**Supplementary Table S1. Protein sequences used in the phylogenetic relationship analysis.**

| Species | Gene name | Locus ID[a] | Transcript name[a] |
|---|---|---|---|
| ***Arabidopsis thaliana*** | *AtLAX3* | AT1G77690 | AT1G77690.1 |
| | *AtLAX2* | AT2G21050 | AT2G21050.1 |
| | *AtAUX1* | AT2G38120 | AT2G38120.1 |
| | *AtLAX1* | AT5G01240 | AT5G01240.1 |
| ***Glycine max*** | *GmLAX1* | Glyma.01G114000 | Glyma.01G114000.1 |
| | *GmLAX2* | Glyma.02G255800 | Glyma.02G255800.1 |
| | *GmLAX3* | Glyma.03G063600 | Glyma.03G063600.1 |
| | *GmLAX4* | Glyma.03G063900 | Glyma.03G063900.1 |
| | *GmLAX5* | Glyma.04G004800 | Glyma.04G004800.1 |
| | *GmLAX6* | Glyma.04G252300 | Glyma.04G252300.1 |
| | *GmLAX7* | Glyma.06G004500 | Glyma.06G004500.1 |
| | *GmLAX8* | Glyma.06G110200 | Glyma.06G110200.1 |
| | *GmLAX9* | Glyma.07G147000 | Glyma.07G147000.1 |
| | *GmLAX10* | Glyma.11G106000 | Glyma.11G106000.1 |
| | *GmLAX11* | Glyma.11G228300 | Glyma.11G228300.1 |
| | *GmLAX12* | Glyma.12G030900 | Glyma.12G030900.1 |
| | *GmLAX13* | Glyma.14G060700 | Glyma.14G060700.1 |
| | *GmLAX14* | Glyma.18G029000 | Glyma.18G029000.1 |
| | *GmLAX15* | Glyma.18G198400 | Glyma.18G198400.1 |
| ***Medicago truncatula*** | *MtLAX1* | Medtr5g082220 | Medtr5g082220.1 |
| | *MtLAX2* | Medtr7g067450 | Medtr7g067450.1 |
| | *MtLAX3* | Medtr3g072870 | Medtr3g072870.1 |
| | *MtLAX4* | Medtr4g415390 | Medtr4g415390.1 |
| | *MtLAX5* | Medtr4g073770 | Medtr4g073770.1 |
| ***Phaseolus vulgaris*** | *PvLAX1* | Phvul.001G241500 | Phvul.001G241500.1 |
| | *PvLAX2* | Phvul.008G106300 | Phvul.008G106300.1 |
| | *PvLAX3* | Phvul.008G225300 | Phvul.008G225300.1 |
| | *PvLAX4* | Phvul.009G120700 | Phvul.009G120700.1 |
| | *PvLAX5* | Phvul.009G122200 | Phvul.009G122200.1 |
| | *PvLAX6* | Phvul.010G003600 | Phvul.010G003600.1 |
| | *PvLAX7* | Phvul.011G034000 | Phvul.011G034000.1 |

|  |  |  |  |
|---|---|---|---|
| ***Lotus japonicus*** | *LjLAX1* | chr3.CM011260.r2.m | chr3.CM0112.160.r2.m |
|  | *LjLAX2* | LjSGA_009163 | LjSGA_009163.1 |
| ***Oryza sativa*** | *OsLAX1* | LOC_Os01g63770 | LOC_Os01g63770.1 |
|  | *OsLAX2* | LOC_Os03g14080 | LOC_Os03g14080.1 |
|  | *OsLAX3* | LOC_Os05g37470 | LOC_Os05g37470.1 |
|  | *OsLAX4* | LOC_Os10g05690 | LOC_Os10g05690.1 |
|  | *OsLAX5* | LOC_Os11g06820 | LOC_Os11g06820.1 |
| ***Sorghum bicolor*** | *SbLAX1* | Sb01g026240 | Sb01g026240.1 |
|  | *SbLAX2* | Sb01g041270 | Sb01g041270.1 |
|  | *SbLAX3* | Sb03g040320 | Sb03g040320.1 |
|  | *SbLAX4* | Sb05g004250 | Sb05g004250.1 |
|  | *SbLAX5* | Sb09g021990 | Sb09g021990.1 |
| ***Zea mays*** | *ZmLAX1* | GRMZM2G149481 | GRMZM2G149481_T01 |
|  | *ZmLAX2* | GRMZM2G129413 | GRMZM2G129413_T01 |
|  | *ZmLAX3* | GRMZM2G127949 | GRMZM2G127949_T01 |
|  | *ZmLAX4* | GRMZM2G045057 | GRMZM2G045057_T01 |
|  | *ZmLAX5* | GRMZM2G067022 | GRMZM2G067022_T02 |

[a], protein sequences from *Lotus japonicus* were retrieved from http://www.kazusa.or.jp/lotus/, and all others were from phytozome 10.3 (http://phytozome.jgi.doe.gov/pz/portal.html).

**Supplementary Table S2. Primers used in qPCR analyses.**

| Gene name | Locus ID | Forward primer (5'-3') | Reverse primer (5'-3') |
|---|---|---|---|
| *GmLAX1* | Glyma.01G114000 | TGTGCCACCACTGTTTTCAT | GTGTGCGTGACATTTTCCAC |
| *GmLAX2* | Glyma.02G255800 | CCGACAGAATGCTGTTGAGA | CCAAATCCAAATCCAACCAC |
| *GmLAX3* | Glyma.03G063600 | CTGGCAGGGTTTTGCATTAT | GCCTGTGCATTTCATAGCAA |
| *GmLAX4* | Glyma.03G063900 | CTCCTTTCTTCATGCCAAGC | GTTCAGGGCATTGGTAGCAT |
| *GmLAX5* | Glyma.04G004800 | TTGTGGTGGTGTGGGTTCTA | GCGGTTGAGTTGATGGAAGT |
| *GmLAX6* | Glyma.04G252300 | GCCAGCCCCTATACGAACTT | GCTACGTAGGGGGAGGAAAG |
| *GmLAX7* | Glyma.06G004500 | AAAATGTTACCAGTGCCCCA | CTAGCTAGCGATGAATGGGC |
| *GmLAX8* | Glyma.06G110200 | TGTCAGCTAAAGGTGCGATG | AGAGGGAGAACGCAAATCAA |
| *GmLAX9* | Glyma.07G147000 | GCCACAGCTCATATGCTCAC | ACCAAAACCCACACCACAAT |
| *GmLAX10* | Glyma.11G106000 | GTGTTACCAATGCCCTCCAC | TAGGGTGCGGCTTCATAGAT |
| *GmLAX11* | Glyma.11G228300 | GCGAGGTTACCTGTGGTGAT | AGCAGGGATGATGTAAACGG |
| *GmLAX12* | Glyma.12G030900 | GTGTTACCAATGCCCTCCAC | CCTAGGGTGTGGCTTCATATA |
| *GmLAX13* | Glyma.14G060700 | AGGGACACATCAGCATCTCC | ACCAAAATGATTCGAAAGCG |
| *GmLAX14* | Glyma.18G029000 | ATTTGGGTTTGCTTGTACGC | ATCACCACAGGTAACCTCGC |
| *GmLAX15* | Glyma.18G198400 | ATTGTGGTGTGGGTTTTGGT | GGCTTGCATTGGTAGCATTT |
| *GmUBI3* | Glyma.20g141600 | GTGTAATGTTGGATGTGTTCCC | ACACAATTGAGTTCAACACAAACCG |

**Supplementary Table S3.** ***GmLAX*****s gene information.**

| Gene Name | Locus ID[a] | Protein[b] | | | Chromosome[a] | Location (Mb)[a] | Strand direction[a] | Transmembrane helices[c] | Subcelluar localization[d] |
|---|---|---|---|---|---|---|---|---|---|
| | | length | MW (kDa) | PI | | | | | |
| *GmLAX1* | Glyma.01G114000 | 483 | 54.5 | 8.63 | Chr01 | 39.29 | - | 10 | plas |
| *GmLAX2* | Glyma.02G255800 | 485 | 54.7 | 8.33 | Chr02 | 44.27 | + | 10 | cyto |
| *GmLAX3* | Glyma.03G063600 | 483 | 54.6 | 8.33 | Chr03 | 10.13 | + | 10 | plas |
| *GmLAX4* | Glyma.03G063900 | 506 | 57.1 | 7.46 | Chr03 | 10.26 | - | 10 | plas |
| *GmLAX5* | Glyma.04G004800 | 476 | 53.8 | 9.02 | Chr04 | 0.41 | + | 10 | plas |
| *GmLAX6* | Glyma.04G252300 | 465 | 52.5 | 8.66 | Chr04 | 51.91 | - | 10 | cyto |
| *GmLAX7* | Glyma.06G004500 | 481 | 54.3 | 8.75 | Chr06 | 0.40 | + | 10 | plas |
| *GmLAX8* | Glyma.06G110200 | 465 | 52.6 | 8.65 | Chr06 | 8.91 | + | 10 | cyto |
| *GmLAX9* | Glyma.07G147000 | 494 | 55.9 | 7.92 | Chr07 | 17.71 | + | 10 | plas |
| *GmLAX10* | Glyma.11G106000 | 488 | 55.1 | 9.01 | Chr11 | 8.06 | - | 10 | plas |
| *GmLAX11* | Glyma.11G228300 | 479 | 54.2 | 8.24 | Chr11 | 32.37 | + | 10 | plas |
| *GmLAX12* | Glyma.12G030900 | 488 | 55.1 | 9.01 | Chr12 | 2.31 | - | 10 | plas |
| *GmLAX13* | Glyma.14G060700 | 482 | 54.3 | 8.28 | Chr14 | 4.92 | - | 10 | plas/cyto |
| *GmLAX14* | Glyma.18G029000 | 479 | 54.3 | 8.38 | Chr18 | 2.19 | - | 10 | plas |
| *GmLAX15* | Glyma.18G198400 | 494 | 55.9 | 7.92 | Chr18 | 47.66 | + | 10 | plas |

[a], the *GmLAX*s gene information was retrieved from the *Glycine max Wm82.a2.v1* genome annotation (phytozome 10.3: http://phytozome.jgi.doe.gov/pz/portal.html)

[b], protein profiles are calculated using the Lasergene (v7.1) software.

[c], transmembrane helices were predicted using the TMHHM Server v2.0 (http://www.cbs.dtu.dk/services/TMHMM/).

[d], subcellular localization was predicted by WoLF PSORT (http://www.genscript.com/psort/wolf_psort.html).

**Supplementary Table S4. Percent ORF nucleotide (bottom-left) and amino acid (up-right, bold) identities of *GmLAX*s.** Colored cells highlight data of duplicated gene paires.

| | ***GmLAX1*** | ***GmLAX2*** | ***GmLAX3*** | ***GmLAX4*** | ***GmLAX5*** | ***GmLAX6*** | ***GmLAX7*** | ***GmLAX8*** | ***GmLAX9*** | ***GmLAX10*** | ***GmLAX11*** | ***GmLAX12*** | ***GmLAX13*** | ***GmLAX14*** | ***GmLAX15*** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ***GmLAX1*** | *** | **83.5** | **97.1** | **87.6** | **78.3** | **79.3** | **77.9** | **79.5** | **90.9** | **79.2** | **84** | **79.2** | **85.7** | **83.8** | **91.1** |
| ***GmLAX2*** | 75.4 | *** | **84.2** | **78.3** | **74.6** | **77.8** | **74.5** | **77.6** | **82** | **75.7** | **87.7** | **75.7** | **95.9** | **87.5** | **82.9** |
| ***GmLAX3*** | 96.6 | 75.7 | *** | **88.4** | **78.1** | **79.7** | **77.7** | **80** | **91.7** | **79** | **84.8** | **79** | **86.8** | **84.6** | **91.9** |
| ***GmLAX4*** | 90.5 | 74.7 | 90.8 | *** | **74.5** | **76.1** | **74.7** | **76.3** | **86** | **76** | **80.7** | **75.8** | **80.4** | **80.1** | **86.2** |
| ***GmLAX5*** | 71 | 72.6 | 71.3 | 70.1 | *** | **84.5** | **97.1** | **84.5** | **78.1** | **89.7** | **75.3** | **90.5** | **75.7** | **75.3** | **78.1** |
| ***GmLAX6*** | 72.1 | 71.6 | 72 | 71.6 | 75.2 | *** | **84.1** | **98.3** | **77.4** | **85.1** | **78.3** | **85.3** | **79.2** | **79** | **77.4** |
| ***GmLAX7*** | 70.8 | 71.9 | 71.1 | 69.6 | 96.6 | 75.1 | *** | **84.1** | **77.3** | **90** | **75.1** | **91.1** | **75.6** | **74.9** | **77.3** |
| ***GmLAX8*** | 71.9 | 71.7 | 72.1 | 71.4 | 74.5 | 97.6 | 74.5 | *** | **77.2** | **85.1** | **77.9** | **85.3** | **79** | **78.5** | **77.2** |
| ***GmLAX9*** | 86.6 | 76.1 | 87.3 | 84.3 | 70.8 | 71.6 | 70 | 71.1 | *** | **78.8** | **82.7** | **78.5** | **84** | **82.7** | **99** |
| ***GmLAX10*** | 71.6 | 71.4 | 71.9 | 69.5 | 87.8 | 75.2 | 87.8 | 75 | 70.8 | *** | **76.4** | **98.6** | **76.4** | **76.6** | **78.8** |
| ***GmLAX11*** | 76 | 85.1 | 76.6 | 74.8 | 72.2 | 71.4 | 71.6 | 71.1 | 76.7 | 71.1 | *** | **76.4** | **90.2** | **97.3** | **83.1** |
| ***GmLAX12*** | 71.3 | 71.9 | 71.4 | 69.1 | 88.5 | 74.8 | 88.7 | 74.8 | 70.3 | 97.5 | 71.4 | *** | **76.9** | **76.6** | **78.5** |
| ***GmLAX13*** | 76.5 | 96.4 | 76.7 | 75.4 | 72.3 | 71.4 | 71.5 | 71.4 | 76.8 | 71.4 | 86.1 | 71.9 | *** | **90.2** | **84.4** |
| ***GmLAX14*** | 75.4 | 85.1 | 76 | 74.4 | 72.1 | 71.4 | 71.6 | 71.2 | 76.5 | 70.9 | 97.6 | 71.4 | 86.2 | *** | **83.1** |
| ***GmLAX15*** | 86.6 | 75.9 | 87.1 | 84.6 | 70.9 | 71.7 | 70.3 | 71.2 | 98 | 70.8 | 76.5 | 70.3 | 76.3 | 76.5 | *** |