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Reporting Summary

Nature Research wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Research policies, see our Editorial Policies and the Editorial Policy Checklist.

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St	at	ıst	$1 \cap S$

101	an statistical analyses, commit that the following items are present in the figure regend, table regend, main text, or Methods section.
n/a	Confirmed
	\square The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement
	🔀 A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
	The statistical test(s) used AND whether they are one- or two-sided Only common tests should be described solely by name; describe more complex techniques in the Methods section.
\boxtimes	A description of all covariates tested
\boxtimes	A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
	A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
	For null hypothesis testing, the test statistic (e.g. <i>F</i> , <i>t</i> , <i>r</i>) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> value noted <i>Give P values as exact values whenever suitable.</i>
\boxtimes	For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
\boxtimes	For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
	Estimates of effect sizes (e.g. Cohen's <i>d</i> , Pearson's <i>r</i>), indicating how they were calculated
	Our web collection on <u>statistics for biologists</u> contains articles on many of the points above.
So	ftware and code
D - I:	

Policy information about <u>availability of computer code</u>

Data collection

No software was used to collect this data.

Data analysis

Python 3.7, including os, matplotlib, re, statistics, glob, math, seaborn, and scipy.

R 3.6, including tidyverse, ggplot2, scales, data.table, foreach, plyr, doMC, GenomicRanges, and stringr.

Customized version of ichorCNA algorithm (copy number alteration prediction and purity and ploidy estimation): https://github.com/GavinHaLab/pdx_evolution_study/ichor_run.

All scripts used in this study can be found at https://github.com/GavinHaLab/pdx_evolution_study.

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research guidelines for submitting code & software for further information.

Data

Policy information about availability of data

All manuscripts must include a data availability statement. This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A list of figures that have associated raw data
- A description of any restrictions on data availability

The copy number profiles analyzed in this study are available in Supplementary Data I of Woo et al., https://doi.org/10.1101/861393.

Please select the one below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection. If see deficiency Selections Selections Social sciences Stolegical, evolutionary & environmental sciences	Field-specific reporting				
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Population characteristics

Recruitment

N/A

Ethics oversight

N/A

Note that full information on the approval of the study protocol must also be provided in the manuscript.