



Additional File 7: Genome duplication amplification events observed in *cysK*, *carA*, and *ptsI* experiments. Read depth coverage (y-axis) is plotted against the genome position (x-axis) for flask 1 population samples for A. *cysK*, B. *carA*, C. and *ptsI* experiments. For *cysK* and *carA* samples (on the left), the regions of amplification are flanked by IS elements, IS186 and IS2, respectively. These regions of amplification contain the genes (*cysM* and *carB*) associated with a model-predicted alternate isozyme (*cysM*) or a previously reported multi-copy suppressor (*carB*). For the *ptsI* experiment (on the right), a smaller region is amplified and this region is magnified in the bottom plot. This region of amplification is flanked by ribosomal RNA genes and the identified metabolic gene of interest within this region is *cyaA*.