

Supporting information for:

Conifers exhibit a characteristic inactivation of auxin to maintain tissue homeostasis

Federica Brunoni, Silvio Collani, Rubén Casanova-Saéz, Jan Šimura, Michal Karady, Markus Schmid, Karin Ljung and Catherine Bellini

Email: karin.ljung@slu.se or catherine.bellini@umu.se or catherine.bellini@inra.fr

The following Supporting Information is available for this article:

Table S1

Fig. S1 to S7

Table S1: Primers used in this work.

Purpose	Name	Gene ID	Primer sequence (5'→3')		
			Forward	Reverse	
RT-qPCR	PaGH3.16_q	MA_10434772g0010	GCTACCACCGAGCGTAACAAG	CACTGAACCATAGCGTTGAAG	
	PaGH3.17_q	MA_16777g0010	CGGTCGAATCGATAACAAATCG	CTGTGAAGCTCCTCGGGAAT	
	PaGH3.gII.1_q	MA_100975g0010	CACGAGGTGGTATAAGAGTCG	GAACCCAGAAGCAAAGATGGC	
	PaGH3.gII.2_q	MA_10432413g0010	CACTGGATGAGAAAGAGCGAC	GCGTCGATACTCAGCACAA	
	PaGH3.gII.3_q	MA_580596g0010	CTATCTATCGCCAAGGAAGAGC	GGAGTTTAGCAGCTCAACGA	
	PaGH3.gII.4_q	MA_66253g0010	GACGATCTCAAGTCTGAG	CGGGCATGAGAAGACTATACAG	
	PaGH3.gII.5_q	MA_6467862g0010	GGTCACTACGTCTATACTG	CCCTCTACTGAGAGCATAATCC	
	PaGH3.gII.7_q	MA_212507g0010	CGTCGTATTGTAACGAGAGAC	CCCTTGCAAGTCTTGCA	
	PaGH3.gII.8_q	MA_10432413g0020	CTGCTCATCCAGTTCCGAA	GGAGTCTTTGCCCTCCGATT	
	PaGH3.gII.9_q	MA_10330250g0010	CGAGAATACGAGCTTGTCG	CAGCTCTGCTTCATCCGTTT	
	PaGH3.gI.1_q	MA_10429520g0010	CATCTGCGTCATGAAGGCTT	CGGTAACCTTCACGACATCACC	
	PaGH3.gI.2_q	MA_376158g0010	GACTGGAGACGAAACCAGAA	CCAAGTCCACTTGCAATTGC	
	PaIF4A_q	MA_50378g0010	TTGGTCGGAGTGGACGATTTGG	TGACGAGAGAATGCTGCAGGAC	
	Cloning	PaGH3.16_clo	MA_10434772g0010	TCCCCTCTAGAAATAATTTTGATTTAACTTTAAGAAGGAGATATACCATGCATCACCATCACCATCACGCGATGGGAGAGAAAGCGAAAGC	CTCGAGTGC GGCCG CAGCAAGCTTCTAGCTAGCTTATTATTACCTCACAAATTTAGCAACAAAC
		PaGH3.17_clo	MA_16777g0010	TCCCCTCTAGAAATAATTTTGATTTAACTTTAAGAAGGAGATATACCATGCATCACCATCACCATCACGCGATGGAGATGAATATTCGCTGC	CTCGAGTGC GGCCG CAGCAAGCTTCTAGCTAGCTTATTATTAATAAAGCTGAGAATTTGG
PaGH3.gII.8_clo		MA_10432413g0020	TCCCCTCTAGAAATAATTTTGATTTAACTTTAAGAAGGAGATATACCATGCATCACCATCACCATCACGCGATGAGTTCTTCTG GAAACGAGG	CTCGAGTGC GGCCG CAGCAAGCTTCTAGCTAGCTTATTATTATGCCAAATTTCTGCATCCTGG	
PaGH3.gII.9_clo		MA_10330250g0010	TCCCCTCTAGAAATAATTTTGATTTAACTTTAAGAAGGAGATATACCATGCATCACCATCACCATCACGCGATGAGTTCTGCTATGGGAAAC	CTCGAGTGC GGCCG CAGCAAGCTTCTAGCTAGCTTATTATTACGCCAATTTCTGCATCC	
5'-RACE	PaGH3.gII.9_gsp	MA_10330250g0010		TGAGCCATTGCACCAGTGACGATGACAT	

Fig. S1

Full-length coding sequence of *PaGH3.16*, *PaGH3.17*, *PaGH3.gII.8* and *PaGH3.gII.9*.

>PaGH3.16_CDS

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>PaGH3.17_CDS

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>PaGH3.grII.9_CDS

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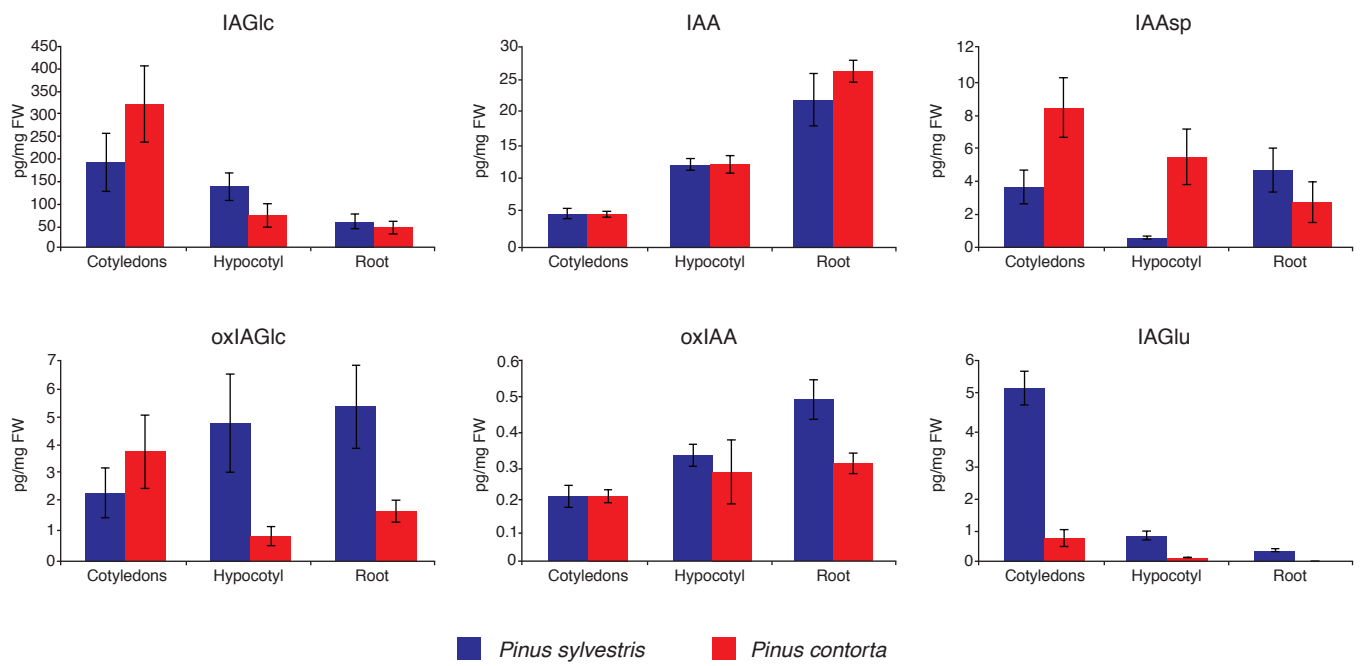


Figure S2

Levels of IAA metabolites in different organs of *Pinus sylvestris* and *Pinus contorta* seedlings.

IAA and IAA metabolites oxIAA, oxIAGlc, IAGlc, IAAsp and IAGlu were quantified in cotyledons, hypocotyl and root from 2-week-old pine seedlings. The level of IAGlu in *P. contorta* root was under the detection limit of the used LC-MS/MS method. Blue indicates *P. sylvestris* and red indicates *P. contorta*. The concentrations of all metabolites are in picograms per milligram fresh weight (FW). Error bar indicates \pm SD (n = 4).

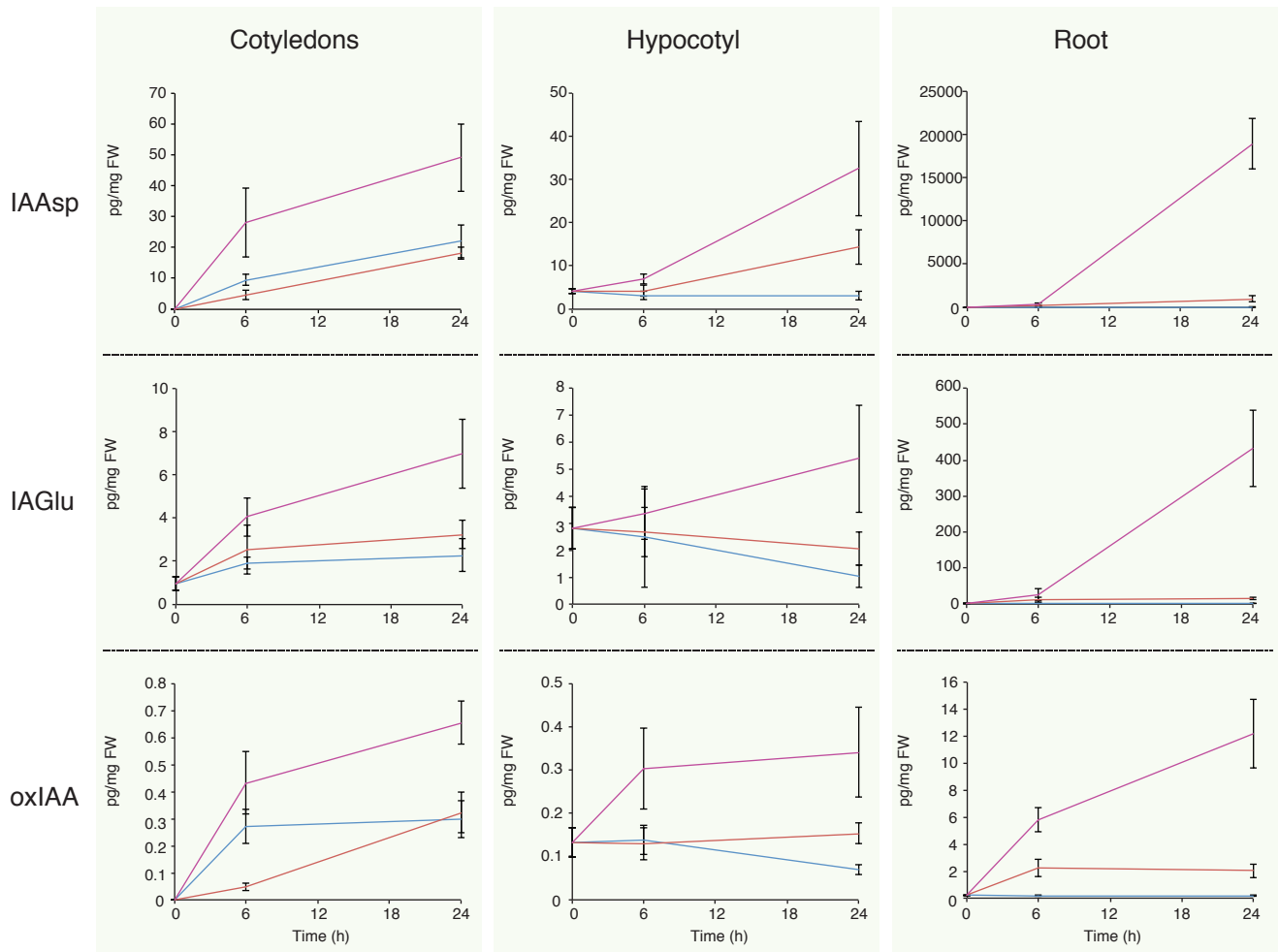


Figure S3

Concentrations of IAA metabolites in different organs of *Picea abies* after feeding with unlabeled IAA.

Two-week-old spruce seedlings were incubated with 1 (red line), 10 μM (pink line) or without (blue line) unlabeled IAA and the levels of IAA and IAA metabolites IAAsp, IAGlu and oxIAA were quantified in cotyledons, hypocotyl and root after different incubation times. The concentrations of all metabolites are in picograms per milligram fresh weight (FW). Error bars indicate ±SD (n = 4).

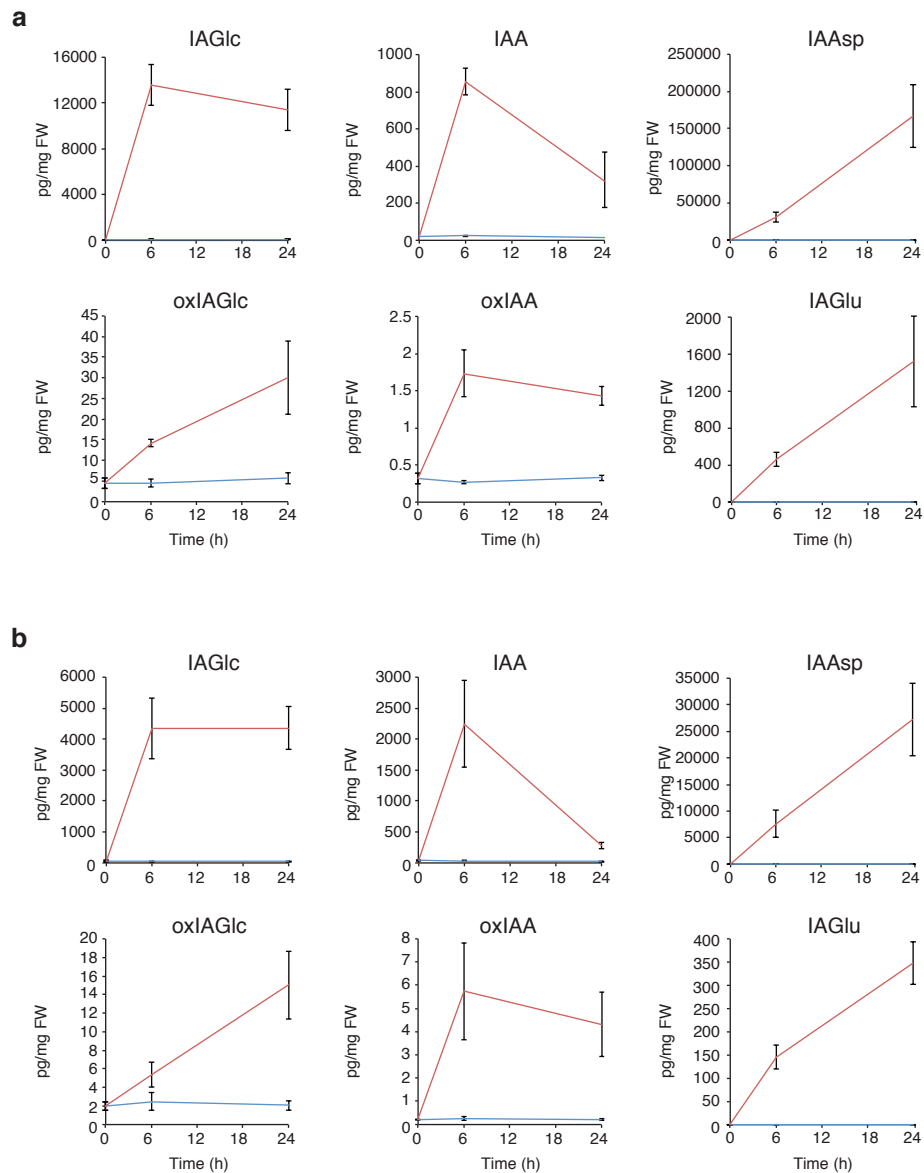


Figure S4

Concentrations of IAA metabolites in *Pinus sylvestris* and *Pinus contorta* roots after feeding with unlabeled IAA.

Two-week-old pine seedlings were incubated with (red line) or without (blue line) 10 μ M unlabeled IAA and the levels of IAA and IAA metabolites oxIAA, oxIAGlc, IAGlc, IAAsp and IAGlu were quantified in roots after different incubation times. Panel **a** indicates *P. sylvestris* and panel **b** indicates *P. contorta*. The concentrations of all metabolites are in picograms per milligram fresh weight (FW). Error bars indicate \pm SD (n = 4).

AtGH3.1	1	-----
AtGH3.2	1	-----
AtGH3.3	1	-----
AtGH3.4	1	-----
AtGH3.5	1	-----
AtGH3.6	1	-----
PpinGH3.16	1	-----
PaGH3.16	1	-----
PaGH3.gII.1	1	-----
PaGH3.gII.2	1	-----
PaGH3.gII.3	1	-----
PaGH3.gII.4	1	-----
PaGH3.gII.5	1	-----
PaGH3.gII.6	1	-----
PaGH3.gII.7	1	-----
PaGH3.gII.8	1	-----
PaGH3.gII.9	1	-----
PaGH3.gII.10	1	-----
AtGH3.9	1	-----
AtGH3.17	1	-----
PaGH3.17	1	-----
AtGH3.11	1	-----
AtGH3.10	1	-----
PaGH3.gI.1	1	-----
PaGH3.gI.2	1	MPGSIDSHEEVIREFEAMAQNAEEVIREFEAIAQNAERDNMKNRSEGGKRIEGEEGVKDE

AtGH3.1	1	-----MAV
AtGH3.2	1	-----MAVD
AtGH3.3	1	-----MTV
AtGH3.4	1	-----MAVD
AtGH3.5	1	-----MPEAP
AtGH3.6	1	-----MPEAP
PpinGH3.16	1	-----MPQAKREEG
PaGH3.16	1	-----MPQAKREES
PaGH3.gII.1	1	-----
PaGH3.gII.2	1	-----
PaGH3.gII.3	1	-----
PaGH3.gII.4	1	-----
PaGH3.gII.5	1	-----
PaGH3.gII.6	1	-----
PaGH3.gII.7	1	-----
PaGH3.gII.8	1	-----
PaGH3.gII.9	1	-----
PaGH3.gII.10	1	-----
AtGH3.9	1	-----
AtGH3.17	1	-----
PaGH3.17	1	-----
AtGH3.11	1	-----MDALK
AtGH3.10	1	-----
PaGH3.gI.1	1	-----
PaGH3.gI.2	61	SRRSNMTGSVDSHEEVIRELEAMTLKAERVQRETLEDNMNKGSEGGKMIIEGKEGALLNRV

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 AtGH3.2 5 SPLQSRMVSATTSEKDVKALKFIEEMTRNPDSVQEKVLGEILTRNSNTEYLKRFDLG---
 AtGH3.3 4 DSALRSPMMHSPSTKDVKALRFIEEMTRNVDFVQKKVIREILSRNSDTEYLKRFGLK---
 AtGH3.4 5 SLQSGMASPTTSETSEVKALEFIEEITRNPDVQEKVLGEILSRNSNTEYLKRFDLN---
 AtGH3.5 6 KKESEVFDLTLDOKKNKQKLFIEELTNSADQVQVLEEILTRNADVEYLRRHDLN---
 AtGH3.6 6 KIAALEVSDSESLAEKKNKQLQFIEDVTNADDVORVLEEILSRNADVEYLRRHGLE---
 PpinGH3.16 10 IESVQESIIATTEERNKALDFIEHATHAAEVQAEVLEILTRNAYTEYLERYQLT---
 PaGH3.16 10 MESVQECISIIATTEERNKALDFIEHATHAAEVQAEVLEILTRNAYTEYLERYQLT---
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 PaGH3.gII.2 1 -----
 PaGH3.gII.3 1 -----
 PaGH3.gII.4 1 MPEAPMRMGNRANDRDKRALDFIENVTTNADDEQVRVLSAILTRNANTEYLKRYGLS---
 PaGH3.gII.5 1 -----
 PaGH3.gII.6 1 -----
 PaGH3.gII.7 1 -----INGANDRHKAALFEIENVTRNADEVQARVLCSSILTRNGDTEYLKRHGLS---
 PaGH3.gII.8 1 ---MSSSLGNEVDDRNRKRALFEIETVTTDADEVQTVLSSILSRNADTEYLKRYGLN---
 PaGH3.gII.9 1 ---MSSAMGNGVSDRDKRALDFIESVTTNADDVQIRVLSILSRNADTEYLKRYGLN---
 PaGH3.gII.10 1 -----
 AtGH3.9 1 -----MDVMKLDHDSVLEKELERITSKAAEVQDNILRGILERNKDTTEYLSKY-MN---
 AtGH3.17 1 -----MIPSYDPNDTEAGLKLLEDLTTNAEAIQQQVLHQILSONSGTQYLRALF-LD---
 PaGH3.17 1 ----MEMNIRCAKDKGEAALQLIENLTARADEVQKQVLYEILRNAAETEYLNKFLN---
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 AtGH3.10 1 -----METVEAGHDDVIGWFEHVSSENACKVQSETLRRILELNSGVEYLRKWLGTVDV
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 PaGH3.gI.2 121 KDESRRSDMPGSVDSHEEVIREFEAMTHNAERVQRETLEAILQRNSGTEYLKKGWVGF---

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 AtGH3.2 62 GVVDR--KT--FKSKVPVITYEDLKPEIQRISNGDCSPILSSHPITEFLTSSGTSAGERK
 AtGH3.3 61 GFTDR--KT--FKTKIPVITYDDLKPEIQRIANGDRSMILSSYPITEFLTSSGTSAGERK
 AtGH3.4 62 GAVDR--KS--FKSKVPVITYEDLKTDIQRIANGDRSPILSSHPITEFLTSSGTSAGERK
 AtGH3.5 63 GRTDR--ET--FKNIMPVITYEDIPEINRIANGDKSPILSSKPISEFLTSSGTSAGERK
 AtGH3.6 63 GRTDR--ET--FKHIMPVITYEDIQPEINRIANGDKSQVLCNSPISEFLTSSGTSAGERK
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 PaGH3.16 67 GRTDR--ES--FKECFPVITYEDLQPEILRIANGDTSPILSAHPISEFLTSSGTSAGERK
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 PaGH3.gII.5 1 -----
 PaGH3.gII.6 1 -----
 PaGH3.gII.7 51 GRTNR--ST--FKKCLPVITYDDLKPEIRRIANGDTSPILSAHPVSEFLTSSGTSAGERK
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 PaGH3.gII.9 55 GRTDR--AT--FKECLPVITYDDLQPDIRRVGRDTSPILSAHPVSEFLTSSGTSAGERK
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 PaGH3.17 53 GRIDN--KS--FKINVPVNYEDIKPYIQRIANGDASAIISAEPISELLTSSGTSAGQPK
 AtGH3.11 63 GNATDPEEA--FKSMVPLVTDVELEPYIKRMVDGDTSPILTGHVPVPAISLSSGTSAGRPK
 AtGH3.10 53 EKMDDYTLETLETSLVPIVSHADLPYIQRIADGETSPILLTQEPITVLSLSSGTEGRQK
 PaGH3.gI.1 1 -----
 PaGH3.gI.2 178 QGSTDPDPLQHFKSCVPVVCYPDLAPYMQRIADGDTSPILTADPITAFSLTAGTGDGNQK

AtGH3.1 117 LMPTI**KEELD**-----RRQLLYS**LLMPVMNL**-YVPGLDKGKGM**YFLFVKS**
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 AtGH3.3 117 LMPTI**EDMD**-----RRQLLYS**LLMPVMNL**-YVPGLDKGKAL**YFLFVKT**
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 AtGH3.5 119 LMPTI**EEELD**-----RRSLLYS**LLMPVMSQ**-FVPGL**ENKGM**YFLFIKS
 AtGH3.6 119 LMPTI**EEELD**-----RRSLLYS**LLMPVMDQ**-FVPGLDKGKGM**YFLFIKS**
 PpinGH3.16 123 IMPTI**HEELK**-----RR**TLLYS**LLMPVMNQ-YMKGLDKGKGM**YFLFVKS**
 PaGH3.16 123 IMPTI**HEELE**-----RR**TLLYS**LLMPVMNQ-YMEGLDKGKGM**YFLFIKS**
 PaGH3.gII.1 110 LVPTI**EDME**-----RR**ALLIS**LVMPIMSQ-YMEGLDKGKGM**YFLFINS**
 PaGH3.gII.2 1 -----
 PaGH3.gII.3 1 -----
 PaGH3.gII.4 114 LMPTI**QEELE**-----R**KTLLYS**LLMPVMNQ-----
 PaGH3.gII.5 1 -----
 PaGH3.gII.6 1 -----
 PaGH3.gII.7 107 LMPTI**QEEWE**-----R**RNLLYK**LLMPVMNQ-YVQGLDKGKGM**YFYFIKS**
 PaGH3.gII.8 111 LMPTI**QEELE**-----R**KALLY**SLLMPVMNQ-YMKGLDEGKGM**YFFFIKS**
 PaGH3.gII.9 111 LMPTI**QEELE**-----R**KALLY**SLLMPVMNQ-YMQGLDKGKGM**YFFFIKS**
 PaGH3.gII.10 1 -----
 AtGH3.9 105 LMPTI**PEDLD**-----R**RTFLYNLI**PIV**NK**-YITGLDKGKAM**YLN**FVKA
 AtGH3.17 109 LM**PS**T**A**E**E**L**E**-----R**K**T**FFYS**M**L**V**P**I**M**N**K**-YVDGLDEGKGM**YLL**FIKP
 PaGH3.17 109 IM**PS**I**P**E**E**L**H**R**K**T**F**L**Y**N**L**L**M**P**I**M**N**K**Y**R**K**T**F**L**Y**N**L**L**M**P**I**M**N**K**Y**-YVPGLDKGKGM**Y**LQFIKT
 AtGH3.11 121 F**I**P**F**T**D**E**L**M**E**-----N**T**L**Q**L**F**R**T**A**F**A**F**R**N**R-D**F**P**I**D**D**N**G**K**A**L**Q**F**I**F**S**S**K**
 AtGH3.10 113 Y**V**P**F**T**R**H**S**A**Q**-----T**T**L**Q**I**F**R**L**S**A**A**Y**R**S**R-F**Y**P**I**R**E**G**G**R**I**L**E**F**I**Y**A**G**K**
 PaGH3.gI.1 1 -----L**F**P**I**K**P**G**G**R**V**L**E**F**V**Y**G**S**K**
 PaGH3.gI.2 238 L**V**P**F**N**D**S**V**I**A**-----S**K**L**Q**Y**R**I**T**N**A**Y**T**A**R**Q**F**P**P**P**Q**S**Q**S**R**F**L**Q**F**I**Y**G**S**R

AtGH3.1 160 E**T**K**T**P**G**G**L**P**A**R**P**V**L**T**S**Y**Y**K**S**E**H**F**R**S**R**--P**Y**D**P**Y**N**V**Y**T**S**P**N**E**A**I**L**C**P**D**S**F**Q**S**M**Y**T**Q**M**L**C**G**L**
 AtGH3.2 161 E**S**K**T**S**G**G**L**P**A**R**P**V**L**T**S**Y**Y**K**S**D**H**F**K**R**R**--P**Y**D**P**Y**N**V**Y**T**S**P**N**E**A**I**L**C**S**D**S**S**Q**S**M**Y**A**Q**M**L**C**G**L**
 AtGH3.3 160 E**S**K**T**P**G**G**L**P**A**R**P**V**L**T**S**Y**Y**K**S**E**Q**F**K**R**R**--P**N**D**P**Y**N**V**Y**T**S**P**N**E**A**I**L**C**P**D**S**S**Q**S**M**Y**T**Q**M**L**C**G**L**
 AtGH3.4 161 E**S**T**T**S**G**G**L**P**A**R**P**A**L**T**S**Y**Y**K**S**D**Y**F**R**T**S**---D**S**D**S**V**Y**T**S**P**K**E**A**I**L**C**D**S**S**Q**S**M**Y**T**Q**M**L**C**G**L
 AtGH3.5 162 E**S**K**T**P**G**G**L**P**A**R**P**V**L**T**S**Y**Y**K**S**S**H**F**K**E**R**--P**Y**D**P**Y**T**N**Y**T**S**P**N**E**T**I**L**C**S**D**S**Y**Q**S**M**Y**S**Q**M**L**C**G**L**
 AtGH3.6 162 E**S**K**T**P**G**G**L**P**A**R**P**V**L**T**S**Y**Y**K**S**S**H**F**K**N**R**--P**Y**D**P**Y**T**N**Y**T**S**P**N**Q**T**I**L**C**S**D**S**Y**Q**S**M**Y**S**Q**M**L**C**G**L**
 PpinGH3.16 166 E**T**R**T**P**G**G**L**L**A**R**P**V**L**T**S**Y**Y**K**S**Q**D**F**I**E**R**--P**Y**D**P**Y**N**V**Y**T**S**P**M**E**A**I**L**C**S**D**S**Y**Q**S**M**Y**C**Q**L**L**C**G**L**
 PaGH3.16 166 E**T**R**T**P**G**G**L**L**A**R**P**V**L**T**S**Y**Y**K**S**Q**H**F**R**E**R**--P**Y**D**P**Y**N**V**Y**T**S**P**I**E**A**I**L**S**A**D**S**Y**Q**S**M**Y**C**Q**L**L**C**G**L**
 PaGH3.gII.1 153 E**S**K**T**P**G**G**L**L**A**R**Y**S**S**T**R**W**Y**K**S**R**F**L**K**D**K**P**L**P**Y**D**P**Y**N**V**Y**T**S**P**I**E**T**I**L**C**P**D**A**Y**Q**S**M**Y**C**Q**L**L**C**G**L**
 PaGH3.gII.2 1 -----
 PaGH3.gII.3 1 -----
 PaGH3.gII.4 1 -----
 PaGH3.gII.5 1 -----M**C**D-----
 PaGH3.gII.6 1 -----
 PaGH3.gII.7 150 E**A**K**T**P**G**G**L**L**A**R**P**V**L**T**S**Y**Y**K**S**S**H**Y**F**R**E**R--P**Y**D**P**Y**N**V**C**T**S**P**I**Q**T**I**L**C**P**D**A**Y**Q**S**M**Y**S**Q**L**L**C**G**L**
 PaGH3.gII.8 154 E**A**K**T**P**G**G**L**L**A**R**P**V**L**T**S**Y**Y**K**S**D**Y**F**K**E**R**--P**Y**D**P**Y**N**V**Y**T**S**P**N**Q**T**V**L**C**Q**D**A**Y**Q**S**M**Y**S**Q**L**L**C**G**L**
 PaGH3.gII.9 154 E**A**K**T**P**G**G**L**P**A**R**P**V**L**T**S**Y**Y**K**S**P**H**F**R**E**R**--P**Y**D**P**Y**N**V**Y**T**S**P**N**Q**T**V**L**C**P**D**A**Y**Q**S**M**Y**S**Q**L**L**C**G**L**
 PaGH3.gII.10 1 -----
 AtGH3.9 148 E**T**S**T**P**C**G**L**P**I**R**A**V**L**T**S**Y**Y**K**S**K**H**F**Q**C**R**--P**Y**D**P**F**N**D**L**T**S**P**I**Q**T**I**L**C**E**D**S**N**Q**S**M**Y**C**Q**L**L**A**G**L**
 AtGH3.17 152 E**I**K**T**P**S**G**L**M**A**R**P**V**L**T**S**Y**Y**K**S**Q**H**F**R**N**R**--P**F**N**K**Y**N**V**Y**T**S**P**D**Q**T**I**L**C**Q**D**S**K**Q**S**M**Y**C**Q**L**L**C**G**L**
 PaGH3.17 168 E**V**T**T**P**S**G**L**K**A**R**P**V**L**T**S**Y**Y**K**S**S**N**F**R**D**R**--P**F**D**K**F**N**V**Y**T**S**P**D**E**T**I**L**C**P**D**S**R**Q**S**M**F**C**Q**L**L**C**G**L**
 AtGH3.11 164 Q**Y**I**S**T**G**G**V**P**V**G**T**A**T**T**N**V**Y**R**N**P**N**F**K**A**G**--M**K**S**I**T**S**P**S**C**S**P**D**E**V**I**F**S**P**D**V**H**Q**A**L**Y**C**H**L**L**S**G**I**
 AtGH3.10 156 E**F**K**T**L**G**G**L**T**V**G**T**A**T**H**Y**A**S**E**E**F**K**T**K**--Q**E**T**T**K**S**F**T**C**S**P**Q**E**V**I**S**G**G**D**F**G**Q**C**T**Y**C**H**L**L**L**G**L**
 PaGH3.gI.1 19 E**S**S**T**K**G**G**L**V**A**S**T**A**T**T**N**I**Y**R**S**E**S**F**K**I**Y**--K**K**N**I**Q**I**L**G**C**S**P**D**E**V**I**F**G**F**D**S**R**Q**S**M**Y**C**H**I**L**C**G**L**
 PaGH3.gI.2 282 Q**F**L**T**K**G**G**L**E**A**S**N**A**S**G**L**G**L**R**S**K**G**F**K**K**Y**--K**E**S**N**Q**W**L**A**C**S**P**E**E**V**V**F**G**F**N**Y**E**Q**S**L**Y**C**H**L**L**C**G**L**

AtGH3.1 218 IDRLSVLRVGVAVFASGLLRRAIRFLQLHWSRFAHDIELGCLDS-EITDPSIRQCMG-ILK
 AtGH3.2 219 IMRHEVLRIGAVFASGLLRRAISFLQNNWKEKARDISTGTLSS-RIFDPAIKNRMSKILTK
 AtGH3.3 218 IMRHEVLRIGAVFASGLLRRAIGFLQTNWKEKARDISTGTLSS-RISDPAIKESMSKILTK
 AtGH3.4 217 IMRHEVLRIGAVFASGLLRRAISFLQNNWKEKARDISTGTLSS-KIFDHAIAKTRMSNILNK
 AtGH3.5 220 CQHQEVLRVGVAVFASGFIRAIKFLFKHWIELVRDIRTGTLS-LITDPSVREAVAK-ILK
 AtGH3.6 220 CQHKEVLRVGVAVFASGFIRAIKFLFKHWIELVRDIRTGTLS-LITDPSVREAVAK-ILK
 PpinGH3.16 224 AQNHEVLRVGVAVFASGLLRRAIRFLEEHWQSLCQDIRSGTVNDEEVTDPCLRESVMK-LLH
 PaGH3.16 224 AQNHEVLRVGVAVFASGLLRRAIRFLEEHWQSLCQDIRSGTINDEEVTDPCLRESVMK-ILR
 PaGH3.gII.1 213 IQNYEVLRMGAVFASGFIRAIKFLFKHWIELVRDIRTGTLS-LITDPSVREAVAK-ILK
 PaGH3.gII.2 1 -----
 PaGH3.gII.3 1 -----
 PaGH3.gII.4 -----
 PaGH3.gII.5 4 -----
 PaGH3.gII.6 1 -----
 PaGH3.gII.7 208 IQNNE-----
 PaGH3.gII.8 212 IQNNEVLRMGAIVFASGFIRAIKFLFKHWIELVRDIRTGTLS-LITDPSVREAVAK-LLH
 PaGH3.gII.9 212 IQNNEVLRMGAIVFASGFIRAIKFLFKHWIELVRDIRTGTLS-LITDPSVREAVAK-LLH
 PaGH3.gII.10 1 -----
 AtGH3.9 206 IHRHKVLRVGVAVFASAFIRRAISYLEKKWSQLCEDIRTGSLNP-MITDPPGCOMAMSCLLMS
 AtGH3.17 210 VQRSHVLRVGVAVFASAFIRRAIKFLFKHWIELVRDIRTGTLS-LITDPSVREAVAK-LLH
 PaGH3.17 226 IQRDEVLRVGVAVFASAFIRRAIKFLFKHWIELVRDIRTGTLS-LITDPSVREAVAK-LLH
 AtGH3.11 222 LFRDQVQYVFAVFAHGLVHAFRTFEQVWEIIVTDIKDGVLSN-RITVPSVRTAMSK-LLT
 AtGH3.10 214 HYSQVEFVSAFYSYTIIVQAFSFEIIRREICADIKEGNLS-RITLPMRKAVALA-LIR
 PaGH3.gI.1 77 LYSNEVQFMSSTFSYSIVFAFRTFEGVWQQLCTDIKEGTLNK-EITVPSMRASVSK-LLK
 PaGH3.gI.2 340 LYSNEVQFMSSTFSYSIVFAFRTFEGVWQQLCTDIKEGTLNK-EITVPSMRASVSK-LLK

AtGH3.1 276 PDPVLAELFIRRECKSD--N--WEKIITRIWPNTKYLDVIVTGAMAQYIPTLEYYS-GGLP
 AtGH3.2 278 PDQELAELFVGVCSQE--N--WEGIIITKIWPNTKYLDVIVTGAMAQYIPTLEYYS-GGLP
 AtGH3.3 277 PDQELADFITSVCGQD--N--WEGIIITKIWPNTKYLDVIVTGAMAQYIPMLEYYS-GGLP
 AtGH3.4 276 PDQELAELFLIGVCSQE--N--WEGIIITKIWPNTKYLDVIVTGAMAQYIPMLEYYS-GGLP
 AtGH3.5 278 PSPKLADFVEFECKKS--S--WQGIITRLWPNTKYVDVIVTGTMSQYIPTLDYYS-NGLP
 AtGH3.6 278 PDPKLADFVESECRKT--S--WQGIITRLWPNTKYVDVIVTGTMSQYIPTLDYYS-NGLP
 PpinGH3.16 283 PNTQLADLIRTECSKE--S--WQGIITRLWPNTKYVDVIVTGTMSQYIPTLDYYS-NGLP
 PaGH3.16 283 PKIQLADLIRTECSKE--S--WQGIITRLWPNTKYVDVIVTGTMSQYIPTLDYYS-NGLP
 PaGH3.gII.1 272 PNPELAELIQRNCSAP--S--WQGIITRLWPNTKYIKTVVTGAMAQYIPTLDYYS-GGLP
 PaGH3.gII.2 1 -----
 PaGH3.gII.3 1 -----
 PaGH3.gII.4 -----
 PaGH3.gII.5 4 -----W-----FP
 PaGH3.gII.6 1 -----
 PaGH3.gII.7 213 -----YIPTLDYYS-AGLP
 PaGH3.gII.8 270 PNPELADLIRRECKSAQ--S--WQGIITRLWPNTKYIDVIVTGAMAQYIPTLDYYS-GGLP
 PaGH3.gII.9 270 PNPELADLIRRECKSAQ--S--WQGIITRLWPNTKYIDVIVTGAMAQYIPTLDYYS-GGLP
 PaGH3.gII.10 1 -----
 AtGH3.9 265 PNPELASEIEEICGRS--S--WKGIIICQLWPKAKFIEAVVTGSMQYIPALEFFSQGKIP
 AtGH3.17 269 PNQELAELIESECAEK--S--WEGILRRIWPNTKYVEVIVTGTMSQYIPTLEFYS-GGLP
 PaGH3.17 284 PNPQLAEIIEHGECSSK--S--WQGIITRLWRKTIYIDVIVTGTMSQYIPTLDYYS-GGLP
 AtGH3.11 280 PNPELAELIRTKCMSL--S--NWYGLIPALFPNAKYVYVIMTGSMEPYVPKLRHYA-GDLP
 AtGH3.10 272 PNPSLASHIEEICLELETNLGWFGLISKLWPKAKFISSIMTGSMLPYLNKLRHYA-GDLP
 PaGH3.gI.1 135 PDPDLADATYKCKNI--G--NWHGVIPLWPKAKFISSIMTGSMEPYVPKLRHYA-GDLP
 PaGH3.gI.2 398 PNPELAQSIIFETCEKLLTN--NWYGVVHKLWPKAKFISSIMTGSMEAYVKKLRHYA-GDLP

AtGH3.1 331 MACTMYASSECYFGINLNPMSKPSSEVSYTIMPNMAYFEFIPLG-----
 AtGH3.2 333 MACTMYASSESYFGINLKPCKPSEVSYTIMPNMAYFEFLPHNHGDG-----GA
 AtGH3.3 333 MACTMYASSESYFGINLKPCKPSEVSYTIMPNMAYFEFLPHHEVPTE-----
 AtGH3.4 331 MASMITYASSESYFGINLNPCKPSEVSYTIFPNMAYFEFLPHNHGDG-----
 AtGH3.5 333 IVCTMYASSECYFGVNLRLPCKPSEVSYTLIPSMAYFEFLPVHRNNG----VTNSINLPK
 AtGH3.6 333 IVCTMYASSECYFGVNLRLPCKPSEVSYTLIPSNMAYFEFLPVHRNSG----VTSSISLPK
 PpinGH3.16 338 QVCTMYASSECYFGINLKPCKPSEVSYTLIPNMAFFFEFLPVYRNKNEAG-----PV
 PaGH3.16 338 QVCTMYASSECYFGINLKPCKSSEVSYTLMPNMAFFFEFLPVYRNNDDA-----AP
 PaGH3.gII.1 327 IVCTMYSSSEGSFGINLNPCKPTEVSYTLIPNMAFFFEFLPVHRQEFG--LSIESPAIPK
 PaGH3.gII.2 1 -----MAYFEFLPVHRKQEEAGATLES PAITK
 PaGH3.gII.3 1 -----
 PaGH3.gII.4 1 -----
 PaGH3.gII.5 7 QRCA-----
 PaGH3.gII.6 1 -----
 PaGH3.gII.7 226 IVCTMYASSECYFGINLKPCKPSEVSYTLIPNMAFFFEFLPVHRKQLQLEAQE-----CP
 PaGH3.gII.8 325 IVCTMYASSECYFGINLKPCKPSEVSYTLIPNMAFFFEFLPVHRKQEEAGLTIESSTIPK
 PaGH3.gII.9 325 IVCTMYASSECYFGINLKPCKPFEVSYTLIPNMAFFFEFLPVHRKQEEAGVTLES---PG
 PaGH3.gII.10 1 -----
 AtGH3.9 321 IVCPMYASSETYFGVNVPELSPKPSDVVFTLLPNMCFEYFIPLGKNGTLSFD-----LD
 AtGH3.17 324 IVSTMYASSECYFGINLNPCLDPADVSYTLIPNMAFFFEFLPVDDKSHEEIHFATHSNTDD
 PaGH3.17 339 IVSTMYASSECYFGVNLKPL-----KVLDLQSNNGTE-----
 AtGH3.11 336 IVSHDYGSSEGWIAANVTPRLSPPEATFAVIPNLGYFEFLPVSETGEG-----
 AtGH3.10 331 IVSADYGSSESWIGVNVDPHLPEDVSVFAVIPTFSYFEFIPLYRRQNQSDICI-----
 PaGH3.gI.1 191 LLTSEYCGATEGWIAANIDPTSSPENTIYTVVVDIGYFEFIPHLRHEGLKLDN-----SV
 PaGH3.gI.2 456 ILPGGYAVSEGYLAVNIDS----ATTFTVVPSTAFFEFIPQDKEG-----

AtGH3.1 374 -----GTKAVELVDVNIKKEYELVVTTYAGLCRYRVGDIILRVTFGHNSAPQFHFVRRKN
 AtGH3.2 382 AEASLDETSILVELANVEVGKEYELVITTYAGLYRYVGDILRVTFGHNSAPQFKFIRRN
 AtGH3.3 381 -----KSELVELADVEVGKEYELVITTYAGLNRVYVGDILQVTFGFYNSAPQFKFVRRKN
 AtGH3.4 379 ---GVEATSILVELADVEVGKEYELVITTYAGLYRYVGDILRVTFGHNSAPQFKFIRREN
 AtGH3.5 389 ALTEKEQQELVDLVDVKLGOEYELVVTTYAGLCRYRVGDILRVTFGFKNKAPQFSFICRKN
 AtGH3.6 389 ALTEKEQQELVDLVDVKLGOEYELVVTTYAGLYRYVGDVLSVAGFKNNAPQFSFICRKN
 PpinGH3.16 391 TTATEQPAELVDLVDVKVGOEYELVITTYSGLYRYRVGDVLRVTFGHNAAPQFQFVCRKN
 PaGH3.16 389 VTMATEQQELVDLADVTVGQYELVITTYAGLYRYVGDVLRVTFGFYNAAPQFQFVCRKN
 PaGH3.gII.1 385 AVDEKEEKDLVLDLVDVKVGOEYELVVTTYAGLYRYVGDVLRVTFGHNAAPQFHFVCRQN
 PaGH3.gII.2 28 TLDEKEREELVELVDVKLGOEYELVVTTYAGLNRVYVGDVLRVTFGFYNAAPQFHFVCRQN
 PaGH3.gII.3 1 -----
 PaGH3.gII.4 1 -----
 PaGH3.gII.5 11 -----SIPCRQN
 PaGH3.gII.6 1 -----MTGFHNNTAPQFHFVYRQN
 PaGH3.gII.7 280 TLNEKDQDELVDLVDVKLGOEYELVITTYAGLYRYVGDVLRVTFGHNAAPQFHFVCRQN
 PaGH3.gII.8 385 TLDDKEREELVELVDLKLGOEYELVVTTYAGLNRVYVGDVLRVTFGHNAAPQFHFVCRQN
 PaGH3.gII.9 382 TLDEKEREELVELADVKLGOEYELVVTTYAGLNRVYVGDVLRVTFGFYNAAPQFHFVCRQN
 PaGH3.gII.10 1 -----MHNS----NFVCRQN
 AtGH3.9 374 DDEQVPCDKVLDLVDVNLKGRYELVVTTFAGLYRYRIGDVLQVAGFYNGAPQFRFICRRN
 AtGH3.17 384 DDDALKEDLIVNLVNVVEVGQYEVITTFITGLYRYRVGDILKVTGFHNKAPQFRFVQRN
 PaGH3.17 370 -NGKKIEDLVDLVDVKVGHYELVVTTYAGLYRYVGDILLVTFGFYNRAPQFEFVYRRN
 AtGH3.11 384 -----EEKPVGLTQVKIGEEYEVVITNYAGLYRYRIGDVVKVIGFYNNTPQLKFI CRN
 AtGH3.10 384 -DGDFVEDKPVPLSQVKLGOEYELVLTTFITGLYRYRIGDVVEVTSFHKGTPKLSFIYRRK
 PaGH3.gI.1 246 ATADYIESLPVGLTFVKVGOEYEVVLTTFAGLYRYRIGDVVKVTGFYNSPQLSYICRKN
 PaGH3.gI.2 498 -----QAEPIGLTFEVIIGKEYEVVITTFGG-----

AtGH3.1 428 VLLSIDSDKTDESELQKAVENAS--SILHEECGSRVAEYTSYADTSTIPGHYVLYWELLV
 AtGH3.2 442 VLLSVEESDKTDEAEELQKAVENAS--RLFAEQ-GTRVIEYTSYAETKTIPGHYVIYWELLG
 AtGH3.3 435 VLLSIESDKTDEAEELQSAVENAS--LLLGEQ-GTRVIEYTSYAETKTIPGHYVIYWELLV
 AtGH3.4 436 VLLSIESDKTDEADLQKAVENAS--RLLAEQ-GTRVIEYTSYADTKTIPGHYVIYWELLS
 AtGH3.5 449 VVLSIDSDKTDEVELQNAVKNV--THLVPF-DASLSEYTSYADTSSIPGHYVLFWELCL
 AtGH3.6 449 VVLSIDSDKTDEVELQNAVKNV--THLVPF-DASLSEYTSYADTSSIPGHYVLFWELCL
 PpinGH3.16 451 VMLSIDADKTDEAEELHNAVNAV--KHLEPL-EATLVEYTSYTDSTIPGHYVLYWELRT
 PaGH3.16 449 VMLSIDSDKTDEAEELHSAVKNV--KHLEPF-EASLVEHTSYAETSTIPGHYVLYWELRN
 PaGH3.gII.1 445 VVLSIHIIDKTDEAEELQSSVEKSI--KHLKPF-DITLMDYTSYADTSTIPGHYVLYWELRF
 PaGH3.gII.2 88 VVLSIDADKTDEAEELHSAVENS--KHLEPF-DAQLIEYTSYADTSTIPGHYVLYWELRF
 PaGH3.gII.3 1 -----MDEAEELHSAVENSA--KHLEPF-DAQLIEYTSYADTATIPGHYMLYWELHF
 PaGH3.gII.4 -----
 PaGH3.gII.5 18 VVLSIDSDKTDEAEERHSAVENSA--KHLEPF-DAQLIEYTRYSDTATIPGHYVLYWELHF
 PaGH3.gII.6 19 VVLSIDSDKRDEVELHSAVENFA--KHLEPF-NAQLIEYTSYADIATIPGHYVLYWELRF
 PaGH3.gII.7 340 VVLSIDSDKTDEAEELQSAVENS--KHLEPF-DSKLEIYTSYADTSTIPGHYVLYWELGS
 PaGH3.gII.8 445 VVLSIDSDKTDEVELHSAVENS--KHLEAF-DAQLIEYTSYADTGTIPGHYVLYWELRF
 PaGH3.gII.9 442 VVLSIDSDKTDEAEELHSAVENSA--KHLVPF-HAQLVEYTSYADTATIPGHYVLYWELRF
 PaGH3.gII.10 12 VVLSIDSNKTDEVELHSAIENS--KHLEAF-DAQLIEYTSYAETGTIPGHYVLYWELRF
 AtGH3.9 434 VVLSIDLDKTNEEDLHRSTLAK--KKLGS--NAFLAEYTSYADTSSVPGHYVLFWEIQG
 AtGH3.17 444 VVLSIDIDKTSEEDLNAVTAQLNHLQHP--SLLLTEYTSYADTSSIPGHYVLFWELKP
 PaGH3.17 429 VVLSIDIDKTNEEDLLKAVTKAK--KLELPE-NALLSEYTSYADTSTLPGHYVLFWELNT
 AtGH3.11 438 LILSINIDKNTERDLQLSVESAA--KRLSEE-KIEVIDFSSYIDVSTDPGHYAFWEISG
 AtGH3.10 443 LILINIDKNTKDLQRVVDKAS--QLLSRSTRAEVVDFTSHADVIARPGHYVIYWEIRG
 PaGH3.gI.1 306 LILTVNIDKTEKDLQISVDKAT--ELLKEE-NVDLVDFTSYADLSTVPGHYVIFWELSD
 PaGH3.gI.2 523 -----AFYINL--

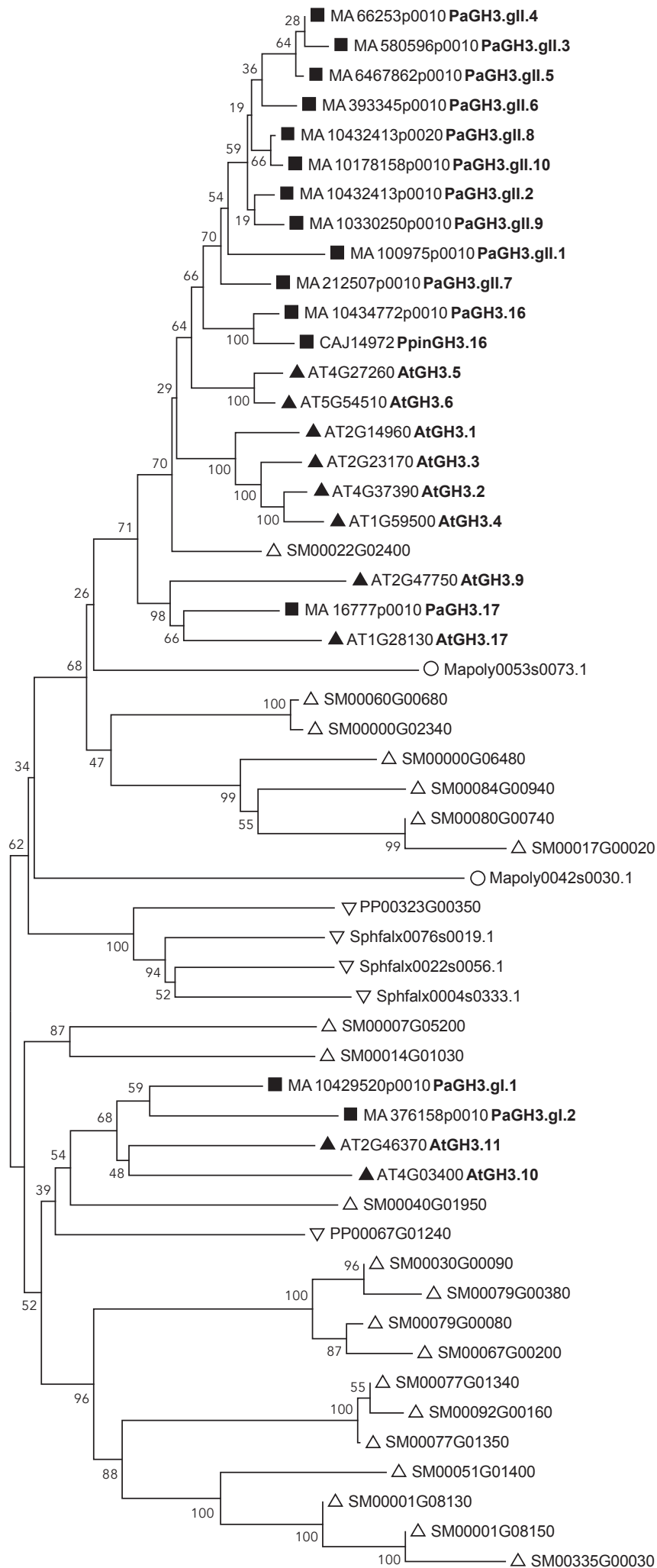
AtGH3.1 486 RDGA---RQPSHETLTRCCLGMEESLNSVYRQSRVADNSVGPLEIRVVRNGTFEELMDYA
 AtGH3.2 499 RDQSN--ALMSEEVMAKCCLEMEESLNSVYRQSRVADKSIGPLEIRVVRNGTFEELMDYA
 AtGH3.3 492 KDQT---NPPNDEVMARCCLEMEESLNSVYRQSRVADKSIGPLEIRVVKNGTFEELMDYA
 AtGH3.4 493 RDQSN--ALPSDEVMARCCLEMEESLNAVYRQSRVSDKSIGPLEIRVVQNGTFEELMDFS
 AtGH3.5 506 DGNT---PIPP-SVFEDCCLAVEESFNTVYRQGRVSDKSIGPLEIKIVEPGTFDKLMDYA
 AtGH3.6 506 NGNT---PIPP-SVFEDCCLTVEESLNSVYRQGRVSDKSIGPLEIKMVESGTFDKLMDYA
 PpinGH3.16 508 SAL----PVPP-SVFEDCCLTVEESLNSVYRQCRVADKSIGPLEIKVVEMGTDFDKLMDYA
 PaGH3.16 506 STV----PVPA-SVFEDCCLTVEESLNSVYRQCRVADKSIGPLEIKVVETGTDFDKLMDYA
 PaGH3.gII.1 502 NNKEVAGAVPS-SVFEDCCLTVEESLNFVYRQGRGADKSIAPLEIRVVEEGTFEQLMDRA
 PaGH3.gII.2 145 NTKSVADAVPS-SVFEDCCLTVEESLNSVYRQGRASDNSIA-----
 PaGH3.gII.3 49 NTKTV--EVPF-SVFEDCCLTAEESLNSIYRQGRASDKSIGPMEIRVVEEGMFDELMDYA
 PaGH3.gII.4 -----
 PaGH3.gII.5 75 STKTV--EVPF-SVFEDCCLTAEESLNSIYRQGRASDKSIDPMEIRVVEEETFDELMDYA
 PaGH3.gII.6 76 NTKAV--EVPS-LVFEDCCLTVEESLNFVYRQGRAFDKSIGPLEIRVVEEGTFDELMDYA
 PaGH3.gII.7 397 KEVAL--TIPP-SVFEDCCLTVEESLNSVYRQGRVSDKSIGPLEIRVVEDGTDFDELMDYA
 PaGH3.gII.8 502 NTKAI--EVPS-SVFEDCCLTAEESLNSVYRQGRASDKSIGPLEIRVVEEGTFNELMDYA
 PaGH3.gII.9 499 DTKAV--AFPS-SVFEDCCLTVEESLNSVYRQGRASDRSIGPLEIRVVEEGTFDQLMDYA
 PaGH3.gII.10 69 NTKAI--EVPS-SVFEDCCLTAEESLNSVYRQGRASDKSIGPLEIRVVEEGTFDELMDYA
 AtGH3.9 490 HLEP-----KLMEECCVAEEELDYTYRQCRTKERSIGALEIRVVKPGTFEKLMDLI
 AtGH3.17 503 RHSNDPPKDD-KTMECCSEVEDCLDYVYRRCRNRDKSIGPLEIRVVS LGTFDSLMDFC
 PaGH3.17 486 RE-----EFLDASVLES CCSTIEESLDSIYRRCRTKDKSIGPLEIRLVKPGTFD LLMDYC
 AtGH3.11 495 ETNE-----DVLQCCNCLDRAFIDAGYVSSRKCKTIGALELRVVAKGTFRKI QEHF
 AtGH3.10 501 EADD-----KALEECCREMDTAFVDYGYVSSRRMNSIGPLELRVVERGTFGKVAERC
 PaGH3.gI.1 363 SLNE-----GIVKRCCSIMDETFIDPGYVSSRKANTIGPLELRIVERGTFRKI IDYY
 PaGH3.gI.2 -----

AtGH3.1 543 ISRGASINQYKVPRCVN-F-TPIVELLDSRVVSAHFSPSLPHWTPERRRR-----
 AtGH3.2 557 ISRGASINQYKVPRCVS-F-TPIVELLDSRVVSAHFSPSLPHWSPERRR-----
 AtGH3.3 549 ISRGASINQYKVPRCVS-F-TPIVELLDSRVVSTHFSPALPHWSPERRR-----
 AtGH3.4 551 ISRGSINQYKVPRCVS-L-TPIMKLLDSRVVSAHFSPSLPHWSPERRH-----
 AtGH3.5 562 ISLIGASINQYKTPRCVK-F-APIIELLNSRVVDSYFSPKCPKWVPGHKQWGSN-----
 AtGH3.6 562 ISLIGASINQYKTPRCVK-F-APIIELLNSRVVDSYFSPKCPKWVPGHKQWGSN-----
 PpinGH3.16 563 ISRGSINQYKAARCVK-F-APMVDILNSRVASASYFSPRCPKWTAGRTQWGALPR---
 PaGH3.16 561 ISRGSINQYKAPRCVK-F-APMVDLLKSRVSAASYFSPRCPKWTPGRTQWGAITRLI-
 PaGH3.gII.1 561 VCQKASINQYKAPRCVK-S-TSMVELLNSRVVHSYFSPRSPMWWVPGSAVSKLVGS---
 PaGH3.gII.2 -----
 PaGH3.gII.3 106 ISRGASINQYKAPRCIK-F-APIVELLNSRVVHSYFNPHNGLSDAEIGHNISLLK---
 PaGH3.gII.4 -----
 PaGH3.gII.5 132 ISRGASINQ-----
 PaGH3.gII.6 133 E-----
 PaGH3.gII.7 454 ISRGASINQYKVPRCVK-C-SPIVGLLNSRVVHSYFSPKCPQWAPGCRKWA-----
 PaGH3.gII.8 559 ISRGASINQYKAPRCIK-F-TPIVELLNSRVVHSYFSPQPPQWAPGCRNWA-----
 PaGH3.gII.9 556 ISRGASINQYKAPRCVK-F-TPIVELLNSRVVHSYFSTQPPQWAPGCREWA-----
 PaGH3.gII.10 126 ISRGASINQYKAPRCIK-F-TPIVELLNSRVVHSYFSPQPPQWAPGCRNWA-----
 AtGH3.9 542 ISQGGSEINQYKTPRCVK-SNSATFKLLNGHVMAFFSPRDPTWVP-----
 AtGH3.17 562 VSQGSSEINQYKTPRCVK-S-GGALEILDNRVIGRFFSKRVPOWEPLGLDS-----
 PaGH3.17 541 INQGSSEINQYKTPRCIK-S-LHVLGLLNSKVTAKYFSKRLPSWTPYNPGLNPNNSQLY
 AtGH3.11 547 IGLGSAGQFKMPCVKPSNAKVLQILCENVVSSYFSTAF-----
 AtGH3.10 553 VGECCGLNQFKTPRCT--TNSVMLDILNDSTIKRFRSSAYD-----
 PaGH3.gI.1 415 TSHGCAVNQFKTPRCIS-TNQALLDILNKNTIQTCFSTLFS-----
 PaGH3.gI.2 -----

Fig. S5

Multiple sequence alignment of predicted amino acid sequences of PaGH3 and AtGH3 proteins.

The multiple sequence alignment was obtained with MUSCLE software. Black shading indicates conserved residues, gray shading indicates residues with similar properties, - indicates a gap inserted to maximize the alignment. Letters with different colors indicate motif 1 (red), motif 2 (blue) and motif 3 (orange) involved in ATP/AMP binding that are conserved in the acyl-adenylate/thioester-forming enzyme superfamily (Staswick *et al.*, 2002). Bold letters represent conserved motif variation in members of Group I.



Group II

Group I

0.1

Fig. S6

Phylogenetic relationships of GH3 proteins between *Picea abies* and other land plants.

Predicted proteins sequences (both full-length and partial) from *P. abies* (Pa), *Pinus pinaster* (Ppin), Arabidopsis (AT), *Selaginella moellendorffii* (SM), *Physcomitrella patens* (PP), *Sphagnum fallax* (Sphfalx) and *Marchantia polymorpha* (Mapoly) were aligned using MUSCLE program. The phylogenetic tree was constructed using MEGA6 program and the Neighbor-Joining method with predicted GH3 proteins. Bootstrap support is indicated at each node. Closed triangle indicates angiosperms, closed square represents gymnosperms, up-pointing open triangle indicates lycophytes, down-pointing open triangle represents mosses and open circle indicates liverworts.

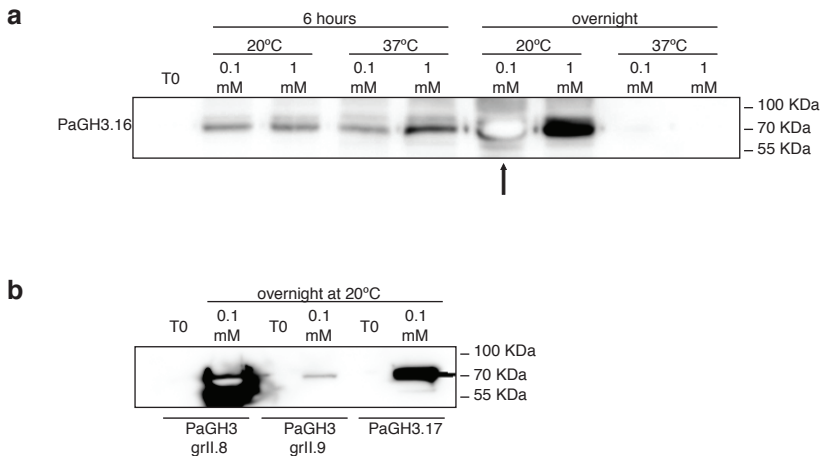


Figure S7

Western blot analysis of IPTG-induced PaGH3.16, PaGH3.gIII.8, PaGH3.gIII.9 and PaGH3.17 recombinant proteins.

(a) PaGH3.16 was used to test the optimal condition for expression of PaGH3 proteins. Bacterial cultures were treated with either 0.1 or 1 mM IPTG and incubated at 20°C or 37°C for 6 hours or overnight. Bacterial cultures that were sampled before the IPTG induction were used as non-induced control (at time 0, T0). The optimal condition was set to 0.1 mM IPTG overnight at 20°C (indicated by a black arrow) and used to induce the expression of other PaGH3 proteins. **(b)** PaGH3.gIII.8, PaGH3.gIII.9 and PaGH3.17 proteins expression. Calculated molecular weight (MW) of 6x His-recombinant proteins: 70.84 kDa (PaGH3.16),