

Supplementary Material

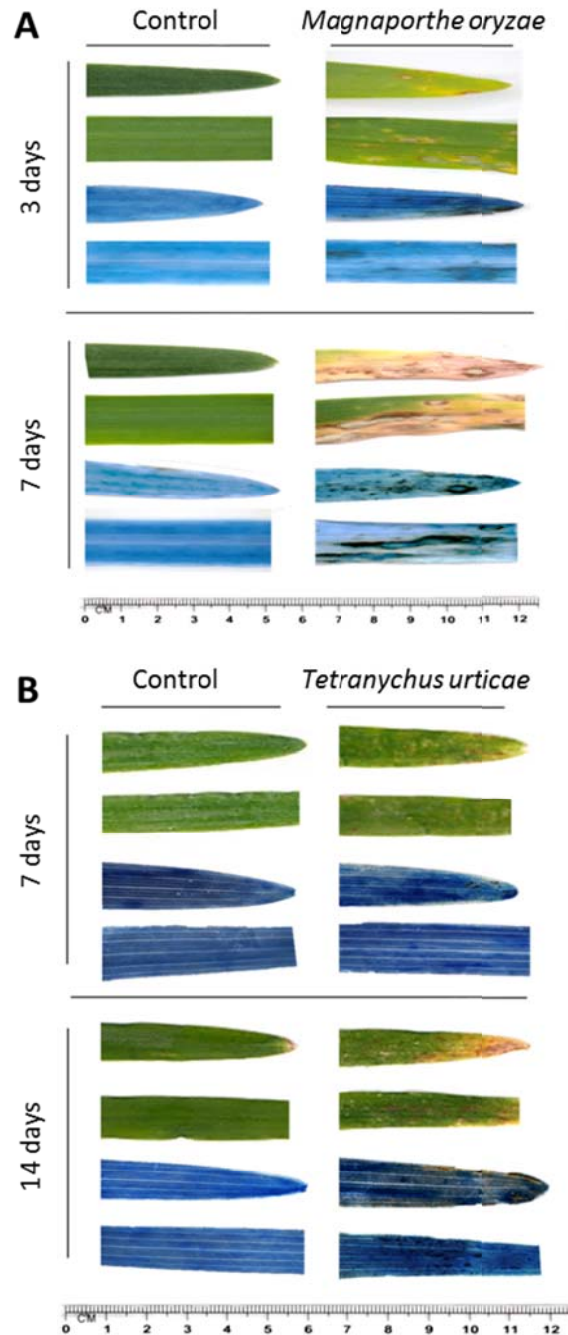
HvPap-1 C1A protease participates differentially in the barley response to a pathogen and an herbivore

Mercedes Diaz-Mendoza, Blanca Velasco-Arroyo, M. Estrella Santamaria, Isabel Diaz, Manuel Martinez*

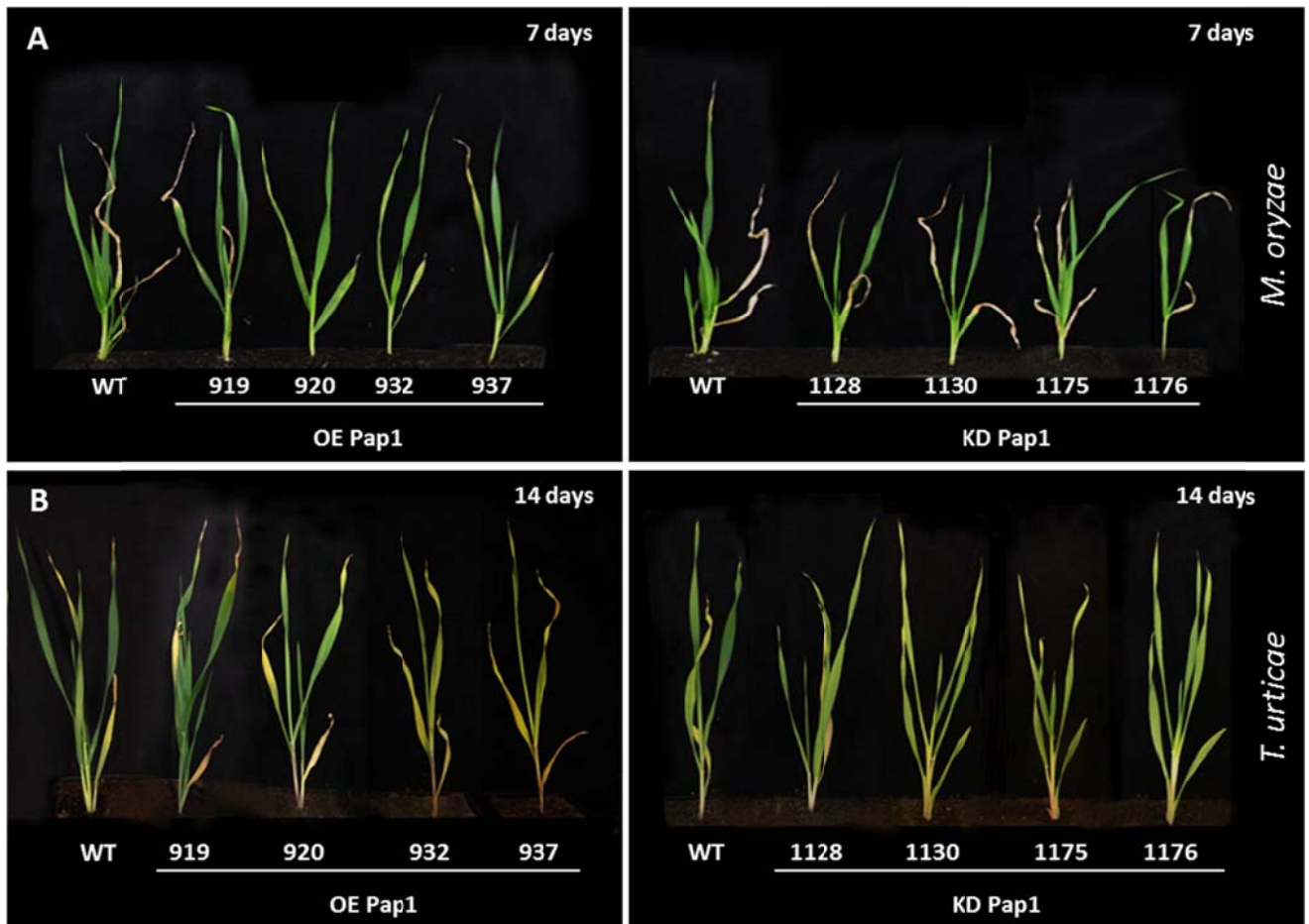
*** Correspondence:** Corresponding Author: m.martinez@upm.es

1 Supplementary Figures and Tables

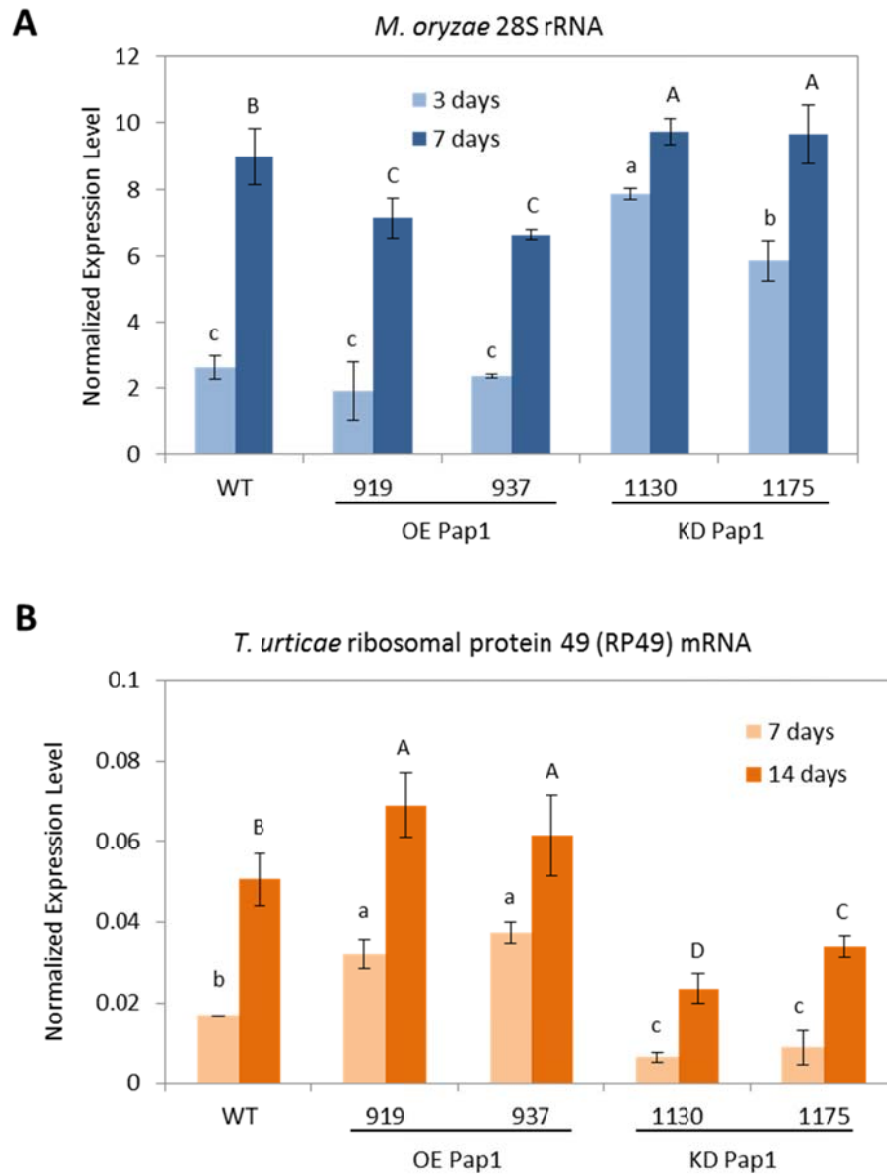
1.1 Supplementary Figures



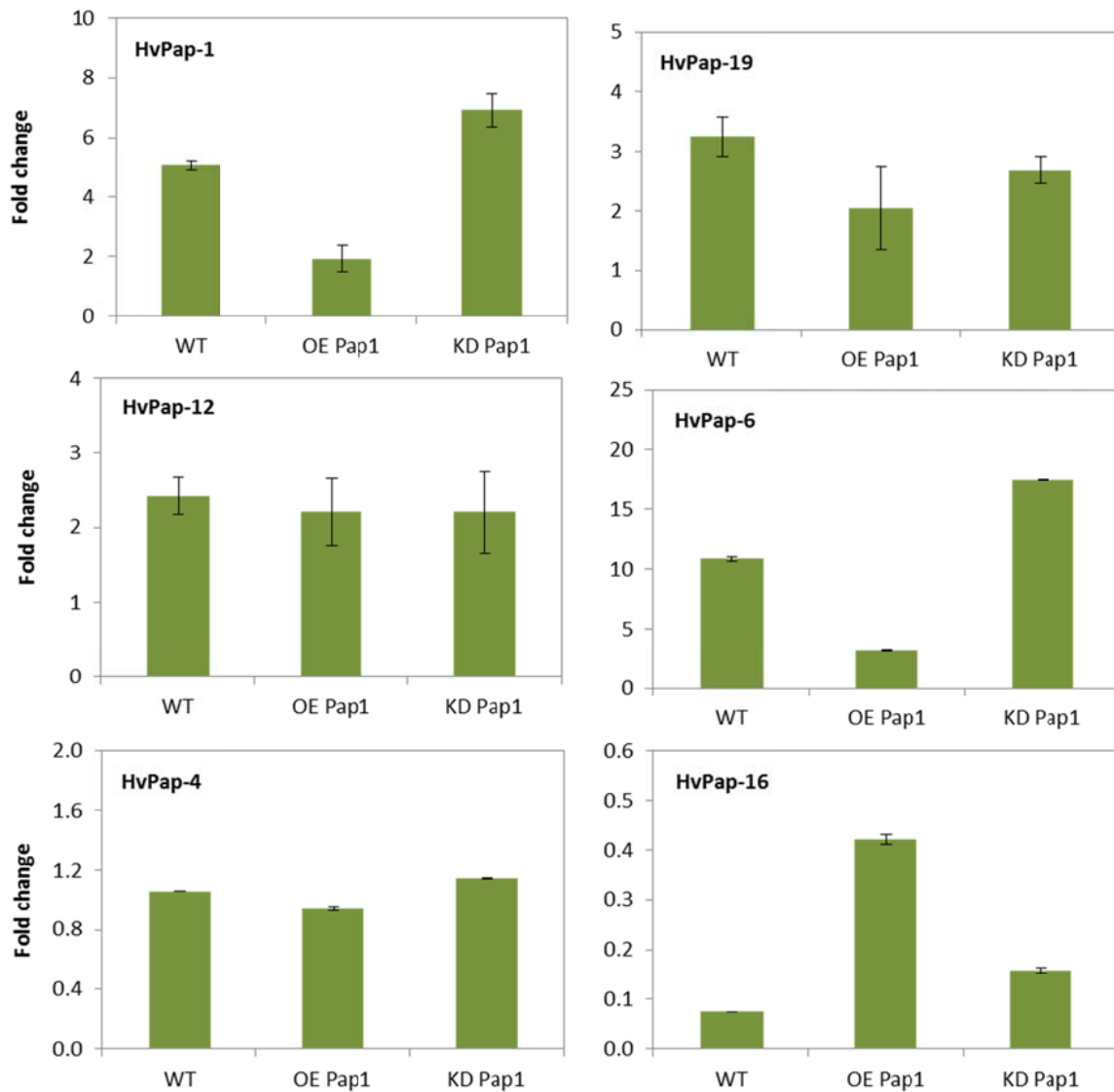
Supplementary Figure 1. Images of the apical and intermediate parts of the oldest leaf of barley plants after **(A)** 3 d and 7 d of *M. oryzae* infection and **(B)** 7 d and 14 d of *T. urticae* infestation, compared to controls without infection/infestation. In blue color, Trypan blue staining showing cell dead to highlight the damaged area.



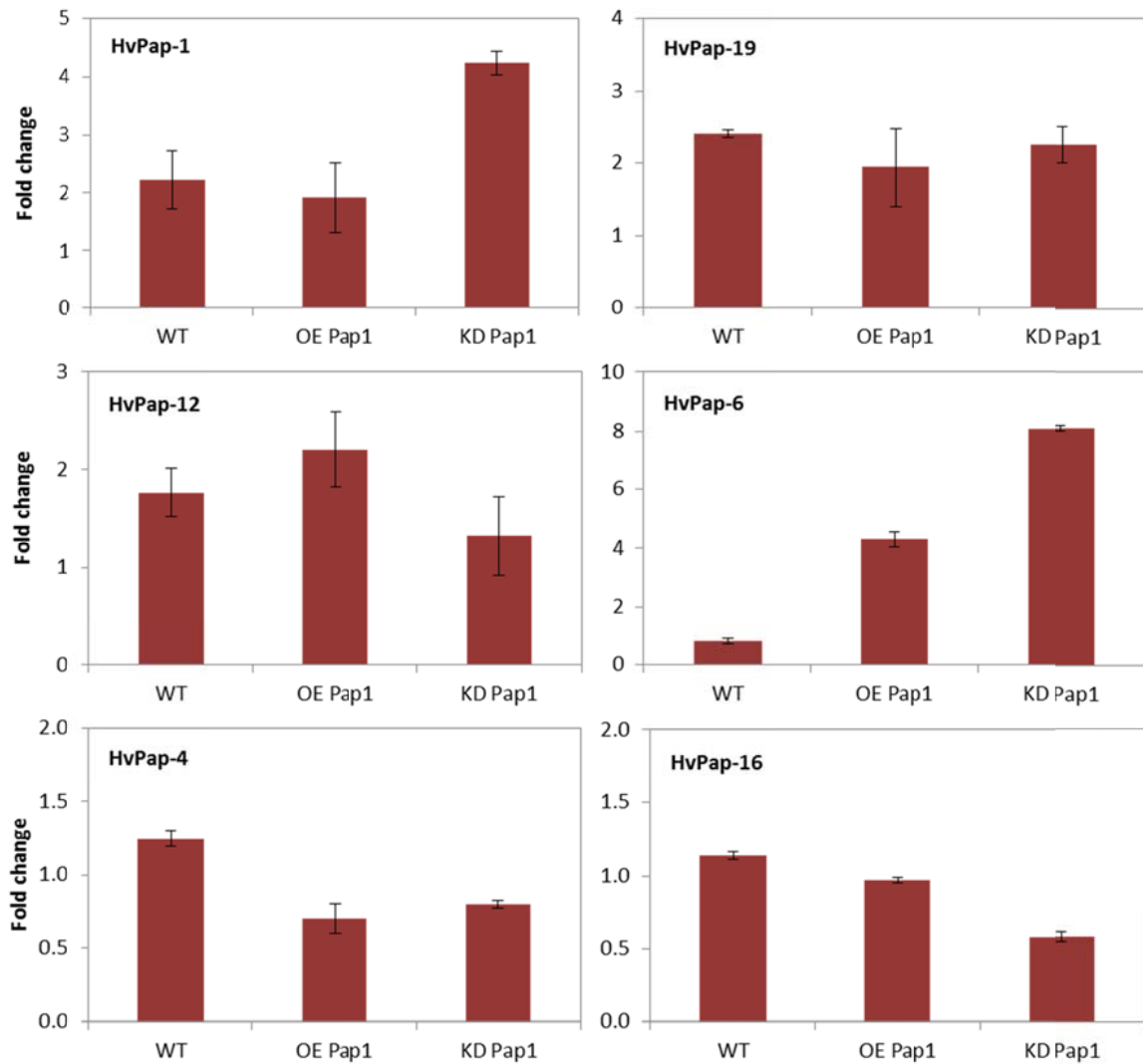
Supplementary Figure 2. Images of the whole barley plant after **(A)** 7 d of *M. oryzae* infection and **(B)** 14 d of *T. urticae* infestation from wild-type (WT), *HvPap-1* overexpressing lines (OE Pap1 919, 920, 932 and 937) and *HvPap-1* silencing lines (KD Pap1 1128, 1130, 1175 and 1176).



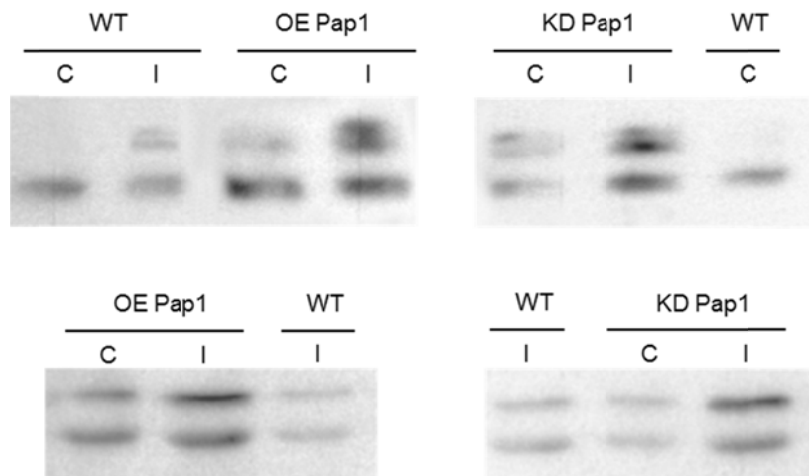
Supplementary Figure 3. Effect of transgenic barley lines overexpressing (OE Pap 919 and 937) or silencing (KD Pap1 1130 and 1175) the *HvPap-1* gene, and wild-type (WT) plants on *M. oryzae* and *T. urticae* performance. **(A)** Quantification of *M. oryzae* small subunit of ribosomal RNA (*Mo28S-rRNA*) mRNA expression levels, at 3 (light blue) and 7 (dark blue) d after *M. oryzae* infection. **(B)** Quantification of *T. urticae* Ribosomal Protein 49 (*TuRP49*) mRNA expression levels, at 7 (light orange) and 14 (dark orange) d after *T. urticae* infestation. Different letters indicate significant differences ($P < 0.01$, one-way ANOVA Student Newman-Keuls test).



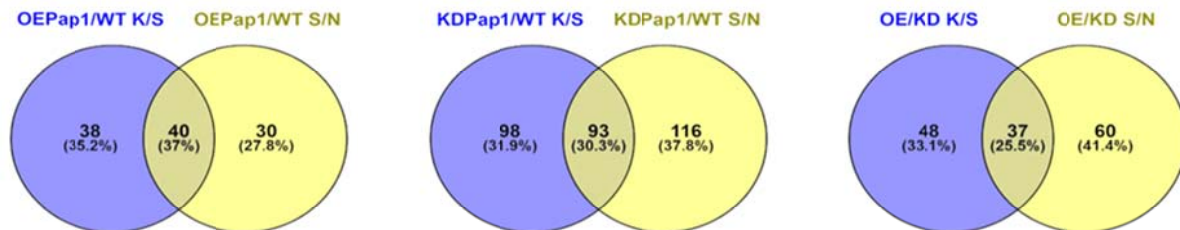
Supplementary Figure 4. Fold change in the expression of C1A CysProt genes (*HvPap-1*, -19, -12, -6, -4 and -16) in transgenic *HvPap-1* overexpressing (OE Pap1, 919) and silencing (KD Pap, 1175) lines, and wild-type (WT) barley plants after 7 d of *M. oryzae* infection, assayed by RT-qPCR. Data were expressed as relative expression to the mRNA levels of C1A CysProt genes in non-treated plants normalized to barley *cyclophilin* mRNA content.



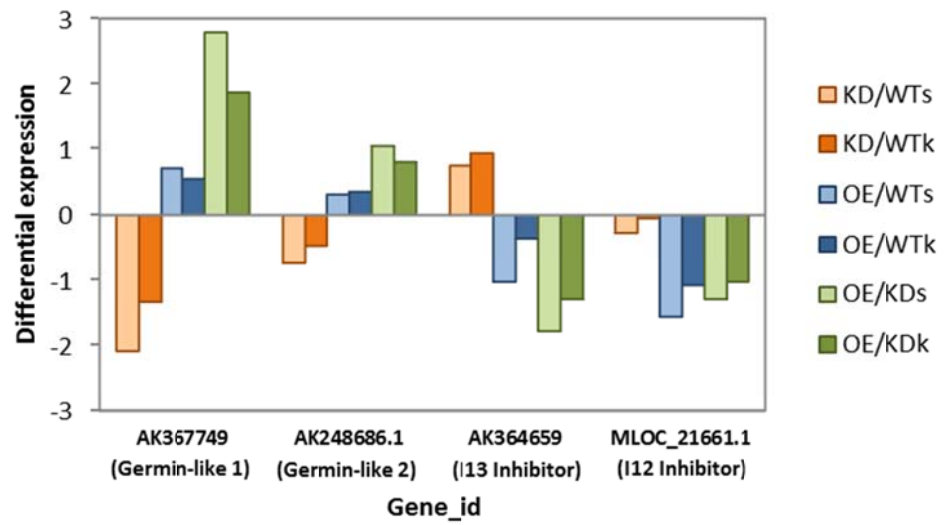
Supplementary Figure 5. Fold change in the expression of C1A CysProt genes (*HvPap-1*, *-19*, *-12*, *-6*, *-4* and *-16*) in transgenic *HvPap-1* overexpressing (OE Pap1, 919) and silencing (KD Pap, 1175) lines, and wild-type (WT) barley plants after 14 d of *T. urticae* infestation, assayed by RT-qPCR. Data were expressed as relative expression to the mRNA levels of C1A CysProt genes in non-treated plants normalized to barley *cyclophilin* mRNA content.



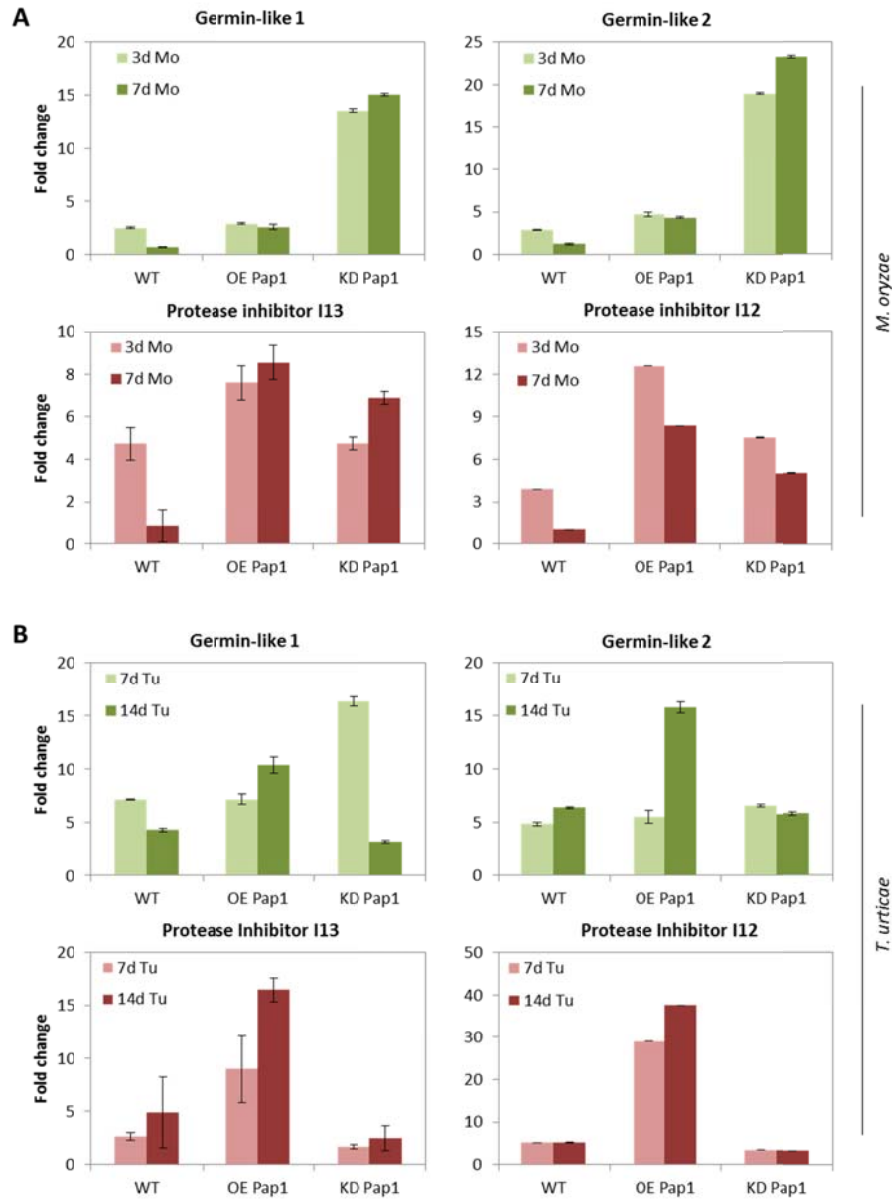
Supplementary Figure 6. Photographs from different gels showing protein accumulation patterns of HvPap-6 in transgenic (OE Pap1 and KD Pap1) and wild-type (WT) barley plants during *T. urticae* infestation assayed by immunoblot. Total protein was extracted from leaves after 14 d of infestation (I) and non-infested leaves (C).



Supplementary Figure 7. Differentially expressed genes (DEGs) in overexpressing (OE Pap1 919) and silencing (KD Pap1 1175) *HvPap-1* transgenic lines. Venn diagrams show shared detected DEGs between SOAP/NOISeq (S/N) and Kallisto/Sleuth (K/S) RNA-seq analyses.



Supplementary Figure 8. Differential RNA-seq expression of selected DEGs between genotypes. Bars represent log2Ratios or b values obtained using the SOAP/NOISeq (s) and Kallisto/Sleuth (k) analyses.



Supplementary Figure 9. Fold change in the expression of germin-like genes and protease inhibitors genes from I12 Bowman-Birk and I13 Potato Inhibitor I families, in transgenic HvPap-1 overexpressing (OE Pap1, 919) and silencing (KD Pap1, 1175) lines, and wild-type (WT) barley plants, assayed by RT-qPCR. Total RNA was extracted from leaves after (A) three (3d) or seven (7d) days of *M. oryzae* infection (light and dark green) or (B) seven (7d) or fourteen (14d) days of *T. urticae* infestation (light and dark red). Data were expressed as relative expression to the mRNA levels of the same genes in non-treated plants normalized to barley *cyclophilin* mRNA content.

1.2 Supplementary Tables

Supplementary Table 1. Primer sequences used for the amplification of barley genes by RT-qPCR assays. *HvPap-4*, *HvPap-6* and *HvPap-16* genes (cathepsin L-like proteases), *HvPap-1* gene (cathepsin F-like protease), *HvPap-19* gene (cathepsin B-like protease) and *HvCycl* (cyclophilin). *Mo28S-rRNA* gene (*Magnaporthe oryzae* small subunit of ribosomal RNA). *TuRP49* gene (*Tetranychus urticae* Ribosomal Protein 49). *HvI12* (Bowman-Birk) and *HvI13* (Potato Inhibitor I) genes (protease inhibitors). *HvGerm1* and *HvGerm2* genes (germin-like).

Genes	Primers
<i>HvCycl</i>	forward: 5'-TCCACCGGAGAGGAAGTACAGT-3' reverse: 5'-AATGTGCTCAGAGATGCAAGGA-3'
<i>HvPap-1</i>	forward: 5'-TCCTGGAGTCGATCTTTGGTTTC-3' reverse: 5'-CAAGCATACTGTTGCGGCTTC-3'
<i>HvPap-4</i>	forward: 5'-CCTTGAGAGTCCTTGTTCCTGA-3' reverse: 5'-CCATGTTCTGTCGTTTAAACCGA-3'
<i>HvPap-6</i>	forward: 5'-TGCAATTGACGGCAAGAAGA-3' reverse: 5'-TGGATCACCAGGTGATCATTG-3'
<i>HvPap-12</i>	forward: 5'-ATGTGCGCTATTGCTACCTGC-3' reverse: 5'-CACCTTATTCATGTCTGGCGAA-3'
<i>HvPap-16</i>	forward: 5'-CTGGATCGGTAAGAACTCGTGG-3' reverse: 5'-TGATGGAGGTGCCATCATATGA-3'
<i>HvPap-19</i>	forward: 5'-CACCTTATTCATGTCTGGCGAA-3' reverse: 5'-TGCCCGCTTAATTTGACAGG-3'
<i>Mo28S-rRNA</i>	forward: 5'-TACGAGAGGAACCGCTCATTCAGATAATT-3' reverse: 5'-TCAGCAGATCGTAACGATAAAGCTACTC-3'
<i>TuRP49</i>	forward: 5'-CTTCAAGCGGCATCAGAGC-3' reverse: 5'-CGCATCTGACCCTTGAAGTTC-3'
<i>HvI12</i>	forward: 5'-AGGACAAGGCGAGAGGTTTG-3' reverse: 5'-GAAGAACCTGCAGTTGTCGC-3'
<i>HvI13</i>	forward: 5'-CTCACCGTGAATCCTGTCCC-3' reverse: 5'-TTAGCCAATGCGGGGAAGTT-3'
<i>HvGerm1</i>	forward: 5'-CGCATCGACTATGCTCCCTT-3' reverse: 5'-TGAAGGTGAATGAGCCCCAC-3'

<i>HvGerm2</i>	forward: 5'- ATGGCATCCTCCCCTACCTT-3' reverse: 5'- CGGCAACACAAAAGTCCTGG-3'
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Supplementary Table 2. CysProt amino acid sequences used for specific antibody production.

Barley proteases	Peptides
HvPap-1	SGFAPSRFKEKPYWIIKN
HvPap-6	IDSEEDYPYKERDNRC
HvPap-16	RLRSYKKVTPPGNEAGLKE
HvPap-19	CQEKKHFSIDAYQVNSDPHD

Supplementary Table 3. List of the top ten significant results obtained from the enrichment gene ontology (GO) analysis of the Biological Process assigned to the DEGs.

Kallisto/Sleuth						
	GO.ID	Term	Annotated	Significant	Expected	classicFisher
1	GO:0009052	pentose-phosphate shunt, non-oxidative b...	3	1	0,01	0,01
2	GO:0009245	lipid A biosynthetic process	4	1	0,01	0,01
3	GO:0042822	pyridoxal phosphate metabolic process	4	1	0,01	0,01
4	GO:0042823	pyridoxal phosphate biosynthetic process	4	1	0,01	0,01
5	GO:0046493	lipid A metabolic process	4	1	0,01	0,01
6	GO:1901269	lipooligosaccharide metabolic process	4	1	0,01	0,01
7	GO:1901271	lipooligosaccharide biosynthetic process	4	1	0,01	0,01
8	GO:0019566	arabinose metabolic process	5	1	0,02	0,02
9	GO:0046373	L-arabinose metabolic process	5	1	0,02	0,02
10	GO:0019321	pentose metabolic process	10	1	0,04	0,04
SOAP/NOISeq						
	GO.ID	Term	Annotated	Significant	Expected	classicFisher
1	GO:0051186	cofactor metabolic process	139	4	0,54	0,002
2	GO:0006732	coenzyme metabolic process	112	3	0,44	0,01
3	GO:0006637	acyl-CoA metabolic process	3	1	0,01	0,01
4	GO:0009052	pentose-phosphate shunt, non-oxidative b...	3	1	0,01	0,01
5	GO:0035383	thioester metabolic process	3	1	0,01	0,01
6	GO:0008152	metabolic process	7509	35	29,24	0,01
7	GO:0042822	pyridoxal phosphate metabolic process	4	1	0,02	0,02
8	GO:0042823	pyridoxal phosphate biosynthetic process	4	1	0,02	0,02
9	GO:1901564	organonitrogen compound metabolic proces...	875	8	3,41	0,02
10	GO:0019566	arabinose metabolic process	5	1	0,02	0,02

Supplementary Table 4. Differentially expressed genes between overexpressing OEPap-1 and silencing KDPap-1 plants obtained by Kallisto/Sleuth method (qval<0.01; b>±1).

target_id	pval	qval	b	BARLEX
AK360179	8,13E-23	5,65E-20	4,43	Nucleic acid-binding-like protein
AK371503	0,00039246	0,00967949	4,35	DCN1-like protein 4
MLOC_43997.1	5,48E-16	1,90E-13	4,02	F-box-like protein
AK371117	2,86E-07	2,31E-05	3,70	ATP-dependent zinc metalloprotease FtsH 2
MLOC_81902.1	1,39E-07	1,24E-05	3,39	Unknown protein
MLOC_47391.1	1,02E-07	9,51E-06	3,38	ATP synthase subunit-like protein
MLOC_79498.2	1,48E-82	1,29E-78	3,03	Cysteine proteinase cathepsin F
MLOC_72300.1	4,06E-05	0,00153465	3,00	GrpE protein homolog
MLOC_56246.1	4,29E-06	0,00023329	2,91	Retrotransposon protein, putative, unclassified
MLOC_80436.1	0,00020482	0,00573598	2,45	Unknown protein
MLOC_497.1	8,32E-07	5,64E-05	2,33	Transposon protein, putative, CACTA, En/Spm sub-class
AK370563	2,48E-42	6,15E-39	2,30	Alpha-N-arabinofuranosidase A
AK251542.1	1,15E-17	5,10E-15	2,28	Retrotransposon protein, putative, Ty3-gypsy subclass
MLOC_13731.1	0,00011963	0,00374678	2,28	BLE2 protein
AK363961	1,41E-07	1,25E-05	2,13	Ubiquitin carboxyl-terminal hydrolase
MLOC_26926.1	4,85E-08	4,99E-06	2,11	Unknown protein
AK367749	8,64E-33	1,36E-29	1,88	Germin-like protein 4d
AK250005.1	1,88E-17	7,94E-15	1,71	Ribonuclease 3
AK374357	1,02E-05	0,00048168	1,69	Zinc finger protein-like protein
MLOC_55511.1	3,43E-06	0,00019318	1,65	Unknown protein
MLOC_37652.5	0,0001061	0,00340368	1,58	Esterase/lipase/thioesterase-like protein
MLOC_33258.3	5,24E-12	1,17E-09	1,56	FAR1-related sequence 5
MLOC_57450.1	0,00022915	0,00625586	1,42	Subtilase
MLOC_69589.1	3,69E-08	3,86E-06	1,39	PBSP domain-containing protein
AK368795	5,97E-05	0,00212782	1,38	Cytochrome P450 family protein
MLOC_18260.2	3,82E-05	0,00147274	1,30	Receptor-like kinase
MLOC_74854.1	1,62E-05	0,0007092	1,29	Flowering locus T3
MLOC_64435.2	4,16E-06	0,00022808	1,29	Resistance protein, putative
AK356201	3,35E-05	0,00131577	1,29	Proline-rich protein
MLOC_78131.2	6,25E-07	4,43E-05	1,26	Transposon protein, putative, Mutator sub-class
AK375581	3,16E-07	2,51E-05	1,25	Major facilitator superfamily protein
AK251585.1	4,30E-07	3,23E-05	1,22	B3 domain-containing protein
MLOC_13987.1	1,99E-10	3,41E-08	1,17	ATP-dependent DNA helicase mph1
MLOC_14895.1	5,75E-05	0,00206897	1,17	Cytochrome P450 family protein
MLOC_17984.1	0,00021738	0,00600052	1,13	Cytochrome P450 family protein
AK363296	4,88E-09	6,24E-07	1,12	Chaperone protein dnaJ
AK372606	0,00013141	0,00403131	1,11	FAD-binding Berberine family protein
AK376278	0,00011506	0,00362563	1,11	Terpenoid cyclases/Protein prenyltransferases superfamily
AK369808	5,60E-06	0,00029487	1,10	-
MLOC_36824.4	0,00018679	0,00536078	1,07	Serine carboxypeptidase family protein

MLOC_14999.1	0,00015418	0,00457623	1,05	Leucine-rich receptor-like protein kinase family protein
AK252681.1	6,30E-23	4,75E-20	1,05	Ribonuclease 3
MLOC_53792.1	0,00038359	0,0095147	1,04	Lysine decarboxylase-like protein
AK365122	6,80E-50	2,36E-46	-1,00	-
MLOC_44822.1	1,10E-09	1,59E-07	-1,00	Beta-lactamase-like protein
MLOC_21661.1	0,00032614	0,00843921	-1,03	Wound induced protein homolog BBI
AK363223	2,03E-05	0,00086853	-1,05	G-type lectin S-receptor-like serine/threonine-protein kinase
MLOC_66756.1	3,37E-15	1,08E-12	-1,05	Pyridoxal biosynthesis lyase pdxS
MLOC_33244.1	0,00025964	0,00696787	-1,06	Flowering promoting factor-like 1, putative
MLOC_58847.1	5,85E-19	2,99E-16	-1,07	60S ribosomal protein L13a-2, putative
MLOC_62134.5	8,83E-05	0,00293763	-1,10	FAR1-related sequence 3 LENGTH=851
MLOC_5129.1	1,10E-30	1,59E-27	-1,14	60S ribosomal protein L35
MLOC_74604.1	0,0001953	0,00551383	-1,15	F-box domain containing protein
AK360713	7,12E-05	0,00247875	-1,18	Early light-induced protein
MLOC_58359.1	7,96E-07	5,49E-05	-1,21	CsAtPR5
MLOC_64967.1	1,63E-24	1,49E-21	-1,21	Eukaryotic aspartyl protease family protein
AK374103	1,44E-07	1,27E-05	-1,25	RNA polymerase-associated protein LEO1, putative
MLOC_53106.1	3,22E-10	5,22E-08	-1,25	Gibberellin receptor GID1L2
MLOC_62844.2	2,17E-66	9,43E-63	-1,26	basic helix-loop-helix (bHLH) DNA-binding superfamily protein
AK369503	5,61E-05	0,00203418	-1,29	Glutamate receptor
AK364659	2,16E-16	8,33E-14	-1,29	Chymotrypsin inhibitor-2
MLOC_55770.2	0,00014885	0,00443698	-1,33	O-methyltransferase
MLOC_7958.1	2,03E-05	0,00086853	-1,41	Tetratricopeptide repeat (TPR)-like superfamily protein
MLOC_18321.1	1,62E-06	0,00010294	-1,44	Protein of unknown function, DUF642
MLOC_13047.1	2,52E-06	0,00014816	-1,46	Leucine-rich receptor-like protein kinase family protein
MLOC_56456.1	2,20E-06	0,00013351	-1,49	exocyst subunit exo70 family protein H6
MLOC_73695.2	2,70E-05	0,00109902	-1,59	Protein kinase family protein
MLOC_80345.1	0,00024517	0,00662037	-1,62	Transposon protein, putative, unclassified
AK357833	9,87E-10	1,46E-07	-1,73	Early light-induced protein
AK355828	9,28E-08	8,81E-06	-1,73	O-methyltransferase
MLOC_72140.1	4,83E-05	0,00177984	-2,17	Lipoxygenase
AK357115	1,02E-06	6,75E-05	-2,18	F-box domain containing protein
MLOC_56951.2	4,25E-06	0,00023232	-2,28	FBD-associated F-box protein
MLOC_26429.1	8,02E-06	0,00040462	-2,43	Transposon protein, putative, ping/pong/SNOOPY sub-class
AK248248.1	8,08E-06	0,00040619	-2,72	Early light-induced protein
MLOC_52920.4	9,71E-09	1,16E-06	-2,89	H-ATPase
MLOC_80344.1	2,12E-75	1,23E-71	-2,95	GRF zinc finger family protein
MLOC_61767.1	8,51E-05	0,00284604	-3,08	FAR1-related sequence 3 LENGTH=851
MLOC_75728.1	1,14E-05	0,0005305	-3,11	Unknown protein
AK371482	1,15E-165	2,01E-161	-3,19	Translation initiation factor eIF-2B gamma subunit
MLOC_77197.1	1,95E-10	3,38E-08	-3,21	Transposon protein, putative, Mutator sub-class
MLOC_7444.1	6,04E-07	4,31E-05	-3,30	HAT family dimerisation domain containing protein
MLOC_49726.1	9,98E-15	3,04E-12	-3,73	Retrotransposon protein, putative, unclassified
MLOC_3164.1	3,33E-13	8,14E-11	-3,87	Replication protein A 32 kDa subunit

MLOC_28203.1 6,14E-41 1,33E-37 -4,87 Enoyl-CoA hydratase/isomerase family protein, expressed

Supplementary Table 5. Differentially expressed genes between overexpressing OEPap-1 and silencing KDPap-1 plants obtained by SOAP/NOISeq method ($\log_2\text{Ratio} > \pm 1$; Probability > 0.80).

Gene_id	log2Ratio	Probability	BARLEX annotation
MLOC_56568.1	10.15	0.94	OJ1005_B10.23 protein
MLOC_81902.1	9.91	0.93	Unknown protein
MLOC_47391.1	8.86	0.85	ATP synthase subunit-like protein
MLOC_43997.1	8.70	0.84	F-box-like protein
MLOC_26534.1	8.39	0.80	Wound induced protein
AK360179	6.61	0.97	Nucleic acid-binding-like protein
MLOC_79498.2	4.49	0.95	Cysteine proteinase cathepsin F
AK251542.1	3.41	0.90	Retrotransposon protein, putative, Ty3-gypsy subclass
AK370563	3.34	0.91	Alpha-N-arabinofuranosidase A
MLOC_26926.1	2.98	0.87	Unknown protein
AK367749	2.79	0.91	Germin-like protein 4d
AK250005.1	2.56	0.91	Ribonuclease 3
MLOC_55511.1	2.42	0.87	Unknown protein
MLOC_23736.1	2.29	0.82	Unknown protein
MLOC_33258.3	2.14	0.87	FAR1-related sequence 5
MLOC_69589.1	2.08	0.84	PBSP domain-containing protein
MLOC_57450.1	2.02	0.81	Subtilase
MLOC_74854.1	1.89	0.87	Flowering locus T3
AK369808	1.67	0.86	-
AK252681.1	1.59	0.88	Ribonuclease 3
AK370706	1.47	0.85	ATP-dependent zinc metalloprotease FtsH 2
AK248581.1	1.46	0.80	Beta-glucosidase, putative
AK251990.1	1.41	0.85	Cysteine-rich secretory protein
AK248844.1	1.41	0.85	Acyl-CoA thioesterase family protein
MLOC_11817.1	1.37	0.85	Receptor kinase 1
MLOC_39318.1	1.35	0.80	Pathogenesis-related thaumatin-like protein
MLOC_61601.1	1.31	0.84	Pyrimidine 5'-nucleotidase
MLOC_65311.2	1.27	0.84	Chitinase
AK250430.1	1.24	0.86	GDSL esterase/lipase
MLOC_72157.3	1.24	0.84	Leucine-rich repeat receptor-like protein kinase family protein
MLOC_70817.1	1.20	0.85	Ribulose biphosphate carboxylase/oxygenase activase
MLOC_63556.4	1.15	0.84	CBL-interacting protein kinase 3
AK360763	1.13	0.83	-
MLOC_81131.1	1.07	0.80	WRKY transcription factor 20
MLOC_71275.2	1.06	0.84	Lipoxygenase
AK248686.1	1.05	0.84	Germin-like protein 4
AK250046.1	-1.00	0.83	Alanine aminotransferase
AK360133	-1.00	0.81	cell wall protein precursor, putative

MLOC_57069.4	-1.01	0.82	tRNA-dihydrouridine synthase
AK253095.1	-1.02	0.83	Proline-rich protein
MLOC_63089.10	-1.02	0.80	Asparagine synthetase
AK250831.1	-1.02	0.82	Oxidoreductase, zinc-binding dehydrogenase family protein
MLOC_21619.1	-1.03	0.83	CASP-like protein
MLOC_3702.1	-1.04	0.84	Preprotein translocase subunit SECE1
MLOC_63184.1	-1.04	0.81	WRKY transcription factor 10
AK252852.1	-1.05	0.84	Proline-rich protein
AK373369	-1.05	0.82	RNA polymerase-associated protein LEO1, putative
AK371226	-1.05	0.80	Type 1 phosphatases regulator YPI1
AK365909	-1.06	0.82	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
MLOC_54272.1	-1.07	0.82	1-aminocyclopropane-1-carboxylate oxidase
MLOC_56451.1	-1.07	0.81	Siroheme synthase
MLOC_64063.2	-1.08	0.83	Nuclear transport factor 2 (NTF2) family protein with RNA binding (RRM-RBD-RNP motifs) domain LENGTH=460
MLOC_59790.1	-1.10	0.83	Eukaryotic aspartyl protease family protein, expressed
MLOC_12849.1	-1.11	0.84	Tobamovirus multiplication-like protein
MLOC_64953.2	-1.11	0.82	Thioredoxin-like protein
MLOC_218.1	-1.14	0.84	cell wall protein precursor, putative
AK358692	-1.14	0.80	40S ribosomal protein S8
MLOC_3743.1	-1.14	0.81	Peroxidase 1
MLOC_38648.2	-1.17	0.83	Concanavalin A-like lectin
AK369436	-1.19	0.85	Protein phosphatase 2C containing protein
AK372602	-1.21	0.83	Protein of unknown function, DUF538
MLOC_79958.1	-1.24	0.86	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2
MLOC_63045.1	-1.27	0.86	Glycosyl transferase, group 1 family protein
AK364337	-1.28	0.82	Cation diffusion facilitator family transporter
MLOC_57751.1	-1.28	0.83	cell wall protein precursor, putative
AK362753	-1.28	0.81	HXXXD-type acyl-transferase family protein
MLOC_33244.1	-1.32	0.80	Flowering promoting factor-like 1, putative, expressed
AK376140	-1.32	0.82	Mediator of DNA damage checkpoint protein
AK252382.1	-1.35	0.86	Actin associated protein
AK363562	-1.35	0.86	UDP-glycosyltransferase
AK370024	-1.39	0.83	60S ribosomal protein l35a
AK365122	-1.40	0.87	-
MLOC_66756.1	-1.44	0.87	Pyridoxal biosynthesis lyase pdxS
MLOC_78302.1	-1.51	0.80	Unknown protein
MLOC_58847.1	-1.56	0.88	60S ribosomal protein L13a-2, putative, expressed
MLOC_5129.1	-1.58	0.88	60S ribosomal protein L35
AK360713	-1.61	0.85	Early light-induced protein
MLOC_64967.1	-1.68	0.87	Eukaryotic aspartyl protease family protein
AK251817.1	-1.69	0.81	Histone H2B
MLOC_53106.1	-1.72	0.87	Gibberellin receptor GID1L2
MLOC_62844.2	-1.75	0.89	basic helix-loop-helix (bHLH) DNA-binding superfamily protein

Supplementary Material

MLOC_7958.1	-1.83	0.85	Tetratricopeptide repeat (TPR)-like superfamily protein
MLOC_4531.2	-1.89	0.84	RNA binding protein-like
MLOC_4180.1	-2.04	0.82	Acyl transferase
MLOC_15383.1	-2.32	0.86	Eukaryotic aspartyl protease family protein
AK357833	-2.45	0.90	Early light-induced protein
MLOC_6294.1	-2.64	0.90	GDSL esterase/lipase
MLOC_26429.1	-3.29	0.85	Transposon protein, putative, ping/pong/SNOOPY sub-class
MLOC_61767.1	-3.34	0.85	FAR1-related sequence 3
MLOC_80344.1	-4.22	0.94	GRF zinc finger family protein
AK371482	-4.59	0.95	Translation initiation factor eIF-2B gamma subunit
MLOC_77197.1	-5.04	0.87	Transposon protein, putative, Mutator sub-class
MLOC_7444.1	-8.70	0.84	HAT family dimerisation domain containing protein, expressed
MLOC_23209.1	-8.87	0.85	Unknown protein
MLOC_3164.1	-9.23	0.89	Replication protein A 32 kDa subunit
MLOC_75728.1	-9.41	0.90	Unknown protein
MLOC_28203.1	-11.13	0.97	Enoyl-CoA hydratase/isomerase family protein, expressed