



CNV analysis of indigenous sheep reveals genes linked to disease resistance and adaptation

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Outcomes of the study

- Two gene groups were identified: Group 1 – interferons linked to disease resistance
- Group 2 - transmembrane pathways, sensory perceptions, metabolic precursors.
- TMC-1 - plays a role in deafness
- 206 CNVs identified after filtering and QC (See Table 1) of which 27% are found on the X-chromosome.

Materials and methods

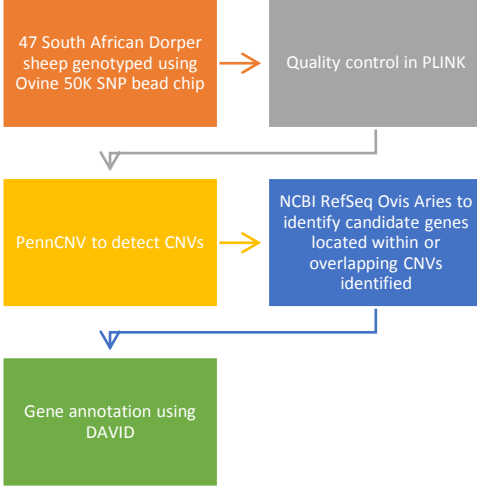


Figure 1. Heatmap of cluster 5 from the functional annotation clustering tool in DAVID for genes overlapping with identified CNVs.

Implications of the study

- CNVs effects important biological processes which influence disease resistance exhibited by indigenous sheep.
- Understanding the CNVs responsible for disease resistance can be of value to the sheep industry in Africa

Background

- Smallholder sheep farmers in Africa mainly uses low-input farming systems
- Needs sheep that are robust, adaptable and disease resistant
- Indigenous sheep may be more adaptable may be due to the presence of advantageous mutations or genetic structural variants, namely copy number variations (CNV's)

Table 1. The number of CNVs and the average length of CNVs on the various chromosomes of the sheep genome.

Copy number	Number of CNV's	Average length (kb)	Chromosomes
1	42	160,48	1, 2, 4, 6, 8-10, 12, 15-18, 22, X
2	47	2047,24	X
3	116	183,02	1-11,15-18, 20-22, X
4	1	150,35	1

*Copy number; 1=deletion of one copy, 2=copy-neutral with LOH, 3=single copy duplication, 4=double copy duplication

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