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.). 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.	Manuscript pages 29 - 30 (“Data and materials availability”)	

Antibodies	indicate where provided: page no/section/legend)	n/a
For commercial reagents, provide supplier name, catalogue number and RRID, if available.	Supplementary materials section pages 3 - 4 (“Processing of single cell suspension for scRNA-seq”) and Supplementary data table S33	

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.		x

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.		x
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.		x
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 constraints report on age, sex and gender or ethnicity for all study participants.	Supplementary data tables 1, 2 and 6	

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	Supplementary data tables 1, 2 and 6	
Randomisation		x
Blinding		x
Inclusion/exclusion criteria	Supplementary data tables 1, 2 and 6 Supplementary materials sections "Ethics and sample acquisition" "Processing samples for imaging and single cell sequencing" "Alignment, quality control, filtering, and preprocessing of scRNA-seq and CITE-seq data"	

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.		x
Define whether data describe technical or biological replicates.	Supplementary data tables 1, 2 and 6	

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.	Supplementary materials section "Ethics and sample acquisition"	
Studies involving experimental animals: State details of authority granting ethics approval (IRB or equivalent committee(s), provide reference number for approval.		x
Studies involving specimen and field samples: State if relevant permits obtained, provide details of authority approving study; if none were required, explain why.		x

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.	Supplementary data tables 1, 2 and 6 Supplementary materials section "Alignment, quality control, filtering, and preprocessing of scRNA-seq and CITE-seq data"	

Statistics	indicate where provided: page no/section/legend	n/a
Describe statistical tests used and justify choice of tests.	Supplementary materials sections: "Alignment, quality control, filtering, and preprocessing of scRNA-seq and CITE-seq data" "Integration and batch correction of scRNA-seq and CITE-seq datasets" "Clustering and annotation of scRNA-seq and CITE-seq data" "Dimensional reduction and marker expression visualisation" "Differential abundance testing and FACS correction" "Clustered gene-set enrichment analysis" "Cell state predictions using probabilistic low-dimensional ElasticNet regression" "Differential lineage priming and progenitor cell fate predictions" "pySCENIC for regulon analysis"	

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.	Manuscript pages 29 - 30 ("Data and materials availability") Supplementary data tables 1, 2 and 6	
If newly created datasets are publicly available, provide accession number in repository **OR** DOI **OR** URL and licensing details where available.	Processed is available at: https://developmental.cellatlas.io/yolk-sac All novel raw sequencing data from this study are made publicly available at ArrayExpress as FASTQs and count matrices as follows: i) Human embryonic liver and yolk sac 10x scRNA-seq (E-MTAB-10552) ii) Human embryonic yolk sac 10x scRNA-seq (E-MTAB-11673) iii) Human embryonic yolk sac Smart-seq2 scRNA-seq (E-MTAB-10888) iv) Human embryonic yolk sac CITE-seq (E-MTAB-11549) v) Human embryonic liver CITE-seq (E-MTAB-11618) vi) Human fetal liver CITE-seq (E-MTAB-11613)	
If reused data is publicly available provide accession number in repository **OR** DOI **OR** URL, **OR** citation.	Processed is available at: https://developmental.cellatlas.io/yolk-sac	

	External data accession numbers and URLs are available in Supplementary data tables S6	

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.	Manuscript pages 29 - 30 (“Data and materials availability”)	
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.	https://github.com/haniffalab/FCA_yolkSac	
If reused code is publicly available provide accession number in repository **OR** DOI **OR** URL, **OR** citation.	https://github.com/haniffalab/FCA_yolkSac	

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.		x