

Abstract Submitted
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Dissecting the heterogeneity of gene expressions in mouse embryonic stem cells¹ LING-NAN ZOU, MATT THOMSON, S. JOHN LIU, FAS Center for Systems Biology, Harvard University, SHARAD RAMANATHAN, Department of Molecular and Cellular Biology, FAS Center for Systems Biology, Harvard University — A population of genetically identical cells, of the same nominal cell type, and cultured in the same petri dish, will nevertheless often exhibit varying patterns of gene expression. Taking mouse embryonic stem (ES) cells as a model system, we use immunofluorescence and flow cytometry to examine in detail the distribution of expression levels for various transcription factors key to the maintenance of the ES cell identity. We find the population-level distribution of many proteins, once rescaled by the average expression level, have very similar shapes. This suggest the largest component of observed heterogeneity comes from a single source. More subtly, we find the expression many of genes appears to modulate with the cell cycle. This may suggest that the program for maintaining ES cell identity is tightly coupled to the cell cycle machinery.

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