Supplementary Material

Fig. S1 KEGG pathway







Supplementary Table S1-S5

Table S1. Specific primers of the genes

|  |  |  |
| --- | --- | --- |
| **Symbol** | **primer F** | **primer R** |
| 16S rRNA | TAACTTCGTGCCAGCAGC | GGAAATTCCACCACCCTC |
| PA0156 | GCGCTTTTCATTCCAAAG | ACACGGACGTGTTCCTCG |
| PA1435 | CTGACCATCGACAACCAG | TAGACGAAATTGCCCTCC |
| mexC | AGGTGATGGTGGTGGGCG | CAGGTGACTGGGCTTGCG |
| PA2018 | GGTGGAGGGCGTGGGCAA | GGTGAGGCGGGCGTTGTG |
| mexB | GTCAAGCAATTGCCGAAA | CAGCGACAGCGCATACAG |
| PA4396 | GGCGGAGACCGACGATTT | CGACCAGGATGCTGAGAT |
| parR | CAGGCAGGGGAAATACTT | AGCGGGTTGAACAGGTAG |
| phoB | AGACAATCCTCATCGTTG | CTGCTGGGTATTTTCCGC |
| PA3573 | CATCGATTTCTACCTGCC | AAGATACTCACCCCCACC |
| motB | TGGCGTTCTTCCTGGTGC | CTGCGGATTGAGGGTCTT |

Table S2. Statistical reads of Clean Data mapped to reference genome

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **#SampleID** | **Total reads** | **Mapped reads** | **Unmapped reads** | **Multiple mapped reads** | **Unique mapped reads** |
| PA1.2620 (1) | 25588060 | 23568822 (92.11%) | 2019238 (7.89%) | 514967 (2.01%) | 23053855(90.10%) |
| PA1.2620 (2) | 28884424 | 26610272 (92.13%) | 2274152 (7.87%) | 1596802(5.53%) | 25013470(86.60%) |
| PA1.2620 (3) | 24775104 | 22686017 (91.57%) | 2089087 (8.43%) | 891827(3.60%) | 21794190(87.97%) |
| PA-99 (1) | 21049038 | 18448745 (87.65%) | 2600293 (12.35%) | 451663(2.15%) | 17997082(85.50%) |
| PA-99 (2) | 21204412 | 19832210 (93.53%) | 1372202 (6.47%) | 870487(4.11%) | 18961723(89.42%) |
| PA-99 (3)  | 22675272 | 19875769 (87.65%) | 2799503 (12.35%) | 1060369(4.68%) | 18815400(82.98%) |

Table S3. Correlation statistics of biological duplicate

|  |  |  |
| --- | --- | --- |
| **sample1** | **sample2** | **R2** |
| PA1.2620 (1) | PA1.2620 (2) | 0.4689 |
| PA1.2620 (1) | PA1.2620 (3) | 0.4735 |
| PA1.2620 (2) | PA1.2620 (3) | 0.9931 |
| PA-99 (1) | PA-99 (2) | 0.9982 |
| PA-99 (1) | PA-99 (3) | 0.9977 |
| PA-99 (2) | PA-99 (3) | 0.997 |

Table S4. GO enrichment categorization of tachyplesin-resisitant responsive DEGs uinigenes vs. all uinigenes

|  |  |  |  |
| --- | --- | --- | --- |
| #GO\_classify1 | GO\_classify2 | All Unigene | DEG Unigene |
| #Total\_gene |  | 4761 | 1004 |
| CCs | extracellular region | 29 | 6 |
| CCs | cell | 1489 | 266 |
| CCs | nucleoid | 6 | 1 |
| CCs | membrane | 1149 | 238 |
| CCs | virion | 5 | 0 |
| CCs | membrane-enclosed lumen | 1 | 0 |
| CCs | macromolecular complex | 226 | 38 |
| CCs | organelle | 127 | 16 |
| CCs | extracellular region part | 5 | 0 |
| CCs | organelle part | 75 | 7 |
| CCs | virion part | 5 | 0 |
| CCs | membrane part | 738 | 165 |
| CCs | cell part | 1489 | 266 |
| MFs | protein binding transcription factor activity | 31 | 4 |
| MFs | nucleic acid binding transcription factor activity | 345 | 76 |
| MFs | catalytic activity | 2976 | 624 |
| MFs | receptor activity | 116 | 15 |
| MFs | structural molecule activity | 78 | 8 |
| MFs | transporter activity | 604 | 114 |
| MFs | binding | 2268 | 467 |
| MFs | electron carrier activity | 143 | 25 |
| MFs | antioxidant activity | 47 | 14 |
| MFs | channel regulator activity | 1 | 0 |
| MFs | metallochaperone activity | 1 | 1 |
| MFs | enzyme regulator activity | 12 | 3 |
| MFs | molecular transducer activity | 219 | 43 |
| BPs | reproduction | 36 | 6 |
| BPs | cell killing | 4 | 2 |
| BPs | immune system process | 1 | 1 |
| BPs | metabolic process | 3339 | 700 |
| BPs | cellular process | 2834 | 585 |
| BPs | biological adhesion | 14 | 0 |
| BPs | signaling | 243 | 50 |
| BPs | multicellular organismal process | 4 | 1 |
| BPs | developmental process | 2 | 0 |
| BPs | growth | 1 | 1 |
| BPs | locomotion | 90 | 15 |
| BPs | single-organism process | 2801 | 576 |
| BPs | response to stimulus | 570 | 124 |
| BPs | localization | 964 | 193 |
| BPs | multi-organism process | 51 | 14 |
| BPs | biological regulation | 828 | 181 |
| BPs | cellular component organization or biogenesis | 173 | 30 |

Table S5. COG classification

|  |  |  |
| --- | --- | --- |
| #ID | Class\_Name | Numbers |
| J | Translation, ribosomal structure and biogenesis | 57 |
| A | RNA processing and modification | 0 |
| K | Transcription | 130 |
| L | Replication, recombination and repair | 32 |
| B | Chromatin structure and dynamics | 1 |
| D | Cell cycle control, cell division, chromosome partitioning | 9 |
| Y | Nuclear structure | 0 |
| V | Defense mechanisms | 17 |
| T | Signal transduction mechanisms | 89 |
| M | Cell wall/membrane/envelope biogenesis | 69 |
| N | Cell motility | 27 |
| Z | Cytoskeleton | 0 |
| W | Extracellular structures | 0 |
| U | Intracellular trafficking, secretion, and vesicular transport | 36 |
| O | Posttranslational modification, protein turnover, chaperones | 64 |
| C | Energy production and conversion | 85 |
| G | Carbohydrate transport and metabolism | 64 |
| E | Amino acid transport and metabolism | 145 |
| F | Nucleotide transport and metabolism | 29 |
| H | Coenzyme transport and metabolism | 50 |
| I | Lipid transport and metabolism | 63 |
| P | Inorganic ion transport and metabolism | 91 |
| Q | Secondary metabolites biosynthesis, transport and catabolism | 53 |
| R | General function prediction only | 194 |
| S | Function unknown | 101 |