Table S2. Details of mutations identified Tp2 antigenic epitopes.

Source of samples	**Tp2 epitopes** (^{27}SHEELKKLGML^{37}, ^{40}DGFDRDALF^{48}, ^{49}KSSHGMGKVGK^{59}, ^{50}SSHGMGKVGK^{59}, ^{96}FAQSLVCVL^{104}, ^{98}QSLVCVLMK^{106}, ^{138}KTSIPNPCKW^{147}) **mutation details**								
	Coverage	**Alt#**	**Alt# (F;R)**	**Reference**	**Mutation call**	**Reference nucleotide position**	**Overall mutation score**	**Epitope variants**	**Function**
Nakuru cattle	31195	30693	11433;19260	TP01_0056	C>G	210	34.60	S**D**EELKKLGML	Missense
	28425	27154	5066;22088		A>AT	224	34.90	SHEEL**N**KLGML	Missense
Mbarara cattle	1671	1662	1383;279		A>C	543	20.90	K**P**SIPNPCKW	Missense
	1840	1832	1501;331		A>G	549	26.40	KTS**V**PNPCKW	Missense
	2061	2025	1609;416		A>T	560	21.10	KTSIPN**P**CKW	Synonymous
	2153	2143	1706;437		A>G	564	20.60	KTSIPN**P**C**E**W	Missense
Karamoja cattle	817	740	3;737		A>AG	302	18.80	KSSHGMGKV**G**K SSHGMGKV**G**K	Synonymous
	3223	3061	2323;738		A>C	543	16.80	K**P**SIPNPCKW	Missense
	3616	3593	2625;968		A>G	549	25.40	KTS**V**PNPCKW	Missense
	4195	4131	2785;1346		A>T	560	23.20	KTSIPN**P**CKW	Synonymous
	4396	4381	2961;1420		A>G	564	23.30	KTSIPN**P**C**E**W	Missense
Simanjiro cattle	66074	13469	3027;10442		A>AG	214	28.30	SH**G**ELKKLGML	Missense
Tanga cattle	94312	92999	23797;69202		C>G	210	37.20	S**D**EELKKLGML	Missense
	94958	90300	12573;77727		A>AT	224	39.00	SHEEL**N**KLGML	Missense
Non-clinical *T. parva*-positive cases	-	-	-		-	-	-	-	-
CD clinical cases	7629	7397	2455;4942		C>CG	210	23.00	S**D**EELKKLGML	Missense
	7256	6941	1801;5140		A>AT	215	22.50	SH**D**ELKKLGML	Missense
	8362	1216	272;944		A>AC	223	22.60	SHEEL**T**KLGML	Missense
	11160	861	220;641		T>AT	276	21.80	K**T**SHGMGKVGK **T**SHGMGKVGK	Missense
	10843	507	140;367		G>CG	286	23.80	KSSH**A**MGKVGK SSH**A**MGKVGK	Missense
	10838	10107	3920;6187		T>AT	287	28.30	KSSH**G**MGKVGK SSH**G**MGKVGK	Synonymous
	6021	5865	2814;3051		C>G	420	17.00	**E**SLVCVLMK	Missense

NB: Detail on interpretation is provided in Table S1 footnotes.