Table S1. Details of mutations identified on Tp1 antigenic epitope.

Sample group	11-mer $Tp1_{214-224}$ (VGYPKVKEEML) epitope mutation details								
	Coverage	**Alt#**	**Alt# (F;R)**	**Reference**	**Mutation call**	**Reference nucleotide position**	**Overall mutation score**	**Epitope variants**	**Function**
Nakuru cattle	73,728	71367	39841;31526	TP03_0849	delGCinsTA	807_808	35.30	VGYPKVKEE**II**	Missense
Mbarara cattle	73,226	31938	18046;13892		delGCinsTA	807_808	35.10	VGYPKVKEE**II**	Missense
Karamoja cattle	17,972	-	-		None	-	-	VGYPKVKEEML	-
Tanga cattle	21,550	20821	11061;9760		delGCinsTA	807_808	39.50	VGYPKVKEE**II**	Missense
Simanjiro cattle	73,820	-	-		None	-	-	VGYPKVKEEML	-
CD clinical cases	44,813	12424	6347;6077		delGCinsTA	807_808	30.10	VGYPKVKEE**II**	Missense
Non-clinical *T. parva*-positive cases	13,052	-	-		None	-	-	VGYPKVKEEML	-

Coverage - the total number of reads that aligned at the variant location.

Alt # - the total number of reads that contained the alternate (variant) nucleotide at the variant position.

Alt # (F; R) - the number of reads that showed the alternate (variant) nucleotide in the forward (F) direction and the number of reads that showed the alternate (variant) nucleotide in the reverse (R) direction.

Overall mutation score - an empirical estimation of the likelihood that a given variant/mutation call is real and not an artifact of sequencing or alignment errors. A score ≥12.00 (95% confidence) is considered statistically significant.

delGCinsTA - deletion of GC and insertion of TA at the indicated reference nucleotide position(s).

C>AC - at the indicated reference nucleotide position, the reference sequence has a "C" whereas the alternate/variant sequence has either an "A" or "C".

NB: Bolded and underlined shows the variant amino acid residue.