Fig. 4. Structural representation of *Pseudomonas aeruginosa* PA2192, C3719 and PA14 genomes. Chromosomes are shown as black circles with adjacent colored tracks (PA2192-green; C3719-red; PA14-purple). Each set of tracks is paired with the outer track representing the predicted ORFs on the forward strand and the inner track being those on the reverse strand. Green, outlined arrowheads in the inner track represent ribosomal RNA operons and their orientation. The location of the *dnaA* gene and the *dif* termination site are marked with black arrows. Plots in the center of the maps show GC-skew (inner plot: green bars, + skew; purple bars, - skew) and GC-bias (outer plot: black trace). In PA2192, the relative changes in the positioning of the rRNA operons, the asymmetry in the GC-skew, and the shift in the location of the *dif* site can be explained by the large inversion. Scale is shown with major ticks of 500 Kb and minor ticks of 100 Kb.

Fig. 5. Phylogenetic analysis of genomes of various *P. aeruginosa* strains. A maximum parsimony tree was generated from concatenating 1836 ORFs that are common to *P. fluorescens* and six strains of *P. aeruginosa* (PAO1, PA14, PA2192, C3719, PACS2, and LES). Bootstrap support values from 100 trials are also shown.

Fig. 6. Relationship between genes present in five *P. aeruginosa* strains. Total number of genes in each genome were shown in parentheses. Ortholog clusters were computed for the five genomes (see SI Materials and Methods). The accessory genes (two, three, four-way clusters) are indicated by red, blue, and green. There are 5,021 genes that have orthologs in all genomes (5-way clusters), which we refer to as the core genes (black). Unique genes are represented by yellow. In particular, note the large number of unique genes in PA2192.

Fig. 7. Comparison of RGPs among five *P. aeruginosa strains*. ORFs flanking each RGP (referred to as anchor sequences) and common to each set of RGPs are shown in black. Genes that share homology between each of the species for a given RGP are shown in blue. Genes with orthologs that are not in syntenic locations are colored green. Genes with no orthologs are colored red. Each coding sequence is shown with a specific orientation based on the terminating arrowhead. The shaded gray regions that connect the different maps in each panel represent ortholog assignments between RGPs. All genes are labeled with their unique identifiers.

Fig. 8. Functional categories of products encoded in the total, core and accessory genomes of various *P. aeruginosa* strains. The distribution of the functional annotations for the ORFs are shown for the following sets of ORFs: all ORFs from PA2192, C3719, PAO1, and PA14, all core genes from the four strains, and all ORFs from the accessory genomes from PA2192, C3719, PA01, PACS2, and PA14 (Color key is shown at top). The 26 functional categories (and the corresponding symbols) used for the annotation are also shown.

Fig. 9. Functional categories of protein products encoded in the various RGPs. The distribution of functional annotations for all RGPs are shown. Functional categories are the same as in SI Fig. 8 with the corresponding color key shown at top.

Fig. 10. Schematic Representation of RGP29**.** The ORFs on the right and left (black) ends are the anchoring ORFs that are conserved between all strains. In PAO1, two ORFs, the *arr* gene and *PA2819* occupy this locus. It is likely that *PA2819* is a mis-annotation as a significant portion of this *ORF* overlap with the three tRNAs genes, an arrangement that has not been seen in any prokaryotic genome. PA14 and C3719 have nine ORFs at the same location. Orthologs are color-coded. The Dit Island is from PA2G_01975 to PA2G_02069 whereas the genes more closely related to those in *C. metallidurans* spans from PA2G_02070 to PA2G_02184. The ORFs PA2G_02064, PA2G_02069, and PA2G_02148 code for integrase (gray). The ORFs PA2G_02073, PA2G_02079 and PA2G_02148 code for *Soj*, *Ssb* and relaxase, respectively.

Fig. 11. RGP29 Junction Sequences. The common regions shared by all the strains are shown in black. The variable Insertion1 sequence is indicated in purple. The PAGI-2 island is indicated in blue and the DIT island is indicated in green. Fragments with dotted underlines represent direct repeats. The region at the 3' end underlined by a continuous black line is the tRNA^{Gly}.

Fig. 12. Genetic organization of the Dit Island and comparison to the similar loci in *P. abietaniphila* and *B. xenovorans*. Genes encoding paralogous families of proteins are shown in the same color.