Mixed-species RNA-seq for elucidating non-cell-autonomous control of gene transcription

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- The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement
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- The statistical test(s) used AND whether they are one- or two-sided
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- For null hypothesis testing, the test statistic (e.g. F, t, r) with confidence intervals, effect sizes, degrees of freedom and P value noted
- Give P values as exact values whenever suitable.
- For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
- For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
- Estimates of effect sizes (e.g. Cohen’s d, Pearson’s r), indicating how they were calculated
- Clearly defined error bars
- State explicitly what error bars represent (e.g. SD, SE, CI)

Software and code

Policy information about availability of computer code

Data collection

No software was used.

Data analysis


For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors/reviewers upon request. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research guidelines for submitting code & software for further information.
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- Accession codes, unique identifiers, or web links for publicly available datasets
- A list of figures that have associated raw data
- A description of any restrictions on data availability

The RNA-seq data produced and used in the Anticipated Results section of this protocol can be downloaded from the European Nucleotide Archive (accession number E-MTAB-5987). Other publicly-available RNA-seq data sets that were used are downloadable from Gene Expression Omnibus series GSE85839 and ArrayExpress accession E-MTAB-5489.

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Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

| Sample size | Example data for the Anticipated Results section was based on n=3, found to be sufficient in our prior publication Hasel et al (2017). Nat Commun. |
| Data exclusions | No data were excluded |
| Replication | This is a Protocol paper, experimental finding and their replication is not a facet of the manuscript. |
| Randomization | All experimental conditions (con vs LPS) were applied to culture material derived from the same animals, therefore the allocation of animals to one or another treatment is not applicable. |
| Blinding | RNA-seq and analysis of reads was done blind to the experimental condition |

Reporting for specific materials, systems and methods

Materials & experimental systems

| n/a | Involved in the study |
| - | Unique biological materials |
| - | Antibodies |
| - | Eukaryotic cell lines |
| - | Palaeontology |
| - | Animals and other organisms |
| - | Human research participants |

Methods

| n/a | Involved in the study |
| - | ChIP-seq |
| - | Flow cytometry |
| - | MRI-based neuroimaging |

Animals and other organisms

Policy information about studies involving animals. ARRIVE guidelines recommended for reporting animal research

| Laboratory animals | P1 Long Evans rat pups were used of both sexes. E17.5 CD1 mouse embryos were used of both sexes |
| Wild animals | n/a |
| Field-collected samples | n/a |