

TVAG_137940	-----MARTKQTARKSTGGKTPRKSLGAKAARKSTPTID	-----SQGAKKQHRFRPGTVALREIRKYQKSTDLLIR	66
TVAG_211260	-----MARTKQTARKSTGGKTPRKSLGAKAARKSTPTID	-----SQGAKKQHRFRPGTVALREIRKYQKSTDLLIR	66
TVAG_224650	-----MARTKQTARKSTGGKTPRKSLGAKAARKSTPTID	-----SQGAKKQHRFRPGTVALREIRKYQKSTDLLIR	66
TVAG_239330	-----MARTKQTARKSTGGKTPRKSLGAKAARKSTPTID	-----SQGAKKQHRFRPGTVALREIRKYQKSTDLLIR	66
TVAG_270800	-----MARTKQTARKSTGGKTPRKSLGAKAARKSTPTID	-----SQGAKKQHRFRPGTVALREIRKYQKSTDLLIR	66
TVAG_270890	-----MARTKQTARKSTGGKTPRKSLGAKAARKSTPTID	-----SQGAKKQHRFRPGTVALREIRKYQKSTDLLIR	66
TVAG_315320	-----MARTKQTARKSTGGKTPRKSLGAKAARKSTPTID	-----SQGAKKQHRFRPGTVALREIRKYQKSTDLLIR	66
TVAG_341360	-----MARTKQTARKSTGGKTPRKSLGAKAARKSTPTID	-----SQGAKKQHRFRPGTVALREIRKYQKSTDLLIR	66
TVAG_399370	-----MARTKQTARKSTGGKTPRKSLGAKAARKSTPTID	-----SQGAKKQHRFRPGTVALREIRKYQKSTDLLIR	66
TVAG_414480	-----MARTKQTARKSTGGKTPRKSLGAKAARKSTPTID	-----SQGAKKQHRFRPGTVALREIRKYQKSTDLLIR	66
TVAG_445270	-----MARTKQTARKSTGGKTPRKSLGAKAARKSTPTID	-----SQGAKKQHRFRPGTVALREIRKYQKSTDLLIR	66
TVAG_452730	-----MARTKQTARKSTGGKTPRKSLGAKAARKSTPTID	-----SQGAKKQHRFRPGTVALREIRKYQKSTDLLIR	66
TVAG_470690	-----MARTKQTARKSTGGKTPRKSLGAKAARKSTPTID	-----SQGAKKQHRFRPGTVALREIRKYQKSTDLLIR	66
TVAG_497330	-----MARTKQTARKSTGGKTPRKSLGAKAARKSTPTID	-----SQGAKKQHRFRPGTVALREIRKYQKSTDLLIR	66
TVAG_499020	-----MARTKQTARKSTGGKTPRKSLGAKAARKSTPTID	-----SQGAKKQHRFRPGTVALREIRKYQKSTDLLIR	66
TVAG_270080	-----MARTKQTARKSTGGKTPRKSLGAKAARKSTPTID	-----SQGAKKQHRFRPGTVALREIRKYQKSTDLLIR	66
TVAG_087830	-----MARTKQTARKTGGKTPRKSLGAKAARKAIPVTD	-----SQGAKKQHRFRPGTVALREIRKYQKSTDLLIR	66
TVAG_185390	-----MEEEPRIHRGKRRIPSSGAARPPDNSSDKSESQKKQRKR--NSWLREIHFYQKTDNLLIR	62	
TVAG_224460	MASTRYADDWSFFDDPDNRSSRLEFSIPSQWSQLDVIKPAKKQLKKKKLPNPDQPKPKKHNHVLKEIRTYQNSVDLLIP	80	

TVAG_137940	KLPFQRLVREIASGFR	GDLRFQSSAIAALQEASEAYLVGLFEDTNLCAIHANRVTIMERDVQLAQRIRGERN	-- 138
TVAG_211260	KLPFQRLVREIASGFR	GDLRFQSSAIAALQEASEAYLVGLFEDTNLCAIHANRVTIMERDVQLAQRIRGERN	-- 138
TVAG_224650	KLPFQRLVREIASGFR	GDLRFQSSAIAALQEASEAYLVGLFEDTNLCAIHANRVTIMERDVQLAQRIRGERN	-- 138
TVAG_239330	KLPFQRLVREIASGFR	GDLRFQSSAIAALQEASEAYLVGLFEDTNLCAIHANRVTIMERDVQLAQRIRGERN	-- 138
TVAG_270800	KLPFQRLVREIASGFR	GDLRFQSSAIAALQEASEAYLVGLFEDTNLCAIHANRVTIMERDVQLAQRIRGERN	-- 138
TVAG_270890	KLPFQRLVREIASGFR	GDLRFQSSAIAALQEASEAYLVGLFEDTNLCAIHANRVTIMERDVQLAQRIRGERN	-- 138
TVAG_315320	KLPFQRLVREIASGFR	GDLRFQSSAIAALQEASEAYLVGLFEDTNLCAIHANRVTIMERDVQLAQRIRGERN	-- 138
TVAG_341360	KLPFQRLVREIASGFR	GDLRFQSSAIAALQEASEAYLVGLFEDTNLCAIHANRVTIMERDVQLAQRIRGERN	-- 138
TVAG_399370	KLPFQRLVREIASGFR	GDLRFQSSAIAALQEASEAYLVGLFEDTNLCAIHANRVTIMERDVQLAQRIRGERN	-- 138
TVAG_414480	KLPFQRLVREIASGFR	GDLRFQSSAIAALQEASEAYLVGLFEDTNLCAIHANRVTIMERDVQLAQRIRGERN	-- 138
TVAG_445270	KLPFQRLVREIASGFR	GDLRFQSSAIAALQEASEAYLVGLFEDTNLCAIHANRVTIMERDVQLAQRIRGERN	-- 138
TVAG_452730	KLPFQRLVREIASGFR	GDLRFQSSAIAALQEASEAYLVGLFEDTNLCAIHANRVTIMERDVQLAQRIRGERN	-- 138
TVAG_470690	KLPFQRLVREIASGFR	GDLRFQSSAIAALQEASEAYLVGLFEDTNLCAIHANRVTIMERDVQLAQRIRGERN	-- 138
TVAG_497330	KLPFQRLVREIASGFR	GDLRFQSSAIAALQEASEAYLVGLFEDTNLCAIHANRVTIMERDVQLAQRIRGERN	-- 138
TVAG_499020	KLPFQRLVREIASGFR	GDLRFQSSAIAALQEASEAYLVGLFEDTNLCAIHANRVTIMERDVQLAQRIRGERN	-- 138
TVAG_270080	KLPFQRLVREIASGFR	GDLRFQSSAIAALQEASEAYLVGLFEDTNLCAIHANRVTIMERDVQLAQRIRGERN	-- 138
TVAG_087830	KLPFQRLVREIASGFR	GDLRFQSSAIAALQEAAEAYLVGLFEDTNLCAIHANRVTIMERDVQLAMRIRGERN	-- 138
TVAG_185390	KLPFCRLVKEITQSVSICEFRYTTGAMEALQEASEAFILIKLLEDGOVCAIHARRITLMNRDLQLAQRIRGDR	---	134
TVAG_224460	RLSFRQRLVREIAHQNN-PTIKFQETAIQALQEASEAFILVGMMEDGNLCTIHAQRVITMKKDMKLAERIRGDSITE		154

Figure S1. Sequence alignment of H3 histones identified in the *T. vaginalis* genome database TrichDB (<http://trichdb.org/trichdb>). Histones highlighted in red were used in experiments: TVAG_270080 (core H3); TVAG_087830 (H3.3 variant); TVAG_185390 (H3T); TVAG_224460 (cenH3). Identical amino acids are shaded in grey.

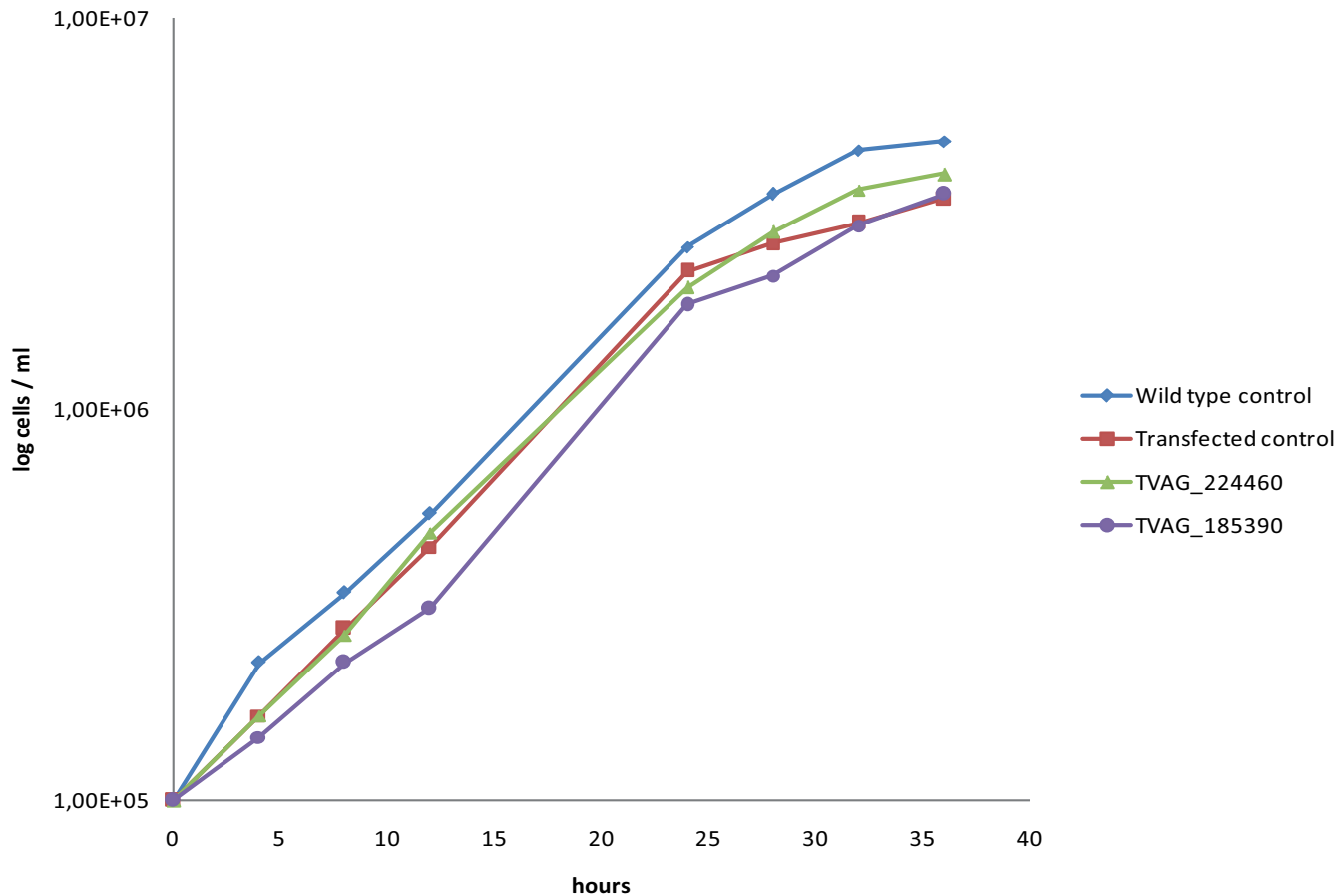


Figure S2: Effect of transfection on the growth of *Trichomonas vaginalis* cells.

The numbers of non-transfected cells (blue, rhombs) and cells transfected with TagVag vector (HA-tagged histones TVAG_224460 – green, triangles; TVAG_185390 – purple, circles; control gene TVAG_206500 – red, squares) are indicated. Cell numbers were determined using a cell counter (Z2, Beckman Coulter). Values represent means of two determinations.

Table S1. List of sequences used for *T. vaginalis* genome searches.

Organism	Name	Accession number	<i>T. vaginalis</i> orthologues	Probability value
<i>Homo sapiens</i>	H2A	NP_066544	17	$\leq 3.1e-36$
<i>Giardia intestinalis</i>	H2A	AAF00590	17	$\leq 1.1e-17$
<i>Homo sapiens</i>	H2B	CAA41051	14	$\leq 2.0e-18$
<i>Giardia intestinalis</i>	H2B	ABV60242	14	$\leq 1.3e-12$
<i>Homo sapiens</i>	H3	NP_003520	23	$\leq 2.9e-24$
<i>Encephalitozoon cuniculi</i>	H3	XP_955598	23	$\leq 4.8e-15$
<i>Giardia intestinalis</i>	H3B	GL50803_3367	23	$\leq 9.3e-12$
	CenH3	GL50803_20037	23	$\leq 1.9e-13$
	H3	XP_001707235	23	$\leq 1.1e-17$
<i>Trypanosoma brucei</i>	H3	XP_001218954	23	$\leq 4.8e-15$
<i>Mastigamoeba balamuthi</i>	H3	AAF00588	23	$\leq 1.5e-18$
<i>Entamoeba dispar</i>	H3	EDI_160110	23	$\leq 1.4e-17$
<i>Toxoplasma gondii</i>	H3	AAO23911	23	$\leq 5.3e-25$
	H3.3	AAM95790	23	$\leq 5.1e-20$
<i>Arabidopsis thaliana</i>	H3	NP_196659	23	$\leq 3.7e-24$
<i>Drosophila melanogaster</i>	CenH3 (Cid)	Q9V6Q2	23	$\leq 7.4e-10$
<i>Homo sapiens</i>	H4	NP_778224	21	$\leq 3.7e-33$
<i>Giardia intestinalis</i>	H4	GL50803_135003	21	$\leq 5.1e-27$

T. vaginalis genome searches for orthologues of histone H2A, H2B, H3 and H4 using protein sequences of selected members of main eukaryotic groups as queries. BLAST searches were performed using TrichoDB tools (<http://trichodb.org>). In BLAST searches, all other sequences identified with queries listed above displayed probability values $> 0,023$.

Table S2. List of histones H2A, H2B, and H4 in *T. vaginalis*.

H2A	H2B	H4
TVAG_021440	TVAG_026390	TVAG_014920
TVAG_026380	TVAG_045410	TVAG_085660
TVAG_045400	TVAG_075290	TVAG_100580*
TVAG_055220	TVAG_105960	TVAG_129720
TVAG_075280	TVAG_144040	TVAG_137930
TVAG_105970*	TVAG_195300	TVAG_191680
TVAG_144030	TVAG_226780	TVAG_211270
TVAG_195310	TVAG_228640	TVAG_224660
TVAG_226790	TVAG_268820	TVAG_239320
TVAG_321400	TVAG_321390**	TVAG_270070
TVAG_329280	TVAG_329270	TVAG_270900
TVAG_380930	TVAG_380920	TVAG_315310
TVAG_381770	TVAG_447850	TVAG_341350
TVAG_389620	TVAG_464720	TVAG_351560
TVAG_447860*		TVAG_392270
TVAG_462660		TVAG_399380
TVAG_464710		TVAG_414470
		TVAG_445260
		TVAG_452720
		TVAG_470680
		TVAG_499010

* a single amino acid substitution

** truncated protein lacking the first 63 amino acids