

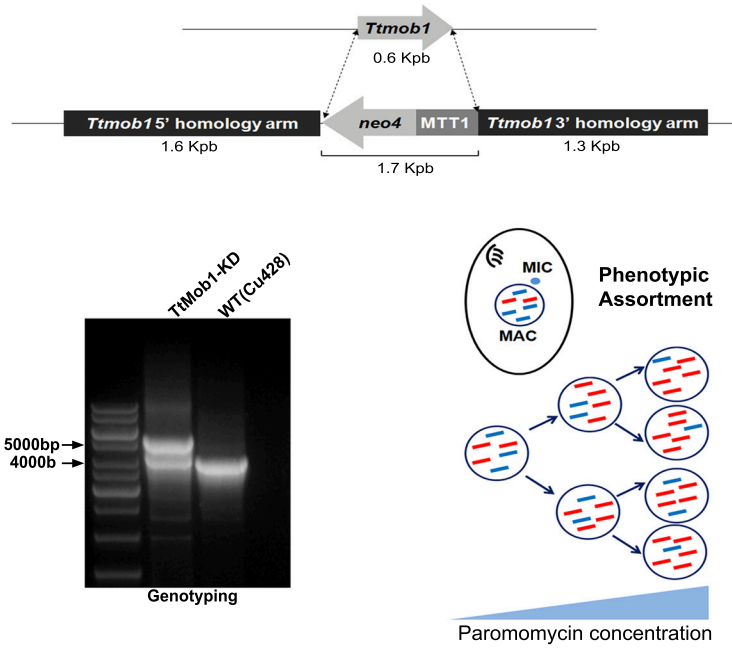
Figure S1

A

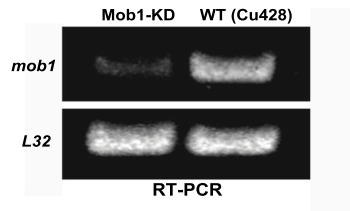
Mobl	<i>T.thermophila</i>	-----		
Mobl	<i>H. sapiens</i>	-----		
Mobl	<i>M. musculus</i>	-----		
Mobl	<i>G.gallus</i>	-----		
Mobl	<i>X. laevis</i>	-----		
Mobl	<i>D. rerio</i>	-----		
Mobl	<i>D. melanogaster</i>	-----		
Mobl	<i>A. thaliana</i>	-----		
Mobl	<i>Z. mays</i>	-----		
Mobl	<i>S. cerevisae</i>	MSFLQNFHISPGQTI RSTRGFKWNTANAANNAGSVSPTKATPHNNTINGNNNNANTINNR	60	
Mobl	<i>D. fasciculatum</i>	-----		
Mobl	<i>T.thermophila</i>	-----MSQKTYKPKQ-IEK	13	
Mobl	<i>H. sapiens</i>	-----MSFLFGSRSSKTFKPKKNIPE	21	
Mobl	<i>M. musculus</i>	-----		
Mobl	<i>G.gallus</i>	-----MSFLYGSRRSSKTFKPKKNIPE	21	
Mobl	<i>X. laevis</i>	-----MSFLFGNRSSKTFKPKKSLPE	21	
Mobl	<i>D. rerio</i>	-----MSFLFGSRSSKTFKPKKNIPE	21	
Mobl	<i>D. melanogaster</i>	-----MDFLFGSRSSKTFKPKKNIPE	21	
Mobl	<i>A. thaliana</i>	-----MSFLGGLGRNQKTFRPKKSAPS	21	
Mobl	<i>Z. mays</i>	-----MSFLGGLGRNQKTFRPKKSAPS	21	
Mobl	<i>S. cerevisae</i>	ADFTNNPVNGYNESDHGRMSPVLTTPKRHAPPEQLQNVTDENYTPSHQKPFLLQPAGTT	120	
Mobl	<i>D. fasciculatum</i>	-----MFSKKS-QTFKPKKNIQE	17	
Mobl	<i>T.thermophila</i>	GSRGWGLKHHIAQMTLGS-GNMSLAVELPQGEKNEWLAVNTIEFYNEISILYGLTLMFECT	72	
Mobl	<i>H. sapiens</i>	GSHQYELLKHA EATLGS-GNLRMAVMLPEGEDLNEWVAVNTVDFFNQINMLYGTITDFCT	80	
Mobl	<i>M. musculus</i>	-----LYGTITDFCT	10	
Mobl	<i>G.gallus</i>	GSHQYELLKHA EATLGS-GNLRMAVMLPEGEDLNEWVAVNTVDFFNQINMLYGTITDFCT	80	
Mobl	<i>X. laevis</i>	GSHQYELLKHA EATLGS-GNLRMAVMLPEGEDLNEWVAVNTVDFFNQINMLYGTITDFCT	80	
Mobl	<i>D. rerio</i>	GSHQYELLKHA EATLGS-GNLRMAVMLPDGEDLNEWVAVNTVDFFNQINMLYGTITDFCT	80	
Mobl	<i>D. melanogaster</i>	GTHQYDLMKHA AATLGS-GNLRNAVALPDGEDLNEWVAVNTVDFFNQINMLYGTITDFCT	80	
Mobl	<i>A. thaliana</i>	GSKGAQLRKHIDATLGS-GNLR EAVRLPPGEDANEWLAVNTVDFFNQVNLlyGLTLTEFCT	80	
Mobl	<i>Z. mays</i>	GSKGAQLRKHIDATLGS-GNLR EAVRLPPGEDINEWLAVNTVDFFNQVNLlyGLTLTEFCT	80	
Mobl	<i>S. cerevisae</i>	VTTHQDIKQIVEMTLGSEGLNQA VKLPRGEDENEWLAVHCVDFYQINMLYGSITDFCS	180	
Mobl	<i>D. fasciculatum</i>	GSKQYQLKQYAEATLGS-GNLR LAVSLPAGEDLNEWLAVNTVDFFNQINMLYGTITDFCT	76	
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Mobl	<i>T.thermophila</i>	PEACPIMSAGPKY EYLWADGQV R TPLKVSASEYIDY LMTWVETQINNESLFPCQIGVPF	132	
Mobl	<i>H. sapiens</i>	EESCVPMSAGPKY EYHWADGTNIKKPIKCSAPKYIDY LMTWVQDQLDDETLFPSKIGVPF	140	
Mobl	<i>M. musculus</i>	EESCVPMSAGPKY EYHWADGTNIKKPIKCSAPKYIDY LMTWVQDQLDDETLFPSKIGVPF	70	
Mobl	<i>G.gallus</i>	EESCVPMSAGPKY EYHWADGTNIKKPIKCSAPKYIDY LMTWVQDQLDDETLFPSKIGVPF	140	
Mobl	<i>X. laevis</i>	EESCVPMSAGPKY EYHWADGTNIKKPIKCSAPKYIDY LMTWVQDQLDDETLFPSKIGVPF	140	
Mobl	<i>D. rerio</i>	EESCPLMSAGPKY EYHWADGTNIKKPIKCSAPKYIDY LMTWVQDQLDDETLFPSKIGVPF	140	
Mobl	<i>D. melanogaster</i>	EETCGIMSAGPKY EYHWADGLTVKKPIKCSAPKYIDY LMTWVQDQLDDETLFPSKIGVPF	140	
Mobl	<i>A. thaliana</i>	PDNCPMTAGPKY EYRWADGVQIKKPIEVSAPKYVEY LMDWIE TQDDETLFPQLGAPF	140	
Mobl	<i>Z. mays</i>	PESCPMTAGPKY EYRWADGVQIKKPIEVSAPKYVEY LMDWIE TQDDETLFPQLGAPF	140	
Mobl	<i>S. cerevisae</i>	PQTCPRMIATNEYEYLWAFQ-KGQPPVSVSAPKYVECLMRWQDQDDESLFPSKIVGTF	239	
Mobl	<i>D. fasciculatum</i>	TSECPMSAGPKY EYHWADGTTVKKAIKVSAP EYVDY LMTWVQSQDDESLFPSKIGVLF	136	
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Mobl	<i>T.thermophila</i>	PKNFLS-VIKVIFKRLFRVYAH IYHSHFQHIMSLGLE YHLNLCFKHF IYFID EFDLVDK	191	
Mobl	<i>H. sapiens</i>	PKNFMS-VAKTILKRLFRVYAH IYHQHFD PVIQLQEEAHLNLSFKHF IFFVQEFNLIDRR	199	
Mobl	<i>M. musculus</i>	PKNFMS-VAKTILKRLFRVYAH IYHQHFD PVIQLQEEAHLNLSFKHF IFFVQEFNLIDRR	129	
Mobl	<i>G.gallus</i>	PKNFMS-VAKTILKRLFRVYAH IYHQHFD PVIQLQEEAHLNLSFKHF IFFVQEFNLIDRR	199	
Mobl	<i>X. laevis</i>	PKNFMS-VAKTILKRLFRVYAH IYHQHFD S VIQLQEEAHLNLSFKHF IFFVQEFNLIDRR	199	
Mobl	<i>D. rerio</i>	PKNFMS-VAKTILKRLFRVYAH IYHQH FESVIQLQEEAHLNLSFKHF IFFVQEFNLIDRK	199	
Mobl	<i>D. melanogaster</i>	PKNFHS-SAKTILKRLFRVYAH IYHQH FTEVVTLGEAHLNLSFKHF IFFVQEFNLIERR	199	
Mobl	<i>A. thaliana</i>	PQNFKD-VVKTIFKRLFRVYAH IYHSHFQKIVSLKEEAHLNLCFKHF ILFTH EFGIDKK	199	
Mobl	<i>Z. mays</i>	PPNFKE-VVKTIFKRLFRVYAH TYHSHFQKIVSLKEEAHLNLCFKHF ILFTNEFGLIDKK	199	
Mobl	<i>S. cerevisae</i>	PEGFIQRVIQPI LRRFRVYAH IYCHHFNE ILELNLQTVLNTSFRHFCLFAQEFELLRPA	299	
Mobl	<i>D. fasciculatum</i>	PKNFQS-IVKTIFKRLFRVYAH IYHSHFQKIVNLGEEAHLNLSLKHFIFFIQEFNLVDK	195	
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Mobl	<i>T.thermophila</i>	ELAPLAE LIQQFKARKEVPQTQQ	214	
Mobl	<i>H. sapiens</i>	ELAPLQELIEKLT SKDR-----	216	
Mobl	<i>M. musculus</i>	ELAPLQELIEKLT SKDR-----	146	
Mobl	<i>G.gallus</i>	ELAPLQELIEKLT SKDR-----	216	
Mobl	<i>X. laevis</i>	EQAPLQELIEKLT SKDR-----	216	
Mobl	<i>D. rerio</i>	ELAPLQELIEKLT SKDR-----	216	
Mobl	<i>D. melanogaster</i>	ELAPLQELIDKLTAKDERQI---	219	
Mobl	<i>A. thaliana</i>	ELAPLQELIESIISPY-----	215	
Mobl	<i>Z. mays</i>	ELAPLQELIESIIVPY-----	215	
Mobl	<i>S. cerevisae</i>	DFGPLELVMELRDR-----	314	
Mobl	<i>D. fasciculatum</i>	ELGPLSELIE TLIKN-----	210	
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Figure S1

B



C



**Figure S1. The creation of the *Tetrahymena thermophila* TtMob1 knockdown strain.** (A) Amino acid sequence alignment of *Tetrahymena thermophila* TtMob1 (XP\_001031965), *Homo sapiens* (NP\_775739.1), *Mus musculus* (AAI04404.1), *Gallus gallus* (XP\_420601.1), *Xenopus laevis* (NP\_001085265.1), *Danio rerio* (NP\_956494.1), *Drosophila melanogaster* (AAF55993.2), *Arabidopsis thaliana* (NP\_199368.1), *Zea mays* (ACG45985.1), *Saccharomyces cerevisiae* (DAA08447.1) and *Dictyostelium fasciculatum* (EGG23319.1). These proteins share an amino-acid sequence identity in the range of 49% to 62%. (B) (Top) Schematic representation of the construct used to disrupt the *Ttmob1* locus, originating the TtMob1-KD strain. (Left) PCR analysis of genomic DNA (gDNA) obtained from WT (Cu428 strain) and TtMob1-KD to confirm their genotype. gDNA was amplified with specific primers to the homology arms of 5' and 3' flanking regions of *Ttmob1* gene. For WT strain it was observed only one band corresponding to WT allele (4 kb), whereas in TtMob1KD cells an additional band corresponding to the disrupted-alleles *Ttmob1* is visible (5 kb). (Right) Schematic representation of phenotypic assortment in *Tetrahymena* macronuclear genome. The larger circle represents the MAC and the small blue circle indicates the MIC. For simplicity the MAC genetic content is represented by six copies of one autonomous replicating piece with WT *Ttmob1* allele (blue lines) and the knockout *Ttmob1* allele (red lines). In cells reproducing asexually, the MAC (45n) divides amitotically, which leads to a random distribution of allelic copies into daughter cells. Genetically transformed cells in the MAC can be pressed to increase the number of disrupted allelic copies by increasing the concentration of the selection drug, paromomycin, in the growth media. (C) RT-PCR analysis of *Ttmob1* expression in TtMob1-KD and in WT (Cu428 strain) cells showing the *Ttmob1* decreased levels in TtMob1-KD cells. The ribosomal protein *L32* coding gene was used as control.