

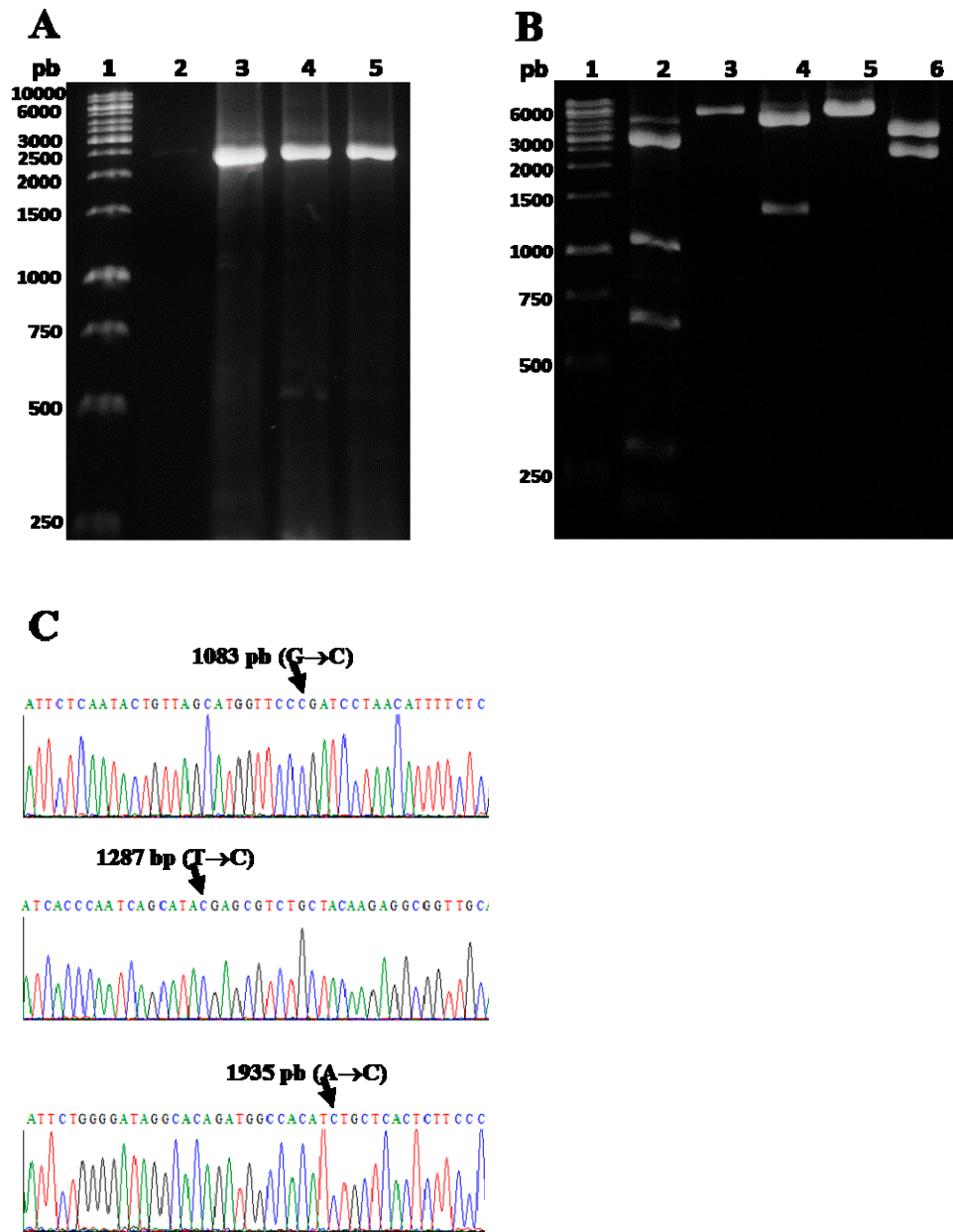


Figure S1. The cloning and site-directed mutagenesis of the *g6pd::6pgl* gene from *G. lamblia*. (A) Analysis of the restriction enzyme digestion of the plasmid containing the *g6pd::6pgl* gene with different mutations generated by site-directed mutagenesis. Lane 1, GeneRuler 1 kb DNA ladder (Thermo Scientific, USA); lane 2, the *NdeI* and *BamHI* double digested *g6pd::6pgl* gene in the pJET2.1 plasmid; lane 3, the *g6pd::6pgl* gene with the mutated *BamHI* restriction site and digested with *BamHI*; lanes 4 and 5, the *g6pd::6pgl* gene containing the first and second mutated *NdeI* restriction sites and digested with *NdeI*; lane 6, confirmation of the mutations made to the *g6pd::6pgl* gene by digestion of the pJET-*g6pd::6pgl* vector with *NdeI* and *BamHI*. A single fragment was released. (B) Electropherograms of the mutated sequences indicating the bases that were changed to eliminate the internal *BamHI* and *NdeI* restriction sites in the *g6pd::6pgl* gene.

Table S1. Comparative analysis of G6PD region protein sequence of *G. lamblia* and the G6PD proteins from other species with the program BLASTp.

Identification	Species	Score	Ident	Gap	e-value
XP_001704441.1	<i>Giardia lamblia</i>	1546	100%	0%	0.0
ESU38278.1	<i>Giardia intestinalis</i>	1543	99%	0%	0.0
EFO63133.1	<i>Giardia lamblia</i> P15	1488	96%	0%	0.0
KWX15280.1	<i>Giardia intestinalis</i> assemblage B	1415	90%	0%	0.0
ESU45561.1	<i>Giardia intestinalis</i>	1414	90%	0%	0.0
EES98494.1	<i>Giardia intestinalis</i> ATCC 5081	1414	90%	0%	0.0
XP_001321978.1	<i>Trichomonas vaginalis</i> (G3)	341	32%	10%	4e-103
OHT05904.1	<i>Tritrichomonas foetus</i>	338	32%	9%	6e-102
OHT00007.1	<i>Tritrichomonas foetus</i>	333	32%	10%	3e-100
XP_001583274.1	<i>Trichomonas vaginalis</i> (G3)	327	32%	8%	1e-97
WP_010872081.1	<i>Synechocystis</i> sp. PCC 6803	698	35%	9%	5e-82
NP_274406.1	<i>Neisseria meningitidis</i> MC58	695	34%	9%	8e-82
WP_004162784.1	<i>Microcystis aeruginosa</i>	681	34%	10%	2e-79
NP_295319.1	<i>Deinococcus radiodurans</i> R1	645	33%	9%	2e-73
NP_228961.1	<i>Thermotoga maritima</i> MSB8	638	33%	11%	2e-73
NP_416366.1	<i>Escherichia coli</i> str. K-12	635	33%	11%	5e-73
NP_001241264.1	<i>Glycine max</i>	626	33%	7%	2e-71
XP_644436.1	<i>Dictyostelium discoideum</i> AX4	624	32%	9%	2e-71
NP_626202.1	<i>Streptomyces coelicolor</i> A3(2)	618	33%	9%	2e-70
NP_718076.1	<i>Shewanella oneidensis</i> MR-1	613	33%	9%	62-70
NP_189366.1	<i>Arabidopsis thaliana</i>	605	33%	8%	2e-68
NP_593344.2	<i>Schizosaccharomyces pombe</i> 972h	602	32%	8%	4e-68
NP_032088.1	<i>Mus musculus</i>	578	32%	10%	1e-64
NP_251873.1	<i>Pseudomonas aeruginosa</i> PAO1	573	32%	10%	3e-64
XP_003864173.1	<i>Leishmania donovani</i>	577	32%	9%	5e-64
NP_502129.1	<i>Caenorhabditis elegans</i>	563	30%	10%	2e-62
NP_014158.1	<i>Saccharomyces cerevisiae</i> S288c	558	31%	11%	6e-62
NP_001035810.1	<i>Homo sapiens</i> isoform b	553	32%	15%	4e-61
NP_000393.4	<i>Homo sapiens</i> isoform a	552	32%	15%	9e-61
NP_215963.1	<i>Mycobacterium tuberculosis</i> H37Rv	546	30%	11%	4e-60
NP_358715.1	<i>Streptococcus pneumoniae</i> R6	471	30%	12%	8e-50
XP_001348685.1	<i>Plasmodium falciparum</i> 3D7	514	30%	11%	8e-43

Multiple alignment of amino acid sequences alignment. The alignment of the deduced amino acid sequences of *Giardia lamblia* ATCC 50803 (XP_001704441.1), *Giardia intestinalis* (ESU38278.1), *Giardia lamblia* P15 (EFO63133.1), *Giardia intestinalis* assemblage B (KWX15280.1), *Giardia intestinalis* (ESU45561.1), *Giardia intestinalis* ATCC 50581 (EES98494.1), *Trichomonas vaginalis* G3 (XP_001321978.1), *Tritrichomonas foetus* (OHT05904.1), *Tritrichomonas foetus* (OHT00007.1), *Trichomonas vaginalis* G3 (XP_001583274.1), *Synechocystis* sp. PCC 6803 (WP_010872081.1), *Neisseria meningitidis* MC58 (NP_274406.1), *Microcystis aeruginosa* (WP_004162784.1), *Deinococcus radiodurans* R1 (NP_295319.1), *Thermotoga maritima* MSB8 (NP_228961.1), *Escherichia coli* str. K-12 (NP_416366.1) *Glycine max* (NP_001241264.1), *Dictyostelium discoideum* AX4 (XP_644436.1), *Streptomyces coelicolor* A3(2) (NP_626202.1), *Shewanella oneidensis* MR-1 (NP_718076.1), *Arabidopsis thaliana* (NP_189366.1), *Schizosaccharomyces pombe* 972h (NP_593344.2), *Mus musculus* (NP_032088.1), *Pseudomonas aeruginosa* PAO1 (NP_251873.1), *Leishmania donovani* (XP_003864173.1), *Caenorhabditis elegans* (NP_502129.1), *Saccharomyces cerevisiae* S288c (NP_014158.1), *Homo sapiens* isoform b (NP_001035810.1), *Homo*

sapiens isoform a (NP_000393.4), *Mycobacterium tuberculosis* H37Rv (NP_215963.1), *Mycobacterium tuberculosis* H37Rv (YP_177789.1), *Streptococcus pneumoniae* R6 (NP_358715.1), *Plasmodium falciparum* 3D7 (XP_001348685.1). Multiple sequence alignment was executed using the online program ClustalW Content in the MEGA7 (v. 7.0.21) software and highly conserved amino acids with the WebLogo program. Fully three conserved regions are shown as colors boxes.

Table S2. Comparative analysis of 6PGL region sequence of *G. lamblia* with the 6PGL proteins from other species in the program BLASTp.

Identification	Species	Score	Ident	Gap	E-value
XP_001704441.1	<i>Giardia lamblia</i>	1546	100%	0%	0.0
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(WP_004162784.1), *Deinococcus radiodurans* R1 (NP_295319.1), *Thermotoga maritima* MSB8 (NP_228961.1), *Escherichia coli* str. K-12 (NP_416366.1) *Glycine max* (NP_001241264.1), *Dictyostelium discoideum* AX4 (XP_644436.1), *Streptomyces coelicolor* A3(2) (NP_626202.1), *Shewanella oneidensis* MR-1 (NP_718076.1), *Arabidopsis thaliana* (NP_189366.1), *Schizosaccharomyces pombe* 972h (NP_593344.2), *Mus musculus* (NP_032088.1), *Pseudomonas aeruginosa* PAO1(NP_251873.1), *Leishmania donovani* (XP_003864173.1), *Caenorhabditis elegans* (NP_502129.1), *Saccharomyces cerevisiae* S288c(NP_014158.1), *Homo sapiens* isoform b (NP_001035810.1), *Homo sapiens* isoform a (NP_000393.4), *Mycobacterium tuberculosis* H37Rv (NP_215963.1), *Mycobacterium tuberculosis* H37Rv (YP_177789.1), *Streptococcus pneumoniae* R6 (NP_358715.1), *Plasmodium falciparum* 3D7 (XP_001348685.1). Multiple sequence alignment was executed using the online program ClustalW Content in the MEGA7 (v. 7.0.21) software and highly conserved amino acids with the WebLogo program. Fully three conserved regions are shown as colors boxes.