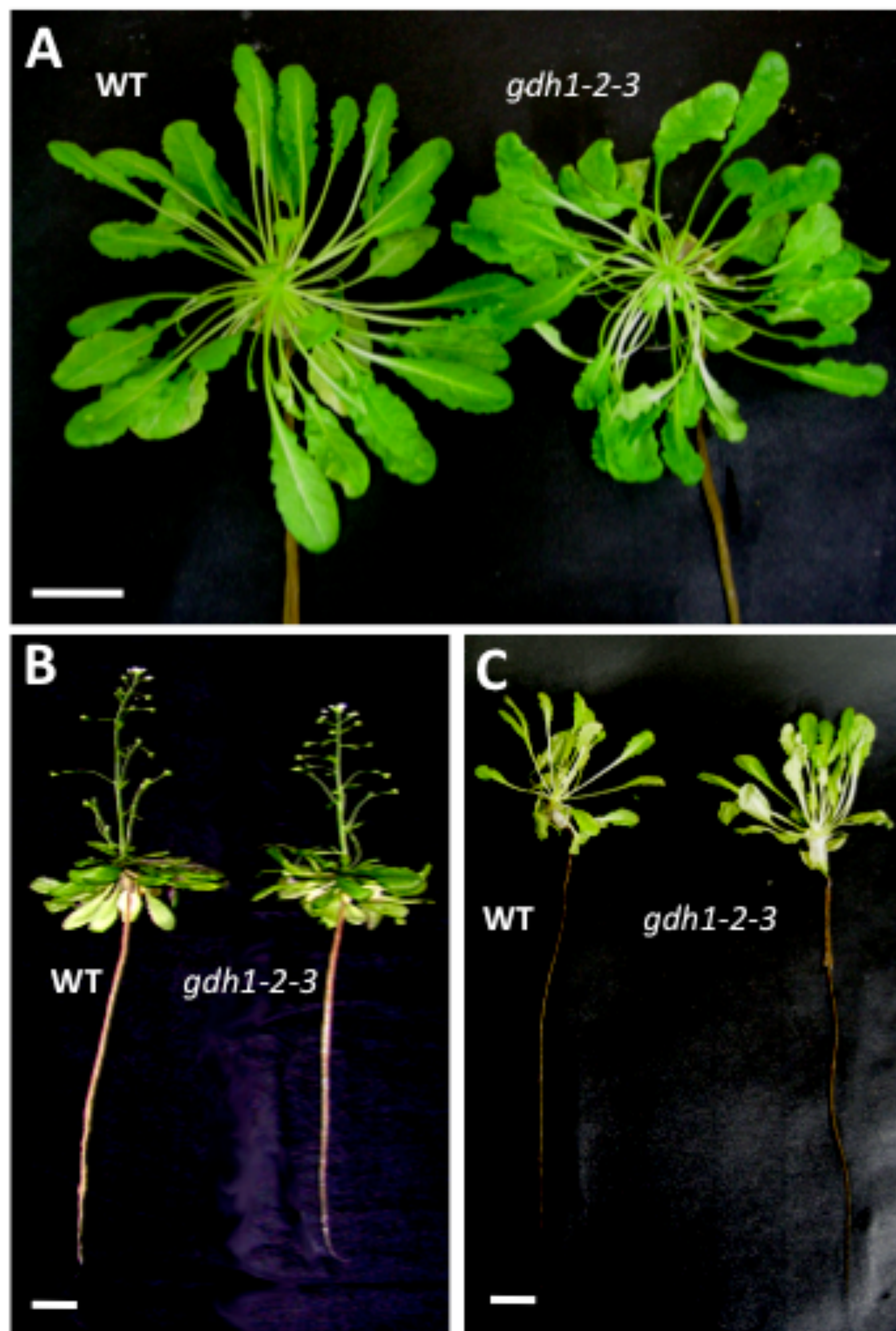
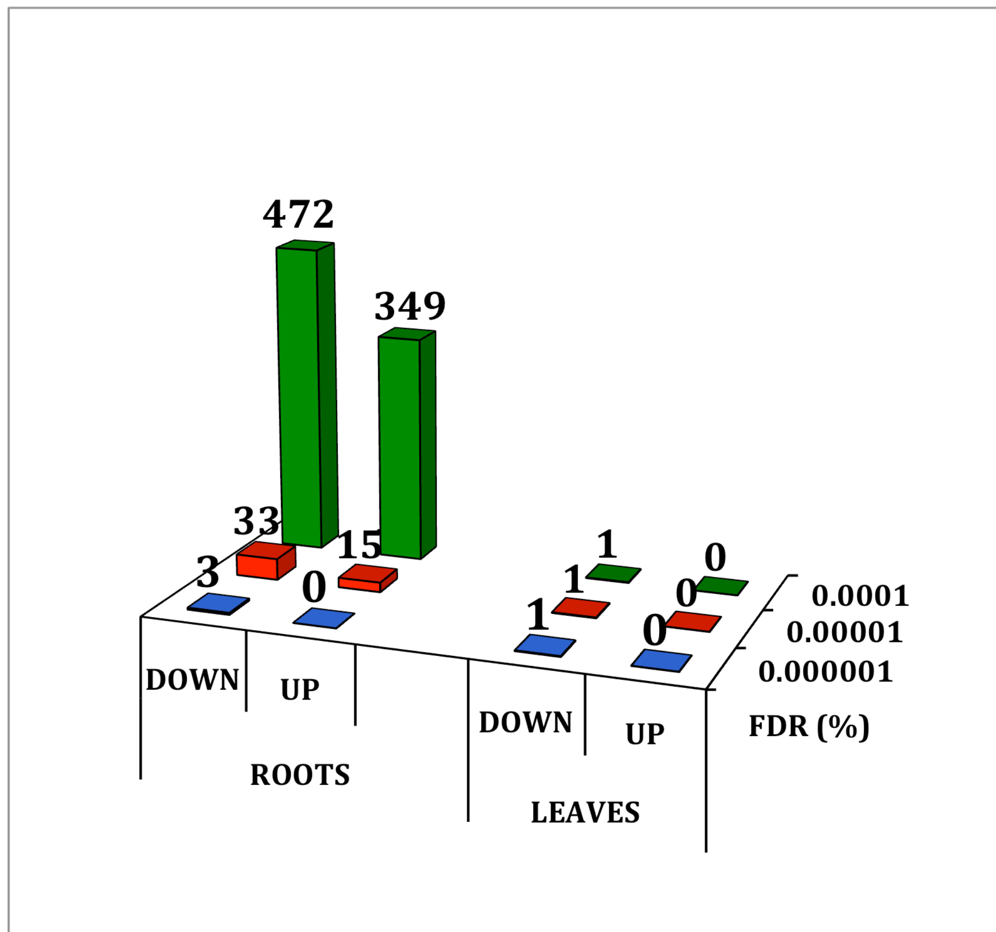
```
           1       10        20        30        40        50        60        70        80
           |--------+---------+---------+---------+---------+---------+---------+---------|
     GDH1
     GDH3
     GDH2
  NADPGDH  MFGPTGGLGMNPSMDDMNLIQQAQRHQLVVSNLGEEIDLEIGPGEDDAAFANNSLIGGPPREPSTGEHDETKHMVLVSDL
Consensus  ................................................................................

           81      90        100       110       120       130       140       150       160
           |--------+---------+---------+---------+---------+---------+---------+---------|
     GDH1
     GDH3
     GDH2
  NADPGDH  PSEDQDISKGTPAKRKKKVVKRWREEWADTYKWAYVDMKDGTARIFCSICREYGRKHRRNPYGNEGSRNMQMSALEEHNN
Consensus  ................................................................................

           161     170       180       190       200       210       220       230       240
           |--------+---------+---------+---------+---------+---------+---------+---------|
     GDH1                                                  MNALAATNRNFKLAARLLGLDS---KLEKSLL
     GDH3                                                  MNALAATNRNFKLASRLLGLDS---KLEKSLL
     GDH2                                                  MNALAATNRNFRHASRILGLDS---KIERSLM
  NADPGDH  SLLHKEALRLQTASKDKIVVDKPIYVKTVMSKSAGSIVEGALKRDPNEIEFVQSVQESVHALERVIAKNSHYVNIMERLL
Consensus  ................................................m#alaat#rnf..a.R.lgl#S...kie.sL$

           241     250       260       270       280       290       300       310       320
           |--------+---------+---------+---------+---------+---------+---------+---------|
     GDH1  IPFREIKVECTIPKDDGTLASFVGFRVQHDNARGPMKGGIRYHPEVDPDEVNALAQLMTWKTAVAKIPYGGAKGGIGCDP
     GDH3  IPFREIKVECTIPKDDGTLASFVGFRVQHDNARGPMKGGIRYHPEVEPDEVNALAQLMTWKTAVAKIPYGGAKGGIGCDP
     GDH2  IPFREIKVECTIPKDDGTLVSYIGFRVQHDNARGPMKGGIRYHPEVDPDEVNALAQLMTWKTAVADIPYGGAKGGIGCSP
  NADPGDH  EPERMIVFRVPWIDDRGETHVNRGFRVQFNQALGPCRGGIRFHPSMNLSIAKFLGFQQTLKNALSPYKLGGASGGSDFDP
Consensus  iPfReIkvectipkDdGtl.s..GFRVQh##ArGPmkGGIR%HPev#pdevnaLaqlmTwKtAva.ipyGGAkGGigcdP

           321     330       340       350       360       370       380       390       400
           |--------+---------+---------+---------+---------+---------+---------+---------|
     GDH1  SKLSISELERLTRVFTQKIHDLIGIHTDVPAPDMGTGPQTMAWILDEYSKFHGYSPAVVTGKPIDLGGSLGRDAATGRGV
     GDH3  SELSLSELERLTRVFTQKIHDLIGIHTDVPAPDMGTGPQTMAWILDEYSKFHGHSPAVVTGKPIDLGGSLGRDAATGRGV
     GDH2  RDLSLSELERLTRVFTQKIHDLIGIHTDVPAPDMGTNAQTMAWILDEYSKFHGHSPAVVTGKPIDLGGSLGREAATGRGV
  NADPGDH  KGKSDNEIMRFCQSFMNEMYRYMGPDKDLPSEEVGVGTREMGYLFGQYRRLAGQFQGSFTGPRIYWAASSLRTEASGYGV
Consensus  ..lS.sEleRltrvFt#kihdliGihtDvPap#mGtg.qtMawild#YskfhG.spavvTGkpIdlggSlgR.aAtGrGV

           401     410       420       430       440       450       460       470       480
           |--------+---------+---------+---------+---------+---------+---------+---------|
     GDH1  MFGTEALLNEHGKTISGQRFVIQGFGNVGSWAAKLISEKGGKIVAVSDITGAIKNKDGIDIPALL---KHTKEHRGVKGF
     GDH3  LFATEALLNEHGKTISGQRFAIQGFGNVGSWAAKLISDKGGKIVAVSDVTGAIKNNNGIDILSLL---EHAEENRGIKGF
     GDH2  VFATEALLAEYGKSIQGLTFVIQGFGNVGTWAAKLIHEKGGKVVAVSDITGAIRNPEGIDINALI---KHKDATGSLNDF
  NADPGDH  VYFARLILADMNKEIKGLRCVVSGCGKIAMHVVEKLIACGAHPVTVSDSKGYLVDDDGFDYMKLAFLRDIKSQQRSLRDY
Consensus  v%.tealLa#.gK.I.Glrfv!qGfGn!g.waakli..kGgk.VaVSD.tGai.#.#GiDi..L.....hk...rsl.d%

           481     490       500       510       520       530       540       550       560
           |--------+---------+---------+---------+---------+---------+---------+---------|
     GDH1  DG----ADPIDPNSILVEDCDILVPAALGGVINRENANEIK---AKFIIEAANHPTDPDADEILSKKGVVILPDIYANSG
     GDH3  DG----ADSIDPDSILVEDCDILVPAALGGVINRENANEIK---AKFIIEGANHPTDPEADEILKKKGVMILPDIYANSG
     GDH2  NG----GDAMNSDELLIHECDVLIPCALGGVLNKENAGDVK---AKFIVEAANHPTDPDADEILSKKGVIILPDIYANAG
  NADPGDH  SKTYARAKYFDELKPWNERCDVAFPCASQNEVDQADAINLVNAGCRLLVEGSNMPCTAEAVDVFRKANVLIAPAIAAGAG
Consensus  .g....ad..#....l.e.CD!l.PcAlggv.#.e#A.#.k...akfi!EgaNhPtdp#Ad#!l.KkgV.IlPdIyAnaG

           561     570       580       590       600       610       620       630     638
           |--------+---------+---------+---------+---------+---------+---------+-------|
     GDH1  GVTVSYFEWVQNIQGFMWEEEKVNDELKTYMTRSFKDLKEMCKTHSCD------LRMGAFTLGVNRVAQATILRGWGA
     GDH3  GVTVSYFEWVQNIQGFMWDEEKVNRELKTYMTRGFKDLKEMCQTHSCD------LRMGAFTLGINRVAQATTIRGWGS
     GDH2  GVTVSYFEWVQNIQGFMWEEEKVNLELQKYMTRAFHNIKTMCHTHSCN------LRMGAFTLGVNRVARATQLRGWEA
  NADPGDH  GVAAGEIEVLRESNSMQWSAEDFESRLQEALKQTYEKALKAANDFGYQKESPEALLHGATIAAFLNIAQAMTDQGCV
Consensus  GVtvsyfEwvq#i#gfmW.eEkv#.eLq.y$tr.%...k.mc.thsc#......LrmGAftlg.nr!AqAtt.rGw..
```

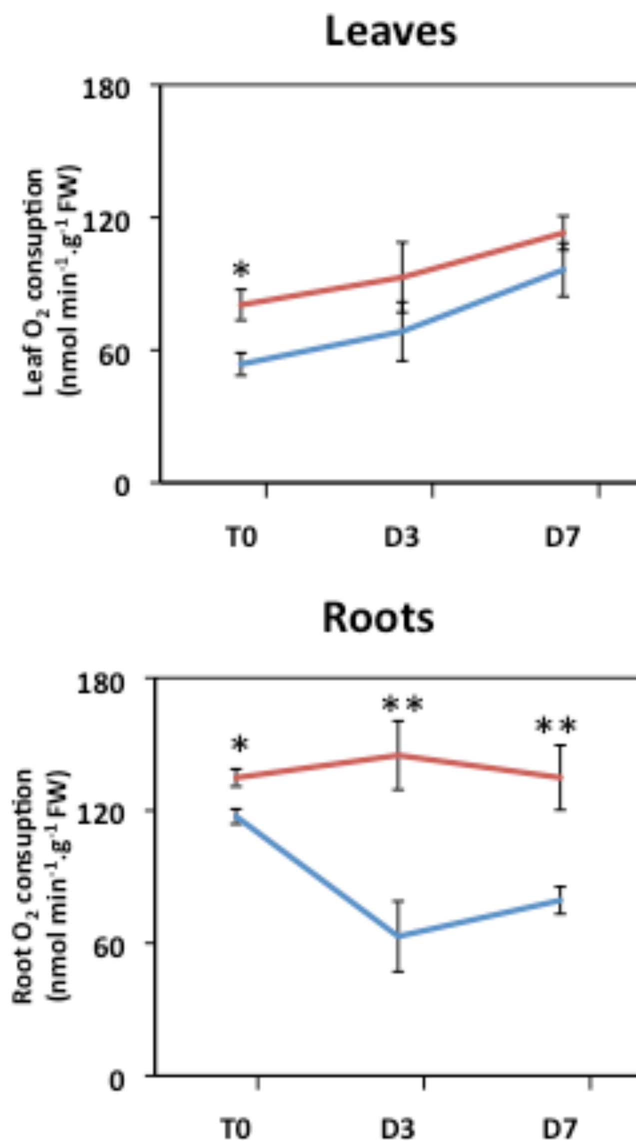
Supplemental Figure 1. Alignment of Deduced Protein Sequences of *Arabidopsis GDH* Genes Encoding the Three NADH-dependent Enzymes and the NAD(P)H-dependent enzyme. An additional consensus protein sequence for the four GDH proteins is also presented.



Supplemental Figure 2: Phenotype of the WT and of the *gdh1-2-3* Mutant
(**A**) Phenotype of the WT and of the *gdh1-2-3* mutant at the rosette stage grown for 28 days under hydroponic conditions and corresponding to T0 in the dark-induced experiment.
(**B**) Phenotype of the WT and of the *gdh1-2-3* mutant after floral induction.
(**C**) Phenotype of the WT and of the *gdh1-2-3* mutant after 7 days in the dark
Bars = 1cm



Supplemental Figure 3. Overall Changes in Transcript Accumulation in Roots and Leaves of *gdh1-2-3* Mutants. The rank product method was used to detect differentially expressed genes according to different levels of False Discovery Rate (FDR). Numbers on top of the columns indicate the number of differentially expressed genes.



Supplemental Figure 4. Respiration in Leaves and Roots of the WT and *gdh1-2-3* Mutant Plants FollowingProlonged Darkness. T0 = plants grown under short day conditions and harvested 2 h after the beginning of the light period, D3 = after 3 continuous days in the dark, D7 = after 7 continuous days in the dark. Respiration was measured by monitoring 0_2 consumption of fresh roots and leaves for 30 to 45 min. The red line corresponds to the *gdh1-2-3* mutant and the blue line to the WT.
Results are presented as mean values for five plants with standard errors. Asterisks indicate a bilateral t-test P-value <0.01(**) and <0.05(*) for statistically significant differences.

Supplemental Table 1. Quantification of GDH Protein in Different Tissue Sections of NADH-GDH Mutant Plants. Immunolocalization of the enzyme was performed using transmission electron microscopy on roots and leaves of the Wild Type (WT), and of the gdh1-2 double mutant and ghd1-2-3 triple mutant.

	Number of gold particles/µm^2 ± sd in mitochondria of phloem companion cells			
	WT	*gdh1-2*	*gdh1-2-3*	Preimmune serum
Leaf	100±35	10±6 [a]	7±4 [a]	6±3 [a]
Root	310±40	100±30	6±3 [a]	6±4 [a]

[a] statistically not different

Supplemental Table 2. Comparison of the Results Obtained with the CATMA Microarray and a qRT-PCR Experiment for Trancripts Abundance in the *Arabidopsis gdh1-2-3* Mutant Compared to the Wild Type (WT).

AGI[d]	Target transcript	qRT-PCR Average FC[e] *gdh1-2-3*/WT	SD[f]	Microarray FC[e] *gdh1-2-3*/WT
AT3G02470	S-ADENOSYLMETHIONINE DECARBOXYLASE[a]	3.14	0.90	2.34
AT1G20840	TONOPLAST MONOSACCHARIDE TRANSPORTER1	1.76	0.51	1.93
AT1G65960	GLUTAMATE DECARBOXYLASE 2	1.78	0.29	1.76
AT3G48450	[b]nitrate-responsive NOI protein, putative	0.68	0.16	0.29
AT1G72060	Serine-type endopeptidase inhibitor	0.75	0.12	0.30
AT4G31730	GLUTAMINE DUMPER 1	0.73	0.05	0.59
AT5G08290	YLS8[c]	1.16	0.07	1.00
AT4G13420	K TRANSPORTER	1.14	0.07	1.00
AT1G61800	Gluc6PT = GPT2	1.19	0.22	1.00

[a,b,c]Three transcripts exhibiting an increase[a], a decrease[b] or no changes[c] in the *gdh1-2-3* mutant in comparison to the WT were selected from those listed in Supplementary Datset 3 and 4.

[d]Arabidopsis gene identification

[e] Average fold change (FC) between the two replicated experiments

[f] Standard deviation (SD)

Supplemental Table 3: Oligonucleotides Used for Screening *Arabidopsis GDH* Mutant Plants. *GDH1*, *GDH2* and *GDH3* indicate the three primers pairs used in the tested gene. "+ ins" indicates the primer pair used to test the presence of the T-DNA in the tested gene with primers located at the intersection between the insertion of the T-DNA and the gene encoding GDH.

Gene	Primer	Primer sequence	Fragment size (bp)
GDH1	Forward	TTCTGATCAAAACTCCAGTGAAA	1559
	Reverse	TGATGACACCACCAAGTGCT	
GDH1 + ins	Forward	CGGCTACTGGAAGAGGAGTG	1381
	Reverse	TCGCAAGACCCTTCCTCTA	
GDH2	Forward	ACAAGGACGCAACTGGAAGT	736
	Reverse	TCCATTTCGGAAAGCTCAAT	
GDH2 + ins	Forward	ACAAGGACGCAACTGGAAGT	1227
	Reverse	TCGCAAGACCCTTCCTCTA	
*GDH*3	Forward	GACTCTCTGATCAAATAAACCCAAA	2103
	Reverse	AAGGTTAAACTGCAATTAGCACA	
GDH3 + ins	Forward	GACTCTCTGATCAAATAAACCCAAA	1256
	Reverse	TCGCAAGACCCTTCCTCTA	

Supplemental Table 4: Oligonucleotides Used for Amplification of RNA to Obtain DNA Fragments Specific for the Three Genes Encoding NADH-GDH and for the β-actin Genes Used as Controls.

Gene	Primer	Primer sequence	Fragment size (bp)
GDH1	Forward	*TGGCTCAAGCTACCATTCTCAGA*	141
	Reverse	*TCGCTCAAGCTACCACTATCAG*	
GDH2	Forward	GTGGTTGGGAAGCTTAATTCAGTT	122
	Reverse	TCGCTCAAGCTACCACTATCAG	
GDH3	Forward	TCGCTCAAGCTACCACTATCAG	151
	Reverse	CTGCAATTAGCACATAGTTTTTATTACTC	
ß-actin-2	Forward	AGTGGTCGTACAACCGGTATTGT	93
	Reverse	GATGGCATGGAGGAAGAGAGAAAC	
ß-actin-7	Forward	AGTGGTCGTACAACCGGTATTGT	95
	Reverse	GAGGAAGAGCATTCCCCTCGTA	
ß-actin-8	Forward	AGTGGTCGTACAACCGGTATTGT	96
	Reverse	GAGGATAGCATGTGGAACTGAGAA	

Supplemental Table 5: Oligonucleotides Used for Amplification of RNA to Obtain DNA Fragments for the qRT-PCR Used to Validate the Microarray Experiment.

Gene	Primer	Primer sequence
PP2A3	Forward	GCAATCTCTCATTCCGATAGTC
	Reverse	ATACCGAACATCAACATCTGG
Q-TIP41	Forward	GCTCATCGGTACGCTCTTTT
	Reverse	TCCATCAGTCAGAGGCTTCC
UBI-10	Forward	GGCCTTGTATAATCCCTGATGAATAAG
	Reverse	AAAGAGATAACAGGAACGGAAACATAGT
SAMDC	Forward	GCAATCGGTTTCGAAGGTTA
	Reverse	TCCTTTAGCTCCACCTCGAA
TMT	Forward	ACCCCTATTTCAACGCCTCT
	Reverse	GAGAGTCGCTCCCTTCATTG
GAD2	Forward	GAGAGTCGCTCCCTTCATTG
	Reverse	TCCTTTAGCTCCACCTCGAA
YLS8	Forward	ACTGGGATGAGACCTGTATG
	Reverse	TGTTGTTGTTACCAGTTCCA
HAK5	Forward	TGTTTTCGGACATTTCGTG
	Reverse	ACCGGCTTTCGAAGTCATAC
G6T	Forward	GACTTTCCCTCTTCCTGTCT
	Reverse	AATGGAGTGAGGATCACAAG
NOI	Forward	CAATAAAGCTCGCGATGACA
	Reverse	TCTTTGATCTTGGGGTTTGG
ENDOP	Forward	AAGCTTCCTCCAAGATGCAA
	Reverse	GAAATCGATGAGTGGGAGGA
GDU1	Forward	AATCGCCTTTGCTCTTCTCA
	Reverse	CAAATCTTCTCCGGCCATTA