

A



B

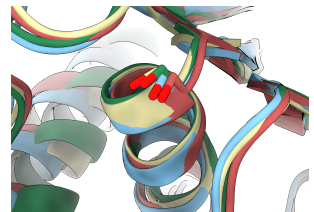
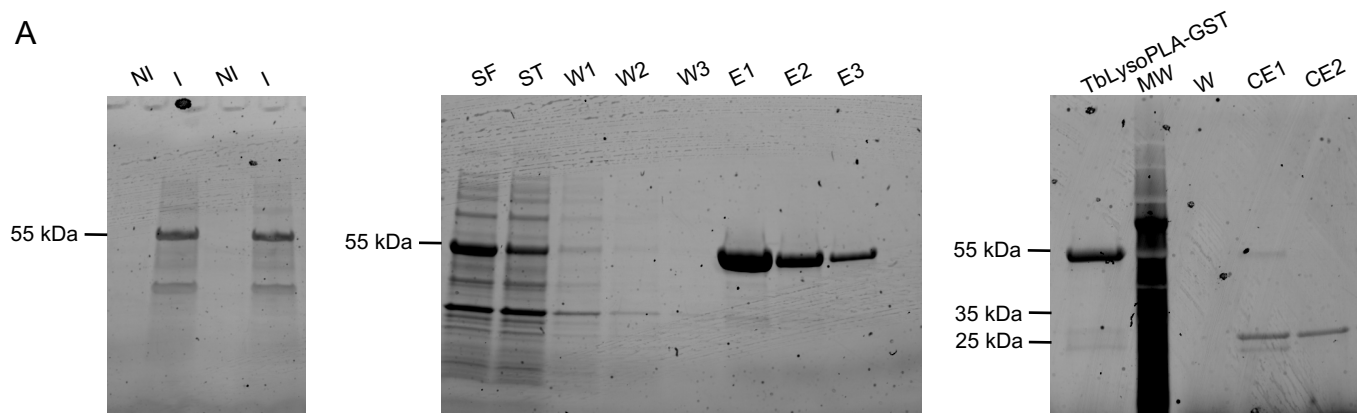
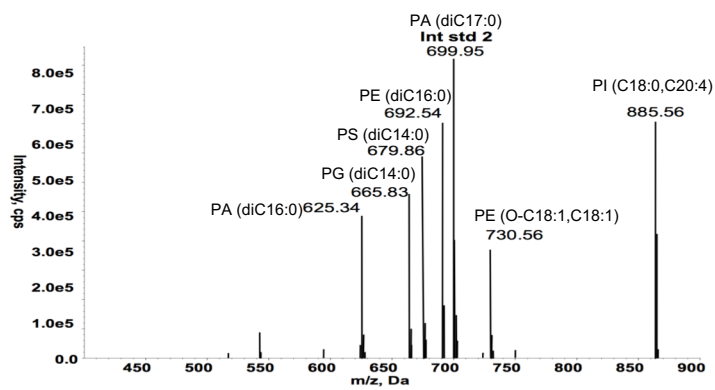


Fig S1

A



B



C

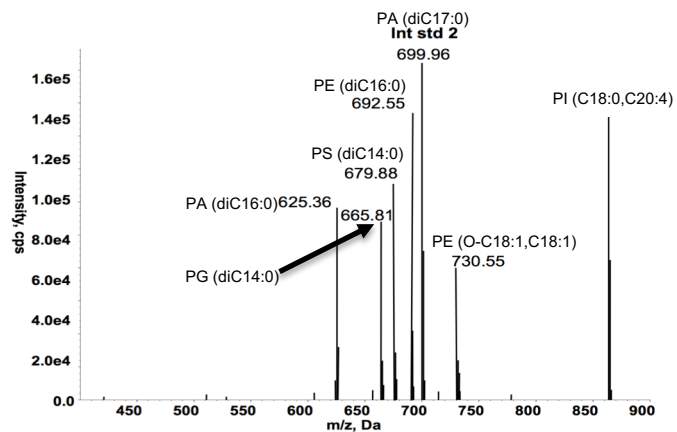


Fig S2

A

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TbLysoPLA -----MFGTPV-----ENLTANQI KEELRTL YGVSDVSGCIEQKDLQEKLEKTRETETLI THGLKYGPLLQI GNRQSPSGI VTLTHGLGDSANGWESVAVELSRRL ---PHL--LF--LLP--
TbPLA1 -----MS-----ESVDQLKTYLQSCDYSDSS-----R-----KKALEM--SOLCCHVYGGEGHLPDGLVCTREVGLKKRDESCGFRSELYTNG
TcPLA1 -----MRRR-----RTM-----TVVVVIL-----LILCGEDVRADYSVRLAT-----R-----ALYAKAAAYCKAEAISW--TCVSGASN-----PGMQ-----KVRVFTNA
LbrPLA1 MSIAITLERRMPQLHSCALCVTL LLSLMMLLAFFLFTSLTKKSESIISNTASLDYNTTEGR-----K-----ALYFKSAAYCPVKSVEW--NGGSACSN-----ATPNFR-----VFNVYDNT
Consensus -----MRR-----TV-----P-----E-----LLEERDYV-----S-----K-----ALYKAYCPKKEW-----C-----CSGSGSNGG-----GW-----EPG-----FLYTN
MSIAITM+RRMPQLHSC+++CVTT+V+M++++P+FTSLE++++LLI+E++++DYSV+++SGCIEQKDLQEKLEKTRETALY++K+AYCP+K+I+EWQS+CGSC+SN+G+G++++GW+++++E+PG++KRD+++GF+F+YTN+
TbLysoPLA -----TASMQPVGINSGAVMNSWYDIRNV-----SSGNGVTEDA--EAIIMSANLYKSLAYTASRRYQVPAGRVVYAGFSGQAVISLAAGLTARIPAGVAALSGYFAAAEKILPQLCNKSLPVLCHGTMNDIIP
TbPLA1 -----SKYVLAFAAGVHDNRSAFES-----ALQLVQKSDA-----YKLAANAALVVSAGFLSNVSGFTGHSGLGGGLATAAVFTGAP--AI-----TFNPAWLSST-----
TcPLA1 KHSTQAFVGVNN--SMIVVSRGTVDLNNWLYDLDFIPVPI RDGCV-GCLVHAGFHCESLWAE--RGYLOELVAGKIEGILITGHSLGGAMANIAANLMSQ--N-----
LbrPLA1 STGNFGYSGIDNDAGRIVVVRGTHNTENWIQDLDFWISIPYPNPSCGNCR IHRGFYRAYSSVRYQL-IYDVL SMLERHPSYTLFI TGHSLGGAMALLAIDFATW--NV-----SK-PEVVDNSV
Consensus -----GNSASVWFAG-----GTHDNNWDLDF-----PY-----SCNGCLHAGFA-----S-----Y-----L-----AYASV-----G-----V-----TGSLGG-----AA-----AA-----P-----S
+++++++G+N+ASMI VV+FRGTHD+N+W+DLDF+++PY+++SCNGCL+HAGF++A++S++Y+L++AY+AS+V+++++V+ITGHSLGGAMALAAA+++++PANVAALSGYFAAAE+++P+++++S+PVLCHGTMNDIIP
TbLysoPLA FSAAEKTKETLESLVGVPVTLVSYPM-----EMSHPK--EINDL-----E-----ASDLAASSLHED--VM-----
TbPLA1 -----RSELLKFPSEVINIYFAEALDVFQRHPQLLNSVPAGAF FAGLSNSKIQQFGTFKYIYCKVIHDPHPYIDAHL--IETIIEELRKENGEKIS-----ASDLAASSLHED--VM-----
TcPLA1 -----PLFPGAPKVLTYTFGQ-----PRVG-----NEAFANWLLAS--FCRDGHESYRVTHKRDVPHLLPMLFGFYHAPNEVWYDNDGDTVHKNCDTIFGTPCSALTAEDEPNCSDSIVSTSI EDHLKYLGVCTRCSC
LbrPLA1 -----QPSSAAPKPSHLAPVMLTYFGE-----PRVG-----NQYFTNWSTSV-LA--NEKQFRITHAKDVPVPHLPPLSWSYVHPQEVWYPADAEAVL-----LCQDNSTEDPLCSNSVYATRVADHLIYFGICTRCEC
Consensus -----SE LKFPQV-----V-----LYFGE-----P-----RVG-----N-----FANWLL-----S-----G-----YR-----H-----DPVPHLP-----L-----H-----P-----E-----VWY-----DC-----E-----V-----C-----EDP-----CS-----S-----ATS-----DHL-----Y-----G-----CTRC-----C
FSA++++SE++KFPGV+PV+LYTFGEALDVFQRHPRVGNVSPAN++FANWLL++SK++++G++++YR+TH+++VPVHLP+L+++++H+P+EVWY++DGE+V+KNCTDIFGT+C+++++EDP+CS+S++ATS++DHL+Y+G+CTRC+C
TbLysoPLA -----KFLQQVLPGPS-----KS--
TbPLA1 -----GGMAQLVQQKMSVIME-V--VASVMSKQFSAGGFGS-----S-----
TcPLA1 DPGEAMSDEELRLEPELERVVAMDYIYQQRNMRFRPPF PARHRES
LbrPLA1 TAAEMEEIYKYKLPPEYTSLLALDYVMNRSRPTVR-----
Consensus -----GEM-----OQKLP-----PE-----E-----V-----A-----DYVM-----SR-----RF-----
++GEM+++++OQKLPPE+E+V+A+DYVM++SR+++RF+++FPA++++ES

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B

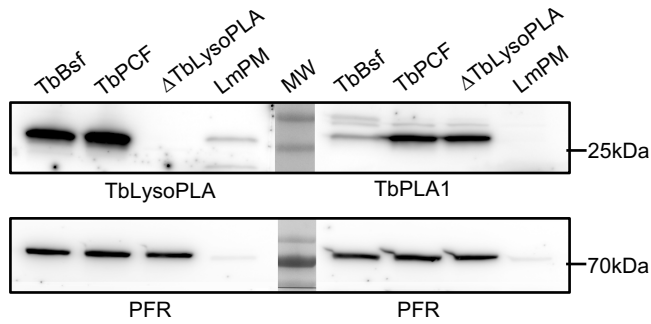
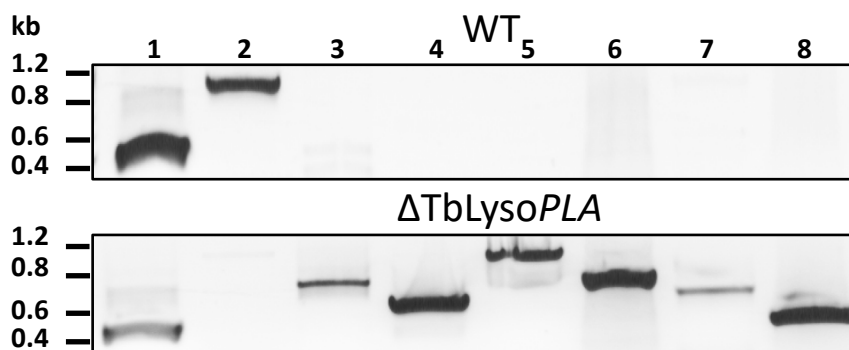


Fig S3

A



B

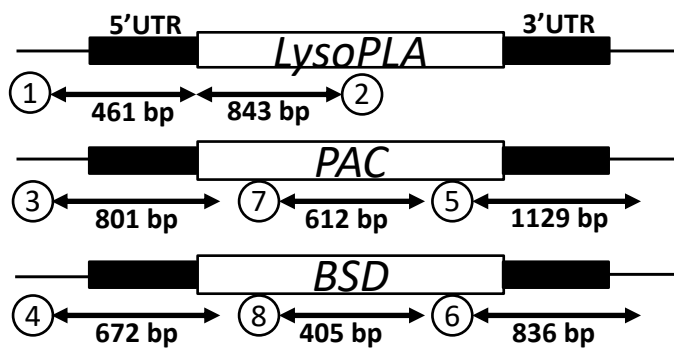


Fig S4

	TbLysoPLA	TbgLysoPLA	TevLysoPLA	TcoLysoPLA	TviLysoPLA	TcrLysoPLA	LmLysoPLA
TbLysoPLA	100						
TbgLysoPLA	99.64	100					
TevLysoPLA	99.64	99.64	100				
TcoLysoPLA	70.61	70.61	70.61	100			
TviLysoPLA	52.17	52.17	52.17	51.19	100		
TcrLysoPLA	62.86	62.50	62.50	63.44	54.33	100	
LmLysoPLA	53.82	53.82	53.82	53.28	43.60	57.61	100

Table S1

	TbLysoPLA	TbPLA1a	TcrPLA1	LbrPLA
TblysoPLA	100			
TbPLA1a	16.06	100		
TcrPLA1	16.29	20.83	100	
LbrPLA	18.27	17.25	37.50	100

Table S2

Name	Sequence	Purpose
PLA1bpGEXfw	AGCT <b>CGAG</b> ATGTTTGGCACGCCGGTTGAGAAT	Heterologous expression in E.coli
PLA1bpGEXfw	AGG <b>CGGCCGCTT</b> ACGATTTTCGATGAAGGTCCGGG	
PLA1bMDfw	TGCCGATTTCGCGCAAGGTGC	
PLA1bMDrev	GCACCTTGCGCGAATCCGGCA	
PLA1bRNAisens5p	GCA <b>AGCTT</b> ATGTTTGGCACGCCGGTTGA	Interference RNA
PLA1bRNAisens3p	GC <b>CTCGAGT</b> ACTCCATTCCTGAGCTCA	
PLA1bRNAiantisens5p	GCA <b>AGCTT</b> GAA <b>CTCGAG</b> AGACTTTTGAGGTAATTGGC	
PLA1bRNAiantisens3p	G <b>CTCTAGA</b> ATGTTTGGCACGCCGGTTGA	
PLA1b5UTRfw	GTTGTG <b>CCATGG</b> GTGCC <b>ATTA</b> ACTCAACTAT	Knock-out
PLA1b5UTRrev	CAACCG <b>GAATTC</b> CAAACATT <b>CTAG</b> ACAACCTTTCAGTGAGGTTTCGTAATG	
PLA1b3UTRfw	CCTTCAT <b>CTAGAT</b> CGTAA <b>CTCGAGT</b> GGAGTTGTAAGAAAGAGAGGTGAATG	
PLA1b3UTRrev	AACGG <b>GCCTT</b> ATAAT <b>GCAA</b> ACGTGTTTGGTGCTTGCTCCTACGGC	
PLA1bTyNterfw	GCA <b>AGCTT</b> ATGGAGGTCCATACTA <b>ACCA</b> AGATCCACTTGACGCCTTTGGCACGCCGGTTGAGAAT	Expression in Trypanosomes
PLA1bTyNterrev	GC <b>CTCGAGT</b> TACGATTTTCGATGAAGGTCCGGG	
PLA1bnoSKSrev	GC <b>CTCGAGT</b> TATGAAGGTCCGGGGAGGACTTGCT	
PLA1bSKLrev	GC <b>CTCGAGT</b> TACAATTTTCGATGAAGGTC	

In **bold**: restriction sites for cloning

Underlined: sequence TY tag

*Italic*: change to create a mutation

Table S3