eLife's transparent reporting form

We encourage authors to provide detailed information *within their submission* to facilitate the interpretation and replication of experiments. Authors can upload supporting documentation to indicate the use of appropriate reporting guidelines for health-related research (see EQUATOR Network), life science research (see the BioSharing Information Resource), or the ARRIVE guidelines for reporting work involving animal research. Where applicable, authors should refer to any relevant reporting standards documents in this form.

If you have any questions, please consult our Journal Policies and/or contact us: editorial@elifesciences.org.

Sample-size estimation
- You should state whether an appropriate sample size was computed when the study was being designed
- You should state the statistical method of sample size computation and any required assumptions
- If no explicit power analysis was used, you should describe how you decided what sample (replicate) size (number) to use

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn't apply to your submission:

> A total of 6 tumor specimens (esPHEO_T1, esPHEO_T2, esPHEO_T3, PHEO_T, ACA_T1, and ACA_T2) and 1 peritumoral specimen(esPHEO_adj) were collected from 3 cases, i.e., pheochromocytoma with ectopic ACTH and CRH secretion (Case 1), common pheochromocytoma (Case 2) and adrenocortical adenoma (Case 3), as shown in Fig. 1a.

Replicates
- You should report how often each experiment was performed
- You should include a definition of biological versus technical replication
- The data obtained should be provided and sufficient information should be provided to indicate the number of independent biological and/or technical replicates
- If you encountered any outliers, you should describe how these were handled
- Criteria for exclusion/inclusion of data should be clearly stated
- High-throughput sequence data should be uploaded before submission, with a private link for reviewers provided (these are available from both GEO and ArrayExpress)

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn't apply to your submission:

> Since the combination of dual ACTH/CRH secreting pheochromocytoma with CS is extremely rare, we reported only one patient (case1). But we collected three dissected tumor specimens (esPHEO_T1, esPHEO_T2, esPHEO_T3) from different anatomic sites of adrenal medulla, mass, and kidney, and a control (esPHEO_adj) from adjacent tissue to tumor.

Statistical reporting

- Statistical analysis methods should be described and justified
- Raw data should be presented in figures whenever informative to do so (typically when N per group is less than 10)
- For each experiment, you should identify the statistical tests used, exact values of N, definitions of center, methods of multiple test correction, and dispersion and precision measures (e.g., mean, median, SD, SEM, confidence intervals; and, for the major substantive results, a measure of effect size (e.g., Pearson's r, Cohen's d)
- Report exact p-values wherever possible alongside the summary statistics and 95% confidence intervals. These should be reported for all key questions and not only when the p-value is less than 0.05.

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn't apply to your submission:

> We performed cell clustering analysis on all cells from all seven specimens in Seurat (v3.1.5). It identified clusters of cells by a shared nearest neighbour (SNN) modularity optimization based clustering algorithm.

(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.)

Group allocation

- Indicate how samples were allocated into experimental groups (in the case of clinical studies, please specify allocation to treatment method); if randomization was used, please also state if restricted randomization was applied
- Indicate if masking was used during group allocation, data collection and/or data analysis

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn't apply to your submission:

> The allocation was not random. We reported the rare case, with dual ACTH/CRH secreting pheochromocytoma associated with CS. Three different anatomic tumor tissues from the rare case were allocated into the rare pheochromocytoma group (esPHEO group) and one peritumoral tissue was allocated into adjacent group (esPHEO_adj group). For comparison, other adrenal tumor subtypes were also collected and studied, namely, a common pheochromocytoma (without ectopic ACTH or CRH secretion function) as a PHEO group and two adrenocortical adenomas as a ACA group.

Additional data files ("source data")

- We encourage you to upload relevant additional data files, such as numerical data that are represented as a graph in a figure, or as a summary table
- 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
- Include model definition files including the full list of parameters used
- Include code used for data analysis (e.g., R, MatLab)
- Avoid stating that data files are "available upon request"

Please indicate the figures or tables for which source data files have been provided:

The raw sequence data reported in this paper have been deposited in the Genome Sequence Archive (Genomics, Proteomics & Bioinformatics 2017) in National Genomics Data Center (Nucleic Acids Res 2020), Beijing Institute of Genomics (China National Center for Bioinformation), Chinese Academy of Sciences, under accession number HRA000403, that are temporary shared at http://bigd.big.ac.cn/gsa-human/s/pHJNFF6a. The data will be publicly accessible after the article is accepted.