Supplemental Material

Fission yeast poly(A) polymerase active site mutation Y86D alleviates the *rad24*Δ *asp1-H397A* synthetic growth defect and upregulates mRNAs targeted by MTREC and Mmi1

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Supplemental Figures S1, S2, S3

Supplemental Tables S1 and S2 are separate .xlsx files

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Spo      TTKQWGITPPISTAPATEQENALNTALINELKNQNLFESPAESEKRVKVLDELQQITTEF  61
Sce      SQKVFGITGPVSTVGATAAENKLNDSLIQELKKEGSFETEQETANRVQVLKILQELAQRF  62

         .  ..  . . . .. ................. ..................   .
Spo      VKKVSLAKHMNEKMANEAGGKIFTYGSYRLGVYGPGSDIDTLVVVPKHVSRDNFFQDLEP  121
Sce      VYEVSKKKNMSDGMARDAGGKIFTYGSYRLGVHGPGSDIDTLVVVPKHVTREDFFTVFDS  122

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Spo      MLREREEVTDLAAVPDAYVPIIKFKFLGISIDLIFARLSVPRVPRDLELSDNNLLKGVEE  181
Sce      LLRERKELDEIAPVPDAFVPIIKIKFSGISIDLICARLDQPQVPLSLTLSDKNLLRNLDE  182

         . .  ..............   ... ...... .......... ..............
Spo      RCVLSLNGTRVTDQILQLVPNRAVFKHALRAIKFWAQRRAIYANVVGFPGGVAWAMMVAR  241
Sce      KDLRALNGTRVTDEILELVPKPNVFRIALRAIKLWAQRRAVYANIFGFPGGVAWAMLVAR  242

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Spo      ICQLYPNAVSSVIVAKFFRILHQWNWPQPILLKPIEDGPLQVRIWNPKLYPSDKAHRMPI  301
Sce      ICQLYPNACSAVILNRFFIILSEWNWPQPVILKPIEDGPLQVRVWNPKIYAQDRSHRMPV  302

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Spo      ITPAYPSMCATHNITLSTQTIILREMVRAGEIADQIMVKALPWSALFQKHDFFHRYKHYL  361
Sce      ITPAYPSMCATHNITESTKKVILQEFVRGVQITNDIFSNKKSWANLFEKNDFFFRYKFYL  362

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Spo      TITAAAKTAEAQ-LKWAGLVESKLRHLVTRLELVDAIALAHPFNKGFDKVYNCSSEEEAQ  420
Sce      EITAYTRGSDEQHLKWSGLVESKVRLLVMKLEVLAGIKIAHPFTKPFESSYCCPTEDDYE  422

          .              .  ..  .   ..       ..             . .. .....
Spo      QVASGVTLEVAYESTDHEKLANDTVNEEKADNTESKADGSENGEKQIFPVYTTTCYIGLE  480
Sce      MIQDKYGSHKTETALNALKLVTDENKEEESIKDAPKA-------------YLSTMYIGLD  469

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Spo      --LEKKKGHPIKRLDISWPTQEFYELCKKW--DKYDDTLMNVFIKNTKNTALPDEVFEPG  536
Sce      FNIENKK----EKVDIHIPCTEFVNLCRSFNEDYGDHKVFNLALRFVKGYDLPDEVFDEN  525

         . ..    ..   .  . .  ... .   .
Spo      EERPKATKKRSTADTAHSTEQLKRQKVSTA*                  566
Sce      EKRPSKKSKRKNLDARHET--VKRSKSDAASGDNINGTTAAVDVN*  568
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Figure S1. Primary structure alignment of the poly(A) polymerases of fission yeast *S. pombe* (Spo; Pla1) and budding yeast *S. cerevisiae* (Sce; Pap1). Positions of side chain identity/similarity are indicated by dots. Gaps in the alignment are denoted by dashes. The conserved Tyr86 and metal-binding Asp153 residues of Pla1 that were mutated in the present study are highlighted in cyan and yellow, respectively.

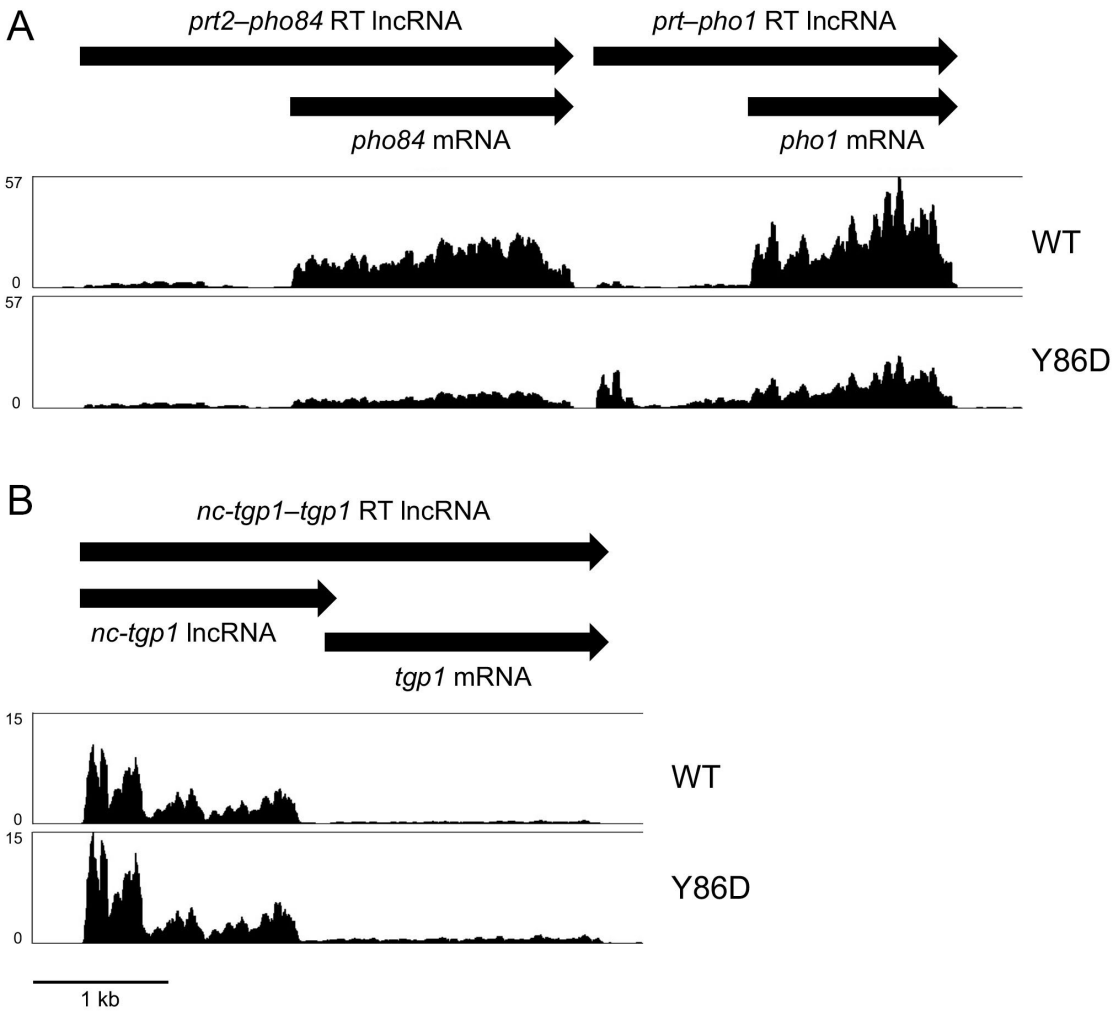

Figure S2. Strand-specific RNA-seq read densities (counts/base/million) from phosphate-replete *pla1*$^{+}$ wild-type (WT) or *pla1-Y86D* cells are plotted as a function of position across the *prt2-pho84–prt-pho1* (A) and *nc-tgp1-tgp1* (B) genomic loci. The common x-axis scale is shown on the bottom left. The RNA-seq read densities were determined from cumulative counts of three RNA-seq replicates. The mRNAs, lncRNAs, and RT (read-through) lncRNAs are shown as arrows in direction of their synthesis.

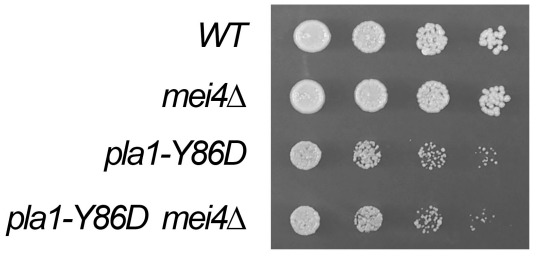

Figure S3. Deleting *mei4*$^{+}$ does not rescue the slow-growth phenotype of *pla1-Y86D*.