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1      10      20      30      40      50      60      70      80      90
MpPSAT MAAISVLSVVQEAAMALSSVPLVGNAGSLKSSVAMRSSFSGGTRLKA SCLKPRASCSAPGSLVTRCTA .TVFASSTAKSIDTANIDARVYNFAAGPATLLEAN
AtPSAT MAAITLNSF.....L VGSNNITQIA LKPKRS.SQSPLHLKSKPNVNFVSKTKPVAVRQVASTTQVQDGVRS GSVGSQB RVEYNFAAGPATLLEAN

100     110     120     130     140     150     160     170     180     190
MpPSAT VVVKQAQADLFNWRGSGMSVMEHRGKFFLSIIQKABADLRRLKLPENVEVLFLOGGASSQESAFIPNLCTPE DTADEFIVTGSWGDKAYKEAQKYCHAN
AtPSAT VVVKQAQADLVNWRGSGMSVMEHRGKFFLSIIQKABADLRRLKLPENVEVLFLOGGATLQESAFIPNLCKSDITVDFVVTGSWGDKAYKEAKKYCHAN

200     210     220     230     240     250     260     270     280     290
MpPSAT LLSFTGHPGKYTNLPSSEFTKLPFGAKFVHICANETIQGVFFRBYFNVGDAI LVADMSSNFCSKPVDSKFGVLIYGGVQRNIGHAGVIVTIIRKDLLGNAQ
AtPSAT VVWISGASEKYTKVPSFELEQDFEAKHLHICANETIHGVFFRBYFNPKNGFLVADMSSNFCSKPVDSKFGVLIYGGVQRNIGHAGVIVTIIRKDLLGNAQ

300     310     320     330     340     350     360     370     380     390
MpPSAT POFPTTFDYKIHAEENKSLYNTPPCFPIYVCGLVFDLLAQGGLEAAEERINIKASLLYDITEGNGEYKCFVEKSVRSLMNVFFTMQTE SLEAEFIKEAA
AtPSAT DIFPVLLDYKIHDENSLYNTPPCFPIYVCGLVFDLLAQGGLEAAEERINIKASLLYDITEGNGEYKCFVEKSVRSLMNVFFTEKSELEAEFIKEAA

400     410     420     430     440
MpPSAT AQCMLVQLKGRHSVGGVRSIYNAMPKAGVEKLVALLMSEQSKHSS
AtPSAT KEKMLVQLKGRHSVGGVRSIYNAMPKAGVEKLVALLMSEQSKHSA.

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1      10      20      30      40      50      60      70      80      90
MpPSP  M V C S G A L G A T G A I F C M R S Q G T L S R R L R S L Q P N L C H C S S A S F A L T N G A L F T S V A D Q R K A V G Q Q R L R V R A G A E E . E L D L V K A K S N I M . D P G V L D L W R N A E
AtPSP  . . . M E A L T T S R V V V . . . Q V P C R K I S E L F A N F S G L E R R Y P . . . C R G . . L V S I M N H P K L . . . . . L R P V T S V Q E H E L S T L G H E G N I V P S K E L L D L W R S V E

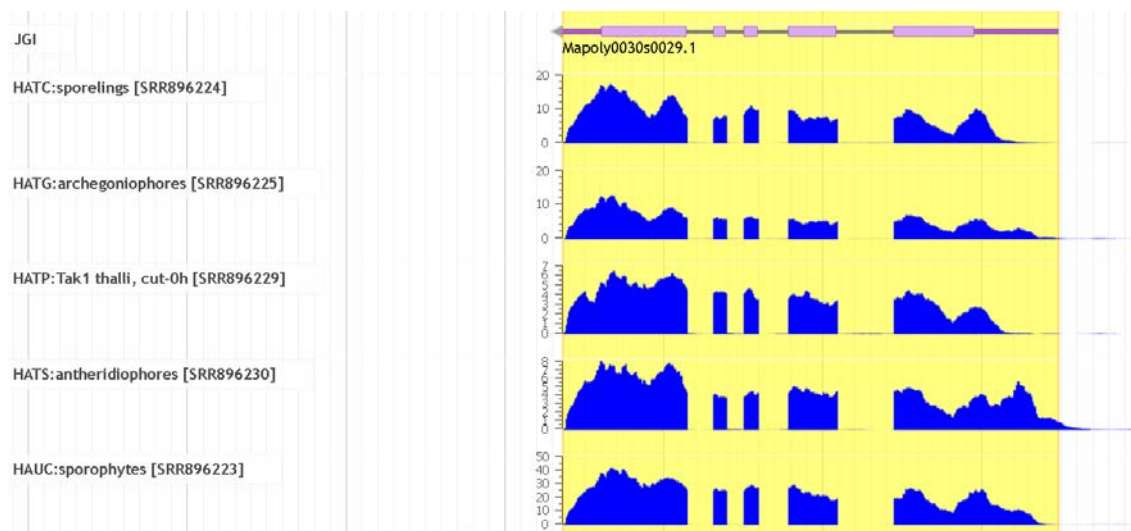
100     110     120     130     140     150     160     170     180     190
MpPSP  A V C F D V D S T V C E D E G I D E L A A F C G A G E A V A A W T A R A M G G S V P F E V A L A A R L D L F K P S A S D V A K L L A S K P P R L S T G L K D L V N K L H S K G T H V Y I V S G G F R O M
AtPSP  A V C F D V D S T V C V D E G I D E L A E F C G A G R A V A E W T A R A M G G S V P F E A L A A R L S L F K P S E S K V E E Y L D K R P P R L S P G I E L V K K L R A N N I D V Y E L S G G F R O M

200     210     220     230     240     250     260     270     280     290
MpPSP  I E F A A E L L N T S K D R I Y A N N L L F G E N G E F T G F D A T E P T S R S G G K A K V I E K I R A E F G Y T K L I M I G D G A T D L E A R R F G G A D M F I C Y G G V A V S P K V I E G S D V F V
AtPSP  I N F V A S I L G I P R E N I F A N N L L F G N S G E F L G F D E N E P T S R S G G K A K A V Q O I R K R G R I Y K T M A M I G D G A T D L E A R R F G G A D M F I C Y A G V O L R E A V A N A D N L L

300
MpPSP  T T T D L I N G L .
AtPSP  F K E S L I N S L D

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Supplementary Figure 1. Multiple amino acid sequence alignments of PSAT and PSP. Amino acid sequences of PSAT and PSP from *A. thaliana* (AtPSAT1 and AtPSP) and *M. polymorpha* (MpPSAT and MpPSP) were aligned.



Supplementary Figure 2. *In silico* expression analysis of *MpPGDH*.

The expression levels of *MpPGDH* (Mapoly0030s0029.1) are graphically indicated using MarpolBase (<http://marchantia.info/>).