

Materials Design Analysis Reporting (MDAR)

Checklist for Authors

The MDAR framework establishes a minimum set of requirements in transparent reporting applicable to studies in the life sciences (see Statement of Task: [doi:10.31222/osf.io/9sm4x](https://doi.org/10.31222/osf.io/9sm4x)). The MDAR checklist is a tool for authors, editors, and others seeking to adopt the MDAR framework for transparent reporting in manuscripts and other outputs. Please refer to the MDAR Elaboration Document for additional context for the MDAR framework.

For all that apply, please note where in the manuscript the required information is provided.

Materials:

Newly created materials	indicate where provided: page no/section/legend)	n/a
The manuscript includes a dedicated "materials availability statement" providing transparent disclosure about availability of newly created materials including details on how materials can be accessed and describing any restrictions on access.	'Data and materials availability' section.	
Antibodies	indicate where provided: page no/section/legend)	n/a
For commercial reagents, provide supplier name, catalogue number and RRID , if available.	Antibodies are listed throughout 'Materials and Methods' section.	
DNA and RNA sequences	indicate where provided: page no/section/legend)	n/a
Short novel DNA or RNA including primers, probes: Sequences should be included or deposited in a public repository.	RNA-Seq data is uploaded under BioProject PRJNA1099138 and plasmid sequences have been made publicly available, GenBank accession numbers are listed in table S8 of 'Materials and Methods'.	
Cell materials	indicate where provided: page no/section/legend)	n/a
Cell lines: Provide species information, strain. Provide accession number in repository OR supplier name, catalog number, clone number, OR RRID.	Transfections were carried out with HEK293 cells (Supplier ATCC) listed in 'Cell culture and transfection' subheading in 'Materials and Methods'.	
Primary cultures: Provide species, strain, sex of origin, genetic modification status.		X
Experimental animals	indicate where provided: page no/section/legend)	n/a
Laboratory animals or Model organisms: Provide species, strain, sex, age, genetic modification status. Provide accession number in repository OR supplier name, catalog number, clone number, OR RRID.	Listed in 'Materials and Methods' section under 'Animal breeding' subheading, captive bred flock.	
Animal observed in or captured from the field: Provide species, sex, and age where possible.		X
Plants and microbes	indicate where provided: page no/section/legend)	n/a
Plants: provide species and strain, ecotype and cultivar where relevant, unique accession number if available, and source (including location for collected wild specimens).		X
Microbes: provide species and strain, unique accession number if available, and source.		X
Human research participants	indicate where provided: page no/section/legend) or state if these demographics were not collected	n/a
If collected and within the bounds of privacy		X

constraints report on age, sex and gender or ethnicity for all study participants.		
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Design:

Study protocol	indicate where provided: page no/section/legend)	n/a
If study protocol has been pre-registered, provide DOI. For clinical trials, provide the trial registration number OR cite DOI.		X

Laboratory protocol	indicate where provided: page no/section/legend)	n/a
Provide DOI OR other citation details if detailed step-by-step protocols are available.		X

Experimental study design (statistics details)		
For in vivo studies: State whether and how the following have been done	indicate where provided: page no/section/legend. If it could have been done, but was not, write not done	n/a
Sample size determination		X
Randomisation		X
Blinding	Blinding applied in behavior scoring, described in 'Materials and Methods'	
Inclusion/exclusion criteria		X

Sample definition and in-laboratory replication	indicate where provided: page no/section/legend	n/a
State number of times the experiment was replicated in laboratory.	In 'Materials and Methods' section	
Define whether data describe technical or biological replicates.	In 'Materials and Methods' section	

Ethics	indicate where provided: page no/section/legend	n/a
Studies involving human participants: State details of authority granting ethics approval (IRB or equivalent committee(s), provide reference number for approval.		X
Studies involving experimental animals: State details of authority granting ethics approval (IRB or equivalent committee(s), provide reference number for approval.	Stated in 'Materials and Methods' section, 'Animal breeding' subheading: Animal Care Committee of Simon Fraser University (permit #1232B-17)	
Studies involving specimen and field samples: State if relevant permits obtained, provide details of authority approving study; if none were required, explain why.	All samples were collected from a captive population in Canada and were exported to Germany, using the following permits: In 2017 Export BC-17-0036, Environment Canada Import 46f-G8787-2017/145-2, Bayerisches Staatministerium für Umwelt und Verbraucherschutz In 2018 Export BC-18-0039, Environment Canada Import 46f-G8787-2018/179-2, Bayerisches	

	Staatministerium für Umwelt und Verbraucherschutz In 2019 *Import 46f-G8787-2019/118-2, Bayerisches Staatministerium für Umwelt und Verbraucherschutz	
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Dual Use Research of Concern (DURC)	indicate where provided: page no/section/legend	n/a
If study is subject to dual use research of concern regulations, state the authority granting approval and reference number for the regulatory approval.		X

Analysis:

Attrition	indicate where provided: page no/section/legend	n/a
Describe whether exclusion criteria were preestablished. Report if sample or data points were omitted from analysis. If yes report if this was due to attrition or intentional exclusion and provide justification.	Low RNA-quality was an exclusion criteria and this is mentioned in the 'Materials and Methods' section.	
Statistics	indicate where provided: page no/section/legend	n/a
Describe statistical tests used and justify choice of tests.	Fisher's exact test, Kruskal-Wallis (when data did not follow a normal distribution), Two-tailed binomial test, Spearman correlation, Benjamini-Hochberg and Bonferroni corrections were applied for multiple testing. Statistical tests employed for RNA-Seq data analysis are described in 'Materials and Methods'. Sample sizes are stated in all Figure legends and table s4 summarizes RNA-Seq sample sizes.	
Data availability	indicate where provided: page no/section/legend	n/a
For newly created and reused datasets, the manuscript includes a data availability statement that provides details for access or notes restrictions on access.	All data used for analyses is publicly available. The manuscript includes a data availability statement on page 11.	
If newly created datasets are publicly available, provide accession number in repository OR DOI OR URL and licensing details where available.	RNA-Seq data accession code: BioProject PRJNA1099138 Plasmid accession codes: all available in GenBank, accession numbers listed in table S8 Genome accession code: RefSeq GCF_001431845.1 Additional datasets deposited at GitHub: https://github.com/azemella/Ruff_adults_RNASeq_gene_expression_2024 Zenodo: 10.5281/zenodo.13694203	
If reused data is publicly available provide accession number in repository OR DOI OR URL, OR citation.	Plasma testosterone and androstenedione were measured in https://doi.org/10.3389/fgene.2021.641620 and https://doi.org/10.1016/j.yhbeh.2020.104877	
Code availability	indicate where provided: page no/section/legend	n/a
For all newly generated custom computer code/software/mathematical algorithm or re-used code essential for replicating the main findings of the study, the manuscript includes a data availability statement that provides details for access or notes restrictions.	All code used for data analysis and visualization is publicly available. The manuscript includes a code availability statement on page 11.	
If newly generated code is publicly available, provide accession number in repository, OR DOI OR URL and licensing details where available. State any restrictions on code availability or accessibility.	GitHub: https://github.com/azemella/Ruff_adults_RNASeq_gene_expression_2024 Zenodo: 10.5281/zenodo.13694203	
If reused code is publicly available provide accession number in repository OR DOI OR URL, OR citation.		X

Reporting

MDAR framework recommends adoption of discipline-specific guidelines, established and endorsed through community initiatives. Journals have their own policy about requiring specific guidelines and recommendations to complement MDAR.

Adherence to community standards	indicate where provided: page no/section/legend	n/a
State if relevant guidelines (e.g., ICMJE, MIBBI, ARRIVE) have been followed, and whether a checklist (e.g., CONSORT, PRISMA, ARRIVE) is provided with the manuscript.	ARRIVE E10 guidelines were followed. No checklist provided.	