

Patterns, Volume 4

Supplemental information

**Paired evaluation of machine-learning models
characterizes effects of confounders and outliers**

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Supplementary information

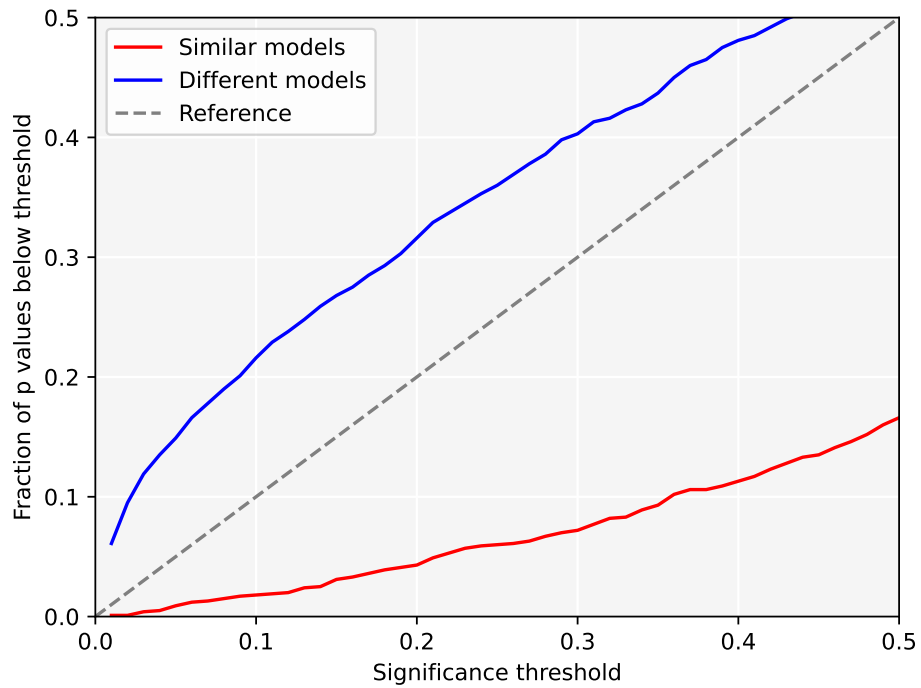


Figure S1. The probability of paired evaluation rejecting the null hypothesis that two models have the same performance. Shown is the fraction of p values from 1,000 two-sided Fisher's Exact tests that fall below a given significance threshold. Each p value was derived on a random 80/20 train/test split of the breast cancer dataset (see Results) by comparing the performance of two random forest models trained with identical hyperparameter values (red) or one random forest model and one linear regression model (blue). The expected "no information" rate is presented as a dashed line for reference.

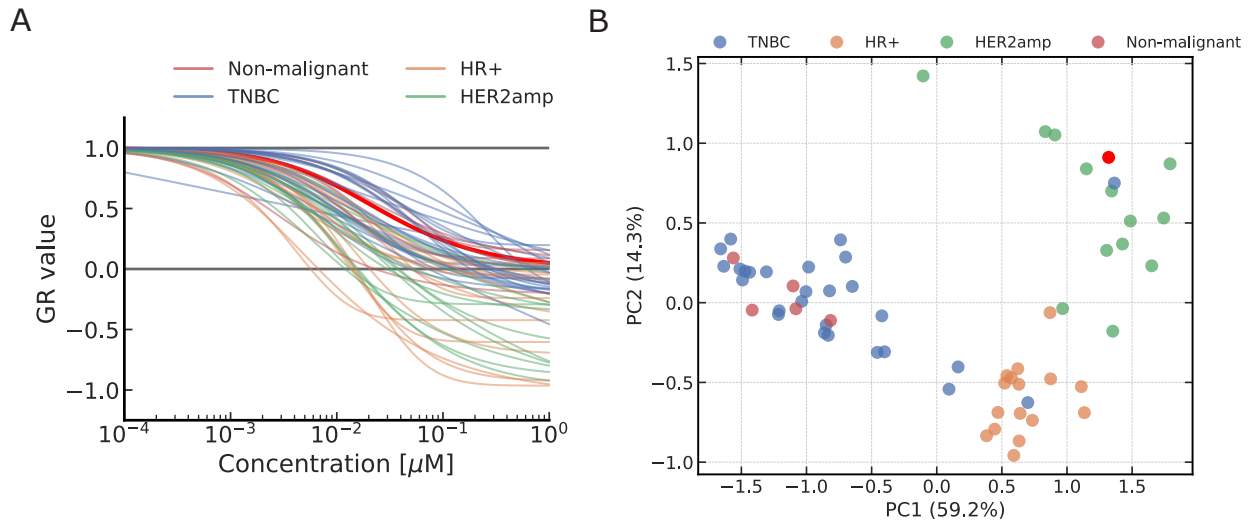


Figure S2. The location of ZR7530 data relative to other cell lines. A.) Growth rates curves for torin2 across all breast cancer cell lines. **B.)** Principal components analysis of the baseline RNA-seq data, computed in the space of the top 20 most important genes (Figure 3). The “outlier” cell line ZR7530 is highlighted in red, all other cell lines are colored by their subtypes.

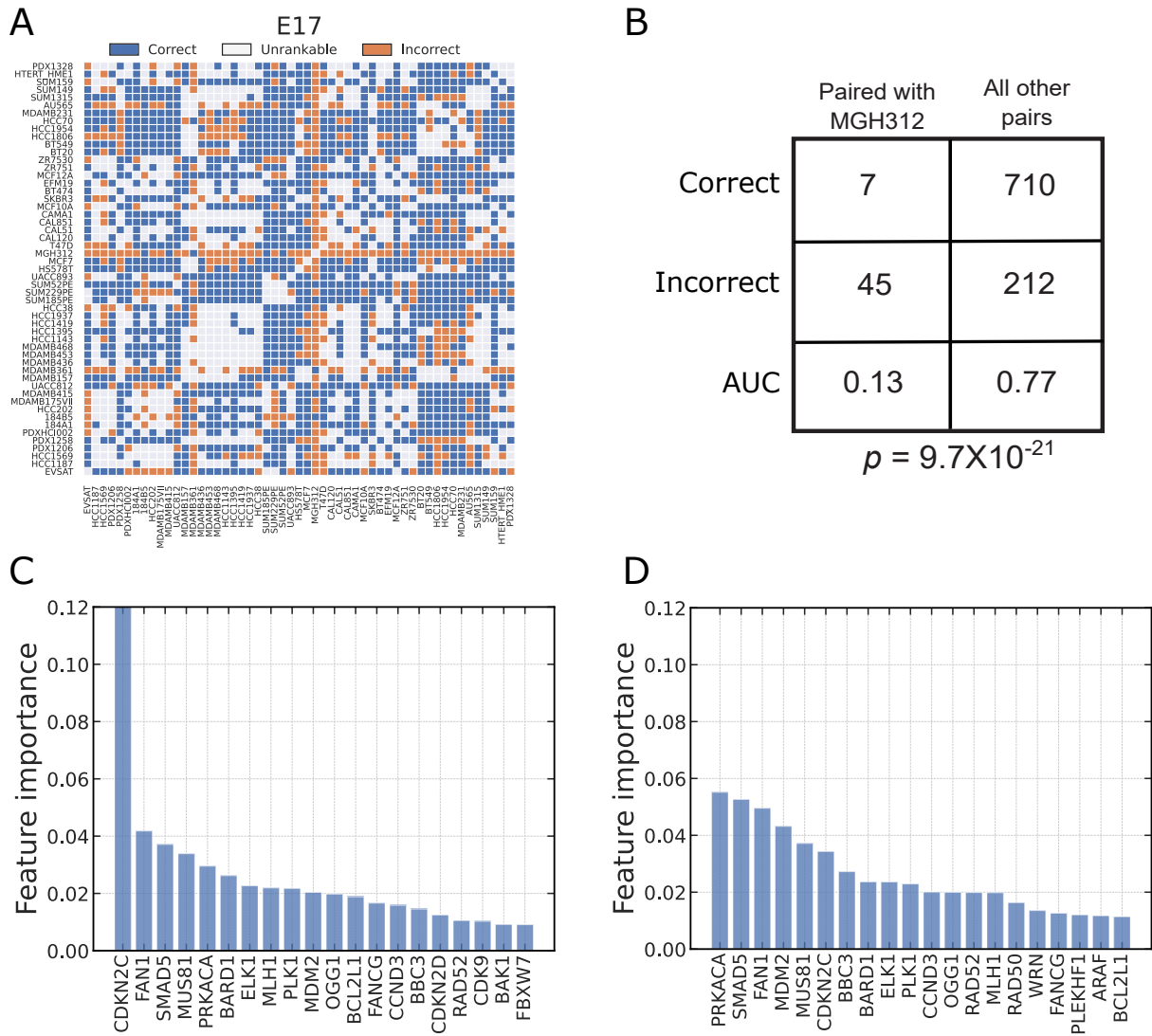


Figure S3. Outlier detection for E17. The interpretation of all panels is analogous to Figure 3.

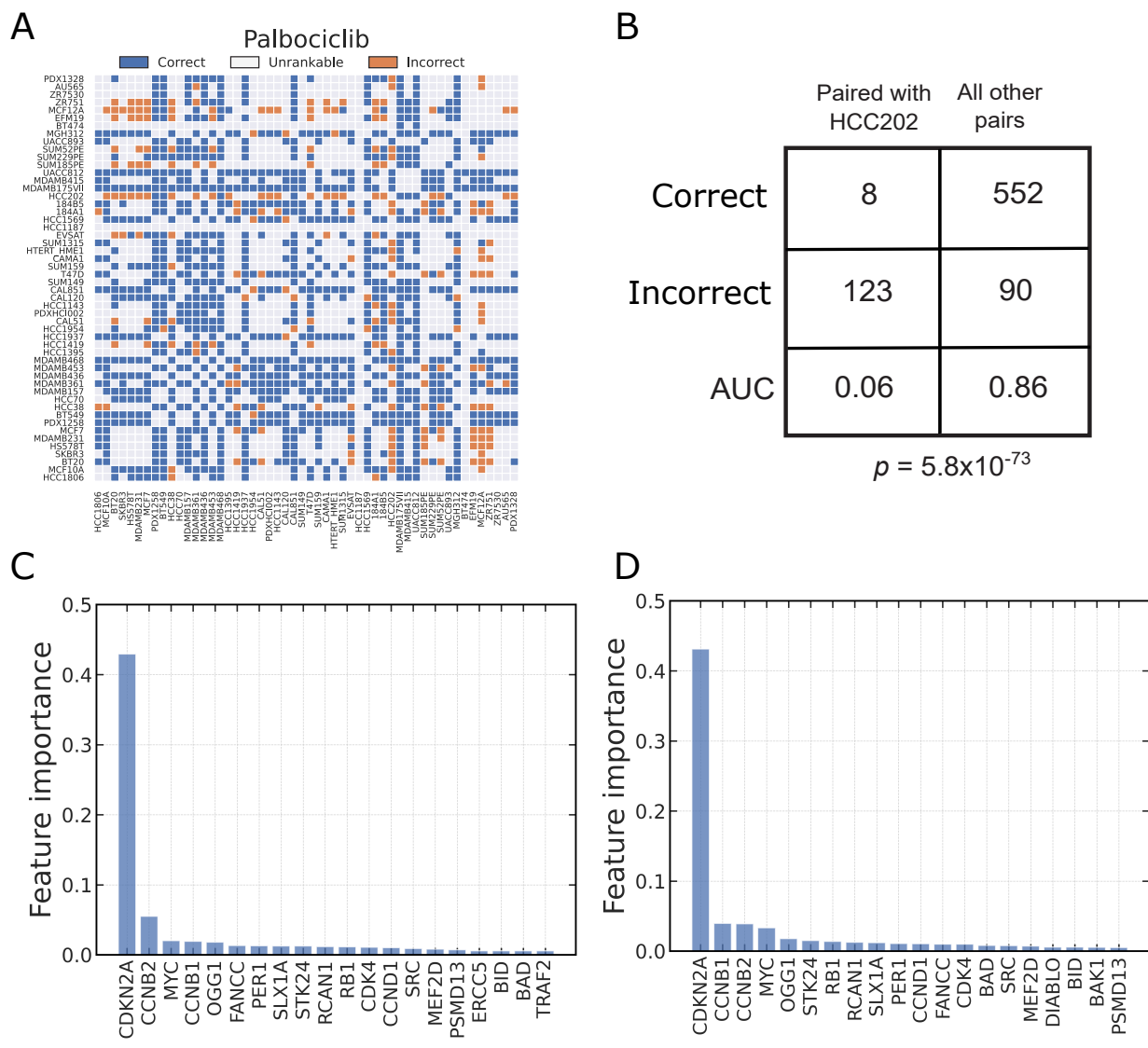


Figure S4. Outlier detection for palbociclib. The interpretation of all panels is analogous to Figure 3.

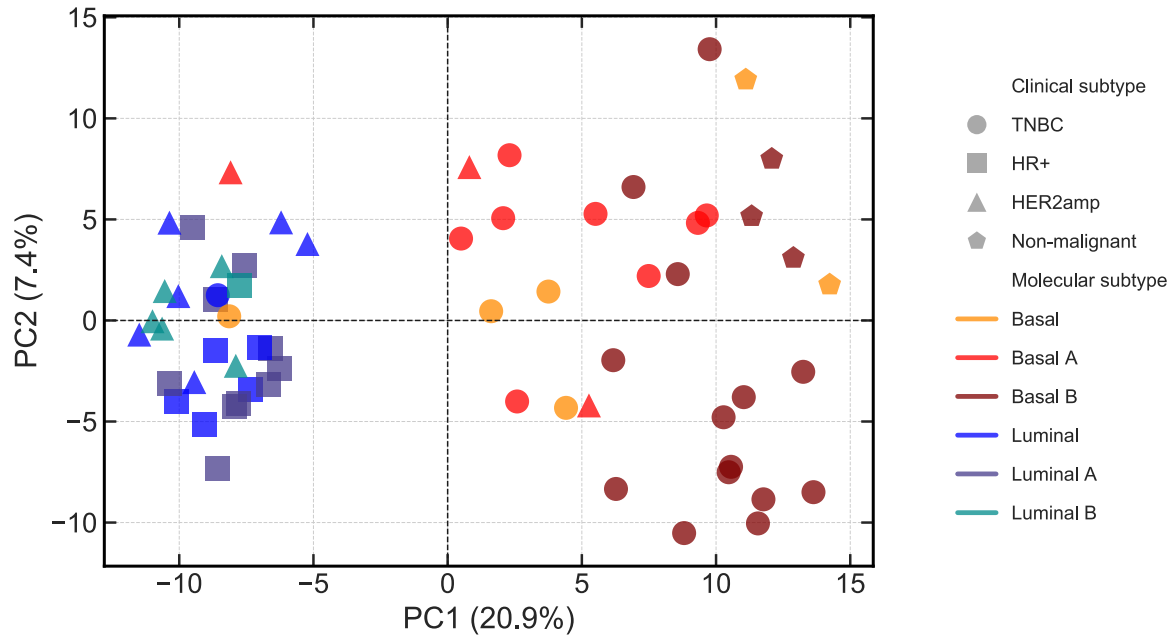


Figure S5. Principal components analysis of baseline RNAseq expression. The points represent individual breast cancer cell lines, shaped according to clinical subtype and colored by molecular subtype.

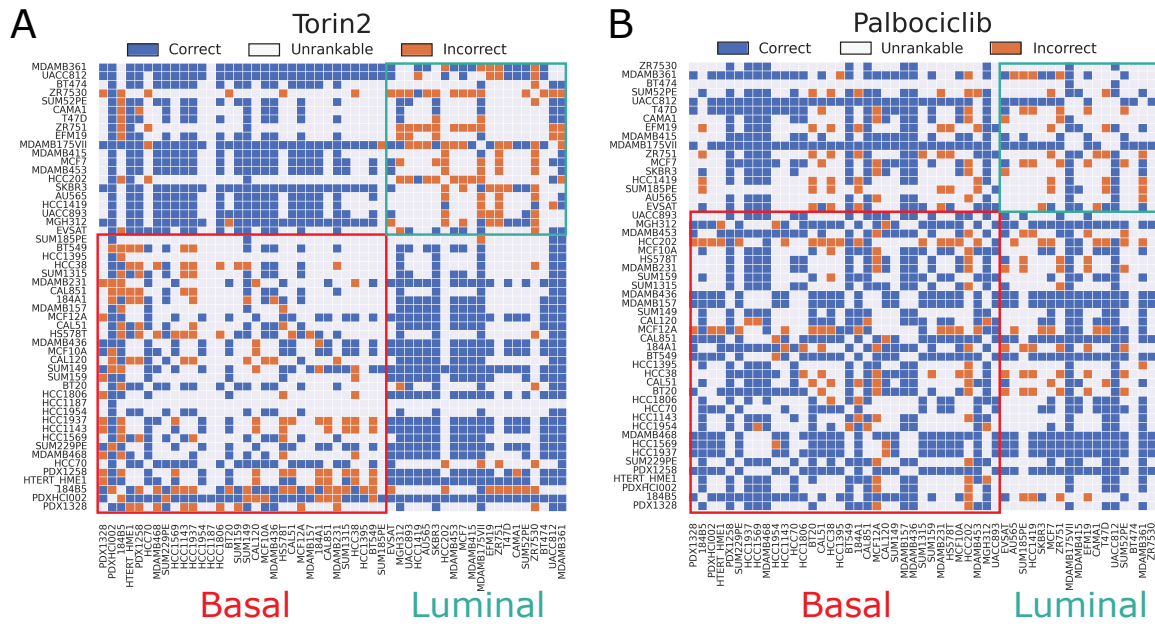


Figure S6. Effect of subtype in model prediction for torin2 and palbociclib.

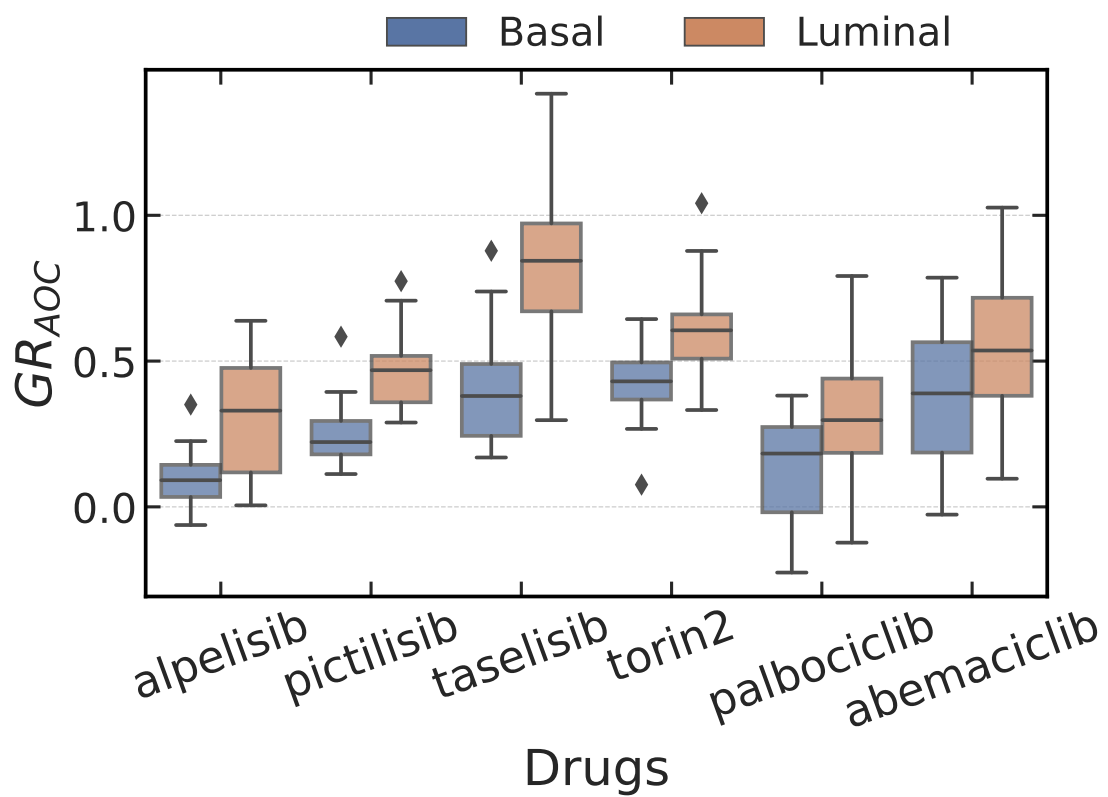
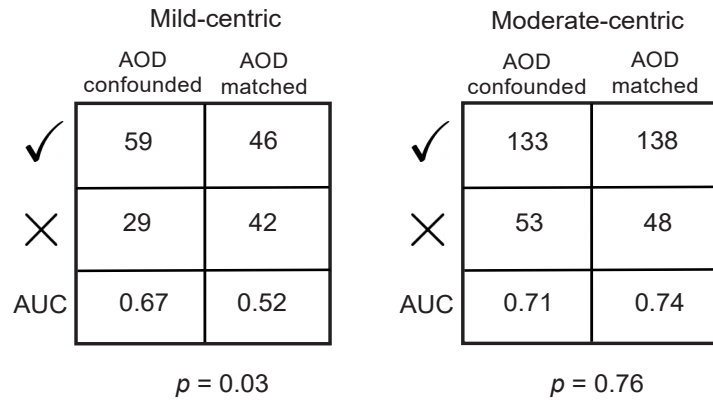


Figure S7. The distribution of GR_{AOC} for selected drugs. The values are plotted separately for basal (blue) and luminal (orange) cell lines.

Moderate vs mild



Moderate vs severe

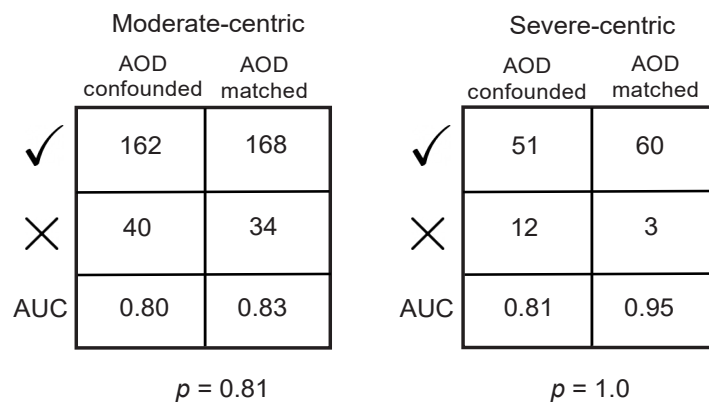


Figure S8. 2x2 contingency tables showing the performance of logistic regression models trained to distinguish between mild, moderate and severe stages of Alzheimer's Disease in the presence of Age of Death (AOD) as a confounder.

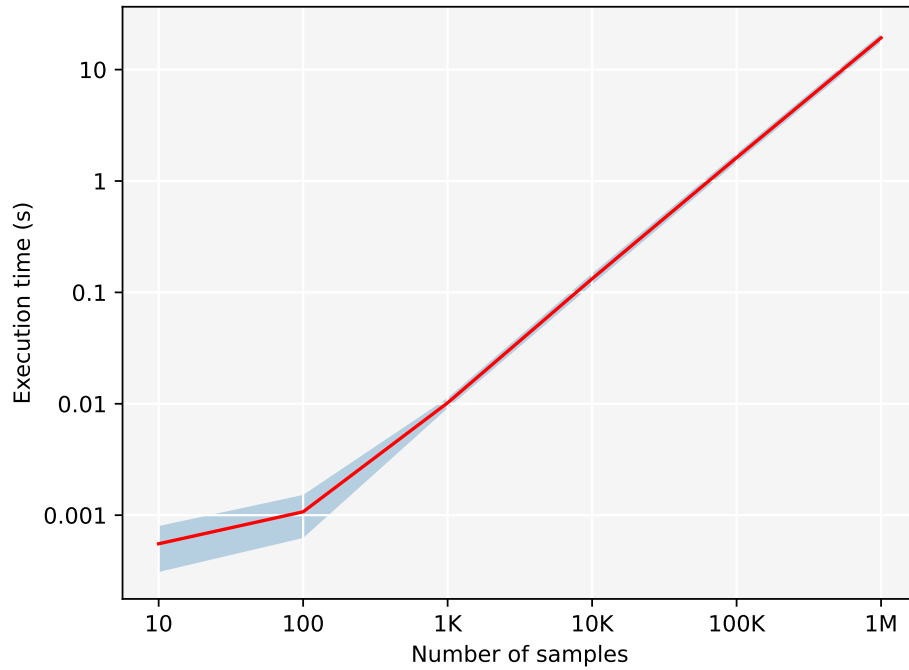


Figure S9. Execution time of the $O(n \log n)$ paired evaluation implementation as a function of dataset size. Shown are statistics collected over 30 runs of the method on randomly-generated sets of scores and labels. The shaded areas (blue) are one standard deviation away from the mean (red). All measurements were made in a standard Gitpod execution environment (4 vCPU, 8GB RAM) using the Python `time()` function.

Table S1: The total number of rankable pairs used to evaluate predictors of drug sensitivity from mRNA expression.

Agent	Number of pairs	Agent	Number of pairs
Paclitaxel	443	BSJ-01-175	616
Doxorubicin	469	BSJ-03-123	304
Taselisib_GDC0032	714	BSJ-03-124	435
Pictilisib_GDC0941	358	BVD523	138
Torin2	389	CFI-400945	553
Vorinostat	112	E17	702
Ipatasertib_GDC0068	333	FMF-03-145-1	705
Everolimus	535	FMF-03-146-1	42
Tivantinib_ARQ197	125	FMF-04-107-2	787
Cabozantinib	66	FMF-04-112-1	7
Saracatinib_AZD0530	296	Flavopiridol	99
Dasatinib	570	GSK2334470	366
Palbociclib_PD0332991	428	LEE011_Ribociclib	524
Dinaciclib_SCH727965	224	LY2606368	747
AZD7762	592	LY3023414	721
Olaparib_AZD2281	50	MFH-2-90	837
Alpelisib_BYL719	367	Pin1-3	50
A-1210477	7	R0-3306	125
Buparlisib_NVP-BKM120	188	Rucaparib	198
INK128_MLN0128	526	SHP099	61
PF-4708671	65	SY-1365	735
Neratinib_HKI272	588	THZ-P1-2	356
Cediranib_AZD2171	220	THZ-P1-2R	37
Ceritinib_LDK378	205	THZ1	399
Trametinib_GSK1120212	460	THZ531	352
Luminespib_NVP-AUY922	322	YKL-5-124	570
Abemaciclib_LY2835219	559	ZZ1-33B	852
Volasertib_BI6727	363	senexin b	150
ABT-737	131		
TGX221	190		
AZD1775	668		
AZD2014	693		
AZD5363	531		
AZD6738	294		
BJP-6-5-3	0		
BMS-265246	689		