

Stat-Pak model

Effect likelihood ratio tests

SNP	d.f.	X ²	P value
Tcl136C	1	9.52	0.0020*
Tcl297C	1	3.72	0.0539
TcII98C	1	4.19	0.0407*
TcV130C	1	16.50	<.0001*
TcV164C	1	8.11	0.0044*
TcV260A	1	13.30	0.0003*

Model summary: X²= 25.54, d.f.=6,
P=0.0003, R²=0.37

Logistic prediction

Predicted diagnostic		
Actual diagnostic	Discordant	Positive
Discordant	8 (57.1%)	6 (42.9%)
Positive	2 (3.8%)	51 (96.2%)

Correctly classified: 59/67 (88.0%)

T-Detect model

Effect likelihood ratio tests

SNP	d.f.	X ²	P value
Tcl275C	1	5.30	0.0213*
TcII673	1	9.73	0.0018*
TcII164T	1	5.38	0.0203*
TcII260G	1	7.67	0.0056*
TcV75C	1	3.70	0.0543

Model summary: X²= 17.28, d.f.=5,
P=0.004, R²=0.27

Logistic prediction

Predicted diagnostic		
Actual diagnostic	Discordant	Positive
Discordant	4 (33.3%)	8 (66.6%)
Positive	1 (1.8%)	54 (98.2%)

Correctly classified: 58/67 (86.6%)

Wiener ELISA model

Effect likelihood ratio tests

SNP	d.f.	X ²	P value
Tcl136C	2	10.09	0.0064*
Tcl297C	2	7.44	0.0243*
TcV102G	2	6.96	0.0308*

Model summary: X²= 26.50, d.f.=6,
P=0.0002, R²=0.26

Logistic prediction

Predicted diagnostic		
Actual diagnostic	Discordant	Positive
Discordant	11 (44.0%)	14 (56.0%)
Positive	3 (7.0%)	40 (93.0%)

Correctly classified: 51/68 (75.0%)

Supplementary Figure 1. Models associating *T. cruzi* SNPs with diagnostic outcome for specific assays. Multivariate logistic models associating diagnostic outcome (positive or serodiscordant) with combinations of parasite SNPs were elaborated. SNPs within Tcl, TcII and TcV are major determinants of diagnostic performance for each individual assay.