

**Table S3.** Details of mutations identified on Tp3 antigenic region.

Sample group	Tp3 gene mutation details								
	Coverage	Alt#	Alt# (F;R)	Reference	Mutation call	Reference Nucleotide position	Overall mutation score	Amino acid change	Function
Nakuru cattle	30020	-	-	TP01_0868	-	-	-	-	-
Mbarara cattle	43604	-	-		-	-	-	-	-
Karamoja cattle	73632	16050	8809;7241		C>CT	406	35.80	p.P136PS	Missense
Non-clinical <i>T. parva</i> -positive cases	84113	43563	20645;22918		A>AG	435	33.00	p.T145TT	Synonymous
	84980	44231	21138;23093		G>AG	438	33.10	p.P146PP	Synonymous
	87673	45412	22510;22902		T>GT	450	33.60	p.V150VV	Synonymous
	90533	89766	43153;46613		C>T	465	38.10	p.T155T	Synonymous
	78134	76886	42398;34488		C>T	507	38.40	p.P169P	Synonymous
CD clinical cases	32169	12397	9984;2413		C>AC	600	33.00	p.T200TT	Synonymous
	70760	70498	34476;36022		T>C	404	38.00	p.M135T	Missense
	78344	77903	39793;38110		G>A	438	37.60	p.P146P	Synonymous
	72587	71190	41225;29965		C>T	507	38.10	p.P169P	Synonymous

p.M135TM - “p” refers to protein sequence. At the indicated reference amino acid position (135), the reference sequence has an amino acid residue “M” where are the alternate/variant sequence has a “T” or “M”. The resulting non-synonymous substitution (with amino acid residue “T”) is due to the corresponding nucleotide substitution (T>CT) at the indicated reference nucleotide position.

p.T155TT - the nucleotide substitution (C>CT) at the indicated reference nucleotide position results in synonymous amino acid residue substitution with a “T” due to degeneracy.

p.V172L - at the indicated reference amino acid position, the reference sequence has an amino acid residue “V” whereas the alternate/variant sequence has a “L”.

**NB:** Additional detail on interpretation is provided in Table S1 footnotes.