**Supplementary Material for ShinyOmics: Collaborative Exploration of Omics Data**

Table S1. Metadata variables included in the example application, and their descriptions

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| **Organism** | **Metadata Variable** | **Description** |
| *S. pneumonaie* T4/19F | Tag1 | Primary functional tag |
| Tag2 | Secondary functional tag (if present) |
| Tag3 | Tertiary functional tag (if present) |
| Category1 | Primary functional category |
| Category2 | Secondary functional category |
| Category3 | Tertiary functional category |
| No..of.Categories | Number of functional tags/categories a gene belongs to (maximum 3) |
| SequenceDiameter | Average pairwise distance between homologs of the same gene across different strains |
| SequencePrevalence | Number of strains that have a homolog of the gene |
| Essential | Whether the gene is essential |
| ExpressionPlasticity | Variability in expression across different experimental conditions |
| Location.Tag | Subcellular compartment the gene product localizes to |
| Gene.Name | Common name of the gene or gene product |
| Gene.Description | Description of the gene or gene product |
| *M. tuberculosis* | start | Gene start position on the chromosome |
| end | Gene end position on the chromosome |
| strand | Gene strand |
| na\_length | Length of gene (nucleotide) |
| gene.name | Common name of the gene or gene product |
| product | Description of the gene or gene product |

Figure S1. Lack of overlap between different omics data. A. For the TIGR4 KAN experiment, RNA-Seq (Experiment 1) is plotted against Tn-seq (Experiment 2). B. For the M. tuberculosis hypoxia experiment, microarray data (Experiment1) is plotted against proteomics data (Experiment 2).

