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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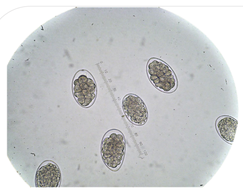
INTRODUCTION

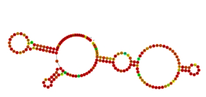


Haemonchus contortus eggs
(Retrieve from Jacob Avula)

Haemonchus contortus
Teladorsagia circumcincta
Trichostrongylus spp.

- 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



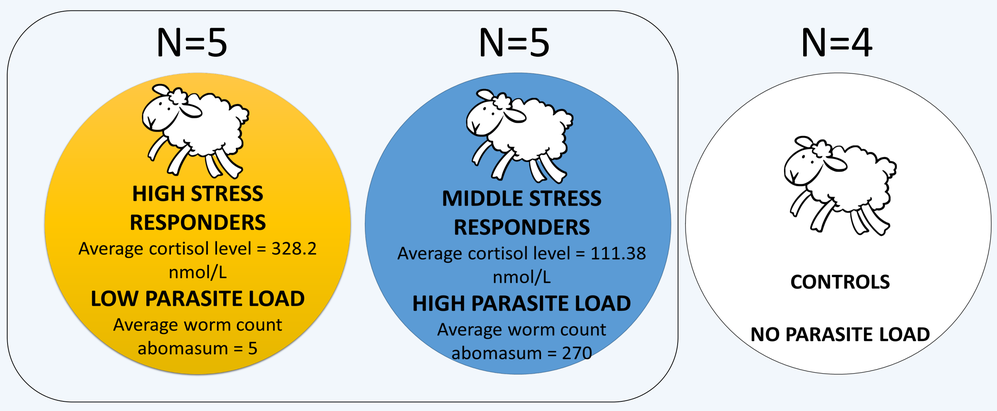
lncRNA

OBJECTIVE

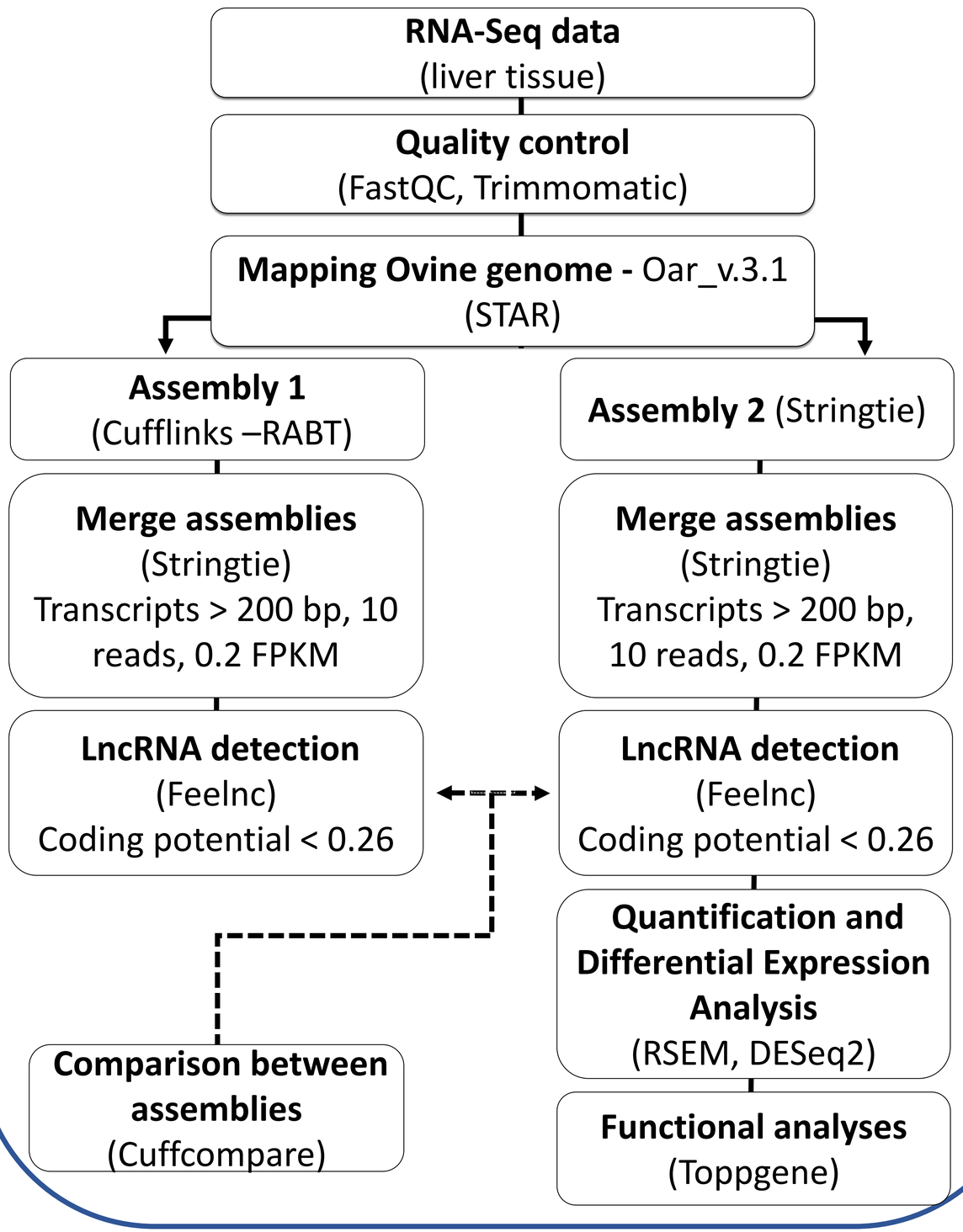
To characterize lncRNA changes in the liver transcriptome of parasitized sheep with variable stress responses

MATERIAL AND METHODS

Experimental design



Long non-Coding RNA Detection Workflow



RESULTS

1. Comparison between Cufflinks and Stringtie transcriptome assemblies:

Cufflinks	Stringtie
1443 lncRNAs	**875 lncRNAs**
1.6 transcripts/lncRNA	1.3 transcripts/lncRNA
Comparison with annotated lncRNA (Oar_v.3.1) : **31 matching loci** Sn= 1.7 Sp= 2.1	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)

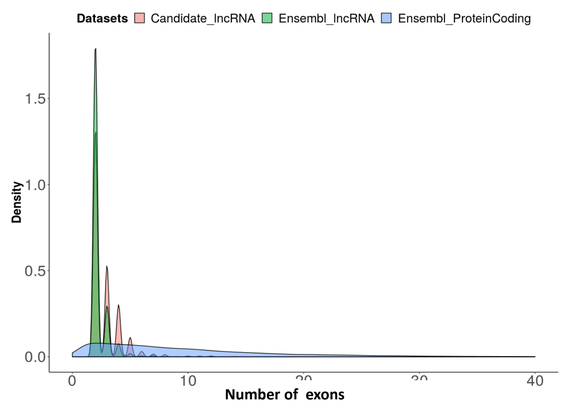


Figure1. Density plot for the number of exons.

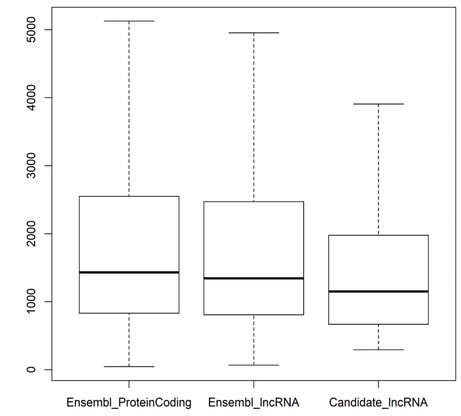


Figure 2. Box plot for the length of the transcripts.

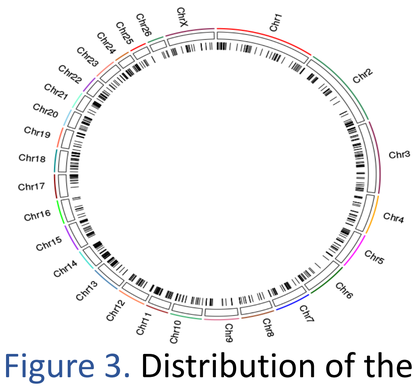
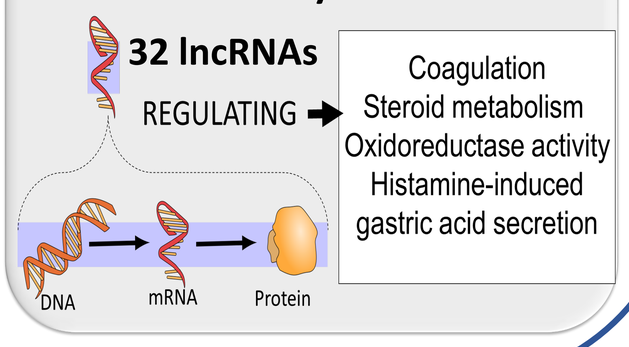


Figure 3. Distribution of the candidate lncRNA across the genome.

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