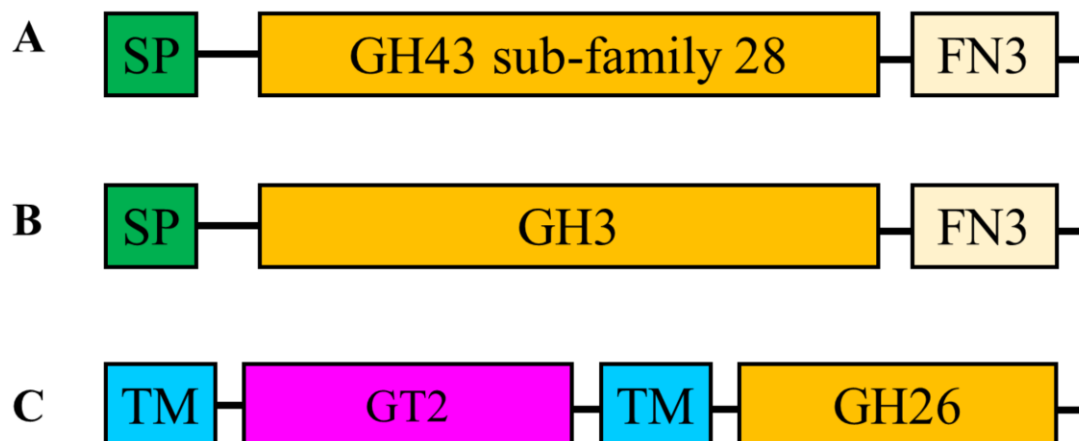
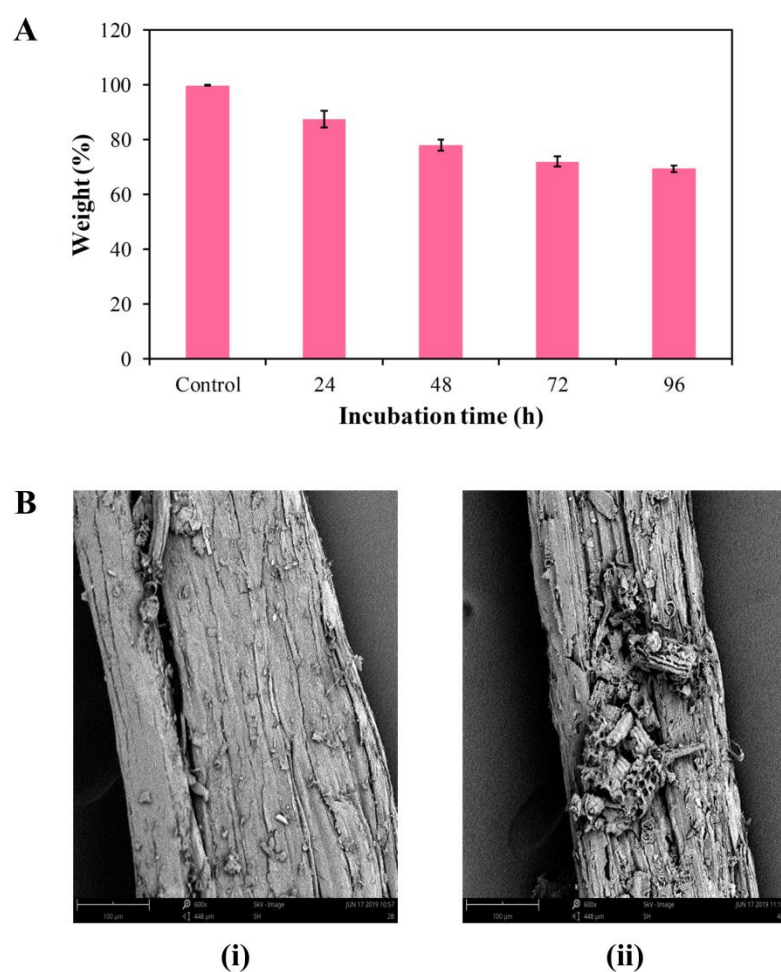


## Supplementary materials



**Figure S1** Domain organization of GH43 sub-family 28 (A), GH3 (B) and GH26 with GT2 (C) annotated in the genome of *Robertkochia solimangrovi*. SP, signal peptide; FN3, fibronectin type 3 domain; TM, transmembrane helix.



**Figure S2** Oil palm empty fruit bunch (EFB) deconstruction by *Robertkochia solimangrovi* as indicated by total biomass weight loss (A) and EFB structural changes (B). Scanning electron micrographs of EFB structure before strain inoculation (i) and after 96 h of incubation (ii).

**Table S1.** Classification of protein coding genes according to Clusters of Orthologous Groups (COGs) for *R. solimangrovi* and *R. marina*.

| Code | Description of COG functional categories                      | <i>R. solimangrovi</i> |                | <i>R. marina</i> |                |
|------|---|------------------------|----------------|------------------|----------------|
|      |   | Number of genes        | Percentage (%) | Number of genes  | Percentage (%) |
| R    | General function prediction only                              | 379                    | 13.35          | 318              | 13.60          |
| E    | Amino acid transport and metabolism                           | 236                    | 8.32           | 225              | 9.59           |
| M    | Cell wall/membrane/envelope biogenesis                        | 231                    | 8.15           | 209              | 8.93           |
| S    | Function unknown  | 224                    | 7.89           | 179              | 7.65           |
| K    | Transcription   | 198                    | 6.97           | 119              | 5.09           |
| P    | Inorganic ion transport and metabolism                        | 192                    | 6.76           | 124              | 5.29           |
| G    | Carbohydrate transport and metabolism                         | 186                    | 6.55           | 134              | 5.73           |
| C    | Energy production and conversion                              | 160                    | 5.62           | 152              | 6.49           |
| J    | Translation, ribosomal structure and biogenesis               | 151                    | 5.33           | 159              | 6.80           |
| T    | Signal transduction mechanisms                                | 148                    | 5.22           | 76               | 3.25           |
| H    | Coenzyme transport and metabolism                             | 129                    | 4.54           | 110              | 4.70           |
| O    | Posttranslational modification, protein turnover, chaperones  | 126                    | 4.44           | 111              | 4.73           |
| L    | Replication, recombination and repair                         | 101                    | 3.54           | 102              | 4.35           |
| I    | Lipid transport and metabolism                                | 100                    | 3.52           | 89               | 3.79           |
| F    | Nucleotide transport and metabolism                           | 73                     | 2.58           | 69               | 2.95           |
| V    | Defense mechanisms  | 66                     | 2.32           | 45               | 1.94           |
| Q    | Secondary metabolites biosynthesis, transport and catabolism  | 60                     | 2.12           | 50               | 2.14           |
| U    | Intracellular trafficking, secretion, and vesicular transport | 50                     | 1.75           | 40               | 1.71           |
| D    | Cell cycle control, cell division, chromosome partitioning    | 19                     | 0.67           | 21               | 0.91           |
| N    | Cell motility   | 8                      | 0.30           | 7                | 0.32           |
| B    | Chromatin structure and dynamics                              | 1                      | 0.03           | 1                | 0.04           |

**Table S2.** Similarity of lignocellulose degrading genes of *R. solimangrovi* to other related sequences based BLASTp search.

| CAZy family        | Locus tag accession | Top hit sequence  | Identity |
|--------------------|---------------------|---|----------|
| GH5 sub-family 46  | DMZ48_08160         | carbohydrate binding module (family 6) of <i>Leeuwenhoekiella marinoflava</i> DSM 3653            | 58.00%   |
| GH9                | DMZ48_13260         | glycosyl hydrolase family 9 of <i>Draconibacterium orientale</i>                                  | 63.48%   |
| GH3                | DMZ48_01605         | glycosyl hydrolase of <i>Flavobacteriaceae</i> bacterium CG17_big_fil_post_rev_8_21_14_2_50_33_15 | 62.69%   |
|                    | DMZ48_08150         | beta-glucosidase of <i>Salinimicrobium sediminis</i>  | 77.32%   |
|                    | DMZ48_09610         | beta-glucosidase of <i>Pseudozobellia</i> sp. CCMM003   | 73.40%   |
|                    | DMZ48_13440         | glycosyl hydrolase of <i>Marivirga lumbricoides</i>   | 67.84%   |
|                    | DMZ48_13560         | beta-glucosidase of <i>Joostella marina</i> DSM 19592   | 67.63%   |
|                    | DMZ48_14810         | glycosyl hydrolase family 3 of <i>Flavobacterium subsaxonicum</i> WB 4.1-42                       | 67.90%   |
|                    | DMZ48_14815         | glycosyl hydrolase of <i>Gramella</i> sp. SH35  | 60.38%   |
| GH30               | DMZ48_08155         | glucosylceramidase of <i>Salinimicrobium sediminis</i>  | 64.03%   |
|                    | DMZ48_08165         | glucosylceramidase of <i>Flavobacteriia</i> bacterium   | 64.42%   |
| GH5 sub-family 13  | DMZ48_12810         | 1,4-beta-xylanase of <i>Salegentibacter</i> sp. T436  | 77.95%   |
| GH10               | DMZ48_13420         | 1,4-beta-xylanase of <i>Muricauda</i> sp. 72  | 63.71%   |
| GH43 sub-family 29 | DMZ48_01140         | glycosyl hydrolase family 43 of <i>Lutibacter oceani</i>  | 75.47%   |
|                    | DMZ48_12865         | glycoside hydrolase of <i>Tamlana nanhaiensis</i>   | 84.45%   |
| GH43               | DMZ48_04615         | beta-xylosidase of <i>Joostella marina</i> DSM 19592  | 63.94%   |
|                    | DMZ48_15560         | glycosyl hydrolase of <i>Lacibacter</i> sp. TTM-7   | 66.15%   |
| GH43 sub-family 31 | DMZ48_12790         | beta-xylosidase of <i>Joostella marina</i> DSM 19592  | 64.78%   |
|                    | DMZ48_12800         | glycosyl hydrolases family 43 of <i>Salegentibacter salinarum</i>                                 | 57.06%   |
| GH43 sub-family 1  | DMZ48_13400         | alpha-N-arabinofuranosidase of <i>Marivirga lumbricoides</i>                                      | 69.86%   |

|                           |             |   |        |
|---------------------------|-------------|---|--------|
| GH43 sub-family 10        | DMZ48_09800 | beta-xylosidase of <i>Joostella marina</i> DSM 19592                                  | 72.31% |
| GH43 sub-family 26        | DMZ48_12795 | putative beta-xylosidase of <i>Joostella marina</i> DSM 19592                         | 78.27% |
|                           | DMZ48_15550 | glycosyl hydrolase family 43 of <i>Flavobacterium</i> sp. Leaf82                      | 64.33% |
|                           | DMZ48_18410 | alpha-N-arabinofuranosidase of <i>Pontibacter diazotrophicus</i>                      | 68.87% |
| GH43                      | DMZ48_15515 | beta-xylosidase of <i>Zhouia amylolytica</i> AD3                                      | 79.31% |
| GH43 sub-family 17        | DMZ48_15280 | glycosyl hydrolases family 43 of <i>Cyclobacterium lianum</i>                         | 77.24% |
| GH43 sub-family 18        | DMZ48_12805 | glycosyl hydrolase family 43 of <i>Salagentibacter</i> sp. T436                       | 80.77% |
| GH43 sub-family 18 + CE10 | DMZ48_04720 | beta-galactosidase of <i>Flavobacteriaceae</i> bacterium FS1-H7996/R                  | 62.50% |
| GH43 sub-family 19        | DMZ48_14390 | hypothetical protein DSM04_101529 of <i>Leeuwenhoekiella</i> sp. R-50232              | 81.42% |
| GH43 sub-family 19 + GH43 | DMZ48_07370 | beta-xylosidase of <i>Joostella marina</i> DSM 19592                                  | 75.88% |
| GH51                      | DMZ48_01125 | alpha-N-arabinofuranosidase of <i>Flavobacterium</i> sp. 123                          | 66.92% |
|                           | DMZ48_01150 | alpha-N-arabinofuranosidase of <i>Flavobacterium</i> sp. 11                           | 76.06% |
|                           | DMZ48_08775 | alpha-N-arabinofuranosidase of <i>Leeuwenhoekiella marinoflava</i> DSM 3653           | 60.62% |
| GH67                      | DMZ48_13435 | alpha-glucuronidase of <i>Sinomicrobium oceani</i>                                    | 62.27% |
| GH115                     | DMZ48_04675 | hypothetical protein IIF7_17427 of <i>Zunongwangia atlantica</i> 22II14-10F7          | 53.34% |
| GH43 sub-family 28        | DMZ48_07195 | F5/8 type C domain-containing protein of <i>Fabibacter pacificus</i>                  | 81.15% |
|                           | DMZ48_17740 | F5/8 type C domain-containing protein of <i>Porphyromonadaceae</i> bacterium KH3CP3RA | 59.55% |
| CE1                       | DMZ48_16570 | esterase family protein of <i>Muricauda</i> sp. 72                                    | 63.81% |
| CE2                       | DMZ48_07320 | hypothetical protein APR42_08025 of <i>Salagentibacter mishustinae</i>                | 42.45% |
| CE4                       | DMZ48_03780 | polysaccharide deacetylase family protein of <i>Tenacibaculum litoreum</i>            | 52.58% |
| GH113                     | DMZ48_11390 | hypothetical protein SAMN04488008_102204 of <i>Maribacter orientalis</i>              | 50.49% |

|                         |             |  |        |
|-------------------------|-------------|--|--------|
| GH26 + GT2 sub-family 3 | DMZ48_06700 | family 2 glycosyl transferase of <i>Galbibacter marinus</i>                | 51.12% |
| GH27 with CBM51         | DMZ48_12870 | hypothetical protein PK35_02670 of <i>Tamlana nanhaiensis</i>              | 79.50% |
| GH5 sub-family 4        | DMZ48_14940 | aryl-phospho-beta-D-glucosidase BglC of <i>Cytophaga xylanolytica</i>      | 55.56% |
| GH2                     | DMZ48_03505 | hypothetical protein DDZ16_13090 of <i>Marinilabilia</i> sp. WTE           | 61.46% |
|                         | DMZ48_04665 | beta-galactosidase/beta-glucuronidase of <i>Joostella marina</i> DSM 19592 | 70.24% |
|                         | DMZ48_07180 | beta-galactosidase of <i>Flaviramulus basaltis</i>                         | 75.19% |
|                         | DMZ48_07385 | beta-galactosidase of <i>Pustulibacterium marinum</i>                      | 68.82% |
|                         | DMZ48_14580 | beta-glycosidase of <i>Zunongwangia atlantica</i> 22II14-10F7              | 67.31% |
|                         | DMZ48_14795 | DUF4982 domain-containing protein of <i>Sinomicrobium pectinilyticum</i>   | 65.00% |
|                         | DMZ48_14865 | beta-galactosidase of <i>Gramella</i> sp. SH35                             | 52.13% |
|                         | DMZ48_15505 | beta-galactosidase of <i>Reichenbachella</i> sp. 5M10                      | 63.13% |
|                         | DMZ48_15590 | beta-galactosidase of <i>Joostella marina</i> DSM 19592                    | 75.16% |
|                         | DMZ48_16090 | beta-galactosidase of <i>Zhouia amylolytica</i>                            | 57.00% |
|                         | DMZ48_16435 | beta-glucuronidase of <i>Mariniflexile</i> sp. TRM1-10                     | 74.84% |
| GH43 sub-family 24      | DMZ48_07375 | glycosyl hydrolases family 43 of <i>Pustulibacterium marinum</i>           | 72.27% |
| GH29                    | DMZ48_02920 | alpha-L-fucosidase of <i>Flavobacteriia</i> bacterium                      | 62.30% |
| GH29 with CBM32         | DMZ48_16630 | alpha-L-fucosidase of <i>Arenibacter</i> sp. C-21                          | 68.04% |
| GH95                    | DMZ48_14070 | alpha-L-fucosidase of <i>Mangrovimonas</i> sp. DI 80                       | 63.26% |
|                         | DMZ48_14845 | alpha-L-fucosidase 2 of <i>Lutibacter flavus</i>                           | 60.86% |
| GH31                    | DMZ48_14800 | alpha-xylosidase of <i>Confluentibacter</i> sp. 3B                         | 79.80% |
| GH16                    | DMZ48_07400 | hypothetical protein SAMN02927921_00688 of <i>Sinomicrobium oceani</i>     | 57.43% |
|                         | DMZ48_16450 | hypothetical protein JoomaDRAFT_0386 of <i>Joostella marina</i> DSM 19592  | 71.50% |

|                               |             |   |        |
|-------------------------------|-------------|---|--------|
| GH28                          | DMZ48_04685 | pectate lyase superfamily protein of <i>Leeuwenhoekiella palythoae</i>                    | 68.11% |
|                               | DMZ48_04700 | glycoside hydrolase family protein of <i>Galbibacter marinus</i>                          | 72.09% |
|                               | DMZ48_09805 | endopolygalacturonase of <i>Joostella marina</i> DSM 19592                                | 73.56% |
| GH43 sub-family 4             | DMZ48_01145 | arabinan endo-1,5-alpha-L-arabinosidase of <i>Gramella</i> sp. SH35                       | 70.33% |
| GH43 sub-family 5             | DMZ48_01135 | arabinan endo-1,5-alpha-L-arabinosidase of <i>Flavobacteriaceae</i> bacterium FS1-H7996/R | 71.74% |
| GH43 sub-family 37 with CBM61 | DMZ48_08955 | beta-xylosidase of <i>Zunongwangia atlantica</i> 22II14-10F7                              | 67.70% |
| GH53                          | DMZ48_07175 | arabinogalactan endo-1,4-beta-galactosidase of <i>Flaviramulus basaltis</i>               | 68.39% |
| GH88                          | DMZ48_16440 | glycosyl hydrolase family 88 of <i>Joostella marina</i> DSM 19592                         | 71.96% |
| GH105                         | DMZ48_02835 | putative unsaturated glucuronyl hydrolase of <i>Joostella marina</i> DSM 19592]           | 71.13% |
|                               | DMZ48_04715 | family 88 glycosyl hydrolase of <i>Flavobacterium</i> sp. IMCC34759                       | 75.40% |
| GH106                         | DMZ48_04710 | glycoside hydrolase of <i>Galbibacter marinus</i>   | 60.57% |
| GH145                         | DMZ48_16445 | neuraminidase of <i>Flavobacterium daejeonense</i>  | 61.00% |
| GH127                         | DMZ48_01130 | hypothetical protein SAMN05216294_1503 of <i>Muricauda zhangzhouensis</i>                 | 68.92% |
|                               | DMZ48_14480 | DUF1680 family protein of <i>Larkinella arboricola</i>                                    | 60.88% |
|                               | DMZ48_15545 | hypothetical protein JoomaDRAFT_0361 of <i>Joostella marina</i> DSM 19592                 | 64.77% |
| GH146                         | DMZ48_12780 | protein of unknown function DUF1680 of <i>Muricauda ruestringensis</i> DSM 13258          | 72.94% |
| CE12                          | DMZ48_02845 | rhamnogalacturonan acetyltransferase of <i>Flaviramulus basaltis</i>                      | 64.11% |
|                               | DMZ48_04660 | rhamnogalacturonan acetyltransferase of <i>Sinomicrobium pectinilyticum</i>               | 56.08% |
| CE12 + CE12                   | DMZ48_04670 | Lysophospholipase L1 of <i>Salegentibacter salinarum</i>                                  | 64.53% |
| CE12 + CE10                   | DMZ48_09795 | esterase/lipase of <i>Joostella marina</i> DSM 19592                                      | 61.72% |

|                           |             |  |        |
|---------------------------|-------------|--|--------|
| PL1 sub-family 2          | DMZ48_09815 | hypothetical protein<br>JoomaDRAFT_1172 of <i>Joostella marina</i> DSM 19592 | 68.08% |
| PL1 sub-family 2 +<br>CE8 | DMZ48_09810 | Pectinesterase A precursor of<br><i>Mariniflexile</i> sp. TRM1-10            | 65.91% |
| PL10 + CE8                | DMZ48_02840 | pectinesterase of <i>Maribacter polysiphoniae</i>                            | 53.28% |
| PL22                      | DMZ48_04705 | hypothetical protein C7S20_10175<br>of <i>Gramella</i> sp. SH35              | 59.17% |
| CBM4                      | DMZ48_13415 | hypothetical protein of <i>Lewinella nigricans</i> DSM 23189                 | 46.24% |
| CBM9                      | DMZ48_08015 | Carbohydrate family 9 binding<br>domain of <i>Leeuwenhoekiella palythoae</i> | 56.61% |

**Table S3.** Putative horizontal transferred genes of *R. solimangrovi* related to lignocellulose degradation, inferred from genomic data.

| Enzyme family         | Gene annotation                                      | Origin  |
|-----------------------|--|---|
| GH2                   | $\beta$ -galactosidase                               | <i>Tangfeifania diversioriginum</i> DSM 27063   |
| GH5 sub-family 4      | Xyloglucan-specific endo- $\beta$ -<br>1,4-glucanase | <i>Prolixibacter denitrificans</i> DSM 27267    |
| GH9                   | Endoglucanase/ exoglucanase                          | <i>Draconibacterium orientale</i> DSM 25947     |
| GH16                  | Xyloglucan-specific endo- $\beta$ -<br>1,4-glucanase | <i>Chitinophagaceae</i> bacterium PMP191F       |
| GH43                  | $\beta$ -xylosidase                                  | <i>Echinicola vietnamensis</i> KMM 6221         |
| GH43 sub-family<br>17 | $\alpha$ -L-arabinofuranosidase                      | <i>Cyclobacterium lianum</i> CGMCC 1.6102       |
| GH43 sub-family<br>28 | Uncharacterized xylanase                             | <i>Porphyromonadaceae</i> bacterium<br>KH3CP3RA |
| GH127                 | $\beta$ -L-arabinofuranosidase                       | <i>Larkinella arboricola</i> DSM 21851          |



**Table S4.** List of potential genes involved in uptake and metabolism of sugars, inferred from genome of *R. solimangrovi*.

| Category             | Gene annotation                        | Number of genes | NCBI accession |
|----------------------|--|-----------------|----------------|
| Sugar transporters   | Na <sup>+</sup> /glucose cotransporter | 3               | TRZ45902       |
|                      |  |                 | TRZ42504       |
|                      |  |                 | TRZ42552       |
|                      | ABC transporter                        | 9               | TRZ46117       |
|                      |  |                 | TRZ45189       |
|                      |  |                 | TRZ45190       |
|                      |  |                 | TRZ44474       |
|                      |  |                 | TRZ43527       |
|                      |  |                 | TRZ43218       |
|                      |  |                 | TRZ42752       |
|                      |  |                 | TRZ42238       |
|                      |  |                 | TRZ42030       |
|                      |  |                 | TRZ45892       |
|                      | MFS transporter                        | 16              | TRZ46281       |
|                      |  |                 | TRZ45171       |
|                      |  |                 | TRZ43987       |
|                      |  |                 | TRZ43544       |
|                      |  |                 | TRZ43734       |
|                      |  |                 | TRZ43151       |
|                      |  |                 | TRZ43247       |
|                      |  |                 | TRZ43248       |
|                      |  |                 | TRZ43275       |
|                      |  |                 | TRZ43297       |
|                      |  |                 | TRZ42558       |
|                      |  |                 | TRZ42286       |
|                      |  |                 | TRZ41998       |
|                      |  |                 | TRZ41888       |
|                      |  |                 | TRZ41890       |
| Glucose conversion   | MFS transporter AraJ                   | 1               | TRZ41988       |
|                      | Glucose/galactose MFS transporter      | 1               | TRZ42054       |
|                      | EamA/RhaT family transporter           | 5               | TRZ45859       |
|                      |  |                 | TRZ43560       |
|                      |  |                 | TRZ42617       |
|                      |  |                 | TRZ41572       |
|                      |  |                 | TRZ41062       |
|                      |  |                 | TRZ42724       |
|                      |  |                 | TRZ45841       |
| Mannose conversion   | Polyphosphate glucokinase              | 1               | TRZ45050       |
|                      | Glucose-6-phosphate isomerase          | 1               | TRZ41776       |
| Galactose conversion | Carbohydrate kinase                    | 1               | TRZ42808       |
|                      | Mannose-6-phosphate isomerase          | 1               | TRZ42233       |
|                      | Galactose-1-epimerase                  | 4               | TRZ42045       |
|                      |  |                 | TRZ45903       |

|                            |  |   |          |
|----------------------------|--|---|----------|
|                            | Galactokinase                                | 2 | TRZ44284 |
|                            |  |   | TRZ44304 |
|                            | Galactose-1-phosphate<br>uridylyltransferase | 1 | TRZ44283 |
|                            | phospho-sugar mutase                         | 1 | TRZ43683 |
| Xylose conversion          | Xylose isomerase                             | 1 | TRZ42503 |
|                            | Xylulokinase                                 | 1 | TRZ42502 |
| Arabinofuranose conversion | Arabinose isomerase                          | 1 | TRZ45904 |
|                            | Ribulokinase                                 | 1 | TRZ45906 |
|                            | Ribulose-5-phosphate 4-epimerase             | 1 | TRZ45905 |
| Pentose phosphate pathway  | Transketolase                                | 2 | TRZ41575 |
|                            |  |   | TRZ41576 |