SUPPLEMENTARY INFORMATION

Supplementary Table S1. Primers used in this study.

Primers used to construct protein expression vectors

AmtriPGDH1-F	AAAGCTTTGACTAGTGCGAAGCCCACGGTTTTGGTGGCGGAGAAG
AmtriPGDH1-R	CGGGCTTATGCGGCCCTACAAGTTGAGGAAAACAAACTCTTCAAC
AhPGDH-F	CAAAGCTTTGACTAGTGCAAAAGTTTTAGTTTCAGACTCTGTGGATC
AhPGDH-R	CGGGCTTATGCGGCCTTAGAGTTTAATGGTGTAAGCATCACGAATCCC
OsPGDH1-F	AAGCTCTTCAAAGCTTTGACTAGTGCCGTACCGGGGAAGCCGAC
OsPGDH1-R	CGGGCTTATGCGGCCCTAGAGCTTGAGGAAAAC
OsPGDH2-F	AAGCTCTTCAAAGCTTTGACTAGTGCGCTGTGGCCGAAGCCG
OsPGDH2-R	CGGGCTTATGCGGCCTCATAGCTCGAGGAAGAC
OsPGDH3-F	AAAGCTTTGACTAGTGGAAGGCCGACGGTGCTTGTGACGGAGAAG
OsPGDH3-R	CGGGCTTATGCGGCCCTAAAGCTTAATAAAGACAAACTCCTCAAC
PpPGDH2-F	AAAGCTTTGACTAGTAACCCTGATCTTGCTACCGTCTTGG
PpPGDH2-R	CGGGCTATGCGGCCTCAAAGCCGAAGAAACACCA
PpPGDH3-F	AAAGCTTTGACTAGTTCTGTAGCGAAGCCCACCGTGTTGG
PpPGDH3-R	CGGGCTTATGCGGCCTTACAGTTTGAGGAATACAAACTCC
PpPGDH4-F	AAAGCTTTGACTAGTAACCCCGATCTTGCCACTGTTCTCG
PpPGDH4-R	CGGGCTTATGCGGCCTCACAACTTCAAAAATACC

Primers used to construct complementation vectors

AmtriPGDH1-F	AGGAAACAGACCATGGCGAAGCCCACGGTTTTGGTGGCGGAGAAG
AmtriPGDH1-R	CTAGAGGATCCCCGGCTACAAGTTGAGGAAAACAAACTCTTCAAC
OsPGDH1-F	AGGAAACAGACCATGGCCGTACCGGGGAAGCCGACGGTGCTCGTGG
OsPGDH1-R	CTAGAGGATCCCCGGCTAGAGCTTGAGGAAAACGAATTCTTCAATCG
OsPGDH2-F	AGGAAACAGACCATGGCGCTGTGGCCGAAGCCGGCGGTGCTGGTGG
OsPGDH2-R	CTAGAGGATCCCCGGTCATAGCTCGAGGAAGACGAACTCCTCGATCG
OsPGDH3-F	AGGAAACAGACCATGGGAAGGCCGACGGTGCTTGTGACGGAGAAG
OsPGDH3-R	CTAGAGGATCCCCGGCTAAAGCTTAATAAAGACAAACTCCTCAAC
PpPGDH2-F	AGGAAACAGACCATGAACCCTGATCTTGCTACCGTCTTGGTGTCTG
PpPGDH2-R	CTAGAGGATCCCCGGTCAAAGCCGAAGAAACACCAGCTCTTCAATCG
PpPGDH3-F	AGGAAACAGACCATGTCTGTAGCGAAGCCCACCGTGTTGGTAGCTG
PpPGDH3-R	CTAGAGGATCCCCGGTTACAGTTTGAGGAATACAAACTCCTCCACGGC
PpPGDH4-F	AGGAAACAGACCATGAACCCCGATCTTGCCACTGTTCTCGTGGC
PpPGDH4-R	CTAGAGGATCCCCGGTCACAACTTCAAAAATACCAATTCACCAATGG

Primers used for site-directed mutagenesis experiments

AtPGDH1-N556A-F	GGAGAGTCTAATGTC**GCT**GTTAACTTCATGAGC
AtPGDH1-N556A-R	GCTCATGAAGTTAAC**AGC**GACATTAGACTCTCC
AtPGDH1-D538A-F	CTGTGCAGGCAGGTG**GCT**CAACCTGGTATGATC
AtPGDH1-D538A-R	GATCATACCAGGTTG**AGC**CACCTGCCTGCACAG
AtPGDH1-Q536A-F	ATCATACTGTGCAGG**GCT**GTGGATCAACCTGGT
AtPGDH1-Q536A-R	ACCAGGTTGATCCAC**AGC**CCTGCACAGTATGAT

Primer sequences are written in the 5′ to 3′ direction. Underlined, double-underlined, and bold sequences denote pPAL7 vector sequence, pTV118N vector sequence, and mutated codon sequences of AtPGDH1 for N556, D538, and Q536, respectively.

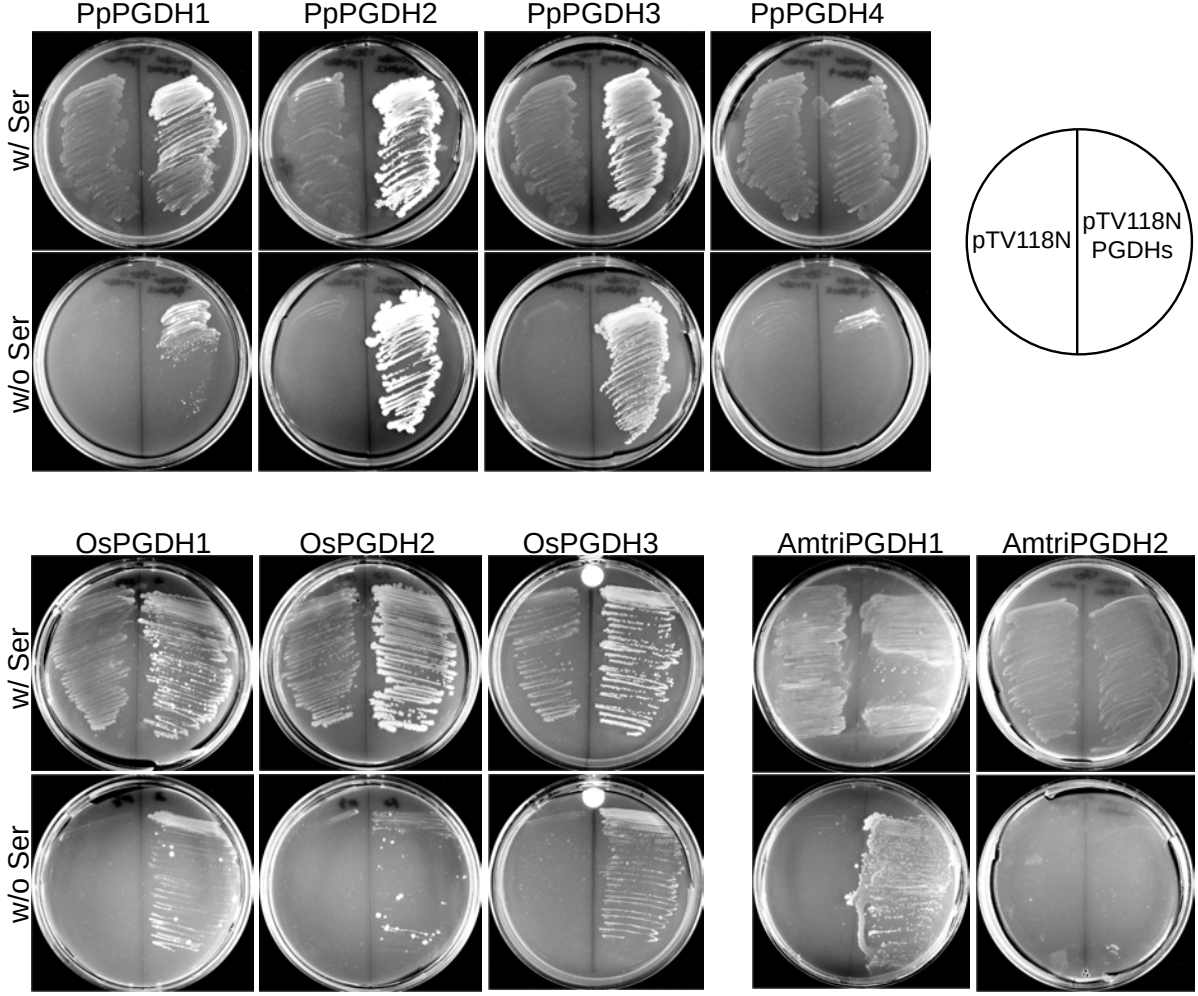


Figure S1. Complementation of a PGDH-defective *E. coli* mutant with *PGDH* cDNAs. *E. coli* strain JW2880 (TG1Δ*serA*::KmFRT) was transformed with the expression vector pTV118N carrying *PGDH* cDNAs (*PpPGDH1*, *PpPGDH2*, *PpPGDH3*, and *PpPGDH4* from *P. patens*; *OsPGDH1*, *OsPGDH2*, and *OsPGDH3* from *O. sativa*; *AmtriPGDH1* and *AmtriPGDH2* from *A. trichopoda*) or with the empty pTV118N as negative control. PGDHs without the transit peptide were used. The transformed *E. coli* were cultured on M9 minimal medium agar plates with or without L-serine.

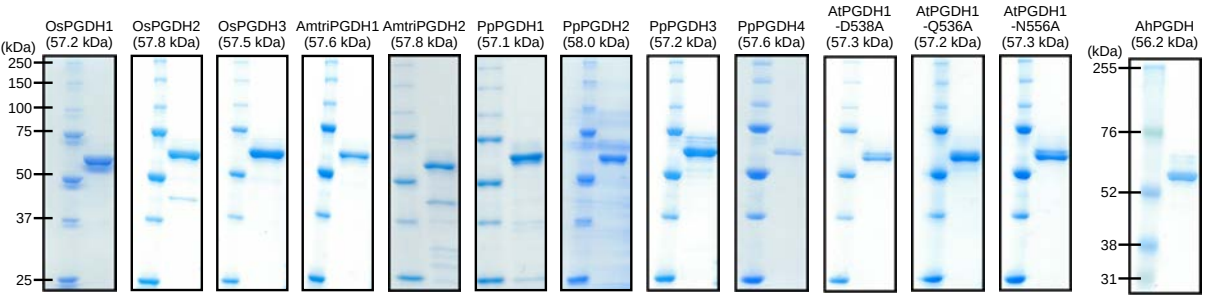
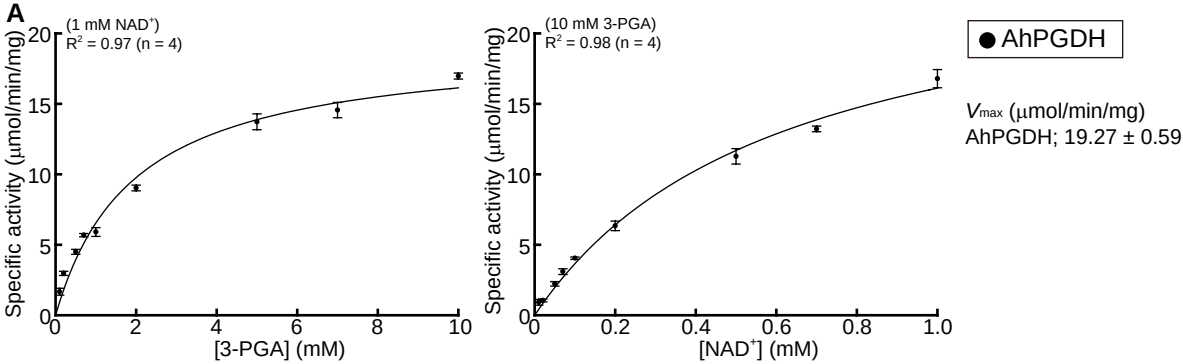


Figure S2. SDS-PAGE analysis of the recombinant PGDHs. The purified recombinant PGDH proteins were subjected to SDS-PAGE analysis (right lane) along with a molecular weight marker (left lane) and were stained with Coomassie Brilliant Blue. The theoretical molecular weight of PGDHs without the transit peptide are shown in parentheses.

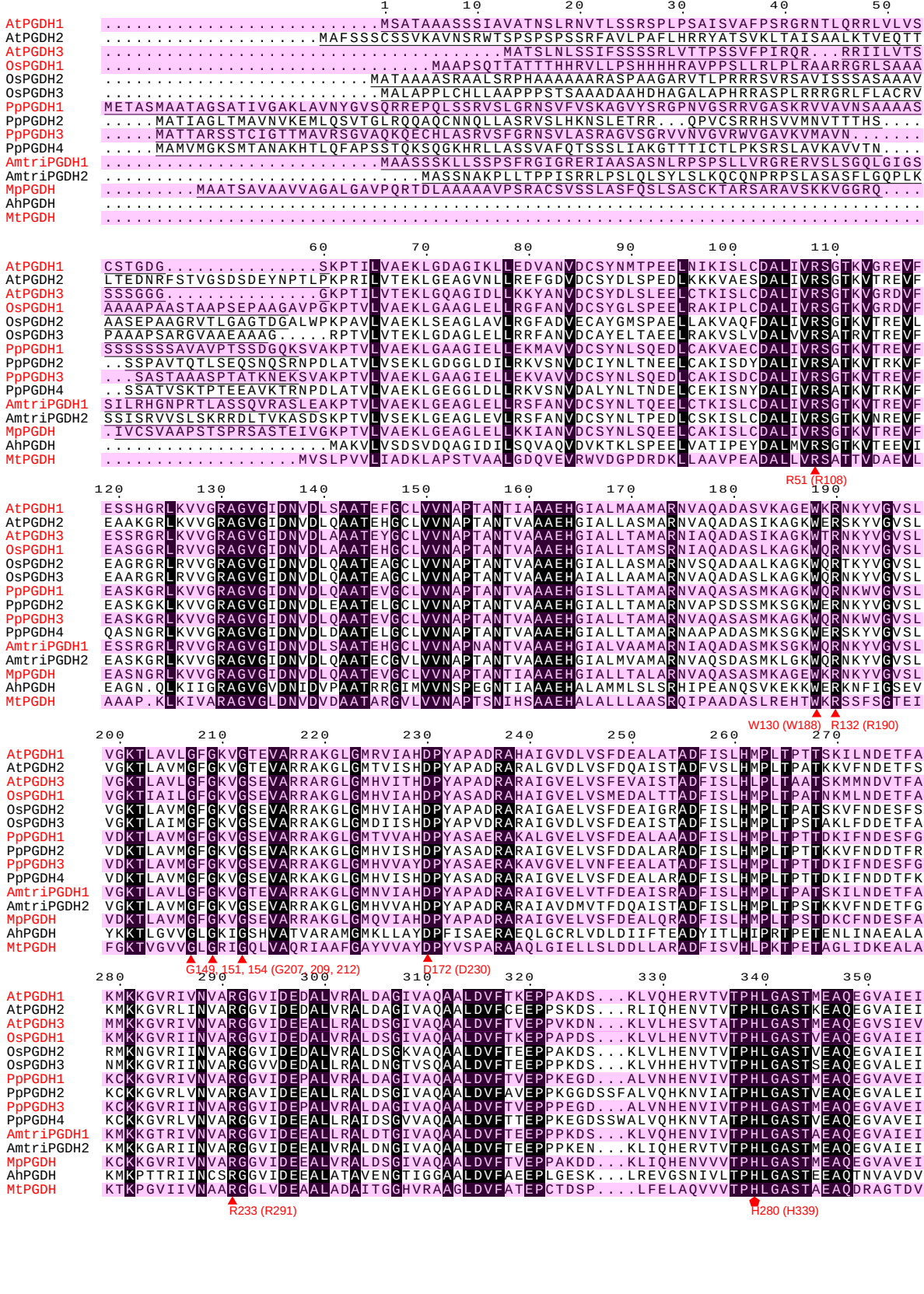
A



B

	k_{cat} (s^{-1})	K_m^{app} (mM)		k_{cat} / K_m ($M^{-1}\cdot s^{-1}$)	
		3-PGA	NAD^+	3-PGA ($\times 10^4$)	NAD^+ ($\times 10^5$)
AhPGDH	72.5 ± 2.25	1.94 ± 0.17	0.608 ± 0.069	3.73 ± 0.34	1.19 ± 0.14

Figure S3. Michaelis-Menten plot and kinetic parameters of AhPGDH. (A) Specific activities at various concentrations of 3-PGA (left) and NAD^+ (right) are shown. Data are presented as the means and standard error from two technical replicates, using enzymes purified from two independent batches of cells (n = 4). (B) Kinetic parameters of AhPGDH. The apparent Michaelis constants (Km^{app}) were calculated from Fig. S3A. Standard errors (SE) are shown.


AtPGDH1
AtPGDH2
AtPGDH3
OsPGDH1
OsPGDH2
OsPGDH3
PpPGDH1
PpPGDH2
PpPGDH3
PpPGDH4
AmtriPGDH1
AmtriPGDH2
MpPGDH
AhPGDH
MtPGDH
R51 (R108)
W130 (W188)
R132 (R190)
G149, 151, 154 (G207, 209, 212)
D172 (D230)
R233 (R291)
H280 (H339)

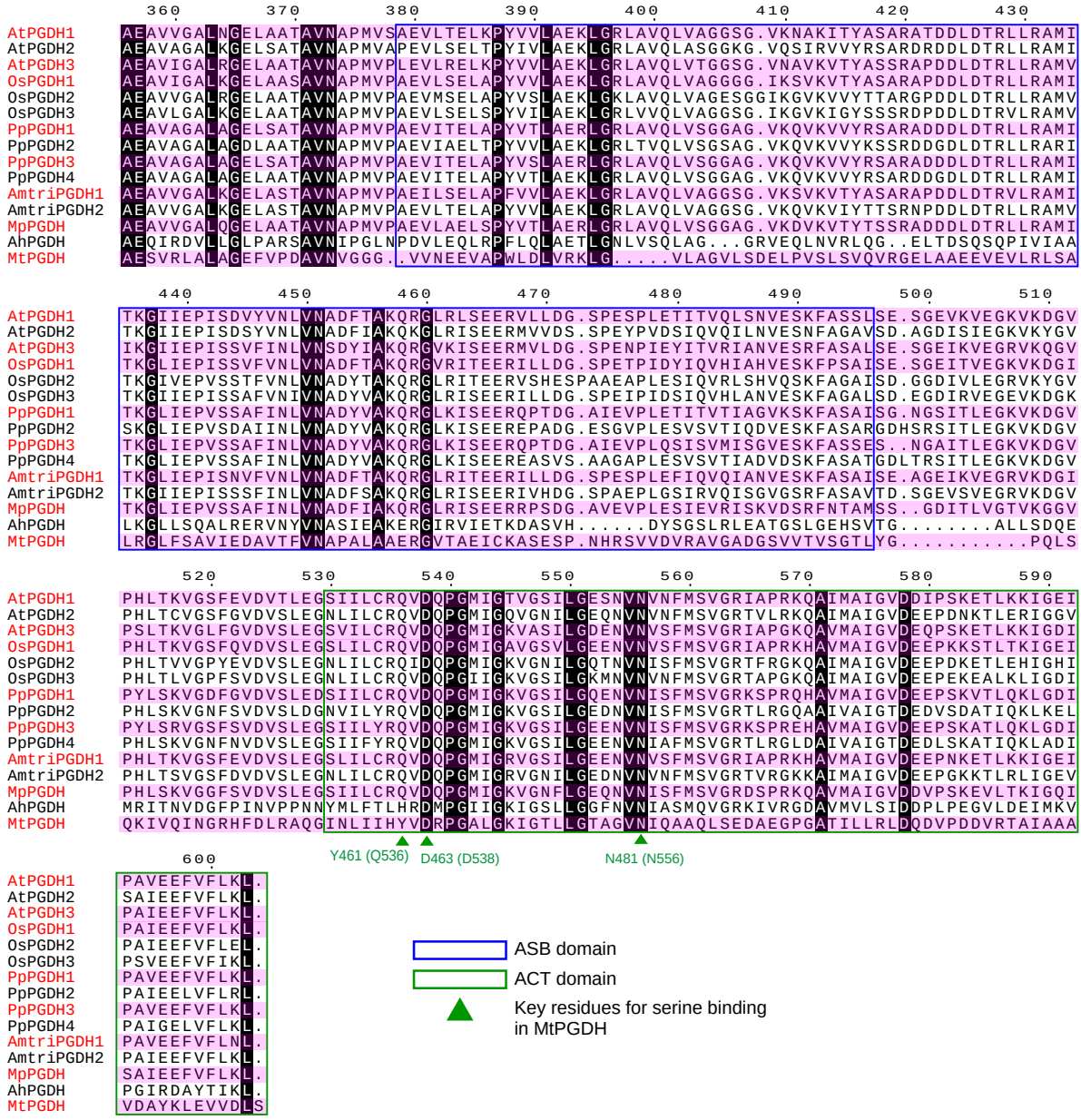


Figure S4. Multiple sequence alignments of full-length amino acid sequences of PGDH isozymes. The full-length amino acid sequences of PGDHs from *A. thaliana* (AtPGDHs), *O. sativa* (OsPGDHs), *A. trichopoda* (AmtriPGDHs), *P. patens* (PpPGDHs), *M. polymorpha* (MpPGDH), *A. halophytica* (AhPGDH), and *M. tuberculosis* (MtPGDH) are shown. Isozymes regulated by all six effector amino acids are highlighted by red font and pink shading. The predicted transit peptides are underlined. The predicted ASB domains and ACT domains are surrounded by blue and green rectangles, respectively. Green triangles, red triangles and red pentagon with number represent key residues for serine binding, substrate binding and active site histidine in MtPGDH, respectively. Correspound residues on AtPGDH1 are also shown in parentheses.

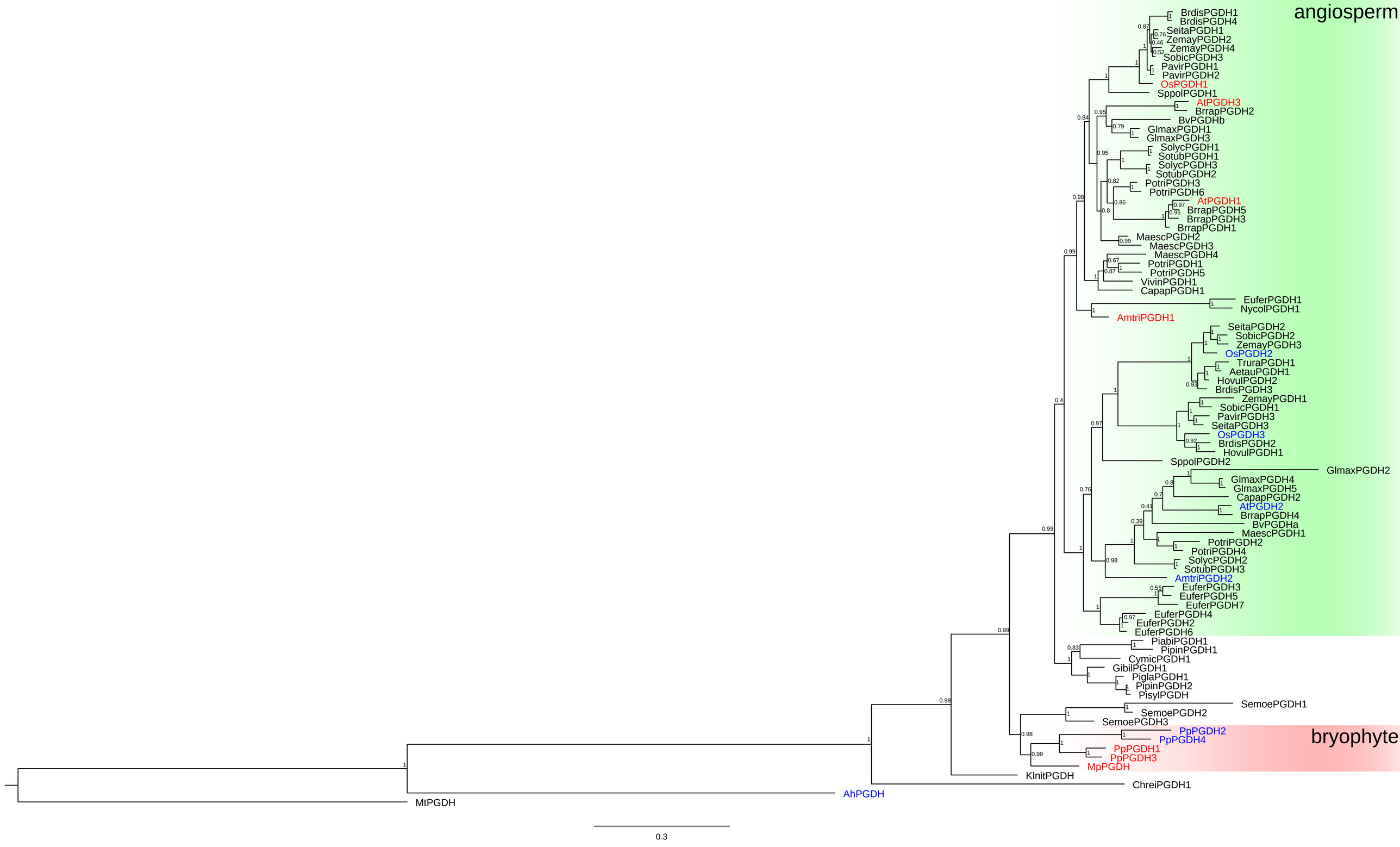

angiosperm
BrdisPGDH1
BrdisPGDH4
SeitaPGDH1
ZemayPGDH2
ZemayPGDH4
SobicPGDH3
PavirPGDH1
PavirPGDH2
OsPGDH1
SppolPGDH1
AtPGDH3
BrrapPGDH2
BvPGDHb
GlmaxPGDH1
GlmaxPGDH3
SolycPGDH1
SotubPGDH1
SolycPGDH3
SotubPGDH2
PotriPGDH3
PotriPGDH6
AtPGDH1
BrrapPGDH5
BrrapPGDH3
BrrapPGDH1
MaescPGDH2
MaescPGDH3
MaescPGDH4
PotriPGDH1
PotriPGDH5
VivinPGDH1
CapapPGDH1
EuferPGDH1
NycolPGDH1
AmtriPGDH1
SeitaPGDH2
SobicPGDH2
ZemayPGDH3
OsPGDH2
TruraPGDH1
AetauPGDH1
HovulPGDH2
BrdisPGDH3
ZemayPGDH1
SobicPGDH1
PavirPGDH3
SeitaPGDH3
OsPGDH3
BrdisPGDH2
HovulPGDH1
SppolPGDH2
GlmaxPGDH2
GlmaxPGDH4
GlmaxPGDH5
CapapPGDH2
AtPGDH2
BrrapPGDH4
BvPGDHa
MaescPGDH1
PotriPGDH2
PotriPGDH4
SolycPGDH2
SotubPGDH3
AmtriPGDH2
EuferPGDH3
EuferPGDH5
EuferPGDH7
EuferPGDH4
EuferPGDH2
EuferPGDH6
PiabiPGDH1
PipinPGDH1
CymicPGDH1
GibilPGDH1
PiglaPGDH1
PipinPGDH2
PisylPGDH
SemoePGDH1
SemoePGDH2
SemoePGDH3
PpPGDH2
PpPGDH4
PpPGDH1
PpPGDH3
MpPGDH
bryophyte
KlnitPGDH
ChreiPGDH1
AhPGDH
MtPGDH
0.3

Figure S5. Phylogenetic tree of PGDHs across multiple plant lineages. Amino acid sequences of PGDHs from eudicots, monocots, basal angiosperms, gymnosperms, lycophyte, bryophytes, charophyte, chlorophyte, cyanobacterium, and actinobacterium were obtained from databases (Supplementary Table S2). Red and blue letters indicate the isozymes sensitive to six effector amino acids and those insensitive or sensitive to some effectors, respectively. Posterior probabilities are indicated at the nodes. Bar indicates substitutions per site.