Table Legends

Table 1. A collection of study metadata containing descriptions of experimental perturbations, growth conditions, accession numbers, and research institutions for all RNA-Sequencing data sets stored in the compendium. Each row corresponds to an individual study (n = 392)

Table 2. A collection of metadata describing all samples stored in the compendium that are present in the Gene Expression Omnibus (GEO). Samples are described in terms of experimental perturbations, growth conditions, and accession numbers. Each row corresponds to an individual sample (n = 3754)

Table 3. A collection of metadata for all compendium studies in which a particular gene (or set of genes) was perturbed (n = 83), either by knockout or experimentally induced over-expression. Each perturbed gene is listed by its common name (e.g., relA) and by its more formal ID (e.g., PA0934)

Table 4. A lookup table that matches all individual genes perturbed in Table 3 with their associated KEGG pathway(s) (if known) and function. Both pathway and function were extracted programmatically from the KEGG online database using the R package KEGGREST.

Table 5. A set of metadata gathered manually to describe all compendium studies that are not present in GEO but do have Bioproject and SRA identifiers so that metadata can be accessed, albeit not programmatically. Studies are described in terms of experimental perturbations, growth conditions, and accession numbers. Each row corresponds to an individual study (n = 182)

Table 6. A legend table that identifies elements of tables 1-5 worthy of further explanation and provides notes to clarify their meaning.