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Materials Design Analysis Reporting (MDAR) Checklist for Authors

The MDAR framework establishes a minimum set of requirements in transparent reporting mainly applicable to studies in the life sciences.

eLife asks authors to **provide detailed information within their article** to facilitate the interpretation and replication of their work. Authors can also upload supporting materials to comply with relevant reporting guidelines for health-related research (see EQUATOR Network), life science research (see the BioSharing Information Resource), or animal research (see the ARRIVE Guidelines and the STRANGE Framework; for details, see *eLife*'s Journal Policies). Where applicable, authors should refer to any relevant reporting standards materials in this form.

For all that apply, please note **where in the article** the information is provided. Please note that we also collect information about data availability and ethics in the submission form.

Materials:

Newly created materials	Indicate where provided: section/figure 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. Genetically engineered BICC1 KO, BICC1-S240P and BICC1-G821E HEK293 cells	Availability is addressed in the 'DATA SHARING STATEMENT". In accordance with the guidelines about the sharing of unique research resources, we will make the designed cells available to the scientific community after completion of MTA. Requests from for-profit corporations will need to go through the Cleveland Clinic Innovations office.	

Antibodies	**Indicate where provided: section/figure legend**	**N/A**
For commercial reagents, provide supplier name, catalogue number and RRID, if available. anti-Polycystin-1 (7e12) anti-Polycystin-1 (2b7) anti-PC2 (YCC2) anti-Polycystin-2 (D-3) anti-Polycystin-2 (G20) anti-myc Rat IgG1 anti-GST anti-BICC1 (A-12) anti-BICC1 g-Tubulin anti-HA (3F10) anti-V5tag (SV5-Pk1) anti-MBP anti-GST anti-GAPDH (14C10)	anti-Polycystin-1 (7e12), Santa Cruz Biotech, SC-130554, RRID:AB_2163355 anti-Polycystin-1 (2b7), published in Newby et. al. 2002 (PMID:11901144) anti-PC2 (YCC2), provided by Dr. S. Somlo anti-Polycystin-2 (D-3), Santa Cruz Biotech, SC-28331, RRID:AB_672377 anti-Polycystin-2 (G20), Santa Cruz Biotech, SC-10376, RRID:AB_654304 anti-myc Rat IgG1, Clone JAC6, Bio-Rad, MCA1929, RRID:AB_322203 anti-GST, Santa Cruz Biotech, SC-459, RRID:AB_631586 anti-BICC1 (A-12), Santa Cruz Biotech, SC-514846 anti-BICC1, Sigma-Aldrich, HPA045212, RRID:AB_10959667 anti-g-Tubulin, Sigma-Aldrich, T6557, RRID:AB_477584 anti-HA (3F10), Roche, 11867423001, RRID:AB_390918 anti-V5tag (SV5-Pk1), Bio-Rad, MCA1360, RRID:AB_322378	

	anti-MBP, NEB, E8030S, RRID:AB_1559728 anti-GST, Santa Cruz, sc-138, RRID:AB_627677 anti-GAPDH (14C10), Cell Signaling, 2118, RRID:AB_561053	

DNA and RNA sequences	Indicate where provided: section/figure legend	N/A
Short novel DNA or RNA including primers, probes: Sequences should be included or deposited in a public repository. mRNA-seq of HEK293 cell lines Primers for engineered cell lines	The mRNA-seq data are deposited into the Gene Expression Omnibus (GEO) database (GSE262417). The primers for the genomically engineered cells are included in the Supplemental Methods section entitled “Cell Culture Studies”.	

Cell materials	Indicate where provided: section/figure legend	N/A
Cell lines: Provide species information, strain. Provide accession number in repository OR supplier name, catalog number, clone number, OR RRID. HEK293 UCL-93	HEK293 – human embryonic kidney cell line, available from ATTC #CRL1573 UCL-93 - normal human kidney cortical epithelial cell line, available from the University of Sheffield	
Primary cultures: Provide species, strain, sex of origin, genetic modification status.		N/A

Experimental animals	Indicate where provided: section/figure 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 *Xenopus* laevis	*Xenopus* - purchased from *Xenopus* Express PKD2 knockout mice - provided by Dr. S. Somlo	

PKD2 knockout mice PKD1Fl/FL:Pkhd1-Cre mice Bicc1 knockout mice	PKD1Fl/FL:Pkhd1-Cre mice - provided by Drs. S. Somlo and P. Igarashi Bicc1 knockout mice - generated by Drs. E.M. De Robertis and O. Wessely	
Animal observed in or captured from the field: Provide species, sex, and age where possible.		N/A

Plants and microbes	**Indicate where provided: section/figure 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).		N/A
Microbes: provide species and strain, unique accession number if available, and source.		N/A

Human research participants	**Indicate where provided: section/figure legend) or state if these demographics were not collected**	**N/A**
If collected and within the bounds of privacy constraints report on age, sex, gender and ethnicity for all study participants.		N/A

Design:

Study protocol	**Indicate where provided: section/figure legend**	**N/A**
If the study protocol has been pre-registered, provide DOI. For clinical trials, provide the trial registration number OR cite DOI.		N/A

Laboratory protocol	**Indicate where provided: section/figure legend**	**N/A**
Provide DOI OR other citation details if detailed step-by-step protocols are available.		N/A

Experimental study design (statistics details) *

For in vivo studies: State whether and how the following have been done	**Indicate where provided: section/figure legend. If it could have been done, but was not, write "not done"**	**N/A**
Sample size determination	Yes - see the Supplemental Methods section entitled "*Xenopus* Embryo Manipulations" and "Mouse Studies".	
Randomisation	Yes - see the Supplemental Methods section entitled "*Xenopus* Embryo Manipulations".	
Blinding	Yes - see the Supplemental Methods section entitled "*Xenopus* Embryo Manipulations".	
Inclusion/exclusion criteria	Yes - see the Supplemental Methods section entitled "*Xenopus* Embryo Manipulations" and "Mouse Studies".	

Sample definition and in-laboratory replication	**Indicate where provided: section/figure legend**	**N/A**
State number of times the experiment was replicated in the laboratory.	Experiments were replicated at least 3 times. Sample sizes are shown in Tables and Figure legends and represent biological replicates (individual cells or animals).	
Define whether data describe technical or biological replicates.	Data describe biological replicates (individual cell experiments or animals).	

Ethics	**Indicate where provided: section/submission form**	**N/A**
Research was performed following written informed consent and according to the declaration of Helsinki and oversight was provided by the Medizinische Genetik Mainz.	This is addressed in the Methods section entitled "International Diagnostic Clinical Cohort".	
Mouse and Xenopus laevis studies were approved by the Institutional Animal Care and Use Committee at the Cleveland Clinic Foundation and LSU Health Sciences Center (present and former employer of Dr. Wessely) and adhered to the National Institutes of Health Guide for the Care and Use of Laboratory Animals. Experimental design and data interpretation followed the ARRIVE1 reporting guidelines.	This is addressed in the Methods section entitled "Animal Studies".	
Studies involving specimen and field samples: State if relevant permits obtained, provide details of authority approving study; if none were required, explain why.		N/A

Dual Use Research of Concern (DURC)	**Indicate where provided: section/submission form**	**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.		N/A

Analysis:

Attrition	**Indicate where provided: section/figure legend**	**N/A**
Describe whether exclusion criteria were pre-established. 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.	Exclusion criteria were for the *Xenopous* experiments are described in the Supplemental Methods section entitled "*Xenopus* Embryo Manipulations".	

Statistics	**Indicate where provided: section/figure legend**	**N/A**
Describe statistical tests used and justify choice of tests.	See the Methods section entitled "Statistical analysis".	

Data availability	**Indicate where provided: section/submission form**	**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 associated with this study are present in the paper or the Supplementary Materials. The "Data Sharing Statement" provides the information for the deposited mRNA-seq data.	
When newly created datasets are publicly available, provide accession number in repository OR DOI and licensing details where available.	The mRNA-seq data are deposited into the Gene Expression Omnibus (GEO) database (GSE262417).	
If reused data is publicly available provide accession number in repository OR DOI, OR URL, OR citation.		N/A

Code availability	**Indicate where provided: section/figure legend**	**N/A**

For any computer code/software/mathematical algorithms essential for replicating the main findings of the study, whether newly generated or re-used, the manuscript includes a data availability statement that provides details for access or notes restrictions.	Rosetta software is publicly available at: https://www.rosettacommons.org/software/license-and-download	N/A
Where 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.		N/A
If reused code is publicly available provide accession number in repository OR DOI OR URL, OR citation.	The software used for the mRNA-sequencing analysis is included in the Supplementary Methods section entitled "Transcriptome Analysis".	

Reporting:

The MDAR framework recommends adoption of discipline-specific guidelines, established and endorsed through community initiatives.

Adherence to community standards	**Indicate where provided: section/figure legend**	**N/A**
State if relevant guidelines (e.g., ICMJE, MIBBI, ARRIVE, STRANGE) have been followed, and whether a checklist (e.g., CONSORT, PRISMA, ARRIVE) is provided with the manuscript.	ARRIVE checklist is provided	

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* We provide the following guidance regarding transparent reporting and statistics; we also refer authors to Ten common statistical mistakes to watch out for when writing or reviewing a manuscript.

Sample-size estimation

- You should state whether an appropriate sample size was computed when the study was being designed
- You should state the statistical method of sample size computation and any required assumptions ● If no explicit power analysis was used, you should describe how you decided what sample (replicate) size (number) to use

Replicates

- You should report how often each experiment was performed
- You should include a definition of biological versus technical replication
- The data obtained should be provided and sufficient information should be provided to indicate the number of independent biological and/or technical replicates
- If you encountered any outliers, you should describe how these were handled
- Criteria for exclusion/inclusion of data should be clearly stated

- High-throughput sequence data should be uploaded before submission, with a private link for reviewers provided (these are available from both GEO and ArrayExpress)

Statistical reporting

- Statistical analysis methods should be described and justified
- Raw data should be presented in figures whenever informative to do so (typically when N per group is less than 10)
- For each experiment, you should identify the statistical tests used, exact values of N, definitions of center, methods of multiple test correction, and dispersion and precision measures (e.g., mean, median, SD, SEM, confidence intervals; and, for the major substantive results, a measure of effect size (e.g., Pearson's r, Cohen's d)
- Report exact p-values wherever possible alongside the summary statistics and 95% confidence intervals. These should be reported for all key questions and not only when the p-value is less than 0.05.

Group allocation

- Indicate how samples were allocated into experimental groups (in the case of clinical studies, please specify allocation to treatment method); if randomization was used, please also state if restricted randomization was applied
- Indicate if masking was used during group allocation, data collection and/or data analysis