

Krzywinski and Cairo reply: We are in full agreement with the core of Katz's argument that "distortion," "embellishment," "concealment" and "unrepresentative displays" have no place in principled communication of scientific information¹. There is no controversy here—Katz extrapolates our storytelling metaphor beyond the intended scope of our column and argues against a position we did not take.

The Points of View series offers effective strategies for visual presentation of complex data. The scope of the Storytelling column² was limited to the construction of multipanel figures, which summarize as much as they support detailed exposition of the text. The column did not address how this text should be composed or the broad subject of motivation and design of scientific experiments. We described an approach to structure the flow of concepts and data across panels in a figure as a way to achieve a narrative, not confabulation.

The design of visual communication requires a distinct approach because we organize and interpret images very differently than words (Gestalt principles of perception³). Whereas text is a natural place for nuance and alternative interpretations, multiple lines of argument in a figure can easily interfere with our perception of all its parts. Our suggestion to "leave out detail that does not advance the plot" speaks to controlling the amount of information to avoid an incomprehensible image and deferring it to the text, where it can be more suitably framed. To interpret it as "inconvenient truths are [to be] swept away" is a misrepresentation.

Readers often look to the abstract and then the figures to provide them with an initial impression and overview of the findings. These are not the only elements that are reported, merely the first elements to be read. At each step, from abstract to figure to text, the level of detail is expanded to accommodate the preparedness of the reader to assimilate new information. It is often impossible to "do justice to experimental complexities and their myriad of interpretations" with a figure.

We support Katz's position that authors should include all the details necessary to appreciate, understand and reproduce the science through the use of visual and written communication that is clear, concise and thoughtful.

COMPETING FINANCIAL INTERESTS

The authors declare no competing financial interests.

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TCPA: a resource for cancer functional proteomics data

To the Editor: Functional proteomics represents a powerful approach to understand the pathophysiology and therapy of cancer. However, comprehensive cancer proteomic data have been relatively limited. As a part of The Cancer Genome Atlas (TCGA) Project and other efforts, we have generated protein expression

data over a large number of tumor and cell line samples using reverse-phase protein arrays (RPPAs). RPPA is a quantitative, antibody-based technology that can assess multiple protein markers in many samples in a cost-effective, sensitive and high-throughput manner^{1,2}. This technology has been extensively validated for both cell line and patient samples^{3–5}, and its applications range from building reproducible prognostic models⁶ to generating experimentally verified mechanistic insights⁷.

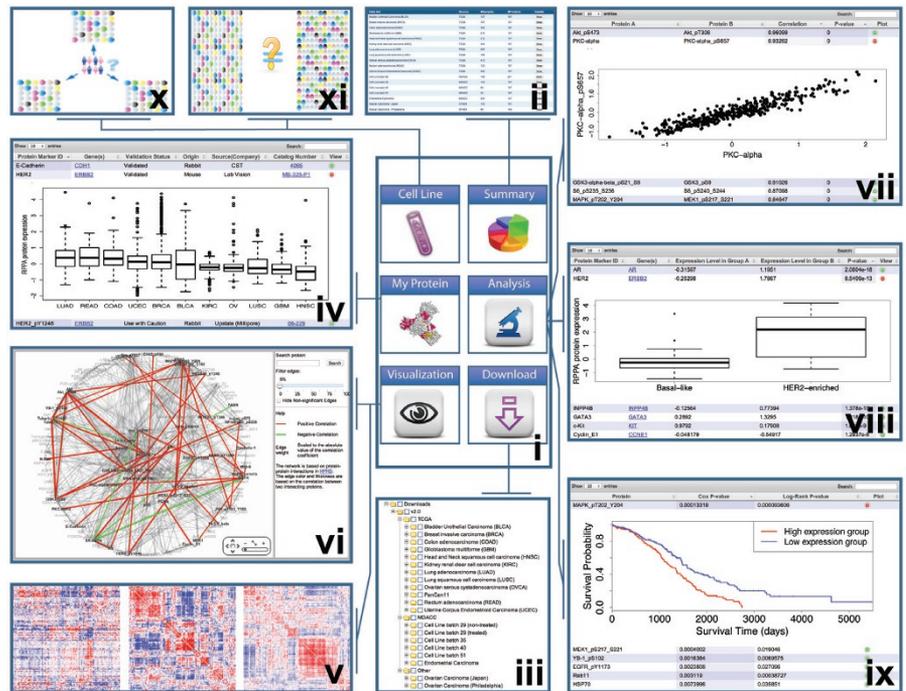
Our RPPA profiling platform includes extensively validated antibodies to nearly 200 proteins and phosphoproteins (**Supplementary Methods** and **Supplementary Table 1**). We are in the process of extending it to 500 independent proteins, covering all major signaling pathways, including PI3K, MAPK, mTOR, TGF- β , WNT, cell cycle, apoptosis, DNA damage, Hippo and Notch pathways. The current data release covers 4,379 tumor samples and consists of three parts (**Supplementary Table 2**). These are (i) TCGA tumor tissue sample sets: 3,467 samples from 11 cancer types, to be extended to 25 cancer types; (ii) independent tumor tissue sample sets: one endometrial tumor set (244 samples)⁷ and two ovarian tumor sets (99 and 130 samples, respectively)⁶, with other independent sets to be added soon; and (iii) tumor cell lines: 439 samples in four cell line sets, including both baseline and drug-treated cell lines. To our knowledge, this represents the largest publicly available collection of cancer functional proteomics data with parallel DNA and RNA data.

To facilitate broad access to these RPPA data sets, we developed a user-friendly data portal, The Cancer Proteome Atlas (TCPA; <http://bioinformatics.mdanderson.org/main/TCPA:Overview>). TCPA provides six modules: Summary, My Protein, Download, Visualization, Analysis and Cell Line (**Fig. 1, i**). The Summary module provides an overview of the RPPA data with detailed descriptions of each set (**Fig. 1, ii**). The Download module allows users to obtain any RPPA data set for analysis through a tree-view interface (**Fig. 1, iii**). The My Protein module provides detailed information about each RPPA protein: protein name, corresponding gene symbol, antibody status and source for the antibody. Users can examine the expression pattern of a protein of interest across different tumor types (for example, HER2 expression shown in **Fig. 1, iv**).

The Visualization module provides two ways to examine global protein expression patterns in a specific RPPA data set. One is through a "next-generation clustered heat map" (**Fig. 1, v**), which allows users to zoom, navigate and scrutinize clustering patterns of samples or proteins and link those patterns to relevant biological information sources. The other is through a network view (**Fig. 1, vi**), which overlays the correlation between any two interacting partners in the protein interaction network (curated in the Human Protein Reference Database⁸).

The Analysis module provides three analysis methods. (i) For correlation analysis, given a user-specified data set, correlations between any pair of proteins are presented in a table (**Fig. 1, vii**). Users can search the results by protein name, rank correlations or visualize the scatter plot of a correlation of interest (for example, there is a strong correlation between PKC- α and its phosphorylated form PKC- α _pS657 in endometrial cancer, as shown in **Fig. 1, vii**). (ii) For differential analysis, differentially expressed protein markers between two tumor types or subtypes can be identified. Given user-defined comparison groups, the

Figure 1 | Overview of the TCGA data portal. TCGA contains six modules (i): the Summary module (ii); the Download module (iii); the My Protein module, which has a table view (iv); the Visualization module, which has a “next-generation clustered heat map” view (v) and network view (vi); the Analysis module, which offers correlation analysis (vii), differential analysis (viii) and survival analysis (ix); and the Cell Line module, which offers cell line–patient BLAST analysis (x) and drug treatment effect analysis (xi).



results are displayed in a table view, and for a protein of interest, users can visualize the box plots for the comparison (for example, the much higher expression of HER2 in the HER2-enriched subtype of breast cancer than in the basal-like subtype shown in **Fig. 1, viii**). (iii) For survival analysis, protein markers or pathway events significantly correlated with patient survival can be identified. The table view shows the univariate Cox proportional hazards model, log rank-test *P* values and a Kaplan-Meier plot for each protein in the data set (for example, phosphorylated MAPK, MEK, EGFR and YB are the top predictors of patient survival in ovarian cancer, which suggests a strong prognostic value of the tyrosine kinase receptor–RAS–MAPK pathway in this disease, as shown in **Fig. 1, ix**).

The Cell Line module provides two analyses for RPPA data from tumor cell lines. (i) For cell line–patient BLAST, cell lines with RPPA profiles that are most similar to those of a patient sample of interest can be selected (**Fig. 1, x**). The returned cell lines are externally linked with Cancer Cell Line Encyclopedia (CCLE)⁹, from which selected mutations, transcriptomic profiles and sensitivity to specific drug treatments can be obtained. (ii) For drug treatment analysis, drug effects on RPPA profiles are provided (**Fig. 1, xi**).

Compared with other proteomic databases such as The Human Protein Atlas¹⁰, an advantage of TCGA is the availability of quantitative protein expression data over large cohorts of well-characterized TCGA patient tumors, with linked DNA and RNA analyses. TCGA allows the validation of findings from TCGA RPPA data through independent sample cohorts and will help users select model tumor cell lines for further functional investigation. TCGA complements nucleic acid–centric cancer genomic data resources such as the CCLE, the Memorial Sloan-Kettering Cancer Center’s cBioPortal for Cancer Genomics, OncoPrint and the UCSC Cancer Genomics Browser. TCGA is also complementary to other protein-driven resources such as the Human Protein Reference Database, search tool for the retrieval of interacting genes/proteins (STRING) and Human Interactome Project. We will include additional data sets from TCGA and other independent cancer studies as they become available, and we will also accept (and help curate as necessary) cancer proteomic data from other groups.

Note: Any Supplementary Information and Source Data files are available in the online version of the paper (doi:10.1038/nmeth.2650).

ACKNOWLEDGMENTS

We gratefully acknowledge contributions from the TCGA Research Network and its TCGA Pan-Cancer Analysis Working Group (contributing consortium members

are listed in **Supplementary Note**). The TCGA Pan-Cancer Analysis Working Group is coordinated by J.M. Stuart, C. Sander and I. Shmulevich. This study was supported by the US National Institutes of Health (U24CA143883 to J.N.W. and G.B.M and P30CA016672); UTMACC–G.S. Hogan Gastrointestinal Research Fund and NCI/UTMDACC Uterine SPOR Career Development Award (to H.L.); Susan G. Komen Foundation (KG081694 to G.B.M.); and Lorraine Dell Program in Bioinformatics for Personalization of Cancer Medicine (to J.N.W.).

AUTHOR CONTRIBUTIONS

G.B.M. and H.L. conceived of and supervised the project. Y.L., R.A., Z.J., W.L., J.-Y.Y., R.G.W.V. and J.L. generated the data, and J.L., P.L.R., B.M.B., D.W.K., C.W., J.N.W., G.B.M. and H.L. developed the data portal. Y.L., G.B.M. and H.L. wrote the manuscript with input from all the other authors.

COMPETING FINANCIAL INTERESTS

The authors declare no competing financial interests.

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PUBLISHED ONLINE 15 SEPTEMBER 2013; DOI:10.1038/NMETH.2650

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