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**Sample-size estimation**

* You should state whether an appropriate sample size was computed when the study was being designed
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* If no explicit power analysis was used, you should describe how you decided what sample (replicate) size (number) to use

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**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)

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This information can be found in the section of Materials and methods and in figure legends. High-throughput sequence can be found via the link: https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE165321.

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* 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.

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(For large datasets, or papers with a very large number of statistical tests, you may upload a single table file with tests, Ns, etc., with reference to sections in the manuscript.)

**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
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**Additional data files (“source data”)**

* We encourage you to upload relevant additional data files, such as numerical data that are represented as a graph in a figure, or as a summary table
* Where provided, these should be in the most useful format, and they can be uploaded as “Source data” files linked to a main figure or table
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Please indicate the figures or tables for which source data files have been provided:

Source data for figure 1:

Source data 1. qRT-PCR data for miR-21-5p relative expression.

Source data 2. Uncropped Western blots for Figure 1E.

Source data 3. The quantitative band intensities for Figure 1E.

Source data 4. Uncropped Western blots for Figure 1F.

Source data 5. The quantitative band intensities for Figure 1F.

Source data for figure 2:

Source data 1. qRT-PCR data for hsa\_circ\_0003764 relative expression.

Source data 2. Uncropped gels for Figure 2F.

Source data 3. qRT-PCR data for circPTPN12 and PTPN12 relative expression with or without RNase R treatment.

Source data 4. qRT-PCR data for circPTPN12 and PTPN12 relative expression with actinomycin D at the indicated time points.

Source data 5. qRT-PCR data for circPTPN12, GAPDH and U6 relative expression in the nuclear and cytoplasmic fractions of EECs.

Source data for figure 3:

Source data 1. qRT-PCR data for circPTPN12 relative expression.

Source data 2. qRT-PCR data for miR-21-5p relative expression.

Source data 3. Data on luciferase activity in HEK-293T cells transfected with miR-21-5p mimic or inhibitor.

Source data 4. Data on luciferase activity of Luc-circPTPN12 containing single or all mutated sites of three putative miR-21-5p binding sites in HEK-293T cells transfected with miR-21-5p mimic.

Source data 5. qRT-PCR data for miR-21-5p relative expression in EECs with Ad-control or Ad-circPTPN12 treatment.

Source data 6. Uncropped Western blots for Figure 3I.

Source data 7. The quantitative band intensities for Figure 3I.

Source data 8. Uncropped Western blots for Figure 3J.

Source data 9. The quantitative band intensities for Figure 3J.

Source data for figure 4:

Source data 1. Data on luciferase activity of Luc-ΔNp63α wild or mut in HEK-293T cells transfected with miR-21-5p mimic or inhibitor.

Source data 2. qRT-PCR data for ΔNp63α relative expression in EECs transfected with miR-21-5p mimic.

Source data 3. Uncropped Western blots for Figure 4D and Figure 4E.

Source data 4. The quantitative band intensities for Figure 4D.

Source data 5. The quantitative band intensities for Figure 4E.

Source data 6. Data on luciferase activity of Luc-ΔNp63α wild or mut in HEK-293T cells transfected with circ-control or circPTPN12.

Source data 7. Uncropped Western blots for Figure 4G.

Source data 8. The quantitative band intensities for Figure 4G.

Source data 9. qRT-PCR data for E-cad, N-cad, α-SMA and FN relative expression.

Source data 10. Uncropped Western blots for Figure 4J.

Source data 11. The quantitative band intensities for Figure 4J.

Source data for figure 5:

Source data 1. qRT-PCR data of circPTPN12 relative expression for Figure 5A.

Source data 2. qRT-PCR data of miR-21-5p relative expression for Figure 5B.

Source data 3. qRT-PCR data of E-cad, N-cad, α-SMA and FN relative expression for Figure 5C.

Source data 4. qRT-PCR data of ΔNp63α relative expression for Figure 5E.

Source data 5. qRT-PCR data of miR-21-5p relative expression for Figure 5F.

Source data 6. qRT-PCR data of E-cad, N-cad, α-SMA and FN relative expression for Figure 5G.