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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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Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn’t apply to your submission:

This information does not apply to our submission because our manuscript is a description of curated computational model and related validation, sensitivity analyses, and drug target screens. We did not sample field data to conduct any analyses for this submission.

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This information does not apply to our submission because the model predictions presented are deterministic, and therefore repeated simulations of a given state yield the same outputs. We additionally did not exclude data or generate high-throughput sequence data in this manuscript.

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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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All relevant statistical analysis methods were placed in the Figure legends for the given analysis, and we expanded on these methods in the Materials and Methods section as referenced in the main text. We reported exact p-values in figure supplements where indicated in the main text.

(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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This information does not apply to our submission because we did not allocate samples into experimental groups. All conditions for model analyses are listed in the relevant Figures as well as the Materials and Methods section. No masking was used for data analysis.

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* 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
* Include model definition files including the full list of parameters used
* Include code used for data analysis (e.g., R, MatLab)
* Avoid stating that data files are “available upon request”

Please indicate the figures or tables for which source data files have been provided:

Our model, datasets used for analysis, and scripts necessary to reproduce all analysis and figures is available at <https://github.com/SysMechBioLab/Fibroblast_Signaling_Network_Model>.