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.	Footnote includes a materials availability statement.	

Antibodies	indicate where provided: page no/section/legend)	n/a
For commercial reagents, provide supplier name, catalogue number and RRID, if available.	In Methods sections '*H3K36me3 chromatin immunoprecipitation' and 'CRISPR/Cas9-mediated gene depletions'* supplier names and RRIDs are given.	

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.	sgRNA sequences are given in supplement table 1. RT-qPCR primers are available upon request to the corresponding author.	

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.	Information concerning the cell lines used including RRIDs are given in Methods sections '*cell lines'* and '*Correlation and Gene Ontology analyses'*	
Primary cultures: Provide species, strain, sex of origin, genetic modification status.	Not used	

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.	Not used	n/a
Animal observed in or captured from the field: Provide species, sex, and age where possible.	Not used	n/a

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).	Not used	n/a
Microbes: provide species and strain, unique accession number if available, and source.	Not used	n/a

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.	No human subjects were included in this study. We however note usage of public available data for lung cancer patients from The Cancer Genome Atlas. This is described in the Methods section.	

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.	This is not a clinical trial/study.	

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.	Protocols from manufacturers are cited by name of the product and the company in the Methods section. Novel protocols are described in details and/or with reference in the Methods section.	

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	This is not a clinical trial/study.	n/a
Randomisation	This is not a clinical trial/study.	n/a
Blinding	This is not a clinical trial/study.	n/a
Inclusion/exclusion criteria	This is not a clinical trial/study.	n/a

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.	Listed in appropriate figure legends and in Methods section. For OMICs data determined using biological replicates the information is given in the Methods section.	
Define whether data describe technical or biological replicates.	Omics data are from biological replicates. MTS cell viability assays are from two biological replicates each performed in duplicate. RT-qPCR experiments are at least technical triplicates of one biological sample and performed several times for results confirmation. Details specified in appropriate figure legends.	

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.	No human subjects were involved in the study	n/a
Studies involving experimental animals: State details of authority granting ethics approval (IRB or equivalent committee(s), provide reference number for approval.	No animals were involved in the study	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.	No specimen or field samples were involved	n/a

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.	No subject to dual use research of concern	n/a

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.	No data points were excluded from the analysis. Exceptions are RT-qPCR data with a ct above 35 and RNA-seq, ChIP-seq, and DNA methylation data filtered as described in the Methods section. Moreover, in case of experimental failure was evaluated to be present due to material problems, human failures or instrumental failures data points were excluded. Following revision of the manuscript, data for ZEB1 sgRNA 3 and FGFR1 sgRNA 2 were removed relative to the original submission. For FGFR1 sgRNA 2 this is a consequence of lack of reduction of FGFR1 protein amounts following sgRNA 2 genomic processing which questioned the efficiency. In this line, FGFR1 sgRNA 2 resulted in a gene-expression profile, as well as MTS profile, differing to the more common observations with sgRNA1 and sgRNA3. For ZEB1 sgRNA 3 this is a consequence of generation of a truncated ZEB1 protein following sgRNA 3 genomic processing which is a product of unclear functionality. In this line, ZEB1 sgRNA 3 resulted in a gene-expression profile following erlotinib, which differed to the common profile observed with sgRNA1 and sgRNA2.	

Statistics	indicate where provided: page no/section/legend	n/a
Describe statistical tests used and justify choice of tests.	This is described throughout the Methods section for the relevant type of experiments.	

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.	A data availability statement is present as a footnote.	
If newly created datasets are publicly available, provide accession number in repository **OR** DOI **OR** URL and licensing details where available.		n/a
If reused data is publicly available provide accession number in repository **OR** DOI **OR** URL, **OR** citation.		n/a

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.	No newly generated code or software generated. Used software is described including reference and RRID if available.	
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.		n/a
If reused code is publicly available provide accession number in repository **OR** DOI **OR** URL, **OR** citation.		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.

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.	ICMJE guidelines were followed, as the journal follows ICMJE recommendations for publication.	n/a

Article Information: https://dx.doi.org/10.21037/tlcr-22-507