

Figure S1. A schematic presentation of the pRT99/35S-Pt4CL1-a plasmid vector used in the biolistic transformation of silver birch clones A, E5382 and E5396.



Figure S2. The scatterplots presenting CV% and concentration values of stem samples. The CV% ($SD_{Cq}/mean_{Cq}$) values were calculated from two technical replicates of each utilized primer pair and the concentration values were generated with Abs Quant/2nd Derivative Max for All Samples Analysis of Lightcycler 480 Software release 1.5.0 SP3. A, *Atub*; B, *PP2A*; C, *Bp4CL1*; D, *Bp4CL2*; E, *Bp4CL3*; F, *Bp4CL4*; G, *Pt4CL1*.



Figure S3. The scatterplots presenting CV% and concentration values of leaf samples. The CV% ($SD_{Cq}/mean_{Cq}$) values were calculated from two technical replicates of each utilized primer pair and the concentration values were generated with Abs Quant/2nd Derivative Max for All Samples Analysis of Lightcycler 480 Software release 1.5.0 SP3. A, *Atub*; B, *PP2A*; C, *Bp4CL1*; D, *Bp4CL2*; E, *Bp4CL3*; F, *Bp4CL4*; G, *Pt4CL1*.



Figure S4. The Cq values of *Atub* **and** *PP2A* **in undamaged and wounded leaves.** The Cq values represent crossing point values generated with Abs Quant/2nd Derivative Max for All Samples Analysis of Lightcycler 480 Software release 1.5.0 SP3 of *Atub* (A) and *PP2A* (B) in non-treated leaves (c) and leaves collected immediately after mechanical wounding (w0) and 1 (w1h), 3 (w3h), 12 (w12h), 24 (w24h), 72 (w3d) and 168 (w7d) hours after the wounding treatment.



Figure S5. Southern blot analysis of regenerated silver birch lines. Lines A1, A2, A5 and E5382/3 were transformed with pRT99/35S-*Pt4CL1*-a plasmid vector and probed for the presence of the 35S-*Pt4CL1* and *nptII*. A genomic DNA sample of 15 μ g digested with *Bam*HI (figures on the left) or *Xba*I (figures on the right) was loaded to each lane.



Figure S6. Southern blot analysis of regenerated silver birch line E5396/4. Line was transformed with pRT99/35S-*Pt4CL1*-a plasmid vector and probed for the presence of the *nptII*. A genomic DNA sample of 15 μ g digested with *Bam*HI (figures on the left) or *Xba*I (figures on the right) was loaded to each lane.



Figure S7. Northern blot analysis of transgenic silver birch lines. RNA samples of 15 μ g were isolated from the leaf (L), phloem (P) and xylem (X) of clones A and E5382 and lines A1, A2, A5 and E5382/3. The probes were 1.1 and 0.8 kb for Pt4CL1 and nptII, respectively.



Figure S8. The leaf morphology of Pt4CL1a line E5382/3. During the first growing season in the greenhouse, the leaf margins of Pt4CL1a line E5382/3 (on the left) differed in from clone E5382 (on the right).



Figure S9. The autumn leaf senescence of silver birch clones and lines. The clone A, line A2, line A5, line E5382/3, and clone E5382 (from left to right) at the end of first growing season at the greenhouse of Finnish Forest Research Institute Punkaharju Unit (photographed on the 6^{th} of October).

| Bpl 4CL 1 Bp4CL 1 Bl 4CL Poptr 4CL 3 Poptr 4CL 5 We4CL 2 We4CL 2 Grr4CL 2 Grr4CL 2 Grr4CL 6 Bpl 4CL 1 Bp4CL 1 | 1 1 1 1 1 1 1 1 5 9 59 | WAI QAK WAI QAK WAI QAK MAI QAK MNP MDAI MNS MDTI TKQ METQLI NQ METQLI NQ METQULKQ WADDGS WAVVER | E F F F F F F F F F F F F F F F F F F F | SKLPDI SKLPDI SKLPDI SKLPDI SKLPDI SKLPDI SKLPDI SKLPDI SKLPDI I QKGDV | YI PKH YI PKH YI PKK YI PKK DI PKK YI PKH YI PKH YI PKH YI PKH | LPIHS LPIHS LPIHS LPIHS LPIHS LPIHS LPIHS MPLHS LPIH PNSPE PNSPE | YCFEN YCFEN YVLEN YVLEN YVLEN YVFEN YLFEN YCFEN YCFEN YCFEN | S KV GS S KV GS S KV GS S KHS S KHS S KY S S S HS S S HS S S HS L P E Y G L G A S Y I L G A S Y I | SRPCL SRPCL SRPCL SKPCL SRPCL SRPCL SRPCL SRPCL SRPCL SRPCL SRPCL | I NGLT I NGLT I NGLT I NGAN I NGAN I NGAT I NGAT I NAPT T AANP T AANP | GKVYT GKVYT GDVYT GDVYT GDVYT GDVYT GDVYT GDVYS GDVYS GDVYS FCTAC | YYDV YYDV YYDV YYA |
|--|--|---|--|---|--|---|---|--|---|--|---|--|
| BI 4CL Pt 4CL 1 Poptr 4CL 3 Poptr 4CL 5 Me 4CL 2 Me 4CL 2 Grr4CL 2 Grr4CL 2 Grr4CL 6 | 59 55 60 61 61 59 59 | ELTARKVA ELTARRVA ELTARRVA ELTARRAA ELTGRRVA ELTARRVA DSTARKVA ESTARKVA | S GL S KL G S GL NK I G S GL NK I G S GL NK L G S GL NK L G S GL NN L G R GL K K E G R GL K K E G | | | PNSPE PSSPE PSSPE PSSPE HNSPE HNSPE PNCPE PNCPE | F | L GASY L GASH L GASH L GASH L GASF L GASF L GASH L GASH | GAMI RGAI V RGAI T RGAI A RGAI A RGAMA RGAMA | T AANP T AANP T AANP T AANP T AANP T AANP T AANP | F CTAC FSTPA FSTPA FFTPA FFTPA FFTPA | |
| Bpl 4CL1 Bp4CL1 Bl 4CL Pt 4CL1 Popt r 4CL3 Popt r 4CL5 Me4CL2 Me4CL2 Gm4CL2 Gm4CL2 Gm4CL6 | 119 119 115 120 120 121 121 119 | QAKSANAK QAKSANAK HAKASRAK HAKASRAK QAKASRAK QAKASNTK QAKASNT QAHASNAK QAHASNAK | I VVTQAC I VVTQAC LLI TQAC LLI TQAC LLI TQAC LLI TQAC LI TQAA LI TQAS LLI TQAS LLI TQAS | YYDRVK YYDRVK YYEKVK YYEKVK YYEKVK YYDKVK YAEKVK YYDKVK YYDKVK | DYT NE DYT NE DYANE DFARE DFARE DYAQQ DLARD DLARD DLR DLR | NGVKI NGVKI NGVKI SDVKV SDVKV SDVKV SDVKV YGI KV YGI FDI FI FI KL | I CI DS I CI DS I CI DS MCVDS MCVDS MCVDS LCI DS VF VDS VF VDS | PPE PPE APD APD APD APD CPPHTI CPP | DC DC GA GC GC GC GC GC QH | L HF S E L HF S E S L F R A L HF S E L HF S E L HF S E L HF S F L HF S C | LTKAC LTKAC LTKAC LTKAC LTQAC LTQAC LSEAC LSEAC LSEAC LCEDN LCEDN | DE ND- DE ND- DE NE- DE NE- DE NE- DE ND- DE RD- DE RD- DE RD- IGDAD |
| Bpl 4CL 1 Bp4CL 1 Bl 4CL Pt 4CL 1 Popt r 4CL 3 Popt r 4CL 5 Me4CL 2 Gr4CL 2 Gr4CL 2 Gr4CL 2 | 173 173 169 174 174 175 175 176 168 | - VAEVDIS - VAEVDIS - VAEVDIS - VPOVDIS - VPOVDIS - MPOVDIR - MPOVDIS - MPOVDIS - MPOVDIS - VDVDVDIK | P DDVVAL P DDVVAL P DDVVAL P DDVVAL P DDVVAL P DDVVAL S E DVVAL P DDVVAL P DDVVAL P DDVVAL | PYSSGT PYSSGT PYSSGT PYSSGT PYSSGT PYSSGT PYSSGT PYSSGT PYSSGT | TGL PK TGL PK TGL PK TGL PK TGL PK TGL PK TGL PK TGL PK | GVMLT GVMLT GVMLT GVMLT GVMLT GVMLT GVMLT GVMLS GVMLS | HKGL V HKGL V HKGL V HKGL I HKGL I HKGL V HKGL V HKGL V | T S V A Q T S V | QVDGE QVDGE QVDGD QVDGD QVDGD QVDGD QVDGE QVDGE QVDGE QVDGD QVDGD | NP NL Y NP NL Y | YHSED YHSED FHSED FHSED FHSED FHSED FHSED FHSDD YHCHD YHCHD | 0VI LC |
| Bpl 4CL 1 Bp4CL 1 Bl 4CL Pt 4CL 1 Popt r 4CL 3 Popt r 4CL 5 We4CL 2 Me4CL 2 Gr4CL 2 Gr4CL 6 | 232 232 228 233 233 234 234 234 236 227 | VLPLFHIY VLPLFHIY VLPMFHIY VLPMFHIY VLPMFHIY VLPMFHIY VLPMFHIY VLPMFHIY VLPLFHIY | S L NS V F L S L NS V F L A L NS W V L A L NS I W L S L NS V L L S L NS V L L | CGLRAG CGLRAG CGLRAG CGLRVG CGLRVG CGLRVG CGLRVG CGLRAK CGLRAK | GASILI GASILI GASILI GASILI GASILI GAAILI GAAILI GAAILI ATILL | L P K F E E P P K F E E N P K F F E N P K F F E N P K F F E N P K F F N P K F N P K F N P K F D N P K F | VSLL(VSLL(VSLL(GTLL(GTLL(GALL(GALL(NSLL) NSLL) | QLIQK QQLIQK QQLIQK QQLIEK QQLIEK QQLIEK QCL | HKVTV HKVTV HKVTV YKVSI YKVSI YKUTV YKUTV HKVTI HKVTI | NP VP NP VP AP VVP AP VVP AP VVP AP VVP AP I VP AP VVP AP VVP | PPIVLA PPIVLA PVMLA PVMLA PVMVA PVVVA PIVLS PPIVLA PPIVLA | I TKF I TKF I AKS I AKS I AKS I AKS I AKS I SKS I S |
| Bpl 4CL 1 Bp4CL 1 Bl 4CL Pt 4CL 1 Popt r 4CL 3 Popt r 4CL 5 We4CL 2 Gr4CL 2 Gr4CL 2 Gr4CL 2 | 292 292 288 293 293 294 294 294 296 287 | P DL DKYDL P DL DKYDL P DL DKYDL P DL DKHDL P DF DKHDL P DT DKYDL P DT EKYDL P DL HKYDL P DL HKYDL | S S V K ML K S S V K ML K S S V K ML K S S L R ML K S S L R ML K S S I R ML K S S I R VL K | S GGAPL S GGAPL S GGAPL S GGAPL S GG <mark>S</mark> PL S G <mark>A</mark> APL S G <mark>A</mark> APL S GAPL S GGAPL | GKELE GKELE GKELE GKELE GKELE GKELE GKELE GKELE GKELE | ETVKA ETVKA DTVRA DTVRA DTVRA DTVRA DTVRA DTVRA DTLRA | K F P NA K F P NA | F GQG' F GQG' F GQG' L F GQG' L GQG' L GQG' F L GQG' K L GQG' K L GQG' | Y GMT E Y GMT E | AGPVL AGPVL AGPVL AGPVL AGPVL AGPVL AGPVL AGPVL | ANCLA ANCLA ANCLA ANCLA ANCLA ANCLA ANCLA ANCLA TMSLA TMSLA | KFAKE KFAKE KFAKE KFAKE KFAKE KFAKE KFAKE |

Figure S10. Alignment of predicted amino acid sequence of silver birch (*Betula pendula*) **putative 4-coumarate:CoA ligase (Bp4CL1, KM099195).** Bp4CL1 aligned with the predicted amino acid sequences of *Betula luminifera* (Bp14CL1, AY792353), *Betula platyphylla* (B14CL, FJ410448), *Glycine max* (Gm4CL2, Glyma13g44950; Gm4CL6, Glyma15g00390), *Manihot esculenta* (Mes4CL2, cassava4.1_005014m; Mes4CL3, cassava4.1_005006m), *Populus tremuloides* (Pt4CL1, AF041049), and *Populus trichocarpa* (Poptr4CL3, grail3.0100002702 LG I; Poptr4CL5, fgenesh4_pg.C_LG_III001773 LG III).

| Pt 4CL2 Popt r 4CL4 Mes 4CL1 Bp4CL2 Ri 4CL3 At 4CL3 Grra 4CL3 | 1 1 1 1 1 1 | MMSVATVEPPKPELSPPQNQNAPSSHETDHIFRSKLP MMSVATVEPPKPELSPPQNQNAPSSHETDHIFRSKLP MTSIASLELEPQNQEFSPKITPGPTQPSETSACVFKSKLP MISVASNSSTEPQNQEFSPKITPGPTQPSETSACVFKSKLP MISIASNNNNNSVVVETPTKPEISPNIISDVISTSQTQPEQKQQPPTTTTHHVFKSKLP MITAALHEPQPRIFRSKLP MSEAAATSFETQHSS-TESCVPKTTTTTSSDVSSPQTT |
|---|---|---|
| Pt 4CL2 Popt r 4CL4 Mes 4CL1 Bp4CL2 Ri 4CL3 At 4CL3 Gma 4CL3 | 38 38 33 42 61 41 47 | DIT-ISNDLPLHAYCFENLSDFSDRPCLISGSTGKTYSFAETHLISRKVAAGLSNLGIKK DIT-ISNHLPLHAYCFENLSDFSDRPCLISGSTGKTYSFAETHLISRKVAAGLSNLGIKK DIP-ISNHLSLHAYCFENLSFADRPCLISGSTGKTYSFAETHLVSOKCAAGLSNLGINK EIP-ISDHLPLHTYCFEHLAEFSDRPCLIVGSTGKTYSFAETHLVSOKIAAGLSNLGIKK DIPNISNHLPLHTYCFENISDFS⊡RPCLIIGSTGKSYTFSETRLLSOKTGVGLSKLGIHK DID-IPNHLPLHTYCFEKLSSVSDKPCLIVGSTGKSYTYGETHLICRRVASGLYKLGIRK DIP-IPNNLPLHTYCFEKLSSVSDKPCLIVGSTGKSYTYGETHLICRRVASGLYKLGIRK |
| Pt 4CL2 Popt r 4CL4 Mes 4CL1 Bp4CL2 Ri 4CL3 At 4CL3 Gma 4CL3 | 97 97 92 101 121 100 104 | GDVIMTLLQNCPEFVFSFLGASMIGAVLTTANPFYTQSEIFKQFSASRAKLIITQSQYVN GDVIMTLLQNCPEFVFSFNGASMIGAVTTTVNPFYTPGEIFKQFSASRAKLIITQSQHVN GDVVMLLQNCPEFVFSFMGASMIGAVTTTÄNPFYTSNEIFKQFTSSRAKLIITQSQYVD GDVIMVLLQNCAEFVFSFLGASMLGAVTTTANPFYTSAEVFKQLNSSKAKLIITQSQYVD GDVIMILLQNCAEFVFAFMGASMIGAVTTTANPFYTASETFKQLEASNAKLIITQSQYVD GDVIMILLQNCAEFVFAFMGASMIGAVTTTANPFYTASETFKQLEASNAKLIITQSQYVD GDVIMILLQNSAEFVFSFMGASMIGAVTTTANPFYTASETFKQLAASKAKLIITMSQYVD GDVIMILLQNSAEFVFFFMASSMLGAVATTANPFYTASETFKQLAASKAKLVVTLSAHVH |
| Pt 4CL2 Popt r 4CL4 Mes 4CL1 Bp4CL2 Ri 4CL3 At 4CL3 Gma 4CL3 | 157 157 152 161 181 160 164 | KLGDS DCHENNOKP GEDFI VITIDDPPENCLHFNVLVEASESEMPTVSILPDDPVA KLRDS DCHENNOKP EEDFI VITIDDPPENCLHFNVLVEANESEMP-TVSIHPDDPVA KLRDSQENQPKLGQDFNVITIDDP-PENCLHFTVLSEAKESEUP-TVSIHPDDPVA KLRETGENFPKLGEDFTVITVDDP-PEKCLHFSVISEANEGEFSSSTVSIDPDDPVA KLRQPGQHFQVVTIDDP-PENCLHFSVISDANENELP-QVSIDPDDPVA KLKNLGENLTLITTDEPTPENCLPFSTLITDETNPFQETVDIGGDDAAA KLDQQQGLKVVTVDEPAADENCWSFREGEESEVAEVEISAEDAVA |
| Pt 4CL2 Popt r 4CL4 Mes 4CL1 Bp4CL2 Ri 4CL3 At 4CL3 Gma 4CL3 | 213 213 206 217 228 210 209 | L P F S S G T T G L P K G VI L T H K S L I T S V A Q Q V D G E I P N L Y L K Q D D V V L C V L P L F H I F S L N S V L L P F S S G T T G L P K G VI L T H K S L I T S V A Q Q V D G E I P N L Y L K Q D D V V L C V L P L F H I F S L N S V L L P F S S G T T G L P K G VI L T H K S L I T S V A Q Q V D G E N P N L Y L K Q E D V V L C V L P L F H I Y S L N S V L L P F S S G T T G L P K G V I L T H K S L I T S V A Q Q V D G E N P N L Y L K Q E D V V L C V L P L F H I Y S L N S V L L P F S S G T T G L P K G V I L T H K S L I T S V A Q Q V D G E N P N L Y L K G D D V V L C V L P L F H I Y S L N S V L L P F S S G T T G L P K G V I L T H K S L I T S V A Q Q V D G E N P N L Y L K G D D V V L C V L P L F H I F S L N S V L L P F S S G T T G L P K G V I L T H K S L I T S V A Q Q V D G D N P N L Y L K S N D V L C V L P L F H I Y S L N S V L L P F S S G T T G L P K G V V L T H K S L V T G V A Q N M E G E N P N V L K E E D V V L C V L P L F H I F S M S V M |
| Pt 4CL2 Poptr 4CL4 Mes 4CL1 Bp4CL2 Ri 4CL3 At 4CL3 Gma 4CL3 | 273 273 266 277 288 270 269 | LCSLRAGSAVLLNQKFEIGSLLELIQKHNVSVAAVVPPLVLALAKNPLEANFDLSSIRVV LCSLRAGSAVLLNQKFEIGSLLELIQKHNVSVAAVVPPLVLALAKNPNVANFDLSSIRVV LCSLRAGAAVLENQKFEIGALLELIQKHNVSVAAVVPPLVLALAKNPNVAGFDLSSIRVV LCSLRAGAAVLENQKFEIGALLELIQRHRVSVAAVVPPLVLALAKNPVVANFDLSSIRVV LCSLRAGAAVLMNPKFEIGTLLELIQRHRVSVAAVVPPLVLALAKNPVVANFDLSSIRVV LCSLRAGAAVLMNPKFEIGTLLELIQRHRVFCGGGWCLAGDSAGEESMVADYDLSSIRVV LNSLRSGATVLLNHKFEIGALLELIQRHRVTIAALVPPLVIALAKNPTVNSYDLSSVRFV MCALRAGSANLLIEKFEIRALLEEIERHRVTVAMVVPPLVVALAKNPAVEEYDLSSIRLV |
| Pt 4CL2 Poptr 4CL4 Wes 4CL1 Bp4CL2 Ri 4CL3 At 4CL3 Grra 4CL3 | 333 326 337 348 330 329 | L S GAAP L GKE L E DAL R'S R V P QAI L G QGY GNT E AGP V L S MC L AF S K QP F P T K S G S C GT V V R L S GAAP L GKE L E E AL R'S R V P QAI L G QGY GNT E AGP V L S MC L AF S K QP L P T K S G S C GT V V R L S GAAP L GKE L E DAL R'S R V P QAI L G QGY GNT E AGP V L S MC L GF A K QP F P T K S G S C GT V V R L S GAAP L GKE L E E AL R'N R V P QAT L G QGY GNT E AGP V L S MC L GF A K QP F P T K S G S C GT V V R L S GAAP L GKE L E E AL R'N R V P QAT L G QGY GNT E AGP V L S MC L GF A K QP F P T K S G S C GT V V R L S GAAP L GKE L E E AL R'N R V P QAY L G QGY GNT E AGP V L S MC L GF A K QP F P T K S G S C G S V V R L S GAAP L GKE L E E AL R'N R V P QAY L G QGY GNT E AGP V L S MS L GF A K P F P T K S G S C G S G AAP L G K E L QD S L R'R L P QAI L G QGY GNT E AGP V L S MS L GF A K P F P T K S G S C G T V V R MS G A AP L G H Q L E E V L R'N R L P NAI L G QGY GNT E AGP V L AMC L GF A K Y P F P T K S G S C G T V V R |
| Pt 4CL2 Popt r 4CL4 Wes 4CL1 Bp4CL2 Ri 4CL3 At 4CL3 Gra 4CL3 | 393 393 386 397 408 390 389 | NAELKVIDPETGRŠLGYNQPGEICIRGSQINKGYLNDAEATANTIDVEGWLHTGDIGYVD NAELKVIDPETGSSLGRNQPGEICIRGSQINKGYLNDAEATANTIDVEGWLHTGDIGYVD NAELKVIDPETGCSLGYNQPGEICIRGQQINKGYLNDLEATANTIDVEGWLHTGDIGYVD NAELKVIDPETGCSLGHNQPGEICIRGSQINKGYLNDGEATATTIDVEGWLHTGDIGFVD NAELKVVEPETGRSLGYNQPGEICIRGQQINKGYLNDGEATATTMDVEGWLHTGDIGYVD NAELKVVEPETGRSLGYNQPGEICIRGQQINKGYLNDGEATATTMDVEGWLHTGDIGYVD NAELKVVEPETGRSLGYNQPGEICIRGQQINKGYLNDFEATSATIDEGWLHTGDIGYVD |

Figure S11. Alignment of predicted amino acid sequence of silver birch (*Betula pendula*) putative 4coumarate:CoA ligase (Bp4CL2, KM099196). Bp4CL2 aligned with the predicted amino acid sequences of *Arabidopsis thaliana* (At4CL3, At1g65060), *Rubus idaeus* (Ri4CL3, AAF91308), *Glycine max* (Gm4CL3, NM_001250341), *Manihot esculenta* (Mes4CL1, cassava4.1_004658m; Mes4CL4, cassava4.1_004136m), *Populus tremuloides* (Pt4CL2, AF041050), and *Populus trichocarpa* (Poptr4CL4, grail3.0099003002 LG IX).

| PoptrACS1 PoptrACS2 Bp4CL3 AtACS6 OsACS1 | 1 1 1 1 | WEKSGYGRDGIYRSLRPTLVLPRDSNLSLVSFLFRNSNSYPHKPALIDADLS-IT MEKSGYGRDGIYRSLRPKLVLPKDPNLSLVSFLFRNSNSYPHKPALIDADLS-IT MEKSGYGRDGIYRSVRPPLVLPKDPNLSMVTFLFRNSSSYPHKPALIDADSS-QT MEKSGYGRDGIYRSLRPTLVLPKDPNTSLVSFLFRNSSSYPSKLAIADSDTG-DS WASASVPAAGYGADGVYRSLRPPAPVASDPGLSLTDLLRRADACPSAVALADAAAGGRA |
|--|------------------|---|
| PoptrACS1 | 55 | LSFSELKSIVIKFAHGLLN-LGISKNDVILIFAPNSYQFPTCFLAITSIGAVATTANPLY |
| PoptrACS2 | 55 | LSFSELKSIVIKVAHGLLN-LGISKNDVVLIFAPNSYQFPICFLAITSTGAIATTANPLY |
| Bp4CL3 | 55 | LSFSQFKSTVATISRGFLG-LGITKNDVVLIFAPNSIQFPLCFLGIVAIGAIATTANPLY |
| AtACS6 | 55 | LTFSQLKSAVARLAHGFHR-LGIRKNDVVLIFAPNSYQFPLCFLAVTAIGGVFTTANPLY |
| OsACS1 | 61 | LTFAELRSAVLSTAVALSSRAGVRPGDAVLLLAPNCVLYPVCFFAVTALGAVGTTVNPDY |
| PoptrACS1 | 114 | TT SELSKQIKDSNPKLVIT VPELWDKVKGFNLPAVFLGPKEVSLPLESGSRIRSFHSL |
| PoptrACS2 | 114 | TT SELSKQIKDSNPKLTIT VPELWDKVKGFNLPAVFLGPKRVSLPLESGSRITSFDSL |
| Bp4CL3 | 114 | TVHELARQVKDSNPKLIIT VPELWDKVKNFNLPAVFLGSNHSSSSSNVIHFDDL |
| AtACS6 | 114 | TVNEVSKQIKDSNPKLIISVNQLFDKIKGFDLPVVLLGSK-DTVEIPPGSNSKILSFDNV |
| OsACS1 | 121 | TPREIAKQVSDARAKLVITISALVPKIAGLRLPVILLDDDANAAAASLPPDATVTLYTNL |
| PoptrACS1 | 172 | VELGGSINSEFPVSDVKQSDIATLLYSSGTTGVSKGVILTHGNFIAASLMVSMDQ |
| PoptrACS2 | 172 | VGLGGSINSQFPSSNVKQSDISTLLYSSGTTGVSKGVILTHGNFIAASLMVTMDQ |
| Bp4CL3 | 168 | VNLGGTWSGSRSGSDFPDSNVKQNDTAALLYSSGTTGMSKGVILTHGNFIAASLMVSMDQ |
| AtACS6 | 173 | MELSEPVSEYPFVEIKQSDTAALLYSSGTTGTSKGVELTHGNFIAASLMVTMDQ |
| OsACS1 | 181 | VAGVKEADYRRPPIKQSDTAALLYSSGTTGDSKGVILTHRNFIAAARMVTSDQ |
| PoptrACS1 | 226 | VMAGEIHNVFLCFLPMFHVFGLAVITYSQLQMGNAVVSMGKFEFEMVLRTIEKYRVTHMW |
| PoptrACS2 | 226 | AMAGEMHDVFLCFLPMFHVFGLAVITYSQLQMGNAVVSMGKFEFEMVLKTIEKHRVTDMW |
| Bp4CL3 | 228 | ELSGEAHNVFLCVLPMFHVFGLAVILYSQLQIGNAVVSMGRFELEKILRAVERYRVSHLW |
| AtACS6 | 227 | DLMGEYHGVFLCFLPMFHVFGLAVITYSQLQRGNALVSMARFELELVLKNIEKFRVTHLW |
| OsACS1 | 234 | DERREGPNVFLCFLPMFHIFGLSVITYAQLHRGNALITAMSRFDINSLMEAVQRHRVTHLF |
| PoptrACS1 | 286 | VVPPVILAL <mark>S</mark> KQNLVKKYDLSSLRNIGSGAAPLGKDLMKECAKNLPDTTILQGEGMTETC |
| PoptrACS2 | 286 | VVPPVVLALAKQDWVKKYDLSSLRNIGSGAAPLGKDLMKECAKNLPDTILSQGYGMTETC |
| Bp4CL3 | 288 | VVPPVTLALAKQDVVKKYDLSSLKHVGSGAAPLGKDLMEECARNIPQAVVAQGYGMTETC |
| AtACS6 | 287 | VVPPVFLALSKQSIVKKFDLSSLKYIGSGAAPLGKDLMEECGRNIPNVLLMQGYGMTETC |
| OsACS1 | 294 | CVPPVITALAKHGKAGKYDLSSLKFIGSGAAPLGKDVMEVVAKKFPDSETVQGYGMTETC |
| PoptrACS1 | 346 | GIVSLEDPRIG-VRHSGSAGILNAGIEAQILSVETAKPLPPNQLGEIWVRGPNMMRGYFN |
| PoptrACS2 | 346 | GIVSVEDSRLG-VRHSGSAGILAAGIEAQIVSVETLKPLPPNQLGEIWVRGPNMMRGYFN |
| Bp4CL3 | 348 | GVVSVENPRVG-VRHTGSAGLLVSGVESQIVSVDTLKPLPPNQLGEIWVRGPNMMQGYYN |
| AtACS6 | 347 | GIVSVEDPRLG-KRNSGSAGMLAPGVEAQIVSVETGKSQPPNQQGEIWVRGPNMMKGYLN |
| OsACS1 | 354 | GIISLEYPEKGQAREFGSTGTLVSGVEAKIVDIKTLKHLPPNQVGEICVRGPNVMQGYFN |
| PoptrACS1 | 405 | NPQATKDTIDKKGWVHTGDLGYFDDDGQLFVVDRIKELIKYKGFQVAPAELEGLLVSHPE |
| PoptrACS2 | 405 | NPQATKDTMDKKGWVHTGDVGYFDDDGQLFVVDRIKELIKYKGFQVAPAELEGLLVSHPQ |
| Bp4CL3 | 407 | NPQATKLTIDKQGWVHTGDLGYFDGDGHLYVVDRIKELIKYKGFQVAPAELEGLLVSHPD |
| AtACS6 | 406 | NPQATKETIDKKSWVHTGDLGYFNEDGNLYVVDRIKELIKYKGFQVAPAELEGLLVSHPD |
| OsACS1 | 414 | NVQATEFTIFKQGWLHTGDLGYFDGGGQLFVVDRIKELIKYKGFQLAPAELEGLLUSHPE |
| PoptrACS1 | 465 | ILDAVVTPYPDAEAGEVPVAYVVRSPNSALTEEDVQKFISDQVAPFKRLRKVTFINSVPK |
| PoptrACS2 | 465 | ILDAVVIPYPDAEAGEVPVAYVVRSPNSALTEVDVQKFIADQVAPFKRLRKVTFINTVPK |
| Bp4CL3 | 467 | ILDAVVIPFPDAEAGEVPIAYVVRSPNSSLTEVDAMKFIANQVAPFKRLRRVTFINKVPK |
| AtACS6 | 466 | ILDAVVIPFPDEEAGEVPIAPVVRSPNSSLTEQDIQKFIAKQVAPYKRLRRVSFISLVPK |
| OsACS1 | 473 | ILDAVVIPFPDAKAGEVPIAYVVRSPDSSLTEVDVQKFIEKQVAYYKRLKRVTFVGSVPK |
| PoptrACS1 | 5 2 5 | SASGKI LRRELVQKVKSKM- |
| PoptrACS2 | 5 2 5 | SASGKI LRRELI QQVKSKI- |
| Bp4CL3 | 5 2 7 | SASGKI LRRELI EKVGSKM- |
| AtACS6 | 5 2 6 | SAAGKI LRRELVQQVRSKM- |
| OsACS1 | 5 3 3 | SASGKI LRR <mark>Q</mark> LI AQVRSSKL |

Figure S12. Alignment of predicted amino acid sequence of silver birch (*Betula pendula*) **putative 4CL-like acyl-CoA synthetase (ACS) (Bp4CL3, KM099197).** Bp4CL3 aligned with the predicted amino acid sequences of *Arabidopsis thaliana* (AtACS6, At4g05160), *Oryza sativa* (OsACS1, Os03g05780) and *Populus trichocarpa* (PoptrACS1, eugene3.01230068; PoptrACS2, estEXT_fgenesh1_pg_v1.C_LG_IV0024).

| p4CL4 ii 4CL2 optr4CL1 optr4CL2 im4CL7 im4CL8 im4CL1 im4CL9 | 1 1 1 1 1 1 | VE-PQKDLQEFIFRSKLPDIYIPNHLPLHTYCFENLSQFKDRPCLINGADGVTYTY VENKHQDDHEFIFRSKLPDIYIPNHLPLHTYCFENLSQFKDRPCLINGNTGETFTY VEARNDQAQEFIFRSKLPDIHIPNHLPLHTYCFENLSRFKDNPCLINGPTGEIHTY VEANKDQVQEFIFRSKLPDIYIPNHLPLHTYCFEKLSQFKDYPCLINGPTGDIYTY VEANKDQVQEFIFRSKLPDIYIPTHLPLHTYCFEKLSQFKDYPCLINGPTGDIYTY VEQQPTQPQPHHDFIFRSKLPDIYIPTHLPLHTYLFQNLSQFKDLPCLINGTTGETFSY VEQQAHHDFIFHSKLPDIYIPSHLPLHTYLFQNLSQFKDLPCLINGTTGETFSY VELSPQEHIFRSPLPDIPIPTHLPLYSYCFQNLSKFHDRPCLIDGDTGETLTY VELSPQEFIFRSPLPDIPIPTHLPLYSYCFQXLSQFHDRPCLIDGDTSETLTY |
|---|--|---|
| p4CL4 i 4CL2 optr4CL1 optr4CL2 im4CL7 im4CL8 im4CL1 im4CL9 | 56 57 57 57 61 56 54 54 | AQVELTARKVASGEDKLGI KQGEVI MLLLQNCPEFAFAFLGASYI GAVSITANPFYTPAE AEVELTSRRVAAGLDKLGI KQGEVI MLLLQNCPEFAFAFLGASYI GAVSITANPFYTPAE ADVELTSRKVASGLNKLGI KQGDVI LLLLQNSPEFVFAFLGASI I GAI SITANPFYTPAE ADVELTSRKVASGLYKLGVQQDVI LLLLQNSPEFVFALLGASFI GAI SITANPFYTSAE AAVELTARKVASGFNKLGI QKGDVI LLLLQNCPQFVFAFLGASYRGATVTAANPFYTPAE TAI QLTARRVASGLNKLGI QKGDVI LLLLQNCPQFVLAFLGASYRGATVTAANPFYTPAE ADVELTARRVASGLNKLGI QKGDVI LLLLQNCPQFVLAFLGASYRGATVTANPFYTPAE ADVELTARRVASGLNKLGI QKGDVI LLLLQNCPQFVLAFLGASYRGATVTANPFYTPAE ADVELTARRVASGLNKLGI QKGDVI LLLLQNCPQFVLAFLGASYRGATVTANPFYTPAE ADVDLAARRIASGLNKLGI QKGDVI MLVLRNCPQFALAFLGAYRGATVTANPFYTPAE ADVDLSARRI SAGLHKI GI CQGDVI MLVLRNCPQFALAFLGATHRGAVVTTANPFYTPAE |
| <pre>3p4CL4 {i 4CL2 >opt r 4CL1 >opt r 4CL2 Sm4CL7 Sm4CL8 Sm4CL1 Gm4CL9</pre> | 116 117 117 117 121 116 114 114 | / AK QAKASNTKLI I TOS SY VDKV KDF AKENG- VKVMCI DSSLDDEL HF SQLT QADE / AK QAKASNAKLI I TOSAY VDKV KDF AKLND-VKVMCVDETSE DVL HF SELTNS ADE / AK QATASKAKLI I TOAVYAE KVQQF VKENDHVKI VTVDSPPENYL HF SELTNS DE AK QATASKAKLI I TOAVYAE KVQQF AQENDHVKI VTVDSLTENCL HF SELTS SDE / AK QATASKAKLI I TOAVYAE KVQQF AQENDHVKI VTVDSAP DGYL HF SELTS SDE / AK QATASNSKLI I TOASY VDKVKDF AREND-VKVI CVDSAP DGYL HF SVLTEADE / AK QATASNSKLI I TOASY VDKVKDF AREND-VKVI CVDSAP EGYL PF SELTEADE / AK QATASNSKLI I TOASY VDKVKDF AREND-VKVI CVDSAP EGYL PF SELTEADE / AK QATASNSKLI I TOASY VDKVKDF AREND-VKVI CVDSAP EGYL PF SELTEADE . AK QATATKTRLVI TOSAY VEKIKSF ADSSSD VVVVCI DDDF SY ENDGVL HF STLSNADE . AK QAMATKTRLVI TOSAY VEKIKSF ADDS-DVVVVCI DDDF SY ENDGVL HF STLSNADE |
| Bp4CL4 Ri 4CL2 Popt r 4CL1 Gr4CL7 Gr4CL7 Gr4CL8 Gr4CL1 Gr4CL9 | 171 173 173 173 176 171 174 173 | NDI PAVKI NP DDVVAL PYSSGTTGL PKGVML THRGL VTSVAQQVDGE NPNL YFHSGDVIL SETPAVKI NP DDVVAL PYSSGTTGL PKGVML THKGL VTSVAQQVDGE NPNL YFHKEDVIL DDI PAVEI NP DDVVAL PYSSGTTGL PKGVML THKGL VTSVAQQVDGE NPNL YFHEKDVIL DDI PAVEI NP DDVVAL PYSSGTTGL PKGVML THKGL VTSVAQQVDGE NPNL YFHERDVIL GDI PAVKI KPDDVVAL PYSSGTTGL PKGVML THKGL VTSVAQQVDGE NPNL YFHERDVIL GDI PAVKI SQDDVVAL PYSSGTTGL PKGVML THKGL VTSVAQQVDGE NPNL YFRSDDVV GDI PAVKI SQDDVVAL PYSSGTTGL PKGVML THKGL VTSVAQQVDGE NPNL YFRSDDVV GDI PAVKI SQDDVVAL PYSSGTTGL PKGVML THKGL VTSVAQQVDGE NPNL YFRSDDVV GDI PAVKI NP DELVAL PYSSGTTGL PKGVML SHKNL VTTI AQL VDGE NPHQYTHSEDVLL REAPAVKI NP DDLVAL PFSSGTSGL PKGVML SHKNL VTTI SQL VDGE NPHQYTHSEDVLL |
| Bp4CL4 Ri 4CL2 Poptr4CL1 Gr4CL7 Gr4CL7 Gr4CL8 Gr4CL1 Gr4CL9 | 231 233 233 236 231 234 233 | EVLPLEHIYSLNSVELCGLRVGASILI MQKFEIVKLLELVQQYKVTIAPEVPPIVLAIAK EVLPLEHIYSLNSVELCGLRVGAAILI MQKFEINKLLELVEKEKVTIAPEVPPIVLSIAK EVLPLEHIYSLNSVLLCGLRAGSAILLMQKFEIVTLMELVQKYKVTIAPEVPPIVLAVAK EVLPLEHIYSLNSVLLCGLRAGSAILLMQKFEIVSLMDLVQKYKVTIAPEVPPIVLAVAK EVLPLEHIYSLNSVLLCGLRAGSAILLMQKFEIVALLELVQKHNVSVAPEVPPIVLAIAK EVLPLEHIYSLNSVLLCSLRVGAAVLIVPKEEITALLELVQKHNVSVAPEVPPIVLAIAK EVLPLEHIYALNSULLCSLRVGASVLIVPKEEITTLLELIQKHKVSIAPEVPPIVLAIVK EVLPMEHIYALNSILLCGIRSGAAVLIVQKFEITTLLELIEKYKVTVASEVPPIVLALVK |
| Bp4CL4 Ri 4CL2 Poptr4CL1 Poptr4CL2 Gr4CL7 Gr4CL8 Gr4CL8 Gr4CL1 Gr4CL9 | 291 293 293 293 296 291 294 293 | S P DVQWY DVS SI RT V MS GAAP MGRELE DAVRAKL P NAKL GQGY GMT E AGP VL AMCL AF AK P DL HR Y DL S SI R MV MS GAAP MGKELE DT VRAKL P NAKL GQGY GMT E AGP VL S MCL AF AK P PVVDKY DL S SI RT V MS GAAP MGKELE DT VRAKL P NAKL GQGY GMT E AGP VL S MCL AF AK S P VVDQY DL S SI RT VL S GAAP MGKELE DT VRAKL P NAKL GQGY GMT E AGP VL S MCL AF AK S P DVER Y DVS SI R MI MS GAAP MGKELE DS VRAKL P NATL GQGY GMT E AGP VL S MCL AF AK S P DUER Y DU S SI R MI MS GAAP MGKELE DS VRAKL P NATL GQGY GMT E AGP VL S MCL AF AK S P DUER Y DU S SI R MI MS GAAP MGKELE DS VRAKL P NATL GQGY GMT E AGP VL S MCL AF AK S P DL ER Y DL S SI R MI MS GAAP MGKELE DS LRAKL P NAIL L GQGY GMT E AGP VL S MCL AF AK S GET HR Y DL S SI R MV T GAAP L GGEL QE AV KARL P HAT F GQGY GMT E AGP - L AI S MAF AK S GET HR Y DL S SI R AV VT GAAP L GGEL QE AV KARL P HAT F GQGY GMT E AGP - L AI S MAF AK |
| Bp4CL4 Ri4CL2 Poptr4CL1 Poptr4CL2 Gm4CL7 Gm4CL8 Gm4CL1 Gm4CL9 | 351 353 353 353 356 351 353 352 | AFEIKSGACGTVVRNAQMKIVDPDTGASLPRNQAGEICIRGSQIMKGYLNDPEATERTI PYEIKSGACGTVVRNAEMKIDPDTNESLPRNQSGEICIRGSQIMKGYLNDPEATENTI PFEIKSGACGTVVRNAEMKIVDPDTGRSLPRNQAGEICIRGSQIMKGYLNDPEATERTV PFEIKSGACGTVVRNAEMKIVDPTGQSCPRNKAGEICIRGCQIMKGTLSK PMQVKSGACGTVVRNAEMKIDPDTGASLHRNQAGEICIRGNQIMKGYLNDQEATERTI PMQVKSGACGTVVRNAEMKIVDPTGASLHRNQAGEICIRGNQIMKGYLNDQEATERTI PSKIKPGACGTVVRNAEMKIVDTETGDSLPRNKHGEICIRGAKMKGYLNDPEATERT |

Figure S13. Alignment of predicted amino acid sequence of silver birch (*Betula pendula*) **putative 4-coumarate:CoA ligase (Bp4CL4, KM099198).** Bp4CL4 with the predicted amino acid sequences of *Rubus idaeus* (Ri4CL2, AAF91309), *Glycine max* (Gm4CL7, Glyma17g07170; Gm4CL8, Glyma17g07180; Gm4CL1, Glyma17g07190; Gm4CL9, Glyma13g01080), and *Populus trichocarpa* (Poptr4CL1, estExt_fgenesh4_pg.C_1210004 scaffold3; Poptr4CL2, gw1.XVIII.2818.1 LG_XVIII).



Figure S14. Relative expression of *Pt4CL1* in stems and leaves of **Pt4CL1a lines A1, A5 and E5282/3.** Values represent means and standard deviations calculated using *PP2A* gene as reference gene (n = 3-14).



Figure S15. Relative expression of *Bp4CL1-4* **genes in mechanically wounded silver birch** (*Betula pendula*) **leaves.** The *Bp4CL1* (A, C) and *Bp4CL2* (B, D) expression in leaves collected immediately (w0) and 1 (w1), 3 (w3), 12 (w12), 24 (w24), 72 (w3d), and 162 (w7d) h after mechanical wounding of clones A, E5382, E5396 and R and transgenic lines A1, A5, E5382/3 and E5396/4. Values represent means and standard errors calculated from the target/referce ratios. A and C, *PP2A* was used as the reference gene; B and D, *Atub* was used as the reference gene.



Figure S16. Relative expression of *Bp4CL3* (A, B), and *Bp4CL4* (C, D) in wounded leaves. The leaves were collected immediately (w0) and 1, 3, 12, 24, 48, and 162 h after mechanical wounding of silver birch (*Betula pendula*) clones A and R and transgenic lines A1 and A5 (A, C) and clones E5382 and E5396 and transgenic lines E5382/3 and E5396/4 (B, D). Values represent means and standard errors calculated using the mean of control leaves as normalizer within each line/clone and *PP2A* as reference.