### 图A

- **Title**: Cell cycle (KEGG sce04110)
- **Graph**: Shows the fraction of pathway recovered as a function of total graph size. The x-axis represents the number of proteins recovered, while the y-axis shows the fraction of the pathway recovered.

### 图B

- **Title**: Ribosome (KEGG sce03010)
- **Graph**: Similar to A, this graph compares the fraction of the pathway recovered against total graph size.

### 图C

- **Title**: ATP synthesis (KEGG sce00193)
- **Graph**: Consistent with A and B, this graph evaluates the fraction of the pathway recovered versus total graph size.

### 图D

- **Graph**: Represents the performance of individual evidence types. The x-axis is the recall (TP/[TP + FN]), and the y-axis is precision (TP/[TP + FP]). Different lines indicate different evidence types.

### 图E

- **Graph**: Compares bioPIXIE recovery, Binary recovery, and Countingbased recovery against recall and precision. The x-axis is recall, and the y-axis is precision.

### 图F

- **Graph**: Shows a comparison with existing methods, similar to E but with additional lines for SEEDY and Complexpander recovery.