**Materials Design Analysis Reporting (MDAR)**

**Checklist for Authors**

The [MDAR framework](https://osf.io/xfpn4/) 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](http://www.equator-network.org/%20)), life science research (see the [BioSharing Information Resource](http://biosharing.org/)), or animal research (see the [ARRIVE Guidelines](http://www.plosbiology.org/article/info%3Adoi/10.1371/journal.pbio.1000412) and the [STRANGE Framework](https://doi.org/10.1038/d41586-020-01751-5); for details, see *eLife*’s [Journal Policies](https://reviewer.elifesciences.org/author-guide/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. | Renilla luciferase reporters possessing the 5' UTR of interest were generated in this study. Corresponding cloned 5' UTRs and plasmid’s names are indicated in key resource table. The data with the use of these reporters is shown in figure 2; figure 4; figure 2. - supplemental figure 2. Plasmids can be requested at the European Plasmid Repository. (Described in Materials & Methods).HeLa-eIF2A-KO and HEK293T-H2-Kb-eIF2A-KO cell lines were generated in this study and can be obtained on request. |  |
|  |  |  |
| **Antibodies** | **Indicate where provided: section/figure legend** | **N/A** |
| For commercial reagents, provide supplier name, catalogue number and [RRID](https://scicrunch.org/resources), if available. | anti-ATF-4 (D4B8) (Rabbit monoclonal) Cell Signaling cat. No #11815 Lot#6 RRID:AB\_2616025 used in Figure 1 supplement figure 1; Figure 4 supplement figure 1anti-C-Myc (Rabbit monoclonal) Cell Signaling cat. No. #13987 Lot#6 RRID: n/a used in Figure 1 supplement figure 1anti-CCND3 (Rabbit polyclonal) invitrogen cat no. #PA5-80416 Lot#UH2828593 RRID:AB\_2787735 used in Figure 2anti-eIF2A (3A7A8) (mouse monoclonal) santa cruz cat. No. sc-517214 Lot#B0821 RRID: n/aused in Figure 1-3; Figure 1 supplement figure 1; Figure 2 supplement figure 2; Figure 3 supplement figure 1; Figure 4 supplement figure 1anti-FLAG (Rabbit polyclonal) SIGMA cat. No. F7425-.2MG Lot#0000252651 RRID:AB\_439687 used in Figure 1 supplement figure 1; Figure 3 supplement figure 1;anti-GAPDH (Rabbit monoclonal) Cell Signaling cat. No. #2118 LOT#16 RRID:AB\_561053 used in Figure 1 supplement figure 1; Figure 4 supplement figure 1anti-HSP90 (Rabbit monoclonal) Cell signaling cat. No. 4877 Lot#6 RRID:AB\_2233307used in Figure 1; Figure 1 supplement figure 1anti-Lamin A/C (636) (mopuse monoclonal) santa cruz cat. No. sc-7292 Lot#C0218 RRID:AB\_627875used in Figure 1 supplement figure 1;anti-NCAPH2 (Rabbit polyclonal) Proteintech cat. No. 26172-1-AP Lot#00039440 RRID:AB\_2880411 used in Figure 2anti-p-p38 (Rabbit polyclonal) Cell Signaling cat. No. #9211 Lot#25 RRID:AB\_331641used in Figure 1 supplement figure 1;anti-PPFIA1 (Rabbit polyclonal) Proteintech cat. No. 14175-1-AP Lot#00005224 RRID:AB\_2171592 used in Figure 2anti-puromycin (mouse monoclonal) Sigma cat. No. MABE343 Lot#3484967 RRID:AB\_2566826used in Figure 1; Figure 1 supplement figure 1;anti-RPS6KB2 (Rabbit polyclonal) Proteintech cat. No. 26194-1-AP Lot#00040692 RRID:AB\_2880419 used in Figure 2anti-Tubulin Sigma cat. No. T9026 LOT#0000307925 RRID:AB\_477593 used in Figure 2-3; Figure 1 supplement figure 1; Figure 2 supplement figure 2; Figure 3 supplement figure 1;anti-G3BP1 (mouse monoclonal) santa cruz cat. No. sc-81940 Lot@G0617 RRID:AB\_1123055 used in Figure 4 supplement figure 1 |  |
|  |  |  |
| **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. | sequences of oligos used for cloning and qRT-PCR DNA are listed in the key resource table of the paper. |  |
|  |  |  |
| **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. | HeLa wt cell line was obtained from DSMZ;HeLa eIF2A-KO cells were generated in this study;HEK293T-H2-Kb were gift from Rienk Offringa lab;HEK293T-H2-Kb-eIF2A-KO were generated in this study |  |
| 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. |  | N/A |
| 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 |  | N/A |
| Randomisation |  | N/A |
| Blinding |  | N/A |
| Inclusion/exclusion criteria |  | N/A |
|  |  |  |
| **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 described in Figure legends, and each dot on graphs represents one biological replicate (individual cells; to gain biological replicates, the experiment was carried out on different days).  |  |
| Define whether data describe technical or biological replicates. | Data describe biological replicates (individual cells). |  |
|  |  |  |
| **Ethics** | **Indicate where provided: section/submission form** | **N/A** |
| Studies involving human participants: State details of authority granting ethics approval (IRB or equivalent committee(s), provide reference number for approval. |  | N/A |
| Studies involving experimental animals: State details of authority granting ethics approval (IRB or equivalent committee(s), provide reference number for approval. |  | N/A |
| 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. |  | N/A |
|  |  |  |
| **Statistics** | **Indicate where provided: section/figure legend** | **N/A** |
| Describe statistical tests used and justify choice of tests. | The exact statistic tests used for the data analysis are indicated in each figure legend. For the next generation data analysis we used DESeq2 package that is commonly used for such type of data analysis. DESeq2 package relies on the Wald test and adjustment of p-values for multiple comparison. Luciferase reporters and quantification of western blots were analyzed with either Dunnett’s multiple comparison test ANOVA or by unpaired, two-sided, t-test. ns = not significant. |  |
|  |  |  |
| **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 source data files. The next generation sequencing underlying the scatter plots in figure 2 and figure 3 and used for metagene profiles generation are deposited at NCBI GEO: GSE282509 |  |
| When newly created datasets are publicly available, provide accession number in repository OR DOI and licensing details where available. | The next generation sequencing data are deposited at NCBI GEO: GSE282509 |  |
| 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. | Software for the ribosome profiling data analysis was developed previously in the lab and is deposited at - https://github.com/aurelioteleman/Teleman-Lab |  |
| 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. | https://github.com/aurelioteleman/Teleman-Lab |  |

**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. |  | N/A |

\* 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](https://doi.org/10.7554/eLife.48175).

**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