













signatures, with 58% of the complexes exhibiting nonrandom TPCA signatures in at least one of the cell lines profiled. Membrane-embedded complexes are included in CORUM but are likely not amenable to the protocol adopted in this work (13). Nonsignificant TPCA signatures could arise for protein complexes with very low interaction stoichiometry—increased assembly can be monitored by changes in TPCA signature. TPCA profiling suggests that many complexes can remain intact yet thermally destabilized in the absence of interaction with DNA and LMW ligands such as ATP (Fig. 2, A and E). We observed many mitochondrial proteins that seem more temperature-resistant in intact cells, as observed previously (11). It is unclear whether TPCA is intrinsic and captured by the recent limited proteolysis and MS methodology (38).

We observed many more complexes with significant TPCA signature in cells than in lysates, suggesting that TPCA could potentially aid the intracellular studies of weak or transient protein-protein interactions that are not preserved in lysate, including protein complexes that depend on the integrity of chromatin-DNA, membrane, and associated structures for stability. TPCA could be used to validate complexes identified by other proteome-wide methodologies and help in their functional characterization across different cell states and conditions. TPCA also permits studying chemical modulators of protein complexes and interactions directly in nonengineered cells and tissues. Analogous to quantifying expression of genes and proteins from a reference genome and reference proteome, respectively, we envisage TPCA-based profiling with reference interactomes as a system-wide discovery strategy for modulated cellular processes. The method therefore can facilitate the discovery of protein complexes involved in diseases, some as potential therapeutic targets or, by TPCA profiles in patient

tissue samples, for prognosis of disease progression or optimization of therapy.

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#### ACKNOWLEDGMENTS

We thank H. Y. Chang for support and A. Larsson for suggestions. **Funding:** This research was funded directly by Young Investigator Grant (1610151038) awarded to C.S.H.T. by the Biomedical Research Council of the Agency for Science, Technology and Research (A\*STAR). Support for this research was provided by a startup grant from Nanyang Technological University and grants from the Swedish Research Council, the Swedish Cancer Society, and the Knut and Alice Wallenberg foundation awarded to P.N., and by National Medical Research Council (NMRC) grant MOHIAFCAT2/004/2015 to P.N. and R.M.S. Research in the lab of V.T. is supported by grant NRF2016NRF-CRP001-024 from the National Research Foundation Singapore. P.K. and X.B. are supported by the Biomedical Research Council, A\*STAR, and NMRC-CBRG14nov086 grants. **Authors contributions:** P.N. initiated the study; C.S.H.T. conceptualized TPCA and designed and implemented associated algorithms; C.S.H.T., X.B., P.K., V.T., R.M.S., and P.N. designed and supervised experiments; C.S.H.T. and C.H.Y. performed computational analysis; K.D.G., C.S.H.T., X.B., M.B.O., L.D., N.P., Y.T.L., and L.S. performed experiments; R.M.S. and J.L. supervised MS analysis; C.S.H.T. wrote the original manuscript; and C.S.H.T. and P.N. reviewed and edited the manuscript. **Competing interests:** P.N. is the inventor of a patent controlled by Pelago Biosciences AB and Evitra Proteoma AB covering the basic CETS method. J.L. is a paid consultant of Pelago Biosciences AB for MS analysis. All other coauthors declare no competing interests. **Data and materials availability:** All data are available in the supplementary materials.

#### SUPPLEMENTARY MATERIALS

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Materials and Methods  
Supplementary Text  
Figs. S1 to S27  
Tables S1 to S27

22 February 2017; resubmitted 28 September 2017  
Accepted 27 January 2018  
Published online 8 February 2018  
10.1126/science.aan0346