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* High-throughput sequence data should be uploaded before submission, with a private link for reviewers provided (these are available from both GEO and ArrayExpress)

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(For large datasets, or papers with a very large number of statistical tests, you may upload a single table file with tests, Ns, etc., with reference to sections in the manuscript.)

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* Where provided, these should be in the most useful format, and they can be uploaded as “Source data” files linked to a main figure or table
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Please indicate the figures or tables for which source data files have been provided:

*Data availability* (described in the omonym section): All raw data included in this study are available at gene expression omnibus (GEO). For 3-CePs, raw RNA-seq data and count matrix are under the GEO accession number GSE179057. Raw ATAC-seq data and peak matrix are available under the accession number GSE179059. Both datasets are collected in a GEO SuperSeries (GSE179064). Cisplatin RNA-seq data and count matrix are available at the accession number GSE207611, the raw ATAC-seq data and peak matrix are available under the number GSE207607. Both are collected in a GEO SuperSeries (GSE207612).

The cell line expression data employed in the prediction pipeline were downloaded from https://www.proteinatlas.org/about/download. The file *RNA HPA cell line gene data* contains transcript expression levels summarized per gene in 69 cell lines and is based on the Human Protein Atlas version 20.0 and Ensembl version 92.38.

Similarly, the TCGA expression data from cancer cell samples (the Cancer Genome Atlas) were downloaded from the same web page of the Human Cell Atlas (Transcript expression levels summarized per gene in 7932 samples from 17 different cancer types). Data are based on The Human Protein Atlas version 20.0 and Ensembl version 92.38.

Cisplatin IC50s in different cell lines can be accessed through the Genomics of Drug Sensitivity in Cancer database (https://www.cancerrxgene.org/compound/Cisplatin/1005/overview/ic50) (Yang et al., 2013). Codes to reproduce both pre-processing and downstream analyses reported in this manuscript are available at the public repository <https://github.com/ccarraro/3-CePs_prediction>. The hCoCena script is accessible at <https://github.com/MarieOestreich/hCoCena> (vertical integration code available upon request).

*Supplementary Data* are available as .xlsx or .pdf files.