Supplementary Data

Supplementary Table 1

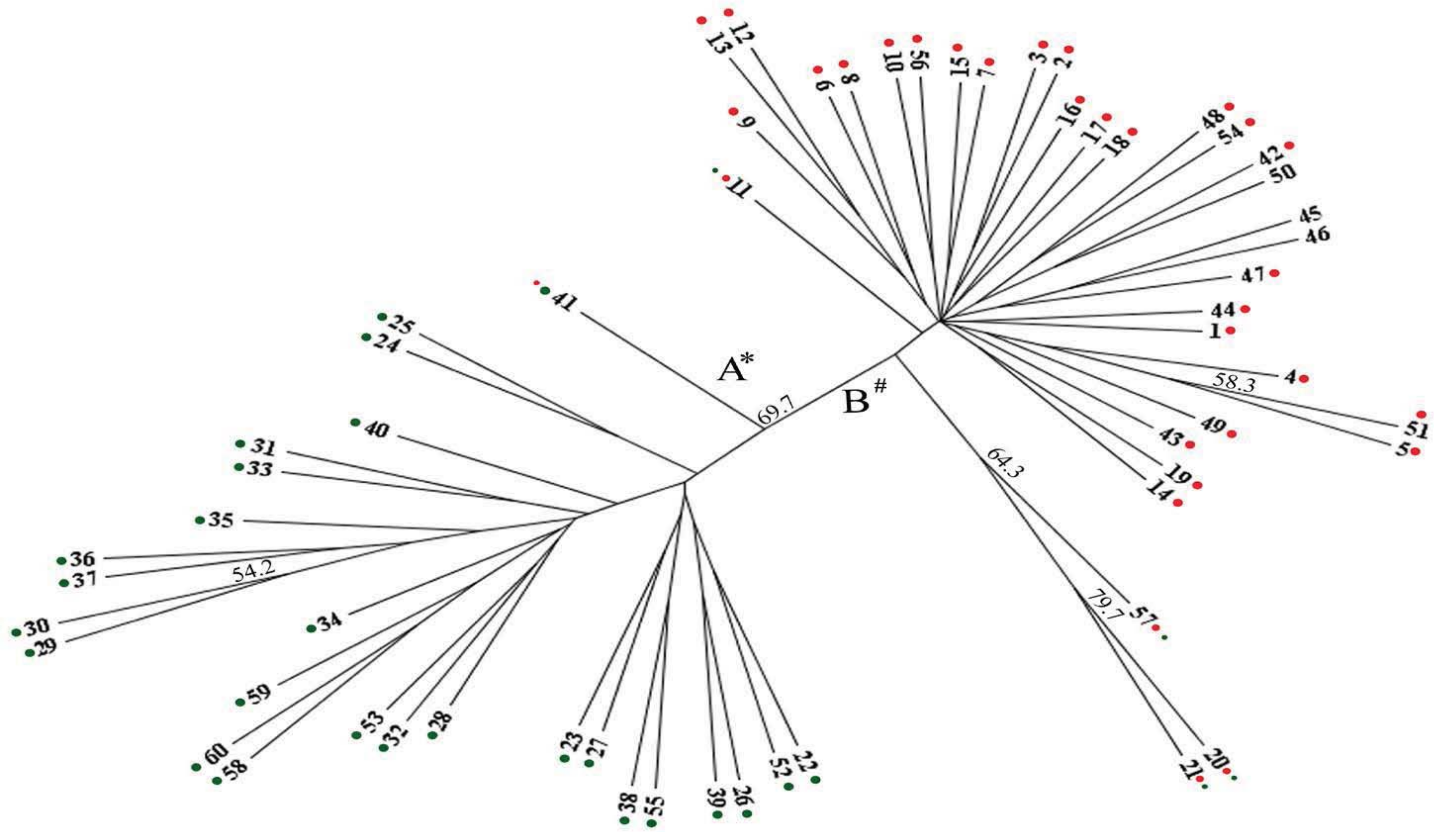
Candidate Loci for *T. vaginalis* MLST Scheme			
Gene ID	Locus Name	Gene Sequence Length (bp)	Accession Nos.
TVAG_299450	**Alanyl-tRNA Synthetase**	**3075**	**XM_001315470**
TVAG_433470	Aldehyde oxidase	3997	XM_001307868
TVAG_005070	**DNA mismatch Repair Protein** [a]	**1758**	**XM_001301638**
TVAG_423490	Eukaryotic Translation Initiation Factor 2 Gamma Subunit	1403	XM_001328484
TVAG_258340	**Family T2, Asparaginase-like Threonine Peptidase**	**990**	**XM_001323020**
TVAG_206250	Gamma Tubulin Complex Protein	1920	XM_001325645
TVAG_134820	**Glutaminase**	**886**	**XM_001295355**
TVAG_184360	Glycerate Kinase	1188	XM_001322722
TVAG_343390	**Mannose 6-Phosphate Isomerase**	**1128**	**XM_001325698**
TVAG_187730	mRNA Capping Enzyme	1686	XM_001327910
TVAG_102430	n6- DNA Methyltransferase	654	XM_001321682
TVAG_296220	NADH Dehydrogenase 24kDa Subunit	652	XM_001312167
TVAG_109540	**Serine Hydroxymethyltransferase**	**1356**	**XM_001322558**
TVAG_346790	Succinate Semialdehyde Dehydrogenase	1398	XM_001310606
TVAG_054490	**Tryptophanase** [b]	**1451**	**XM_001330582**
TVAG_341080	Tubulin Specific Chaperone B	657	XM_001328402

Supplementary Table 1.
Sixteen candidate loci screened for inclusion in MLST scheme for *Trichomonas vaginalis*. The seven loci chosen for final MLST scheme are **bolded**.

[a] Single-copy gene used for population genetics analysis of *T. vaginalis* by Conrad, et al. (10, 11).

[b] Determined to have likely resulted from lateral gene transfer (9).

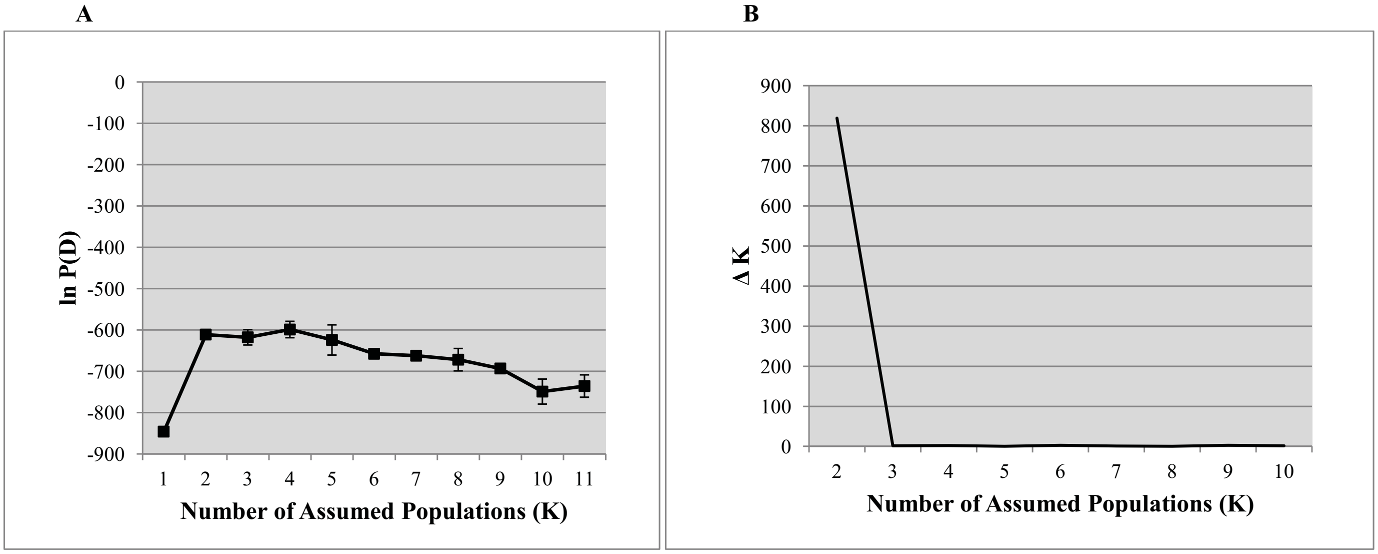
Supplementary Figure 1



Supplementary Figure 1. Unrooted phylogram

Clustering analysis based on the neighbor-joining method. *Trichomonas vaginalis* sequence types (STs) clustered into two phylogenetic clades (A and B). Numbers on branches indicate bootstrap proportions based on 1000 replicates. Green and red dots correspond to the coloring scheme of Figure 1. STs with two dots indicate STs with < 85% ancestry in either population based on the Bayesian population assignments of Figure 3A.

Supplementary Figure 2



Supplementary Figure 2. **Detecting the number of populations in *T. vaginalis* with STRUCTURE analysis.**
A. Log probability of data [ln P(D)] for K populations using the admixture model. Average and standard deviation over 5 replicates are shown.
B. Rate of change in the log probability of the data between consecutive K values [ΔK].