FW106-02\_bin.8 | g\_\_Burkholderia\_(UID4006) | 96.03 | 1.24 | 505 | 4.02 | 49,011 | 11,325 |
| FW106-10\_bin.23 | f\_\_Xanthomonadaceae\_(UID4214) | 95.81 | 0.95 | 86 | 5.90 | 284,499 | 125,043 |
| GW715\_bin.26 | f\_\_Rhodocyclaceae\_(UID3972) | 95.64 | 2.21 | 115 | 2.57 | 122,073 | 52,424 |
| FW021\_bin.3 | f\_\_Xanthomonadaceae\_(UID4214) | 95.6 | 1.7 | 78 | 3.62 | 189,940 | 75,682 |
| FW300\_bin.31 | c\_\_Alphaproteobacteria\_(UID3305) | 95.59 | 6.67 | 197 | 3.87 | 92,024 | 31,056 |
| se\_bin.2 | o\_\_Burkholderiales\_(UID4001) | 95.56 | 1.99 | 457 | 5.27 | 68,769 | 16,270 |
| FW021\_bin.26 | k\_\_Bacteria\_(UID3187) | 95.51 | 0.85 | 22 | 3.30 | 588,991 | 360,040 |
| GW715\_bin.46 | o\_\_Rhodospirillales\_(UID3754) | 95.45 | 0.25 | 176 | 5.16 | 197,652 | 46,428 |
| DP16D\_bin.41 | k\_\_Bacteria\_(UID2982) | 95.44 | 0.71 | 85 | 2.53 | 221,299 | 78,422 |
| FW215\_bin.17 | c\_\_Gammaproteobacteria\_(UID4388) | 95.33 | 3.79 | 566 | 2.76 | 34,001 | 6,904 |
| DP16D\_bin.30 | c\_\_Gammaproteobacteria\_(UID4274) | 95.14 | 0.92 | 353 | 4.65 | 75,019 | 21,150 |
| FW106-02\_bin.14 | f\_\_Xanthomonadaceae\_(UID4214) | 95.12 | 2.85 | 21 | 3.04 | 430,515 | 356,845 |
| FW021\_bin.20 | k\_\_Bacteria\_(UID1453) | 95.01 | 1.28 | 213 | 2.51 | 74,937 | 17,364 |
| FW021\_bin.4 | c\_\_Betaproteobacteria\_(UID3959) | 95 | 3.67 | 339 | 3.20 | 79,786 | 15,732 |
| FW215\_bin.19 | p\_\_Bacteroidetes\_(UID2605) | 94.85 | 0.89 | 412 | 3.49 | 45,037 | 12,920 |
| FW106-10\_bin.9 | k\_\_Bacteria\_(UID203) | 94.83 | 4.47 | 70 | 4.42 | 335,701 | 123,597 |
| FW021\_bin.54 | k\_\_Bacteria\_(UID3187) | 94.66 | 5.13 | 29 | 5.21 | 565,568 | 346,509 |
| GW715\_bin.28 | c\_\_Gammaproteobacteria\_(UID4202) | 94.57 | 1.49 | 63 | 3.57 | 199,209 | 99,515 |
| FW106-02\_bin.5 | g\_\_Burkholderia\_(UID4006) | 94.53 | 3.32 | 119 | 4.75 | 372,874 | 88,031 |
| FW300\_bin.19 | k\_\_Bacteria\_(UID2495) | 94.32 | 2.25 | 96 | 4.89 | 307,891 | 76,736 |
| FW021\_bin.37 | p\_\_Bacteroidetes\_(UID2591) | 94.09 | 1.48 | 625 | 4.98 | 62,909 | 11,185 |
| FW106-10\_bin.6 | g\_\_Burkholderia\_(UID4006) | 93.97 | 1.55 | 400 | 3.08 | 235,300 | 12,296 |
| FW300\_bin.41 | o\_\_Burkholderiales\_(UID4000) | 93.65 | 1.97 | 677 | 4.63 | 46,754 | 9,315 |
| GW928\_bin.19 | k\_\_Bacteria\_(UID3187) | 93.58 | 4.75 | 613 | 2.75 | 23,892 | 5,539 |
| FW021\_bin.35 | f\_\_Xanthomonadaceae\_(UID4214) | 93.4 | 1.4 | 29 | 2.98 | 308,486 | 179,307 |
| GW715\_bin.13 | k\_\_Bacteria\_(UID3187) | 93.35 | 3.64 | 613 | 4.20 | 46,154 | 9,597 |
| GW199\_bin.3 | k\_\_Archaea\_(UID2) | 93.13 | 6.63 | 393 | 1.56 | 23,002 | 5,356 |
| FW106\_bin.11 | o\_\_Burkholderiales\_(UID4000) | 92.93 | 5.3 | 22 | 3.26 | 463,761 | 267,194 |
| FW300\_bin.11 | o\_\_Actinomycetales\_(UID1593) | 92.83 | 3.69 | 425 | 2.27 | 108,177 | 7,809 |
| GW715\_bin.24 | f\_\_Xanthomonadaceae\_(UID4214) | 92.77 | 1.17 | 318 | 2.42 | 42,221 | 10,893 |
| FW021\_bin.42 | k\_\_Bacteria\_(UID1452) | 92.56 | 3.19 | 362 | 3.16 | 153,586 | 14,622 |
| DP16D\_bin.23 | c\_\_Betaproteobacteria\_(UID3971) | 92.07 | 2.37 | 576 | 3.12 | 25,766 | 6,981 |
| FW602\_bin.24 | c\_\_Betaproteobacteria\_(UID3971) | 91.96 | 5.56 | 492 | 4.02 | 70,999 | 12,771 |
| DP16D\_bin.2 | c\_\_Deltaproteobacteria\_(UID3216) | 91.94 | 1.33 | 313 | 2.13 | 36,266 | 8,991 |
| FW215\_bin.51 | c\_\_Gammaproteobacteria\_(UID4274) | 91.88 | 5.36 | 950 | 4.09 | 39,936 | 5,812 |
| GW928\_bin.17 | k\_\_Archaea\_(UID2) | 91.76 | 2.91 | 126 | 1.68 | 71,974 | 24,692 |
| FW305\_bin.6 | k\_\_Bacteria\_(UID1452) | 91.42 | 3.3 | 323 | 2.52 | 38,548 | 12,311 |
| FW301\_bin.2 | c\_\_Gammaproteobacteria\_(UID4266) | 90.4 | 1.31 | 356 | 4.58 | 154,330 | 19,863 |
| FW021\_bin.53 | c\_\_Betaproteobacteria\_(UID3959) | 90.05 | 0.24 | 125 | 2.99 | 101,654 | 38,336 |
| FW106-02\_bin.11 | c\_\_Betaproteobacteria\_(UID3959) | 89.91 | 1.29 | 280 | 4.20 | 92,148 | 30,501 |
| FW602\_bin.31 | f\_\_Xanthomonadaceae\_(UID4214) | 89.52 | 6.36 | 229 | 2.54 | 646,747 | 236,695 |
| FW602\_bin.52 | k\_\_Bacteria\_(UID1452) | 89.18 | 6.22 | 143 | 3.09 | 252,083 | 48,834 |
| GW928\_bin.5 | o\_\_Rhodospirillales\_(UID3754) | 89.06 | 2.11 | 775 | 4.69 | 31,369 | 8,637 |
| FW301-02\_bin.13 | k\_\_Bacteria\_(UID2982) | 88.85 | 3.08 | 1574 | 5.62 | 18,943 | 4,119 |
| FW215\_bin.33 | k\_\_Bacteria\_(UID2569) | 88.81 | 8.06 | 911 | 4.01 | 35,054 | 5,413 |
| DP16D\_bin.1 | c\_\_Betaproteobacteria\_(UID3959) | 88.48 | 3.01 | 462 | 2.34 | 27,705 | 6,812 |
| FW300\_bin.36 | o\_\_Actinomycetales\_(UID1663) | 88.28 | 1.35 | 745 | 3.26 | 24,798 | 5,210 |
| FW305\_bin.15 | k\_\_Bacteria\_(UID2495) | 87.44 | 5.25 | 577 | 4.10 | 43,895 | 9,881 |
| FW106-02\_bin.6 | f\_\_Xanthomonadaceae\_(UID4214) | 87.1 | 5.4 | 126 | 3.17 | 337,657 | 70,375 |
| GW715\_bin.45 | c\_\_Alphaproteobacteria\_(UID3422) | 86.85 | 4.26 | 514 | 3.21 | 81,823 | 9,340 |
| FW300\_bin.53 | c\_\_Gammaproteobacteria\_(UID4443) | 85.48 | 3.2 | 736 | 2.57 | 22,511 | 4,506 |
| FW602\_bin.25 | p\_\_Bacteroidetes\_(UID2591) | 85.44 | 2.53 | 778 | 4.80 | 32,653 | 7,987 |
| FW021\_bin.59 | k\_\_Bacteria\_(UID1452) | 85.24 | 1.85 | 507 | 2.11 | 16,683 | 4,931 |
| GW928\_bin.9 | k\_\_Bacteria\_(UID2565) | 85.13 | 1.08 | 816 | 4.43 | 33,802 | 7,094 |
| FW602\_bin.19 | k\_\_Bacteria\_(UID2570) | 84.88 | 6.47 | 717 | 3.84 | 32,534 | 6,958 |
| FW602\_bin.38 | k\_\_Bacteria\_(UID1452) | 82.73 | 4.55 | 84 | 3.25 | 116,370 | 59,107 |
| FW301\_bin.11 | c\_\_Alphaproteobacteria\_(UID3305) | 81.63 | 1.16 | 958 | 4.62 | 27,636 | 6,084 |
| FW021\_bin.52 | o\_\_Rhizobiales\_(UID3450) | 81.47 | 3.7 | 1067 | 4.62 | 27,666 | 5,143 |
| GW928\_bin.20 | k\_\_Bacteria\_(UID1452) | 81.35 | 3.3 | 439 | 2.66 | 57,125 | 8,732 |
| FW305\_bin.14 | k\_\_Bacteria\_(UID203) | 80.46 | 0 | 8 | 0.79 | 279,925 | 135,229 |
| FW300\_bin.13 | p\_\_Bacteroidetes\_(UID2591) | 80.31 | 1.89 | 855 | 3.09 | 21,801 | 4,314 |
| GW715\_bin.11 | c\_\_Alphaproteobacteria\_(UID3305) | 80.2 | 1.17 | 636 | 2.76 | 29,778 | 5,385 |
| GW715\_bin.20 | k\_\_Bacteria\_(UID3187) | 80.2 | 8.59 | 1081 | 4.14 | 26,280 | 4,431 |
| DP16D\_bin.15 | k\_\_Bacteria\_(UID2565) | 79.98 | 0 | 299 | 1.63 | 40,723 | 7,081 |
| FW602\_bin.17 | k\_\_Bacteria\_(UID1452) | 79.74 | 2.31 | 802 | 3.06 | 22,599 | 4,770 |
| FW106-10\_bin.24 | o\_\_Burkholderiales\_(UID4000) | 79.69 | 0.7 | 90 | 3.93 | 154,575 | 75,430 |
| FW300\_bin.39 | k\_\_Bacteria\_(UID1452) | 79.66 | 5.59 | 597 | 2.61 | 35,333 | 5,566 |
| GW715\_bin.47 | k\_\_Bacteria\_(UID2495) | 79.35 | 0 | 129 | 0.79 | 44,991 | 12,251 |
| FW602\_bin.30 | c\_\_Betaproteobacteria\_(UID3971) | 79.3 | 1.72 | 361 | 2.34 | 30,352 | 8,843 |
| FW021\_bin.24 | f\_\_Xanthomonadaceae\_(UID4214) | 78.81 | 0.82 | 46 | 2.65 | 158,767 | 99,477 |
| DP16D\_bin.55 | o\_\_Rhodospirillales\_(UID3754) | 78.79 | 3.06 | 850 | 3.10 | 22,657 | 4,059 |
| FW215\_bin.14 | k\_\_Bacteria\_(UID203) | 77.87 | 0.86 | 18 | 0.67 | 118,038 | 73,222 |
| FW215\_bin.29 | k\_\_Archaea\_(UID2) | 77.57 | 3.74 | 124 | 0.74 | 28,687 | 8,137 |
| FW602\_bin.41 | k\_\_Bacteria\_(UID1452) | 77.23 | 0 | 2 | 1.09 | 855,898 | 855,898 |
| FW602\_bin.51 | k\_\_Bacteria\_(UID3187) | 77.08 | 3.51 | 362 | 2.82 | 43,032 | 10,591 |
| FW021\_bin.39 | f\_\_Xanthomonadaceae\_(UID4214) | 76.96 | 3.46 | 814 | 2.99 | 19,587 | 4,200 |
| GW715\_bin.51 | k\_\_Bacteria\_(UID203) | 76.89 | 3.61 | 568 | 4.08 | 126,688 | 14,285 |
| FW104\_bin.10 | k\_\_Bacteria\_(UID2565) | 76.65 | 0.2 | 272 | 1.32 | 50,942 | 5,939 |
| DP16D\_bin.42 | p\_\_Euryarchaeota\_(UID49) | 75.48 | 0.73 | 419 | 1.34 | 21,160 | 3,491 |
| DP16D\_bin.6 | k\_\_Bacteria\_(UID203) | 75.29 | 5.49 | 145 | 0.92 | 159,544 | 39,264 |
| FW215\_bin.27 | k\_\_Archaea\_(UID2) | 75 | 1.86 | 279 | 1.11 | 17,919 | 4,691 |
| FW021\_bin.43 | k\_\_Bacteria\_(UID203) | 74.48 | 1.88 | 521 | 2.79 | 33,050 | 6,838 |
| FW305\_bin.8 | k\_\_Bacteria\_(UID2495) | 74.13 | 0 | 91 | 0.72 | 27,166 | 11,245 |
| GW928\_bin.18 | k\_\_Archaea\_(UID2) | 73.62 | 2.32 | 445 | 1.54 | 31,611 | 4,481 |
| DP16D\_bin.29 | k\_\_Bacteria\_(UID203) | 73.12 | 7.21 | 1121 | 3.85 | 21,209 | 3,766 |
| FW300\_bin.57 | k\_\_Bacteria\_(UID1452) | 73.1 | 2.92 | 250 | 1.41 | 48,451 | 13,646 |
| DP16D\_bin.14 | k\_\_Bacteria\_(UID1452) | 72.52 | 0.99 | 75 | 1.16 | 72,611 | 23,677 |
| GW928\_bin.3 | k\_\_Bacteria\_(UID2565) | 72.03 | 1.17 | 355 | 1.22 | 10,582 | 4,063 |
| GW928\_bin.10 | f\_\_Rhodocyclaceae\_(UID3972) | 71.77 | 3.14 | 563 | 2.18 | 22,772 | 4,525 |
| FW300\_bin.56 | k\_\_Bacteria\_(UID1452) | 70.83 | 0.93 | 2 | 0.77 | 494,791 | 494,791 |
| FW215\_bin.7 | k\_\_Bacteria\_(UID1452) | 70.79 | 1.98 | 73 | 1.00 | 93,230 | 19,827 |
| FW602\_bin.45 | k\_\_Bacteria\_(UID1452) | 70.7 | 0 | 2 | 0.98 | 842,311 | 842,311 |
| FW300\_bin.23 | k\_\_Bacteria\_(UID1453) | 70.6 | 1.8 | 38 | 0.89 | 93,980 | 51,973 |
| FW215\_bin.11 | k\_\_Bacteria\_(UID1452) | 70.3 | 0.99 | 97 | 1.01 | 40,847 | 15,215 |
| DP16D\_bin.9 | k\_\_Bacteria\_(UID1453) | 70.09 | 0 | 27 | 1.03 | 214,539 | 159,463 |

**Table S6.** Genome sizes of *Patescibacteria* and non-*Patescibacteria* members including well-established phyla, newly defined phyla and genome bins of this study.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Group** | **Bactterial Phylum/Genome Bin** | **Genome size / Calibrated (for genome bins) genome size (Mbp)** | **No. of genomes for genome size summary** | **Representative genomes / bins** | **Completeness of representative genomes / bins (%)** | **Contamination of representative genomes / bins (%)** |
| Patescibacteria | Azambacteria | 0.83 | 1 | LCFX01000000 | 71.6 | 3.4 |
| Brennerbacteria | 0.81 | 3 | MHHX01000000 | 81.2 | 0 |
| Campbellbacteria | 0.99 | 4 | CP011215 | 75.7 | 1.1 |
| Doudnabacteria | 1.25 | 8 | MFEF01000000 | 70.3 | 1 |
| Giovannonibacteria | 1.07 | 4 | LCFO01000000 | 74.4 | 5.2 |
| Harrisonbacteria | 1.06 | 2 | MHJL01000000 | 80.3 | 8.5 |
| Jorgensenbacteria | 0.99 | 2 | LCQG01000000 | 75.7 | 4.5 |
| Kerfeldbacteria | 1.4 | 6 | MHKI01000000 | 76.2 | 4 |
| Komeilibacteria | 1.24 | 1 | MHKS01000000 | 73.4 | 0 |
| Liptonbacteria | 1.02 | 3 | MHLE01000000 | 72.7 | 1 |
| Magasanikbacteria | 1.48 | 5 | LCFY01000000 | 78.7 | 1.1 |
| Moranbacteria | 1.5 | 7 | LBYD01000000 | 89.5 | 0 |
| Nomurabacteria | 0.94 | 23 | LBRL01000000 | 80.1 | 2.3 |
| Roizmanbacteria | 1.33 | 2 | LBST01000000 | 75.6 | 0 |
| Shapirobacteria | 1.16 | 3 | LBTB01000000 | 74.8 | 0 |
| Uhrbacteria | 1.77 | 1 | LCAU01000000 | 70.8 | 5.9 |
| Vogelbacteria | 0.94 | 1 | MHTK01000000 | 57.8 | 0 |
| Woesebacteria | 1.22 | 13 | CP011214 | 73.8 | 0 |
| Yonathbacteria | 1 | 3 | MHUZ01000000 | 72.9 | 1.1 |
| DP16D\_bin.9 | 1.03 | 1 |  | 70.09 | 0 |
| FW215\_bin.11 | 1.01 | 1 |  | 70.3 | 0.99 |
| FW215\_bin.7 | 1 | 1 |  | 70.79 | 1.98 |
| FW305\_bin.14 | 0.79 | 1 |  | 80.46 | 0 |
| GW715\_bin.47 | 0.79 | 1 |  | 79.35 | 0 |
| DP16D\_bin.14 （JOE2） | 1.16 | 1 |  | 72.52 | 0.99 |
| Other phyla | Acidobacteria | 5.31 | 6 | Terriglobus saanensis (NC\_014963) | 100 | 1.7 |
| Actinobacteria | 4.48 | 741 | Mycobacterium tuberculosis (NC\_000962) | 99.9 | 0 |
| Armatimonadetes | 5.23 | 1 | Chthonomonas calidirosea (NC\_021487) | 95.7 | 0 |
| Bacteroidetes | 3.71 | 268 | Bacteroides fragilis (NC\_006347) | 99.3 | 0 |
| Chlamydiae | 1.14 | 124 | Chlamydia trachomatis (NC\_000117) | 98.9 | 0 |
| Deinococcus | 2.94 | 27 | Thermus-Deinococcus geothermalis (NC\_008025) | 98.3 | 0 |
| Elusimicrobia | 1.64 | 1 | Elusimicrobium minutum (NC\_010644) | 96.6 | 0 |
| Firmicutes | 3.3 | 1570 | Bacillus subtilis (NC\_014976) | 99.8 | 0.1 |
| Fusobacteria | 2.42 | 22 | Fusobacterium nucleatum subsp. nucleatum (NC\_003454) | 100 | 0 |
| Gemmatimonadetes | 5.61 | 3 | Gemmatimonas aurantiaca (NC\_012489) | 98.9 | 4.4 |
| Ignavibacteriae | 3.3 | 1 | Melioribacter roseus (NC\_018178) | 100 | 1.1 |
| Nitrospinae | 3.1 | 1 | Nitrospina gracilis HG422173 | 94.9 | 3.9 |
| Planctomycetes | 6.21 | 17 | Rhodopirellula baltica (NC\_005027) | 99.9 | 0 |
| Proteobacteria | 4.3 | 3924 | Pseudomonas aeruginosa (NC\_002516) | 99.7 | 0.1 |
| Saccharibacteria | 1.38 | 1 | Saccharibacteria bacterium (MKSO00000000) | 65.1 | 0.9 |
| Spirochaetes | 2.58 | 72 | Treponema denticola (NC\_002967) | 100 | 0 |
| Synergistetes | 2.31 | 5 | Jonquetella anthropi (NZ\_CM001376) | 100 | 0 |
| Verrucomicrobia | 3.59 | 11 | Methylacidiphilum fumariolicum (NZ\_LM997411) | 99.3 | 1 |