

Supplementary materials

This document included the supplementary materials for:

A genome-wide analysis of the *ASYMMETRIC LEAVES2/LATERAL ORGAN BOUNDARIES (AS2/LOB)* gene family in barley (*Hordeum vulgare* L.)

Table S1 Amino acid sequence of the *ASL/LBD* genes in barley

>HvASL1/LBD1

MAGGSPCASCKLLRRRCKDCIFAPFFPADDPHKFAIVHKVFGASNVSKMLLELPVQQRG
DAVSSLVYEANARVRDPVYGCVGAIQFLQNVSQLQMLAVAQAEILCIQMQRDGCQS
QDDAGRNDGHSLAAMQMQMVVDDTAAAEAFMQNGGGGFPPQLMSSYGGAPASNVHH
YGQDHLKRESLWT

>HvASL2/LBD2

MASSASSFPGSVITMASSAAAAGAASSGAAGTGSPCAACKFLRRKCQPDVCFAPYFPPD
NPQKFVHVHRVFGASNVTKLLNELNPYQREDAVNSLAYEADMRLRDPVYGCVGVISVLQ
HQLRQLQQDLARARYELSKYQAAA AVASVGCNGTPAMADFIGNTVPNCTQNF
STAIGAGLGFHDQFAAVQMLARSYEGEGAVARLGVNNGSGGGYDFGYTSGMGPVSGLG
PLGGGPFLKHGTAGGDERHTAAQ

>HvASL3/LBD3

MSTASDWQQDHEVGGKIKSESTAEADRMMAAARRSSSLPAAGAGPASTPSFNTMTPCAA
CKLLRRRCAQECFPSPFFSPLPHKFAVHKVFGASNVSKMLLEVHESQRGDAANSLVYE
ANLRLRDPVYGCMGAILTLQQQVHALEAELAAVRAEILKHRYRPAAAAAA AVPNVPPSSH
ASQLLAAGGHRPAGAMGLPAPAVGPVASASSSTTVYAAASSSTDYSSITHENAPYFG

>HvASL4/LBD4

MESSGDTAPLHSSPTPTSPAMATGTAVVMSPCAACKILRRRCVDRCVLAPYFPPTDPHKF
ATAHRVFGASNIKLLQDLPEEQRADAVSSMVYEAAARARDPVYGSAGAICQLQRQVDGL
KAQLARAQAEAAARAHHAHLVALLCVEVATAAATPPQDAYCSGGGSQSQLAAPPVVG
SAPADALYVVDGSAAGGGGIMQAGHVGWADEPLWT

>HvASL21/LBD5

MRGSERAAVSTSTSGMSCNGCRVLRKGCNDACMLRPCLLWIEGADAQGHATIFAAKFFG
RAGLMSFLTAVPESQRPAVFQSLLYEAAGRITNPVGGAVGLLWAGSWHLCEAAVQTVLRG
GAIRPLPELAGGVPEGVGGSDLFASSRRRAVVCSTYSMAKRVTPRKTWAPAAASHHQE
PSCDLGLFLTPGSAAA AEGERRARRAGTPSMSSDGSVTTTAGAGADGDKEPELLNLFV

>HvASL20/LBD6

MRLSCNGCRVLRKGCSEDCSIRPCLQWIKSPEAQANATVFLAKFYGRAGLMNLINAGTDD
SLRPGIFRSLLYEACGRIVNPIYGSVGLLWSNNWQMCQAAVEAVLSGKPIVQVSSDAAA
DRTPLKAYDIRHVSTSPAADGRLHKVAKPGRTRFRKRASSASSHHNPSSDSNNKPKPQPRP
PTAEELDRQHRKEMEEGAFQRAPSHSSDSRHEDPVEPHSQQEASADTEAEAGSHVSQA
EQEQEQSTEPADHAEEVEKDDEELGLELTLGFAPVAARPAGCHLSVRTAAEPFVGLRFL

>HvASL22/LBD7

MRMSCNGCRVLRKGC GEGCTIRPCLEWIRSPDAQANATVFLAKFYGRAGLLNLLAAVPD
AGLRPPLFRSLLYEACGRMANPVYGSV GMLWSAQWEACQAAVEAVLKGRPIVRVSSDAP
LAPCDIRHVAKPDRPAAAGTLPGVSRAGRTRFKRASSSTAKTKSSFS DANKHDDGLDQAP
SHEESAGSHVEDGGMAVEQAREEELSEGTEVDAGSHVSQAEHSPAPPVAKDEEAHGDEIG
LELTLGIQTVAPRLVVRSPACFGASSSNAQSSHIGLLEL PVS

>HvASL5/LBD8

MASPSSTGNSIVSVVVA AATTPGAGAPCAACKFLRRKCLPGCVFAPYFPPEEPQKFANVHK
VFGASNVTKLLNELPPHQREDAVSSLAYEAEARVKDPVYGC VGAISVLQRQVHRLQKEL
DAAHTELLRYACGELGSIPTALPVVTAGVPSGRLSSAVMPCPGQLAGGMYSGGGGGGFRR
LGLVDAIVPQPPLSAGCYYNMRSNNNAGGSVAADVAPVQIPYASMANWAVNAISTITTT S
GSESIGMDHKEGGDSSM

>HvASL6/LBD9

MASSASSLPAPGGSVITLAASSAGGNGAGGVC GTGSPCAACKFLRRKCQPD CVFAPYFP
PDNPQKFVHVHRVFGASNVTKLLNELHPYQREDAVNSL AYEADMRLRDPVYGCVAVISIL
QRNLRQLQQDLARAKYELSKYQSAAGPNGSQAMA EFIGSAVPNGVASFINVGHSAALGS
VGGVTGFGQDQQA AVQMLSRSYEAAEPIARLGLNGSY EFGYSASAMTGAGSV PGLGML
GGSPFLKPGIAGSDERGGAGQ

>HvASL7/LBD10

MTSSSATSSSHLHITITNASSTITNTK SQSQHNHSSSVSPRSGGSGGGSGSGSGS GTTNQ
ACAACKYQRRKCNPDCLAPYFPADQQRFLNAHRLFGVSNILKTLRRLKPELCEAAMQ
TLIYQAEMRAMDPVGGCCRMIDLEHTSELLAAEL AALNQHLDLRQAASGVAGGDVMD
GPCADLEVTSSNHQQEQLLLHADQDQVVDALYVAQEGADPVIQNGADHDDNRQPQYHG
GQQQQQLYDYFYEATGAGGDEAGRKPGGSGVDINVDVMQHFDYDSSCEVDDHHKVD
QLEPMISSSLDEHYPIGQKEYEMKVASFVDVLDVRPEMQAVDGNADIGVKEELQEEEDPK
NNIELSKATHMAESSDCRLGLGF

>HvASL8/LBD11

MPCLLSTLSFLAIPNFTLLYHVPVRLSSPRSQLFLCHSPSPKRGEHASMSTERERLDEIGKKI
KREPDPAAIAGVVAVSPTTEHHVHRLGPGIGGAVNIATPCAACKLLRRRCAHECPFAPYF
SPHEPHKFAAVHKVFGASNVS KM LLEVPEAERADAASSLVYEANLRLRDPVYGC MGAIS
MLQQQVNALEAELEAVRAEIFKHRYRQAGVGVGVGAANLIVDDGAAAAGGFMPSTTL
VHTADVVSVAEAGQEVATLPATPTATAYAAGQPSSADYSSLNTSEHDAYFG

>HvASL12/LBD12

MIQFTGCKEQEYTTNIDQAPEAMTGFSSPCGACKFLRRKCVSGCVFAPHFCHEQGAAHFA
AIHKVFGASNASKLLMSLPATDRREAAVTISYEAQARLHDPVYGCVAHIFALQQQVVTLQ
AQLESLKTGAPQLVSSLEEDSIKAKIMAYEKGEARMPQLGESVKIESES YFGDDVMACTS
MPYSQGYSSHIYTTDYTDSFNDDSINRSTMFVPDMQEYLQENGY Y

>HvASL11/LBD13

MKEVVAAGGGGGVSPCAACKLLRRRCSPGCVFAPYFPAGEPHRFASVHKVFGASNISKLL
QEIPAEHRGDAVSSLVYEANARVRDPIYGCVAITSLQRQVESLQTQLALAQAE MVRLRM
ANAYGAARRNGGGSSASGSPSSISSPTKATPDHHHMAAVNRPGVMELELECSR FWSF

>HvASL23/LBD14

MSCNGCRVLRKGCSDACVLRPSIEWIDGAQPQANATV FVAKFFGRAGLVA SLAAVPLHHR
PALFRSLLYEACGR TINPVSGAIGLMWTSNWDLCQAAADAVLRGDSLRSLSAVPAAFTDR
DMAGLYGSGVTNTGSSSSLHSSPENSTSAPAGKR SKNYCGAAAGQQVKLP GPVLPSCELD

LCLTPLSSPLAGRRGGASDEYSTTTCCEEASGDAAEAGAPALLNLFN

>HvASL18/LBD15

MTSVQNIETLFQVGDGRWTKDKVAQALGAANNSPNRAATLLSSAPGQANVPKIASLIISES
KVPEAPDFPGPSSLSSPEQPILKKQKAKSTGVQIPSTALLASSDVSDSSSPSSKQVDGKKP
KKVNTCARCRRQKQGCKDCVFADVFTTETQSDYDKASELFGIKSMQNRLSLVQPQDRLQ
VREAIMWRVAAWANDPLHGPLGRFRNLEREAAAAAASAAAARLAACSFLTTKKHSTIVL
CHLLLVHIKSQLAKK

>HvASL9/LBD16

MDYSNEATNTAAAQPYGRSMSPSRVSSCSPPPVFPLMGNAPSSPPTIVLSPCAACKVLR
RCADGCMLAPYFPPTPEAKFTTAHRVFGASNIKLLQDLPESSRADAVSSMVYEAEARLRD
PVYGCAGAVCRLQKEANELKVDLARAQADLLSIQTQHANLLALVCVEFAANHRGDQQH
QHQPPLADQLNSIGGSGGGALYQQLYDSLDSASWEEARQLWT

>HvASL19/LBD17

MSSNSPCAACKLLRRKCTQGCVFAPYFPPDQPAKFANVHKVFGASNVSKLLNELPVVQR
EDAVNSLAYEAEARLRDPVYGCVAYISVLQLKIKQVREEIANARKELSGYIGQAAYAPIVP
VQHPHAAAAAAQYAAMGLVQPHPHQHQQMAMQQQPYHQQIAEAQHLLAAVEVA
RSGGQGHQHHQHXXXQHQQHEMMMRQTYGNVHGAAAGPTIAVDPP
QGAAYDGTAPFLIQQQPSPSALTYRMEEPSPPQSSGSHVDMRAPQQHHQHTDGSDE
GSGGAPPS

>HvASL13/LBD18

MAGAGVTTTGGSPCGACKFLRRRCAAECVFAPYFCAEDGASQFAAIHKVFGASNAKLLQ
QVAPGDRSEAAATVTYEAQARLRDPVYGCVAHIFALQQQVAALQAQVAHARTQAQLGAA
ATAMHPLLQQAWQAAAAEHDDHSITSTQSSSGCYSGAHQRSDDGSSLHGAEMYACGY
GEQEEGSY

>HvASL14/LBD19

MALGRPLHPNHPQQQQRSPQHRRQQRSGRPPSDPAVITDRLMSMTGLGSPCGACKFLRR
KCARGCVFAPYFCHEQGAHFHAAIHKVFGASNVSKLLAHLPISDRAEA AVTVSYEAQARL
RDPVYGCVAHIFALQQQVMTLQAQLASLKAHAPPAPQGMQQHQDDVKGYVGGGAADQ
YGHGAYQWYNGNGAAAQQCAYGGNGGAVAGHDSITALLSGSAASDYMMYHALEQSA
SDDDRHAAAAFEAADQSSFGTEESGWRSSSGYQDCEDLQSVAYAYLNRS

>HvASL24/LBD20

MRASCNGCRVLRKGCTDDCTIRPCLAWIRGADAQANATVFLAKFYGRAGLLNLLAAGTD
AALRPALFRSLLYEACGRVANPVYGATGLFCMGRWEACQDAVQAVFEGRRIAVQSEAVRH
PGLVAAFDVRHVPKPMVVPAPPGLGVSRAGRTMFKRASSSSTAKPTISSGAKHGDLDR
PSHEEPAGSHDHVVEDGGMAVAVAVAAKQVRGESSADTGAEAHSHVSQAEQNLMPQLA
QGGDDEVGLELTLGFGPATRLLRSPPARPDAARRSSAECGHIGLLELPLV

>HvASL15/LBD21

MSSGVGSSTLGGCGGPGSGSGGGGGGLGGGGGGPCGACKFLRRKCVSECFAPYFDSEQ
GAAHFVAHVHKVFGASNVSKLLQIPAHKRLDAVVTICYEAQARLRDPVYGCVAHIFALQQ
QVNNLQAEITYLQTHLATLELPSPLPAAPQLPMAMPAQFSISDLPTTNIPTTIDLSALFEP
PAQPQWALQQHHQHQLRQPSYGAMAHRGGSSMAEGSAGSGGDLQTLARELLDRHGRS
GVKPELQPPPPHPR

>HvASL10/LBD22

MAGAQTGSSATPCASCKLLRRRCARDCVFAPYFPPEDPHRFATVHRVFGASNVSKMLQEL

PAAQRADAVSSLVYEATARMRDPVYGCAGAISYLQQQVSQLQVQLAVAQAEIIQRINHPS
SAAFHLQELQQRQAQQQQMQMDDDDKAYSSLVMQNDLMSTLLLQEACLKKE
>HvASL16/LBD23

MAAAPGGGGGGVAGVAGSPCGACKFLRRRCVAECVFAPYFSSEQGAARFAAIHKVFGA
SNAKLLAHLPLADRCEAVVTITYEAQSRLRDPVYGCVAQIFALQQQVAILQAQLMQARA
QIACGVQSTTSPVSVSHHQQQPWSQDTSIAALLRQQENVSSFAAGGALLPELMSGDVSML
QQHCGGKVEGGGGGAGDLQYLAQAMMQSSNYSL
>HvASL17/LBD24

MSGSTSVGVGVGAMLSGSSGGPCGACKFLRRKCTDDCIFAPYFSDQGV EHF TAVHKVF
GASNVSKLLNQTPPKRLDAAITICYEAKARLRDPAYGCVADIFALQQQVENLQAEVGF
HARLRTLQQTSPPPFSPPYMPMTTEFSISEMASLSNVPNTIDISSLFDPSMQWAFQQQEH
HQRHQPCGQTEEGSGGIGNTNSNSGDLQALARELLDRRSTRSTP