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AtIAA16.....NHGGEMAGKNG...KRGFSET.VDLKLNLSSTAMDSVSK.....VDLEN.....MKEKV
AtIAA14.....GTETVESPAKSGVGNKRGFSET.VDLKLNLS...NKQGH.....VDLNTNG.....APKEKTFLK
AtIAA17.....G.DTV.APVT...GNKRGFSET.VDLKLNLNNEPANKEGS.....TTHDVVTF.....DSKEKSACPK
AtIAA7.....GAEAVESPAKSAVGSKRGFSET.VDLMLNLS...NKEGS.....VDLKNVSA.....VPKEKT.LK
BrIAA.....GAEANENLEKSAVGNKRGFSET.VDLMLNLS...NKEGA.....VDLNNVAS.....ASKDKTLLK
VvIAA.....GSEGSE.....VVRKRGFSET.VDLKLNLSG...KEAG.....VDDNKVKSL...QKEK...SKSLPCGN
GmIAA14.....GGSEVETPRT...AGKRGFSET.VDLKLNLS...KEDL.....NENLKNV.....SKEKTLK
MpIAA14.....GGTTTVAEPETAKTGKRGFSET.IDLKLNLS...KE.....DLNDNVKN...SKDKNNFLSCTK
CrIAA1.....GGGGGTGEITDQSMRTGKRGFSET.VDLKLNLS...DQSSVDLNEKVKN..PPSKE.TNSK
PtIAA.....GASNGNDGEAAKGNKRGFSET.VDLKLNLS...KE.TGKDG...SDQEKVV.....MKEKTVAPRPN
RcIAA16.....GSNV.NDSEFAKVNKRGFSET.VDLKLNLS...KEPSGKDVIVGEE.....TMKEKATVPSSSN
NtIAA28.....AINGNEGEMTSKNNKRVFSET.VDLKLNLS...KDS.....TVDN.....QVDNIKEKKNIAPT
StIAA3.....ANGNEVESTNKNNGKRVFSET.VDLKLNLS...KDSTLMDNINQVDN.....MKEKNNIVVPSN
SaIAA.....AGDQKSSG...SYGKRGFAET.VDLKLNLS...KEI.....GDLDRGGLERKDLCKEKNLMPSPTESAR
InIAA1.....GG.GGNDGEAVKSNKRAFSDT.VDLKLNLS...KES.....NVDQVEN.....LKDNNNNVVTSPS
PmIAA7.....GAAAAGEKTNNNNYKRGYEQT.VDLKLNLS...KDL....PNQTDLAE.....NKKND
LlIAA.....GGET...EMAKSLGKRGFSET.IDLKLNLS...LETTTVDGKKNPVPVAN
MjIAA1.....LGFSGKTSAGVAGNKRGFSETL.VDLKLNLS...LNKSSPPSDDLQDTATSDLIMMKNMKNKSGGGVIKDVNDNTKVNANNA
OsIAA11.....AGEL...AAR...SSGKRGFAET.IDLKLNLS...QPAAPAAVSGEEGAQEDKEDADAAAAAADEKMS.....MKRSASQSSVVTAE
SbIAA.....GGGE..VVGEGRSSVSSGKRGFAET.IDLKLNLS...LEPATPAAVLKAAEADEHQDGVAAAKEDAGCVAAAEAAVGGKMKRSPSQSSVVTAAAVQA
ZmIAA30..GGGGEPALGGEGRSSSSASGKRGFAET.IDLKLNLS...LEPA..AVVEAEEDH..GVA.....VALEKEEEAGMKRSPSQSSV.AAAVLA

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**Supplemental Figure S6.** Amino acid sequences between conserved domains I and II for IAA proteins that contain a second LxLxL motif.

Amino acid sequence comparison of Arabidopsis (*At*) *IAA7* (AT3G23050), *IAA14* (AT4G14550), *IAA16* (AT3G04730), and *IAA17* (AT1G04250) with those from other plant species (*BrIAA*, *Brassica rapa* BAF81520; *GmIAA14*, *Glycine max* FJ534642; *PtIAA*, *Populus trichocarpa* XP\_002328494; *InIAA*, *Ipomoea nil* BAG55005; *MpIAA14*, *Malus prunifolia* BAH15071; *VvIAA*, *Vitis vinifera* XP\_002281771; *RcIAA16*, *Ricinus communis* XP\_002531288; *NtIAA28*, *Nicotiana tabacum* AF123508\_1; *CrIAA1*, *Catharanthus roseus* ADJ68049; *StIAA3*, *Solanum tuberosum* ACV31209; *SaIAA*, *Striga asiatica* ABD98055; *LlIAA*, *Lycoris longituba* ADG58023; *PmIAA7*, *Plantago major* CAH59413; *MjIAA1*, *Mirabilis jalapa* ACL81167; *OsIAA11*, *Oryza sativa* NM\_001057248; *ZmIAA30*, *Zea mays* NP\_001150626; *SbIAA*, *Sorghum bicolor* XP\_002443496). GenBank accession numbers are given for each example of the IAA proteins related to Arabidopsis *IAA7*, *IAA14*, *IAA16*, and *IAA17*. The conserved DLxLxL motif is boxed in yellow. Identical amino acids in the alignments that are found in four or more of the IAA proteins listed are boxed in grey. The sequences were aligned with Clustal W method and adjusted manually.