***eLife’s* transparent reporting form**

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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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* You should report how often each experiment was performed
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* 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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* Statistical analysis methods should be described and justified
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* 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
* Indicate if masking was used during group allocation, data collection and/or data analysis

N/A – This study used cultured cells. Sample groups were defined by the constructs transfected into them and/or by the treatments administered.

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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
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RAW and MaxQuant processed data have been deposited in the PRIDE proteomeXchange repository and can be accessed at https://www.ebi.ac.uk/pride/login, using the accession PXD023441, username reviewer\_pxd023441@ebi.ac.uk and password w3onMUjZ. The reactions, rate equations, differential equations and parameter sets required to reproduce the models can be found in the Supplementary File 1. The code for the modelling has been deposited to github and can be accessed at [https://github.com/NguyenLab-IntegratedNetworkModeling/Akt-IRS-negative-feedback.git](https://protect-au.mimecast.com/s/rdiqCxngwOf1B8WgRt8zDsg?domain=github.com). Plasmids generated in this study will be made available upon request. Any further information and requests for resources should be directed to james.burchfield@sydney.edu.au or david.james@sydney.edu.au.