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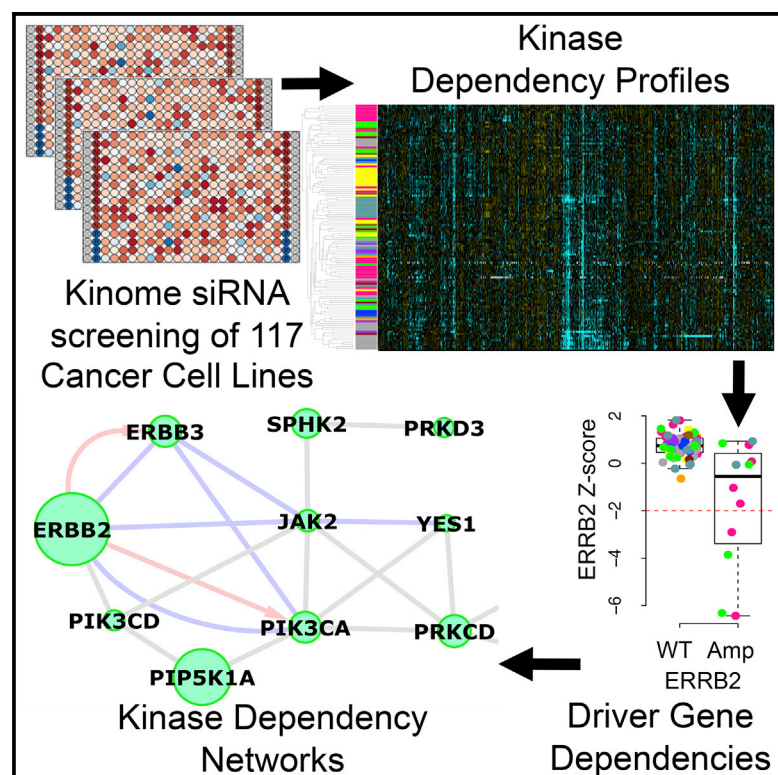
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Large-Scale Profiling of Kinase Dependencies in Cancer Cell Lines

Graphical Abstract



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In Brief

Campbell et al. use parallel siRNA screens to identify the kinase dependencies of 117 cancer cell lines from ten cancer types. They use this resource to identify kinase dependencies associated with specific cancer types or driver genes and show that the integration of protein interaction networks facilitates the interpretation of these dependencies.

Highlights

- Kinome-wide (714 gene) siRNA screens in 117 cell lines from ten cancer histotypes
- Integrating genotype data reveals cancer driver gene dependencies
- Integrating protein interaction data aids the interpretation of genetic dependencies
- Identified dependencies enable prediction of mutant cell line responses to drugs



Large-Scale Profiling of Kinase Dependencies in Cancer Cell Lines

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SUMMARY

One approach to identifying cancer-specific vulnerabilities and therapeutic targets is to profile genetic dependencies in cancer cell lines. Here, we describe data from a series of siRNA screens that identify the kinase genetic dependencies in 117 cancer cell lines from ten cancer types. By integrating the siRNA screen data with molecular profiling data, including exome sequencing data, we show how vulnerabilities/genetic dependencies that are associated with mutations in specific cancer driver genes can be identified. By integrating additional data sets into this analysis, including protein-protein interaction data, we also demonstrate that the genetic dependencies associated with many cancer driver genes form dense connections on functional interaction networks. We demonstrate the utility of this resource by using it to predict the drug sensitivity of genetically or histologically defined subsets of tumor cell lines, including an increased sensitivity of osteosarcoma cell lines to FGFR inhibitors and SMAD4 mutant tumor cells to mitotic inhibitors.

INTRODUCTION

The phenotypic and genetic changes that occur during tumorigenesis alter the set of genes upon which cells are dependent. The best known example of this phenomenon of “genetic dependency” is oncogene addiction where tumor cells become dependent upon the activity of a single oncogene, which when inhibited leads to cancer cell death. Alternatively, tumor cells can become addicted to the activity of genes other than

oncogenes, effects known as non-oncogene addictions (Luo et al., 2009), induced essential effects (Tischler et al., 2008), or synthetic lethal interactions (Kaelin, 2005). From a clinical perspective, identifying genetic dependencies in tumor cells could illuminate vulnerabilities that might be translated into therapeutic approaches to treat the disease. Examples of this approach include the development of drugs that target oncogene addiction effects, such as imatinib in the case of *ABL* addiction, and therapeutic approaches that exploit synthetic lethal effects, such as PARP inhibitors for *BRCA*-deficient cancers (Lord et al., 2015).

A number of groups have used high-throughput screening approaches such as RNAi or small molecule sensitivity screens to systematically identify genetic dependencies in tumor cell lines (Barretina et al., 2012; Brough et al., 2011; Cowley et al., 2014; Garnett et al., 2012; Koh et al., 2012). A particular focus has been in dissecting genetic dependencies that involve kinases (Brough et al., 2011; Grueneberg et al., 2008), as these enzymes play key roles in a number of oncogenic processes (Greenman et al., 2007) and are pharmacologically tractable (Sakharkar and Sakharkar, 2007; Workman and Al-Lazikani, 2013; Zhang et al., 2009). Previously, we used high-throughput short interfering (si)RNA screening to identify the kinase dependencies in a panel of 20 breast cancer derived cell lines (Brough et al., 2011). Here, we describe as a resource an expansion of this approach, namely parallel siRNA screens targeting 714 genes in 117 genetically and histologically diverse tumor cell lines. Building on our previous work (Brough et al., 2011), we extend our analytical approach to describe how this data set may be used as a hypothesis-generating tool for identifying candidate therapeutic targets associated with specific tumor histotypes or mutations in cancer driver genes. We also illustrate how, by integrating this functional data with orthogonal data sources such as protein-protein interaction data sets, these genetic dependencies might be dissected mechanistically.

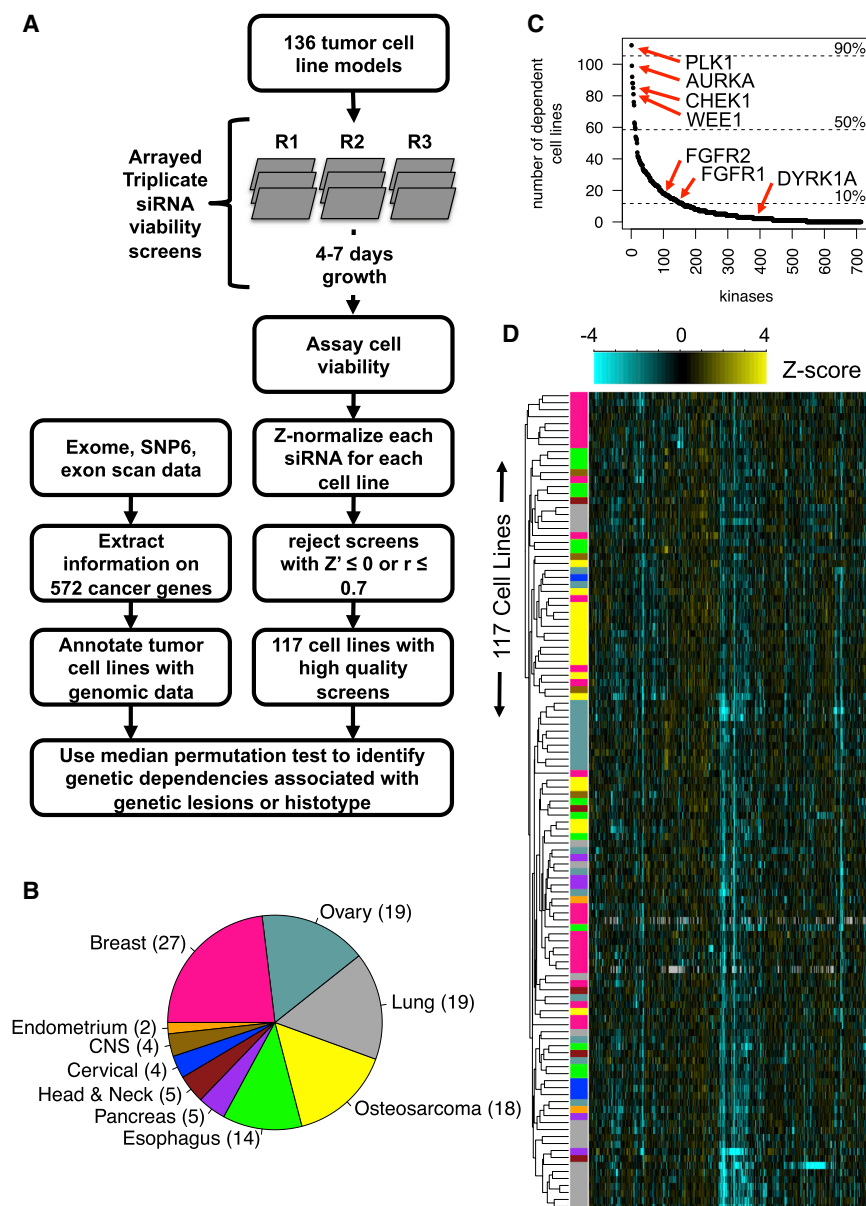


Figure 1. Screening Overview

(A) Schematic of siRNA screening, data processing, and genomic data integration.

(B) Piechart illustrating histotypes for 117 cell lines that passed QC (CNS).

(C) Frequency plot depicting the number of cell lines in which each kinase siRNA caused a significant growth defect ($Z \leq -2$).

(D) Clustered heatmap summarizing the KGDs of 117 cell lines. The average linkage hierarchical clustering was used with Pearson's correlation as the similarity metric. Only the 20% most variable siRNA Z scores were used for the calculation of correlations. The histotype of each cell line is indicated by the color blocks to the left of the heatmap and corresponds to the scheme shown in (B).

fluency (on average 4-7 days), at which point cell viability was assessed using the CellTiter-Glo assay. Following data processing and the application of quality control filters to ensure the reproducibility and high dynamic range of each screen (see [Supplemental Information](#); [Figure 1A](#); [Table S1A](#)), we retained 117 high quality screens for further analysis. The resulting resource ([Table S1B](#)) features tumor cell line models from ten different cancer types (breast, ovarian, lung, osteosarcoma, esophageal, pancreatic, head, and neck, cervical, CNS, and endometroid; [Figure 1B](#)), and includes data for 69 lines not profiled in prior large-scale RNAi screens ([Brough et al., 2011](#); [Cowley et al., 2014](#); [Koh et al., 2012](#)).

To allow data to be compared between different cell lines, the viability data from each screen were standardized by the use of a robust Z score statistic ([Table S1B](#)). We considered candidate kinase genetic dependencies (KGDs) in the data set as those where the siRNA elicited $Z < -2$ effects. 76% of the kinases pro-

filed in the screening library represented KGDs in at least one tumor cell model. Additionally, 53% and 26% represented KGDs in ≥ 5 and ≥ 10 cell lines, respectively ([Figure 1C](#) and [Table S1C](#)). On average, each tumor cell line model exhibited 51 KGDs. A set of six kinase-coding genes (*PLK1*, *AURKA*, *WEE1*, *CHEK1*, *CDK11A*, and *GUCY2D*) represented KGDs in $>70\%$ of the cell lines screened and four of these (*PLK1*, *AURKA*, *WEE1*, and *CHEK1*) are known to be involved in the mitotic cell-cycle -checkpoint.

Candidate KGDs Associated with Tumor Histotypes

Using average linkage hierarchical clustering to cluster the siRNA Z score data ([Figure 1D](#)), we found that tumor cell lines frequently clustered according to tumor histotype. For example,

RESULTS

Kinase Genetic Dependencies Identified by Parallel siRNA Screens

We screened a panel of 136 tumor cell lines in triplicate in a plate-arrayed format using an siRNA library designed to target 714 genes (see [Experimental Procedures](#) and [Figure 1A](#)). The genes targeted with this library included 500 protein kinases ([Manning et al., 2002](#)), with the remaining targets comprising metabolic kinases (e.g., ATP-dependent 6-phosphofructokinases), lipid kinases (e.g., PIK3C2A), as well as proteins that lack kinase activity, but directly impact kinase signaling (e.g., the cyclin dependent kinase inhibitor CDKN1C). Cells were reverse transfected with siRNA and then cultured until cells reached 70% con-

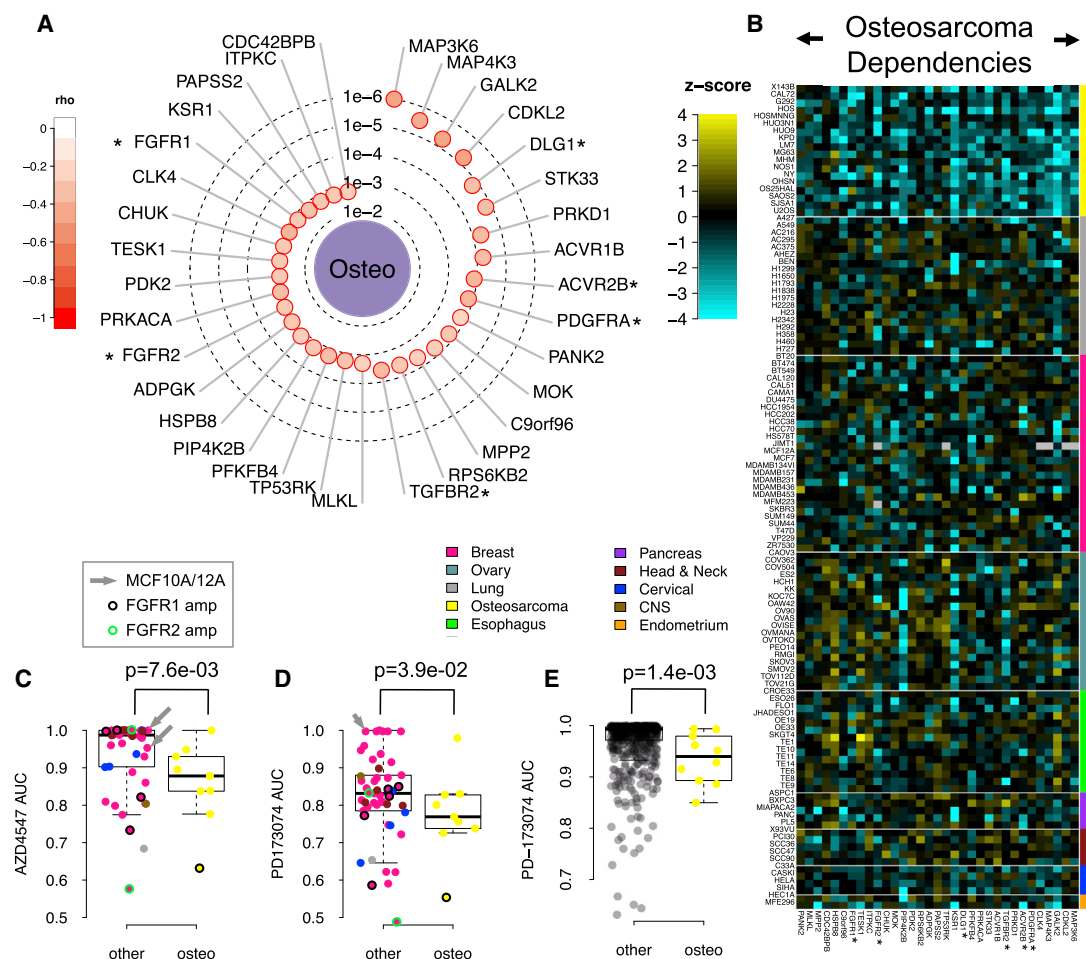


Figure 2. Kinase Dependencies Associated with Histotypes

(A) Radar plot summarizing the KGDs associated with the osteosarcoma histotype. The concentric circles indicate the statistical significance and the depth of color indicates the separation of Z scores between the osteosarcoma histotype and the non-osteosarcoma group of cell lines. A set of six kinases annotated as involved in skeletal system morphogenesis in the Gene Ontology are annotated with asterisks.

(B) Heatmap of KGDs enriched in osteosarcoma cell lines are shown as a heatmap representing siRNA Z scores. The asterisks indicate kinases involved in skeletal system morphogenesis as in (A).

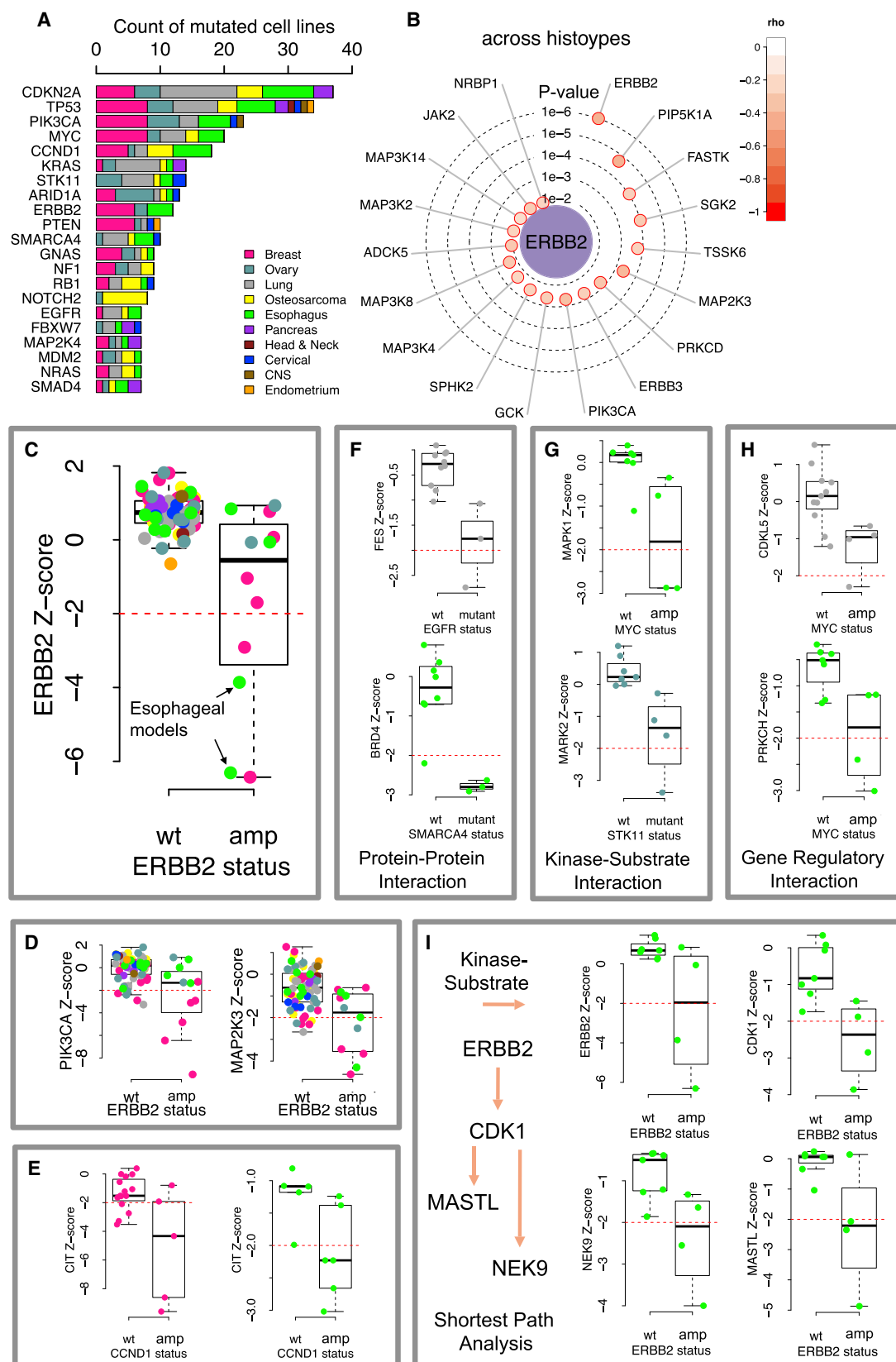
(C and D) Box plots of area under curve (AUC) estimates for 58 cell lines exposed to the FGFR inhibitor AZD4547 (C) and PD173074 (D) at eight different concentrations. *FGFR1* and *FGFR2*-amplified cell lines are indicated with black and green circles, respectively. The non-tumor epithelial cell lines MCF10A and MCF12A are indicated with gray arrows.

(E) Box plot of AUC estimates for a panel of cell lines exposed to the FGFR inhibitor PD173074 (Garnett et al., 2012).

In each box plot (C–E), the top and bottom of the box represents the third and first quartiles and the box band represents the median (second quartile); whiskers extend to 1.5 times the interquartile distance from the box. See also Figures S1 and S2.

the majority of ovarian cancer cell lines formed a single cluster, as did those models derived from osteosarcomas (Figure 1D). Using median permutation (MP) tests on the Z score data, we found 151 KGDs associated with specific histotypes at a false discovery rate (FDR) of 0.1 (Table S1D). As expected, the number of KGDs associated with each histotype was correlated with the number of cell lines screened for that histotype (Spearman's $\rho = 0.82$), reflecting the increased statistical power resulting from a larger sample size. In breast cancer models, we found an increased requirement for *ERBB3* and *PIK3CA*, members of the *ERBB2* and *PI3*-kinase signaling pathways that are frequently dysregulated in this cancer histology (Miller et al.,

2011). In contrast, models of osteosarcoma were more reliant upon genes involved in “skeletal system morphogenesis”, including *PDGFRA*, *ACVR2B*, *TGFBR2*, *DLG1*, *FGFR1*, and *FGFR2* (Su et al., 2008) (Gene Ontology enrichment $p < 0.001$ after correcting for multiple hypothesis testing, Berriz et al., 2009; Figures 2A and 2B). The *FGFR1* and *FGFR2* KGDs suggested that osteosarcoma models might be especially sensitive to small molecule FGFR inhibitors. Testing a set of 58 tumor cell lines for FGFR inhibitor sensitivity, we found AZD4547 (Gavine et al., 2012) and PD173074 (Bansal et al., 2003) to be more selective for osteosarcoma models (AZD4547, $p = 7.6 \times 10^{-3}$, PD173074 $p = 3.9 \times 10^{-2}$; Figures 2C and 2D; Table S1E) and



(legend on next page)

to have minimal effects in two non-tumor epithelial models (Figure S1). This osteosarcoma selective effect was independent of *FGFR1* or *FGFR2* amplification status and was also apparent when *FGFR1* or *FGFR2* amplified tumor cell lines were excluded from the analysis (AZD4572, $p = 7.2 \times 10^{-3}$ and PD173074, $p = 4.3 \times 10^{-2}$; Figures 2C and 2D). Furthermore, the osteosarcoma selective nature of PD173074 was confirmed by a reanalysis of PD173074 sensitivity data derived from 660 tumor cell lines (Garnett et al., 2012) (Figure 2E; $p = 1.4 \times 10^{-3}$). Taken together, these results suggested that FGFR inhibitors might show some utility in osteosarcoma, but that factors in addition to *FGFR1* and *FGFR2* amplification might explain drug sensitivity in this setting.

We also assessed the possibility that KGDs could be identified that were associated with specific subtypes of cancer. We, and others, have previously used RNAi data to identify KGDs associated with distinct breast cancer subtypes (Brough et al., 2011; Marcotte et al., 2012). To illustrate the utility of the expanded data set described here, we used MP tests to identify KGDs associated with the clear cell subtype of ovarian cancer (OCC). We found three kinases (*CAMK2N1*, *GRK2*, and *MAP3K9*) to be KGDs in OCC models, compared to other ovarian cancer histologies such as serous ovarian cancer (Figure S2; Table S1F).

Candidate KGDs Associated with Driver Gene Alterations

By integrating the siRNA data with exome sequencing (Forbes et al., 2015) and copy number profiling data (Barretina et al., 2012), we identified KGDs associated with mutations in each of 200 candidate cancer driver genes (see Supplemental Information; Table S1G). We identified 4,247 putative dependencies associated with driver gene mutations (uncorrected MP test $p \leq 0.05$; Table S1H). As the large number of tests performed using these 200 driver genes prohibited correction for multiple hypothesis testing, we focused our subsequent analysis on 21 key cancer driver genes (12 tumor suppressor genes and nine oncogenes; Futreal et al., 2004; Vogelstein et al., 2013) (Figure 3A) mutated in at least seven tumor cell lines in our panel. This identified 211 KGDs at an FDR of 0.5 (Table S1I) that could form the basis for subsequent validation experiments.

This approach reconfirmed the well-established *ERBB2* oncogene addiction in models of breast cancer, but also established *ERBB2* addiction/KGD in models of esophageal cancer (Figures 3B and 3C), where *ERBB2* is recurrently amplified/over-expressed in 20% of tumors (Bang et al., 2010). This suggested

that this particular genetic dependency was relatively independent of the underlying histotype. *ERBB2* amplification was also associated with dependency upon other members of the *ERBB2* signaling network including the *ERBB2* binding partner *ERBB3* ($p = 2 \times 10^{-3}$), *JAK2* ($p = 1 \times 10^{-2}$), and the downstream effector of *ERBB2*, *PIK3CA* ($p = 4 \times 10^{-3}$; Figure 3D). We found other KGDs associated with *ERBB2* amplification, including a strong dependency upon the stress response kinase *MEK3* (*MAP2K3*, $p = 4 \times 10^{-4}$; Figure 3D) (Dérjard et al., 1995) and *PIP5K1A* ($p = 2 \times 10^{-5}$), a kinase involved in inositol phosphate metabolism (Loijens and Anderson, 1996).

We assessed the possibility that some KGDs associated with cancer driver gene mutations might be private to or more profound in particular histotypes. For example, *BRAF* p.V600E mutant melanomas are extremely sensitive to *BRAF* inhibition, whereas colorectal cancers with the same mutation show little response (Prahallad et al., 2012). We used a similar analysis as above to identify KGDs associated with driver gene mutations within particular histotypes and identified 943 KGDs (Tables S1J and S1K), compared to 211 in the prior analysis that combined all histotypes. Together, these 1,154 candidate dependencies could inform the design of subsequent validation studies. As an example of this, we selected for validation one of the KGDs associated with *RB1* mutation in osteosarcoma (Kansara et al., 2014), *DYRK1A* ($p = 6.8 \times 10^{-3}$; Figure S3A), a component of the DREAM complex (Sadasivam and DeCaprio, 2013) previously identified as a protein interaction partner of *RB1* (Varjosalo et al., 2013). To confirm the dependency of *RB1* null osteosarcoma models upon *DYRK1A*, we selected 14 osteosarcoma models and characterized these according to their *RB1* mutation and protein expression status and established that multiple distinct *DYRK1A* siRNAs could replicate the *RB1* selectivity observed in the initial screen as well as eliciting *DYRK1A* silencing (Figure S3). These results suggest that *DYRK1A* might represent a valid genetic dependency in *RB1* defective osteosarcoma cells.

We also noted from our analysis of the siRNA data that some genetic dependencies associated with cancer driver gene mutations were observed independently in multiple histotypes. These included KGDs associated with *ERBB2* amplification in breast and esophageal cancer models (e.g., *ERBB2* $p = 7.9 \times 10^{-5}$ [breast] and $p = 9.2 \times 10^{-3}$ [esophageal] and *MAP2K3* $p = 3.3 \times 10^{-2}$ [breast] and $p = 4.4 \times 10^{-3}$ [esophageal]; Figure S4A), but also a dependency upon the microtubule associated

Figure 3. KGDs Associated with Cancer Driver Mutations

(A) Bar chart indicating the frequency of driver gene alterations observed in the cell line panel. The colored segments in each bar indicate the histotypes in which alterations were detected.
(B) Radar plot summarizing the KGDs associated with *ERBB2* amplification (the scheme as per Figure 2A).
(C) Box plot showing the *ERBB2* Z scores for cell lines grouped according to *ERBB2* amplification status. The colors indicate cell line histotypes as in (A).
(D) Box plots showing additional KGDs associated with *ERBB2* amplification.
(E) Box plots summarizing *CCND1* KGDs upon *CIT*.
(F) Examples of KGDs that are supported by protein-protein interactions.
(G) Examples of KGDs that are supported by kinase-substrate relationships.
(H) Examples of KGDs that are supported by gene regulatory relationships.
(I) Examples of KGDs associated with *ERBB2* amplification status in esophageal cancer models supported by kinase-substrate relationships that form a shortest path between the mutated driver gene and kinases.
In each box plot (C–I), the top and bottom of the box represents the third and first quartiles and the box band represents the median (second quartile); whiskers extend to 1.5 times the interquartile distance from the box. See also Figures S3 and S4 and Tables S1I and S1K.

serine/threonine kinase *MAST1* in *CCND1* amplified breast or esophageal cancer models ($p = 1.1 \times 10^{-2}$ [breast] and $p = 1.3 \times 10^{-2}$ [esophageal]; Figure S3B). Likewise, a KGD upon Citron Rho-interacting kinase (*CIT*), a regulator of cytokinesis (Madaule et al., 1998) was also seen in *CCND1* amplified breast or esophageal cancer models ($p = 2. \times 10^{-3}$ [breast], $p = 2.6 \times 10^{-3}$ [esophageal]; Figure 3E). In both osteosarcoma ($p = 1.4 \times 10^{-3}$) and lung cancer models ($p = 3.5 \times 10^{-2}$; Figure S1C), we identified an association between mutation/deletion of *CDKN2A* and dependency upon the cyclin dependent kinase gene *CDK11A*, which encodes a CDKN2A interacting protein (Varjosalo et al., 2013). In total, we identified 63 kinase dependencies associated with driver gene mutation status that were observed independently in more than one histotype (Table S1K).

Integrating Data on Protein-Protein and Regulatory Interactions Facilitates the Interpretation of Genetic Dependencies

The set of KGDs associated with cancer driver gene alterations can be used to frame testable hypotheses, such as “mutation in gene *A* drives dependency upon a gene *B*.” However, without further information, there are a number of potential mechanistic explanations for each genetic dependency. In model organisms, the problem of interpreting such dependencies has been addressed by integrating information from protein-protein (Beyer et al., 2007) and kinase-substrate interaction databases (Fiedler et al., 2009). To facilitate a mechanistic understanding of KGDs and to provide additional guidance for the design of subsequent experiments, we annotated our list of KGDs according to whether they involved known protein-protein interactions (Chatr-Aryamontri et al., 2015; Das and Yu, 2012), known kinase-substrate relationships (Lachmann and Ma’ayan, 2009), or known regulatory relationships (Cerami et al., 2011) between the driver gene and the identified dependency (see Experimental Procedures). Doing this, we found 113 KGDs involved pairs of genes with a previously reported functional relationship between the mutated driver gene and kinase target (Tables S1I and S1K). For example, mutation/amplification of *EGFR* in lung cancer cell lines was associated with an increased dependency upon *FES* ($p = 3 \times 10^{-2}$; Figure 3F), previously identified as an *EGFR* binding partner (Jones et al., 2006). Similarly, in esophageal cancer models, we identified a significant association between mutation of the chromatin remodeling factor gene *SMARCA4* and dependency upon the bromodomain protein *BRD4* ($p = 6 \times 10^{-3}$; Figure 3F), previously identified as a protein interaction partner of *SMARCA4* (Rahman et al., 2011). Among the dependencies associated with a kinase-substrate interaction, we found that mutation of *STK11* (*LKB1*) in ovarian cancer models was associated with an increased dependency upon *MARK2* ($p = 2 \times 10^{-3}$; Figure 3G), an *LKB1* substrate (Lizcano et al., 2004). Similarly, we found that *MYC* (*cMYC*) amplified esophageal models had an increased dependency upon *MAPK1* (ERK-2, $p = 1.2 \times 10^{-2}$; Figure 3G), which is known to phosphorylate and stabilize the cMYC protein (Sears et al., 2000). We also identified a series of dependencies between cancer driver genes and their transcriptional targets, the majority of which focused upon *MYC*. In lung cancer models, we found that *MYC* amplification was associated with an increased dependency upon *CDKL5* (5.6×10^{-3} ; Fig-

ure 3H), a gene whose expression is regulated by *MYC*. Similarly, in esophageal models, we found *MYC* amplification to be associated with an increased dependency upon the *MYC* transcriptional target *PRKCH* (Zeller et al., 2006) ($p = 6.7 \times 10^{-3}$; Figure 3H).

For KGDs where a direct relationship between the driver gene and the kinase was not known, we used a simple information-flow type analysis to identify the shortest known molecular paths between driver gene and the kinase dependency (Tables S1I and S1K). For example, one of the strongest dependencies identified across all histotypes was between *STK11* and *SRP72* (Figure S4C). We found no evidence of a direct relationship between the two genes, but found that *STK11* has been shown to regulate the expression of *MYC* (Nath-Sain and Marignani, 2009), which in turn has been shown to regulate *SRP72* (Zeller et al., 2006), suggesting a putative path linking the driver gene and the kinase dependency. In esophageal cancer models, we found that *ERBB2* amplification is associated with *MASTL* (Voets and Wolthuis, 2010) and *NEK9* (Belham et al., 2003) KGDs (Figure 3I). We found no direct link between *ERBB2* and either of these kinases, but both are CDK1 substrates and CDK1 itself is an *ERBB2* substrate. In this instance, all members of the path (*ERBB2*/*CDK1*/*NEK9*/*MASTL*) were identified as *ERBB2* dependencies. In total, 163 dependencies not supported by a direct link could be reached by adding one intermediate connection (e.g., CDK1 is an intermediate connection between *ERBB2* and *NEK9*).

Pathway and Network Level KGDs

Work in model organisms has shown that a genetic mutation often results in an increased dependency on not just one gene, but multiple genes involved in a specific pathway or complex (Collins et al., 2007; Kelley and Ideker, 2005; Ryan et al., 2012). To explore the utility of this concept in interpreting our KGD data, we mapped the nominally significant KGDs ($p \leq 0.05$) identified for each cancer driver gene across all histotypes onto the high-confidence STRING functional interaction network (Franceschini et al., 2013) (see Experimental Procedures). For 11 of the 21 driver genes analyzed (*KRAS*, *ERBB2*, *CCND1*, *PIK3CA*, *SMAD4*, *NOTCH2*, *ARID1A*, *NF1*, *FBXW7*, *MAP2K4*, and *RB1*), we found that the dependencies associated with each driver gene were significantly more connected on the STRING interaction network than would be expected by chance (see Experimental Procedures; Figure S5; Table S1L). This suggested that these 11 driver genes might induce dependencies not just on individual genes, but on functional subnetworks. For two of these networks, we added known protein-protein and kinase-substrate interaction data to aid their interpretation. In the case of the network associated with *ERBB2* amplification, this suggested that *ERBB2* amplification might induce dependencies on direct binding partners and substrates of *ERBB2* (*JAK2*, *ERBB3*, and *PIK3CA*), but also a network of genes involved in MAPK signaling (e.g., *MAP2K3*, *MAP3K4*, and *MAP3K2*) and inositol phosphate metabolism (including *PIP5K1A*, *PIK3CA*, and *PIK3CD*) (Figure 4A). Similarly, we found significantly more functional interactions among the kinases identified as dependencies associated with mutation of the tumor suppressor *SMAD4*, a member of the TGF- β pathway that

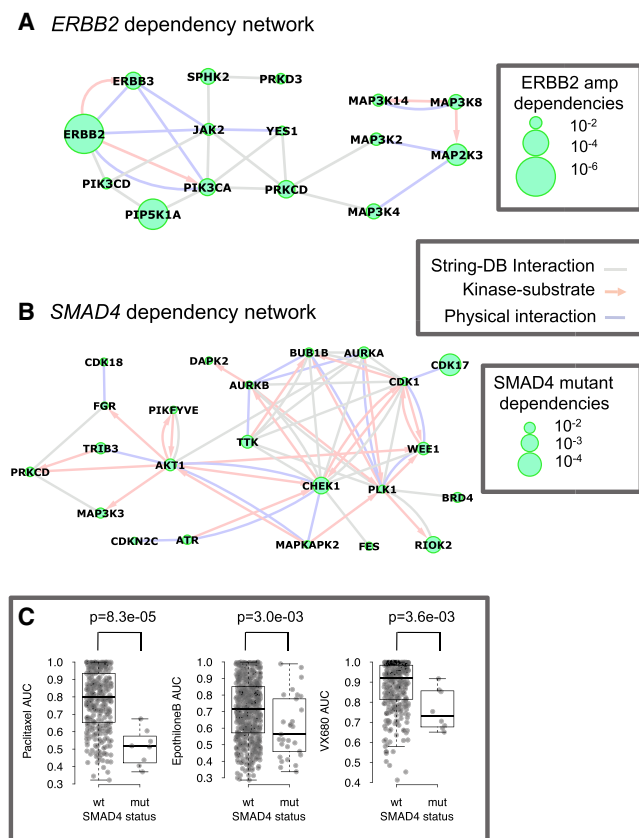


Figure 4. Driver Gene KGDs and Functional Interaction Networks

(A) Functional interaction network showing interactions between *ERBB2* amplification-associated KGDs. The nodes correspond to kinases that are identified as KGDs in *ERBB2* amplified cell lines. The nodes are scaled to indicate the significance of the KGD association p value. The blue edges correspond to experimentally determined protein-protein interactions, the pink arrows indicate the direction of experimentally determined kinase-substrate interactions, and the gray edges reflect high-confidence STRING functional interactions. Only KGDs that interact with at least one other *ERBB2* dependency are shown.

(B) Functional interaction network showing interactions among KGDs identified in *SMAD4* mutated cancer cell lines. Details as for *ERBB2* network in (A).

(C) Box plot showing AUC values of a panel of cell lines exposed to compounds targeting microtubules (paclitaxel and etoposide B) or Aurora Kinases (VX680) and classified into *SMAD4* mutant or wild-type groups. The top and bottom of the box represents the third and first quartiles and the box band represents the median (second quartile); whiskers extend to 1.5 times the interquartile distance from the box.

See also Figure S5 and Table S1L.

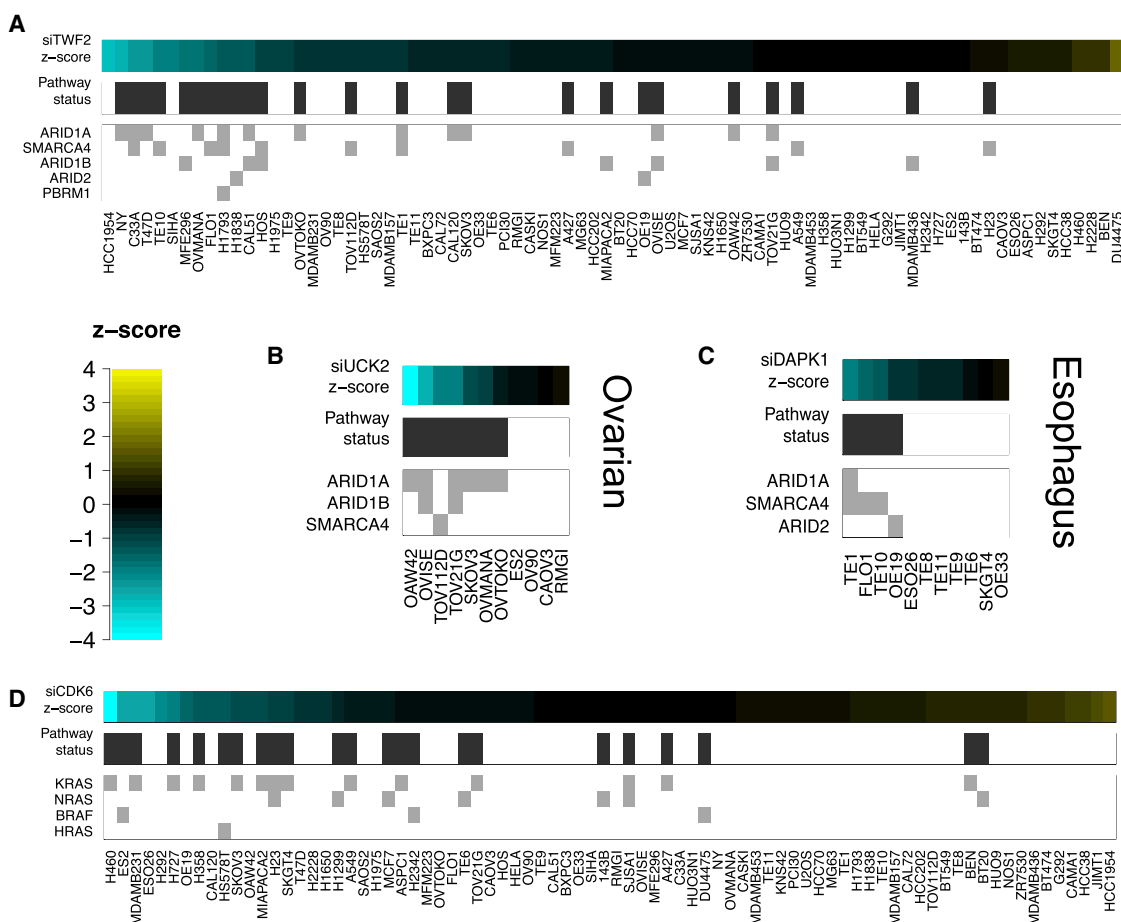
is frequently mutated or homozygously deleted in colorectal (Thiagalingam et al., 1996), pancreatic (Hahn et al., 1996), and esophageal (Dulak et al., 2013) cancers (Figure 4B). The integrated network we constructed from *SMAD4* KGDs revealed that *AKT1* and a number of its substrates (*FGR*, *MAP3K3*, *PIKFYVE*, *CHEK1*, and *WEE1*) were *SMAD4* mutation associated KGDs. Consistent with this, loss of *SMAD4* has been shown to be associated with increased AKT activation in colorectal and pancreatic tumor cell lines (Chen et al., 2014; Zhang et al., 2014). Furthermore, a recent large-scale drug screen identified

SMAD4 as the only driver gene significantly associated with sensitivity to A-443654, a pan-AKT inhibitor (Garrett et al., 2012). In addition to *AKT1* and its substrates, we found a densely connected group of kinases that regulate the mitotic cell cycle in the *SMAD4* dependency network (Figure 4B), suggesting that *SMAD4* mutant tumor cell lines may have an increased sensitivity to perturbation of this process. To test this hypothesis, we analyzed a compendium of drug sensitivity profiles (Garrett et al., 2012) and found that *SMAD4* mutant cell lines have increased sensitivity to the Aurora Kinase inhibitor VX-680 (Harrington et al., 2004) ($p = 4 \times 10^{-3}$; Figure 4C). Furthermore, we found that *SMAD4* mutant cell lines also exhibited an increased sensitivity to the mitotic inhibitors paclitaxel ($p = 8.3 \times 10^{-5}$) and epothilone B ($p = 3 \times 10^{-3}$; Figure 4C), suggesting a general sensitivity to drugs that target the mitotic checkpoint.

We present the functional interaction networks for the dependencies associated with each driver gene in Figure S5 and Table S1L. In addition to aiding the interpretation of dependencies, these subnetworks may be useful in alleviating some of the problems associated with false-positive effects in high-throughput genetic screens. Although there is a possibility of any given dependency being the result of off-target siRNA effects (Jackson and Linsley, 2010), the likelihood of an entire pathway being identified through off-target effects is likely to be much lower.

In the examples described above, we used the siRNA data to identify KGDs associated with defects in individual driver genes. Although there are hundreds of reported driver genes in cancer, some of these can be grouped into a small number of recurrently altered pathways (Garraway and Lander, 2013). Furthermore, it is possible that mutation in any member of such a pathway might have similar phenotypic effects. With this in mind, we considered whether we could identify candidate “pathway level” dependencies by grouping tumor cell lines according to mutations in any one of a set of driver genes belonging to the same pathway or complex. We obtained a previously curated list of pathways associated with driver gene mutations (Garraway and Lander, 2013) and manually updated this using literature information on well-established pathways (e.g., homologous recombination). For each pathway, tumor cell lines were grouped using a logical OR argument, i.e., if a cell line possessed a functional mutation of any gene member of the pathway then that cell line was considered mutated in that pathway. This resulted in a set of 15 pathway groupings (Table S1M) that were perturbed in at least seven tumor cell lines. Associating pathway mutations with KGDs was then performed in the same way as for individual genes using the MP test approach. This resulted in the identification of an additional 338 dependencies across all histotypes (Table S1N) and 748 histotype-specific dependencies (Table S1O).

As with individual driver genes, we found that the mutation of pathways was often associated with dependencies that were densely connected on the STRING functional interaction network. Indeed, using the dependencies identified across all histotypes, we found that nine of the 15 pathways (HR, PRC2, PI3K signaling, Cell Cycle Oncogenes, Cell Cycle Merged, TOR Signaling, MAPK Signaling, TGF B Signaling, and RAS/RAF Signaling) were associated with dependencies that were more functionally connected than would be expected by chance.



models were combined as a group ($\rho = -0.43$). CDKs, including CDK6, have been identified by a number of groups as putative non-oncogene addictions for *KRAS* mutant cancers (Barbie et al., 2009; Puyol et al., 2010). Our results suggest that CDK6 might be a non-oncogene addiction not just for *KRAS* mutant models, but also for cell lines with any one of a variety of MAPK activating mutations (*NRAS*, *HRAS*, and *BRAF*). We tested this hypothesis using published drug screening results for a CDK4/6 inhibitor (PD0332991) in 628 cell lines (Garnett et al., 2012) and found a significant association between mutation of the MAPK pathway and sensitivity to this inhibitor ($p = 2.5 \times 10^{-3}$, Mann-Whitney U [MW U]-test). None of the individual members of this pathway showed as strong an association with this inhibitor (*KRAS* $p = 1.9 \times 10^{-1}$, *HRAS* $p = 5.8 \times 10^{-2}$, *NRAS* $p = 1.7 \times 10^{-2}$, *BRAF* $p = 2.8 \times 10^{-2}$, and MW U-test).

DISCUSSION

A key challenge in the study of cancer biology is to understand how driver mutations alter the cellular state to promote tumor progression and how these altered states may be exploited in the development of targeted therapeutic approaches to the disease (Yaffe, 2013). Here, we have used siRNA screening to quantitatively estimate the kinase requirements of tumor cell lines in an attempt to understand better the genetic dependencies present. By integrating our siRNA data with molecular and histotype classifications, we have identified KGDs associated with particular cancer histologies or the presence of particular driver gene mutations. By integrating the KGD data with additional sources of annotation, such as protein-protein interaction data, we have tried to exemplify how testable hypotheses can be framed to explain the associations between a biomarker, such as a driver gene mutation, and a kinase dependency. Our aim in providing this data and illustrating its potential utility is to present starting points for further work.

As with any large functional data set, it is important to point out where elements of the technology used might influence the interpretation of the data. In general, siRNA mediated gene silencing is transient, when compared to, for example, short hairpin (sh) RNA mediated RNAi. With this in mind, we used a relatively short cell culture period between transfection and cell viability assessment (a 4 to 7 day period). Nevertheless, we cannot predict whether longer-term cell culture or longer-term gene silencing might result in a somewhat different profile of genetic dependencies. Furthermore, we used an ATP-based assay of cell viability in the screens. Some modes of cell inhibition exist that might have been missed using this method. As with any high-throughput technique, siRNA screens also have inherent false-positive and false-negative effects. Addressing false positives is especially important given the well-documented off-target effects associated with RNAi reagents (Jackson and Linsley, 2010). Consequently, we recommend that subsequent work that builds on the dependencies we have identified encapsulates some form of orthogonal validation. Individual siRNAs designed to target a gene (as we have shown in the case of *DYRK1A* dependency in *RB1* null cell lines) or small molecule inhibitors (as we have shown for the FGFR sensitivity of osteosarcoma cell lines) might be used as a form of validation. Alternatively,

methods such as CRISPR-Cas9 mediated gene targeting (Sander and Joung, 2014) might be appropriate. We also note that like all genetic screen data sets, the negative predictive value of our data (i.e., the prediction that a particular genetic dependency does not exist) might be somewhat limited, given the transient and sometimes incomplete nature of gene silencing by siRNA.

In carrying out functional screens in cancer cell lines, we have tried to use some of the lessons learned from studies in model organisms to aid the interpretation of our identified dependencies. For example, integrating protein-protein interaction data with functional data (Figure 5) was an approach pioneered in the study of yeast genetic interaction screens (Beyer et al., 2007; Kelley and Ideker, 2005). Here, we have integrated this type of data to help frame testable hypotheses relating to the observed dependencies. A more sophisticated level of protein-protein interaction data for human tumor cell lines (Krogan et al., 2015) will undoubtedly enhance our ability to understand genetic dependencies. Similarly the availability of phosphoproteomic data for the cell lines in our panel may facilitate a more mechanistic reconstruction of the signaling networks active in each cell line. A number of approaches (e.g., So et al., 2015; Terfve and Saez-Rodriguez, 2012) have been developed to integrate siRNA or small molecule perturbations with time-course phosphoproteomics data sets to reconstruct signaling networks. Currently phosphoproteomic data for cancer cell line panels are relatively limited (e.g., Casado et al., 2013; Creixell et al., 2015), but as the overlap of cell lines covered by these phosphoproteomic resources and our siRNA resource increases there will be opportunities for the development of further integrative modeling approaches. Similarly, the increased availability of protein expression data sets (e.g., Lawrence et al., 2015; Moghaddas Gholami et al., 2013) may provide further opportunities for the development of additional integrative approaches.

Finally, to make our resource as useful to the community as possible, we have made all of the data described in this manuscript available (<https://cansar.icr.ac.uk/>), alongside the computational scripts used to integrate data (https://github.com/GeneFunctionTeam/cell_line_functional_annotation).

EXPERIMENTAL PROCEDURES

siRNA and Small Molecule Screening

Cell lines were transfected with a plate-arrayed siRNA library targeting 714 kinases and kinase-related genes (Dharmacon SMARTpools). Positive control (siPLK1) and multiple negative controls (siCON1 and siCON2; Dharmacon, catalog numbers D-001210-01-20 and D-001206-14-20) and AllStar (QIAGEN, catalog number 1027281) were included on every plate. 20 breast cancer models were screened in a 96-well-plate format while the remaining cell lines were screened in a 384-well-plate format (Table S1A). All screens were performed in triplicate. Cell viability was estimated as cells reached 70% confluency (normally 4–7 days after transfection) using a CellTiter-Glo assay (Promega). Data processing and quality control was performed using the cellHTS2 R package (Boutros et al., 2006). Further details, including small molecule sensitivity testing, are provided in the Supplemental Information.

Association Testing

To identify associations between specific features (histotype or driver gene mutation) and sensitivity to specific siRNAs, a one-sided MP test was used. For each siRNA, we compared the observed difference between the median

Z score of the interest group and the median Z score of the “other” group to that expected based on random permutation. There were one million random samples that were created with the same sample sizes as the interest and other groups and the difference in the medians of the two groups calculated, allowing an empirically determined p value to be calculated. Correction for multiple testing was performed using the Benjamini and Hochberg FDR (Benjamini and Hochberg, 1995) and only those at an FDR of 50% are reported. For all small molecule association tests, we used a one-sided MW U test on area under the dose response curve values.

Data Access

All siRNA Z score data can be found in Table S1B and also at <https://cansar.icr.ac.uk/>.

Data Integration

Data from HINT (Das and Yu, 2012), BioGRID version 3.4.128 (Chatr-Aryamontri et al., 2015), and KEA protein-protein interaction databases were used (Lachmann and Ma'ayan, 2009). Kinase-substrate interactions were obtained from KEA (Lachmann and Ma'ayan, 2009), PhosphoSitePlus (Hornbeck et al., 2015) and (Cheng et al., 2014). High confidence (combined score >0.7) functional interactions were obtained from the STRING database (Version 9.1; Franceschini et al., 2013). Gene expression relationships were obtained from Pathway Commons (Cerami et al., 2011). The shortest_path function in NetworkX (Hagberg et al., 2008) was also used. Further details are provided in the Supplemental Information.

ACCESSION NUMBERS

The accession number for the exome sequencing data of 11 ovarian cancer cell lines reported in this study is ENA: PRJEB9639.

SUPPLEMENTAL INFORMATION

Supplemental Information includes Supplemental Experimental Procedures, five figures, and one table and can be found with this article online at <http://dx.doi.org/10.1016/j.celrep.2016.02.023>.

AUTHOR CONTRIBUTIONS

C.J.L., A.A., C.J.R., and J.C. designed the experiments and wrote the manuscript. J.C. and C.J.R. performed statistical analyses and data integration. H.H., H.N.P., I.B., I.Y.C., J.F., R.B., R.M., R.R., S.C.-C., and S.P.-V. performed siRNA screens. C.T.W., H.H., H.N.P., and R.R. performed drug profiling. H.H. and R.B. performed protein quantitation. H.N.P. performed RT quantitative (q) PCR. A.G., J.C., and W.W. processed the siRNA and small molecule inhibitor screen data. J.T., B.A.-L., R.N., S.J.S., T.F., and D.A.Q. contributed materials, reagents, and analysis tools. A.A. and C.J.L. secured funding. All authors read and approved the final manuscript.

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