

INF-BIOx121 2017

RNA-seq

differential expression analysis

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Sep 18-20, 2017

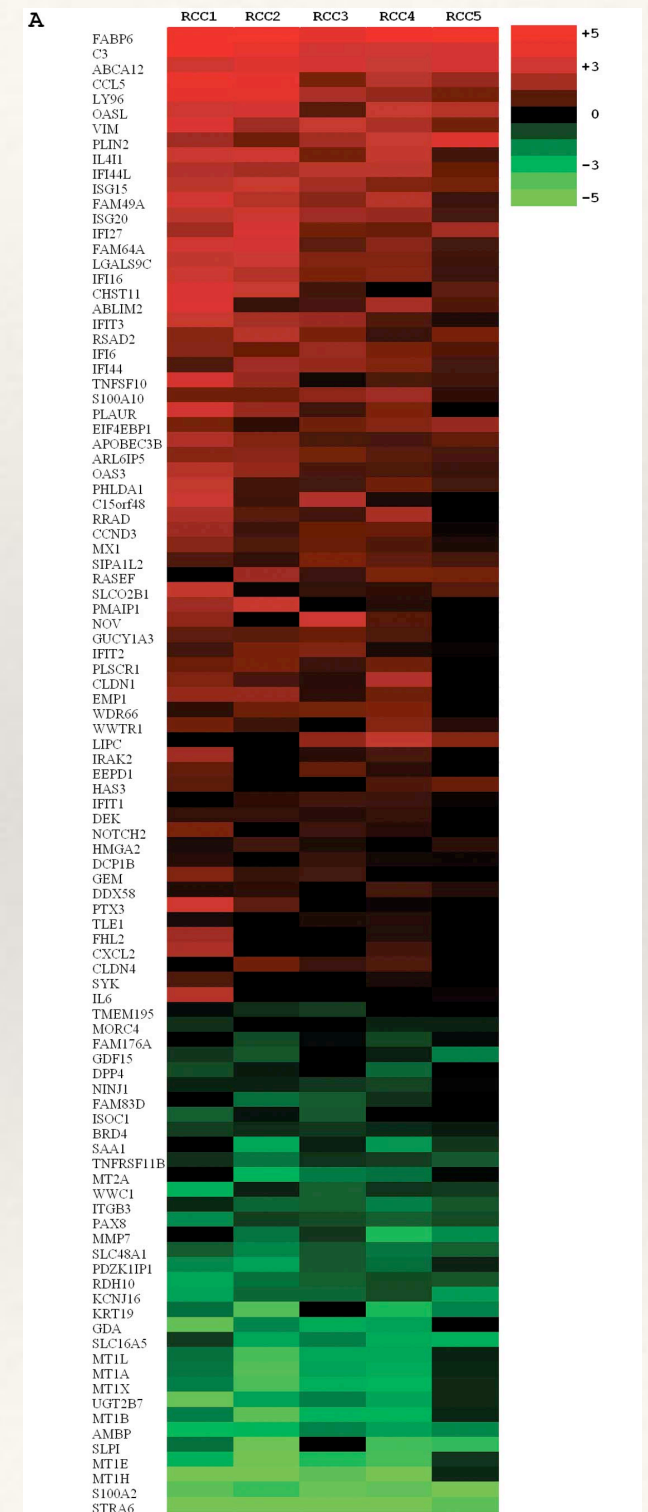
RNA-seq analysis

After DE list

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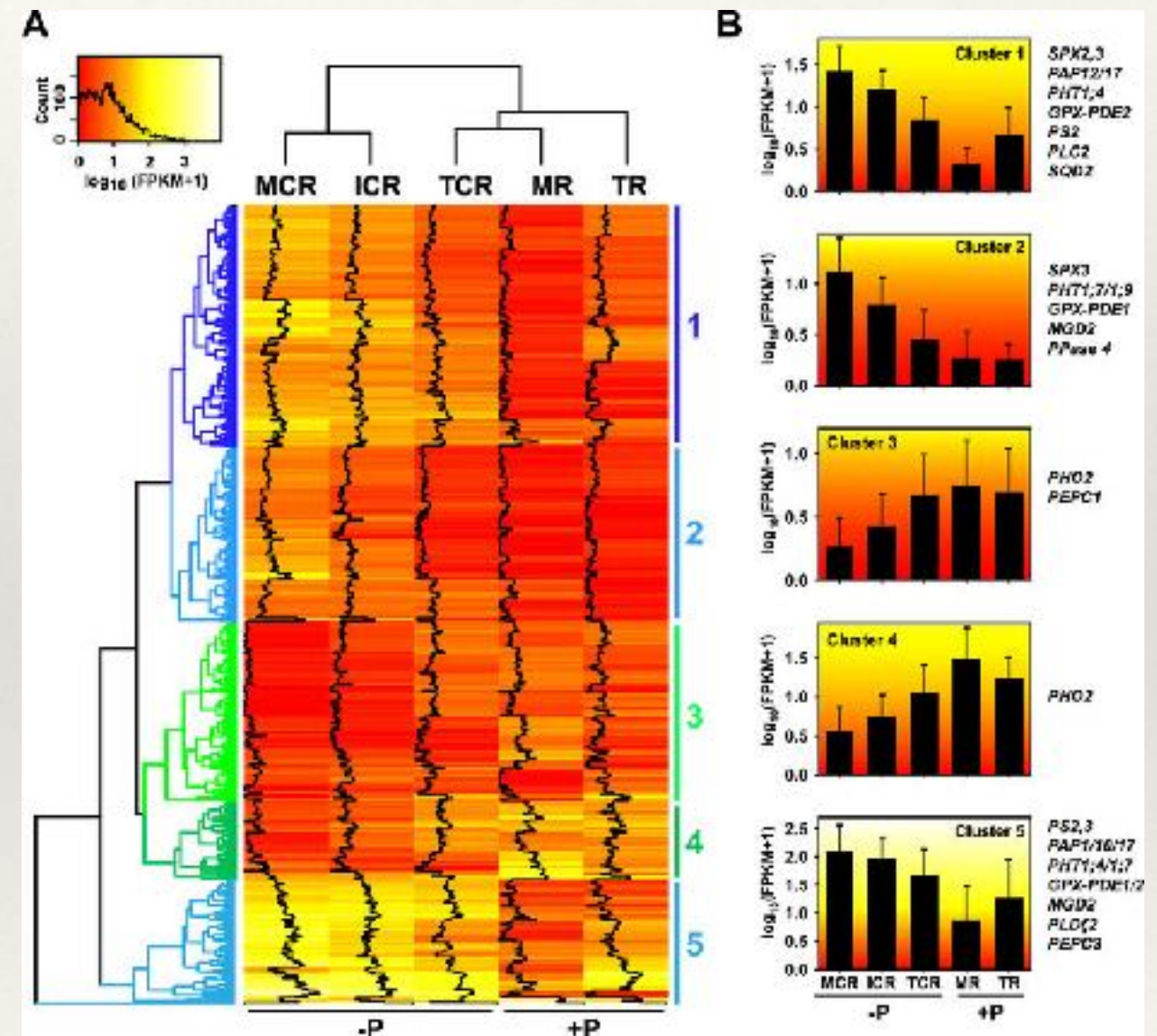
DE list. What next?

- ❖ Heatmap
 - ❖ Possible to make heatmaps using cummeRbund, DESeq2 and edgeR or in R
 - ❖ Personal favorite - MeV TM4
- ❖ cummeRbund code for extracting FPKM matrix
 - ❖ `repFpkmMatrix(genes(cuff))`
 - ❖ FPKM + 1



DE list. What next?

- ❖ Clustering
 - ❖ Gene (feature level)
 - ❖ Sample level
 - ❖ Hierarchical
 - ❖ CAST: Clustering Affinity Search Technique
 - ❖ Personal favorite - MeV TM4
 - ❖ Possible in R



DE list. What next?

- ❖ Functional profiling of gene lists
 - ❖ Gene Ontology (GO) enrichment analysis
 - ❖ Biological process
 - ❖ Cellular components
 - ❖ Molecular function
 - ❖ KEGG pathway enrichment analysis



- ❖ Tools
 - ❖ GOrilla (<http://cbl-gorilla.cs.technion.ac.il/>)
 - ❖ Comprehensive tool - g:Profiler (<http://biit.cs.ut.ee/gprofiler/>)

DE list. What next?

- ❖ Annotation
 - ❖ BLAST if only sequence is available (*de novo* assembly)
 - ❖ Use the “gene_id”
 - ❖ Ensemble / UCSC
 - ❖ NCBI / RefSeq
 - ❖ Uniprot