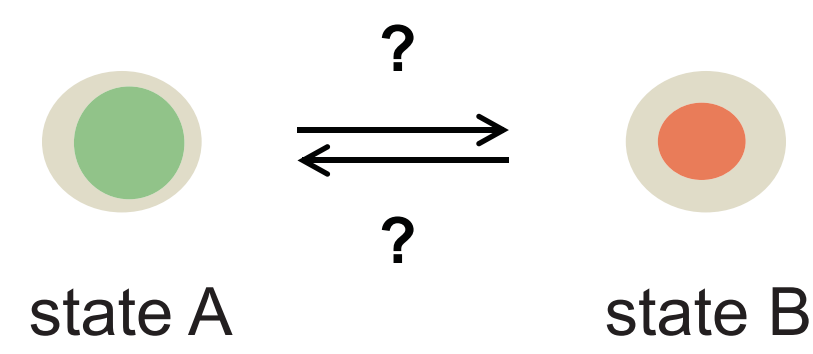


Nac1 Coordinates a Sub-network of Pluripotency Factors to Regulate Embryonic Stem Cell Differentiation

Mohan Malleshaiah¹, Megha Padi², Pau Rué³, John Quackenbush², Alfonso Martinez-Arias³ and Jeremy Gunawardena¹

¹Department of Systems Biology, Harvard Medical School, Boston, USA. ²Biostatistics and Computational Biology, Dana-Farber Cancer Institute, Boston, USA. ³Department of Genetics, University of Cambridge, Cambridge, UK.

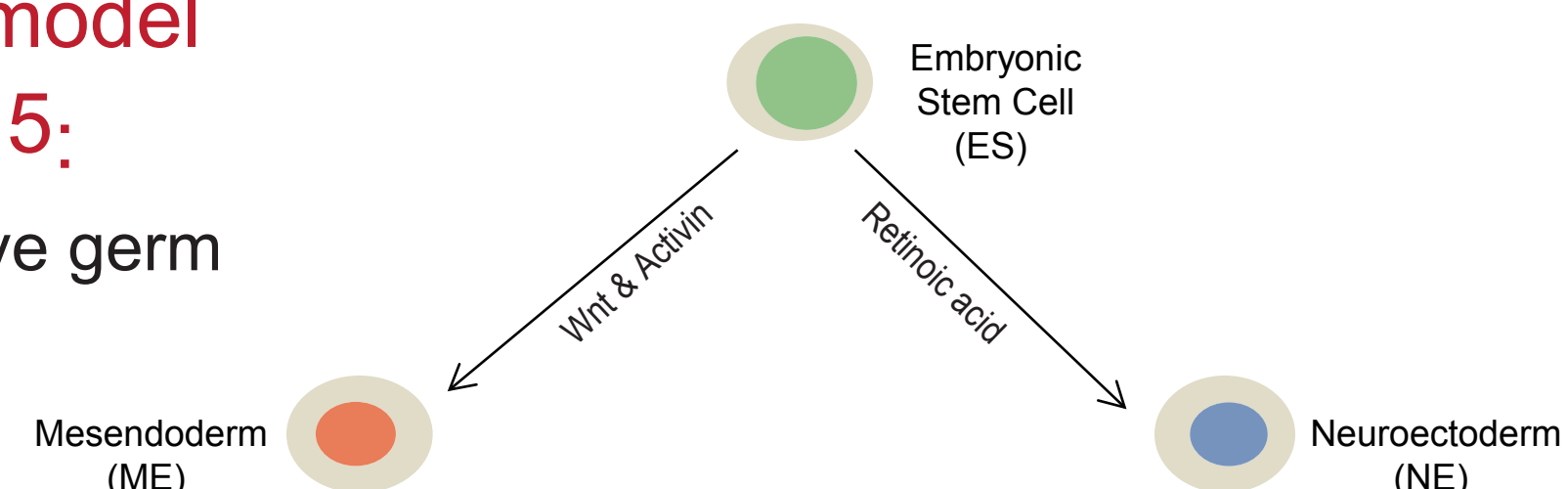
Primary Research Focus:



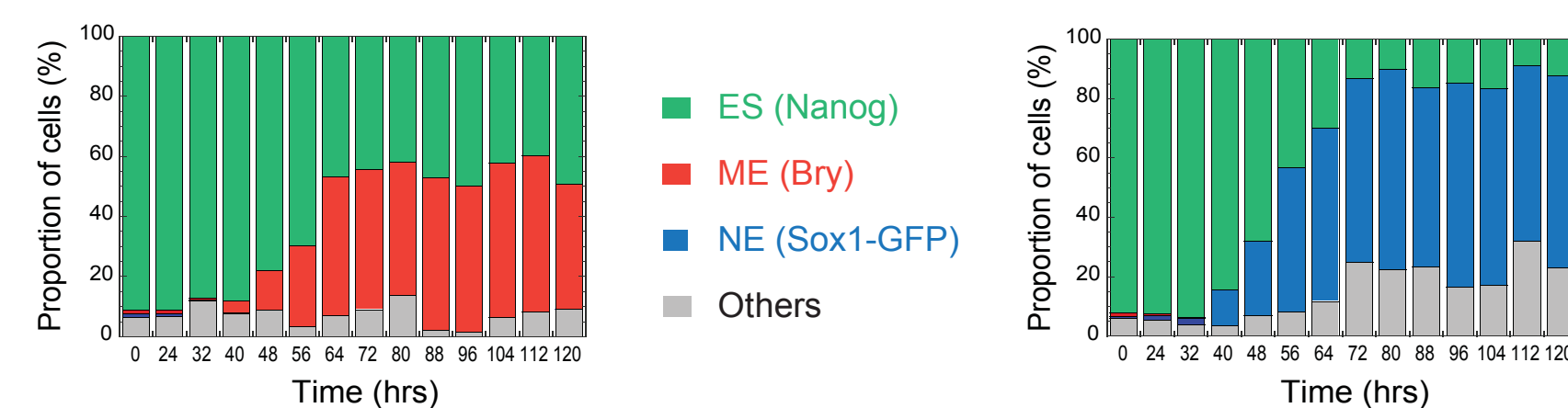
Discovering the mechanisms which control cell states¹ and their transitions

Embryonic stem cells (ESC) model system to study cell states²⁻⁵:

ESC differentiation into the alternative germ layer precursors - Mesendoderm and Neuroectoderm.

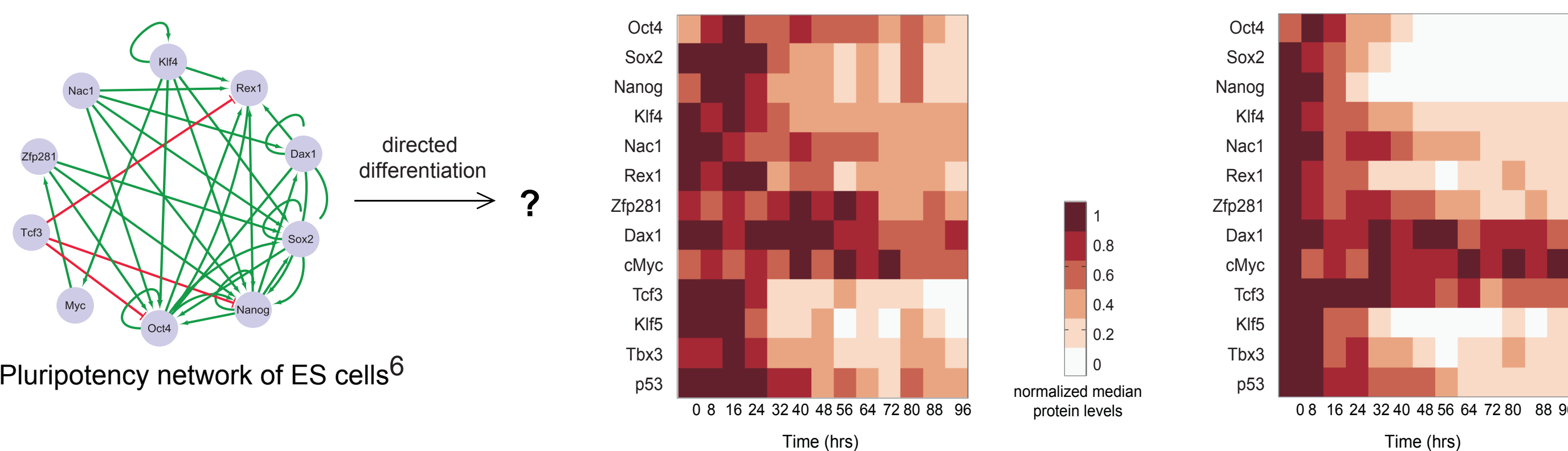


Efficient differentiation of ESCs into ME or NE



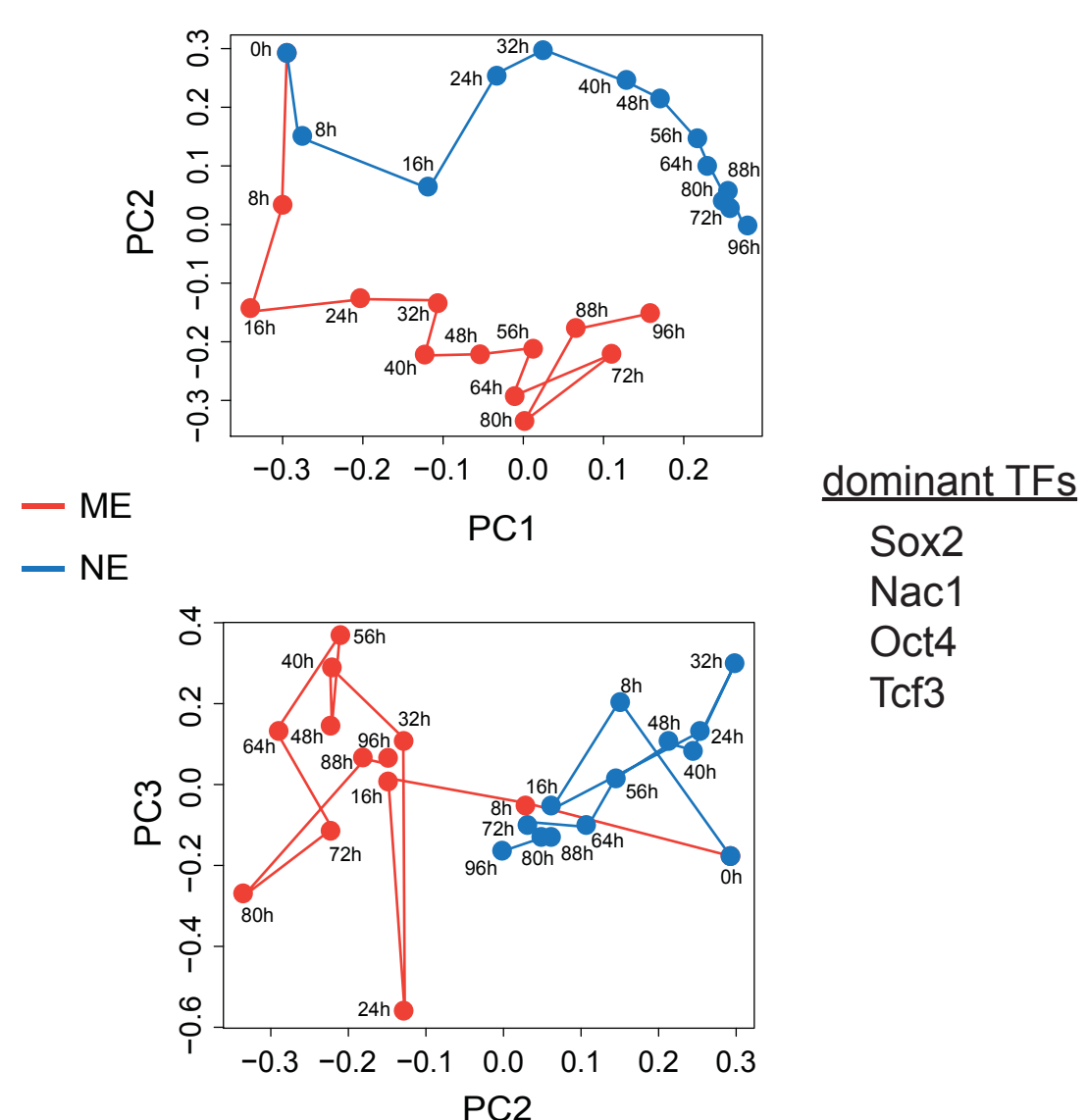
1. Reorganization of ESC TFs network during differentiation:

Quantitative changes in the level of pluripotency factors during ESC differentiation

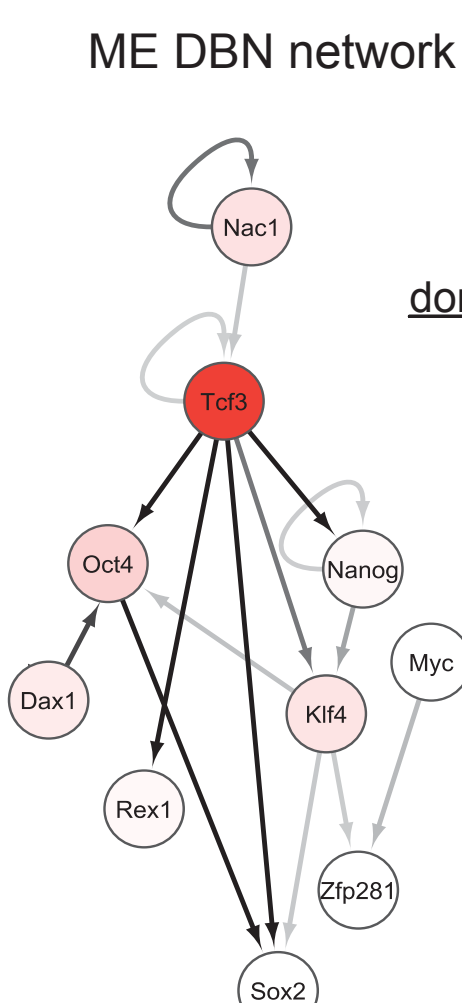


Principal component analysis (PCA)

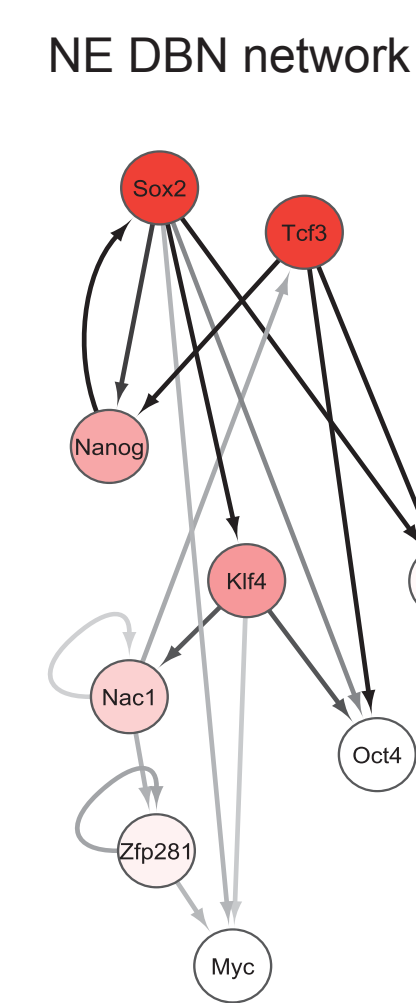
Dynamic Bayesian network (DBN) analysis



dominant TFs
Sox2
Nac1
Oct4
Tcf3



dominant TFs
Tcf3
Nac1
Oct4
Klf4

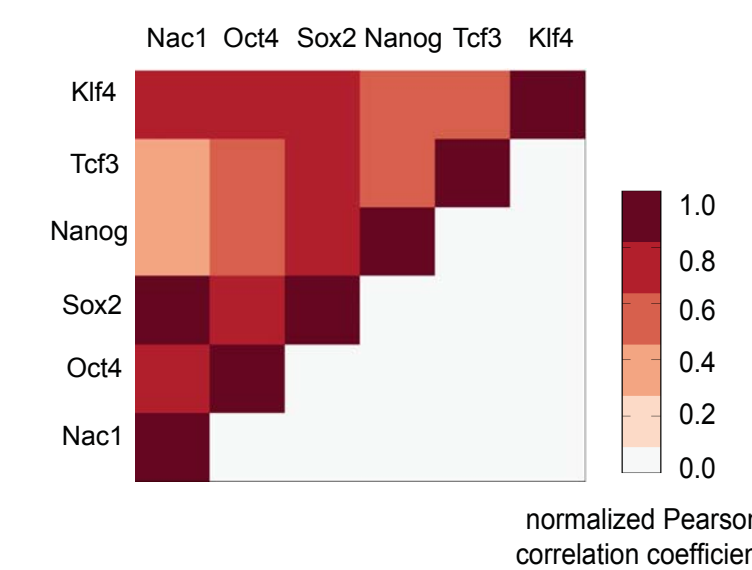


dominant TFs
Sox2
Tcf3
Nanog
Klf4

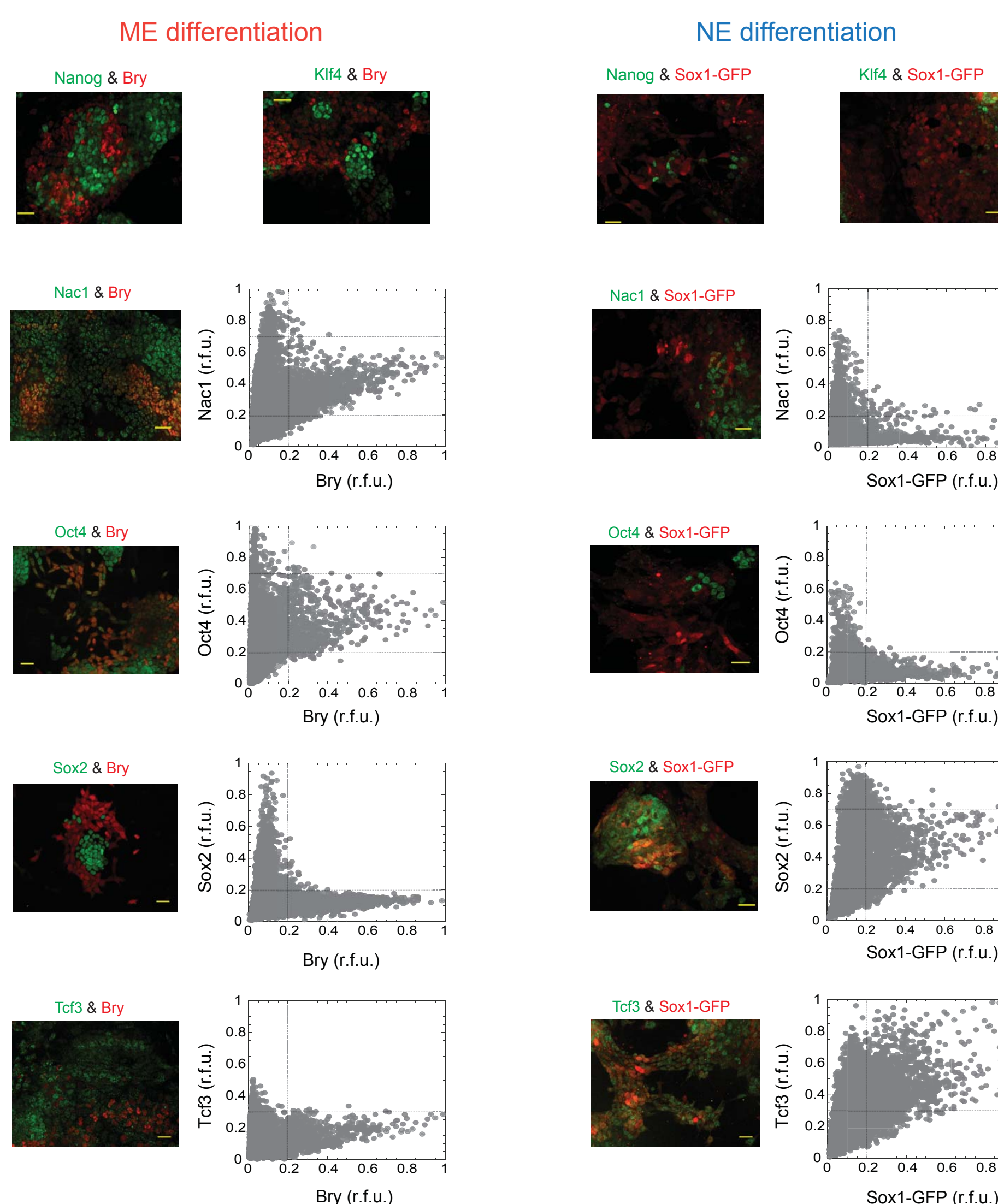
Nodes: white (<= 0.5), red gradient (0.5 - 1) and red (1)
Edges: off-white (0.25), gray scale (0.25 - 0.5) and black (> 0.5)

2. Key pluripotency TFs also regulate ESCs fate choice

Key TFs, identified by PCA & DBN, protein correlations in ES cells

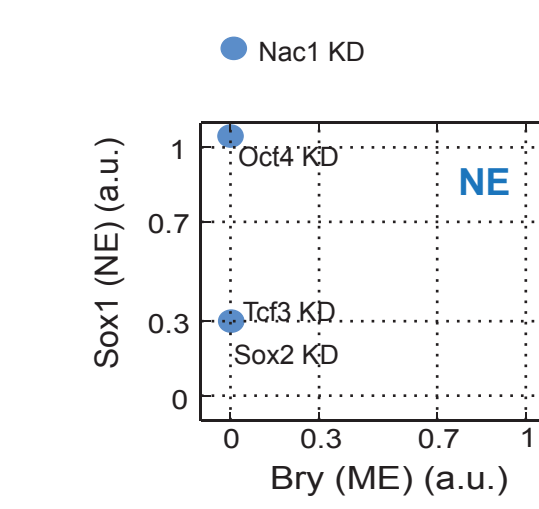
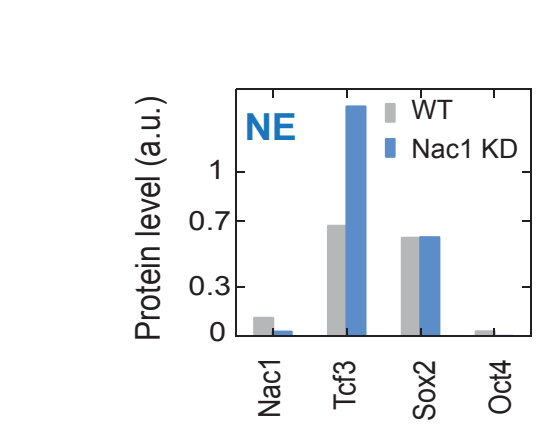


Distinct requirement of key TFs for the ME or NE choice

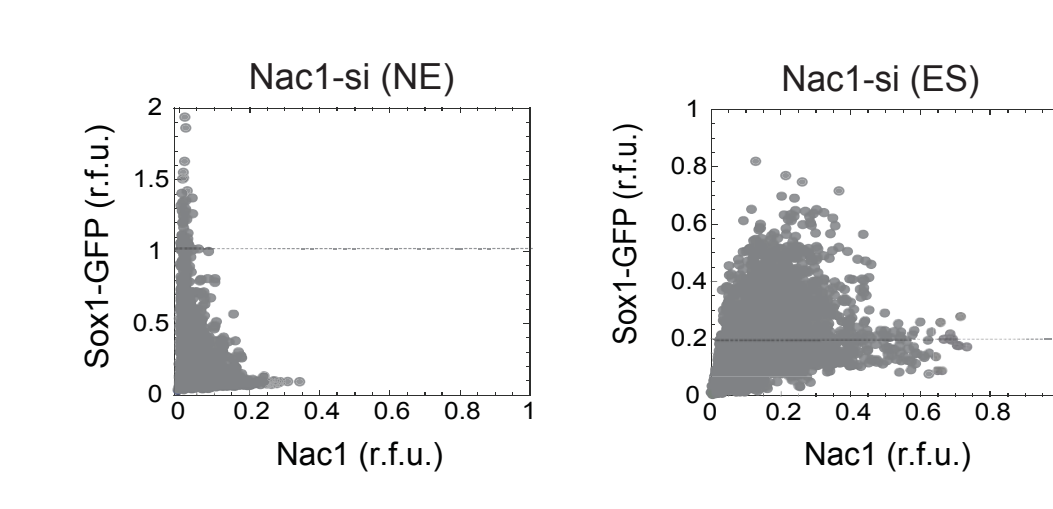
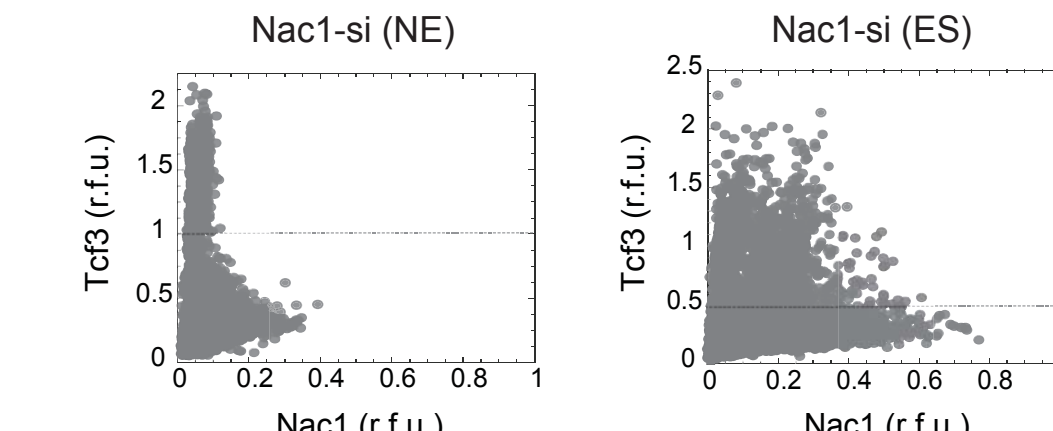


3. Nac1 controls the key TFs sub-network

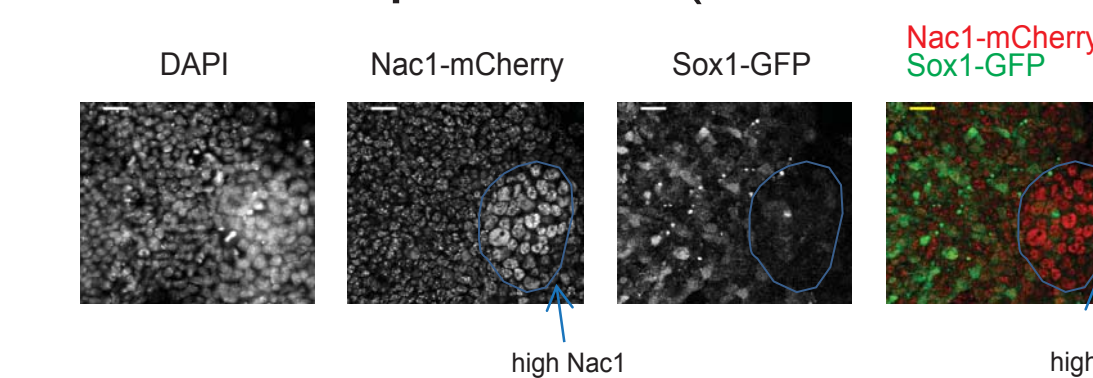
Model predictions



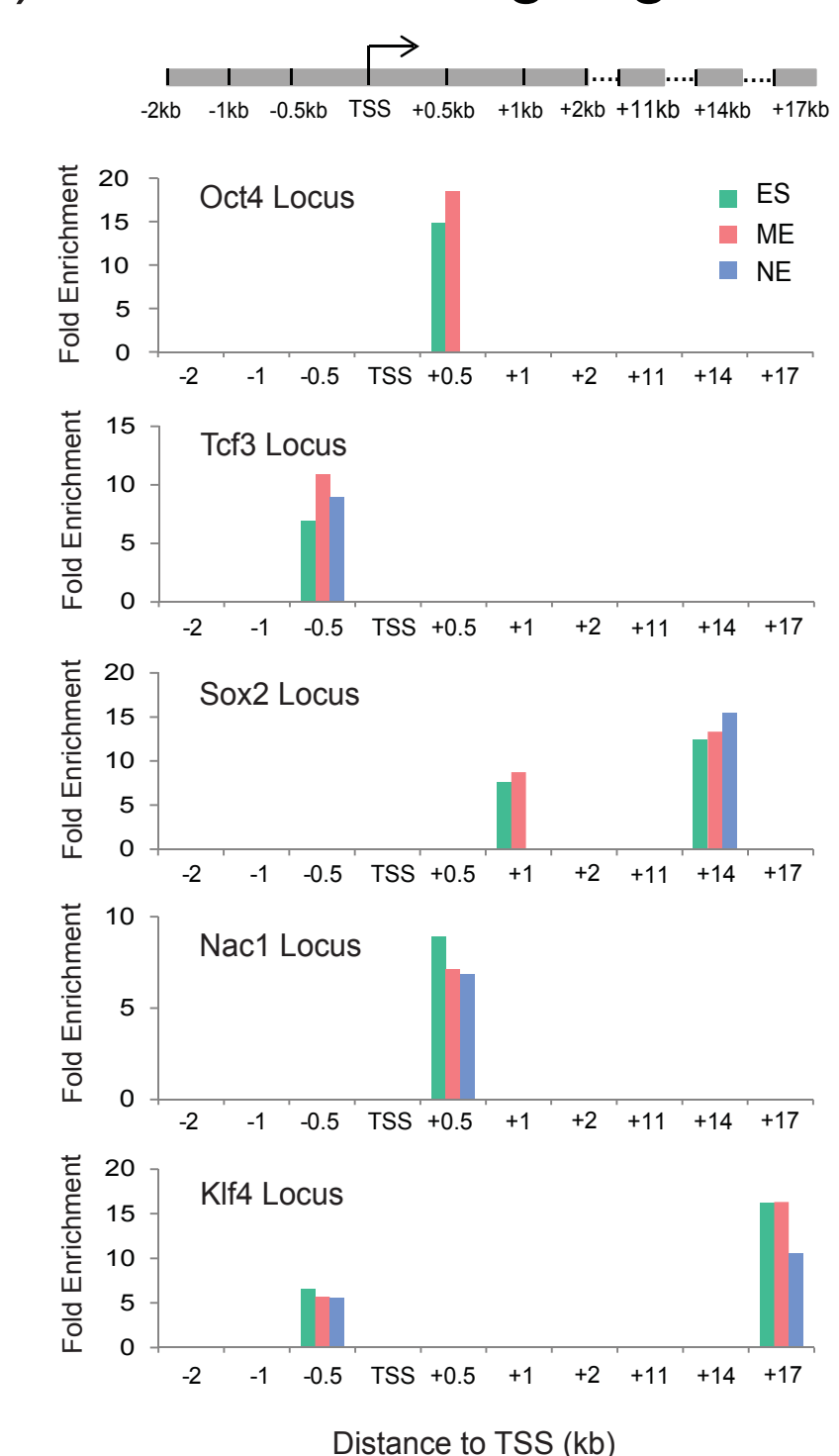
Experimental verification



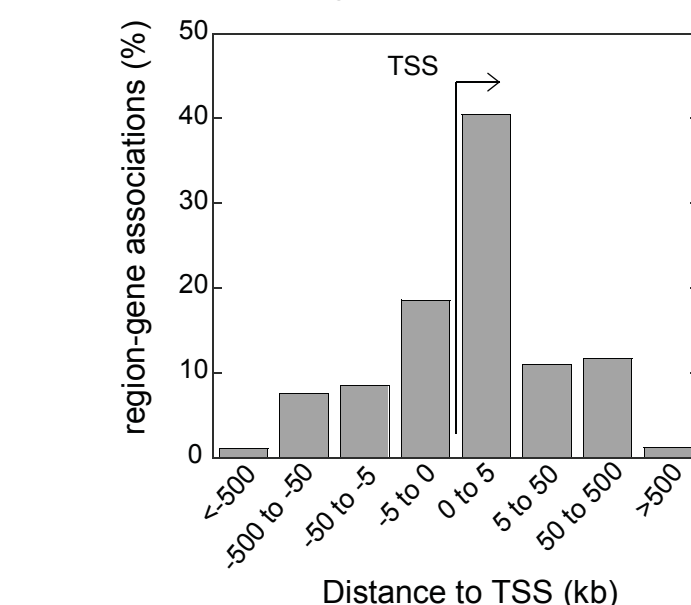
Nac1 over-expression (NE differentiation)



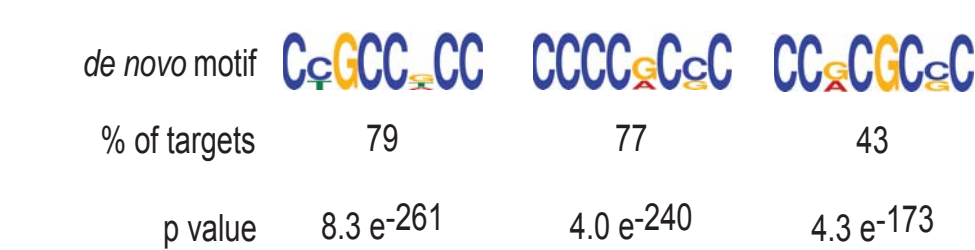
Nac1 binding regions



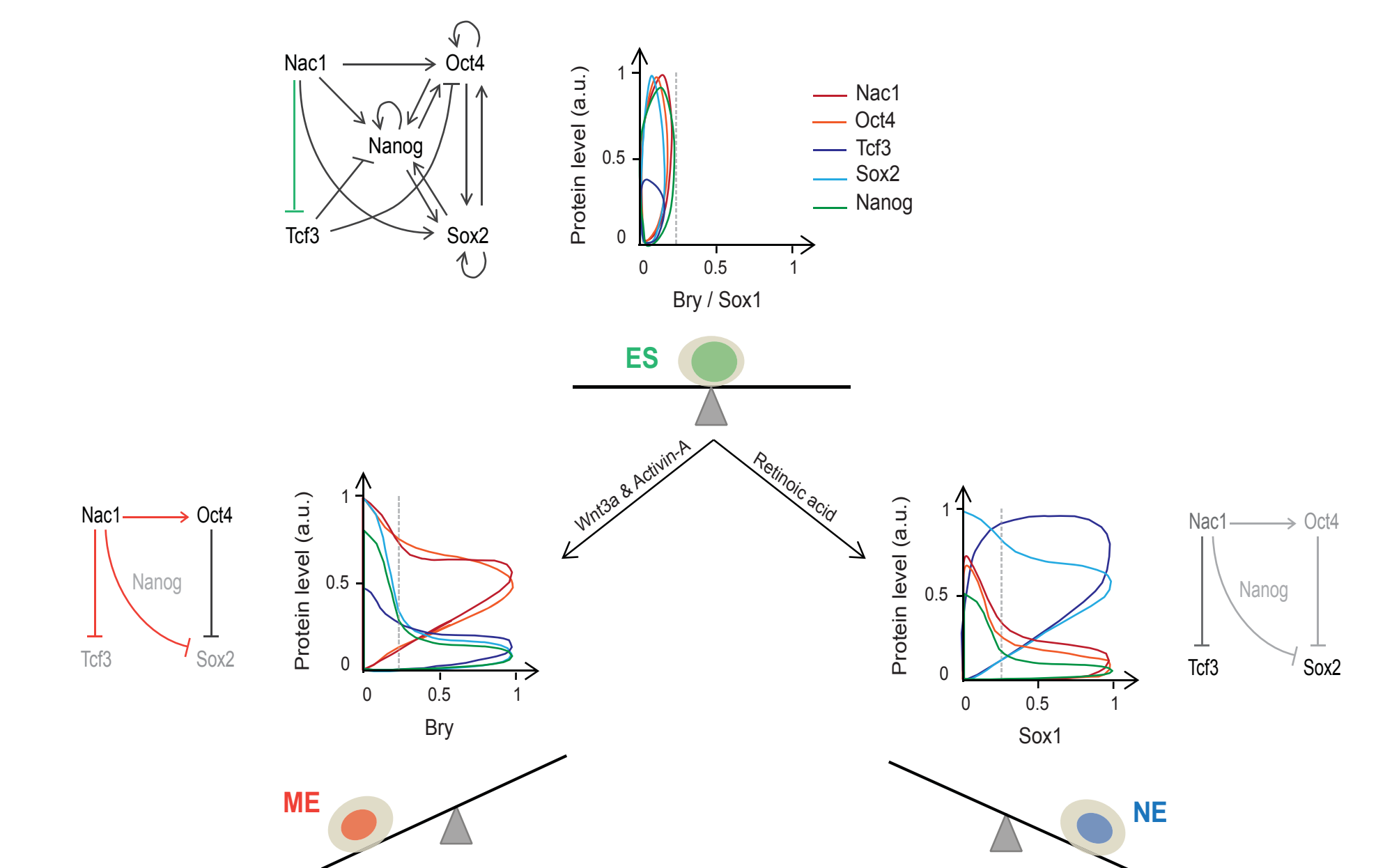
ChIP-Seq analysis for Nac1 binding



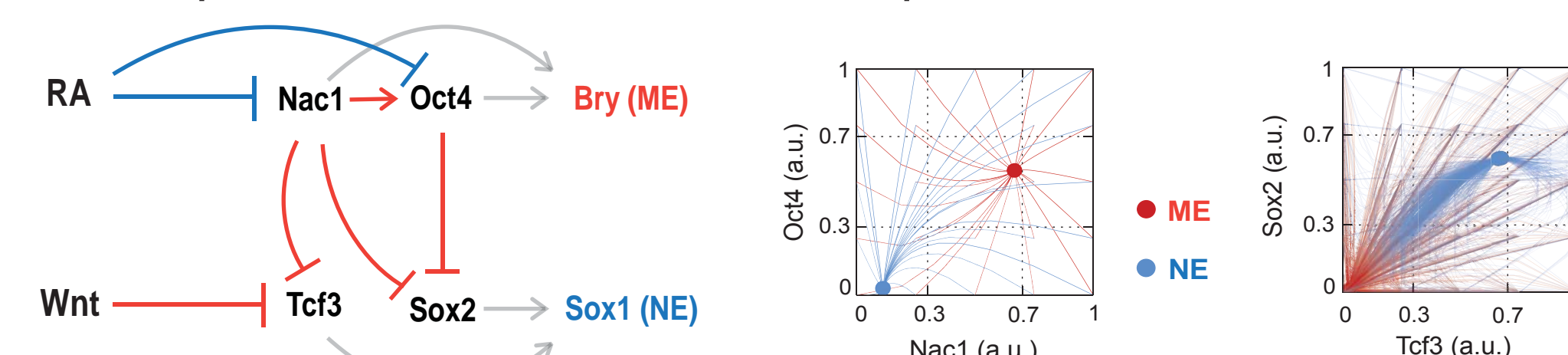
Nac1 binding motifs



Summary of ES, ME and NE cell states regulation by the key TFs



Simple mathematical model recapitulates the above results



Conclusion and perspectives:

1. A sub-network of pluripotency TFs consisting of Nac1, Oct4, Tcf3, and Sox2 promotes ESC differentiation.
2. Nac1 controls the sub-network to promote ME and repress NE fate selection.
3. Quantitatively constrained Nac1 and Oct4 favor the ME, and Tcf3 and Sox2 favor the NE, fate choice.
4. Similar mechanisms among shared TFs may govern cell-fate decisions during development and in disease states such as cancer.

References:

1. Graf T & Enver T. Nature 462, 587-594 (2009).
2. Young RA. Cell 144, 940-954 (2011).
3. Ying QL. et.al. Nature 453, 519-523 (2008).
4. Silva J & Smith A. Cell 132, 532-536 (2008).
5. Takahashi K & Yamanaka S. Cell 126, 663-676 (2006).
6. Kim J. et.al. Cell 132, 1049-1061 (2008).

Alfonso Martinez-Arias, Ph.D. Department of Genetics, University of Cambridge, Cambridge, UK.

Nikon Imaging Center, HMS.
FACS Facility, Systems Biology
Biopolymers Facility

Pau Rué, Ph.D.
Megha Padi, Ph.D.
Rebecca Ward, Ph.D.

Marc Kirschner, Ph.D.
Stephen Michnick, Ph.D.
John Quackenbush, Ph.D.

Tathagata Dasgupta, Ph.D.
Satabhisa Mukhopadhyay, Ph.D.
Victor Li, Ph.D.

Human Frontier Science Program (HFSP)
European Research Council (ERC)
National Human Genome Research Institute
National Institutes of Health (NIH)

Acknowledgements: Jeremy Gunawardena, Ph.D. Department of Systems Biology, Harvard Medical School, Boston, USA.

Anna-Katerina Hadjantonakis, Ph.D. Sloan Kettering Institute, New York, USA.