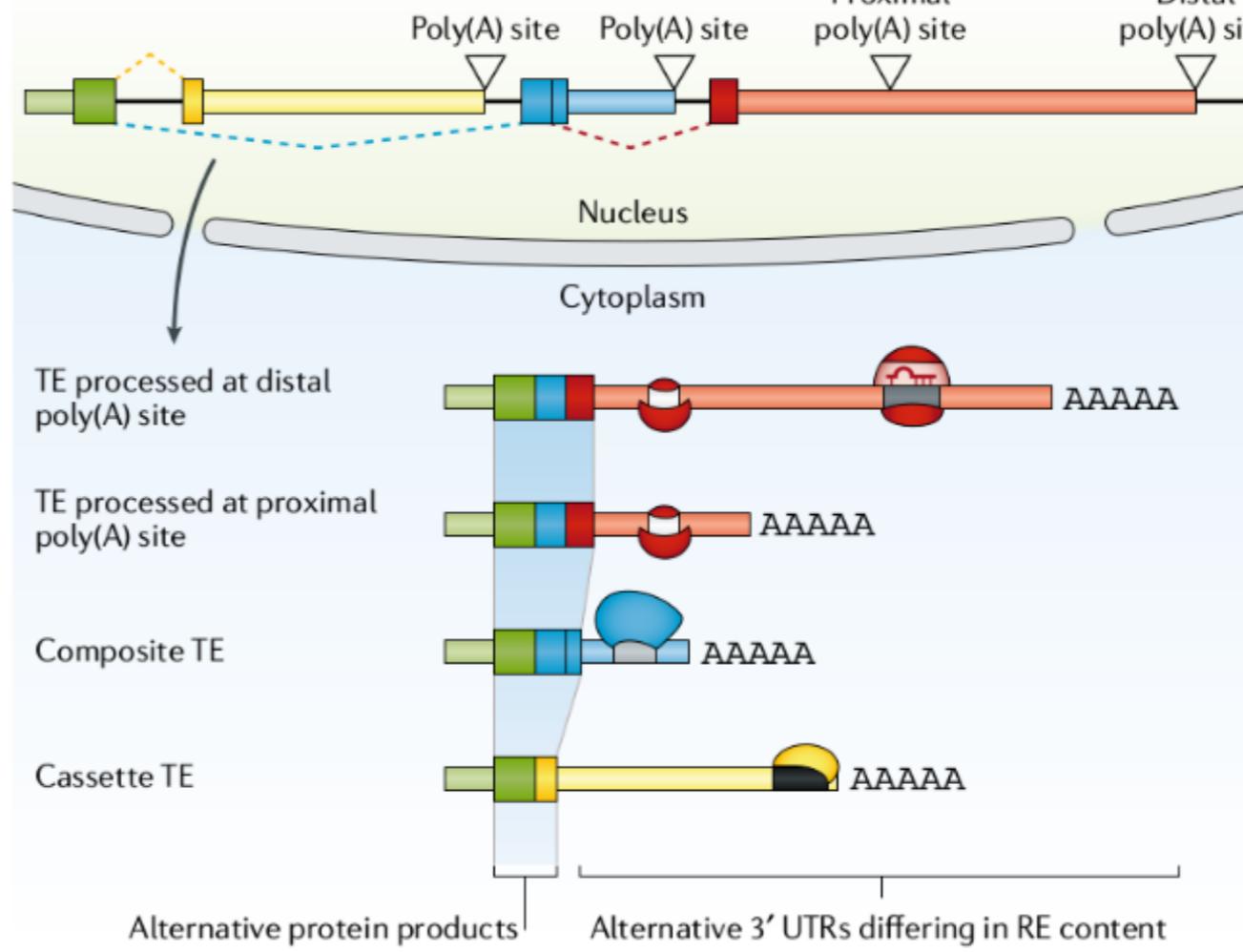
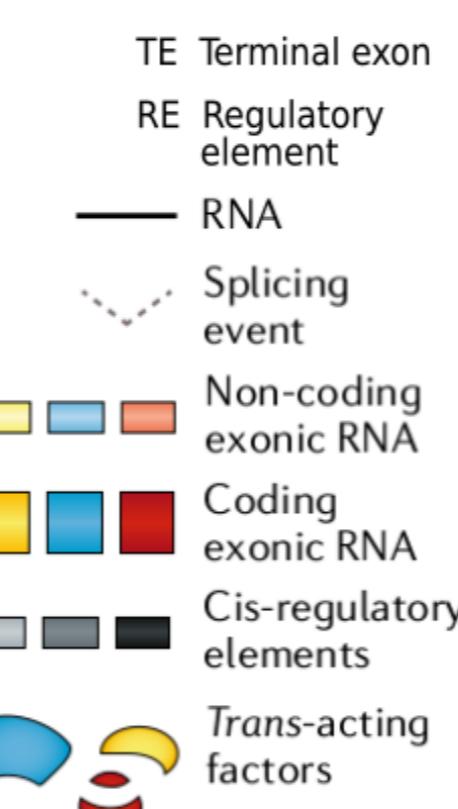


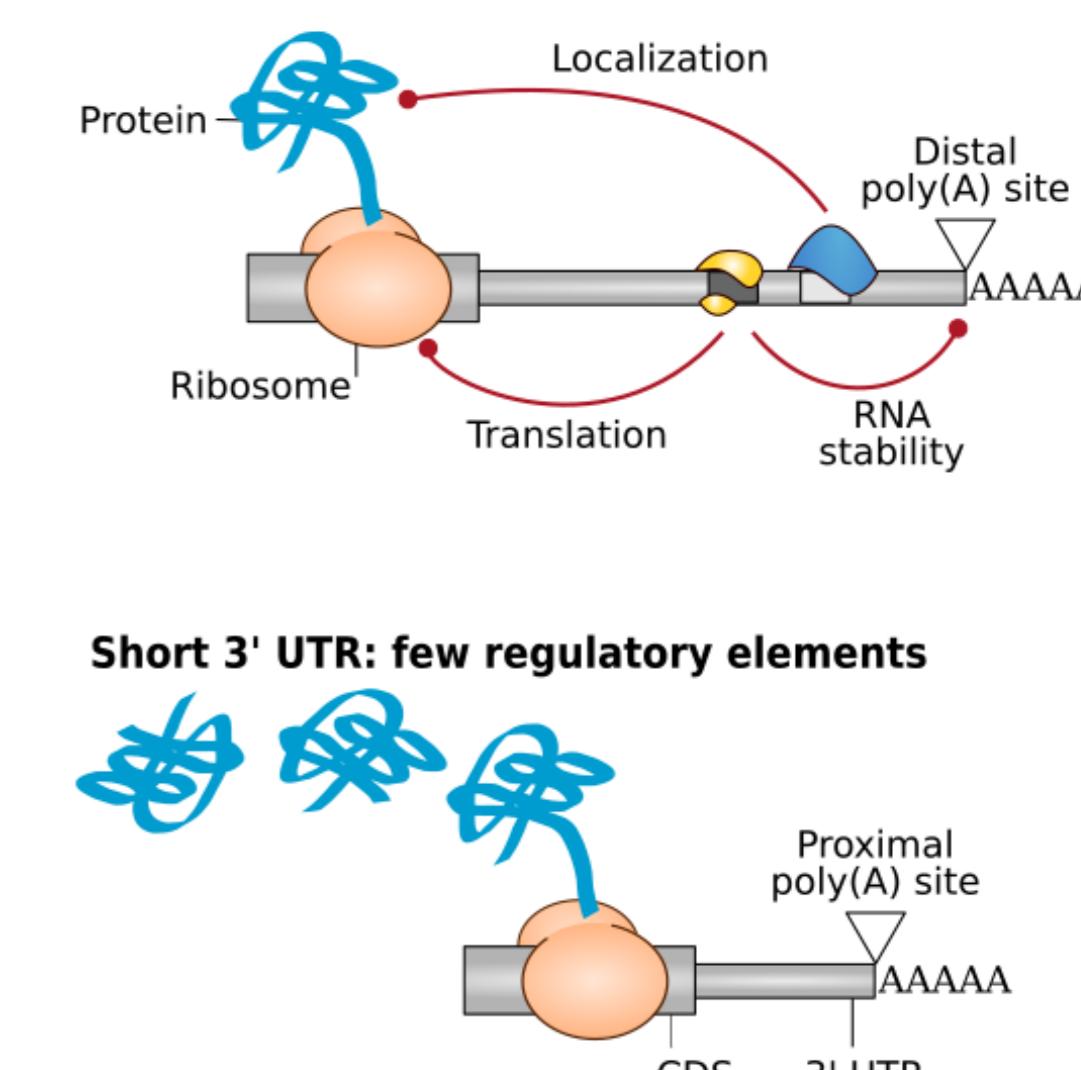
Alternative Polyadenylation (APA) is an important source of transcriptome diversity¹

Most genes have multiple poly(A) sites (PAS), which are differentially processed across cell types.

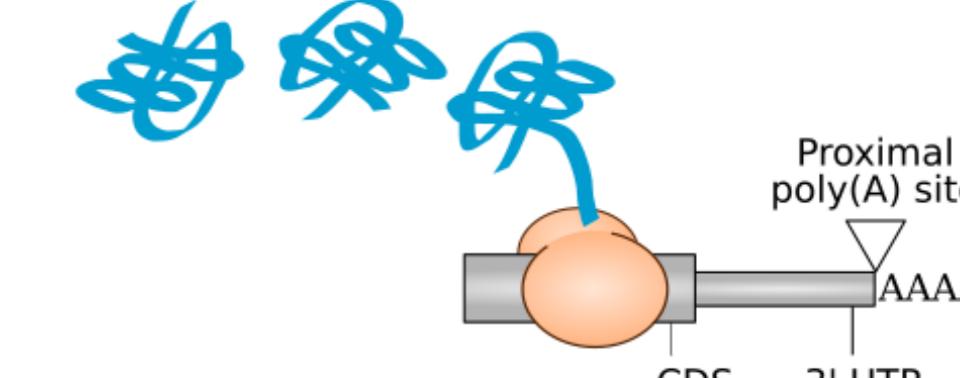
APA contributes to human diseases, including cancer and haematological, immunological and neurological diseases.



Long 3' UTR: many regulatory elements

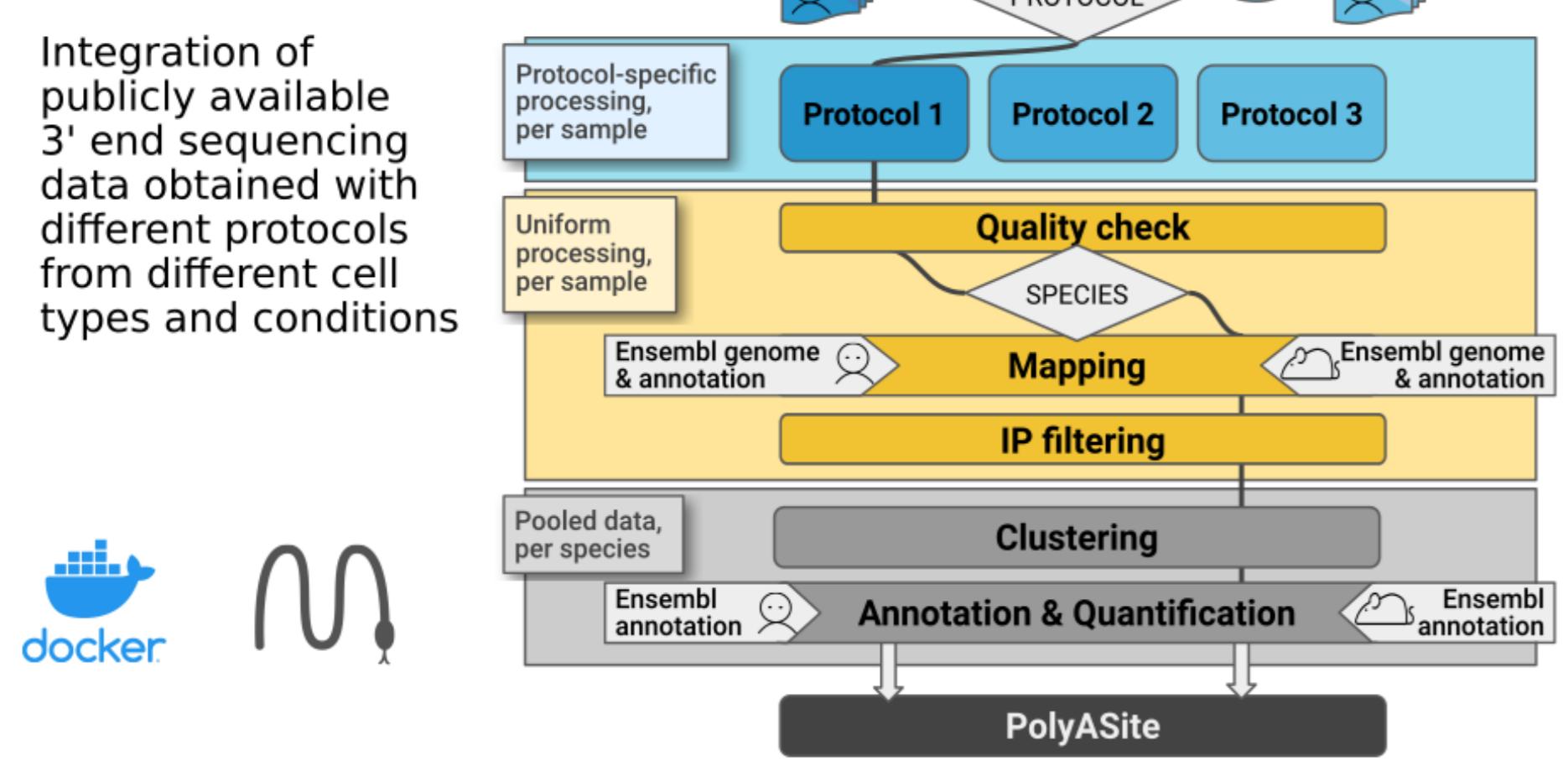


Short 3' UTR: few regulatory elements

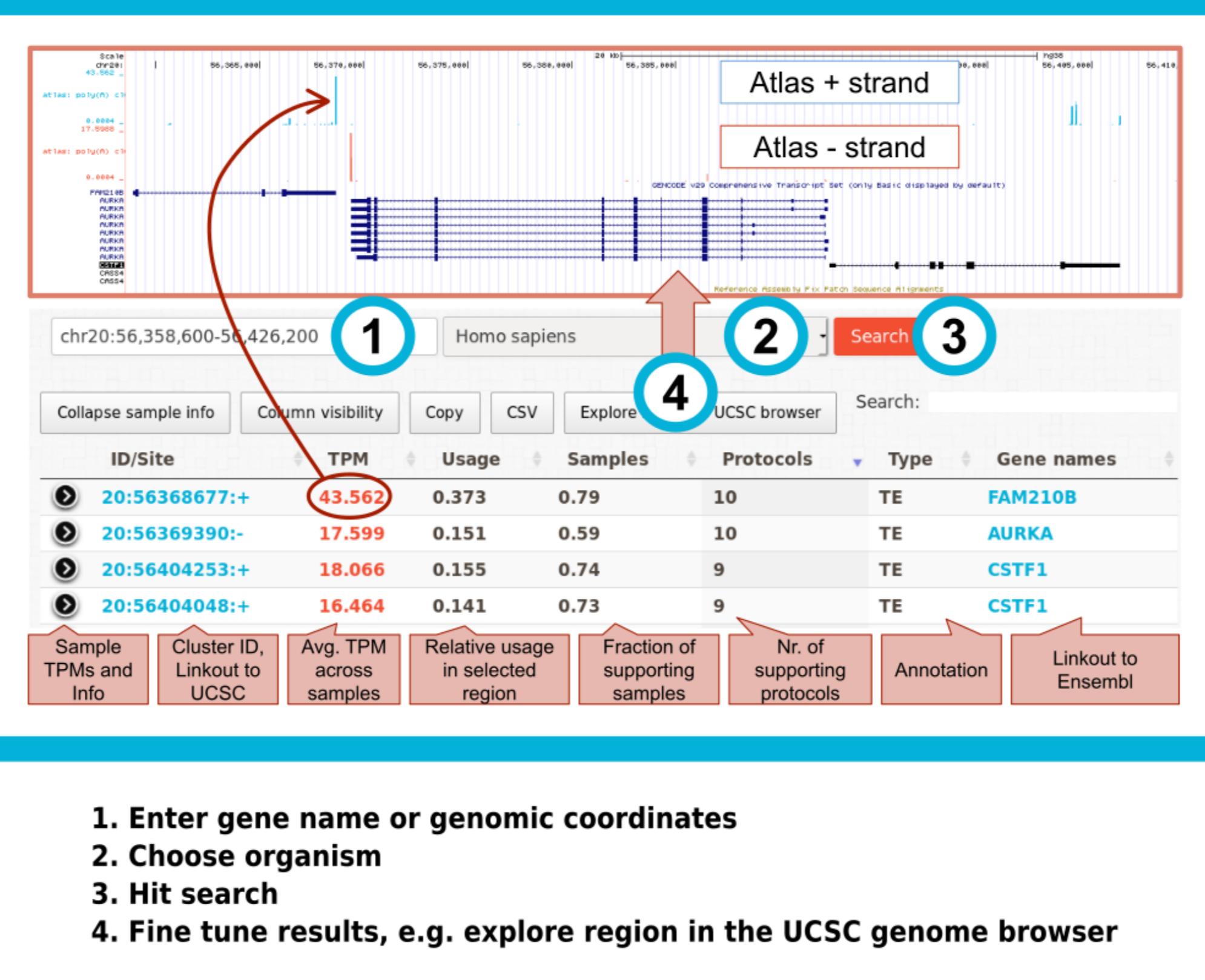


polyasite.unibas.ch

PolyASite²: A comprehensive atlas of poly(A) sites



/Search



/Atlas

	Human	Mouse	Worm
Distinct protocols	10	9	2
No. of samples	221	178	22
Total no. of reads	1,104,077,259	1,167,552,603	67,268,436
No. of poly(A) site clusters	569,005	301,001	20,931
% of clusters with poly(A) signal	76	72	81

- Download poly(A) sites or view them in UCSC genome browser
- Get background information & processing statistics
- Check out samples contributing to the atlas
- Learn more about available 3' end sequencing protocols

Probing the RNA 3' end landscape

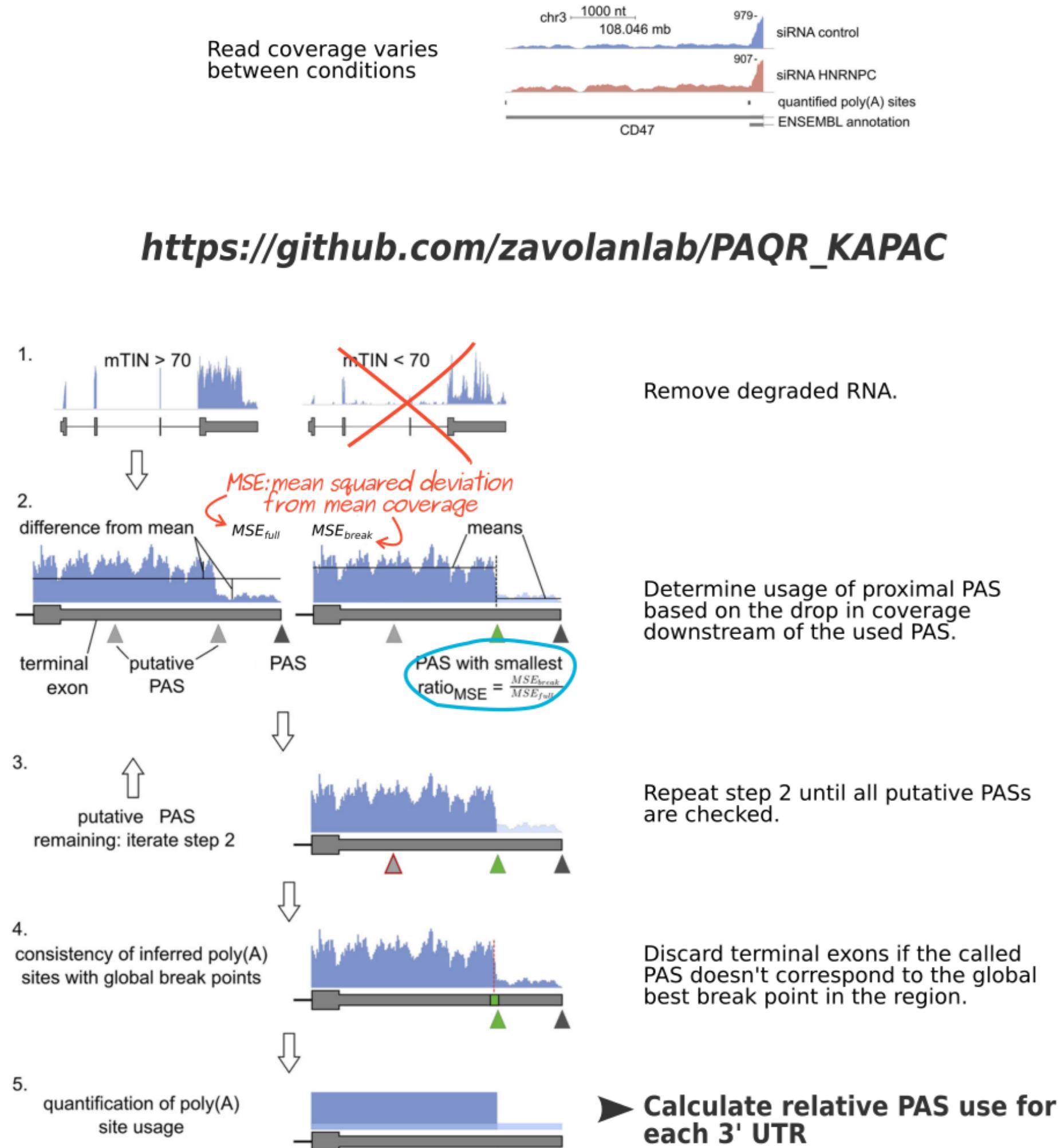
C.J. Herrmann, D. Burri, R. Schmidt, A.J. Gruber, F. Gypas,

A. Kanitz, M. Zavolan

Biozentrum, University of Basel, Switzerland

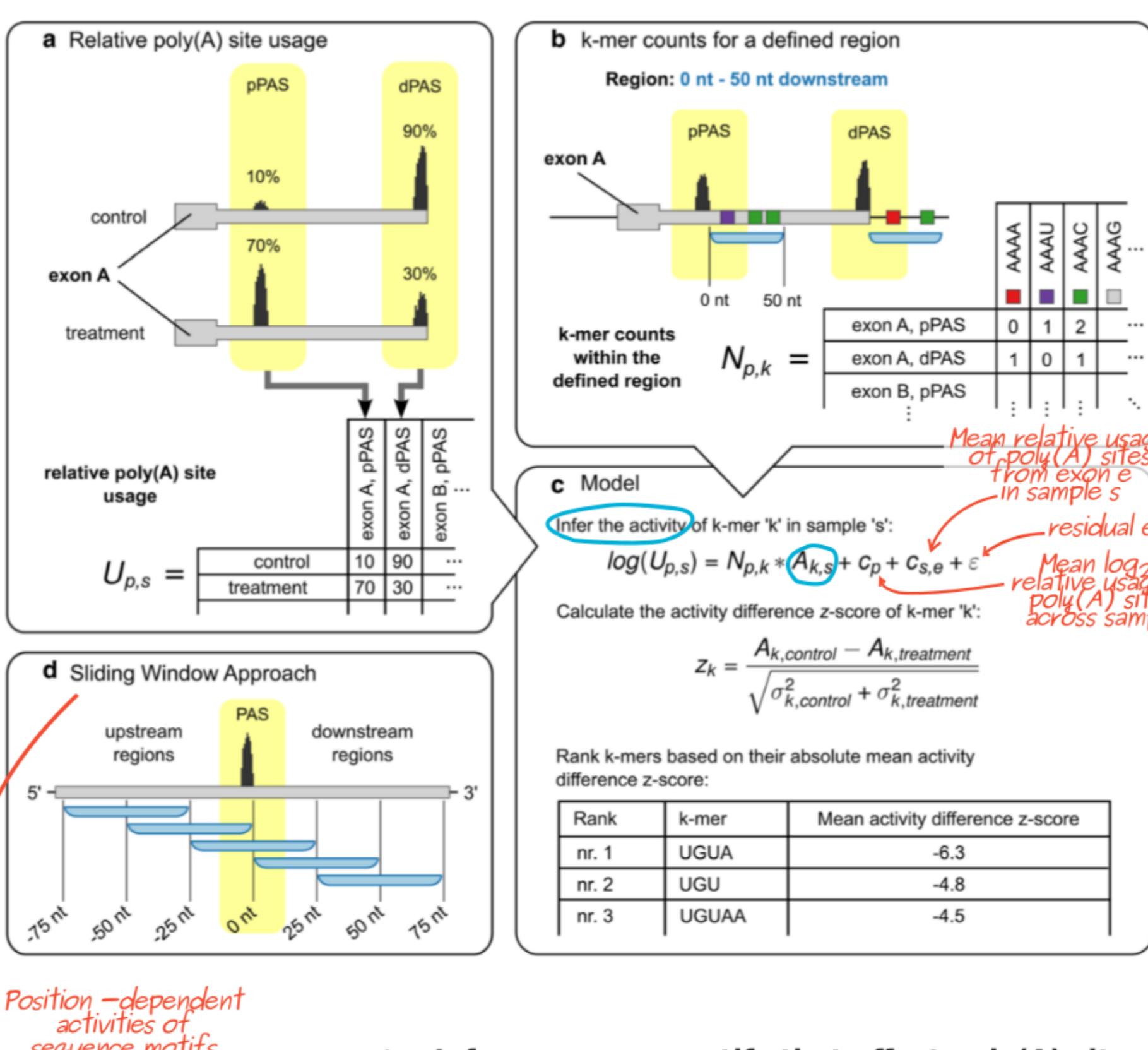
- Atlas of RNA 3' ends
- Computational tools
- Future focus on cell type specificity of APA isoforms

PAQR³: How to quantify poly(A) site use from RNA-seq data?

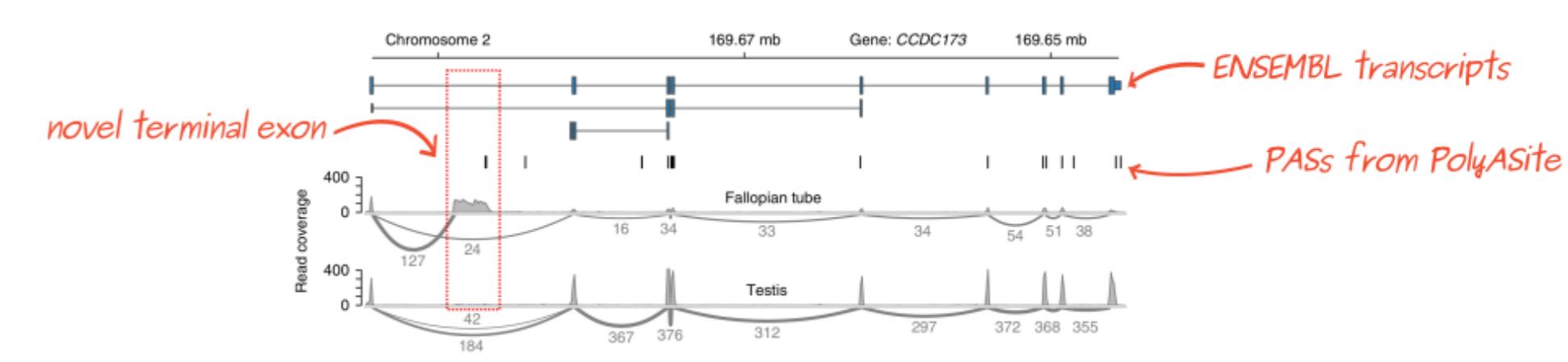


KAPAC³: Which sequence motifs influence poly(A) site selection?

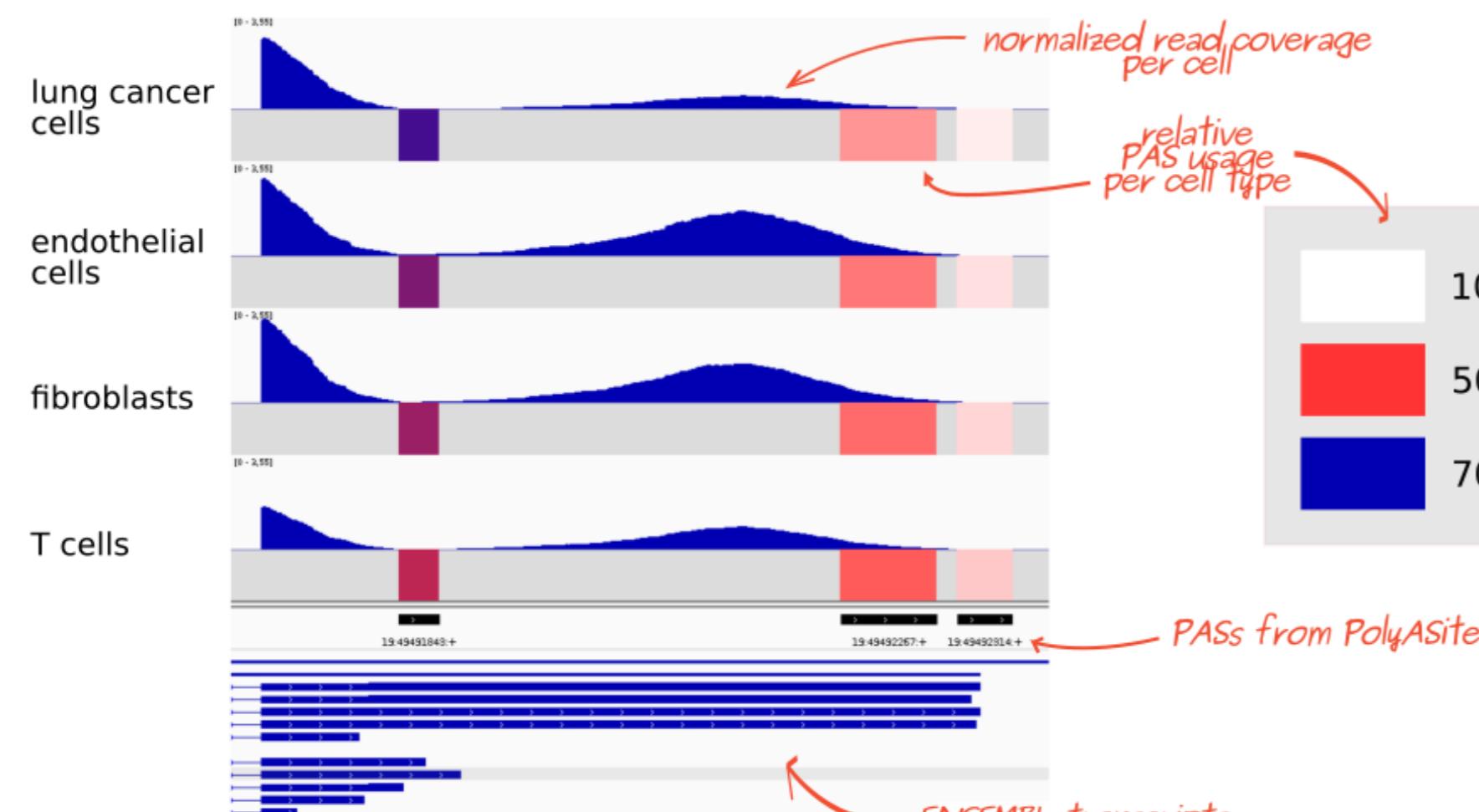
https://github.com/zavolanlab/PAQR_KAPAC



TECtool⁴: Why 'intrinsic' poly(A) sites?



Outlook: How to quantify and compare poly(A) site use in different cell types?



Poly(A) site usage in individual cell types, inferred from single-cell sequencing data⁵ (10x Genomics).

Example: Terminal exon of ribosomal protein L13a (RPL13A), preferred use of proximal PAS in lung cancer cells.

Cancer cells express transcripts with shortened 3' UTRs.

<https://polyasite.unibas.ch>



If you have any questions, please drop us a line at polyasite-biozentrum@unibas.ch. Looking forward to hearing from you!

Github: <https://github.com/zavolanlab>

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