**Supplemental data: Expression of homeobox genes during in vitro culture of Lactuca sativa P. FARINA ET AL.**

**Supporting Information Table S1.** List of primers used in this study.

|  |  |  |  |
| --- | --- | --- | --- |
| Use | Primer name | Primer sequence 5’-3’ | Amplicon (bp) |
| Full-length amplification of *LsWUS1L* gene | WUS1FFWUS1RR | forward, 5’-GTTCTCTAGGTGTTTTGTGATTAGG-3’reverse, 5’-CAGAGGTTAAACTGACGACCAC-3’ | 1,445 |
| Full-length amplification of *LsWUS2L* gene | WUS2FFWUS2RR | forward, 5’-CTCTTTCTTCCATGTGCCATCTCC-3’reverse, 5’-GGCAGATAATACATAATTCCCATCC-3’ | 1,439 |
| Full-length amplification of *LsSTM1L* gene | LAT1FSTM1RR | forward, 5’-GACACGTAAGTCCTCCATATCC-3’reverse, 5’-TCCCTTACGGTTCACACAAACTTGC-3’ | 3,207 |
| Transcription analysis of *LsWUS1L*, *LsWUS2L*, *LsSTM1L* and *Ls18S mRNA* genes | WUS1QFWUS1QRWUS2QFWUS2QRSTM1Q1FSTM1Q1R18QF18QR | forward, 5’-CACATCACATTGGGGTTGGTTC-3’reverse, 5’-CAATTGATCCAGTGGCCCTACT-3’forward, 5’-ATCTCACCTTCGGAGGGAGG-3’reverse, 5’-GTTCCTCCGACGACTCTAGAT-3’forward, 5’-AGCACTATGTCTTCCTCCACCTC-3’reverse, 5’-AGCAGAAGTCGAAGTCCCACAG-3’forward, 5’-TGACTCAACACGGGGAAAC-3’reverse, 5’-GACAAATCGCTCCACCAAC-3’ | 134141130120 |

**Supporting Information Figure S1.** List of amino acid sequences of WUSCHEL Homeobox (WOX) transcription factors (TFs) used for phylogenetic analysis. Ls: *Lactuca sativa* ‘Romana’; Ha: *Helianthus annuus* L.; Cc: *Cynara cardunculus* L. var. *scolymus*; C×m: *Chrysanthemum* × *morifolium* Ramat.; Pp: *Prunus persica* (L.) Batsch; Na: *Nicotiana attenuata* Torr. ex S. Watson; Pa: *Prosopis alba* Griseb.; Gm: *Glycine max* L. (Merr.); Md: *Malus domestica* Borkh.; Mt: *Medicago truncatula* (Gaertn.); At: *Arabidopsis thaliana* (L.) Heynh. The GenBank accession numbers are in brackets.

>LsWUS1L (MN623284)

METQQQPSDIQDLGNKTSSTYVCRQSSTRWTPTSDQIRILKELYYNNGIRSPTADQIQRIAAQLRQYGKIEGKNVFYWFQNHKARERQKKRFTPAPPPPSPFSDHINHHLPTAPAMQIQSHHHHYHHQEPPHVYNHQHKLYTTHHIGVGSSSSQGVMAVGCGYGSVAMEKSFRECSISPPGESRATGSIGRNFGSRSRVGVESFSFFENIKPKRYEILENHHQEEEHQEEGDSSTQIETLPLFPIHGGTHHDFFSMKAADLSSEHTTGGYYTRGNWYRKDGRASLELSLNSYGYYN

>LsWUS2L (MN623285)

METQQQEQDLGNKNNTSYLCRQSSTRWTPTSDQIRILKELYYNNGIRSPTADQIQRIAARLRHYGKIEGKNVFYWFQNHKARERQKKRFTPVPVTPPPPPPPPPPPPSTATLLPSPFSDHRHHHHHMHVNSHHPPQFYSQQHKLYTTHQISPSEGGSSSTGFMPVGYGYGSVAMEKSFKECSISQGESRVVGGTSQNFGSWVGSDSYSYEKIKPEYEAPEEDDDRGGELSAQMETLPLFPVNGGATMGGSHHDIINMKAPVAVESPLMSEHSNGGCYTGGNWFRSDGRTSLELSLNSYGYYN

>HaWUS (LN811433.1)

METQQQQADIQDFGNKNSNTYACRQSSTRWTPTSDQIRILKELYYNNGIRSPTADQIQRIAAQLRQYGKIEGKNVFYWFQNHKARERQKKRFTPTAPPPPSHFSDHINHHLPNAAPMQIPSHHHHYHHQEPPHVYAHPHKLYTTHHIGVGSSSQGVMGVGCGYGSVAMEKSFRKCSISPPGESKATGGIGRNIGSRSRISVDSCSFFDTIKPKTYEMFENHDQDEEQGEPSTEIETLPLFPIHDGNHHDFFGMRTANLQLEQGTGGYYTGGSWYRSDERASLELSLNSYGYYN

>CcWUSL (XM\_025106474.1)

METQQQQQQQTDIQDLGNKNSSSYVCRQSSTRWTPTSDQIRILKELYYNNGIRSPTADQIQRIAAQLRQYGKIEGKNVFYWFQNHKARERQKKRFTPAPPPPSSTTTLLPSPFSDHTHQHINHHLPTAAAMQIQSHHPHYHHQEPPHVYSHQHKLYTTHHIGVGSSSSSSQGVMAVGCGYGSVAMEKSFRECSISPPEESMATGGVGRNFGSRSRVGVDSCSFFDTIKPTTYDILENHNQDEEQEEGETSTQIETLPLFPIHGGTHHDFFSMKSADLSSDGGYYTGGNWYRSDGRASLELSLNSYGYYN

>C×mWUSL (MK124768.1)

MKNTMETQHHQQQDIHDHLGNKNSSNYVCRQSSTRWTPTSDQIRILKELYYTSGIRSPTAEQIQRIAAQLRQYGKIEGKNVFYWFQNHKARERQKKIFTPTVPPPQPPSSHYSTDHINHHIPTAAMHIQSHNYHHELPSSHVYGHPHKLYTTHHIGVGSSSSSQGMMTVGCGYGSVAMEKSFRECSISPPGENRATEGIGRNFGSRSRVGVGSFSFFDKIKPKRFEIVENNREDEDQEGKNSPEIETLPLFPIHGGSHQDFFGMKTDLSSEHSVGGYYTGGNWYRPDGRASLELTLNTYGYND

>PpWUSL (XM\_007203116.1)

MEPQQTQQQPNEDGSNKGTSSGTNFLCRQSSTRWTPTSDQIRILKDLYYNNGVRSPSAEQIQRISARLRQYGKIEGKNVFYWFQNHKARERQKKRFIDVPAPPIMQRSGLGINNNNAPTAYEPINHSNKYPNSSASAGVSPSSAGVIAVGQMGSHGYGSMTMEKSFRDCSISAAGGTSSGHVGGSNNNIGHNFGSWVGVDAYSSPYTLFDKRSSSRQVFGDQENTMDEEDHEYQENLQGSPEIETLPLFPMHGEDIHGFGNIKSTSDGYYSGWYRSDDGNNGRTSLELSLNSYGHMTRDYFRSY

>NaWUS (XM\_019395955.1)

MEAAQQQNQQHYLHQQHLSIGQVANNIEDGVGGNSSKNNSSSFMCRQSSTRWTPTTDQIRILKDLYYNNGVRSPTAEQIQRISAKLRQYGKIEGKNVFYWFQNHKARERQKKRLIAAAATDSNNNIPMQMRGVWRSADDPIHHKYNNTTGIHCPSASSHGVLAVGQNGNYGYGTLAMEKSFRDCSISPGGNSNGSMGHQNITWVGVDPYTSHQAYPFLEKTKHFDETLVDDYEELQQEEENYQRASALETLPLFPMHEENISSFCNIKHESSGGFYTEWYRSDDHNLAAAARASLELSLNSFIGRSPNSS

>PaWUSL (XM\_028918678.1)

MEPQQQQAANEDAGGSGRGGYLCRQSSTRWTPTSDQIRILKDLYYNNGVRSPNAEQIQRISARLRQYGKIEGKNVFYWFQNHKARERQKKRFTSTSDHLPSPMHLQRPPSSATTNWKPDHESILHPKYSNIPPSHGVSSASSSTAGMVSLGQMGNYGYGSVTMEKCFRDCSISAAGSSGTISHNLGWVGMDPYSNYTNFLDKIRPGDQETLKEEQEGEDGAPEIETLPLFPMHGEDVHGYCNLRSDSSYYGGGWYHGDEYGFKNNGSHRTSLELTLNSYTRRSPDSS

>GmWUS (XM\_003517132.4)

MMEPQQQQQQAQGSQQQQQNEDGGSGKGGFLSRQSSTRWTPTNDQIRILKELYYNNGIRSPSAEQIQRISARLRQYGKIEGKNVFYWFQNHKARERQKKRFTSDHNHNNVPMQRPPTNPSAAWKPDLADPIHTTKYCNISSTAGISSASSSVEMVTVGQMGNYGYGSVPMEKSFRDCSISAGGSSGHVGLINHNLGWVGVDPYNSSTYANFFDKIRPSDQETLEEEAENIGATKIETLPLFPMHGEDIHGYCNLKSNSYNYDGNGWYHTEEGFKNASRASLELSLNSYTRRSPDYA

>MdWUSL (XM\_017335783.2)

MDPQQNPNELLDGGNRQGGGVMCRQSSTRWTPTTDQIKILKDLYYNNGIRSPSAEQIHRISAKLRQYGKIEGKNVFYWFQNHKARERQKKRFTSSSTPDHHAAPPMPAVPPQADNIRQRSSGFGIDINATAAAAYEQLPINHHSKYSNISGSPAGFSSTSSSVGVNVSAGAQMGNYGYGSMAMEKSFRDCSLSSGGSTSTGHVGGSNYNNFNHNPGSWVGVDPYSSPYSIFDKKSPSKQVFGDQENMTEEEYYNQQQASPEIETLPLFPMHGEDIHGFGNIKSSSMEGYYSGWYRSDGSNDGGSRTSLELSLNSYGHMAPDCFRSC

>MtWUS (XM\_003612110.2)

MEQPQQQQQPQTQQHSPNNGIMGSRQSSTRWTPTTDQIRILKDLYYNNGIRSPSAEQIQRISARLRQYGKIEGKNVFYWFQNHKARERQKKRFTSDVNVVPIIQRAPNNNTIISAANWKPDHHEQQQNINVHTNHSTYNISSAGLSSASCSSAEMVTVGQIGNYGYGSVPMEKSFRECTISAGCSSSQVGSTINPHIGWIGHHVDPYSSAYANLFEKIRPNEEIMEEYDQGQENGSPEIETLPLFPMHGEDIHGGYCNLKSNSSNYGGWYQAEDAGFMYGSRTTSLELSLNSYGCRSPDYAN

>AtWUS1 (OAP09268.1)

MEPPQHQHHHHQADQESGNNNNKSGSGGYTCRQTSTRWTPTTEQIKILKELYYNNAIRSPTADQIQKITARLRQFGKIEGKNVFYWFQNHKARERQKKRFNGTNMTTPSSSPNSVMMAANDHYHPLLHHHHGVPMQRPANSVNVKLNQDHHLYHHNKPYPSFNNGNLNHASSGTECGVVNASNGYMSSHVYGSMEQDCSMNYNNVGGGWANMDHHYSSAPYNFFDRAKPLFGLEGHQDEEECGGDAYLEHRRTLPLFPMHGEDHINGGSGAIWKYGQSEVRPCASLELRLN

>AtWOX1 (AY251394.1)

MWTMGYNEGGADSFNGGRKLRPLIPRLTSCPTAAVNTNSDHRFNMAVVTMTAEQNKRELMMLNSEPQHPPVMVSSRWNPTPDQLRVLEELYRQGTRTPSADHIQQITAQLRRYGKIEGKNVFYWFQNHKARERQKRRRQMETGHEETVLSTTSLVSNHGFDKKDPPGYKVEQAKNWICSVGCDTQPEKPSRDYHLEEPANIRVEHNARCGGDERRSFLGINTTWQMMQLPPSFYSSSHHHHQRNLILSPTVSSNMSNSNNAVSASKDTVTVSPVFLRTREATNTETCHRNGDDNKDQEQHEDCSNGELDHQEQTLELFPLRKEGFCSDGEKDKNISGIHCFYEFLPLKN

>AtWOX2 (OAO90278.1)

MEHEVNAGTASSSRWNPTKDQITLLENLYKEGIRTPSADQIQQITGRLRAYGHIEGKNVFYWFQNHKARQRQKQKQERMAYFNRLLHKTSRFFYPPPCSNVGCVSPYYLQQASDHHMNQHGSVYTNDLLHRNNVMIPSGGYEKRTVTQHQKQLSDIRTTAATRMPISPSSLRFDRFALRDHCYAGEDINVNSSGRKTLPLFPLQPLNASNADGMGSSSFALGSDSPVDCSSDGAGREQPFIDFFSGGSTSTRFDSNGNAL

>AtWOX3 (NM\_128422)

MSPVASTRWCPTPEQLMILEEMYRSGIRTPNAVQIQQITAHLAFYGRIEGKNVFYWFQNHKARDRQKLRKKLAKQLHQQQHQLQLQLQQIKPKPISSMISQPVNKNIIDHHNPYHHHHHNHHHNHHRPYDHMSFDCCSHPSPMCLPHQGTGVGEAPSKVMNEYYCTKSGAEEILMQKSITGPNSSYGRDWMMMMDMGPRPSYPSSSSSPISCCNMMMSSPKIPLKTLELFPISSINSKQDSTKL

>AtWOX4 (FJ440850)

MKVHEFSNGFSSSWDQHDSTSSLSLSCKRLRPLAPKLSGSPPSPPSSSSGVTSATFDLKNFIRPDQTGPTKFEHKRDPPHQLETHPGGTRWNPTQEQIGILEMLYKGGMRTPNAQQIEHITLQLGKYGKIEGKNVFYWFQNHKARERQKQKRNNLISLSCQSSFTTTGVFNPSVTMKTRTSSSLDIMREPMVEKEELVEENEYKRTCRSWGFENLEIENRRNKNSSTMATTFNKIIDNVTLELFPLHPEGR

>AtWOX5 (AY251398)

MSFSVKGRSLRGNNNGGTGTKCGRWNPTVEQLKILTDLFRAGLRTPTTDQIQKISTELSFYGKIESKNVFYWFQNHKARERQKRRKISIDFDHHHHQPSTRDVFEISEEDCQEEEKVIETLQLFPVNSFEDSNSKVDKMRARGNNQYREYIRETTTTSFSPYSSCGAEMEHPPPLDLRLSFL

>AtWOX6 (AY251399)

MGYISNNNLINYLPLSTTQPPLLLTHCDINGNDHHQLITASSGEHDIDERKNNIPAAATLRWNPTPEQITTLEELYRSGTRTPTTEQIQQIASKLRKYGRIEGKNVFYWFQNHKARERLKRRRREGGAIIKPHKDVKDSSSGGHRVDQTKLCPSFPHTNRPQPQHELDPASYNKDNNANNEDHGTTEESDQRASEVGKYATWRNLVTWSITQQPEEINIDENVNGEEEETRDNRTLNLFPVREYQEKTGRLIEKTKACNYCYYYEFMPLKN

>AtWOX7 (AIR72305.1)

MSSRGFNIKARGLCNNNNGGGGTGAKCGRWNPTVEQVKLLTDLFKAGLRTPSTDQIQKISMELSFYGKIESKNVFYWFQNHKARERQKCRKISTVKFDHRQDTDLSKPRRDNVRRHQLPAKVCKVEEKMIETLQLFPLSKVERVRANVTAASHNEYTREQAYTTAFSTFSTCGAEMEHSPLDLRLSFL

>AtWOX8 (AY251400)

MSSSNKNWPSMFKSKPCNNNHHHQHEIDTPSYMHYSNCNLSSSFSSDRIPDPKPRWNPKPEQIRILESIFNSGTINPPREEIQRIRIRLQEYGQIGDANVFYWFQNRKSRAKHKLRVHHKSPKMSKKDKTVIPSTDADHCFGFVNQETGLYPVQNNELVVTEPAGFLFPVHNDPSAAQSAFGFGDFVVPVVTEEGMAFSTVNNGVNLETNENFDKIPAINLYGGDGNGGGNCFPPLTVPLTINQSQEKRDVGLSGGEDVGDNVYPVRMTVFINEMPIEVVSGLFNVKAAFGNDAVLINSFGQPILTDEFGVTYQPLQNGAIYYLI

>AtWOX9 (AY251401)

MASSNRHWPSMFKSKPHPHQWQHDINSPLLPSASHRSSPFSSGCEVERSPEPKPRWNPKPEQIRILEAIFNSGMVNPPREEIRRIRAQLQEYGQVGDANVFYWFQNRKSRSKHKLRLLHNHSKHSLPQTQPQPQPQPSASSSSSSSSSSSKSTKPRKSKNKNNTNLSLGGSQMMGMFPPEPAFLFPVSTVGGFEGITVSSQLGFLSGDMIEQQKPAPTCTGLLLSEIMNGSVSYGTHHQQHLSEKEVEEMRMKMLQQPQTQICYATTNHQIASYNNNNNNNNIMLHIPPTTSTATTITTSHSLATVPSTSDQLQVQADARIRVFINEMELEVSSGPFNVRDAFGEEVVLINSAGQPIVTDEYGVALHPLQHGASYYLI

>AtWOX10 (NM\_101923)

MEQESLNGRYGSRVMTDEQMETLRKQIAIYAVLCDQLVFLHNSLSSVPLLSSGMNPMRGEYFDPMVASSSAHGMSTRPRWTPTTTQLQILENIYKEGSGTPNPRRIKEITMELSEHGQIMEKNVYHWFQNRRARSKRKQPPTTTITSSQADDAAVTTTEERGRCGDDSGGFESYEHILFPSPDLGIEHLLNRDKFID

>AtWOX11 (AAP37140.1)

MDQEQTPHSPTRHSRSPPSSASGSTSAEPVRSRWSPKPEQILILESIFHSGMVNPPKEETVRIRKMLEKFGAVGDANVFYWFQNRRSRSRRRQRQLQAAAAAAAATTNTCDQTMMVSNSLPHHSGSDLGFGGCSTSSNYLFASSSSSYGGGCDNQSNSGMENLLTMSGQMSYHEATHHHYQNHSSNVTSILCPSDQNSNFHYQQGAITVFINGVPTEVTRGGIDMKATFGEDLVLVHSSGVPLPTDEFGFLMHSLQHGEAYFLVPRQT

>AtWOX12 (AY251403)

MNQEGASHSPSSTSTEPVRARWSPKPEQILILESIFNSGTVNPPKDETVRIRKMLEKFGAVGDANVFYWFQNRRSRSRRRHRQLLAATTAAATSIGAEDHQHMTAMSMHQYPCSNNEIDLGFGSCSNLSANYFLNGSSSSQIPSFFLGLSSSSGGCENNNGMENLFKMYGHESDHNHQQQHHSSNAASVLNPSDQNSNSQYEQEGFMTVFINGVPMEVTKGAIDMKTMFGDDSVLLHSSGLPLPTDEFGFLMHSLQHGQTYFLVPRQT

>AtWOX13 (AY251404)

MMEWDNQLQPNNHHSSNLQGIDVNGGSGAGGGMYVKVMTDEQYETLRKQIAIYGTICERLVEMHKTLTAQQDLAGGRMGGLYADPMMSSLGHKMTARQRWTPTPVQLQILERIFDQGTGTPSKQKIKDITEELSQHGQIAEQNVYNWFQNRRARSKRKQHGGGSSGNNNGESEVETEVEALNEKRVVRPESLLGLPDGNSNNNGLGTTTATTTAPRPEDLCFQSPEISSDLHLLDVLSNPRDEHLVGKMGLAESYNLYDHVEDYGMSG

>AtWOX14 (OAP12283.1)

MDREIQNGAYSGRVMTEEQMEILRKQIAVYAVICDQLVLLHNSLSSYHPLSSGVRPMVGGYFDPMGASSSSHRISTRHRWTPTSTQLQILESIYDEGSGTPNRRRIREIATELSEHGQITETNVYNWFQNRRARSKRKQPQTTTANGQADDVAVTTEERRSCGDSGGLESYEHILFPSPDLGIEHLLSIGKFMET

**Supporting Information Figure S2.** List of amino acid sequences of class 1 and 2 of KNOTTED-LIKE Homeobox (KNOX) transcription factors (TFs) used for phylogenetic analysis. Ls: *Lactuca sativa* ‘Romana’; Ha: *Helianthus annuus* L.; Aa; *Artemisia annua* L.; At: *Arabidopsis thaliana* (L.) Heynh.; Bo: *Brassica oleracea* L.; Tc: *Theobroma cacao* L.; Gh: *Gossypium hirsutum* L.; Rc: *Ricinus communis* L.; Vv: *Vitis vinifera* L.; Hb: *Hevea brasiliensis* (Willd. ex A. Juss.) Müll. Arg.; Jr: *Juglans regia* L.; Si: *Setaria italic* (L.) Beav.; Zm: *Zea mays* L.; Sb: *Sorghum bicolor* (L.) Moench.; Ta: *Triticum aestivum* L.; Sl: *Solanum lycopersicum* L.; St: *Solanum tuberosum* L.; Cc: *Capsicum chinense* Jacq.; Dc: *Daucus carota* L. The GenBank accession numbers are in brackets.

>LsSTM1L (MN623286)

MEGDAGGGGGTSSCLMSFGDSNIINTSSNSNNNNVGALCLPPPPVSYNNNNNNLIFADQDHHHHHHHHHHSTCGTSTSAMMLENSAININDGGELAFMSSSSCSSSAKAKIMSHPHYPRLLSAYLNCQKIGAPPEVVERLEDACRASVVAAMSSRSGSAGCEAGTSDGGGGGGMNMMIIGQDPALDQFMEAYCEMLIKYEQELAKPFKEAMLFLSRVESQFKAISISTSDSAGGEVGMDKNGSSEEEVDVNNNLIDPQAEDQELKGQLLRKYSGYLGSLKQEFMKKRKKGKLPKEARQQLLDWWTRHYKWPYPSEAQKLALAESTGLDQKQINNWFINQRKRHWKPSEDMQFVVMDAAHPHHYFMENILGNPYPMDVSLL

>HaKNOT1L (AAM28231.1)

MESDGDGGGTSSCLMSFGDTTNNINNNSSNNNNSNNNIGSLCLPPNPPGAYNTTTNNNNLIFSDHHPSAMMLEDNNININDGVGLAFMNPSSSVKAKIMSHPHYPRLLSAYLNCQKIGAPPEVVERLEEACRASVVAAMSSCSGGAGTSDGSGGGMNMIIGQDPALDQFMEAYCEMLIKYEQELSKPFKEAMLFLSRIESQFKAISISTSDSAGGEGGMDKNGSSEEEVDVNNNLIDPQAEDRELKGQLLRKYSGYLGSLKQEFMKKRKKGKLPKEARQQLLDWWTRHYKWPYPSEAQKLALAESTGLDQKQINNWFINQRKRHWKPSEDMQFVVMDAAHPHYFMENMNILGNPYPMDVSLL

>AaKNOT1L (PWA89621.1)

MEGGDGGTSSSCLMSFGDNNNINNNTNNNNIGSLCLVPISYNNNNNLIFSNNNNNCGTSSASGMMLQDNNIKAKIMSHPHYPRLLSAYLNCQKIGAPPEVVERLEEACRASVVAAMSSREGGGSSSDGGMMMIGQDPALDQFMEAYCEMLIKYEQELSKPFKEAMLFLSRVESQFKAISISTSDSAGGDGGLDRNGSSEEEVDVSNNLVDPQAEDRELKGQLLRKYSGYLGSLKQEFMKKRKKGKLPKEARQQLLDWWTRHYKWPYPSEAQKLALAESTGLDQKQINNWFINQRKRHWKPSEDMQFVVMDAAHPHYFMESMLGNPYPMDVSLL

>AtSTM (NP\_176426.1)

MESGSNSTSCPMAFAGDNSDGPMCPMMMMMPPIMTSHQHHGHDHQHQQQEHDGYAYQSHHQQSSSLFLQSLAPPQGTKNKVASSSSPSSCAPAYSLMEIHHNEIVAGGINPCSSSSSSASVKAKIMAHPHYHRLLAAYVNCQKVGAPPEVVARLEEACSSAAAAAASMGPTGCLGEDPGLDQFMEAYCEMLVKYEQELSKPFKEAMVFLQRVECQFKSLSLSSPSSFSGYGETAIDRNNNGSSEEEVDMNNEFVDPQAEDRELKGQLLRKYSGYLGSLKQEFMKKRKKGKLPKEARQQLLDWWSRHYKWPYPSEQQKLALAESTGLDQKQINNWFINQRKRHWKPSEDMQFVVMDATHPHHYFMDNVLGNPFPMDHISSTML

>BoSTM (Q9M6D9)

MESGSNSTSCPMAFAGDNSDGPMCPMMMMMMPVITSHQQHHGHDQQHQHQQQHDGYAYQSHHQHSSLLFLQSLTPPSQEAKNKVRSSCSPSSGAPAYSFMEINHQNELLAGGLQSPVLSSLLVKAKIMAHPHYHRLLLAYVNCQKVGAPPEVQARLEETCSSAAAAAASMGPTGSLGEDPGLDQFMEAYCEMLVKYEQELSKPFKEAMVFLQHVECQFKSLSLSSPSSLGYGEAAIERNNNGSSEEEVDMNNEFVDPQAEDRELKGQLLRKYSGYLGSLKQEFMKKRKKGKLPKEARQQLLDWWSRHYKWPYPSEQQKLALAESTGLDQKQINNWFINQRKRHWKPSEDMQFVVMDATHPLHYFMGNVLGNPFPIDHISGTML

>TcSBH1 (XM\_007026123.2)

MEGGSNSTSCMIAFGHNSHGLCPMTMMPLMTSHPHHQHHHHHHPPNSDSNSLFLPLPPTNNQDQNHNSSSGSSMILDDHNNNNNSTNNNTGCYFMETNDGSSSSVKAKIMAHPHYHRLLAAYVNCQKVGAPPEVVARLEEACASAATMGPSGTGCLGEDPALDQFMEAYCEMLTKYEQELSKPFKEAMLFLQRVECQFKALTVSSPSSACGEAADRNGSSEEEVDVNNNFIDPLAEDRELKGQLLRKYSGYLGSLKQEFMKKRKKGKLPKEARQQLLDWWGRHYKWPYPSESQKIALAESTGLDQKQINNWFINQRKRHWKPSEDMQFVVMDATHPHYYMDNVLGNPFPMDLSPTLL

>GhSBH1L (XM\_016837791.1)

MEGGSNSTSCMMAFGHNSNGLCPMTMMHHPMTSHLHPQHQHHHHHPNSGSSSLFLPQPPTNNQDQNHNSSSGSSMILDDQHNTTTSNNNNTGCYFMESNDGSSSVKAKIMAHPHYHRLLAAYVNCQKVGAPPEVVARLEEACASAATMGPTRTGCIGEDPALDQFMEAYCEMLTKYEQELTKPFKEAMLFLQRVECQFKALTVSSPNPACGEGVDRNASSEEDVDVNNNFIDPLAEDRELKGQLLRKYSGYLGSLKQEFMKKRKKGKLPKEARQQLLDWWSRHYKWPYPSESQKLALAESTGLDQKQINNWFINQRKRHWKPSEDMQFVVMDAAHPHYYMDNVLGNPFPMDLSPTLL

>RcSBH1 (XM\_002518374.3)

MEGGSNSTSCMMAFGDNSNGLCPMMMMMPLMTSSHQHHHHHHHPNADLSSNTLFLPLPPTNNQDQNRNSSSGSSMILDDHNPNTNTGCYFMDNNDAAAASVKAKIMAHPHYHRLLAAYINCQKVGAPPEVVTRLEEACASAATMGQAGTSCIGEDPALDQFMEAYCEMLTKYEQELSKPFKEAMLFLQRVECQFKALTVASPNSALGEASDRNGSSEEEVDVNNNFIDPQAEDQELKGQLLRRYSGYLGSLKQEFMKKRKKGKLPKEARQQLLDWWSRHYKWPYPSESQKLALAESTGLDQKQINNWFINQRKRHWKPSEDMQFVVMDATHPHYYMDNVLGNPFPMDISPALL

>VvSBH1 (XM\_002271908.3)

MEGGSSSTACLMAFGDNSSNGLCPMMMMPLMTTSNPNAADANTLFLPLPPNHNHDLNRNSSRGSSLILENHNHNQHTTTTSTNNHHGSDPGCYFMETHGNNDGSTSSVKAKIMAHPHYHRLLAAYANCQKVGAPPEVVARLEEACASEAAMVRTGTSCIGEDPALDQFMEAYCEMLTKYEQELSKPFKEAMLFLSRVECQFKALTVSSSDSAGGEGLDRNGSSEEEVDVNNNFIDPQAEDRELKGQLLRKYSGYLSSLKQEFMKKRKKGKLPKEARQQLLDWWSRHYKWPYPSESQKLALAESTGLDQKQINNWFINQRKRHWKPSEDMQFVVMDATHPGHYYMDNVLGNPFPMDLSPTLL

>HbSBH1 (XM\_021813596.1)

MEGGSNSTSCMMAFGDNSDGLCPMMMMMPLMTSHHHPPPPPPPPNADSSSNTLFLPLPSTNNQHQNRNSGSGSSVLLDEHNHNSNSNTGCYFMDNNDDSTASVKAKIMAHPHYPRLLVAYINCQKVGAPPEVVTGLEEACASAAAMGPTGTSCIGEDPTLDQFMEAYCEMLTKYEQELLKPFKEAMLFLQRVECQFKALTVSSPNSACGEANERNGSSEEEVDVNNNFIDPQAEDQELKGQLLRRYSGYLGSLKQEFMKKRKKGKLPKEARQQLLDWWSRHYKWPYPSESQKLALAESTGLDQKQINNWFINQRKRHWKPSEDMQFVVMDATHSHYYMDNVLSNPFPMDISPTFL

>JrSBH1 (XM\_018952762.1)

MDSGSNGTSCMMSFGENSYGLCPVMMMPLMSSHQSHHHHNPNADANSLIPLPPTNNHDQNRNRNTDNSSAFFLHDQTNNSNTGCYFMESNTNMNNHESSSSAEKVKIMAHPHYQRLLAAYVNCQKVGAPPEVVARLEETCASAATMGHPGTGSIGEDPALDQFMEAYCEMLTKYEQELSKPYKEAVLFLQRIECQFKALTVSSSDSACGEAVDRSGSSEEEVDLNNNFIDPHAEDRELKGQLLRKYSGYLGSLKQEFMKKKKKGKLPKEARQQLLDWWSRHYKWPYPSESQKLALAESTGLDQKQINNWFINQRKRHWKPSEDMQFVVMDAAHQHYYMDNVLGNPFPMDISPTSLL

>SiKN1 (XM\_004981856.4)

MEEITHHFGVGASGGHGHVQHHLHHHHPWGSSLSAVVAPPPQTPPSAGLPLTLNTAATGNSGGAGGNPVLQLANGGGLLDACVKAKEPSSSSPYAGDVDAIKAKIISHPHYYSLLAAYLECQKVGAPPEVSARLTAMAQELEARQRTALGGLGAATEPELDQFMEAYHEMLVKFREELTRPLQEAMEFMRRVESQLNSLSISGRSLRNILSSGSSEEDQEGSGGETEIPEVDAHGVDQELKHHLLKKYSGYLSSLKQELSKKKKKGKLPKEARQQLLSWWDLHYKWPYPSETQKVALAESTGLDLKQINNWFINQRKRHWKPSEEMHHLMMDGYHTTGAFYMDGHFINDGGLYRLG

>ZmKN1 (NM\_001111966)

MEEITQHFGVGASSHGHGHGQHHHHHHHHHPWASSLSAVVAPLPPQPPSAGLPLTLNTVAATGNSGGSGNPVLQLANGGGLLDACVKAKEPSSSSPYAGDVEAIKAKIISHPHYYSLLTAYLECNKVGAPPEVSARLTEIAQEVEARQRTALGGLAAATEPELDQFMEAYHEMLVKFREELTRPLQEAMEFMRRVESQLNSLSISGRSLRNILSSGSSEEDQEGSGGETELPEVDAHGVDQELKHHLLKKYSGYLSSLKQELSKKKKKGKLPKEARQQLLSWWDQHYKWPYPSETQKVALAESTGLDLKQINNWFINQRKRHWKPSEEMHHLMMDGYHTTNAFYMDGHFINDGGLYRLG

>SbKN1 (XM\_002463907.2)

MEEITHHFGVGASSHSHGHGHGQHHHHHHPWASSLSAVVAPPPQQPPTAGLPLTLNTVAATGNSGASGNPVLQLANGGSLLDACVNVKAKGEPSSSSPYAGDLEAIKAKIISHPHYYSLLAAYLECKKVGAPPDVSARLTAMAQELEARQRTALSGLGAATEPELDQFMEAYHEMLVKFKEELTRPLQEAMEFMRRVESQLNSLSISGRSLRNILSSGSSEEDQEGSGGETELPEVDVHGVDQELKHHLLKKYSGYLSSLKQELSKKKKKGKLPKEARQQLLSWWDLHYKWPYPSETQKVALAESTGLDLKQINNWFINQRKRHWKPSEEMHHLMMDGYHTNTFFMDGHFINDGGLYRLG

>OsOSH1 (D16507.1)

MEEISHHFGVVGASGVHGGHQHQHHHHPWGSSLSAIVAPPPPPQLQQQQTQAGGMAHTPLTLNTAAAAVGNPVLQLANGSLLDACGKAKEASASASYAPDVEAIKAKIISHPHYSSLLAAYLDCQKVGAPPEVAARLTAVAQDLELRQRTALGVLGAATEPELDQFMEAYHEMLVKYREELTRPLQEAMEFLRRVETQLNTLSISGRSLRNILSSGSSEEDQEGSGGETELPEIDAHGVDQELKHHLLKKYSGYLSSLKQELSKKKKKGKLPKDARQQLLNWWELHYKWPYPSESQKVALAESTGLDLKQINNWFINQRKRHWKPSDEMQFVMMDGYHPTNAAAFYMDGHFINDGGLYRLG

>TaKNOX1L (AF224498.1)

MEEIGHHFGLGATAHGQHHSQLPWGSSPLSAVIAPPPQQQQQQQSAGYLAHSPLSLNTAPPSGSHGGGTGCSNPVLQLANGSLLEACAKAAKEPSSSSYAADVEAIKAKIISHPHYSSLLAAYLDCQKVGAPPEVLARLTAVAQDLELRQRTALGSFGTATEPELDQFMEAYHEMLVKYREELTRPLQEAMEFLRRVETQLNSLSISGRSLRNILSSGSSEEDQEGSGGETELPEIDAHGVDQELKHHLLKKYSGYLSSLKQELSKKKKKGKLPKDARQQLLSWWEMHYKWPYPSESQKVALAESTGLDLKQINNWFINQRKRHWKPSDEMQFVMMDAYHPPNAAFYMDGHFVNDSGLYRFG

>SlLET12 (NM\_001247016.2)

MEFQDHFSQEMVLHQQQQQQQQQQNAVLRSMLPESPHHDARKSPPTWLNTSLLRQQHSQFGNASSPSSAAAAAAVAGGNNFLHLQTSNSDSSNSNQWLSPTAAAGGGGNGGGGGHNDELSESMNFAKKMSQQHSGGGEENNNNNNNNNNNNNNEEENSWEREKCKADILNHPLYDQLLSAHVSCLRIATPVDQLPRIDAQLAQSQNVVAKYSVLGQGQPPLDDKDLDQFMTHYVLLLSSFKEQLQQHVRVHAMEAVMACWELEQSLQSLTGVAPGEGTGATMSDDDDDQADSDTNFLDGGFDGPDSMGFGPLVPTESERSLMERVRQELKHELKQGYKEKIVDIREEILRKRRAGKLPGDTTSVLKAWWQSHSKWPYPTEEDKARLVQETGLQLKQINNWFINQRKRNWHSNPSTSSSQKSKRKSAGEIKQ

>StLET12 (NM\_001318614.1)

MEFQDHFSQEMALHQQQQQQQQQQQQQNAVLRSMLPESPHHDARKSPPTWLNTSLLRQQHSQFANSSSPSSAAAAAARGGHFLHLQTSNSDSSNSNQWLSPTAAAGGGGGVTGGGGGHNDELSESMNFAKKMSQQHSGGGEENNNNNNEEENSWEREKCKADILNHPLYDQLLSAHVSCLRIATPVDQLPRIDAQLAQSQNVVAKYSVLGQGQPPLDDKDLDQFMTHYVLLLSSFKEQLQQHVRVHAMEAVMACWELEQSLQSLTGVAPGEGTGATMSDDDDDQADSDTNFLDGGFDGPDSMGFGPLVPTESERSLMERVRQELKHELKQGYKEKIVDIREEILRKRRAGKLPGDTTSVLKAWWQSHSKWPYPTEEDKARLVQETGLQLKQINNWFINQRKRNWHSNPSTSSSQKSKRKSAGEIKQ

>CcHKN1-3 (PHU11234.1)

MEFQDHFSQEIALHHHQQQQQQQQHPNVAVLRSMLPNESPDNNNNNNNNNKLQPTWLNTSLLRQQHFAAAAAAAASSPSGGGNNNNNNFLHLQTSNSDSSNSNQWLSPTGGELSKMNQAAAGGGGGGEDSNNINNSNTNNNNEEEHSWEREKCKADILNHPLYDQLLSAHVSCLRIATPVDQLPRIDAQLAQSQNVVAKYSVLGQGQPPLDDKDLDQFMTHYVLLLSSFKEQLQQHVRVHAMEAVMACWELEQSLQSLTGVAPGEGTGATMSDDDDDQADSDTNFLDGGFDGPDSMGFGPLVPTESERSLMERVRQELKHELKQGYKEKIFDIREEILRKRRAGKLPGDTTSVLKAWWQSHSKWPYPTEEDKARLVQETGLHLKQINNWFINQRKRNWHSNPSTSSSQKSKRKSAGEIKQ

>DcLET12 (XM\_017398413.1)

MAFNDHISQAMALQHYTDQQLTADVSPEVKTGPPTWLNNAILRQQNHHHYAGETNFLHLQTTNSDSSASNQWLSRPINIENDVDHNNSMMQISDDEKKFNHMSGLNDVADGGDWQSVKCKAEILSHPLYDELLSAHVSCLRIATPVDQLPRVDAQLAQSHQVVAKYSGLGDSINQPLDDKDLDHFMTHYVLLLSSFKEQLQQHVRVHAMEAVMACWELEQSLQSLTGIAPGEGTGSTMSDDDDDQAESDTNLFEGSLDGQDSMGFGPLVPTESERSLMERVRQELKHELKQGYKEKIVDIREEILRKRRAGKLPGDTTSLLKAWWQSHSKWPYPTEEDKARLVQETGLQLKQINNWFINQRKRNWHSNPSSSTVPKSKRKSNAGERNAEPFM

>AtKNOX5 (NP\_194932.1)

MSFNSSHLLPPQEDLPLRHFTDQSQQPPPQRHFSETPSLVTASFLNLPTTLTTADSDLAPPHRNGDNSVADTNPRWLSFHSEMQNTGEVRSEVIDGVNADGETILGVVGGEDWRSASYKAAILRHPMYEQLLAAHVACLRVATPVDQIPRIDAQLSQLHTVAAKYSTLGVVVDNKELDHFMSHYVVLLCSFKEQLQHHVCVHAMEAITACWEIEQSLQSLTGVSPSESNGKTMSDDEDDNQVESEVNMFDGSLDGSDCLMGFGPLVPTERERSLMERVKKELKHELKQGFKEKIVDIREEIMRKRRAGKLPGDTTSVLKEWWRTHSKWPYPTEEDKAKLVQETGLQLKQINNWFINQRKRNWNSNSSTSSTLTKNKRKRTGKS

>ZmKNOX6 (NM\_001176502.1)

MSFHYPDHGLSMDAAAAAAAAAAASSPNPSGFSPGVGGEREKAAIAAHPLYERLLEAHVACLRVATPVDQLPRIDAQIAARPPPLAAAAGAAAAGGPSGGEELDLFMTHYVLLLCSFKEQLQQHVRVHAMEAVMGCWELEQSLQSLTGASPGEGTGATMSDDEDNQVDSEANMFDGNDGSDGMGFGPLMLTEGERSLVERVRQELKNELKQGYKEKLVDIREEIMRKRRAGKLPGDTASVLKAWWQAHSKWPYPTEDDKARLVQETGLQLKQINNWFINQRKRNWHSNPTSSGEKTKKKR

**Supporting Information Figure S3.** Representation of the *LsWUSCHEL1-LIKE* (*LsWUS1L*) and *LsWUS2L* genes of *Lactuca sativa* ‘Romana’. A: Pairwise Sequence Alignment (EMBOSS Needle) of the coding sequences of the *LsWUS1L* and *LsWUS2L* genes; B: ClustalW2 alignment (MUSCLE) of the nucleotide sequences of the *LsWUS1L* and *LsWUS2L* genes. The start and stop codons are highlighted in green and magenta, respectively. The non-coding intronic regions are highlighted in yellow. Asterisks indicate identical nucleotides; C: schematic representation of the *LsWUS1L* and *LsWUS2L* genes. ATG and TAA or TGA represent the translation start and stop codons, respectively. The rectangles represent the three exons joined by introns depicted as lines.

A

*LsWUS1L* 1 ATGGAAACACAACAACAACCATCAGATATTCAAGATTTAGGGAACAAAAC 50

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*LsWUS2L* 1 ATGGAAACTCAACAACAAGAA---------CAAGATTTAGGAAACAAAAA 41

*LsWUS1L* 51 CAGCAGCACTTATGTATGCAGGCAAAGCAGCACGAGGTGGACACCCACAA 100

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*LsWUS2L* 42 CAATACCAGTTATTTATGTAGGCAAAGTAGTACAAGGTGGACACCCACAA 91

*LsWUS1L* 101 GTGATCAGATCAGAATTTTGAAAGAACTTTACTACAACAATGGAATCAGA 150

 |.||.|||||..||||..|.|||||||||||.|||||||||||||||||.

*LsWUS2L* 92 GCGACCAGATTCGAATACTTAAAGAACTTTATTACAACAATGGAATCAGG 141

*LsWUS1L* 151 TCACCAACGGCTGATCAGATCCAGAGAATCGCTGCCCAACTCAGACAGTA 200

 ||||||||.|||||.|||||.||||||||||||||.|...|.|||||.||

*LsWUS2L* 142 TCACCAACTGCTGACCAGATTCAGAGAATCGCTGCTCGTTTAAGACATTA 191

*LsWUS1L* 201 CGGAAAGATTGAAGGCAAGAATGTGTTTTATTGGTTTCAGAACCATAAAG 250

 .||.||.||.||||||||.|||||||||||||||||||||||||||||||

*LsWUS2L* 192 TGGGAAAATCGAAGGCAAAAATGTGTTTTATTGGTTTCAGAACCATAAAG 241

*LsWUS1L* 251 CTCGTGAAAGGCAGAAAAAACGATTCAC------TCCTGCTCCTCCACCA 294

 ||||||||||.|||||||||.||||||| .||||...|||||||.

*LsWUS2L* 242 CTCGTGAAAGACAGAAAAAAAGATTCACCCCGGTACCTGTAACTCCACCT 291

*LsWUS1L* 295 CCATCTCCGTTCTCTGATCATATCAACCACCATCTAC--CCACCGCC-CC 341

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*LsWUS2L* 292 CCACCTCC-TCCTC-------CTCCACCTCCTCCTCCTTCCACCGCCACC 333

*LsWUS1L* 342 CGCCATGCAAATTCAGT------CTCACCATCATCACTACCACCATCAAG 385

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*LsWUS2L* 334 CTCC-TCCCATCTCCGTTTTCCGATCACCGCCATCACCATCACCA-CATG 381

*LsWUS1L* 386 AA---------CCACCAC--------ATGTCTATAACCACCAACACAAAC 418

 .| ||||||| || ||||.|.|||.||||||||.|

*LsWUS2L* 382 CATGTTAATTCCCACCACCCACCTCAAT-TCTACAGCCAACAACACAAGC 430

*LsWUS1L* 419 TCTACACCACACATCACAT---------TGGGGTTGGTTCTTCTTCTTCA 459

 ||||||||||.|||||.|| .|.||..||||||||||

*LsWUS2L* 431 TCTACACCACTCATCAAATCTCACCTTCGGAGGGAGGTTCTTCTT----- 475

*LsWUS1L* 460 CAA--GGAGTGATGGCTGTTGGGTGTGGCTATGGATCTGTCGCCATGGAG 507

 ||| |||.|.|||.|||||||||.||||||||||||||||||||||||.

*LsWUS2L* 476 CAACGGGATTCATGCCTGTTGGGTATGGCTATGGATCTGTCGCCATGGAA 525

*LsWUS1L* 508 AAGAGTTTCAGGGAGTGTTCAATATCACCGCCGGGAG-----AGAGTAG- 551

 ||||||||||.|||||||||.|||||| |..|||| |||||.|

*LsWUS2L* 526 AAGAGTTTCAAGGAGTGTTCTATATCA---CAAGGAGAATCTAGAGTCGT 572

*LsWUS1L* 552 -GGCCACTGGATCAATTGGCCGGAATTTCGGATCAAGATCACGGGTTGG- 599

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*LsWUS2L* 573 CGG----AGGAACAA---GTCAGAATTTTG------GGTCATGGGTGGGA 609

*LsWUS1L* 600 TGTCGAATCATTTTCTTTCTTTGAAAATATCAAGCCAAAAAGATACGAG- 648

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*LsWUS2L* 610 AGT-GATTCGTATTCTTAC---GAGAAGATAAAGCC---------GGAGT 646

*LsWUS1L* 649 ATCTTAGAGAATCATCATCAAGAGGAAGA-----ACATCAAGAAGAAGGA 693

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*LsWUS2L* 647 AT------GAAGCA----CCGGAGGAAGACGACGACA-----GAGGAGGA 681

*LsWUS1L* 694 GATAGT--TCAACACAGATTGAAACGCTTCCTTTATTTCCAAT------- 734

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*LsWUS2L* 682 G--AGTTGTCAGCCCAGATGGAGACTCTTCCTCTCTTTCCAGTCAACGGT 729

*LsWUS1L* 735 -------TCAT-GGAGGCACCCACCATGATTTCTTCAGCATGAAGGCG-- 774

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*LsWUS2L* 730 GGCGCCACCATGGGAGGCAGCCATCATGATATCATCAACATGAAGGCGCC 779

*LsWUS1L* 775 ---------------GCAGATT--TGTCATCGGAGCATACCACGGGAGGT 807

 ||.| || ||||| |||||||..|..||||||

*LsWUS2L* 780 TGTGGCTGTGGAGTCGCCG-TTGATGTCA---GAGCATAGTAATGGAGGT 825

*LsWUS1L* 808 TACTACACCAGAGGAAACTGGTACCGCAAGGACGGCCGTGCTTCCCTTGA 857

 |.|||.|||.|||||||.||||..|||...||.|||||..||||.|||||

*LsWUS2L* 826 TGCTATACCGGAGGAAATTGGTTTCGCTCCGATGGCCGGACTTCACTTGA 875

*LsWUS1L* 858 GCTCAGTCTCAACTCGTATGGATATTATAACTAA 891

 .||.||.||||||||.||||||||||||||||.|

*LsWUS2L* 876 ACTTAGCCTCAACTCATATGGATATTATAACTGA 909

B

*LsWUS1L* ATGGAAACACAACAACAACCATCAGATATTCAAGATTTAGGGAACAAAACCAGCAGCACT

*LsWUS2L* ATGGAAACTCAACAACAAGAA---------CAAGATTTAGGAAACAAAAACAATACCAGT

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*LsWUS1L* TATGTATGCAGGCAAAGCAGCACGAGGTGGACACCCACAAGTGATCAGATCAGAATTTTG

*LsWUS2L* TATTTATGTAGGCAAAGTAGTACAAGGTGGACACCCACAAGCGACCAGATTCGAATACTT

 \*\*\* \*\*\*\* \*\*\*\*\*\*\*\* \*\* \*\* \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\* \*\* \*\*\*\*\* \*\*\*\* \*

*LsWUS1L* AAAGAACTTTACTACAACAATGGAATCAGATCACCAACGGCTGATCAGATCCAGAGAATC

*LsWUS2L* AAAGAACTTTATTACAACAATGGAATCAGGTCACCAACTGCTGACCAGATTCAGAGAATC

 \*\*\*\*\*\*\*\*\*\*\* \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\* \*\*\*\*\*\*\*\* \*\*\*\*\* \*\*\*\*\* \*\*\*\*\*\*\*\*\*

*LsWUS1L* GCTGCCCAACTCAGACAGTACGGAAAGATTGAAGGCAAGAATGTGTTTTATTGGTTTCAG

*LsWUS2L* GCTGCTCGTTTAAGACATTATGGGAAAATCGAAGGCAAAAATGTGTTTTATTGGTTTCAG

 \*\*\*\*\* \* \* \*\*\*\*\* \*\* \*\* \*\* \*\* \*\*\*\*\*\*\*\* \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

*LsWUS1L* AACCATAAAGCTCGTGAAAGGCAGAAAAAACGATTCACTCCTGCTCCTCCACCACCATCT

*LsWUS2L* AACCATAAAGCTCGTGAAAGACAGAAAAAAAGATTCACCCCGGTACCTGTAACTCCACCT

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*LsWUS1L* CCGTTCTCTGATCATATCAACCACCATCTAC--CCACCGCCCCCGCCATGCAAATTCAGT

*LsWUS2L* CCACCTCCTCCTC--CTCCACCTCCTCCTCCTTCCACCGCCACCCTCCTCCCATCTCCGT

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*LsWUS1L* C------TCACCATCATCACTACCACCA---------------TCAAGAACCACCACATG

*LsWUS2L* TTTCCGATCACCGCCATCACCATCACCACATGCATGTTAATTCCCACCACCCACCTCAAT

 \*\*\*\*\* \*\*\*\*\*\* \* \*\*\*\*\* \*\* \* \*\*\*\*\* \*\*

*LsWUS1L* TCTATAACCACCAACACAAACTCTACACCACACATCACATTGGTAATTAATTTATGATCA

*LsWUS2L* TCTACAGCCAACAACACAAGCTCTACACCACTCATCAAATC-----TCACCTTCGGGT--

 \*\*\*\* \* \*\*\* \*\*\*\*\*\*\*\* \*\*\*\*\*\*\*\*\*\*\* \*\*\*\*\* \*\* \* \* \*\* \* \*

*LsWUS1L* AAATAAATCCCGTTTCA----TATATCTGTATTATGCATAGTCATTTCCTAGTT--TTGA

*LsWUS2L* --ATTTGTCACATCCCACCATTGTGTTCATATT-TGTATAA--ATTTTGTATTTTGTTCG

 \*\* \*\* \* \* \*\* \* \* \* \*\*\*\* \*\* \*\*\* \*\*\*\* \*\* \*\* \*\*

*LsWUS1L* ATATTTTTCTCTTGTAAAGATTGTATTTT---TCTAATAATTTTTGGCTAAATTTTGAAT

*LsWUS2L* TTAATTTTCACCTTCACATAGCATATTTCATGTCGACTTATTT----ACATATTTCAGAT

 \*\* \*\*\*\*\* \* \* \* \* \* \*\*\*\*\* \*\* \* \* \*\*\*\* \* \*\*\*\* \*\*

*LsWUS1L* TTTGTGAGATCTTTCGCAGGGGTTGGTTCTTCTTCTTCACAAGGAGTGATGGCTGTTGGG

*LsWUS2L* TTTCT------TTGTACAGAGGGAGG---TTCTTCTTCAACGGGATTCATGCCTGTTGGG

 \*\*\* \* \*\* \*\*\* \*\* \*\* \*\*\*\*\*\*\*\*\*\* \*\*\* \* \*\*\* \*\*\*\*\*\*\*\*

*LsWUS1L* TGTGGCTATGGATCTGTCGCCATGGAGAAGAGTTTCAGGGTATATATTTATAAATATAAA

*LsWUS2L* TATGGCTATGGATCTGTCGCCATGGAAAAGAGTTTCAAGGTATGCCTACACAAACATATA

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*LsWUS1L* TATA---AACAAACATAC----TTTACACACACTTCATTTAATGTATAAGACGCTC----

*LsWUS2L* TGCATATAGCATGCATACACCATTGATCGAAACTT-ACGGAATGGAAAAAGAACTCATGT

 \* \* \* \*\* \*\*\*\*\* \*\* \* \* \*\*\*\* \* \*\*\*\* \* \*\* \*\*\*

*LsWUS1L* -------TCTAAATAAAATACTTTTGAATATTCTCGTCGAACATGTTCATTAGAATTTCA

*LsWUS2L* GTGATAATCTTAGACTAAAACTTTTGGGTATTTGTGTTTCTTATCTTCTTCACTAAATCT

 \*\*\* \* \*\* \*\*\*\*\*\*\* \*\*\*\* \*\* \*\* \*\*\* \* \* \* \*\*

*LsWUS1L* TGGGGAATGT-GAAAATTTATTCTGGGGTTAGGGTTTAAATGATTATTTTCGCTATTTGT

*LsWUS2L* TGAATATTATCGGAAAAGTATT---------GAACTCAAA------------CTCTCTAG

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*LsWUS1L* AAAAATGATAAAGATAATGCCACTTTTTAAACACCGAAAAAGTAAACAAATACTACTATT

*LsWUS2L* AACAACGGAAAAG---------CATTTGAAACGTATAAAAACTA---AAAT----TTCTT

 \*\* \*\* \* \*\*\*\* \* \*\*\* \*\*\*\* \*\*\*\*\* \*\* \*\*\*\* \* \*\*

*LsWUS1L* GACAAAAGGATATAACAAAACTGCCCTTTGTGTTGTATATATATAGGAGTGTTCAATATC

*LsWUS2L* GAAAAA----------------------TGTGCAATGTATGTATAGGAGTGTTCTATATC

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*LsWUS1L* ACCGCCGGGAGAGAGTAGGGCCACTGGATCAATTGGCCGGAATTTCGGATCAAGATCACG

*LsWUS2L* A---CAAGGAGAATCTAGAGTCGTCGGAGGAACAAGTCAGAATTTTG------GGTCATG

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*LsWUS1L* GGTTGGTGTCGAATCATTTTCTTTCTTTGAAAATATCAAGCCAAAAAGATACGAGATCTT

*LsWUS2L* GGTGGGAAGTGATTCGTATTCTTAC---GAGAAGATAAAGCC------------------

 \*\*\* \*\* \*\* \*\* \* \*\*\*\*\* \* \*\* \*\* \*\* \*\*\*\*\*

*LsWUS1L* AGAGAATCATCATCAAGAGGAAGAACATCAAGAAGAAGGAGATAGTTCAACACAGATTGA

*LsWUS2L* GGAGTATGAAGCACCGGAGGAAGACGACGACAGAGGAGGAGAGTTGTCAGCCCAGATGGA

 \*\*\* \*\* \* \* \*\*\*\*\*\*\*\* \* \* \*\* \*\*\*\*\*\* \*\*\* \* \*\*\*\*\* \*\*

*LsWUS1L* AACGCTTCCTTTATTTCCAATTCAT---------------GGAGGCACCCACCATGATTT

*LsWUS2L* GACTCTTCCTCTCTTTCCAGTCAACGGTGGCGCCACCATGGGAGGCAGCCATCATGATAT

 \*\* \*\*\*\*\*\* \* \*\*\*\*\*\* \* \* \*\*\*\*\*\*\* \*\*\* \*\*\*\*\*\* \*

*LsWUS1L* CTTCAGCATGAAGGCG---------GCAGATTTGTC------ATCGGAGCATACCACGGG

*LsWUS2L* CATCAACATGAAGGCGCCTGTGGCTGTGGAGTCGCCGTTGATGTCAGAGCATAGTAATGG

 \* \*\*\* \*\*\*\*\*\*\*\*\*\* \* \*\* \* \* \* \*\* \*\*\*\*\*\*\* \* \*\*

*LsWUS1L* AGGTTACTACACCAGAGGAAACTGGTACCGCAAGGACGGCCGTGCTTCCCTTGAGCTCAG

*LsWUS2L* AGGTTGCTATACCGGAGGAAATTGGTTTCGCTCCGATGGCCGGACTTCACTTGAACTTAG

 \*\*\*\*\* \*\*\* \*\*\* \*\*\*\*\*\*\* \*\*\*\* \*\*\* \*\* \*\*\*\*\* \*\*\*\* \*\*\*\*\* \*\* \*\*

*LsWUS1L* TCTCAACTCGTATGGATATTATAACTAA

*LsWUS2L* CCTCAACTCATATGGATATTATAACTGA

 \*\*\*\*\*\*\*\* \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\* \*

C

**ATG TAA**

148 bp 288 bp

439 bp 372 bp

*LsWUS1L* (1,327 bp)

80 bp

**ATG TGA**

460 bp 372 bp

126 bp 247 bp

*LsWUS2L* (1,282 bp)

77 bp

**Supporting Information Figure S4.** Representation of the *LsSHOOT MERISTEMLESS1-LIKE* gene (*LsSTM1L*) of *Lactuca sativa* ‘Romana’. A: nucleotide sequences of *LsSTM1L*. The start and stop codons are highlighted in green and magenta, respectively. The non-coding intronic regions are highlighted in yellow; B; schematic representation of the *LsSTM1L* gene. ATG and TAG represent the translation start and stop codons, respectively. The rectangles represent the four exons joined by introns depicted as lines.

A

ATGGAGGGTGATGCTGGAGGTGGAGGGGGTACTTCATCATGTTTGATGAGTTTTGGAGACAGCAACATCATTAATACTAGCAGTAATAGTAATAATAACAACGTTGGAGCACTATGTCTTCCTCCACCTCCTGTTTCATATAACAACAACAACAACAACCTAATTTTCGCCGATCAAGATCACCATCATCATCATCATCATCATCATCATAGTACCTGTGGGACTTCGACTTCTGCTATGATGCTTGAAAACAGCGCCATTAATATCAACGATGGAGGAGAGTTAGCCTTCATGAGCTCCTCCTCGTGTTCTTCTTCTGCTAAAGCAAAGATCATGTCTCATCCTCATTACCCTCGTCTCTTATCAGCTTATCTTAACTGTCAAAAGGTATATCTAGCTACTTCTTAACCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCGTGTGTTTGTTTGTGCGCGCTCGCCTATCAGCAAACACGGATCTATATAGTTCTCTATATATATAGTTCACAACTGAAACAAGTGGTGGAATTTTGTATCTTCAGGTTTCAGCATATCTTTTTATACGTGTTTACTGGTTTCTGCATTTGGTACAATCTAATAAGAAATCCTGAGTAAAAATCAAGTTGTGTTTTTTCAGGGGTTTGTGTGTTTGATTCAATAGCTATTGCTTGATTTAGTAGTGTAATAGAGACACTCTTAAAAGCAAACAACTTGTAAGAAGGAACCTAGAAGTGGGTTTTCTAGATTTGTGTGTTTCTGTGTGCGTGACATCATTTCTTTTAGTTCTTTCTTCATTTGGTAGCATAATATACTTTCTTGAAGAGAGAATAAAAAAAATGCAAGGCAAAACCCTTATTTAGACGCAGAAAGTTTATTCTTTCACTTTCGTAACGTATATTTGATATATGAAGCATGTGTTTGTGTTTAATTAAGAGTAATATGAAAGATTTTTTCTTTAATTAATTAATACAAAATACAGATAGGAGCACCGCCTGAAGTAGTGGAAAGACTAGAAGATGCTTGCAGAGCGTCGGTGGTGGCTGCGATGTCCAGTCGTTCCGGCTCCGCAGGTTGTGAGGCTGGTACCAGTGATGGCGGTGGTGGTGGAGGAATGAATATGATGATCATCGGACAAGATCCAGCACTTGATCAGTTCATGGAAGCTTACTGTGAGATGCTCATTAAATACGAGCAAGAACTCGCCAAACCCTTCAAAGAAGCCATGCTTTTTCTCTCAAGAGTTGAATCCCAGTTCAAGGCAATCTCCATTTCTACTTCAGATTCTGGTGCATCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTATAAATTTTATGATTCTGGGGAATTGTTTAATAAACTACAGATTACTCTTGATTTCATCATAAAACTTTTAAAAGAAGTTCTGTTTCCAGCACAAAAGCGCTTCTTTGAATGTTCTTCATGCTTAGGAACTAGATGCGATTCTGTTTTCTTAGAACAGTTTATTGTCTTCATTAATGCTATCTGGTTCTTAAATTATTTTTTACAATAGTAATCACCAAAAAGTACTATTAATATATATCATGTATAGATCTTAAATTTGTTTTCAAATTTTGTCCATAGCACAATTTCCAAGACTTGACAATAGTTTGCCTACAGTTTCATATCACATGAATTCTTGTGAAAGTTCCTTTTTCCAAAAGTTTATAATTTTCATGTATACAAACATGAAAAAATCTTTGATATATGAGGCTCATCTATGATCTATTTTATGACACTATACGGCTATGTCTGATCCATTTACGTGTATAATGTAAAAGATTTGTAGGGGAGGACCCTAAACGACGATGTATATGTGTGGAGGCCTATTGTGATGAATCTTTCACTCCATCCTGGAAGCTTTGCACTGTTTTTCTAGTAAAATAACCTGTACAAATTTCCAGTTTTTCACCCCTTGAATGTAGAGATATATATATATACAAGTACAATTATATGTTCCTTTTATTGGCAGCATCCTGTCCAATATTACATTGTTTTTTACCCTGGGAGATTTTTTTGTTGCAATTAACATAAGGTTGATTGTCGGCATTTCCACCCAAAGCACCCAAGGGAAAAAAATAACCCTATATCTTTGGTTCGGATGATTGCATTCCAACCATTTTGGTGGAAATTAAAGGTGCATCTACTGTCTGTTCATTGGCAATGTGATCAGATGCATGCATTTACGAGTAGTGTTACAGGTTGAATTGCGATCAAATAAAAAAAATAACTCATGTGCATATAACTGTGCTTTTATTTATGTGATGTATATACAACAAATAAGCTTTAGTCTTAAAATCGGATTCTTATAGCAGACCATATGGAAGAAAACAGTAGTCTATTTGTTCCATATGATCTAGATACATGTACCTTGTTGCATCTAAGAATTGTTCATAACTGCATTTTGTGCCTAAAATCTCCTTTAAAGTTGCTTTGTCTTTGATAATTTCTGTTTTAATTTGATGCAAACTTCAGCGGGTGGCGAAGTAGGTATGGATAAAAATGGATCATCCGAGGAAGAGGTGGATGTAAATAACAATCTCATAGATCCTCAAGCTGAAGATCAGGAACTGAAGGGTCAGCTGTTACGCAAGTATAGTGGTTATTTAGGTAGTCTCAAGCAAGAGTTCATGAAGAAGAGAAAGAAAGGAAAGTTGCCCAAAGAAGCACGTCAACAATTACTCGACTGGTGGACTAGGCATTACAAATGGCCATACCCTTCGGTAACTATAATACTGTTTTCTTGATTAAAACAAAATCTATCTGCCAAAAAAGAAAAACTTTACATTTCTCTTAACGTACTCTACTGTCTCTTGTGAACAGGAGGCTCAGAAGTTGGCACTGGCTGAGTCAACAGGACTAGACCAGAAGCAGATAAACAACTGGTTCATAAACCAAAGGAAGCGACATTGGAAGCCATCTGAGGATATGCAGTTTGTGGTAATGGATGCTGCTCATCCTCATCACTATTTCATGGAGAACATCCTCGGGAACCCTTATCCCATGGACGTTTCGTTGCTATAG

B

**ATG TAG**

387 bp 307 bp 248bp 201 bp

602 bp 1,226 bp

*LsSTM1L* (3,071 bp)

100 bp