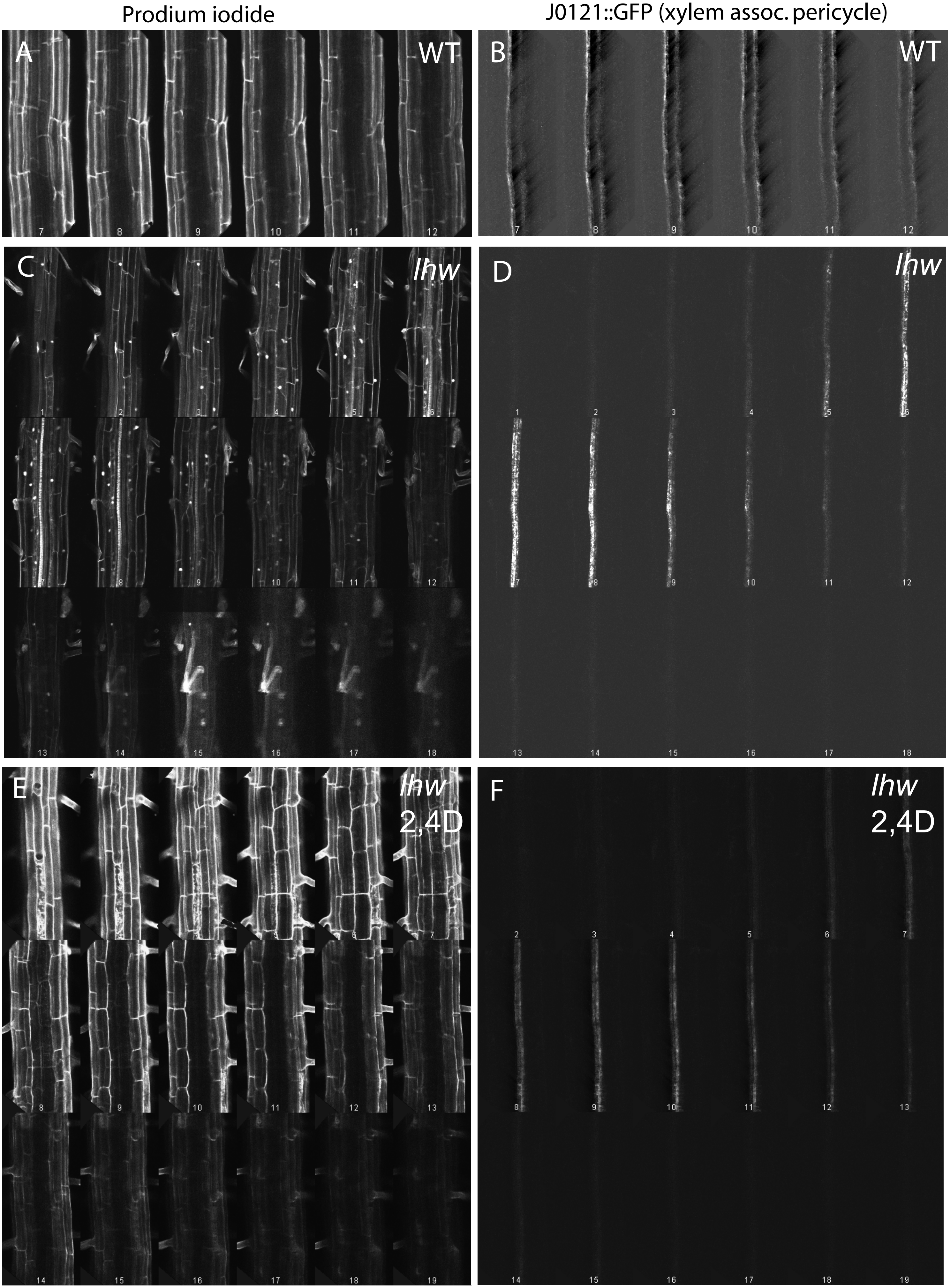
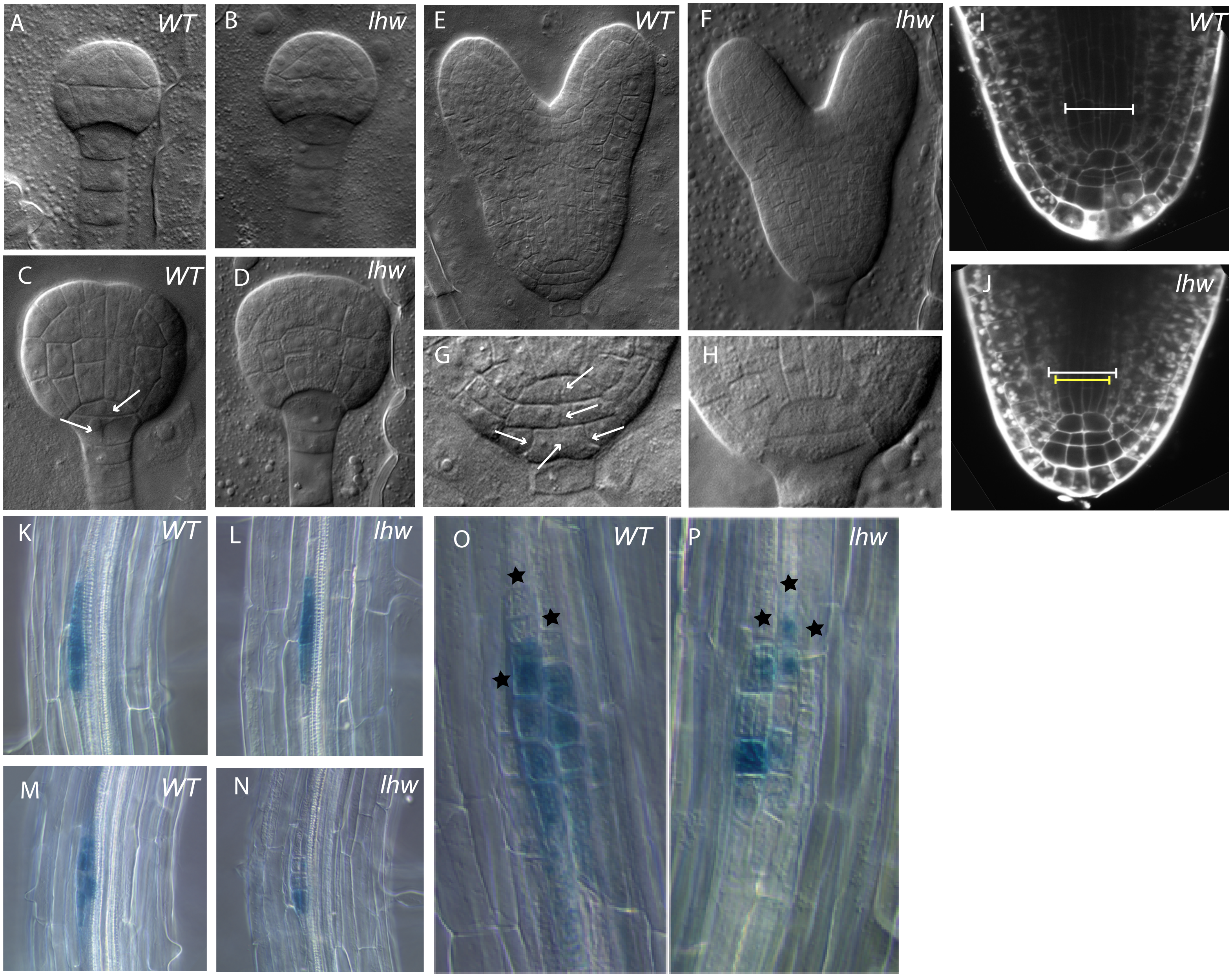
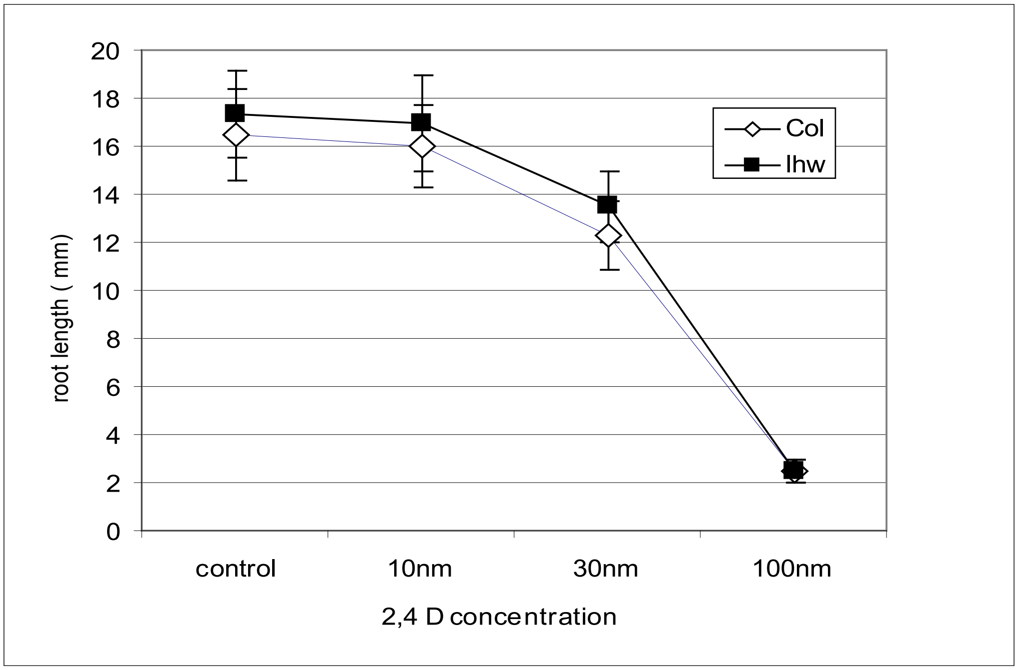
Figure S1: Montages of J0121::GFP expression



Supplemental Figure 2



Supplemental Figure 3



Supplemental Figure 2: CLUSTAL W (1.83) multiple sequence alignment of LHW and relatives from Arabidopsis and Rice

```
Os11g06010.1      --MAVGDALRRLCEEVGWSYAVFWKAIGAADPVHLVWEDGYCGHASCPAGSDPSEALPTD 58
Os12g06330.1      --MAVGDALRRLCEEARWSYAVFWKAIGAADPVHLVWEDGFCGHASCSAGSEAS-----E 53
lhw               MGVLLREALRSMCVNNQWSYAVFWK-IGCQNSSLLIWEECYNETESSSNPRRLCG----- 54
At1g64625         ------------------------------------------------------------
At1g06150         MGYTLQQILRSICSNTDWNYAVFWKLNHH-SPMVLTLEDVYCVNHERGLM---------P 50
At2g31280         MGSTSQEILKSFCFNTDWDYAVFWQLNHRGSRMVLTLEDAYYDHHG-------------- 46


Os11g06010.1      VGCAAAADTMTMCSLVNKVMASQVHVVGEGTVGRAAFTGNHQWIIHGTAN---DHGIPSE 115
Os12g06330.1      AGCESGG---AVCTLVRKIMASQVHVVGEGTIGRAAFTGNHQWIVHETAN---DHGLRSE 107
lhw               LGVDTQGNEKVQLLTNRMMLNNRIILVGEGLVGRAAFTGHHQWILANSFN---RDVHPPE 111
At1g64625         --------------------------------------GNHQWLFSDTLFQWEHEFQNQF 22
At1g06150         ESLHGGRHAHDPLGLAVAKMSYHVHSLGEGIVGQVAISGQHQWIFSEYLN----DSHSTL 106
At2g31280         TNMHG---AHDPLGLAVAKMSYHVYSLGEGIVGQVAVSGEHQWVFPENYN----NCNSAF 99
                                                        *.***:.         .

Os11g06010.1      V-AAEMSYQFRVGIQTIAIIPVLPRGVLQLGSTGVVLENKSFMTHAKKLCSQLNNRSSMA 174
Os12g06330.1      VVAAEMNNQFRAGIKTIAIIPVLPRGVLQLGSTSVILENISSVQQYKKLCCQLNNRSSMV 167
lhw               V-INEMLLQFSAGIQTVAVFPVVPHGVVQLGSSLPIMENLGFVNDVKGLILQLG------ 164
At1g64625         LCGFKILIRQFTYTQTIAIIPLGSSGVVQLGSTQKILESTEILEQTTRALQETCLKP--- 79
At1g06150         QVHNGWESQISAGIKTILIVAVGSCGVVQLGSLCKVEEDPALVTHIRHLFLALTDPLAD- 165
At2g31280         EFHNVWESQISAGIKTILVVAVGPCGVVQLGSLCKVNEDVNFVNHIRHLFLALRDPLAD- 158
                          :  .  :*: :..: . **:****   : *.   : .

Os11g06010.1      VSSSVKNSSSQQGRSRPLHGASNVQSTENRSKLFSQFPVTCEQYNHPDTMAVSGSTSLNA 234
Os12g06330.1      ASASAKNDLSQKVQSRSLHGLPSIHP--------------YEQCYGHDARALSSSTSANT 213
lhw               -------------------------------------------------CVPG------ 168
At1g64625         ------------------------------------------------------------
At1g06150         ------------------------------------------------------------
At2g31280         ------------------------------------------------------------


Os11g06010.1      CMNGSLLKIAQLNGQAVREHIVYSKPDVRFIQQV-YRDGQLGSNAQSI-----AMSSDLI 288
Os12g06330.1      GRNTSLLKVAQRNDQAIREQVLYA-PDMRFRQQLPYSDRRVDINTHSS-----AMSSGFI 267
lhw               -------------------------------------ALLSENYRTY-----EPAADFI 185
At1g64625         -----------------------------------HDSGDLDTLFESLGDCEIFPAES-- 102
At1g06150         -----------------------------------HASNLMQCDINSPSDRPKIPSKCLH 190
At2g31280         -----------------------------------HAANLRQCNMNNSLCLPKMPSEGLH 183
                                                               ..        :

Os11g06010.1      SSSLRSVQKQPLLMNNISQLEYGDGAETSADLRKNVLLKPPVCLDPFIHDR-NINISHGI 347
Os12g06330.1      SSISASVEKYPLLTNNIGQVEHGNMEESSG--PRNVLLKSLSCRNPVVHENTNTSLFHGG 325
lhw               G----------------------------------------------------------- 186
At1g64625         ------------------------------------------------------------
At1g06150         -EASPDFSG--------------------------------------------------- 198
At2g31280         AEAFPDCSG--------------------------------------------------- 192


Os11g06010.1      TEVSNVINDHGNFDFLSGGARVVRANLCTSATS-QVLDRRSHSVSGMLLHREPIVSCEVP 406
Os12g06330.1      DEVPAFLNSHGSFDFLQAGPRVVEANLYNNGTSSQVLDQRCSSTSGMAGY-KPSVSYKFP 384
lhw               VPVSRIIPSQ--------GHKILQSSAFVAETSKQHFNSTGSSDHQMVEE---------- 228
At1g64625         ------------------FQGFSFDDIFAEDNPPSLLSPEMISSEAASSN---------- 134
At1g06150         -EFDKAMDMEGLNIVSQNTSNRSNDLPYNFTPTYFHMERTAQVIGGLEAVQPSMFGSNDC 257
At2g31280         -EVDKAMDVEESNILTQYKTRRSDSMPYNTPSSCLVMEKAAQVVGGREVVQGSTCGSYSG 251
                                                  .   :.

Os11g06010.1      QSSEFSTKMGSLERGSFQISSAPSSESDVQISNGLNTSISRENQLSVSNHICQDQKINGV 466
Os12g06330.1      HSAQFIVKMENPRRQSFQDPAAPSSGSDVQVSSGLKTTTRQFN----PEHMCQNKKTNEV 440
lhw               ----SPCNLVDEHEGGWQSTTGFLTAGEVAVPS--------------------NPDAWL 263
At1g64625         ------QDLTNGDDYGFDILQSYS-----------------------------------L 153
At1g06150         VTSGFSVGVVDTKHKNQVDISDMSKVIYDEETGGYRYSRELDPN---FQHYSRNHVRNSG 314
At2g31280         VTFGFPVDLVGAKHENQVGTNIIRDAPHVGMTSGCKDSRDLDPN---LHLYMKNHVLNDT 308
                          : .    .

Os11g06010.1      NDLSATLSTERMNNMDGCKPPGLSLERTSPLFMEQSVENDLFDILGPQFHHLCHNAGADL 526
Os12g06330.1      NDSSAAVSTQDVKNMDRHKILDISNERTSSFVMDPSTENDLFDIFGTDFHQLHRSLDGDL 500
```

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lhw               NQNFSCMSNVDAAEQQQIPCEDISSKRS-------LGSDDLFDMLGLDDKNKGCDNSWGV 316
At1g64625         DDLYQLLADPPEQNCSSMVIQGVD--------------KDLFDILGMN------------ 187
At1g06150         GTSALAMESDRLKAGSSYPQLDSTVLTALKTDKDYSRRNEVFQPSESQGSIFVKDTEHRQ 374
At2g31280         STSALAIEAERLITSQSYPRLDSTFQATSRTDKESSYHNEVFQLSENQGNKYIKETERML 368
                  .     :        .     .                .::*:    :

Os11g06010.1      VP----------------------WTDAKPESSDRDVPESSIHADSAPLFSSRDNEL-YS 563
Os12g06330.1      S-----------------------WNTAKPQSSDRDAPESSIYLDSSPAFGAQEDEFSYS 537
lhw               S-------------------------QMRTEVLTRELSDFRIIQEMDPEFG--------S 343
At1g64625         -----------------------------SQTPTMALPPKGLFS---------------- 202
At1g06150         EEKSESSQLDALTASLCSFSGSELLEALGPAFSKTSTDYGELAKFESAAAIRRTNDMSHS 434
At2g31280         GRNCESSQFDALISSGYTFAGSELLEALGSAFKQTNTGQEELLKSEHGSTMRPTDDMSHS 428
                                               .           :

Os11g06010.1      GIFSLTDTDQLLDAVISNVNPAGKQSSDD---SASCKTSLTDIPATSYLCSKEMKQCGSS 620
Os12g06330.1      GIFSLTDTDQLLDAVISNVNPGGKQISGD---SASCKTSLTDIPSTSYCGSKETKQCKSS 594
lhw               SGYELSGTDHLLDAVVSGACSSTKQISDET--SESCKTTLTKVSNSSVTTPSHSSPQGSQ 401
At1g64625         ---------ELISSSLSNN---------------TCSSSLTNVQEYSGVNQSKRRKLDTS 238
At1g06150         HLTFESSSENLLDAVVASMSNGDGNVRREISSSRSTQSLLTTAEMAQAEPFGHNKQNIVS 494
At2g31280         QLTFDPGPENLLDAVVANVCQRDGNARDDMMSSRSVQSLLTN--MELAEPSGQKKHNIVN 486
                           .*:.: ::.                : .: **           .      .

Os11g06010.1      GVPSVLIKNESAQ--FIKQPCLAENAEDGCLSQNNGMHKSQIRLWIESGQSMKCESASAS 678
Os12g06330.1      GAPPLLIKNELAVSNFVKQPCFLEKAEDGCLSQNNGVQKSQIRLWIESGQNMKCESVSAS 654
lhw               ---------------------LFEKKHGQPLGPSS-VYGSQISSWVEQAHSLKREGSPRM 439
At1g64625         ------------------------SAHSSSLFPQEETVTSRS-LWIDDD-----ERSSIG 268
At1g06150         ------------------TVDSVISQPPLADGLIQQNPSNICGAFSSIGFSSTCLSSSSD 536
At2g31280         ------------------PINSAMNQPPMAEVDTQQNSSDICGAFSSIGFSSTYPSSSSD 528
                                        .         .    .    : .          .

Os11g06010.1      NSKGLDTPSKANRKRSRPGESPKPRPKDRQLIQDRIKELREMVPNGAKCSIDALLEKTVK 738
Os12g06330.1      NSKGLDTANKANRKRSRPGESPKPRPKDRQLIQDRIKELRELVPNGAKCSIDALLEKTIK 714
lhw               VNKNETAKPANNRKRLKPGENPRPRPKDRQMIQDRVKELREIIPNGAKCSIDALLERTIK 499
At1g64625         GNWKKPHEEGVKKKRAKAGESRRPRPKDRQMIQDRIKELRGMIPNGAKCSIDTLLDLTIK 328
At1g06150         QFPTSLEIPKKNKKRAKPGESSRPRPRDRQLIQDRIKELRELVPNGSKCSIDSLLECTIK 596
At2g31280         QFQTSLDIPKKNKKRAKPGESSRPRPRDRQLIQDRIKELRELVPNGSKCSIDSLLERTIK 588
                             ::** :.**. :***:***:****:**** ::***:*****:**: *:*

Os11g06010.1      HMLFLQSVTKHADKLKDSTESKILGN-ENGPVWKDYFEGGATWAFDVGSQSMTCPIIVED 797
Os12g06330.1      HMVFLQSVTKHADNLKDSNESKIHGGGENGPLLKDYFEGGATWAFDVGSQSMTCPIIVED 774
lhw               HMLFLQNVSKHSDKLKQTGESKIMKE----------DGGGATWAFEVGSKSMVCPIVVED 549
At1g64625         HMVFMQSLAKYAERLKQPYESKLVKE------------KERTWALEVGEEGVVCPIMVEE 376
At1g06150         HMLFLQSVSQHADKLTKSASSKMQHK-DTGTLGISSTEQGSSWAVEIGGHLQVCSIMVEN 655
At2g31280         HMLFLQNVTKHAEKLSKSANEKMQQK-ETG-------MQGSSCAVEVGGHLQVSSIIVEN 640
                  **:*:*.::::::.*... ..*:                  : *.::* .  ...*:**:

Os11g06010.1      LDRPRQMLVEMICEDRGIFLEIADFIKGLGLTILRGAMEARKSKIWARFTVEAN------ 851
Os12g06330.1      LDRPRQMLVEMLCEDRGIFLEIADFIKGLGLTILRGVMEARKNKIWARFTVEAN------ 828
lhw               INPPRIFQVEMLCEQRGFFLEIADWIRSLGLTILKGVIETRVDKIWARFTVEAS------ 603
At1g64625         LNREGEMQIEMVCEEREEFLEIGQVVRGLGLKILKGVMETRKGQIWAHFIVQAK------ 430
At1g06150         LDKEGVMLIEMLCEECSHFLEIANVIRSLELIILRGTTEKQGEKTWICFVVEG------- 708
At2g31280         LNKQGMVLIEMLCEECGHFLEIANVIRSLDLVILRGFTETQGEKTWICFVTEVGSRITQF 700
                  ::    . :**:**:   ****.: ::.* * **:*  * :  : *  * .:

Os11g06010.1      -------------RDVTRMEIFLSLVRLLEPNCDSSG--AAENANNVNMPLGLVHQPVIP 896
Os12g06330.1      -------------RDVTRMEIFLSLMRLLEPSCDGGGGGVGDNPNNVKIPPGIVQHPVIP 875
lhw               -------------RDVTRMEIFMQLVNILEQTMKCGG-------NSKTILDGIKATMPLP 643
At1g64625         -------------PQVTRIQVLYSLVQLFQHHTKHDDLLS-------------------- 457
At1g06150         ----------QNNKVMHRMDILWSLVQIFQPKATNR------------------------ 734
At2g31280         MKEIPKQIKSQNSKVMQRMDILWSLVQIFQPKANEKG----------------------- 737
                                 : *:::: .*:.:::

Os11g06010.1      ATGRIQ- 902
Os12g06330.1      ATGHLR- 881
lhw               VTGGCSM 650
At1g64625         -------
At1g06150         -------
At2g31280         -------
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