

Additional file 11. Number of genes in RAST subcategory shown to be significantly over-represented in clade II genomes as compared to clade III genomes. For each RAST subcategory, gene numbers were color coded as representing (i) high number of genes in a specific subcategory (light gray) and (2) low number of genes in a given subcategory (dark gray); the cut-off between these categories were arbitrary. The two non cold-adapted clade III strains are shown above the three cold-adapted clade II strains.