

RNA structuredness of viral genomes

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Computational Approaches to RNA Structure and Function
Benasque

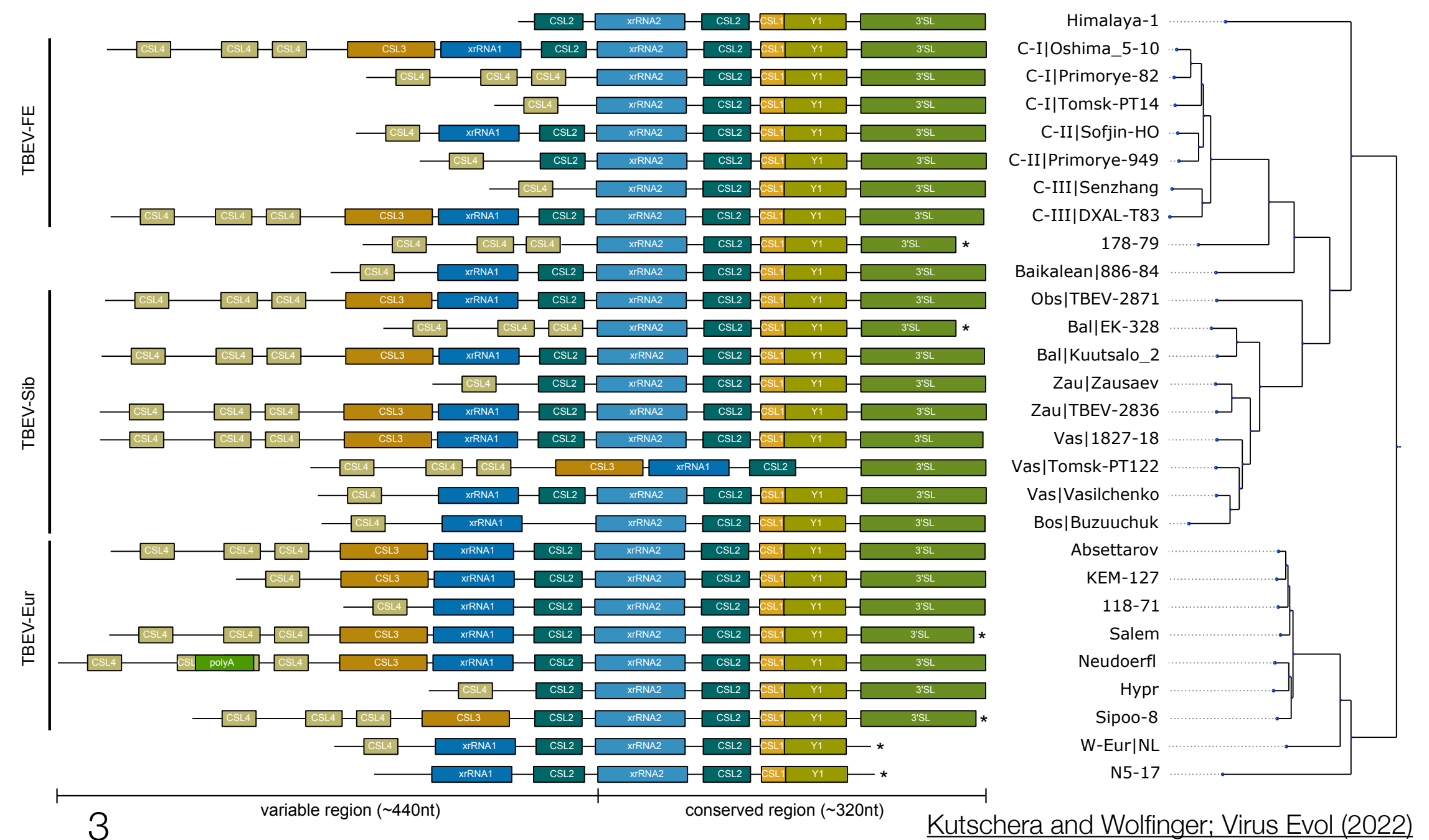
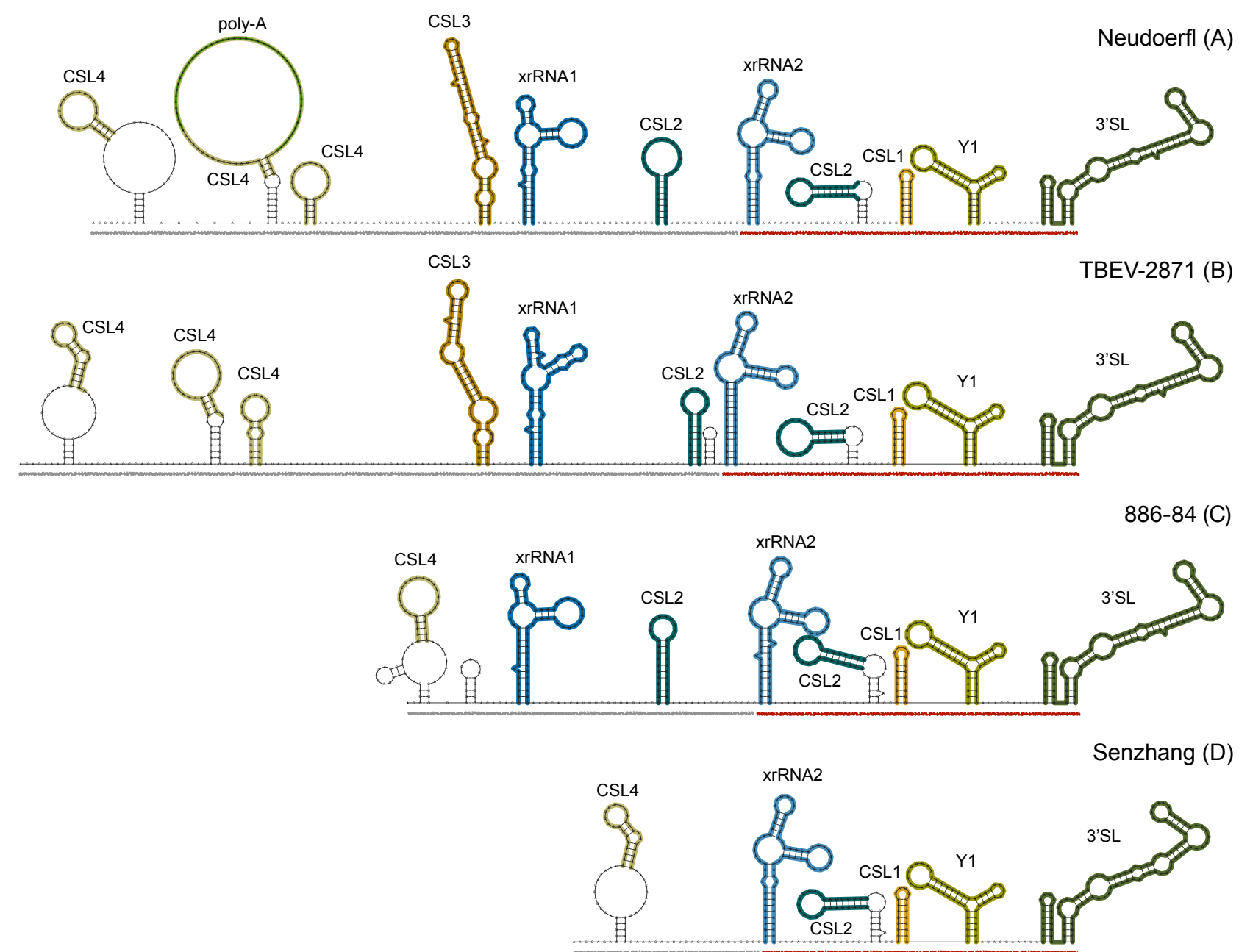
12 August 2022

RNA structuredness of viral genomes

- Many examples of structured, functional RNAs in untranslated regions
- Some known examples of (conserved) RNA structures in coding regions
- Different evolutionary pressures on RNA structure in coding/non-coding regions

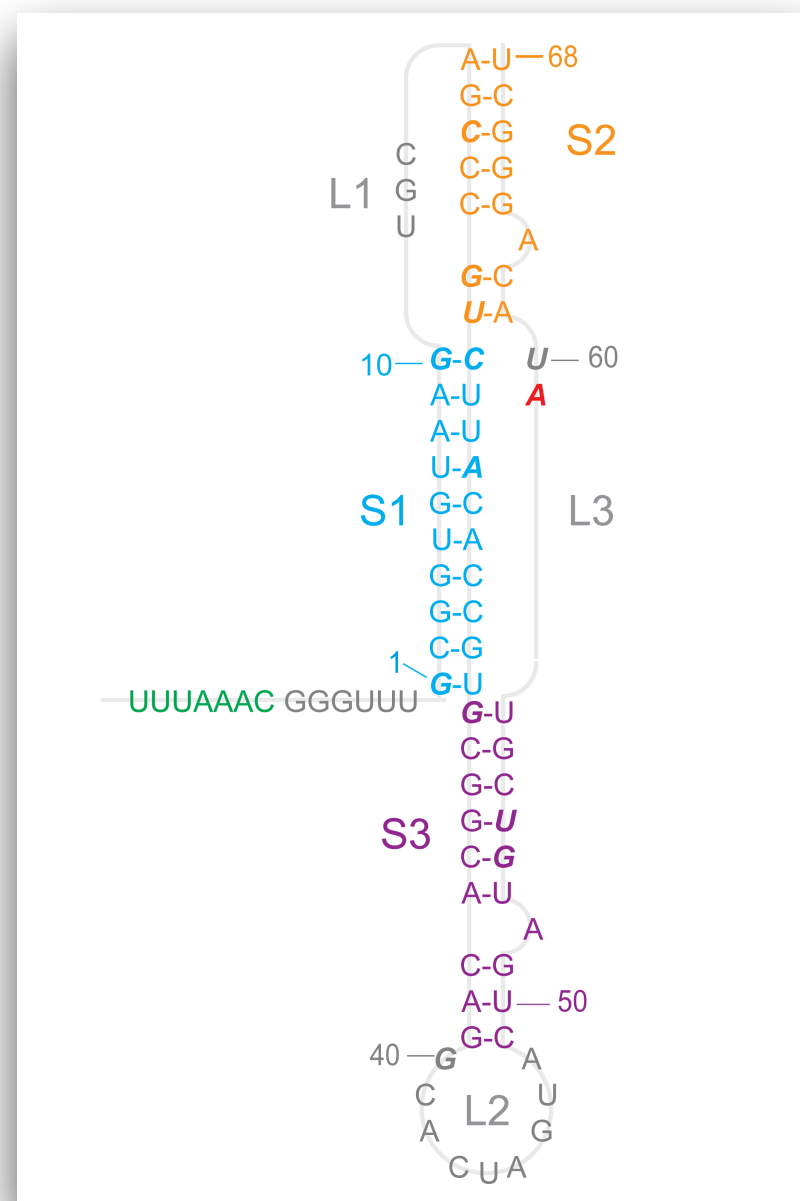
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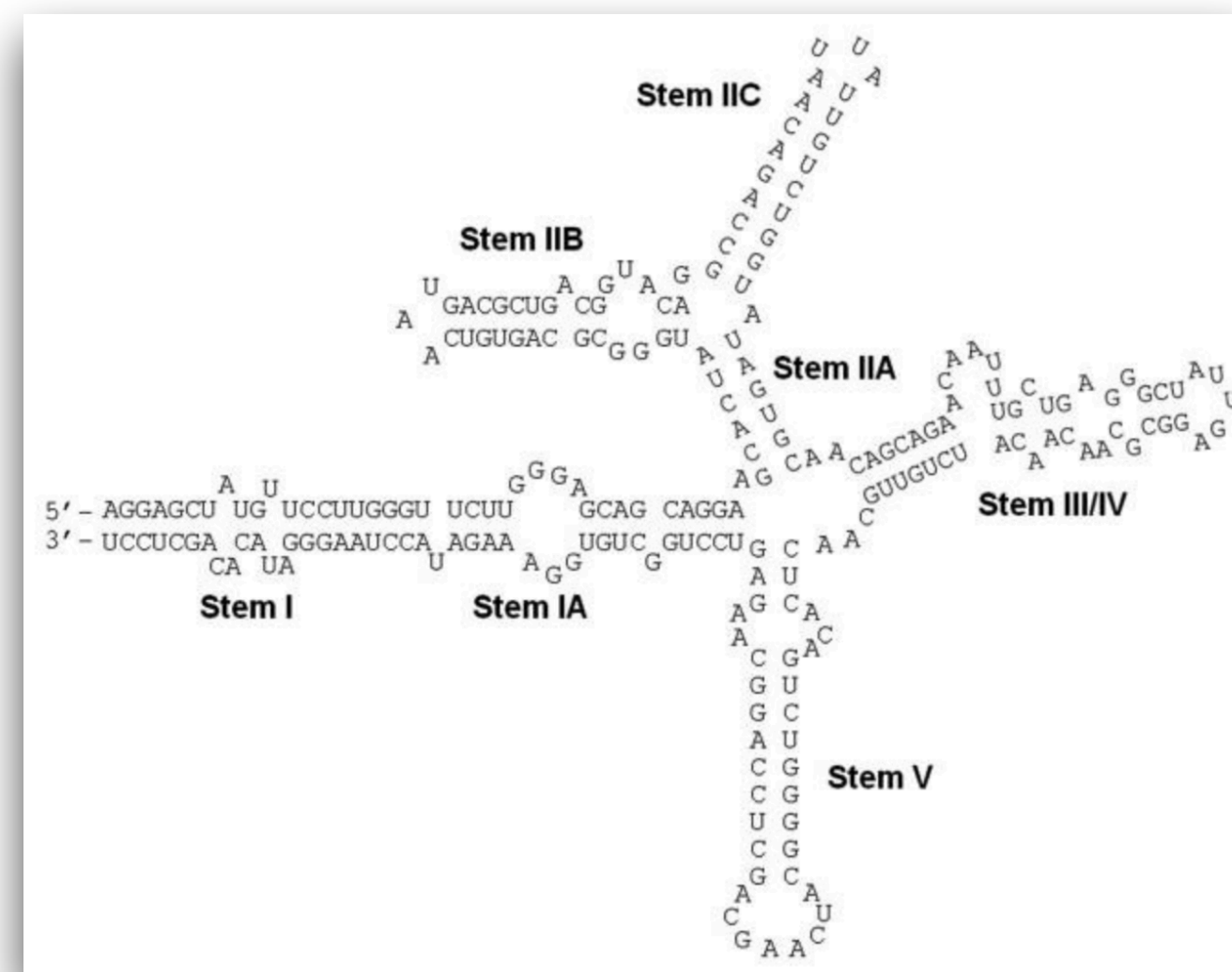


RNA structuredness of viral genomes

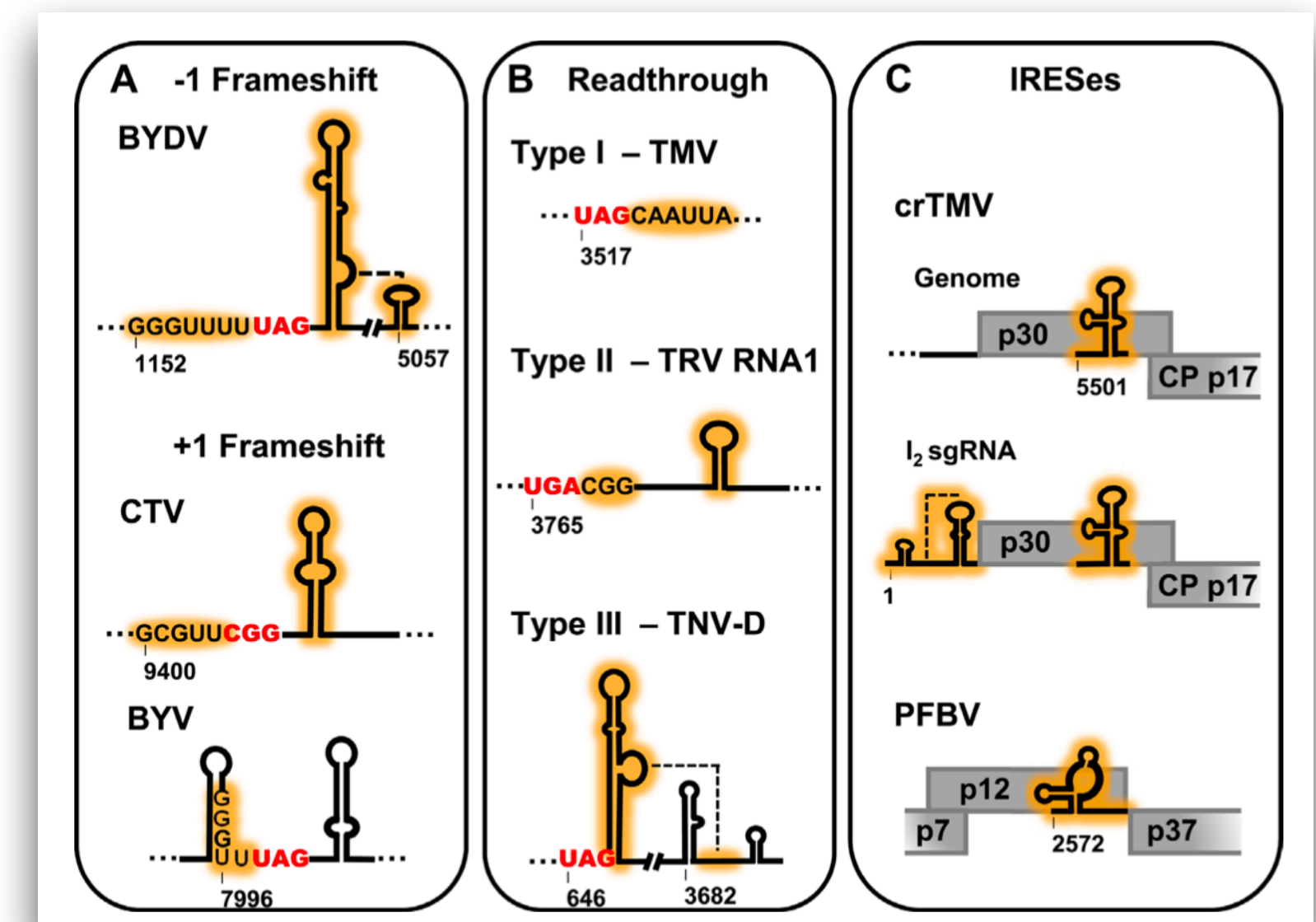
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Omar et al.; PLoS Comput Biol (2021)



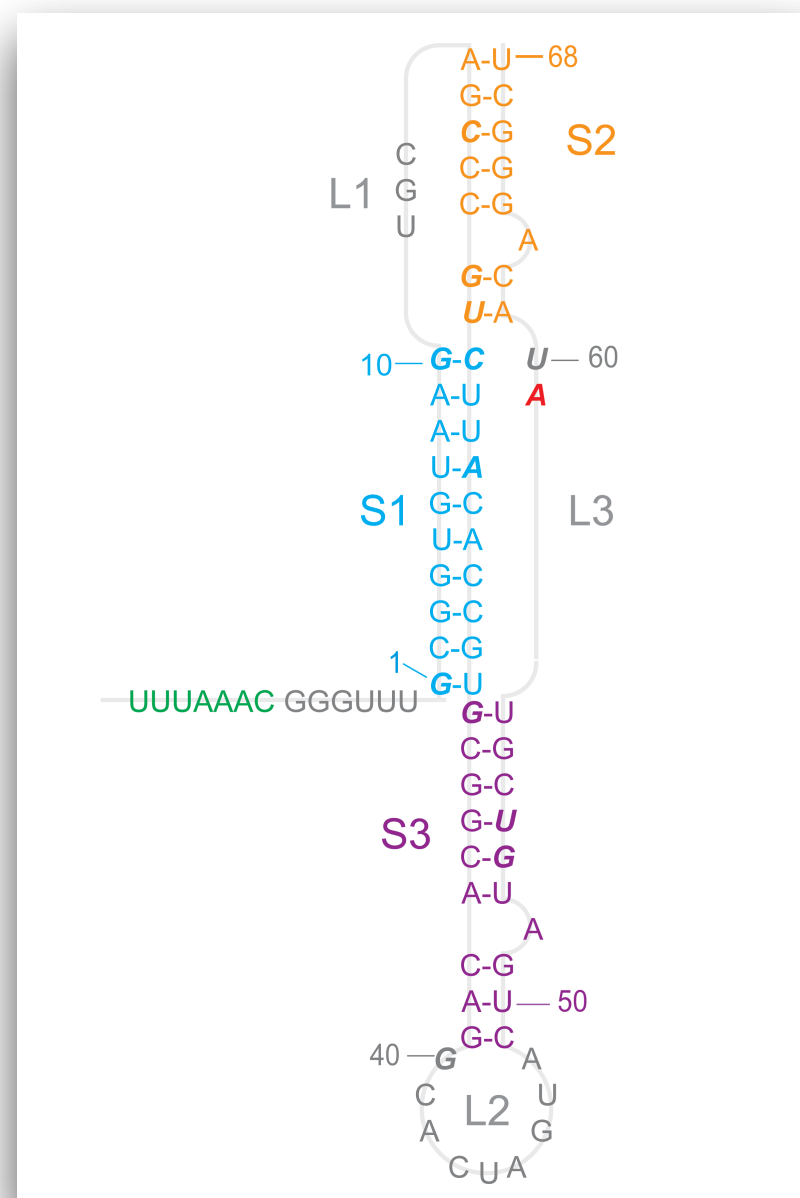
Fernandes et al.; RNA Biol (2012)



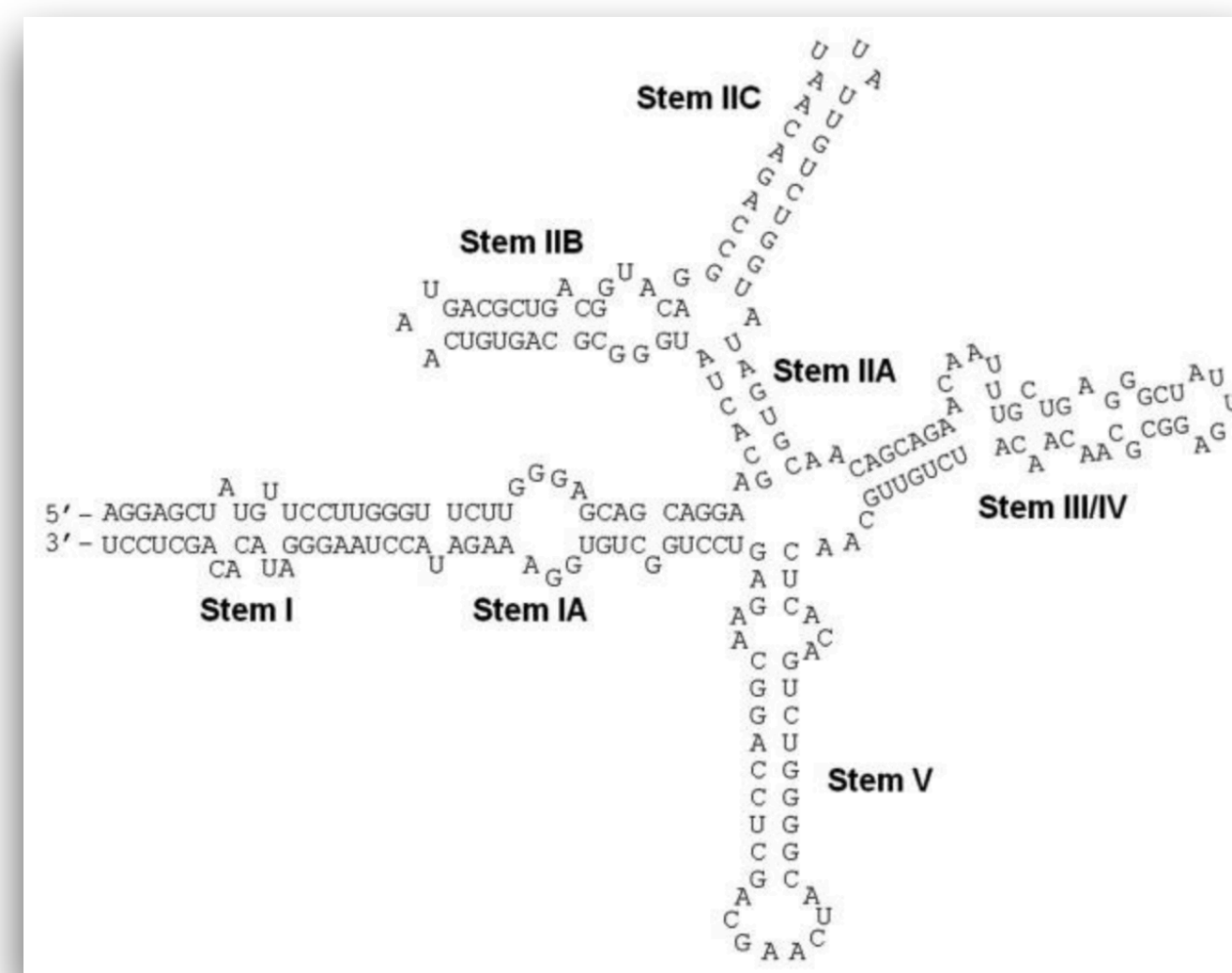
Newborn and White; Virology (2015)

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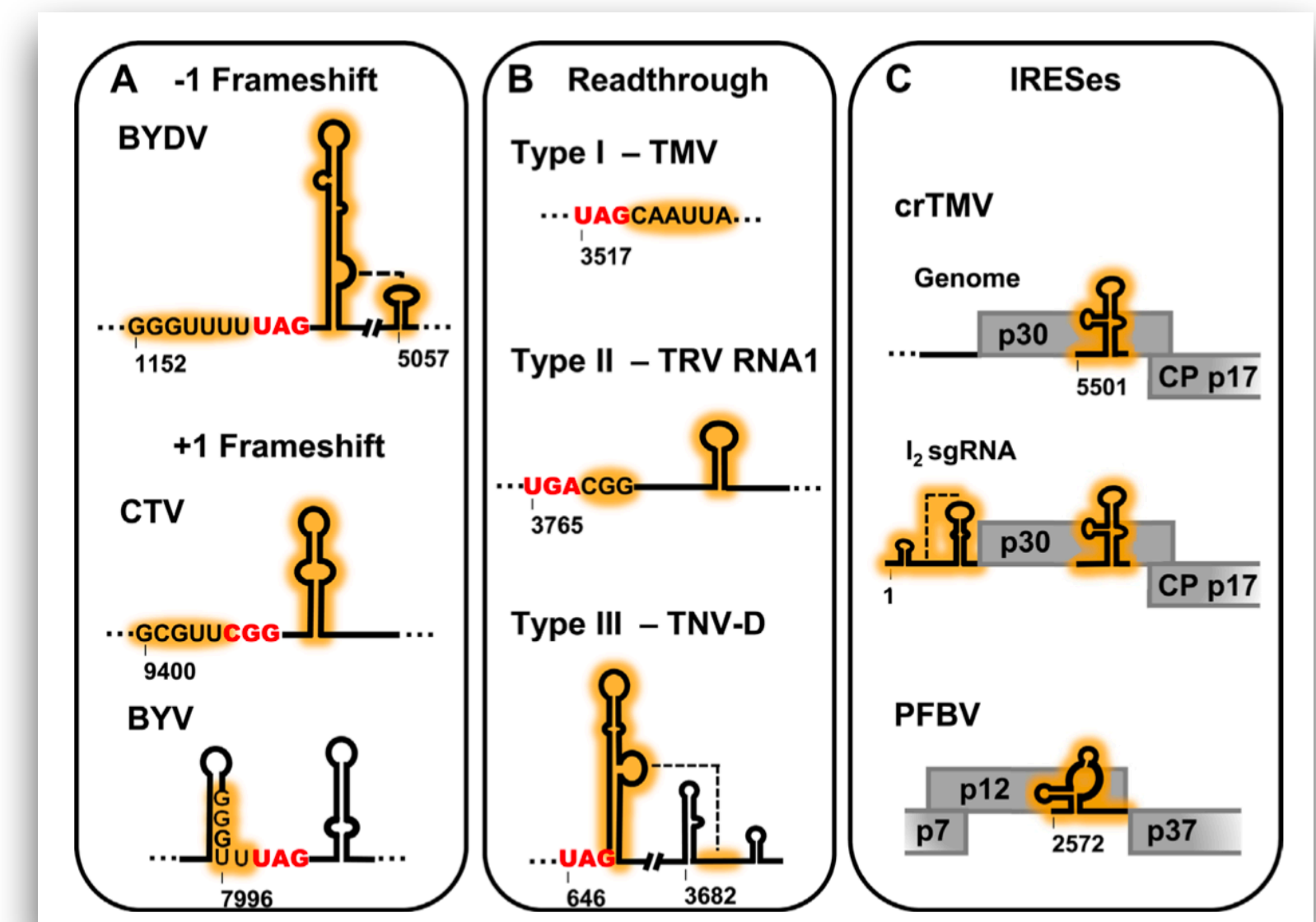
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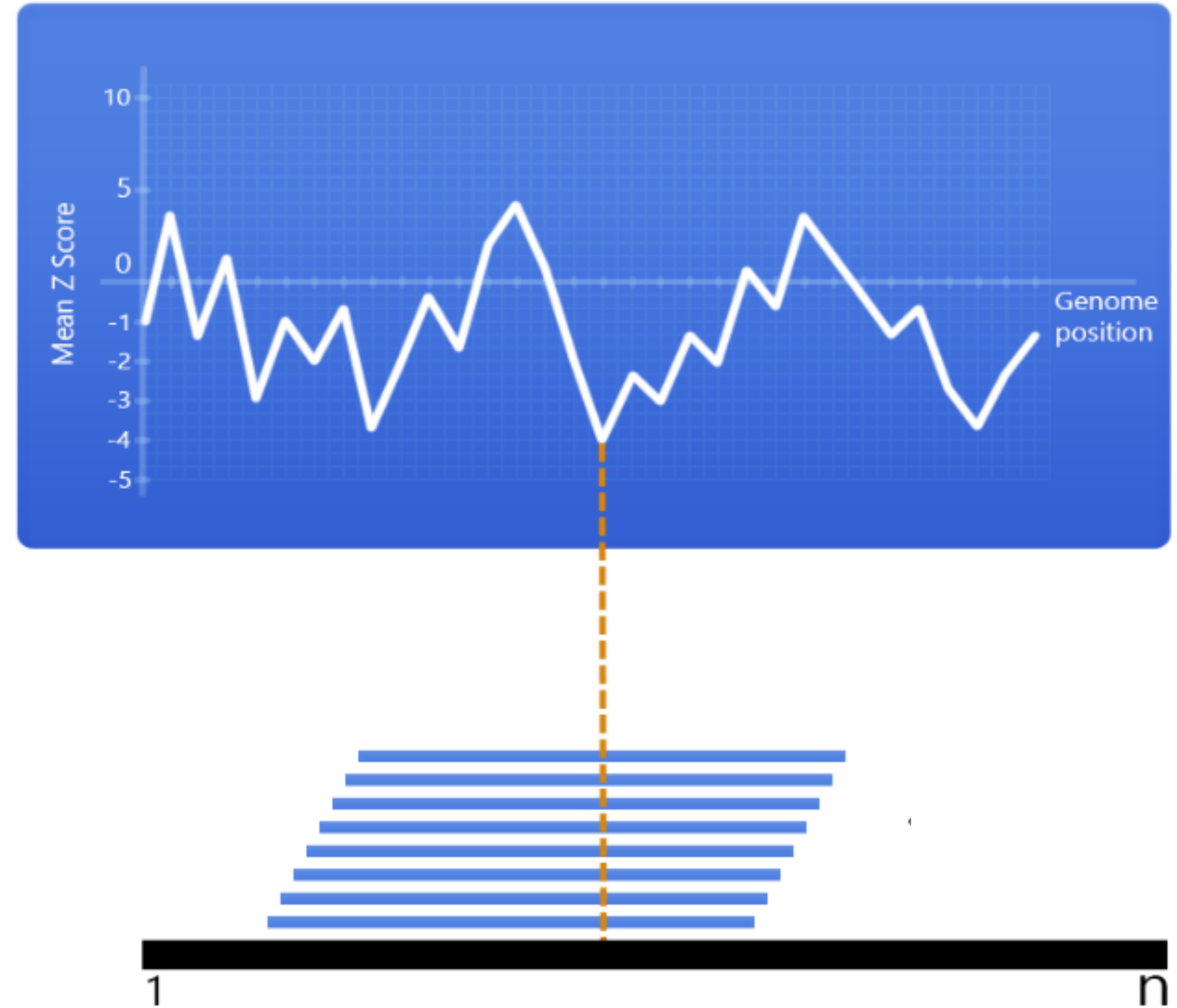


Newborn and White; Virology (2015)

How to assess global RNA structuredness?

- MFE Z scores as a proxy for RNA structuredness

$$z = \frac{m - \mu}{\sigma}$$



How to assess global RNA structuredness?

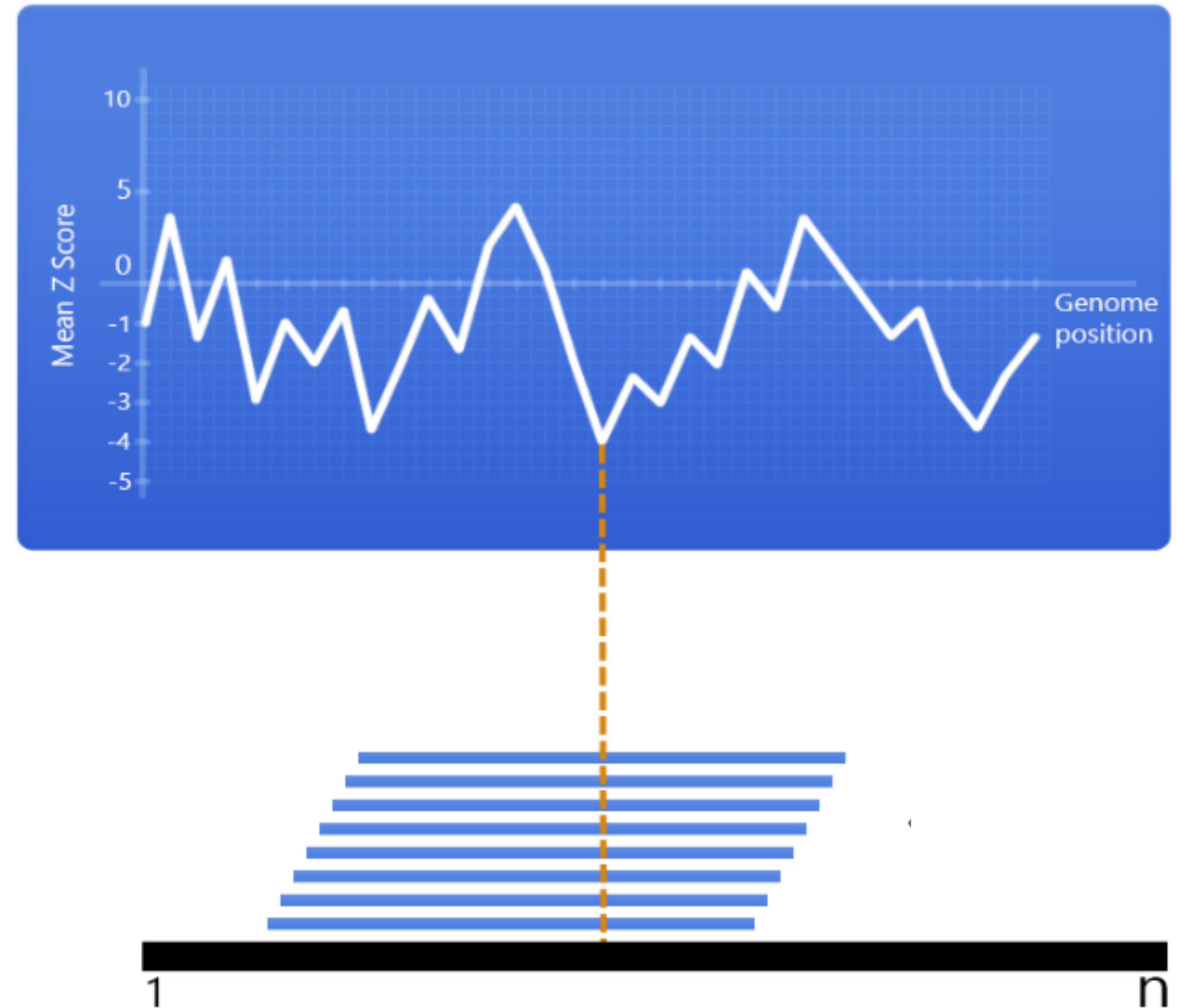
- MFE Z scores as a proxy for RNA structuredness

$$z = \frac{m - \mu}{\sigma}$$

- Opening energy

$$\Delta G_{\text{open}} = -RT \ln P(\text{unpaired})$$

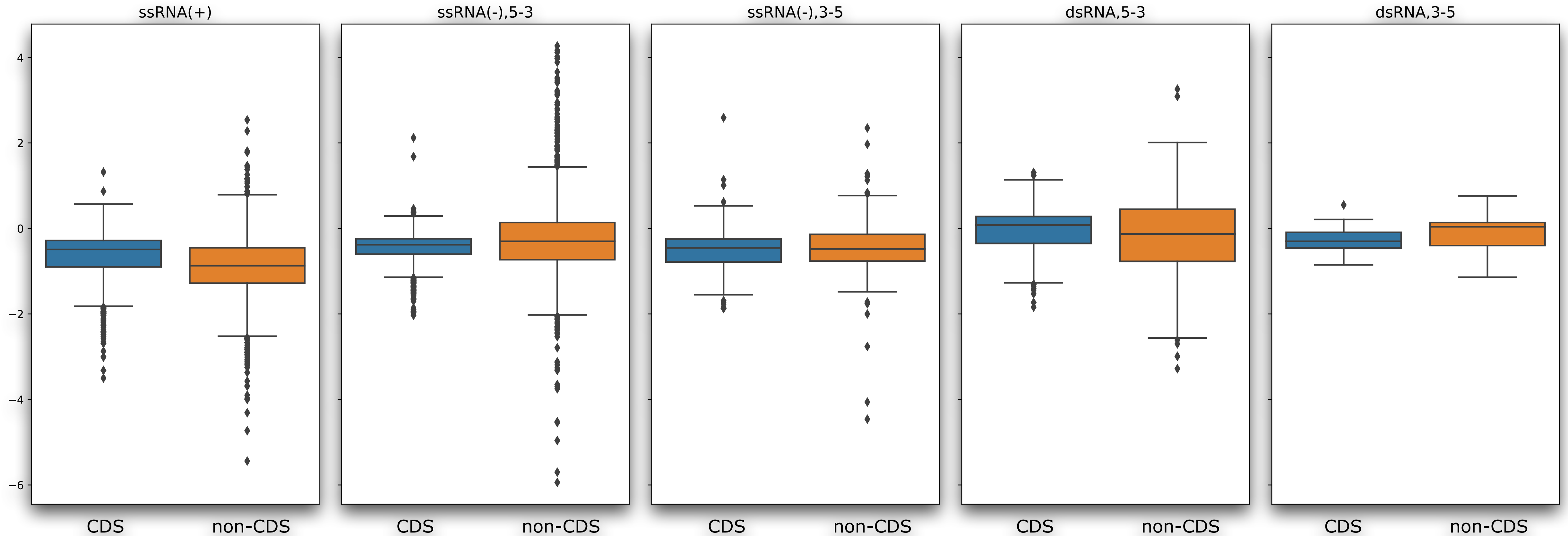
- GC content



Data Set

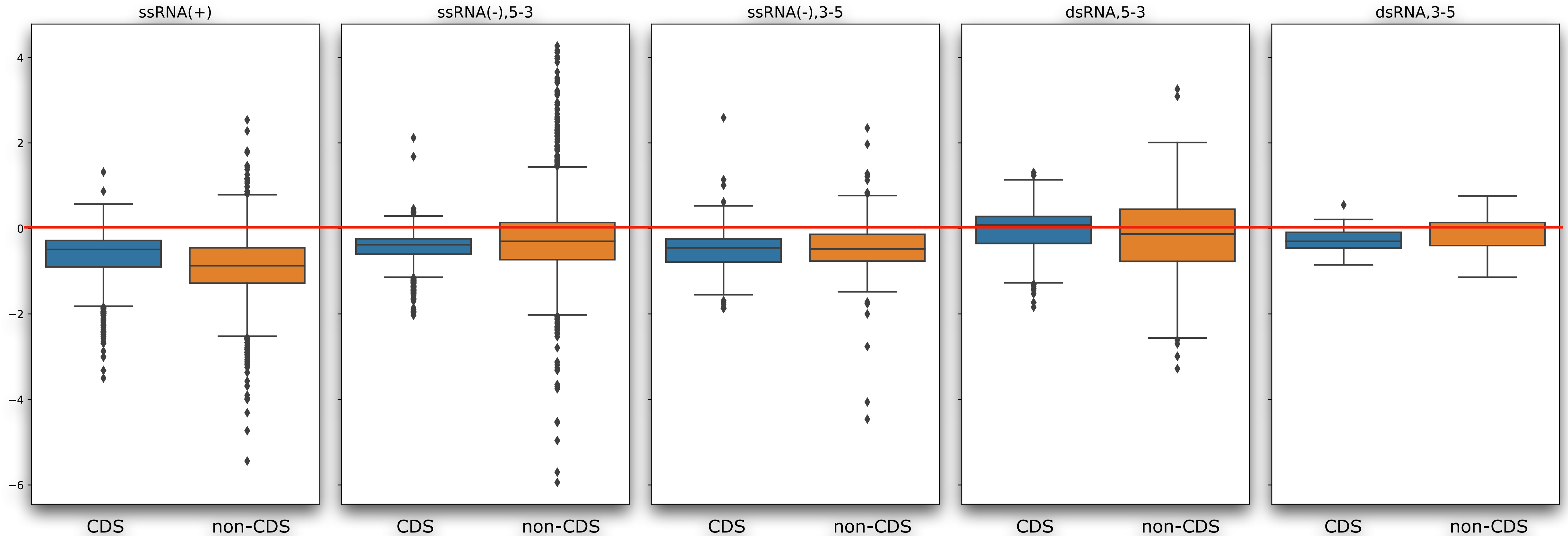
| Baltimore classification | Unsegmented | Segmented | Total |
|---------------------------------|--------------------|------------------|--------------|
| ssRNA(+) | 1333 | 373 | 1706 |
| ssRNA(-) | 355 | 1118 | 1473 |
| dsRNA | 73 | 890 | 963 |
| dsDNA | 714 | 0 | 714 |
| | 2475 | 2381 | 4856 |

Structuredness coding/non-coding regions



MFE Z scores

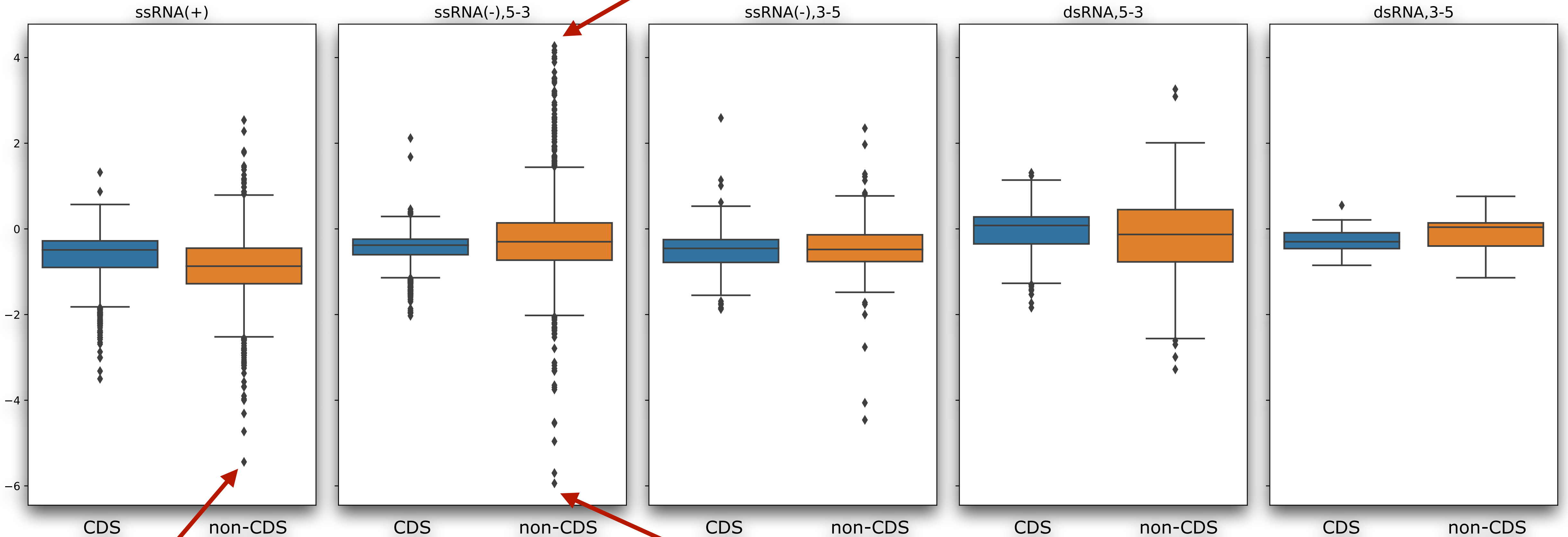
Structuredness coding/non-coding regions



MFE Z scores

Structuredness coding/non-coding regions

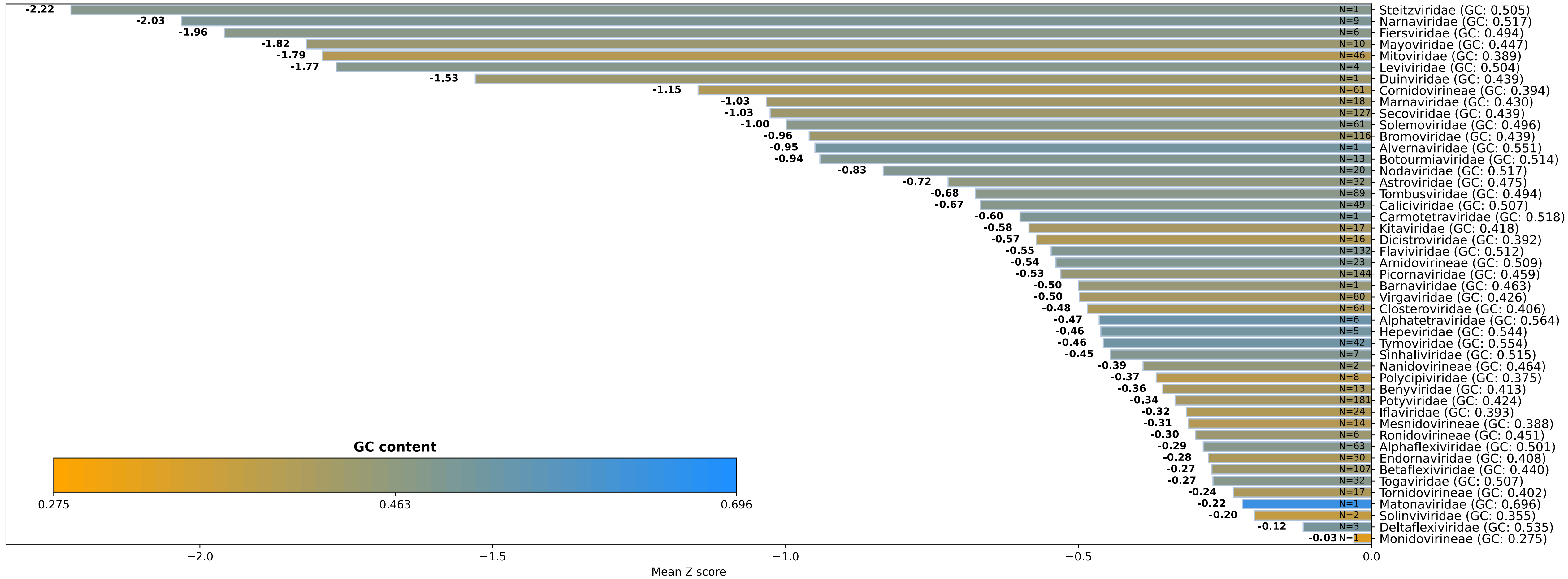
Anhembi virus, segment L (Bunyavirus)



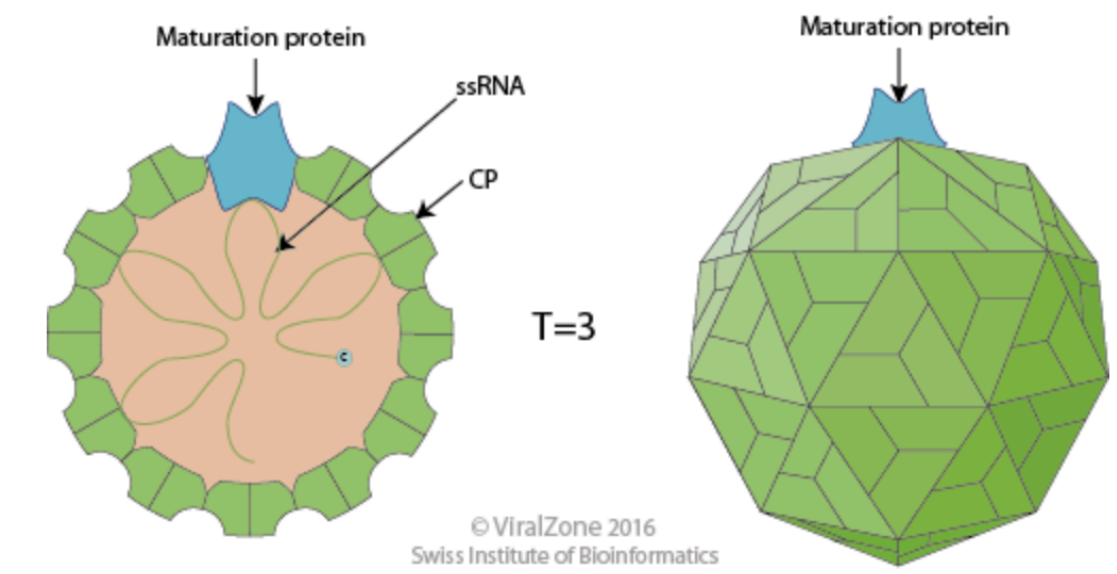
Blechmonas luni narnavirus 1

Uukuvirus (Bunyavirus)

Mean Z score of ssRNA(+) families

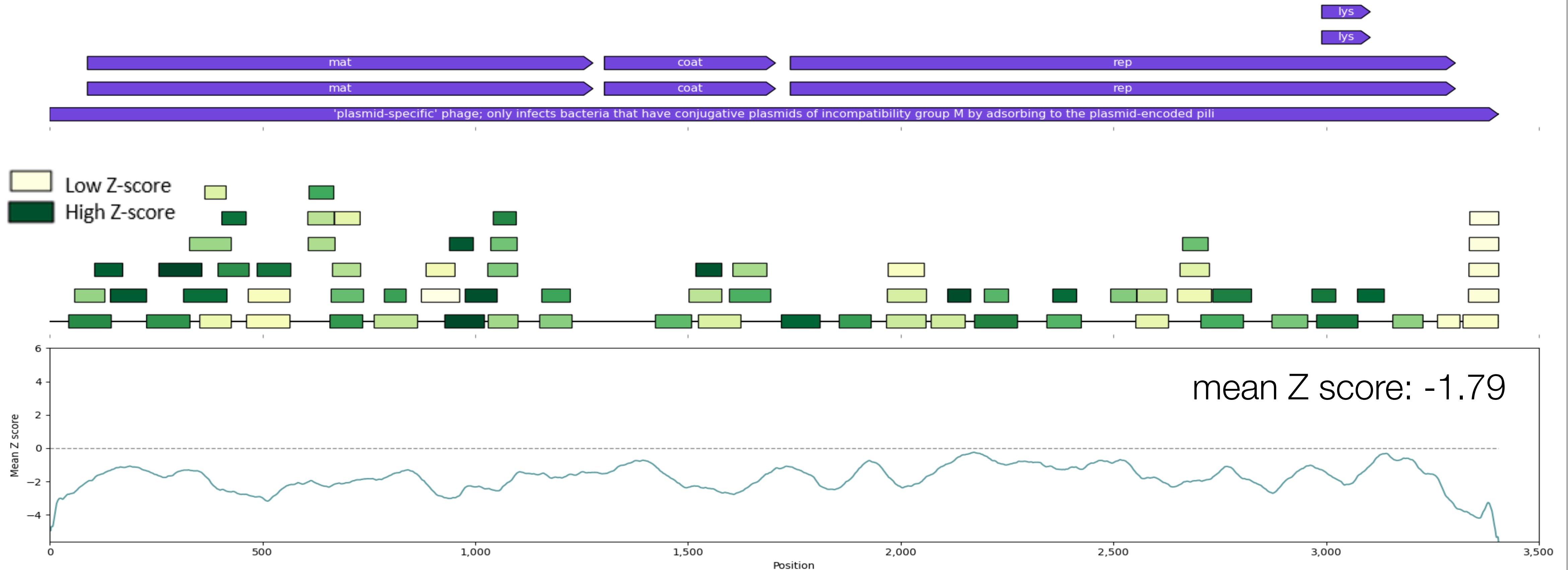


Phage example [ssRNA(+)]

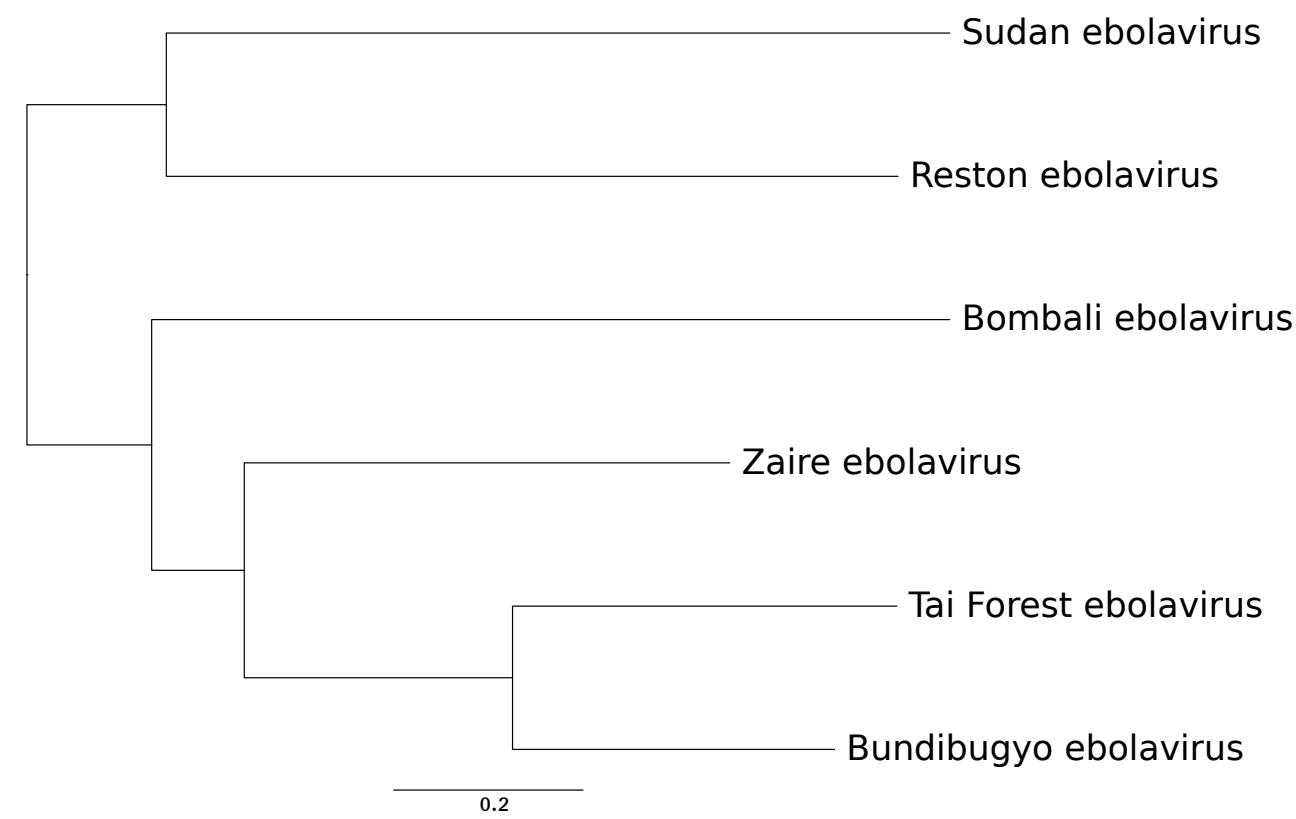


<https://viralzone.expasy.org/163>

Viruses|Orthornavirae|Lenarviricota|Leviviricetes|Norzivirales|Fiersviridae|Enterobacteria phage M

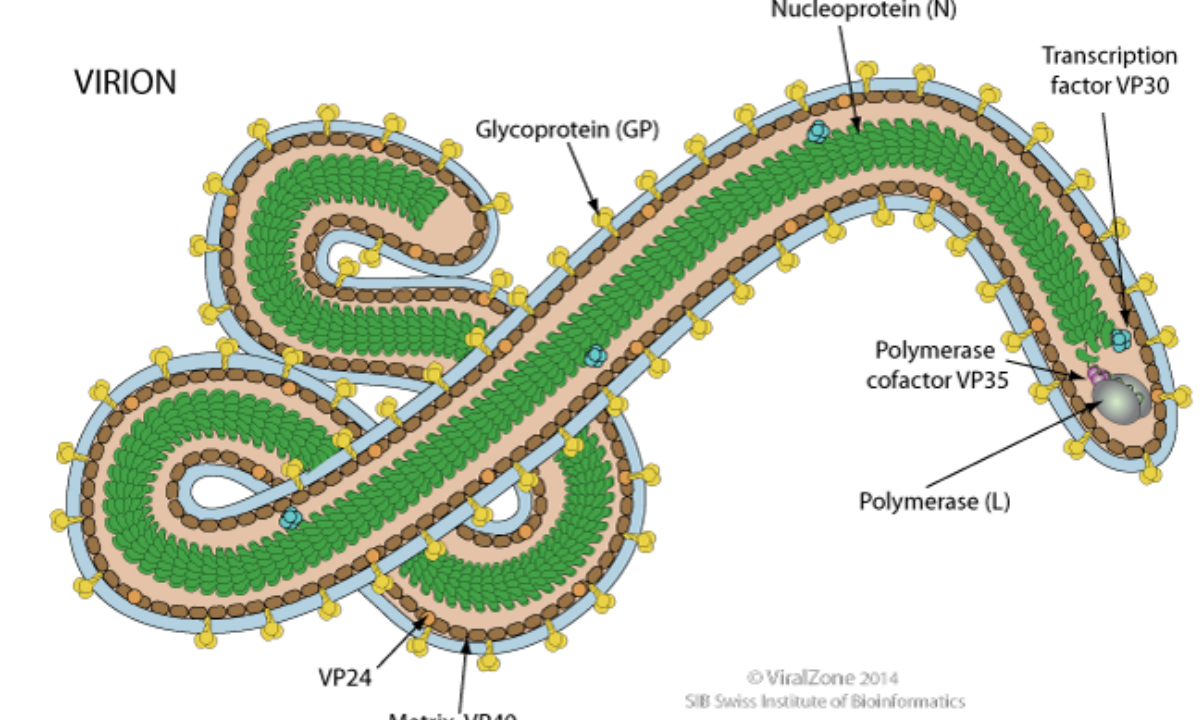


Ebolavirus example [ssRNA(-)]

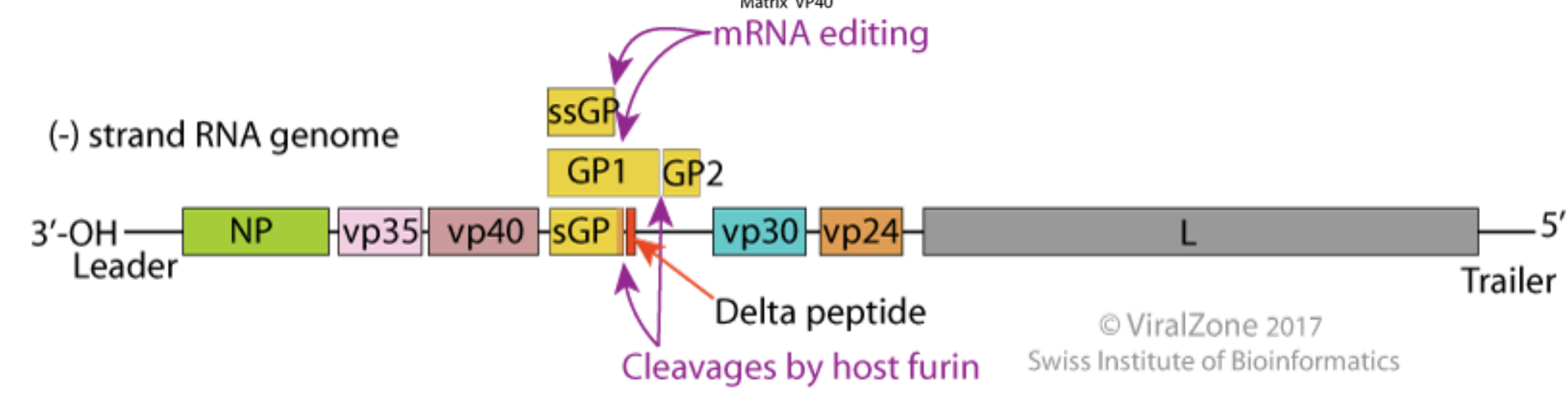


| | BDBV | BOMV | EBOV | RESTV | SUDV | TAFV |
|-------|-------|-------|-------|-------|-------|------|
| TAFV | 0.678 | 0.603 | 0.634 | 0.598 | 0.596 | 1 |
| SUDV | 0.597 | 0.578 | 0.6 | 0.594 | 1 | |
| RESTV | 0.597 | 0.582 | 0.602 | 1 | | |
| EBOV | 0.633 | 0.605 | 1 | | | |
| BOMV | 0.602 | 1 | | | | |
| BDBV | 1 | | | | | |

nucleotide identity
0.6 0.7 0.8 0.9 1.0

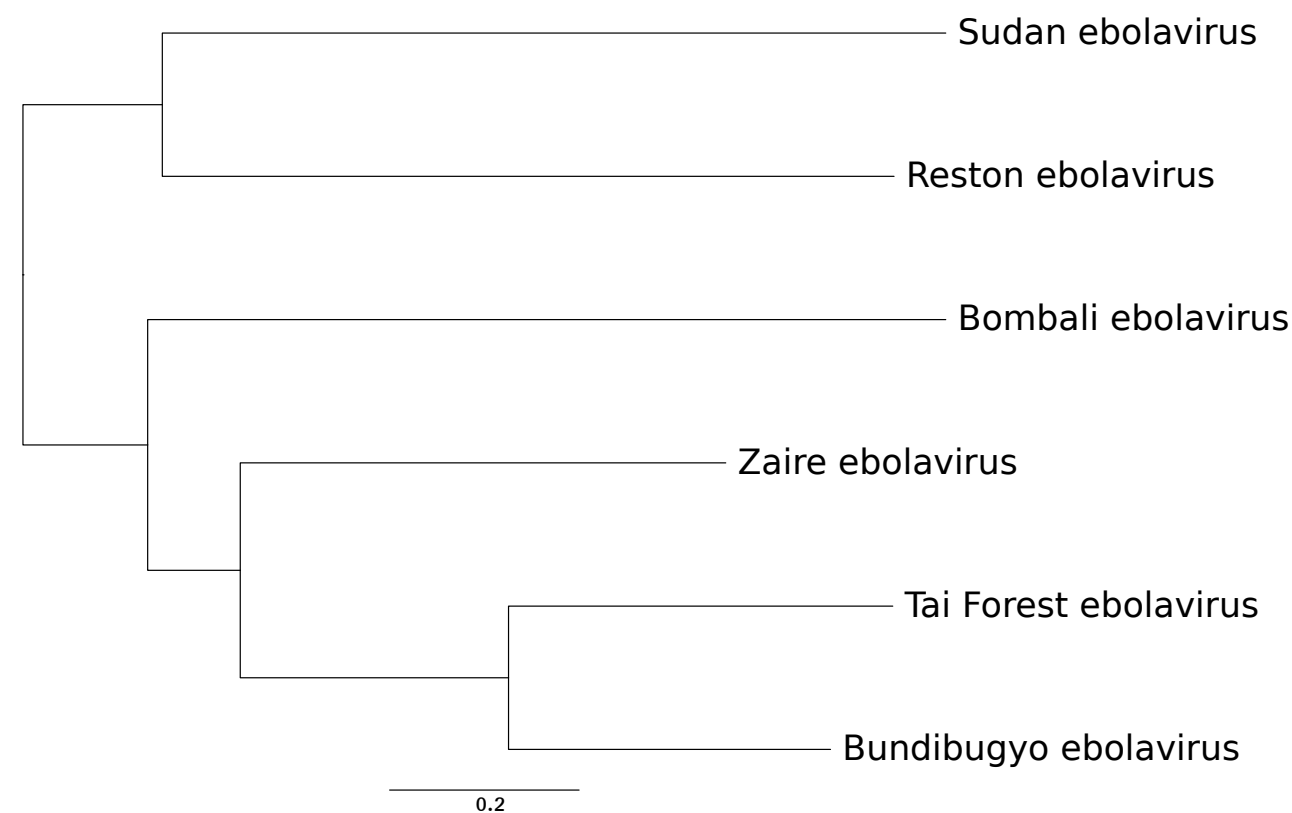


<https://viralzone.expasy.org/207>



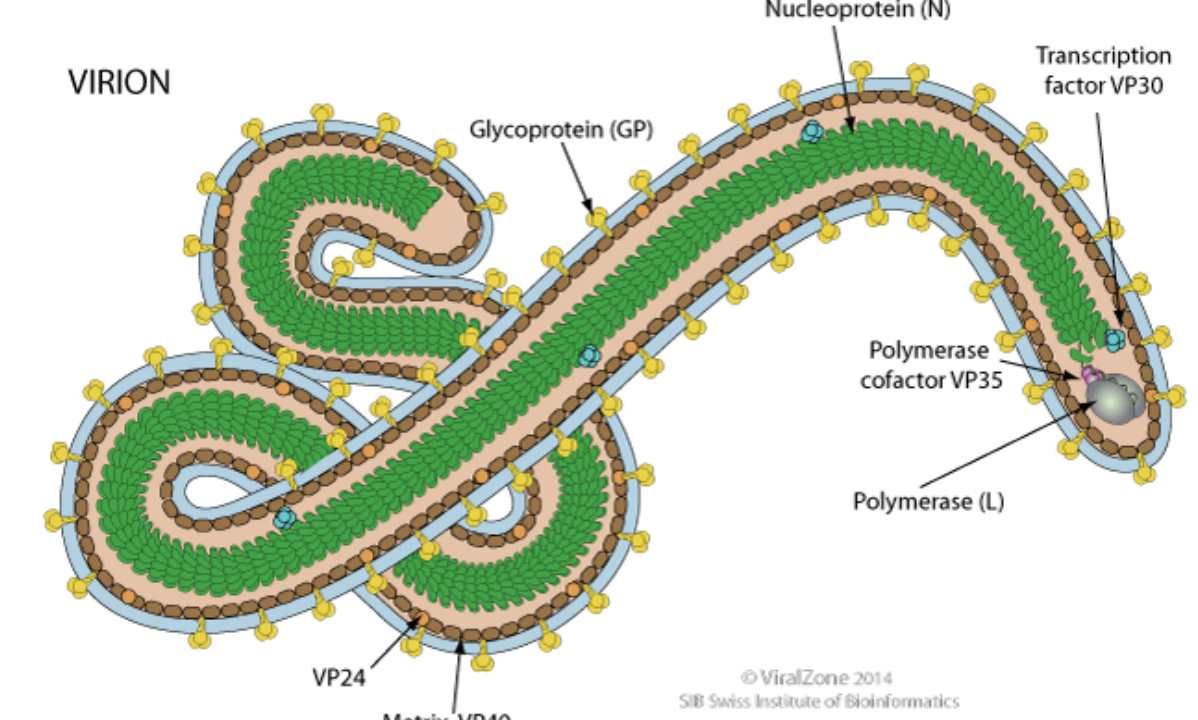
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Ebolavirus example [ssRNA(-)]

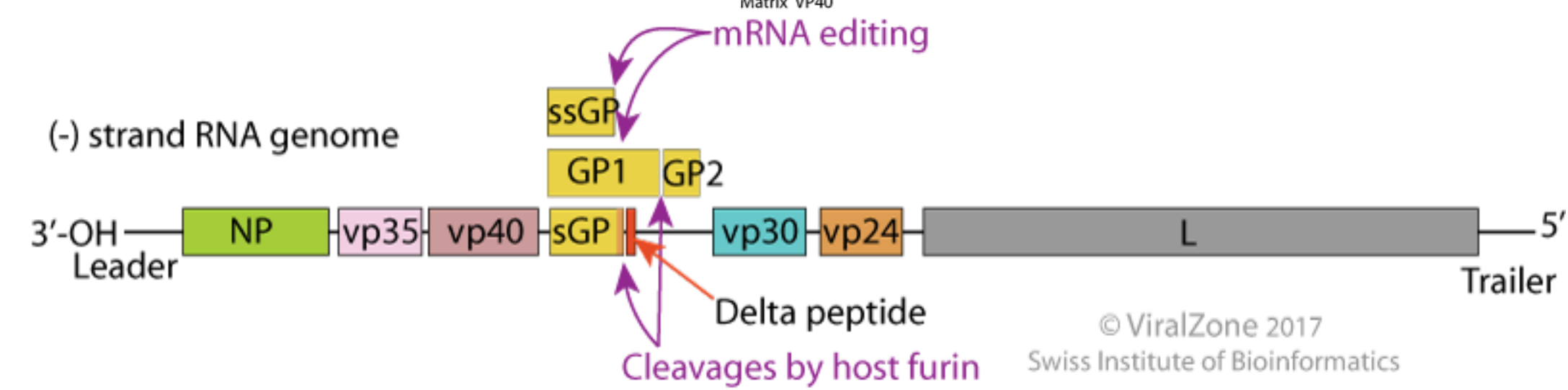


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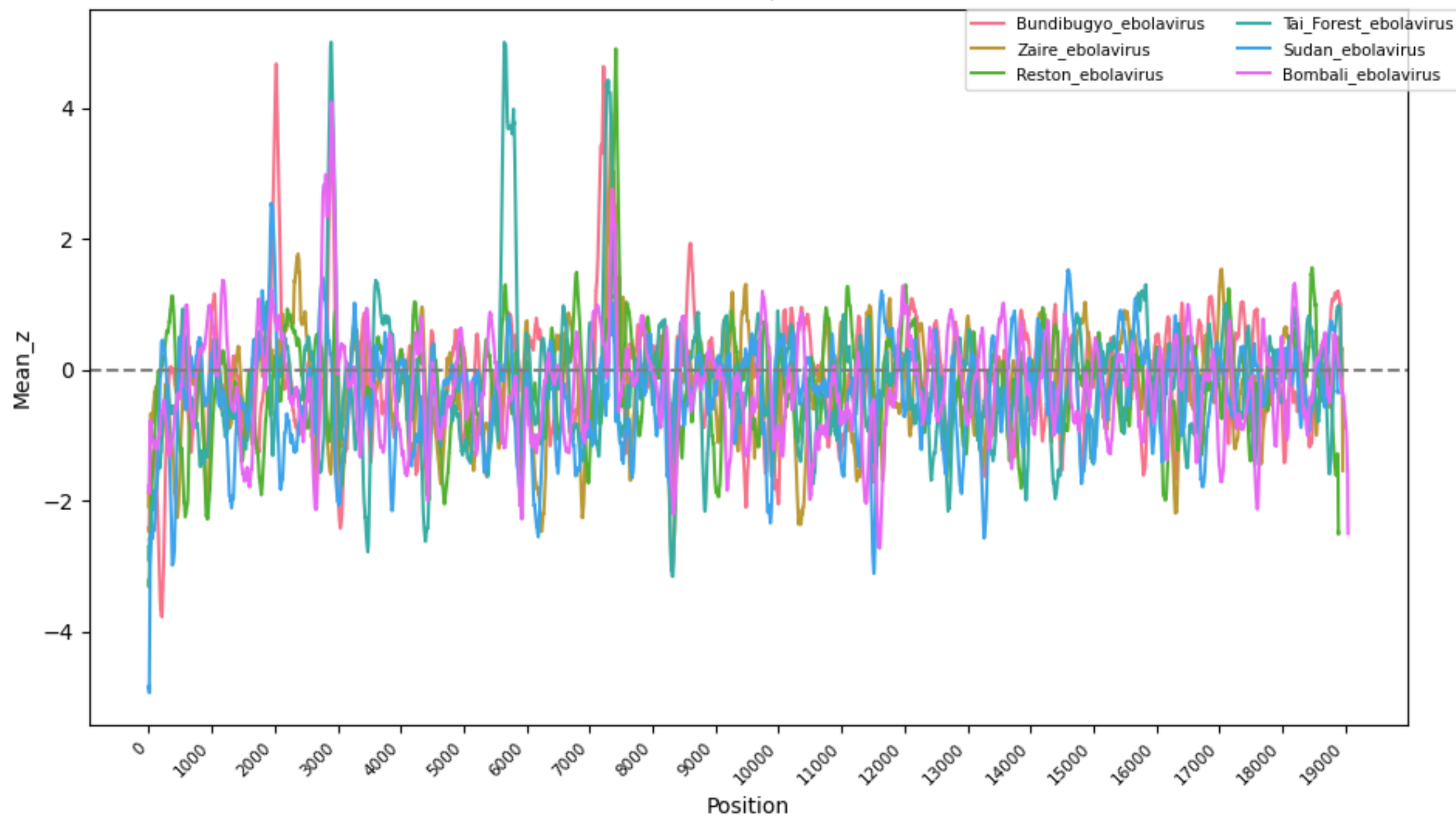


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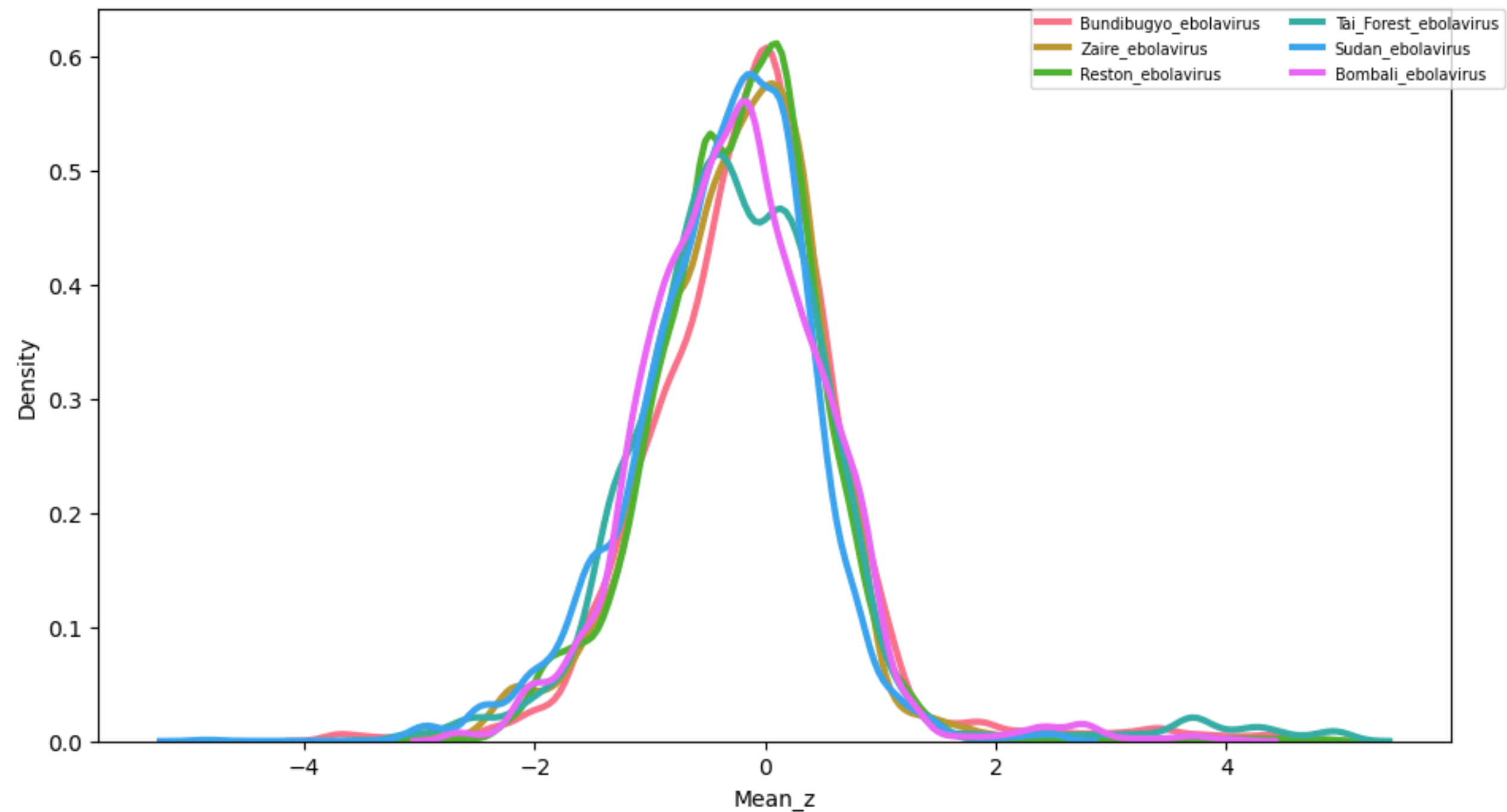


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All Ebolavirus, wlen 100

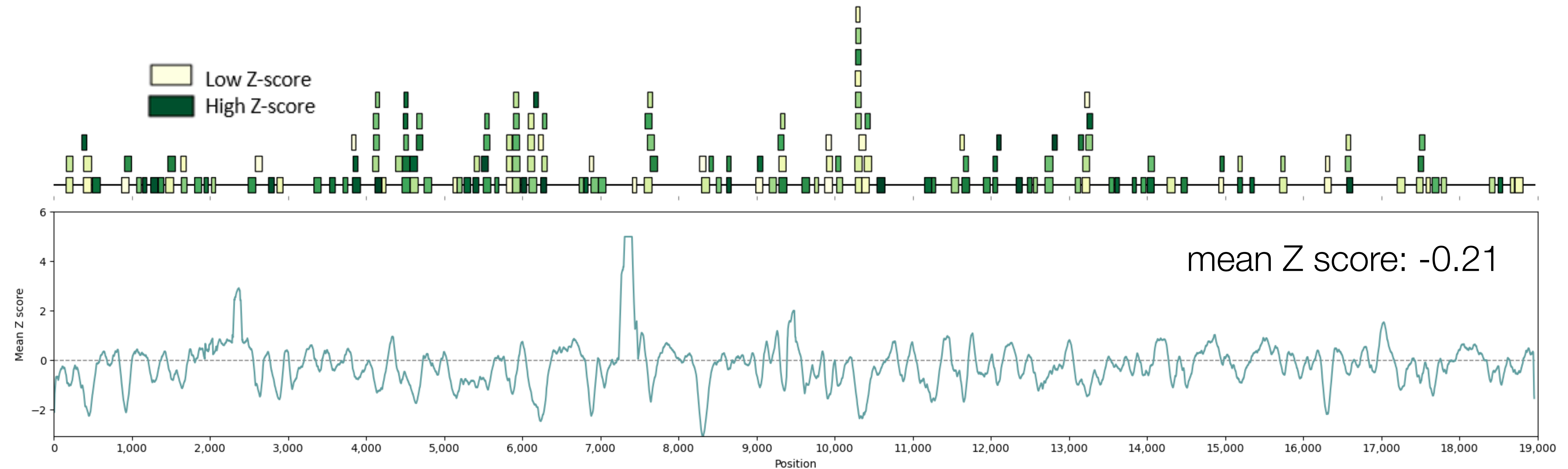
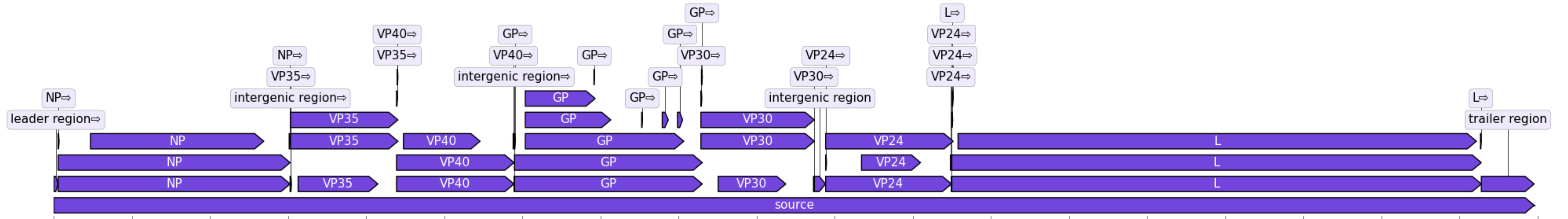


All densities Ebolavirus, wlen 100



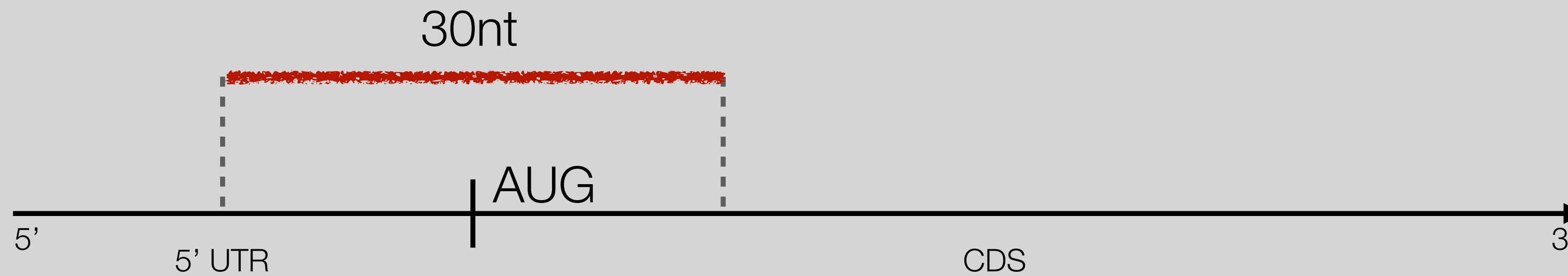
Ebolavirus example [ssRNA(-)]

RNALfold (filtered for $z=-2$) with Mean Z, wlen100 - Zaire ebolavirus

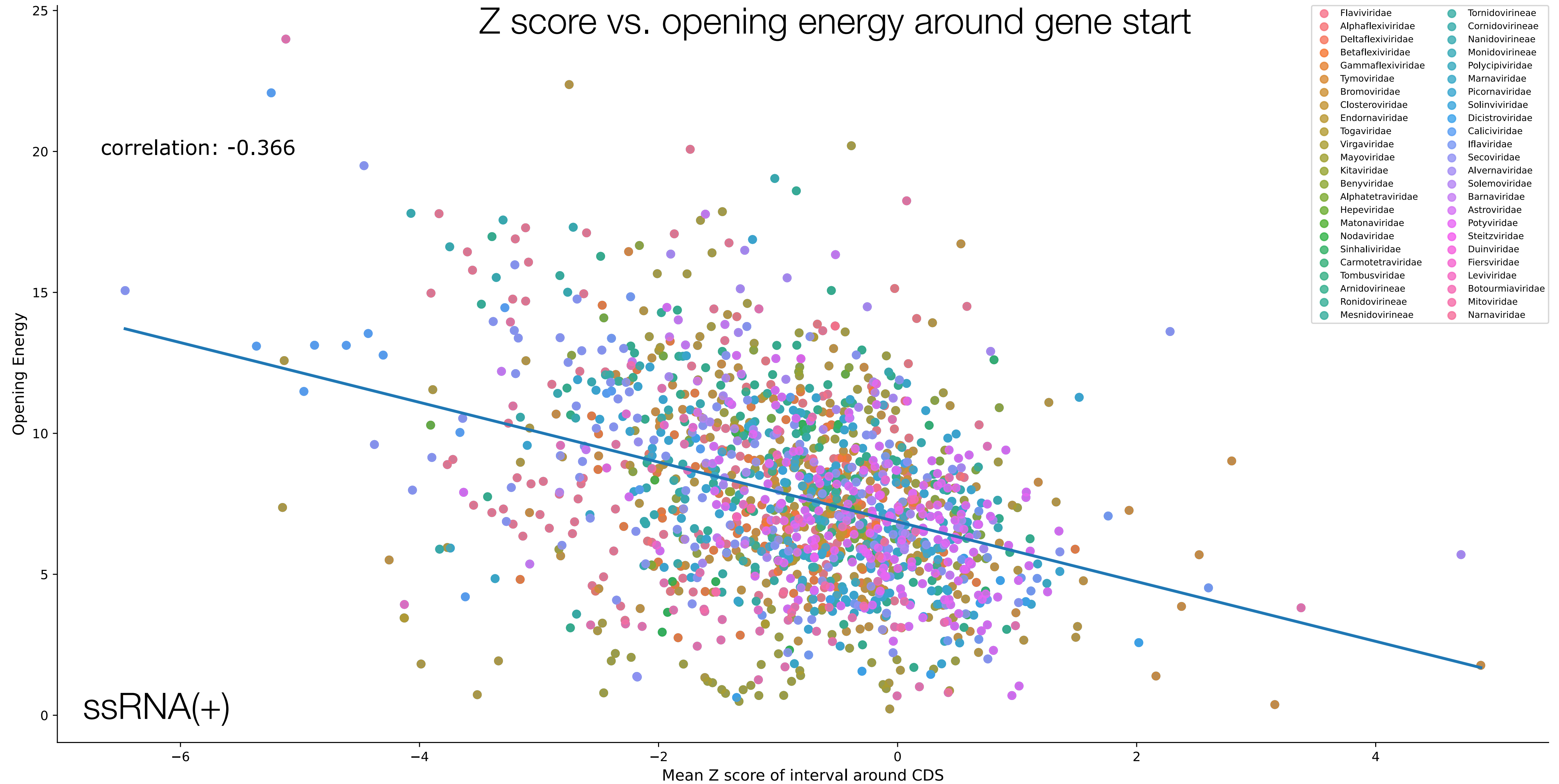


Structuredness of gene start regions

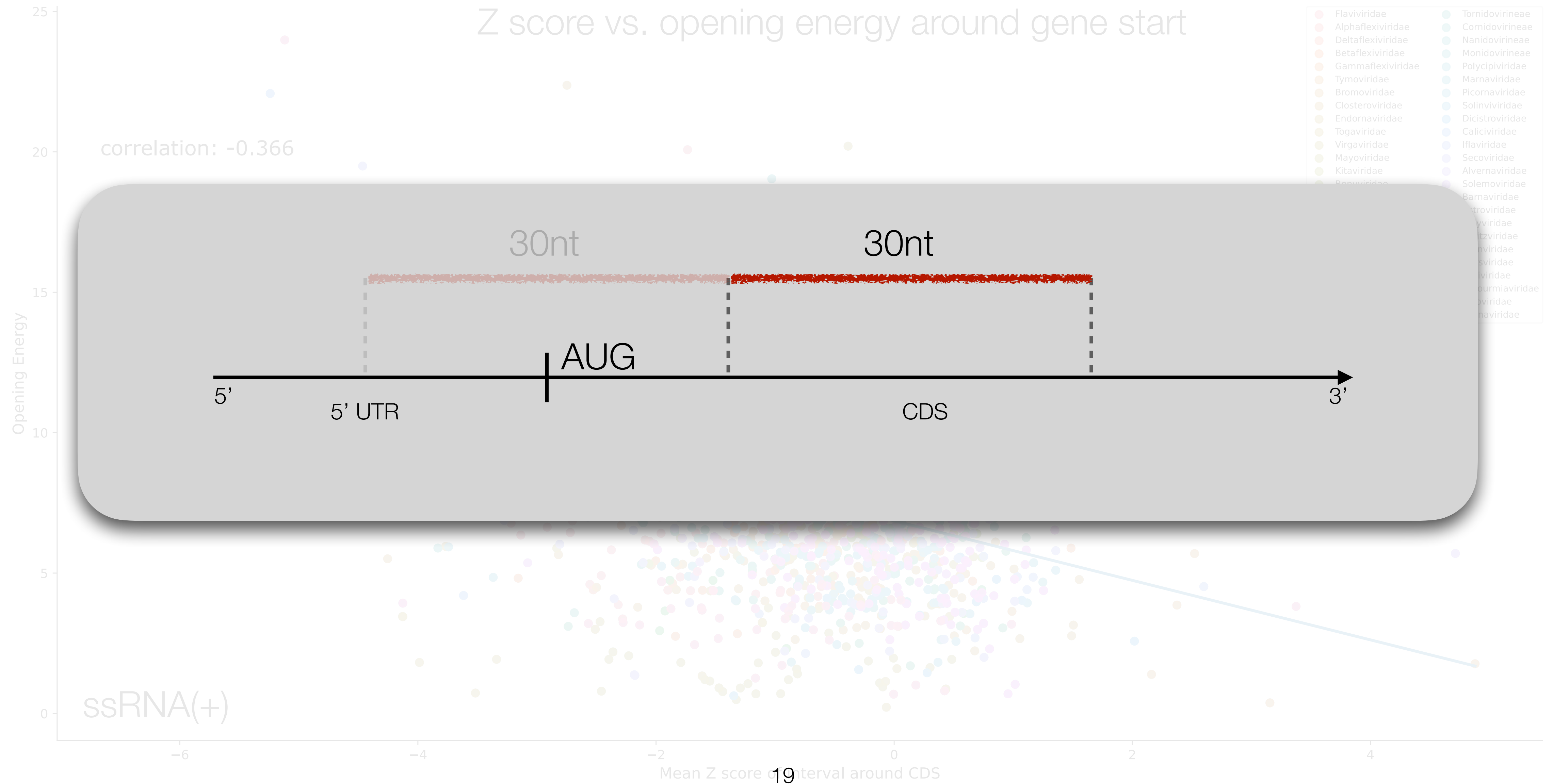
Are they accessible?



Structuredness of gene start regions

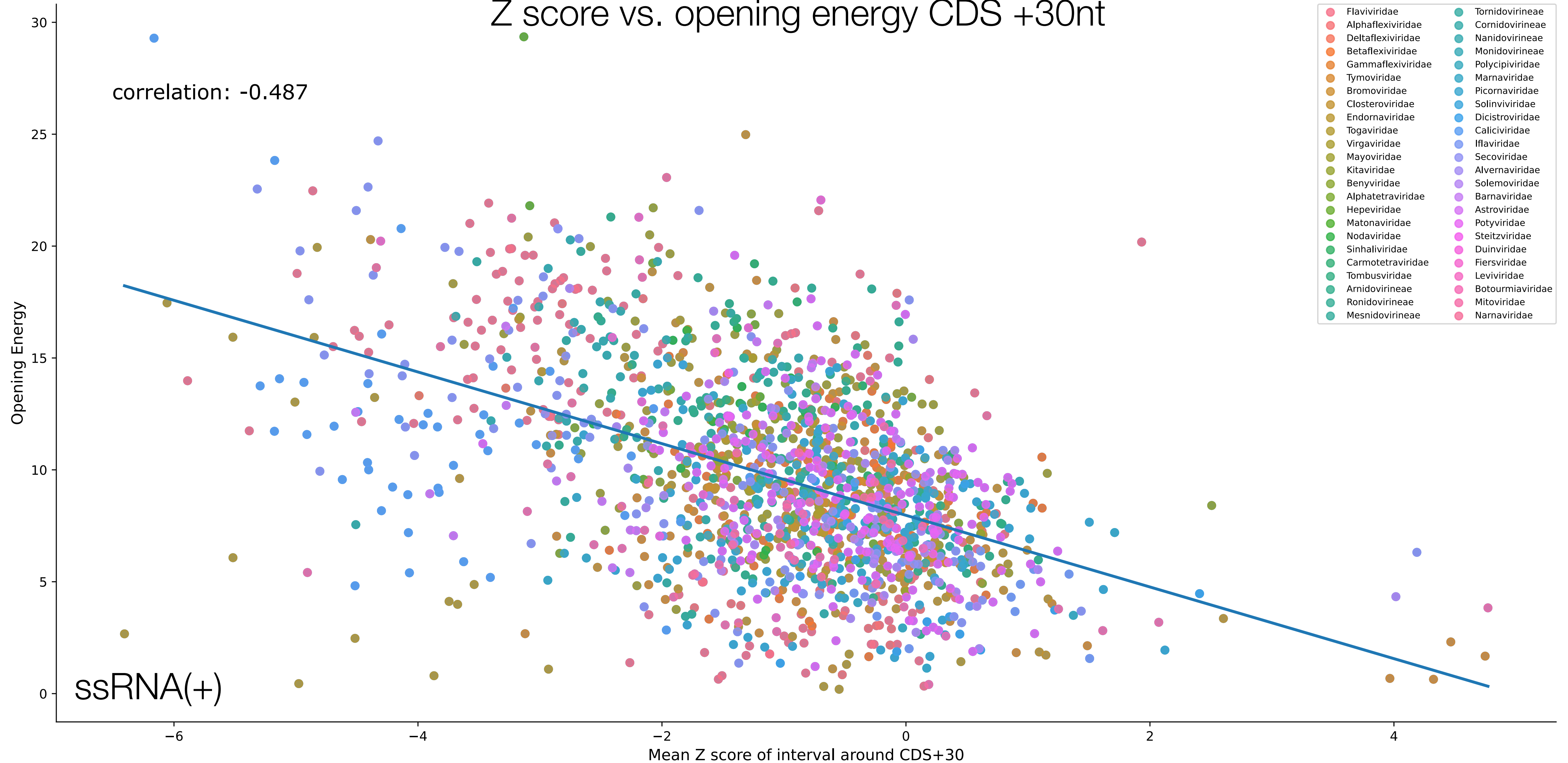


Structuredness of gene start regions

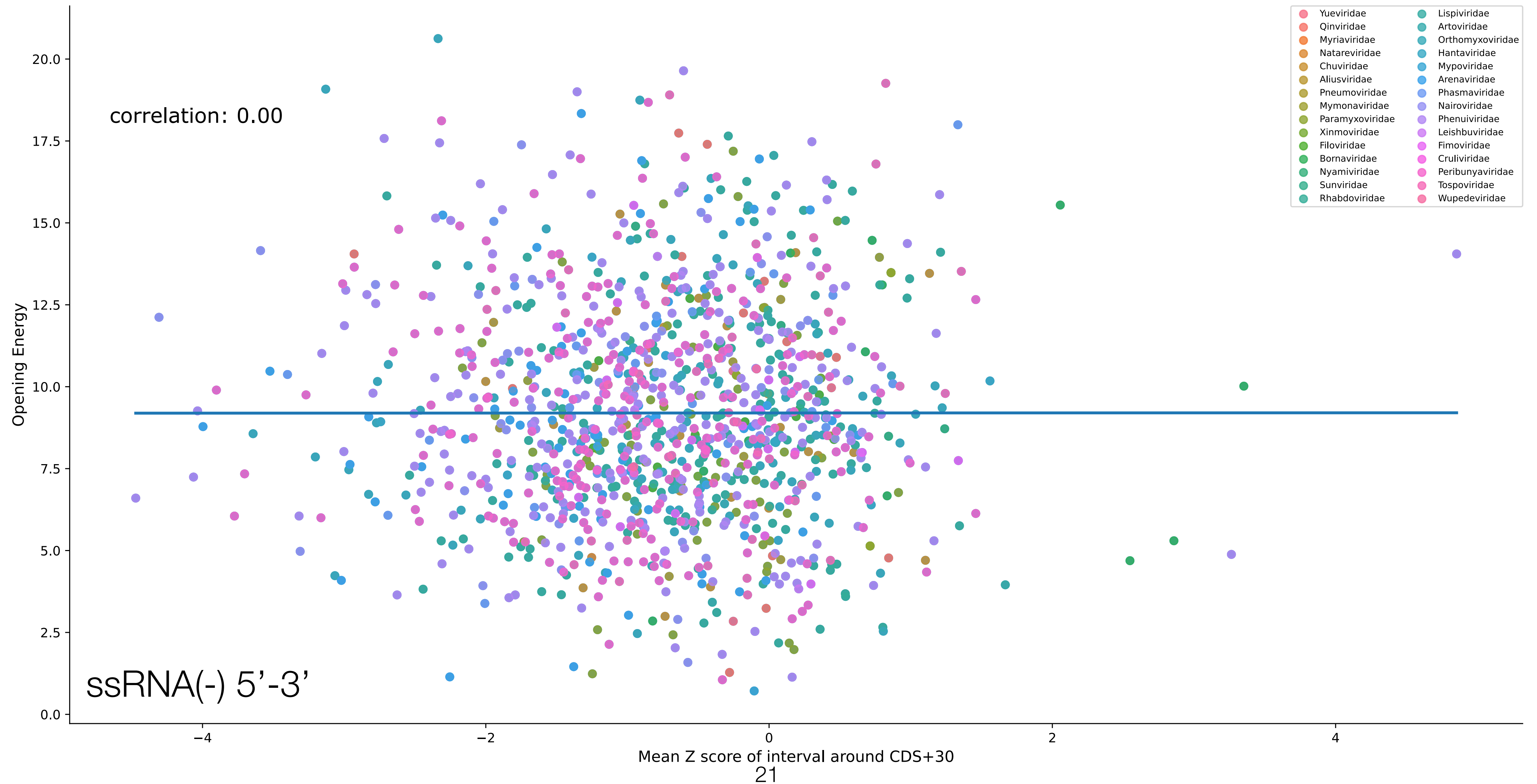


Structuredness of gene start regions

Z score vs. opening energy CDS +30nt



Structuredness of gene start regions



Where we are

- Viruses differ in their RNA structuredness; many viruses are more structured than expected
- GC content is not always a proxy for RNA structuredness
- Some viruses achieve high structuredness despite low GC content

The next steps

- Analyse structuredness of human mRNAs
- Assess the impact of codon usage bias on RNA structuredness
- Synbio: Study the impact of alternative genetic codes on RNA structuredness

Acknowledgements

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