Table 1 Suppl. List of primers used for the experiments.

Primer name	Sequences
degUGDH-F1	5'-GGI GCIGGITAYGTIGGIGG-3'
degUGDH-F2	5'-GGIGCIGGIAARGCIGCIG-3'
degUGDH-R1	5'-GGRTGRTCCCARTCRAAYTT-3'
degUGDH-R2	5'-GCIGGIGTYTCICKIGTRTC-3'
3'RACE-F1	5'-TGTCAGCACTGTGTGAAGCA-3'
3'RACE-F2	5'-GCGTGGTTTCCTCAATGTTC-3'
M13M4	5'-GTTTTCCCAGTCACGAC-3'
5'RACE-R1	5'-ACATCTGCCCCAGTTGCTTCACACA-3'
5'RACE-R2	5'-CCGGCCTCCAATAAGAA CACGATCA-3'
UGDH-Full-F	5'-ATGGTGAAGATCTGCTGTCT-3'
UGDH-Full-R	5'-GGCATAGGCAATTAAGTATCACAAGTC-3'
LgUGDH-*Bam*HI-F	5'-TA<u>GGATCC</u>ATGGTGAAGATCTGCTGTCT-3'
LgUGDH-*Bam*HI-R	5'-CG<u>GGATCC</u>GAGGAAAAAGAAGTCAAAC-3'
NPT II-F	5'-TTGTCACTGAAGCGGGAAGG-3'
NPT II-R	5'-CGGCGATACCGTAAAGCAC-3'
LgUGDH-SP-F	5'-GTTGGTTTTGGTGGGTCTTGTT-3'
LgUGDH-SP-R	5'-CTCCTTTCCAGTA GTTTGCCACTT-3'
LgActin-F	5'-GAAGCCAAATGCTCTTTCT CGT-3'
LgActin-R	5'-TCTCCTGTATTGTATTGCGTTGCT-3'
Atactin2-F	5'-CTGGATTCTGGTGATGGTGTGTCT-3'
Atactin2-R	5'-GAACCACCGATCCAGACACTGTAC -3'

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At  MVKICCIGAGYVGGPTMAVIALKCPDVEVAVVDISVPRINAWNSDTLPIYEPGLDDVVKQCRGKNLFFSTDVEKHVREADI  81
Os  MVKICCLGAGYVGGPTMAVIALKCPDVEVVVVDISAARIDAWNSDALPIYEPGLDDVVRRCRGRNLFFSSDVERHVGEADI  81
Gm  MVKICCIGAGYVGGPTMAVIALKCPSIEVAVVDISKSRIAAWNSDQLPIYEPGLDGVVKQCRGKNLFFSTDVEKHVFEADI  81
Pt  MVKICCIGAGYVGGPTMAVIALKCPSIEVVVVDIWEPRIAAWNSDQLPIYEPGLYDVVKECRGRNLFFSKDVEKHVAEADI  81
Eg  MVKICCIGAGYVGGPTMAVIALKCPSVEVAVVDISVSRIQAWNSEQLPIYEPGLDAVVKQCRGKNLFFSTDVEKHVFEADI  81
Ps  MVKICCLGAGYVGGPTMAIIALKCPAIEVVVVDISSARIAAWNSDQLPIYEPGLDEVVKSCRGKNLFFSSDVEKHVLEADI  81
Co  MVKICCIGAGYVGGPTMAVIALKCPSIEVVVDISVARIAAWNSEQLPIYEPGLDDVVKQCRGRNLFFSTDIEKHISEADI   81
Bn  MVKICCIGAGYVGGPTMAVIALKCPAIEVAVVDISVSRITAWNSDQLPIYEPGLDAVVKQCRGKNLFFSTDVEKHVSEADI  81
Lg  MVKICCLGAGYVGGPTMAIIALKCPAIEVVVVDISAARIAAWNSDQLPIYEPGLDEVVKSCRGKNLFFSSDVEKHVLEADI  81

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Os  VFVSVNTPTKARGLGAGKAADLTYWESAARMIAAVATSDKVVVEKSTVPVKTAEAIEKILDHNGRDGVGFQILSNPEFLAE  162
Gm  VFVSVNTPTKTQGLGAGKAADLTYWESAARMIADVSKSDKIVVEKSTVPVKTAEAIEKILTHNSK.GIKFQILSNPEFLAE  161
Pt  VFVSVNTPTKTQGLGAGKAADLTYWESAARTIADVSKSDKIVVEKSTVPVKTAEAIEKILTHNSK.GIKFQILSNPEFLAE  161
Eg  VFVSVNTPTKTRGLGAGKAADLTYWESAARMIADVSKSDKIVVEKSTVPVKTAEAIEKILTHNSK.GIKFQILSNPEFLAE  161
Ps  IFVSVNTPTKTRGLGAGKAADLTYWESAARMIADVSRSDKIVVEKSTVPVKTAEAIEKILTHNTK.GINFQILSNPEFLAE  161
Co  IFVSVNTPTKTRGLGAGKAADLTYWESAARMIADVSKSDKIVVEKSTVPVKTAEAIEKILTHNSR.GINFQILSNPEFLAE  161
Bn  VFVSVNTPTKTSGLGAGKAADLTYWESAARMIADVSKSDKIVVEESTVPVKTAEAIEKILTHNSK.GIKFQILSNPEFLAE  161
Lg  IFVSVNTPTKTRGLGAGKAADLTYWESAARMIADVSKSDKIVVEKSTVPVKTAEAIEKILTHNTK.GINFQILSNPEFLAE  161

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Pt  GTAIGDLFQPDRVLIGGRETPEGQKAIQALKDVYAHWVPEDRILTTNLWSAELSKLAANAFLAQRISSVNAMSALCEATGA  242
Eg  GTAIQDLFAPDRVLIGGRETPEGQKAIQTLKDVYAHWVPEDRILTTNLWSAELSKLAANAFLAQRISSVNAMSSLCEATGA  242
Ps  GTAIDLLNPDRVLIGGRETPEGQKAVEALKAVYANWVPEDRIIATNLWSAELSKLAANAVLAQRISSVNAMSALCEATGA   242
Co  GTAIEDLFKPDRVLIGGRETPEGQKAIKTLKDVYAHWVPEDRILATNLWSAELSKLAANAVLAQRISSINAMSALCEATGA  242
Bn  GTAIQDLFSPDRVLIGGRETPEGEKAIQALKAVYANWVPEDRILTTNLWSAELSKLAANAFLAQRISSVNAMSALCEATGA  242
Lg  GTAIQDLLNPDRVLIGGRQSPEGQKAVEALKAVYANWVPEDRIIATNLWSAELSKLAANAVLAQRISSVNAMSALCEATGA  242

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Os  DVAEVAYAVGKDSRIGAKFLNASVGFGGSCFQKDILNLVYICECNGLPEVANYWKQVIKINDYQKSRFVNRVVSSMFNTVA  324
Gm  NVQQVSYSVGTDSRIGPKFLNASVGFGGSCFQKDILNLVYICECNGLPEVAEYWKQVIKINDYQKSRFVNRVVASMFNTVS  323
Pt  DVAEVSYAVGKDSRIGPKFLNASVGFGGSCFQKDILNLVYICECNGLPEVAEYWKQVIKINDYQKSRFVNRVVSSMFNTVS  323
Eg  DVAQVSYAVGKDSRIGPKFLNASVGFGGSCFQKDILNLVYICECNGLPEVAEYWKQVIKINDYQKARFVNRVVSSMFNTVS  323
Ps  DVTEVAYAVGKDSRIGPKFLNASVGFGGSCFQKDILNLIYICECNGLVEVANYWKGVIKINDYQKSRFVNRVVSSMFNTVS  323
Co  DVTEVSYAVGKDSRIGPKFLNASVGFGGSCFQKDILNLVYICECNGLPEVANYWKQVIKINDYQKNRFVNRVVASMFNTVS  323
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Lg  DVTEVAYAVGKDSRIGPKFLNASVGFGGSCFQKDILNLIYICECNGLMEVANYWKGVIKINDYQKSRFVNRVVASMFNTVS  323
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Os  GKKIAVLGFAFKKDTGDTRETPAIDVCKGLIGDKAKVSIYDPQVTEDQVQRDLAMSKFDWDHPVHLQPMSP.TAIKQVSVA  404
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Pt  QKKIAILGFAFKKDTGDTRETPAIDVCQGLLGDKALLSIYDPQVQKEHIQRDLIMKKFDWDHPLHLQPKSASSAVEQVTVT  404
Eg  NKKIAILGFAFKKDTGDTRETPAIDVCKGLLGDKARLSIYDPQVTEEQIQRDLTMNKFDWDHPLHLQPMSP.TTVKQVSVV  403
Ps  GKKIAVLGFAFKKDTGDTRETPAIDVCKGLLGDKANISIYDPQVTEDQIQRDLSMNKFDWDHPPHLQPMSP.SAIKQVSVV  403
Co  GKKIAVLGFAFKKDTGDTRETPAIDVCKGLLGDKAKISIYDPQVTEDQIQRDLAMNKFDWDHPIHLQPMSP.TTVKQVSVT  403
Bn  NKKIAVLGSAFKKDTGDTRETPAIDVCKGLLGGKARLSIYDPQVTEDQIQRDLVMNKFDWDHPLHLQPMSP.TTVKRVSVV  403
Lg  GKKIAVLGFAFKKDTGDTRETPAIDVCKGLLGDKANISIYDPQVTEDQIQRDLSMNKFDWDHPPHLQPMSP.SAIKQVSVV  403
                                                            •••
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Os  WDAYEAARAAHGVCILTEWDEFRSLDYARIYGMQKPAFVFDGRNVVDAEKLREIGFIVYSIGKPLDAWLKDMPAV  480
Gm  WDAYEATKDAHGLCILTEWDEFKTLDYQKIFDNMQKPAFVFDGRNIVDADKLREIGFIVYSIGKPLDPWLKDMPAV  479
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Co  WDAYEATKDAHGVCILTEWDEFKALDYQKIYDNMQKPAFVFDGRNIVDVEKLRKIGFIVFSIGKPLDPWLKDMPAV  479
Bn  WDAYEATKGAHGVCILTEWDEFKNLDYKKIYDNMQKPAFIFDGRNIADMDKLREIGFIVYSIGKPLDGWLKDMPAV  479
Lg  WDAYEATKDAHGVCILTEWDEFKTLDYQKIYDNMQKPAFIFDGRNIVDLEKLRKIGFIVYSIGKPLDPWVKDLPAS  479
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Fig. 1. Suppl. The alignment of amino acid sequences of uridine diphosphate glucose dehydrogenase (UGDH) proteins from *Larix gmelinii* (*Lg*), *Arabidopsis thaliana* (*At*, BAB02581.1), *Oryza sativa* (*Os*, AAS07200.1), *Glycine max* (*Gm*, AAB58398.1), *Populus tomentosa* (*Pt*, AAR32717.1), *Eucalyptus grandis* (*Eg*, ABP04019.1), *Picea sitchensis* (*Ps*, ABR17780.1), *Cinnamomum osmophloeum* (*Co*, AAR84297.1), and *Boehmeria nivea* (*Bn*, ABM55267.3). The amino acids are numbered on the *right* of each protein. The putative NAD^{+} cofactor-binding motif (G-A-G-Y-V-G-G) is *underlined*. The key catalytic site (G-F-G-G-S-C-F-Q-K-D-I-L) is indicated by the *dash line* and Cys-272, which is supposedly involved in enzyme catalysis during the second-half reaction catalyzed by UGDH, is the *solid triangle*. Two putative N-glycosylation motifs (N-A-S and N-I-S), which may be involved in membrane-binding activity, are indicated by the *solid circles* under the sequences.
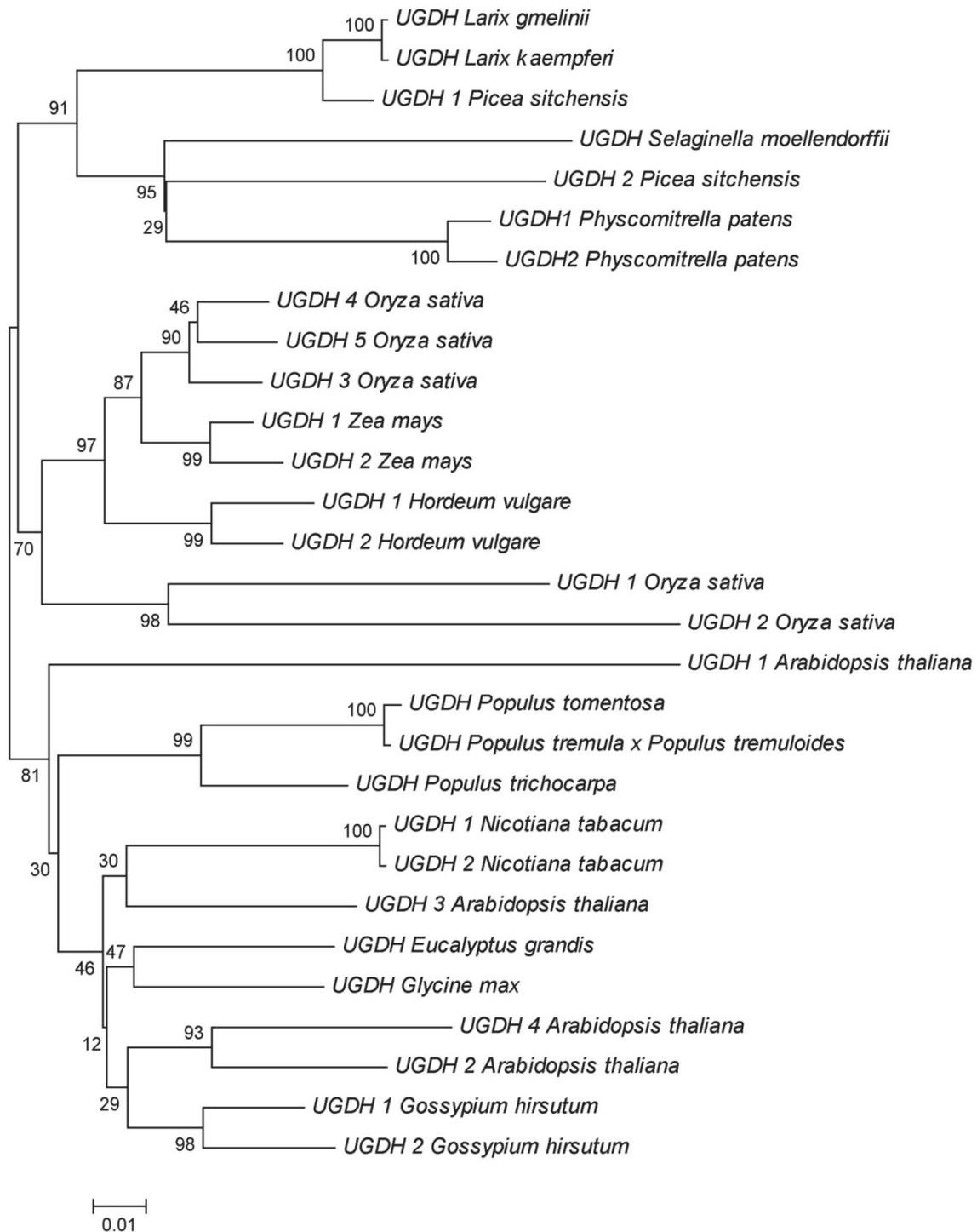
Fig. 2 Suppl. A phylogenetic tree of plant uridine diphosphate glucose dehydrogenase (UGDH) sequences constructed as described in the methods. The following protein sequences are included: *Oryza sativa* (UGDH 1, ABF96712.1; UGDH 2, ABF97514.1; UGDH 3, ABF98973.1; UGDH 4, ABA97736.1; UGDH 5, ABG22007.1), *Nicotiana tabacum* (UGDH 1, AAT40105.1; UGDH 2, AAT40106.1), *Arabidopsis thaliana* (UGDH 1, NP_173979.1; UGDH 2, AAL11570.1; UGDH 3, AAU90084.1; UGDH 4, AAP21188.1), *Zea mays* (UGDH 1, 658123 in the GnpSeq database; UGDH 2, 658125 in the GnpSeq database), *Glycine max* (UGDH, AAB58398.1), *Eucalyptus grandis* (UGDH, ABP04019.1), *Populus tomentosa* (UGDH, AAR32717.1), *Populus trichocarpa* (UGDH, XP_002324103.1), *Populus tremula × Populus tremuloides* (UGDH, AAF04455.1), *Picea sitchensis* (UGDH 1, ABR17780.1; UGDH 2, ABR17492.1), *Gossypium hirsutum* (UGDH 1. ACJ11712.1; UGDH 2, ADB24766.1), *Hordeum vulgare* (UGDH 1, BAJ85096.1; UGDH 2, BAJ88568.1), *Larix kaempferi* (UGDH, AHA44517.1), *Selaginella moellendorffii* (UGDH, XP_002965664.1), and *Physcomitrella patens* (UGDH1, XP_001782554.1; UGDH2, XP_001761641.1).
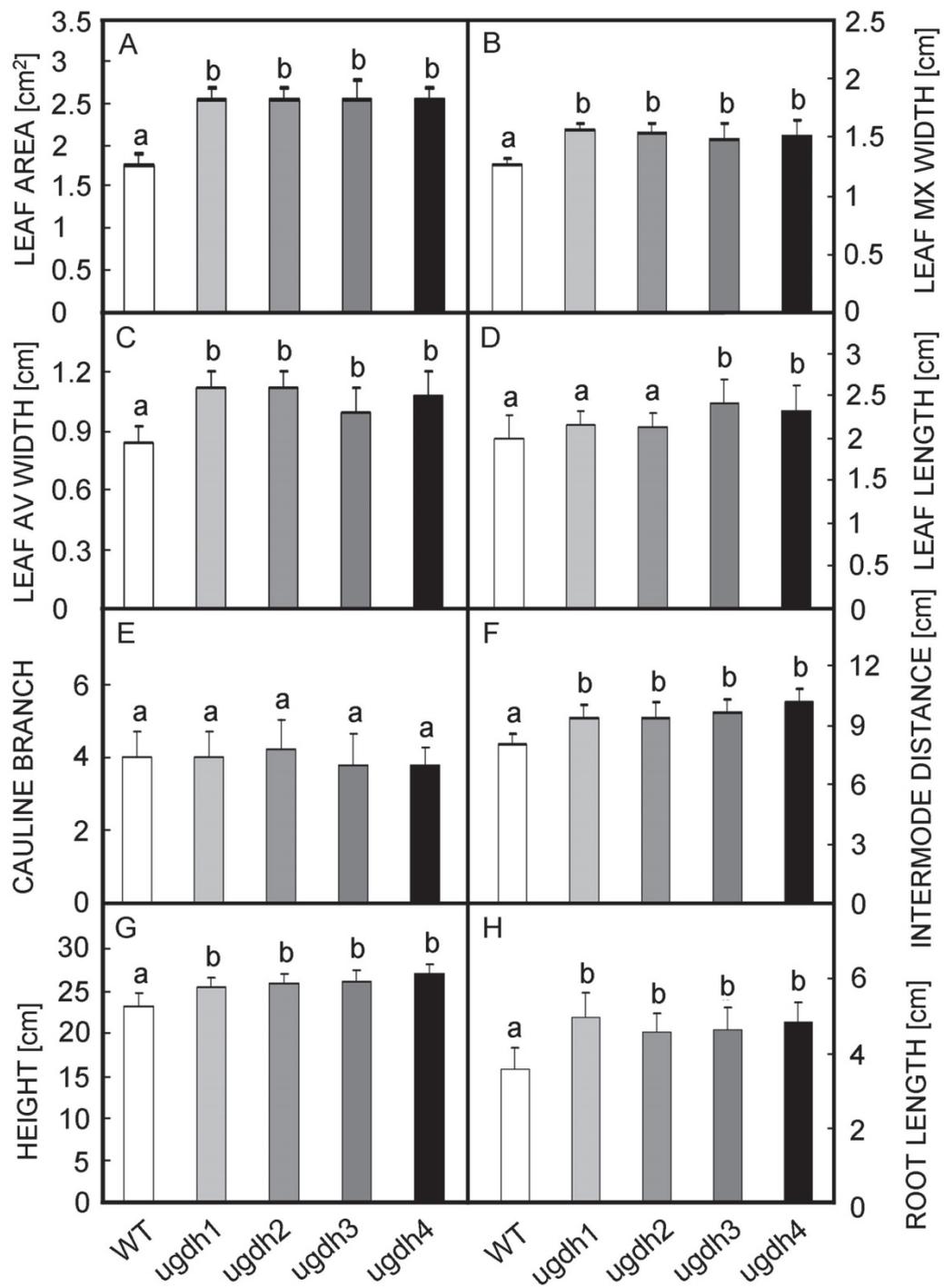
Fig. 3 Suppl. Morphological analysis of wild type (WT) and transgenic *Arabidopsis thaliana* plants. Leaf area (*A*), maximum width (*B*), average width (*C*), and length (*D*) of the fifth rosette, the number of cauline branches (*E*), internode distances (*F*), and plant height (*G*) were measured in 40-d-old plants, and roots length (*H*) was measured in 14-d-old plants. Means ± SDs were calculated from five plants per line; different letters indicate significant differences according to Fisher's least significant difference test (*P* < 0.05).
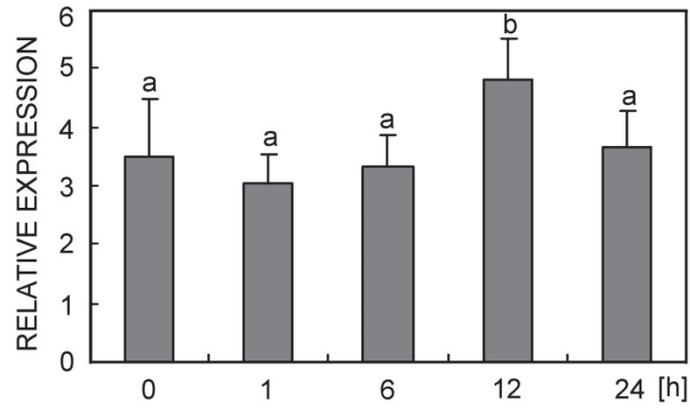
Fig. 4 Suppl. Real-time PCR was used to measure relative expression of the *LgUGDH* gene in *L. gmelinii* seedlings cultivated at 4 °C for 0 - 24 h. Means ± SDs were calculated from five plants per line; different letters indicate significant differences according to Fisher's least significant difference test ($P < 0.05$).