

Mouse embryonic stem cells serve as an in-vitro model for early embryonic development. They enable us to sample the transcriptome at very high time resolution to shed light on gene regulation during development. In this work, transcriptome data from differentiating mouse embryonic stem cells is used to gain insight into different layers of gene regulation. Operating at the chromosome, sub-megabase domain and individual promoter level, these layers are studied with a focus on the interplay between X chromosome inactivation and pluripotency. The analysis of different regulatory mechanisms illustrates the importance of gene dosage fine-tuning, feedback control and functional modularity for proper gene regulation during differentiation.

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