

## **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:**

<b>Newly created materials</b>	<b>indicate where provided: page no/section/legend)</b>	<b>n/a</b>
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.	Reagents will be available upon request. There are MTA's and patents associated with some of the cell lines and mouse lines.	
<b>Antibodies</b>	<b>indicate where provided: page no/section/legend)</b>	<b>n/a</b>
For commercial reagents, provide supplier name, catalogue number and <a href="#">RRID</a> , if available.	This is all available in the materials and methods section.	
<b>DNA and RNA sequences</b>	<b>indicate where provided: page no/section/legend)</b>	<b>n/a</b>
<b>Short novel DNA or RNA including primers, probes:</b> Sequences should be included or deposited in a public repository.		N/A
<b>Cell materials</b>	<b>indicate where provided: page no/section/legend)</b>	<b>n/a</b>
<b>Cell lines:</b> Provide species information, strain. Provide accession number in repository <b>OR</b> supplier name, catalog number, clone number, <b>OR</b> RRID.	This information is provided in the M&M. The parental HL60 cell line was a kind gift from Henry Bourne.	
<b>Primary cultures:</b> Provide species, strain, sex of origin, genetic modification status.	All this information is provided in detail in the M&M.	
<b>Experimental animals</b>	<b>indicate where provided: page no/section/legend)</b>	<b>n/a</b>
<b>Laboratory animals or Model organisms:</b> Provide species, strain, sex, age, genetic modification status. Provide accession number in repository <b>OR</b> supplier name, catalog number, clone number, <b>OR</b> RRID.	GNB4 KO mice were created in house at MSKCC. Male and female mice were used for these experiments between the ages of 6-8 weeks. Genetic modifications were made on the C57BL/6 background.	
<b>Animal observed in or captured from the field:</b> Provide species, sex, and age where possible.		N/A
<b>Plants and microbes</b>	<b>indicate where provided: page no/section/legend)</b>	<b>n/a</b>
<b>Plants:</b> provide species and strain, ecotype and cultivar where relevant, unique accession number if available, and source (including location for collected wild specimens).		N/A
<b>Microbes:</b> provide species and strain, unique accession number if available, and source.	FLARE fungal strains were provided by Dr. Tobias Hohl at MSKCC.	
<b>Human research participants</b>	<b>indicate where provided: page no/section/legend) or state if these demographics were not collected</b>	<b>n/a</b>
If collected and within the bounds of privacy constraints report on age, sex and gender or ethnicity for all study participants.		N/A

## Design:

<b>Study protocol</b>	<b>indicate where provided: page no/section/legend)</b>	<b>n/a</b>
If study protocol has been pre-registered, provide DOI. For clinical trials, provide the trial registration number <b>OR</b> cite DOI.		N/A
<b>Laboratory protocol</b>	<b>indicate where provided: page no/section/legend)</b>	<b>n/a</b>
Provide DOI <b>OR</b> other citation details if detailed step-by-step protocols are available.	All experimental details are contained in the M&M.	
<b>Experimental study design (statistics details)</b>		
<b>For in vivo studies:</b> State whether and how the following have been done	<b>indicate where provided: page no/section/legend. If it could have been done, but was not, write not done</b>	<b>n/a</b>
Sample size determination	Sample size was determined in consultation with IRB/IACUC for animal experiments. This is part of the process of getting approval for these mouse experiments.	
Randomisation		N/A
Blinding	Blinding was done for mouse flow experiments at 18 and 24 hours. Blinding wasn't done for 24 hour experiment. This could have been done but wasn't.	
Inclusion/exclusion criteria		N/A
<b>Sample definition and in-laboratory replication</b>		
<b>Sample definition and in-laboratory replication</b>	<b>indicate where provided: page no/section/legend</b>	<b>n/a</b>
State number of times the experiment was replicated in laboratory.	Experiments were replicated 3 times at least.	
Define whether data describe technical or biological replicates.	Most experiments there were 2 to three technical replicates included in each of the 3 biological replicates.	
<b>Ethics</b>		
<b>Ethics</b>	<b>indicate where provided: page no/section/legend</b>	<b>n/a</b>
<b>Studies involving human participants:</b> State details of authority granting ethics approval (IRB or equivalent committee(s), provide reference number for approval.	IRB	
<b>Studies involving experimental animals:</b> State details of authority granting ethics approval (IRB or equivalent committee(s), provide reference number for approval.	IRB/IACUC	
<b>Studies involving specimen and field samples:</b> State if relevant permits obtained, provide details of authority approving study; if none were required, explain why.		N/A
<b>Dual Use Research of Concern (DURC)</b>		
<b>Dual Use Research of Concern (DURC)</b>	<b>indicate where provided: page no/section/legend</b>	<b>n/a</b>
If study is subject to dual use research of concern regulations, state the authority granting approval and reference number for the regulatory approval.		N/A

## Analysis:

<b>Attrition</b>	<b>indicate where provided: page no/section/legend</b>	<b>n/a</b>
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.		N/A
<b>Statistics</b>	<b>indicate where provided: page no/section/legend</b>	<b>n/a</b>
Describe statistical tests used and justify choice of tests.	All statistics were performed using GraphPad Prism packages either using a t-test or ANOVA paired tests.	
<b>Data availability</b>	<b>indicate where provided: page no/section/legend</b>	<b>n/a</b>
For newly created and reused datasets, the manuscript includes a data availability statement that provides details for access or notes restrictions on access.	Data will be available upon request.	
If newly created datasets are publicly available, provide accession number in repository <b>OR</b> DOI <b>OR</b> URL and licensing details where available.	RNAseq data can be found Bioproject: PRJNA1106430 Biosample: SAMN41132906 SRA:	
If reused data is publicly available provide accession number in repository <b>OR</b> DOI <b>OR</b> URL, <b>OR</b> citation.		N/A
<b>Code availability</b>	<b>indicate where provided: page no/section/legend</b>	<b>n/a</b>
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 is provided on GitHub.	
If newly generated code is publicly available, provide accession number in repository, <b>OR</b> DOI <b>OR</b> URL and licensing details where available. State any restrictions on code availability or accessibility.	<a href="https://github.com/benjaminwiner/GSEA_analysis/blob/main/BYW_GSEA_analysis">https://github.com/benjaminwiner/GSEA_analysis/blob/main/BYW_GSEA_analysis</a>  <a href="https://github.com/benjaminwiner/RNAseq_volcanoplotcode/blob/main/RNAseq_Volcano_plot_code">https://github.com/benjaminwiner/RNAseq_volcanoplotcode/blob/main/RNAseq_Volcano_plot_code</a>  <a href="https://github.com/benjaminwiner/Migration_analysis_code/commit/734f21019633e1267362cbbd4d6086340f4a268a">https://github.com/benjaminwiner/Migration_analysis_code/commit/734f21019633e1267362cbbd4d6086340f4a268a</a>	
If reused code is publicly available provide accession number in repository <b>OR</b> DOI <b>OR</b> URL, <b>OR</b> citation.	There are no restrictions on any of the code or its use.	N/A

## **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.

<b>Adherence to community standards</b>	<b>indicate where provided: page no/section/legend</b>	<b>n/a</b>
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.		N/A