

**>Thaumatococcus-like protein (BCF79772)**

MSNLIISFFLFSILFSVSTNAATFTITNNCPYTIWAAAVPGGGKQLNSGGTWTITAPGGTTGARIWGRTGCTVT  
GPNGLRCNTGDCGGLFQCQGYQPPNTLAEYALNQFDNLDFFDISLVDGFNVPMQFVPSVGGCTSGPICSANII  
AQCPVSLQTQGGCNPCTVFKTPEYCTSGSCGPTQYSEFFKGLCPNAYSYPKDDATSTYTCKTGANYKVVFCP

**>Unknown (Contig\_14 (Fragment))**

MAMASPSLHKIVFACGAIITIMLMAIGAIIPSTDAAMFIFTNPLYCYCRDCIANGAKASLLSWGTCCPGLCDLAK  
TLATSKARLVKQLGCLGMSQYLSEIPGYSYV

**>S-like RNase (BAE16663)**

MENYSMIKLLVWQSLAAMALCQSPGFDFFYFVQQWPGAYCDTSRGCCNPTSGKPPSDFGIHGLWPNYNSGGYP  
SNCDSSNPFDPSTQIQDLLSLOLQWPSLTCPPSSDGTSTFWTHEWNKHGTCSESVLTEHAYFAAALNLKSQANTLA  
SLTNAGITPNNSTFYNSDLVLAIAIKQGTGHDAVYQCNTEENGNSQLYQIYICVDDTTGANFIECPVAPNQCPSI  
EFPSP

**>Lipid transfer protein (BAW35429)**

MAAGLKLATLAIWSCLVIVGVAPQASAAAFIGYDWGTTFFYCCKDYIQTGIDCALDYACCPVIAQFAGAVNKAS  
TKDEISYSCLAMKSALYSMPYNYTATATMVAKCGYTLPYNVAKTAPCY

**>Cysteine protease (BAW35427)**

MAFTNTTFHQFLLFAILLICIGLSSFOSSAISHEPSMVKRHEEWMVQHRRTYKDNVEKERRFQIFQKNVNLIEAHN  
KKNKSYSLSVNQFADLTDEEFKMYASAKVPESTRHSNSQRTPFKYEGYTSVPASINWVTMGAVTPIRNQGTCSG  
CWAFAAIATVESLTIWIKTGKSYDLSEQQIVDCDRYKDRGCNGGYADGAYNWIINNRGVTTEASYPYVGYQOYY  
CYRAQSAVTIKGYQFVNNSEAMQAVANQPIAVYVESKGYNFKYSSGGLFTGQCGTATDHVVAVVGYGTTTDD  
GYPYWLKNSWGTGWGENGYMRMLRNVDPRGLCGIALYPTYPTN

**>Lipid transfer protein (Contig\_35636)**

MAGFSVKFSAALLISILLVAGIASFTAASVCGQVAVVSRECMPIVMDKAPSVTSSCCSATVGLASLLNTAANK  
KQACQCLKDIASKMPGIDYNRVKSIPSKCGIKHFPLPLDPNAKC

**>Unknown (Contig\_1360)**

MAMATSRSVLHLKFAACIAALVILAMNPAHFVDAGIFTFTDNCLYYCQDCLAHGAIASVFSWLGCCPGMQRDAK  
KLNTPGCDMRDKAFACGTGYKAYLMDFSGYNNDNTQYTLKRCNASFPFPVSTSVDCFKAVS

**>Class I chitinase (BAR13254)**

MKISLLLLLFFVPLLSGTSAQOCQGYQAGGALCPNGLCCSKYGYCGTTSAYCGDGCQSQCQGGSSPPPAPPSPSP  
SGGGDVSSIITSQIFNQMLLHRNDNACPANGFYSYQAFINAARKFSGFGTGDTNTRKNELAFFGQTSHETT  
GWSTAPDGPYAWGYCFKQEQGNPDYCAPSSTYPCAPGQKYGRGPIQISYNYNYGLCGAAINQPLLSNPGLVA  
SDADISFETAIFWMTPOGNKPSCHAVATGQWNPSSADQAAGRVPYGYVITNIINGGVECGQGEKAEVADRIGF  
YQRYCSIFGISPGQNLDCYNQRPFS

**>Cysteine-rich repeat secretory protein (Contig\_23860)**

MSGNSSFLSLVFYIFLMLHSFAFADPLFQNCSSGNLASNTAYNNLISVNLDLNKTPPYTGFTIVADVTGQKADG  
VYGLALCRGDISLQDCATCVGQGSIDSALCQNKTSAILWYDHCLYKYNQDFFGQIDSTNKFVLYSGDVAGNP  
TSFNQKTSDFLTLAKNASSNTPTRFATGVSGPVDGSTTLFGLTQCTWDLSSDACFRCLQEIIISGIPTCCSGKL  
GARIFYGSCNVRYETYNFIGT

**>Lipid transfer protein (Contig\_25610 (Fragment))**

FDYRFTTHIITTTMASSTLKLICMAFAVVILVAPHAETFDYDAPNPITAVATTFGVSFCEYLRTGRGDGLFF  
FKPFCCLGLEFIKELAYSSEASLHDTICICLQNLQIFFDISDKYSTSILTFCNITTDYIITRNTDCNKLTL

**> $\beta$ -1, 3-glucanase (BAR13253)**

MELSSCASSNDGRYSMAITTLVIGLLLSNVVDTANAIGTCYGMGLNDLPSQRVVSDYNYRNIKGMRIYGPVSS  
LSQALQGSPIAVMVGVPNQDLPGIAMSQSTADSWVQNNIMKYPGVRWKYISAGNEIRPNLNDGGAQYARYVLP  
MQLNQTSTVNFGLRIKVTALLETGICINTYPPSQGFDPSSISGYILPIVKFLAANGSPLFLNVYPYFAYIYTPN  
MDIRYALFTSPNVVVQDQGYQNLFDIAIVDSVYSALEKAGTGMVQIVVTETGWPTAGDKATSIANAQTYNNNL  
IQHVKNGTPKRPSKAIETFIIDMYNENLKTPEREKHWGLFKSNGEQKYPIDFN

**>S1/P1 nuclease (Contig\_14977 (Fragment))**

GAQDLASLCSWADQVRFRFWSSALHFADIQDPNACNFQYDRDCIDTNGVLGRCVVGAIYNYTGQLLDYVNGTE  
TGNYNTQSLFLSHFMGDVHQPLHCGHAVDKGGNTIEVHWYR

**>Lipid transfer protein (Contig\_29120)**

MAGSTMLKLIATSFVVCVILVAPQAKAHYTCDPITYVVEVTVILSPCYGFLKTGKTDALFYNELFCCLAARLVNSF  
AYSSPTALKDTCYILENSVSLYKFNVPVYQQLFKKCGVNSTYAFDPSLDCSTLKL

**>Hevein-like protein (BAR13255)**

MESKGLRFAFLICLVAGAVSQQCGSQAGGQLCPNNLCCSQYGYCGSTDAYCSTANHCQSNCHGGGNTPPSPSSD  
IGEGANNVRATYHLYNPQDNGWSLYAVSAYCSTWDGDQSYAWRSKYGWTAFCGPVGPHGQAACGQCLLVNTAT  
GAQATVRIVDQCSNGGLDLVNVFNAIDTNGQGYAQGHLLTVNYQFVNCGD

**>GDSL lipase (Contig\_30899)**

MGTNDWIRNYFIPENPCLRALTYTVDQYADFLVGVFNHLSLEVLYKGGCRRFIVYSVPATGCMPTVKTIAGNFSG  
KCVDRFNNAAVIHNAKIQQALSQFNQTHDVKTIVYVSFYDLLLDATQNPSTYGFTESLIPCCGALLSPRAILCNP  
LLLTCPDASKHVYWDVHPTAEFYELLANKTMEALTLDF

**>Polyvinylalcohol dehydrogenase (FAA01288)**

MAPLTKESIFGTCFRIYLVVSCLLATLEGGSAQWPNHGGNLDNTRSPILPQPSINPSKISSLKLKWKFFVGNDI  
SATPALWSGNLYFPAWNGVLYAVNALTGVPWIQQNLGQLTGLTPTGTVVNVTVSRATPVVAGDLLIIGIYGPVAV  
VIAVSRFTGKLVWMTKLDPHALALITMSGTACLDIYVGVSSLEELLPAEQCCTFRGSMAKLDIKTGKLLWQTY  
TVPDNNKLGGYAGAAIWGSSPSIDVVRNLVYVGTGNLYTAPAAALECQAKQNNETTKPAHPDQCTSPDAHGNS  
VLAFLDMGTGNIKWYRQLGGYDVVFYFACLVPNNPSCPPGPNVDADFGEAPMLLTIQYNGILRDVAVLGQKSGFVW  
ALERSGGDIWFTLAGPGGTEGGGTWGAATDGKRIYTNIVNNNRENFTLAPSTATTTAGGWVALDANTGKILWS  
TANPSNDTTNGPVTVVGGVVFAGSVAPNGPFYGM DARTGKVIWYNTNATIYGGASSSYGCVYIG

**>Lipid transfer protein (Contig\_30505)**

MAGSSVEFIRAFILGILFFATVASITAEASVCSQVDVVSGECPYAMGKASSVTSSCCSAVKGLAVLLNTSANK  
EQACKCIKAILSNMPLDINKVKAVPSKCGITDFPLSSC

**>Polygalacturonase inhibitor (Contig\_23225 (Fragment))**

YSPIYGALPSSSLTKLKYLTAIRVSGTNLNSTIPSFNGMNTLQSIDLSSNSLYGTIPSSLGNLVGLNRLDLSNN  
HLSGQIPESLGSCKNLDTLDFSNQLTGDVPKSLSHVNMAVVALGSNQLTGDASHLFQSNQNTGLTYLYGNRFKFN  
FSNVIVDANLAYFDMSNNLVYGGFPPSINDPLFEFVSNNRLCGPIPEGGSLQQFQADAFDNNLCLCGRPLPP  
CSGS

**>Valine-tRNA ligase (Contig\_1096 (Fragment))**

MSEKTETMELSAEELDKKKKKEEKAREKELKKQKAAQKAEAAKLQVQPSNASKKSERKNQRRSAEEENADDYI  
DPQTSFGEKKLLSRMAKQYNPSVVEASWYAWWEKSGFFVADAKSSKPPFVIVLPPPNVTGALHIGHALTSAIQ  
DTIIRWRQMSGYNTLWVPGMDHAGIATQVVVEKKIMRERKLRHDLGRDKFVSEVWNWKNKEYGGTILRQORRLG  
SSLDWSRECFMDEKRCLAVTEAFVRLFKEGLIYRDIRLVNWDVLRTAISDIEVDYQDIKERTLLKVPGYEKD  
VEFGVLTSAFAYPLEGNLGEIVVATTRVETMLGDTAIAVHPEDTRYQHILGKFAIHPFNGRKLPIIPDPILVDRN  
FGTGAVKITPAHDPNDFEVGKRHKLEFINIFTDDGKINGNGGPEFEGMPFRAREAITKALQEKGLYRGAKNNE  
MRLGVCSSRSRDVVEPMIKPQWYVNCSSMAKDALNAVMDENQRIEIIIPKQYASDWKRWLENIRDWCVSRQLWWG  
HRIPAWYVSLENDERKELGSYNHWHVVARNEEEARKEANERYPGKKFTISQDPDVLDTWFSGLFPLTVLGWPD  
ETEDLKAFYPTSVLETGHDILFFWVARMVLMGKLGDPVFRKVYLHPMIRDAHGRKMSKSLGNVIDPLEVING  
ITLQGLHKRLEEGNLERAEKLTAKAGQEKDFPNGISECGADALRFALVSYTAQSDKINLDIQRVVGQRWCNKL  
WNAIRFAMSKLGDYTPPTNIVPEILPFCCQWILSVLNKAIGETVASFEAYEFSDAATAVYSWWQFKLCDVYIE  
VIKPYFVGSDDSSAASSKRFAQDVLWLCLETGLRLLHPFMPFVTEELWQRLPHPKDSVRKESIMISEYPSVVKSW  
TNEKVEQMDLIESAVKALRYLRSLMPVKERHERRPAFALCQTDEVAEIIINLHELEICTLANVTSLVSSVDD  
APVGSTVSVVNE

**>Class IV chitinase (Contig\_23195 (Fragment))**

MISPKYIPNYTPIQTMALSIRTRFAIICVIIIVVFSSSSLAQNCGCDSSLCCSQYGYCGTSDAYCGIGCQEGPC  
KYPVNNTKNDVSVPGVVSDAFFNGIIDQAAPTCEGIGFYSSRAAFLCAWENYTFD

**>S1/P1 nuclease (Contig\_3798)**

MGSRVGIWVCGAVVFLHLIPLSILSWGQHGHYATCKIAEGYISKDAMIAVKQLLPESAGGELAAVCSWPDQIRFH  
YPWSGPLHYIDTPDFRCQYDYNRDCHDSAGNKGRCVAGAIYNYTEQLVLGCQNSSFPNSTKYNLTEALMFLAHP  
IGDVHQPLHVGFSDGGGNTIRVRWFRQMSNLHHVWDTSIIDTALKRFYKSDLSDFIREIQLNITGSWADDLVG  
WESCASNKTVCPDYPASESISLACRYAYRNATSGSTLGGDYFLSRLPVVEQRLAQGGIRLAATLNRI FSPRLIQ  
PHEDTQDCGSESGITI

**>Basic secretory protein (BAR13256)**

MARIFLILSSILFLASTQQQAVIYTVTNNAADTPGGIRFATQIGLDYSRQTLASATAFIWRLFQENSPAERKN  
TQHVTLIVESMDGVAYTSADQIHLISANYVQGYSGDVKREITGVLYHEMTHVWQWDGNGQAPGGLIEGMADYVRL  
KAGYAPSHWVKPGQGDRWDQGYDVTAYFLDYCDSLRPGFVALLNKMMRSGYSDGFFNQQLLGLSVKQLWSNYKAK  
YNH

**>Serine/threonine-protein kinase (Contig\_9565 (Fragment))**

MEQYEILEQIGKGAFGSALLVRHKIEKKKYVLKKIRLARQTDRTRRSAHQEMELISKIRNPFVVEYKDSWVERG  
CYVCIVIGYCEGGDMAEAIKKANNVHFSEEKLCCKWLQLLMALDYLHTNHILHRDVKCSNIFLTKERDIRLGDF  
GLAKLLTSDDLASSVVGTPSYMCPPELLADIPYGSKSDIWSLGCCYIEMSALMPAFKAFDMQALINKINKSIIISP  
LPTMYSGAFRGLVKSMRLRKNPELRPSAAELLKHPHLQSHVLKINLKYGNPRRNSLPISDFHNRRTTRFTEPDEV  
LEKRRLSLGNDRTLNPVSLTEHYSPSSIKEDQFSEHLGRRLEDLSVSSVHREVGVNDIAMSKVNTTTRTSRLS  
TPAKASATLRRESAPSKFSSPGFNRSFPPVTNAS

**>Class III peroxidase (Contig\_31040 (Fragment))**

LGRFDSLSTSLNDTSPALTMDLDELTAFAERNFTQIDMIALFGSHTVGHACHGTFNRLYNFSSSSSVDPTL  
NPEYAKQLQAECPVNVDPSVEASLDPV

**>Calmodulin-binding protein (Contig\_21026 (Fragment))**

KLPTIRSLTSEIEGVASDRPETGCFCHKLDKLPKFLREIADQIEEFTAQARENFSCPARLGSAVVCERLNHEVT  
EAAYPNYLELRILNLTLLHPIFTNDEVTGKDGEESIVALVDAMGKVFGSFPEVILNVVLEGNFNCSNDEKWSKE  
DFDMHIVKKRENNALLVGDLOVTLKRGVAKLGLDFKFTDNSSFWVSKKFRLLGLQVAPSSCKGMRIREAITEPFKV  
KDCRVKINGKHDAPQFNDEIWRLLKSIKGGVHHKLNKGVATVEDFLRLWVINEQELRQLLLVGMGMKSKQW  
KDLINHAKTCSPGSKLYFVPTANADIGTIIILNRFYELSELIIGGRHLSAVSLTDYQKAQARALVKEAYQKKTIM  
EYDDSHASQSQHVCNNSITPSMDVVWGVQDIHRPTPVANDGNVPLTECPPCCLPDHGNSTTMEQPRELQNPCK  
HTYTSFHHGECSTFQSHISSFSVDNNLQHSVPVGPSSADIEWFWSMEETSSYQDYPPVITGARQHINHNGRFKFK  
TVLAHLLSVEIFLKEVRV

**>Class III peroxidase (Contig\_46408 (Fragment))**

ANRIYNFSATSPVDPTLVPQFAAHLQELCPVNVDPSVRVPLDAVTPDVFDNQYYKNLINHMGLLSVDQMLYSDD  
RTRTYVVDWAQNQQHFYDALSAAMVKMGRIGVLSIDGNIRTH

**Figure S1** FASTA file of amino acid sequences of the proteins subjected to the LC-MS/MS analysis. Names in the parentheses indicate the protein ID. The letters starting from "Contig" indicate sequences obtained by *de novo* assembly based on the DRA data DRR051750 (Fukushima *et al.*, 2017) , and the others indicate sequences registered with NCBI.

## Cysp1

-400 GTGTTGAATTTTTATGGATTTTGATAAAAAAAAAATTTAATAATGATAGTG  
ARRIAT GT1CONSENSUS

-350 GGGTTTACGGTAACAATTATGAGAGAAGATAATGAGGTATACTGTATATT  
GT1CONSENSUS

-300 ATAGCAGGAAATGATGATTTAATATTTTGTAAGATGAAAAATTTACTCAA  
GT1CONSENSUS ARRIAT GT1CONSENSUS

-250 ATAGAAAAGGATTGTAAGTATATTGAGATATACCAAATAAAAAAGATTG  
ARRIAT ARRIAT

-200 CAAAGATTATGGAAAAAGGGAGTATAAGTTTTAGAAAGTTGAGCGATGCC  
ARRIAT  
GT1CONSENSUS

-150 GATTTTCTGGCTCCCTATTCGTCGGCAGTAAATTAATTAGAATAGTGAGG  
ARRIAT GT1CONSENSUS

-100 ACCAGCTTCGTTTATTACGCAACGAGAAGTTTGTTACTGAACATATTGAT  
GAREAT

-50 CTTTATGTGCCTATAAATAGAACAGATCACGTTGGTTCCTCATTACCAGT  
CARGCW8GAT  
RHERPATEXPA7  
T/GBOXATPIN2  
ABRELATERD1  
GT1CONSENSUS

## Chi1

-400 CAGGTATACAGTGACCATATAACAGGAAGATTATGTTTGCCTTTTTAGTT  
ARRIAT

-350 CTCATTTTTTCATGGGCAATCCAATTTTATAACTTCTGGCTTAAGAGCAAC  
GT1CONSENSUS ARRIAT

-300 CTCTAAATTTTTCTTGGTCGGCTCGCTGTAGCTTCCAACGTAAAGATAT  
GT1CONSENSUS

-250 AGCATGACAAATAGGTTGTTAATATTTGCGCCAACCTGTGTGATAAATTT  
GT1CONSENSUS

-200 CACTCATGCTTTGCCCTCCTAGTGATTTTCATTGACCATAGGATCCTAATA  
PREATPRODH ARRIAT WBOXATNPR1

-150 CAGCATAAAAAATAGTAAGCATTGTCCATGGTCCATGAAATCTATAGATT  
ARRIAT ARRIAT

-100 ATGAAATTGTCATTAGAAGACTAATCAATCGAAAATCCCGTGCAGGAAG  
ARRIAT  
GT1CONSENSUS  
ARRIAT

-50 TCCCTATTTATACACCTCCTGTATCCTAACTTTCACCAGGTCATAATAAA



## Hel1

.....  
-400 TCAAATAAATCTTGAAGGGAATCCTATTTTCCTACCTATGAACTCAA  
ARR1AT ARR1AT GT1CONSENSUS  
-350 TTTGAGTTTTTTGTGATTTCAATGCCAGGTTTGCCGATATATAGGTACTGG  
ARR1AT  
-300 AGCGGGTGACTTTTAGCGGCGAAGAGGCGAATATCCGCAAGACGGATCCT  
PIBS  
-250 TGATCTATCTTCAGAAGCCAAAATTTAATGCTGCAAGTATTTTCAACC  
GT1CONSENSUS MYBPLANT  
-200 AAACAAAACATCATATGT CAGTTAGTATATAGATTAGACTTGGTACCTTC  
ANAERO1CONSENSUS MYB2CONSENSUSAT ARR1AT  
-150 TTCTAATCTAAGTATACATGTGCGACTATTATCATCATAGGTCCATATTTT  
ARR1AT GT1CONSENSUS GT1CONSENSUS  
-100 CCTTGTGAAGATGTTGTTGCTCCGTGGCGACTAGTCAAGATTGTAATTC  
SORLIP1AT WBOXATNPR1 ARR1AT  
-50 TTCCCTATAAATATGGTGACCCTTGTTTCATTCTTTCTATCAACCAGAAA

**Figure S2** Upstream sequences and *cis*-DNA elements of *Cysp1*, *Chi1*, *Glu1*, *Tlp1* and *Hel1*. Numbers are relative to transcription start site (+1). PlantPAN3.0 (Chow et al., 2019)-based analyses identified the following elements: ABRELATERD1 (etiolation-responsive element), ANAERO1CONSENSUS (involved in the fermentative pathway), ANAERO3CONSENSUS (involved in the fermentative pathway), ANAERO4CONSENSUS (involved in the fermentative pathway), ARR1AT (ARR1 binding element involved in response to cytokinin, CARGCW8GAT (flower-specific responsive element), GAREAT (GA-responsive element), GT1CONSENSUS (consensus GT-1 binding site in many light-regulated genes), LEAFYATAG (target sequence of LEAFY involved in flowering), MYB1AT (MYB recognition site involved in dehydration-response), MYB2CONSENSUSAT (MYB recognition site involved in dehydration-response), MYBPLANT (plant MYB binding site involved in anthocyanin biosynthesis), PIBS (PHR1-binding sequence found in the upstream regions of phosphate starvation responsive genes from several plant species), PREATPRODHD (pro- or hypoosmolarity-responsive element), RHERPATEXPA7 (root hair-specific element), SORLIP1AT (sequence over-represented in light-induced promoter), SREATMSD (sugar-repressive element), SURECOREATSULTR11 (core of sulfur-responsive element), TBOXATGAPB (light-responsive element), T/GBOXATPIN2 (involved in jasmonate signaling), WBOXPCWRKY1 (pathogen/elicitor response element), WBOXATNPR1 (involved in SA-response).

**Table S1** Summary of iBAQ values in the Asp-N digestion

<b>Protein name <sup>a</sup></b>	<b>iBAQ value</b>	<b>Abundance rank</b>
Thaumatococcus-like protein (BCF79772)	2.09E+05	1
Lipid transfer protein (BAW35429)	1.22E+05	2
S-like RNase (BAE16663)	1.10E+05	3
Unknown (Contig_14 (Fragment))	3.60E+04	4
Cysteine protease (BAW35427)	2.54E+04	5
Lipid transfer protein (Contig_35636)	2.15E+04	6
Unknown (Contig_1360)	1.94E+04	7
Class I chitinase (BAR13254)	1.58E+04	8
Cysteine-rich repeat secretory protein (Contig_23860)	9.17E+03	9
Lipid transfer protein (Contig_25610 (Fragment))	7.38E+03	10
Hevein-like protein (BAR13255)	5.83E+03	11
$\beta$ -1, 3-glucanase (BAR13253)	5.05E+03	12
Polyvinylalcohol dehydrogenase (FAA01288)	4.69E+03	13
Lipid transfer protein (Contig_29120)	3.95E+03	14
GDSL lipase (Contig_30899)	3.65E+03	15
Lipid transfer protein (Contig_30505)	2.57E+03	16
Polygalacturonase inhibitor (Contig_23225 (Fragment))	1.92E+03	17
Class IV chitinase (Contig_23195 (Fragment))	1.38E+03	18
Basic secretory protein (BAR13256)	9.31E+02	19
Class III peroxidase (Contig_31040 (Fragment))	8.82E+02	20
Class III peroxidase (Contig_46408 (Fragment))	6.56E+02	21

<sup>a</sup>Names in the parentheses indicate the protein ID. The letters starting from "Contig" indicate sequences obtained by *de novo* assembly based on the DRA data DRR051750 (Fukushima *et al.*, 2017), and the others indicate sequences registered with NCBI.

**Table S2** Summary of iBAQ values in the chymotrypsin digestion

<b>Protein name <sup>a</sup></b>	<b>iBAQ value</b>	<b>Abundance rank</b>
Thaumatococcus-like protein (BCF79772)	6.43E+04	1
Unknown (Contig_14 (Fragment))	5.53E+04	2
S-like RNase (BAE16663)	3.09E+04	3
Cysteine protease (BAW35427)	1.89E+04	4
Lipid transfer protein (BAW35429)	1.53E+04	5
Unknown (Contig_1360)	1.08E+04	6
Class I chitinase (BAR13254)	1.05E+04	7
Cysteine-rich repeat secretory protein (Contig_23860)	9.45E+03	8
Lipid-transfer protein (Contig_29120)	4.90E+03	9
S1/P1 nuclease (Contig_14977 (Fragment))	2.61E+03	10
GDSL lipase (Contig_30899)	1.54E+03	11
Hevein-like protein (BAR13255)	1.32E+03	12
Polyvinylalcohol dehydrogenase (FAA01288)	8.34E+02	13
Valine-tRNA ligase (Contig_1096 (Fragment))	3.00E+02	14
S1/P1 nuclease (Contig_3798)	1.17E+02	15
Serine/threonine protein kinase (Contig_9565 (Fragment))	1.15E+02	16
Calmodulin-binding protein (Contig_21026 (Fragment))	5.75E+01	17

<sup>a</sup> Names in the parentheses indicate the protein ID. The letters starting from "Contig" indicate sequences obtained by *de novo* assembly based on the DRA data DRR051750 (Fukushima *et al.*, 2017), and the others indicate sequences registered with NCBI.



**Table S3** PCR primers used in the Real-Time PCR

<b>Gene name</b>	<b>Primer sequence (5' to 3')</b>
<i>actin</i>	F: TGAGGCACCACTCAACCCTA R: AGAGAAAGCACCGCCTGAA
<i>eIF4A</i>	F: ATTGGCCCGTGGTATTGATGTC R: TTGATTGCCACACCCTTTCTCC
<i>TIP41</i>	F: TTGGCTGCAAAGGAACCCATTC R: AACCAACCACTCGGCATAACTC
<i>Cysp1</i>	F: CAGAGGAGTCACCACCGAAG R: CCCGTTTCGCTATTGTTTGA
<i>da-1</i>	F: ATGGAACAAGCACGGAACCT R: TAGGCTGGCAAGGGTATTGG
<i>Chi1</i>	F: TTGTGCCGCTTCTTTCAGG R: CAGCATAGCCCGTTAGGACA
<i>Glu1</i>	F: GGACATCAGGTATGCTCTATTCACC R: TTCCAGTTCCCGCCTTCTC
<i>Tlp1</i>	F: GGGTCGTACAGGATGCACAGT R: CCGCCAGAGTATTAGGAGGTTG
<i>Hel1</i>	F: GCGACGGTAAGGATTGTGGA R: CATAGCCTTGTCGGTTGGTG
<i>DaMET1</i>	F: GGTGCTGATTGGCGTGA R: TGGCGGTGTTTGGGAGA
<i>DaCMT3</i>	F: TCTCCCTCAATTTTCGCCTTC R: GGGACGACACCCCTCATAAC
<i>DaDRM2</i>	F: AGTAGGACAGACCGCTACAAATCAC R: CCAATGCCTGAGAAGAGAGACA
<i>DaROS1</i>	F: AAAGAAAGACTGCCCCATCAC R: TGTTGTTCAATCCCCTCTCCT
<i>DaDME</i>	F: TCCACCACAGAAATCGAAGG R: GGTGAAGCGTTAGCAGTCGT

**Table S4** PCR primers used in the bisulfite sequencing

Gene name	Primer sequence (5' to 3') <sup>a</sup>
<i>Cysp1</i>	F: <u>ACACTCTTTCCCTACACGACGCTCTTCCGATCT</u> AATTATGAGAGAAGATAATGAGGTA
	R: <u>GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT</u> TCTTTTCACCATTRATRRTTCAT
<i>Chi1</i>	F: <u>ACACTCTTTCCCTACACGACGCTCTTCCGATCT</u> GAAGTATTATYAYAGTATTGTTGTG
	R: <u>GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT</u> ARAAATCTTCATRTTTTTTAATCCC
<i>Glu1</i>	F: <u>ACACTCTTTCCCTACACGACGCTCTTCCGATCT</u> TTTTTGYTGTTGAAYTYGGATG
	R: <u>GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT</u> CCATTRAATATCTTCCATCATT
<i>Tlp1</i>	F: <u>ACACTCTTTCCCTACACGACGCTCTTCCGATCT</u> ITYATTTYTTGGTTTAATATTGTGAT
	R: <u>GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT</u> CAATTRCTTRTTATATACCTTCTAT
<i>Hel1</i>	F: <u>ACACTCTTTCCCTACACGACGCTCTTCCGATCT</u> TTAGGATGGTYATTAYTGATTAAG
	R: <u>GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT</u> CARATCAARAATRCAAACCTC

<sup>a</sup> The underlined portions indicate overhangs.

**Table S5** C5-MTases and DNA demethylases identified in *D. adelsae*

Name	Gene		Length (aa)	kDa	pI
	Name	Accession number			
DNA (cytosine-5)-methyltransferase 1	<i>DaMET1</i>	YAAA01000001	1579	177.2	5.70
DNA (cytosine-5)-methyltransferase CMT3	<i>DaCMT3</i> <sup>a</sup>	YAAA01000002	765	-	-
DNA (cytosine-5)-methyltransferase DRM2	<i>DaDRM2</i>	YAAA01000003	613	68.5	4.97
DNA glycosylase/AP lyase ROS1	<i>DaROS1</i>	YAAA01000004	1902	211.0	5.84
Transcriptional activator DEMETER	<i>DaDME</i>	YAAA01000005	2005	223.2	6.95

<sup>a</sup> Sequence is partial.