OVERVIEW OF THE SUPPLEMENTARY MATERIAL OF THE ARTICLE

In vitro discovery of promising anti-cancer drug combinations using maximization of a therapeutic index

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The supplementary material is divided into 4 files and 3 movies, these are 1-SupplementaryData.pdf, that includes

- **a)** Table S1: A set of 13 clinical/experimental drugs used in the iterative search using the MACS algorithm (pilot experiment).
- b) Table S2: Results of generation 0 of pilot experiment.
- c) Table S3: Results of generation 1 of pilot experiment.
- **d)** Table S4: Results of generation 2 of pilot experiment.
- e) Table S5: Results of generation 3 of pilot experiment.
- f) Table S6: Results of generation 0 of main experiment.
- g) Table S7: Results of generation 1 of main experiment.
- h) Table S8: Results of generation 2 of main experiment.
- i) Figure S1: Optimization overview of all iterations of pilot experiment.
- **j)** Figure S2: Factorial concentration-response and TS (therapeutic synergy) study of combination (Sunitinib, 17-AAG, Afungin, Trichostatin A).
- **k)** Figure S3: Factorial concentration-response study of combination (Sunitinib, 17-AAG, Afungin, Trichostatin A) in patient cells.
- I) Figure S4: Factorial concentration-response and TS study of combination (Rapamycin, 17-AAG, Trichostatin A).
- **m)** Figure S5: Factorial concentration-response study of combination (Rapamycin, 17-AAG, Trichostatin A) in patient cells.
- **n)** Figure S6: Factorial concentration-response and TS study of combination (Rapamycin, 17-AAG).
- **o)** Figure S7: Factorial concentration-response study of combination (Rapamycin, 17-AAG) in patient cells.
- **p)** Figure S8: Factorial concentration-response and TS study of combination (Sunitinib, 17-AAG, Afungin).
- **q)** Figure S9: Factorial concentration-response study of combination (Sunitinib, 17-AAG, Afungin) in patient cells.
- **r)** Figure S10: Analysis of patient data for the combination (17-AAG, Afungin, Trichostatin A).

2- SupplementaryMethods-I-II-III.pdf, consists of

Supplementary Methods I

- a) Gene expression analysis of combination (17-AAG, Afungin, Trichostatin A).
- b) Statistical variability calculations.
- c) Performance monitoring of experimental/computational pipeline.
- **d)** Supplementary Figure S11: Performance monitoring of experimental/computational pipeline.

Supplementary Methods II

- a) Beckman Coulter® Biomek 2000 cherry picking program
- **b)** Matlab® code for prediction of IC10 and IC20 values from concentration response data
- c) Supplementary Figure S12: Cell plate layout.

Supplementary Methods III

a) Theory for determination for the number of degrees of freedom related to t-test for therapeutic synergy.

3- Gene Expression Data.xls, includes

- **a)** Contains differential gene expression signature of combination (17-AAG, Afungin, Trichostatin A).
- **b)** Compounds matching that signature when run CMap 02 (https://www.broadinstitute.org/cmap/).

4- Movies

- **a)** Supplementary Movie S1.mov, combination (17-AAG, Afungin, Trichostatin A) treatment of MelJuso^{YFP}.
- **b)** Supplementary Movie S2.mov, MelJuso^{YFP} treated with 17-AAG.
- c) Supplementary Movie S3.mov, MelJuso YFP treated with Bortezomib.