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A genome wide RNAz screen for structured RNA elements in mouse

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Overview

- ▶ Introduction
 - RNAz, LocARNA
- Our pipeline
- Preliminary results

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Introduction »

RNAz

- Uses alifold
- A machine learning approach
- Based on
 - Structure Conservation Index
 - Thermodynamic Stability

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Introduction »

RNAz 2.0

- Dinucleotide shuffled z-scores
- Windows > 400nt
- >10 species

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Introduction »

Challenges

- Highly dependent on alignment quality

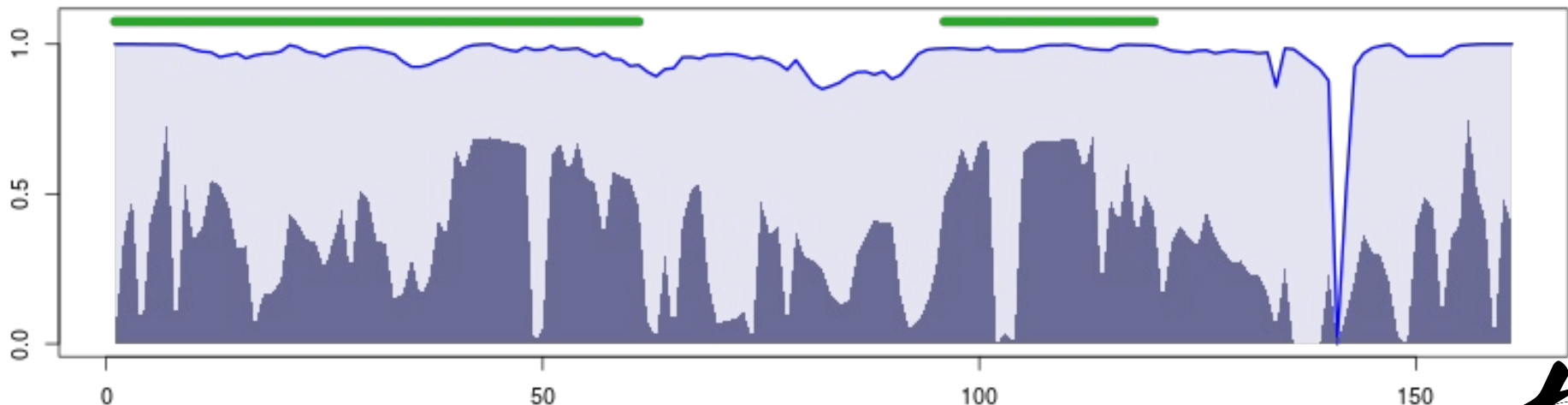
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Introduction »

LocARNA

- Structure based multiple sequence alignment
- LocARNA-P
 - Column wise reliabilities for boundary prediction

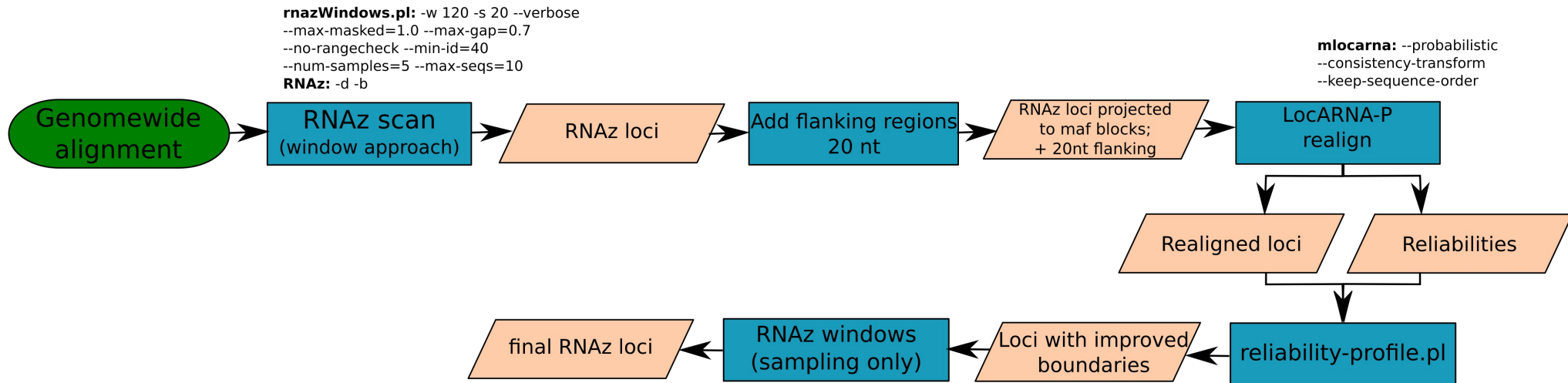


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Our Pipeline »

Flowchart



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Preliminary results » False Positive Rate

- Reduced False Positive Rate

Approach	FDR	Method
Preliminary experiment 1	58%	MultiZ alignments; Multiperm; Low confidence results; Alignments filtered; Chr 11
Preliminary Experiment 2	72%	MultiZ alignments; Multiperm; Low confidence results; Alignments unfiltered ; Chr 11
Experiment 2 Loci realigned	26%	LocARNA realigned; Boundaries predicted; Multiperm; Low confidence results;
Genome wide alignment	71%	MultiZ alignments; Multiperm; Low confidence results; Alignments unfiltered ;
Genome wide Loci realigned	53%	LocARNA realigned; Boundaries predicted; Multiperm+flanking regions; Low c. results;
Washietl et al.	50%	ENCODE region (1% of human genome); High confidence Predictions; MultiZ alignment; filtered
Smith et al.	22%	High Confidence Results; Multiperm; EPO Alignments

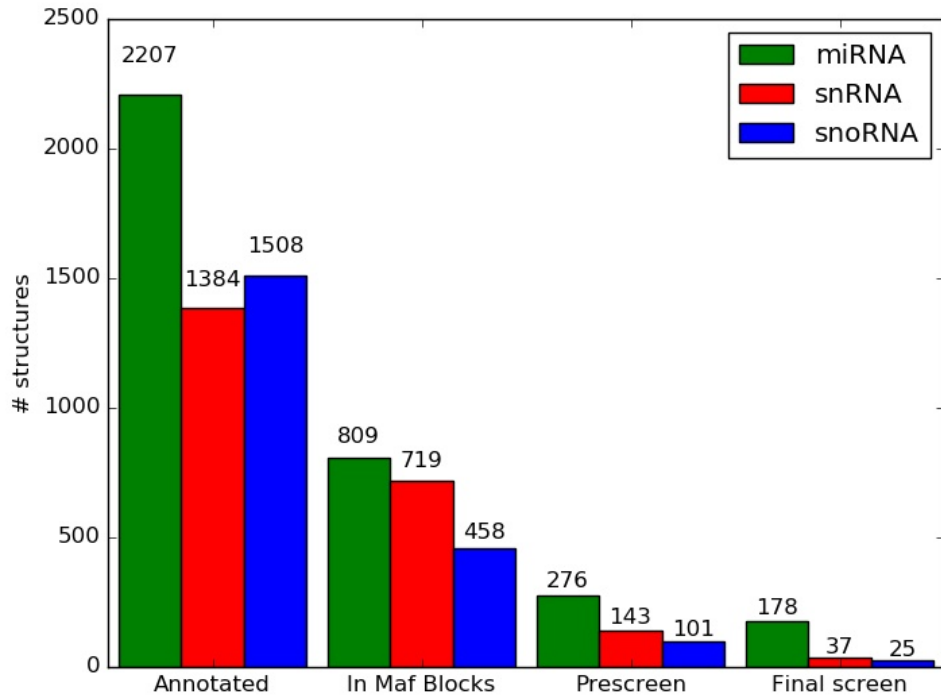
Washietl et al. *Genome Res.* **2007**. 17: 852-864

Smith et al. *Nucleic Acids Res.* **2013**. 41(17): 8220-36.

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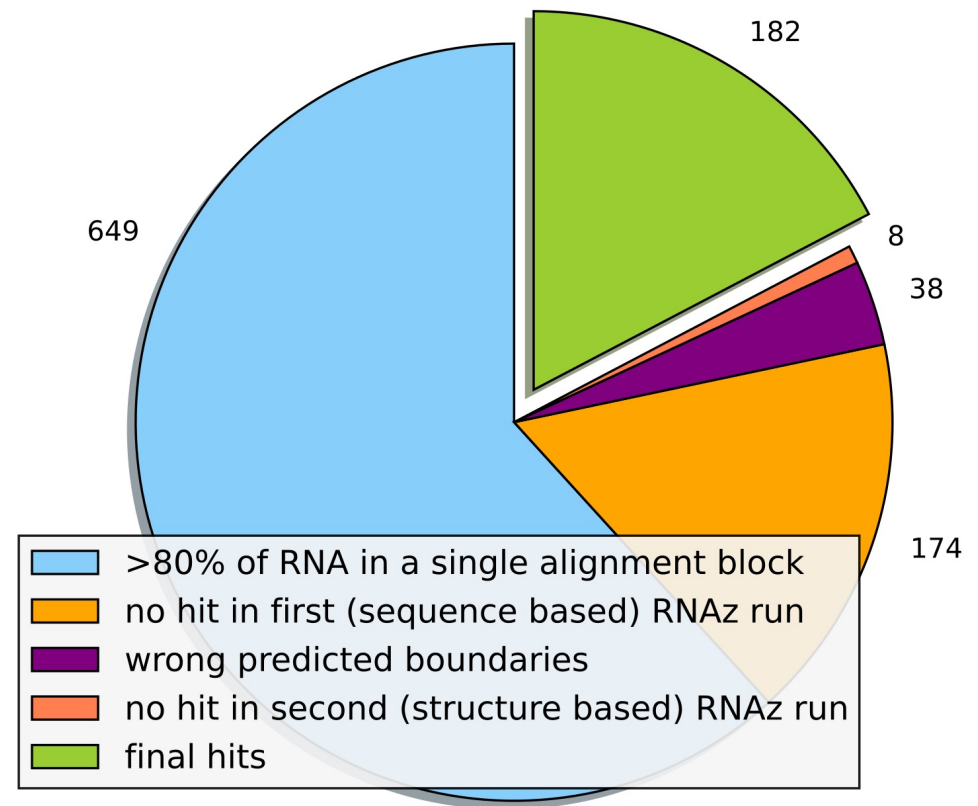
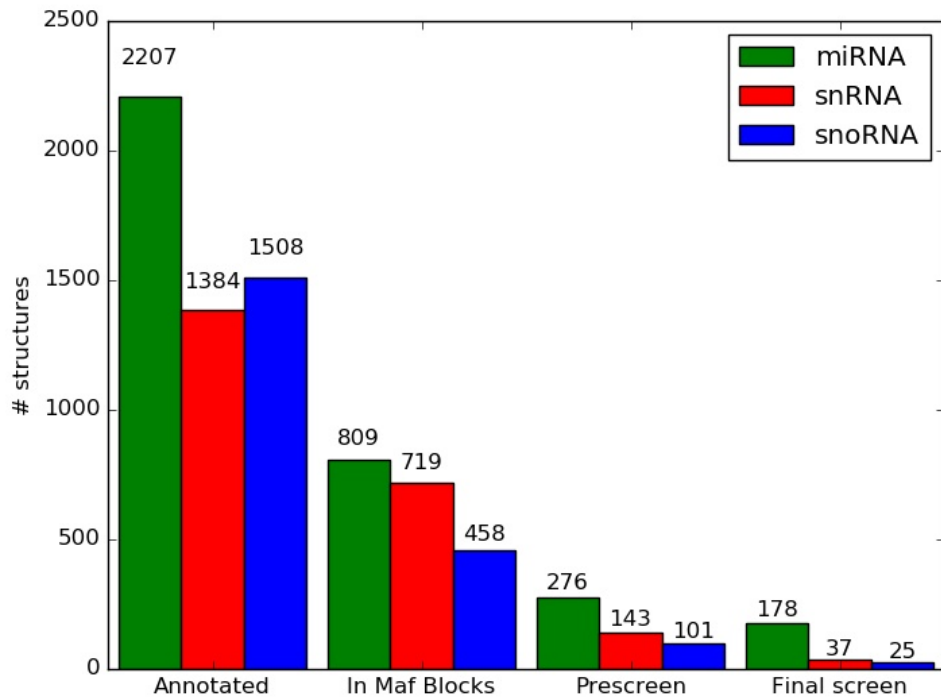
Preliminary results » Annotated RNAs



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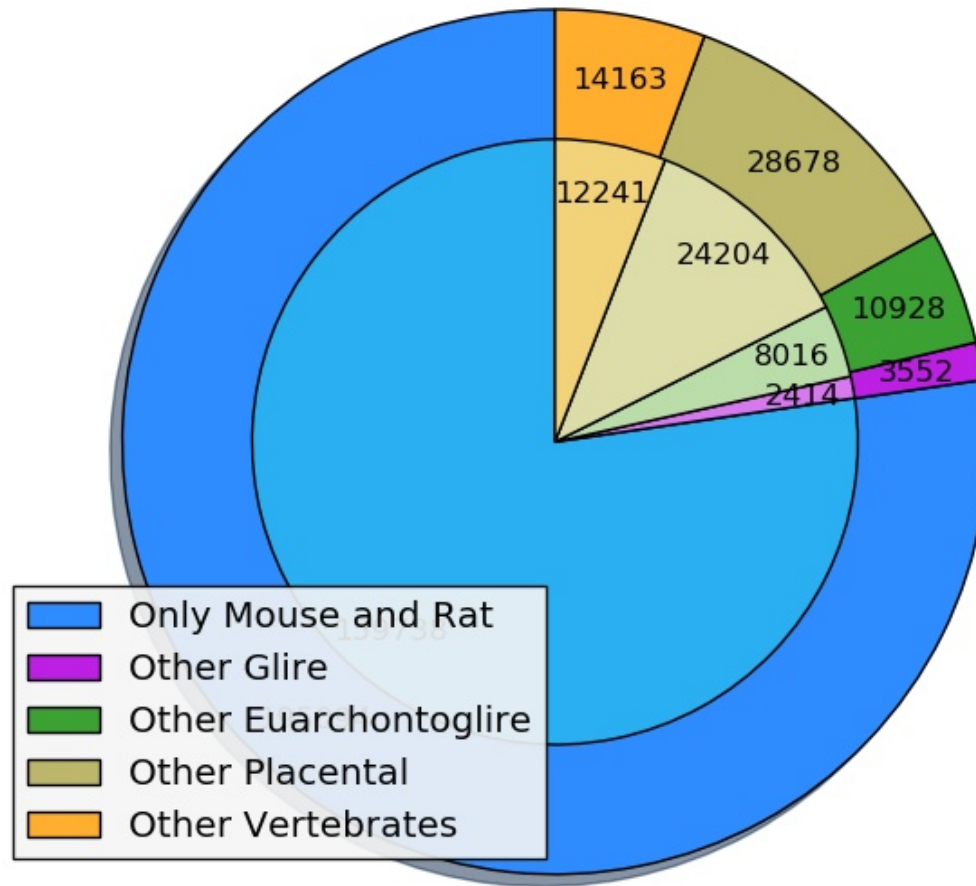
Preliminary results » Annotated RNAs



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Preliminary results » Phylogenetic information

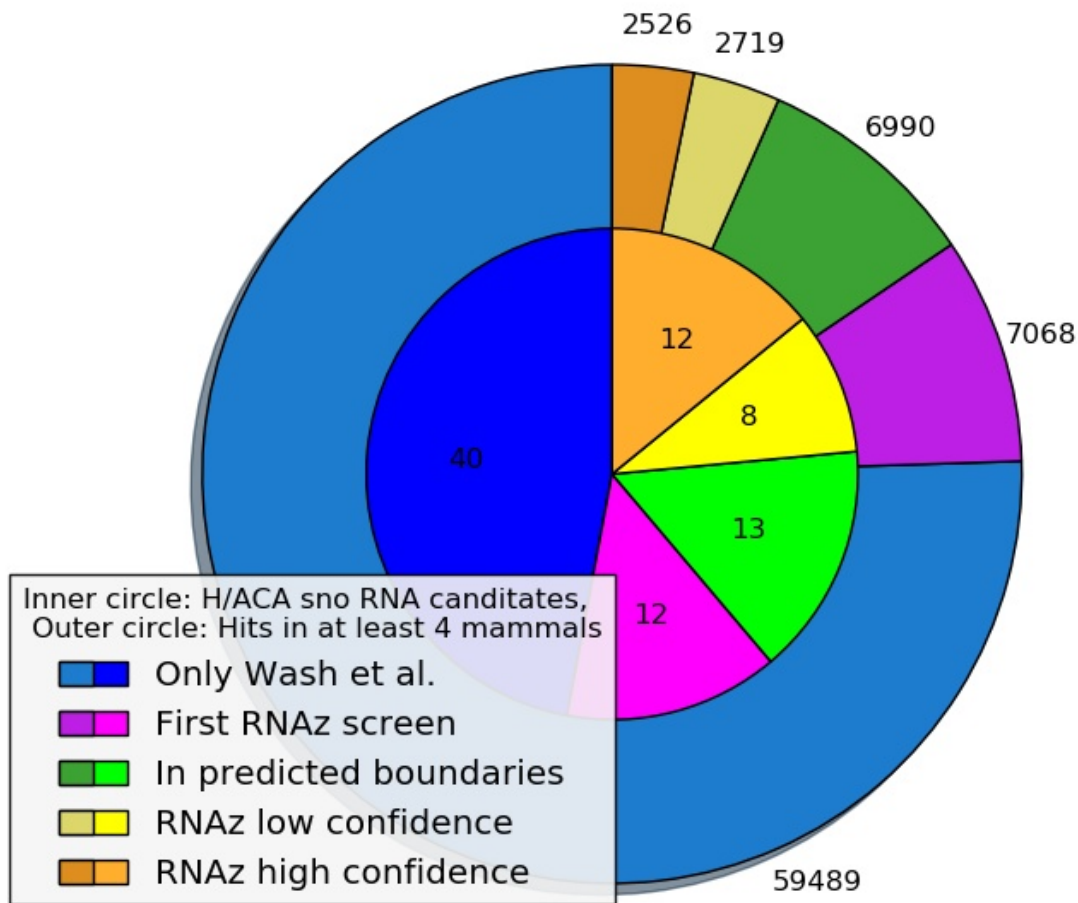


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Preliminary results »

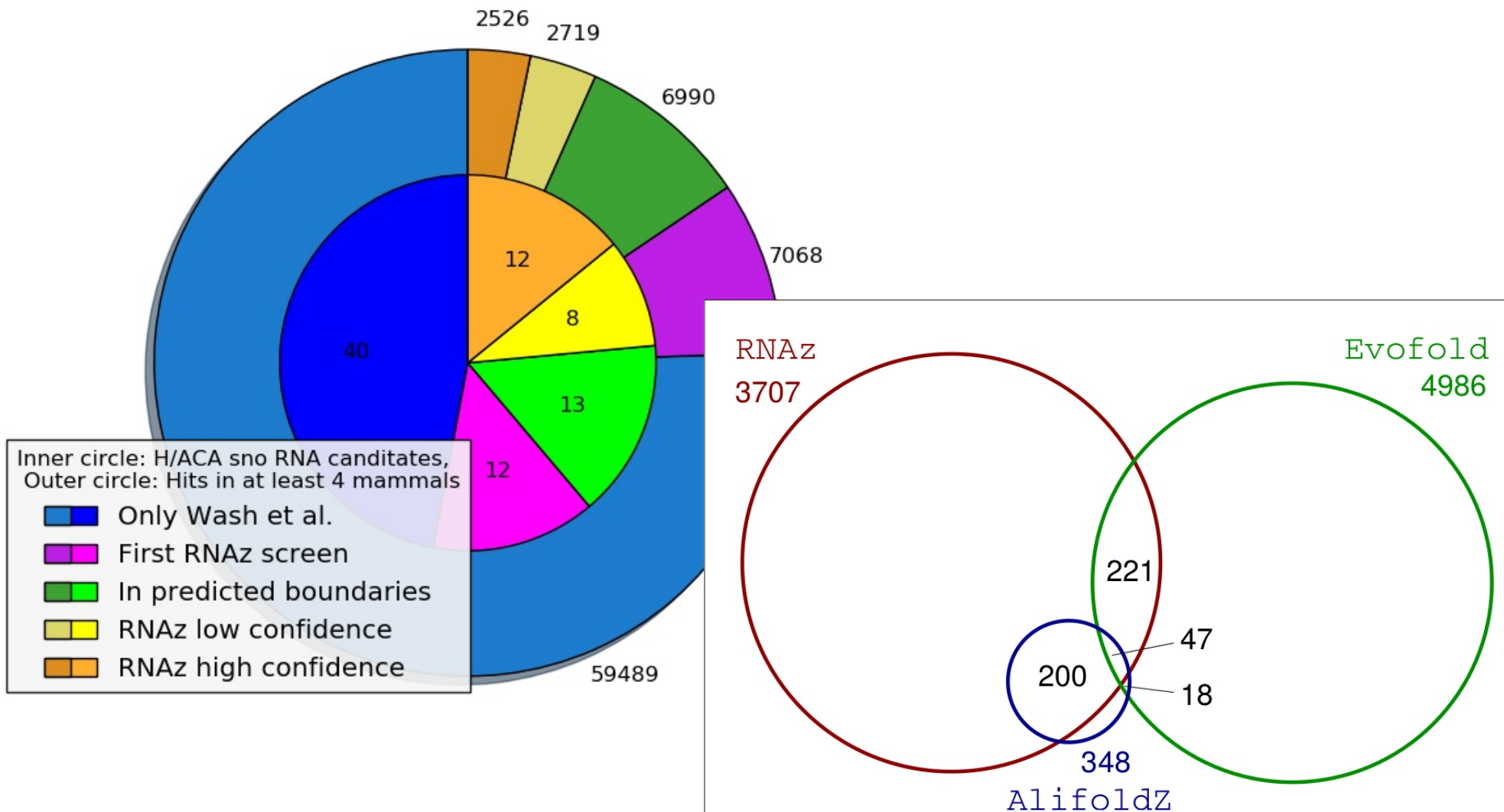
Comparing to Washietl et al.



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Preliminary results » Comparing to Washietl et al.



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