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

Dataset:
  Num of genes in input gene set: 13
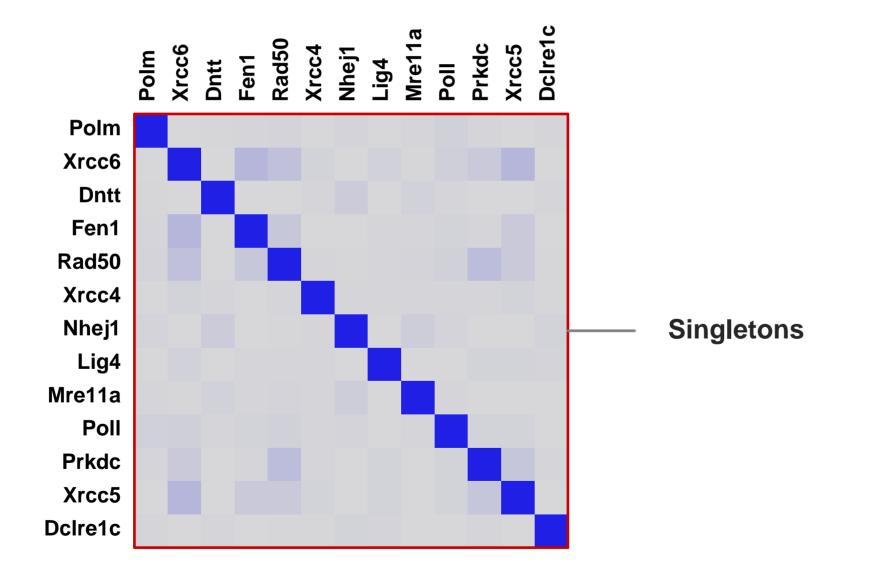 Total number of genes: 16493

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: 13.   Num of CEMs: 0.

Scale of average Pearson correlations

0.0   0.2   0.4   0.6   0.8   1.0

Singletons