



## Identification of lncRNAs regulating variable stress-responding sheep naturally exposed to gastrointestinal nematode parasites

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# Identification of lncRNAs regulating variable stress-responding sheep naturally exposed to gastrointestinal nematode parasites



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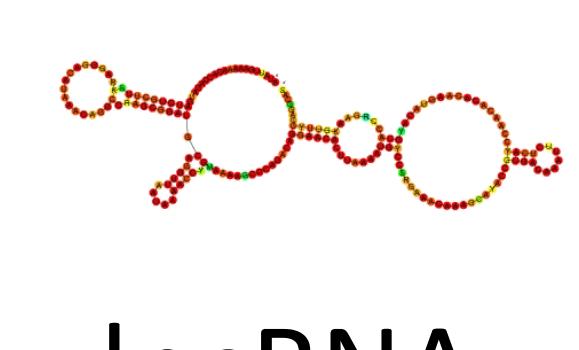
**Haemonchus contortus**  
**Teladorsagia circumcincta**  
**Trichostrongylus spp.**

Haemonchus contortus eggs  
(Retrieve from Jacob Avula)

- Gastrointestinal nematode (GIN) parasites are a common cause of morbidity and mortality in livestock, causing important agricultural losses
- Emergence of anthelmintic-resistant gastrointestinal nematode parasite strains → Research on alternative parasite control approaches

- RNA sequencing technology (RNA-Seq) has allowed the discovery of thousands of previously unannotated noncoding functional elements
- Long non-Coding RNAs (lncRNAs) → large proportion of the transcriptome (approx. 70%)

Regulatory elements  
of gene expression  
Important in immune  
response



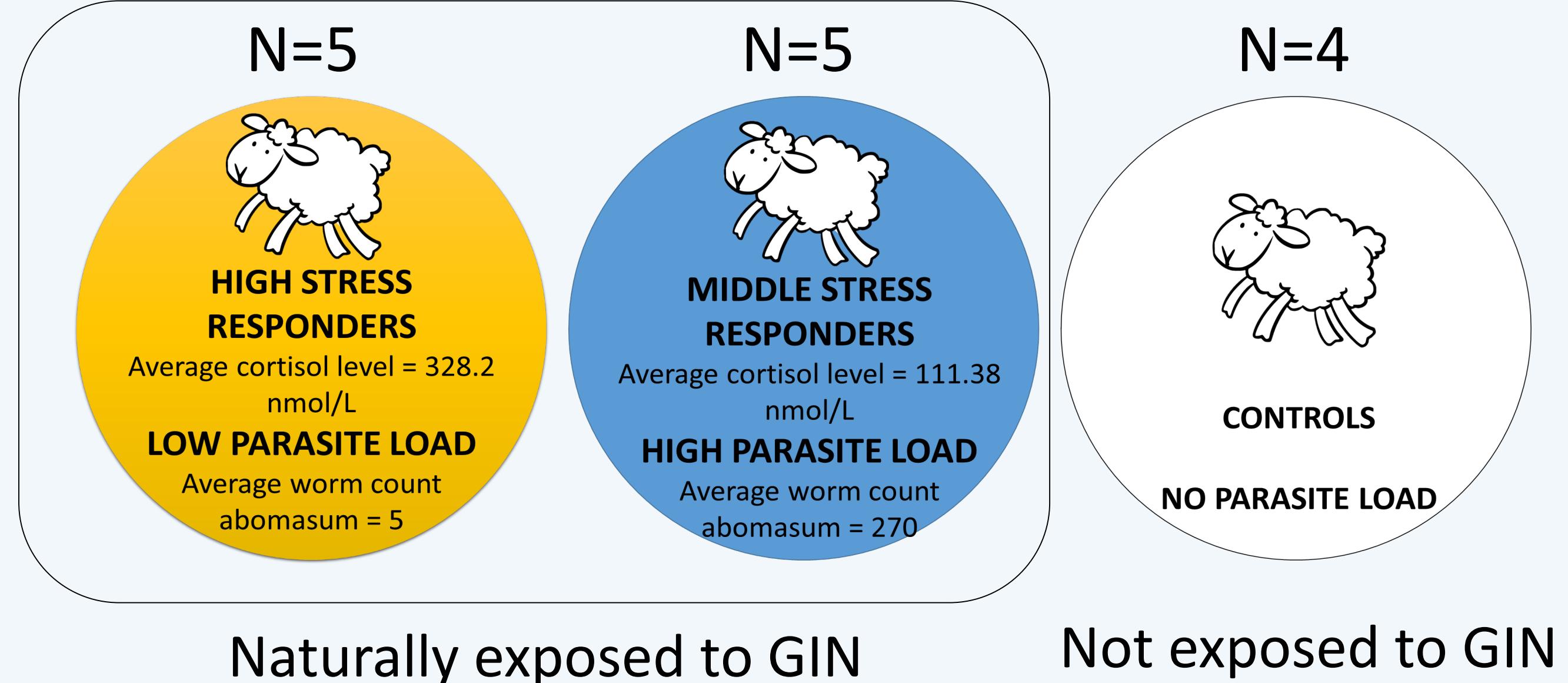
lncRNA

## OBJECTIVE

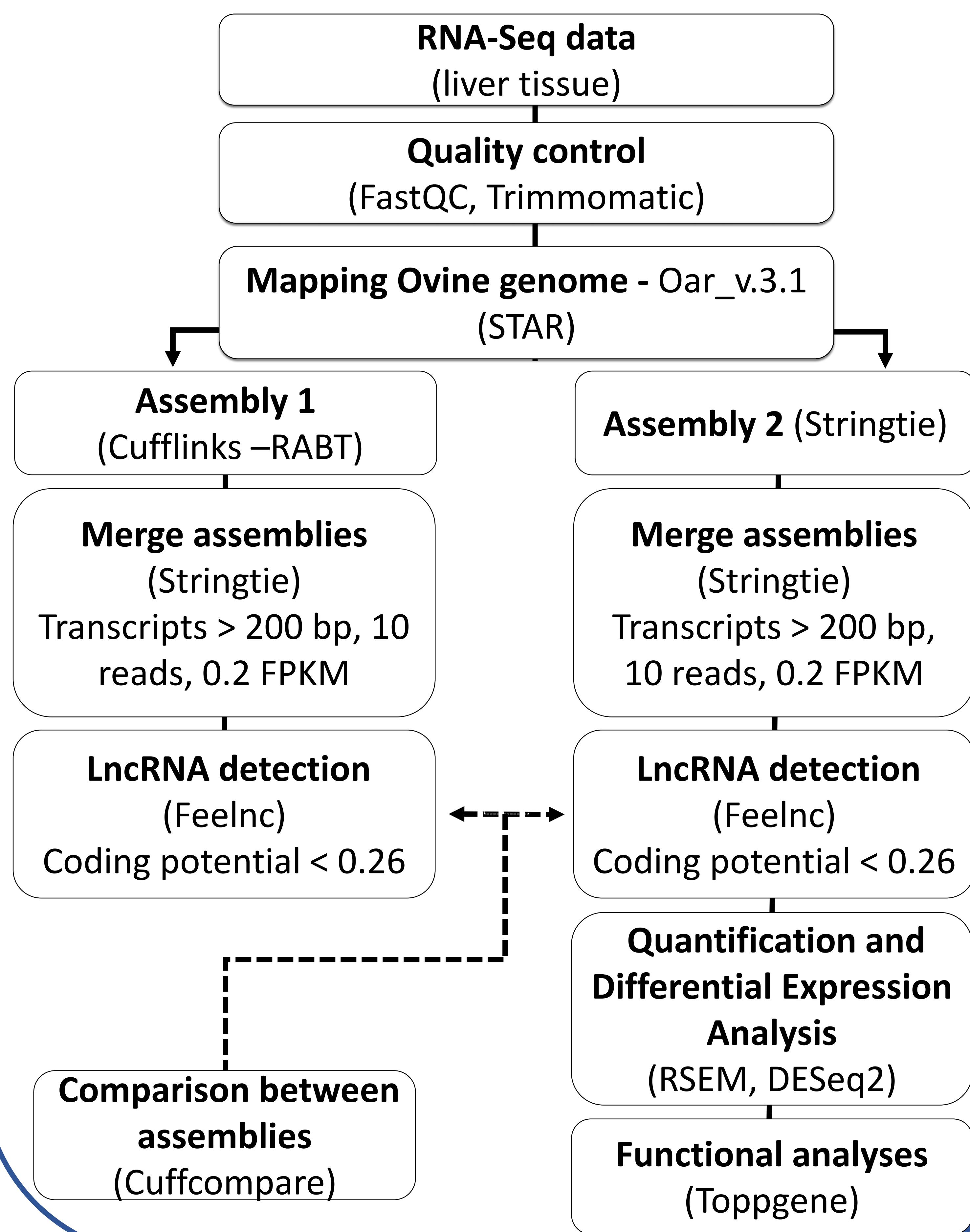
To characterize lncRNA changes in the liver transcriptome of parasitized sheep with variable stress responses

## MATERIAL AND METHODS

### Experimental design



### Long non-Coding RNA Detection Workflow



## INTRODUCTION

- Gastrointestinal nematode (GIN) parasites are a common cause of morbidity and mortality in livestock, causing important agricultural losses
- Emergence of anthelmintic-resistant gastrointestinal nematode parasite strains → Research on alternative parasite control approaches

## RESULTS

### 1. Comparison between Cufflinks and Stringtie transcriptome assemblies:

Cufflinks  
1443 lncRNAs  
1.6 transcripts/lncRNA

Comparison with annotated lncRNA (Oar\_v.3.1) :  
31 matching loci  
Sn= 1.7 Sp= 2.1

Stringtie  
875 lncRNAs  
1.3 transcripts/lncRNA

Comparison with annotated lncRNA (Oar\_v.3.1) :  
49 matching loci  
Sn= 2.6 Sp= 5.6

### 2. Genomic properties of the candidate lncRNAs compared to the ovine reference genome:

- We observed that lncRNAs have lower numbers of exons (median = 2) than mRNAs (median = 7; Fig. 1)
- The most frequently observed length of lncRNA (median = 1,149 bp) was smaller (Fig. 2) than the length of mRNAs (median = 1,431 bp)
- The distribution of candidate lncRNAs across the genome exhibited a pattern similar to the distribution of protein-coding genes (Fig. 3)

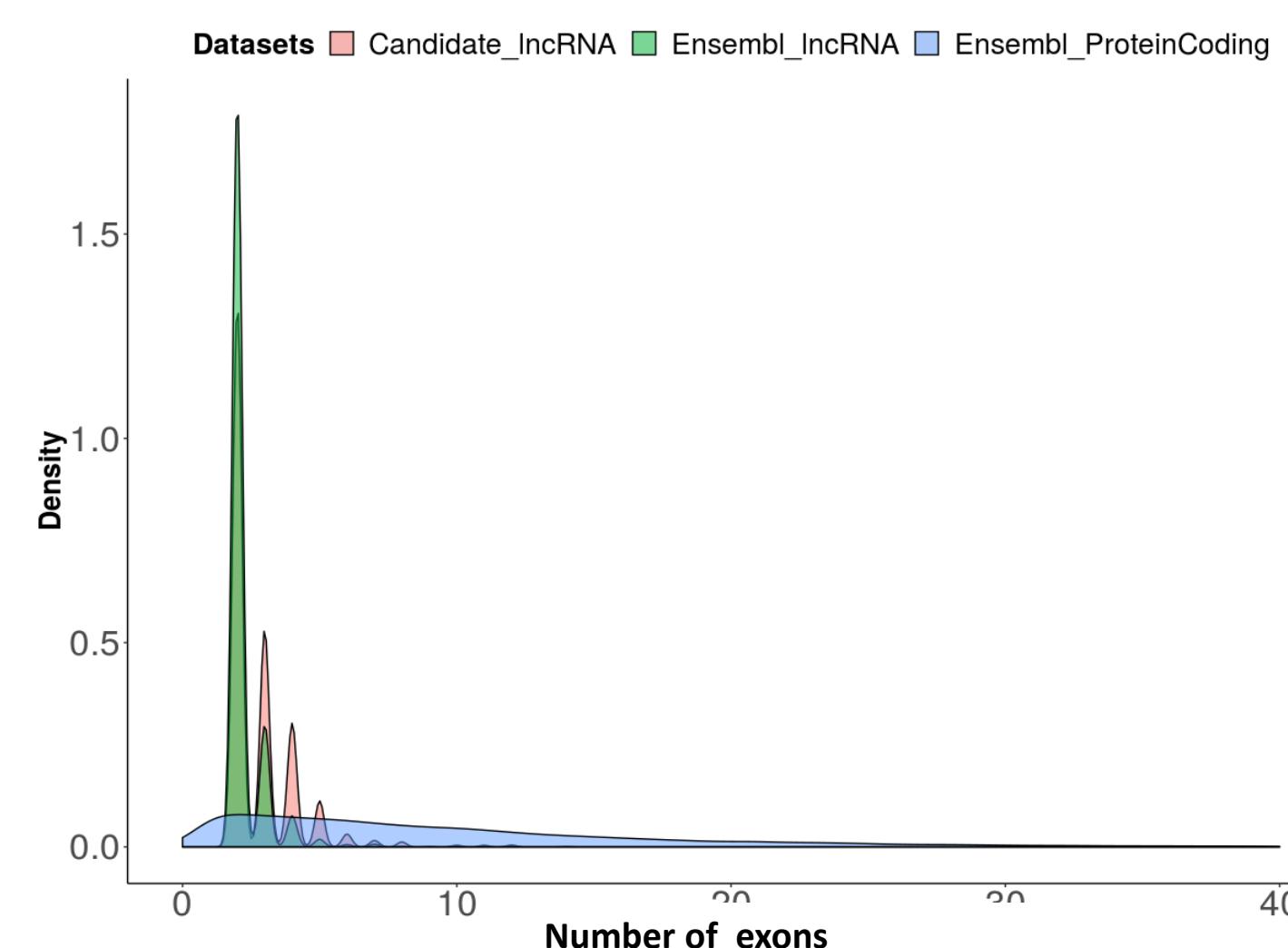


Figure 1. Density plot for the number of exons.

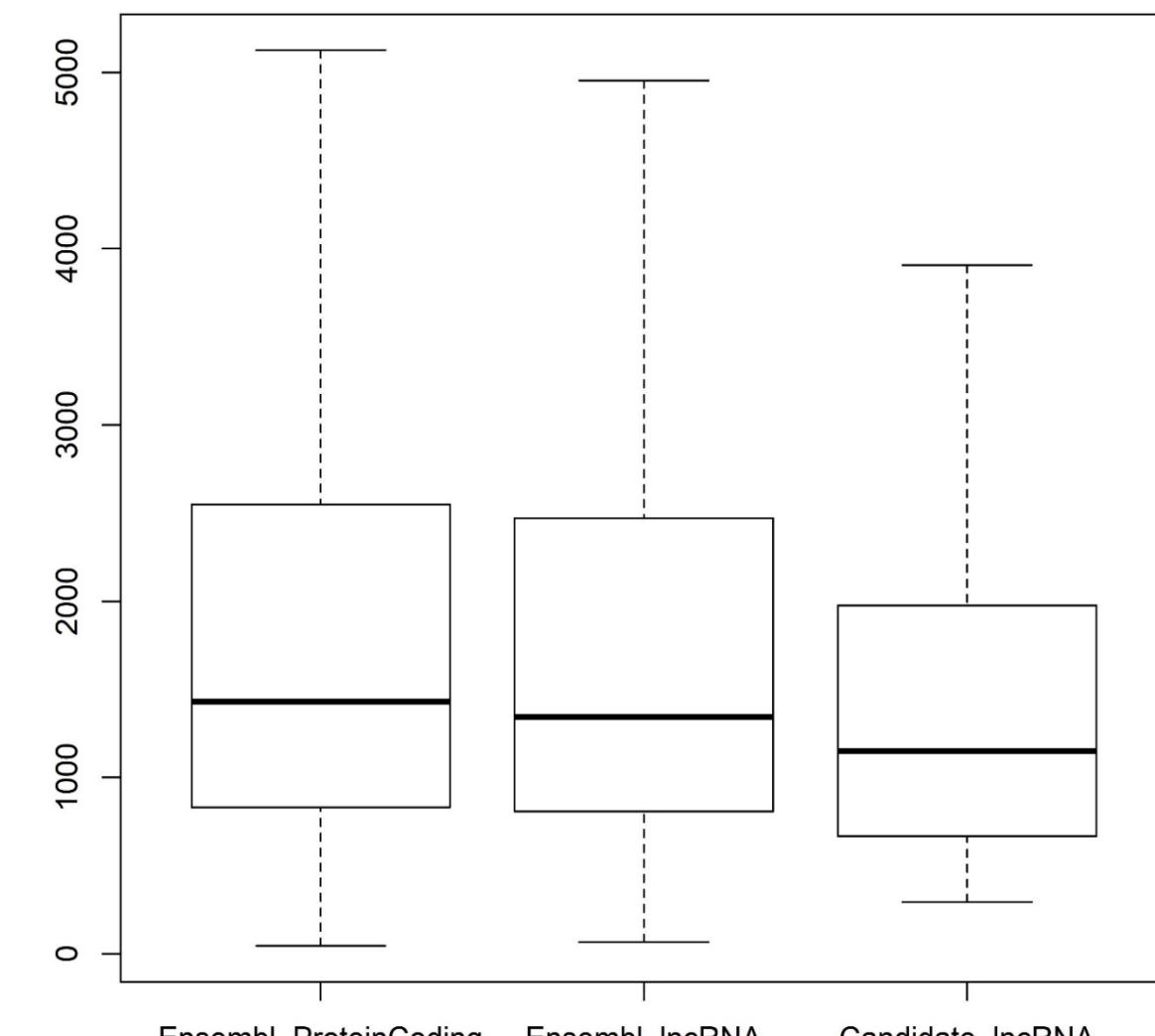


Figure 2. Box plot for the length of the transcripts.

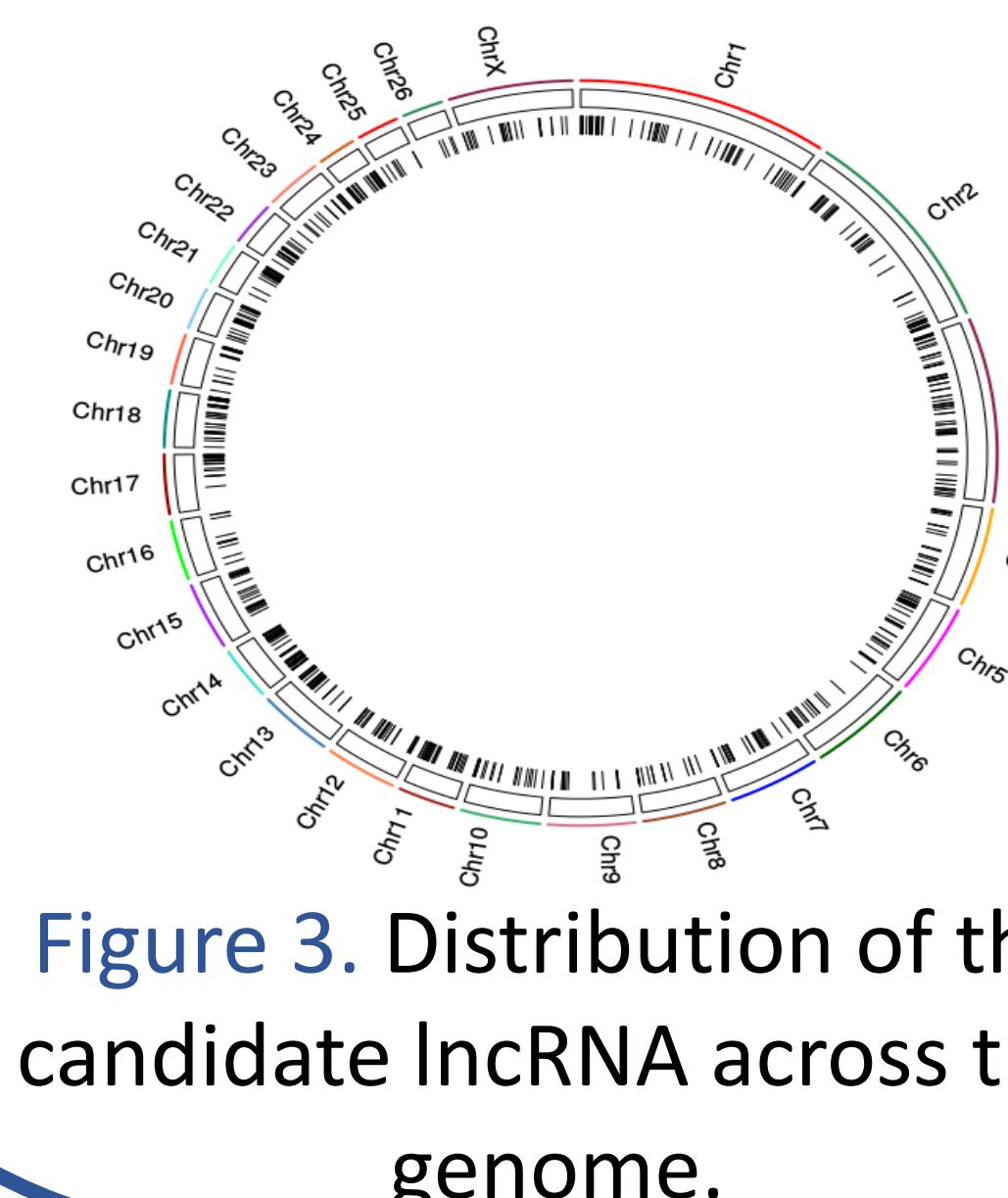
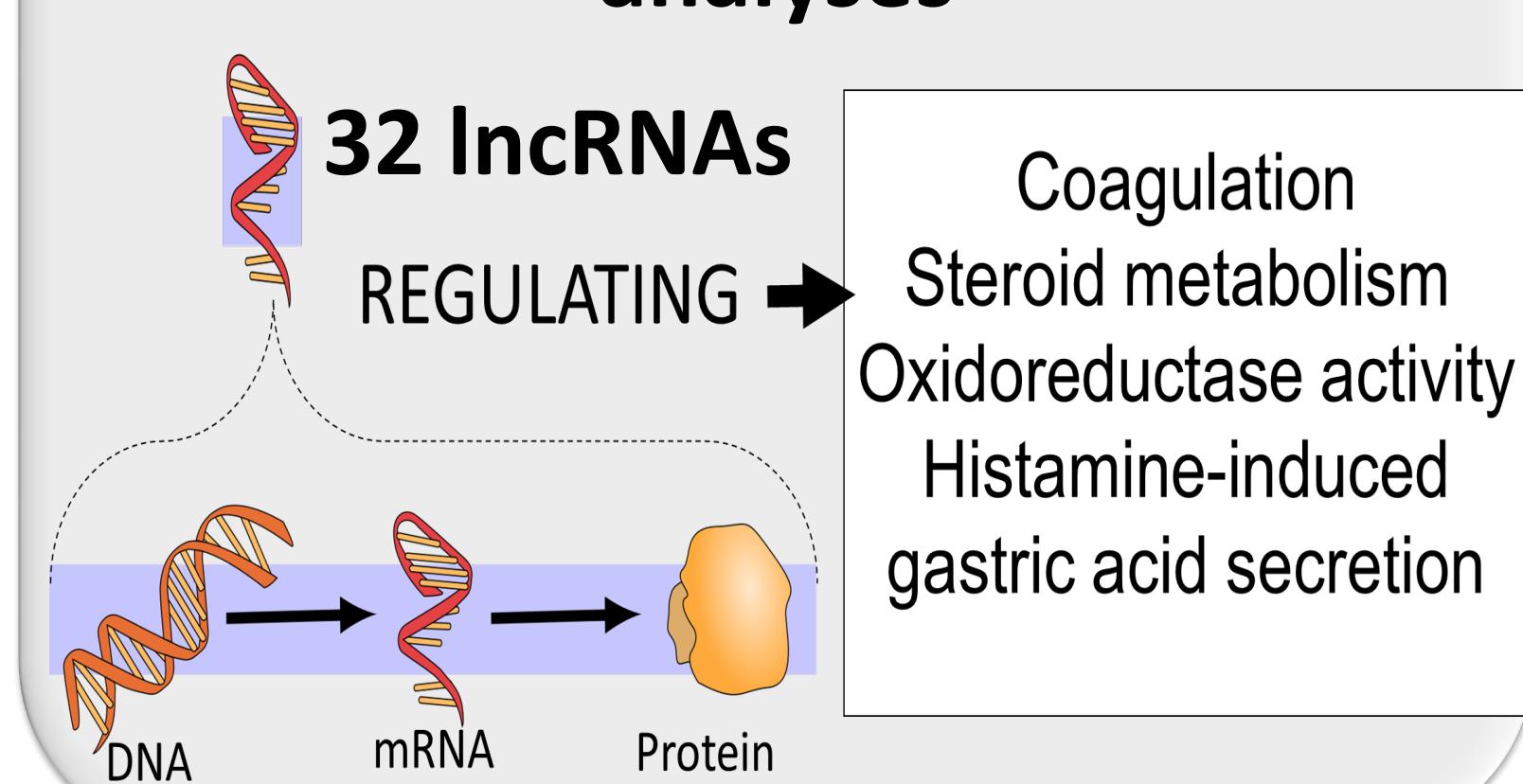


Figure 3. Distribution of the candidate lncRNA across the genome.

### 3. Differential expression analyses



## CONCLUSION

Potential candidate lncRNAs identified as differentially expressed may be associated to genes (cis-regulation) playing crucial functions in host response to parasites

The outcomes from this research could be used to better understand ovine immune response against GIN