**Fig. S1.** **Confirmation of transposon integration in PGPR2 mutant library.** (A) Integration of mariner transposon was confirmed with PCR to amplify the transposon. Lane M, 1-kb molecular weight DNA marker (Thermo Fisher Scientific, USA); “-”, negative control (gDNA from *P*. *aeruginosa* PGPR2); “+”, positive control (pSAM\_BT plasmid DNA); lane 3-14, PCR amplification of GmR antibiotic cassette from gDNA of individual mutants of *P*. *aeruginosa* PGPR2. (B) PCR for the same samples using *himar* transposase gene primers should be lost in mutants upon proper integration of transposon.

**Fig. S2. Southern blot analysis of PGPR2 INSeq library mutants.** Genomic DNA of wild type PGPR2 (WT) and 13 INSeq mutants were digested with *Hin*dIII restriction enzyme and resolved on an 0.8% agarose gel. A gentamicin resistance gene used as a probe revealed a single insertion and random integration of the transposon.

**Fig. S3.** Genome map of *P. aeruginosa* PGPR2 showing transposon insertion sites. The outer circle represents the forward strand (red), the inner circle represents the reverse strand (blue), and the purple bars represent the transposon insertion sites.

**Fig. S4.** Functional categorization of essential genes responsible for growth of PGPR2. The functional classification was done according to protein annotation by COG database using WebMGA.

**Fig. S5.** Functional categorization of genes responsible for the fitness of PGPR2 during corn root colonization. The functional classification was done according to protein annotation by COG database using WebMGA.

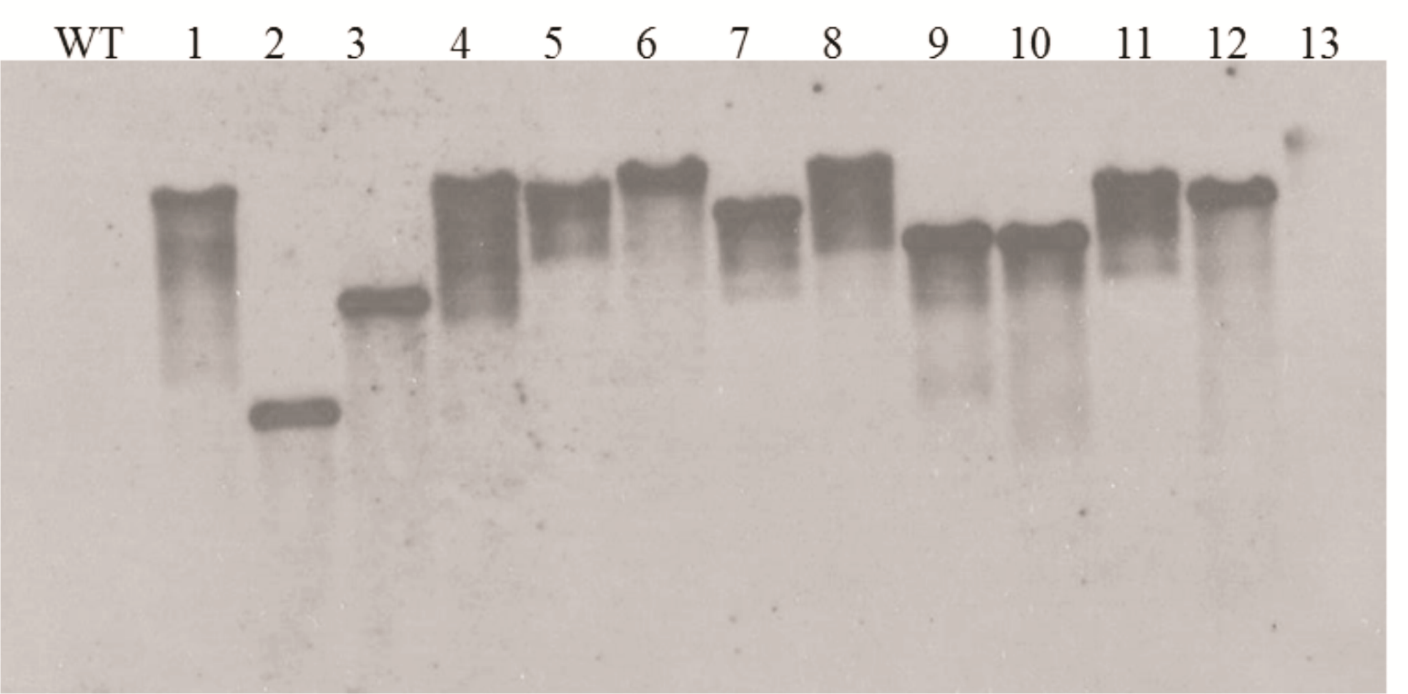


Fig. S2

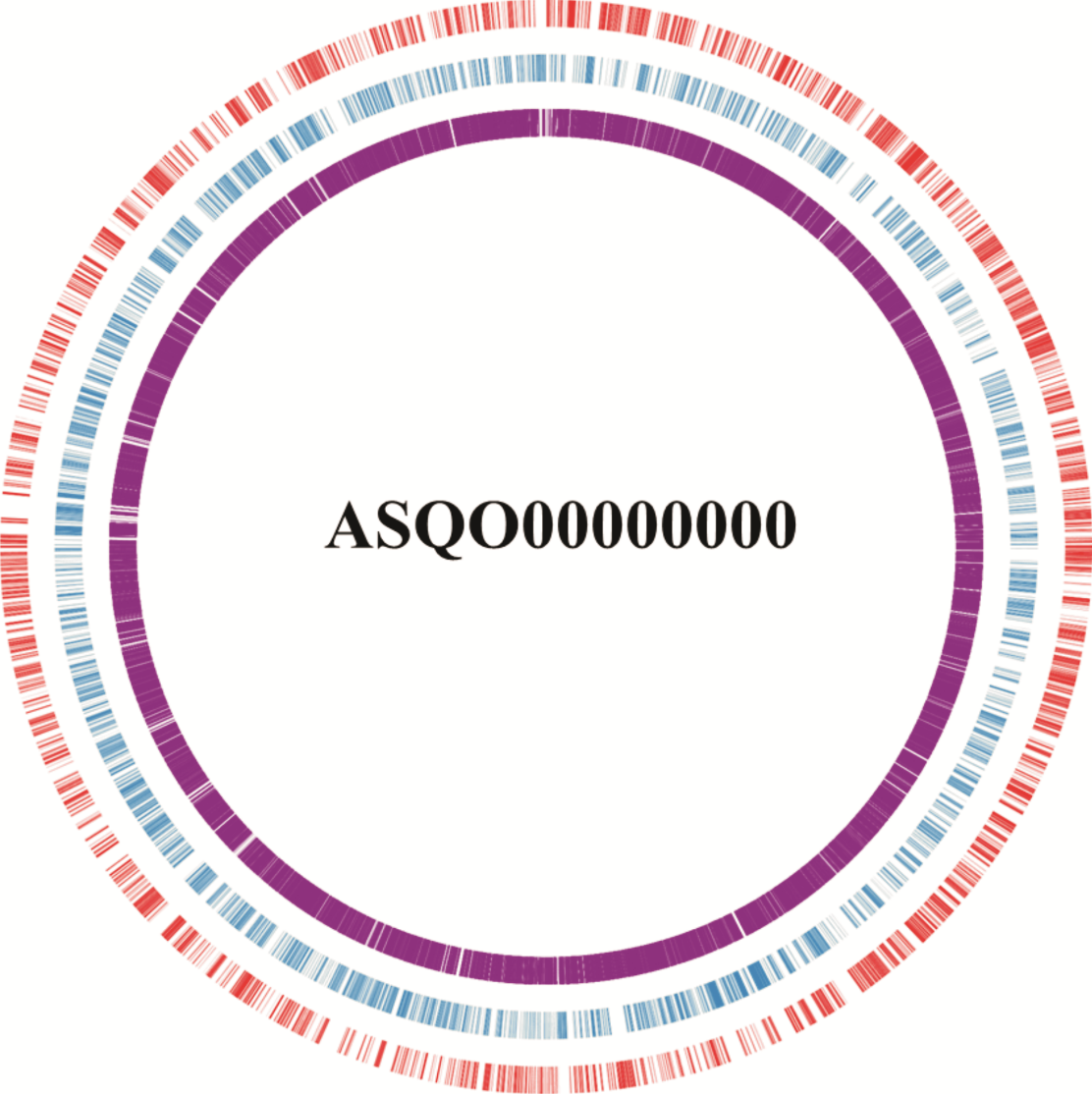


Fig. S3

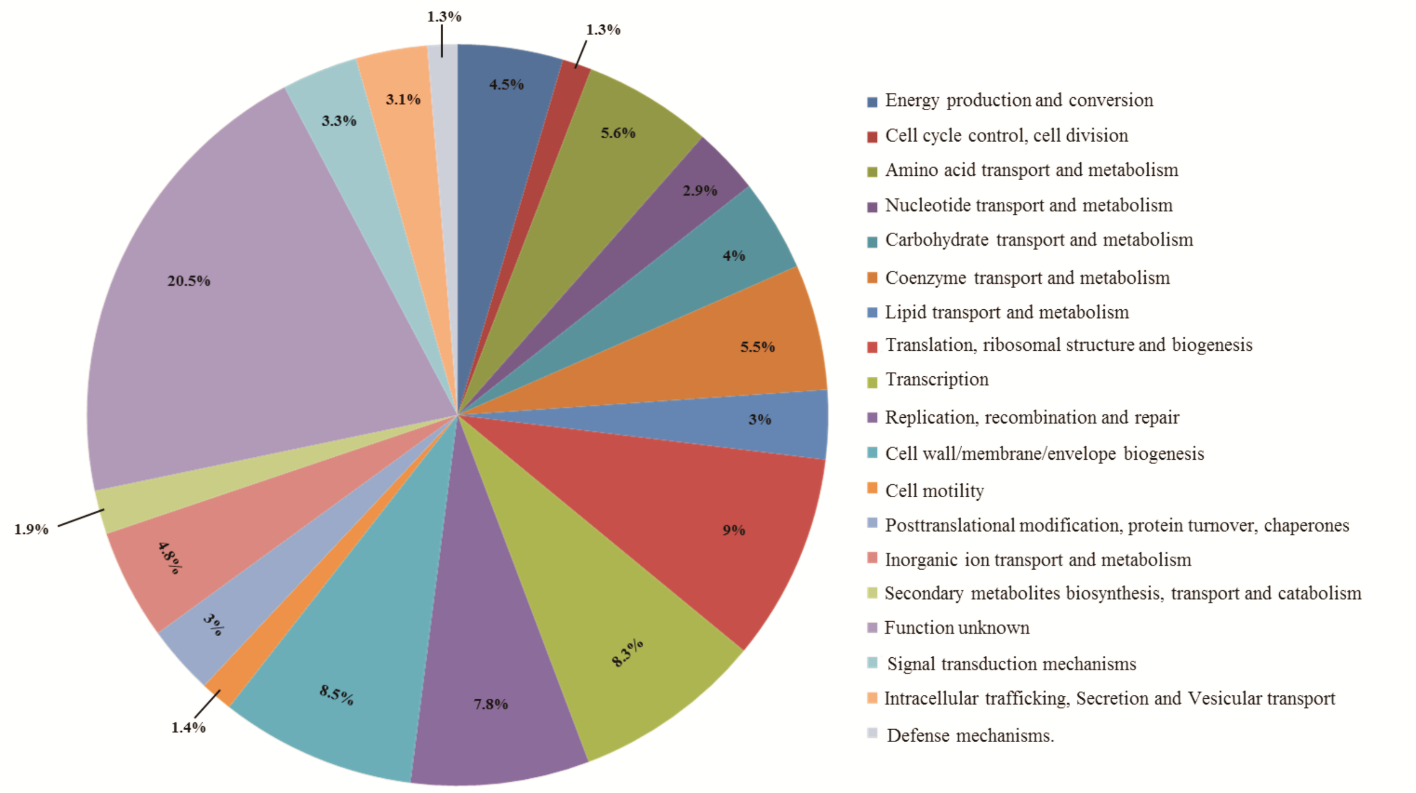


Fig. S4

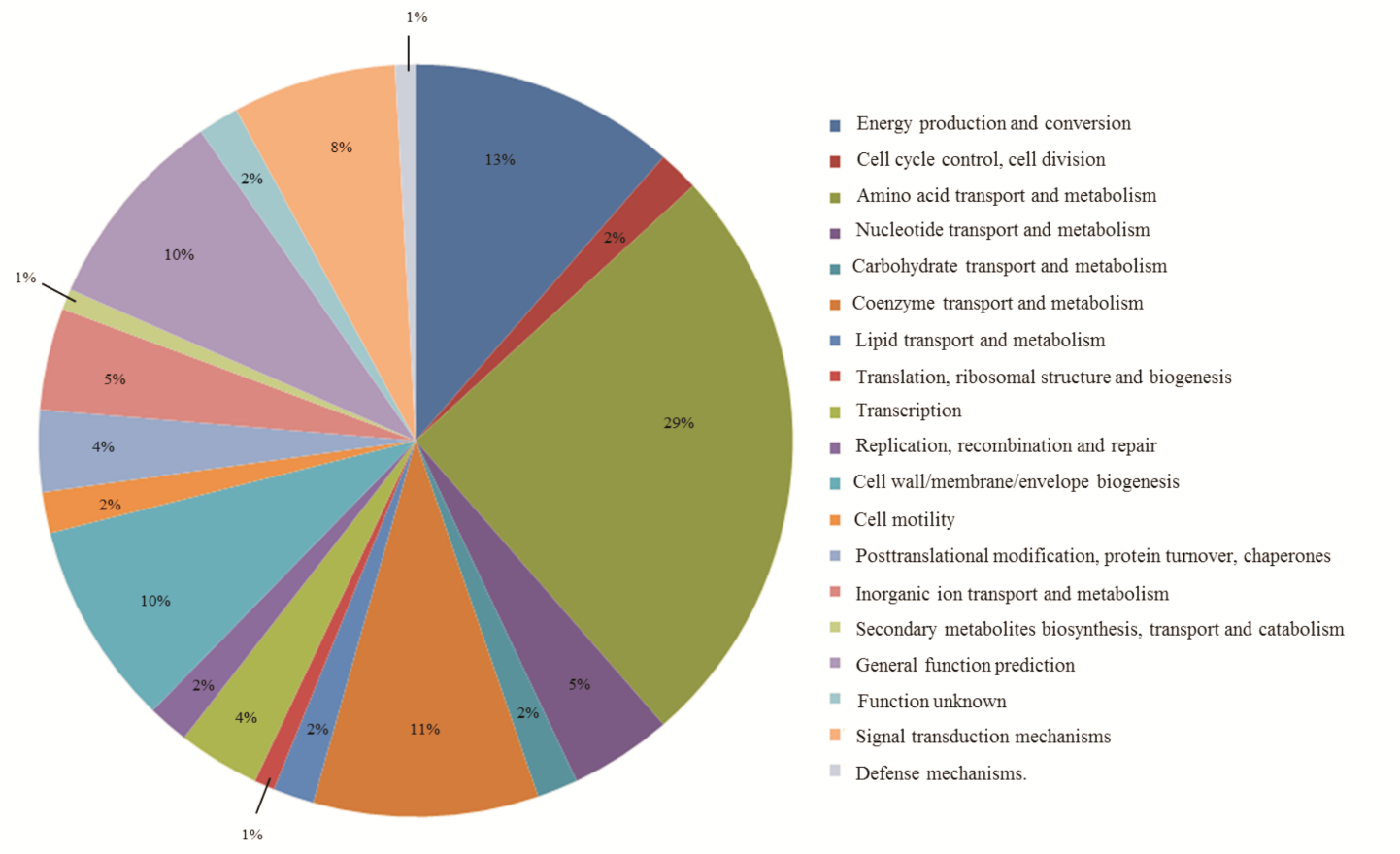


Fig. S5

**Table S1** List of primers used in this study

|  |  |  |
| --- | --- | --- |
| Primer | Sequence (5’-3’)a | Purpose |
| Gen F | TA**CTCGAG**CGCGTCAATTCTCGAATTGACA | GmR PCR |
| Gen R | CA**GCGGCCGC**AGGGTTTTCCCAGTCAC | GmR PCR |
| Trans F | CACC**GGATCC**CAGTGTGATGGATTGACACATAG | Transposase PCR |
| Trans R | TA**GCGGCCGC**AGGGTTTTCCCAGTCACG | Transposase PCR |
| *trpD* F | GAA**CTCGAG**ATGGATATCAAGGGAGCCCTC | TrpD deletion |
| trpD R1 | TAT**AAGCTT**CACGAAGGACGCCGCCGAGGA | TrpD deletion |
| *trpD* F1 | GTT**AAGCTT**GAAGTGCGTCCCGAGGACTTC | TrpD deletion |
| trpD R | ATT**CTCGAG**TCACTGTGCGTTCTCCTCTCT | TrpD deletion |
| *hom* F | GAA**CTCGAG**GTGAAACCGGTCAAAGTAGGC | Hom deletion |
| *hom* R1 | CAT**AAGCTT**GCCTTGGCGAAGATCTCGTTG | Hom deletion |
| *hom* F1 | GTT**AAGCTT**TGACCTCCGATCCGGAGAACC | Hom deletion |
| *hom* R | GCG**CTCGAG**TCAATTCAGTTGTTCGACACG | Hom deletion |
| *oprF* F | GCG**CTCGAG**ATGAAACTGAAGAACACCTTA | OprF deletion |
| *oprF* R1 | AAT**AAGCTT**GTGGTAGATGGCGTCCAGAGA | OprF deletion |
| *oprF* F1 | GCT**AAGCTT**AAAGAGAACAGCTACGCTGAC | OprF deletion |
| *oprF* R | GCG**CTCGAG**TTACTTGGCTTCAGCTTCTAC | OprF deletion |
| *cbrA* F | TAA**CTCGAG**ATGCTGACGAGCTTTAGCCTG | CbrA deletion |
| *cbrA* R1 | ATT**AAGCTT**CGAGCATCACCAGCTTGACCA | CbrA deletion |
| *cbrA* F1 | ATT**AAGCTT**GAACGCGAAGGCGACGGCGAG | CbrA deletion |
| *cbrA* R | ATT**CTCGAG**CTACAGCTCGGCCGTCGGGCC | CbrA deletion |

a Relevant restriction sites are given in bold letters.