Figure S1. The double mutant *hae hsl2* is totally deficient in abscission. **(a)** Inflorescence of wild type Arabidopsis plant. Red arrow points to first siliques with absciced floral organs. **(b)** *hae hsl2* double mutant. Orange and yellow arrows indicate silique positions 16 and 20, respectively, counting from the top of the inflorescense. **(c)** Attached floral organs of the *hae hsl2* double mutant are turgid at least until position 16.

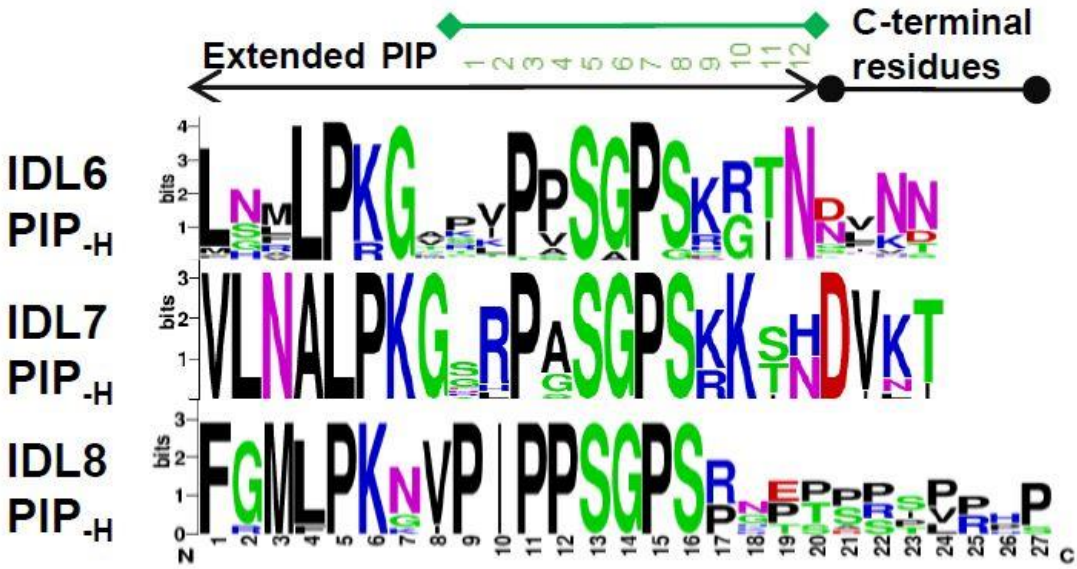

Figure S2. Conserved residues in propeptides of angiosperm IDL 6 8 orthologues numbered from the start of the extended PIP motif to the C terminal end. Sequences were aligned using Muscle, and consensus sequences were generated with logo@compbio berkeley edu The PIP residues are numbered 1 12 Compared to IDA and IDLA 1 5 IDL 6 8 lack the His (in position 11 The Arg His Asn (of IDA has been shown to interact with the co receptor SERK 1 22.

LRR		*Arabiopsis thaliana* HAE LxxLxxLxLxxNxLSGx-IPxx-LGx		*Arabidopsis thaliana* HSL2 LxxLxxLxLxxNxLSGxIPxx-LGx		*Elais guineensis* EgHSL2 LxxLxxLxLxxNxLS-GxIPxxLGx
1	88	LPSLHSLSLYNNSINGS-LSADDFDT	97	IRTLINITLSQNNLNGTIDSAPLSL	121	IPTLRHLSLAWNDLGGGLPAADVAL
2	113	CHNLISLDLSENLLVGS-IPKSLPFN	122	CSKLQNLILNQNNFSGKLPEF-SPE	118	CSGLEVLNLSNNFFV-GRLPEFSGE
3	138	LPNLKFLEISGNNLSDT-IPSS-FGE	146	FRKLRVLELESNLFTGEIPQS-YGR	142	FPRLRLLDLSGNNFS-GDIPPSFGR
4	162	FRKLESLNLAGNFLSGT-IPAS-LGN	170	LTALQVLNLNGNPLSGIVPAF-LGY	166	FPSLRVLSLYSNLIS-GRIPSFLAN
5	186	VTTLKELKLAYNLFSPSQIPSQ-LGN	190	LTELTHLDLAYISDPSPIPST-LGN	190	LTELIEFNLGFNPFRSGSLPPEIGN
6	211	LTELQVLWLAGCNLVGP-IPPS-LSR	219	LSNLTDLRLTHSNLVGEIPDS-IMN	215	LTKLEVLWLPFVNLV-GEIPDSVGN
7	235	LTSLVNLDLTFNQLTGS-IPSW-ITQ	243	LMLLENLDLAMNGLTGEIPES-IGT	239	LANLKILDLSNNGLT-GRIPASIGR
8	259	LKTVEQIELFNNSFSGE-LPES-MGN	267	LESVYQIRLYDNRLSGKLPES-IGN	263	LRSVEKMELWRNQLS-GELPQSLGN
9	283	MTTLKRFDASMNKLTGK-IPDN-LN-	291	LTELRNFDVSQNNLTGELPEK-IA-	287	LTSLFAFDASENKLT-GKLPE-GLA
10	306	LLNLESLNLFENMLEGP-LPES-ITR	314	ALQLISFNLNDNFFTGGLPDV-VAL	310	GLNLTSLALNDNRMD-GEISTVLAQ
11	330	SKTLSELKLFNNRLTGV-LPSQ-LGA	338	NPNLVEFKIFNNSFTGTLPRN-LGK	334	NPHLVELKLFNNNFS-GELPSGLGR
12	354	NSPLQYVDLSYNRFSGE-IPAN-ICG	362	FSEISEFDVSTNRFSGELPPY-LCY	358	YSYLTNVDVSGNQFA-GRLPPDLCS
13	378	EGKLEYLILIDNSFSGE-ISNN-LGK	386	RRKLQKIITFSNQLSGEIPES-YGD	382	RGMLESLVAFGNRFS-GELPQSYAD
14	402	CKSLTRVRLSNNKLSGQ-IPHGFWG-	410	CHSLNYIRMADNKLSGEVPAR-FWE	409	CRTLDYVRIQNNELS-GKVPDLFWS
15	426	LPRLSLLELSDNSFTGS-IPKTIIG-	434	LPLTRLELANNNQLQGSIPPS-ISK	430	LPKLYHLELRGNKLE-GSLPPNISR
16	450	AKNLSNLRISKNRFSGS-IPNE-IGS	458	ARHLSQLEISANNFSGVIPVK-LCD	454	AKNLTQIIISDNKFS-GQIPPEICD
17	474	LNGIIEISGAENDFSGE-IPES-LVK	482	LRDLRVIDLSRNSFLGSIPSC-INK	478	LMELRTFDAGNNQFS-SGLPLCIAD
18	498	LKQLSRLDLSKNQLSGE-IPRE-LRG	506	LKNLERVEMQENMLDGEIPSS-VSS	502	LTKLQVLDLQQNNFS-GEIPA-GG-
19	522	WKNLNELNLANNHLSGE-IPKE-VGI	530	CTELTELNLSNNRLRGGIPPE-LGD	524	WTELARINLSMNRFS-GEIPRSLGD
20	546	LPVLNYLDLSSNQFSGE-IPLE-LQN	554	LPVLNYLDLSNNQLTGEIPAE-LLR	548	LPVLTYLDLSGNQLS-GEIPPELTN-
21	570	L-KLNVLNLSYNHLSGK-IPPL-YA-	578	L-KLNQFNVSDNKLYGKIPS--FQ-	572	L-KLNHLNLSGNDLS-GKIPD--GF-
22	592	NKIYAHDFIGNPGLCVD-LDG--LCR	600	QDIFRPSFLGNPNLCAPNLDPIRPC	594	DTSFFLPSLLGNPDLCSSSGLKTFRRC

Figure S3. Structure-based sequence alignment of the 21 leucine-rich repeats (LRRs) comparing Arabidopsis AtHAE and AtHSL2 with EgHSL2 from oil palm. Residue numbers are found in the columns to the left of the respective alignments. The plant LRR consensus sequence making up the scaffold of the ectodomain is shown on top of the alignments and is shaded in grey throughout the LRRs. Residues shown from the AtHAE-AtIDA crystal structure to mediate hydrophobic interactions with AtIDA, and corresponding conserved residues in AtHSL2 and EgHSL2, are highlighted in blue, residues contributing to hydrogen bond interactions and/or salt bridges are shown in red. N-glycosylation sites are indicated in green, cysteine residues involved in disulphide bridge formation in orange, and residues involved in binding of AtSERK1 in yellow.