

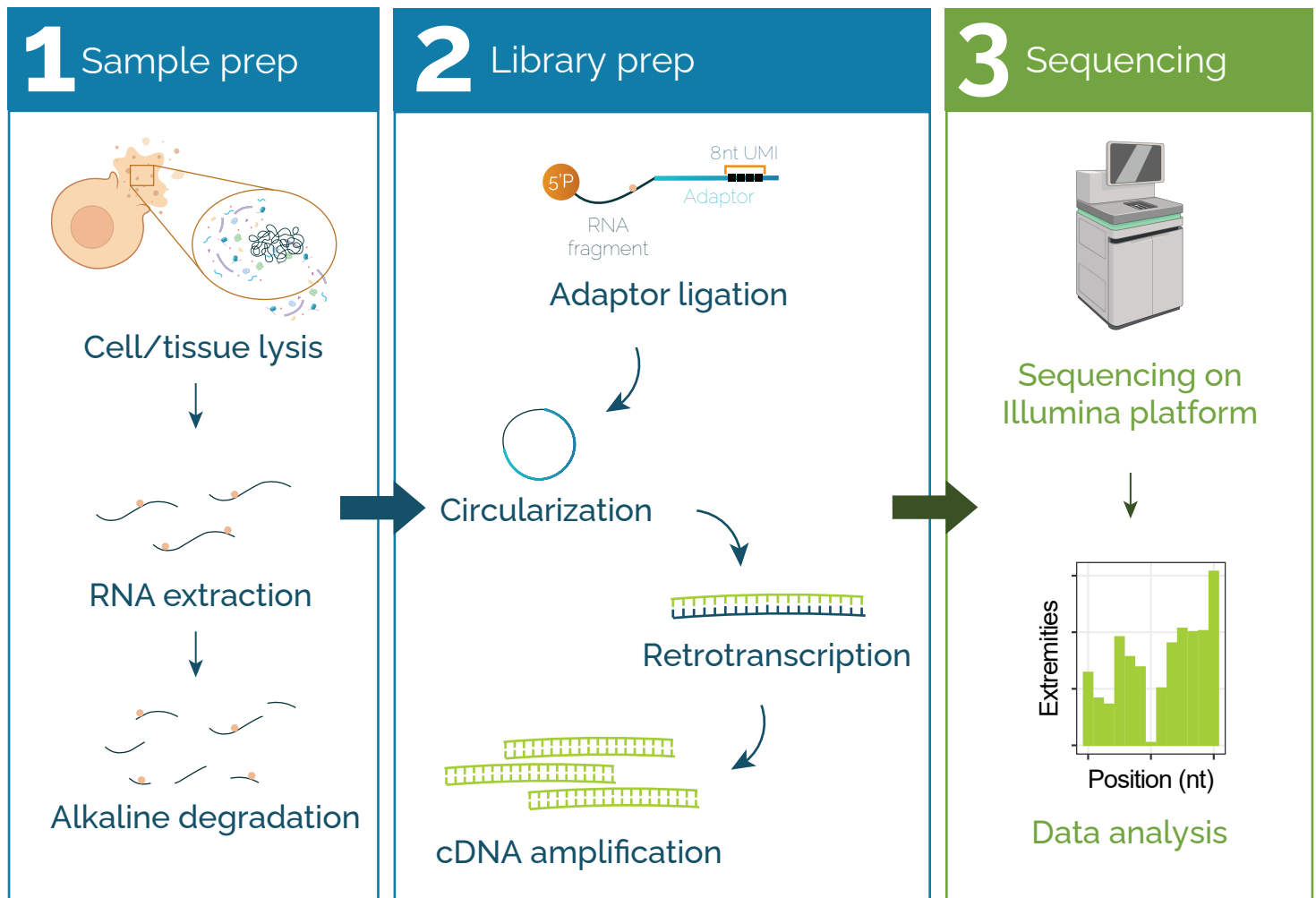
# RiboMe

Enhanced  
ribosome  
innovations



Unlock the power of RNA 2'-O-Me epitranscriptome

Introducing RiboMe: the **first commercial kit** enabling **standardized** analysis of RNA 2'-O-methylome. Start directly from total RNA and precisely quantify 2'-O-methylation levels thanks to the presence of **unique molecular identifiers** (UMIs). With 12 ready-to-use reactions, everything you need is right in the box to explore the epitranscriptomic code of RNA. Streamlined. Sensitive. Reliable. Discover what your RNA has been hiding.



## Specifications

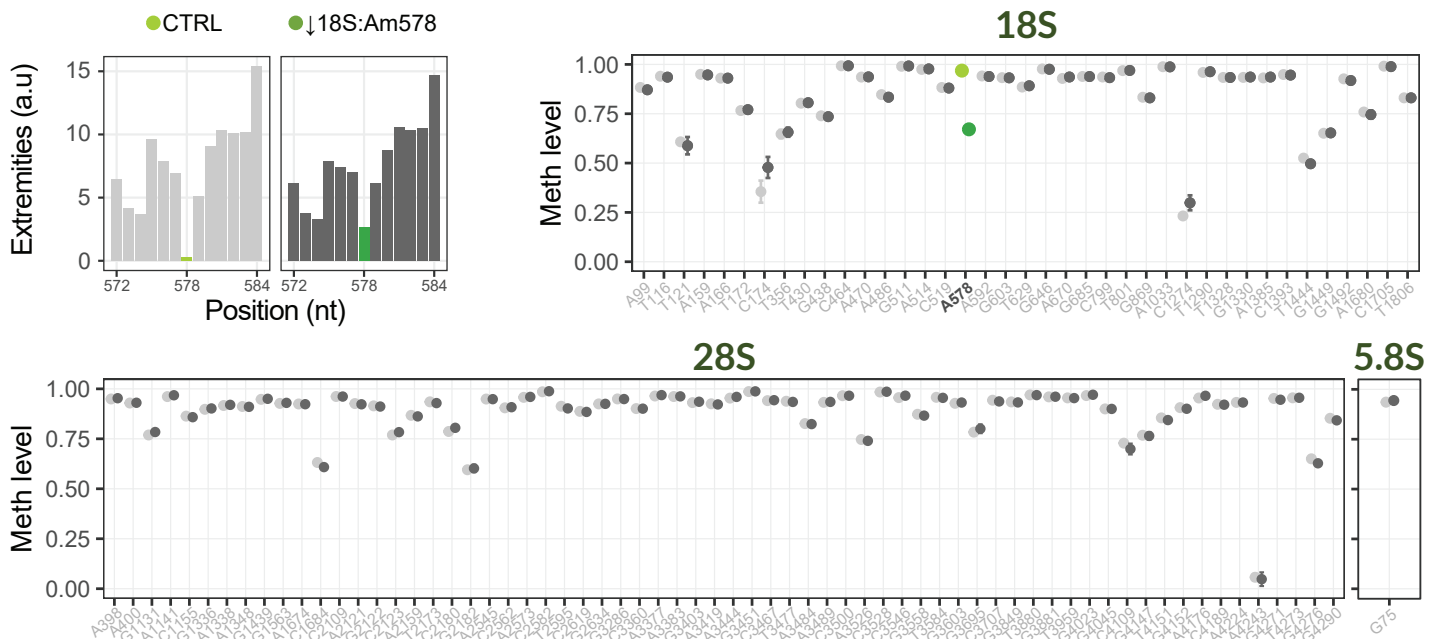
|                 |                   |               |         |
|-----------------|-------------------|---------------|---------|
| Species         | All species*      | Kit size      | 12 rxns |
| Total RNA input | ≥ 40 ng total RNA | Workflow time | 2 days  |

\*all species with annotated genome



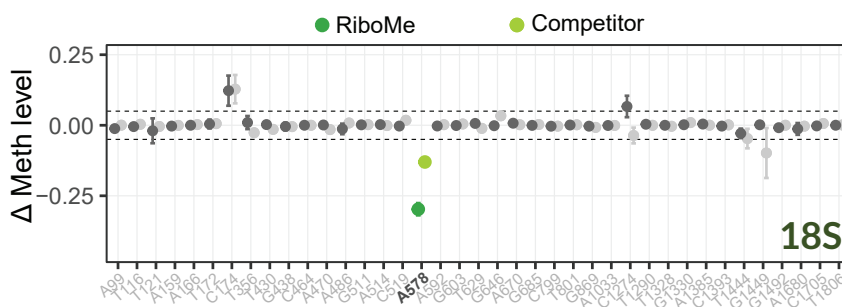
# Proof-of-concept studies

## (A) RiboMe detects site-specific variations in 2'-O-methylation level



RiboMe provides robust, and accurate quantification of 2'O methylation levels. Following the perturbation of methylation seposition at site 18S:A578, RiboMe exhibits strong specificity by detecting a clear reduction at the target site, with no other equally substantial changes observed.

## (B) RiboMe has a higher sensitivity compared to available methods



Compared to other kits, RiboMe demonstrates superior sensitivity in detecting methylation changes at the perturbed site compared to CTRL.

# Highlights



Precise 2'-O  
methylome  
quantification



Standardized



Reliable



Increased  
sensitivity



Fast  
workflow



Imagine what you can discover. Immagina.

eRIS