Supporting information

**Supplementary Tables**

Table S1  Information collected on the reference genome sequences. The short name used in this study, their reference, the number of contigs, the proportions of completeness and contamination, estimated by CheckM and the number of 16S rRNA gene sequences (16S).

| Name                                      | Short name | Reference                    | Total length [Mbp] | Number of contigs | completeness (%) | contamination (%) | 16S |
|-------------------------------------------|------------|------------------------------|--------------------|-------------------|------------------|-------------------|-----|
| Ca. Accumulibacter phosphatis str. UW-1   | ACC_UW1    | (Martin et al., 2014)       | 5.3                | 4*                | 99.8             | 0.2               | 2   |
| Ca. Accumulibacter sp. BA-93              | ACC_BA93   | (Skennerton et al., 2015)   | 4.6                | 85                | 100.0            | 0.3               | 1   |
| Ca. Accumulibacter aalborgensis          | ACC_aalb   | (Albertsen et al., 2016)    | 4.7                | 181               | 99.5             | 0.1               | 1   |
| Dechloromonas aromatica                   | DEC_arom   | (Coates et al., 2001)       | 4.5                | 1                 | 99.6             | 0.3               | 4   |
| Dechloromonas sp.                         | DEC_sp     | (Parks et al., 2017)        | 3.3                | 1                 | 99.8             | 0.2               | 3   |
| Ca. Propionivibrio aalborgensis          | POV_aalb   | (Albertsen et al., 2016)    | 3.8                | 405               | 93.8             | 3.8               | 1   |
| Propionivibrio dicarboxylicus             | POV_dica   | (Varghese et al., 2016)     | 4.5                | 47                | 96.4             | 0.9               | 2   |
| Propionivibrio limicola                   | POV_limi   | (Wang et al., 2020)         | 3.1                | 57                | 97.7             | 1.4               | 1   |
| Dokdonella koreensis                      | DOK_kore   | (Yoon et al., 2006)         | 4.4                | 1                 | 99.2             | 0.6               | 2   |
| Ca. Saccharimonas aalborgensis            | SAC_aalb   | (Albertsen et al., 2013)    | 1.0                | 1                 | 67.1             | 0.9               | 1   |

* one chromosome and three plasmids
Table S2 Number of 16S rRNA genes extracted from PacBio contigs for each sample and the best match in MiDAS 16S rRNA gene database vS123.2.1.3 (McIlroy et al., 2017). The taxonomy *Dechloromonas* here also includes 16S rRNA sequences classified as *Ferribacterium* in MiDAS.

| Acronym | d71 | d322 | d427 | d740 | taxonomy |
|---------|-----|------|------|------|----------|
| ACC | 10 | 7 | 9 | 3 | k._Bacteria;p._Proteobacteria;c._Gammaproteobacteria;o._Betaproteobacterales;f._Rhodocyclaceae;g._Candidatus Accumulibacter;s._ |
| ALC | 2 | | | | k._Bacteria;p._Proteobacteria;c._Gammaproteobacteria;o._Betaproteobacterales;f._Alcaligenaceae;g._uncultured;s._ |
| BFA | 1 | | | | k._Bacteria;p._Proteobacteria;c._Alphaproteobacteria;o._Rhizobiales;f._B142;g._s._ |
| CMA | 1 | | | | k._Bacteria;p._Proteobacteria;c._Gammaproteobacteria;o._Betaproteobacterales;f._Comamonadaceae;g._uncultured;s._ |
| COM | 1 | | | | k._Bacteria;p._Proteobacteria;c._Gammaproteobacteria;o._Xanthomonadales;f._Competibacteriaceae;g._Candidatus Competibacter;s._ |
| CPC | 2 | | | | k._Bacteria;p._Proteobacteria;c._Gammaproteobacteria;o._Xanthomonadales;f._Competibacteriaceae;g._CPB;CB2;F32;s._ |
| CPS | 1 | | | | k._Bacteria;p._Proteobacteria;c._Gammaproteobacteria;o._Xanthomonadales;f._Competibacteriaceae;g._CPB;S18;s._ |
| CYC | 4 | | | | k._Bacteria;p._Bacteroidetes;c._Sphingobacteria;o._Sphingobacteriales;f._Saprosiraceae;g._CYCU-0281;s._ |
| CYT | 4 | 1 | | | k._Bacteria;p._Bacteroidetes;c._Cytophagia;o._Cytophagales;f._Cytophagaceae;g._uncultured;s._ |
| DBO | 1 | | | | k._Bacteria;p._Proteobacteria;c._Alphaproteobacteria;o._DB1-14;f._s._ |
| DEC | 3 | 1 | | | k._Bacteria;p._Proteobacteria;c._Gammaproteobacteria;o._Betaproteobacterales;f._Rhodocyclaceae;g._Dechloromonas;s._ |
| DEF | 1 | | | | k._Bacteria;p._Proteobacteria;c._Alphaproteobacteria;o._Rhodobacterales;f._Rhodobacteraceae;g._Defluviimonas;s._ |
| DOK | 2 | | | | k._Bacteria;p._Proteobacteria;c._Gammaproteobacteria;o._Xanthomonadales;f._Xanthomonadaceae;g._Dokdonella;s._ |
| FER | 1 | | | | k._Bacteria;p._Bacteroidetes;c._Sphingobacteria;o._Sphingobacteriales;f._Chitinophagaceae;g._Ferruginibacter;s._ |
| FLA | 1 | 1 | | | k._Bacteria;p._Bacteroidetes;c._Flavobacteria;o._Flavobacteriales;f._Flavobacteriaceae;g._Flavobacterium;s._ |
| HAC | 2 | | | | k._Bacteria;p._Bacteroidetes;c._Sphingobacteria;o._Sphingobacteriales;f._Haliscomenobacter;s._ |
| LED | 2 | | | | k._Bacteria;p._Bacteroidetes;c._Cytophagia;o._Cytophagales;f._Cytophagaceae;g._Leadhiltherella;s._ |
| LEP | 1 | | | | k._Bacteria;p._Proteobacteria;c._Gammaproteobacteria;o._Betaproteobacterales;f._Burkholderiaceae;g._Leptothrix;s._ |
| NGA | 2 | | | | k._Bacteria;p._Proteobacteria;c._Gammaproteobacteria;o._Betaproteobacterales;f._Gallionellaceae;g._Candidatus Nitrotoga;s._ |
| NIA | 2 | | | | k._Bacteria;p._Bacteroidetes;c._Sphingobacteria;o._Sphingobacteriales;f._Chitinophagaceae;g._Niabella;s._ |
| NIT | 1 | | | | k._Bacteria;p._Nitrospira;c._Nitrospira;f._Nitrospiraceae;g._Nitrospira;s._sublineage I |
| OMC | 1 | | | | k._Bacteria;p._Planctomycetes;o._OM190;f._g._s._ |
| PER | 1 | | | | k._Bacteria;p._Bacteroidetes;c._Cytophagia;o._Cytophagales;f._Cytophagaceae;g._Penicicilea;s._ |
| POV | 2 | | | | k._Bacteria;p._Proteobacteria;c._Gammaproteobacteria;o._Rhodocyclaceae;f._Rhodocyclaceae;g._Propionivibrio;s._ |
| PRO | 1 | 3 | | | k._Bacteria;p._Actinobacteria;c._Actinobacteria;o._Propionibacteria;f._Propionibacteriaceae;g._Propionicilibrata;s._ |
| PSE | 1 | | | | k._Bacteria;p._Proteobacteria;c._Gammaproteobacteria;o._Xanthomonadales;f._Xanthomonadaceae;g._Pseudoxanthomonas;s._ |
| QED | 2 | | | | k._Bacteria;p._Bacteroidetes;c._Sphingobacteria;o._Sphingobacteriales;f._Saprosiraceae;g._QEDRSBF09;s._ |
| ROB | 1 | 3 | | | k._Bacteria;p._Proteobacteria;c._Alphaproteobacteria;o._Rhodobacterales;f._Rhodobacteraceae;g._Rhodobacter;s._ |
| ROD | 1 | 1 | 2 | | k._Bacteria;p._Proteobacteria;c._Gammaproteobacteria;o._Betaproteobacterales;f._Rhodocyclaceae;g._uncultured;s._ |
| SAC | 1 | 10 | | | k._Bacteria;p._Bacteroidetes;c._Sphingobacteria;o._Sphingobacteriales;f._Saprosiraceae;g._Sbr-gs28;s._ |
| SAP | 1 | | | | k._Bacteria;p._Bacteroidetes;c._Sphingobacteria;o._Saprosiraceae;g._uncultured;s._ |
| SBR | 1 | 1 | | 1 | k._Bacteria;p._Proteobacteria;c._Alphaproteobacteria;o._Rhizobiales;f._Rhizobaceae;g._Shinella;s._ |
| SHI | 1 | | | | k._Bacteria;p._Chlorobi;f._Chlorobiaceae;g._Chlorobiaceae;f._s._ |
| SKA | 1 | | | | k._Bacteria;p._Gemmatismonadetes;c._Gemmatismonadetes;o._Gemmatismonadaceae;f._Gemmatismonadaceae;g._Skagen138;s._ |
| SPB | 1 | 1 | | | k._Bacteria;p._Proteobacteria;c._Gammaproteobacteria;o._Betaproteobacterales;f._Burkholderiaceae;g._spb280;s._ |
| TER | 1 | | | | k._Bacteria;p._Bacteroidetes;c._Sphingobacteria;o._Chitinophagaceae;g._Terrimonas;s._ |
| THI | 2 | 2 | | | k._Bacteria;p._Proteobacteria;c._Gammaproteobacteria;o._Thiotrichales;f._Thiotrichaceae;g._Thiotrix;s._ |
| ZOO | 6 | | | | k._Bacteria;p._Proteobacteria;c._Gammaproteobacteria;o._Betaproteobacterales;f._Rhodocyclaceae;g._Zoogloea;s._ |
Table S3  Accession ID, reference, clone ID and clade information of the \textit{ppk1} sequences included in the this study.

| accession number | reference       | clone ID | clade |
|------------------|-----------------|---------|-------|
| EF559322.1       | He et al.2017   | DUR_D9  | I     |
| EF559324.1       |                 | DUR_F9  | IIB   |
| EF559331.1       |                 | DUR_B11 | IIA   |
| EF559333.1       |                 | LV_E6   | IIC   |
| EF559340.1       |                 | NAN_A3  | IIC   |
| EU432594.1       | Peterson et al.2008 | BpbwW_20 | IIC |
| EU432628.1       |                 | BPBW2416 | IC    |
| EU432630.1       |                 | BPBW2421 | IA    |
| EU432639.1       |                 | BPBW2443 | IA    |
| EU432673.1       |                 | BPBW2524 | IA    |
| EU432696.1       |                 | BPBW2573 | IC    |
| EU432711.1       |                 | BPBW2691 | IC    |
| EU432715.1       |                 | BPBW2702 | IIE   |
| EU432717.1       |                 | BPBW2707 | IIIG  |
| EU432719.1       |                 | BPBW2717 | IIIG  |
| EU432735.1       |                 | BPBW2774 | IIA   |
| EU432747.1       |                 | BPBW3567 | IIC   |
| EU432817.1       |                 | BPBW3118 | IIID  |
| EU432854.1       |                 | BPBW2806 | IIE   |
| EU432859.1       |                 | BPBW2832 | IIIG  |
| EU432881.1       |                 | BPBW2889 | IB    |
| EU432887.1       |                 | BPBW2897 | ID    |
| EU432891.1       |                 | BPBW2902 | ID    |
| EU432902.1       |                 | BPBW2921 | IE    |
| EU432907.1       |                 | BPBW2929 | ID    |
| EU432910.1       |                 | BPBW2935 | IE    |
| EU432916.1       |                 | BPBW2945 | IB    |
| EU432919.1       |                 | BPBW2950 | IE    |
| EU432920.1       |                 | BPBW2951 | IB    |
| EU432933.1       |                 | BPBW2973 | IE    |
| EU432966.1       |                 | BPBW3245 | II    |
| EU433049.1       |                 | BPBW3353 | IID   |
| EU433059.1       |                 | BPBW3461 | II    |
| EU433074.1       |                 | BPBW3482 | IID   |
| EU433088.1       |                 | BPBW3496 | II    |
| EU433103.1       |                 | BPBW3513 | IIE   |
| EU433138.1       |                 | BPBW3651 | IIB   |
| EU433140.1       |                 | BPBW3653 | II    |
| EU433159.1       |                 | BPBW3676 | IIB   |
| EU433242.1       |                 | BPBW3772 | IIF   |
| EU433263.1       |                 | BPBW3805 | IIF   |
| EU433286.1       |                 | BPBW3834 | IIF   |
| KP737882.1       | Mao et al.2015  | TK_5    | II-I  |
| KP737888.1       |                 | TK_11   | II-I  |
| KP737919.1       |                 | TK_64   | II-I  |
| KP737990.1       |                 | DT_138  | IIH   |
| KP738013.1       |                 | DT_48   | IIH   |
| KP738084.1       |                 | GZ_16   | IIH   |
Table S4 Primer sequence and contig coordinates.

| Primer name | Primer sequence (5' - 3') | Contig UNC4029 | Contig UNC4079 |
|-------------|---------------------------|----------------|----------------|
| F1          | GCCTGGCTGGTTCTGTATTA      | 138 204-138 223| 128 859-128 878|
| FR2         | CTGCAGCGGCTAAGTAG         | 139 054-139 037| 286 432-286 449|
| R3          | CGCCAGCCGCTATCTGTT        | 123 621-123 604| 131 051-131 034|
| R4          | TCAGGTGTTGGTTGATTCC       | 294 769-294 750| 287 578-287 559|

Table S5 Main characteristics of the assemblies of the PacBio long-reads and/or Illumina short-reads sequencing data. Only the contigs longer or equal to 2000 kbp were considered.

| Day | sample name                        | Total length [Mbp] | number of contigs | N50 contig length [Mbp] | max contig length [Mbp] | average gene length [Mbp] | 16S detected per 10 [Mbp] | proportion of complete 16S [%] |
|-----|------------------------------------|-------------------|-------------------|-------------------------|-------------------------|---------------------------|----------------------------|--------------------------------|
| 71  | d71_A long-reads assembly         | 69.3              | 1485              | 65 018                  | 3.46                    | 808                       | 3.5                       | 96                             |
|     | d71_A hybrid assembly             | 196.6             | 19 277            | 17 044                  | 1.62                    | 709                       | 2.7                       | 45                             |
|     | d71_A short-reads assembly        | 101.2             | 16 031            | 9056                    | 1.40                    | 859                       | 1.3                       | 41                             |
| 322 | d322_A long-reads assembly        | 29.8              | 548               | 76 706                  | 0.83                    | 844                       | 4.0                       | 100                            |
|     | d322_A hybrid assembly            | 199.4             | 21 309            | 16 668                  | 1.85                    | 786                       | 3.0                       | 46                             |
|     | d322_A short-reads assembly       | 135.2             | 19 901            | 10 910                  | 1.40                    | 874                       | 1.1                       | 34                             |
| 427 | d427_A long-reads assembly        | 75.6              | 1997              | 55 509                  | 3.50                    | 863                       | 3.8                       | 86                             |
|     | d427_A hybrid assembly            | 284.4             | 29 679            | 15 754                  | 2.41                    | 720                       | 2.3                       | 40                             |
|     | d427_A short-reads assembly       | 155.3             | 24 142            | 10 083                  | 2.17                    | 870                       | 1.0                       | 32                             |
| 740 | d740_A long-reads assembly        | 123.7             | 1300              | 211 407                 | 3.90                    | 798                       | 5.1                       | 100                            |
|     | d740_A hybrid assembly            | 409.0             | 34 726            | 21 228                  | 1.34                    | 691                       | 2.3                       | 39                             |
|     | d740_A short-reads assembly       | 197.3             | 25 320            | 19 743                  | 0.77                    | 897                       | 1.1                       | 44                             |
Table S6  Characteristics of all MAGs containing at least one 16S rRNA gene related to *Ca*. Accumulibacter, obtained with the four individual binning tools tested: MuLoBiSC, MetaBAT2, MaxBin2 and CONCOCT, from metagenomic samples taken at four different days of reactor operation (d71, d322, d427, d740). The *Ca*. Accumulibacter 16S rRNA genes with different numbers have a sequence difference of at least three nucleotides. Different contigs containing the same *Ca*. Accumulibacter 16S rRNA gene are distinguished with distinct lowercase letters. Completeness and contamination percentages were determined with CheckM. The weighted silhouette coefficient (WSC) are expressed in millions.

| Sample | Binning tool | Contigs containing at least one *Ca*. Accumulibacter 16S rRNA gene | Number of contigs | Bin length [Mbp] | N50 [kbp] | Number of rRNA operon | Number of tRNA | Number of CDS | Completeness [%] | Contamination [%] |
|--------|--------------|---------------------------------------------------------------|-------------------|-----------------|-----------|----------------------|---------------|---------------|----------------|-----------------|
| d71    | MuLoBiSC    | ACC003a ACC003b                                              | 52                | 4.7             | 108       | 2                    | 47            | 4139          | 86.4           | 1.3             |
|        |              | ACC005a ACC005b                                              | 14                | 4.3             | 361       | 2                    | 45            | 3898          | 84.3           | 1.4             |
|        | MetaBAT2    | ACC001a ACC001c                                              | 55                | 5.9             | 144       | 1                    | 59            | 5306          | 96.6           | 20.3            |
|        |              | ACC003a ACC003b                                              | 166               | 7.6             | 56        | 2                    | 60            | 7032          | 48.3           | 36.2            |
|        |              | ACC005a ACC005b                                              | 57                | 4.8             | 107       | 3                    | 48            | 4276          | 86.9           | 1.5             |
|        |              | ACC005a ACC005b                                              | 8                 | 3.1             | 452       | 2                    | 39            | 2833          | 44.8           | 0               |
| d322   | MuLoBiSC    | ACC001a                                                      | 71                | 4.4             | 79        | 1                    | 42            | 4105          | 42.5           | 5.8             |
|        |              | ACC003a ACC003b                                              | 92                | 6.8             | 346       | 4                    | 68            | 7084          | 99.0           | 21.3            |
|        | MetaBAT2    | ACC003a ACC003b                                              | 140               | 9.0             | 141       | 3                    | 86            | 8526          | 96.6           | 37.9            |
|        |              | ACC003a ACC003b ACC003c ACC010                                | 173               | 8.7             | 74        | 4                    | 64            | 8482          | 89.9           | 20.6            |
|        |              | ACC009 COM001 CPS001                                          | 4                  | 1               | 49        | 3                    | 50            | 4592          | 93.6           | 2.6             |
| d427   | CONCOCT     | ACC001a ACC001b ACC001c ACC005a ACC005b ACC009 ACC010 ACC003c | 473               | 4.3             | 315       | 8                    | 186           | 23417         | 100.0          | 202.1           |
|        |              | ACC003a ACC003b                                              | 46                | 4.3             | 115       | 2                    | 45            | 3853          | 83.1           | 1.1             |
| d740   | MuLoBiSC    | ACC007a                                                      | 13                | 4.8             | 409       | 1                    | 50            | 4181          | 94.8           | 4.4             |
|        |              | ACC007b ACC007c                                              | 20                | 5.1             | 325       | 2                    | 47            | 4396          | 97.8           | 5.6             |
|        | MetaBAT2    | ACC007a                                                      | 15                | 4.9             | 409       | 1                    | 50            | 4285          | 95.7           | 5.5             |
|        |              | ACC007b ACC007c                                              | 27                | 5.6             | 300       | 2                    | 48            | 4916          | 98.3           | 5.6             |
|        |              | ACC007a ACC007b ACC012                                       | 4                  | 1               | 324       | 3                    | 102           | 10879         | 100.0          | 104.2           |
|        | CONCOCT     | ACC007a ACC007b ACC012                                       | 73                | 12.2            | 324       | 3                    | 102           | 10879         | 100.0          | 104.2           |
Table S7  Characteristics of the good quality MAGs containing at least one 16S rRNA gene related to *Ca. Accumulibacter*, obtained with the four individual binning tools tested: MuLoBiSC, MetaBAT2, MaxBin2 and CONCOCT.

| Sample | Binning tool | Contigs containing at least one *Ca. Accumulibacter* 16S rRNA gene | Number of contigs | Bin length (Mbp) | Completeness (%) | Contamination (%) | WSC *d* |
|--------|--------------|----------------------------------------------------------------|-------------------|-----------------|------------------|------------------|---------|
| d71 MaLoBiSC | ACC003a | ACC003b | 52 | 4.7 | 86.4 | 1.3 | 2.1 |
| | ACC005a | ACC005b | 14 | 4.3 | 84.1 | 1.4 | 1.8 |
| | MetaBAT2 | ACC003a | ACC003b | ACC010 | 57 | 4.8 | 86.9 | 1.5 | 1.9 |
| | MaxBin2 | ACC009 | COM001 | CPS001 | 41 | 4.9 | 93.6 | 2.6 | 1.3 |
| | CONCOCT | ACC003a | ACC003b | 46 | 4.3 | 83.1 | 1.1 | 2.5 |
| d322 MuLoBiSC | ACC003a | ACC003b | 10 | 5.1 | 96.7 | 0.4 | 3.2 |
| | MetaBAT2 | ACC003a | ACC003b | 13 | 5.4 | 98.6 | 0.4 | 2.8 |
| | CONCOCT | ACC003a | ACC003b | 43 | 6.8 | 98.6 | 0.4 | < 0 |
| d427 MuLoBiSC | ACC003a | ACC003b | ACC003c | 17 | 5.4 | 98.1 | 2.7 | 4.2 |
| | ACC004a | 5 | 5.2 | 98.6 | 1.5 | 3.5 |
| | ACC005a | ACC005b | ACC005c | 19 | 4.7 | 97.9 | 2.2 | 3.1 |
| | MetaBAT2 | ACC003a | ACC003b | ACC003c | 21 | 5.6 | 98.1 | 4.1 | 3.9 |
| | ACC004a | 4 | 5.2 | 98.0 | 1.4 | 3.4 |
| | ACC005a | ACC005b | ACC005c | 38 | 5.3 | 98.5 | 5.5 | 1.2 |
| | MaxBin2 | ACC003a | ACC003b | ACC003c | 47 | 6.8 | 98.2 | 3.7 | 1.8 |
| | ACC005a | ACC005b | ACC005c | 50 | 5.6 | 96.6 | 7.3 | 2.6 |
| | CONCOCT | ACC004a | 5 | 5.5 | 98.0 | 1.5 | 3.5 |
| d740 MuLoBiSC | ACC007a | ACC010 | 13 | 4.8 | 94.8 | 4.4 | 3.0 |
| | ACC007b | ACC012 | 20 | 5.1 | 97.8 | 5.6 | 2.9 |
| | MetaBAT2 | ACC007a | ACC007b | ACC012 | 15 | 4.9 | 95.7 | 5.4 | 2.6 |
| | 27 | 5.6 | 98.3 | 5.6 | 2.1 |

*a* Metagenomic samples taken at four different days of reactor operation (d71, d322, d427, d740)

*b* The *Ca. Accumulibacter* 16S rRNA genes with different numbers have a sequence difference of at least three nucleotides. The letters indicate different contigs containing the same *Ca. Accumulibacter* 16S rRNA gene.

*c* Completeness and contamination percentages were determined with CheckM

*d* WSC = weighted silhouette coefficient (expressed in millions)
Table S8: Characteristics of all MAGs containing at least one 16S rRNA gene related to *Ca. Accumulibacter*, obtained with the metaWRAP and the default combination of binning tool, MetaBAT2, MaxBin2 and CONCOCT (BXC) and the combination MetaBAT2, MaxBin2, MuLoBiSC (BXM).

| Sample<sup>a</sup> | Binning tool | Contigs containing at least one *Ca. Accumulibacter* 16S rRNA gene<sup>b</sup> | Number of contigs | Bin length [Mbp] | N50 [kbp] | Number of rRNA operon | number of tRNA | number of CDS | Completeness [%] | Contamination [%] |
|-------------------|--------------|---------------------------------|------------------|------------------|-----------|----------------------|---------------|---------------|----------------|-----------------|
| **d71**           | BXC          | ACC003a ACC003b ACC010          | 57               | 4.8              | 107       | 3                    | 48            | 4276          | 87.7           | 1.8             |
|                   | BXM          | ACC003a ACC003b                 | 51               | 4.6              | 108       | 2                    | 47            | 4135          | 86.4           | 1.3             |
|                   |              | ACC005a ACC005b                 | 14               | 4.3              | 361       | 2                    | 45            | 3898          | 84.1           | 1.4             |
| **d322**          | BXC          | ACC003a ACC003b                 | 13               | 5.4              | 637       | 3                    | 55            | 4660          | 98.6           | 0.4             |
|                   | BXM          | ACC001                          | 47               | 2.9              | 73        | 1                    | 29            | 3030          | 59.0           | 0.0             |
|                   |              | ACC003a ACC003b                 | 13               | 5.4              | 637       | 3                    | 55            | 4660          | 98.6           | 0.4             |
|                   |              | ACC005a ACC005b                 | 71               | 4.3              | 69        | 2                    | 46            | 4024          | 76.2           | 10.3            |
| **d427**          | BXC          | ACC003a ACC003b ACC003c         | 45               | 6.7              | 445       | 3                    | 56            | 6075          | 98.2           | 2.7             |
|                   |              | ACC004a                         | 4                | 5.2              | 3459      | 2                    | 48            | 4598          | 98.0           | 1.4             |
|                   |              | ACC004b DEC002 ROD005           | 182              | 3.9              | 25        | 2                    | 52            | 4586          | 73.7           | 26.5            |
|                   |              | ACC005a ACC005b ACC005c         | 35               | 5.2              | 331       | 2                    | 54            | 4551          | 98.5           | 3.9             |
| **d740**          | BXC          | ACC003a ACC003b ACC003c         | 17               | 5.4              | 549       | 3                    | 56            | 4654          | 98.1           | 2.7             |
|                   |              | ACC004a                         | 5                | 5.2              | 3459      | 2                    | 48            | 4615          | 98.6           | 1.5             |
|                   |              | ACC005a ACC005b ACC005c         | 19               | 4.7              | 48        | 2                    | 53            | 4116          | 97.9           | 5.5             |
|                   | BXM          | ACC007a ACC007b ACC012          | 15               | 4.9              | 409       | 1                    | 50            | 4285          | 95.7           | 5.4             |
|                   |              | ACC007b ACC012                  | 27               | 5.6              | 300       | 2                    | 48            | 4916          | 98.3           | 5.6             |
|                   |              | ACC007b ACC012                  | 13               | 4.8              | 409       | 1                    | 50            | 4181          | 94.8           | 4.4             |
|                   |              | ACC007b ACC012                  | 27               | 5.6              | 300       | 2                    | 48            | 4916          | 98.3           | 5.6             |

<sup>a</sup> Metagenomic samples taken at four different days of reactor operation (d71, d322, d427, d740)

<sup>b</sup> The *Ca. Accumulibacter* 16S rRNA genes with different numbers have a sequence difference of at least three nucleotides. The letters indicate different contigs containing the same *Ca. Accumulibacter* 16S rRNA gene.

<sup>c</sup> Completeness and contamination percentages were determined with CheckM
Table S9  Characteristics of the good quality *Ca*. Accumulibacter related MAGs obtained with the metaWRAP and the default combination of binning tool, MetaBAT2, MaxBin2 and CONCOCT, combined with MuLoBiSC (BXC_M) and the combination MetaBAT2 and MuLoBiSC (BM).

| Sample \(^{a}\) | Binning tool | Contigs containing at least a *Ca*. Accumulibacter 16S rRNA gene \(^{b}\) | Number of contigs | Bin length (Mbp) | Completeness (%) | Contamination (%) | WSC \(^{d}\) |
|-----------------|--------------|----------------------------------|------------------|-----------------|------------------|------------------|--------|
| d71             | BXC_M        | ACC003a, ACC003b, ACC010         | 51               | 4.6             | 86.4             | 1.3              | 2.6    |
|                 | ACC005a      | ACC005b                          | 14               | 4.3             | 84.1             | 1.4              | 3.1    |
|                 | BM           | ACC003a, ACC003b                 | 51               | 4.6             | 86.4             | 1.3              | 2.6    |
|                 | ACC005a      | ACC005b                          | 14               | 4.3             | 84.1             | 1.4              | 3.1    |
| d322            | BXC_M        | ACC003a                         | 13               | 5.4             | 98.6             | 0.4              | 2.8    |
|                 | BM           | ACC003a, ACC003b, ACC003c        | 13               | 5.4             | 98.6             | 0.4              | 2.8    |
| d427            | BXC_M        | ACC003a, ACC003b, ACC003c        | 45               | 6.7             | 98.2             | 2.7              | 1.7    |
|                 | ACC004b      |                                  | 5                | 5.2             | 96.5             | 1.5              | 3.6    |
|                 | ACC005a      | ACC005b, ACC005c                 | 19               | 4.7             | 97.9             | 2.2              | 3.2    |
|                 | BM           | ACC003a, ACC003b, ACC003c        | 17               | 5.4             | 98.2             | 2.7              | 4.4    |
|                 | ACC004a      |                                  | 5                | 5.2             | 96.5             | 1.5              | 3.6    |
|                 | ACC005a      | ACC005b, ACC005c                 | 19               | 4.7             | 97.9             | 2.2              | 3.2    |
| d740            | BXC_M        | ACC007a, ACC007b, ACC012         | 13               | 4.8             | 94.8             | 4.4              | 3.0    |
|                 | BM           | ACC007a, ACC012                  | 27               | 5.6             | 98.3             | 5.6              | 2.2    |
|                 |              |                                  |                  |                 |                  |                  |        |

\(^{a}\) Metagenomic samples taken at four different days of reactor operation (d71, d322, d427, d740)  
\(^{b}\) The *Ca*. Accumulibacter 16S rRNA genes with different numbers have a sequence difference of at least three nucleotides. The letters indicate different contigs containing the same *Ca*. Accumulibacter 16S rRNA gene.  
\(^{c}\) Completeness and contamination percentages were determined with CheckM  
\(^{d}\) WSC = weighted silhouette coefficient (expressed in millions)

Table S10  Similarity between ACC005 MAG extracted from samples d71, d322 and d427. On the left, the average nucleotide identity [%] computed with fastani. On the right, the percentage of aligned bases between the two genomes.

| Query\(\text{ref}\) | ACC005\_d71 | ACC005\_d322 | ACC005\_d427 |
|-------------------|-------------|-------------|-------------|
| ACC005\_d71       | 68.87       | 89.77       |             |
| ACC005\_d322      | 98.56       | 73.30       |             |
| ACC005\_d427      | 99.58       | 99.10       |             |

Table S11  Similarity between the ACC003 MAG extracted from samples d71, d322 and d427. On the left, the average nucleotide identity [%] computed with fastani. On the right, the percentage of aligned bases between the two genomes.

| Query\(\text{ref}\) | ACC003\_d71 | ACC003\_d322 | ACC003\_d427 |
|-------------------|-------------|-------------|-------------|
| ACC003\_d71       | 84.20       | 84.02       |             |
| ACC003\_d322      | 98.53       | 96.32       |             |
| ACC003\_d427      | 98.52       | 99.85       |             |
Table S12  Similarity between *Ca.* Accumulibacter, *Dechloromonas* and *Propionivibrio* MAG and chosen reference genomes. On the left, the average nucleotide identity [%] computed with fastani. On the right, the percentage of aligned bases between the two genomes.

| Query ref | ACC001a_d71 | ACC003_d322 | ACC004_d427 | ACC005_d427 | ACC007_d740 | ACC012_d740 | ACC_BA-93 | ACC_UW1 | POV001002 | POV_aalb | POV_lim | POV_dica | DEC001_d71 | DEC_sp | DEC_arom |
|-----------|-------------|-------------|-------------|-------------|-------------|-------------|------------|---------|------------|----------|---------|----------|-----------|---------|---------|
| ACC001a_d71 | 19.3 | 5.4 | 17.8 | 17.2 | 14.8 | 18.2 | 76.5 | 3.6 | 3.6 | 3.9 | 3.4 | 2.1 | 2.3 | 2.0 |
| ACC003_d322 | 80.2 | 6.5 | 36.1 | 36.1 | 34.5 | 36.4 | 19.9 | 4.3 | 4.8 | 3.8 | 3.7 | 2.3 | 2.3 | 2.3 |
| ACC004_d427 | 78.0 | 78.3 | 6.8 | 6.5 | 4.8 | 7.3 | 6.6 | 10.6 | 11.3 | 10.4 | 8.3 | 3.6 | 3.0 | 4.0 |
| ACC005_d427 | 79.9 | 82.3 | 78.5 | 81.0 | 57.7 | 88.8 | 19.4 | 4.8 | 4.5 | 4.1 | 3.6 | 2.4 | 2.5 | 2.3 |
| ACC007_d740 | 79.9 | 82.3 | 78.4 | 95.8 | 56.9 | 80.2 | 20.6 | 4.6 | 4.5 | 3.6 | 3.3 | 2.3 | 2.2 | 2.2 |
| ACC012_d740 | 79.5 | 82.4 | 77.9 | 86.2 | 86.5 | 57.3 | 16.7 | 5.16 | 4.1 | 3.2 | 2.8 | 2.0 | 2.1 | 2.2 |
| ACC_BA-93 | 79.9 | 82.3 | 78.6 | 98.9 | 95.8 | 86.3 | 20.3 | 4.7 | 4.6 | 3.7 | 2.5 | 2.6 | 2.3 | 2.3 |
| ACC_UW1 | 95.3 | 80.1 | 78.2 | 80.0 | 80.1 | 79.8 | 80.1 | 3.9 | 4.2 | 4.3 | 3.7 | 2.9 | 2.6 | 2.8 |
| POV001002 | 77.4 | 78.2 | 79.2 | 77.9 | 78.3 | 78.9 | 77.9 | 77.8 | 97.3 | 4.8 | 3.31 | 2.1 | 1.8 | 2.0 |
| POV_aalb | 77.4 | 77.9 | 78.9 | 77.8 | 78.0 | 77.8 | 77.9 | 77.5 | 97.3 | 4.8 | 3.31 | 2.1 | 1.8 | 2.0 |
| POV_lim | 78.0 | 77.6 | 79.0 | 77.7 | 77.4 | 77.6 | 77.8 | 78.0 | 77.7 | 77.6 | 8.8 | 4.4 | 3.9 | 4.1 |
| POV_dica | 77.7 | 77.8 | 78.8 | 77.5 | 77.5 | 77.8 | 77.7 | 77.9 | 77.5 | 77.7 | 78.9 | 3.2 | 3.4 | 2.9 |
| DEC001_d71 | 77.2 | 77.1 | 78.2 | 77.3 | 77.5 | 77.3 | 77.2 | 77.8 | 77.3 | 77.0 | 77.9 | 77.6 | 42.1 | 38.1 |
| DEC_sp | 77.2 | 77.8 | 77.7 | 77.5 | 77.3 | 77.4 | 77.4 | 77.3 | 77.7 | 77.1 | 78.1 | 78.1 | 83.1 | 36.3 |
| DEC_arom | 76.9 | 77.3 | 78.1 | 77.2 | 77.2 | 77.1 | 77.6 | 78.5 | 77.2 | 78.3 | 77.5 | 82.9 | 82.1 | 82.1 | 82.1 |

*a* from sample d71
Table S13 Number of recombinase and transposase genes per 1000 coding DNA sequences (CDS) detected by prokka in the MAG obtained with metaWRAP combining the binning from MetaBAT2, MaxBin2 and the in house binning. The bins are ordered by the normalized sum of the two first columns. The taxonomic affiliation is here given by checkM.

| bin            | Recombinases 1000 CDS | Transposase 1000 CDS | Taxonomic affiliation | completeness |
|---------------|------------------------|----------------------|-----------------------|--------------|
| ACC003_d427   | 6                      | 42                   | _c._Betaproteobacteria | 98.1         |
| ACC007_d427   | 7                      | 23                   | _c._Betaproteobacteria | 98.3         |
| Bin.1_d322    | 8                      | 21                   | _c._Betaproteobacteria | 94.8         |
| BFA002/ROB004_d427 | 1                  | 42                   | _o._Rhizobiales        | 50.5         |
| ACC005_d427   | 6                      | 17                   | _c._Betaproteobacteria | 97.9         |
| ACC003_d71    | 2                      | 33                   | _c._Betaproteobacteria | 86.4         |
| POV001/002_d71 | 4                    | 24                   | _c._Betaproteobacteria | 78.3         |
| ACC005_d71    | 5                      | 18                   | _c._Betaproteobacteria | 84.1         |
| PRO001_d740   | 6                      | 12                   | _o._Actinomycetales    | 50.6         |
| NGA002_d740   | 2                      | 25                   | _c._Betaproteobacteria | 91.3         |
| Bin.4_d71     | 4                      | 14                   | _c._Betaproteobacteria | 66.9         |
| ACC001_d322   | 4                      | 11                   | _c._Betaproteobacteria | 59.0         |
| ACC005_d322   | 4                      | 9                    | _c._Betaproteobacteria | 76.2         |
| Bin.3_d427    | 4                      | 7                    | _o._Actinomycetales    | 82.7         |
| ZOO001/002_d740 | 2                  | 19                   | _f._Rhodocyclaceae     | 92.9         |
| Bin.4_d427    | 1                      | 17                   | _o._Actinomycetales    | 97.8         |
| Bin.8_d427    | 2                      | 14                   | _c._Betaproteobacteria | 51.9         |
| COM/CSP001_d71 | 2                    | 13                   | _c._Gammaproteobacteria | 93.6         |
| CYC001_d740   | 1                      | 10                   | _p._Bacteroidetes      | 98.8         |
| ROD002/004_d740 | 3                   | 7                    | _c._Betaproteobacteria | 82.7         |
| PRO003_d740   | 1                      | 15                   | _o._Actinomycetales    | 92.1         |
| CPC001_d427   | 3                      | 3                    | _c._Gammaproteobacteria | 90.2         |
| NIA001_d740   | 2                      | 6                    | _p._Bacteroidetes      | 99.0         |
| Bin.1_d427    | 0                      | 14                   | _o._Actinomycetales    | 73.9         |
| Bin.3_d322    | 3                      | 0                    | _k._Bacteria           | 55.2         |
| Bin.11_d71    | 3                      | 3                    | _o._Actinomycetales    | 84.1         |
| DEC001_d71    | 2                      | 7                    | _c._Betaproteobacteria | 98.5         |
| Bin.1_d71     | 2                      | 8                    | _f._Xanthomonadaceae   | 59.9         |
| Bin.15_d427   | 1                      | 11                   | _o._Actinomycetales    | 51.7         |
| CYT001_d740   | 2                      | 4                    | _o._Cytophagales       | 84.5         |
| SBR001_d740   | 1                      | 9                    | _o._Actinomycetales    | 96.6         |
| SBR001_d427   | 1                      | 9                    | _o._Actinomycetales    | 96.4         |
| DOK002_d740   | 2                      | 5                    | _f._Xanthomonadaceae   | 94.3         |
| SBR003_d322   | 1                      | 7                    | _o._Actinomycetales    | 82.0         |
| SAG012_d740   | 2                      | 2                    | _k._Bacteria           | 56.0         |
| DB0001_d71    | 1                      | 4                    | _c._Alphaproteobacteria | 51.0         |
| DEQ001_d740   | 1                      | 4                    | _f._Rhodobacteraceae   | 84.5         |
| Bin.9_d740    | 1                      | 7                    | _p._Bacteroidetes      | 83.8         |
| QED001_d740   | 1                      | 3                    | _p._Bacteroidetes      | 89.3         |
| Bin.12_d427   | 1                      | 3                    | _p._Bacteroidetes      | 72.4         |
| SPB001_d71    | 1                      | 4                    | _o._Burkholderiales    | 68.2         |
| THI001_d322   | 1                      | 6                    | _c._Gammaproteobacteria | 88.6         |
| SAC002_d740   | 2                      | 0                    | _k._Bacteria           | 67.3         |
| DB0002_d740   | 1                      | 4                    | _c._Alphaproteobacteria | 84.0         |
| SAC013_d740   | 1                      | 4                    | _k._Bacteria           | 63.0         |
| PSE002_d427   | 1                      | 4                    | _f._Xanthomonadaceae   | 85.2         |
| SAC015_d740   | 1                      | 2                    | _k._Bacteria           | 65.8         |
| THI001_d427   | 0                      | 6                    | _c._Gammaproteobacteria | 84.2         |
| CYT003_d740   | 1                      | 2                    | _o._Cytophagales       | 94.9         |
| SAC014_d740   | 1                      | 2                    | _k._Bacteria           | 56.0         |
| Bin.7_d71     | 0                      | 5                    | _k._Bacteria           | 78.6         |
| SAC001_d740   | 1                      | 0                    | _k._Bacteria           | 57.7         |
| LED001/002_d740 | 1                  | 1                    | _o._Cytophagales       | 60.8         |
| SAC003_d740   | 1                      | 0                    | _k._Bacteria           | 60.6         |
| HAC001/002_d740 | 1                  | 2                    | _p._Bacteroidetes      | 65.4         |
| CMA001_d740   | 0                      | 1                    | _k._Bacteria           | 50.9         |
Table S14  Putative type F plasmid-related contigs in the PacBio long-read assemblies of samples d71, d322, d427 and d740. The taxonomy of the contigs is provided by CAT. The contigs indicated as circular by the miniasm assembler are considered as circularized. Affiliations to a bin (metaWRAP combining MetaBAT2, MaxBin2 and MuLoBiSC) are indicated for the contigs that were not unbinned.

| contig_name | sample | taxonomy              | len     | circularized | bin     |
|-------------|--------|-----------------------|---------|--------------|---------|
| UNC0046     | d71    | o Betaproteobacteriales | 57566   | no           | -       |
| UNC0085     | d71    | Ca. Accumulibacter     | 37421   | yes          | -       |
| UNC0094     | d71    | p Proteobacteria       | 49953   | no           | -       |
| UNC0157     | d71    | Ca. Accumulibacter     | 39454   | yes          | -       |
| UNC0209     | d71    | Ca. Accumulibacter     | 49912   | yes          | -       |
| UNC0409     | d71    | Ca. Accumulibacter     | 51073   | no           | -       |
| UNC0427     | d71    | Ca. Accumulibacter     | 66331   | no           | -       |
| UNC0491     | d71    | p Proteobacteria       | 24472   | no           | -       |
| UNC0732     | d71    | Ca. Accumulibacter     | 15609   | yes          | -       |
| UNC0872     | d71    | Ca. Accumulibacter     | 21615   | no           | -       |
| UNC0964     | d71    | Ca. Accumulibacter     | 19994   | no           | -       |
| UNC1095     | d71    | p Proteobacteria       | 23891   | no           | -       |
| UNC1106     | d71    | Ca. Accumulibacter     | 23398   | no           | -       |
| UNC1469     | d322   | p Proteobacteria       | 49499   | yes          | -       |
| UNC1481     | d322   | Ca. Accumulibacter     | 39447   | yes          | -       |
| UNC1485     | d322   | Ca. Accumulibacter     | 95818   | no           | -       |
| UNC1487     | d322   | Ca. Accumulibacter     | 75188   | no           | -       |
| UNC1488     | d322   | Ca. Accumulibacter     | 89764   | yes          | -       |
| UNC1496     | d322   | Ca. Accumulibacter     | 16819   | no           | -       |
| UNC1517     | d322   | Ca. Accumulibacter     | 40862   | no           | -       |
| UNC1593     | d322   | Ca. Accumulibacter     | 25761   | yes          | -       |
| UNC1608     | d322   | Ca. Accumulibacter     | 24231   | no Bin.1     | ACC001  |
| UNC1627     | d322   | Ca. Accumulibacter     | 87312   | no ACC012    |        |
| UNC1705     | d322   | Ca. Accumulibacter     | 33216   | no           | -       |
| UNC1816     | d322   | Ca. Accumulibacter     | 33647   | no           | -       |
| UNC2037     | d427   | Ca. Accumulibacter     | 147421  | no           | -       |
| UNC2046     | d427   | Ca. Accumulibacter     | 39428   | yes          | -       |
| UNC2058     | d427   | Ca. Accumulibacter     | 47111   | no           | -       |
| UNC2067     | d427   | Ca. Accumulibacter     | 88157   | no           | -       |
| UNC2068     | d427   | Ca. Accumulibacter     | 75519   | no           | -       |
| UNC2082     | d427   | p Proteobacteria       | 52639   | no           | -       |
| UNC2125     | d427   | Ca. Accumulibacter     | 18325   | no           | -       |
| UNC2127     | d427   | Ca. Accumulibacter     | 42431   | no           | -       |
| UNC2195     | d427   | Ca. Accumulibacter     | 45755   | yes          | -       |
| UNC2239     | d427   | o Betaproteobacteriales| 25751   | yes          | -       |
| UNC2774     | d427   | Ca. Accumulibacter     | 121130  | no           | -       |
| UNC2923     | d427   | Ca. Accumulibacter     | 23264   | no           | -       |
| UNC3052     | d427   | Ca. Accumulibacter     | 19298   | no           | -       |
| UNC3985     | d740   | Ca. Accumulibacter     | 71224   | no           | -       |
| UNC3988     | d740   | Ca. Accumulibacter     | 84405   | no           | -       |
| UNC3992     | d740   | Ca. Accumulibacter     | 30058   | no           | -       |
| UNC4003     | d740   | Ca. Accumulibacter     | 68196   | no ACC012    |        |
| UNC4019     | d740   | Ca. Accumulibacter     | 81770   | no ACC012    |        |
| UNC4201     | d740   | Ca. Accumulibacter     | 104603  | yes          | -       |
| UNC4503     | d740   | o Betaproteobacteriales| 32457   | no           | -       |
| UNC4505     | d740   | Ca. Accumulibacter     | 68949   | yes          | -       |
| UNC5165     | d740   | o Betaproteobacteriales| 29889   | no           | -       |
| UNC5193     | d740   | Ca. Accumulibacter     | 31786   | no           | -       |
| UNC5195     | d740   | o Betaproteobacteriales| 39314   | no           | -       |
Supplementary Figures

Figure S1 MuLoBiSC workflow. General workflow of the MAGs assembly with MuLoBiSC, from DNA extraction to MAGs validation.
Figure S2 Composition of the bacterial communities in the aerobic granular sludge on day 71 (d71), day 322 (d322), day 427 (d427) and day 740 (d740), estimated by 16S rRNA gene amplicon sequencing. The taxonomic affiliation was obtained by comparison with MiDAS2. The genera are colored according to the class they belong to, with the exception of the Betaproteobacteriales, previously the class of Betaproteobacteria, colored in red. They were recently merged with the Gammaproteobacteria (Parks et al., 2018), here colored in light green. Only the most abundant taxa are shown.
Figure S3 GC skew Dechloromonas MAG and reference. GC skew (grey) and cumulative GC skew (green) plots of (A) *Dechloromonas* MAG DEC001 from sample d71 and (B) *Dechloromonas* sp. HYN0024 (CP031842.1; Parks et al., 2017).

Figure S4 GC skew Saccharibacteria MAG and reference. GC skew (grey) and cumulative GC skew (green) plots of (A) Saccharibacteria MAG SAC002 from sample d427, (B) SAC013 from sample d740, (C) SAC015 from sample d740 and (D) Ca. Saccharimonas aalborgensis isolate TM71 (CP005957.1; Albertsen et al., 2013).
Figure S5  GC skew Dokdonella MAG and reference. GC skew (grey) and cumulative GC skew (green) plots of (A) Dokdonella MAG DOK002 from sample d740 and (B) Dokdonella koreensis DS-123 (NZ_CP015249.1; Yoon et al., 2006).

Figure S6  GC skew Sbr-gs28. GC skew (grey) and cumulative GC skew (green) plots of Sbr-gs28 MAG SBR001 from sample d427.
Figure S7 Scatter plot of the $\sqrt{\text{coverage}}$ vs $\log_e(\text{length})$ of the contigs. The contigs affiliated with Ca. Accumulibacter, by CAT v5.2, are colored in red and the bins affiliated with Ca. Accumulibacter are indicated by different shapes. The names of the potentially complete MAGs are indicated on the plot.
Figure S8 Assembly graph of long-read assembly of sample day 71. Assembly graph of the PacBio long-read assembly of sample day 71 visualized in Bandage. The sequences were replaced by the polished sequences, yet the edges of the graph are the relations between the contigs before the polishing. Some of them may therefore be ‘chimeric’, but still provide information about the similarity between the contigs before correction. Only the contig longer than 100 kbp or linked to a contig longer than 100 kbp are shown. The labels indicate the metaWRAP combining MetaBAT2, MaxBin2 and MuLoBiSC (BXM), the taxonomic affiliation provided by CAT (von Meijenfeldt et al.,2019) and the coverage on contigs longer than 100 kbp. Contigs are colored according to the bin they belong to.
Figure S9 Assembly graph of PacBio long-read assembly of sample day 322. Assembly graph of the PacBio long-read assembly of sample day 322 visualized in Bandage. The sequences were replaced by the polished sequences, yet the edges of the graph are the relations between the contigs before the polishing. Some of them may therefore be 'chimeric', but still provide information about the similarity between the contigs before correction. Only the contig longer than 100 kbp or linked to a contig longer than 100 kbp are shown. The labels indicate the metaWRAP combining MetaBAT2, MaxBin2 and MuLoBiSC (BXM), the taxonomic affiliation provided by CAT (von Meijenfeldt et al., 2019) and the coverage on contigs longer than 100 kbp. Contigs are colored according to the bin they belong to.
Figure S10 Assembly graph of PacBio long-read assembly of sample day 427 visualized in Bandage. The sequences were replaced by the polished sequences, yet the edges of the graph are the relations between the contigs before the polishing. Some of them may therefore be chimeric, but still provide information about the similarity between the contigs before correction. Only the contigs longer than 100 kbp or linked to a contig longer than 100 kbp are shown. The labels indicate the metaWRAP combining MetaBAT2, MaxBin2 and MuLoBiSC (BXM), the taxonomic affiliation provided by CAT (von Meijenfeldt et al., 2019) and the coverage on contigs longer than 100 kbp. Contigs are colored according to the bin they belong to.
Figure S11 Assembly graph of PacBio long-read assembly of sample day 740. Assembly graph of the PacBio long-read assembly of sample day 740 visualized in Bandage. The sequences were replaced by the polished sequences, yet the edges of the graph are the relations between the contigs before the polishing. Some of them may therefore be 'chimeric', but still provide information about the similarity between the contigs before correction. Only the contig longer than 100 kbp or linked to a contig longer than 100 kbp are shown. The labels indicate the metaWRAP combining MetaBAT2, MaxBin2 and MuLoBiSC (BXM), the taxonomic affiliation provided by CAT (von Meijenfeldt et al., 2019) and the coverage on contigs longer than 100 kbp. Contigs are colored according to the bin they belong to.
Figure S12 MUMmer plots comparing ACC005 MAGs. MUMmer plots comparing the *Ca. Accumulibacter* MAG ACC005 obtained (A) from samples d71 and d322, (B) from samples d427 and d71 and (C) from samples d427 and d322. Only the alignments bigger than 4 kbp are shown.
Figure S13 MUMmer plots comparing ACC003 MAGs. MUMmer plots comparing the *Ca. Accumulibacter* MAG ACC003 obtained (A) from samples d71 and d322, (B) from samples d427 and d71 and (C) from samples d427 and d322. Only the alignments bigger than 4 kbp are shown.
Figure S14 MUMmer plot comparing MAGs ACC005, ACC007 and Ca. Accumulibacter sp. BA-93. MUMmer plots comparing similar Ca. Accumulibacter MAGs, obtained from this study and (Skennerton et al., 2015): (A) ACC007 from sample d740 and ACC005 from sample d427, (B) Ca. Accumulibacter sp. BA-93 and ACC007 from sample d740 and (C) Ca. Accumulibacter sp. BA-93 and ACC005 from sample d427. Only the alignments bigger than 4 kbp are shown.
Figure S15 MUMmer plot of MAG ACC007 and ACC012 (A) MUMmer plot comparing the Ca. Accumulibacter MAGs ACC007 and ACC012 from samples d740. Only the alignments bigger than 4 kbp are shown. The zone on the part of the MUMmer plot indicated by the red rectangle is enlarged below. (B) Zoom the comparison of two contigs from ACC007 and ACC012 MAGs showing several genomic rearrangement episodes. The presence of recombinases (recR, yer) and transposases (tnpA) is indicated on the top at the edge of the plot. The conserved fragments presented in supplementary Figure 2 are indicated on the MUMmer plot with the corresponding letter.
Figure S16 Mapping of individual granule reads on MAGs. Mapping of short-read sequences of individual granules from (Leventhal et al., 2018). The same protocol was followed but the reference MAGs were replaced by the ones from the present study, except for Ca. Accumulibacter sp. BA-91, for which no similar MAG was assembled in this study.
Figure S17  ACC001 assembly graph  Assembly graph of contigs similar to Ca. Accumulibacter phosphatis str. UW-1 (Martín et al., 2014). (A) metaWRAP BXM bin name and the coverage of illumina reads obtained with extraction method A are indicated for each contig. (B) DNA sequences with at least 90% identity with Ca. Accumulibacter phosphatis str. UW-1 are indicated in blue. (C) colored parts indicate DNA sequences identity with a gene from BUSCO Betaproteobacteria set (Kriventseva et al., 2015) with a minimal coverage of 60%.
Figure S18 ACC001 assembly graph zoom 1
Zoom on potential variants of closely related *Ca. Accumulibacter* populations in the assembly graph of contigs similar to *Ca. Accumulibacter phosphatis* str. UW-1 (Martin et al., 2014). (A) DNA sequences with at least 90 % identity with *Ca. Accumulibacter phosphatis* str. UW-1 are indicated in blue, (B) metaWRAP BXM bin name and the coverage of illumina short-reads obtained with extraction method A are indicated for each contig. Colored parts indicate DNA sequences identity with a gene from BUSCO Betaproteobacteria set with a minimal coverage of 60 %.

Figure S19 ACC001 assembly graph zoom 2
Zoom on the assembly graph of contigs similar to *Ca. Accumulibacter phosphatis* str. UW-1 (Martin et al., 2014). (A) DNA sequences with at least 90 % identity with *Ca. Accumulibacter phosphatis* str. UW-1 are indicated in blue, (B) metaWRAP BXM bin name and the coverage of illumina short-reads obtained with extraction method A are indicated for each contig. Colored parts indicate DNA sequences identity with a gene from BUSCO Betaproteobacteria set with a minimal coverage of 60 %.
Figure S20 Assembly graph of MAGs ACC007 and ACC012 (A) Assembly graph of MAGs ACC007 and ACC012 in sample d740. DNA sequences with at least 90% identity with Ca. Accumulibacter sp. BA-93 (Skennerton et al., 2015) are indicated in red. (B) Zoom on the probable chimeral contig ACC007/012.
Figure S21 Mapping of long-reads on the probable chimera contig. IGV view of the mapping PacBio long-reads from sample d740 on the long-read contig utg000193l. This contig contains a ACC007 16S rRNA gene sequence but it is placed in bin ACC012 by MetaBAT2, the MuLoBiSC and metaWRAP with the MetaBAT2, MaxBin2 and in house binning combination.