Cellular response to drug perturbation – Gliederung

1. **Broad analysis**
2. **Gene expression profiles**

* treated and untreated
* density plots, violin or boxplot, correlation heatmap

🡪 normalized?

🡪 groups?

1. **space of gene expression and dimensionality reduction**

* find main latent factors 🡪 where do they belong to
* PCA, co-variance

1. **individual gene expression signatures**

* find most differentially expressed genes
* log2 fold-change (FC)  
  - treated and untreated   
  - each cell line at each time point

1. **Exploratory analysis with matrix of log2FC**
2. density plots, violin or boxplot, correlation heatmap
3. dimensionality reduction
4. **Specific analysis 🡪 one particular targeted therapy or chemotherapy agent**
5. **Specific data**

* main factors driving the drug mutation
* functional annotation of drug response biomarkers

1. **transcriptional changes of drug perturbation**

* genome-wide t-test   
  - treated and untreated  
  - multiple individual t-test along the transcriptome 🡪 one t-test per gene
* patterns of transcriptome modulation (clusters)  
  - PCA

1. **drug sensitivity based on collected biomarkers**
2. exploratory analysis

* density plots, violin or boxplot, correlation heatmap
* dimensionality reduction

1. model of drug response

* linear models, log-transformation   
  🡪 which biomarkers / covariates explain better the drug response