1. Which count data? Dragen or processed by Ichita and provided to Marc
2. Which thresholds?
   1. Melanocytes vs. DSCs: pval = 0.05, FC = 1.5?
   2. DSC irradiated: pval = 0.05, FC = 1.3?
3. What is our reference group? Melancoytes or DSCs?
4. Functional analysis
   1. Which algorithm?
      1. ORA?
      2. GSEA?
      3. Pathway analysis (with directed biological endpoints): e.g. IPA
   2. Which database?
      1. GO Terms
         1. Biological process
         2. Molecular function
         3. Cellular compartment
      2. KEGG pathways
      3. Reactome pathways
      4. All three?
   3. Suggestion:
      1. ORA on downregulated genes (Biological process) with reduced Terms depicted as treemap if necessay
      2. ORA on upregulated genes (Biological process) with reduced Terms depicted as treemap if necessary
      3. Supplemented by KEGG and Reactome Pathway analysis

Suggestion for publication:

* Fig1: PCA, Volcano Plot, Heatmap
* Fig2: Depiction of GO Terms either in 1 or 2 Figures
  + Supplemented by 1 Figure including KEGG and Reactome Pathways
* Fig1 and Fig2 for Mel vs DSC and trt vs. ctrl or for different papers?
* Fig3: Apoptosis, Cell Cycle, etc?