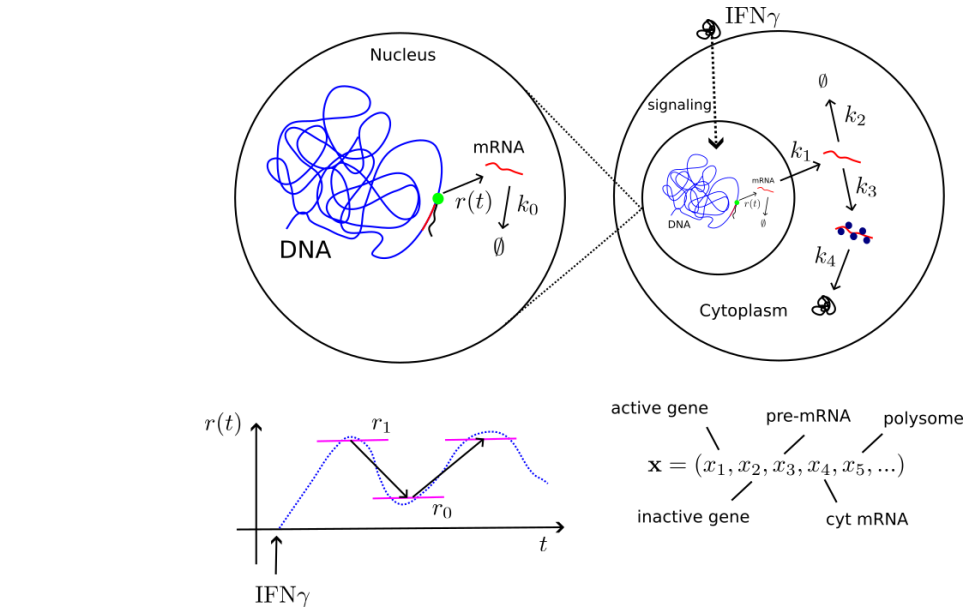# The kinetics of Interferon-γ induced RNA flow

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Summary

- Recap of the compartment model for RNA flow
- Gene selection based on RNA flow
- Brief comments on probe design

A model for RNA Flow

RNA Flow: parameter inference

RNA Flow: parameter inference

Gene selection is based on hypothesized differences in rates k_i or the behavior of $r(t)$ in different experimental conditions

The selection method chosen where is based on expected differences in $r(t)$

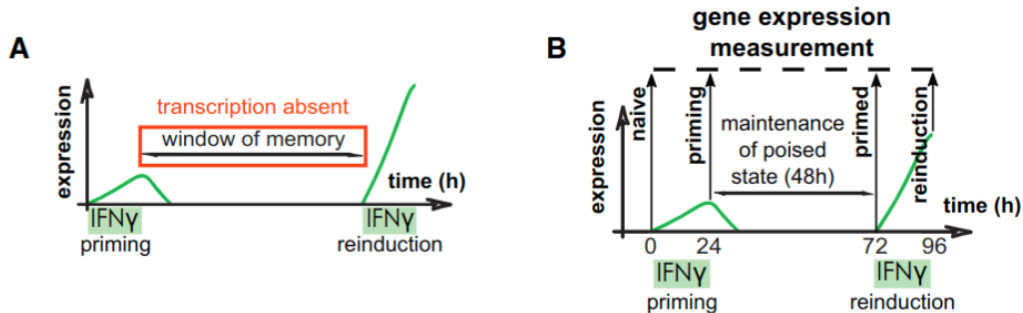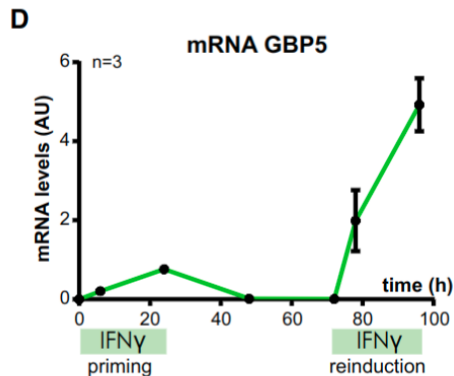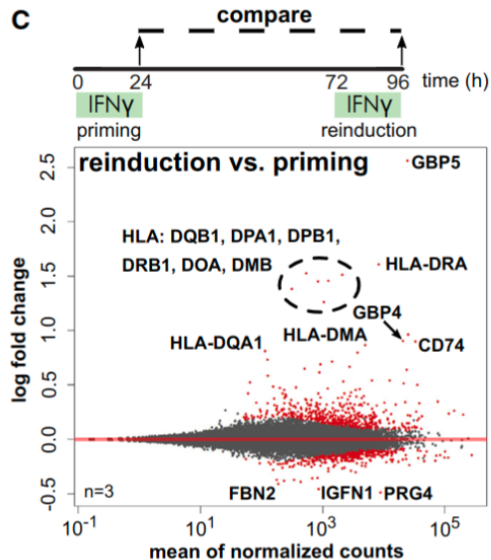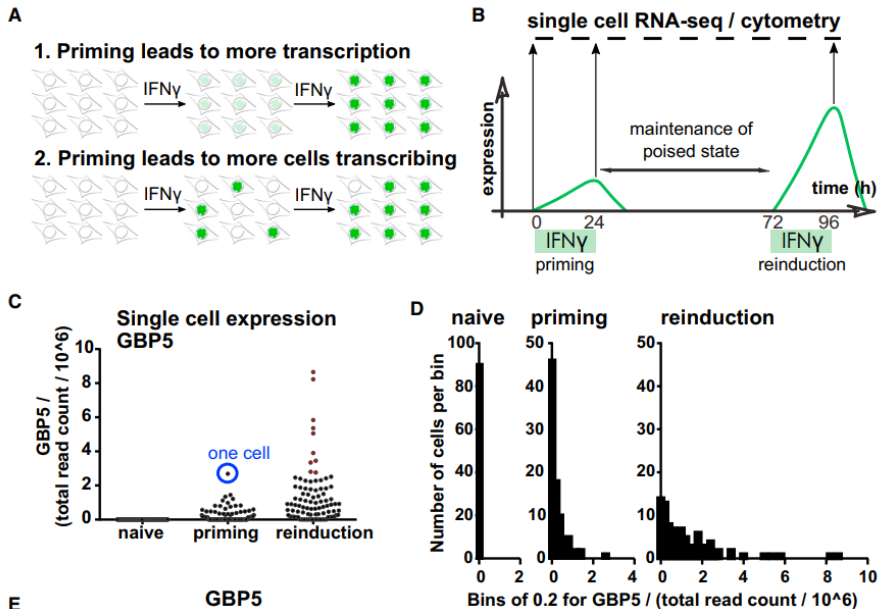# The principle of Interferon-γ induced transcriptional memory

Figure 1

Siwek et al. *Activation of Clustered IFNg Target Genes Drives Cohesin-Controlled Transcriptional Memory*. Molecular Cell 2020

Total RNA-seq identifies GBP5 as a memorized gene

Single-cell RNA-seq identifies GBP5 as a memorized gene

A

1. Priming leads to more transcription

IFNγ → IFNγ →

2. Priming leads to more cells transcribing

IFNγ → IFNγ →

B

single cell RNA-seq / cytometry

expression

maintenance of poised state

time (h)

0   24   72   96

IFNγ   IFNγ
priming   reinduction

C

Single cell expression GBP5

GBP5 / (total read count / 10^6)

one cell

naive   priming   reinduction

D

naive   priming   reinduction

Number of cells per bin

Bins of 0.2 for GBP5 / (total read count / 10^6)

E

GBP5

BLASTing probes for GPB5 and CD274