TITLE	Refitting? Eq? corr bw new and old?	Metric type
Inconsistency in large pharmacogenomic studies (Dec 2013)	No (used reported IC50)	Spearman r for $IC50_{CCLE-GDSC}$ and $AUC_{CCLE-GDSC}$, $gene\text{-}exp_{CCLE-GDSC}$ Cohen's kappa (k) coefficient for sensitivity $calls_{CCLE-GDSC}$ and mutaion $data_{CCLE-GDSC}$
Pharmacogenomic agreement between two cancer cell line data sets (Dec 2015)	No (used reported IC50 after capping at max dosage tested)	Pearson r
Assessment of pharmacogenomic agreement (9 may, 2016)	no	Pearson r
Reproducible pharmacogenomic profiling of cancer cell line panels (19 may 2016)	yes 4-parameter log-logistic model	%age agreement for sensitivity calls on mean viabilty (equivalent to area under the log-dose/response curve)
Integrating heterogeneous drug sensitivity data from cancer pharmacogenomic studies (June 2016)	Yes Log-logistic regression	Pearson and Spearman correlations on IC50, EC50 and adjusted and non adjusted AUC

Drug response consistency in CCLE and CGP (Dec 2016)	No (IC50 re-calculated *for shared dose range)*	Pearson r for m and AUC (shared log-dose range)+ Binary sensitivity calls + SVM(m and AUC as predictors) (tr on 1, te on another and vice-versa) Cohen's kappa (k) for sensitivity calls$_{CCLE-GDSC}$
Revisiting inconsistency in large pharmacogenomic studies (Aug 17)	yes (spearman r>0.93 bw old n new) (IC50 truncated to the maximum concentration used for each drug)	ABC Pearson, Spearman, and Somers' Dxy rank correlation coefficients to quantify the consistency of (AUC-published, AUC-recomputed, AUC*, IC50-published, IC50-recomputed) DXY,; MCC, CRAMERV:,INFORM: Informedness for discretized sensitivity
Genetic and transcriptional evolution alters cancer cell line drug response (Aug 2018)	yes 4-parameter log-logistic function	Spearman drug response distance (ED bw dr res profiles-viabilities) expression distance (ED bw 978 landmark genes) SNV dist: jaccard

Metric values (best achieved)	wise cor/analysis	respo nse score	Inconsistency source
DRUG RESPONSE * median r=0.28 for $IC50_{CCLE\_GDSC}$, median r=0.35 for $AUC_{CCLE-GDSC}$ * BEST:17AAG: r=0.61 for $IC50_{CCLE-GDSC}$, 0.58 for $AUC_{CCLE-GDSC}$ k <0.5 for sensitivity $calls_{CCLE-GDSC}$ (obtained from waterfall) GENE EXPRESSION & MUTATION median r=0.85 for $gene\text{-}exp_{CCLE-GDSC}$ BEST: the urinary tract (median r=0.87) median k=0.65 for $mutation_{CCLE-GDSC}$	yes	No	*pharmacological assay used *therange of drug concentrations tested, and * choice of an estimator for summarizing the drug dose–response curve.
DRUG RESPONSE *BEST: Nilotinib: r=0.89 for $IC50_{CCLE-GDSC}$, 0.75 for $AUC_{CCLE-GDSC}$ Majority compounds has r>0.5 due to which authors say datasets have reasonable consistency Lapatinib: k = 0.65 for sensitivity $calls_{CCLE-GDSC}$ only 40% of drugs had a κ≥0.4,	yes	no	*Paucity of drug-sensitive cell lines in the overlapping set *No of CLs seeded per well, drug conc range , no of cell doubling achieved, cel viability assays, way of calculating sensitivity value *Intrinsic technical and biological noise of pharmacological assays *cannot be attributed solely to the use of different experimental protocol BCZ: authors analyzed the replicated experiments performed by the GDSC using identical protocols to screen camptothecin (pcc r=0.57) and AZD6482 (pcc
…	…	no	
PD0325901: gCSI-CCLE %age areement=96% Lapatinib: gCSI-GDSC %age agreement=98% (GDSC seems to have selected very few cell lines sensitive to erlotinib and lapatinib)	yes	no	assay type, cell seeding density, and growth media.
r for adjusted $AUC_{CCLE-GDSC}$ = 0.69 D-WISE Nilotinib: pearsn r =0.87, spearman r=0.22] adjusted $AUC_{CCLE-GDSC}$ 17-AAG: pearson r=0.64, spearman r=0.64]adjusted $AUCC_{CLE-GDSC}$ Nilotinib: pearsn r =0.63, spearman r=0.20] $AUC_{CCLE-GDSC}$ 17-AAG: pearson r=0.41, spearman r=0.49] $AUC_{CCLE-GDSC}$	yes	Adjust	*most drugs with very low correlation show no or low activity in the proliferation assay * intrinsic noise of the high-throughput screening

DRUG RESPONSE r=0.52 for $m_{CCLE-GDSC}$, r=0.61 for $AUC_{CCLE-GDSC}$ k=0.53 for … (obtained from manual curation) k=0.55 for…(obtained from SVM prediction) overall r=0.69 for $IC50_{CCLE-GDSC}$ only for pairs determined to be sensitive by atleast 1 dataset by SVM Dwise: Best r=0.55 for NVP-TAE684 only for pairs determined to be sensitive by atleast 1 dataset by SVM	no (reports ic50 corr Dwise)		* information loss associated with collapsing a two-dimensional continuous description of drug sensitivity onto a single binary variable. * the different viability assays used, as well as inescapable confounding factors such as cell confluency, clonal variations, genomic drift, different drug suppliers/batches, laboratories/equipment and serum composition.
IC50 All CLs: Nilotinib: pearson r=0.75, spearman r=0.30, somer=0.98]using IC50-published Nilotinib: pearson r=0.92, spearman r=0.30, somer= --]using IC50-recomputed Sensitive (some) Nilotinib: pearson r=0.61, spearman r=0.40, somer=0.45]using IC50-published Nilotinib: pearson r=0.88, spearman r=,0.63 somer= --]using IC50-recomputed	yes	no	* nature of targeted therapies, which are expected to have selective activity against some cell lines * substantial differences in doses used for each drug and in the methods used to both assay cell viability and to estimate drug response parameters.(showed higher consistency is achieved when the same pharmacological assay is used (GSK and CCLE used the CellTiter-Glo assay, while GDSC used Syto60)]
r between drug response distance and expression distance=0.45 r between drug response distance and SNV distance=0.47 see ext fig 11j	no	no	Inconsistencies in drug response studies may be attributed to * genetic variation (. For example, genetic inactivation of PTEN was associated with decreased PTEN and increased AKT expression signatures) *and transcriptomic variability (example, strains sensitive to CDK inhibitors had an upregulated cell cycle signature, and strains sensitive to PI3K inhibitors had an upregulated mTOR signature (Fig. 4f–g and

Combining	Extra info?
no	
	(If sensitivity is limited to a small subset of cell lines, Spearman correlations will be dominated by stochastic values from the many insensitive lines
no	*only one drug (nilotinib) passes the threshold for consistency. *only 40% of drugs had a κ≥0.4, * Used older (2012) release of data [outdated ic50s and missed ~400 pairs]
no	* gCSI data (used CTG) agreed less well with GDSC than with CCLE. * SENSITIVITY CALLS: For targeted agents expected to inhibit only a few lines, fit two-component mixture distributions to assign 'sensitive', 'no-call' or 'resistant' labels
considers AUC at shared dosage	* uses 3 datasets: CCLE, GDSC, CTRP * compared its peason corr with Haibe's spearman, its spearman itself is bad

suggests removing potentially suspect dose–response data, doing so in future efforts could further facilitate data usability.	
no	CONCLUSION: 2 broad eff drugs(PD-0325901 and 17-AAG using spearman r on AUC~0.6) and 3 targeted (Nilo, crizo, PLX using pearson using pearson r on AUC*~0.8) are consistent SIMILAR OBSERVATIONS: Eliminating the insensitive cell lines resulted in decreased consistency for most drugs, which suggests a high level of inconsistency across sensitive cell lines
no	*mutations with AF(allelic fraction)>0.05. *landamrk genes considered *drug response profiles were vaibility values for each pair (only active drugs considered for finding euclidean dist) The high degree of variability in drug response cannot be explained by irreproducibility of the assay.

Limitation

Uses ic50 reported by CCLE and GDSC
GDSC extrapolates ic50 estimated from curve fitting
and CCLE reported max concentration tested for inactive drugs; due to which ic50 values are inconsistent.
Eg: Fig 2 shows Tanespimycin (17AAG) and PD0325901 as medium correlation drugs; others as low correlation
drugs (which is NOT TRUE: the corr is observed to be low bcz of the fact stated above).

correlation since most drugs are inactive (correct way should be extrapolating both). Explanation:
* Case 1: DW (ic50< max dosage) => no capping=> no change in correlation for such drugs (eg: Paclitaxel and 17-AAG/tanespimycin, PD0325901).
* Case 2: DNW (ic50>max dosage)=> ic50 capped=> corr should improve since new capped values of ic50 in gdsc are same as the ccle ic50 values which are also capped to same value in ccle
* Case 3: DW on high dosage (ic50 > gdsc max dosage but < ccle max dosage)=> cor should degrade as extrapolated ic50 values are actually the correct estimate and new values are probably greater than the corresponding ccle ic50 estimate.
Eg: Sorafenib, Erlotinib

…

* omitted unclassified lines or those exhibiting
intermediate response;
*For broadly active compounds, lines divided into the three response categories in equal proportion.

* uses shared dose range to find auc and slope!
loss of info, does not solve the inconsistency problem, may give better corr
* Does Not work for DNW cases (corr is low)

* m and AUC calculated on shared-log dose range separately for each dataset separately;
loss of info, does not solve the inconsistency problem, may give better corr
* Manual curation of sensitivity is not scalable;on new large datasets such as CTRP and GDSC1000

* ABC taken over the intersection of the dose range (then normalized by length of common interval) [loss of info, does not solve the inconsistency problem,]..used it to identify similar drugs using clustering * Filtered out curves which didn't have viability between 0-100% and is not monotonically non-increasing * discretized drug sensitivity values by selecting a common arbitrary threshold ->used AUC ≤ 0.2 (IC50 ≥ 1 μM) and AUC ≤ 0.4 (IC50 ≥ 10 μM) to identify the "insensitive" cell lines for targeted and cytotoxic drugs, respectively,				