

Reporting Summary

Nature Portfolio 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 Portfolio policies, see our [Editorial Policies](#) 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 (<i>n</i>) 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 <i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i>
☐	☒ 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. <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>
☒	☐ 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 <i>d</i> , Pearson's <i>r</i>), 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	1) Zen 2.6 (blue edition) for confocal imaging, 2) LoLigo Autoswim (v1.0.0) and uEye Cockpit (v4.90) for swim endurance and behavior 3) Fragment analyzer controller (v3.1.0.12) and Prosize Data Analysis (v4.0.2.7) for genotyping by capillary electrophoresis
Data analysis	For snRNA-seq analysis: CellRanger (v6.0.0) , R (v4.2.1), Seurat (v4.1.1) , DecontX package (celda v1.16.1), DoubletFinder (v2.0.3) , CellChat (v1.4.0) ,Python (v3.8.10),CellRank (v1.5.1), SeuratDisk (v0.9020), scvelo (v0.2.4),scanpy (v1.9.1), ggvenn (v0.1.9), biomaRT (v2.52.0),Sparse_matrix_homologe_converter_082322 (Custom), s7_marker_comparison_v3 (Custom) . For image analysis and quantification: ImageJ (v1.53t), Cell_Counter_v1-5 (Custom), Cell_Count_Processor_v1_vms (Custom), hcr_celltypespecific_analysis_v3.1_080222 (Custom). For swim behavior analysis: Swim behavior_Tracking_v2 (Custom), SwimBehavior_processing and quantification_v7 (Custom). For statistics: Graphpad Prism (v9.5.1), Github Repository: https://github.com/MokalledLab/Zebrafish_SCI_Atlas/tree/v1.0.0

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 Portfolio [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 description of any restrictions on data availability
- For clinical datasets or third party data, please ensure that the statement adheres to our [policy](#)

Both raw and processed files of the snRNA-seq are deposited in Gene Expression Omnibus (Accession # GSE235395, reviewer token: ydubskqqptytjkb). Additionally, the snRNA-seq data for both all integrated cell types and neuron subset is available to exploring here: https://shiny.path.wustl.edu/SCI_Atlas/. All other raw data related to the manuscript are available upon request.

Research involving human participants, their data, or biological material

Policy information about studies with [human participants or human data](#). See also policy information about [sex, gender \(identity/presentation\), and sexual orientation](#) and [race, ethnicity and racism](#).

Reporting on sex and gender

Reporting on race, ethnicity, or other socially relevant groupings

Population characteristics

Recruitment

Ethics oversight

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

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

Life sciences study design

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

Sample size

Data exclusions

Replication

Randomization

Blinding

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
☐	☒ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology and archaeology
☐	☒ Animals and other organisms
☒	☐ Clinical data
☒	☐ Dual use research of concern
☒	☐ Plants

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ MRI-based neuroimaging

Antibodies

Antibodies used	Primary antibodies used in this study were chicken anti-GFP (AVES, GFP-1020, 1:1000), rabbit anti-dsRed (Takara, 632496, 1:250), mouse anti-HuC/D (Invitrogen, A21271, 1:500), Mouse anti-81.5C10 (MNR2/HB9/Mnx1, DSHB, 1:50), rabbit anti-Pax2 (BioLegend, 901002, 1:500). Secondary antibodies (Invitrogen, 1:250) used in this study were Alexa Flour 488, Alexa Flour 594, and Alexa Flour 647 goat anti-rabbit or goat anti-mouse antibodies.
Validation	All these antibodies were previously utilized in the literature. mouse-anti-HuC/D labels neuronal marker genes HuC and HuD (https://www.thermofisher.com/antibody/product/HuC-HuD-Antibody-clone-16A11-Monoclonal/A-21271). chicken anti-GFP (https://www.aveslabs.com/products/anti-green-fluorescent-protein-antibody-gfp) and rabbit anti-dsRed (https://www.takarabio.com/products/antibodies-and-elisa/fluorescent-protein-antibodies/red-fluorescent-protein-antibodies?catalog=632496) recognized red and green fluorescent proteins and are used here to enhance the signal of respective transgenic lines. HB9 labels motor neurons (https://dshb.biology.uiowa.edu/81-5C10?keywords=MNR2&quantity=1) and Pax-2 labels interneurons (https://www.biolegend.com/en-ie/products/purified-anti-pax-2-antibody-11510).

Animals and other research organisms

Policy information about [studies involving animals](#); [ARRIVE guidelines](#) recommended for reporting animal research, and [Sex and Gender in Research](#)

Laboratory animals	Adult zebrafish of the Ekkwill, Tubingen and AB strains were used in this study. Size matched (~2 cm) male and female animals of ~4 months of age were used. The following previously published zebrafish strains were used: Tg(vglut2a:RFP) (Satou et al., 2013), Tg(gad1b:GFP) (Satou et al., 2013) and Tg(isl1a:GFP) (Higashijima et al., 2000).
Wild animals	Wild animals were not used in this study
Reporting on sex	Within each experiment, equal sex distribution were used.
Field-collected samples	This study did not involve samples collected from the field
Ethics oversight	All animal experiments were performed in compliance with the institutional animal care and use committee (IACUC) at the Washington university in St. Louis.

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

Plants

Seed stocks	Not Applicable
Novel plant genotypes	Not Applicable
Authentication	Not Applicable