

Table S1. Genome feature of strain DHR18.

| Type | Number | Total_len | Average_len | Percentage of genome (%) |
|----------|--------|-----------|-------------|--------------------------|
| Gene | 7,597 | 7,386,926 | 972 | 87.72 |
| CDS | 7,450 | 7,345,767 | 986 | 87.23 |
| tRNA | 73 | 5,772 | 79 | 0.07 |
| 23S rRNA | 6 | 17,274 | 2879 | 0.21 |
| 16S rRNA | 6 | 9,174 | 1529 | 0.11 |
| 5S rRNA | 5 | 535 | 107 | 0.01 |
| tm RNA | 1 | 370 | 370 | 0.00 |

Table S2. The plant growth promotion-associated genes in strain DHR18

| SeqID | KO | Gene | Function | Potential application |
|-----------|--------|-------------------|--------------------------------------|--------------------------|
| ctg_04905 | K01695 | <i>trpA</i> | tryptophan synthase alpha chain | Plant growth regulator |
| ctg_05505 | K00128 | <i>aldh</i> | aldehyde dehydrogenase (NAD+) | Tryptophan metabolism |
| ctg_03473 | K00128 | <i>aldh</i> | aldehyde dehydrogenase (NAD+) | Tryptophan metabolism |
| ctg_07039 | K00128 | <i>aldh</i> | aldehyde dehydrogenase (NAD+) | Tryptophan metabolism |
| ctg_04907 | K01696 | <i>trpB</i> | tryptophan synthase beta chain | Plant growth regulator |
| ctg_00484 | K01609 | <i>trpC</i> | indole-3-glycerol phosphate synthase | Plant growth regulator |
| ctg_02598 | K04751 | <i>glnB</i> | regulating nitrogen utilization | Biofertilizer |
| ctg_03090 | K04751 | <i>glnB</i> | regulating nitrogen utilization | Biofertilizer |
| ctg_03011 | K02806 | <i>ptsN</i> | regulating nitrogen utilization | Biofertilizer |
| ctg_01930 | K03366 | <i>budA, budC</i> | plant defense | Plant resistant elicitor |
| ctg_02269 | K04488 | <i>nifU</i> | nitrogen fixation | Biofertilizer |
| ctg_06505 | K15790 | <i>nifQ</i> | nitrogen fixation | Biofertilizer |



Figure S1. Schematic diagram of *Ganoderma pseudoferreum* inoculation on rubber tree

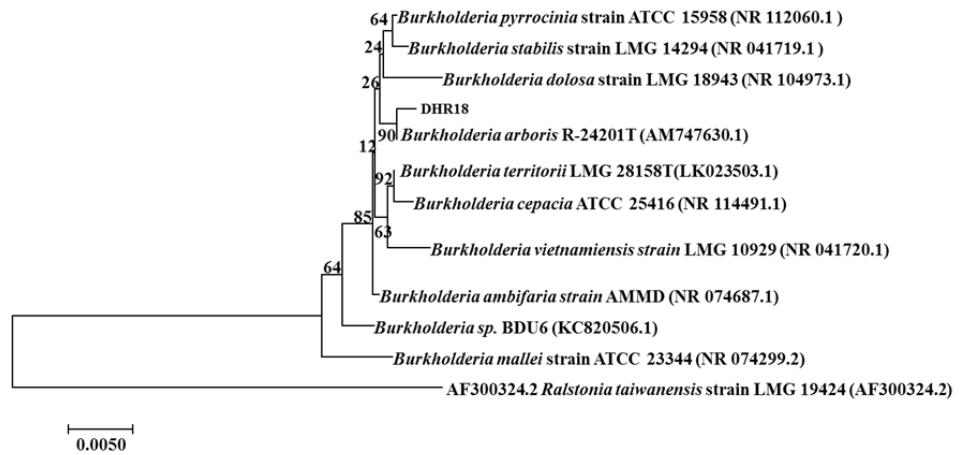


Figure S2. Phylogenetic trees based on the 16S rDNA sequence of DHR18 and their homologous sequences. *Ralstonia taiwanensis* strain LMG 19424 (AF300324.2) was chosen as the out-group.

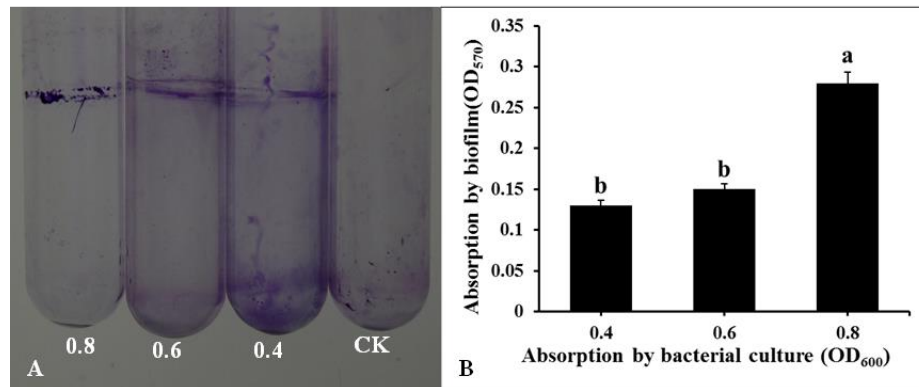


Figure S3. Biofilm formation. Biofilms developing on glass tubes were stained with 0.1% crystal violet (A). The mean amount of biofilm produced by different concentrations culture (OD_{600} = 0.4, 0.6, 0.8) (B). Bars indicate the standard error of the mean. Columns marked with the same letter are not significantly different at $p \leq 0.05$, considering Duncan's Multiple Range Test.

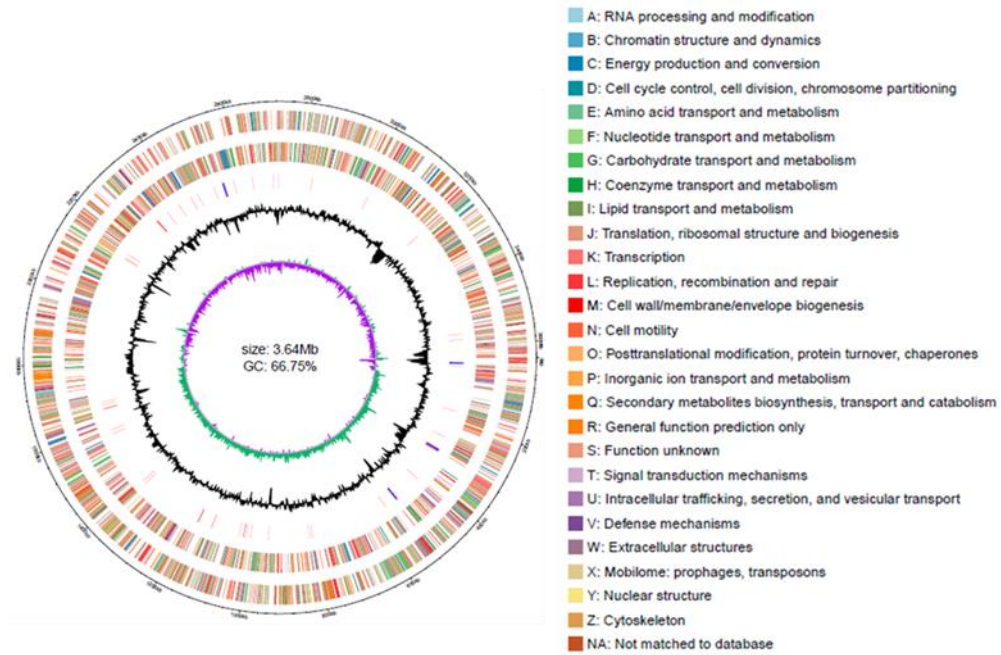


Figure S4. Circular map of strain DHR18 genome

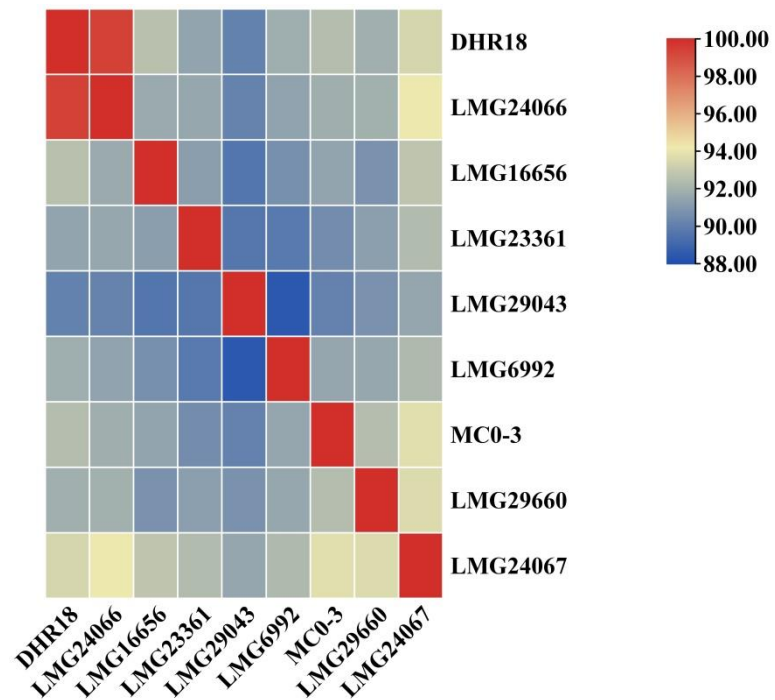


Figure S5. Average Nucleotide Identity (ANI, %) of DHR18 and other type strains. Genome comparison between DHR18 and 8 homologous bacterial strains. LMG24066: *Burkholderia arboris*; LMG16656: *Burkholderia cenocepacia*; LMG23361: *Burkholderia contaminans*; LMG29043: *Burkholderia diffusa*; LMG6992: *Burkholderia lata*; MC0-3: *Burkholderia orbicola*; LMG29660: *Burkholderia puraquae*; LMG24067: *Burkholderia seminalis*.

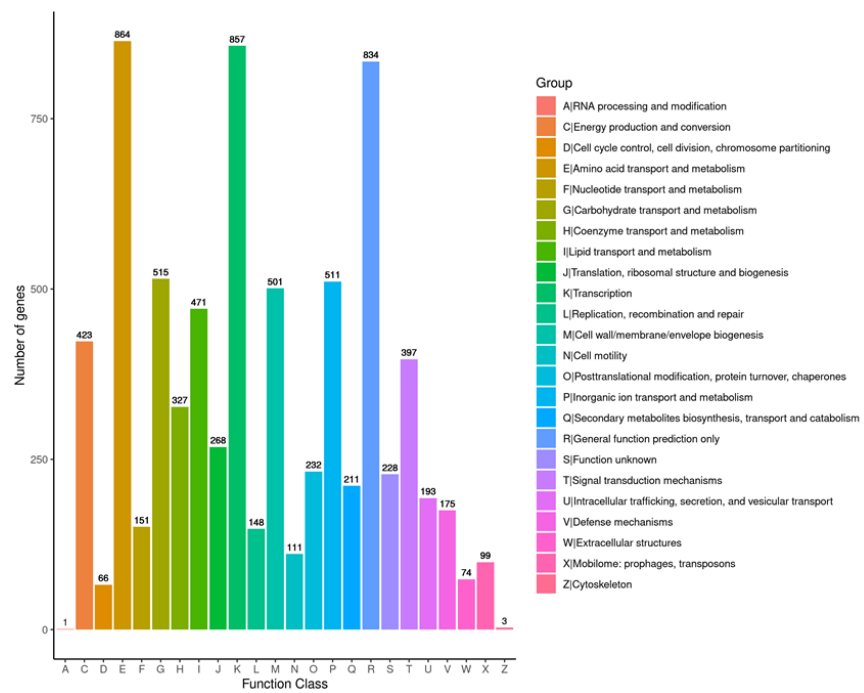


Figure S6. COG annotation of the strain DHR18 genome

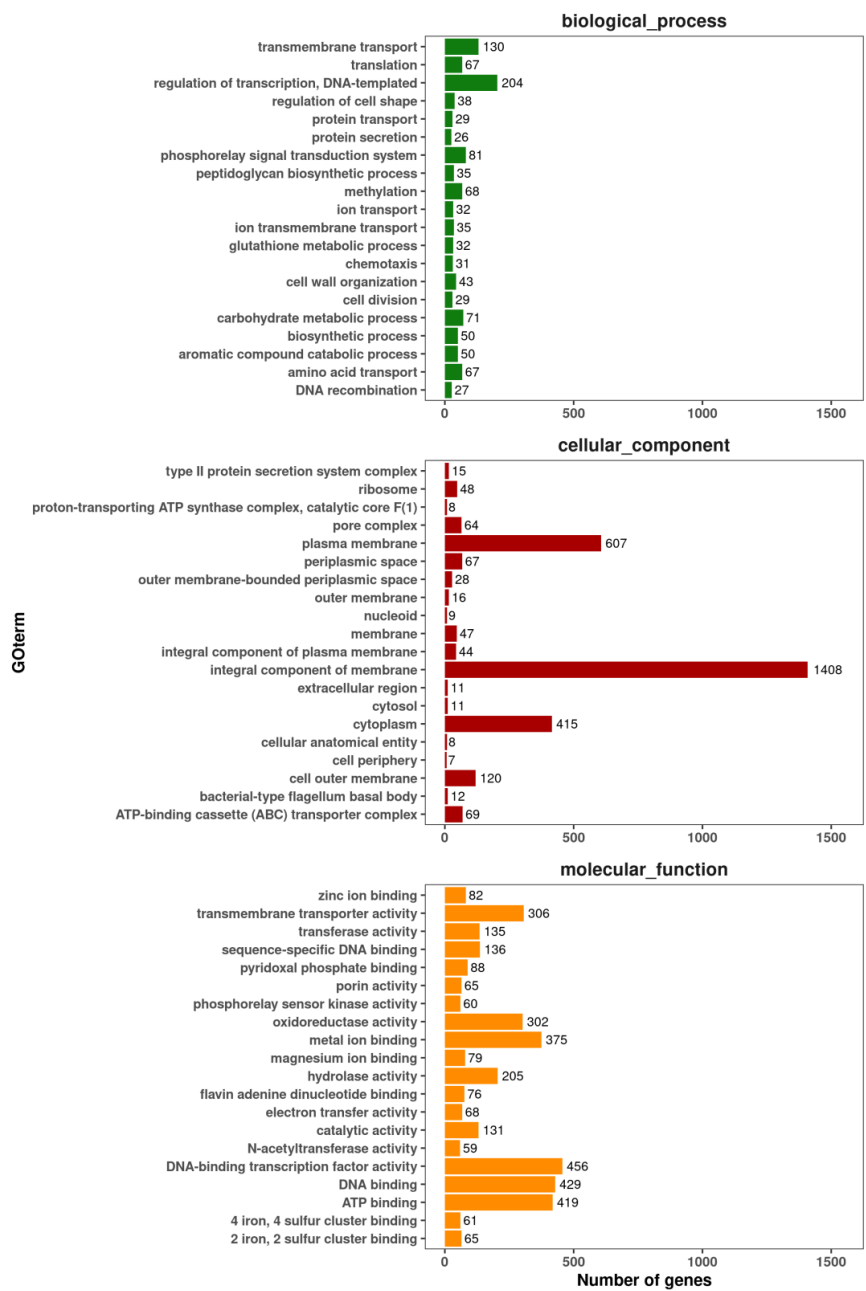


Figure S7. GO annotation of the strain DHR18 genome

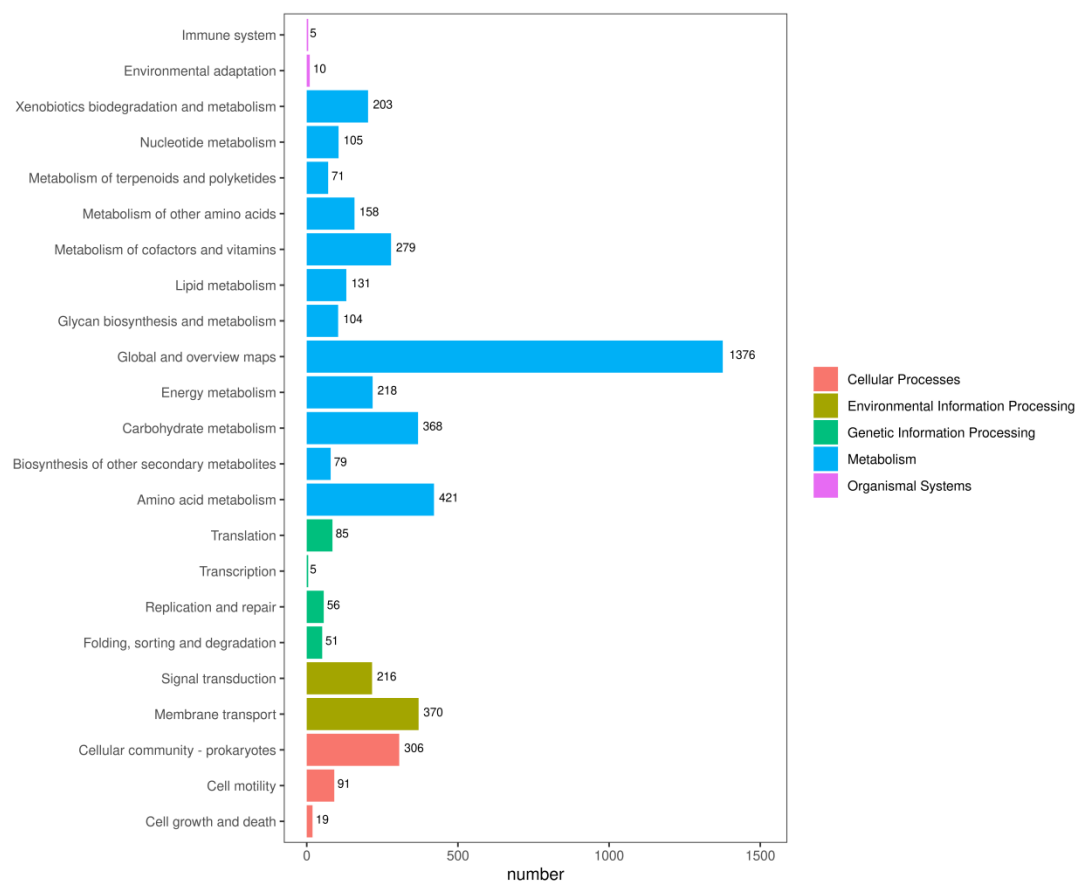


Figure S8. KEGG passageway annotation of the strain DHR18 genome

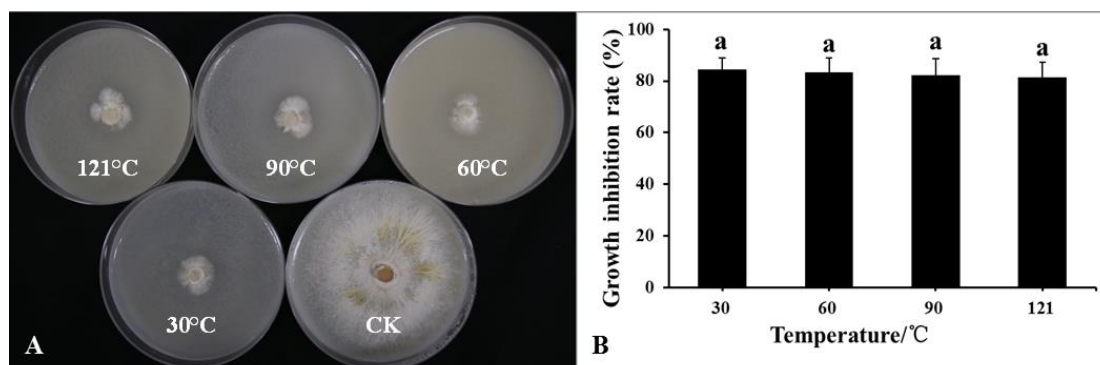


Figure S9. Effect of temperature on antibacterial activity of DHR18 (**A,B**). Bars indicate the standard error of the mean. Columns marked with the same letter are not significantly different at $p \leq 0.05$, considering Duncan's Multiple Range Test (**B**).