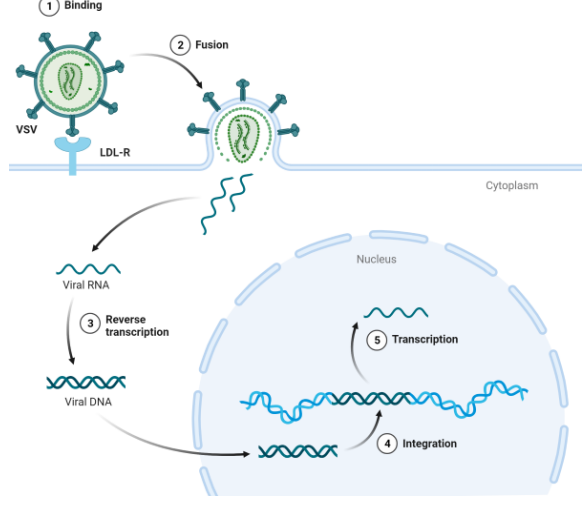


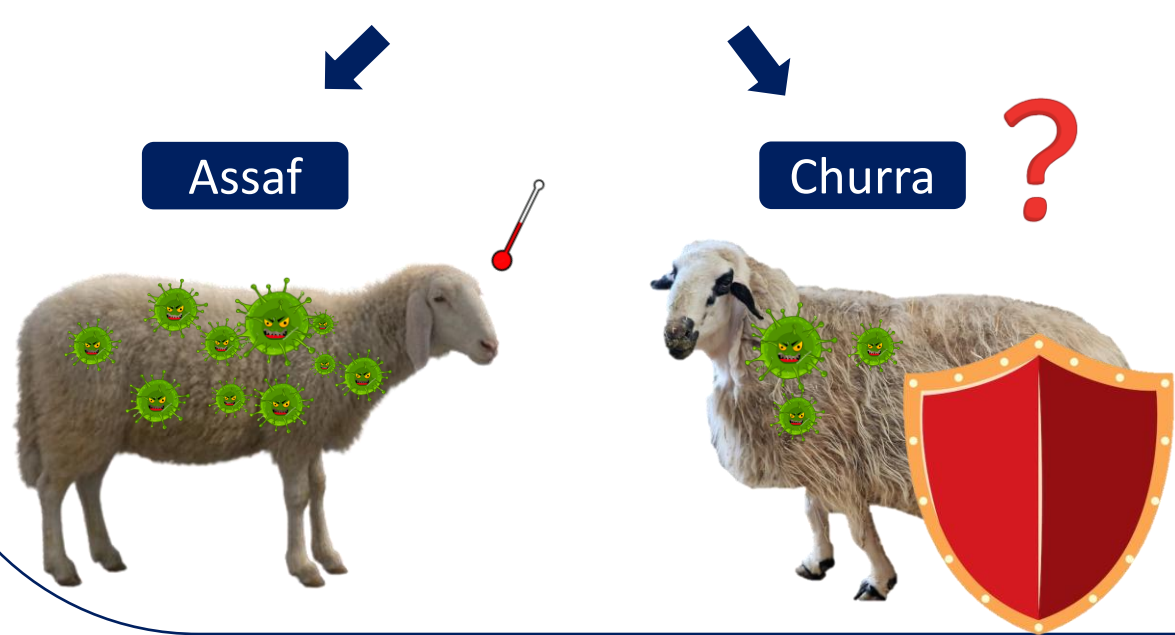
Introduction

- Small ruminant persistent lentivirus causes maedi-visna (MV) in sheep, leading to significant economic losses in the sheep dairy industry.



- TMEM154*, *CCR5*, and *TLR9* are reported as genes associated with susceptibility/resistance to MV in sheep.

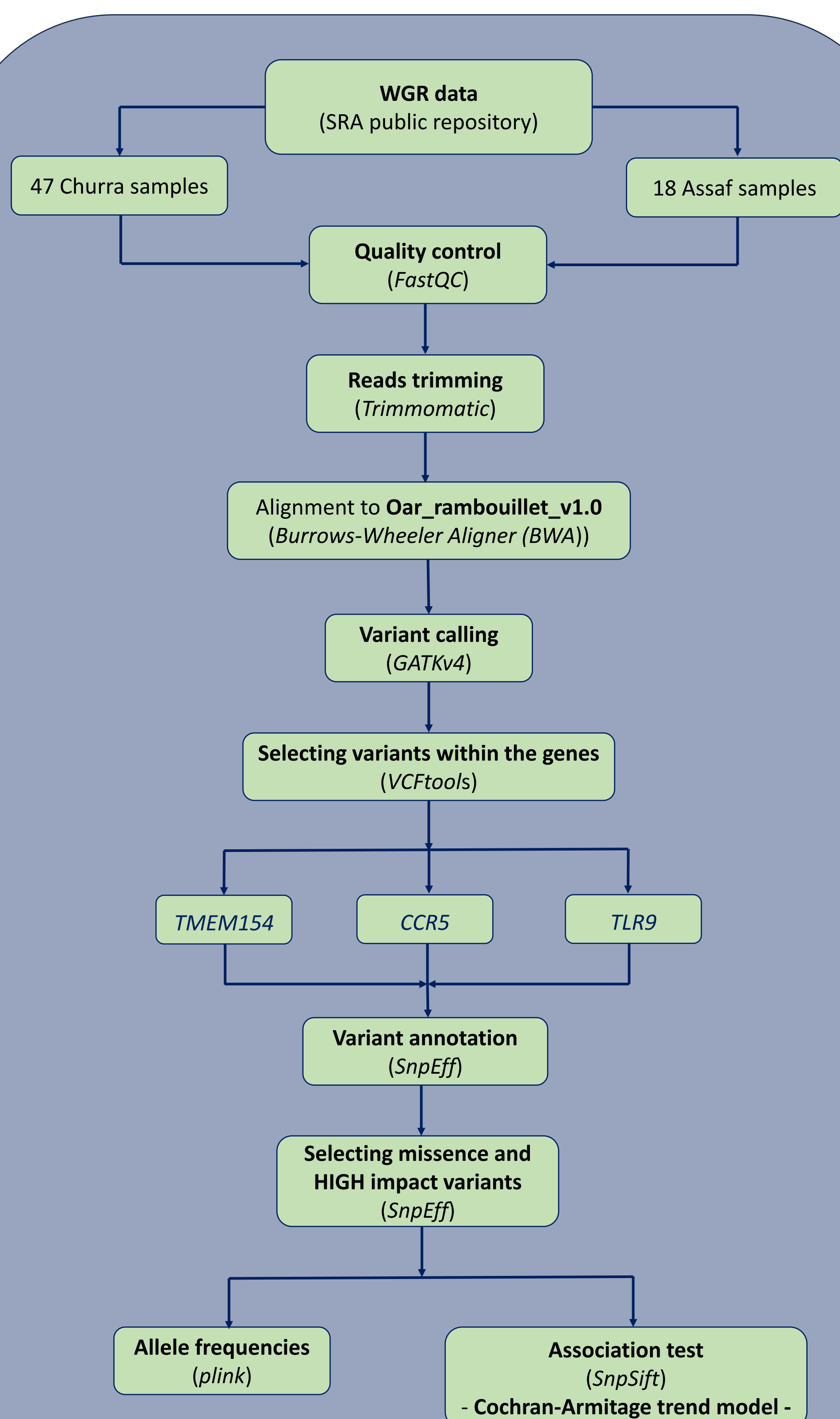
- Spain has a high MV prevalence (around 50%), with notable differences between the Churra and Assaf dairy sheep breeds.



The Aim

To evaluate the genetic diversity of three candidate genes associated with MV susceptibility in two dairy sheep breeds reared in Spain through the analysis of whole genome resequencing (WGR) datasets.

Materials and Methods



Results and Discussion

677 total variants within *TMEM154*, *CCR5*, *TLR9*

51 variants with functional consequences

58,8%

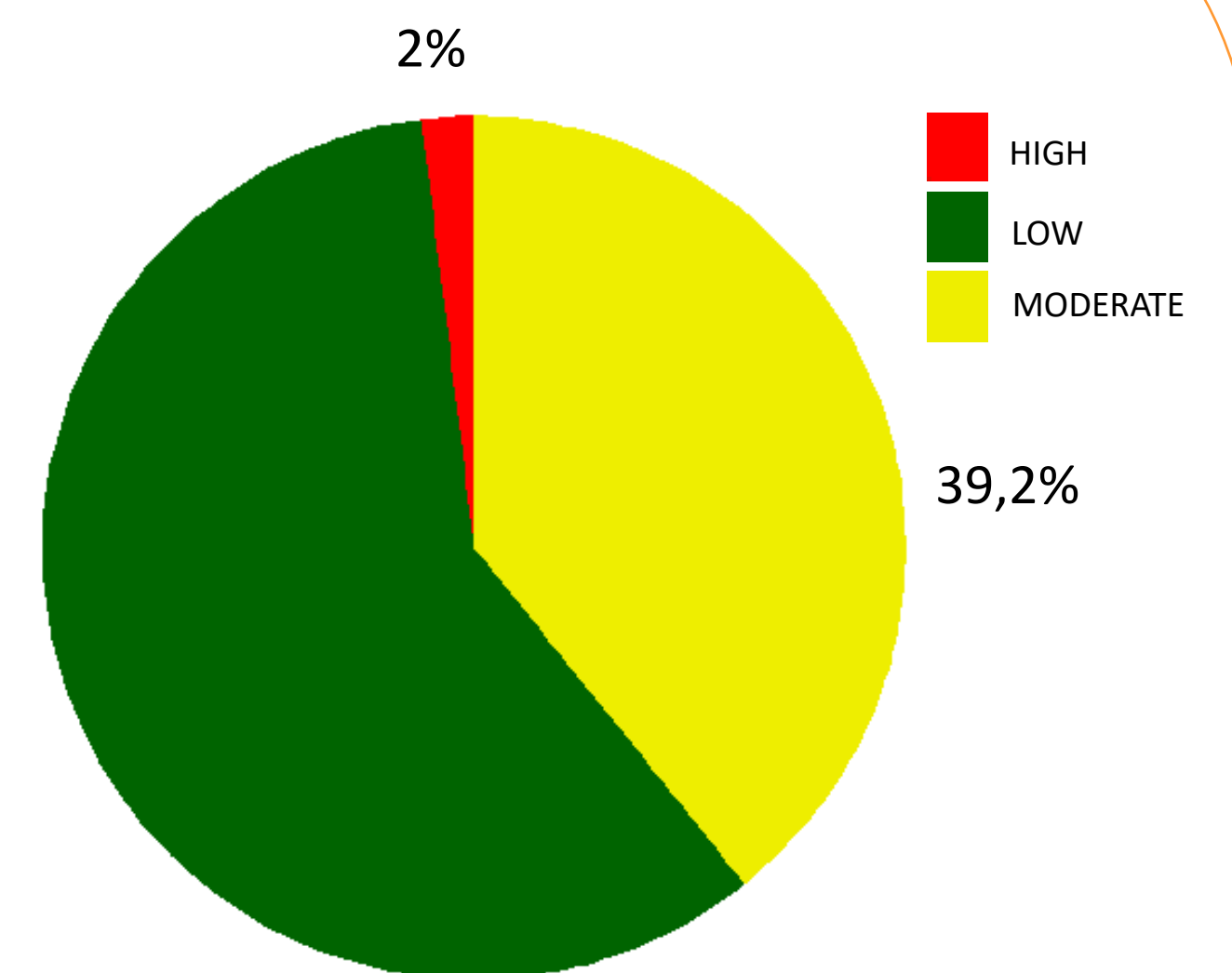
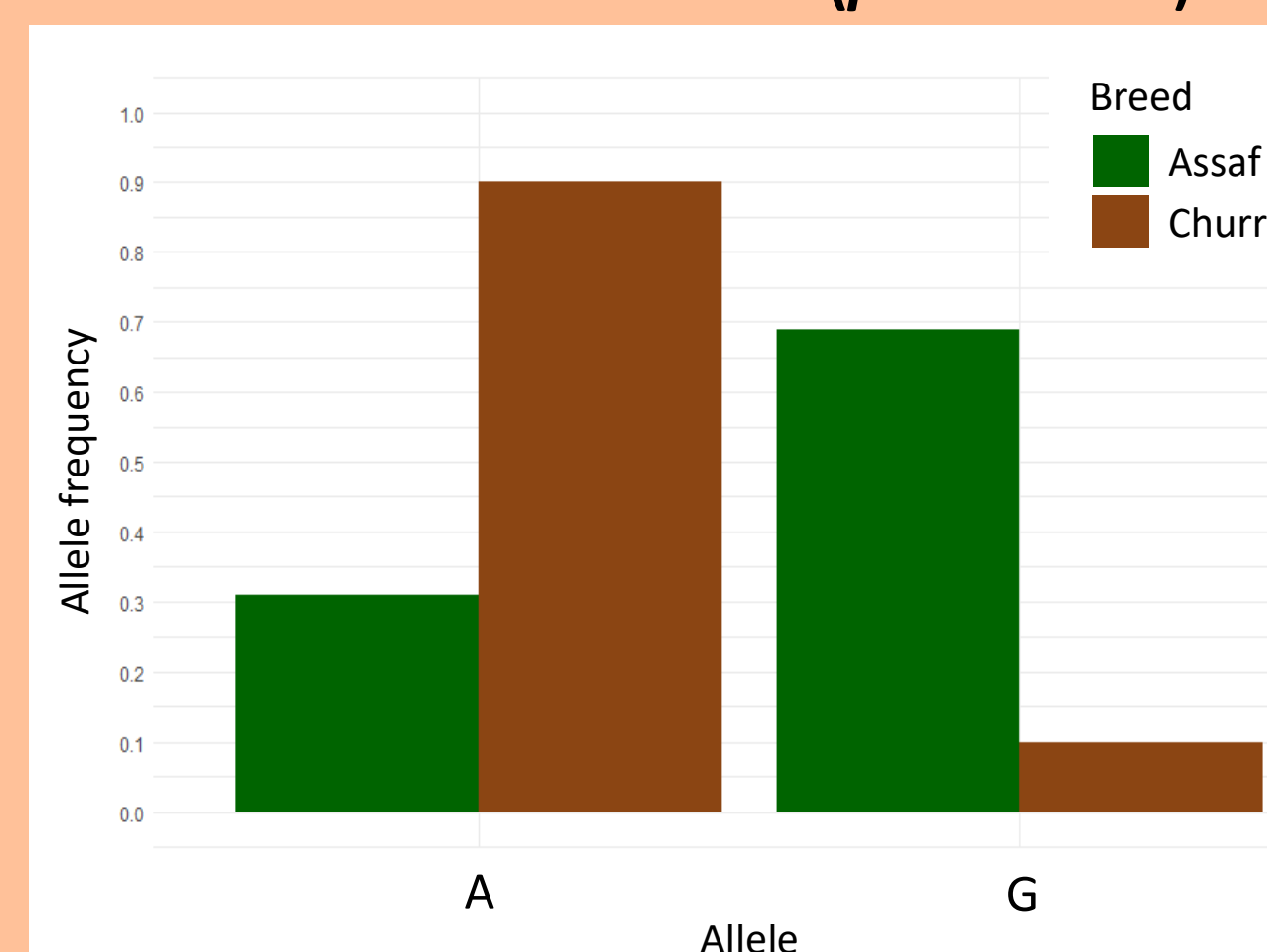


Table 1. Allele frequencies for missense and impact variants.

Genes	Position	Assaf				Churra			
		Allele1	Freq1	Allele2	Freq2	Allele1	Freq1	Allele2	Freq2
<i>TMEM154</i>	5752143	GC	0.944444	G	0.055556	GC	0.955556	G	0.044444
	5752196	C	0.944444	A	0.055556	C	1	A	0
	5776836	G	0.777778	A	0.222222	G	1	A	0
	5776842	A	0.305556	G	0.694444	A	0.904255	G	0.095745 *
	5776870	C	0.944444	T	0.055556	C	0.923913	T	0.076087
<i>CCR5</i>	5776948	A	0.833333	T	0.166667	A	1	T	0
	50634320	C	1	T	0	C	0.968085	T	0.031915
	50635610	A	0.027778	G	0.972222	A	0	G	1
	50635654	G	0.805556	T	0.194444	G	1	T	0
<i>TLR9</i>	50635828	C	0.833333	G	0.166667	C	0.914894	G	0.085106
	54977356	A	0.083333	G	0.916667	A	0.255319	G	0.744681
	54977378	C	0.083333	A	0.916667	C	0.244681	A	0.755319
	54977582	A	0.083333	T	0.916667	A	0.265957	T	0.734043

* *TMEM154_rs408593969* ($p=2.62E-06$)



The *rs408593969* mutation causes an amino acid substitution (K/E) at position 35 of the *TMEM154* protein which has been associated with the serological MV status in sheep populations (Riggio et al., 2023; Souza Rodrigues et al., 2022).

Conclusion

- ✓ The *TMEM154* KK proteotype, found in a higher frequency in Churra, has been related to a lower MV susceptibility and may be associated with the lower prevalence of MV in this breed.
- ✓ These preliminary findings highlight the potential importance of *rs408593969* and the need to further investigate its role in MV susceptibility mechanisms in the breeds analyzed.

Acknowledgement

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