

1    **Supplementary material**

2    **Draft genome of *Tanacetum cinerariifolium*, the natural source of mosquito coil**

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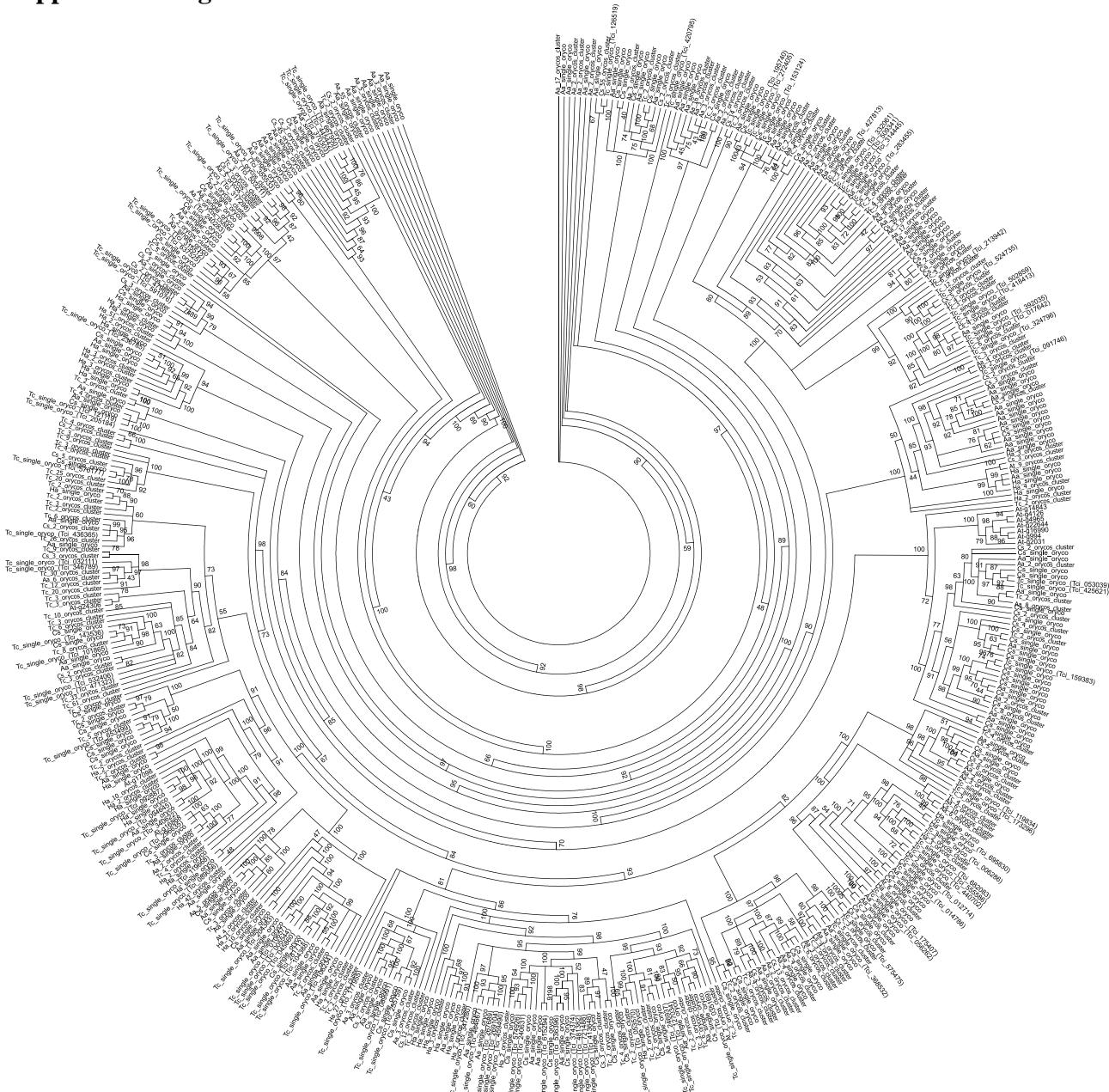
22    FAX: +81-774-98-6262

24      **Supplemental figure 1.**



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26      **Supplemental Figure 1. Molecular phylogenetic analysis of *sire*-clade transposable elements**  
27      (**TEs**). ML tree for sire TEs were generated based on RT domain-encoding sequences. The  
28      bootstrap-supported clusters with same-genus-derived genes are shown in single nodes.  
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## Supplemental Figure 2.



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**Supplemental Figure 2. Molecular phylogenetic analysis of *oryco*-clade transposable elements (TEs).** ML tree for *oryco* TEs were generated based on RT-domain-encoding sequences. The bootstrap-supported clusters with same-genus-derived genes are shown in single nodes.

**Supplemental Figure 3.****A**

Tci_399175 SNA-I (O22415.1)	MRLFATLLLVLVVAIY-LHLGGVQADNKYDKNKFSYNNQMPNIKAYIKLLEELRDRILASG-TDVHGILVTRPARNPILQ MRVVTKLLYLVLAICGLGIHGALTHTRVTPVPSVSFNLTGADTYGFLRALQEKVILGNHTAFDLPVLPESQVSDS	78 80
Tci_399175 SNA-I (O22415.1)	ERFIQVELQNSGYQVITVIIDTVNVVYGVYLSSPLAPIHYLDGDAEALPNTTYIHRPLNFDGRYRSLP----- NRFVLVPLTNPSGDTVTLAIDVNLYVAFSSNG----RSYFFSGSTAVQRDNLFVDT-TQEELNFTGNYISLERQVGE	153 154
Tci_399175 SNA-I (O22415.1)	DRDQTPLGHGALNDAIR----NLYYGQSQ--RSALLVIIQMVAEAVRIRHIEHLILRLRNMYDERNPNFIPDTKAINLENS GRVYIPLGPKSIAQAISLRTYTLSAGDTKPLARGLLVIQMVSEAARFRYIELRIRTSITDAS--EFTPDLMLSMENN	226 232
Tci_399175 SNA-I (O22415.1)	WDALSTQIQSSCESGVFLREVRVQIAPDPSSQLRIRNVEESMALAALALMLYTKPTAIR-----MPVPVPVAV WSSMSSEIQQAQPGGIFP--GVVQLRDERNNPIEVINFRRLFELTYIAVLLYGCAPTSNSYTNNIDAQIICKMPVFRGG	297 310
Tci_399175 SNA-I (O22415.1)	GADEQCPYGEPTTNIIGRDGQCMDVKENQYGNGNPIIIFPCGNAQRNQLWTFKSDGTIRSNGKCLTSGNYIMIFDCDIA GYEKVCSVVEVTRRISGDGLCVDRDGHYIDGNTVOLGPCGN-ECNQLWTFRTDGTIRWLKCLTTSS-SVMYIDCNIV	377 388
Tci_399175 SNA-I (O22415.1)	P-ETTKWILHNAGTIIMNPRLRVIAAESSTPRTVLTAADVDSNSHQAWSAGNYTQPTITI PEPEATKWWVSTDGTITNPRSGVLVTAPQAAEGTALSLENNIHAARQGWITVG-DVEPLVTFIVGYKQMCLTENGENNFWW	456 467
Tci_399175 SNA-I (O22415.1)	ANCVIDITEPRQOWAIYGDRTIRLYSDRILCVTSRGHESVDSIILFKCQGSEQRWTFMADATTINPYAQLVMDVRGSDVS EDCVLNR-VEQEWALYGDGTIRVNSNRSLCVTSEDHEPSDLIVLKCEGSGNQRWFVNNTGTSINPNAKLVMVDVAQSNVS	536 546
Tci_399175 SNA-I (O22415.1)	IQEIIILYPPTGNPNQKWIAF---- 556 LRKILLYPPGTGNPNQOWITTTQPA 570	
		<span style="background-color: cyan; color: black; padding: 2px;">:RIP domain (pfam00161)</span> <span style="background-color: green; color: black; padding: 2px;">:RICIN domain (smart00458)</span> <span style="background-color: yellow; color: black; padding: 2px;">:Q-X-W conserved motif</span>

**B**

Tci_144982 ETR1 (AAA70047.1)	MMDSCDFETQWPADELLVVKYQYISDFFIAFAYFSIPLELIYFVQKSAFFPYRWLMQFGAFIVLCGATHFINLWTFSSH -MEVCNCIEPQWPADELLMKYQYISDFFIAIAYFSIPLELIYFVKKSAFPYRWLVLFQGAFTVLCGATHLINLWTFSSH	80 79
Tci_144982 ETR1 (AAA70047.1)	SKTVAIVMTVAKLSTAFVSCVTALMLVHIIPDLLSVKTRELFLKQRAEDDLREMGLIIKQEEETGRHVRMLTHEIRSTLDR SRTVALVMTTAKVLTAVVSCATALMLVHIIPDLLSVKTRELFLKNKAAELDREMGLIRIQTQEEETGRHVRMLTHEIRSTLDR	160 159
Tci_144982 ETR1 (AAA70047.1)	HTILKTTIELGRTLDEECVLMWPSRKGMILQLSHSLHNLIIFPGSTVPINLPIIIEVFNSAAIRIPHNCPLARIRTPV HTILKTTIELGRTLALEECAWMPTRTGLELQLSYTILRHQHPVEYTVPIQLPVINQVFGTSRAVKISPNSPVARLRPVS	240 239
Tci_144982 ETR1 (AAA70047.1)	GSYIPPEVVAWRVPLLHLSNFEIDNWPDSAKSYAVMILILPBMNGVRKWRDHEMELTVVADQVAVALSHAAILEESMRA GKMLGEVVAWRVPLLHLSNFOINDWPELSTKRYALMVLMLPSDSARQWHVHELELVVADQVAVALSHAAILEESMRA	320 319
Tci_144982 ETR1 (AAA70047.1)	RDQLMDQNFAHLNARQEAEMAIHARNDLFLAVMNHEMRTPMHAIIALSSLLETELTPDQRAMIEILTILKSSNLLAALNDV RDLMEQNVALDLARREAETAIRARNDLFLAVMNHEMRTPMHAIIALSSLQETELTPEQRLMVEITILKSSNLLATLNDV	400 399
Tci_144982 ETR1 (AAA70047.1)	LDLSRLEDGSLELESEVFNHLGLFKEVVTLINPIASVKNNTSMALNCDLDPAGFIGDEKRLMQIIILNNVGNAVKFTKGHH LDLSRLEDGSIQLELGTFNLHTLFREVNLNLIKPIAVVKKLPITLNLPDLPFVVGDEKRLMQIIILNIVGNAVKFSKQGS	480 479
Tci_144982 ETR1 (AAA70047.1)	VSIQASILSPPEYIQLQEWQTPEFCPTLTDGLFYLLVQVKDGGSGIKQQDIPHIIFTKFSEPRSASNRRNGAGLGLAICKRFV ISVTALVTK---SDTRAADFFVVPTGSHFYLRVKVKGDSAGINPQDIPKIFTKFAQTQSILATRSSGGSGLGLAISKRFV	560 555
Tci_144982 ETR1 (AAA70047.1)	NLMGGHIWIESGGLGKGTVAVFLVKLGLCNYPNDPTMQLVPRT--VPKTRPHQGSGLIQLI----- NLMEGNIWIESDGLGKGCTAIFDVKLGISERSNE-SKQSGIPKVPAPRHSNFTGLKVLVMDENGVSRMVTKGLLVHLGC	619 634
Tci_144982 ETR1 (AAA70047.1)	-----HRQLDRGGYQGASSFPFLYNNRIM----- EVTTVSSNEECLRVVSHEHKVVFMDCMPGVENYQIALRIHEKFTKQRHQPPLVALSGNTDKSTKEKCMMSGFLDGVLKK	642 714
Tci_144982 ETR1 (AAA70047.1)	----- PVSLDNIRDVLSLLEPRVLYEGM 738	
		<span style="background-color: cyan; color: black; padding: 2px;">:HATPase_c domain (pfam02518)</span>

**C**

Tci_154278 AtFer1(CAA63932.1)	MSLN-ISISSSFNLLLN-KTDADLG-YVPRKAIGFVKVNGRCRASVGEENAVVS-----SGVLFQPFEEVKKDAFVVPIS MASNALSSFTAANPALSPKPPLPHGSAPSVSLSGFSRKVGGRAVVVAATVDNNMPMTGVVFQPFEEVKKADLAIPIT	72 80
Tci_154278 AtFer1(CAA63932.1)	PQMSLAKQNYFHDEAAINEQINWEYNVSYVHALYAYFDRDNVALKGFAKFFKVSSDEERHAEKIMKYQNMRRGVIL SHASLARQFTADASEAVINEQINWEYNVSYVHSMAYFDRDNVAMGLAKFFKESSEERHAEKEMEYQNRGGRVIL	152 160
Tci_154278 AtFer1(CAA63932.1)	HTIVTPPSEFEHVKEKGDALYAMEALASLEKLVNEKLLAIHAVADRNDPQMAFDIESEFLABQVIAIKKISDYVSQLRRV HPIVSPISEFEHAKGDALYAMEALASLEKLTNEKLLNVHKVASENNPQLADEVESEFLGQVIAIKKISDYITQLRMT	232 240
Tci_154278 AtFer1(CAA63932.1)	GKGHGIVWHFDQMLLEGGVAA 252 GKGHGIVWHFDQMLLN---- 255	
		<span style="background-color: green; color: black; padding: 2px;">:eukaryotic ferritin domain (cd01056)</span> <span style="background-color: blue; color: black; padding: 2px;">:Iron ion channel</span> <span style="background-color: yellow; color: black; padding: 2px;">:Ferroxidase diiron center</span>

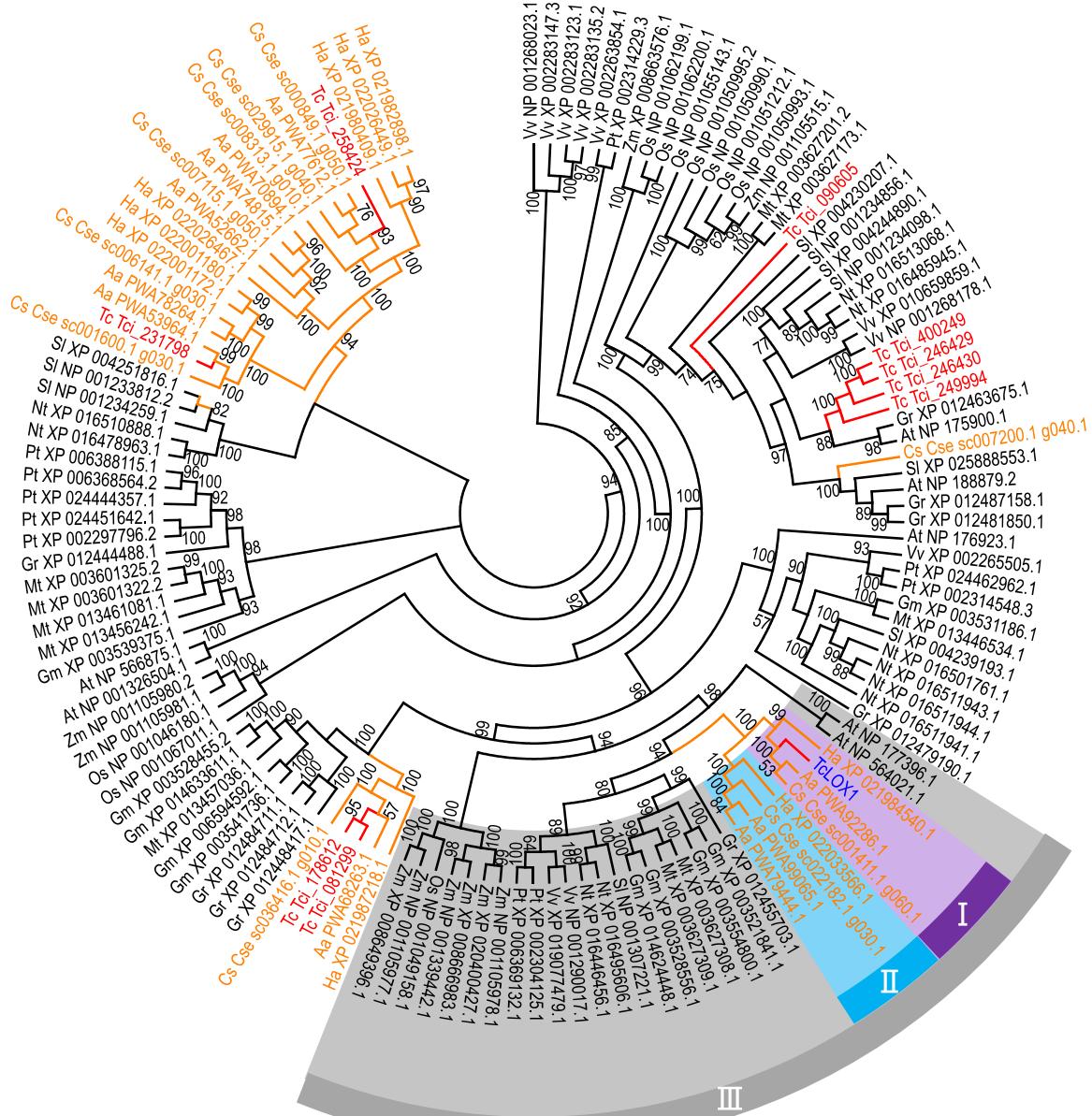
38 **Supplemental Figure 3. Amino acid sequence alignment of ribosome-inactivating protein Tci\_399175**  
39 and *Sambucus nigra* agglutinin I (SNA-I, accession No. O22415.1) (A), signal transduction histidine  
40 kinase Tci\_144982 and *Arabidopsis thaliana* ethylene-response gene (ETR1, accession No. AAA70047.1)  
41 (B), and ferritin-like protein Tci\_154278 and *A. thaliana* ferritin-1 (AtFer-1, accession No. CAA63932.1)  
42 (C). The conserved protein domains are highlighted or underlined.

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## Supplemental Figure 4.

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A



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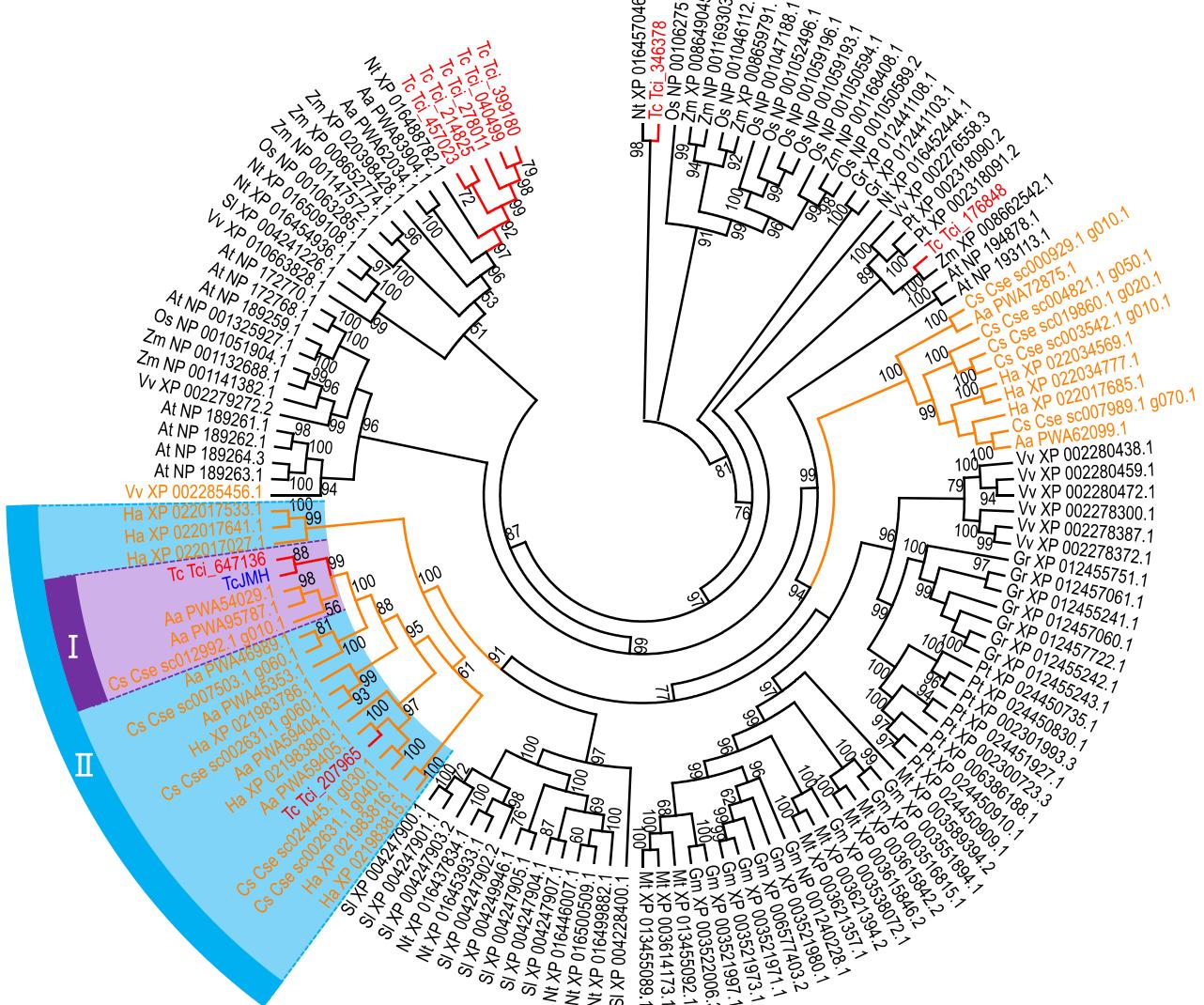
**B**

Aa_PWA79444.1	-MALAKEIMGTSILOEQK--PSFHNSK--SLKPMHH--NHVSISQNGSFQTRF----AKVVKSAISEDIAKFKVKSEKDEKEAVSFKVRALTVRNKVQE	89
Aa_PWA92286.1	-MALTRQIMGTS-LMDKK--TSVFGSN-----LCINHVSINKQHRLRLRK-TRKNGSMMVAISEDILVRLRVKEK---PVTFKVRAVLTVRNKSKE	83
Aa_PWA99065.1	-MALAKEIMGTSILOEQK--PSFHNSK--SLKPMHO--NHVSISQNGSFQTRF----GKVVVKSAISEDIAKFKVKSEKDEKEAVSFKVRALTVRNKVQE	89
Cs_Cse_sc001411.1_g060.1	-MALTRQIMGTS-LMDKK--TSVFGSN-----LCINHVSINKQHRLRLRK-TRKNGSMMVAISEDILVRLRVKEK---PVTFKVRAVLTVRNKSKE	83
Cs_Cse_sc022182.1_g030.1	-MALAKEIMGTSILOEQKQQPSFLN----SLKPMHO--NHVISQNGSFRIR----TKVVKSAISEDIAKFKVKSEKDEKEAVTFKVRALTVRNKVQE	88
Ha_XP_021984540.T	MASLAKDIISASSMVNDK--SSFFGNSNIINONLGRLYVNPNVLIPLDLRKRLRKGVRITTPVVAIASEDLVKLVRVEK---PVSFKVRAVLTVRNKVQE	94
Ha_XP_022033566.1	-MAISQJLMCGSLTEKSQ---FLSSN---ILKSINTYSNQSVSPKRCVRTR-----PVPVKAISIEDLKDLAKFVN-AEKAVTFKVRALTVRNKYQE	86
Tc_TcLOX1	-MALAKQIMGAS-LMDQK--TSVFGSN-----LCINHVLVN-KHRLRLRK-TRKNGSMMVAISEDILVKLXRVKEK--PVTFKVRAVLTVRNKNKE	84
Aa_PWA79444.1	D-FKETLVVKIDAFADQIGRNVVLLELFSEVIDSKTRAPPKSKEGVLKDWSQSKNSLNKEVKVNTSDILVESDFGVPGAITITNKHQKEFYLESETIEGFAC	188
Aa_PWA92286.1	D-FKDTDFRKIDALTDQIGWNVIQLEFSNDIDPDKTRAPRKSNEAVLKDWWSKSKNSNTERVNTADIMVDSDFGIPGAITISNKHQKEFLETITIEGFAC	182
Aa_PWA99065.1	D-FKETLVVKIDAFADQIGRNVVLLELFSEVIDSKTRAPPKSKEGVLKDWSQSKNSLNKEVKVNTSDILVESDFGVPGAITITNKHQKEFYLESETIEGFAC	188
Cs_Cse_sc001411.1_g060.1	D-FKDTDFRKIDALTDQIGWNVIQLEFSNDIDPDKTRAPRKSNEAVLKDWWSKSKNSNTERVNTADIMVDSDFGIPGAITISNKHQKEFLETITIEGFAC	182
Cs_Cse_sc022182.1_g030.1	D-FKETLVVKIDAFADQIGRNVVLLELFSEVIDSKTRAPPKSKEGVLKDWSQSKNSLNKEVKVNTSDILVESDFGVPGAITITNKHQKEFYLESETIEGFAC	187
Ha_XP_021984540.T	D-LTETIVRKLDLDAFDQIGRNVVLLELFSEVIDPDKTRAPPKSKEEALKDWWSKSKNSNTERVNTADILVSEFGIPGAIAITNKHQKEFYLESETIEGFAC	193
Ha_XP_022033566.1	D-FKETLVVKFDALDQIGRNVVLVHSVDIDPDKTRAPPKSKEEALKDWSEKSNLKEVKVNTSDILVGSDFGIPGAISISNKHQKEFYLESETIEGFAC	185
Tc_TcLOX1	DFFKETLVVKFDALDQIGRNVVLVHSVDIDPDKTRAPPKSKEEALKDWSEKSNLKEVKVNTSDILVGSDFGIPGAISISNKHQKEFYLESETIEGFAC	184
Aa_PWA79444.1	GPVYFPFCNSWVQSVNNDHPEPRIFFSNQPYLPDQTTPAGIKLRLREKEELRDLRGDGTVRKLSDRIDYDVNDLGNPDRGNDFTPILLGGQKIPYPRRCRTG	288
Aa_PWA92286.1	GPVHFPFCNSWVQSICKDLPNPRIFFTNQPYLPDPTPAGLKLRLREKEELRDLRGDGTVRKLSDRIDYDVNDLGNPDRGNDFTPILLGGKLPYPRRCRTG	282
Aa_PWA99065.1	GPVYFPFCNSWVQSICKDLPNPRIFFTNQPYLPDPTPAGLKLRLREKEELRDLRGDGTVRKLSDRIDYDVNDLGNPDRGNDFTPILLGGKLPYPRRCRTG	288
Cs_Cse_sc001411.1_g060.1	GPVYFPFCNSWVQSICKDLPNPRIFFTNQPYLPDPTPAGLKLRLREKEELRDLRGDGTVRKLSDRIDYDVNDLGNPDRGNDFTPILLGGKLPYPRRCRTG	282
Cs_Cse_sc022182.1_g030.1	GPVYFPFCNSWVQSICKDLPNPRIFFTNQPYLPDPTPAGLKLRLREKEELRDLRGDGTVRKLSDRIDYDVNDLGNPDRGNDFTPILLGGKLPYPRRCRTG	287
Ha_XP_021984540.T	GPVHFPFCNSWVQSYKDPSKEPRVFSNQPYLPDPTPAGLKLRLREKEELRDLRGDGTVRKLSDRIDYDVNDLGNPDRGNDFTPILLGGKLPYPRRCRTG	293
Ha_XP_022033566.1	GPVYFPFCNSWVQSTNDHPNPRIFFSNQPYLPDPTPAGLKLRLREKEELTLYLRDGDKGVRKLDRIDYDVNDLGNPDRGSEFSRPILGGQKIPYPRRCRTG	285
Tc_TcLOX1	GPVHFPFCNSWVQSTNDHPNPRIFFTNQPYLPDPTPAGLKLRLREKEELTLYLRDGDKGVRKLDRIDYDVNDLGNPDRGSEFSRPILGGQKIPYPRRCRTG	284
Aa_PWA79444.1	RAPSDTDIAESERVEKPFPLYVPRDEQFDESKQNTFTSRSLKAVHLNLLPSMVASISKHHDFKGSQIESLYSEGVLVLLGLQDDLLKKLRLPNLVTRLH	388
Aa_PWA92286.1	RAPSDTDIAESERVEKPFPLYVPRDEQFDESKQNTFTSRSLKAVHLNLLPSMVASISKHHDFKGSQIESLYSEGVLVLLGLQDDLLKKLRLPNLVTRLH	382
Aa_PWA99065.1	RTPSDTDIAESERVEKPFPLYVPRDEQFDESKQNTFTSRSLKAVHLNLLPSMVASISKHHDFKGSQIESLYSEGVLVLLGLQDDLLKKLRLPNLVTRLH	388
Cs_Cse_sc001411.1_g060.1	RTPSDTDIAESERVEKPFPLYVPRDEQFDESKQNTFTSRSLKAVHLNLLPSMVASISKHHDFKGSQIESLYSEGVLVLLGLQDDLLKKLRLPNLVTRLH	382
Cs_Cse_sc022182.1_g030.1	RTPSDTDIAESERVEKPFPLYVPRDEQFDESKQNTFTSRSLKAVHLNLLPSMVASISKHHDFKGSQIESLYSEGVLVLLGLQDDLLKKLRLPNLVTRLH	387
Ha_XP_021984540.T	RAPSDTDIAESERVEKPFPLYVPRDEQFEEKSANAFTRGKVLNHLPSIASISKHHDFKGSQIESLYSEGVLVLLGLQDDLLKKLRLPNLVTRLH	393
Ha_XP_022033566.1	RLPSPDTDILCESERVEKPFPLYVPRDEQFEEKSANAFTRGKVLNHLPSIASISKHHDFKGSQIESLYSEGVLVLLGLQDDLLKKLRLPNLVTRLH	382
Tc_TcLOX1	RVPSPDTDIAESERVEKPFPLYVPRDEQFEEKSANAFTRGKVLNHLPSMTSISKHDFKGSQIESLYSEGVLVLLGLQDDLLKKLRLPNLVTRLH	384
Aa_PWA79444.1	ESSQGGGLLKYDTPKILSKDRFSWLDRDEFARQALAGVNPSVIEKLKLVFPVSHLDPEIYGPOQESALKEEHLIGYLNGMTVQQAIEENKLFIDYHDYL	488
Aa_PWA92286.1	ESSQGGGLLKYDTPKILSKDKFAWLRDEFARQALAGVNPSVIEKLKLVFPVSHLDPEIYGPOQESALKEEHLIGYLNGMTVQQAIEENKLFIDYHDYL	482
Aa_PWA99065.1	ESSQGGGLLKYDTPKILSKDKFAWLRDEFARQALAGVNPSVIEKLKLVFPVSHLDPEIYGPOQESALKEEHLIGYLNGMTVQQAIEENKLFIDYHDYL	488
Cs_Cse_sc001411.1_g060.1	ESSQGGGLLKYDTPKILSKDKFAWLRDEFARQALAGVNPSVIEKLKLVFPVSHLDPEIYGPOQESALKEEHLIGYLNGMTVQQAIEENKLFIDYHDYL	482
Cs_Cse_sc022182.1_g030.1	ESSQGGGLLKYDTPKILSKDKFAWLRDEFARQALAGVNPSVIEKLKLVFPVSHLDPEIYGPOQESALKEEHLIGYLNGMTVQQAIEENKLFIDYHDYL	487
Ha_XP_021984540.T	ESSQGGGLLKYDTPKILSKDKFAWLRDEFARQALAGVNPSVIEKLQVFPVSRLDPEIYGPOQESALKEEHLIGYLNGMTVQQAIEENKLFIDYHDYL	493
Ha_XP_022033566.1	--SQGGGGGLKYDTPKILSKDKFAWLRDEFARQALAGVNPSVIEKLQVFPVSRLDPEIYGPOQESALKEEHLIGYLNGMTVQQAIEENKLFIDYHDYL	480
Tc_TcLOX1	ESSQGGGLLKYDTPKILSKDKFAWLRDEFARQALAGVNPSVIEKLQVFPVSRLDPEIYGPOQESALKEEHLIGYLNGMTVQQAIEENKLFIDYHDYL	484
Aa_PWA79444.1	PFLDRINALDERKAYATRTTFFLTPTSGTLKPAIAEELSPLRALPGSOPKRVLTPTIDATSNWTLQLAHKVCNSDAGVHQLSHWLRTHAAMEPPFTLSAHR	588
Aa_PWA92286.1	PFLDRINALDGRKAYATRTTFFLTPTSGTLKPAIAEELSPLQALPGSESNSRWTPTIDATSNWMLQLAHKVCNSDAGAHQLVHFLRTHAATEPPFTLSAHR	582
Aa_PWA99065.1	PFLDRINALDGRKAYATRTTFFLTPTSGTLKPAIAEELSPLQALPGSESNSRWTPTIDATSNWMLQLAHKVCNSDAGAHQLVHFLRTHAATEPPFTLSAHR	588
Cs_Cse_sc001411.1_g060.1	PFLDRINALDGRKAYATRTTFFLTPTSGTLKPAIAEELSPLQALPGSESNSRWTPTIDATSNWMLQLAHKVCNSDAGAHQLVHFLRTHAATEPPFTLSAHR	588
Cs_Cse_sc022182.1_g030.1	PFLDRINALDGRKAYATRTTFFLTPTSGTLKPAIAEELSPLQALPGSESNSRWTPTIDATSNWMLQLAHKVCNSDAGAHQLVHFLRTHAATEPPFTLSAHR	587
Ha_XP_021984540.T	PFLDRINALDGRKAYATRTTFFLNPSGTLIMPVAIELSPLQALPGTESKRWTPTPADATSNWMLQLAHKVCNSDAGVHQLSHWLRTHASMEPPFTLSAHR	593
Ha_XP_022033566.1	PFLDRINALDGRHTYATRTTIFYLINESGTLPKVAIELSPLP---QSKRVTPTIDATSNWMLQLAHKVCNSDAGVHQLVHFLRTHAIMEPPFTLSAHR	575
Tc_TcLOX1	PFLDRINALDGRHTYATRTTIFYLINESGTLPKVAIELSPLP---QSKRVTPTIDATSNWMLQLAHKVCNSDAGVHQLVHFLRTHAIMEPPFTLSAHR	584
Aa_PWA79444.1	QLSAMHPYKLLDPHMRYTLTINAIRQLNINADGVIEQGFTPGRYMEISAAYAKHWRFDLEGLPADLIRRGMAVPDPSQRHGLKLIIEDDYPYASDGL	688
Aa_PWA92286.1	QLSAMHPYKLLDPHMRYTLTINQLQRNLINADGVIEQGFTPGRYMEISAAYAKHWRFDLEGLPADLIRRGMALPDSKPHGLKLVIEDDYPYASDGL	682
Aa_PWA99065.1	QLSAMHPYKLLDPHMRYTLTINQLQRNLINADGVIEQGFTPGRYMEISAAYAKHWRFDLEGLPADLIRRGMALPDSKPHGLKLVIEDDYPYASDGL	688
Cs_Cse_sc001411.1_g060.1	QLSAMHPYKLLDPHMRYTLTINQLQRNLINADGVIEACFTPGRYMEISAAYAKHWRFDLEGLPADLIRRGMALPDSKPHGLKLVIEDDYPYASDGL	682
Cs_Cse_sc022182.1_g030.1	QLSAMHPYKLLDPHMRYTLTINQLQRNLINADGVIEACFTPGRYMEISAAYAKHWRFDLEGLPADLIRRGMALPDSKPHGLKLVIEDDYPYASDGL	687
Ha_XP_021984540.T	QLSAMHPYKLLDPHMRYTLTINQLQRNLINADGVIECQGFTPGRYMEMSAAAYKNWRFDLEGLPADLIRRGMALPDSKPHGLKLVIEDDYPYASDGL	693
Ha_XP_022033566.1	QLSAMHPYKLLDPHMRYTLTINQLQRNLINADGVIECQGFTPGRYMEMSAAAYKNWRFDLEGLPADLIRRGMALPDSKPHGLKLVIEDDYPYASDGL	675
Tc_TcLOX1	QLSAMHPYKLLDPHMRYTLTINQLQRNLINADGVIECQGFTPGRYMEMSAAAYKNWRFDLEGLPADLIRRGMALPDSKPHGLKLVIEDDYPYASDGL	684
Aa_PWA79444.1	IWEAIQDWVRTYVNRYPPDPSLVCNDRELQAWYAEVINVGHADLRYENWPTLANAEDILTIALTTIWLASAQHAALINFQOQPYGGYIIPNRPPPMRRLIP	788
Aa_PWA92286.1	IWEAIQDWVRTYVNHYPPDPSAQCWNDRQLEQAWYAEVINVGHADLRYENWPTLANAEDILTASADDLTSVLTIIWLASAQHAALINFQOQPYGGYIIPNRPPPMRRLIP	782
Aa_PWA99065.1	IWEAIQDWVRTYVNHYPPDPSLVCNDRELQAWYAEVINVGHADLRYENWPTLANAEDILTASADDLTSVLTIIWLASAQHAALINFQOQPYGGYIIPNRPPPMRRLIP	788
Cs_Cse_sc001411.1_g060.1	IWEAIQNWVKTYVNHYPPDPSAQCWNDRQLEQAWYAEVINVGHADLRYENWPTLANAEDILTASADDLTSVLTIIWLASAQHAALINFQOQPYGGYIIPNRPPPMRRLIP	782
Cs_Cse_sc022182.1_g030.1	IWEAIQNWVRTYVNHYPPDPSLVCNDRELQAWYAEVINVGHADLRYENWPTLANAEDILTASADDLTSVLTIIWLASAQHAALINFQOQPYGGYIIPNRPPPMRRLIP	787
Ha_XP_021984540.T	IWEAIQNWVRTYVNHYPPDPSAQCWNDRQLEQAWYAEVINVGHADLRYENWPTLANAEDILTASADDLTSVLTIIWLASAQHAALINFQOQPYGGYIIPNRPPPMRRLIP	793
Ha_XP_022033566.1	IWEAIQNWVRTYVNHYPPDPSLVCNDRELQAWYAEVINVGHADLRYENWPTLANAEDILTASADDLTSVLTIIWLASAQHAALINFQOQPYGGYIIPNRPPPMRRLIP	775
Tc_TcLOX1	IWEAIQNWVKTYVNHYPPDPSAQCWNDRQLEQAWYAEVINVGHADLRYENWPTLANAEDILTASADDLTSVLTIIWLASAQHAALINFQOQPYGGYIIPNRPPPMRRLIP	784
Aa_PWA79444.1	DENDPEYASFLLEDQFQYFLALPSMLQSTKYMAMVDTLSTHSPDEEYIGERQDFTWSDGAEMEAFYGFASEIQRIKEIEKNRDMSLKNRCCAGVL	888
Aa_PWA92286.1	DQNDPEYASFLHDPPQKRYFLSALPSLQSTKYMAMVDTLSTHSPDEEYIGERQDFTWSDGAEMEAFYGFASEIQRIKEIEKNRDMSLKNRCCAGVL	882
Aa_PWA99065.1	DENDPEYASFLHDPPQKRYFLSALPSLQSTKYMAMVDTLSTHSPDEEYIGERQDFTWSDGAEMEAFYGFASEIQRIKEIEKNRDMSLKNRCCAGVL	888
Cs_Cse_sc001411.1_g060.1	DENDPEYASFLHDPPQKRYFLSALPSLQSTKYMAMVDTLSTHSPDEEYIGERQDFTWSDGAEMEAFYGFASEIQRIKEIEKNRDMSLKNRCCAGVL	888
Cs_Cse_sc022182.1_g030.1	DENDPEYASFLHDPPQKRYFLSALPSLQSTKYMAMVDTLSTHSPDEEYIGERQDFTWSDGAEMEAFYGFASEIQRIKEIEKNRDMSLKNRCCAGVL	887
Ha_XP_021984540.T	DENDPEYASFLHDPPQKRYFLSALPSLQSTKYMAMVDTLSTHSPDEEYIGERQDFTWSDGAEMEAFYGFASEIQRIKEIEKNRDMSLKNRCCAGVL	893
Ha_XP_022033566.1	DENDPEYASFLHDPPQKRYFLSALPSLQSTKYMAMVDTLSTHSPDEEYIGERQDFTWSDGAEMEAFYGFASEIQRIKEIEKNRDMSLKNRCCAGVL	875
Tc_TcLOX1	DVNDPEYASFLHDPPQKRYFLSALPSLQSTKYMAMVDTLSTHSPDEEYIGERQDFTWSDGAEMEAFYGFASEIQRIKEIEKNRDMSLKNRCCAGVL	884
Aa_PWA79444.1	YELLAPSSEPGVTCRGLPNVS-----	
Aa_PWA92286.1	YELLAPSSEPGATCRGVPNVS-----	
Aa_PWA99065.1	YELLAPSSEPGVTCRGLPNVS-----	
Cs_Cse_sc001411.1_g060.1	YELLAPSSEPGATCRGVPNVSINIRRSKDYKPSIPLPPMSYNIQASHTKPLYKELCGNLITIGEVATCLRQOGDEVFIMSHGDVKVVPNALRLS	975
Cs_Cse_sc022182.1_g030.1	YELLAPSSEPGVTCRGLPNVS-----	
Ha_XP_021984540.T	YELLAPSSESGATCRGVPNVS-----	
Ha_XP_022033566.1	YELLAPSSEPGATCRGVPNVS-----	
Tc_TcLOX1	YELLAPSSEPGATCRGVPNVS-----	

**Supplemental Figure 4. Molecular phylogenetic analysis of *T. cinerariifolium* 13-lipoxygenase**

**(TcLOX1).** TcLOX1-related proteins were searched by BLASTP against 14 different plant protein sets and incorporated into maximum likelihood tree analysis (A) using ORTHOSCOPE method<sup>56</sup>. Proteins incorporated into this tree include 9 from *T. cinerariifolium*, 10 from *C. seticuspe*, 10 from *A. annua*, 9 from *H. annuus*, 10 from *Z. mays*, 10 from *V. vinifera*, 10 from *M. truncatula*, 10 from *S. lycopersicum*, 10 from *P. trichocarpa*, 10 from *O. sativa*, 9 from *G. raimondii*, 10 from *N. tabacum*, 10 from *G. max*, and 7 from *A. thaliana*. TcLOX1 nodes are indicated in blue; *T. cinerariifolium* nodes and edges are indicated in red; other Asteraceae nodes and edges are indicated in orange. The amino acid sequence alignments for maximum likelihood tree analysis are shown in panel B.

A



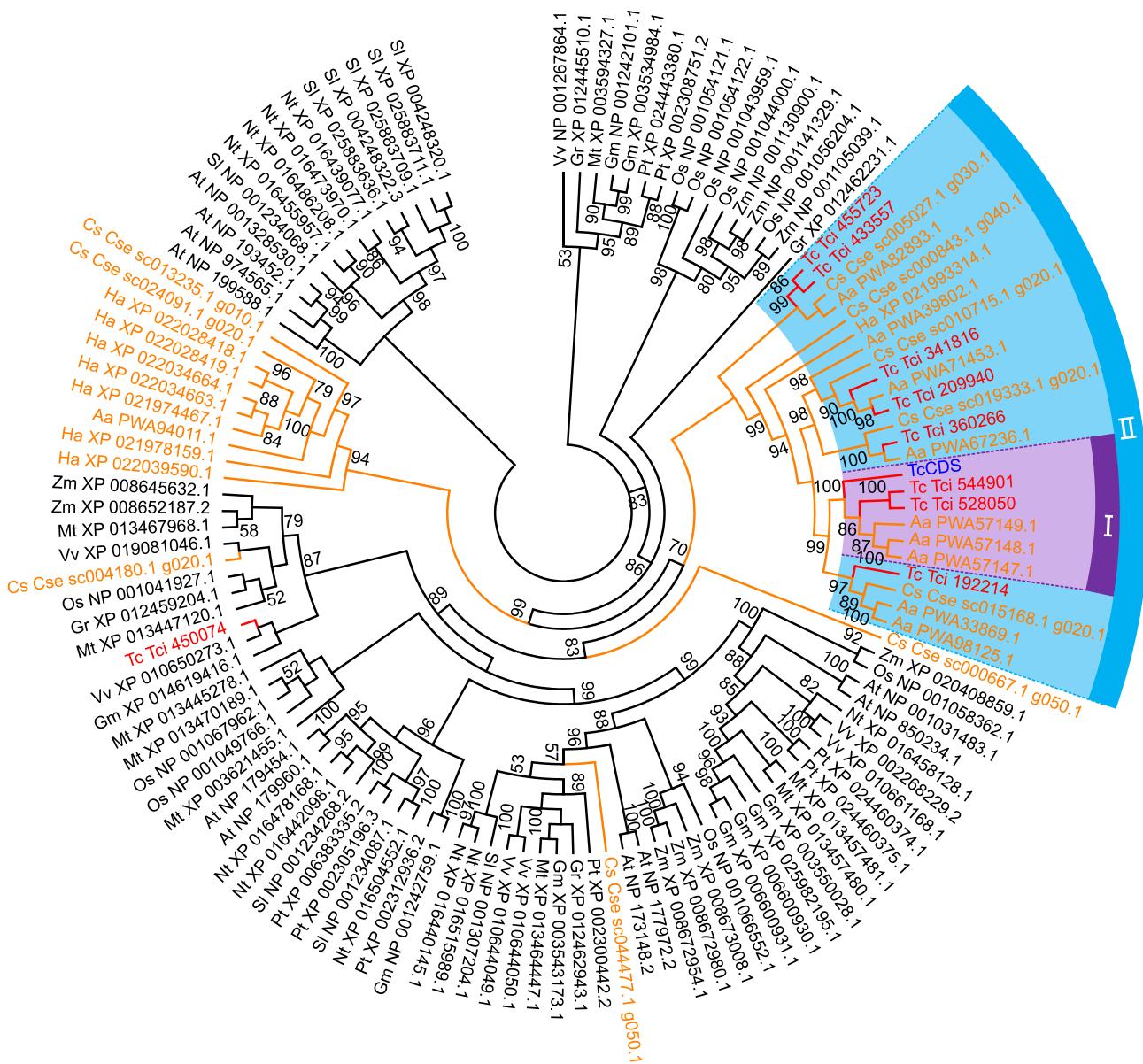
**B**

Aa_PWA45353.1	-----MISIMALLFLYIFLLFPILSLLY-IVPKIIK-NKSrin-----PPGPLGLPFIGNLHQIDS	54
Aa_PWA46989.1	-----MALFFMYIFLLFPILYLY-LLPKINKRSSLRA-----PPGPLGLPFIGNLHQIDS	51
Aa_PWA54029.1	-----MDSLIQFLIASLPLILYOLIPKIIKNKSKSNVHGQFRSPGPGRPHGMPFIGNLHQIDK	58
Aa_PWA59404.1	-----MALLFLFLMSLPLILSLLY-LFPKFIKNKSQFDP-----PGPRLPLFTGNLHQIDQ	50
Aa_PWA59405.1	-----MALFFMYIFLLFPILYLY-LLPKINKRSSLRA-----PPGPLGLPFIGNLHQIDS	51
Aa_PWA95787.1	-----MDSLIQFLIASLPLILFLLY-LLPKIICKSKSSVQGQFRSPGPGRPHGMPFIGNLHQIDK	56
Cs_Cse_sc002631.1_g040.1	-----MDSLIQFLIASLPLILFLLY-LLPKIICKSKSSVQGQFRSPGPGRPHGMPFIGNLHQIDK	56
Cs_Cse_sc002631.1_g060.1	-----MDSLIQFLIASLPLILFLLY-LLPKIICKSKSSVQGQFRSPGPGRPHGMPFIGNLHQIDK	50
Cs_Cse_sc007503.1_g060.1	-----MDSLIQFLIASLPLILFLLY-LLPKIICKSKSSVQGQFRSPGPGRPHGMPFIGNLHQIDK	50
Cs_Cse_sc012992.1_g010.1	-----MALFFMYIFLLFPILYLY-LLPKISK-RSSRLA-----PPGPLGLPFIGNLHQIDS	50
Cs_Cse_sc024445.1_g030.1	-----MALLFLFLMSLPLILSLLY-LFPKFIKNKSQFDP-----PGPRLPLFTGNLHQIDQ	50
Ha_XP_021983786.1	-----MDSLIQFLILVSLFLSFTY-LLPKIICKSKSSVQGQFRSPGPGRPHGMPFIGNLHQIDK	51
Ha_XP_021983800.1	-----MSLILLLFLPLLSTLY-LLPKIICKSKSSVQGQFRSPGPGRPHGMPFIGNLHQIDK	48
Ha_XP_021983815.1	-----MELVEMFILLSLLLSLLY-LLPKIICKSKSSVQGQFRSPGPGRPHGMPFIGNLHQIDQ	50
Ha_XP_021983816.1	-----MELLFLMFLFS--LSIMY-LLPKIICKSKSSVQGQFRSPGPGRPHGMPFIGNLHQINP	47
Ha_XP_022017027.1	-----MISNMLLPFLFLLSSLLY-LIH---KKSKSFNP-----PGPGLPLFTGNLHQIDQ	47
Ha_XP_022017533.1	-----MISNMLLPFLFLLSSLLY-LIH---KKSKSFNP-----PGPGLPLFTGNLHQIDQ	51
Ha_XP_022017641.1	-----MISNMLLPFLFLLSSLLY-LIH---KKSKSFNP-----PGPGLPLFTGNLHQIDQ	51
Tc_TcJMH	-----MMIPIMASVFVYILLPFILYLYIN-LWVKINKNRINRNL-----PPGPLGLPFIGNLHQIDS	56
Tc_Tci_207965	-----PPGPLGLPFIGNLHQIDS-----PGPGLPLFTGNLHQIDQ	92
Tc_Tci_647136	-----MSNEQKYPGKFLRIQRRKQMPARLLVFFAFQKEVEFRNVSTMALLFLFLMSLPLLSSLLY-LLPKIICKNSQFDP-----PGPGLPLFTGNLHQIDQ	56
Aa_PWA45353.1	-----SSIHTSLWNLSRSYGPIVYLSFGFVSCIVVSSASLAKEVLKTODLIFCSRPSMVQAORK-----	112
Aa_PWA46989.1	-----SSIHTSLWNLSRSYGPIVYLSFGFVSCIVVSSASLAKEVLKTODLIFCSRPSMVQAORK-----	109
Aa_PWA54029.1	-----SSLHTSLWNLSKSYSYGPILFLRGFIPSIVVSSASLAKEVLKTODVIFCSRPSVSSQRK-----	109
Aa_PWA59404.1	-----SNFHISLWSLSKSYSYGPVVSINLGFIPAIIVSSASLAKEVLKTODLIFCSRPSVHGLQR-----	116
Aa_PWA59405.1	-----SHLHTLWNLSKSYSYGPVVSINLGFIPAIIVSSASLAKEVLKTODIIFCSRPSVHGLQR-----	108
Aa_PWA95787.1	-----SSLHTSLWNLSKSYSYGPILFLRGFIPSIVVSSASLAKEVLKTODVIFCSRPSVSSQRK-----	109
Cs_Cse_sc002631.1_g040.1	-----SSLHTSLWNLSKSYSYGPVVSINLGFIPAIIVSSASLAKEVLKTODVIFCSRPSVSSQRK-----	156
Cs_Cse_sc002631.1_g060.1	-----SSLHTSLWNLSKSYSYGPVVSINLGFIPAIIVSSASLAKEVLKTODVIFCSRPSVSSQRK-----	109
Cs_Cse_sc007503.1_g060.1	-----SSIHTSLWNLSRSYGPILYLYINFGFVPCIVVSSASLAKEVLKTODLIFCIR-----	109
Cs_Cse_sc012992.1_g010.1	-----CSLHTSLWNLSKSYSYGPILYLYINFGFVPCIVVSSASLAKEVLKTODDHTFCSRPLHGIKK-----	108
Cs_Cse_sc024445.1_g030.1	-----1NLHTSLWNLSKSYSYGPILYLYINFGFVPCIVVSSASLAKEVLKTODDHTFCSRPLHGIKK-----	108
Ha_XP_021983786.1	-----SSLHTSLWKLSKSYSYGPVSVLQFGFIPSTIVSSASLAKEVLKTODDHTFCSRPLHGIKK-----	109
Ha_XP_021983800.1	-----SSLHTSLWNLSKSYSYGPVSVLQFGFIPVPIVSSASLAKEVMKTODLIFCSRPSVHGLQR-----	106
Ha_XP_021983815.1	-----STLHTSLWNLSKSYSYGPVSVLQFGFIPVPIVSSASLAKEVMKTODLIFCSRPSVHGLQR-----	108
Ha_XP_021983816.1	-----SSLHTSLWNLSKSYSYGPVSVLQFGFIPVPIVSSASLAKEVMKTODIIFCSRPSVHGLQR-----	105
Ha_XP_022017027.1	-----SSLHTSLWNLSKSYSYGPVSVLQFGFIPVPIVSSASLAKEVLKTODIIFCSRPSVHGLQR-----	105
Ha_XP_022017533.1	-----SSLHTSLWNLTKSYSYGPVSVLQFGFIPVPIVSSASLAKEVLKTODLIFCSRPSVHGLQR-----	109
Ha_XP_022017641.1	-----SSLHTSLWNLTKSYSYGPVSVLQFGFIPVPIVSSASLAKEVLKTODLIFCSRPSVHGLQR-----	109
Tc_TcJMH	-----SSLHTCLNLWNLSKSYSYGPVSVLQFGFIPVPIVSSASLAKEVYKTODVIFCSRPSVHGLQR-----	114
Tc_Tci_207965	-----SSLHTLWNLSKSYSYGPVSVLQFGFIPVPIVSSASLAKEVYKTODVIFCSRPSVHGLQR-----	150
Tc_Tci_647136	-----SHLHTLWNLSKSYSYGPVSVLQFGFIPVPIVSSASLAKEVYKTODIIFCNRPLTVLGQK-----	150
-----MLPEKLSSP-----		
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Aa_PWA46989.1	-----	
Aa_PWA54029.1	-----	
Aa_PWA59404.1	-----	
Aa_PWA59405.1	-----	
Aa_PWA95787.1	-----	
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Cs_Cse_sc002631.1_g060.1	-----1MGVNSVELFLANLIYSFDWGLPDGTKIEDIDSGQLSCWFFKKSCFALQKVFRNVSTMALPFLFLMSLPLLSSLLYLLPKIICKSKPQS-----VPPGP	549
Cs_Cse_sc007503.1_g060.1	-----	
Cs_Cse_sc012992.1_g010.1	-----	
Cs_Cse_sc024445.1_g030.1	-----	
Ha_XP_021983786.1	-----	
Ha_XP_021983800.1	-----	
Ha_XP_021983815.1	-----	
Ha_XP_021983816.1	-----	
Ha_XP_022017027.1	-----	
Ha_XP_022017533.1	-----	
Ha_XP_022017641.1	-----	
Tc_TcJMH	-----	
Tc_Tci_207965	-----	
Tc_Tci_647136	-----	
Aa_PWA45353.1	-----LLYNCIDVVFSYYNEW-----	147
Aa_PWA46989.1	-----	
Aa_PWA54029.1	-----	
Aa_PWA59404.1	-----	
Aa_PWA59405.1	-----	
Aa_PWA95787.1	-----	
Cs_Cse_sc002631.1_g040.1	-----	
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Cs_Cse_sc012992.1_g010.1	-----LTYNGLDVAFSPYNDYW-----	143
Cs_Cse_sc024445.1_g030.1	-----LSYNGLDMVFSYNEYW-----	143
Ha_XP_021983786.1	-----IGYNGHDVALSPYRNW-----	144
Ha_XP_021983800.1	-----VSYHGLEVIFSPYNDYW-----	141
Ha_XP_021983815.1	-----FSYGGLDVAFSSYDEIW-----	143
Ha_XP_021983816.1	-----FSYGGLDVAFSPYDEIW-----	140
Ha_XP_022017027.1	-----LSYEGLDITFAPYNEHW-----	140
Ha_XP_022017533.1	-----LTYDGLDMAFSPYNEHW-----	144
Ha_XP_022017641.1	-----LTYDGLDMAFSPYNEHW-----	144
Tc_TcJMH	-----RKMRIKFSLHLFSPKRVH-----	149
Tc_Tci_207965	-----FSYNGLDVVFSPSNQYW-----	185
Tc_Tci_647136	-----VLLFLVVRAIN-----	20

Aa_PWA45353.1	-----ASRYIREDEISHAMKKINGLALLSENVNLSAIMKNVTSTIVMRVGFGRYE--DGHERREIILRLIDELQSMITNFFVEDLWPGLPFAGLIDKL	238
Aa_PWA46989.1	-----MKNVISTIVMRVGFGRYE--DGHKRREIILRLIDELOSMITNFFVEDLWPGLPFAGLIDKL	59
Aa_PWA54029.1	-----SSRYIREEEVLHAMKKIHNLSSLKHINLTEIMINVSTIVMRVGFGRYE--DGHERREIIRLIGELOQAMITDFFVADLWPGLPFAASLDRL	235
Aa_PWA59404.1	-----RSSRFIREDEVSNAMEKIHGHLASSKHVNLSSEIAHIVMSNMVTRIGFGKRYE--DGYESKEILRLLHELQATLTNYFISDLWPDFPLVGLIDRL	312
Aa_PWA59405.1	-----SYRYIREEEVSAMKTIFGALITSQVNLSLEITKSVASTIVMRVGFGRYQ--DGHERKEVLRLLLEVQAMMANNFFVSDLWPGLPFAGLADRL	234
Aa_PWA95787.1	-----SSRYIREEEVLHAMKKITHNLSSLKHINLTEIMINVSTIVMRVGFGRYE--DGHERREIIRLIGELOQAMITDFFVADLWPGLPFAASLDRL	235
Cs_Cse_sc002631.1_g040.1	-----SFSYIREDEVSNAMEKTTIHGALLSSKKVNLSEITKRVTSNIMMRVGFGRYQ--DGHESEKVELRLQITELOQAMANFFASDLWPGLPFWVWIDDKL	102
Cs_Cse_sc002631.1_g060.1	-----1LGPKRVRQSRYIREDEVSNAMEKTIHGIALSAKOVNLSEITKSVASTIVMRVGFGRYQ--EGHERKQVLRLLEVQAMMANNFFVSDLWPGLPFAASLDVR	747
Cs_Cse_sc007503.1_g060.1	-----KYIREDEISHAMKKINELAASSKHVNLSSEIMKNTISTIMMRVGFGRYQ--DGHEHEIREILRLIDELQSMITNFFVEDLWPGLPFAASLDVR	189
Cs_Cse_sc012992.1_g010.1	-----SSMYIREDEVLHAMKRTHQALASSKHVNLSSEIMKNTISTIMMRVGFGRYB--DGHERREIIRLIGELOQSMITDFFVADLWPGLPFAASLDRL	234
Cs_Cse_sc024445.1_g030.1	-----CFSYIREDEVSNAMEKTTIHGALLSSKKVNLSEITKRVTSNIMMRVGFGRYQ--DGHESEKVELRLQITELOQAMANFFASDLWPGLPFWVWIDDKL	102
Ha_XP_021983786.1	-----SSRYIREDEVSNAMEKTTIHGALLSSKKVNLSEITKRVTSNIMMRVGFGRYQ--DGHESEKVELRLQITELOQAMANFFASDLWPGLPFWVWIDDKL	234
Ha_XP_021983800.1	-----SFRHIREDEVTTAMKKIHELAASSKEVNLSSEIMKNTISTIMMRVGFGRYB--ECDGSKEILRLLHELQATLTNYFISDLWPGLPFAASLDVR	235
Ha_XP_021983815.1	-----STRDIREDEVSNAMEKTTIHGALLSSKKVNLSEITKSVTSTIMMRVGFGRYQ--DGDHDTIEVLHRLTEVQAMMADFFASDLWPGLPFWVGLVDR	232
Ha_XP_021983816.1	-----STRYIREDEVSNAMEKTTIHGALLSSKKVNLSEITKSVTSTIMMRVGFGRYQ--DENERKVKVLGLLDELOETIVDNYVSDIWPGLPFWVGLVDR	234
Ha_XP_022017027.1	-----SLRYIQGEISAIKKIHDIAAELAEKVNLSKMNLMSNMVRRVCFGKRYHYQNGHERKVKVLGLINEVEQHLLDYLSDIWPGLPFWVGLVDR	233
Ha_XP_022017533.1	-----SFRHIREDEVSTAMKTIHDALSLSGTVNLSEVMKNTMIIIMMRCFGKKYHCRDGLIEKKVGLLINEQEAYLVDLYFSDIWPGLPFWVGLVDR	237
Ha_XP_022017641.1	-----SFRHIREDEVSTAMKTIHDALSLSGTVNLSEVMKNTMIIIMMRCFGKKYHCRDGLIEKKVGLLINEQEAYLVDLYFSDIWPGLPFWVGLVDR	237
Tc_TcJMH	-----SSRYIREDEVSNAMEKTTIHGALLSSKKVNLSEITKSVASTIVMRVGFGRYB--DGHERKEVLRLLLEVQAMMANNFFVSDLWPGLPFWVLDVR	240
Tc_Tci_207965	-----SSRYIREDEVSNAMEKTTIHGALLSSKKVNLSEITKSVASTIVMRVGFGRYQ--DGHERKEVLRLLLEVQAMMANNFFVSDLWPGLPFWVLDVR	276
Tc_Tci_647136	-----S--LIKDEVALAMKKVHKLALLSKKHINLTEIMMNVTISTIVMRVGFGRYE--DGHERREIIRLIGELOQSMITDFFVADLWPGLPFAASLDRL	108
Aa_PWA45353.1	-----TGKIDRLEKCFQDLDLSFYQELIDERLN-AQNAKSCE-EDQDILDILQLKEQQLNNESTEFTNNHHIKAMLT-----VIIQSISHENY	317
Aa_PWA46989.1	-----TGKIDRLEKCFQDLDLSFYQELIDERLN-AQNAKSCE-EDQDILDILQLKEQQLNNESTEFTNNHHIKAMLT-----DVLAGTDASA	138
Aa_PWA54029.1	-----TGKTDRLKECFCQDLDLSFYQELIDERLN-AQNAKSCE-EDQDILDILQLKEQQLNNESTEFTNNHHIKAMLT-----GF	307
Aa_PWA59404.1	-----LGKFYRLEKCLQGLDSFYQNLIDEHLD-TEYSKPNE-EHEDLIDILLQLRNQQLSDSFELTNNDHKMAMLT-----DILVAGTDNSA	391
Aa_PWA59405.1	-----LGKTDRLKECFCQDLDLSFYQNLIDEHLD-RNDK-TSHEEEEDFTDILLRLKDDQDOL-----DILVAGTDNSA	286
Aa_PWA95787.1	-----TGKTDRLKECFCQDLDLSFYQNLIDEHLD-RNDK-TSHEEEEDFTDILLRLKDDQDOL-----DILVAGTDNSA	316
Cs_Cse_sc002631.1_g040.1	-----1SGKSDRLEKCFQYFDLYQDLDLSFYQDLDLSFYQNLIDEHLD-PIFKFSKCEENEYFLDILLRLRKDQHNL--LTYDHIKANLMVFGPLVSSLTVFVFCFLFKNVLAAGTDTSA	198
Cs_Cse_sc002631.1_g060.1	-----1LGKTNRLDRCFQYFDLYQDLDLSFYQNLIDEHLD-RKDQTSHE-QEEDFDIDILLRLRKDQHNL--FNLNDHIKAMLM-----DVLAGTDTS	823
Cs_Cse_sc007503.1_g060.1	-----1TGKIDRLEKCFQDLDLSFYQNLIDEHLD-AQNAKSCE-EDQDILDILQLKEQQLNNESTEFTNNHHIKAMLT-----DVLAGTDNSA	268
Cs_Cse_sc012992.1_g010.1	-----1MGKTDRLKECFCQDLDLSFYQNLIDEHLD-PIFKFSKCEENEYFLDILLRLRKDQHNL--LTYDHIKANLM-----DVLAGTDNSA	315
Cs_Cse_sc024445.1_g030.1	-----1SGKSDRLEKCFQYFDLYQDLDLSFYQNLIDEHLD-HAHP-PIFKFSKCEENEYFLDILLRLRKDQHNL--LTYDHIKANLM-----NVLAAGTDTSA	311
Ha_XP_021983786.1	-----MGKFYRLEKCFKDLDSFYQNLIDEHLD-PQNPKSSE-GEHDLIDILLQLKKDHVLPDPFELTNNDHKALIT-----DILVAGTDNSA	314
Ha_XP_021983800.1	-----SGKTRKDLRDECFLYDFLYQDLDLSFYQNLIDEHLD-PENI-KSREGEFVDIILRLRKDQHNL--LTDHDKANLM-----DVLAGTDTS	308
Ha_XP_021983815.1	-----MGKTDRLKECFCQDLDLSFYQNLIDEHLD-CRNI-KSHEDEDDVIDILLRIMEDDKLFS-----LTDHDKANLM-----NVLSAGTDNSA	310
Ha_XP_021983816.1	-----IGKTDRLKECFCQDLDLSFYQNLIDEHLD-CRNI-RSHEDEDDVIDILLRIMEDDKLFG-----LTDHDKANLM-----NVLAAGTDTSA	307
Ha_XP_022017027.1	-----MGKTNRLKECFCQDLDFFYQNLIDEHLD-PLKDKSEEEEDDDVIDILLRIMEDDKLFG-----LTDHDKANLM-----DVLAGTDTS	310
Ha_XP_022017533.1	-----TGKMNQRDKCFCRSLDSFYQNLIDEHLD-PQEDKSYYEEEEDDDVIDILLQLEKDKLFS-----LTDHDKVMLM-----DVLAGTDTS	314
Ha_XP_022017641.1	-----TGKMNQRDKCFCRSLDSFYQNLIDEHLD-PQEDKSYYEEEEDDDVIDILLQLEKDKLFS-----LTDHDKVMLM-----DVLAGTDTS	314
Tc_TcJMH	-----IGKTARLENCRFLDLYQDLDLSFYQNLIDEHLD-AQNTNSHDQEDKINMDILLHLKKDQVSPPIKLTNDHKAMLT-----DVLAAGTDTSA	320
Tc_Tci_207965	-----LGKTDRLRDECFLYDFLYQDLDLSFYQNLIDEHLD-RKDQ-KTHEEEEDFTDILLRLKKQQLFN--LTDHDKANLM-----DVLAGTDTS	352
Tc_Tci_647136	-----TGKTNRLKECFCQDLDLSFYQNLIDEHLD-AQNAKSHNQEDQDIDMILLQLKKDQVSPPIKLTNDHKAMLT-----DVLAGTDATA	188
Aa_PWA45353.1	-----KFIFF-----	
Aa_PWA46989.1	-----ATVVWAMTALIKNPVKVMKQEEVRNVVGKK--CGINEDELPKLIYLKAIVKEIMRLYPAPLLPVPRVTKKDAILQGYKIKEKTLVYVNAIAGRDPE	235
Aa_PWA54029.1	-----ATLVWAMTTLVKYPKAMKQAAEVRVKMVQNK---DKVDEDDLPKLTLYKAVKEVMRMLYPAAPLLPVPRVTKDAIILDYKIQNQTLVYVNAIAGRDPE	487
Aa_PWA59404.1	-----ATLVWAMTTLVKYPKAMKQAAEVRVKMVQNK---DKVDEDDLPKLTLYKAVKEVMRMLYPAAPLLPVPRVTKDAIILDYKIQNQTLVYVNAIAGRDPE	487
Aa_PWA59405.1	-----ATVVWAMTALIKNPVKVMKQEEEVNRVVGKK--GAIDENDLAQIYLKAIVKEIMRLYPAPLLPVPRVTKDAIILDYKIQNQTLVYVNAIAGRDPE	412
Aa_PWA95787.1	-----ATVVWAMTALIKNPVKVMKQEEEVNRVVGKK--GAIDENDLAQIYLKAIVKEIMRLYPAPLLPVPRVTKDAIILDYKIQNQTLVYVNAIAGRDPE	284
Cs_Cse_sc002631.1_g040.1	-----1ATVVWAMTTLVKYPKAMKQEEEVNRVVGKK--KGKADEDDLPKLTLYMVKAVKEVMTMLYPTVPLLPRETTKETLHGKYKPKTLG-----DSE	919
Cs_Cse_sc007503.1_g060.1	-----1ATVVWAMTALIKNPVKVMKQEEEVNRVVGKK--KGKADEDDLPKLTLYMVKAVKEVMTMLYPTVPLLPRETTKETLHGKYKPKTLG-----DSE	365
Cs_Cse_sc012992.1_g010.1	-----1ATVVWAMTALIKNPVKVMKQEEEVNRVVGKK--GAIDENDLAQIYLKAIVKEIMRLYPAPLLPVPRVTKDAIILDYKIQNQTLVYVNAIAGRDPE	411
Cs_Cse_sc024445.1_g030.1	-----1ATVVWAMTALMKYPKVMKQEEEVNRVVGKK--KGRVDKDLPKLTLYMVKAVKEVMTMLYPSVPLLPRETTKETLHGKYKPKTLVFNVAIAGRDPE	407
Ha_XP_021983786.1	-----ATLVWAMTSLIKNPKEMKVQEEEVNRVVGDK--GKVDDEDDLPKLTLYMVKAVKEVRLYPAAPLLPVPRVTKDAIILDYKIQNQTLVYVNAIAGRDPE	410
Ha_XP_021983800.1	-----ATVVWAMTALIKNPVKMKQEEEVNRVVGDK--KSKVDEDDLPKLTLYMVKAVKEVRLYPTVPLLPRETTKETLNGYIKQOKTLVFNVAIAGRDPE	404
Ha_XP_021983815.1	-----ASVWSMILLIKNPVEMKQAAEVRNMIGK--KGKIDEDDLPLKLTLYMVKAVKEVRLYPAAPLLPVPRVTKDAIILDYKIQNQTLVYVNAIAGRDPE	406
Ha_XP_021983816.1	-----ATVWSLTLMKPNPKVMKQAAEVRNMIGK--KCMIDEDDLPLKLTLYMVKAVKEVRLYPAAPLLPVPRVTKDAIILDYKIQNQTLVYVNAIAGRDPE	403
Ha_XP_022017027.1	-----ATVWWAMTSLIKNPKIMKQEEEVNRVVGK--KGIIEEDDLPLKLTLYMVKAVKEVRLYPAAPLLPVPRVTKDAIILDYKIQNQTLVYVNAIAGRDPE	406
Ha_XP_022017533.1	-----ATVWWAMTLLIRNPVMQKQEEEVNRVVGK--DGKISEDDLPKLTLYMVKAVKEVRLYPAAPLLPVPRVTKDAIILDYKIQNQTLVYVNAIAGRDPE	410
Ha_XP_022017641.1	-----ATVWWAMTLLIRNPVMQKQEEEVNRVVGK--NGKVSDEDDLPKLTLYMVKAVKEVRLYPAAPLLPVPRVTKDAIILDYKIQNQTLVYVNAIAGRDPE	410
Tc_TcJMH	-----ATVWWAMTALMKNPVKVMKQAAEVRVTVGGKK--GAIDENDLAQIYLKAIEIMRLYPAPLLPVPRVTKDAIILDYKIQNQTLVYVNAIAGRDPE	416
Tc_Tci_207965	-----ATVWWAMALMKNPVKMGAJKQEEEVNRVVGK--GAIDENDLAQIYLKAIEIMRLYPAPLLPVPRVTKDAIILDYKIQNQTLVYVNAIAGRDPE	452
Tc_Tci_647136	-----ATVWWAMTALIKNPDKMKAQEEVRNVAGKK--GAIDENDLAQIYLKAIEIMRLYPAPLLPVPRVTKDAIILDYKIQNQTLVYVNAIAGRDPE	264
Aa_PWA45353.1	-----SWENPEEFLPERFLG-SDIDFRGNDFELI PFGAGRRICPGIPGLVVMVELLANLNLVLFDWLPGMKEDIDEYAKPGVIMHKNECLLIAHVY-----	330
Aa_PWA46989.1	-----SWENPEEFLPERFLG-SDIDFRGNDFELI PFGAGRRICPGIPGLVVMVELLANLNLVLFDWLPGMKEDIDEYAKPGVIMHKNECLLIAHVY-----	586
Aa_PWA54029.1	-----SWENPEEFLPERFLG-SDIDFRGNDFELI PFGAGRRICPGIPGLVVMVELLANLNLVLFDWLPGMKEDIDEYAKPGVIMHKNECLLIAHVY-----	586
Aa_PWA59404.1	-----SWENPEEFLPERFLG-SDIDFRGNDFELI PFGAGRRICPGIPGLVVMVELLANLNLVLFDWLPGMKEDIDEYAKPGVIMHKNECLLIAHVY-----	586
Aa_PWA59405.1	-----SWENPEEFLPERFLG-SDIDFRGNDFELI PFGAGRRICPGIPGLVVMVELLANLNLVLFDWLPGMKEDIDEYAKPGVIMHKNECLLIAHVY-----	586
Aa_PWA95787.1	-----SWENPEKFLPERFLG-SDIDFRGNDFELI PFGAGRRICPGIPGLVVMVELLANLNLVLFDWLPGMKEDIDEYAKPGVIMHKNECLLIAHVY-----	507
Cs_Cse_sc002631.1_g040.1	-----1SWDSPEEFLPARFLG-SDIDFRGNDFELI PFGAGRRICPGIPGLVVMVELLANLNLVLFDWLPGMKEDIDEYAKPGVIMHKNECLLIAHVY-----	379
Cs_Cse_sc007503.1_g060.1	-----1SWENPEEFLPERFLG-SDIDFRGNDFELI PFGAGRRICPGIPGLVVMVELLANLNLVLFDWLPGMKEDIDEYAKPGVIMHKNECLLIAHVY-----	101
Cs_Cse_sc012992.1_g010.1	-----1SWENPEEFLPERFLG-SDIDFRGNDFELI PFGAGRRICPGIPGLVVMVELLANLNLVLFDWLPGMKEDIDEYAKPGVIMHKNECLLIAHVY-----	446
Cs_Cse_sc024445.1_g030.1	-----1SWDSPEEFLPERFLG-SDIDFRGNDFELI PFGAGRRICPGIPGLVVMVELLANLNLVLFDWLPGMKEDIDEYAKPGVIMHKNECLLIAHVY-----	502
Ha_XP_021983786.1	-----SWENPEEFLPERFLG-SDIDFRGNDFELI PFGAGRRICPGIPGLVVMVELLANLNLVLFDWLPGMKEDIDEYAKPGVIMHKNECLLIAHVY-----	509
Ha_XP_021983800.1	-----SWDSPEEFLPERFLG-SDIDFRGNDFELI PFGAGRRICPGIPGLVVMVELLANLNLVLFDWLPGMKEDIDEYAKPGVIMHKNECLLIAHVY-----	499
Ha_XP_021983815.1	-----FWSPEDPFYPERFLG-SDIDFRGNDFELI PFGAGRRICPGIPGLVVMVELLANLNLVLFDWLPGMKEDIDEYAKPGVIMHKNECLLIAHVY-----	503
Ha_XP_021983816.1	-----YWRDPEDPFYPERFLG-SDIDFRGNDFELI PFGAGRRICPGIPGLVVMVELLANLNLVLFDWLPGMKEDIDEYAKPGVIMHKNECLLIAHVY-----	498
Ha_XP_022017027.1	-----SWESPEEFLPERFLG-SDIDFRGNDFELI PFGAGRRICPGIPGLVVMVELLANLNLVLFDWLPGMKEDIDEYAKPGVIMHKNECLLIAHVY-----	500
Ha_XP_022017533.1	-----SWNNPGEFFPERFMGKCDIDFKGNDFELI PFGAGRRICPGIPGMSTGIVWELLANLNLVLFDWLPGMKEDIDEYAKPGVIMHKNECLLIAHVY-----	506
Ha_XP_022017641.1	-----SWNNPGEFFPERFMGKCDIDFKGNDFELI PFGAGRRICPGIPGMSTGIVWELLANLNLVLFDWLPGMKEDIDEYAKPGVIMHKNECLLIAHVY-----	506
Tc_TcJMH	-----SWENPEEFLPERFLG-SDIDFRGNDFELI PFGAGRRICPGIPGMSTGIVWELLANLNLVLFDWLPGMKEDIDEYAKPGVIMHKNECLLIAHVY-----	511
Tc_Tci_207965	-----SWENPEEFLPERFLG-SDIDFRGNDFELI PFGAGRRICPGIPGMSTGIVWELLANLNLVLFDWLPGMKEDIDEYAKPGVIMHKNECLLIAHVY-----	551
Tc_Tci_647136	-----SWENPEEFLPERFLG-SDIDFRGNDFELI PFGAGRRICPGIPGMSTGIVWELLANLNLVLFDWLPGMKEDIDEYAKPGVIMHKNECLLIAHVY-----	551

**Supplemental Figure 5. Molecular phylogenetic analysis of *T. cinerariifolium* jasmone hydroxylase (TcJMH).** TcJMH-related proteins were searched by BLASTP against 14 different plant protein sets and incorporated into maximum likelihood tree analysis using ORTHOSCOPE method<sup>56</sup> (A). Proteins incorporated into this tree include 9 from *T. cinerariifolium*, 10 from *C. seticuspe*, 10 from *A. annua*, 10 from *H. annuus*, 10 from *Z. mays*, 10 from *V. vinifera*, 8 from *M. truncatula*, 10 from *S. lycopersicum*, 10 from *P. trichocarpa*, 10 from *O. sativa*, 9 from *G. raimondii*, 10 from *N. tabacum*, 10 from *G. max*, and 10 from *A. thaliana*. TcJMH nodes are indicated in blue; *T. cinerariifolium* nodes and edges are indicated in red; other Asteraceae nodes and edges are indicated in orange. The amino acid sequence alignments for maximum likelihood tree analysis are shown in panel B.

A



**B**

Aa_PWA33869.1	-----MAFSNRVIVGGYLTSKWPWHASSRPSVGQPKNVLHCHQ-----MSSE	4
Aa_PWA39802.1	-----RSSDPLLSTTMSND	53
Aa_PWA57147.1	-----	
Aa_PWA57148.1	-----MACSSSSLSSKWASWNASSFPHPSVOPFVTR-KNWRVYHKOTSES-TITTLSSN	52
Aa_PWA57149.1	-----MAFSNRVIVGGNLTSKWPWHASSQPSVGKLNVLHCHK--RSSDSLLSTTMSND	53
Aa_PWA67236.1	-----MAFSNRVIVGGNLTSKWPWHASSQPSVGKLNVLHCHK--RSSDSLLSTTMSND	53
Aa_PWA71453.1	-----	
Aa_PWA98125.1	-----MNPLIMITYKCFSLVGSLSKWKASWNGSSHQTLSTRPLVAAGKYVVRYQTATDSIYSTLTITMSSE	68
Cs_Cse_sc010715.1_g020.1	-----	
Cs_Cse_sc015168.1_g020.1	-----MAFCNSLVLGGSSKWKASWNGSSHQTLSTRPLVAAGKYVVRYQTATDSIYSTLTITMSSE	60
Cs_Cse_sc01933.1_g020.1	-----MAFSNRVIVGGNLTSKWKASWHAASSRPSVGQPKNVLHCHK--RPSYSLLSTTMSND	53
Ha_XP_021974467.1	-----	
Ha_XP_021993314.1	-----	
Ha_XP_022028418.1	-----	
Ha_XP_022028419.1	-----	
Ha_XP_022034663.1	-----	
Ha_XP_022034664.1	-----MSWCILLCGLSSKWKASWDASSRPHPSVOPFVTR-KNWRVYHKPTSESSYSTLTITMSSE	57
Tc_TcCDS	-----	
Tc_Tci_192214	-----	
Tc_Tci_209940	-----	
Tc_Tci_341816	-----RMQNVPYASVVGSIIMYVRCTRDRDAVFQONITSRFQONPNELCWTWVKTIIKVEIGGGNLTSKWKASCHASSRPSIGTLKVLHCHKTSDSLSTTMSND	750
Tc_Tci_360266	-----TSEHCKRKFKVRIDVGARPSVTIDDLFWADHGFRQYQCLSLVVDLRLWLXVVIAGANLTSKWKASSHASSRPSLGQPKTVLNCHK--WTSDSLSTTMSND	118
Tc_Tci_528050	-----	
Tc_Tci_544901	-----	
Aa_PWA33869.1	-----LNSEFMHVYDTLKSELVHDPAF--ASDDNSCOWVERMIDYNVPG-----GKMVRASFVVDSCOLLKGEKMT--DEVFLACALGWCTEWLQASLUVFDD	94
Aa_PWA39802.1	-----LKSFKMFQVYDQLKSELJHDPAF--AFDDVSROWVDKMDYIVPG-----GKMTRGLSVVDSDYOLLKREELTD--DEAFL--LOAYYLYDD	133
Aa_PWA57147.1	-----MFAVTKMMYA-----GKMVRGYSVVDSDYQLLKQGELELTE--EEAFLVCALGWCTEWLQAFILAHD	59
Aa_PWA57148.1	-----	
Aa_PWA57149.1	-----LNSQFMQVETLKSELJHDPSF--EFDDDSRQWVERMIDYTVPG-----GKMVRGYSVVDSDYQLLKQGELELTE--EEAFLVCALGWCTEWLQAFILAHD	142
Aa_PWA67236.1	-----LKSFKMFQVYDQLKSELJHDPAF--EFDDDSRQWVMDYIVPG-----GKMFRGLSVESYQLLKQGEELAD--GEVFLACALGWCTEWLQAYFLVLD	143
Aa_PWA71453.1	-----MOVYETLKSELJHDPSF--EFDDDSRQWVERMIDYTVPG-----GKMVRGYSVVDSDYQLLKQGELELTE--EEAFPVCALGWCTEWLQAFILAHD	85
Aa_PWA98125.1	-----LNSEFMHVYDTLKSELVHDPAF--VSDDNSCOWVERMIDYNVPG-----GEMVRASFVVDSCOLLKGEKMT--DEVFLACALGWCTEWLQASLUVFDD	151
Cs_Cse_sc010715.1_g020.1	-----MTRGLSVVDNYQLLKQGEELTD--DEAFLVCTLGWCIEWLQVYLYDD	46
Cs_Cse_sc015168.1_g020.1	-----LNSEFMHVYDTLKSELVHDCAF--VSDDNSCOWVERMIDYNVPG-----GKMVRASFVVDSCOLLKGEKMT--DEVFLACALGWCTEWLQASLUVFDD	150
Cs_Cse_sc01933.1_g020.1	-----LKSFKMFQVYDQLKSELJHDPAF--EFDDVSROWVDKMDYIVPG-----GKMFRGLSVESYQLLKQGEELAD--GEVFLVCALGWCTEWLQAYGLVLD	143
Ha_XP_021974467.1	-----MRMEDLISDRKLNNILVIIISNVNVITRYNFP-----VMRSRLWVNWFDPVMSRSLGWCIEWLQANFLVLD	69
Ha_XP_021993314.1	-----	
Ha_XP_022028418.1	-----MFCRYNFDP-----VMRSRLWVNWFDPVMSRSLGWCIEWLQANFLVLD	44
Ha_XP_022028419.1	-----	
Ha_XP_022034663.1	-----MRMEDLISDRKLNNILVIIISNVNVITRYNFP-----VMRSRLWVNWFDPVMSRSLGWCIEWLQANFLVLD	21
Ha_XP_022034664.1	-----MRMEDLISD-----RYNFDP-----VMRSRLWVNWFDPVMSRSLGWCIEWLQANFLVLD	69
Tc_TcCDS	-----LDSQFMQVETLKSELJHDSSF--EFDDDSRQWVERMIDYTVPR-----GKMVRGYSVVDSDYQLLKQGEKMT--DEVFLACALGWCTEWLQASFVLD	147
Tc_Tci_192214	-----MIDYIVPG-----GKMVRASFVVDSCOLMKGEKMT--DEVFLACALGWCTEWWS	48
Tc_Tci_209940	-----MHVYDTLKFELVHDQAF--VSDDNSCOWVERMIDYNVPG-----GKMVRGYSVVDSDYQLLKQGEKMT--DEVFLACALGWCTEWLQASFVLD	85
Tc_Tci_341816	-----LKSFKMFQVYDQLKSELJHDPAF--EFDDVSROWVDKMDYIVPG-----GKMVRGYSVVDSDYQLLKQGEELAD--GEVFLVCTLGWCIEWLQAYFLVLD	847
Tc_Tci_360266	-----LKSFKMFQVYDQLKSELJHDPAF--EFDDVSROWVDKMDYIVPG-----GKMFRGLSVESYQLLKQGEELAD--GEVFLVCTLGWCIEWLQAYFLVLD	208
Tc_Tci_528050	-----MGFLGFLFSSAPISSTF--CDSEECG--TMSDYTIP-----GDMA--SFSIILMQEIN--CLLMCTERLQAFIALED	66
Tc_Tci_544901	-----	
Aa_PWA33869.1	-----IMDDGSHTRRGRCSCWFLRPEVCMTAVNDGMLRNHVRILKKHFHEKAYYVHLVLFNEAEFTQVCQGMIDAIAT--LEGKKDLSKYTMSTPCNLFLPHST	193
Aa_PWA39802.1	-----IMDGSHYRRQPCWFLRPEVCMTAVNDGMLRNHVRILKKHFHEKAYYVHLVLFNEAEFTQVCQGMIDVTT--LVGKEGLSNYSLSLNRIIOYQKCSY	232
Aa_PWA57147.1	-----IMDGSHTRRGRCSCWFLRPEVCMTAVNDGMLRNHVRILKKHFHEKAYYVHLVLFNEAEFTQVCQGMIDVTT--LVGKEGLSNYSLSLNRIIOYQKCSY	158
Aa_PWA57148.1	-----IMDGSHTRRGRCPCWFLRPEVCMTAVNDGMLRNHVRILKKHFHEKAYYVHLVLFNEAEFTQVCQGMIDVTT--LVGKEGLSNYSLSLNRIIOYQKCSY	98
Aa_PWA57149.1	-----IMDGSHTRRGRCPCWFLRPEVCMTAVNDGMLRNHVRILKKHFHEKAYYVHLVLFNEAEFTQVCQGMIDVTT--LVGKEGLSNYSLSLNRIIOYQKCSY	241
Aa_PWA67236.1	-----IIDDGSHTRRGRCPCWFLRPEVCMTAVNDGMLRNHVRILKKHFHEKAYYVHLVLFNEAEFTQVCQGMIDVTT--KFRYGRGEMIDAITT--LVGKEGLSNYSLSLNRIIOYQKCSY	241
Aa_PWA71453.1	-----IMDGSHTRRGRCPCWFLRPEVCMTAVNDGMLRNHVRILKKHFHEKAYYVHLVLFNEAEFTQVCQGMIDVTT--LEGKKDLSKYTMSTPCNLFLPHST	159
Aa_PWA98125.1	-----QTCVQGMIDAIAT--LEGKKDLSKYTMSTPCNLFLPHST	189
Cs_Cse_sc010715.1_g020.1	-----1IMDGSHYRRQPCWFLRPEVCMTAVNDGMLRNHVRILKKHFHEKAYYVHLVLFNEAEFTQVCQGMIDVTT--IJKKHFQAKAYYMHLLDFNE	91
Cs_Cse_sc015168.1_g020.1	-----1IMDGSHTRRGRCSCWFLRPEVCMTAVNDGMLRNHVRILKKHFHEKAYYVHLVLFNEAEFTQVCQGMIDVTT--LDGKKDLSKYTMSLNRRIFYEKSSY	249
Cs_Cse_sc01933.1_g020.1	-----1IIDDGSHTRRGHCPCWFLRPEVCMTAVNDGMLRNHVRILKKHFQAKAYYVHLVLFNEAEFTQVCQGMIDVTT--LVGKEGLSKYSLSLNRIIOYQKCSY	242
Ha_XP_021974467.1	-----IMNESHTHT-----ENFMTCYQLVFYRENLTLCGCSH	100
Ha_XP_021993314.1	-----MIAVNDGALLSNHVRIILKKNFHGKAYAHLLDFNEVELETQTIYQGMIDATTTLVGEKDLSKYTLFLKWRILQYQKSSY	79
Ha_XP_022028418.1	-----IMDESHTNR-----ENFMTCYQLVFYRENLTLCGCSH	75
Ha_XP_022028419.1	-----IMDESHTNR-----ENFMTCYQLVFYRENLTLCGCSH	52
Ha_XP_022034663.1	-----IMNESHTHT-----ENFMTCYQLVFYRENLTLCGCSH	100
Ha_XP_022034664.1	-----IMNESHTHT-----ENFMTCYQLVFYRENLTLCGCSH	81
Tc_TcCDS	-----IMDGSHTRRGRCPCWFLRPEVCMTAVNDGMLRNHVRILKKHFHEKAYYVHLVLFNEAEFTQVCQGMIDVTT--LVGKEGLSNYSLSLNRIIOYQKCSY	246
Tc_Tci_192214	-----	
Tc_Tci_209940	-----IMDASHTRRGRSCWYRLEPEVCMTAVNDGMLRNHVRILKEHFDKAYYQMLVDFNEAEFTQVCQGMIDVTT--LDGKKDLSKYTMSLQHNDIMAACS	184
Tc_Tci_341816	-----IMDGSHYRRQPCWFLRPEVCMTAVNDGMLRNHVRILKKHFHEKAYYVHLVLFNEAEFTQVCQGMIDVTT--EMIDVISTLVG	924
Tc_Tci_360266	-----IIDDGSHTRRGHCPCWFLRPEVCMTAVNDGMLRNHVRILKKHFHEKAYYVHLVLFNEAEFTQVCQGMIDVTT--EMIDVISTLVG	307
Tc_Tci_528050	-----IMDGSHTRRGRCPCWFLRPEVCMTAVNDGMLRNHVRILKKHFHEKAYYVHLVLFNEAEFTQVCQGMIDVTT--IARQKDLLYTTTLNRRILQYQKSSY	165
Tc_Tci_544901	------MDGSHTRRRGRCPCWFLRPEVCMTAVNDGMLRNHVRILKKHFHEKAYYVHLVLFNEAEFTQVCQGMIDVTT--IARQKDLLYTTTLNRRILQYQKSSY	98
Aa_PWA33869.1	-----FNFLNTLPM-----IACALIMFGENLDDHVLAQDVIEIGIYYQVO	290
Aa_PWA39802.1	-----YSFYL-----VACALIMFGENLDDHVLAQDVIEIGIYYQVO	270
Aa_PWA57147.1	-----YSCYLP-----IACALIMFGENLEDHVQVKDILVELGMYYQIO	196
Aa_PWA57148.1	-----YSCYLP-----IACALIMFGENLEDHVQVKDILVELGMYYQIO	136
Aa_PWA57149.1	-----YSCYLP-----IACALIMFGENLEDHVQVKDILVELGMYYQIO	279
Aa_PWA67236.1	-----YSCYLF-----ACALIMLGENLDDHAQVKDIVVEMGYIAQVO	279
Aa_PWA71453.1	-----YSCYLF-----YCLVITVKVQ	170
Aa_PWA98125.1	-----FNFLNTLPM-----IACALIMFGENLDDHVLAQDVIEIGIYYQVO	230
Cs_Cse_sc010715.1_g020.1	-----1YSFYLPEVCMTAVNDGMLRNHVRILKKHFHEKAYYVHLVLFNEAEFTQVCQGMIDVTT--VVCALIMFGENLDDHVLAQDVIEIGIYYQVO	123
Cs_Cse_sc015168.1_g020.1	-----1YSFYLPEVCMTAVNDGMLRNHVRILKKHFHEKAYYVHLVLFNEAEFTQVCQGMIDVTT--IACALIMFGENLDDHVLAQDVIEIGIYYQVO	291
Cs_Cse_sc01933.1_g020.1	-----1YSYP-----SKNLDLHQVNNDLVEVEMDLYQVO	271
Ha_XP_021974467.1	-----SR-----CEYINHF-----FLQTVNVCQPP	121
Ha_XP_021993314.1	-----YSFYL-----CEYINHF-----FLQTVNVCQPP	117
Ha_XP_022028418.1	-----SR-----FGSLSAIREMEGAYRECAVKETST-----	101
Ha_XP_022028419.1	-----SR-----CEYINHF-----FLQTVNVCQPP	78
Ha_XP_022034663.1	-----SR-----CEYINHF-----FLQTVNVCQPP	121
Ha_XP_022034664.1	-----SR-----CEYINHF-----FLQTVNVCQPP	102
Tc_TcCDS	-----YSCYLP-----IACALIMFGENLEDHVQVKDILVELGMYYQIO	284
Tc_Tci_192214	-----YSCYLP-----KDVLIEMGYIYYQVO	62
Tc_Tci_209940	-----KKRPPLM-----APDTYLNLFIMKIHHNDEFSKPLERRYKFDELDYVD	227
Tc_Tci_341816	-----KK-----GLSNYSLSLNRIIOQ	941
Tc_Tci_360266	-----YSCYLP-----CLYFPIILNDQIYFHLCFKFECALMGENLDDHVQVKDILVELGMYYQIO	376
Tc_Tci_528050	-----YSCYLP-----IACALIMFGENLEDHVQVKDILVELGMYYQIO	203
Tc_Tci_544901	-----YSCYLP-----IACALIMFGENLEDHVQVKDILVELGMYYQIO	136

Aa	PWA33869.1	-----NDYLDIFGEPNVFGKTGTDIEECKCSWLIVKAMELANEEQQKILN-----ENYGMDPEKAVVKELY-----RNINP-----
Aa	PWA39802.1	-----DDYFDIFGDPVKVVGKLTGTDIEECKCSWLIAKALELANEEQQKILN-----ENYGKDLDAKAVVKELY-----HTLNLO-GAYE-----343
Aa	PWA57147.1	-----NDYLDIFGDPNVFGKTGTDIEECKCSWLIAKALELSNEEQKKILS-----ENYGKNDPAKAVKVEVY-----HALDLK-SAYE-----269
Aa	PWA57148.1	-----NDYLDIFGDPNVFGKTGTDIEECKCSWLIAKALELSNEEQKKILS-----ENYGKNDPAKAVKVEVY-----HALDLK-SAYE-----209
Aa	PWA57149.1	-----NDYLDIFGDPNVFGKTGTDIEECKCSWLIAKALELSNEEQKKILS-----ENYGKNDPAKAVKVEVY-----HALDLK-SAYE-----352
Aa	PWA67236.1	-----DDYLDIFGDPNVVGKIGTDIENFKCSWLIVAKALELSNEEQKKILS-----KNYGIKDPKVANVKKL-----HTLNLE-GVY-----352
Aa	PWA71453.1	-----YKGS-----YSCYPS---DCVCTPYVG-----EICEDQ-----MLQVKRKK-NSL-----207
Aa	PWA98125.1	-----NDYLDIFGEPNVFGKTGTDIEECKCSWLIVKAMELANEEQQKILN-----ENYGMDPEKAVVKELY-----HTLNLE-GAYE-----303
Cs	Cse sc010715.1_g020.1	-----DDYLDIFGDPVKVVGKSPPIFSFLDDHAFLRNHNLCITCIDS-----NRYRLQVYLIAAFRLRLYLTGRPHMFLLPHLIDDIAYGAYE-----209
Cs	Cse sc015168.1_g020.1	-----NDYLDIFGEPNVFGKTGTDIEECKCSWLIVKAMEQANEQQKILN-----ENYGMDPEKAVAIKELY-----HTLNLE-GAYE-----364
Cs	Cse sc019333.1_g020.1	-----DDYFDIFGDPNVVGKIGTDIENFKCSWLIVAKALELSNEEQNKFLS-----ENYGIKDPKVANVKKL-----RTINLE-RVYE-----344
Ha	XP_021974467.1	-----FVIFIS---FGGYSGLFQTFFKTIMHLRCTNP-----
Ha	XP_021993314.1	-----NDYLDIFGDPNVFGKTGTDIEECKCSWLIVAKALELASEEQQQKILY-----ENYGKDKQACVEVKELY-----HTLNLO-GVYE-----190
Ha	XP_022028418.1	-----LWTYIIKVYYLRTGLDRSIW-----CTNP-----
Ha	XP_022028419.1	-----LWTYIIKVYYLRTGLDRSIW-----CTNP-----
Ha	XP_022034663.1	-----FVIFIS---FGGYSGLFQTFLR-----PLCT-----
Ha	XP_022034664.1	-----FVIFIS---FGGYSGLFQTFLR-----PLCT-----
Tc	TcCDs	-----NDYLDIFGDPNVFKVGTGTDIEECKCSWLIAKALELANEEQQKILS-----ENYGKDPAKAVVKELY-----HALDLK-GAYE-----357
Tc	Tci_192214	-----NDYLDIFGDPNVFGKTGTDIEECKCSWLIVKALELANDEQQQKILS-----ENYGSTDPEKAVVKELY-----QTLKLK-GVY-----135
Tc	Tci_209940	-----NDYLDIFGDPNVFGKTGTDIEECKCSWLIVKALELANDEQQQKILS-----ENYGSTDPEKAVVKELY-----QTLKLK-GVY-----316
Tc	Tci_341816	-----IVDSDMFFLYEWSGMLKELGDNKKIPFTTYRIHMMSMDCLVSIMADGVVIKLLNYVIGCKEIEGLAVGETELY-----MRGVLRPK-GSFL-----975
Tc	Tci_360266	-----YKCS-----YYSFYLP---VACSLLMIGEN-----LDDHVQVK-DILV-----449
Tc	Tci_528050	-----DDYFDIFGDPNVVGKIGTDIESFKCSWLIVAKALELSNEEQKKILS-----ENYGIKDPKVAVVKKL-----HTLNLE-AVYE-----
Tc	Tci_544901	-----NDYLDIFGDPDV-----NDYLDIFGDPDV-----
Aa	PWA33869.1	-----
Aa	PWA39802.1	DYEKSTHEELITSIEAH---PSKALRAVLKSFLEKIYKRQK-----381
Aa	PWA57147.1	DYEINLYEKSMKAIKAL---PSITVQAVLKSCLEKMYEGHK-----307
Aa	PWA57148.1	DYEINLYEKSMKAIKAL---PSITVQAVLKSCLEKMYEGHK-----247
Aa	PWA57149.1	DYEINLYEKSMKAIKAL---PSITVQAVLKSCLEKMYEGHK-----390
Aa	PWA67236.1	DYENKTREELIKSIDVL---PNKAVQAVLRSFLKKLFKRRK-----390
Aa	PWA71453.1	DYEINLYEKSMKAIKAL---PSITVQAVLKSCLEKMYEGHK-----390
Aa	PWA98125.1	DYESNIYAEILKSIEAH---PSKAVQAVLKSCPGKIFYKGKAHSMPPTILR-----350
Cs	Cse sc010715.1_g020.1	DYESNIYAEILLSIEAH---PSKALQAVLKSFLETTIYKRQK-----247
Cs	Cse sc015168.1_g020.1	DYESNIYAEILKSIESV---PSKAVQAVLKSCLGKIFYGHK-----402
Cs	Cse sc019333.1_g020.1	DYENKTTHEELIESIEVL---PNKAVQAVLRSFLKKLFKRRK-----382
Ha	XP_021974467.1	EYEKMTTHEEFMLIESH---PSNVYQO-----215
Ha	XP_021993314.1	EYEKMTTHEEFMLIESH---PSNVYQO-----215
Ha	XP_022028418.1	-----
Ha	XP_022028419.1	-----
Ha	XP_022034663.1	-----
Ha	XP_022034664.1	-----
Tc	TcCDs	DYEINLYEKSMKAIAH---PSISVQAVLKSCLEKMYKGHK-----395
Tc	Tci_192214	EYESNIYADLIKSIEAH---PSKAVQGVLKSCLGKIFYGHN-----173
Tc	Tci_209940	KFVEGDIAGMPPMVYISMFLFSWFAHWEDHDHFHNKYMHKGVGKTRYCA-----366
Tc	Tci_341816	EM-----977
Tc	Tci_360266	DYENKTAKELIKSIEVL---PNKAVQEVLKSFRLKLYKRRK-----487
Tc	Tci_528050	-----
Tc	Tci_544901	-----

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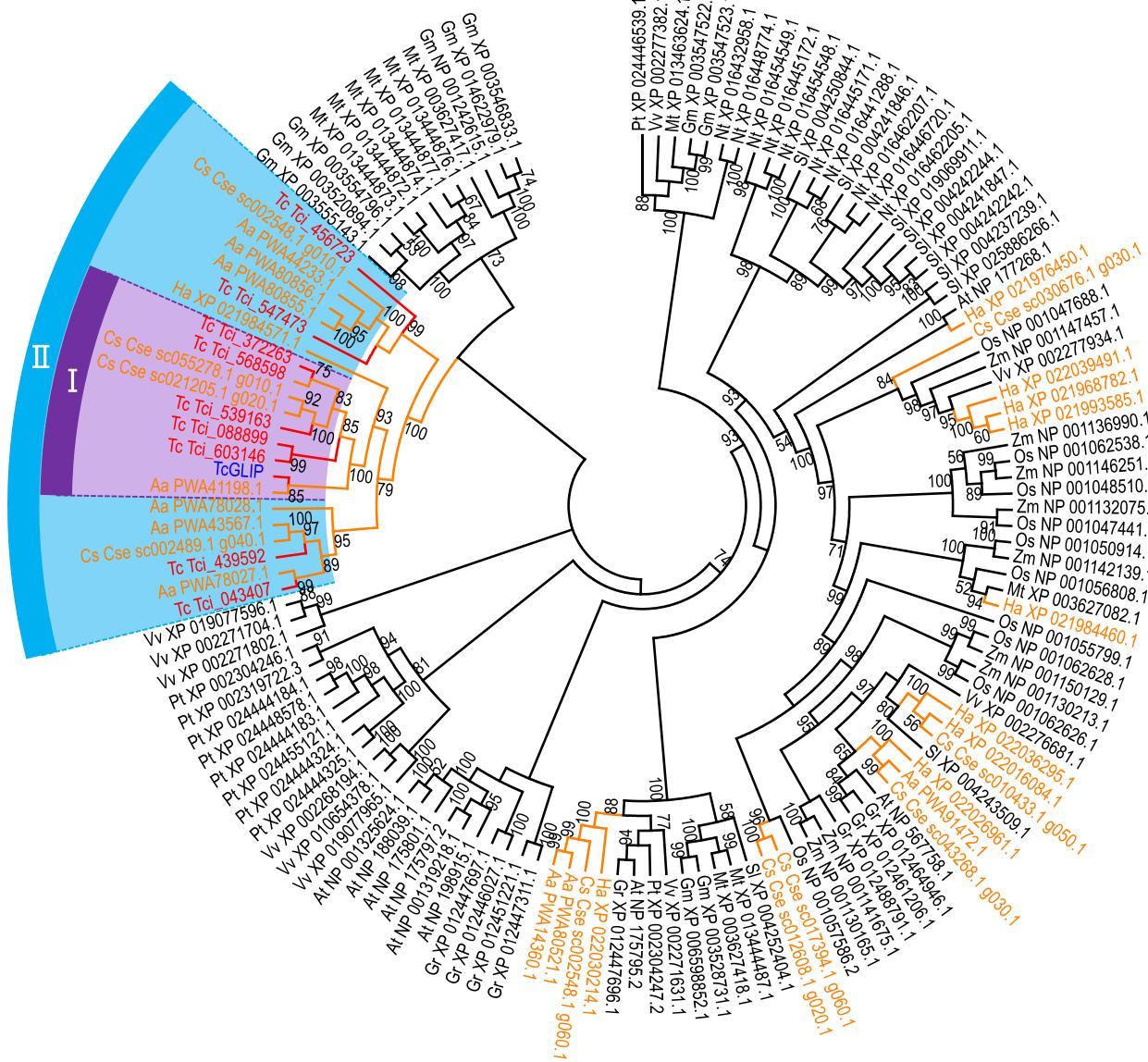
### Supplemental Figure 6. Molecular phylogenetic analysis of *T. cinerariifolium* chrysanthemyl

**diphosphate synthase (TcCDS).** TcCDS-related proteins were searched by BLASTP against 14 different plant protein sets and incorporated into maximum likelihood tree analysis using ORTHOSCOPE method<sup>56</sup> (A). Proteins incorporated into this tree include 9 from *T. cinerariifolium*, 10 from *C. seticuspe*, 10 from *A. annua*, 8 from *H. annuus*, 9 from *Z. mays*, 7 from *V. vinifera*, 9 from *M. truncatula*, 9 from *S. lycopersicum*, 8 from *P. trichocarpa*, 10 from *O. sativa*, 4 from *G. raimondii*, 10 from *N. tabacum*, 9 from *G. max*, and 10 from *A. thaliana*. TcCDS nodes are indicated in blue; *T. cinerariifolium* nodes and edges are indicated in red; other Asteraceae nodes and edges are indicated in orange. The amino acid sequence alignments for maximum likelihood tree analysis are shown in panel B.

95      **Supplemental Figure 7.**

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**A**



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**B**

Aa_PWA41198.1	-----MAIASSKLGALVFVAVLCLSLPTG-----	-----CLSSQQ-AALFVFGDSLFD-----	-----PGNNHHIN-----TT	52	
Aa_PWA43567.1	-----MTVASSKSG--FLVLFVFCLSVPID-----	-----SWGNIEKHIALFVFGDSLFD-----	-----PGNNNYIN-----TT	53	
Aa_PWA78027.1	-----IPDFIAMAIIASSKSSRFAVVIM-CLLIPTK-----	-----CRENIHKQLVLFVLDGSLF-----	-----PGNNNYIN-----TT	141	
Aa_PWA78028.1	-----IEDVFAMAVANRKSSFVLLLIIAVVVLCPLTRI-----	-----DCHENIHKEVAVFVFGDSFFD-----	-----PGNNNYIN-----TT	483	
Aa_PWA80855.1	-----SSHG-----	-----HYDEKEHPLFVFGDSLFD-----	-----PGNNNYIN-----TT	53	
Aa_PWA80856.1	-----SSHG-----	-----HYDEKEHPLFVFGDSLFD-----	-----PGNNNYIN-----TT	53	
Cs_Cse_sc002489.1_g040.1	1FKVINPMVTVAASSKSG--FLVLFVFCLSVPID-----	-----SWGNIEKHIALFVFGDSLFD-----	-----PGNNNYIN-----TT	135	
Cs_Cse_sc002548.1_g010.1	SCHG-----	-----HYDEKEHPLFVFGDSLFD-----	-----PGNNNYIN-----TT	53	
Cs_Cse_sc021205.1_g020.1	-----AELFWKGDPMTGPYNLKALFDAMAVASSKLGALVFVAILCLSILPAVCLSSQOALFV-----	-----FGDSLFD-----	-----PGNNHHIN-----TT	423	
Cs_Cse_sc055278.1_g010.1	-----AELFWKGDPMTGPYNLKALFDG-----	-----CLSSQQALFV-----	-----PGNNHHIN-----TT	400	
Ha_XP_021984571.T	-----MAIADGKSVFLLPIVVVFSLSIPT-----	-----GCLS-----	-----SALFVFGDSFFD-----	-----PGNNNYIN-----TI	51
Tc_TcGLIP	-----MAVASRKLGLALVAVLCLSLPIG-----	-----CLSSQQALFV-----	-----PGNNHHIN-----TI	53	
Tc_Tci_043407	-----MANISSESRRAFVAIIITCLSIPN-----	-----GCLS-----	-----SALFVFGDSFFD-----	-----PGNNNYIN-----TT	55
Tc_Tci_088899	-----	-----CLSSQQALFV-----	-----PGNNHHIN-----TT	55	
Tc_Tci_372263	-----KSG-----	-----CLSSQQALFV-----	-----PGNN-HIN-----TA	30	
Tc_Tci_439592	-----LSIYSRTFT--NRQYTDMVGNLTK-----	-----VIKGJHKGGGRKFGFLTIVXD-----	-----PGNNNFIK-----TI	87	
Tc_Tci_456723	-----NPSPNDGGCIEAASLILHNQALAK-----	-----SIKRLAKHGFVKSYSLYDFHTNLNQRLKHPSKYGYQOGKTAGCGT-----	-----PGNNHHIN-----TT	234	
Tc_Tci_539163	-----AKMFWKGYPPVTGPYNLKALFDG-----	-----CLSSQQALFV-----	-----PGNNHHIN-----TT	101	
Tc_Tci_547473	-----AELFWGDGDSVATPYNLKAFFHASYR-----	-----FGDSLFD-----	-----PGNNNYIN-----TT	108	
Tc_Tci_568598	-----	-----NMISKHVALFVFGDSLSDY-----	-----PGNNNYIN-----TT	108	
Tc_Tci_603146	-----EMIFEEAIGRLKTYEERIKYKGK-----	-----QVDNQDRLLFTRYGEQGR-----	-----RGHG-ESN-----QS	83	
Aa_PWA41198.1	-----RFDQANFWPYG-----	-----RFDSDGRLLIP-----	-----DFIAEYASLP-LIPAYLEP-NNDFTHGV-----	107	
Aa_PWA43567.1	-----ASFQANYWPY-----	-----RFSNGRLLIP-----	-----DFIAEYARLP-LIPPPYLEPGNNEFAYGA-----	109	
Aa_PWA78027.1	-----TAFQANYPY-----	-----RFSNGRLLIP-----	-----DFIAEYAGLP-LIPAYLEPNNEFTHGA-----	197	
Aa_PWA78028.1	-----PVFQANYLWPY-----	-----RFDSDGRLLIP-----	-----DFIAEYARLP-LIPPPYLEPGNNFAFTYGA-----	539	
Aa_PWA80855.1	-----PDFQANWPY-----	-----RFDSDGRLLIP-----	-----DFIAEYAGLP-LIPTYLDPQNDDFLYGA-----	109	
Aa_PWA80856.1	-----PDFQANWPY-----	-----RFDSDGRLLIP-----	-----DFIAEYAGLP-LIPTYLDPQNDDFLYGA-----	109	
Cs_Cse_sc002489.1_g040.1	1ASFQANWPY-----	-----RFSNGRLLIP-----	-----DFIAEYARLP-LIPPPYLEPGNNEFAYGA-----	141	
Cs_Cse_sc002548.1_g010.1	1PDFQANWPY-----	-----RFDSDGRLLIP-----	-----DFIAEYAGLP-LIPTYLDPRNDDFLYGA-----	109	
Cs_Cse_sc021205.1_g020.1	1DFQANFWPY-----	-----RFSNGRLLIP-----	-----DFIAEYASLP-LIPAYLEP-NNDFTHGA-----	478	
Cs_Cse_sc055278.1_g010.1	1ADFQANFWPY-----	-----RFDSDGRLLIP-----	-----DFIAEHASLP-LIPAYLE-----	446	
Ha_XP_021984571.T	-----TDFQANHWPY-----	-----RFDSDGRLLIP-----	-----DFIAEYAKLP-LIPAYLEPSNKEYTHGA-----	107	
Tc_TcGLIP	-----VNFKANFWPY-----	-----RFDSDGRLLIP-----	-----DFIAEYASLP-LIPAYLEP-NNDFTHGA-----	108	
Tc_Tci_043407	-----AAFQANFTPY-----	-----RFSNGRLLMP-----	-----DFIAEYAGLPLIPAYLEPGNNEFETYGA-----	112	
Tc_Tci_088899	-----	-----RFSNGRLLMP-----	-----MIPAYLEP-NNDFTHGA-----	16	
Tc_Tci_372263	-----TDFQANFWPYA-----	-----EYAS-----	-----LP-IIPAYLEP-NNDFTHGA-----	63	
Tc_Tci_439592	-----PVFQANFWPY-----	-----RFSNGRLLIP-----	-----DFIAEYARLP-PIRPYLAPGNTELTYGT-----	143	
Tc_Tci_456723	-----GRFRGTFSCCGKRPVKEFQLCNPNEVYARVLGT-----	-----SMSMSRFLFIAHFLILETITTLTQASKLXIA-----	-----DFIAEYARLP-IIPAYLEP-NNDFTHGA-----	327	
Tc_Tci_539163	-----ADFQANFWPY-----	-----RFDSDGRLLIP-----	-----DFIGR-----	135	
Tc_Tci_547473	-----ADFRANFWPY-----	-----RFDSDGRLLIP-----	-----DFIAEFAGLP-LIPTYLDPRNTEFTYGA-----	164	
Tc_Tci_568598	-----VSYFSPPGG-----	-----	-----MEQI-----	4	
Tc_Tci_603146	-----RGQENNFKKET-----	-----HNNSNKLTHDKSKETITTSTPLLIKRTFSHVNPT-----	-----SVLQLELCMP-IIPAYLEP-NNDFTHGA-----	156	
Aa_PWA41198.1	-----NFASGGAGALIESHAGL-----	-----KNLGDTSKSQLLSNAVYLFCSCGGNDYQSP-----	-----FYP-YTREQYDVLVIRNMTKV-----	173	
Aa_PWA43567.1	-----NFASVGAGALIDITRAGFV-----	-----VDLQTOQLRYLELENRRNQLGDTEARQLLSSAVYLFCSCGGNDYQSP-----	-----Y-HL-FTDEQYTDVMIGNLTVN-----	201	
Aa_PWA78027.1	-----NFASAGAGALIETFAGFV-----	-----VDLQTOQLRYFGDLEDHYRQNLGDTKARQLLSSAVYLFCSCGGNDYQSP-----	-----Y-YP-YTHEQYTDVMIGNLTVN-----	289	
Aa_PWA78028.1	-----NFASSAGATLIDNLAGLV-----	-----VDLQTOLOQYFGDLENLYRQNLGDTKAEQQLLSSAVYLFCSCGGNDYQSP-----	-----I-SH-VENPMLNQGNDYFVSSVGNND-----	634	
Aa_PWA80855.1	-----NFASSGGAGALVESNAGFV-----	-----VDLKTQLEYFGDLEKQFRNLGDAKEQQLLSSAVYMFCGGNDYQSP-----	-----ILY-P-YTHEQYVRMVIGNLTDV-----	201	
Aa_PWA80856.1	-----NFASGGAGALVESNAGFV-----	-----VDLKTQLEYFGDLEKQFRNLGDAKEQQLLSSAVYMFCGGNDYQSP-----	-----ILY-P-YTHEQYVRMVIGNLTDV-----	201	
Cs_Cse_sc002489.1_g040.1	1NFASAGAGALIDITRAGFV-----	-----VDLQTOQLRYGEVENNYPNRLGDKEARLKLLSSAVYLFCSCGGNDYQSP-----	-----Y-HL-FTNEQYTDVMIGNLTVN-----	150	
Cs_Cse_sc002548.1_g010.1	1NFASGGAGALVESNAGFV-----	-----VDLKTQLEYFGDLEKQFRNLGDAKEEQLLSSAVYMFCGGNDYQSP-----	-----YLP-YTHEQYVGVMIGNLTDV-----	201	
Cs_Cse_sc021205.1_g020.1	1NFASGGAGALIESHTGF-----	-----VVDLQTOQLRYFGDLVNLYRQNLGDTKSKQLLSSAVYLFCSCGGNDYQSP-----	-----YLP-YTHEQYDMLVIGNMNTV-----	563	
Cs_Cse_sc055278.1_g010.1	1PNNDFTHGANPGRITDQG-----	-----VVDLQTOQLRYFGDLVNLYRQNLGDTKSKQLLSSAVYLFCSCGGNDYQIP-----	-----YYP-YTREQYDMLVIGNMNTV-----	528	
Ha_XP_021984571.T	-----NFASAGAGALIDITYAGFV-----	-----VDLHTQLRHEDYRQNLGDTKARQLMSSAVYLFCSCGGNDYQSP-----	-----SIYQ-YTHQOYDVMIGNLTTV-----	199	
Tc_TcGLIP	-----NFASAGAGALIASHAGLA-----	-----VGLQTOQLRYFGDLDHYRQNLGDTKSRLDAVYLFSCCGNDYQSP-----	-----YYP-YTQEYQDVIVGNMNTV-----	193	
Tc_Tci_043407	-----NFASAGAGALIGTRAGFV-----	-----VGLQTOQLRYFGDLEDHYRNLGDTKARQLLSSAVYLFCSCGGNDYQSP-----	-----NFASAGAGALIGTRAGFV-----	182	
Tc_Tci_088899	-----NFASAGAGALISSHAGF-----	-----VNLGDAKSRLKLSSTAVYLFSCCGANDYQSP-----	-----YYP-YTHEQYDVTGNTMNV-----	81	
Tc_Tci_372263	-----NFASGGAGALIESHAGF-----	-----VNLGDAKSRLKLSSTAVYLFSCCGANDYQSP-----	-----YYP-YTQEYQANIVIGNITKV-----	137	
Tc_Tci_439592	-----NFASTGSGALNDTDAFV-----	-----VDLQTOLOCHFGDLEDHYRQNLGDTKARQLLSSAVYLFCSCGGNDYQSP-----	-----Y-SR-T-FINRQYTDVMIGNLTVK-----	236	
Tc_Tci_456723	-----NFASGGAGALVETHAGSV-----	-----VDLKTQLOKLYISNLKKHFRRFNFGDLKAEQQLLSSAVYLFCSCGGNDYQSP-----	-----VLYL-YTHEAYVGVMIGNLTVN-----	419	
Tc_Tci_539163	-----AGALINSHAGF-----	-----VVDLQTOQLRYFGDNLYRQNLGDTKSRLDAVYLFSCCGANDYQIP-----	-----YYP-YTQEYQVDMIGNMNTV-----	214	
Tc_Tci_547473	-----NFASGGAGALVESHDFV-----	-----IDLQTOLOQYFGDLEKQFRNLGDAETNRLLSDAVYLFSCCGANDYQSP-----	-----VLYPYTTHEEYGLVIGNLTVN-----	258	
Tc_Tci_568598	-----KLCFRAGALIDSHAGFV-----	-----VLDLQTOQLRYFGDLVNLYRQNLGDAKSRLQLLSDAVYLFSCCGANDYQSP-----	-----YYS-YTQEYQADIVIGNITNV-----	89	
Tc_Tci_603146	-----NFASGGAGALISSHAGF-----	-----VLDLQTOQLRYFGCDLVNLYRQNLGDAKSRLKLLSSAVYLFCSCGGANDYQSP-----	-----YYP-YTHEQYDVTGNTMNV-----	241	
Aa_PWA41198.1	-----IKA-----	-----IYEKGGREFGVLTAPIGLCWPGRIRQPGNTCT-----	-----YAKFDISTAI SN-----	250	
Aa_PWA43567.1	-----IKA-----	-----IYAKGRKRKFGLTIVPLSGCSFGRVIGOPFGYICHKGIDDTARIHNLQKLAITLEHLEKLEGFM-----	-----YAKCDISTAITN-----	278	
Aa_PWA78027.1	-----IKA-----	-----IYDKGGRKFGLTIVPLSGCSFGRVIGOPFGYICHKGIDDTARIHNLQKLAITLEHLEKLEGFM-----	-----YANFDISTAMYN-----	366	
Aa_PWA78028.1	-----IKA-----	-----IYKGGGRKFGLTIVPLIGCFPAIRLQGPGNTCT-----	-----YAKFDISTATIN-----	711	
Aa_PWA80855.1	-----IKA-----	-----IYEGKGRKRKFATIPLLAACWPSVRAGRGRVGNCTNEEDLISLHLQKLAITLEHLEKLEGFM-----	-----YSKFDLANEVNK-----	278	
Aa_PWA80856.1	-----IKA-----	-----IYEKGRKRKFATIPLLAACWPSVRAGRGRVGNCTNEEDLISLHLQKLAITLEHLEKLEGFM-----	-----YSKFDLANEVNK-----	278	
Cs_Cse_sc002489.1_g040.1	IKG-----	-----IYAKGRKRKFGLTIVPLIGCFPAIRLQGPGNTCT-----	-----YAKFDISTAI SN-----	158	
Cs_Cse_sc002548.1_g010.1	IKG-----	-----IYAKGRKRKFGLTIVPLIGCFPAIRLQGPGNTCT-----	-----YAKFDISTAI SN-----	278	
Cs_Cse_sc021205.1_g020.1	IKG-----	-----IYEGKGRKRKFATIPLLAACWPSVRAGRGRVGNCTNEEDLISLHLQKLAITLEHLEKLEGFM-----	-----YSKFDLANEVNK-----	640	
Cs_Cse_sc055278.1_g010.1	IKG-----	-----IYKATVYRGIYEKGRKRKFATIPLLGCGWEGRIRQPGNTCT-----	-----ETYLC-----	596	
Ha_XP_021984571.T	IKG-----	-----IYEVGRRRFGLNVPPLGCPAIRLQGPGNTCT-----	-----LSKLDFYTSMSN-----	276	
Tc_TcGLIP	-----	-----IYEGKGRKFGVNVPGLCWPGRIRQPGNTCT-----	-----YAKFDLSTA IN-----	270	
Tc_Tci_043407	-----	-----IYDKGGRKFGLTIVPLIGCFPAIRLQGPGNTCT-----	-----YAKFDLSTA IN-----	158	
Tc_Tci_088899	-----	-----IYEGKGRKFGLTIVPLIGCFPAIRLQGPGNTCT-----	-----YARFDISTAI SY-----	158	
Tc_Tci_372263	-----	-----IYEGKGRKFGVVTAPlLGCPMRVRQPGNTCT-----	-----IDELTRLHQAHAKRLEHLEKLEGFM-----	232	
Tc_Tci_439592	-----	-----IYEGKGRKFGVVTAPlLGCPMRVRQPGNTCT-----	-----IDELTRLHQAHAKRLEHLEKLEGFM-----	313	
Tc_Tci_456723	-----	-----IYEGKGRKFGVVTAPlLGCPMRVRQPGNTCT-----	-----IYEGKGRKFGVVTAPlLGCPMRVRQPGNTCT-----	496	
Tc_Tci_539163	-----	-----IYEGKGRKFGVVTAPlLGCPMRVRQPGNTCT-----	-----IYEGKGRKFGVVTAPlLGCPMRVRQPGNTCT-----	291	
Tc_Tci_547473	-----	-----IYEGKGRKFGVVTAPlLGCPMRVRQPGNTCT-----	-----IYEGKGRKFGVVTAPlLGCPMRVRQPGNTCT-----	335	
Tc_Tci_568598	-----	-----IYEGKGRKFGVVTAPlLGCPMRVRQPGNTCT-----	-----IYEGKGRKFGVVTAPlLGCPMRVRQPGNTCT-----	165	
Tc_Tci_603146	-----	-----IYEGKGRKRKFVVTAPILGCPMRVRQPGNTCT-----	-----IYEGKGRKRKFVVTAPILGCPMRVRQPGNTCT-----	318	

Aa_PWA41198_1	-----	-RMKSPSKYGFKEGERACCGSGPFG-----	274
Aa_PWA43567_1	-----	-RMNNPSKYGFKDGETACCGSGPFR-----	302
Aa_PWA78027_1	-----	-RMNNPSKYGFKVGDITACCGSGPFK-----	390
Aa_PWA78028_1	-----	-RMNNPSKYGFNEGETACCGNGPLR-----	735
Aa_PWA80855_1	-----	-RMNNPSKYGFVGSACCGTGPFR-----	302
Aa_PWA80856_1	-----	-RMNNPSKY-----	
Cs_Cse_sc002489_1_g040_1	-----	-RMNNPSKYGFKDGETACCGSGPFR-----	160
Cs_Cse_sc002548_1_g010_1	-----	-RMNNPSKYGFKVGSACCGTGPFR-----	302
Cs_Cse_sc021205_1_g020_1	-----	-RMNNPSKYGFKEGERACCGSGPFRGIYSCGGMIGIKEFELCDNATEYL-----	688
Cs_Cse_sc055278_1_g010_1	-----		
Ha_XP_021984571_1	-----	-RMKNPSQYGFKEGETACCGSGPFG-----	300
Tc_TcGLIP	-----	-RMKNPSKYGFKEGESACCGSGPFG-----	294
Tc_Tci_043407	-----	-GDTACCGSGPFR-----	235
Tc_Tci_088899	-----	-RMKNPSKY-----	177
Tc_Tci_372263	LYSCNFLSLCRAPOYFLASLVLVPVPRYFKRQNVFSSEVFHSSSPTKSSPSYFAASVFFLPFFSRSNKVFSHOCVCPRLSSSLCTLFAICRSILGNPOF	-----	332
Tc_Tci_439592	-----	-RMNNPSKYGFKDGETACCGSGPFR-----	337
Tc_Tci_456723	-----	-RMNNPSKYGFVGTSAACCGSGPYR-----	520
Tc_Tci_539163	-----	-RMKNPSKYGFR-----	
Tc_Tci_547473	-----	-RMKNPSKYGFKVGDITACCGSGP-----	357
Tc_Tci_568598	-----	-RMKSHSIYGFKEGERACCGSGPFG-----	189
Tc_Tci_603146	-----	-RMKNPSKYGFKEAERACCGSGPFG-----	342
Aa_PWA41198_1	-----	-GIYSCGGMIGIKEFELCEN-----	314
Aa_PWA43567_1	-----	-GKNSCGGKRGTITEYELCDN-----	342
Aa_PWA78027_1	-----	-GIFSCGGKRGTIDYEYLCD-----	430
Aa_PWA78028_1	-----	-GIYSCGRRRGITDYEYLCDN-----	775
Aa_PWA80855_1	-----	-GIDSCGGKREVKEFELCDN-----	342
Aa_PWA80856_1	-----		
Cs_Cse_sc002489_1_g040_1	-----	-GKNSCGGKRGTITEYELCDN-----	164
Cs_Cse_sc002548_1_g010_1	-----	-GIDSCGGKREVKEFELCDN-----	342
Cs_Cse_sc021205_1_g020_1	-----	-FFDCFHPELASRQFAEMFWGDSMVTPQYNLKALFEAMAVASSKGALAAAIVVLCLSISSDCHENIHKQVLVVLGDSLDPGNINYIN	779
Cs_Cse_sc055278_1_g010_1	-----		
Ha_XP_021984571_1	-----	-GVYSCGGMRRIKEYEVCDN-----	340
Tc_TcGLIP	-----	-GNYDCG-----RIKEFGLCDN-----	331
Tc_Tci_043407	-----	-GITS CGGKRGTITEYELCD-----	275
Tc_Tci_088899	-----	-GIYSCGMRRIKEFELCNN-----	217
Tc_Tci_372263	-----	FITFTCNVKWPEIKRYMAQYPELRTDRADIMCKVFEQVKDFVNFLKKVTFGYVQLIEEYIYAEIPDHVEDPRGYKLVIDLMMHGFCAANLGAPXIP	432
Tc_Tci_439592	-----	-GNFSCGGKRGTQMYEYLCDN-----	377
Tc_Tci_456723	-----	-GIYSCGGKRLQEQYQLCDN-----	560
Tc_Tci_539163	-----	-KAREHVAVVVLLLEG-----	323
Tc_Tci_547473	-----	-GIYSCGMRGIKEFELCDT-----	226
Tc_Tci_568598	-----	-GIYSCGMRRIKEFELCDN-----	382
Tc_Tci_603146	-----	-ATDYLFFDSFHPELASHQFA	
Aa_PWA41198_1	-----	-EMFWD-GDSMVTPQNMKSLFEG-----	348
Aa_PWA43567_1	-----	-EMFWK-GDSKVTAPYNLQALF-----	363
Aa_PWA78027_1	-----	-EMFWE-GDYMTAPYNLQALFEAMIVASSNSGFIVIIVILCLSIPTGSQAH-----	479
Aa_PWA78028_1	-----	-ELFWK-GDPTVTGPYNLQALFDGPK-----	799
Aa_PWA80855_1	-----	-ELFWD-GDSDVTTPYLNKAFQELQGELTTTSRMQL-----	375
Aa_PWA80856_1	-----	-GTSELNRNPSNLV-----	298
Cs_Cse_sc002489_1_g040_1	-----	-EMFWK-GDSVVTGPYNLQALFKGTLLFFPMFMSFGKFAYLFMIEPVDK-----	1697
Cs_Cse_sc002548_1_g010_1	-----	-1ELFWD-GDSDVTTPYLNKAFFQAELAGPLIPTYLDPRRNNEFTYGANFAS-----	391
Cs_Cse_sc021205_1_g020_1	-----	-1TTTSFQSNTFPYGESESYFNPPTRGRFSNGLRIDPDTIAEYAGLPLISAYLEPE-----	829
Cs_Cse_sc055278_1_g010_1	-----		
Ha_XP_021984571_1	-----	-EMFWN-GDSIVTEPNSLEALFDGAASSTTFLVHPNNEL-----	376
Tc_TcGLIP	-----	-EMFSWT-GDSMVTPQNLKALFEG-----	365
Tc_Tci_043407	-----	-EMFWK-GDYMVTAPYNLQALEFKNN-----	298
Tc_Tci_088899	-----	-ETF-----	220
Tc_Tci_372263	-----	-NYIVNTAELQVYIYLEEAIINGFEKSVDFFGLQAPPNLLKDLENKLM-----	482
Tc_Tci_439592	-----	-KMFWK-GNSVVTTPYLNKLF-----	399
Tc_Tci_456723	-----	-QLFWD-ADPNVTTPYLNQTLFXMSSSLQVLPDRPARMLGKQANGG-----T	606
Tc_Tci_539163	-----	-GE-----	325
Tc_Tci_547473	-----		
Tc_Tci_568598	-----		
Tc_Tci_603146	-----	-ETF-----	385

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**Supplemental Figure 7. Molecular phylogenetic analysis of *T. cinerariifolium* GDSL lipase (TcGLIP).**

TcGLIP-related proteins were searched by BLASTP against 14 different plant protein sets and incorporated into maximum likelihood tree analysis using ORTHOSCOPE method<sup>56</sup> (A). Proteins incorporated into this tree include 9 from *T. cinerariifolium*, 10 from *C. seticuspe*, 10 from *A. annua*, 10 from *H. annuus*, 9 from *Z. mays*, 10 from *V. vinifera*, 10 from *M. truncatula*, 10 from *S. lycopersicum*, 10 from *P. trichocarpa*, 10 from *O. sativa*, 8 from *G. raimondii*, 10 from *N. tabacum*, 10 from *G. max*, and 9 from *A. thaliana*. TcGLIP nodes are indicated in blue; *T. cinerariifolium* nodes and edges are indicated in red; other Asteraceae nodes and edges are indicated in orange. The amino acid sequence alignments for maximum likelihood tree analysis are shown in panel B.

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**Supplemental Figure 8.****A**

Tci_094327	---MSFDFSRVGVVCSFSLIAER-----	FPGVLGGSGGSGSISASTESFKDTTKVTKFSVDFG	56
AaSPB (PWA57483.1)	MEWNITKWDWENIAMLPGSKGVASPKKLQSTDWGKEKGQDIDGSSNHSGVLGGSGGSGSISASTESTFKDTTKVTKFSVDFG		80
Tci_094327	GGEINKISPSLQASVFSSDQSIGLKLSERTYCENNLPNSNNSVSTDK-----	KDYHRKHM	121
AaSPB (PWA57483.1)	GGEINKSSPSLEASVCSSDQSIGLKLGKRTYFENNLPNSNNSVSTVKVKLSQLQOSAPIICQVMGCDRLSSAKDYHRKHR		160
Tci_094327	VYDIHLKALKVIVVGLK-----HRLDEFRRWARYCYSRIFCGDNEK-----	LKRRFIV	169
AaSPB (PWA57483.1)	VCDVHSKSLKVIVAGLERRFCQOCSCRFHGLPEFDGKKRSCRKRLADHNARRKPHQETTQFNSRSLSLSSYYDGPROLSFA		240
Tci_094327	FAGSVIVYNERRLQELGN-----	RLIKMNNAFDKGNSHVYVVPFSS	210
AaSPB (PWA57483.1)	FNNGPMVQTCKPAVSSMWENTCNSKHSVATVKAEKYGGHDVLTHSQGVQFPNFSMTPTLSFNRNIISSKGTTAGVFDQGSS		320
Tci_094327	SIYKAILSLPFFPHIGQAVRRLAARGTIFTTRNGD-----	QGSTKRNG	252
AaSPB (PWA57483.1)	LELRRAILSLLSNNSNWGSSESDFGCILDHEMHTNGPNTAQOGMHSAPHGLPLISPEYWQIDHQSVDPHIHGTHFQGSQILKA		400
Tci_094327	CYML-----	256	
AaSPB (PWA57483.1)	PYGIQYSNPMDEIVQPL	417	

**B**

TcGLIP (AFJ04755.1)	-MAVASRKILGALVLVAVLCLSLPTGCLS-SQQAAALFTFGDSVFDPGNNNHINTHVNFKANFWPYQOSYFSSPTGRFSDG	78	
Tci_043407	MANTSSESRRFAAVIITCLSIPTNCHANIKQVLVFGDSLFDPGNNNYINTTAAFQANFTPYGESYFYPPPTGRFSNG	80	
Tci_043410	-----MANFWPYGESYFTSPITGRFSNG	22	
TcGLIP (AFJ04755.1)	RIIPPDFIAEYASLP-IIPAYLEP-NNDFTHGANFASAGAGALIASHAGLAVGLOTOQLRYFGDLVDHYRQNLDIKSRQLL	156	
Tci_043407	RIMPDFIAEYAGLPPLIPAYLEPGNNNEFTYGANFASAGAGALIGTRAGFVVGLOTOQLRYFGDLEDHYRHNLGDTKARQLL	160	
Tci_043410	RLIPPDFIAEYARLP-LIPPYLEPGNNNEFTYGANFASAGAGVLIDTKAGFVVDLQTOQLRYLGDNENKYRENLGDGTGARQLL	101	
TcGLIP (AFJ04755.1)	SDAVYLFS CGGNDYQSPYYP--YTQE QYV DIVIGNMTNVIKGTYEKGGRKFEGVNVNPLIGCWPGMRAKOPGNTCNTEVD	233	
Tci_043407	STAVYLFSCGANDYLSPVG-----NNTGIYDKGGRKFGLNVALLGCFOAIRVGQPGNTCNKEMD	220	
Tci_043410	SSAVYLFSCGINDYVSFVGSNVSNTDEQY TDMVIGSLTTVIRGTYAKGGRKFVTVPLLGCSPGFRISQPGNICNKRID	181	
TcGLIP (AFJ04755.1)	ELTRIHNQAFAKRLEOLEKOLEGFVYAKFDLSTAII NRMKNPSKYGFKEGESACCGSGP-----FGGNYDCG--RIK	303	
Tci_043407	DIV-----GDTACCGSGP-----FRGIFSCGGKRGIT	247	
Tci_043410	DTARLHNRKFAMKLEHLOKQDGFMYAKFDISAIITNRMNNPSEYANRLVDSLQRCFGKGP SKLGF LVL FVFCI WVPID	261	
TcGLIP (AFJ04755.1)	EFGLCDNATEYFFFDPFHPN-----ELASRQFAEMFWDGDSMVQPYNLKALFEGKPSTKYLPNDEL-----	365	
Tci_043407	EYELCDDVTEFFLFEDSSHP-----ELAYRQFAEMFWKGDYMVTAQYNLQALFKNN-----	298	
Tci_043410	SWGNIDKRVALFVFGDSLFDPGNNNYINTTSYQANFWPYGESYFNNPPTGRFSNGRLLPDFIAEYARLPLIPPYLKPGNK	341	
TcGLIP (AFJ04755.1)	--		
Tci_043407	--		
Tci_043410	EF 343		

117 **Supplemental Figure 8. Amino acid sequence alignment of Tci\_094327 and *A. annua* squamosa  
118 promoter-binding (SPB) transcription factor (A), Tci\_043407, Tci\_043410, and TcGLIP (B).**