

Supplementary material

Table S1. Primers used in this study

Primer name	Sequence	Use
DHPS1For	5'-CCAGGATATACCTCCCCAGGTTAT-3'	RT-PCR
DHPS1Rev	5'-ATATCACTCCAGTGGCACCGTG-3'	RT-PCR
DHPS2For	5'-CAAGATATACCGCCTCGTGCC-3'	RT-PCR
DHPS2Rev	5'-GATTCCAATCGGGTTTGGCTCG-3'	RT-PCR
017267-LP	5'-TCTCTGTTCTGGAAGTTTATGCCA-3'	PCR genotyping
017267-RP	5'-AACCTAAAAACCGCCTCGAA-3'	PCR genotyping
017267-LP1	5'-TGCCATACCTGGAAGTTGTTTTG-3'	PCR genotyping
017267-RP1	5'-CATGCGTGCCGTTTCTATCTC-3'	PCR genotyping
147470-LP	5'-TGGCAGGACAAACACAGACGA-3'	PCR genotyping
147470-RP	5'-TGCTCCCTTCCGATTTCTTC-3'	PCR genotyping
147470-LP1	5'-ATCACAGCCATTAAGACACCG-3'	PCR genotyping
147470-RP1	5'-CACAACCAATCTTCAGGGAAG-3'	PCR genotyping
LBb1	5'-GCGTGGACCGCTTGCTGCAACT-3'	PCR genotyping
LBb1.3	5'-ATTTTGCCGATTTTCGGAAC-3'	PCR genotyping

Table S2. Comparison of DHDPS1 and DHDPS2 at un-conserved sites

Difference	Identity			Conservative replacement		
	DHDPS1	DHDP2	Consensus	DHDPS1	DHDP2	Consensus
1	D77	V78	V	D77	V78	V
2	R87	K88	K	R87	K88	K
3	S88	A89	None	S88	A89	None
4	Q84	E85	E	Q84	E85	E
5	T92	I93	M	T92	I93	M
6	E95	Q96	Negative	E95	Q96	Negative
7	R132	S133	Positive	R132	S133	Positive
8	M158	V159	V	M158	V159	V
9	G162	A163	A	G162	A163	A
10	M179	L180	L	M179	L180	L
11	N180	I181	Nonpolar	N180	I181	Nonpolar
12	T185	S186	Hydroxyl	T185	S186	Hydroxyl
13	C202	G203	G	C202	G203	G
14	Q208	R209	None	Q208	R209	None
15	V209	A210	V	V209	A210	V
16	M217	L218	Nonpolar	M217	L218	Nonpolar
17	N227	K228	Negative	N227	K228	Negative
18	K235	N236	K	K235	N236	K
19	I237	V238	I	I237	V238	I
20	Q246	E247	E	Q246	E247	E
21	H254	Y255	Y	H254	Y255	Y
22	A282	S283	None	A282	S283	None
23	A285	S286	None	A285	S286	None
24	D292	A293	Charged	D292	A293	Charged
25	Q296	H297	None	Q296	H297	None
26	V303	I304	L	V303	I304	L
27	A313	S314	Nonpolar	A313	S314	Nonpolar
28	I330	L331	Nonpolar	I330	L331	Nonpolar
29	D347	E348	Negative	D347	E348	Negative
30	R348	K349	Positive	R348	K349	Positive
31	V352	A353	V	V352	A353	V
	13%	29%		61%	65%	

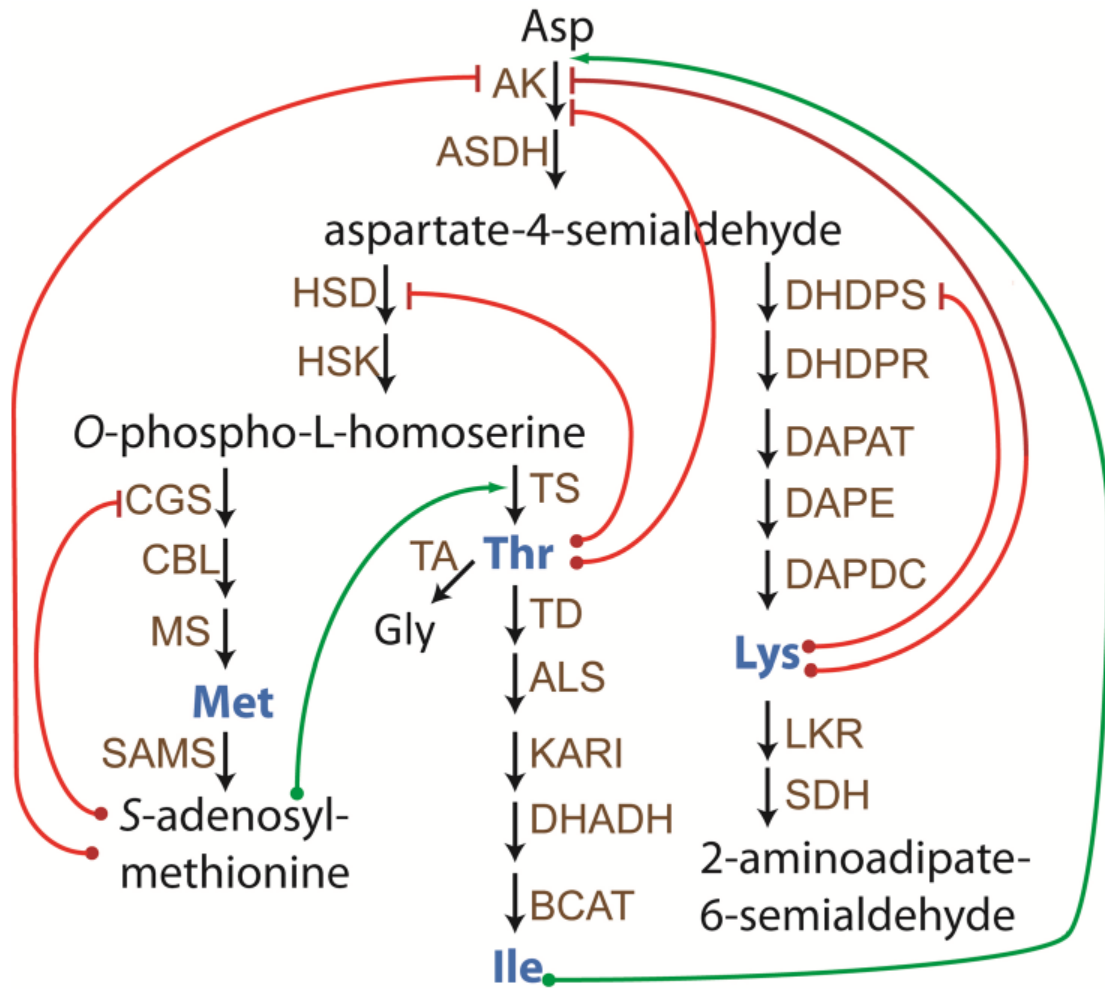


Fig. S1. The aspartate family pathway.

Analysis of SALK_147470 TDNA insertion site in At3g60880 (*DHDPS1*)

22495066 ttaatttagy gttttgaaag ATGTCAGCTT TGA AAAAATTA CGGCTTGATC TCCATTGATT
22495126 CTGCCCTCCA TTTTCCTCGA TCAAAATCAAT TGCCAGAGCTA TAAGAGgtta ctcctctctct
22495186 cctctctctct cctctatgctt aactcttattg ggattatagt tactgggtatt ggatttgggtt
22495246 tgcagcagctc tctatgtgtaa ttgaaatctt tgtatccacag gtgagaacaat gaatatattg
22495306 ctttgggttac taaagcaata actttttctct ttgaaagaatc ggatttggtag ttgtgtttat
22495366 actctgttgat cgtattggcta gattaatgct tagacattgc cttatgatct ctgagtgtat
22495426 gatattattg ctcacaaac cagaagGAAT GCAAAATGGG TCTCTCCAAT AGCAGCTGTT
22495486 GTACCTAATC TCCATCTTCC TATGGGCAGT CTCGAGGATA AAAACAGgtg catctctctat
22495546 tctctctctct tcttctctctt gtttttggctt atactctcagc agctctctctt tgtatttttgg

5'-tgggcagg acaaacacag acga-3' 147470-LP 5'-atcacag ccattaagac
22495606 tggttggcagG ACA AACACAG ACGACATAAG GTCCTTAGA GTGATCACAG CCATTAAGAC

acog-3' 147470-LP1
22495666 ACCCTAITTA COTGATGGAA GATTCGACTC CCAAGCATAc GATGACTTAG TCAACACGCA
22495726 GATAGAAAAC GGTGCTGAAG GTGTGATTGT TGGTGGTACA ACTGGTGAAG GCCAAITGAT
22495786 GAGCTGGGAT GAGCACATAA TGCTTATCGG CCATACTGTA AATTGTTTTG GGGGAAGGAT
22495846 CAAAGTCATT GGAAACACTG GAAGTAACTC GACTAGGGAA GCTATTCTATG CCACCTGAGCA
22495906 AGGATTCCGC ATGGGAATGC ACGGGGCACCT GCACATTAAc CTTACTACTAT GAAAACACATC
22495966 CATTGAAGGC ATGAAATGGCG ATTTTCAAAC CGTCTTTCAT ATGGGAACCGA CTATTATATA
22496026 CAACTGGCCA GGTGGRACGT GCCAGGATAT AACTCCCCAG GTTATCTTTA AACTCTCTCA

Confirmed insertion site SALK_147470 TDNA ↓→
22496086 GAACCCATAT ATGGCTGGGG TTAAGGAATG CGTTGGTAAT AACCGAGTTG ARGAGTATAc
AGTTG AAGAGTATAc...
R V E E Y T
229/364

SIGNAL reported insertion site SALK_147470 TDNA ↓→
22496146 TGAGAAGGGA ATTGTCTGTTT GGAGTGGAAA TGATGATCAG TGCCATGATT CTAGATGGGA
A

22496206 TCACGGTGGC ACTGGAGTGA TATCGGTTAC TAGCAATTTA GTTCCGGGTT TGATGAGGAA
TCACGGTGGC ACTGGAGTGA TATC...

22496266 GTTGATGTTT GAAGGTAGAA ACTCAGCGTT GAACGCAAAg CTTCTTCTT TAATGGATTG
22496326 GCTATTCCAA GAACCGAATC CCATTGGTGT AAACACTGCT TTGGCTCAGT TAGGAGTTGC
22496386 GAGGCCGGTT TTTGGTTTAC CTTATGTGCC ATTGCTCTCG TCCAAAAGGA TTGAGTTCTGT
22496446 TAAACTGGTG AAGGAAATCG GARGGGAGCA TTTTGTAGGA GACAGAGATG TTCAGGTACT
3'-c ttccttttagc cttccctctgt-5' 147470-RP

22496506 TGATGATGAT GACTTCATCT TAATCGGTCG ATATTAGagt cttctccctg aagatttgggt
3'-gaaggagc ttctaaacaa

22496566 ggttttatac tttctctggtt cagttgtttag ttatttagct gatgagaaac tcacagatgg
cac-5' 147470-RP1

Analysis of SALK_017267 TDNA insertion site in At2g45400 (*DHDPS2*)

18731274 gttcctggtt gttttcaaaG ATGGCTGCTT TGA AAGGTTA TGGCTTGTGT TCTATGGACT
18731334 CTGCTCTTCA ATTCOCCTGT CTAARGCTAT TCAATAGCTA CAAGAGgtta tctctctctct
18731394 cctctcatatt ttgcagacat ataacgtttt gctcaagctt ttgtgtgttt ttgttattcc
18731454 aagctagggca taataaatctc tggaaatggc ttgaaatagtc agtccactgct tagttgaaat
18731514 tgaatgttag ttgtcttaga ttgaaagcta ttgattcaat ggtgattctg tcgtaaacct
18731574 gttctaatgta aatttgcact tgaatgtttc tggtttggat ttgaaaaact attacttctct
18731634 ttgtctaatc atatagaaag acttcagttt tataaaaaa gttgcttttt tttcttaca
18731694 ttgagcagta ttgactcaaG ctcactgtgt ttgtttaaacc agAAGCACTC CGAAATGGGT
18731754 CTCTCCCAA GCAGCTGTTG TACCCAATT CCATCTCCCA ATGGCCAGCT TGGAGGTTAA
18731814 AAACAGgtct gtcagataga gtttagctgg accaaagctta tatgattgta caatctcata

5'-tgc catacctgga actgtttttg-3' 017267-LP1
5'-tc tctgttttgg aagtttatgc ca-3' 017267-LP
18731874 gtataatact cctgttctgg aagtttatgc catacctgga actgtttttg tttttgtgct
18731934 tgtcagGACA AACCACGAGC ACATTAAGC TCTACGTGTG ATCACAGCTA TCAAAACACC
18731994 GTATCTACCT GATGGAGAT TCGACTTGA AGCCTACGAT GACTTGGCTA ACATTGAGAT
18732054 ACAAAACGGT GCTGAAGGTT TCATTGTTGG TGGTACAAC TGGTAAGGAC AACTGATGAG
18732114 CTGGGAGCAA CACATTATGC TTATAGGCCA TACCGTTAC TGTTTTGGCG GAAGCATCAA
18732174 AGTCATTGGA AACACTGGAA GCAATTCGAC TAGAGAAGCA ATCCACGGCA CTGAACAAGG
18732234 ATTCGCGGTT GGAATGCAAT CTGCTCTTCA TATAAACCT TACTATGGCA AGACTTCTAT
18732294 TGAGGGACTG ATTCACATT TCCAGTCTGT TCTTCATATG GGACCGAGCA TTATATACAA
18732354 TGTGCTGTGT CGAACAGGGC AAGATATACC GCTCTGTGOC ATOTTCAAAC TTTCTCAGAA

SALK_017267 TDNA ↓→
18732414 TCCGAATTTA GCTGGTGTGA AGGAATGTGT TGGCAACAAG CGAGTCGAAg AGTACACTGA
SIGNAL reported insertion site SALK_017267 TDNA TCGAAG AGTACACTGA...
Confirmed insertion site SALK_017267 TDNA TCGAAG AGTACACTGA...
PROTEIN SEQ _LV E E Y T E_
230/365

18732474 GAATGGGGTT GTTGTGTGGA GTGGAAATGA TGATGAGTGT CATGATTCCA GATGGGATTA
18732534 TGGAGCAACA GGAGTTATAT CAGTACTAGT TAAITTAGTT CCGGGTTTGA TGAGGAAGTT
18732594 GATGTTGAA GGTAGGAATT CACTTTTGA CCAAAAGCTT CTAACCTTGA TGGCTTGGCT
18732654 GTTCCACGAG CCAAAACCGA TTGGAATCAA CACTGCTTTG GCTCAGCTTG GAGTTTCGAG
3'-aagctc
18732714 GCGGTTTTT AGSITACCAT ATGTACCATT GOCAGTGTCT AAGAGGCTTG AGTTTGTGAA
cggccaaaaa tccaa-5' 017267-RP

18732774 ACTGCTCAAG CAGATTGGAC CAGACCAATT TGTGGCTGAG AAAGATGTTc AGCCTCTTGA
18732834 TGATGATGAT TTTATCTTAA TCGGTCGATA TTAGcactact tttttttttt taattttttg
18732894 ttcctttttt ttgtgtgtta atgaagaaga gatggttcta tcaatttgggt ttatgtagctt
18732954 gatgaatgaa tgaaaactca agaatgatt ccatcatatt tcttagcttg ttttggctctc
18733014 ttctctcttt ttactctgtt tttactctgt tttacggttg cctcaaaagga gggagataga
3'-ctctatct

18733074 aacggcagcc aTgtttgata atattgtttg aaacagcatg gctttgcaat ctggaaagcg
ttgcctgtgog tac-5' 017267-RP1

Fig. S2. Positions of TDNA insertions in *DHDPS1* and *DHDPS2*.

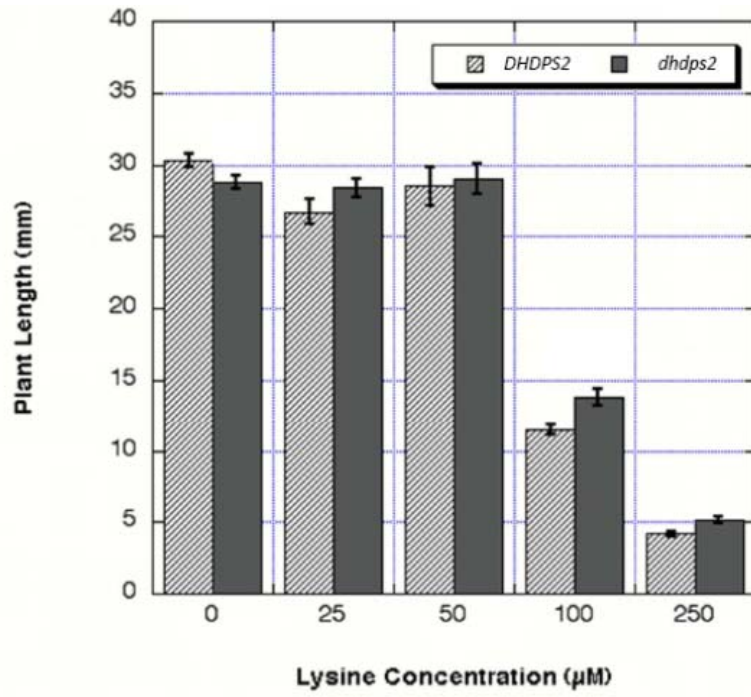


Fig. S3. Root length of Arabidopsis seedlings grown with supplemental Lys.

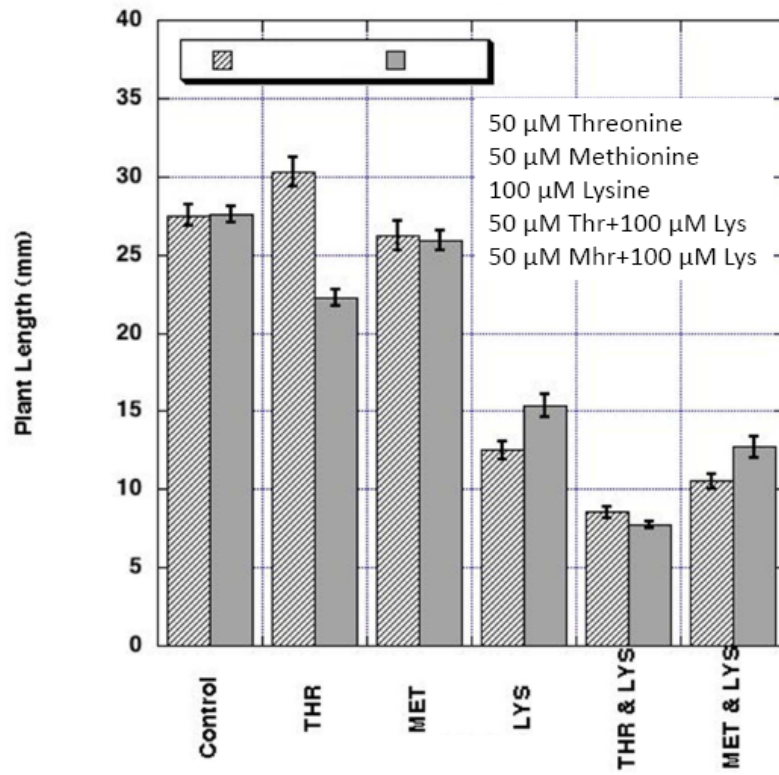


Fig. S4. Root length of Arabidopsis seedlings grown with supplemental Lys, Thr and Met.

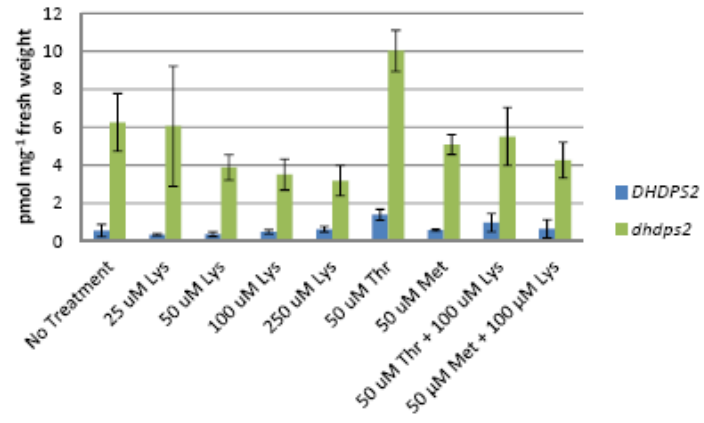
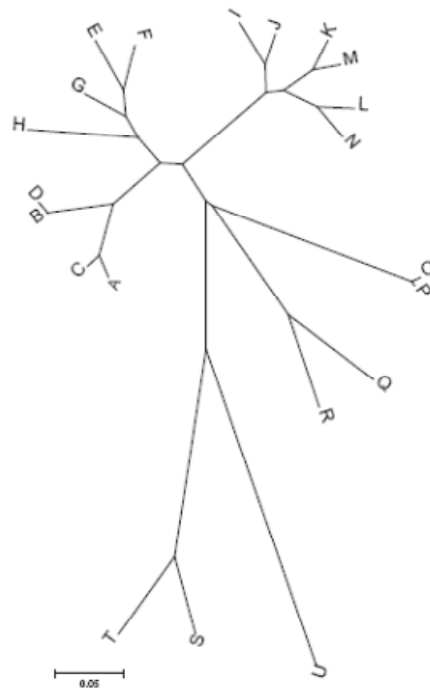


Fig. S5. Thr level in Arabidopsis seedlings grown with supplemental Lys, Thr and Met.

Supplementary
Figure 6A.



- A=>gi|15232971|ref|NP_191647.1| dihydrodipicolinate synthase DHPS1 [Arabidopsis thaliana]
 B=>gi|15225477|ref|NP_182068.1| dihydrodipicolinate synthase DHPS2 [Arabidopsis thaliana]
 C=>gi|297817410|ref|XP_002876588.1| dihydrodipicolinate synthase 1 [Arabidopsis lyrata subsp. lyrata]
 D=>gi|297824595|ref|XP_002880180.1| dihydrodipicolinate synthase 2 [Arabidopsis lyrata subsp. lyrata]
 E=>gi|224127414|ref|XP_002320068.1| predicted protein [Populus trichocarpa]
 F=>gi|224063919|ref|XP_002301301.1| predicted protein [Populus trichocarpa]
 G=>gi|255561405|ref|XP_002521713.1| dihydrodipicolinate synthase, putative [Ricinus communis]
 H=>gi|225453935|ref|XP_002279840.1| PREDICTED: dihydrodipicolinate synthase 2, chloroplastic [Vitis vinifera]
 I=>gi|115457444|ref|NP_001052322.1| Os04g0254000 [Oryza sativa Japonica Group]
 J=>gi|115460042|ref|NP_001053621.1| Os04g0574800 [Oryza sativa Japonica Group]
 K=>gi|242076866|ref|XP_002448369.1| hypothetical protein SORBIDRAFT_06g026060 [Sorghum bicolor]
 L=>gi|242093822|ref|XP_002437401.1| hypothetical protein SORBIDRAFT_10g026260 [Sorghum bicolor]
 M=>gi|226493858|ref|NP_001148623.1| dihydrodipicolinate synthase 2 [Zea mays]
 N=>gi|162462912|ref|NP_001105425.1| dihydrodipicolinate synthase, chloroplastic precursor [Zea mays]
 O=>gi|302802285|ref|XP_002982898.1| hypothetical protein SELMODRAFT_117275 [Selaginella moellendorffii]
 P=>gi|302800325|ref|XP_002981920.1| hypothetical protein SELMODRAFT_179125 [Selaginella moellendorffii]
 Q=>gi|168007999|ref|XP_001756695.1| predicted protein [Physcomitrella patens subsp. patens]
 R=>gi|168026205|ref|XP_001765623.1| predicted protein [Physcomitrella patens subsp. patens]
 S=>gi|159483379|ref|XP_001699738.1| dihydrodipicolinate synthase [Chlamydomonas reinhardtii]
 T=>gi|302831141|ref|XP_002947136.1| dihydrodipicolinate synthase [Volvox carteri f. nagariensis]
 U=>gi|145346467|ref|XP_001417708.1| predicted protein [Ostreococcus lucimarinus CCE9901]

A/1-364 154 GFAMGMHGALHI NPYYGKTS EGMNAHFQTVLHMGPPTI YNVPGRTCQDI PPQVIFKLSRQ
 C/1-365 155 GFAMGMHGALHI NPYYGKTS EGMTAHFQTVLHMGPPTI YNVPGRTSQDI PPQVIFKLSR
 B/1-365 155 GFAVGMHAALHI NPYYGKTS EGLIAHFQSVLHMGPPTI YNVPGRTGQDI PPRALF KLSRQ
 D/1-365 155 GFAVGMHAALHI NPYYGKTS EGLIAHFQSVLHMGPPTI YNVPGRTGQDI PPRALF KLSRQ
 E/1-363 152 GFAVGMHAALHI NPYYGKTS EGMVSHFDSVLPMPGPTI YNVPGRTGQDI PPRVHTIAQ
 F/1-365 155 GFAVGMHAALHI NPYYGKTS EGMVSHFDCVLPMPGPTI YNVPGRTGQDI PPRVHTIAQ
 G/1-367 157 GFAVGMHAALHI NPYYGKTS EGLVSHFDSVLPMPGPTI YNVPGRTGQDI PPQVHTIAQ
 H/1-365 155 GFAVGMHAALHI NPYYGKTS EGLVSHFESVLPMPGPTI YNVPGRTGQDI PPQVHTVAQ
 I/1-380 170 GFAVGMHAALHI NPYYGKTS EGLVSHFEAVLPMGPTI YNVPGRTGQDI PPAVIEAVSS
 J/1-273 63 GFAVGMHAALHI NPYYGKTS EGLVSHFEAVLPMGPTI YNVPGRTGQDI PPAVIEAVSS
 K/1-376 166 GFAVGMHAALHI NPYYGKTS EGLVSHFEAVLPMGPTI YNVPGRSQQDI PPQVIEALSG
 M/1-377 167 GFAVGMHAALHI NPYYGKTS EGLVSHFEAVLPMGPTI YNVPGRSQQDI PPQVIEALSG
 L/1-383 173 GFAVGMHAALHI NPYYGKTS EGMVSHFEAVLPMGPTI YNVPGRSQQDI SPPVIEALSG
 N/1-380 170 GFAVGMHAALHI NPYYGKTS EGMVSHFEAVLPMGPTI YNVPGRSQQDI PPEVIEALSG
 O/1-368 158 GFAMGMHAALHI NPYYGKTS MDGLLHFKSVLAMGPTV YNVPGRTGQDI PPSVIEKIAS
 P/1-368 158 GFAMGMHAALHI NPYYGKTS MDGLLHFKSVLAMGPTV YNVPGRTGQDI PPSVIEKIAS
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 R/1-311 101 GFAMGMHGALHI NPYYGKTS NEGLIKHFESVLEMGPTI YNVPGRTGQDI PPSVIERISV
 S/1-345 136 GFAVGMHASLQI NPYYGKTS KAGL LNHFNAVLNEGPAVVYVNPGRTGQDI PDDVMEICQ
 T/1-344 134 GFAVGMHASLQI NPYYGKTS KAGL LNHFNAVLNEGPAI VYVNPGRTGQDI PDDVMEISK
 U/1-369 159 GFAVGMHASLQI NPYYGKTS RAGLEHFEAVVLDLGPALVYVNPARTSQQDI VPDI MFELAK

A/1-364 214 NPNMAGVKECVGNRRVEEYTEKGI VVWSGNDDQCHDSRWDHGATGVI SVTSLNVPGLMRK
 C/1-365 215 NPNMAGVKECVGNRRVEEYTEKGI VVWSGNDDQCHDSRWDHGATGVI SVTSLNVPGLMRK
 B/1-365 215 NPNMAGVKECVGNKRVEEYTEKGI VVWSGNDDQCHDSRWDY GATGVI SVTSLNVPGLMRK
 D/1-365 215 NPNMAGVKECVGNKRVEEYTEKGI VVWSGNDDQCHDSRWDY GATGVI SVTSLNVPGLMRK
 E/1-363 212 SPNLAGVKECAGNDRVEQYTDKGI VVWSGNDDQCHDARWNHGATGVI SVTSLNVPGLMRK
 F/1-365 215 SPNLAGVKECVGNDRVEQYTDKGI VVWSGNDDQCHDARWNHGATGVI SVTSLNVPGLMRK
 G/1-367 217 SPNLAGVKECVGNDRVEEYTEKGI VVWSGNDDQCHDSRWNHGATGVI SVTSLNVPGLMRQ
 H/1-365 215 SANLAGVKECVGNDRVQOYTDNRV VVWSGNDDQCHDAKMDY GATGVI SVTSLNVPGLMRQ
 I/1-380 230 FTNLAGVKECVGHERVKCYTDKGI TVVWSGNDDQCHDSRWKY GATGVI SVASNLVPGLMHD
 J/1-273 123 FSNMAGVKECVGHERVKCYTDKGI TVVWSGNDDQCHDSRWKY GATGVI SVASNLVPGLMRK
 K/1-376 226 YSNLAGVKECVGHERVKCYTDKGI TVVWSGNDDQCHDSRWKY GATGVI SVASNLVPGLMRN
 M/1-377 227 YPNMAGVKECVGHERVKCYTDKGI TVVWSGNDDQCHDSRWKY GATGVI SVASNLVPGLMRS
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 N/1-380 230 YTNMAGVKECVGHERVKHYADKGI TVVWSGNDDQCHDSRWKY GATGVI SVTSLNVPGLMHS
 O/1-368 218 SPNFLGVKECMGNERVKHYTEQGI AVVWSGNDDQCHDSRWDFGARGVI SVVSNLVPKLMHE
 P/1-368 218 SPNFLGVKECMGNERVKHYTEQGI AVVWSGNDDQCHDSRWDFGARGVI SVVSNLVPKLMHE
 Q/1-311 161 KRNFVGLKECVGNDRVGAAYVKKGLTVVWSGNDDQCHDARWDYGAQGVV SVVSNLVPOLAHK
 R/1-311 161 NSNFVGLKECVGNERVGAAYVEKGF SVVWSGNDDQCHDARWNYGAQGVV SVVSNLVPOLAHK
 S/1-345 196 HSNFLGMKECTGNARIKNYVT RGVNCSGNDDQSHDARHSNGAVGVI SVTSLNVPGLMHK
 T/1-344 194 HSNFLGMKECTGNARIKNYVT RGVNCSGNDDQSHDARHSAGAVGVI SVTSLNVPGLMNG
 U/1-369 219 HANFAGVKECEGNARIKOYTDNGVTCWTVGNDDQCHDARYDAGAVGVI SVTSLNVPGLMRE

A/1-364 274 LMFEG. RNSALNAKLLPLMDWLFQEPNPI GVNTALAQLGVARPVFRLPYVPLPLSKRIEF
 C/1-365 275 LMFEG. RNSALNSKLLPLMDWLFQEPNPI GVNTALAQLGVARPVFRLPYVPLPLSKRIEF
 B/1-365 275 LMFEG. RNSLNSKLLPLMAMLFHEPNPI GLNTALAQLGVS RPVFRPYVPLPLSKRIEF
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 I/1-380 290 LMYEG. ENKTLNEKLEPLMKWLFCCPNPI ALNTALAQLGVARPVFRLPYVPLPLEKRVEF
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 R/1-311 221 LMFEG. KDVDLNEKLLPLMDWLFVFNPI GLNTALAQGLI RPVFRPYVPLPLEKRVEF
 S/1-345 256 LMHGS. PDPQLNADLKELEMAWLFCEPNPI SLNTALAMCGLARPVFRPYVPLSRAQREKQ
 T/1-344 254 LMHGS. QPDTALNSLKELEMAWLFCEPNPI ALNTALAMCGLVQPVFRPYVPLDRQREKQ
 U/1-369 279 LMFEG. PNPELRDRLPLMDWLFVFNPI GLNTALAMCGLVQPVFRPYVPLSRAQREKQ


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A/ 1-364 333 VKLVKEI GREHFVGD RDVQVL DDDDFI LI GRY~
C/ 1-365 334 VRLVKEI GREHFVGD RDVQVL DDDDFI LI GRY~
B/ 1-365 334 VKLVKEI GREHFVGE KDVQAL DDDDFI LI GRY~
D/ 1-365 334 VKLVKEI GREHFVGE KDVQAL DDDDFI LI GRY~
E/ 1-363 331 VNLVKKI GRENFVGE EDVQVL DDDDFI LI ARLC
F/ 1-365 334 VNLVKKI GRENFVGENN VQVL DDDDFI LI SRY~
G/ 1-367 336 VNLVKA I GRENFVGE KDVRVL DDDDFI LI GRY~
H/ 1-365 334 VNI VKEI GRENFVGE KDVKVL DDDDFI LVGRY~
I/ 1-380 349 VRI VESI GRENFVGE NEARVL DDDDFV LVSRY~
J/ 1-273 242 VRI VESI GRENFV GQKEARVL DDDDFV LI SRY~
K/ 1-376 345 VRI VEA I GRGNFV GQKEARVL DDDDFV LI SRY~
M/ 1-377 346 VRI VEA I GRGNFV GQKEARVL DDDDFV LI SRY~
L/ 1-383 352 VRI VEA I GRENFV GEKEACVL DDDDFV LI SRY~
N/ 1-380 349 VRI VESI GRENFV GQKEAPVL DDDDFV LI SRY~
O/ 1-368 337 VKI VEG I GRDNF P GCTEVRL KDDDFL LVERY~
P/ 1-368 337 VKI VEG I GRENF P GCTEVRL KDDDFL LVERY~
Q/ 1-311 280 VQMVNQI GRH HFVGD KDVQV MEDNDF LLLDRF~
R/ 1-311 280 VQMVHDI GREHFVGD NDVQV MEDNDF ALLARF~
S/ 1-345 315 AVLLNKV. QEHI PGCKSV RV MEDHEFI LVGRH~
T/ 1-344 314 AALLMAV. QEHI PGCRGV RV MEDHEFT LVGRH~
U/ 1-369 338 AEHLRAVGL DAVA GDGAI RDLSDADFTI LRDW~

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Fig. S6. Multiple sequence alignment and phylogenetic analysis of plant DHDPS.