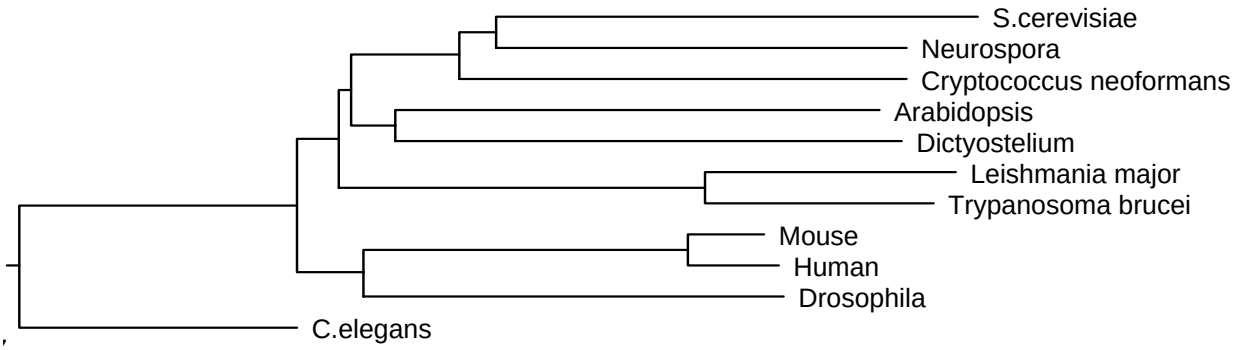
Figure S1.

Evolutionary tree depicting relationships amongst SPLs



An evolutionary tree amongst eukaryotic SPLs was constructed using the ClustalW algorithm as implemented in the DNAstar LaserGene package. Sequences used were Human (CAA09590), Mouse (AAH26135), *Drosophila melanogaster* (CAC10531), *Leishmania major* (AY770983) , *Trypanosoma brucei* (XP_826696), *Neurospora crassa* (XP_327047), *Saccharomyces cerevisiae* (AAB64470), *Cryptococcus neoformans* (EAL17929), *Caenorhabditis elegans* (AAD44756), *Arabidopsis thaliana* (AAM44962) and *Dictyostelium discoideum* (AAP37027).

The percent amino acid identity amongst these species may be found in the matrix below

Percent Identity

1	2	3	4	5	6	7	8	9	10	11		
	39.0	38.2	38.2	37.5	37.0	34.7	37.5	35.4	63.4	37.9	**1**	Leishmania major
		48.0	84.5	41.2	41.4	38.0	40.0	40.2	37.9	38.8	**2**	Mouse
			47.6	39.4	40.2	39.6	38.7	39.0	39.1	39.2	**3**	Drosophila
				43.1	42.2	36.1	38.5	39.6	37.7	38.8	**4**	Human
					37.3	36.3	42.3	40.5	38.6	40.8	**5**	Arabidopsis
						37.6	37.7	38.8	36.3	37.3	**6**	C.elegans
							37.8	45.5	36.3	42.5	**7**	S.cerevisiae
								38.4	38.7	38.9	**8**	Dictyostelium
									36.6	46.4	**9**	Neurospora
										37.7	**10**	Trypanosoma brucei
											11	Cryptococcus neoformans

Figure S2.
Alignment of *Leishmania* SPL with eukaryotic SPLS

Residues show to be essential when mutated in other eukaryotic SPLs are indicated by black triangles. A putative pyridoxal phosphate binding region is boxed. Residues identical in all 5 sequences are shaded and boxed (for specific sequence information see the legend to Fig. S1).

Fig. S3

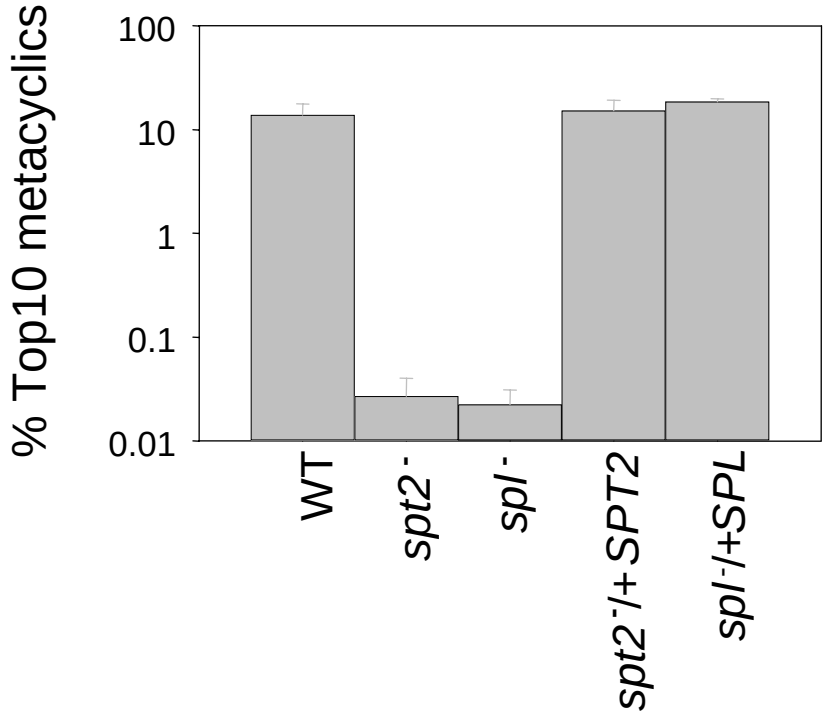


Fig. S3. *Spl*- and *spt2*- mutants are defective in metacyclogenesis. Promastigotes were grown to late stationary phase (three days after reaching maximum density) and the percentage of metacyclics was determined using the density centrifugation method and represented as “Top10 metacyclics”.

Fig. S4

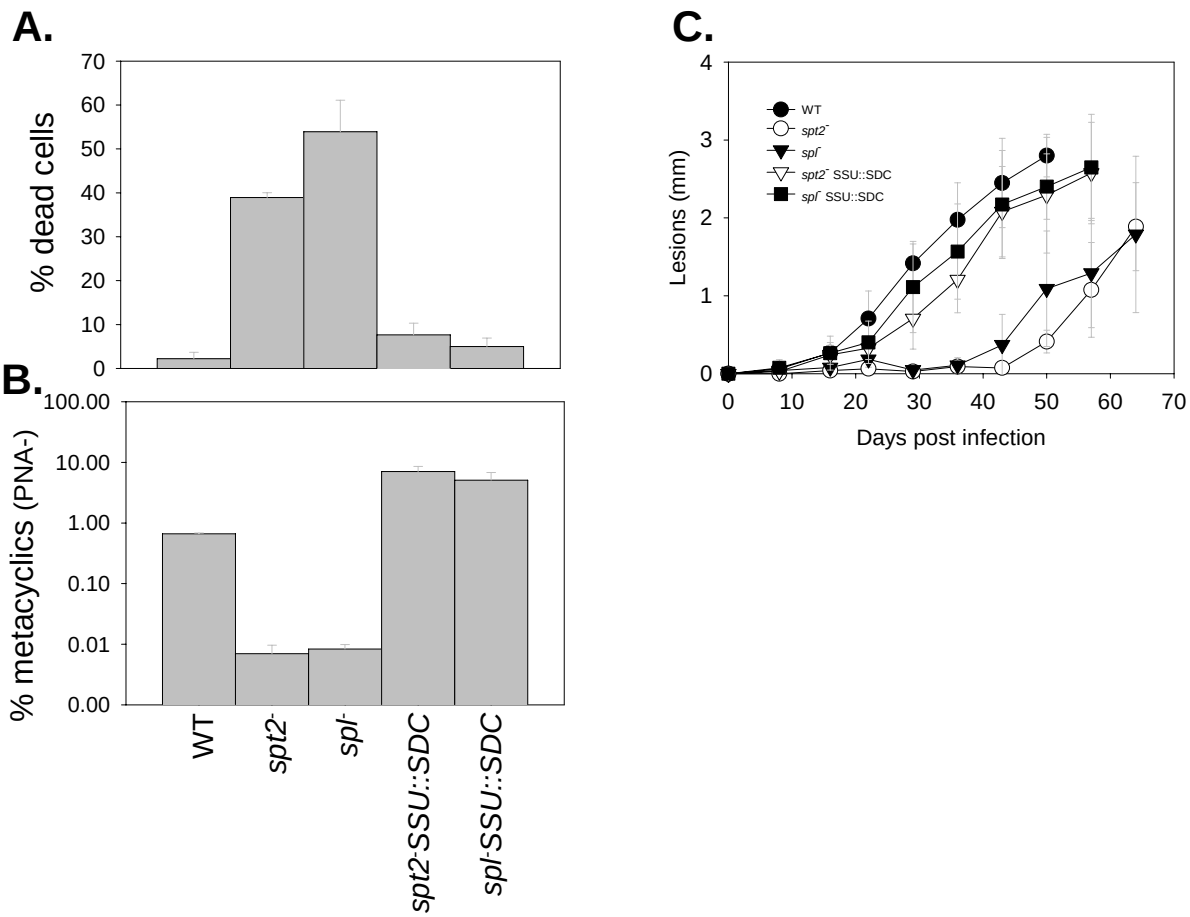


Fig. S4. Overexpression of serine decarboxylase (SDC) restores defects in *spt2*- and *spl*- mutants. WT, *spt2*-, *spl*-, *spt2*- *SSU::SDC*, and *spl*- *SSU::SDC* promastigotes were grown in M199 medium as described in *Materials and Methods*. Three days after entry into stationary phase, the percentage of dead cells (propidium iodide-positive) was determined by flow cytometry (**A**), and the percentage of metacyclics was determined using the peanut agglutination method (**B**). Stationary phase promastigotes were used to infect BALB/c mice at 1.0 x 10^6 cells/mouse and the progression of lesion is shown in (**C**). Error bars represent standard deviations.

Table S1. EtN rescues the defects of *spl*$^{-}$ and *spt2*$^{-}$ mutants.

	Density (#/ml)	% PI $^{+}$	% Top 10
WT control	2.8 x 10^{7}	5.12	13.8
WT + EtN	2.9 x 10^{7}	4.24	10.0
spt2^{-} control	7.4 x 10^{6}	38.0	0.32
spt2^{-} + EtN	2.8 x 10^{7}	11.6	19.5
spl^{-} control	7.3 x 10^{6}	49.5	0.29
spl^{-} + EtN	2.6 x 10^{7}	7.82	17.4

Promastigotes were grown to late stationary phase (three days after reaching maximum density) in the absence or presence of 0.5 mM EtN. Culture density was determined using a Coulter Counter; percentage of dead cells was determined by flow cytometry of parasites stained with propidium iodide (PI + %); and the percentage of metacyclics was determined using the density centrifugation method and represented as “Top10 metacyclics”.