Transcript analysis using RNA-seq

What others call transcriptomics?!

Sven Findeiß

Bioinformatics Group, Department of Computer Science;
and Interdisciplinary Center for Bioinformatics,
University of Leipzig

Bled, February 2010

[Sorek and Cossart, 2010]

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Lederberg:2001

"$\cdots$-OM signifies fullness, completeness as in divinity $\cdots$, it encompasses the entire universe in its unlimitedness."

Transcriptomics in Prokaryotes

Whole transcriptome studies have been started only recently.

- microbial gene structure was regraded as simple
  $\rightarrow$ no introns $\curvearrowright$ no splicing
  $\rightarrow$ no editing
- technical difficulties e.g. for the mRNA enrichment
  $\rightarrow$ lack poly(A) tails
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Gained knowledge:

$\Rightarrow$ 5'UTR annotation

$\Rightarrow$ novel untranslated regulatory elements

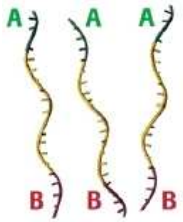
$\Rightarrow$ alternative operon structures

$\Rightarrow$ discovery of novel ncRNAs

[Sorek and Cossart, 2010]

Transcriptome Sequencing (454)

2) Fragment Preparation



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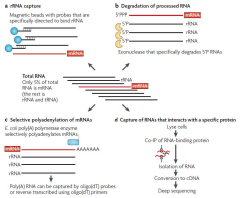

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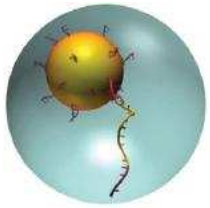

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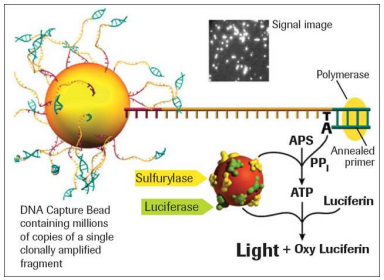

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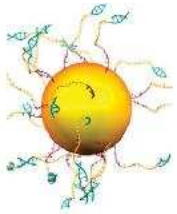

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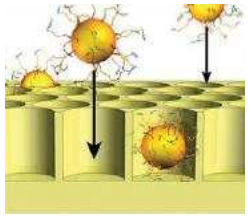

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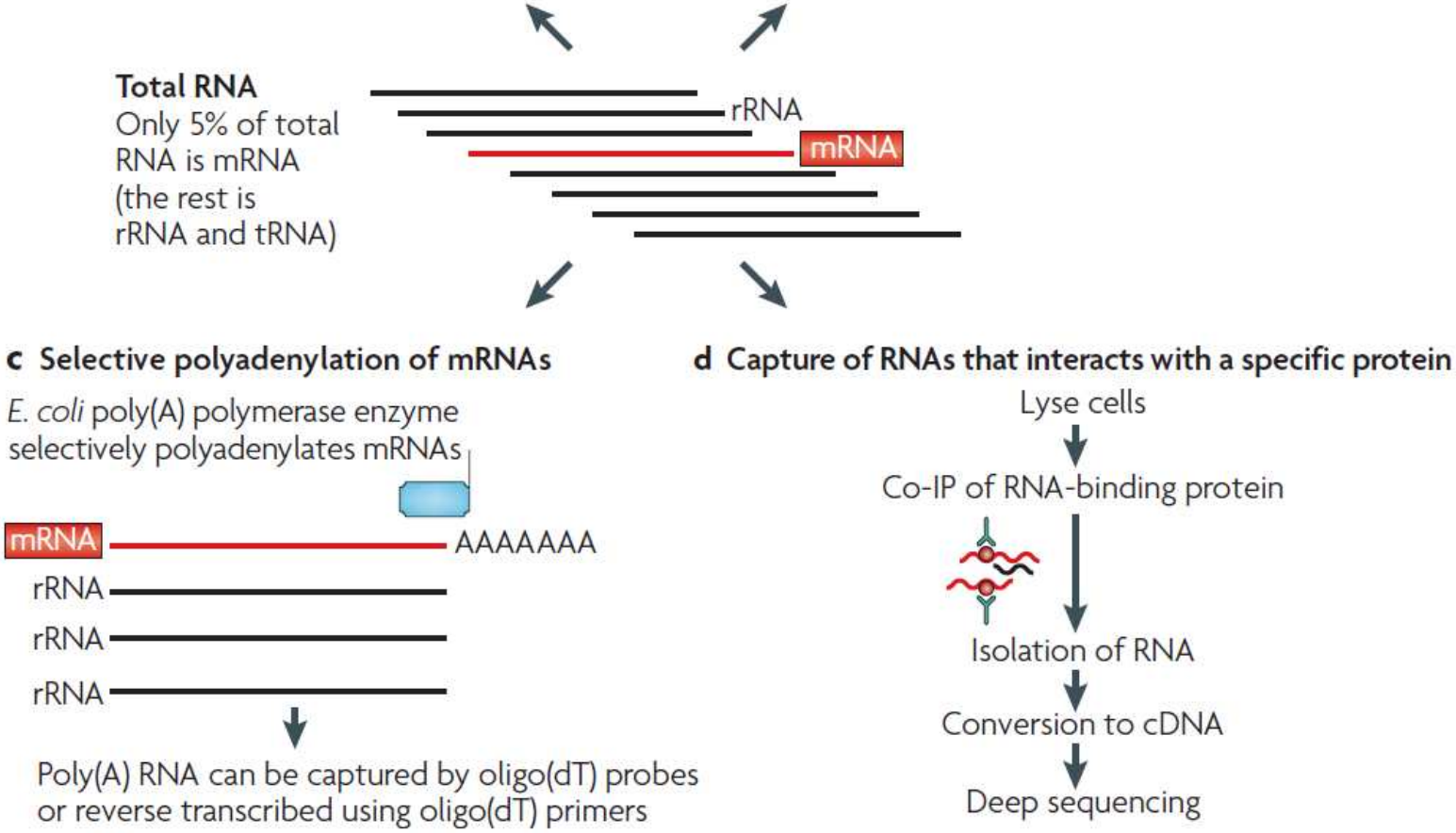

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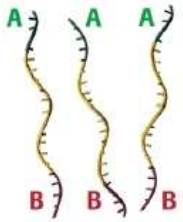

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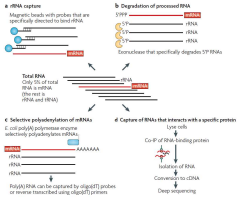

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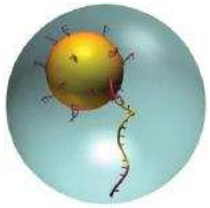

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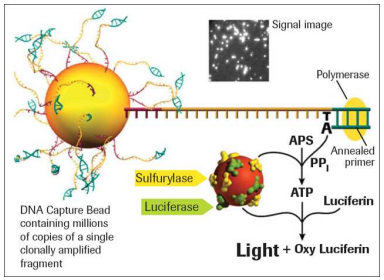

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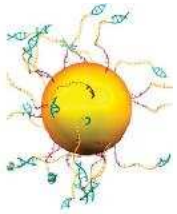

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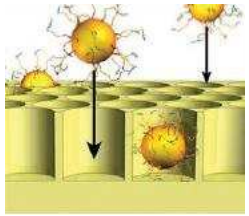

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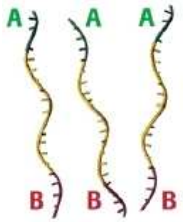

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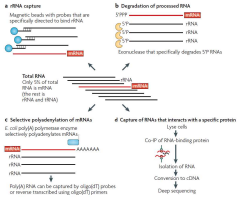

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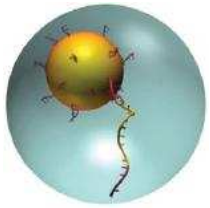

Thousands of sequencing reads

⇓

Post processing steps like clipping, poly-A filtering, etc.

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Mapping with a certain method like Blast, Segemehl, etc.

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90% of mapped sequencing reads

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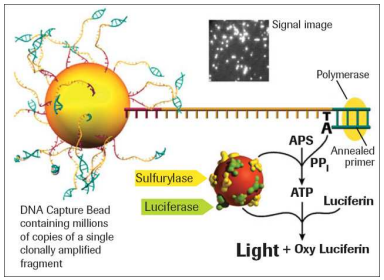

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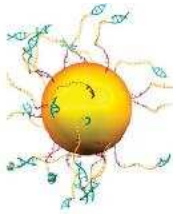

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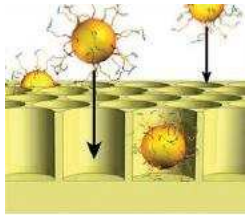

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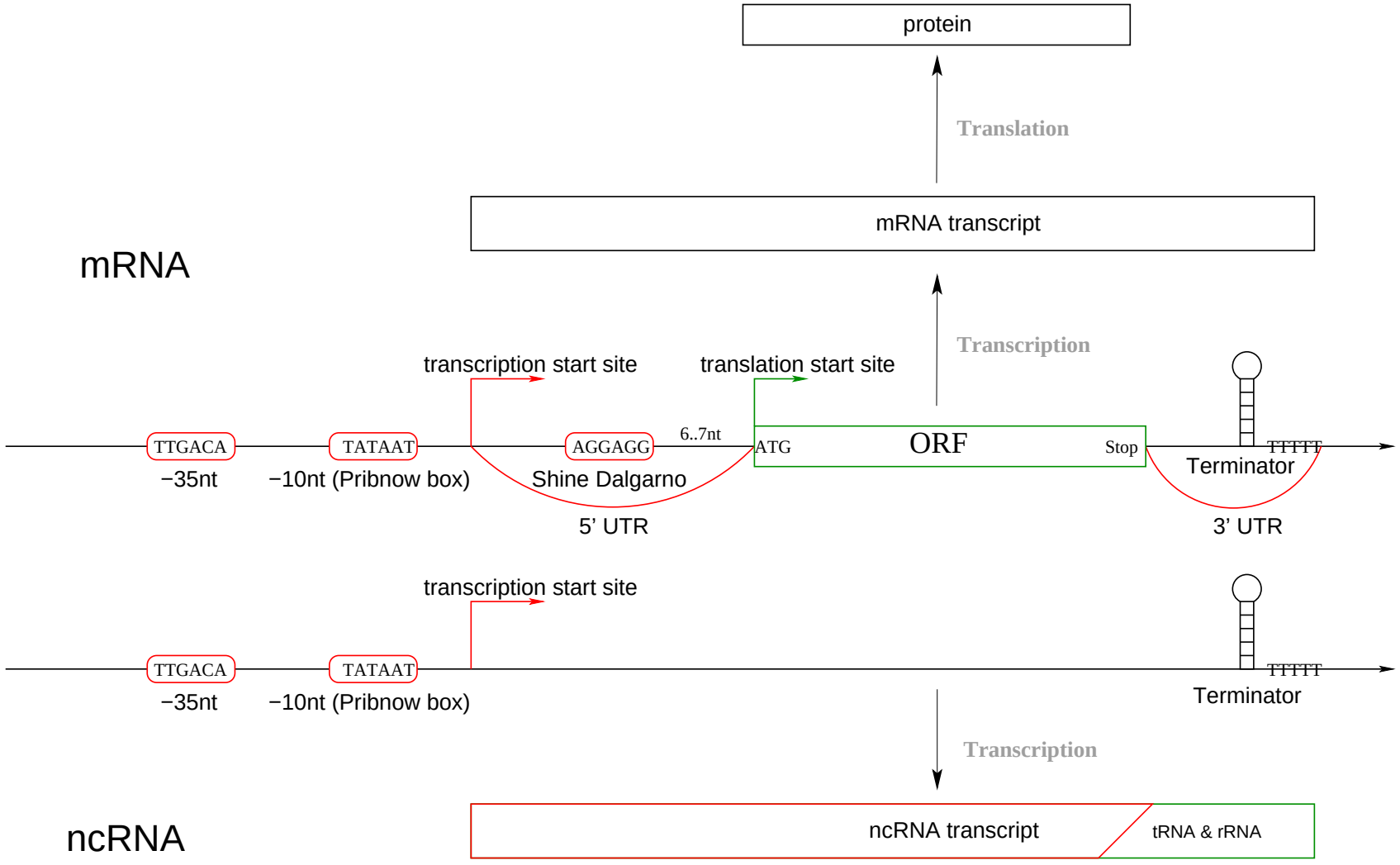

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- library is enriched for primary transcripts
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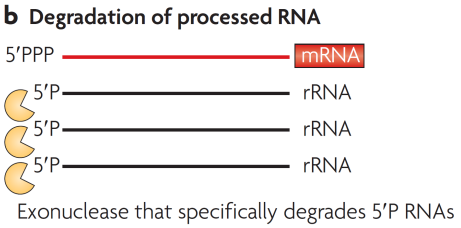

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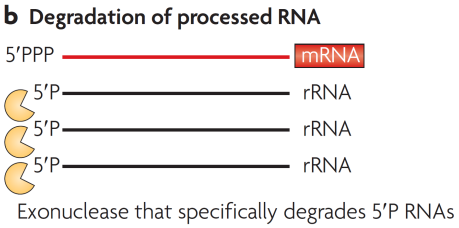

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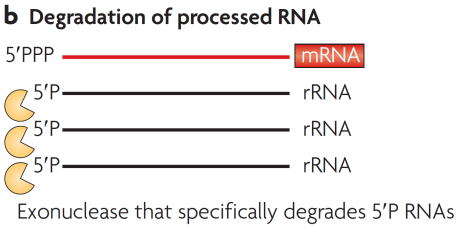

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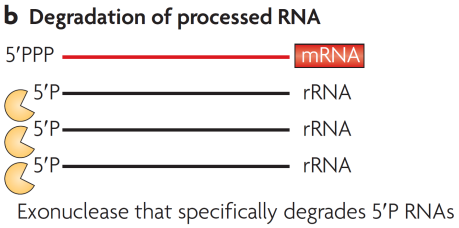

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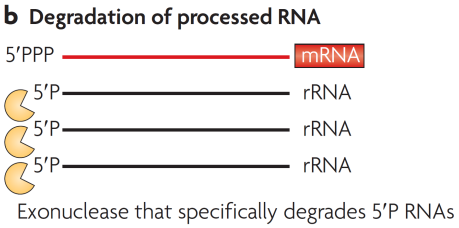

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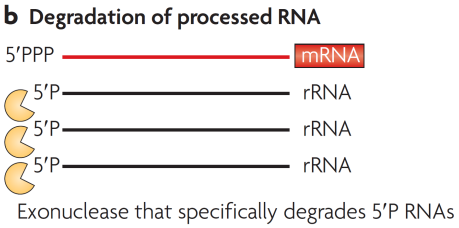

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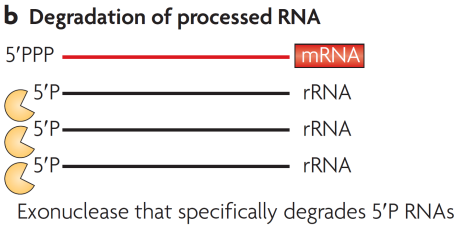

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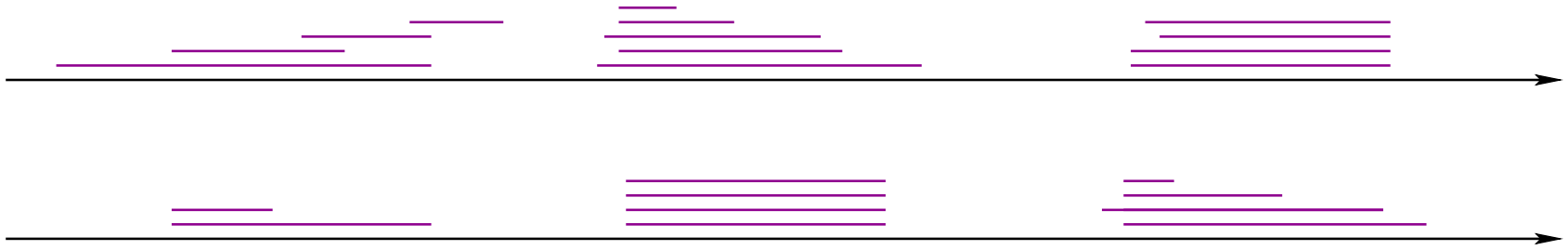

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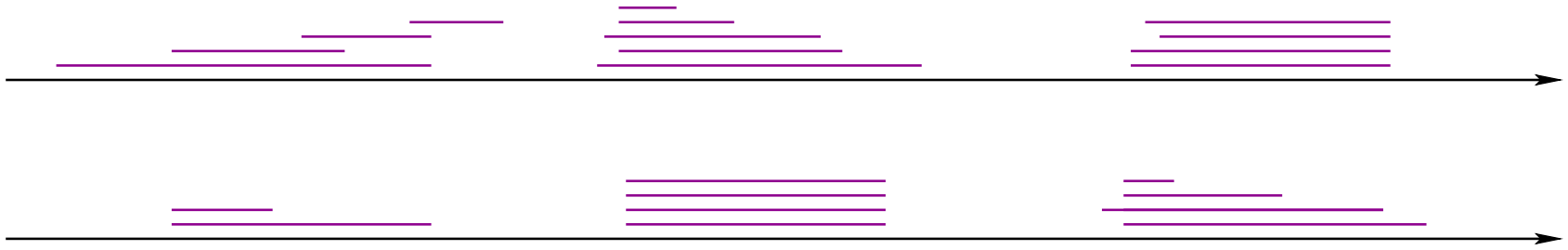

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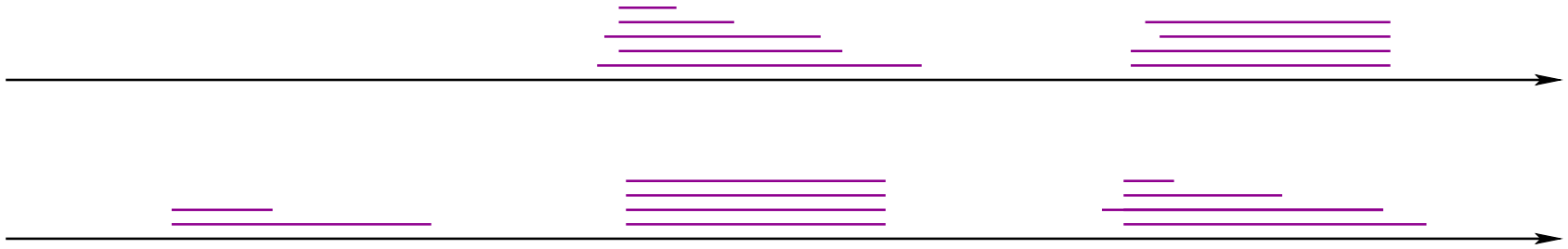

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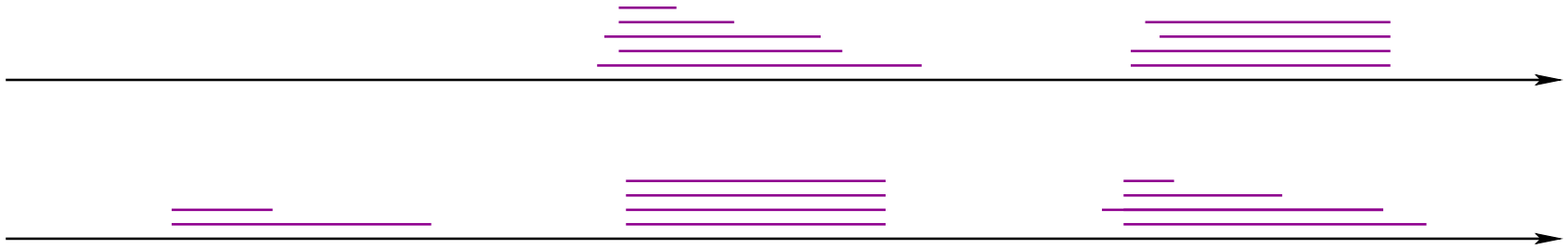

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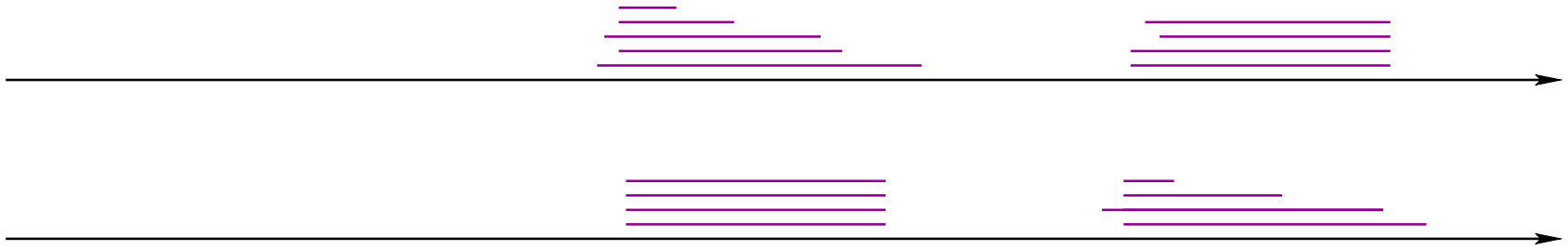

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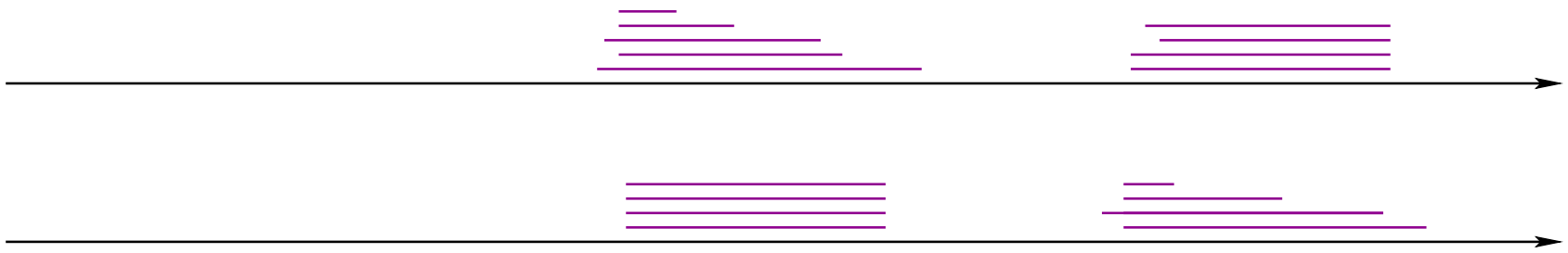

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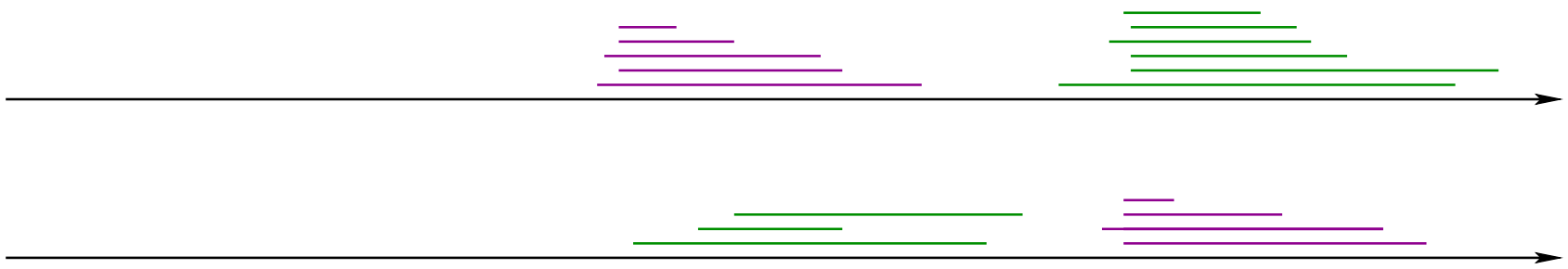

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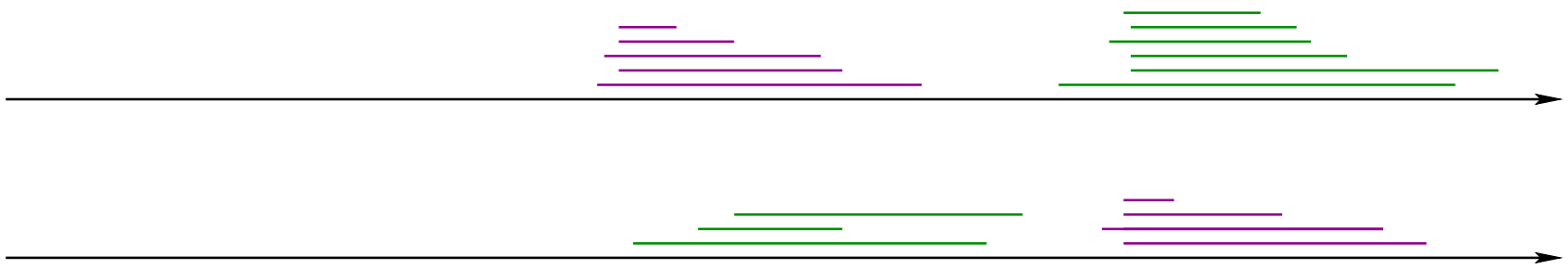

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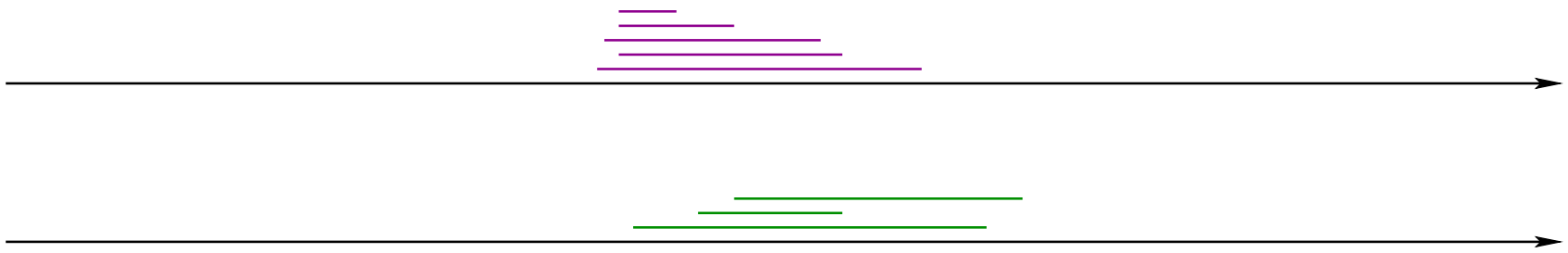

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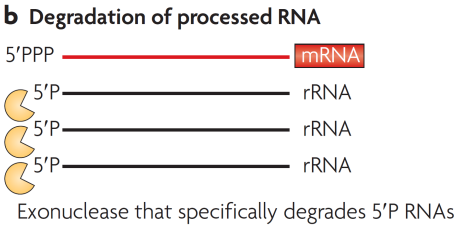

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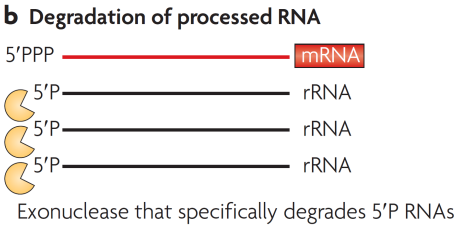

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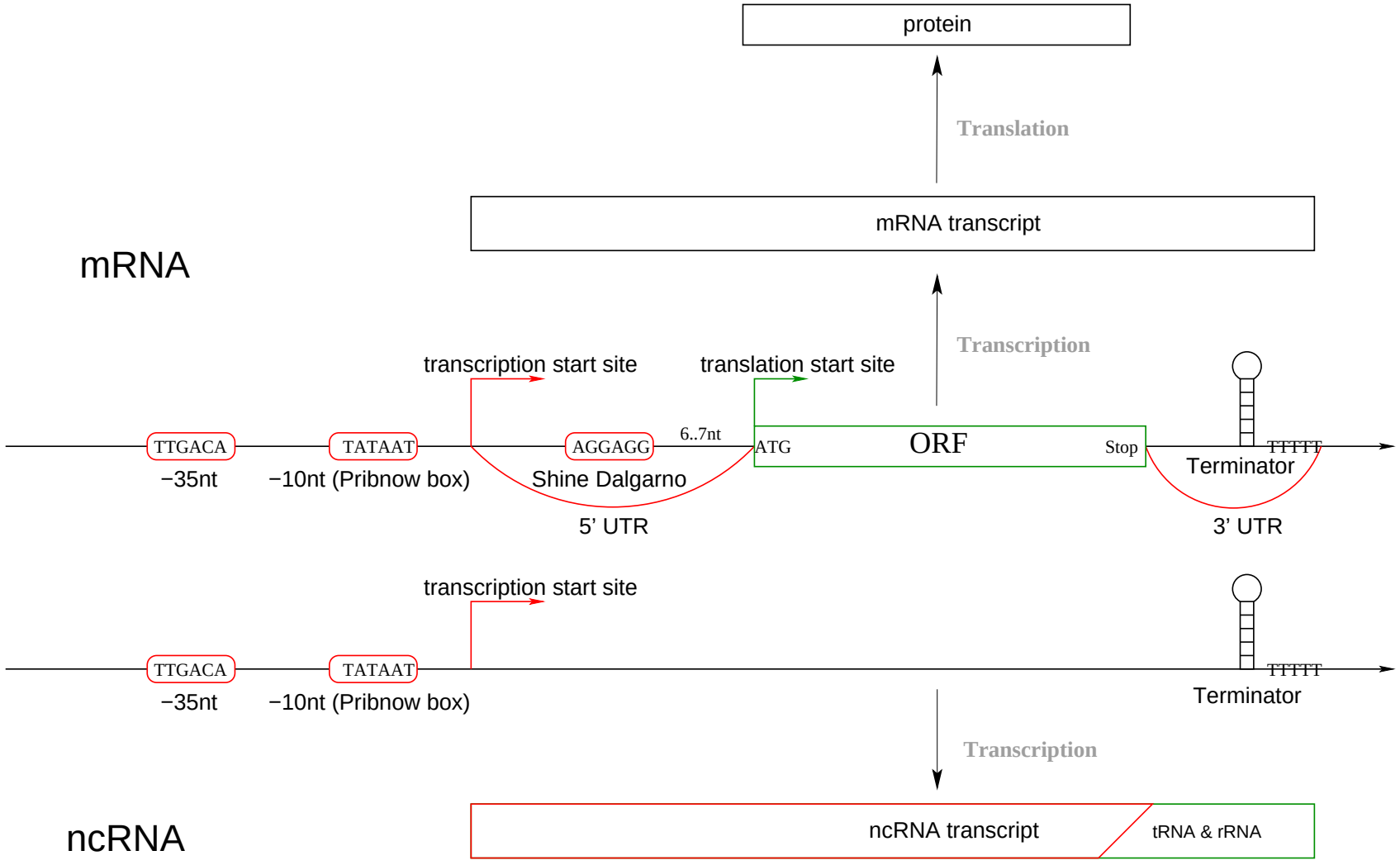
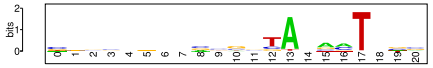
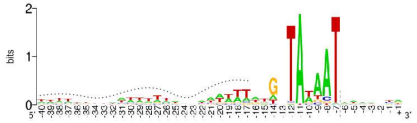


Regulatory motif Detection

Publication	# Library	Enriched/Normal Total	Core Promoter	5’ UTR
Own data	1	45,419/56,257 101,676		
[Albrecht et al., 2009]	2	?/? 249,432		
[Sharma et al., 2010]	5	1,435,974/1,384,949 2,820,923		

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Thanks to...

All the Bleden