Current Research

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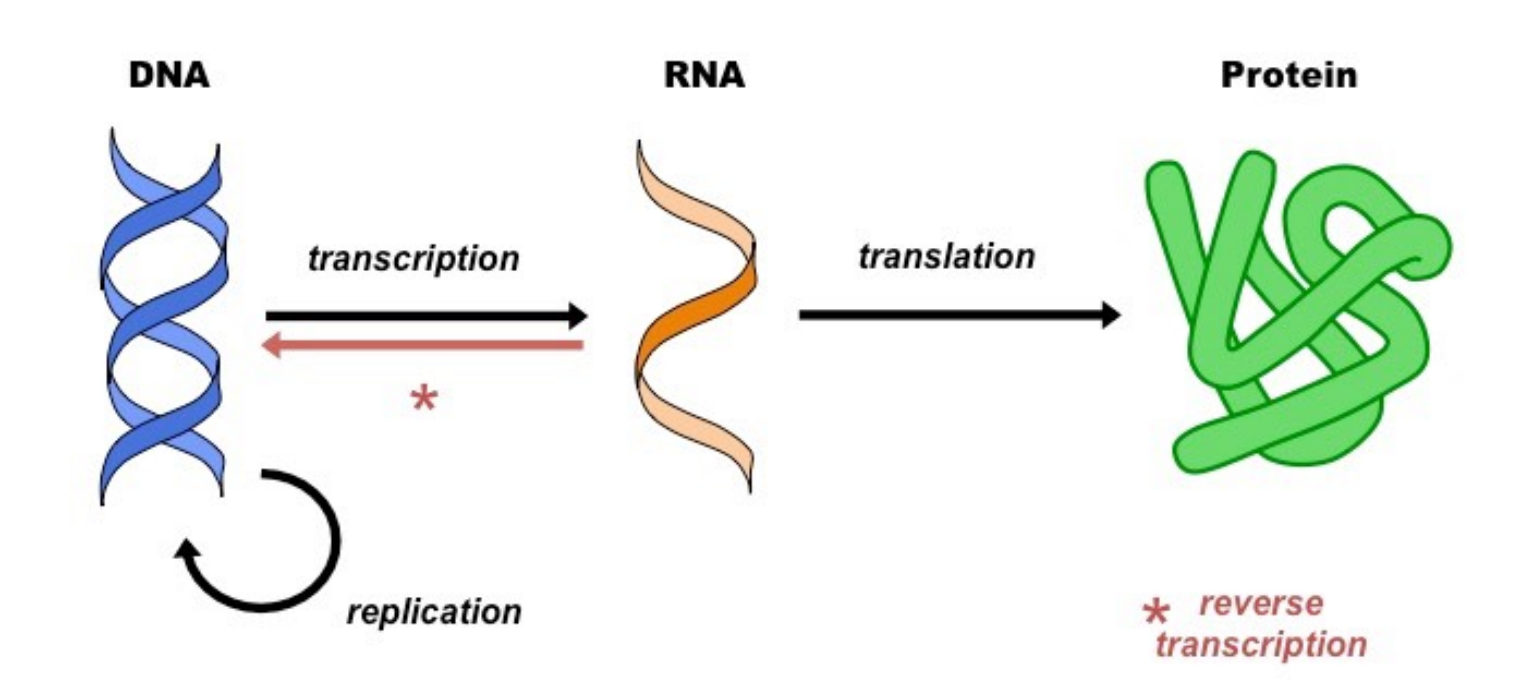
Background

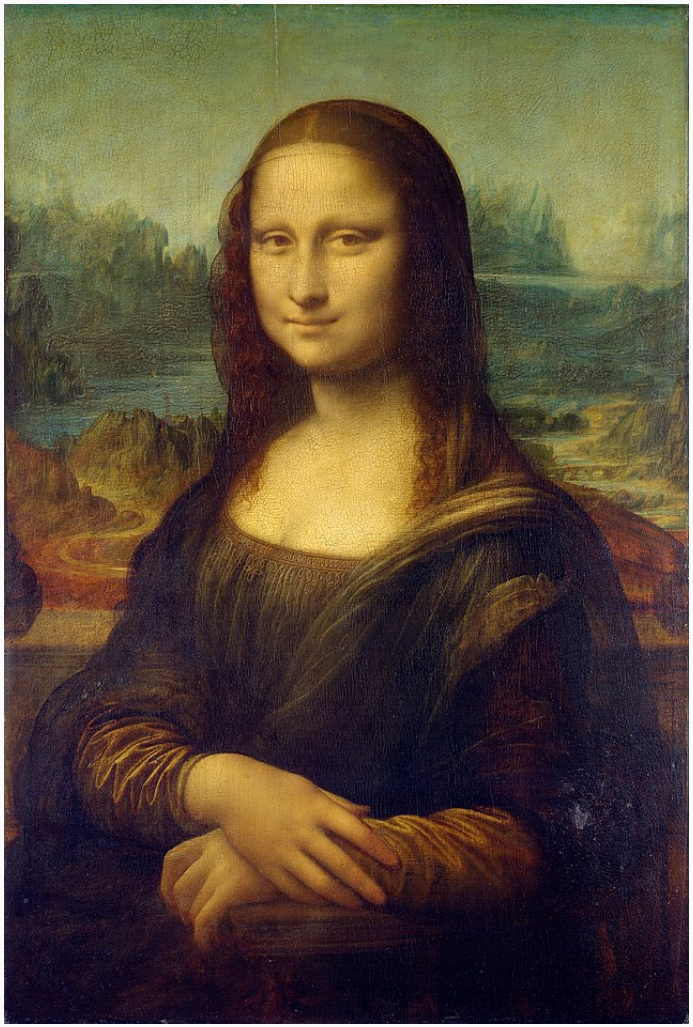
Enhancer intro

Central Dogma of Biology

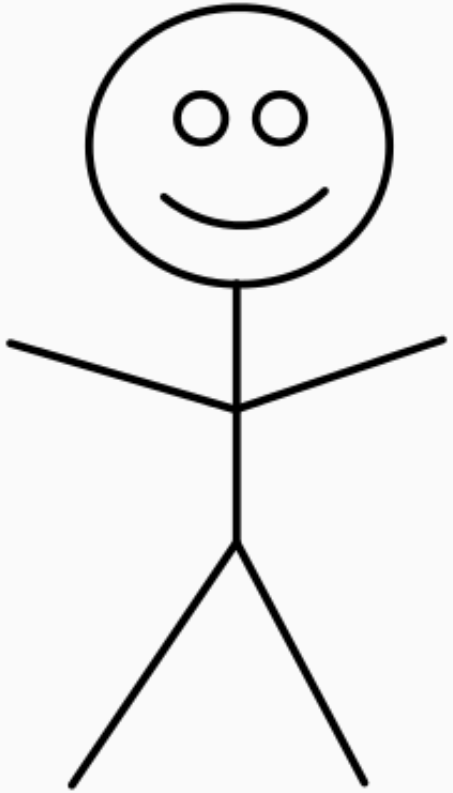


A Simple View of Gene Expression

Gene Expression



Central Dogma



Enhancers Image

Enhancers Fun facts

- Cis-acting DNA sequences that can increase the transcription of genes [1]

[1] (Pennacchio et al. 2013)

Multiple Enhancers can regulate one gene

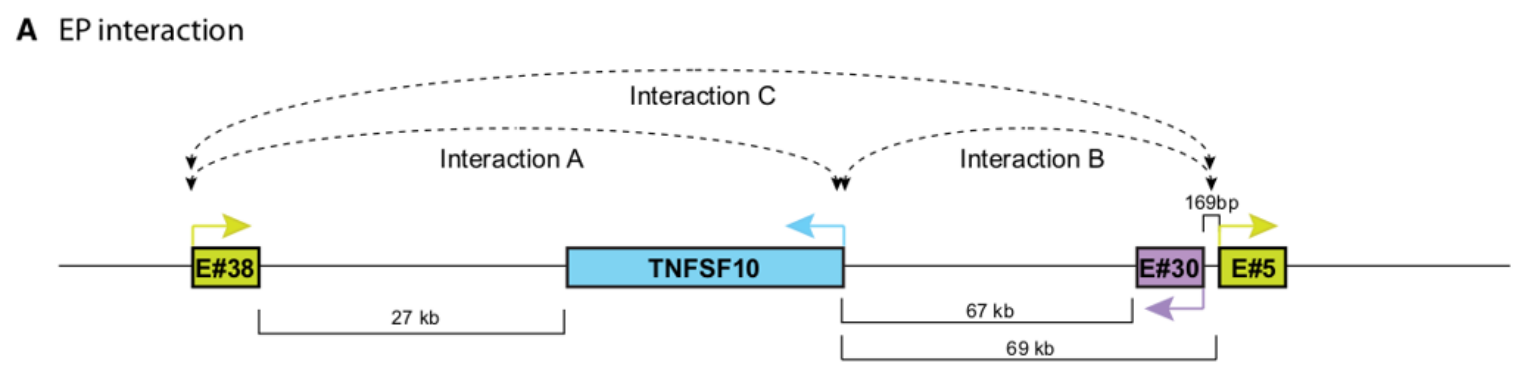


Figure 1: [fn:1: (Kim et al. 2018)]

Enhancers can regulate multiple genes

Topologically Associating Domain (TAD)

Why are Enhancers difficult to identify?

- Scattered across the 98% of the human genome that does not encode proteins [1]
- Enhancers location relative to their target gene (or genes) is highly variable. They can be upstream, downstream, or within introns. [1]
- Enhancers do not necessarily act on the respective closest promoter but can bypass neighbouring genes to regulate genes located more distantly along a chromosome[1]

eRNAs Introduction

Global Transcriptional Activity dynamics reveal functional enhancer rnas

GRO-seq Overview

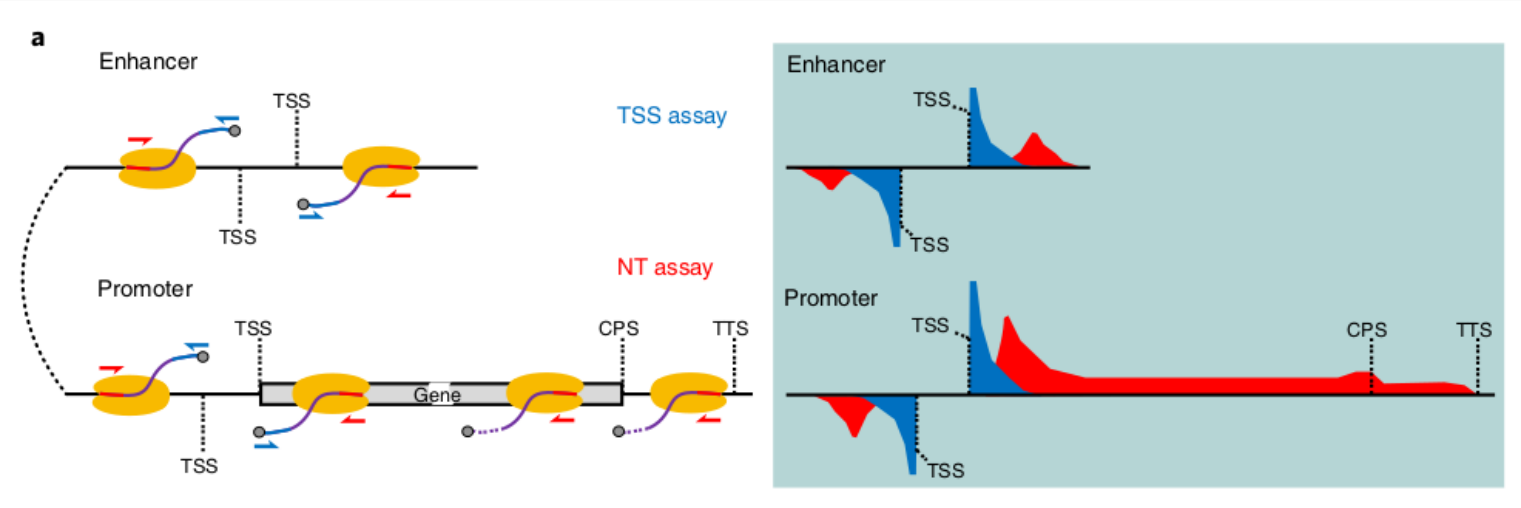


Figure 2: (Yao et al. 2022)

Reproduction with IMR

Hypothesis

Aims

Aim 1 Create a best practice secondary analysis pipeline for nascent transcripts

Aim 2 Take advantage of New Developments to improve eRNA annotation

New developments

CHM13

Epigenetic patterns in a complete human genome - PubMed

PINTS

NT vs TSS

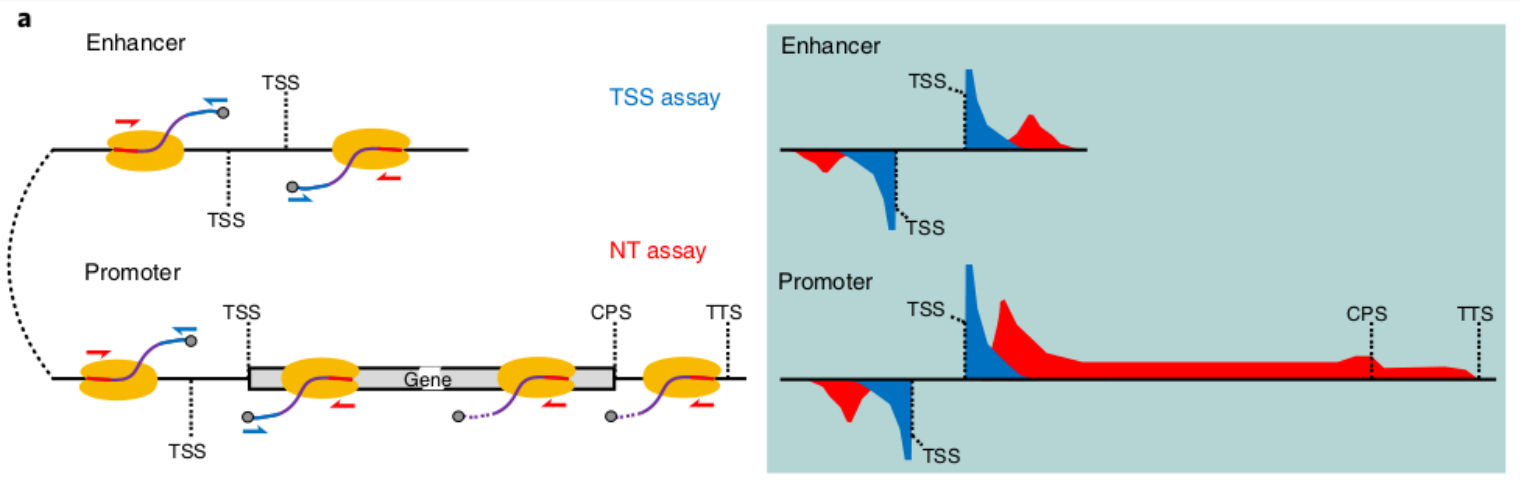


Figure 3: (Yao et al. 2022)

Aim 3 Compare eRNA dynamics between cell lines