

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 [Authors & Referees](#) and the [Editorial Policy Checklist](#).

Statistics

For all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.

n/a Confirmed

- 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.
- A description of all covariates tested
- 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. F , t , r) with confidence intervals, effect sizes, degrees of freedom and P value noted
Give P values as exact values whenever suitable.
- For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
- 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 d , Pearson's r), indicating how they were calculated

Our web collection on [statistics for biologists](#) contains articles on many of the points above.

Software and code

Policy information about [availability of computer code](#)

Data collection

No software was used.

Data analysis

Cell Ranger v1.2.1, R v3.4.4, Seurat v1.4.0, v2.3.0 and v2.3.4, Monocle v2.6.3, CIBERSORT (absolute mode beta).

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/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 datasets generated and analysed during the current study are available in the following repositories: Mouse developmental time points single cell RNAseq (GSE118068), PFB bulk RNAseq (EGAS00001002696, GSE64415), Human tumor single cell RNAseq/PFA/C-PA bulk RNAseq (EGAS00001003170) and MB bulk RNAseq (EGAD00001004435).

Field-specific reporting

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.

Life sciences Behavioural & social sciences Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see [nature.com/documents/nr-reporting-summary-flat.pdf](https://www.nature.com/documents/nr-reporting-summary-flat.pdf)

Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

Sample size	Sample size was determined by the availability of the human samples. The mouse data set sample size was selected in function of important events occurring during mouse cerebellar development time line.
Data exclusions	All of the data acquired was utilized for analysis, unless specified otherwise in the figure legends or text.
Replication	No replicates were performed on the single cell RNA seq mouse data set within the individual time points. Replicates were used for the human RNA seq (bulk and single cell) as described in the figure legends.
Randomization	NA
Blinding	NA

Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

Materials & experimental systems

n/a	Involved in the study
<input checked="" type="checkbox"/>	<input type="checkbox"/> Antibodies
<input checked="" type="checkbox"/>	<input type="checkbox"/> Eukaryotic cell lines
<input checked="" type="checkbox"/>	<input type="checkbox"/> Palaeontology
<input type="checkbox"/>	<input checked="" type="checkbox"/> Animals and other organisms
<input type="checkbox"/>	<input checked="" type="checkbox"/> Human research participants
<input checked="" type="checkbox"/>	<input type="checkbox"/> Clinical data

Methods

n/a	Involved in the study
<input checked="" type="checkbox"/>	<input type="checkbox"/> ChIP-seq
<input checked="" type="checkbox"/>	<input type="checkbox"/> Flow cytometry
<input checked="" type="checkbox"/>	<input type="checkbox"/> MRI-based neuroimaging

Animals and other organisms

Policy information about [studies involving animals](#); [ARRIVE guidelines](#) recommended for reporting animal research

Laboratory animals	The study involved collection of cerebellum and hind brain regions of wild type mice (C57BL6 strain) from multiple embryonic (Embryonic day 10, 12,14,16,18) and postnatal time (Post natal day 0, 5, 7 and 14) points. Both males and females mice were used with no discrimination. Litter mates, specifically for the embryonic time points were pooled when needed.
Wild animals	NA
Field-collected samples	NA
Ethics oversight	AUP 21-0100H approved by The Centre for Phenogenomics (Toronto).

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

Human research participants

Policy information about [studies involving human research participants](#)

Population characteristics	Patients diagnosed with cerebellar pediatric brain tumors were recruited from McGill University Health Centre and the Hospital for Sick Children/The Arthur and Sonia Labatt Brain Tumour Research Centre Biobank.
Recruitment	NA

Ethics oversight

REB MCH003-26 approved by McGill University Health Centre (Montreal). REB 1000055059 approved by The Arthur and Sonia Labatt Brain Tumour Research/Hospital for Sick Children (Toronto).

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