

Supplementary Information for “Deep generative neural network for accurate drug response imputation”

Impact of cell lineage and cancer types on drug response

Some drugs were previously shown to have tissue-specific effect. We tested for the potential association between drug response and cell line lineage or cancer type. Using Fisher’s Exact Test, we found that the haematopoietic and lymphoid cell lines were particularly sensitive to many drugs using both the observed and predicted ActArea in CCLE (Supplementary Figure 9A, the red pies). Such a trend was similarly observed in GDSC data (Supplementary Figure 9B). Several other pairs of tissue/cell lines and MEK inhibitors were observed for sensitivity, including large intestine cell lines with AZD6244 and PD-0325901 and pancreas to PD-0325901. In the cancer data (Supplementary Figure 9C and 9D), HNSC, LGG, and LUSC showed strong sensitivity to many compounds (red boxes), while BRCA, KIRC, KIRP, and LIHC were insensitive to many compounds (blue boxes). From both the cell line data and cancer data, cell lines of skin origin (CCLE) and skin tumors (TCGA) were found sensitive to MEK and BRAF inhibitors, such as AZD6244, PD-0325901, PLX4720, and RAF265.

Supplementary Table 1. Model stability

	Rank	Rank	ZS	ZS	Z01	Z01
	Sigmoid	ReLU	Sigmoid	ReLU	Sigmoid	ReLU
17-AAG	0.756	0.662	0.701	0.670	0.378	0.324
AEW541	0.658	0.623	0.710	0.461	0.166	0.156
AZD0530	0.754	0.587	0.788	0.643	0.589	0.292
AZD6244	0.838	0.674	0.837	0.648	0.419	0.259
Erlotinib	0.881	0.839	0.850	0.756	0.618	0.506
Irinotecan	0.776	0.752	0.708	0.592	0.628	0.364
L-685458	0.907	0.767	0.872	0.722	0.846	0.284
Lapatinib	0.947	0.823	0.950	0.764	0.601	0.593
LBW242	0.368	0.491	0.402	0.351	0.937	0.235
Nilotinib	0.858	0.637	0.782	0.551	0.378	0.152
Nutlin-3	0.829	0.763	0.812	0.784	0.884	0.376
Paclitaxel	0.791	0.773	0.730	0.692	0.659	0.492
Panobinostat	0.792	0.750	0.826	0.661	0.611	0.516
PD-0325901	0.837	0.619	0.854	0.653	0.366	0.223
PD-0332991	0.850	0.779	0.825	0.694	0.784	0.424
PF2341066	0.771	0.816	0.748	0.761	0.671	0.487
PHA-665752	0.833	0.644	0.767	0.529	0.929	0.502
PLX4720	0.921	0.866	0.881	0.826	0.656	0.252
RAF265	0.838	0.742	0.806	0.645	0.472	0.520
Sorafenib	0.904	0.779	0.871	0.786	0.702	0.542
TAE684	0.722	0.570	0.678	0.520	0.293	0.413
TKI258	0.786	0.717	0.807	0.752	0.431	0.402
Topotecan	0.804	0.766	0.811	0.677	0.462	0.532
ZD-6474	0.874	0.603	0.844	0.604	0.564	0.249

*The values were the average Pearson correlation coefficient of the predicted response in all TCGA samples by the top 10 best models.

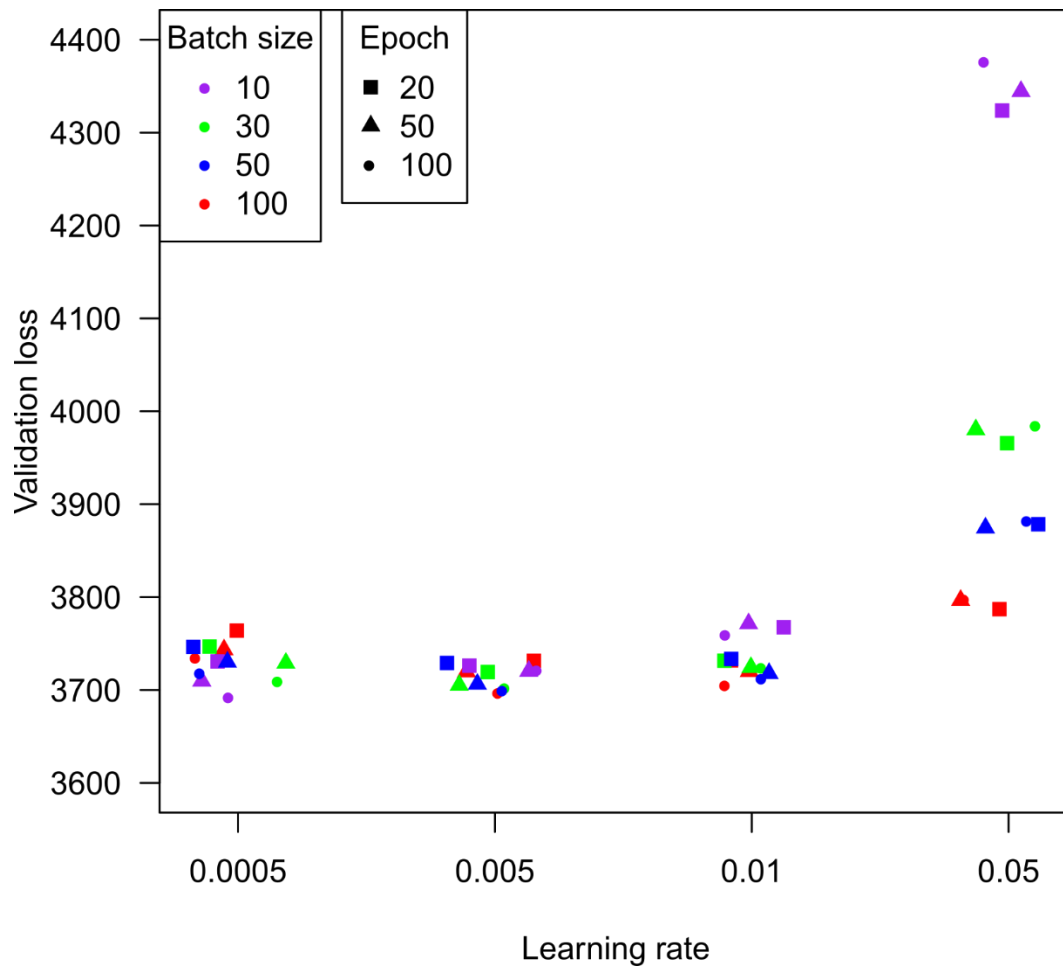
Supplementary Table 2. Model evaluation using TCGA data

	Target	Compound	Rank Sigmoid		ZS Sigmoid		PCA+EN		Gene+EN	
			<i>t</i>	<i>p</i> -value	<i>t</i>	<i>p</i> -value	<i>t</i>	<i>p</i> -value	<i>t</i>	<i>p</i> -value
CCLE	ERBB2	Lapatinib	9.19	2.60E-19	4.93	9.71E-07	9.41	4.11E-20	17.48	3.54E-59
GDSC	ERBB2	Lapatinib	6.02	2.52E-09	2.77	5.71E-03	5.14	3.42E-07	5.36	1.05E-07
CCLE	MET	PF2341066	6.61	9.84E-11	4.02	6.84E-05	6.22	1.02E-09	4.46	9.89E-06
CCLE	ALK [#]	PF2341066	2.68	7.68E-03	4.62	4.87E-06	2.60	0.01	3.13	1.88E-03
CCLE	MET	PHA.665752	3.78	1.75E-04	2.67	7.89E-03	8.16	2.53E-15	2.13	0.03
CCLE	ALK [#]	PHA.665752	2.69	7.38E-03	5.46	7.52E-08	3.26	1.17E-03	1.00	0.32
GDSC	MET	Crizotinib	6.60	1.01E-10	-2.81	5.14E-03	1.62	0.106	-0.81	0.42
GDSC	ALK [#]	Crizotinib	0.88	0.38	-5.17	3.39E-07	-1.76	0.078	-2.11	0.04
GDSC	MET	Foretinib	5.79	1.25E-08	4.95	1.01E-06	4.73	2.86E-06	2.47	0.01
GDSC	ALK	Foretinib	2.54	1.14E-02	1.73	8.49E-02	-1.37	0.17	-1.72	0.09
GDSC	MET	PHA.665752	2.26	0.024	1.51	0.131	-2.32	0.021	-0.02	0.99
GDSC	ALK	PHA.665752	3.85	1.32E-04	-2.21	0.0276	-4.18	3.50E-05	1.27	0.21
CCLE	pCR ^{\$}	Paclitaxel	2.26	0.026	0.08	0.469	0.18	0.86	-1.19	0.24
GDSC	pCR	Paclitaxel	-0.02	0.99	-0.49	0.687	0.30	0.382	-0.02	0.49

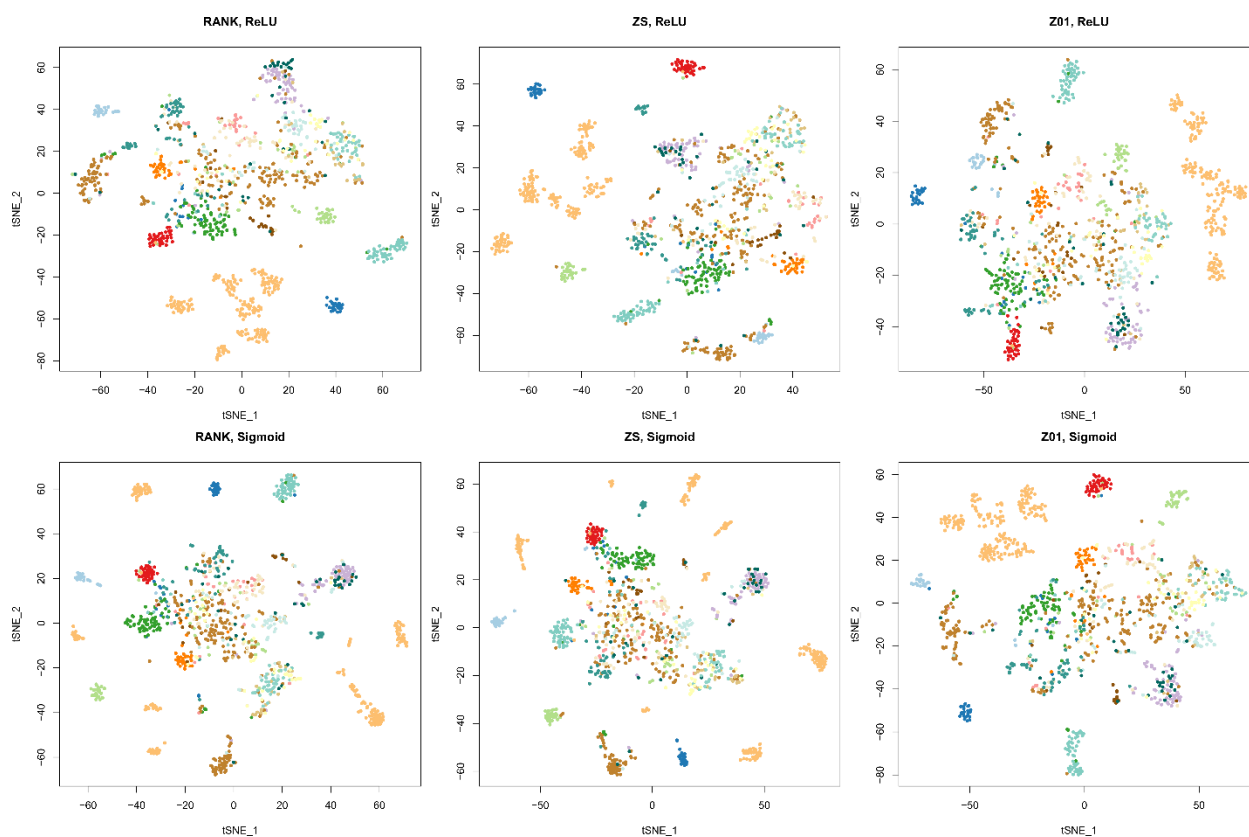
*Grey cells: the direction of the association is opposite, or the association is insignificant.

[#]ALK is not the primary target but could also be targeted by the MET inhibitors. Thus, the association is expected to be moderate.

^{\$}pCR: pathological complete response.

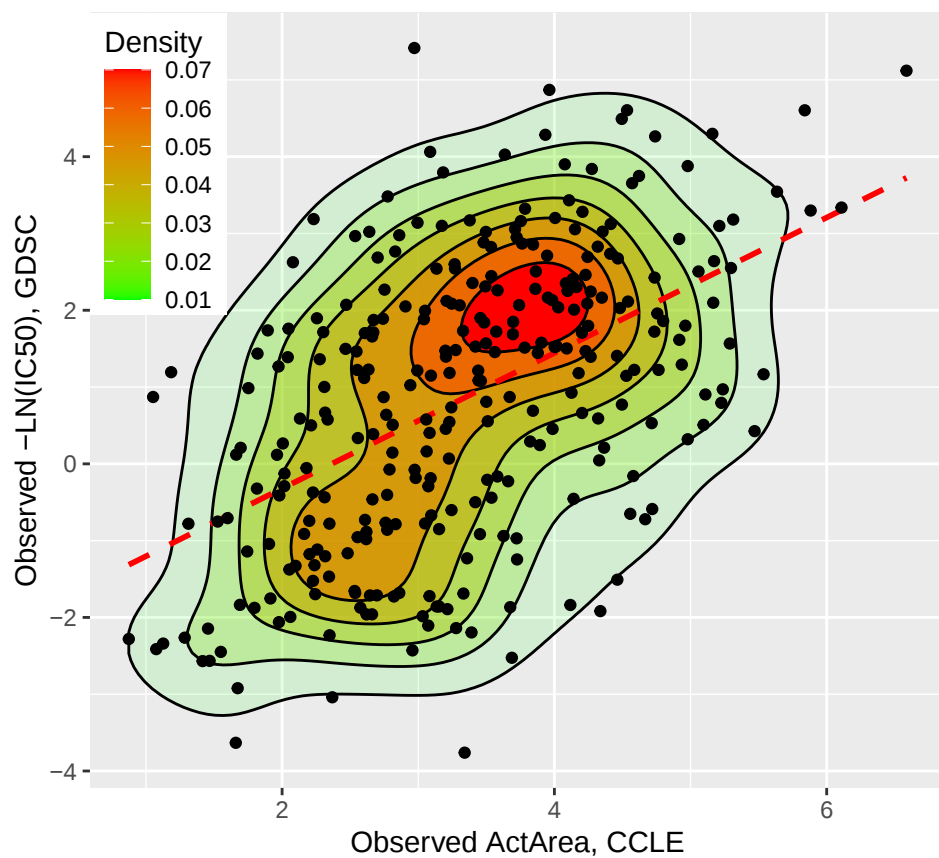


Supplementary Figure 1. The hyperparameter sweep result for different VAE models. The final model was selected with batch size being 100, 100 epochs, and learning rate being 0.0005. See more details in main text.

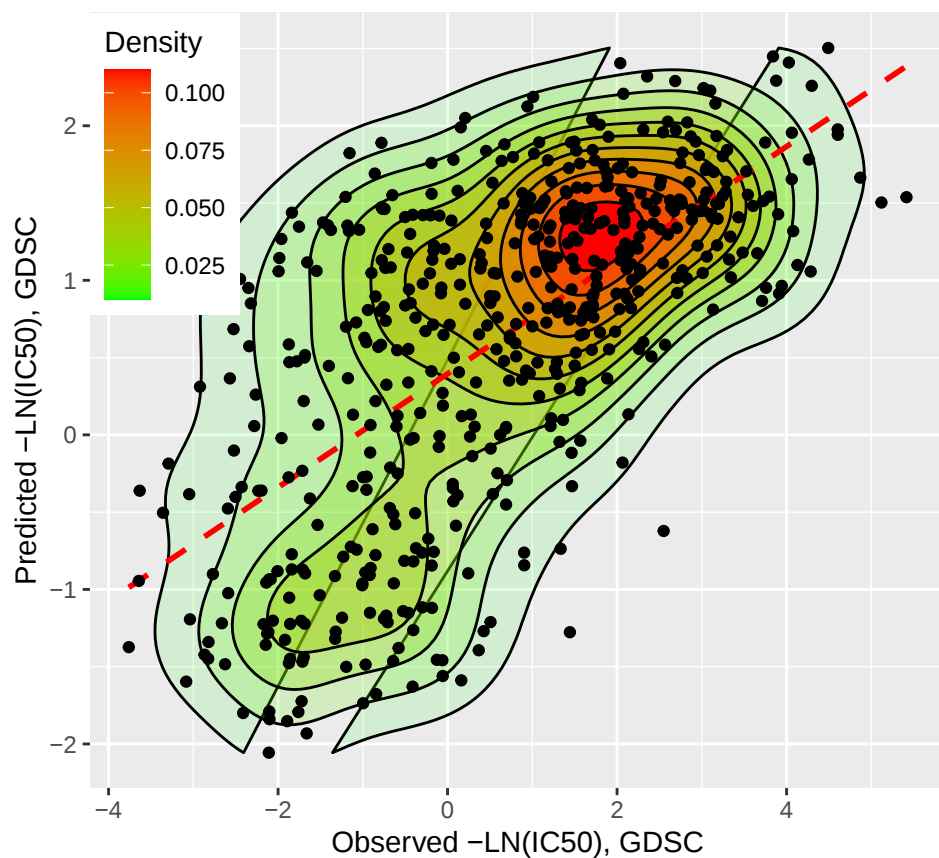


Supplementary Figure 2. tSNE plots of different VAE compression models. tSNE: t-distributed stochastic neighbor embedding. In each panel, a dot represents a cell line. The legend of node color is the same as in Figure 1.

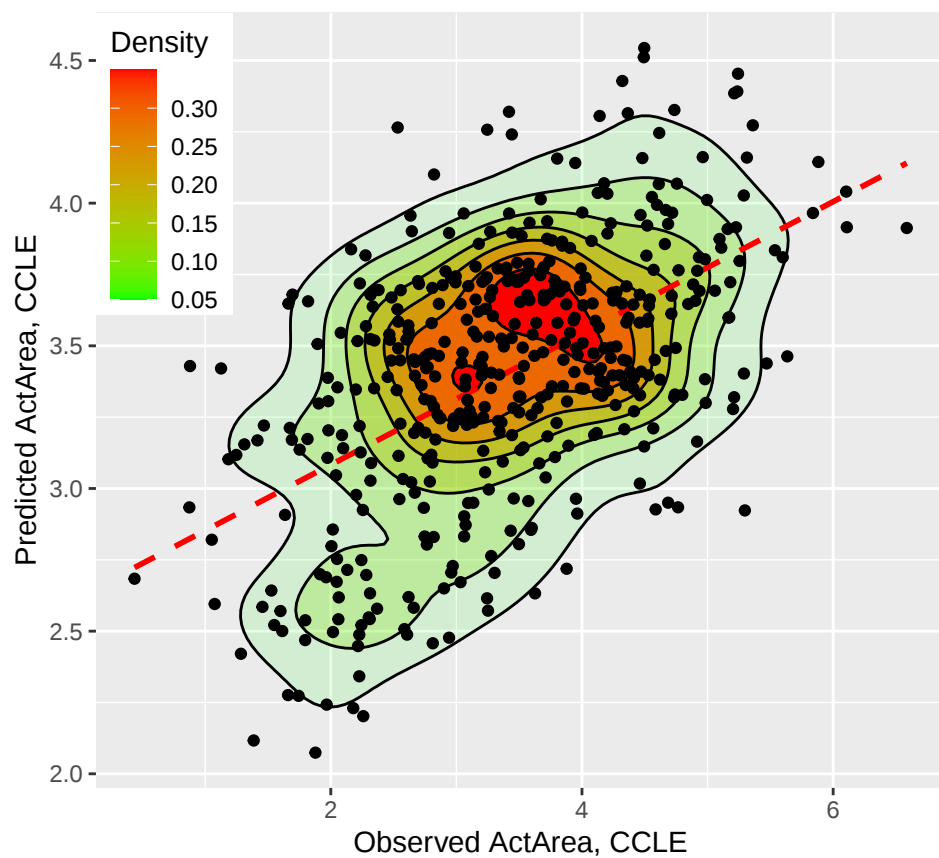
17-AAG
Observed DR, $r = 0.507$, $n = 297$



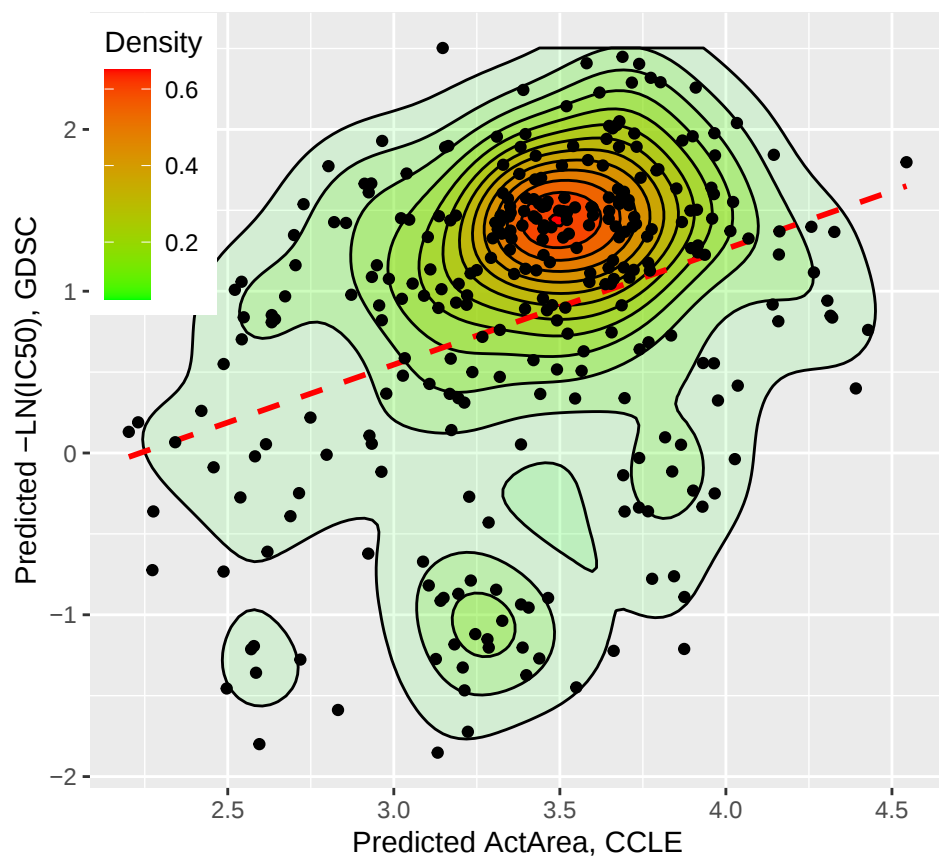
Tanespimycin
GDSC, $r = 0.644$, $n = 529$



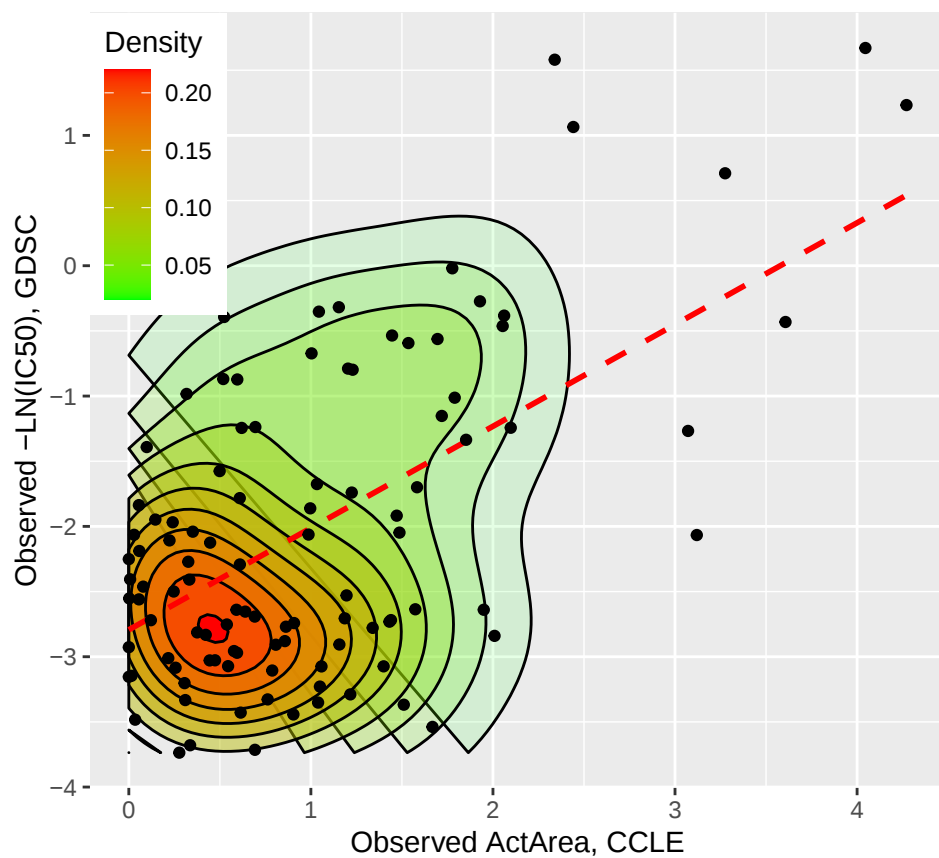
17-AAG
CCLE, $r = 0.535$, $n = 454$



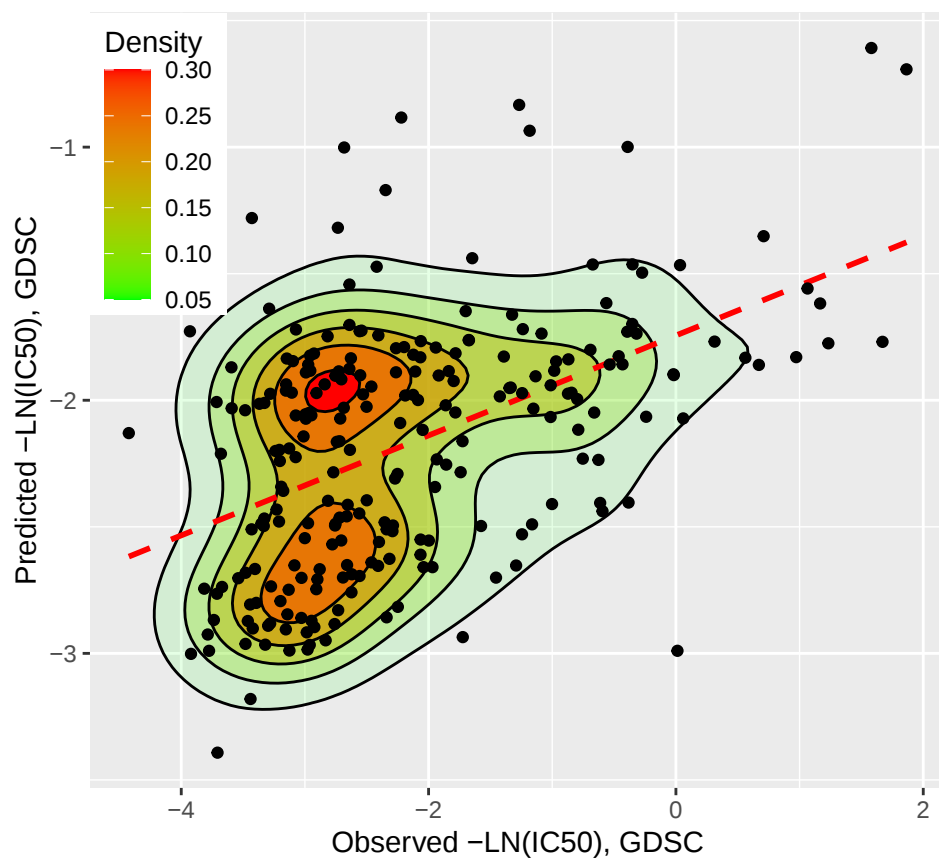
Tanespimycin
Predicted DR, $r = 0.325$, $n = 297$



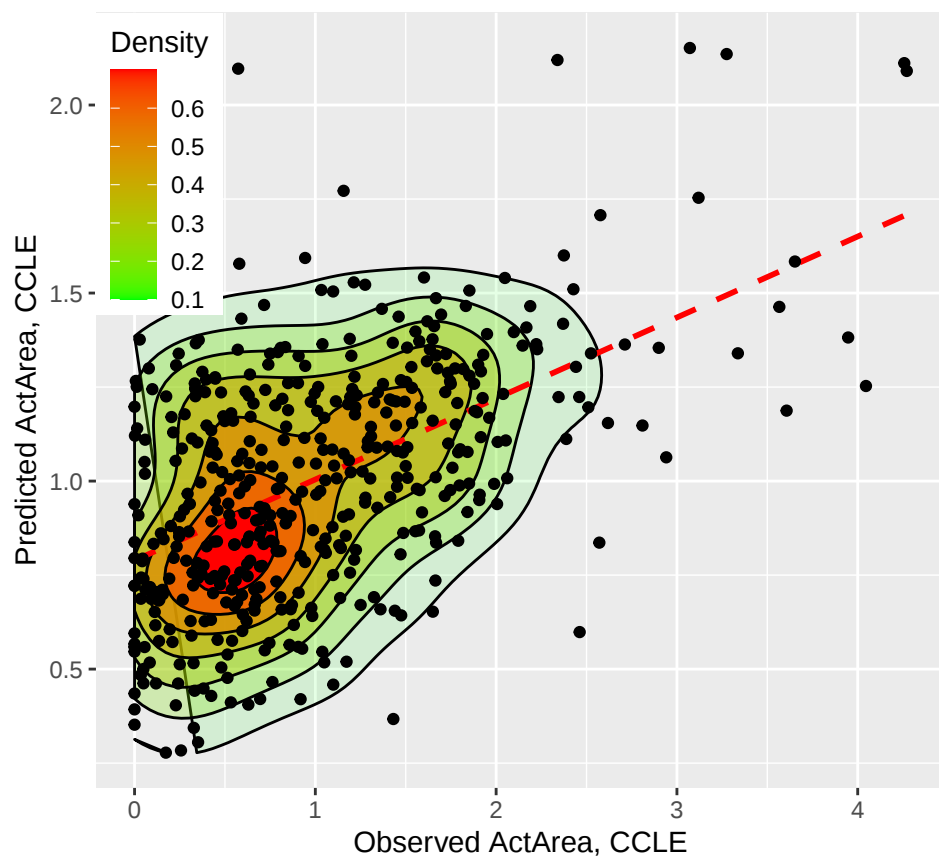
AZD0530
Observed DR, $r = 0.557$, $n = 105$



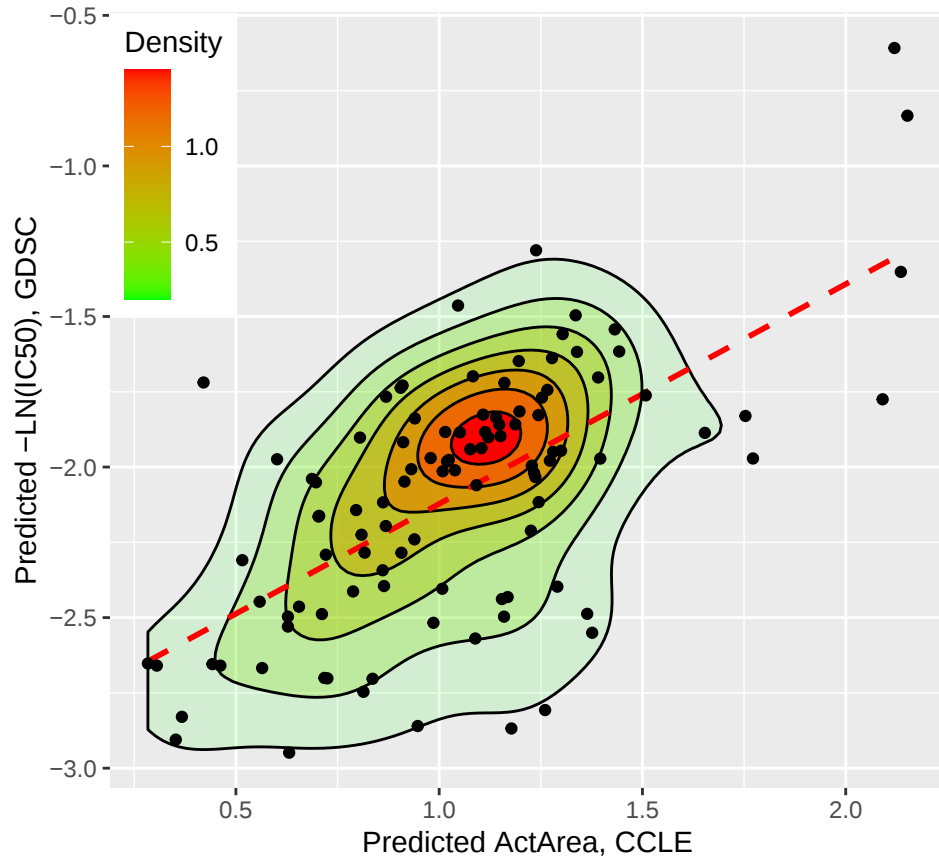
Saracatinib
GDSC, $r = 0.484$, $n = 236$



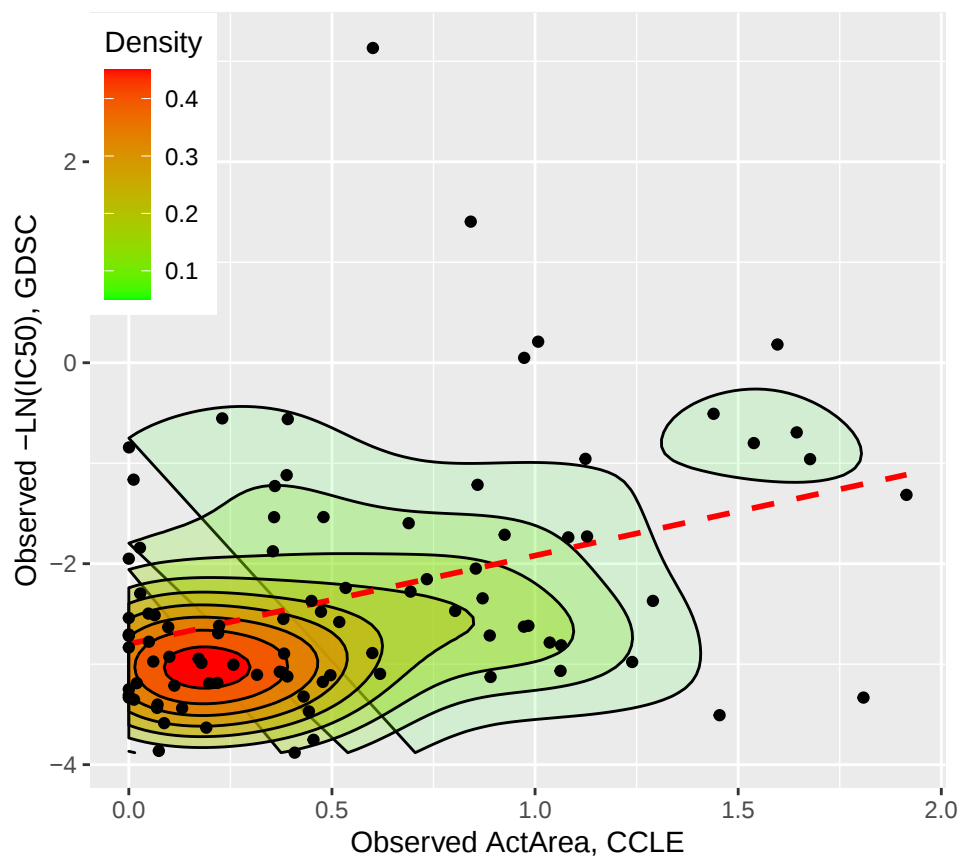
AZD0530
CCLE, $r = 0.515$, $n = 455$



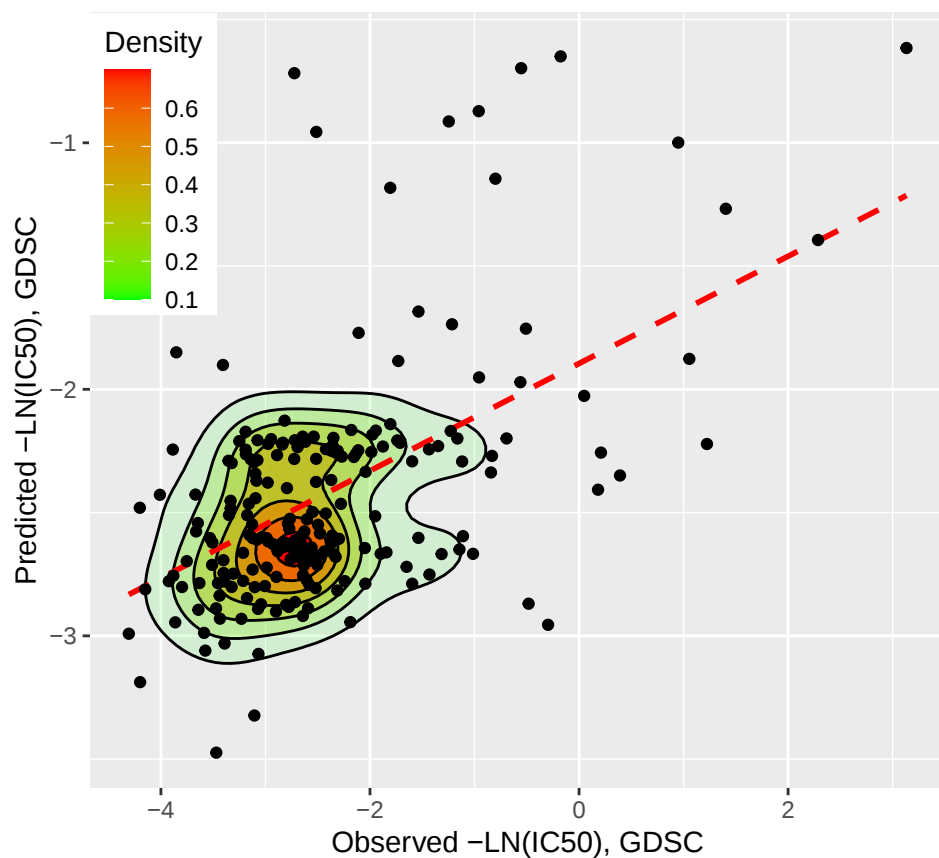
Saracatinib
Predicted DR, $r = 0.637$, $n = 105$



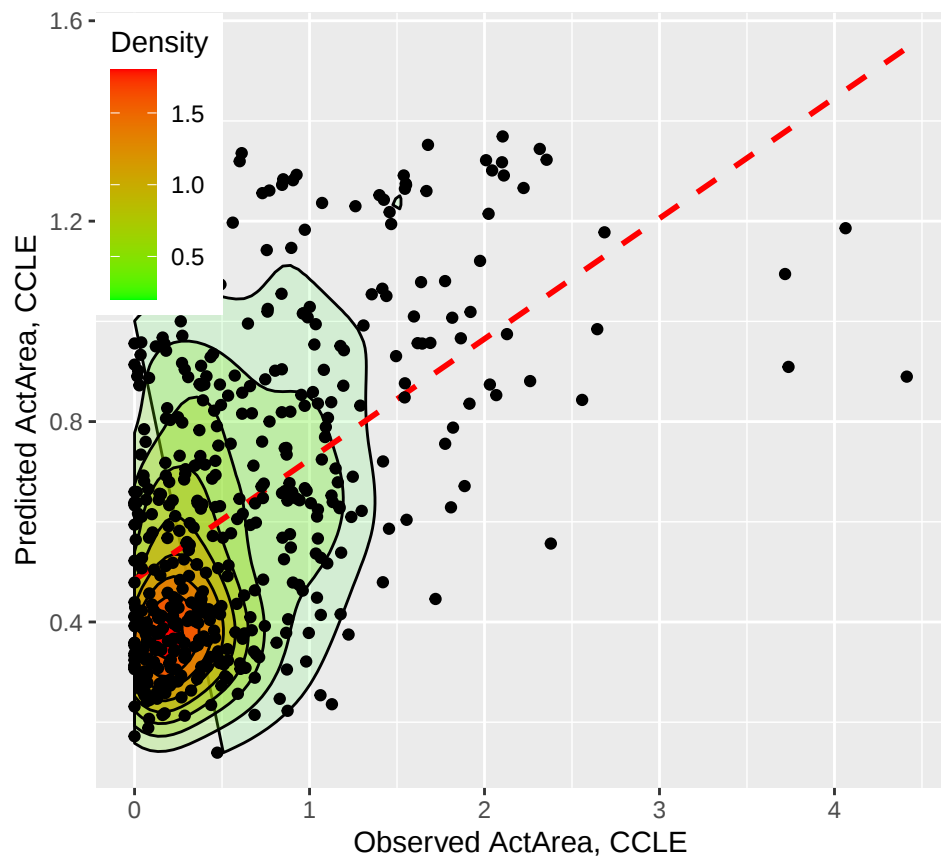
Erlotinib
Observed DR, $r = 0.366$, $n = 92$



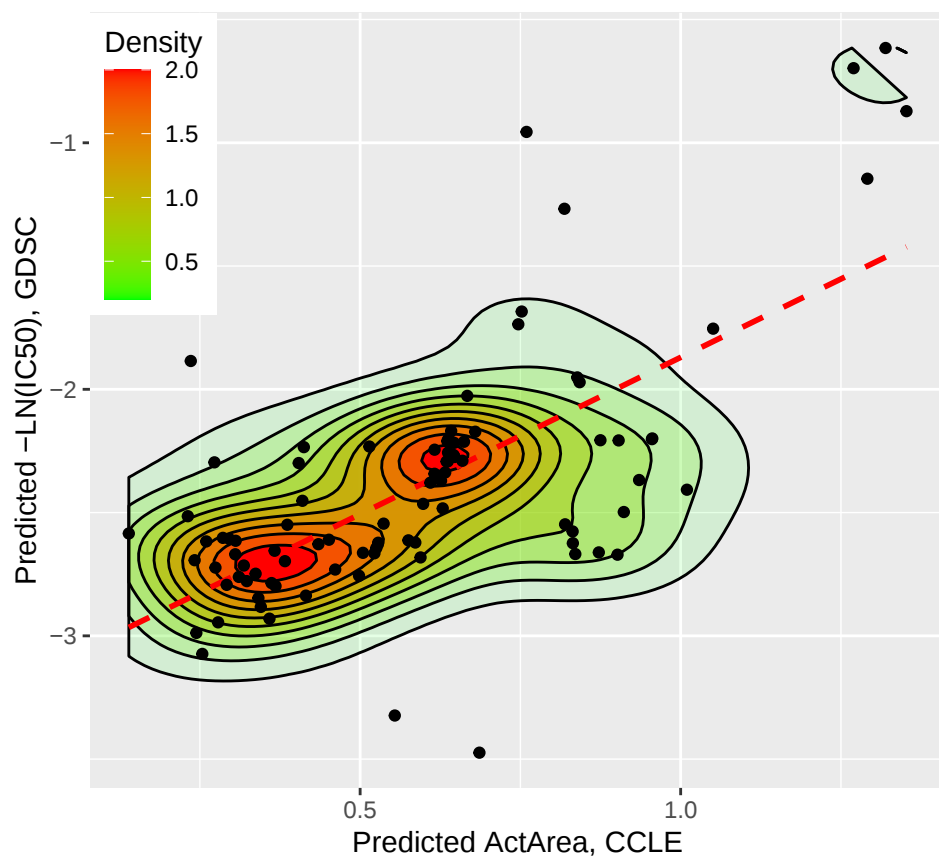
Erlotinib
GDSC, $r = 0.521$, $n = 207$



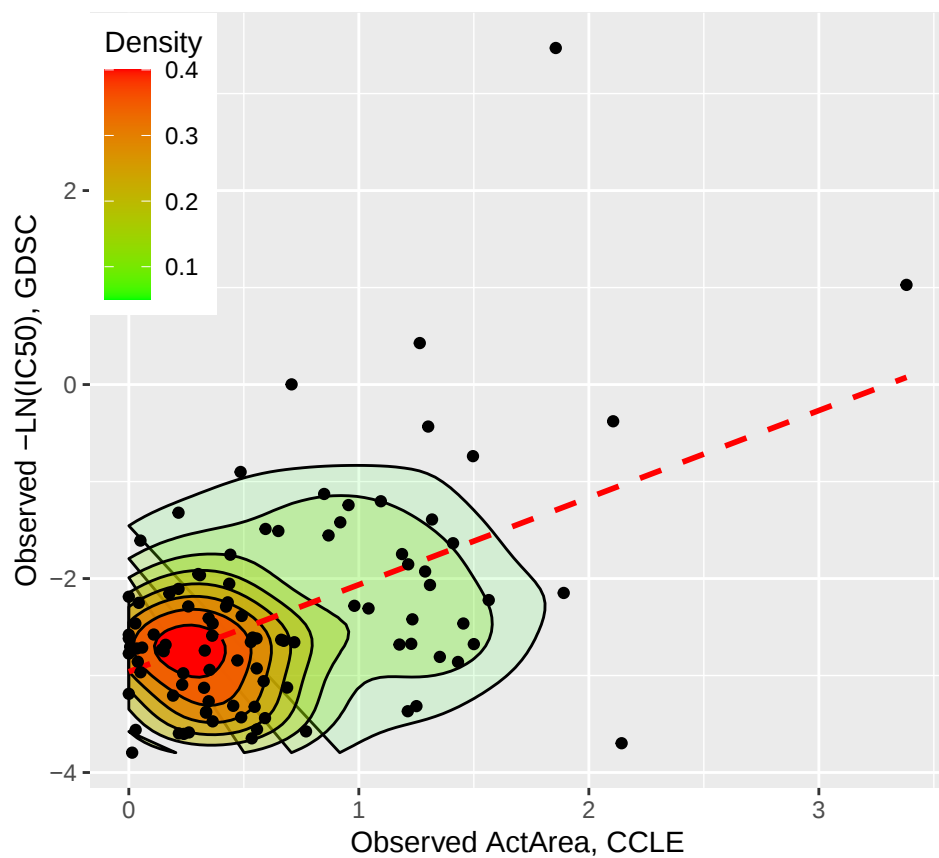
Erlotinib
CCLE, $r = 0.515$, $n = 454$



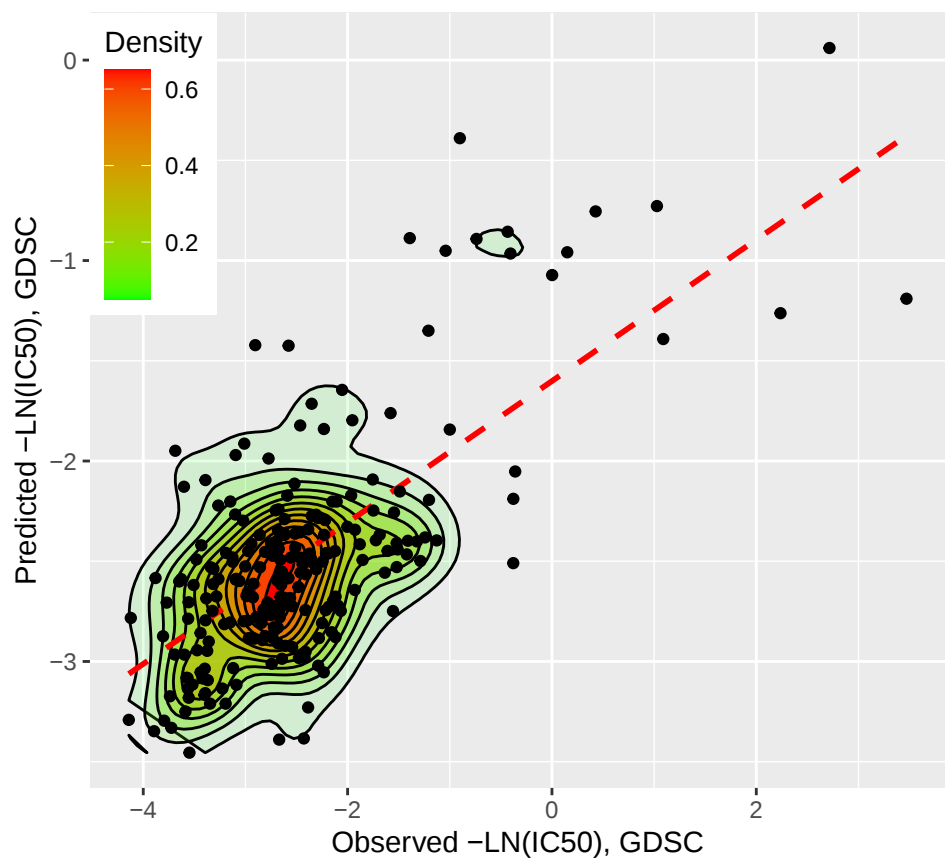
Erlotinib
Predicted DR, $r = 0.674$, $n = 92$



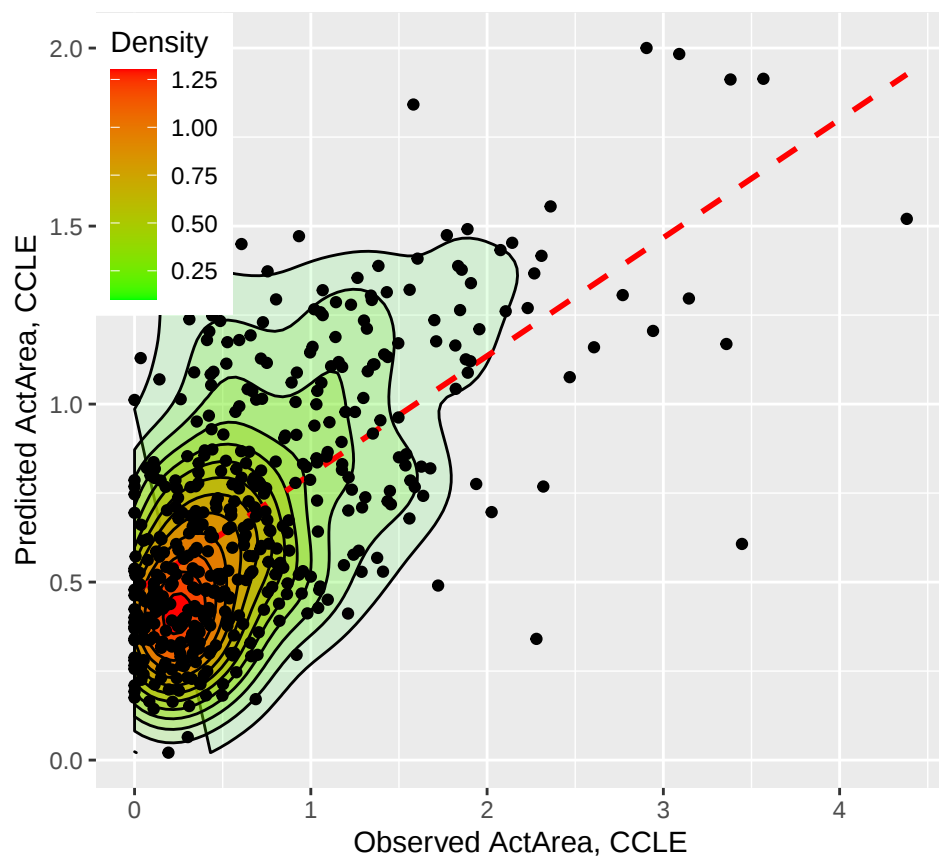
Lapatinib
Observed DR, $r = 0.492$, $n = 98$



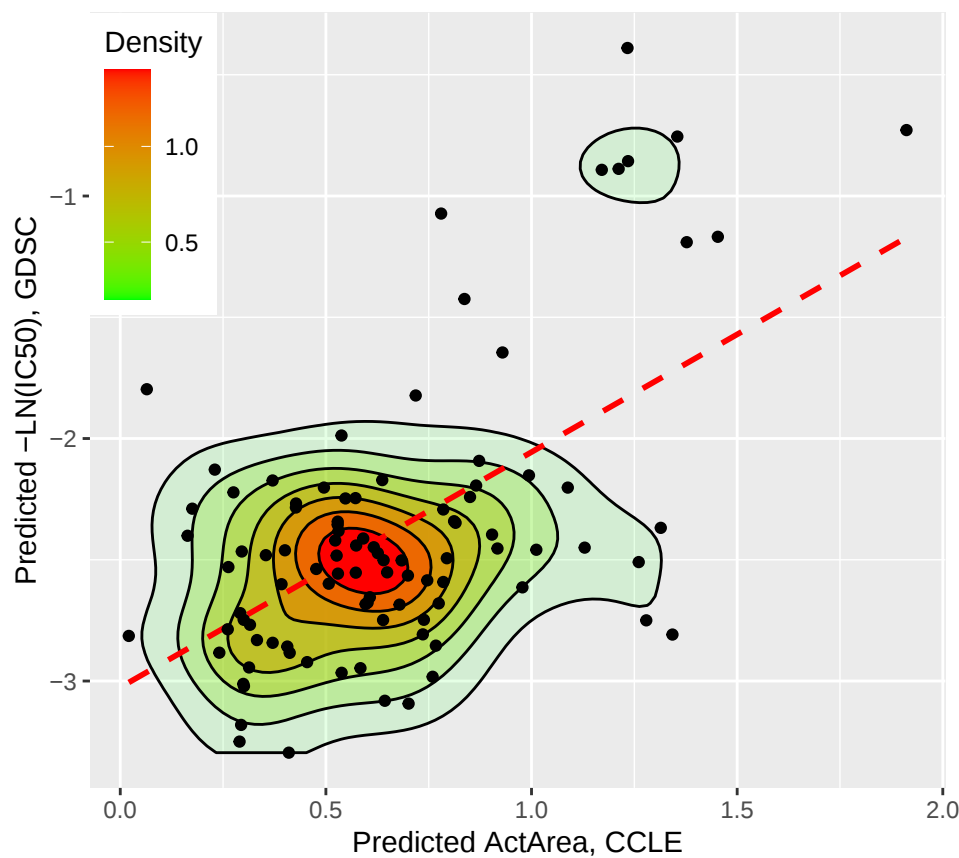
Lapatinib
GDSC, $r = 0.664$, $n = 225$



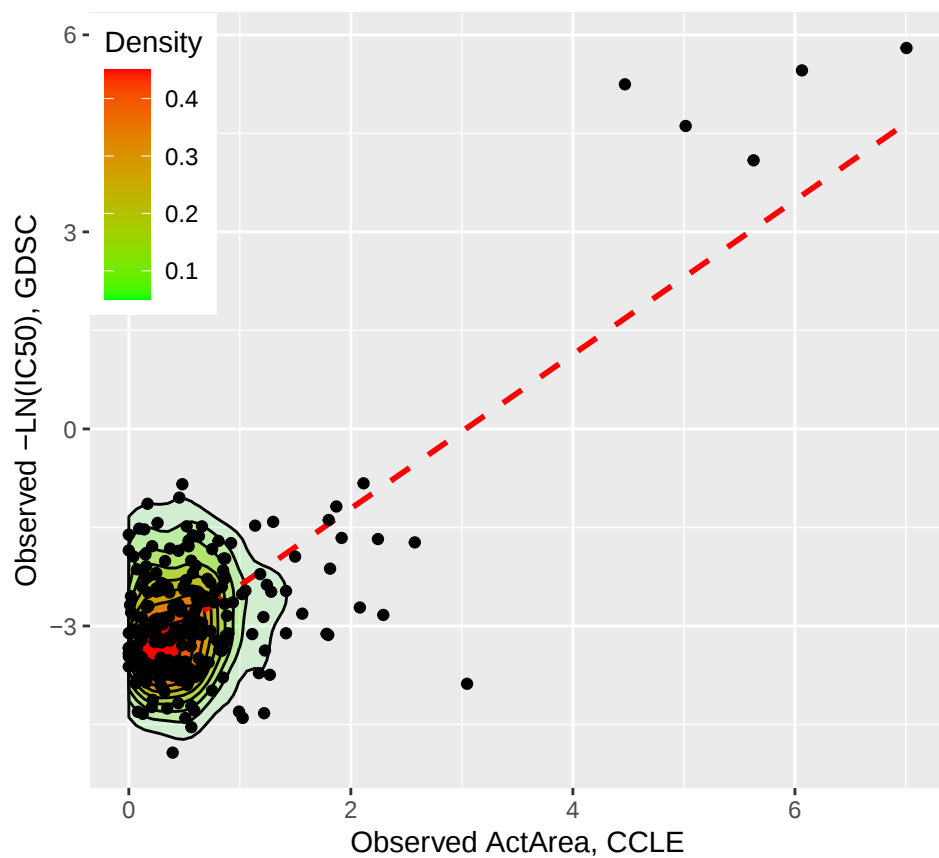
Lapatinib
CCLE, $r = 0.608$, $n = 455$



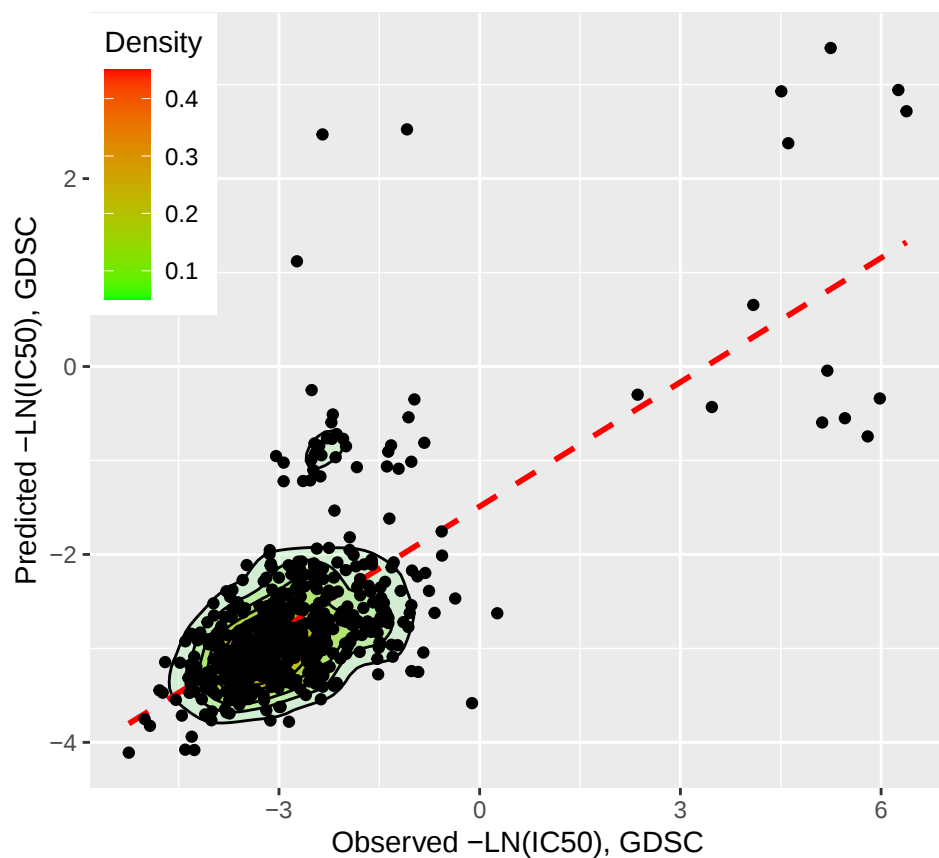
Lapatinib
Predicted DR, $r = 0.577$, $n = 98$



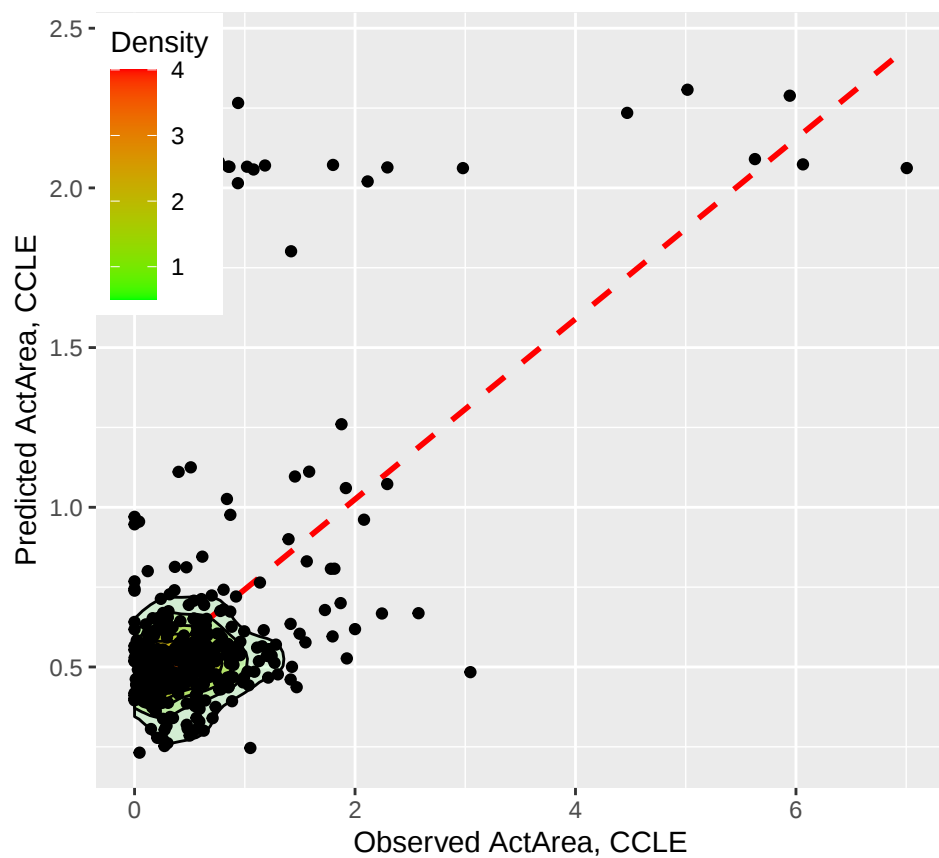
Nilotinib
Observed DR, $r = 0.75$, $n = 228$



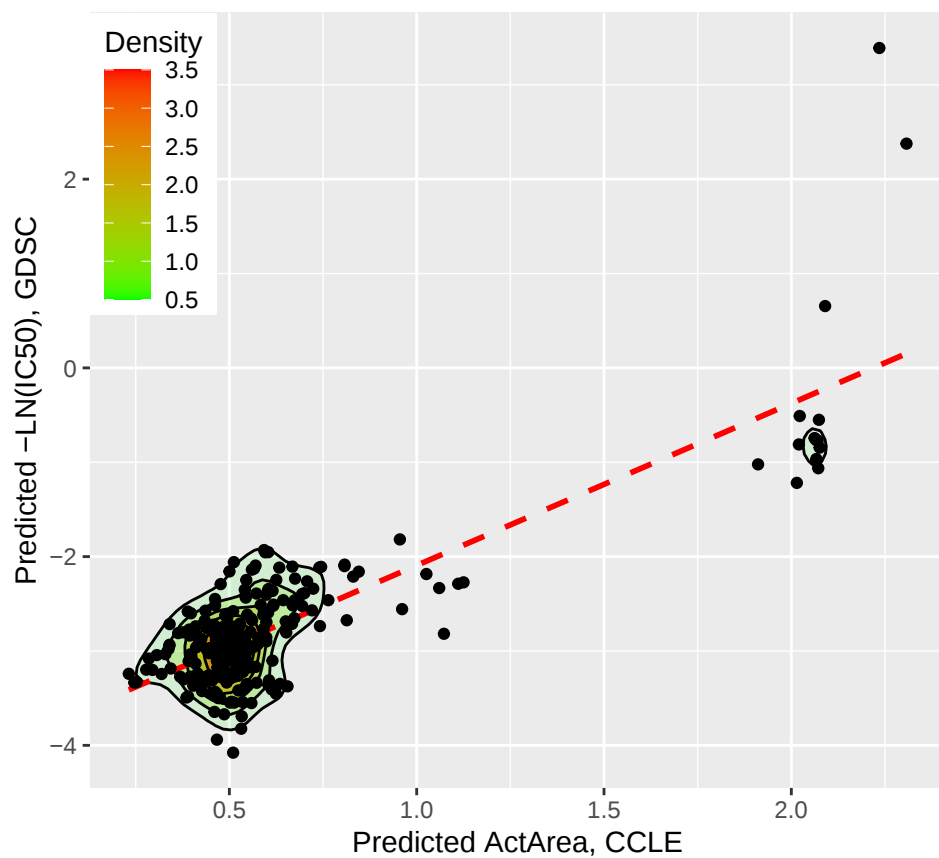
Nilotinib
GDSC, $r = 0.691$, $n = 509$



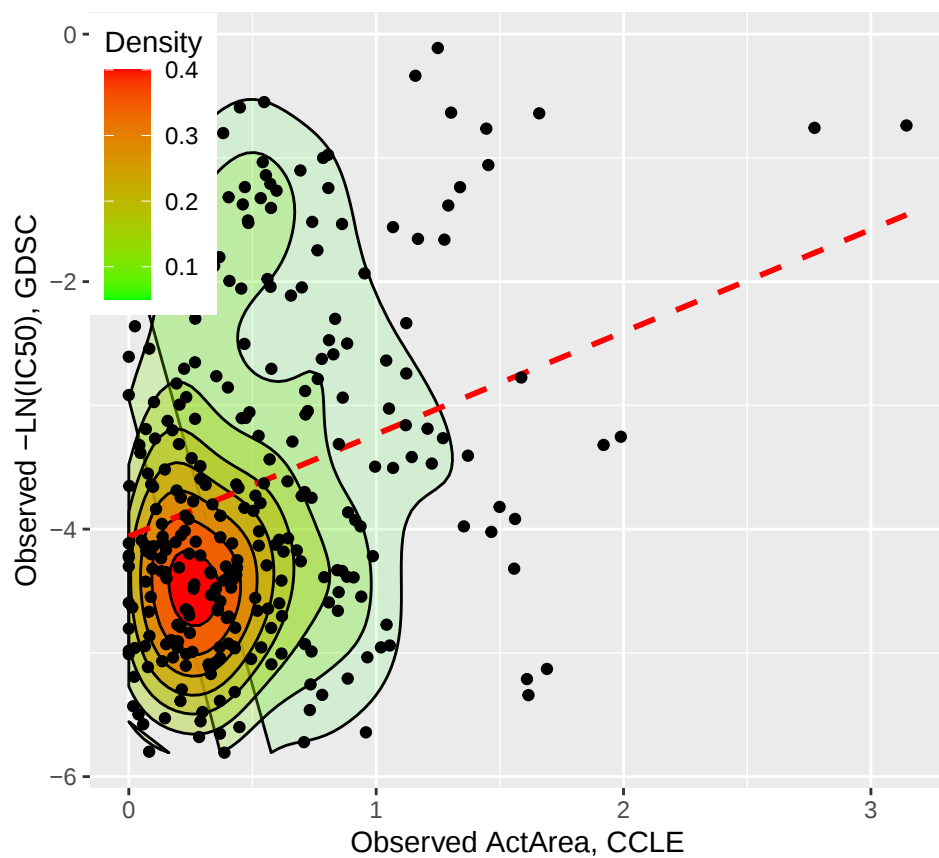
Nilotinib
CCLE, $r = 0.561$, $n = 375$



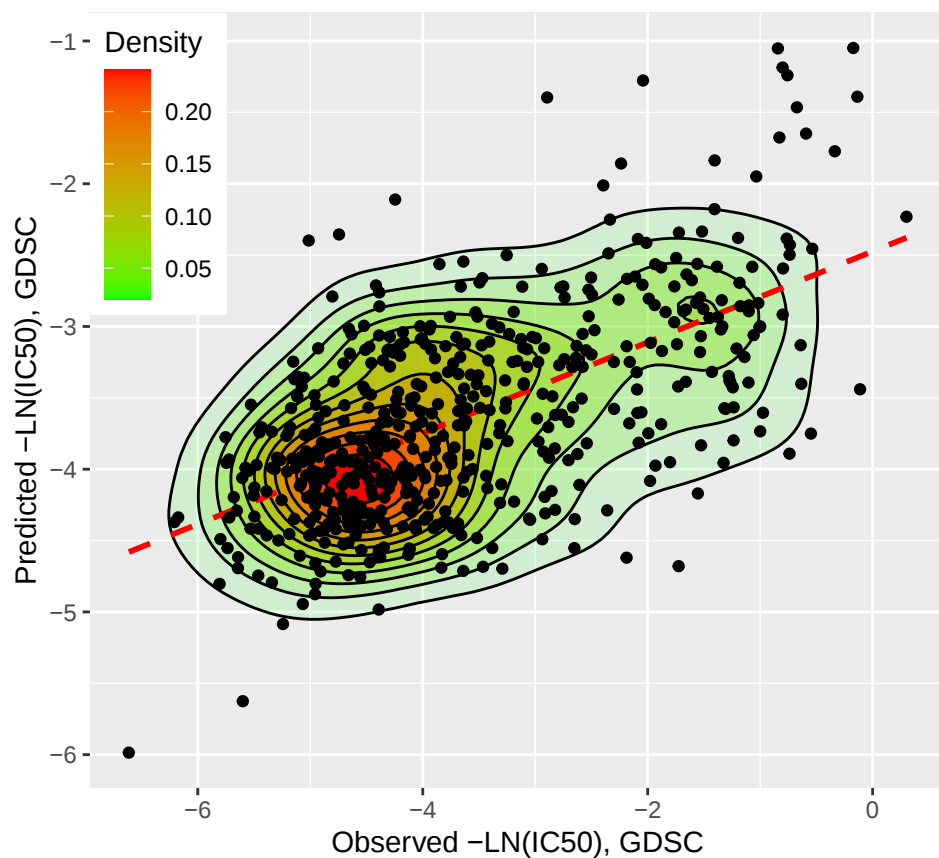
Nilotinib
Predicted DR, $r = 0.83$, $n = 228$



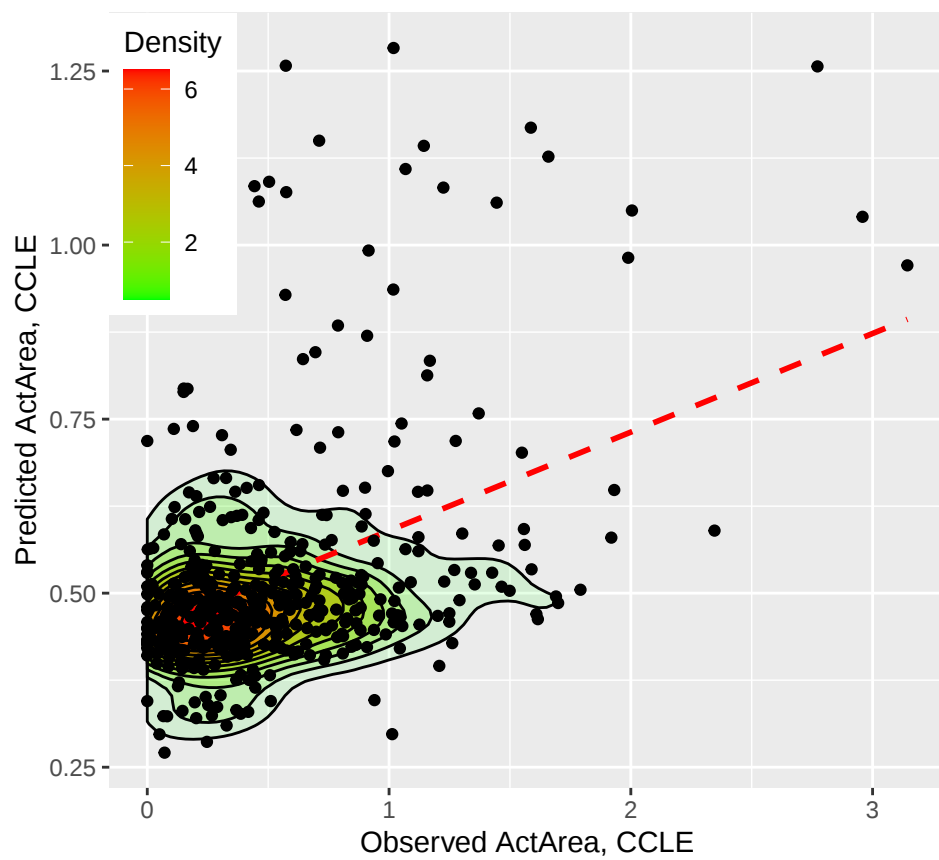
Nutlin-3
Observed DR, $r = 0.277$, $n = 298$



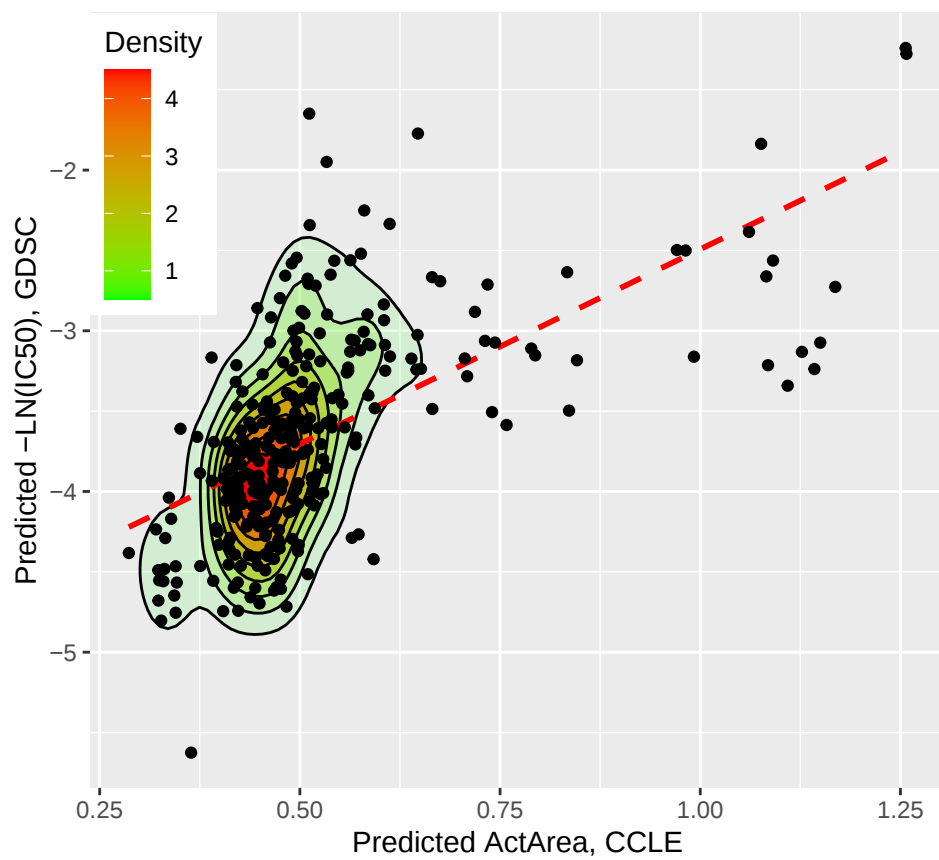
Nutlin-3a (-)
GDSC, $r = 0.61$, $n = 529$



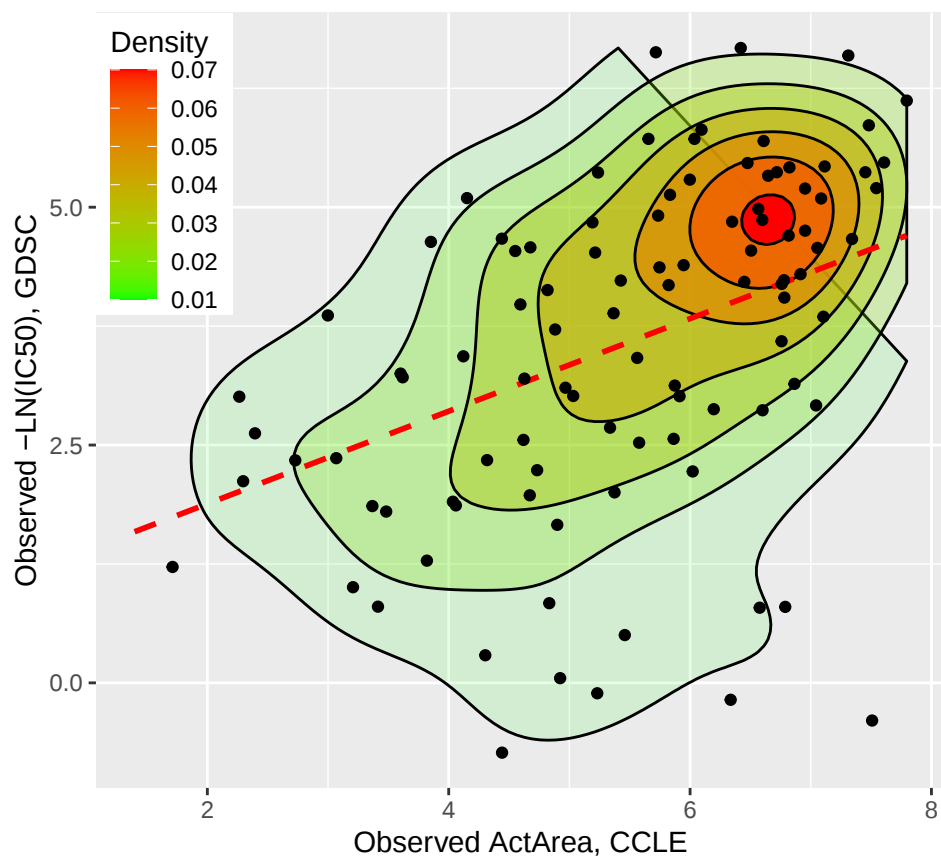
Nutlin-3
CCLE, $r = 0.414$, $n = 455$



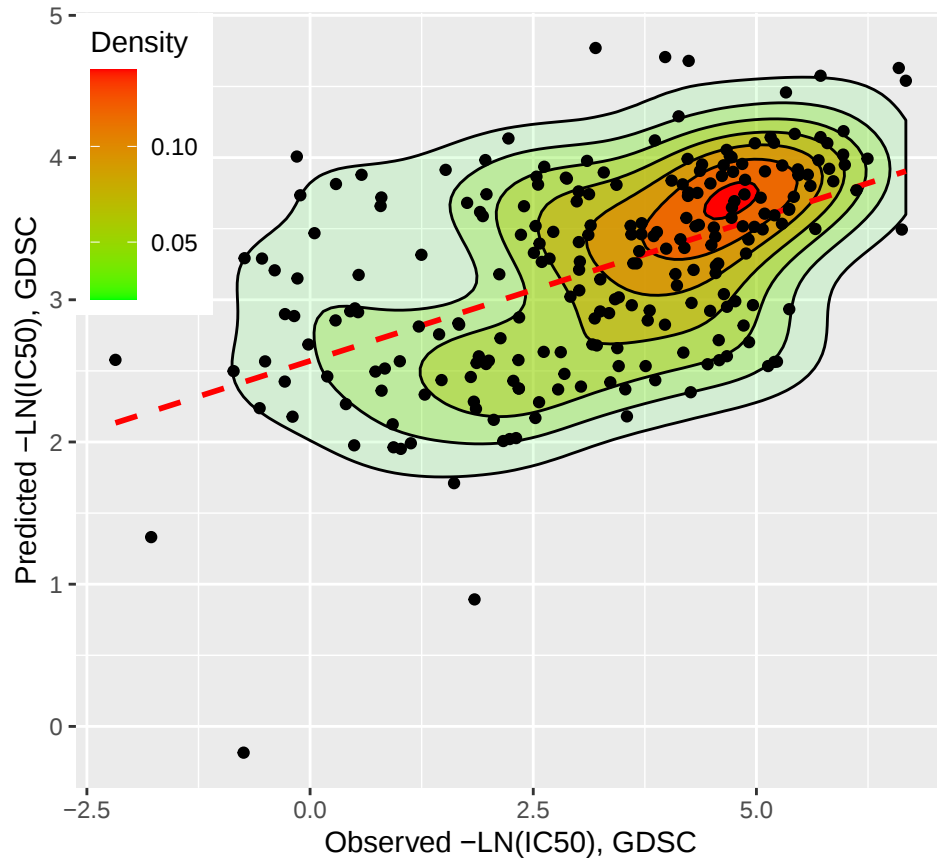
Nutlin-3a (-)
Predicted DR, $r = 0.61$, $n = 298$



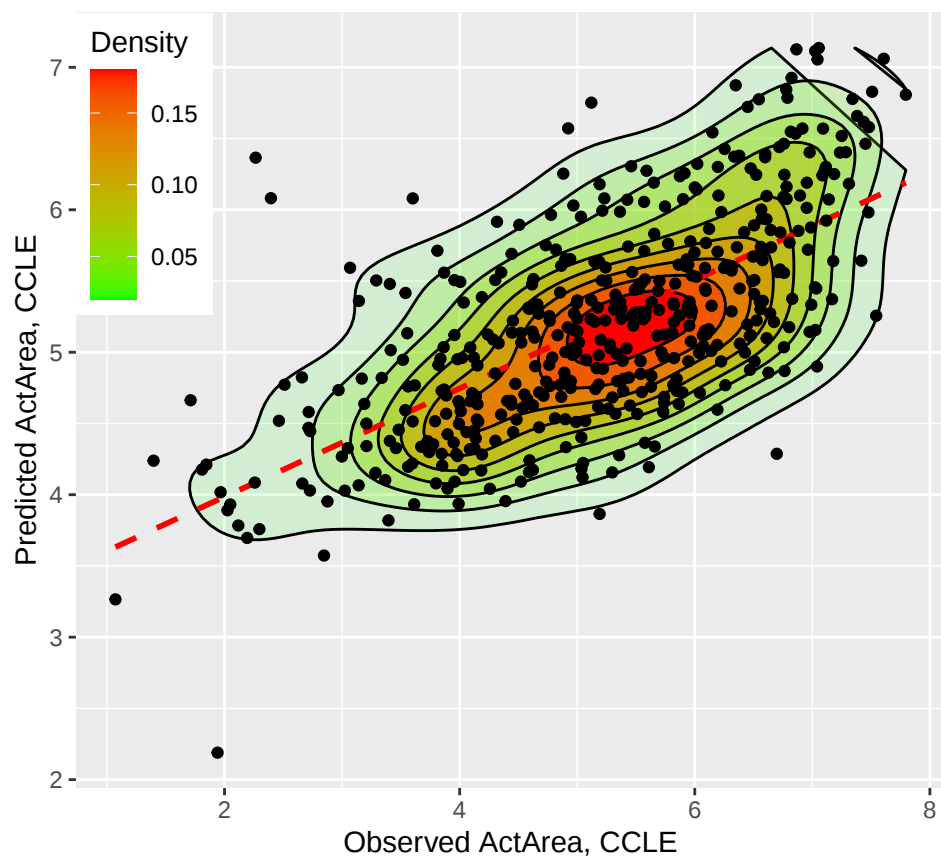
Paclitaxel
Observed DR, $r = 0.404$, $n = 101$



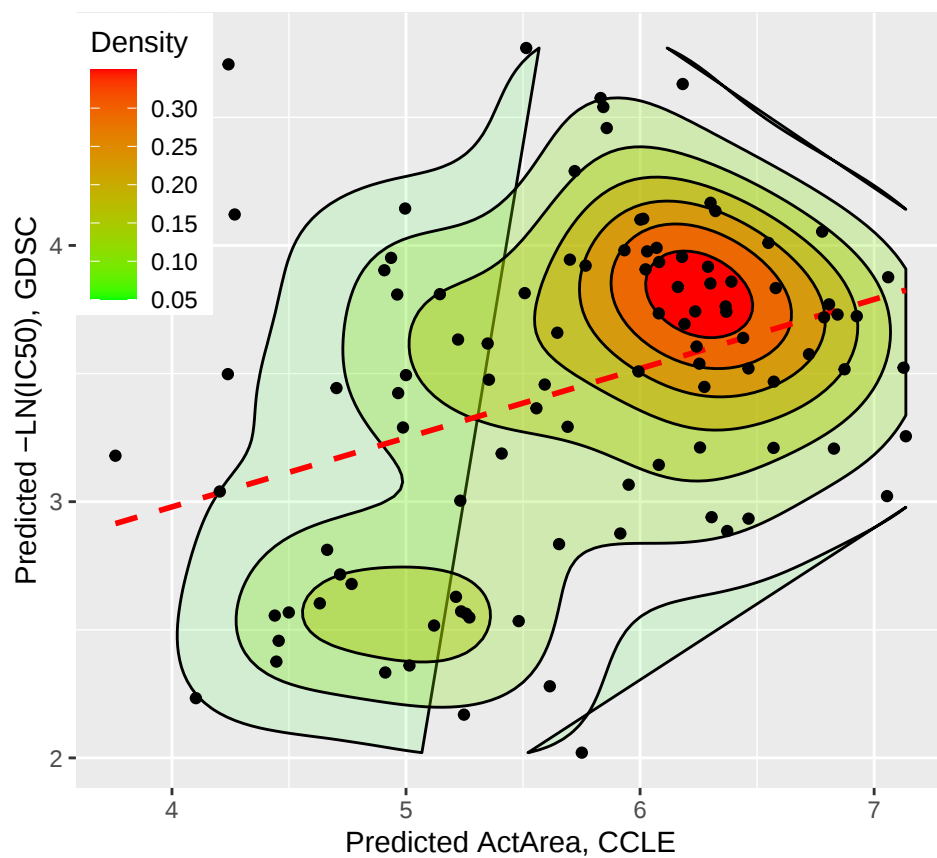
Paclitaxel
GDSC, $r = 0.517$, $n = 231$



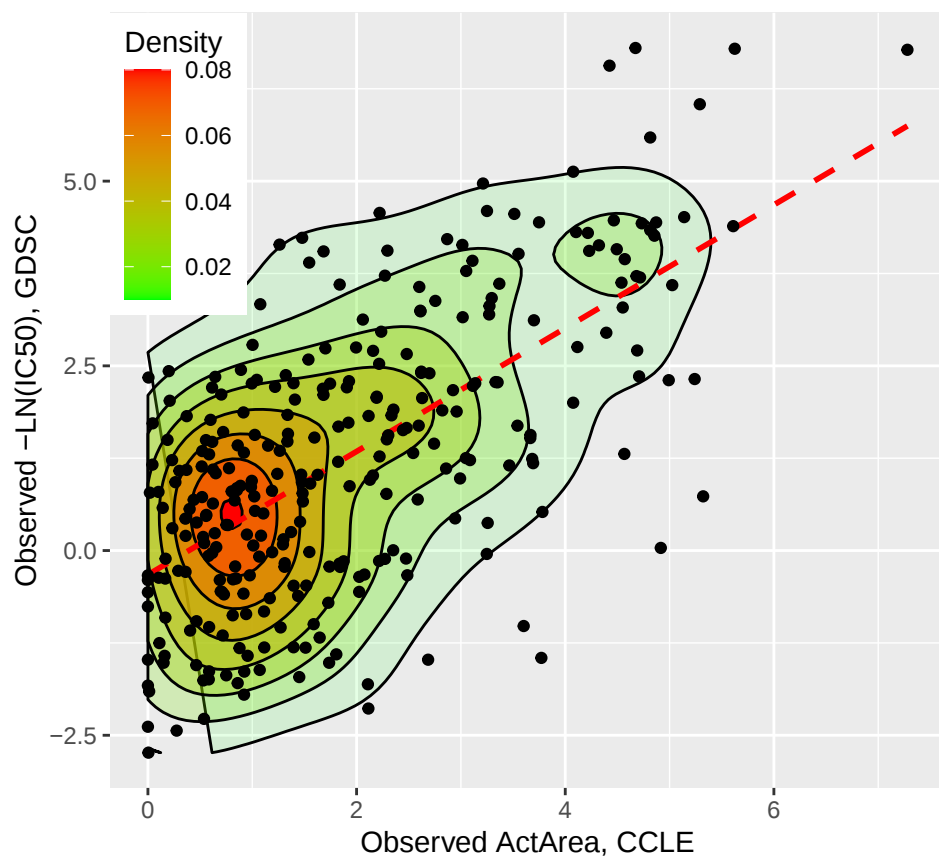
Paclitaxel
CCLE, $r = 0.668$, $n = 454$



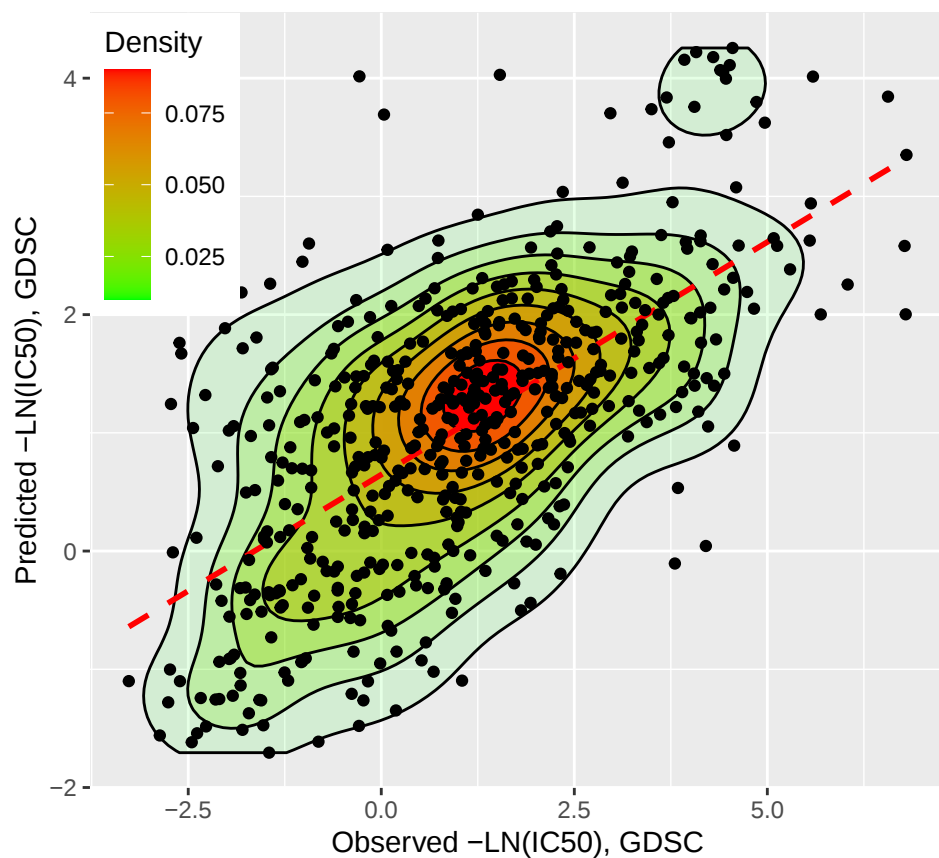
Paclitaxel
Predicted DR, $r = 0.342$, $n = 101$



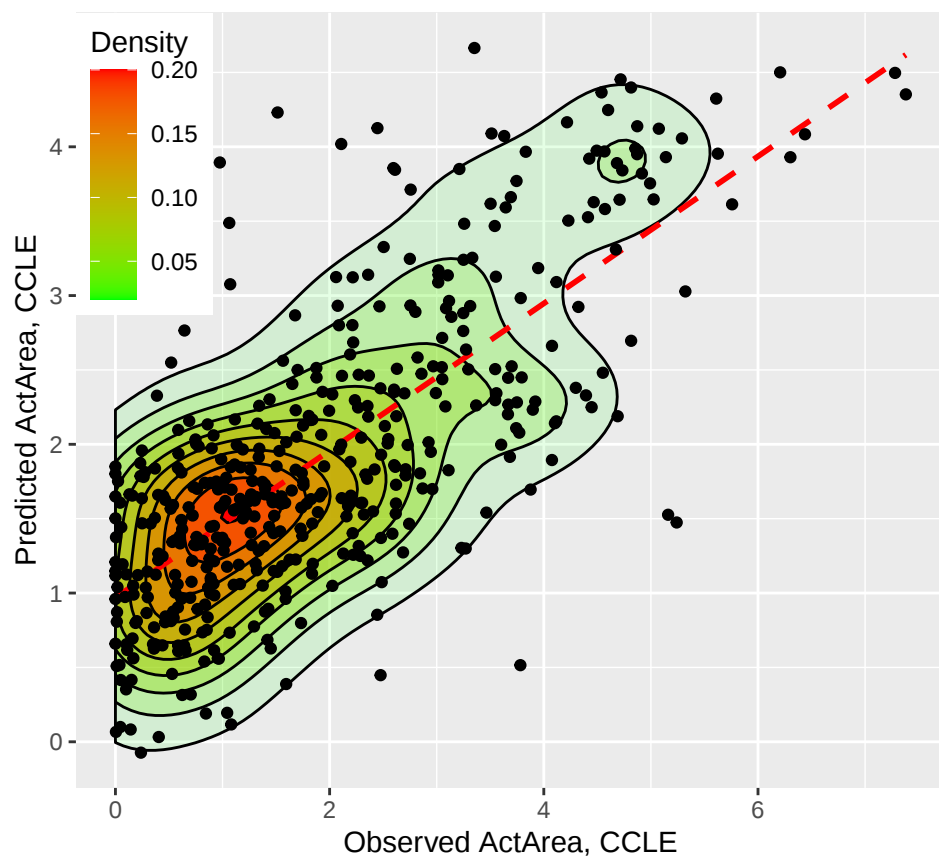
PD-0325901
Observed DR, $r = 0.636$, $n = 294$



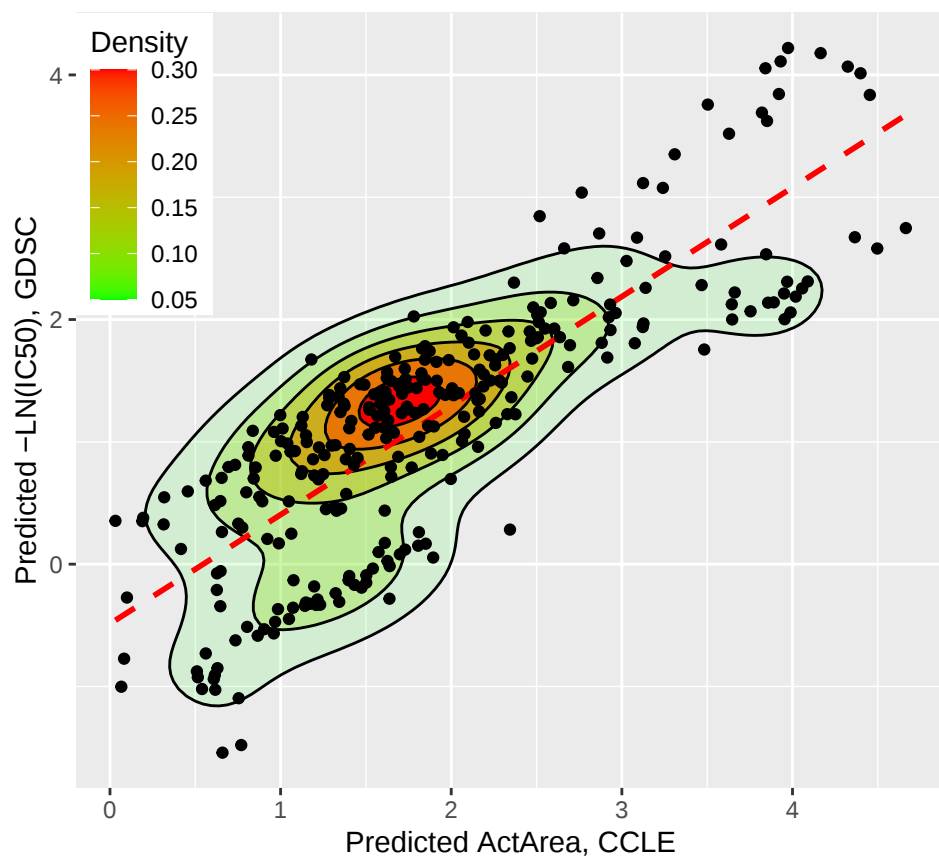
PD0325901
GDSC, $r = 0.647$, $n = 524$



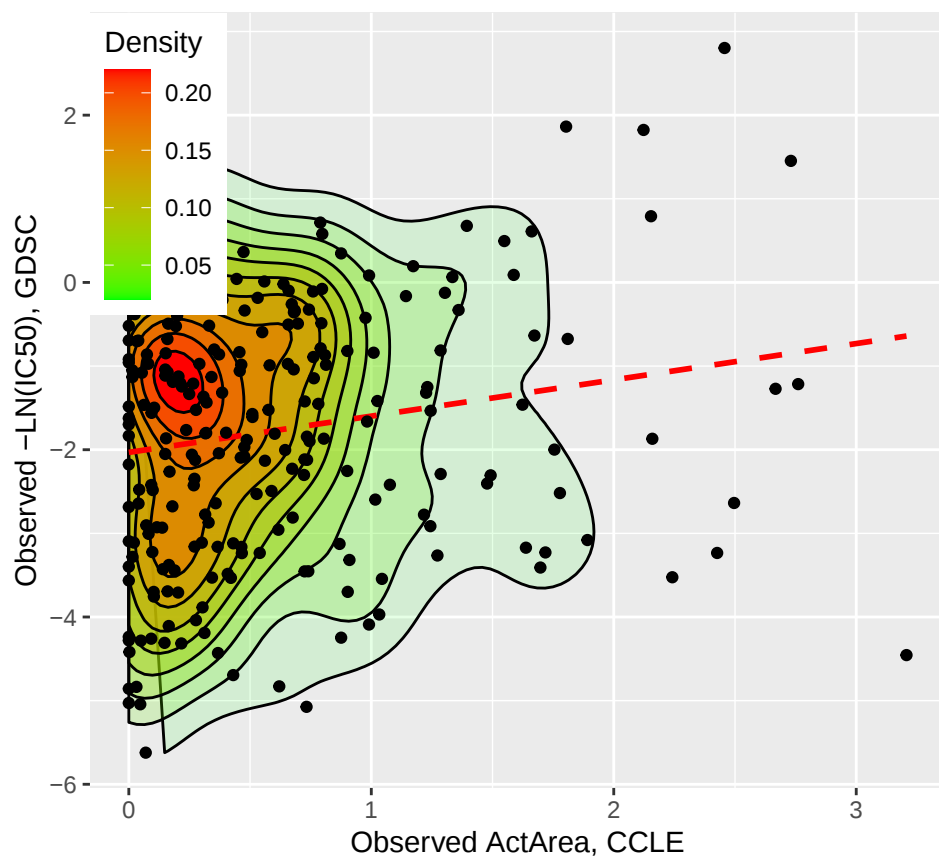
PD-0325901
CCLE, $r = 0.734$, $n = 455$



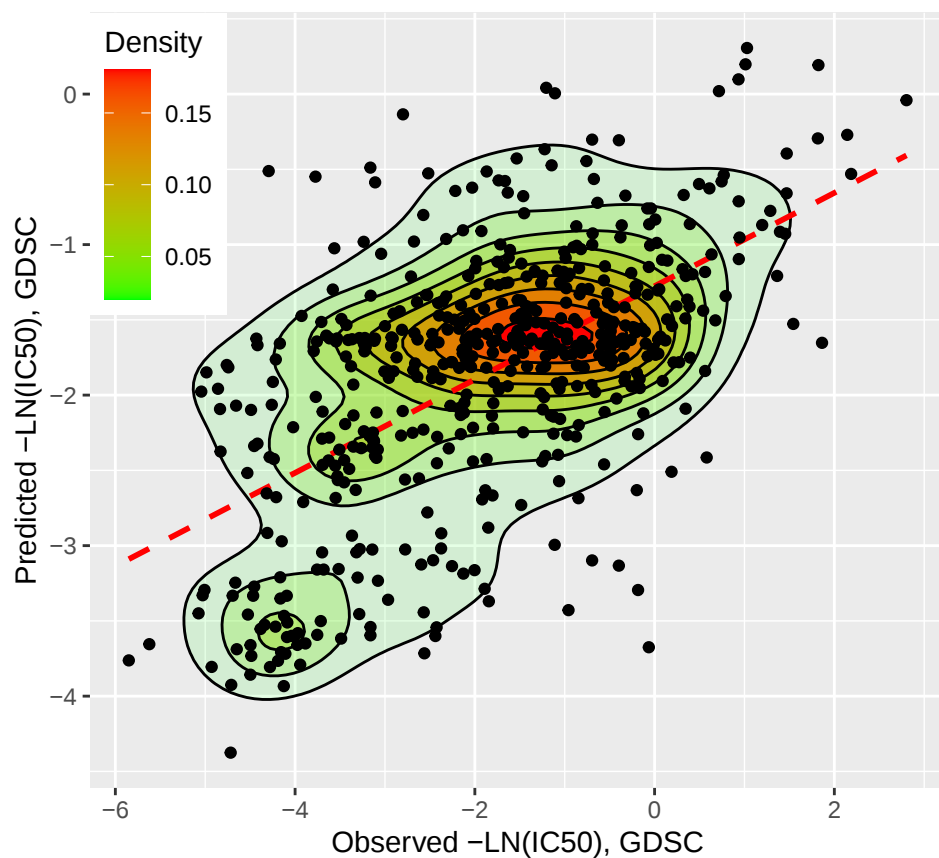
PD0325901
Predicted DR, $r = 0.826$, $n = 294$



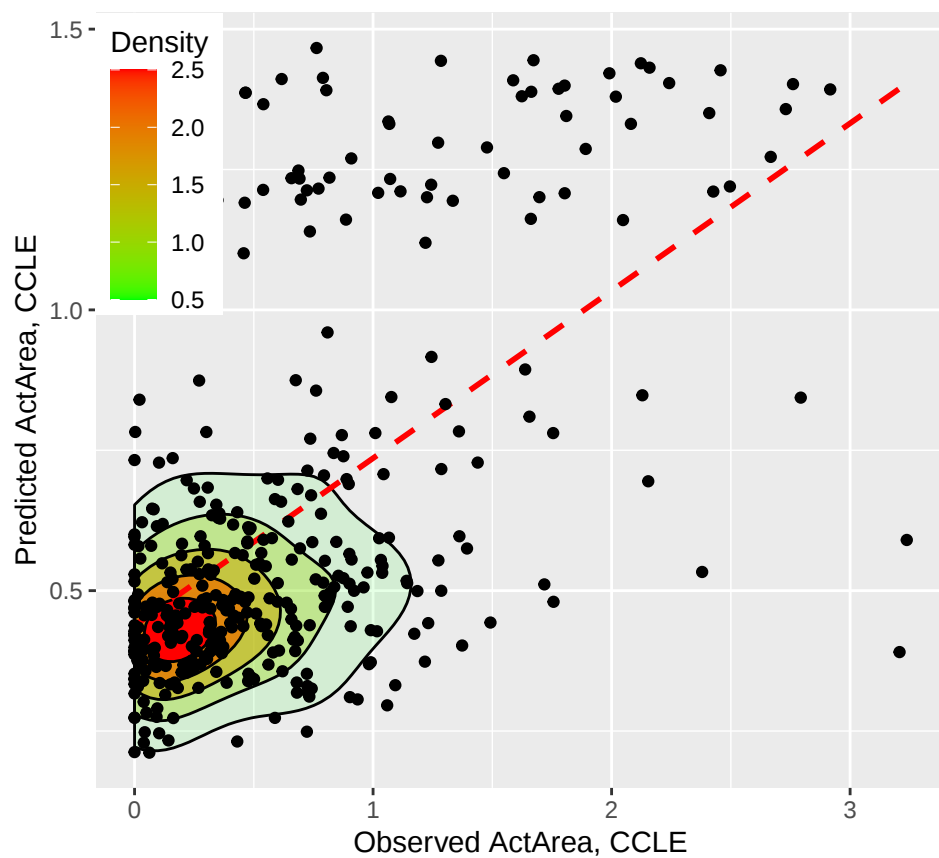
PD-0332991
Observed DR, $r = 0.174$, $n = 240$



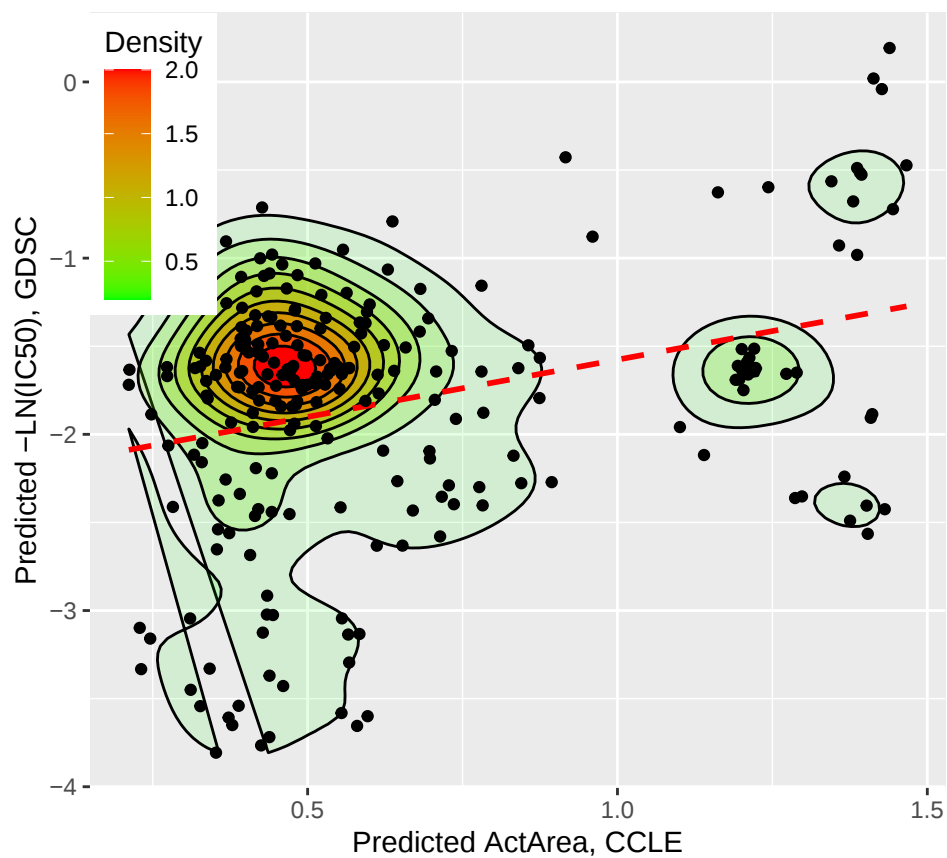
Palbociclib
GDSC, $r = 0.582$, $n = 512$



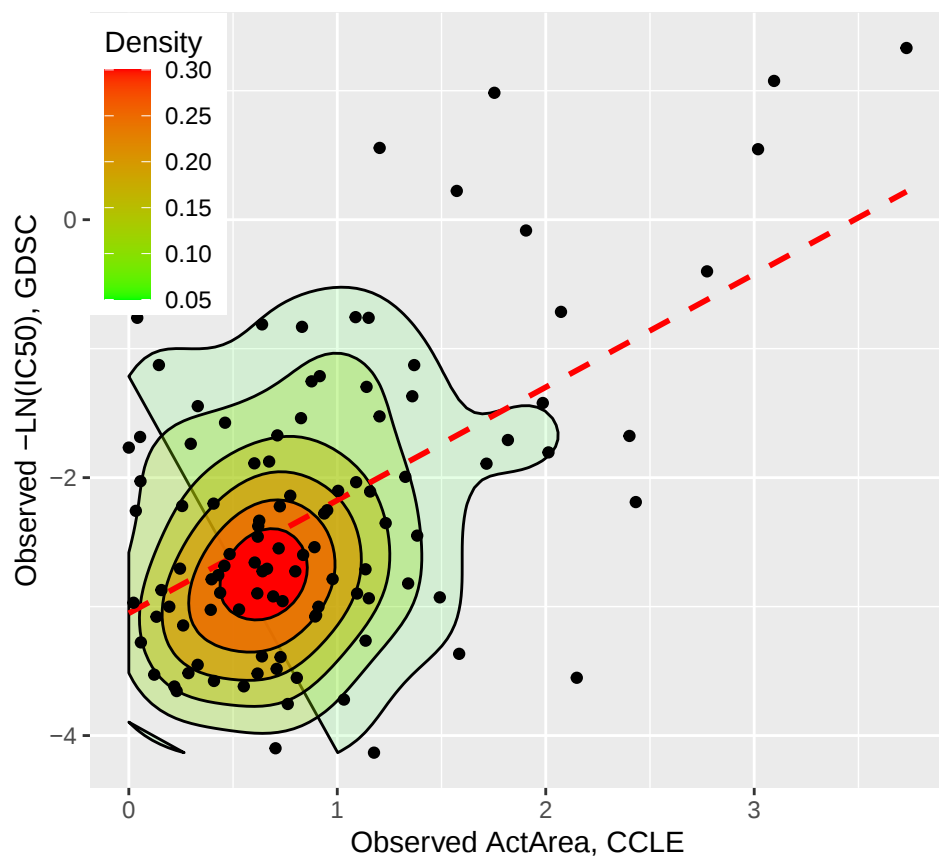
PD-0332991
CCLE, $r = 0.573$, $n = 388$



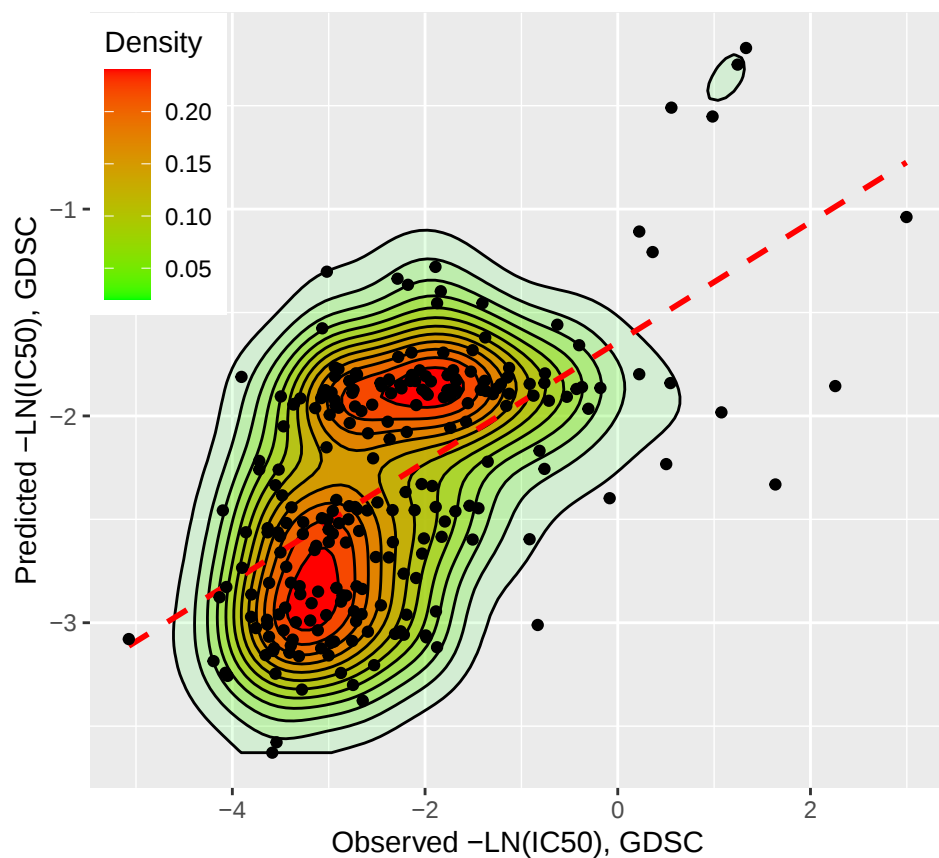
Palbociclib
Predicted DR, $r = 0.296$, $n = 240$



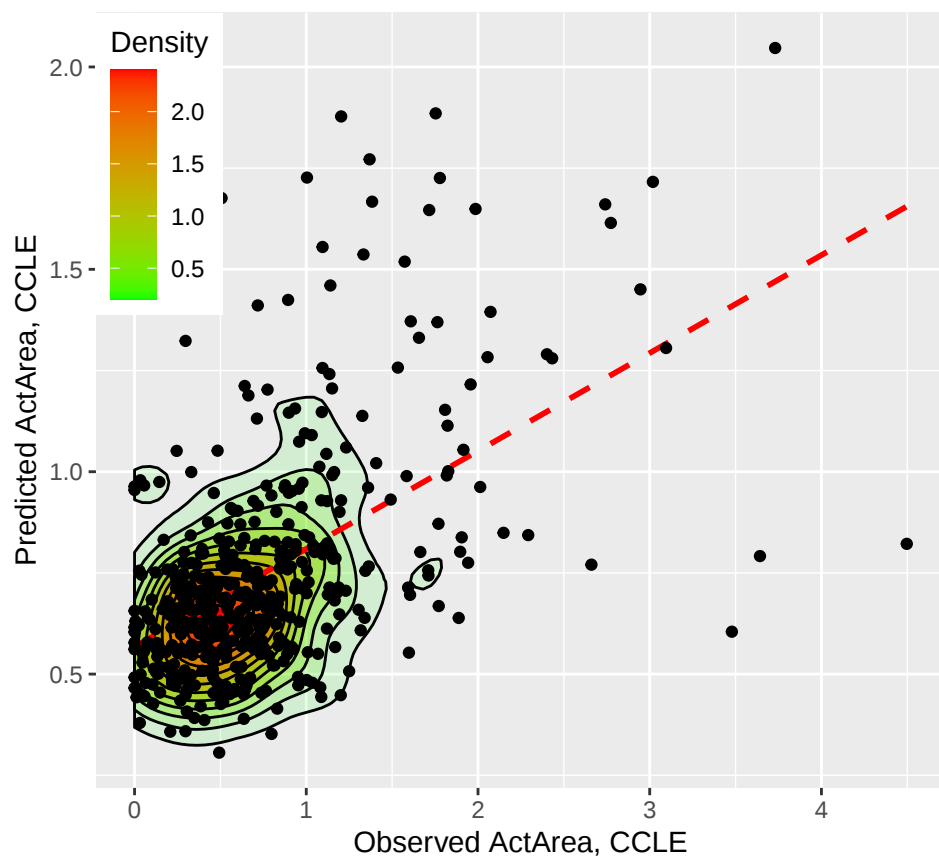
PF-2341066
Observed DR, $r = 0.54$, $n = 105$



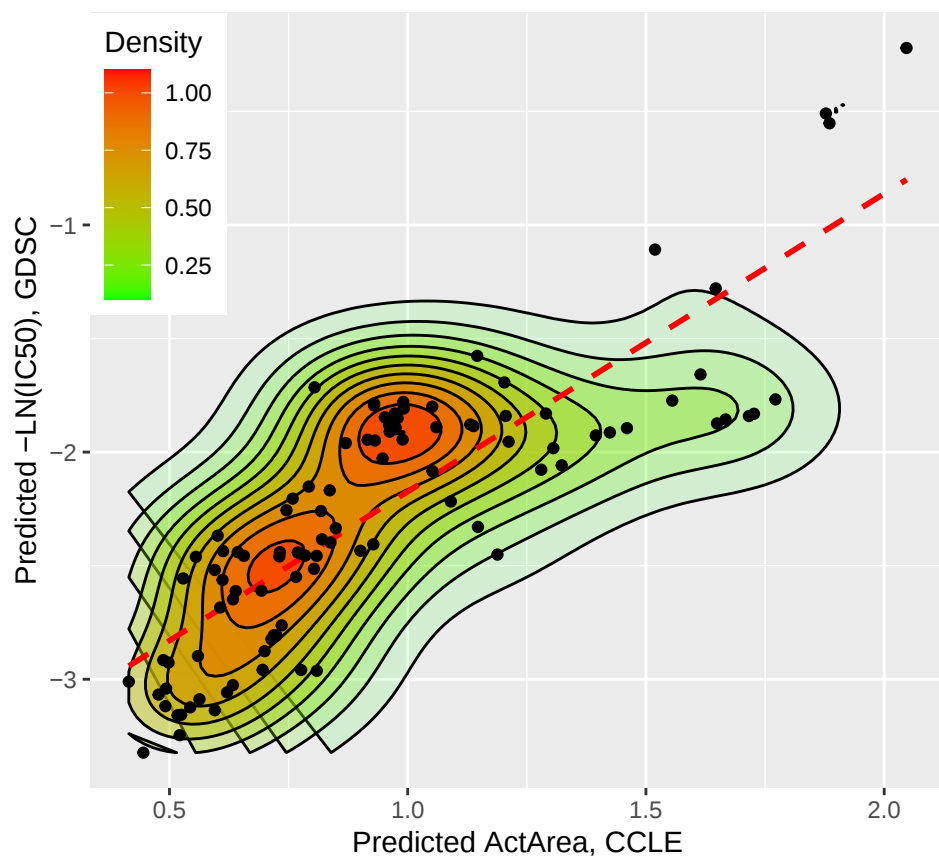
Crizotinib
GDSC, $r = 0.594$, $n = 235$



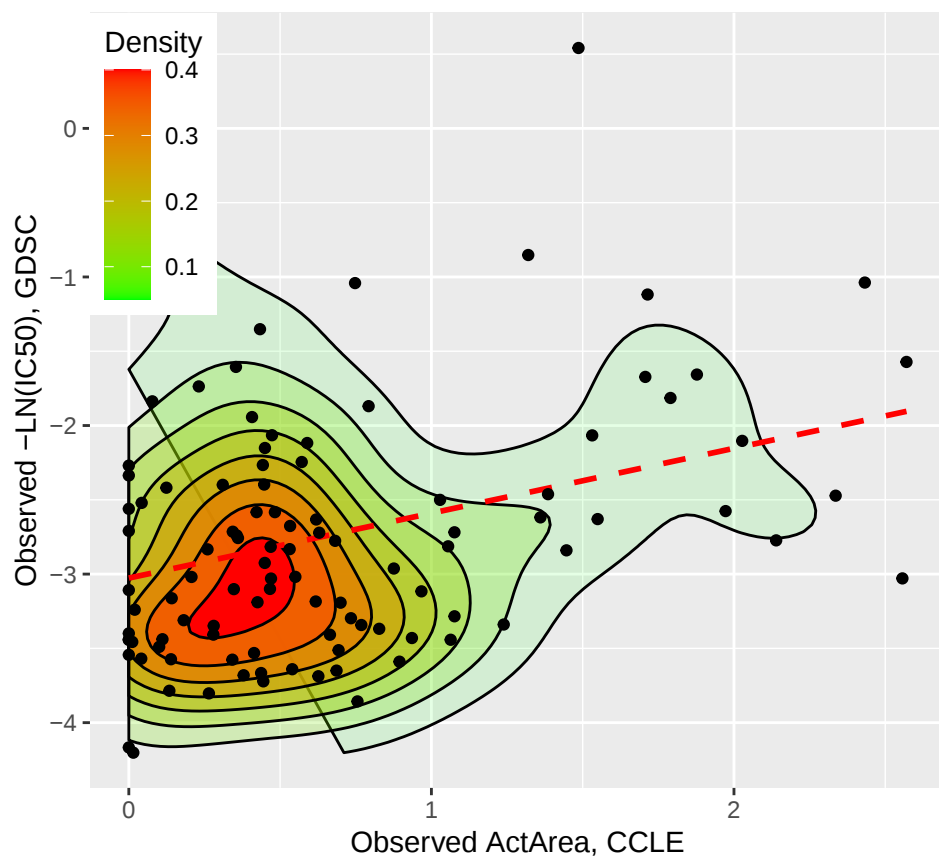
PF2341066
CCLE, $r = 0.526$, $n = 455$



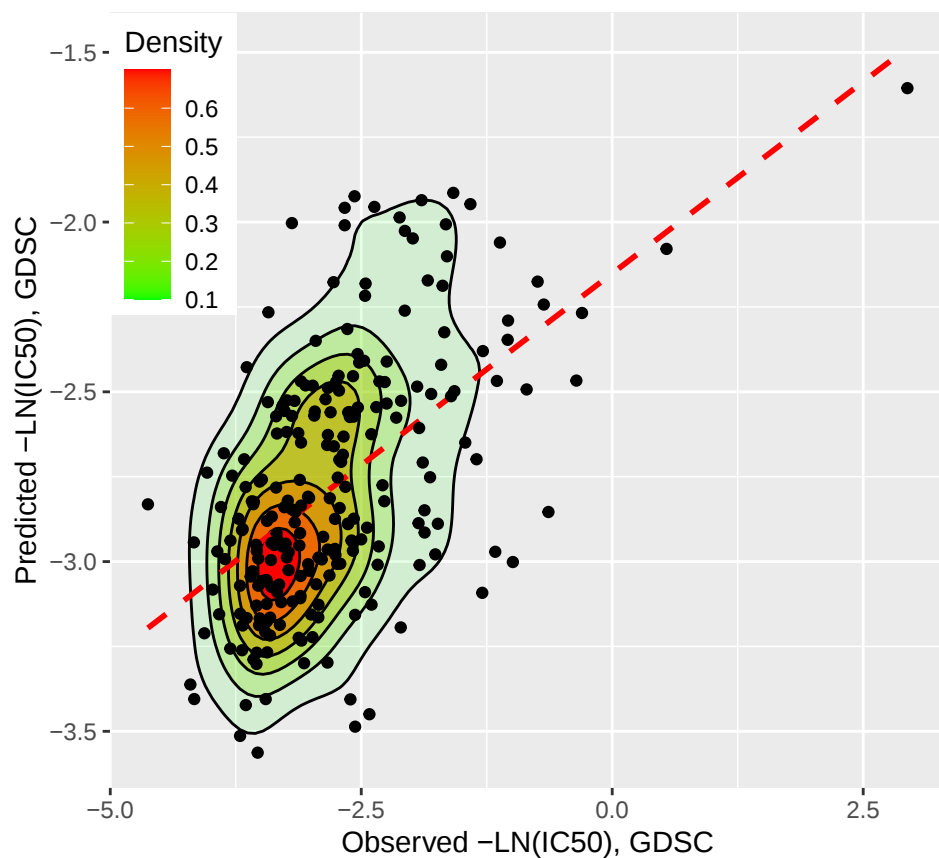
Crizotinib
Predicted DR, $r = 0.837$, $n = 105$



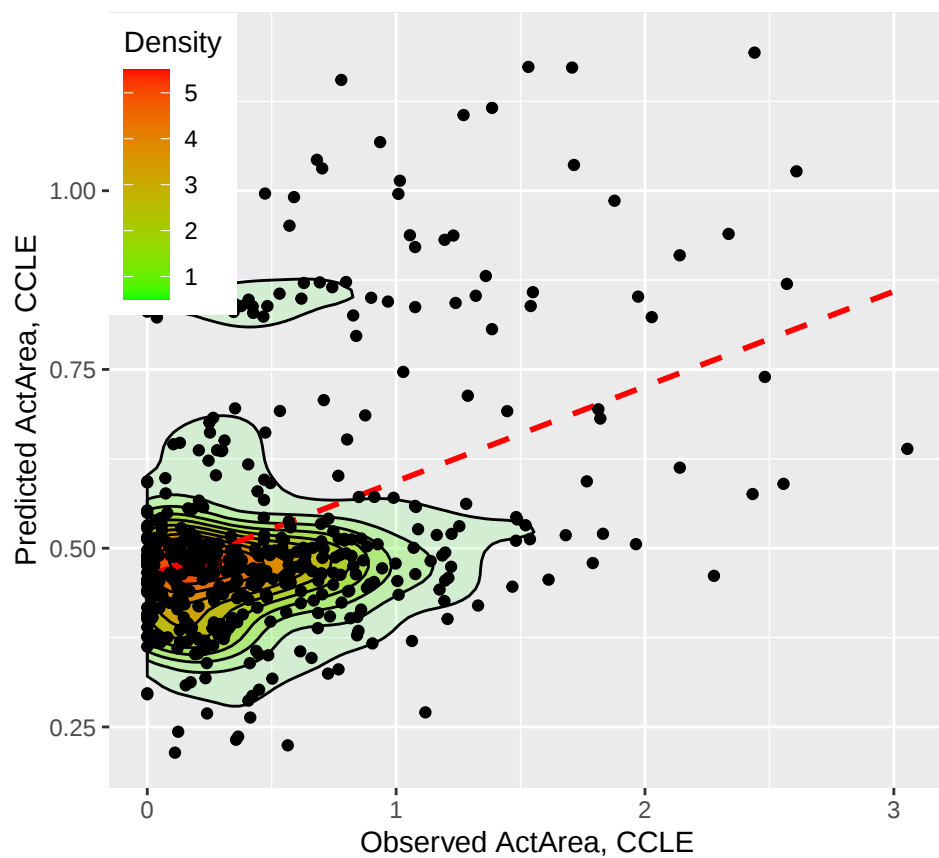
PHA-665752
Observed DR, $r = 0.322$, $n = 105$



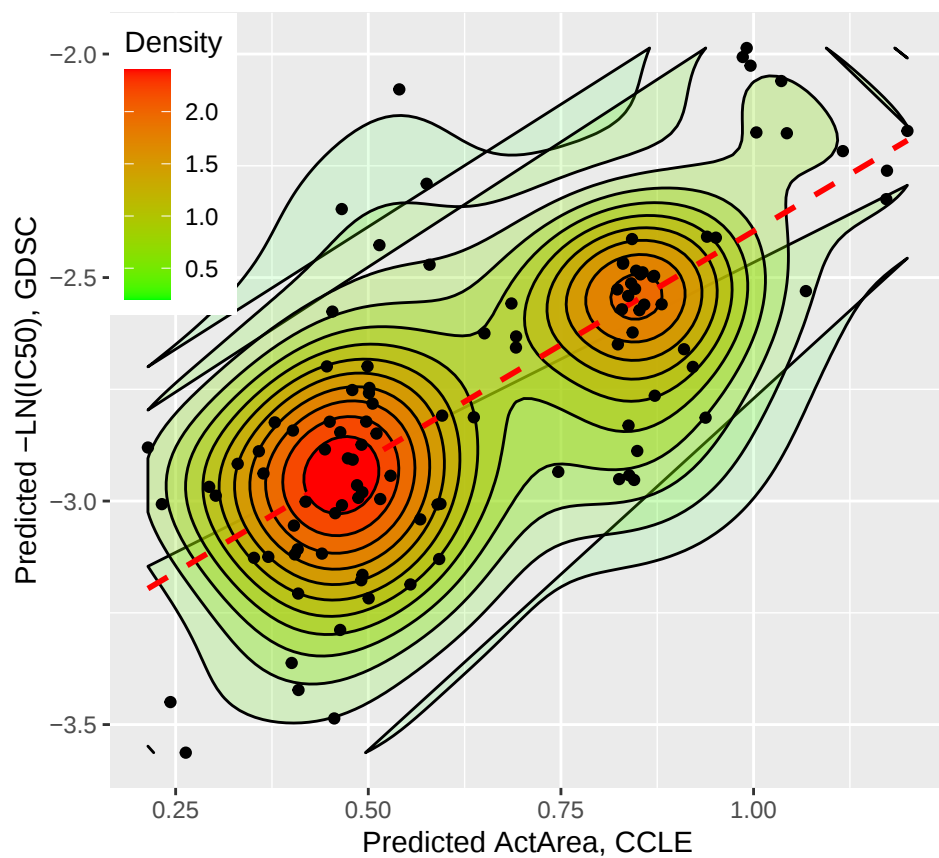
PHA-665752
GDSC, $r = 0.551$, $n = 236$



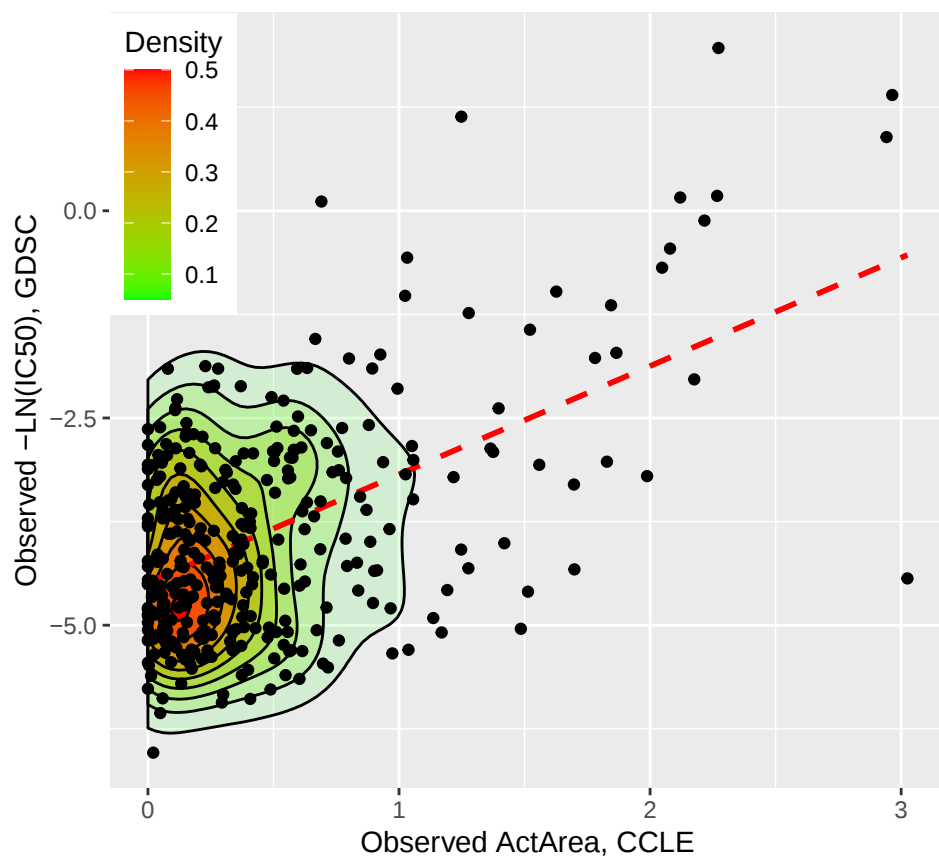
PHA-665752
CCLE, $r = 0.4$, $n = 454$



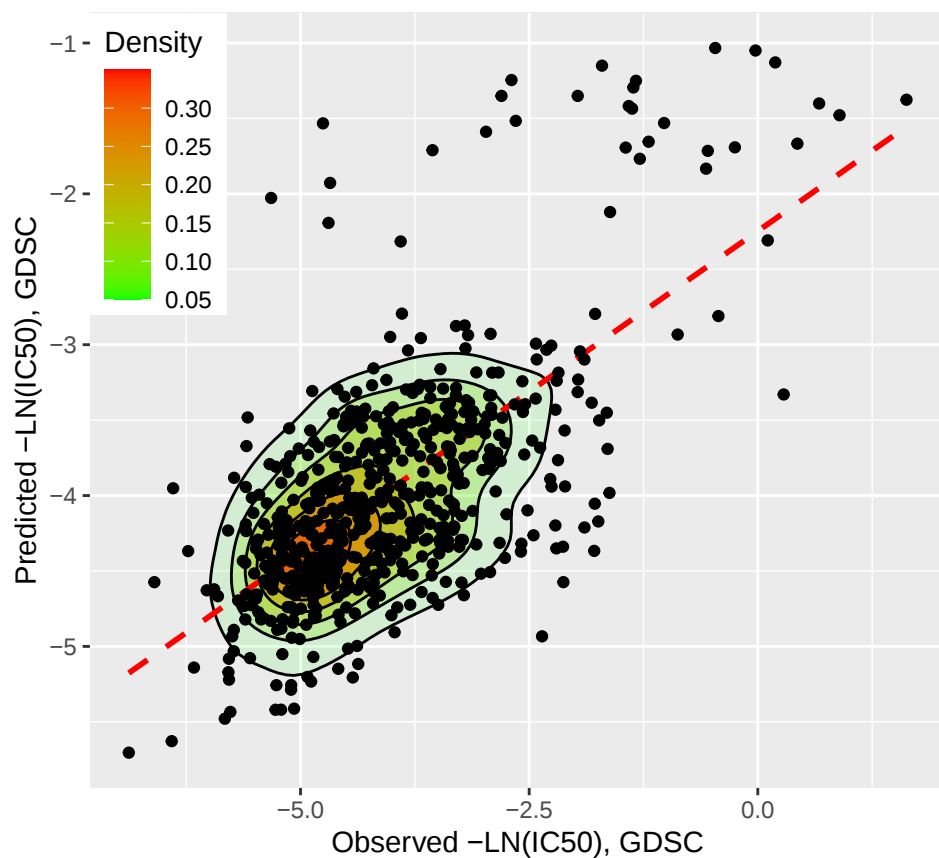
PHA-665752
Predicted DR, $r = 0.725$, $n = 105$



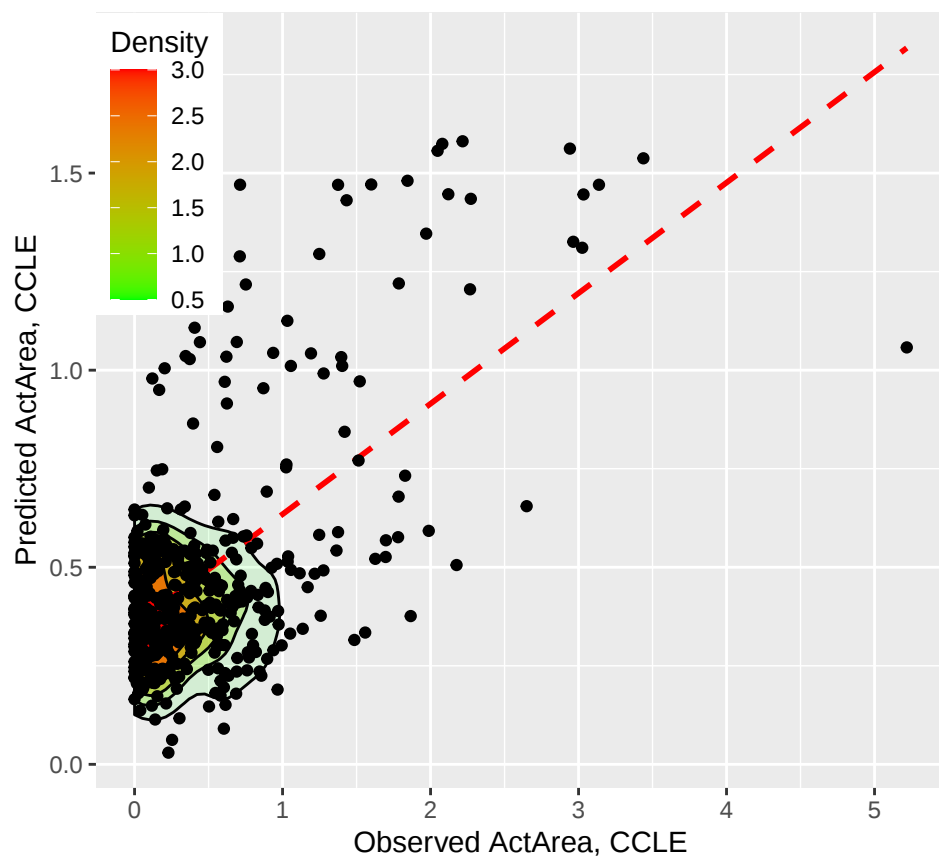
PLX4720
Observed DR, $r = 0.521$, $n = 336$



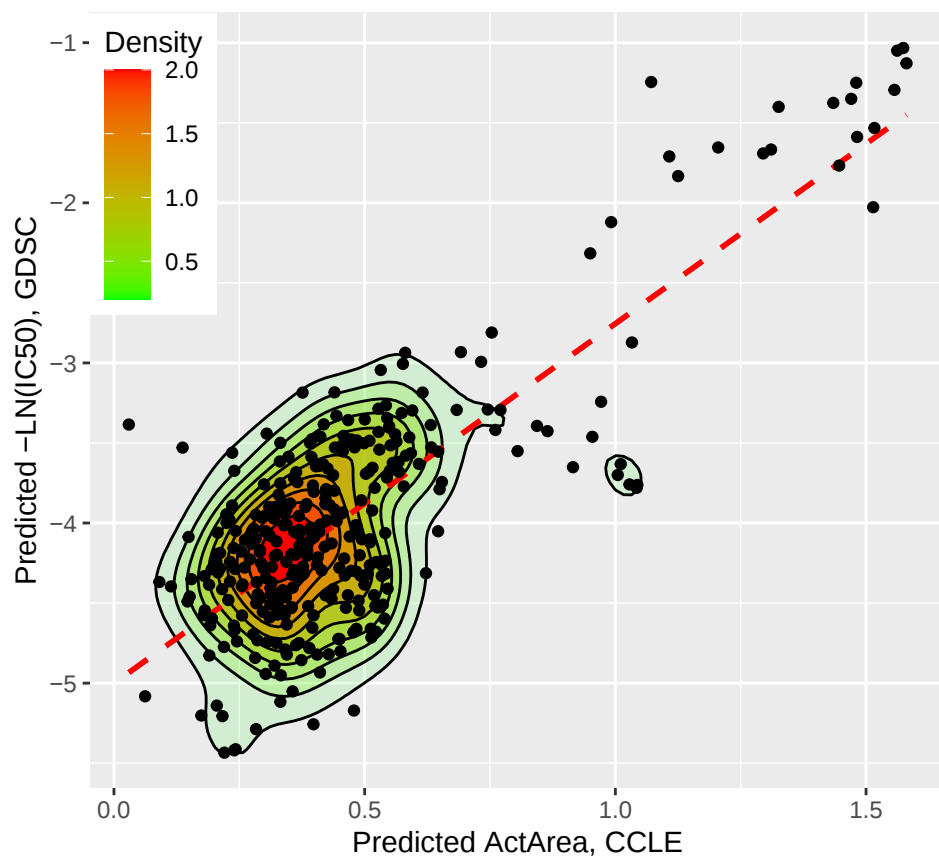
PLX-4720
GDSC, $r = 0.669$, $n = 604$



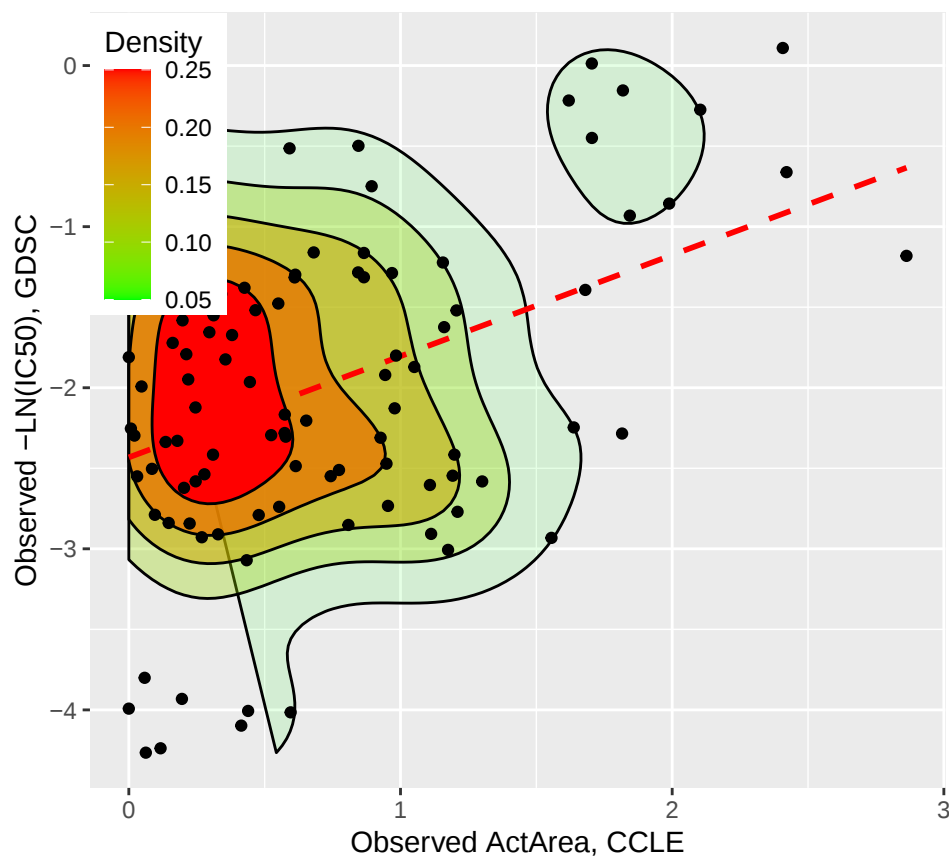
PLX4720
CCLE, $r = 0.561$, $n = 447$



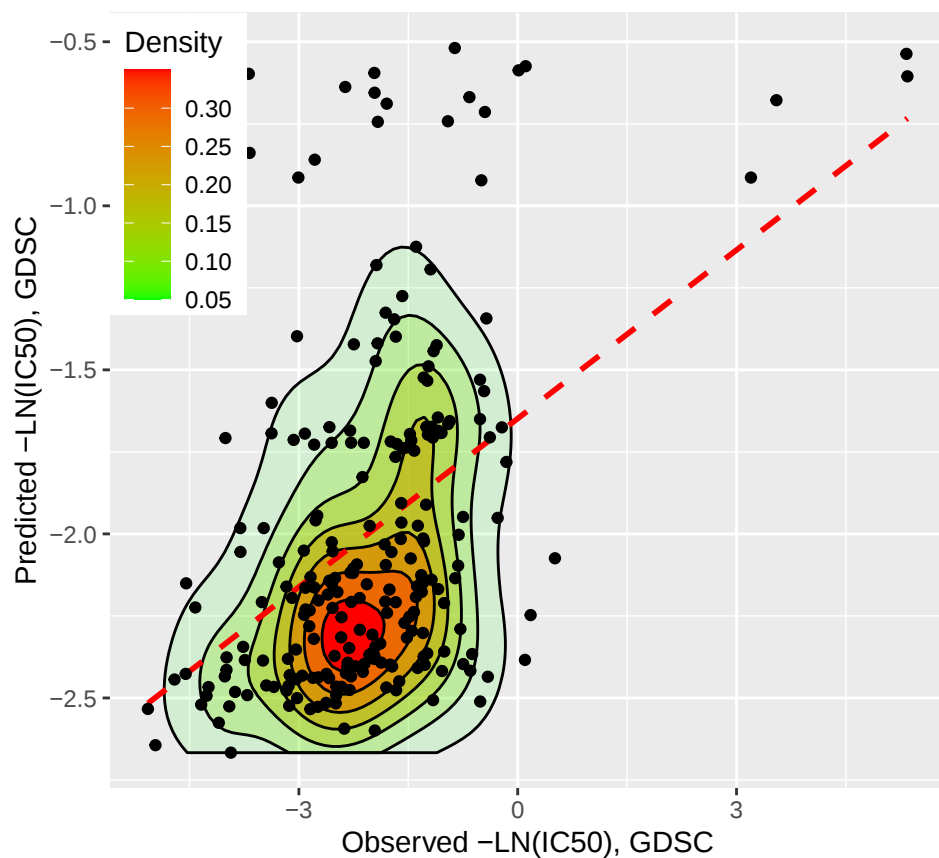
PLX-4720
Predicted DR, $r = 0.806$, $n = 336$



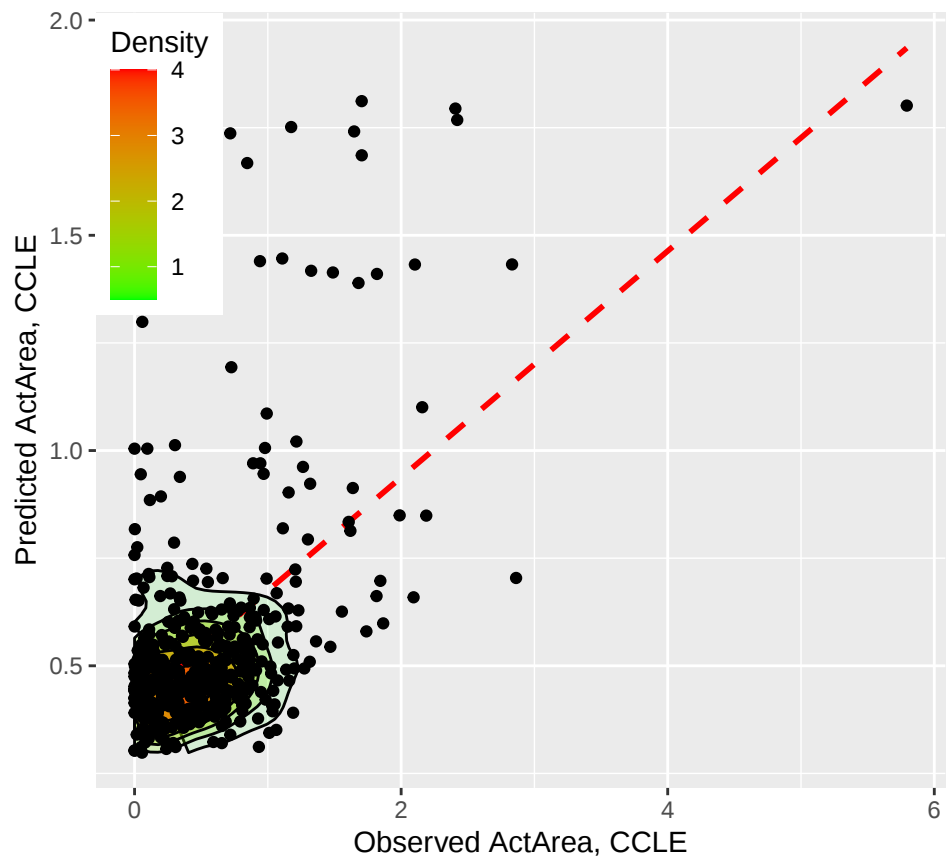
Sorafenib
Observed DR, $r = 0.401$, $n = 101$



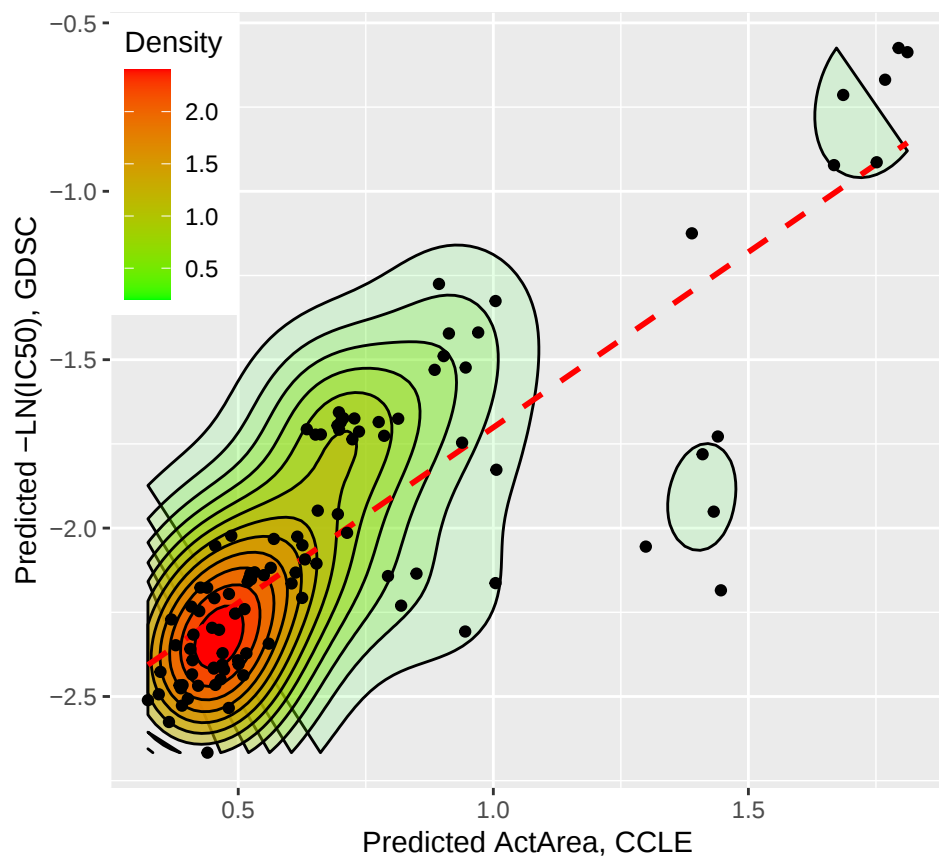
Sorafenib
GDSC, $r = 0.45$, $n = 229$



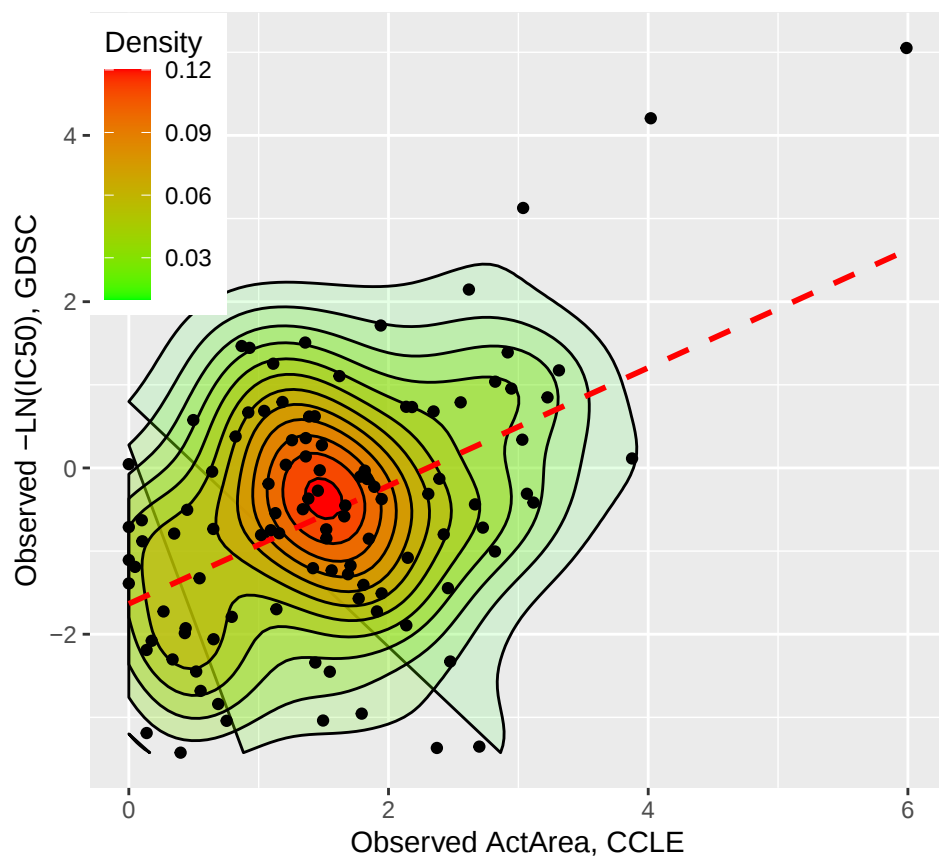
Sorafenib
CCLE, $r = 0.542$, $n = 454$



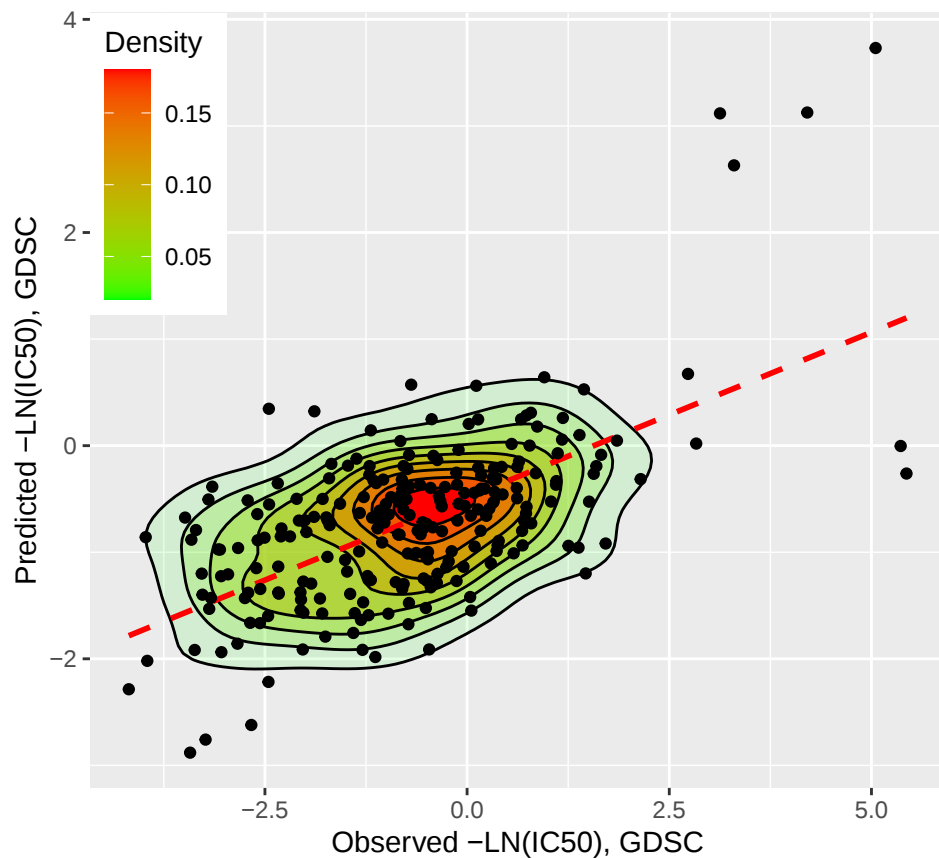
Sorafenib
Predicted DR, $r = 0.828$, $n = 101$



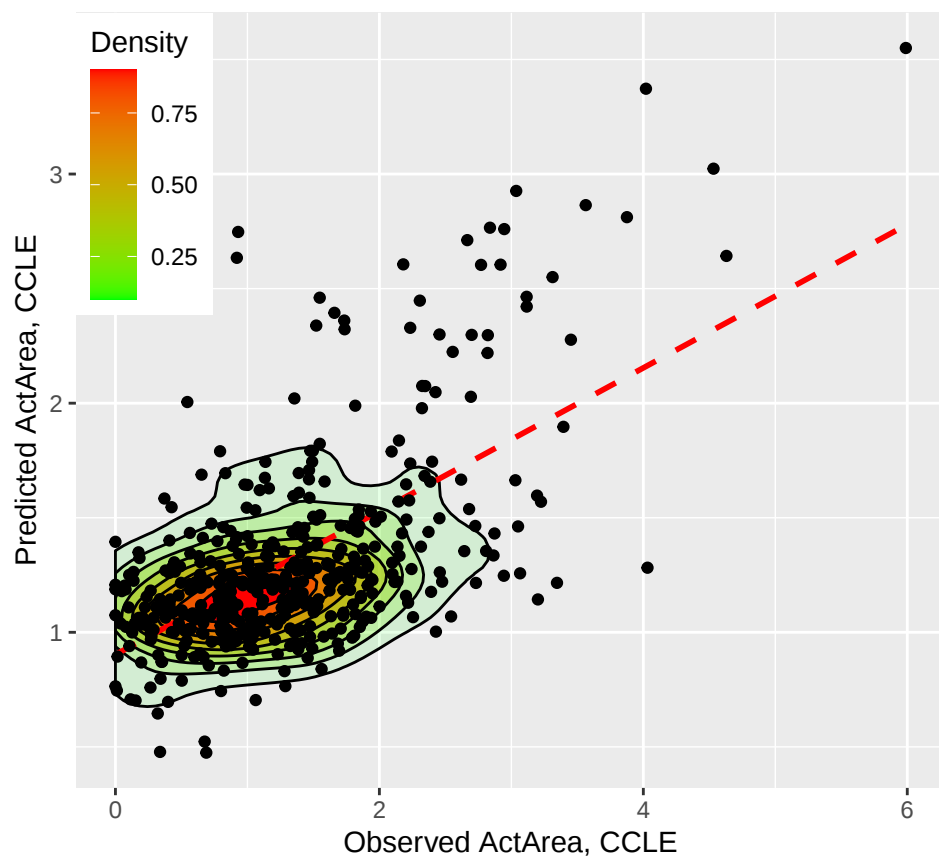
TAE684
Observed DR, $r = 0.486$, $n = 105$



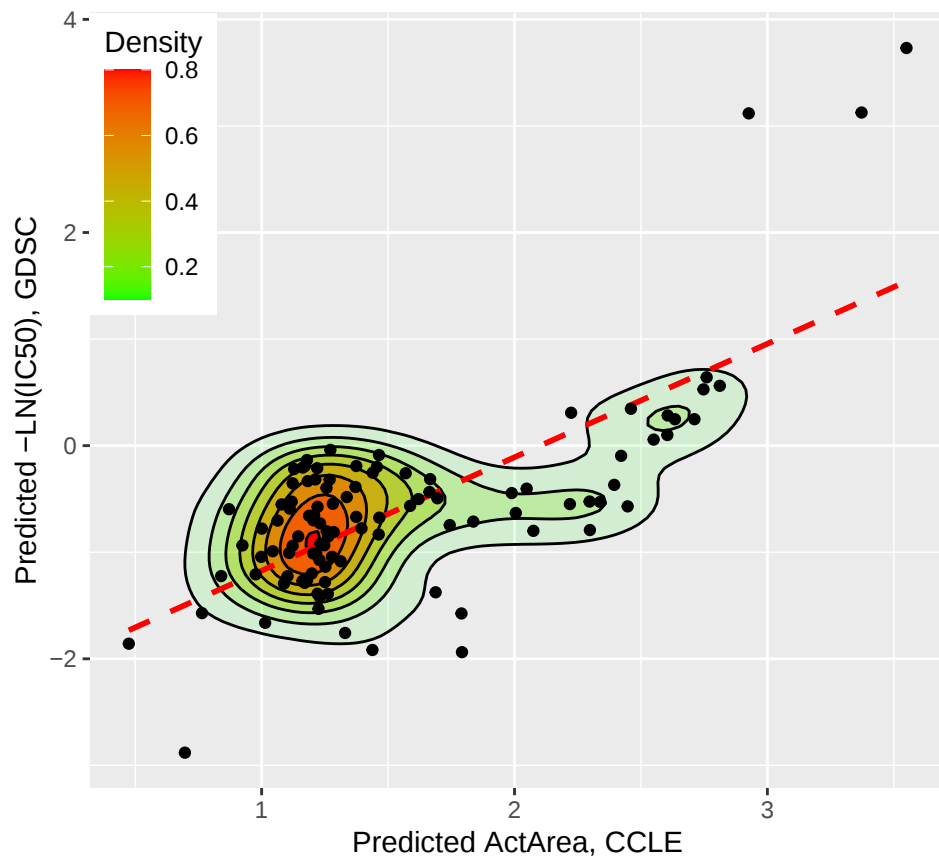
NVP-TAE684
GDSC, $r = 0.618$, $n = 235$



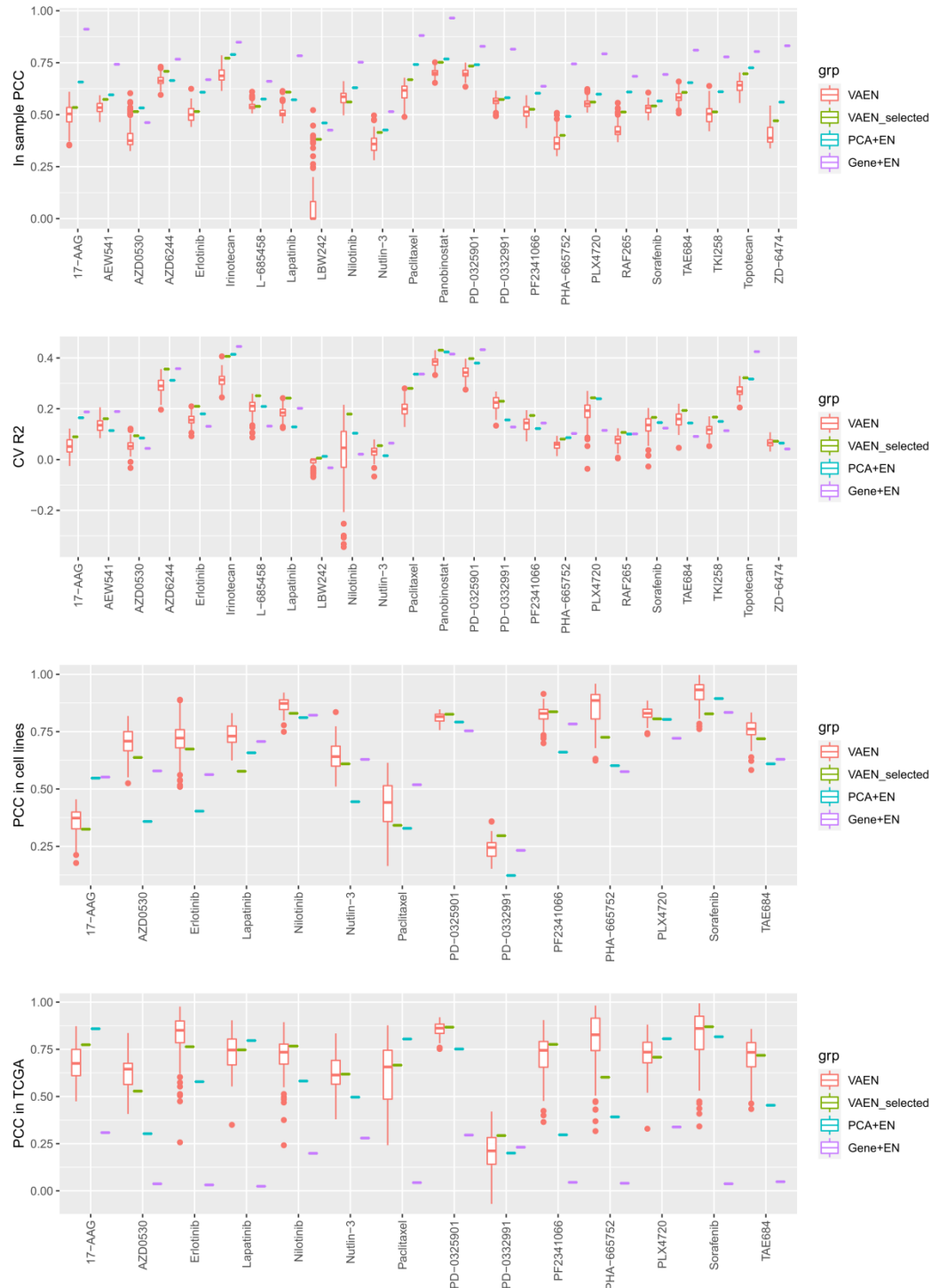
TAE684
CCLE, $r = 0.607$, $n = 455$



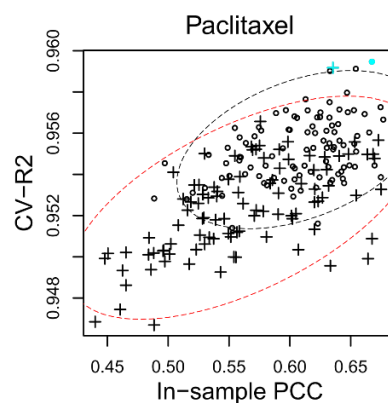
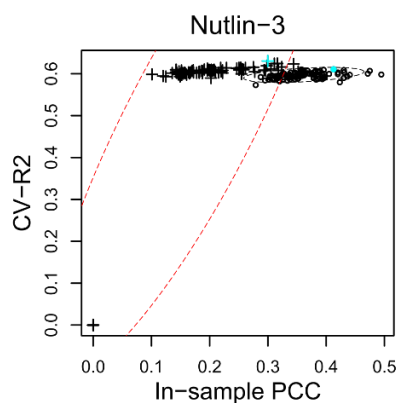
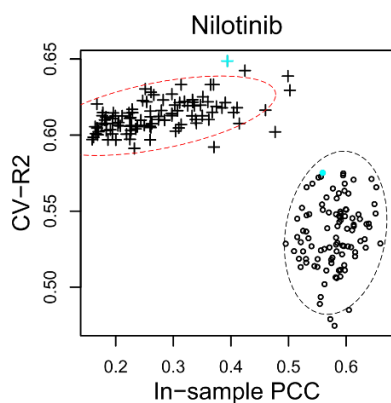
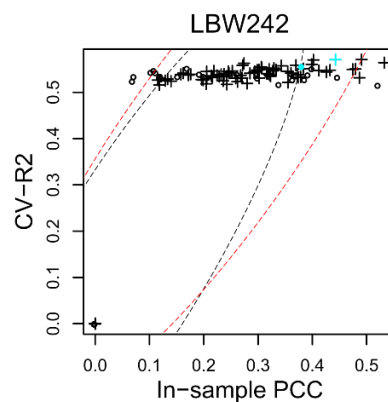
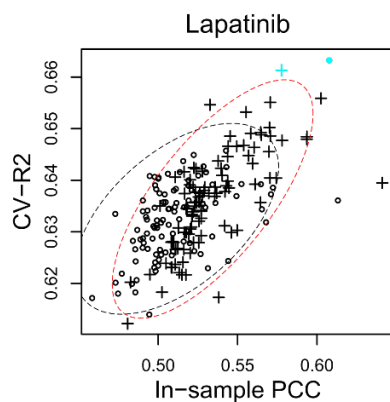
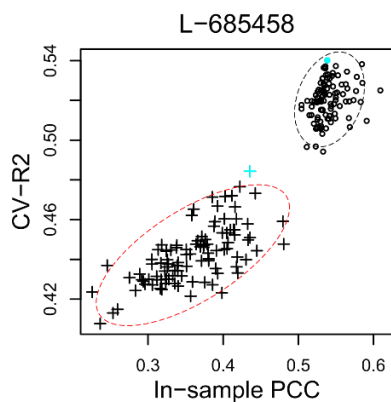
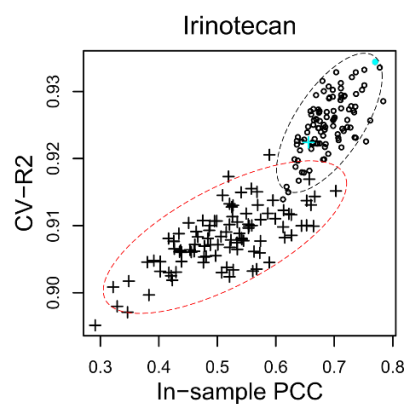
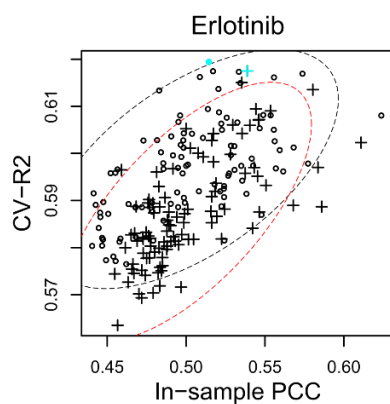
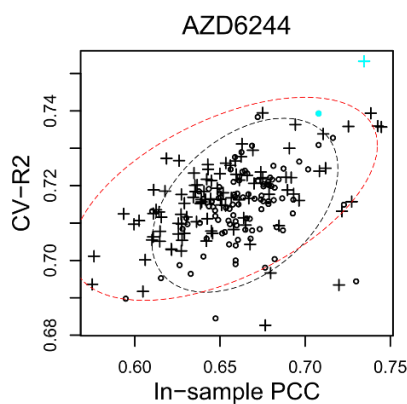
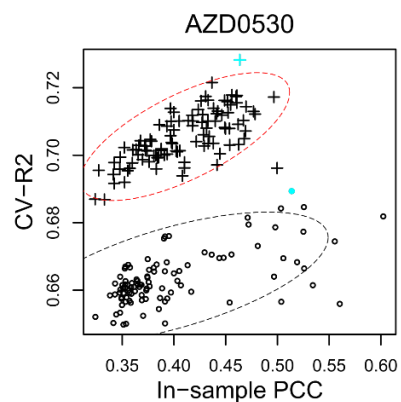
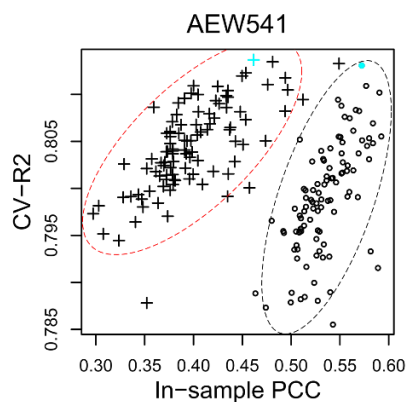
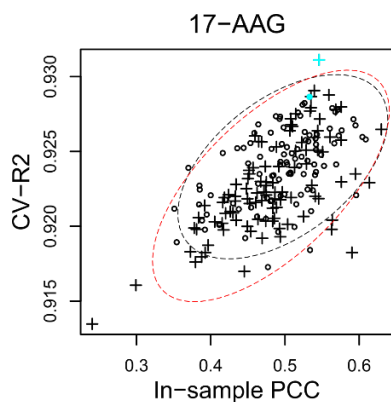
NVP-TAE684
Predicted DR, $r = 0.719$, $n = 105$

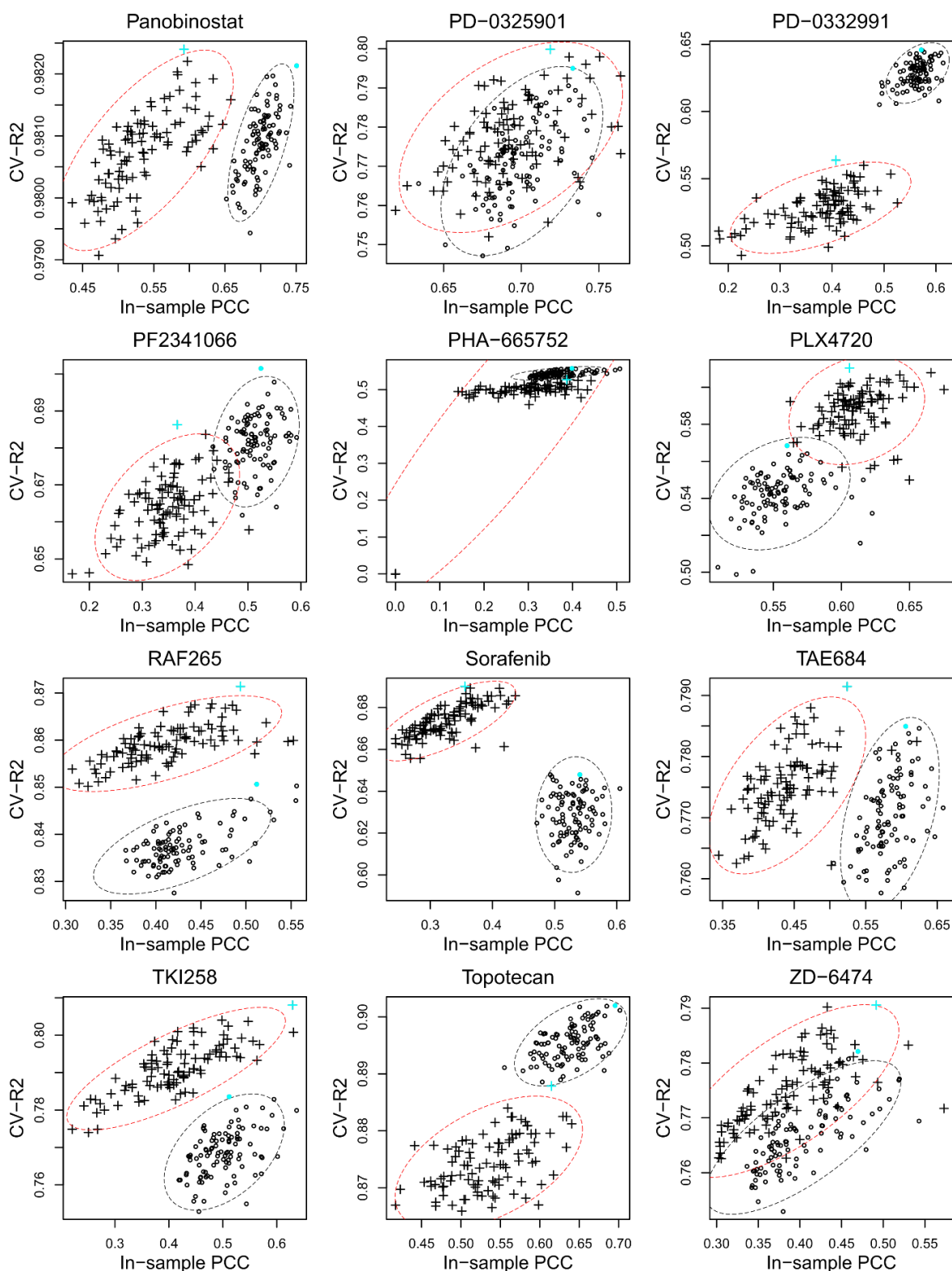


Supplementary Figure 3. Comparison of the observed and predicted drug response for 14 shared drugs between CCLE and GDSC.

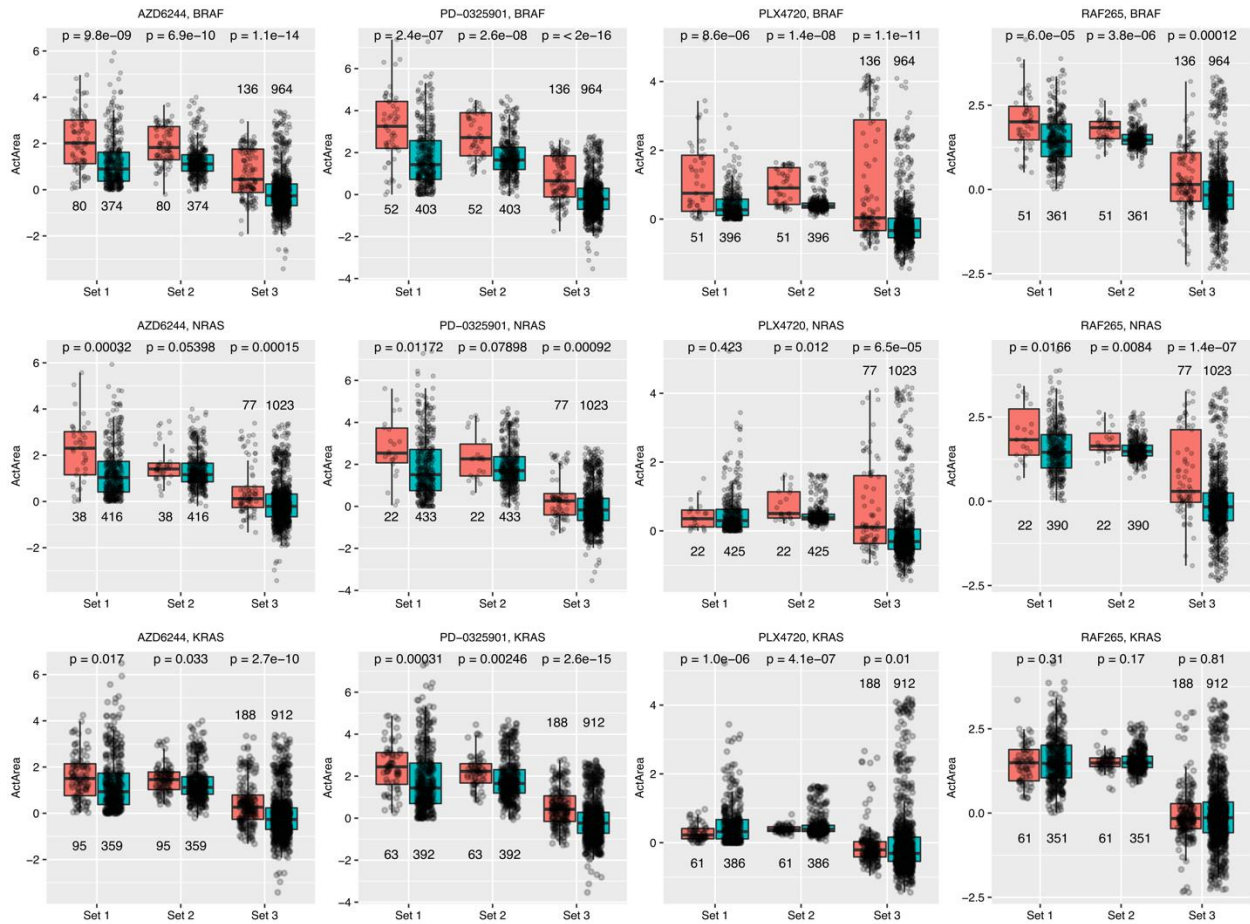


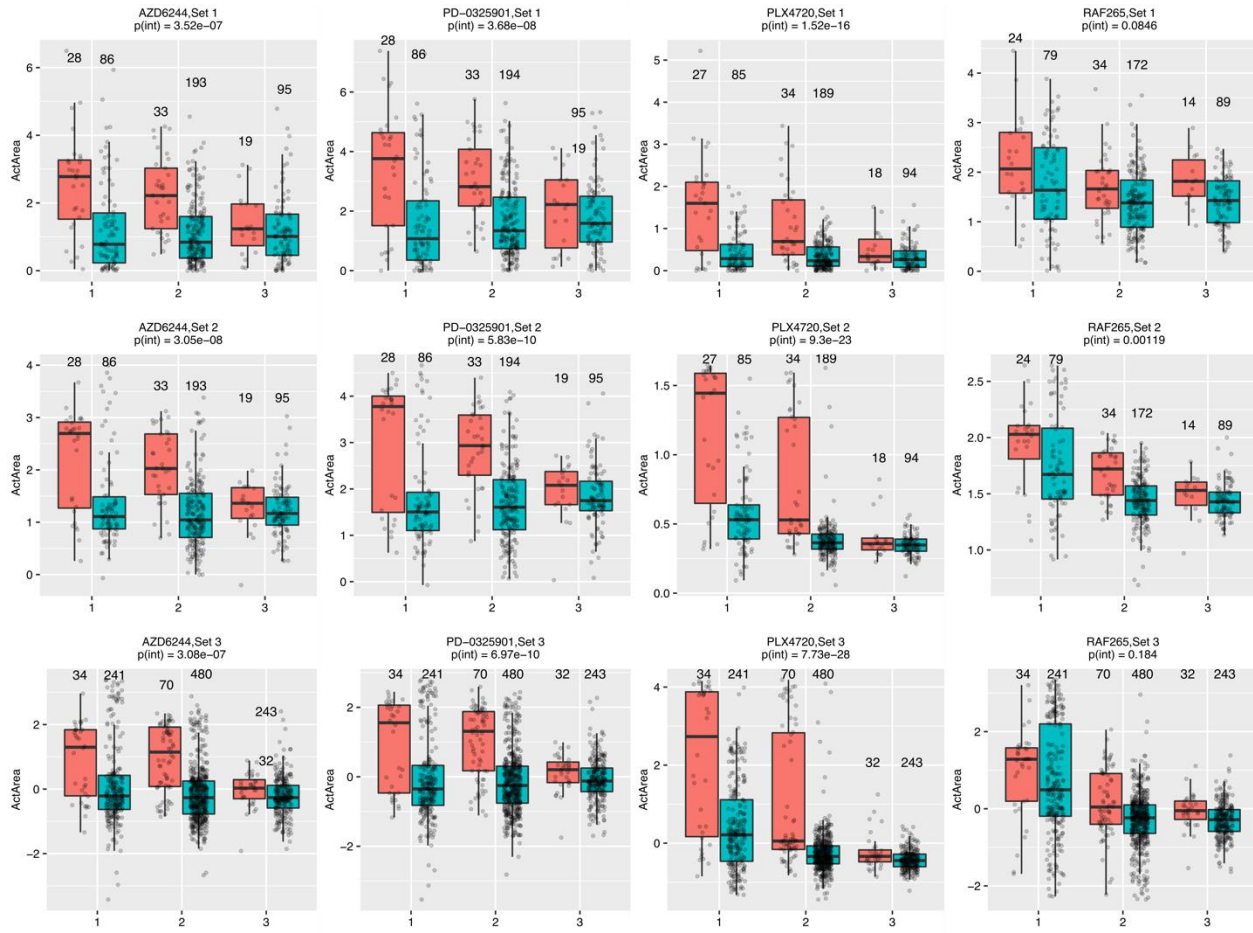
Supplementary Figure 4. Model comparison and evaluation using computational measurements. (A-B) Comparison of models using in-sample PCC (A) and holdout R2 (B). (C-D) Cross-panel model comparison using shared drugs in CCLE cell line data (C) and TCGA (D). Each box shows the inter quartile range (IQR between Q1 and Q3) for the corresponding set. The central mark (horizontal line) shows the median and the whiskers show the rest of the distribution based on IQR [$Q1-1.5 \times IQR$, $Q3+1.5 \times IQR$]. Data outside of this range are considered outliers and represented by solid dots.



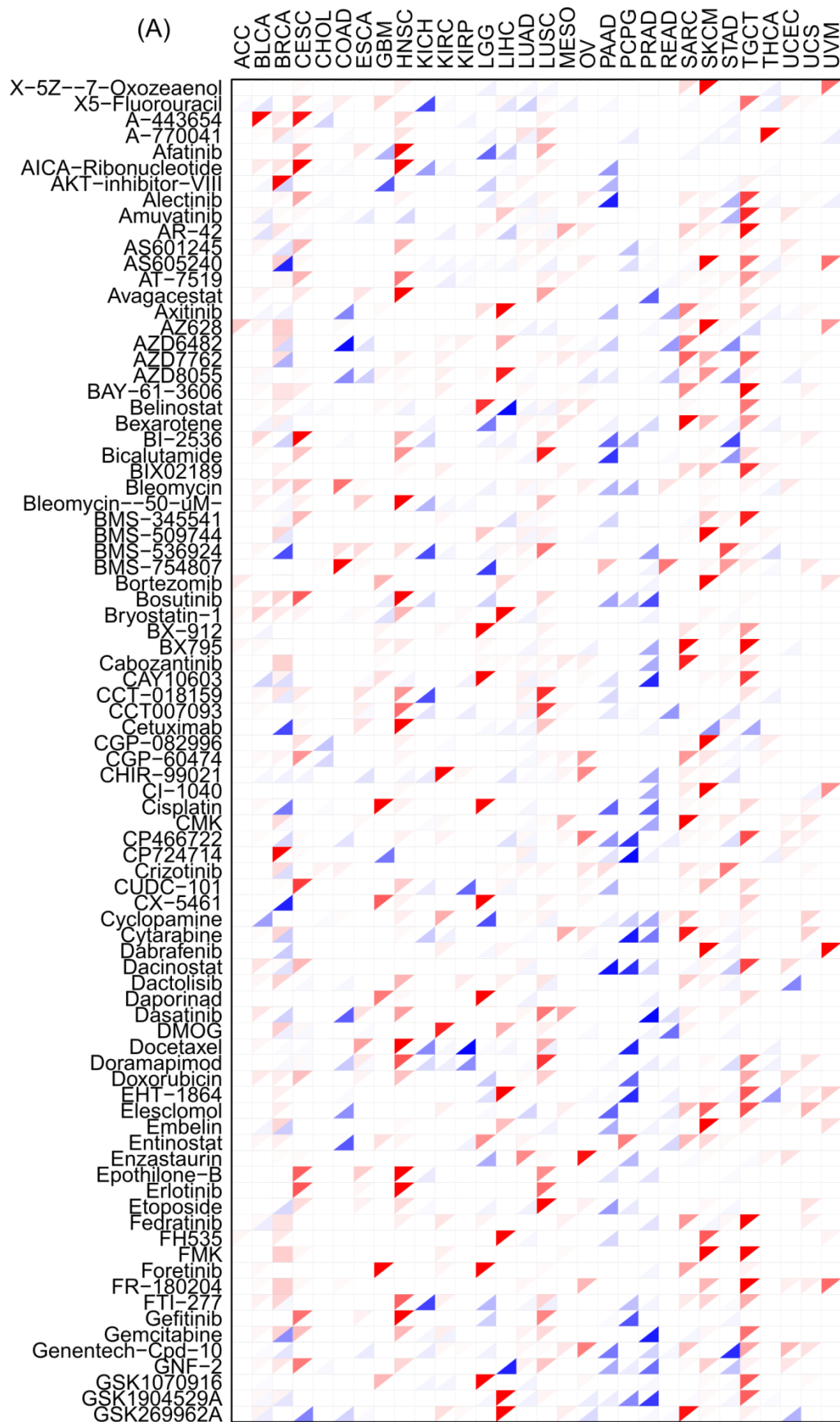


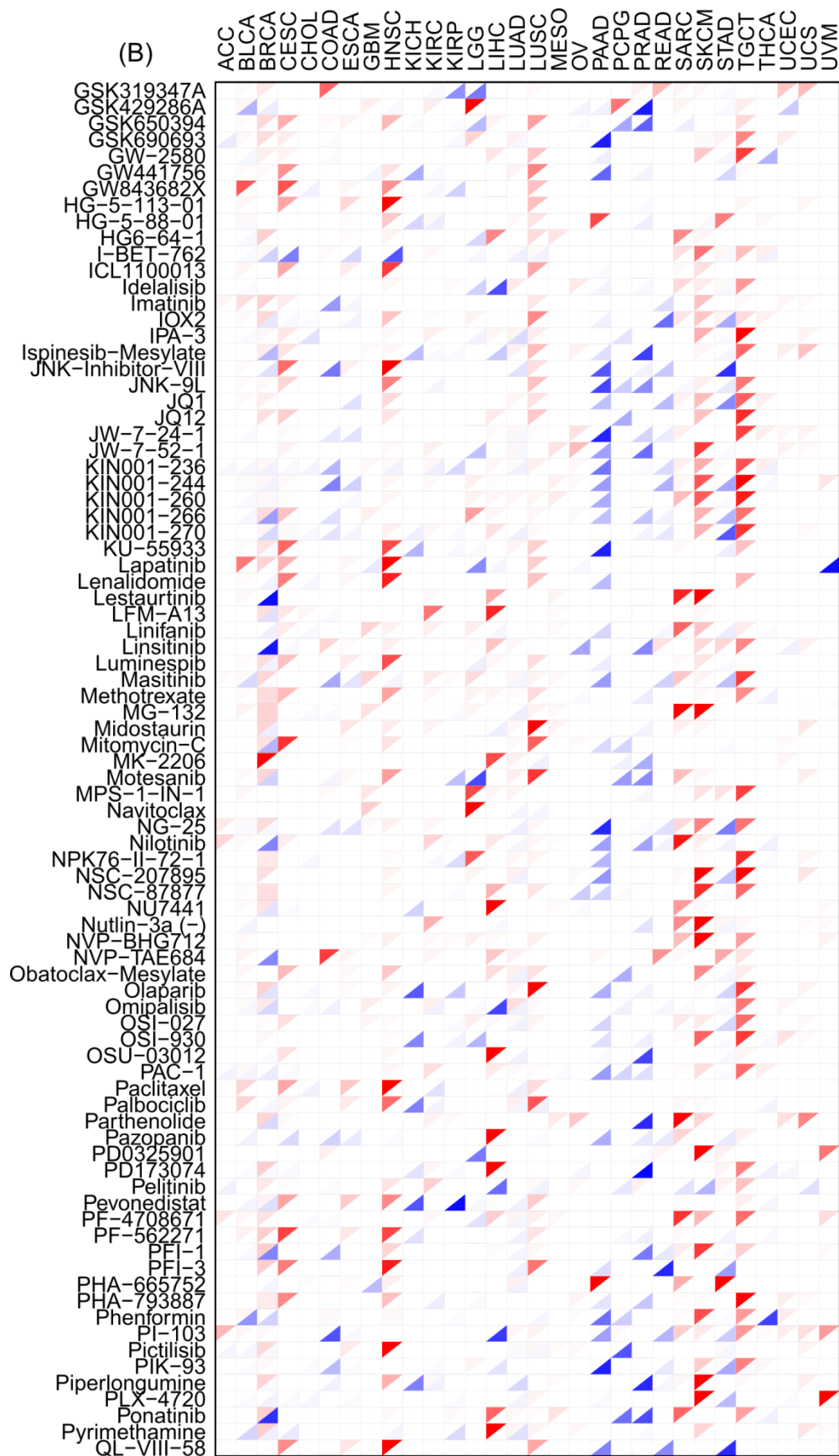
Supplementary Figure 5. Performance comparison for A-models and S-models. Dots in the circle shape: parameters from A-models; dots in the plus (+) shape: parameters from S-models. The dots in cyan: the best models from the A-model (circle) and the S-model (+) respectively. The black (red) dash eclipse: the 95 percent confidence interval of the A-models (S-models).

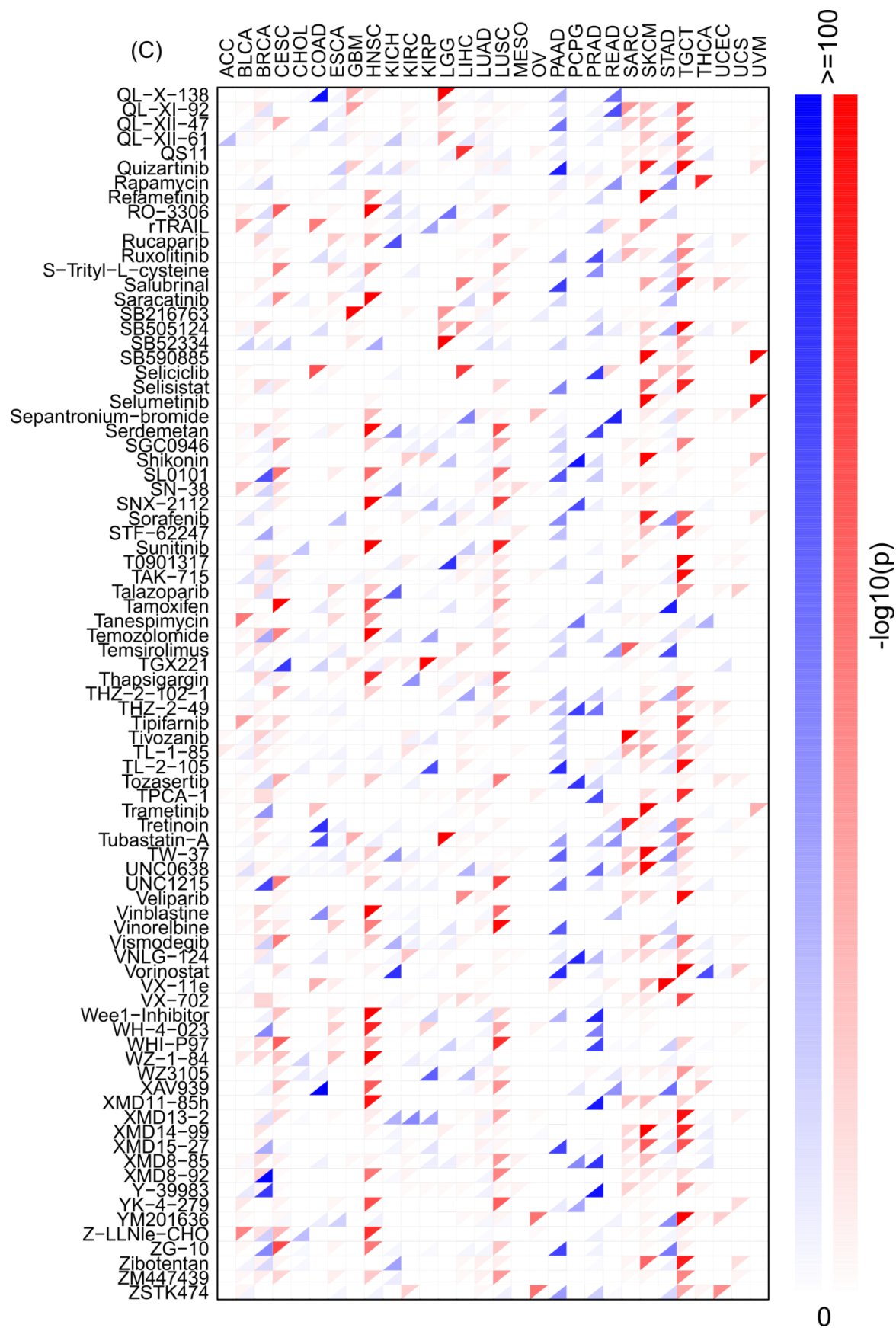




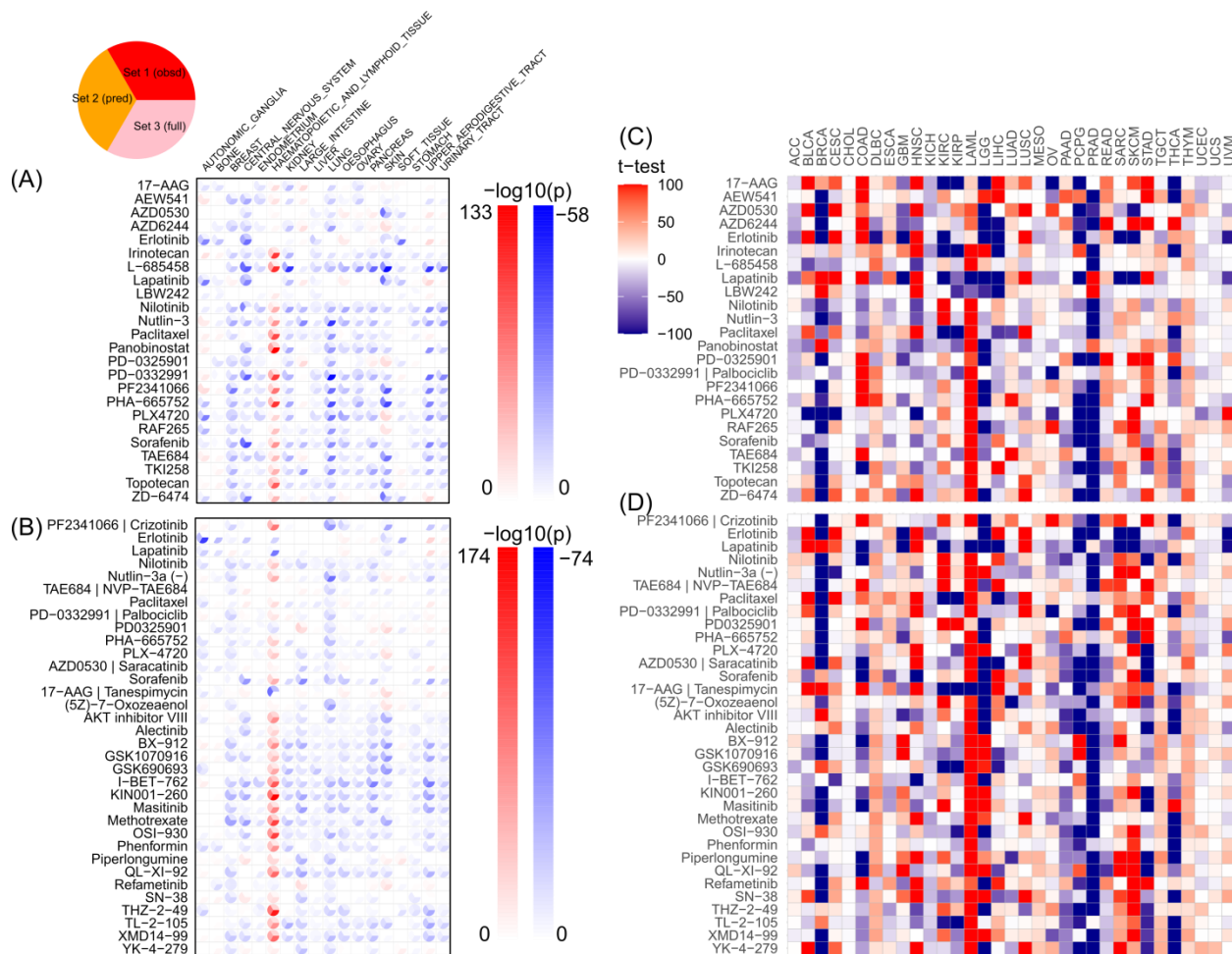
Supplementary Figure 7. Demonstration of the interaction effect between *BRAF* mutations and *EGFR* expression in three sets. In each panel, a regression function was fitted following $Y_{\text{response}} \sim X_{\text{BRAF}} + X_{\text{EGFR}} + X_{\text{BRAF}} \times X_{\text{EGFR}}$, where X_{BRAF} indicated whether a sample harbored a *BRAF* mutation (red: mutant; blue: wild type) and X_{EGFR} was a factor with three levels indicating group information of a sample defined by *EGFR* gene expression. We defined three groups according to *EGFR* gene expression (x-axis): the lower quarter (group 1), the middle half (group 2), and the higher quarter of samples (group 3). *P*-value for the interaction factor was shown in the title. The sample size for each group is annotated above the box. The *p*-value was obtained from the fitted regression model for the interaction effect $X_{\text{BRAF}} \times X_{\text{EGFR}}$. Each box shows the inter quartile range (IQR between Q1 and Q3) for the corresponding set. The central mark (horizontal line) shows the median and the whiskers show the rest of the distribution based on IQR [Q1-1.5×IQR, Q3+1.5×IQR].







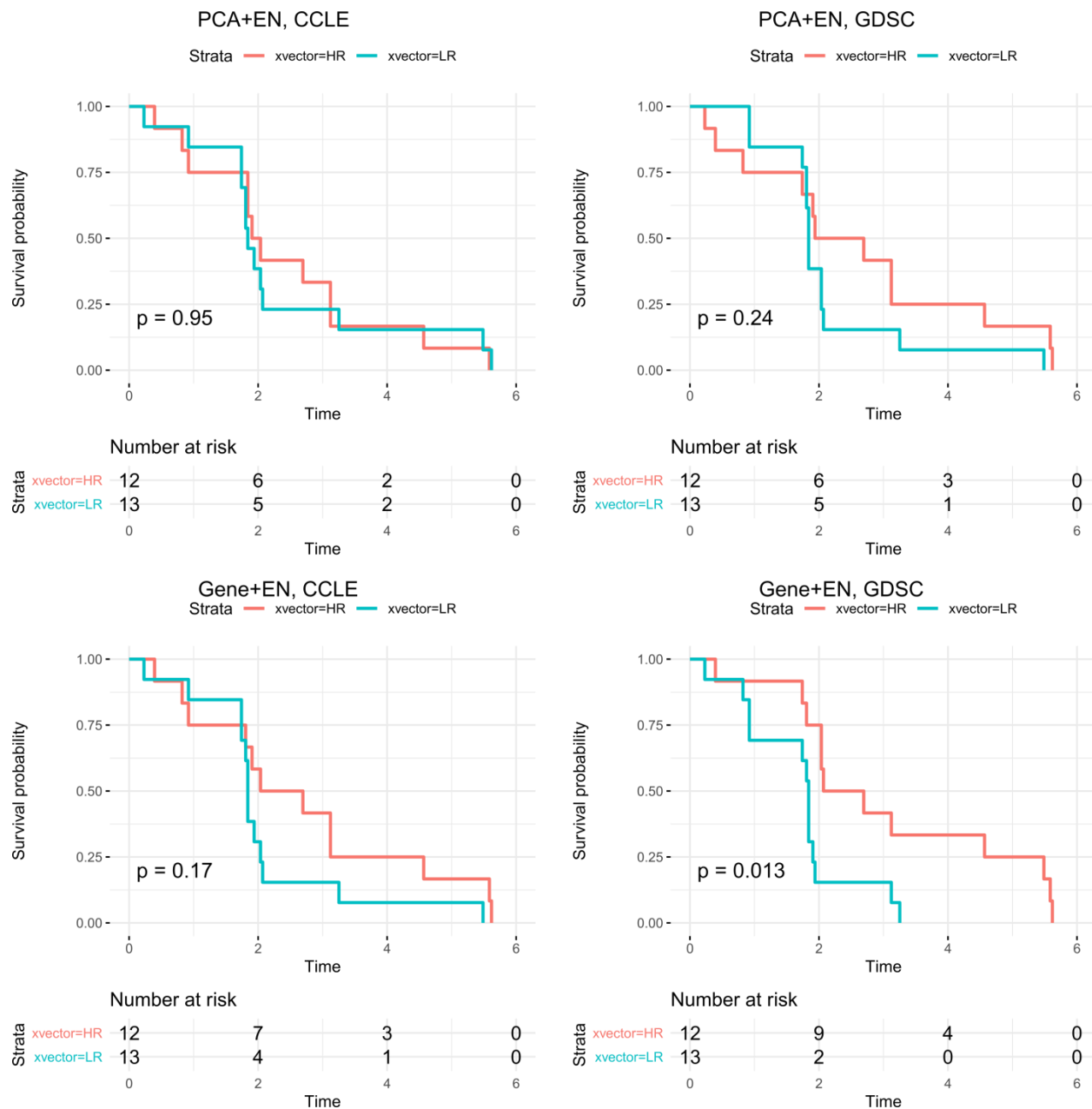
Supplementary Figure 8. Enrichment test results of the sensitive or insensitive samples in each of the 30 cancer types (excluding 3 immune related cancer: DLBC, LAML, and THYM) using 251 GDSC drugs. For each cell, the top left triangle shows the sensitive trend (in red) and the bottom right triangle shows the insensitive trend (in blue), with the color proportional to the p -value. The p -value was similarly calculated as explained in Figure 3C.



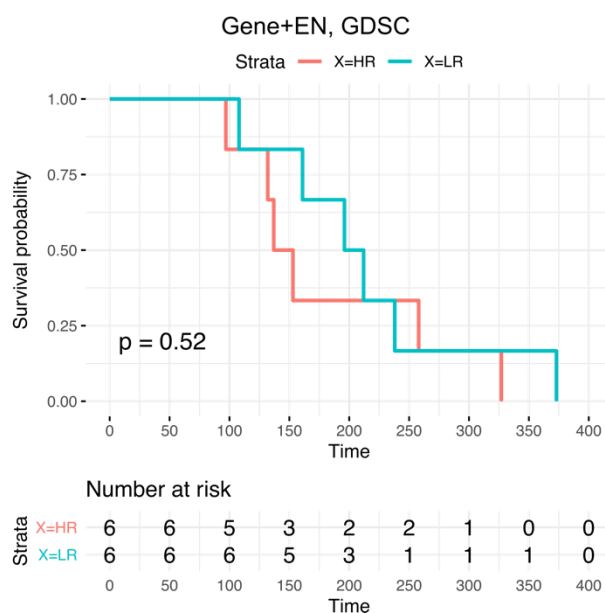
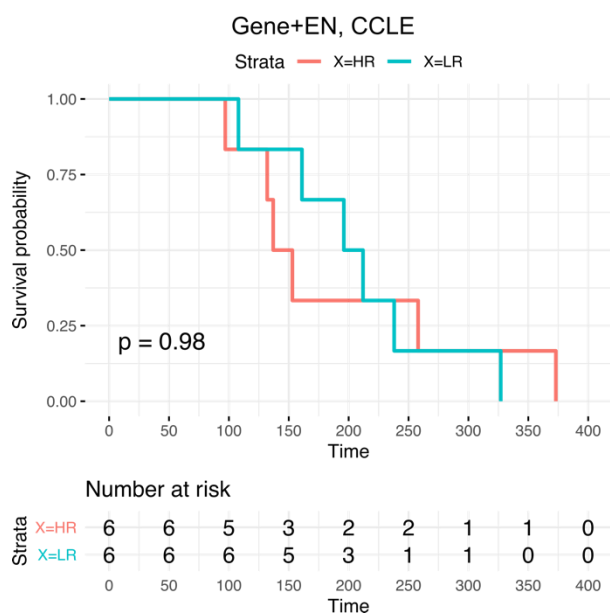
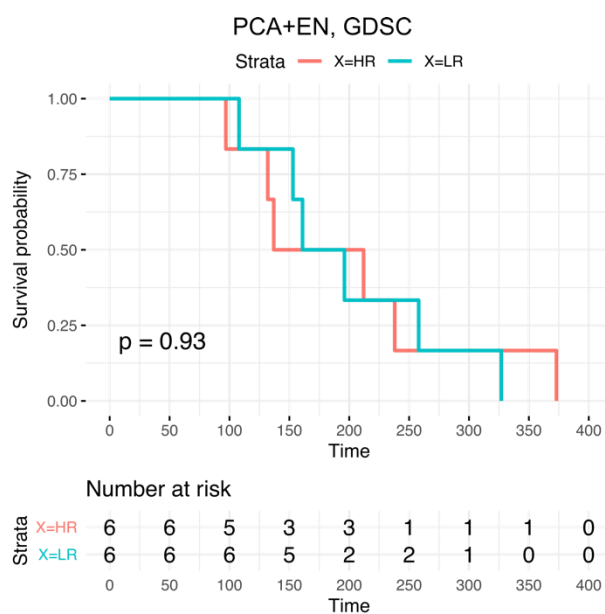
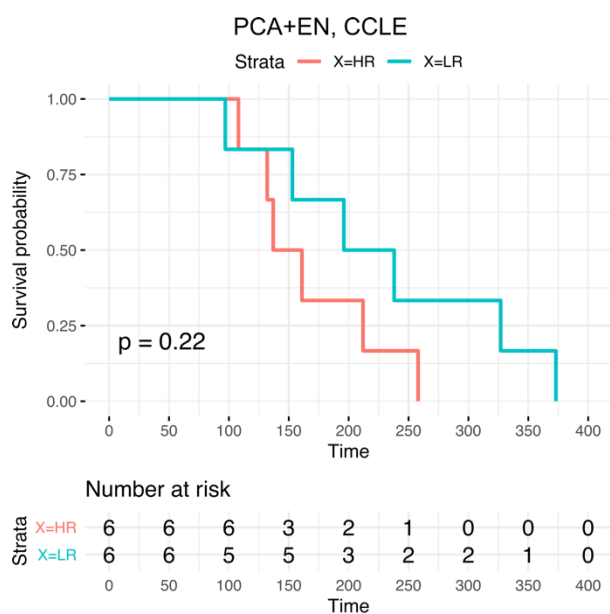
CCLE, catenated

UCEC, KRAS	0.00033	0.95	0.14	0.0011	0.0018	0.94	0.63	0.017	0.17	0.85	0.47	0.83	0.77	0.0058	0.042	1	0.66	0.12	1	0.97	0.96	0.78	1	0.95
THCA, NRAS	1	0.99	0.43	0.23	1	1	0.99	0.75	0.91	0.64	1	0.79	0.98	0.77	1	1	0.99	1	0.42	0.38	1	0.37	0.98	1
THCA, HRAS	0.87	1	0.38	0.035	1	1	1	0.48	0.59	0.87	0.99	0.81	0.98	0.69	1	1	0.99	0.99	0.7	0.68	1	0.68	0.97	0.96
THCA, BRAF	1	0.82	0.023	0.8	1.7e-06	2.1e-05	1	1	2.4e-08	1	0.079	1	1	6e-04	0.94	2.6e-06	0.54	0.94	7.3e-17	0.21	1e-23	1	0.049	0.15
STAD, KRAS	0.00036	1	0.41	0.019	0.083	0.47	1	0.78	0.99	0.94	0.99	1	1	0.0015	0.91	0.01	0.49	1	3.8e-05	0.6	0.4	0.57	0.55	0.95
SKCM, NRAS	0.0043	0.19	0.23	0.00047	0.64	0.36	0.94	0.42	0.7	0.59	0.94	0.96	0.52	0.00012	0.92	0.18	0.97	0.66	0.00019	0.37	0.18	0.84	0.69	0.71
SKCM, BRAF	1.9e-05	0.48	0.87	0.00067	0.83	0.43	0.63	0.55	0.24	0.35	0.2	0.5	0.15	0.0014	0.53	0.1	0.11	0.11	0.0011	0.13	0.041	0.44	0.015	0.99
READ, NRAS	0.24	0.88	0.71	0.66	0.28	0.23	0.71	0.91	0.88	0.8	0.89	0.84	0.65	0.29	0.62	0.8	0.69	0.88	0.43	0.32	0.64	0.88	0.65	0.85
READ, KRAS	0.55	0.98	0.62	0.79	0.49	0.96	0.99	0.99	0.97	0.99	0.97	0.92	0.99	0.66	0.98	1	0.97	0.75	0.18	0.8	0.99	0.87	1	0.78
PCPG, HRAS	8.8e-05	0.83	1	0.2	1	1.1e-07	0.025	1	0.4	0.39	0.077	0.0022	0.087	0.26	0.00051	0.56	0.21	0.27	0.64	0.14	0.79	0.034	0.0038	0.99
PAAD, KRAS	2e-10	0.99	2.3e-06	1.7e-06	1.8e-08	0.93	1	3.3e-08	0.99	1	1	0.32	1	5.6e-07	0.98	3e-04	0.064	1	0.0052	1	0.0088	1	0.98	4.7e-06
LUAD, KRAS	0.017	0.99	0.0065	0.0025	0.22	0.99	0.99	0.0036	0.19	0.94	0.98	1	0.99	0.00071	0.71	0.84	1	0.29	0.99	1	0.3	1	1	0.93
LUAD, EGFR	0.95	0.98	7.6e-05	9e-07	0.046	0.69	0.94	0.53	0.027	0.85	0.59	0.96	0.97	5.8e-10	0.99	0.98	0.99	0.22	0.36	0.82	0.99	0.88	0.84	0.42
LAML, NRAS	0.0087	0.27	0.86	0.13	0.25	0.87	0.065	0.24	0.81	0.89	0.62	0.18	0.75	0.067	0.043	0.082	0.12	0.015	0.45	0.077	0.21	0.14	0.14	0.84
HNSC, HRAS	0.0016	0.82	0.014	0.014	0.99	0.00025	0.37	0.93	0.97	0.051	0.0019	0.0022	0.29	0.019	0.04	9e-05	0.038	5.2e-05	0.015	0.02	0.56	0.0059	0.01	0.91
COAD, KRAS	0.16	0.99	0.12	0.13	0.0029	0.87	0.98	0.99	1	0.65	0.74	0.95	0.97	0.035	0.92	0.92	0.56	0.25	0.00091	0.68	0.86	0.64	1	0.067
COAD, BRAF	0.047	1	0.99	0.96	0.99	0.62	0.27	0.28	0.11	0.32	0.019	0.65	0.056	0.98	0.65	0.47	0.00064	0.13	1.8e-07	0.0048	0.83	0.006	0.017	0.31
CESC, KRAS	0.83	0.16	0.001	0.0012	1	1	0.95	0.83	0.99	1	0.93	1	0.11	0.003	0.092	0.41	0.19	0.98	0.92	0.98	0.11	0.99	0.99	0.81
BLCA, KRAS	0.048	0.29	0.16	0.04	0.99	0.74	0.29	0.99	0.96	0.17	0.16	0.44	0.64	0.024	0.29	0.031	0.76	0.092	0.072	0.18	0.029	0.18	0.56	1
BLCA, HRAS	0.27	0.41	0.0015	0.022	0.012	0.54	0.98	0.12	0.18	0.95	0.99	0.039	0.97	0.01	0.81	0.92	0.87	0.14	0.42	0.92	0.84	0.95	0.93	0.21
	X17.AAG	AEW541	AZD0530	AZD6244	Erlotinib	Irinotecan	L.685458	Lapatinib	LBW242	Nilotinib	Nutlin-3	Paclitaxel	Panobinostat	PD.0325901	PD.032391	PF2341066	PHA.665752	PLX4720	RAF265	Sorafenib	TAE684	TKI258	Topotecan	ZD.6474

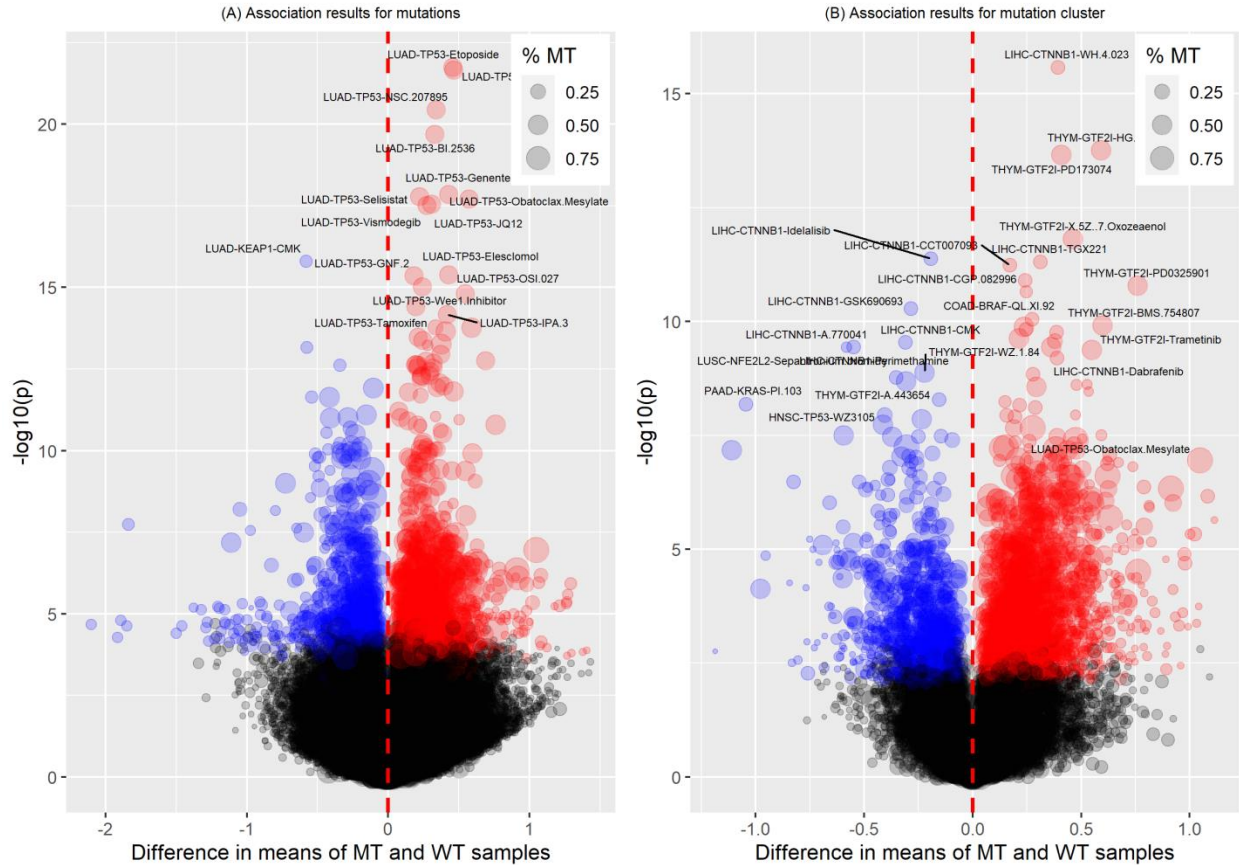
Supplementary Figure 10. Association of *BRAF* (V600E), *EGFR* (positions 719, 746, 858, and 861), and Ras genes (positions 12, 13, and 61) with 24 CCLE drugs. The *p*-value was obtained by a one-sided *t*-test to compare the samples with the corresponding mutations and the samples with pan-negative mutations in all five genes (*BRAF*, *KRAS*, *HRAS*, *NRAS*, and *EGFR*). The alternative hypothesis was that the mutant samples had higher response than the pan-negative samples. The mutant group were required to have more than 10 samples.



Supplementary Figure 11. Survival analysis results using the PCA+EN or gene+EN models for GSE33072: NSCLC samples were treated with Erlotinib, an EGFR inhibitor. The *p*-values were from a log-rank test comparing two groups of samples defined by the predicted response to Erlotinib (HR: high response, greater than the median; LR: low response).



Supplementary Figure 12. Survival analyses using the PCA+EN or gene+EN models for GSE65186 samples who were treated with vemurafenib. We stratified these samples by predicted response to PLX4720, a BRAF inhibitor. HR: high response. LR: low response. The p -values were from a log-rank test comparing the HR group and the LR group.



Supplementary Figure 13. Association of somatic mutations with drug response (GDSC). (A) Volcano plot of drug-gene association. Each dot represents the statistics of the association status of a gene in a cancer type with a drug. The p -value was obtained from a two-sided Wilcoxon test comparing the predicted response in samples with the mutant gene (i.e., those with deleterious missense SNVs or nonsense SNVs) and samples with the wild type gene. The former group was required to have ≥ 10 samples. X-axis: difference of the average drug response in the samples harboring the mutated gene (MT) from that in the wild type (WT) samples. Y-axis: $-\log_{10}(p)$ where the unadjusted p -value was used for plotting. Red (difference > 0) and blue (difference < 0) dots indicate significant associations (BH-adjusted $p < 0.05$). The size of the dots is proportional to the percentage of MT samples. (B) Volcano plot of the associations between drugs and mutation clusters in genes. Each dot represents the statistics of the association status of a mutation cluster in a gene with a drug in a cancer type. The p -value was obtained from a two-sided Wilcoxon test comparing the predicted response in samples with mutations located in the cluster of the gene and samples with the wild type gene. The former group was required to have ≥ 10 samples. X-axis: difference of the average drug response in the samples harboring cluster mutations (MT) from that in the wild samples (WT). Y-axis: $-\log_{10}(p)$ where the unadjusted p -value was used for plotting. Red (difference > 0) and blue (difference < 0) dots indicate significant associations (BH-adjusted $p < 0.05$).