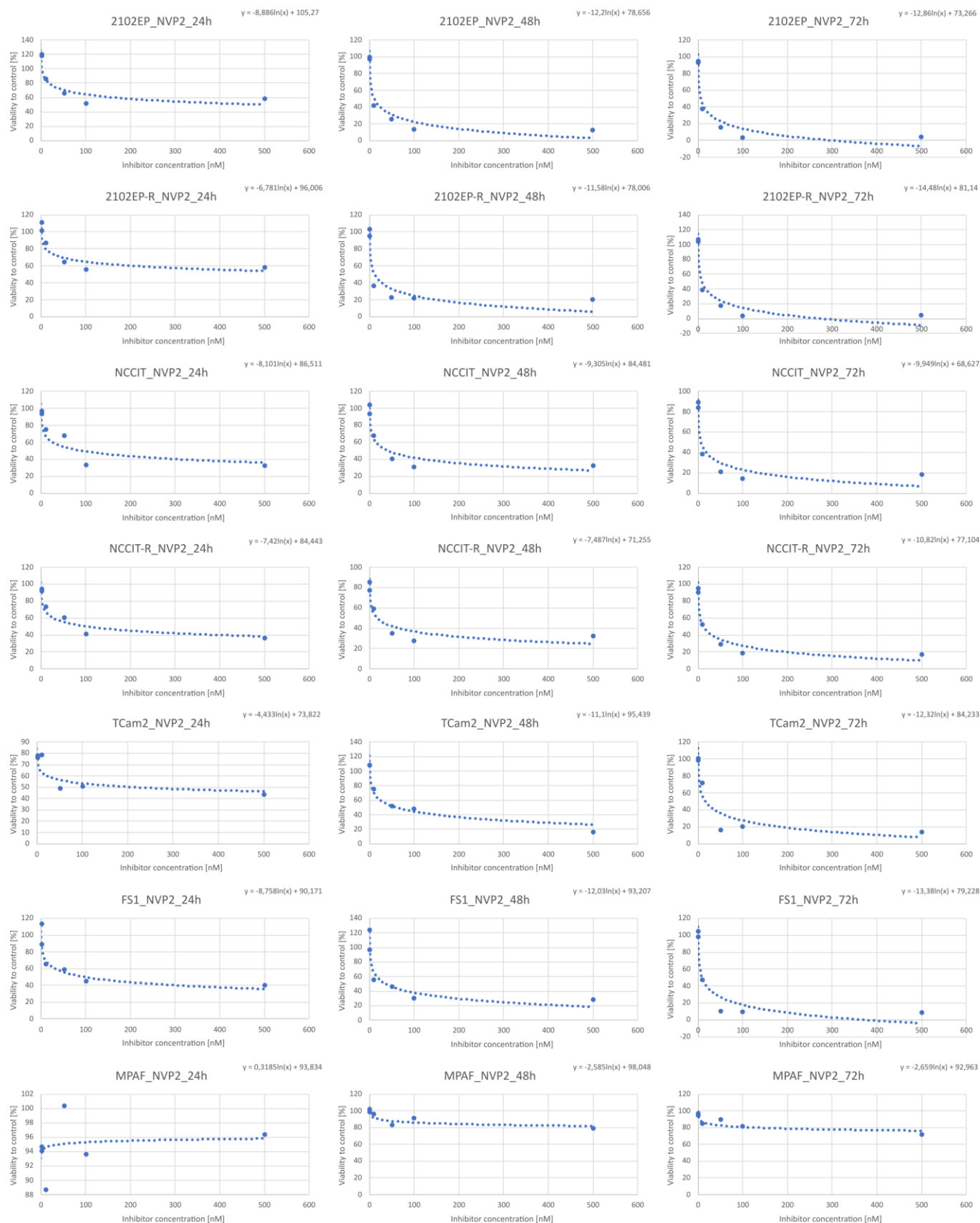
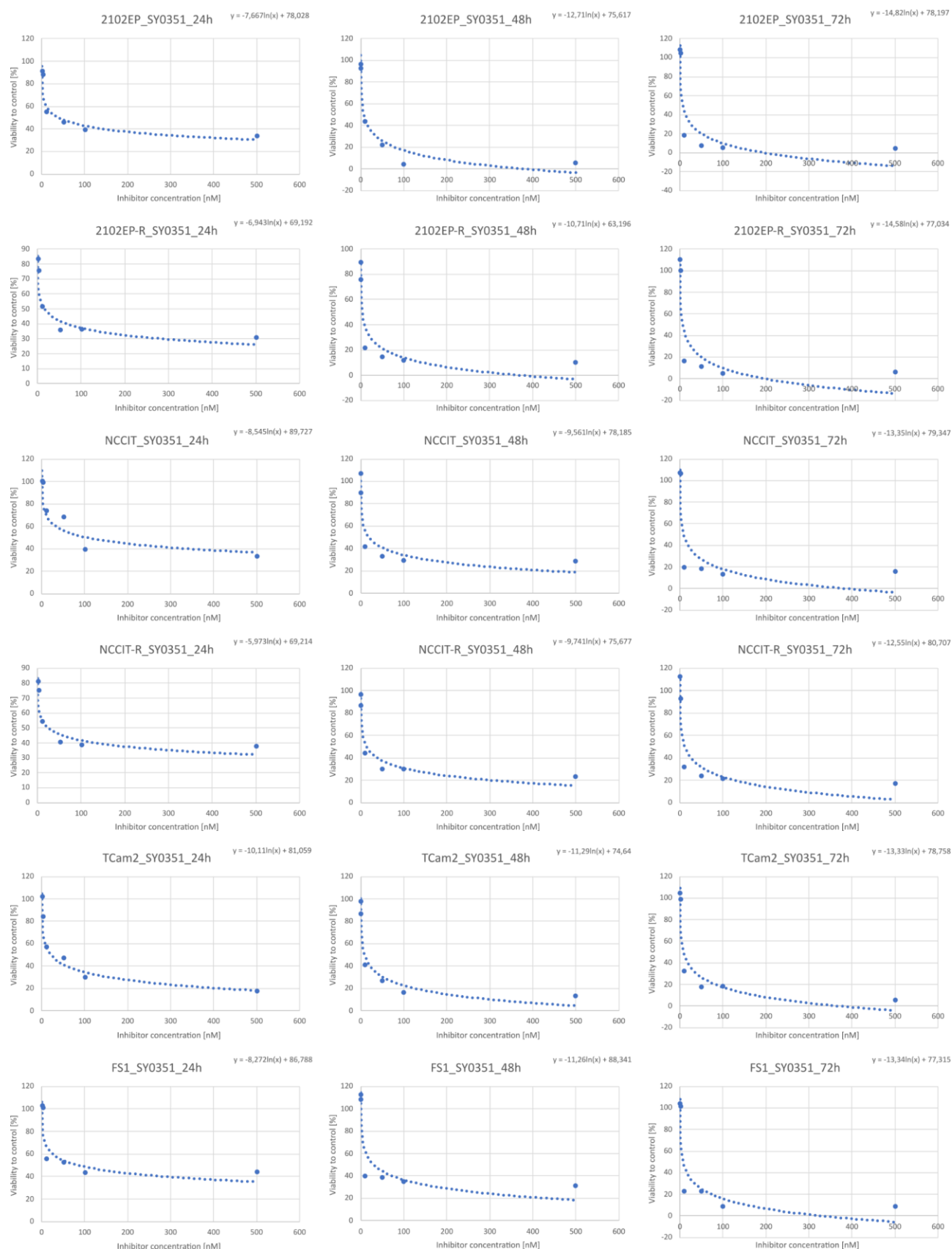


# CDK inhibitors

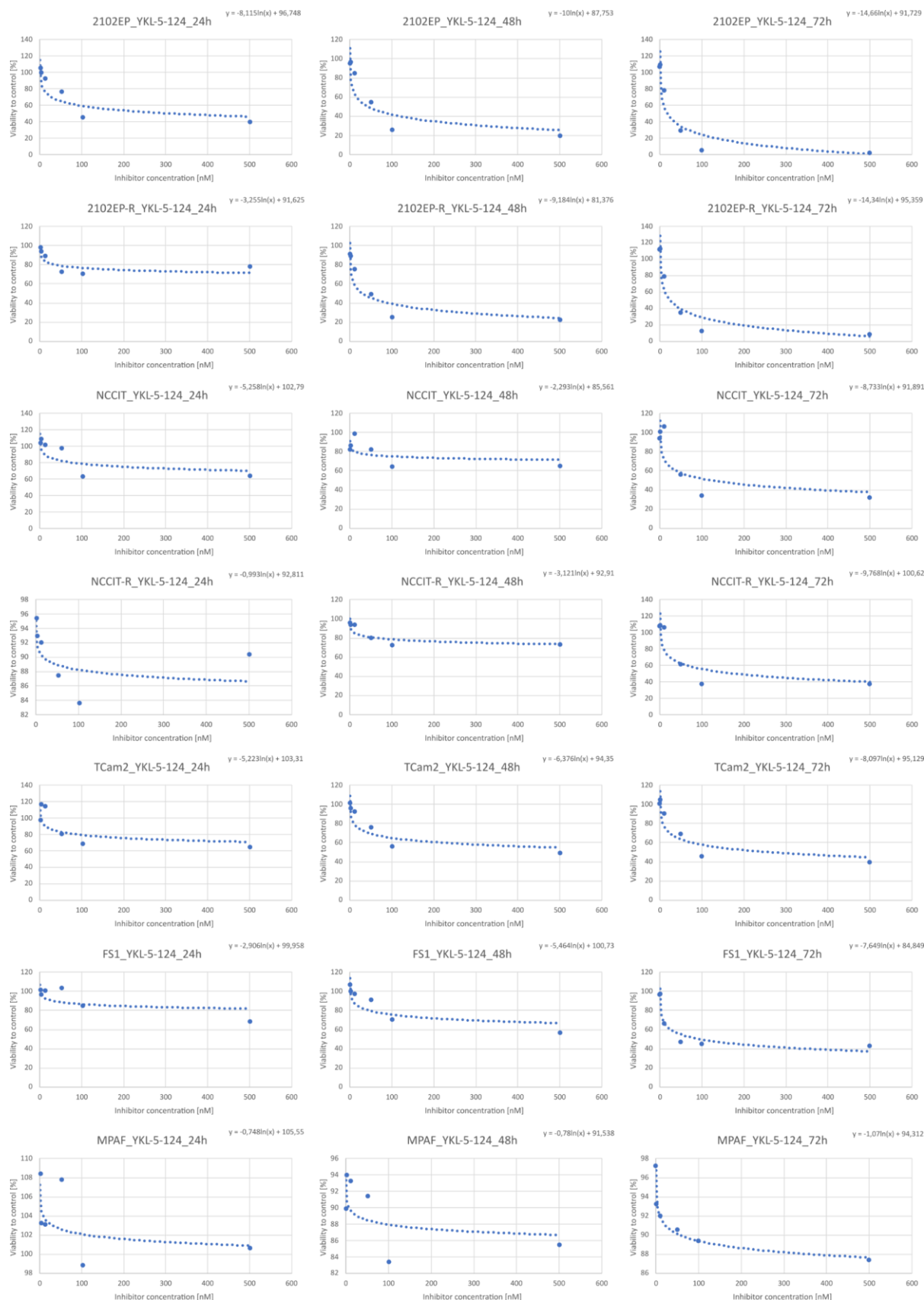
## -Supplementary Figures-



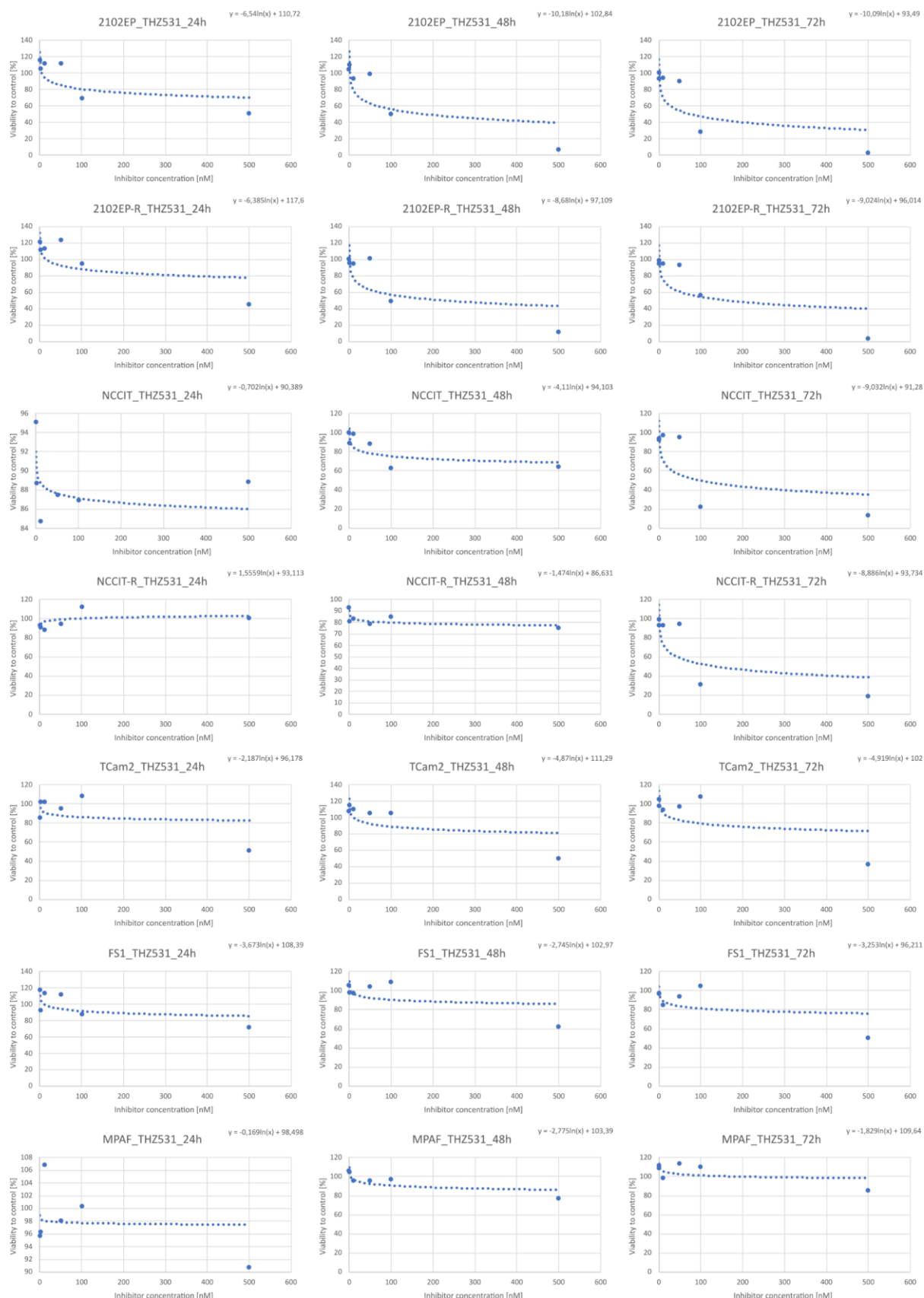
**Supplementary Figure S1: Logarithmic regression for NVP2 IC50 value calculation.**  
 Graphs are based on XTT viability data from Figure 2.



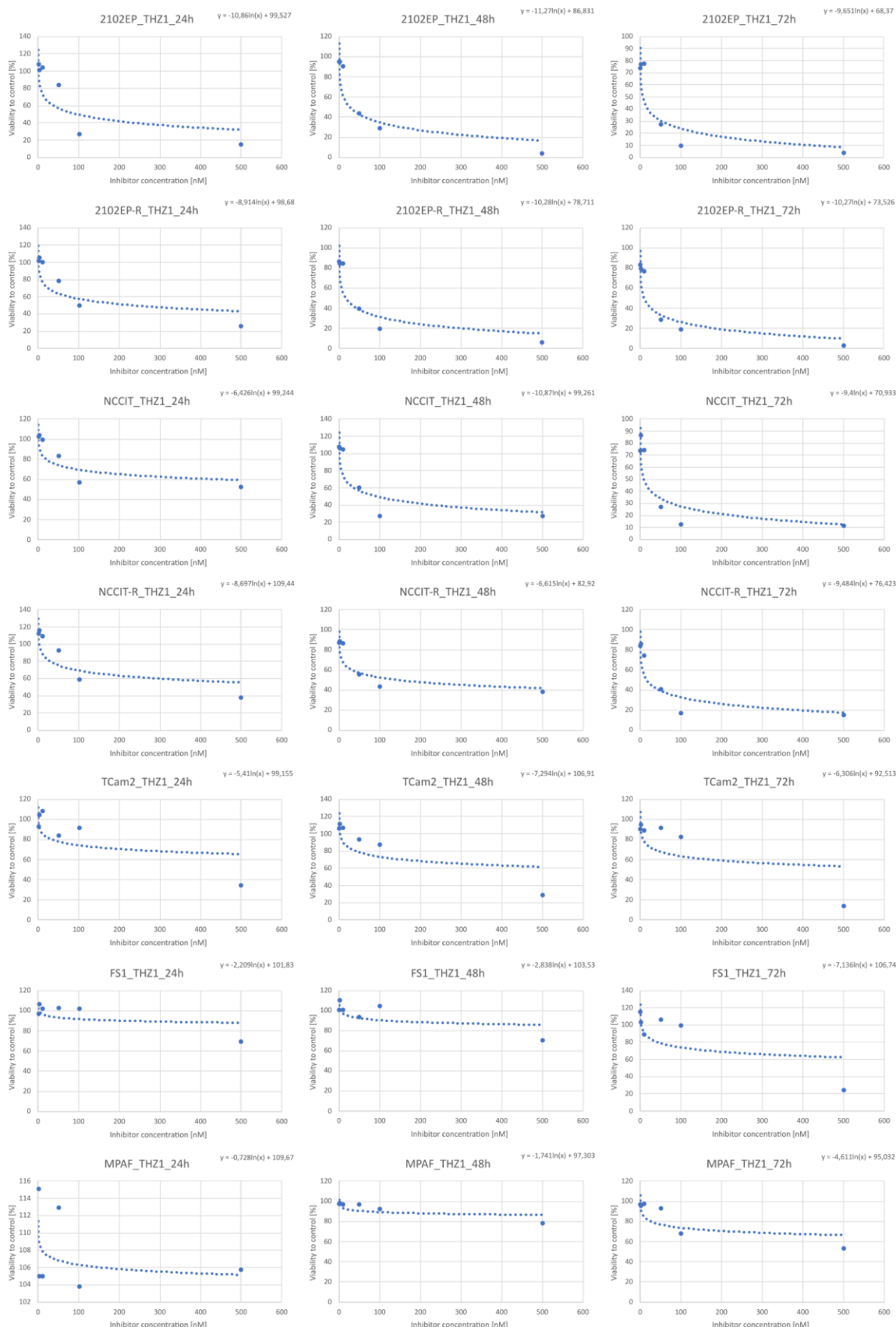
**Supplementary Figure S2: Logarithmic regression for SY0351 IC50 value calculation.** Graphs are based on XTT viability data from Figure 2.



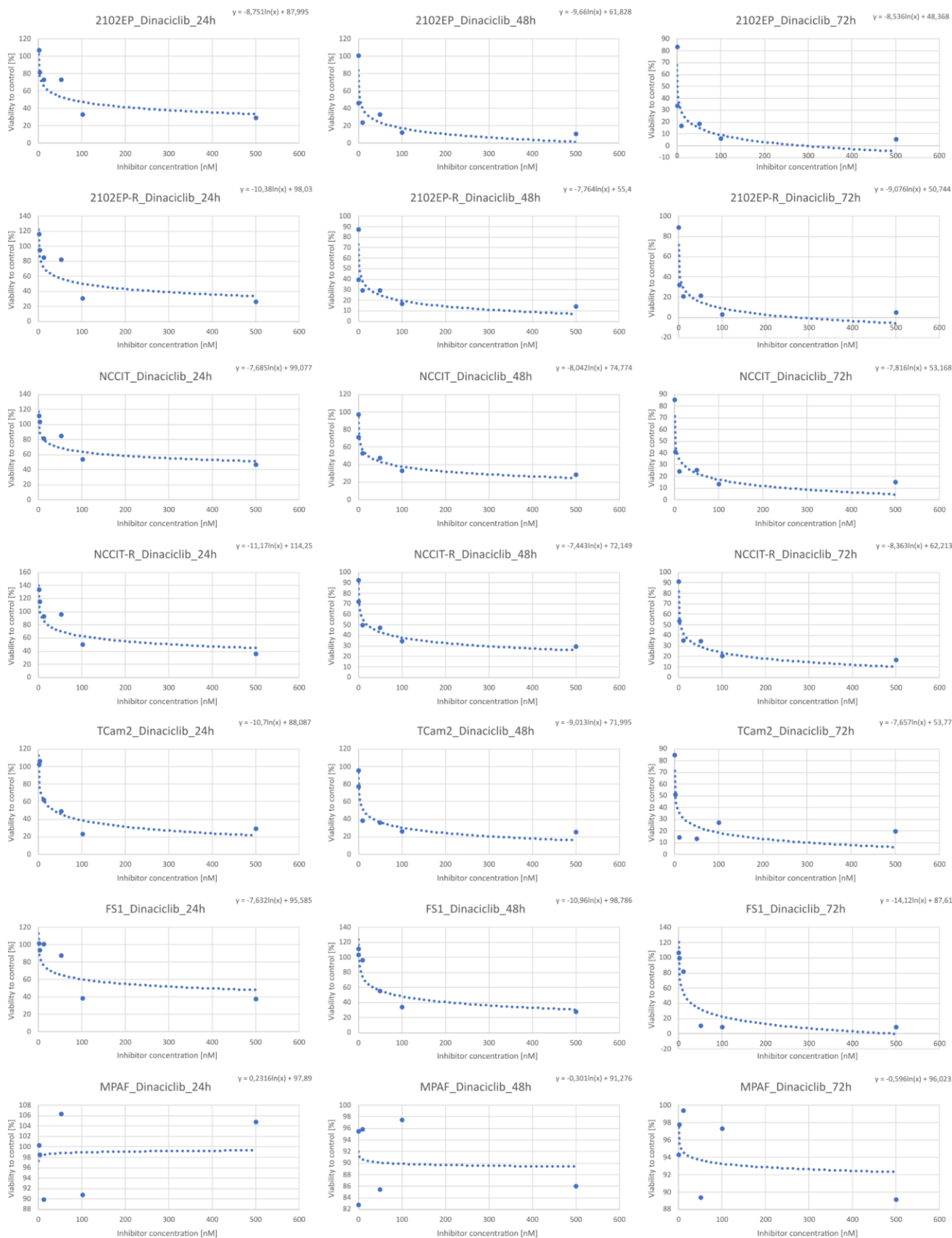
**Supplementary Figure S3: Logarithmic regression for YKL-5-124 IC50 value calculation.** Graphs are based on XTT viability data from Figure 2.



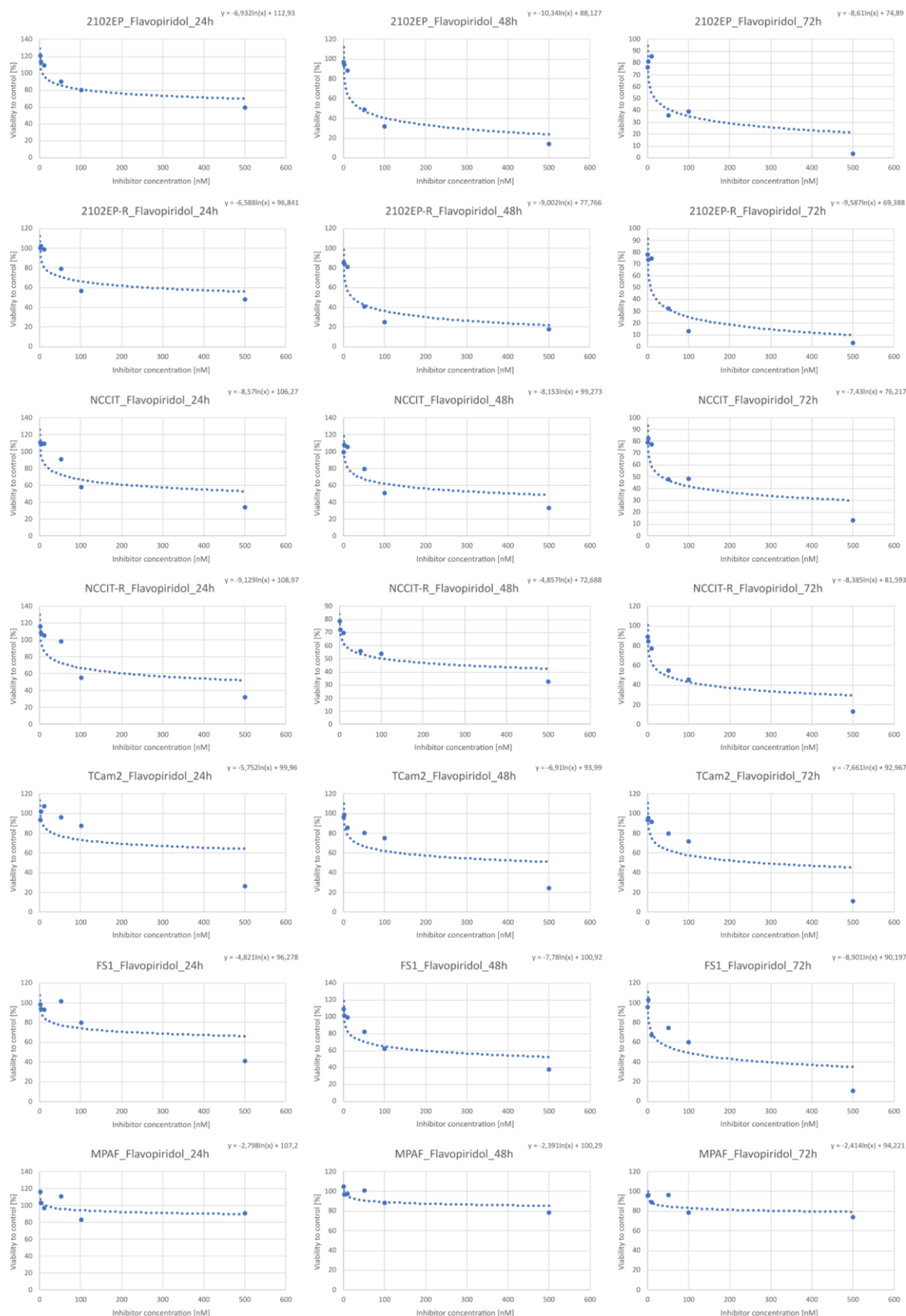
**Supplementary Figure S4: Logarithmic regression for THZ531 IC50 value calculation.** Graphs are based on XTT viability data from Figure 2.



**Supplementary Figure S5: Logarithmic regression for THZ1 IC50 value calculation.** Graphs are based on XTT viability data from Figure 2.

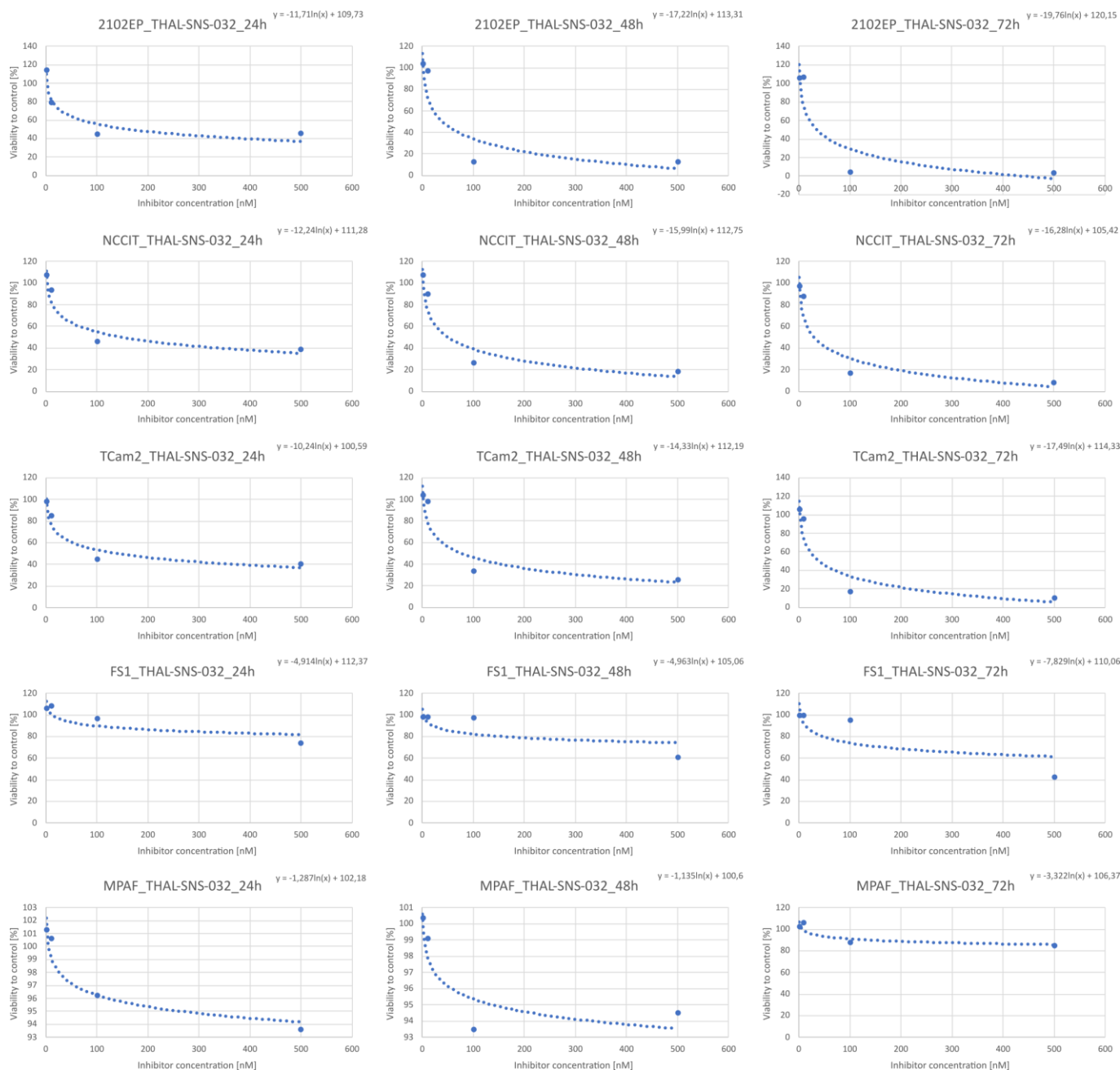


**Supplementary Figure S6: Logarithmic regression for Dinaciclib IC50 value calculation.** Graphs are based on XTT viability data from Figure 2.

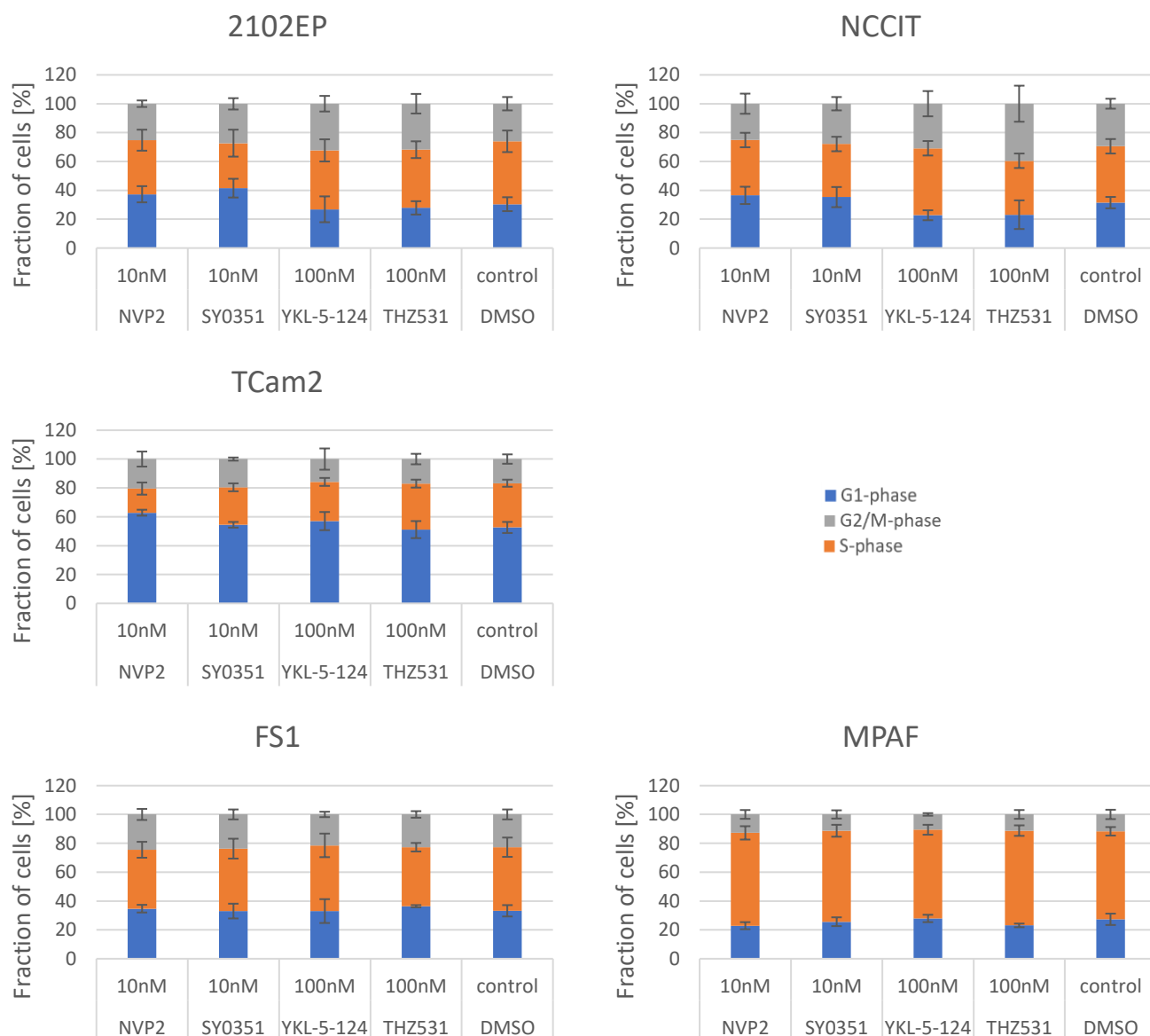


**Supplementary Figure S7: Logarithmic regression for Flavopiridol IC50 value calculation.** Graphs are based on XTT viability data from Figure 2.

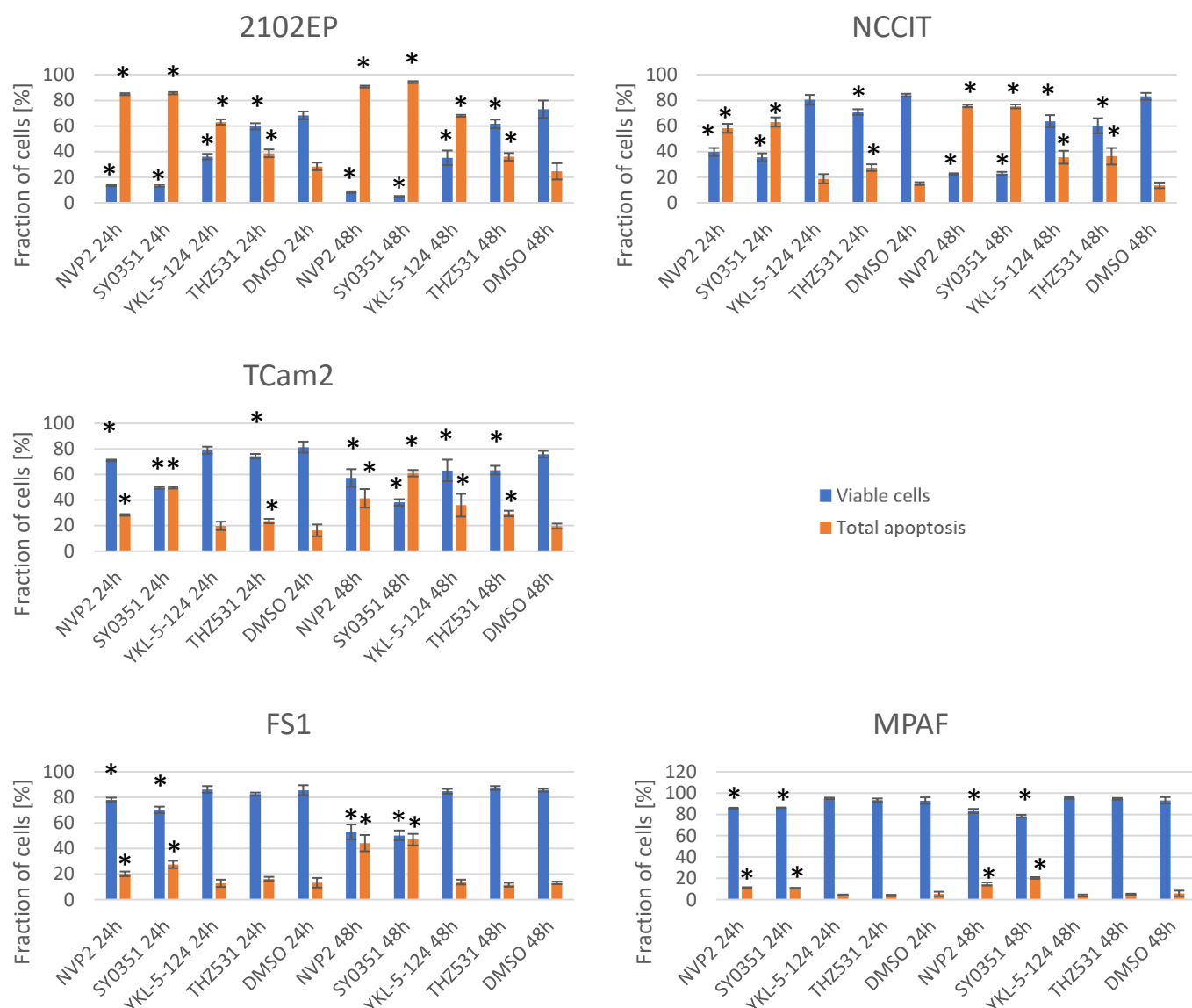




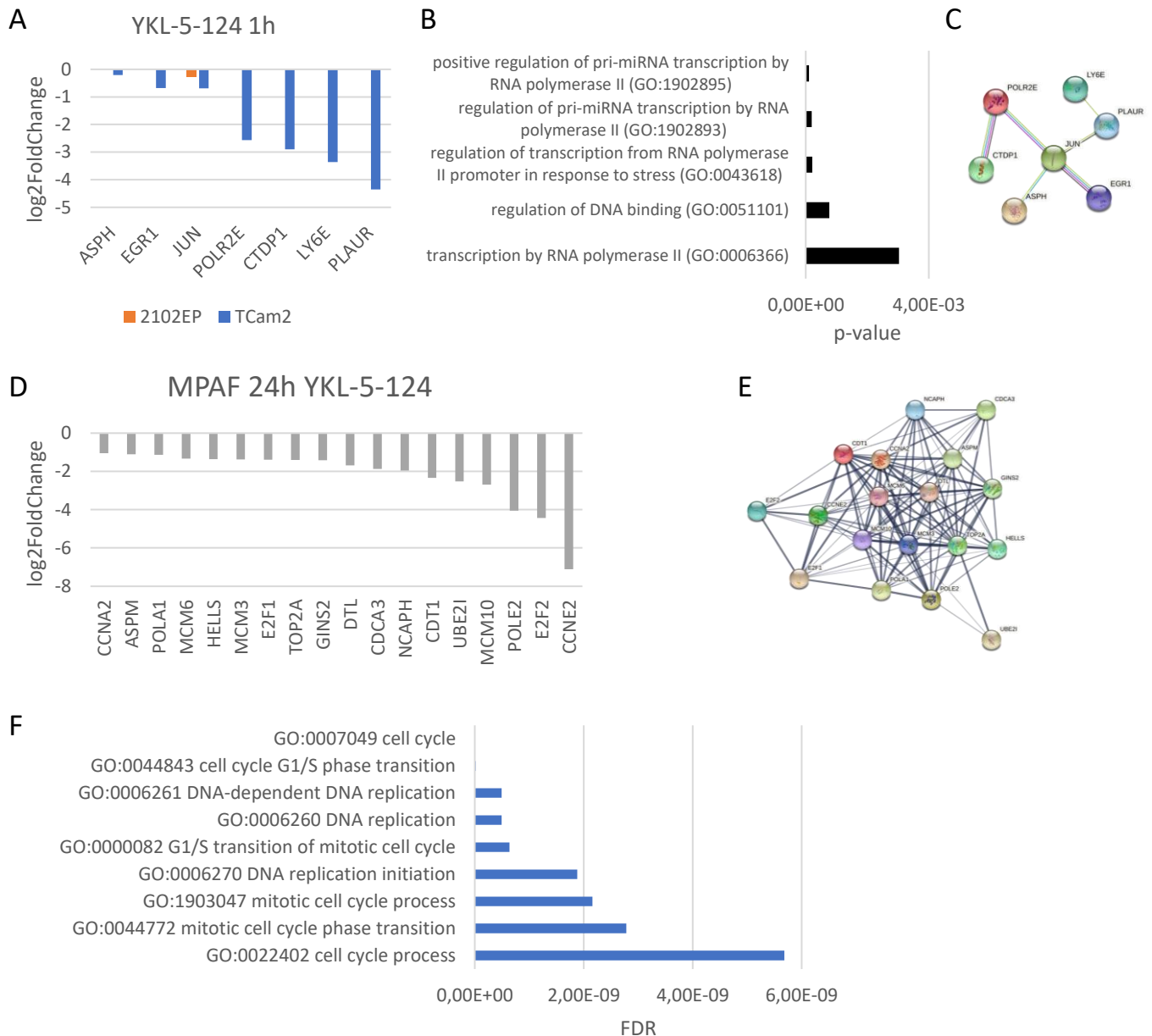
**Supplementary Figure S8: Logarithmic regression for THAL-SNS-032 IC50 value calculation.** Graphs are based on XTT viability data from Figure 2.



**Supplementary figure S9: Cell cycle analysis of TGCT and control cell lines.** Hoechst-FACS based cell cycle analysis after 20 h of CKD inhibitor treatment. Control sample was supplemented with DMSO according to inhibitor dilution (Final DMSO conc. 0.0002 %). n=3-6.



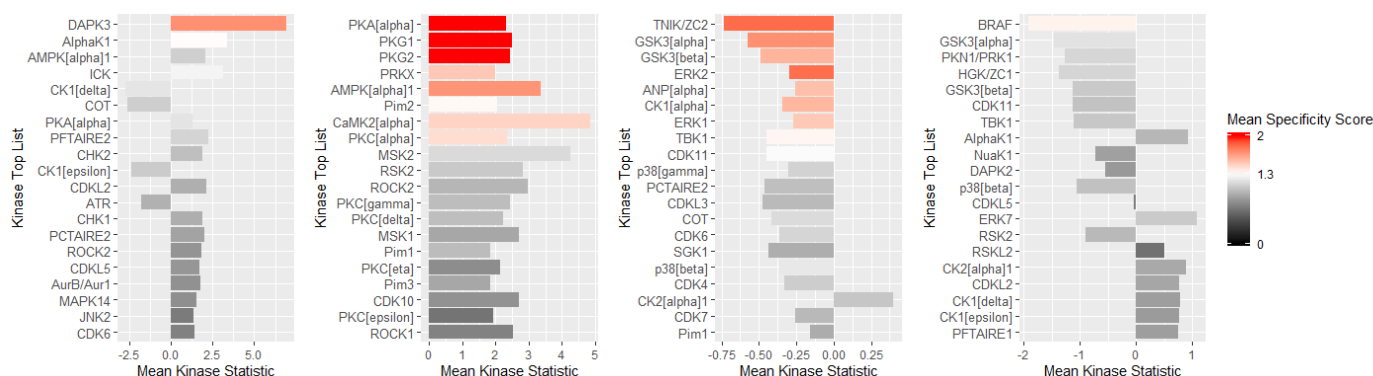
**Supplementary figure S10: Apoptosis analysis of TGCT and control cell lines.** 7AAD/AnnexinV FACS based apoptosis analysis after 24 h and 48 h of CKD inhibitor treatment. Cells which emitted a signal for AnnexinV only or for Annexin and 7AAD were considered to be apoptotic while double negative cells represented the viable cell population. For calculation of p-values by two-tailed Student's t-test each treated sample is referred to the corresponding DMSO control. n=3-6. Significance is given as \*P < 0.05.



**Supplementary figure S11: YKL-5-124 treatment revealed deregulated RNA polymerase II function and downregulation of cell cycle associated genes in TCam2 cells and MPAF cells, respectively.** (A) Downregulated genes after 1 h of YKL-5-124 (100 nM) treatment in 2102EP and TCam2 cells and corresponding (B) Gene Ontology as well as (C) STRING interaction analysis. (D) Downregulated genes in MPAF cells after 24 h of YKL-5-124 exposure with (E) STRING interaction and (F) GO analysis. All samples n=3.

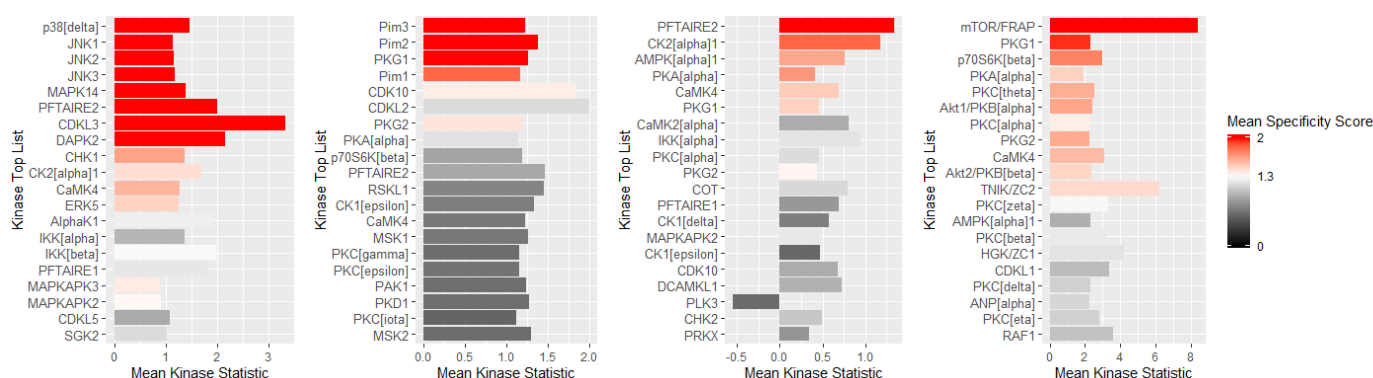
A

2102EP YKL-5-124 1h    2102EP YKL-5-124 24h    TCam2 YKL-5-124 1h    TCam2 YKL-5-124 24h



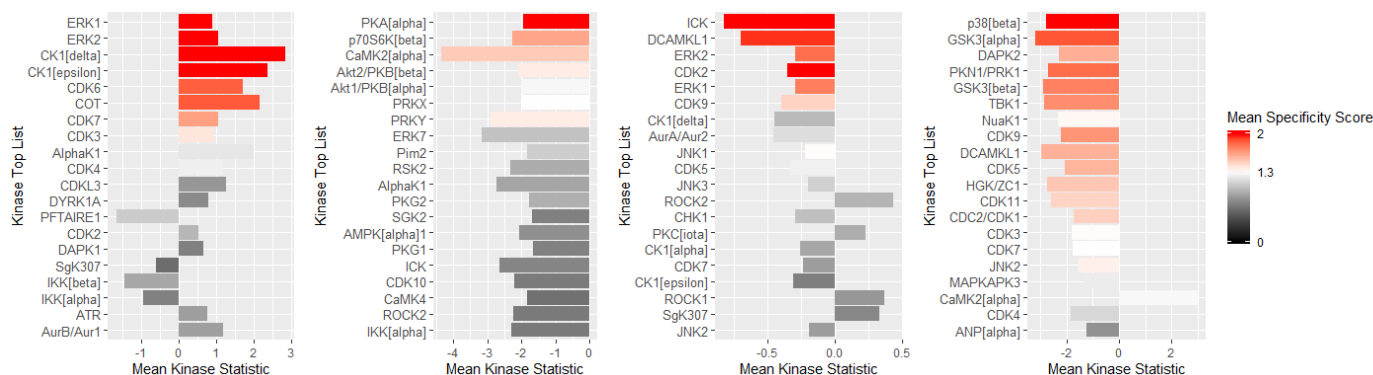
B

2102EP NVP2 1h    2102EP NVP2 24h    TCam2 NVP2 1h    TCam2 NVP2 24h



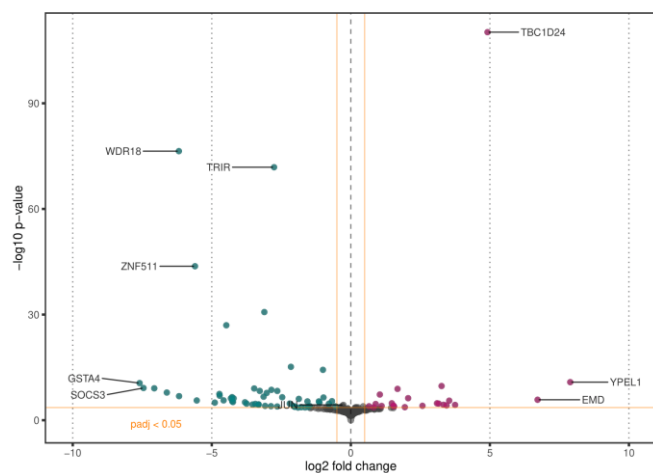
C

2102EP THZ531 1h    2102EP THZ531 24h    TCam2 THZ531 1h    TCam2 THZ531 24h

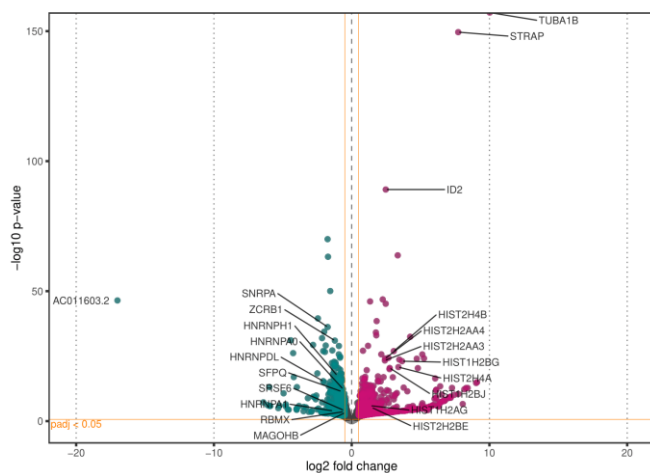


**Supplementary Figure S12: Serine/ threonine kinase activity assay.** Kinase score plots rank-order the top kinases differential between the treated and DMSO control group. 2102EP and TCam2 cells were treated for 1 h or 24 h with (A) YKL-5-124 (100 nM), (B) NVP2 (10 nM) or (C) THZ531 (100 nM). Subsequently, proteins were isolated and analyzed by PAM Gene assay. All samples n=2.

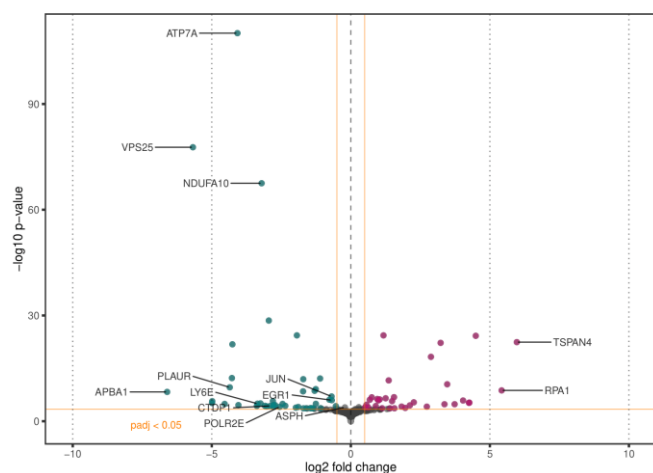
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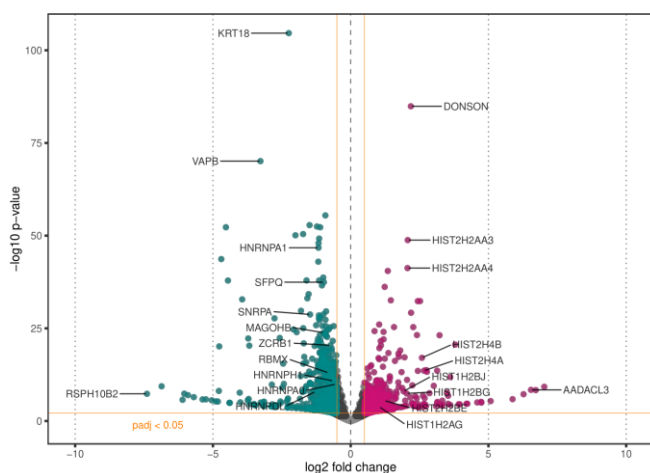
2102EP 24h YKL-5-124



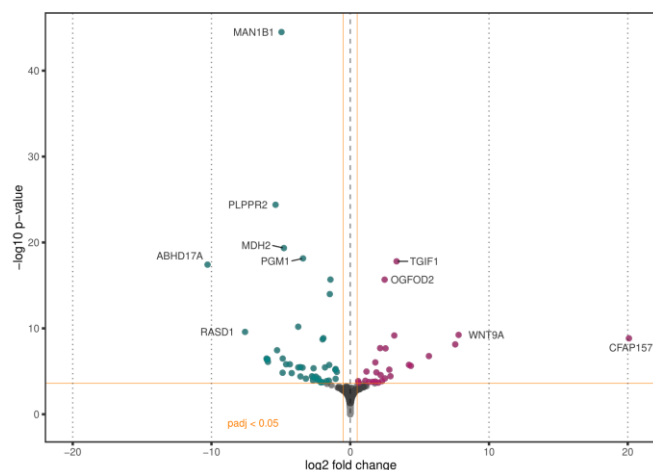
TCam2 1h YKL-5-124



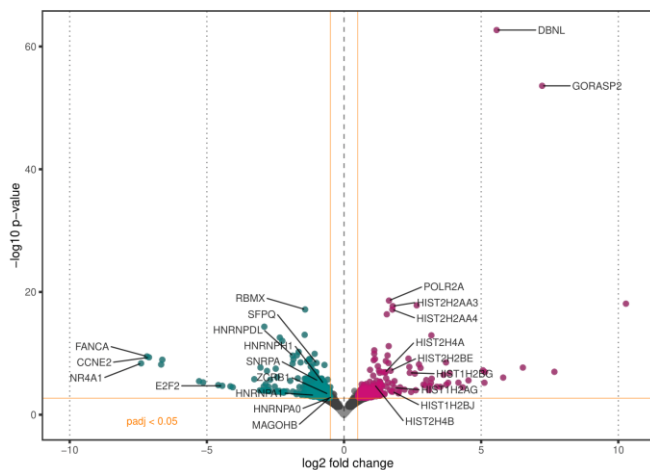
TCam2 24h YKL-5-124



MPAF 1h YKL-5-124

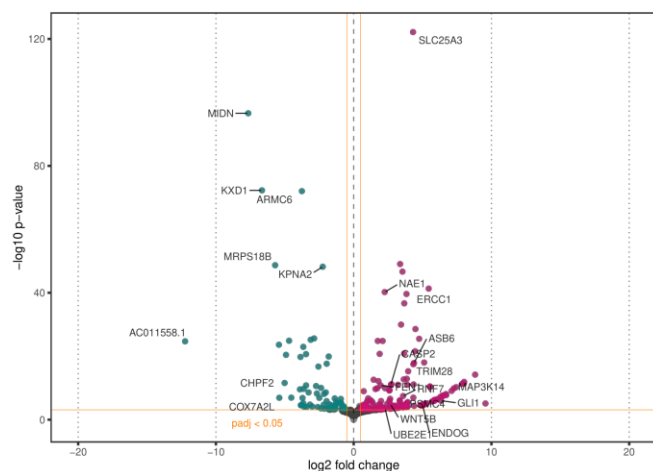


MPAF 24h YKL-5-124

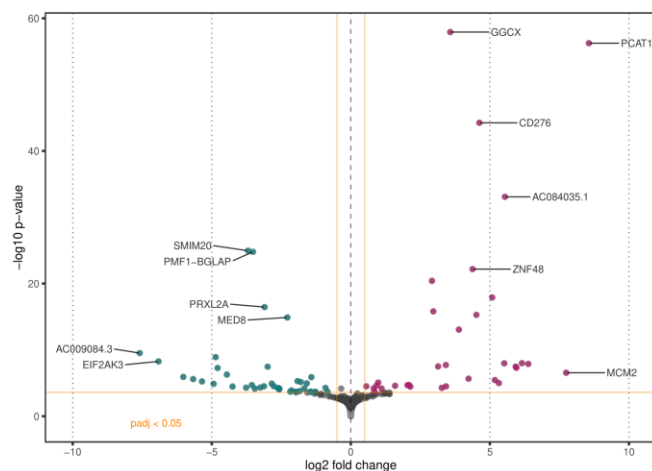


**Supplementary Figure S13: RNA sequencing data distribution of significantly deregulated genes (YKL-5-124).** 2102EP, TCam2 and MPAF cells were treated for 1 h and 24 h with YKL-5-124 (100 nM).

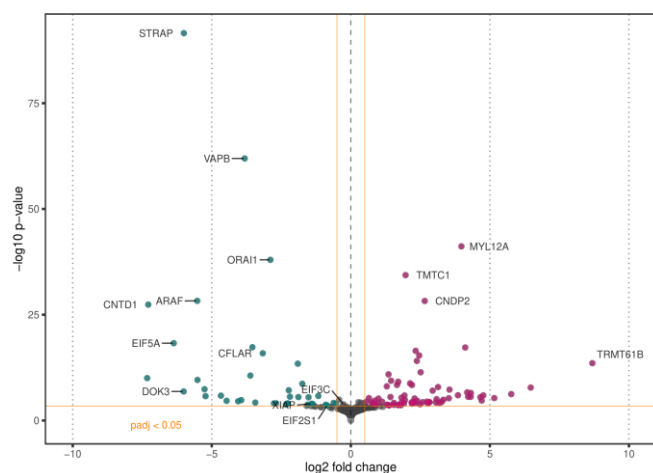
2102EP 1h SY0351



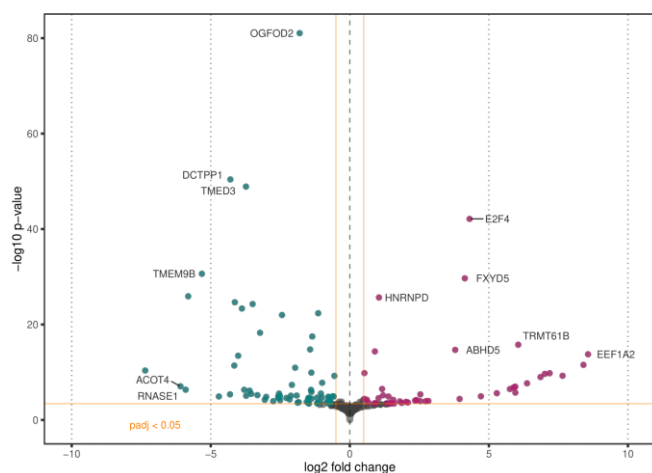
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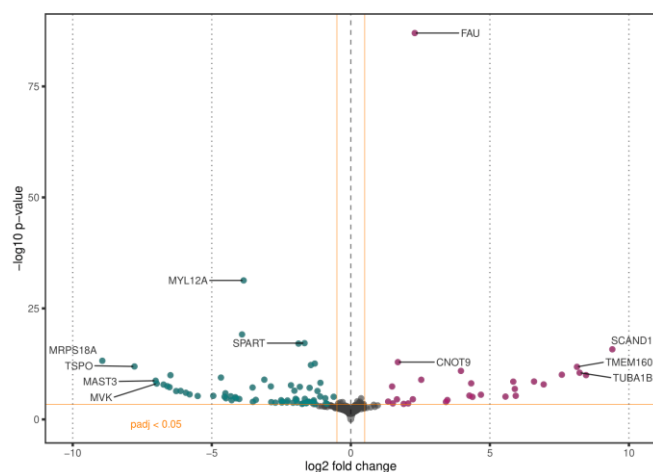
TCam2 1h SY0351



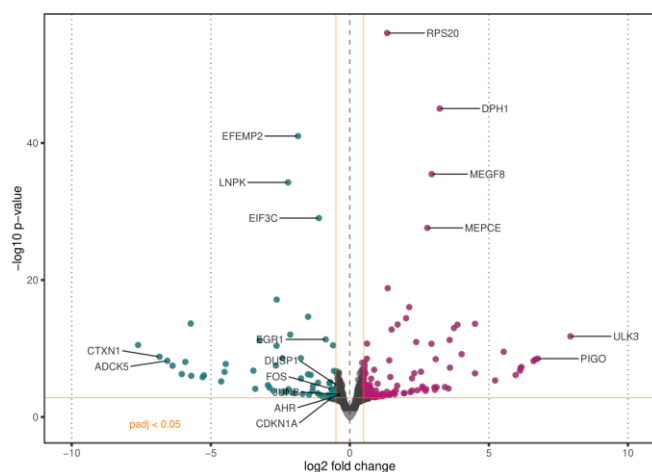
TCam2 24h SY0351



MPAF 1h SY0351

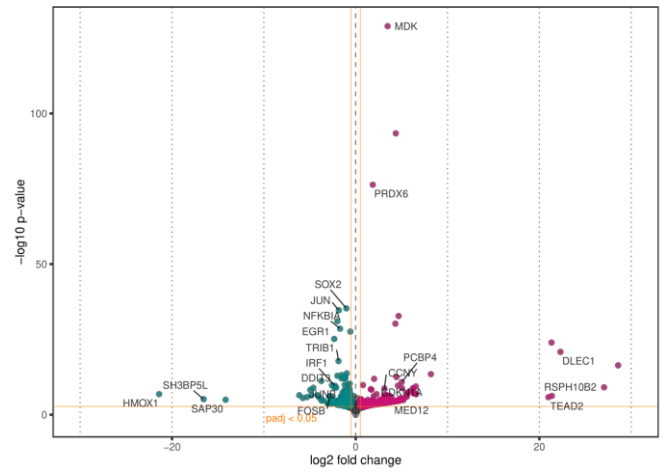


MPAF 24h SY0351

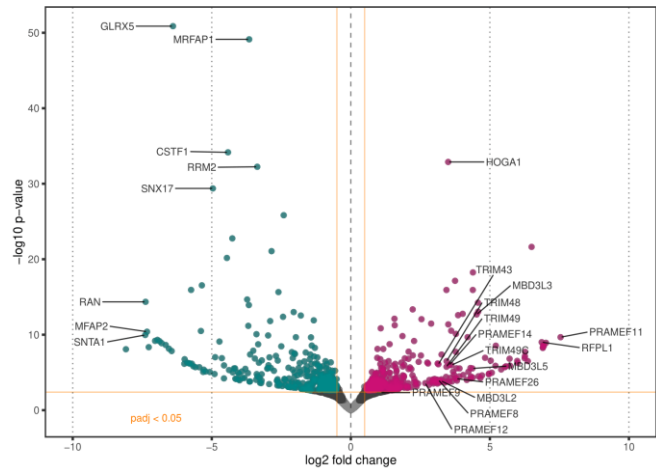


**Supplementary Figure S14: RNA sequencing data distribution of significantly deregulated genes (SY0351).** 2102EP, TCam2 and MPAF cells were treated for 1 h and 24 h with SY0351 (10 nM).

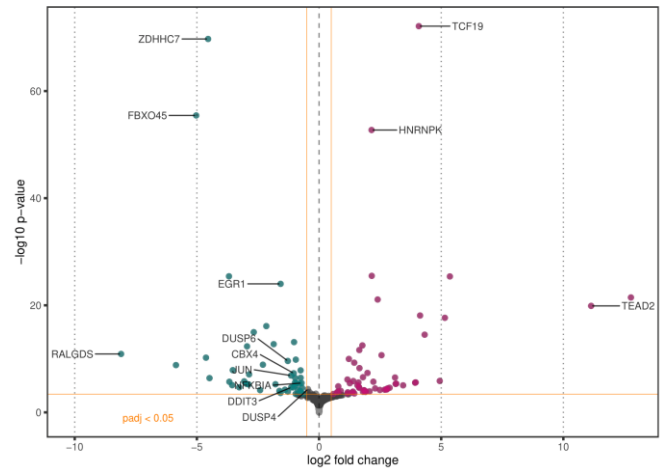
2102EP 1h NVP2



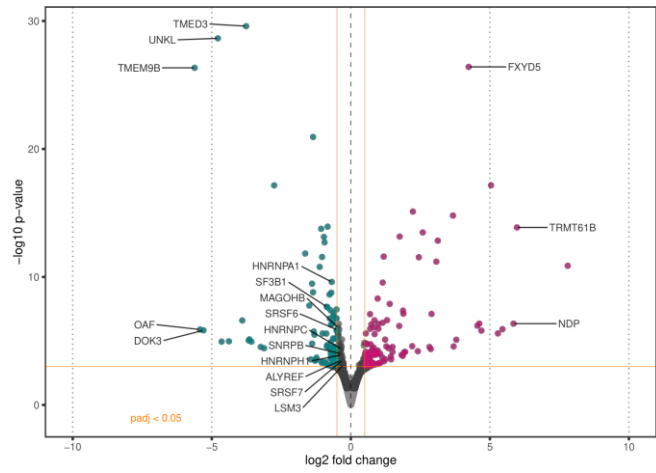
2102EP 24h NVP2



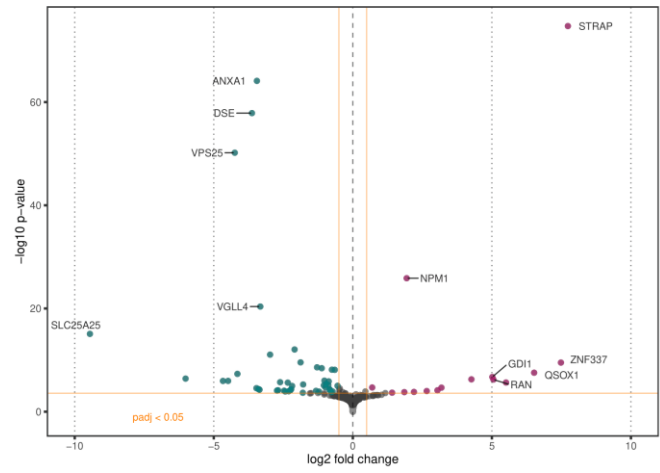
TCam2 1h NVP2



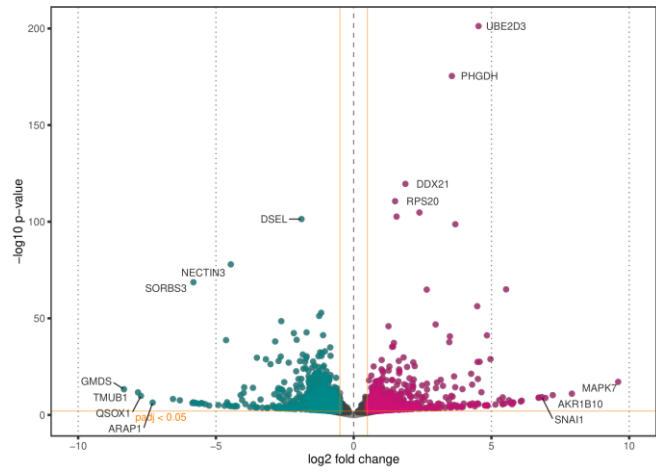
TCam2 24h NVP2



MPAF 1h NVP2



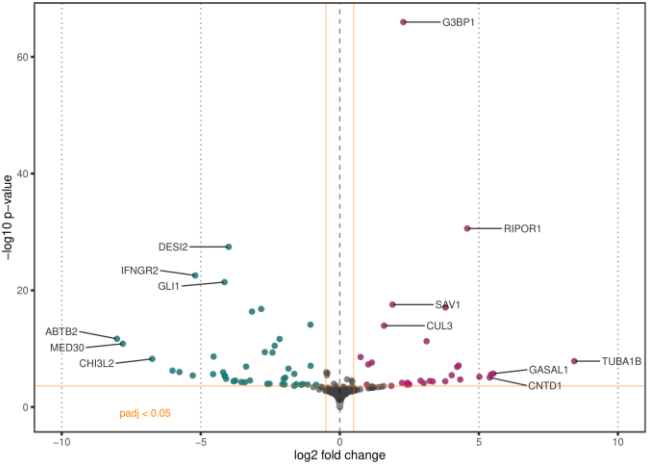
MPAF 24h NVP2



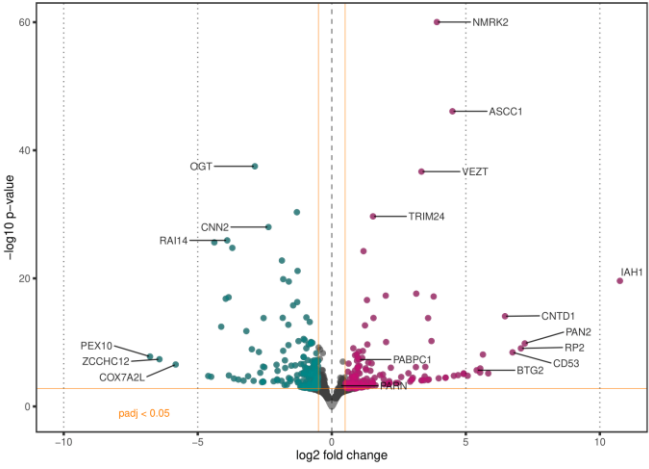
**Supplementary Figure S15: RNA sequencing data distribution of significantly deregulated genes (NVP2).** 2102EP, TCam2 and MPAF cells were treated for 1 h and 24 h with NVP2 (10 nM).



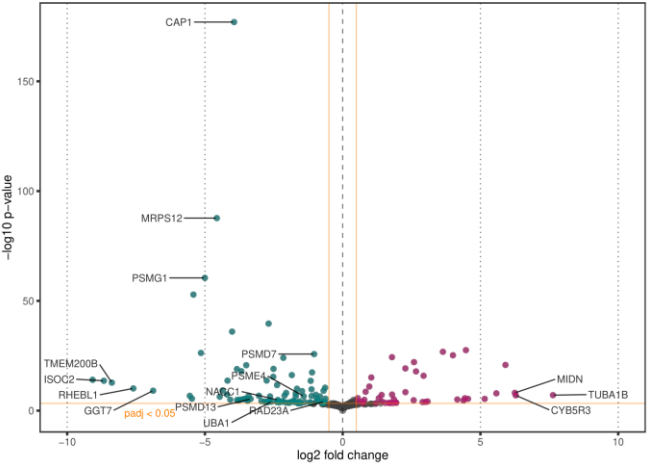
2102EP 1h THZ531



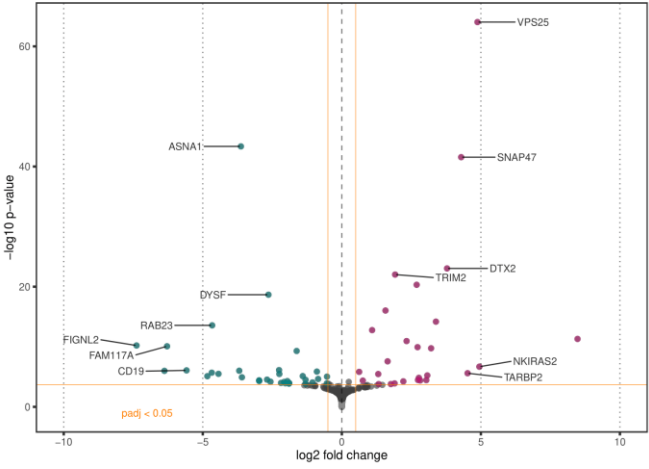
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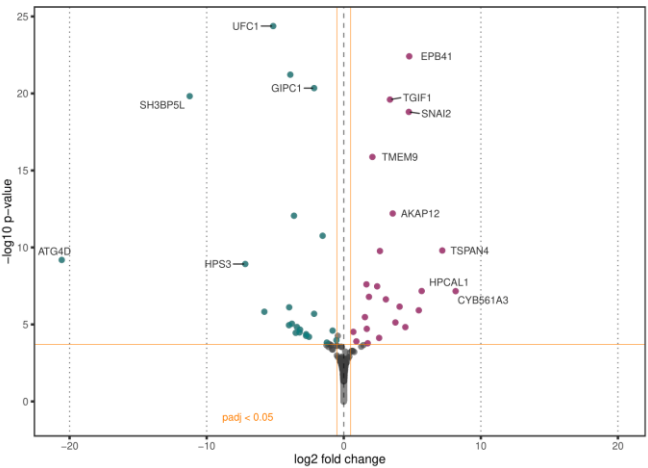
TCam2 1h THZ531



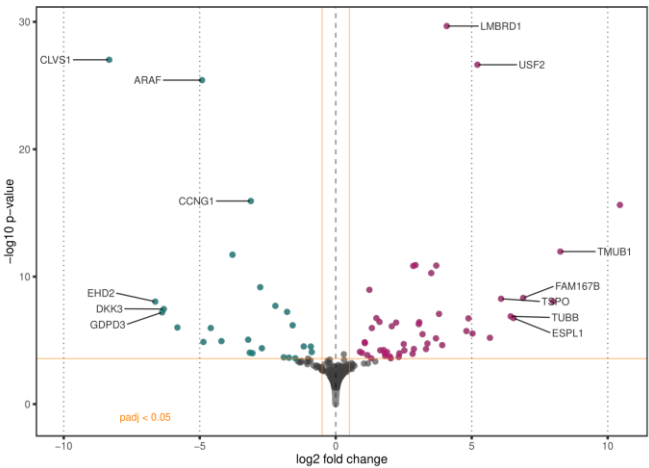
TCam2 24h THZ531



MPAF 1h THZ531



MPAF 24h THZ531



**Supplementary Figure S16: RNA sequencing data distribution of significantly deregulated genes (THZ531).** 2102EP, TCam2 and MPAF cells were treated for 1 h and 24 h with THZ531 (100 nM).