

Reporting Summary

Nature Portfolio wishes to improve the reproducibility of the work that we publish. This form provides structure 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 (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 Custom python and R code: https://github.com/triasteran/nonAUG_manuscript/tree/main/jupyter_notebooks (doi: 10.5281/zenodo.7390032)

Data analysis Trips-viz ORF predictor v1.0: https://github.com/skiniry/Trips-Viz_orfquery_routes.py (doi: 10.5281/zenodo.7390032)
Custom python and R code: https://github.com/triasteran/nonAUG_manuscript/tree/main/jupyter_notebooks (doi: 10.5281/zenodo.7390032)

Other software: CESAR v2.0, PHAST v1.5, GenomicFeatures R package v3.6.1, PhyloCSF v1.0.1

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](#)

All data generated during this study are included in this published article and its supplementary information files: Supplementary Information (Supplementary_Information.pdf), Supplementary table 1 (Supplementary_table_1.xlsx), Supplementary Table 2 (Supplementary_table_2.tsv), Supplementary Table 3 (Supplementary_table_3.xlsx), Supplementary Table 4 (Supplementary_table_4.xlsx), Supplementary Table 5 (Supplementary_table_5.xlsx), Supplementary Table 6 (Supplementary_table_6.xlsx), Supplementary Table 7 (Supplementary_table_7.xlsx), Supplementary Table 8 (Supplementary_table_8.xlsx), Supplementary Table S9 (Supplementary_table_9.xlsx). The datasets analysed during the current study are available in GEO under accession numbers: GSE62247 (<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE62247>), GSE114794 (<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE114794>), GSE79664 (<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE79664>), GSE51584 (<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE51584>), GSE94460 (<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE94460>), GSE73136 (<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE73136>), GSE87328 (<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE87328>), GSE64962 (<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE64962>), GSE65885 (<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE65885>), GSE56887 (<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE56887>), GSE70211 (<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE70211>) and GSE79392 (<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE79392>), GSE77401 (<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE77401>), GSE58207 (<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE58207>) and 4 studies of proteomics data the ProteomeXchange PXD004452 (<http://proteomecentral.proteomexchange.org/cgi/GetDataset?ID=PXD004452>), PXD002395 (<http://proteomecentral.proteomexchange.org/cgi/GetDataset?ID=PXD002395>), PXD002082 (<http://proteomecentral.proteomexchange.org/cgi/GetDataset?ID=PXD002082>), PXD002815 (<http://proteomecentral.proteomexchange.org/cgi/GetDataset?ID=PXD002815>). We used GENCODE v25 (GRCh38.p7, https://www.encodegenes.org/human/release_25.html) fasta and gtf files and GENCODE v35 (GRCh38.p13, https://www.encodegenes.org/human/release_35.html) fastq and gtf files; RefSeq fasta and gtf files (July 1, 2020; GRCh38.p13, 109.20200815, https://ftp.ncbi.nlm.nih.gov/refseq/H_sapiens/). Source data is provided with this paper (Source_data.xlsx).

Human research participants

Policy information about [studies involving human research participants and Sex and Gender in Research](#).

Reporting on sex and gender	n/a
Population characteristics	n/a
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.

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	Fig.3g, N=24 and 28, no sample size calculation was performed since these gene sets are predetermined by certain conditions - taken from another study (you cannot draw more genes from 'population').
Data exclusions	No data was excluded from the analysis.
Replication	the notion of biological and technical replicates is irrelevant here since we are comparing two sets of bioinformatics predictions, not experimental data that can be done in replicates
Randomization	No randomisation is applicable since the study procedure is theoretical (bioinformatics) and no experiments or simulations were conducted.
Blinding	No blinding is applicable since the study procedure is theoretical (bioinformatics) and no experiments or simulations were conducted (no test subjects suitable for blinding participated).

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

Methods

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