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**Supplemental Information**

**Trypanosomatid Deoxyhypusine Synthase Activity  
Is Dependent on Shared Active-Site Complementation  
between Pseudoenzyme Paralogs**

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**Table S1. Role of active site residues, based on published mutational and structural analysis on hDHS (related to Figure 7).**

<b>TbDHSc:DHSp</b>	<b>hDHS</b>	<b>Role and/or mutation effect</b>
H377A-DHSc:DHSp <sup>^</sup>	H288-hDHS(Lee et al., 2001, Liao et al., 1998)	Proposed hydride acceptor in (Step 1, Fig. 2)
DHSc:DHSp-H266A <sup>^</sup>		
DHSc:DHSp-E103A <sup>#</sup>	E136-hDHS(Umland et al., 2004)	Required for binding of spermidine based on GC7 structure
E166A-DHSc:DHSp <sup>#</sup>		
D405A-DHSc:DHSp	D316-hDHS(Umland et al., 2004, Lee et al., 2001)	Required for spermidine binding; H-bond with amino group in GC7; possible catalytic base? (Step 2, Fig. 2)
DHSc:DHSp-E104A	E137-hDHS(Umland et al., 2004, Lee et al., 2001)	Required for spermidine binding; mutants are unable to bind spermidine or catalyze spermidine cleavage (Step 2, Fig. 2); NAD binding unaffected
DHSc:DHSp-D218A	D243-hDHS(Umland et al., 2004, Lee et al., 2001)	Prevents spermidine cleavage (Step 2, Fig. 2) due to lack of spermidine binding; NAD binding unaffected

**Table S2. Thermal stability of *Tb*DHSc:DHSp WT and mutants** (Related to Figure 7). The melting temperature ( $T_m$ ) of each enzyme was measured using a Thermal Shift Assay. All enzymes showed good thermal stability with  $T_m$  above 51°C. Errors represent standard deviation for 6 replicates.

<b>Sample</b>	<b><math>T_m</math> (°C)</b>
<i>Tb</i> DHSc:DHSp	56.0 ± 0.45
E166A-DHSc:DHSp	51.1 ± 0.66
DHSc:DHSp-E103A	56.1 ± 0.20
DHSc:DHSp-E104A	57.2 ± 0.61
DHSc:DHSp-D218A	57.6 ± 0.58
D405A-DHSc:DHSp	55.5 ± 0.84
DHSc:DHSp-H266A	57.4 ± 1.39
H377A-DHSc:DHSp	55.7 ± 0.41

