PDF Output of CLIC (clustering by inferred co-expression)

Dataset:

Num of genes in input gene set: 20
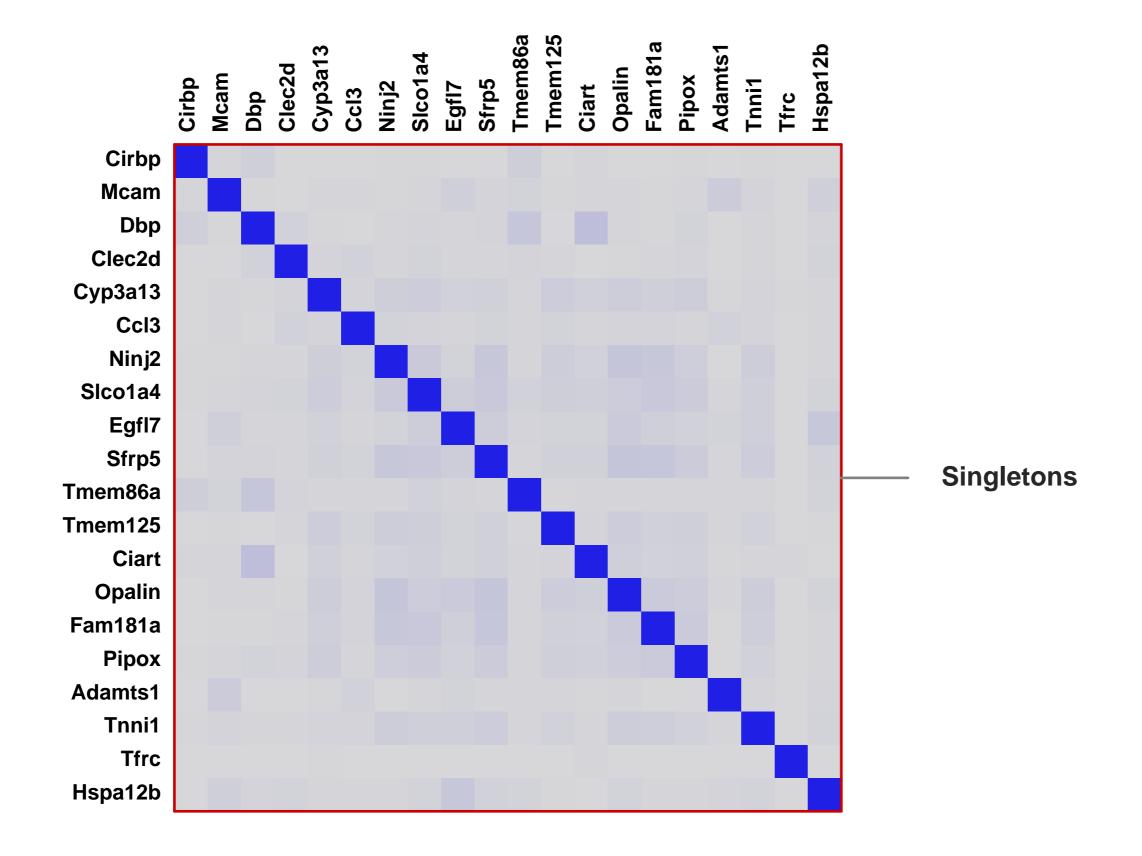
Total number of genes: 16493

CLIC PDF output has three sections:

1) Overview of Co-Expression Modules (CEMs)

- Heatmap shows pairwise correlations between all genes in the input query gene set.

- Red lines shows the partition of input genes into CEMs, ordered by CEM strength.

- Each row shows one gene, and the brightness of squares indicates its correlations with other genes.

- Gene symbols are shown at left side and on the top of the heatmap.

2) Details of each CEM and its expansion CEM+

- Top panel shows the posterior selection probability (dataset weights) for top GEO series datasets.

- Bottom panel shows the CEM genes (blue rows) as well as expanded CEM+ genes (green rows).

- Each column is one GEO series dataset, sorted by their posterior probability of being selected.

- The brightness of squares indicates the gene's correlations with CEM genes in the corresponding dataset.

- CEM+ includes genes that co-express with CEM genes in high-weight datasets, measured by LLR score.

3) Details of each GEO series dataset and its expression profile:

- Top panel shows the detailed information (e.g. title, summary) for the GEO series dataset.

- Bottom panel shows the background distribution and the expression profile for CEM genes in this dataset.

Overview of Co-Expression Modules (CEMs) with Dataset Weighting

Num of Genes in Query Geneset: 20.   Num of CEMs: 0.

Scale of average Pearson correlations