<u>**Supplement:**</u>
These are only suggestions for possible supplemental figures. Please feel free to change or remove anything.

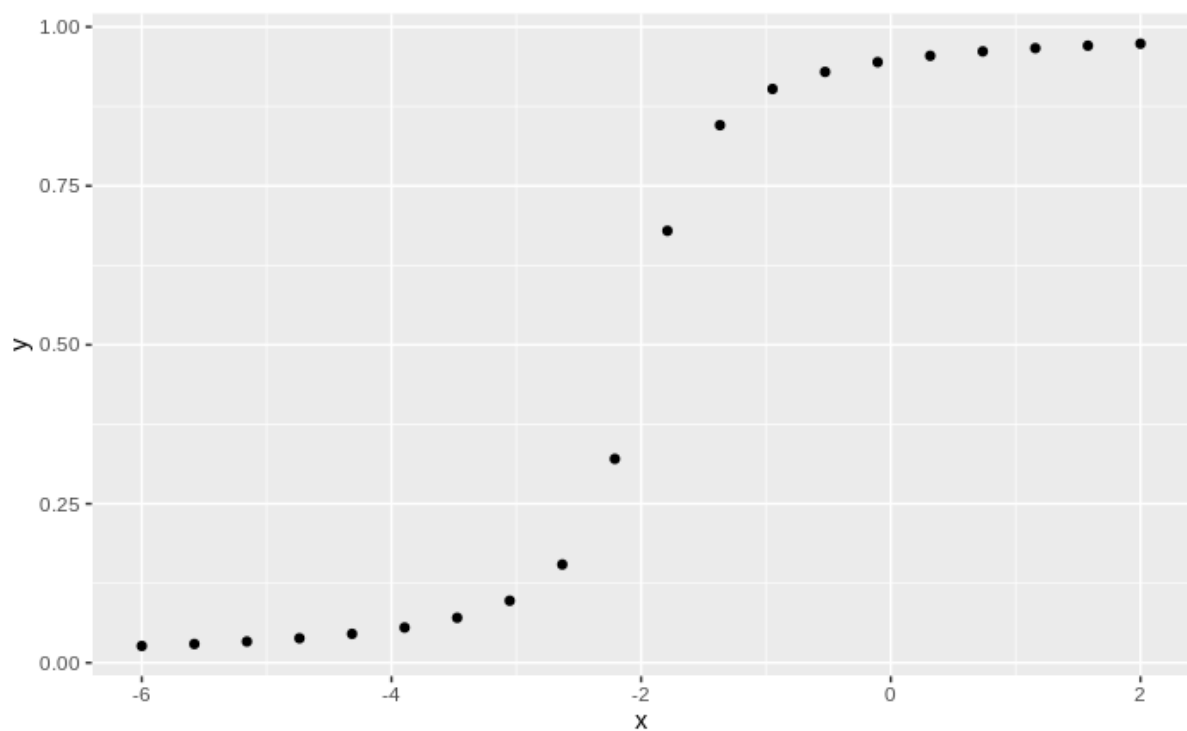- <u>**Figure1: kd value transformation function**</u>
  Kd transformation function
  We could also add the histograms of original and transformed values, but I don't think this is necessary
  - **Code**: depinfer package project:
    /g/huber/users/batzilla/depInfeR/vignettes/analysisWorkflow.Rmd
    Line 77

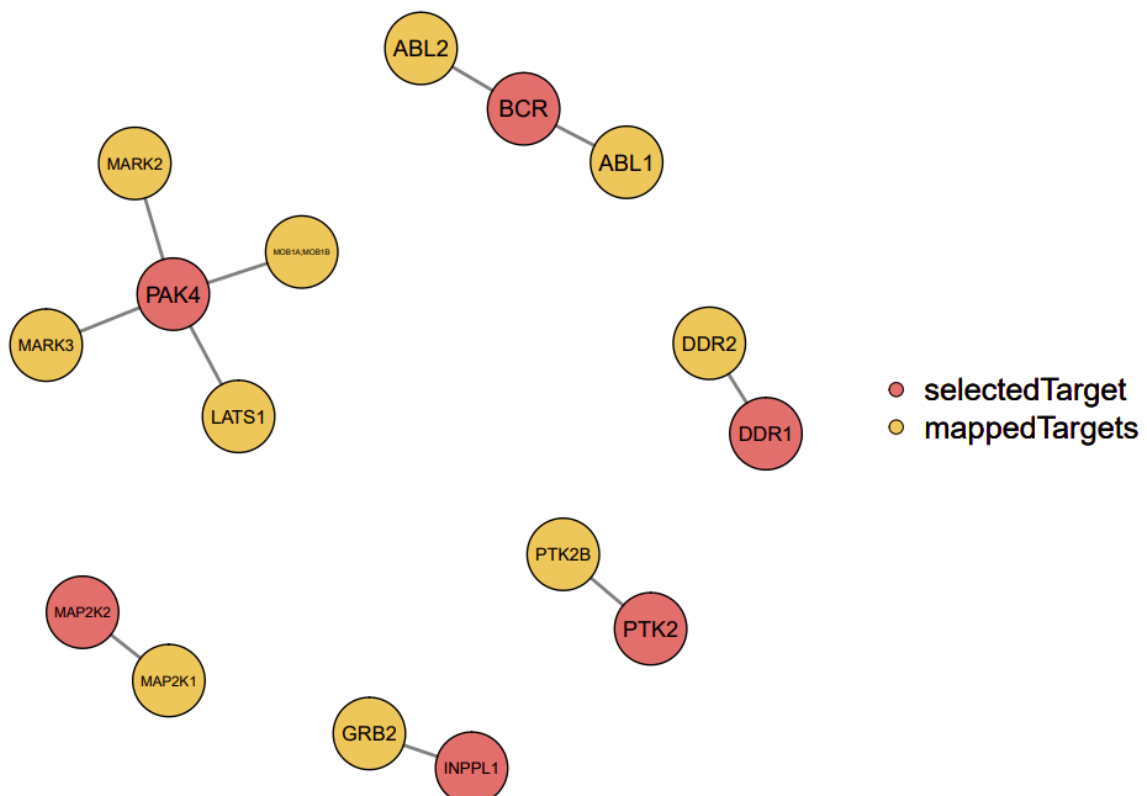- **Figure2: Collapsed kinase sets (for every dataset)**
  - **Code:**

    I think this code still needs to be transferred to the package to capture the actual kinase sets that we refer to in the manuscript
   - GDSC: targetimportance project: /targetimportance/package_modified/analysisGDSC_Sanger_Median.Rmd

      Line 409

    - EMBL2016: /targetimportance/package_modified/analysisEMBL2016_Median.Rmd

      Line 243

    - CTRP: /targetimportance/CTRP_Broad/analysisCTRP_median.Rmd

      Line 358

    - BeatAML: /targetimportance/BEATAML/analysisBeatAML_Median.Rmd

      Line 431

  - **Example**:

Target groups with highly correlated drug affinity profile

- **Figure3: Complete drug-kinase binding network (EMBL dataset)**
  - **Code:**
    I think this code still needs to be transferred to the package to capture the actual drug-kinase bindings that we refer to in the manuscript /g/huber/users/targetimportance/package_modified/targetNetwork_GDSC_EMBL.Rmd
    Line 79
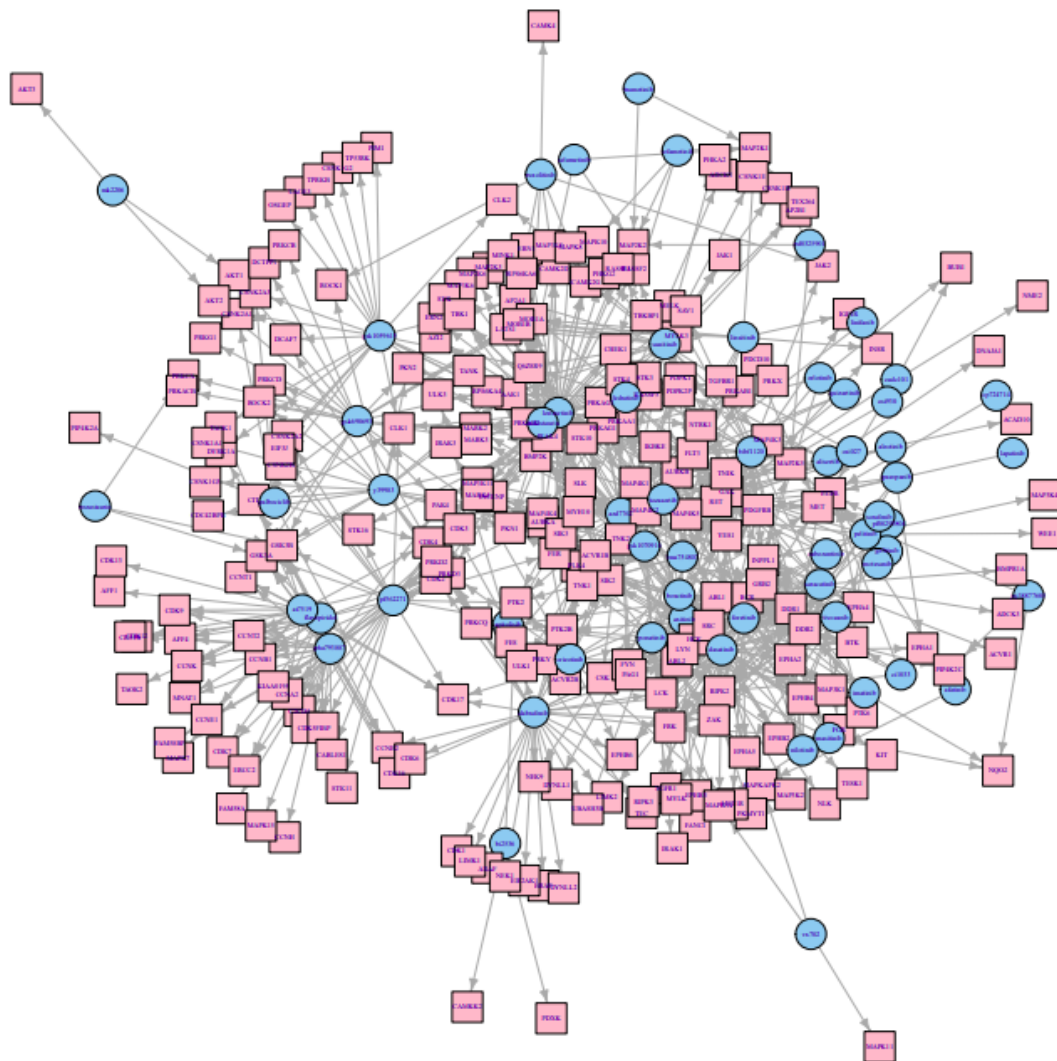
- **Figure4: Protein dependence heatmap GDSC**
  - **I think this figure just needs to be adjusted a little bit.**
  - **Code**: depinfer package project:
    /g/huber/users/batzilla/depInfeR/vignettes/analysisWorkflow.Rmd
    Line 185
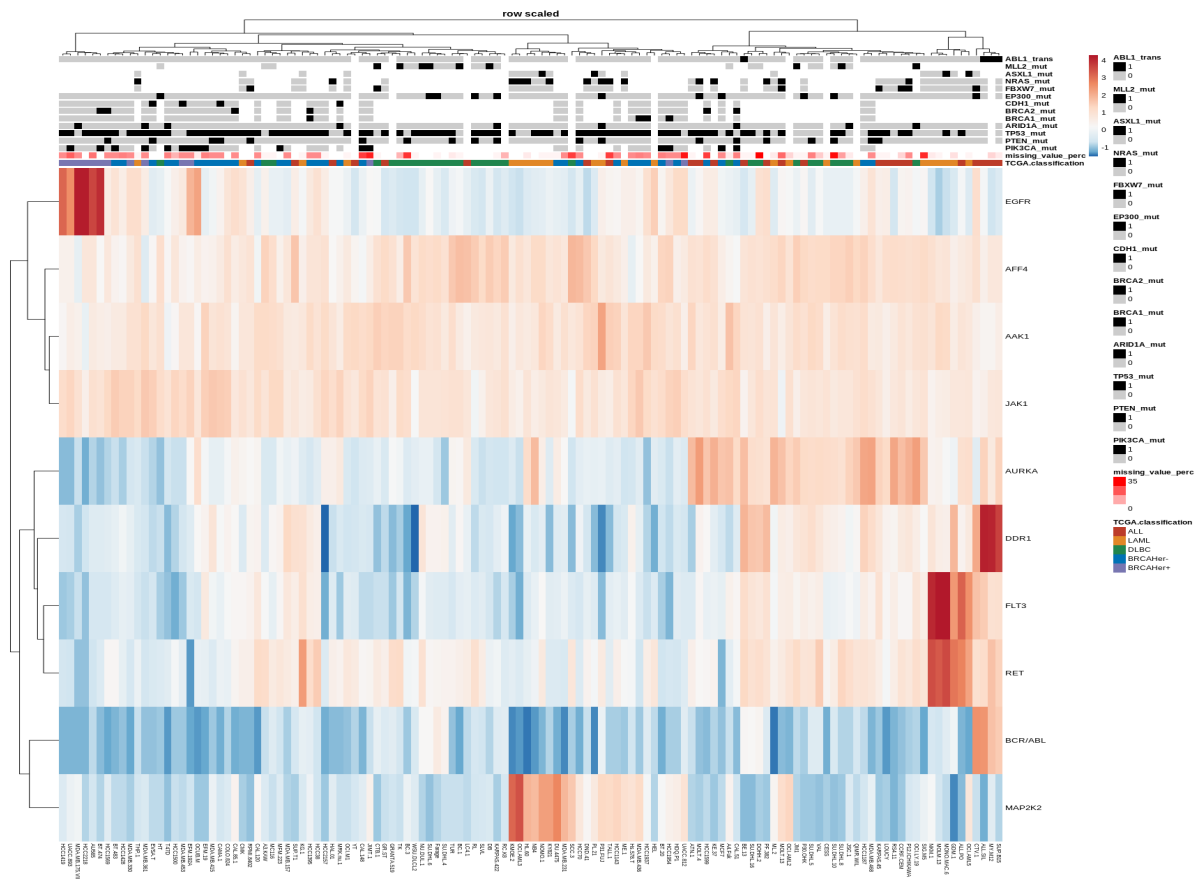
- **Figure5: correlation GDSC CTRP**

  I actually don't think we need a figure here. I just refer to the Pearson correlation in the manuscript. However, I think we need to transfer the code to the depinfer project to use the (reproducible) results that we refer to in the manuscript.
    - **Code:** target importance project: /g/huber/users/batzilla/targetimportance/Validation_Prediction/GDSC_CTRP_Median_Manuscript.Rmd

- **<u>Figure6: BeatAML associations</u>**
- The BeatAML (and CTRP) analysis are currently not yet in the package and only in the targetimportance project. I'm not sure if we should include these analyses in the package or make it available in some other way.
- **Code:** target importance project: /g/huber/users/batzilla/targetimportance/BEATAML/analysisBeatAML_Median.Rmd **Line 1107**
- **These are the associations we refer to in the manuscript - they could look like this:**
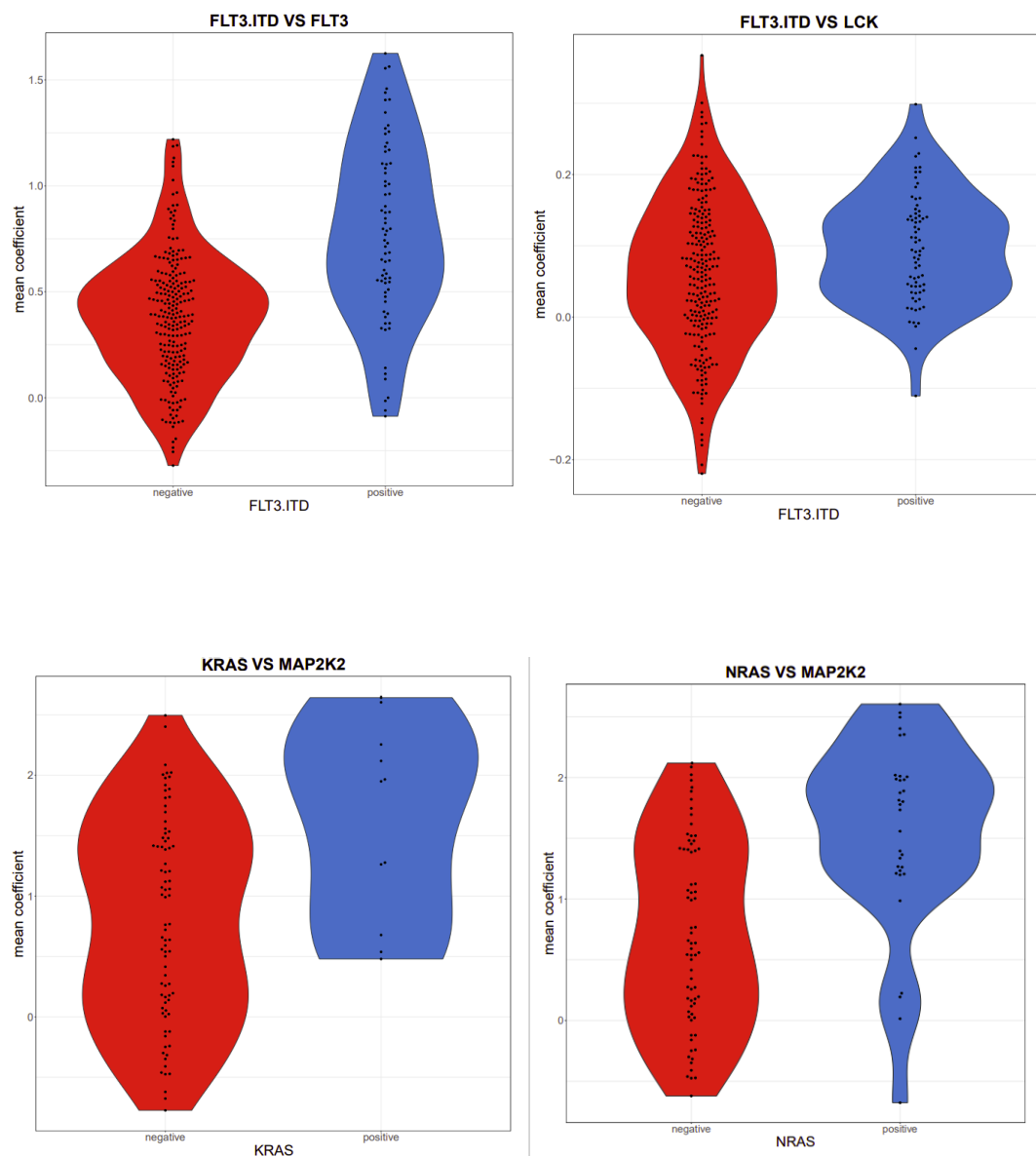
- **<u>Figure7: EMBL2016 disease association (BTK)</u>**
- **I think something like this still needs to be included in the package code.**
- **Code:** target importance project:
  /targetimportance/package_modified/analysisEMBL2016_Median.Rmd
  Line 965

diagnosis VS BTK
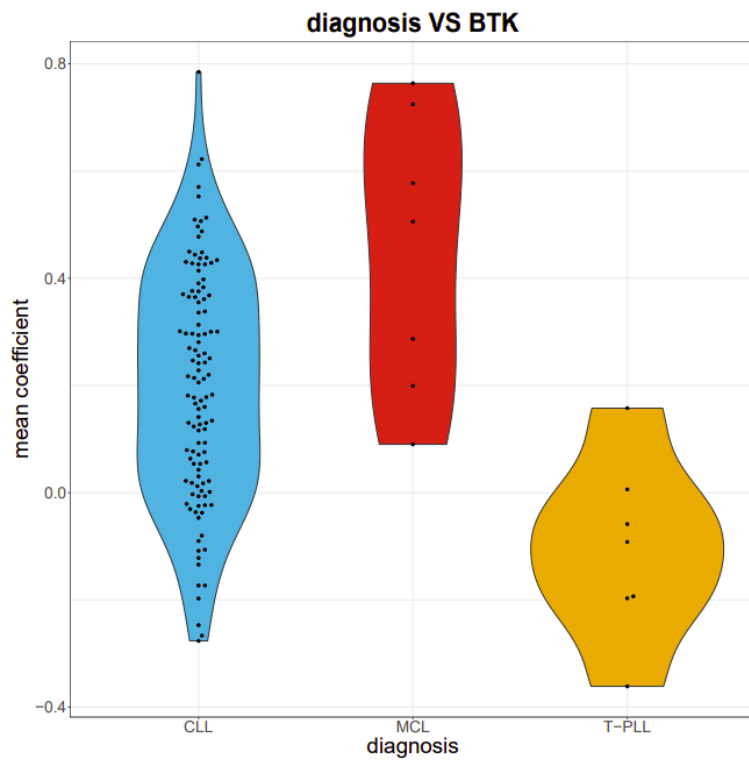
- **Figure8: Protein dependence heatmap EMBL2016**
- **I think this figure just needs to be adjusted a little bit.**
- **Code**: depinfer package project:
  /g/huber/users/batzilla/depInfeR/vignettes/analysisWorkflow.Rmd
  Line 487
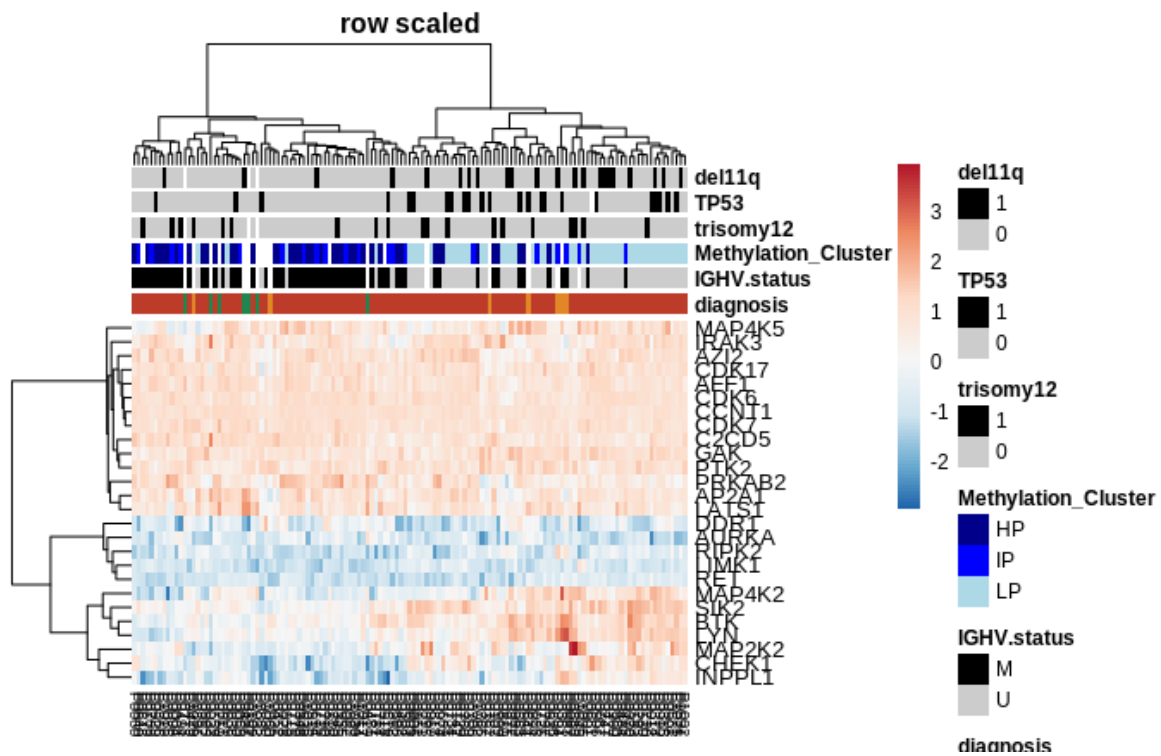
- **Figure9: Differential effect of CHK1 inhibitors without BCR-off-targets**

I still need to write the code for the t-test. I don't really think we need a figure here. But we can still discuss this.

- **Figure10: Upregulated CHK1 genes in U-CLL**
- **I don't think it makes sense to include the RNA sequencing analysis into the package - so I'm not sure where to put the code for a figure like this for example.**
- **Code:** target importance project: /g/huber/users/batzilla/targetimportance/CHK1_analysis/Expression_U-M-CLL.Rmd **Line 203**

Upregulated Hallmarks and Genes in U-IGHV (colored by Log2 Fold Change)