Supplementary Figure S1. 16s rRNA phylogenetic tree. The evolutionary history was inferred using the Neighbor-Joining method. The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed using the p-distance method and are in the units of the number of base differences per site. Evolutionary analyses were conducted in MEGA X.
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Supplementary Table S1. Genome data used in this study

| Species                        | Strain         | Assembly                  | Note                                                                 |
|--------------------------------|----------------|---------------------------|----------------------------------------------------------------------|
| Erythrobacter aquimixticola    | JSSK-14        | ASM360547v1               | https://www.ncbi.nlm.nih.gov/assembly/GCF_00360547v1/                |
| Erythrobacter atlanticus       | s21-N3         | ASM107781v2               | https://www.ncbi.nlm.nih.gov/assembly/GCF_0107781v2/                |
| Erythrobacter citreus          | LAMA 915       | Erythrobacter citreus LAMA 915 v1 | https://www.ncbi.nlm.nih.gov/assembly/GCF_01235865.1/               |
| Erythrobacter flavus            | VG1            | ASM223761v1               | https://www.ncbi.nlm.nih.gov/assembly/GCF_00223761.1/               |
| Erythrobacter gangiinensis      | CGMCC1.15024   | ASM188669v1               | https://www.ncbi.nlm.nih.gov/assembly/GCF_01886695.1/               |
| Erythrobacter litoralis         | DSM 8509       | ASM171916v1               | https://www.ncbi.nlm.nih.gov/assembly/GCF_01719165.1/               |
| Erythrobacter longus            | DSM 6997       | Ery_DSM 6997_v1           | https://www.ncbi.nlm.nih.gov/assembly/GCF_00715015.1/               |
| Erythrobacter luteus            | KA37           | ASM101094v1               | https://www.ncbi.nlm.nih.gov/assembly/GCF_01010945.1/               |
| Erythrobacter lutinarius        | S-5            | ASM336313v1               | https://www.ncbi.nlm.nih.gov/assembly/GCF_01355411/                 |
| Erythrobacter marinus           | KCTC 23554     | ASM102155v1               | https://www.ncbi.nlm.nih.gov/assembly/GCF_01021555.1/               |
| Erythrobacter nanhaiasediminitis| CGMCC 1.7715   | IMG-taxon 2619618819 annoated assembly | https://www.ncbi.nlm.nih.gov/assembly/GCF_900115585.1/               |
| Erythrobacter odorhensis        | KCTC 23981     | ASM360519v1               | https://www.ncbi.nlm.nih.gov/assembly/GCF_003605195.1/              |
| Erythrobacter seohaensis        | SW-135         | ASM279586v1               | https://www.ncbi.nlm.nih.gov/assembly/GCF_02795865.1/               |
| Erythrobacter vulgaris          | O1             | IDBA-UD                   | https://www.ncbi.nlm.nih.gov/assembly/GCF_00756795.1/               |
| Erythrobacter xanthus           | CCTCC AB 2015396 | ASM358401v1             | https://www.ncbi.nlm.nih.gov/assembly/GCF_03584015.1/               |
| Erythrobacter zhengii           | V18            | ASM358412v1               | https://www.ncbi.nlm.nih.gov/assembly/GCF_03584125.1/               |
| Agrobacterium tumefaciens       | MAFF210266     | ASM7000286v1              | https://www.ncbi.nlm.nih.gov/assembly/GCF_0070002865.1              |
| Altererythrobacter mangrovi     | C9-11          | ASM226934v1               | https://www.ncbi.nlm.nih.gov/assembly/GCF_002269345.1/              |
| Altererythrobacter marensis     | KCTC 22370     | ASM102862v1               | https://www.ncbi.nlm.nih.gov/assembly/GCF_01028625.1/               |
| Croceicoccus naphthovorans      | PQ-2           | ASM102870v1               | https://www.ncbi.nlm.nih.gov/assembly/GCF_01028705.1/               |
| Croceicoccus pelagius           | Ery9           | ASM166191v1               | https://www.ncbi.nlm.nih.gov/assembly/GCF_01661915.1/               |
| Porphyrobacter dokdonensis      | DSW-74         | ASM167733v1               | https://www.ncbi.nlm.nih.gov/assembly/GCF_01677335.1/               |
| Porphyrobacter tepidarius       | DSM 10594      | ASM215569v1               | https://www.ncbi.nlm.nih.gov/assembly/GCF_002155695.1/              |
| Sandaracinobacter               | PAMC 28131     | ASM638587v1               | https://www.ncbi.nlm.nih.gov/assembly/GCF_006385875.1/              |
| Sphingobium chlorophenolicum    | L-1            | ASM14783v3                | https://www.ncbi.nlm.nih.gov/assembly/GCF_00147835.2/               |
| Sphingobium herbicidovorans     | MH             | ASM208043v1               | https://www.ncbi.nlm.nih.gov/assembly/GCF_002080435.1/              |
| Sphingomonas koreensis          | ABOJv          | ASM192238v1               | https://www.ncbi.nlm.nih.gov/assembly/GCF_001922385.1/              |
| Sphingomonas melonis            | JJ26           | ASM250426v1               | https://www.ncbi.nlm.nih.gov/assembly/GCF_002504265.1/              |
| Zymomonas mobilis               | ZM4            | ASM710v1                  | https://www.ncbi.nlm.nih.gov/assembly/GCF_00007105.1/               |
**Table S2.** BUSCO genome assembly assessment.

| Strain | BUSCO result | *Erythrobacter sp. 3-20A1M* |  | *Erythrobacter xanthus* |  |
|--------|--------------|-----------------------------|-----------------|------------------------|-----------------|
|        | Count | Ratio (%) | Count | Ratio (%) | Count | Ratio (%) |
| **Complete (C)** | Single-copy (S) | 143 | 96.6 | 139 | 93.9 |
|        | Duplicated (D) | 0 | 0 | 1 | 0.7 |
| **Fragmented (F)** | 0 | 0 | 0 | 0 |
| **Missing (M)** | 5 | 3.4 | 8 | 5.4 |
| **Total** | 148 | 100 | 148 | 100 |
**Supplementary Table S3. Virulence factors of *Erythrobacter* sp. 3-20A1M.**

| Locus tag       | Annotation                                      | Gene name | Note  |
|-----------------|-------------------------------------------------|-----------|-------|
| **Biofilm**     |                                                 |           |       |
| F7D01_05380     | capsular biosynthesis protein                   | epsA      |       |
| F7D01_13520     | UDP-N-acetylglucosamine 2-epimerase (non-hydrolyzing) | epsC      |       |
| F7D01_13155     | protein-tyrosine-phosphatase                    | epsP      |       |
| F7D01_09625     | polysaccharide deacetylase family protein       | pgdA      |       |
| F7D01_05290     | exopolysaccharide biosynthesis polypreynyl glycosylphosphotransferase | pslA      |       |
| F7D01_13545     | polysaccharide biosynthesis tyrosine autokinase | vpsO      |       |
| F7D01_05365     | polysaccharide pyruvyl transferase family protein | wcaK      |       |
| F7D01_10440     | polysaccharide biosynthesis protein             | wza       |       |
| F7D01_13540     | polysaccharide export protein                   | wza       |       |
| F7D01_05355     | exopolysaccharide biosynthesis protein          |           |       |
| F7D01_05390     | diutan polysaccharide export protein            |           |       |
| **Flagella**    |                                                 |           |       |
| F7D01_10115     | AAA domain-containing protein                   | flaM      |       |
| F7D01_10235     | flagellar basal body P-ring formation protein FlgA | flaA      |       |
| F7D01_10285     | flagellar basal body P-ring protein FlgI       | flgI      |       |
| F7D01_10250     | flagellar basal body rod protein FlgB           | flgB      |       |
| F7D01_10255     | flagellar basal body rod protein FlgC           | flgC      |       |
| F7D01_10155     | flagellar basal-body-associated protein FliL    | fliL      |       |
| F7D01_10275     | flagellar basal-body rod protein FlgG           | flgG      |       |
| F7D01_10170     | flagellar biogenesis protein                    | fliO      |       |
| F7D01_10230     | flagellar biosynthesis anti-sigma factor FlgM   | flgM      |       |
| F7D01_10260     | flagellar biosynthesis protein FlgD             | flgD      |       |
| F7D01_10280     | flagellar biosynthesis protein FlgH             | flgH      |       |
| F7D01_10290     | flagellar biosynthesis protein FlgJ             | flgJ      |       |
| F7D01_10305     | flagellar biosynthesis protein FlgL             | flgL      |       |
| F7D01_10180     | flagellar biosynthesis protein FliQ             | fliQ      |       |
| F7D01_10185     | flagellar biosynthetic protein FliR             | fliR      |       |
| F7D01_10195     | flagellar filament capping protein FliD         | fliD      |       |
| F7D01_10295     | flagellar hook-associated protein FlgK          | flgK      |       |
| F7D01_10265     | flagellar hook-basal body complex protein       | flgE      |       |
| F7D01_10270     | flagellar hook-basal body complex protein       | flgG      |       |
| F7D01_10120     | flagellar hook-basal body complex protein FliE  | fliE      |       |
| F7D01_10310     | flagellar motor stator protein MotA             | motA      |       |
| F7D01_10130     | flagellar motor switch protein FliG             | fliG      |       |
| F7D01_10165     | flagellar motor switch protein FliN             | fliN      |       |
| F7D01_10125     | flagellar M-ring protein FliF                   | fliF      |       |
| F7D01_10225     | flagellar protein FlgN                         | flgN      |       |
| F7D01_10175     | flagellar type III secretion system pore protein FliP | fliP      |       |
| F7D01_10215     | flagellar type III secretion system protein FlhA | flhA      |       |
| F7D01_10190     | flagellar type III secretion system protein FlhB | flhB      |       |
| F7D01_10110     | flagellin FliC                                 | fliC      |       |
| F7D01_10140     | Fli/YscN family ATPase                         | fliI      |       |
| F7D01_10300     | hypothetical protein                            | flgK      |       |
| F7D01_10135     | hypothetical protein                            | fliH      |       |
| F7D01_10160     | hypothetical protein                            | fliM      |       |
| F7D01_10200     | hypothetical protein                            | fliS      |       |
| F7D01_10245     | hypothetical protein                            | motA      |       |
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| Accession  | Description                                           | Location   |
|------------|-------------------------------------------------------|------------|
| F7D01_13825 | Hypothetical protein                                  | motB       |
| F7D01_10315 | OmpA family protein                                   | rpoN       |
| F7D01_08885 | RNA polymerase factor sigma-54                       | rpoD       |
| F7D01_00160 | RNA polymerase sigma factor RpoD                      |            |
| F7D01_10210 | Sigma-70 family RNA polymerase sigma factor           | flhA       |
| F7D01_05320 | Type I secretion system permease/ATPase               | eexD       |
| F7D01_05315 | TolC family outer membrane protein                    | tolC       |
| F7D01_10215 | Flagellar type III secretion system protein FlhA      | flhA       |
| F7D01_10175 | Flagellar type III secretion system pore protein      | fliP       |
| F7D01_10370 | Type V secretion protein                              | virB10     |
| F7D01_03725 | Type VI secretion protein                             | virB2      |
| F7D01_11605 | Protein translocase subunit SecD                     | secD       |
| F7D01_11600 | Protein translocase subunit SecE                     | secE       |
| F7D01_03155 | Twin-arginine translocase TatA/TatE family subunit   | tatA       |
| F7D01_03150 | Twin-arginine translocase subunit TatB               | tatB       |
| F7D01_03145 | Twin-arginine translocase subunit TatC               | tatC       |
| F7D01_00885 | Sec-receptor protein                                  |            |
| F7D01_02415 | tRNA (adenosine(37)-N6)-threonylcarbamoyltransferase complex transferase subunit TsaD | tsaD       |
| F7D01_14405 | Preprotein translocase subunit SecG                  | secG       |
| F7D01_01380 | Preprotein translocase subunit SecY                  | secY       |
| F7D01_00885 | Signal recognition particle protein                   |            |
| F7D01_13025 | Cell wall hydrolase                                   |            |
| F7D01_10565 | Cellulase family glycosylhydrolase                    | bgalB      |
| F7D01_10535 | Family 1 glycosylhydrolase                            | bgalB      |
| F7D01_10540 | Family 1 glycosylhydrolase                            | bgalB      |
| F7D01_09485 | 1, 4-beta-D-glucan glucohydrolase                     | bgalX      |
| F7D01_13025 | Beta-glucosidase                                      | bgalX      |
| F7D01_13030 | Beta-glucosidase                                      | bgalX      |
| F7D01_13095 | 1, 4-beta-D-glucan glucohydrolase                     | bgalX      |
| F7D01_06485 | Cell wall hydrolase                                   | cwlJ       |
## Pan-genome analysis of *Erythrobacter* sp. 3-20A1M

| Accession | Description | Gene Symbol |
|-----------|-------------|-------------|
| F7D01_05925 | UTP--glucose-1-phosphate uridylyltransferase | GalU |
| F7D01_04500 | glucokinase | glk |
| F7D01_13105 | ROK family protein | glk |
| F7D01_04785 | DUF3459 domain-containing protein | malZ |
| F7D01_12500 | glycoside hydrolase family 65 protein | mapA |
| F7D01_10545 | alpha/beta hydrolase fold domain-containing protein | mlhB |
| F7D01_10550 | alpha/beta hydrolase fold domain-containing protein | mlhB |
| F7D01_13150 | trehalose-6-phosphate synthase | otsA |
| F7D01_13140 | trehalose-phosphatase | otsB |
| F7D01_10345 | pectate lyase | pelL |
| F7D01_13280 | glucose-6-phosphate isomerase | pgi |
| F7D01_09690 | 6-phosphogluconolactonase | pgi |
| F7D01_05410 | alpha-D-glucose phosphate-specific phosphoglucomutase | pgm |
| F7D01_07065 | phosphomannomutase | pgm |
| F7D01_10375 | alpha/beta hydrolase fold domain-containing protein | pme |
| F7D01_06300 | adenosine kinase | scrK |
| F7D01_13145 | glycoside hydrolase family 15 protein | sga1 |
| F7D01_11430 | HAD-IIB family hydrolase | spp |
| F7D01_01595 | TlyA family rRNA (cytidine-2'-O)-methyltransferase | tlyA |
| F7D01_10570 | alpha, alpha-trehalase TreF | treF |
| F7D01_12505 | trehalose-phosphatase | treF |
| F7D01_10530 | alpha/beta fold hydrolase | |
| F7D01_10555 | hypothetical protein | |
| F7D01_13285 | PEP-CTERM sorting domain-containing protein | |
| F7D01_04780 | glycoside hydrolase family 97 protein | |
| F7D01_10915 | glycoside hydrolase family 97 protein | |
| F7D01_10360 | TRAP transporter small permease subunit | dctQ |
| F7D01_10355 | DctP family TRAP transporter solute-binding subunit | yiaO |
### Supplementary Table S4. AntiSMASH prediction of secondary metabolites biosynthetic gene clusters

| #  | Strain                        | Contig       | Region     | Type               | From    | To       | Most similar known cluster        | Similarity |
|----|-------------------------------|--------------|------------|--------------------|---------|---------|-----------------------------------|------------|
| 1  | Erythrobacter sp. 3-20A1M    | CP045200     | Region 1   | T3PKS, lassopeptide, hserlactone, terpene | 315,403 | 356,446 |                                    |            |
|    |                               | CP045200     | Region 2   | T3PKS              | 1,649,973 | 1,687,811 |                                    |            |
|    |                               | CP045200     | Region 3   | lassopeptide, hserlactone, terpene       | 1,984,024 | 2,008,298 | zeaxanthin                        | 66%        |
| 2  | Erythrobacter aquimisticola   | NZ_RAHX0100001 | Region 1.1 | T3PKS              | 1,032,494 | 1,073,561 |                                    |            |
|    |                               | NZ_RAHX0100001 | Region 1.2 | terpene            | 2,334,005 | 2,358,384 |                                    |            |
| 3  | Erythrobacter flavus          | NZ_CP022528.1 | Region 1   | terpene            | 2,713,680 | 2,738,023 | carotenoid                        | 33%        |
|    |                               | NZ_CP022528.1 | Region 2   | bacteriocin        | 3,023,136 | 3,033,975 |                                    |            |
| 4  | Erythrobacter atlanticus      | NZ_CP011310.1 | Region 1.1 | lassopeptide       | 257,946  | 280,508  | S-layer glycan                    | 20%        |
|    |                               | NZ_CP011310.1 | Region 1.2 | betalactone        | 606,681  | 637,153  |                                    |            |
|    |                               | NZ_CP011310.1 | Region 1.3 | T3PKS              | 1,532,661 | 1,573,740 |                                    |            |
|    |                               | NZ_CP011310.1 | Region 1.4 | terpene            | 2,643,212 | 2,667,666 |                                    |            |
| 5  | Erythrobacter citreus LAMA 915| JYNE01000026.1 | Region 8.1 | terpene            | 237,062  | 257,823  |                                    |            |
|    |                               | JYNE01000028.1 | Region 13.1 | hserlactone       | 396,047  | 416,616  |                                    |            |
| 6  | Erythrobacter ganginensis      | NZ_CP018097.1 | Region 1.1 | lassopeptide       | 489,588  | 512,943  | S-layer glycan                    | 20%        |
|    |                               | NZ_CP018097.1 | Region 1.2 | terpene            | 1,147,944 | 1,172,816 | zeaxanthin                        | 66%        |
| 7  | Erythrobacter littoralis       | CP017057.1   | Region 1   | T1PKS,NRPS-like, terpene | 415,708  | 467,897  | lipopolysaccharide, carotenoid     | 16%        |
|    |                               | CP017057.1   | Region 2   | terpene            | 752,393  | 776,822  |                                    | 16%        |
| 8  | Erythrobacter longus          | NZ_JMW0100001 | Region 1.1 | terpene            | 1,207,151 | 1,232,225 | carotenoid                        | 16%        |
|    |                               | NZ_JMW0100009 | Region 9.1 | bacteriocin        | 43,588   | 54,445   |                                    |            |
|    |                               | NZ_JMW0100009 | Region 9.2 | lassopeptide       | 129,036  | 151,467  | S-layer glycan                    | 20%        |
| 9  | Erythrobacter luteus          | NZ_LBHB0100001 | Region 1.1 | lassopeptide       | 186,723  | 209,331  |                                    |            |
|    |                               | NZ_LBHB0100001 | Region 1.2 | T3PKS              | 1,086,616 | 1,127,713 |                                    |            |
|    |                               | NZ_LBHB0100002 | Region 11.1 | terpene            | 990,801  | 1,015,707 | zeaxanthin                        | 66%        |
| 10 | Erythrobacter nanhalediminis   | NZ_FOWZ0100001 | Region 5.1 | terpene            | 973,100  | 997,416  | zeaxanthin                        | 66%        |
| 11 | Erythrobacter vulgaris         | NZ_CCSI0100003 | Region 3.1 | terpene            | 264,281  | 288,621  | zeaxanthin                        | 66%        |
| 12 | Erythrobacter lutimaris        | NZ_QRB0100001 | Region 4.1 | terpene            | 94,452   | 119,258  | zeaxanthin                        | 66%        |
|    |                               | NZ_QRB0100001 | Region 4.2 | lassopeptide       | 672,213  | 701,326  | capsular polysaccharide           | 3%         |
|    |                               | NZ_QRB0100001 | Region 4.3 | bacteriocin, lanthipeptide | 1,194,495 | 1,218,692 |                                    |            |
| 13 | Erythrobacter seohaensis       | NZ_CP024920.1 | Region 1   | lassopeptide       | 440,381  | 462,679  |                                    |            |
## Pan-genome analysis of *Erythrobacter* sp. 3-20A1M

| Organism                  | Region   | Gene       | Start    | End      | Description                     | Identifier | Percentage |
|---------------------------|----------|------------|----------|----------|----------------------------------|------------|------------|
| *Erythrobacter odishensis* | Region 2 | bacteriocin | 1,859,624 | 1,870,472 |                                  | NZ_CP02492 0.1 |            |
|                          | Region 3 | terpene    | 1,993,945 | 2,018,261 | zeaxanthin                       | NZ_CP02492 0.1 | 66%       |
| *Erythrobacter marinus*   | Region 1.1 | T3PKS      | 252,492  | 293,559  |                                  | NZ_QYOS01 000025 |            |
|                          | Region 2.1 | T3PKS      | 471,232  | 512,296  |                                  | NZ_QYOS01 000024 |            |
| *Erythrobacter zhengii V18* | Region 1.1 | T3PKS      | 468,525  | 509,592  |                                  | NZ_QYOS01 000023 |            |
| *Erythrobacter xanthus*   | Region 20.1 | lassopeptide | 1         | 4,548     |                                  | NZ_QXFM01 000033 |            |
|                          | Region 40.1 | lassopeptide | 9,686     | 12,233    | carotenoid                       | NZ_QXFM01 000005 | 33%       |
|                          | Region 45.1 | lassopeptide | 51,011    | 53,568    |                                  | NZ_QXFM01 000057 |            |
|                          | Region 68.1 | lassopeptide | 58,971    | 61,528    |                                  | NZ_QXFM01 00007 |            |
|                          | Region 74.1 | lassopeptide | 13,793    | 16,350    |                                  | NZ_QXFM01 000083 |            |
|                          | Region 75.1 | lassopeptide | 24,972    | 27,534    |                                  | NZ_QXFM01 000084 |            |
|                          | Region 81.1 | NRPS-like   | 2,198     | 2,456     |                                  | NZ_QXFM01 000090 | 100%      |
|                          | Region 82.1 | NRPS       | 2,288     | 2,546     |                                  | NZ_QXFM01 000091 |            |
|                          | Region 87.1 | lassopeptide | 7,841     | 8,108     |                                  | NZ_QXFM01 000096 |            |
|                          | Region 89.1 | NRPS       | 8,516     | 8,782     |                                  | NZ_QXFM01 000097 |            |
|                          | Region 90.1 | NRPS       | 2,288     | 2,546     |                                  | NZ_QXFM01 000098 |            |
|                          | Region 10.1 | NRPS-like   | 2,159     | 2,417     |                                  | NZ_QXFM01 000115 |            |
|                          | Region 13.1 | NRPS       | 22,399    | 24,957    | acyldepsipeptidase               | NZ_QXFM01 000145 | 15%       |
Supplementary Table S5. Photosynthetic gene clusters of *Erythrobacter* species.

| Strain | Contig | Start  | End    | F/R | Locus tag     | Gene ID | Function                                                                 |
|--------|--------|--------|--------|-----|---------------|---------|--------------------------------------------------------------------------|
| CP017057 | 938351 | 939787 | -      | Ga0102493_111818 | pucC | FMS transporter, BCD family, chlorophyll transporter                      |
| CP017057 | 939784 | 940506 | -      | Ga0102493_111819 | bchM | magnesium-protoporphyrin O-methyltransferase                              |
| CP017057 | 940503 | 941399 | -      | Ga0102493_111820 | chlL | light-independent protochlorophyllide reductase subunit L                |
| CP017057 | 941422 | 945072 | -      | Ga0102493_111821 | bchH | magnesium chelatase subunit H                                            |
| CP017057 | 945062 | 946648 | -      | Ga0102493_111822 | chlB | light-independent protochlorophyllide reductase subunit B                |
| CP017057 | 946652 | 947953 | -      | Ga0102493_111823 | chlN | light-independent protochlorophyllide reductase subunit N                |
| CP017057 | 947950 | 948519 | -      | Ga0102493_111824 | bchF | 3-vinyl bacteriochlorophyllide hydratase                                  |
| CP017057 | 948792 | 949703 | +      | Ga0102493_111825 | btuF | Methanogenic corrinoid protein MtBl                                     |
| CP017057 | 949716 | 951140 | +      | Ga0102493_111826 | ppsR | transcriptional regulator PpsR                                           |
| CP017057 | 951271 | 952173 | +      | Ga0102493_111827 | bchG | chlorophyll synthase                                                      |
| CP017057 | 952173 | 953516 | +      | Ga0102493_111828 | pucC | FMS transporter, BCD family, chlorophyll transporter                      |
| CP017057 | 953513 | 954709 | +      | Ga0102493_111829 | bchP | geranylgeranyl reductase                                                  |
| CP017057 | 954720 | 955202 | +      | Ga0102493_111830 | tspO | tryptophan-rich sensory protein                                           |
| CP017057 | 955447 | 955701 | +      | Ga0102493_111831 |       | hypothetical protein                                                      |
| CP017057 | 955930 | 956853 | -      | Ga0102493_111832 | pufM | photosynthetic reaction center M subunit                                 |
| CP017057 | 956868 | 957692 | -      | Ga0102493_111833 | pufL | photosynthetic reaction center L subunit                                  |
| CP017057 | 957790 | 957984 | -      | Ga0102493_111834 | pufA | light-harvesting complex 1 alpha chain                                   |
| CP017057 | 958053 | 958229 | -      | Ga0102493_111835 | pufB | light-harvesting complex 1 beta chain                                    |
| CP017057 | 958386 | 959831 | -      | Ga0102493_111836 | bchZ | chlorophyllide a reductase subunit Z                                     |
| CP017057 | 959828 | 961429 | -      | Ga0102493_111837 | bchY | chlorophyllide a reductase subunit Y                                     |
| CP017057 | 961434 | 962423 | -      | Ga0102493_111838 | bchX | chlorophyllide a reductase subunit X                                     |
| CP017057 | 962420 | 963355 | -      | Ga0102493_111839 | bchC | 3-hydroxyethyl bacteriochlorophyllide a dehydrogenase                    |
| CP017057 | 963487 | 964608 | -      | Ga0102493_111840 | crtF | demethylspheroidene O-methyltransferase                                  |
| CP017057 | 964693 | 966285 | +      | Ga0102493_111841 | crtD | 1-hydroxycarotenoid 3,4-desaturase                                        |
| CP017057 | 966405 | 967124 | +      | Ga0102493_111842 | crtC | carotenoid 1,2-hydration                                                |
| CP017057 | 967134 | 967286 | -      | Ga0102493_111843 |       | hypothetical protein                                                      |
| CP017057 | 967283 | 968176 | -      | Ga0102493_111844 | bchO | magnesium chelatase accessory protein                                    |
| CP017057 | 968173 | 969984 | -      | Ga0102493_111845 | bchD | magnesium chelatase subunit D                                            |
Pan-genome analysis of *Erythrobacter* sp. 3-20A1M

| Accession     | Start    | End      | Gene Name | Description                                          |
|---------------|----------|----------|-----------|------------------------------------------------------|
| CP017057      | 969981   | 970982   | bchI      | magnesium chelatase subunit I                        |
| CP017057      | 971081   | 972781   | sfuB      | iron(III) transport system permease protein          |
| CP017057      | 2771973  | 2774057  | TolB      | Amino-terminal domain-containing protein              |
| CP017057      | 2774432  | 2775124  | ubqA      | Ubiquinol oxidase                                    |
| CP017057      | 2775180  | 2776211  | bchJ      | Bacteriochlorophyll 4-vinyl reductase                 |
| CP017057      | 2776201  | 2777829  | bchE      | Anaerobic magnesium-protoporphyrin IX monomethyl ester cyclase |
| NZ_JMIW01000003 | 138241   | 139635   | pucC      | MFS transporter                                      |
| NZ_JMIW01000003 | 139671   | 140393   | bchM      | Magnesium protoporphyrin IX methyltransferase        |
| NZ_JMIW01000003 | 140393   | 141289   | chlL      | Ferredoxin:protochlorophyllide reductase (ATP-dependent) iron-sulfur ATP-binding protein |
| NZ_JMIW01000003 | 141306   | 144941   | bchH      | Magnesium chelatase subunit H                        |
| NZ_JMIW01000003 | 144931   | 146496   | chlB      | Ferredoxin:protochlorophyllide reductase (ATP-dependent) subunit B |
| NZ_JMIW01000003 | 146499   | 147794   | chlN      | Ferredoxin:protochlorophyllide reductase (ATP-dependent) subunit N |
| NZ_JMIW01000003 | 147791   | 148366   | bchF      | 2-vinyl bacteriochlorophyllide hydratase              |
| NZ_JMIW01000003 | 148865   | 149461   | btuF      | Cobalamin B12-binding protein                        |
| NZ_JMIW01000003 | 149474   | 150898   | ppsR      | Transcriptional regulator PpsR                       |
| NZ_JMIW01000003 | 151166   | 152131   | bchG      | Chlorophyll synthase ChlG                           |
| NZ_JMIW01000003 | 152131   | 153519   | pucC      | BCD family MFS transporter                           |
| NZ_JMIW01000003 | 153516   | 154739   | bchP      | Geranylgeranyl diphosphate reductase                  |
| NZ_JMIW01000003 | 154797   | 155327   | tspO      | Tryptophan-rich sensory protein                       |
| NZ_JMIW01000003 | 155349   | 155603   | hypothetical | Hypothetical protein                                  |
| NZ_JMIW01000003 | 155708   | 158071   | suaC      | TonB-dependent receptor                              |
| NZ_JMIW01000003 | 158299   | 159225   | pufM      | Photosynthetic reaction center subunit M             |
| NZ_JMIW01000003 | 159225   | 160061   | pufL      | Photosynthetic reaction center subunit L             |
| NZ_JMIW01000003 | 160196   | 160324   | pufA      | Light-harvesting protein                             |
| NZ_JMIW01000003 | 160411   | 160569   | pufB      | Light-harvesting protein                             |
| NZ_JMIW01000003 | 160720   | 162204   | bchZ      | Chlorophyllide a reductase subunit Z                 |
| NZ_JMIW01000003 | 162201   | 163649   | bchY      | Chlorophyllide a reductase subunit Y                 |
| NZ_JMIW01000003 | 163768   | 164757   | bchX      | Chlorophyllide a reductase iron protein subunit X    |
| NZ_JMIW01000003 | 164754   | 165689   | bchC      | Chlorophyll synthesis pathway protein BchC           |
| NZ_JMIW01000003 | 165850   | 166983   | crtD      | Methyltransferase domain-containing protein          |
| NZ_JMIW01000003 | 167104   | 168684   | crtF      | Phytoene desaturase                                  |
## Pan-genome analysis of *Erythrobacter* sp. 3-20A1M

| Accession | Start | End   | Gene      | Description                              |
|-----------|-------|-------|-----------|------------------------------------------|
| NZ_JMIW01000003 | 168798 | 169517 | crtC      | hydroxyneurosporene dehydrogenase        |
| NZ_JMIW01000003 | 169514 | 169732 |           | hypothetical protein                      |
| NZ_JMIW01000003 | 169729 | 170634 | bchO      | alpha/beta fold hydrolase                 |
| NZ_JMIW01000003 | 170631 | 172307 | bchD      | magnesium chelatase subunit D             |
| NZ_JMIW01000003 | 172304 | 173305 | bchI      | magnesium chelatase ATPase subunit I      |
| NZ_JMIW01000003 | 173390 | 175066 | sfuB      | iron ABC transporter permease             |
| NZ_QRBB01000001 | 123476 | 123541 | VOC family protein |                            |
| NZ_QRBB01000001 | 123525 | 123625 | bchI      | magnesium chelatase ATPase subunit I      |
| NZ_QRBB01000001 | 123625 | 123794 | bchD      | magnesium chelatase subunit D             |
| NZ_QRBB01000001 | 123794 | 123882 | bchO      | alpha/beta fold hydrolase                 |
| NZ_QRBB01000001 | 123879 | 123940 | chlB      | gamma-glutamylcyclotransferase            |
| NZ_QRBB01000001 | 123940 | 124015 | crtC      | hydroxyneurosperone dehydrogenase         |
| NZ_QRBB01000001 | 124028 | 124186 | crtD      | phytoene desaturase                       |
| NZ_QRBB01000001 | 124197 | 124305 | crtF      | methyltransferase domain-containing protein|
| NZ_QRBB01000001 | 124306 | 124420 | bchC      | chlorophyll synthesis pathway protein BchC |
| NZ_QRBB01000001 | 124418 | 124593 | bchX      | chlorophyllide a reductase iron protein subunit X |
| NZ_QRBB01000001 | 124598 | 124679 | bchY      | chlorophyllide a reductase subunit Y       |
| NZ_QRBB01000001 | 124690 | 124833 | bchZ      | chlorophyllide a reductase subunit Z       |
| NZ_QRBB01000001 | 124849 | 124865 | pqB       | light-harvesting protein                  |
| NZ_QRBB01000001 | 124873 | 124922 | pqA       | light-harvesting protein                  |
| NZ_QRBB01000001 | 124905 | 124970 | pqL       | photosynthetic reaction center subunit L   |
| NZ_QRBB01000001 | 124988 | 125081 | pqM       | photosynthetic reaction center subunit M   |
| NZ_QRBB01000001 | 125082 | 125180 | tspO      | tryptophan-rich sensory protein           |
| NZ_QRBB01000001 | 125141 | 125160 | bchP      | geranylgeranyl diphosphate reductase      |
| NZ_QRBB01000001 | 125164 | 125284 | pucC      | MFS transporter                           |
| NZ_QRBB01000001 | 125283 | 125415 | pucD      | covalent B12-binding protein              |
| NZ_QRBB01000001 | 125415 | 125507 | bchG      | chlorophyll synthase ChlG                 |
| NZ_QRBB01000001 | 125514 | 125656 | ppsR      | transcriptional regulator PpsR             |
| NZ_QRBB01000001 | 125655 | 125730 | bnaF      | covalent B12-binding protein              |
| NZ_QRBB01000001 | 125756 | 125821 | bchF      | 2-vinyl bacteriochlorophyllide hydratase   |
| NZ_QRBB01000001 | 125821 | 125907 | chlN      | ferredoxin:protochlorophyllide reductase (ATP-dependent) subunit N |
Pan-genome analysis of *Erythrobacter* sp. 3-20A1M

| Accession | Start | End | Gene Name | Description |
|-----------|-------|-----|-----------|-------------|
| NZ_QRBB01000001 | 1259510 | 1261138 | DL238_RS06165 | ferredoxin:protochlorophyllide reductase (ATP-dependent) subunit B |
| NZ_QRBB01000001 | 1261128 | 1264670 | DL238_RS06170 | magnesium chelatase subunit H |
| NZ_QRBB01000001 | 1264681 | 1265568 | DL238_RS06175 | ferredoxin:protochlorophyllide reductase (ATP-dependent) iron-sulfur ATP-binding protein |
| NZ_QRBB01000001 | 1265568 | 1266293 | DL238_RS06180 | magnesium protoporphyrin IX methyltransferase |
| NZ_LDCP01000004 | 33678 | 33998 | AB731_RS12275 | TrbC/VirB2 family protein |
| NZ_LDCP01000004 | 34097 | 35098 | AB731_RS12280 | chlI magnesium chelatase ATPase subunit I |
| NZ_LDCP01000004 | 35095 | 36804 | AB731_RS12285 | chlD magnesium chelatase subunit D |
| NZ_LDCP01000004 | 36804 | 37691 | AB731_RS12290 | bchO alpha/beta fold hydrolase |
| NZ_LDCP01000004 | 37808 | 38527 | AB731_RS12295 | crtC hydroxyneurosporene dehydrogenase |
| NZ_LDCP01000004 | 38647 | 40212 | AB731_RS12300 | pucC MFS transporter |
| NZ_LDCP01000004 | 40293 | 41429 | AB731_RS12305 | bchP geranylgeranyl diphosphate reductase |
| NZ_LDCP01000004 | 41546 | 42478 | AB731_RS12310 | bchC chlorophyll synthesis pathway protein BchC |
| NZ_LDCP01000004 | 42478 | 43464 | AB731_RS12315 | bchX chlorophyllide a reductase iron protein subunit X |
| NZ_LDCP01000004 | 43468 | 45015 | AB731_RS12320 | bchY chlorophyllide a reductase subunit Y |
| NZ_LDCP01000004 | 45012 | 46457 | AB731_RS12325 | bchZ chlorophyllide a reductase subunit Z |
| NZ_LDCP01000004 | 46578 | 46736 | AB731_RS13860 | pufB light-harvesting protein |
| NZ_LDCP01000004 | 46801 | 46968 | AB731_RS13865 | pufA light-harvesting protein |
| NZ_LDCP01000004 | 47095 | 47919 | AB731_RS12330 | pufL photosynthetic reaction center subunit L |
| NZ_LDCP01000004 | 47934 | 48911 | AB731_RS12335 | pufM photosynthetic reaction center subunit M |
| NZ_LDCP01000004 | 48908 | 49963 | AB731_RS12340 | pufC photosynthetic reaction center cytochrome c subunit |
| NZ_LDCP01000004 | 50037 | 50243 | AB731_RS12345 | hypothetical protein |
| NZ_LDCP01000004 | 50319 | 50786 | AB731_RS12350 | tspO tryptophan-rich sensory protein |
| NZ_LDCP01000004 | 50804 | 52000 | AB731_RS12355 | bchP geranylgeranyl diphosphate reductase |
| NZ_LDCP01000004 | 51997 | 53316 | AB731_RS12360 | pucC BCD family MFS transporter |
| NZ_LDCP01000004 | 53313 | 54215 | AB731_RS12365 | chlB ferredoxin:protochlorophyllide reductase (ATP-dependent) subunit B |

*E. marinus*
| Strain | Gene | Start | End | Description |
|--------|------|-------|-----|-------------|
| NZ_LDCP01000004 | 60226 | 63813 | + | $\text{bchH}$ magnesium chelatase subunit H |
| NZ_LDCP01000004 | 63823 | 64722 | + | $\text{chlL}$ ferredoxin:protochlorophyllide reductase (ATP-dependent) iron-sulfur ATP-binding protein |
| NZ_LDCP01000004 | 64722 | 65453 | + | $\text{bchM}$ magnesium protoporphyrin IX methyltransferase |
| NZ_LDCP01000004 | 65453 | 66880 | + | $\text{pucC}$ BCD family MFS transporter |
| NZ_QYOS01000024 | 423580 | 425007 | - | $\text{pucC}$ MFS transporter |
| NZ_QYOS01000024 | 425007 | 425708 | - | $\text{bchM}$ magnesium protoporphyrin IX methyltransferase |
| NZ_QYOS01000024 | 425708 | 426604 | - | $\text{chlL}$ ferredoxin:protochlorophyllide reductase (ATP-dependent) iron-sulfur ATP-binding protein |
| NZ_QYOS01000024 | 426618 | 430166 | - | $\text{bchH}$ magnesium chelatase subunit H |
| NZ_QYOS01000024 | 430156 | 431685 | - | $\text{chlB}$ ferredoxin:protochlorophyllide reductase (ATP-dependent) subunit B |
| NZ_QYOS01000024 | 431690 | 432988 | - | $\text{chlN}$ ferredoxin:protochlorophyllide reductase (ATP-dependent) subunit N |
| NZ_QYOS01000024 | 432985 | 433515 | - | $\text{bchF}$ 2-vinyl bacteriochlorophyllide hydratase |
| NZ_QYOS01000024 | 433726 | 434622 | + | $\text{btuF}$ cobalamin B12-binding protein |
| NZ_QYOS01000024 | 434634 | 436052 | + | $\text{ppsR}$ transcriptional regulator PpsR |
| NZ_QYOS01000024 | 436118 | 437023 | + | $\text{chlG}$ chlorophyll synthase ChlG |
| NZ_QYOS01000024 | 437031 | 438356 | + | $\text{pucC}$ MFS transporter |
| NZ_QYOS01000024 | 438353 | 439549 | + | $\text{bchP}$ geranylgeranyl diphosphate reductase |
| NZ_QYOS01000024 | 439546 | 440025 | + | $\text{tspO}$ tryptophan-rich sensory protein |
| NZ_QYOS01000024 | 440086 | 440280 | + | $\text{pufC}$ photosynthetic reaction center cytochrome c subunit |
| NZ_QYOS01000024 | 440291 | 441406 | - | $\text{pufM}$ photosynthetic reaction center subunit M |
| NZ_QYOS01000024 | 441403 | 442377 | - | $\text{pufL}$ photosynthetic reaction center subunit L |
| NZ_QYOS01000024 | 442392 | 443216 | - | $\text{pufA}$ light-harvesting protein |
| NZ_QYOS01000024 | 443315 | 443491 | - | $\text{pufB}$ light-harvesting protein |
| NZ_QYOS01000024 | 443573 | 443728 | - | $\text{bchZ}$ chlorophyllide a reductase subunit Z |
| NZ_QYOS01000024 | 443847 | 445292 | - | $\text{bchY}$ chlorophyllide a reductase subunit Y |
| NZ_QYOS01000024 | 445289 | 446812 | - | $\text{bchX}$ chlorophyllide a reductase iron protein subunit X |
| NZ_QYOS01000024 | 446843 | 447841 | - | $\text{bchC}$ chlorophyll synthase pathway protein BehC |
| NZ_QYOS01000024 | 447838 | 448773 | - | $\text{crtF}$ methyltransferase domain-containing protein |
| NZ_QYOS01000024 | 448882 | 450042 | - | $\text{crtD}$ phytoene desaturase |
| NZ_QYOS01000024 | 450108 | 451667 | + | $\text{crtC}$ hydroxynaphthoquinone dehydrogenase |
## Pan-genome analysis of *Erythrobacter* sp. 3-20A1M

| Gene ID        | Start Position | End Position | Protein Name                        | Description                                           |
|----------------|----------------|--------------|-------------------------------------|-------------------------------------------------------|
| NZ_QYOS01000024  | 45243          | 45268        | D4Q51_RS11505                       | hypothetical protein                                   |
| NZ_QYOS01000024  | 45249          | 45354        | D4Q51_RS11510                       | alpha/beta fold hydrolase                             |
| NZ_QYOS01000024  | 45355          | 45515        | D4Q51_RS11515                       | magnesium chelatase subunit D                         |
| NZ_QYOS01000024  | 45521          | 45622        | D4Q51_RS11520                       | magnesium chelatase ATPase subunit I                  |
| NZ_QYOS01000024  | 45627          | 45767        | D4Q51_RS11525                       | TolC family protein                                   |
| NZ_QXFL01000004  | 12125          | 12823        | D2V07_RS09550                       | Crp/Fnr family transcriptional regulator              |
| NZ_QXFL01000004  | 12955          | 13956        | D2V07_RS09555                       | bchI magnesium chelatase ATPase subunit I             |
| NZ_QXFL01000004  | 13957          | 15645        | D2V07_RS09560                       | bchD magnesium chelatase subunit D                    |
| NZ_QXFL01000004  | 15642          | 16559        | D2V07_RS09565                       | bchO alpha/beta fold hydrolase                        |
| NZ_QXFL01000004  | 16552          | 17418        | D2V07_RS09570                       | hypothetical protein                                   |
| NZ_QXFL01000004  | 17538          | 19097        | D2V07_RS09580                       | crtC hydroxyneurosporene dehydrogenase                |
| NZ_QXFL01000004  | 19212          | 20321        | D2V07_RS09585                       | crtD phytoene desaturase                              |
| NZ_QXFL01000004  | 20431          | 21366        | D2V07_RS09590                       | bchC chlorophyll synthesis pathway protein BchC       |
| NZ_QXFL01000004  | 21363          | 22361        | D2V07_RS09595                       | bchX chlorophyllide a reductase iron protein subunit X|
| NZ_QXFL01000004  | 22401          | 23924        | D2V07_RS09600                       | bchY chlorophyllide a reductase subunit Y             |
| NZ_QXFL01000004  | 23921          | 25366        | D2V07_RS09605                       | bchZ chlorophyllide a reductase subunit Z             |
| NZ_QXFL01000004  | 25488          | 25643        | D2V07_RS09610                       | pufB light-harvesting protein                         |
| NZ_QXFL01000004  | 25725          | 25898        | D2V07_RS09615                       | pufA light-harvesting protein                         |
| NZ_QXFL01000004  | 26000          | 26824        | D2V07_RS09620                       | pufL photosynthetic reaction center subunit L         |
| NZ_QXFL01000004  | 26839          | 27813        | D2V07_RS09625                       | pufM photosynthetic reaction center subunit M         |
| NZ_QXFL01000004  | 27810          | 28925        | D2V07_RS09630                       | pufC photosynthetic reaction center cytochrome c subunit|
| NZ_QXFL01000004  | 28942          | 29142        | D2V07_RS09635                       | hypothetical protein                                   |
| NZ_QXFL01000004  | 29196          | 29787        | D2V07_RS09640                       | tspO tryptophan-rich sensory protein                   |
| NZ_QXFL01000004  | 29765          | 30871        | D2V07_RS09645                       | bchP geranylgeranyl diphosphate reductase             |
| NZ_QXFL01000004  | 30868          | 32193        | D2V07_RS09650                       | pucC MFS transporter                                   |
| NZ_QXFL01000004  | 32190          | 33095        | D2V07_RS09655                       | bchG chlorophyll synthase ChlG                        |
| NZ_QXFL01000004  | 33161          | 34579        | D2V07_RS09660                       | ppsR transcriptional regulator PpsR                   |
| NZ_QXFL01000004  | 34591          | 35487        | D2V07_RS09665                       | bnuF cobalamin B12-binding protein                    |
| NZ_QXFL01000004  | 35698          | 36228        | D2V07_RS09670                       | bchF 2-vinyl bacteriochlorophyllide hydratase          |
| NZ_QXFL01000004  | 36225          | 37508        | D2V07_RS09675                       | chIN ferredoxin:protochlorophyllide reductase (ATP-dependent) subunit N |
### Pan-genome analysis of *Erythrobacter* sp. 3-20A1M

| Accession   | Start Position | End Position | Orientation | Gene Name | Description                                           |
|-------------|----------------|--------------|-------------|-----------|-------------------------------------------------------|
| NZ_QXFL01000004 | 37513          | 39045        | +           | D2V07_RS09680 | chlB: ferredoxin:protochlorophyllide reductase (ATP-dependent) subunit B |
| NZ_QXFL01000004 | 39035          | 42571        | +           | D2V07_RS09685 | bchH: magnesium chelatase subunit H                  |
| NZ_QXFL01000004 | 42585          | 43481        | +           | D2V07_RS09690 | chlL: ferredoxin:protochlorophyllide reductase (ATP-dependent) iron-sulfur ATP-binding protein |
| NZ_QXFL01000004 | 43481          | 44197        | +           | D2V07_RS09695 | bchM: magnesium protoporphyrin IX methyltransferase   |
| NZ_QXFL01000004 | 44197          | 45624        | +           | D2V07_RS09700 | pucC: MFS transporter                                  |
| NZ_QXFL01000001 | 624664         | 625662       | -           | D2V07_RS03135 | rhodanese-related sulfurtransferase                   |
| NZ_QXFL01000001 | 625906         | 626754       | +           | D2V07_RS03140 | pufL: photosynthetic reaction center subunit L        |
| NZ_QXFL01000001 | 627803         | 628963       | +           | D2V07_RS03150 | pufC: photosynthetic reaction center cytochrome c subunit |

