**Supplementary Figure 2**. Similarity of draft netwoks for *Pseudomons putida* created with 7 reconstructions tools to the manually-curated model iJP962. The Jaccard distance and the ratio between coverage and additional elements was calculated to compare gene sets (A) and reactions sets (B) between draft models and iJP962. In both cases, MetaDraft, AuReMe and RAVEN were the tools that generated the drafts more similar to iJP962 (dots in the top-left of the plot). However, the use of this tools do not ensure obtaining a draft similar to the manually-curated model as other networks created with these tools got lower scores. Thus appropiate parameters have to be set for each tool.

