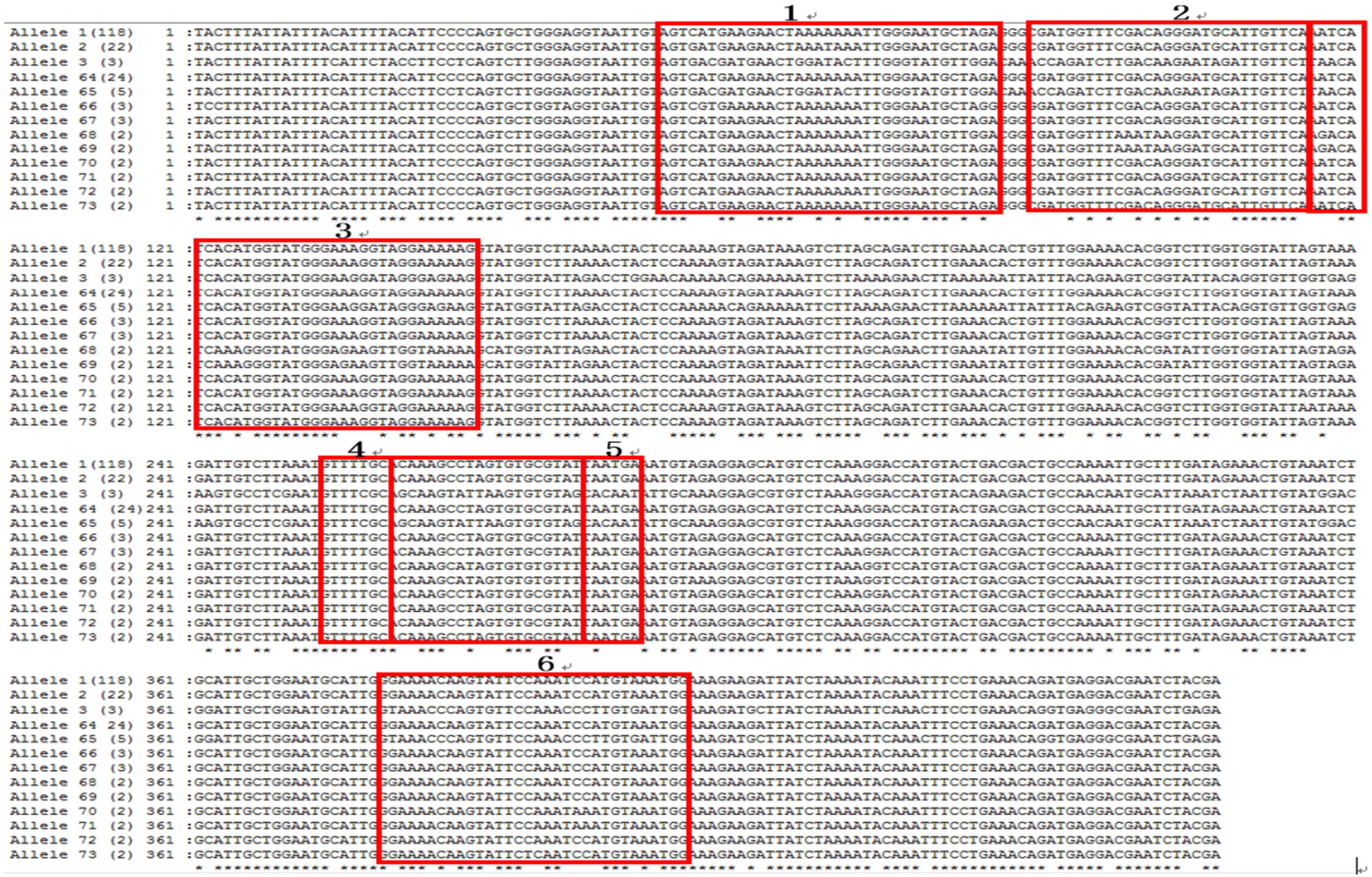
Supplementary Figure 1: Multiple sequence alignment of Tp1 alleles obtained in this study from cattle from Malawi. The naming of the alleles follows the nomenclature by [27]. Alleles 1 and 5 were first described by [27]. The epitope coding region are boxed in red. The number in parenthesis is the number of sequences obtained in the allele.



Supplementary Figure 2: Multiple sequence alignment of Tp2 alleles obtained in this study from cattle from Malawi. The naming of the alleles follows the nomenclature by [27]. Alleles 1 and 2 and 3 were first described by [27]. The epitope coding region are boxed in red. The number in parenthesis is the number of sequences obtained in the allele.

Supplementary Table 1: Tp1 Analysis of molecular variation (AMOVA)

Source of variation	d.f	Sum of squares	Variance components		Percentage of variation
Among groups	1	49.554	4.13637	Va	43.03
Among populations within groups	2	93.706	0.62209	Vb	6.47
Within populations	224	1087.612	4.85541	Vc	50.50
Totals	227	1230.873	9.61387		
Fixed indices					
FSC: 0.11357					
FST: 0.49496					
FCT: 0.43025					

Supplementary Table 2: Tp2Analysis of molecular variation (AMOVA)

Source of variation	d.f	Sum of squares	Variance components		Percentage of variation
Among groups	1	39.384	1.90318	Va	20.06
Among populations within groups	2	40.925	0.26387	Vb	2.78
Within populations	183	1339.381	7.31902	Vc	77.16
Totals	186	1419.690	9.48607		
Fixed indices					
FSC: 0.03480					
FST: 0.22845					
FCT: 0.20063					