Table S3: Predicted processing efficiency and binding affinity to H2-K^b of polymorphic TB10.4$_{4\text{-}11}$ epitopes. Bold letters indicate polymorphic substitution

Variants	15mer	epitope	Proteasome score	TAP score	MHC score	Processing score	Total score	MHC ic50
WT	IMYNYPAMLGHAGDM	IMYNYPAM	0.94	0.23	-0.87	1.17	0.30	7.4
P9S	IMYNY**S**AMLGHAGDM	IMYNY**S**AM	0.82	0.23	-0.75	1.05	0.30	5.6
A10T	IMYNYP**T**MLGHAGDM	IMYNYP**T**M	1.07	0.23	-0.81	1.30	0.49	6.5
A10V	IMYNYP**V**MLGHAGDM	IMYNYP**V**M	1.09	0.23	-0.98	1.32	0.35	9.5
M11I	IMYNYPA**I**LGHAGDM	IMYNYPA**I**	1.07	0.33	-0.88	1.40	0.52	7.6
Nonbinder	IM**ANA**PAMLGHAGDM	IM**ANA**PAM	0.94	0.15	-3.13	1.10	-2.04	1356.5