Supplemental Figure 6

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AT3G47090.1         -----------------------KKRKNNQKINNSAPFTLEIFHEKLSYGDLRNATDGFS
AT3G47580.1         -----------------------RKRRKNQQTNNLVPSKLEIFHEKISYGDLRNATNGFS
AT3G47570.1         -----------------------RKRKKNKETNNPTPSTLEVLHEKISYGDLRNATNGFS
AT3G47110.1         ----------------------------------------------------------FS
AT5G20480.1         -------------------FMKRKKKNNASDGNPSDSTTLGMFHEKVSYEELHSATSRFS
AT5G39390.1         -----------------------KKKN-----------------DKISYEELYNATSGFS
AT2G24130.1         IATPVLCVFGYPLVQRSRFGKNLTVYAKEEVEDEEKQNQNDPKYPRISYQQLIAATGGFN
AT5G46330.1 (FLS2)    ------------------KKKEKKIENSSESSLPDLDSALKLKRFEPKELEQATDSFN 871
                                                                   *   .

AT3G47090.1         SSNIVGSGSFGTVFKALLQTENKIVAVKVLN--MQRRGAMKSFMAECESLKDIRHRNLVK
AT3G47580.1         SSNMVGSGSFGTVFKALLPTESKIVAVKVLN--MQRRGAMKSFMAECESLKDTRHRNLVK
AT3G47570.1         SSNMVGSGSFGTVYKALLLTEKKVVAVKVLN--MQRRGAMKSFMAECESLKDIRHRNLVK
AT3G47110.1         SSNLIGSGNFGAVFKGFLGSKNKAVAIKVLN--LCKRGAAKSFIAECEALGGIRHRNLVK
AT5G20480.1         STNLIGSGNFGNVFKGLLGPENKLVAVKVLN--LLKHGATKSFMAECETFKGIRHRNLVK
AT5G39390.1         SSNLIGSGNFSDVFKGLLGLEEKLVAVKVLN--LLKHGATKSFIAECESFKGIRHRNLAK
AT2G24130.1         ASSLIGSGRFGHVYKGVLRN-NTKVAVKVLDP-KTALEFSGSFKRECQILKRTRHRNLIR
AT5G46330.1         SANIIGSSSLSTVYKGQLED-GTVIAVKVLNLKEFSAESDKWFYTEAKTLSQLKHRNLVK 930
                    ::.::**. :. *:*. *    . :*:***:           *  *.: :   :**** :

AT3G47090.1         LLTACASIDFQGNEFRALIYEFMPNGSLDKWLHPEEVEEIHRPSRTLTLLERLNIAIDVA
AT3G47580.1         LLTACASTDFQGNEFRALIYEYLPNGSVDMWLHPEEVEEIRRPPRTLTLLERLNIVIDVA
AT3G47570.1         LLTACSSIDFQGNEFRALIYEFMPNGSLDMWLHPEEVEEIHRPSRTLTLLERLNIAIDVA
AT3G47110.1         LVTICSSSDFEGNDFRALVYEFMPNGNLDMWLHPDEIEETGNPSRTLGLFARLNIAIDVA
AT5G20480.1         LITVCSSLDSEGNDFRALVYEFMPKGSLDMWLQLEDLERVNDHSRSLTPAEKLNIAIDVA
AT5G39390.1         LITVCSSLDSQGNDFRALVYEFMPKGSLDMWLQPEDLESANNHSRSLTFAEKVNIAIDVA
AT2G24130.1         IITTCSKPG-----FNALVLPLMPNGSLERHLYPGEYS-----SKNLDLIQLVNICSDVA
AT5G46330.1         ILGFAWESG----KTKALVLPFMENGNLEDTIHG-------SAAPIGSLLEKIDLCVHIA 979
                    ::  . . .      .**:   : :*.::  :           .        :::  .:*
                           ↑

AT3G47090.1         SVLDYLHVHCHEPIAHCDLKPSNILLDDDLTAHVSDFGLARLLLKFDQESFFNQLSSAG-
AT3G47580.1         SVLDYLHVHCHEPIAHCDLKPSNVLLEDDLTAHVSDFGLARLLLKFDKESFLNQLSSAG-
AT3G47570.1         SVLDYLHVHCHEPIAHCDLKPSNVLLDDDLTAHVSDFGLARLLLKFDEESFFNQLSSAG-
AT3G47110.1         SALVYLHTYCHNPIAHCDIKPSNILLDKDLTAHVSDFGLAQLLLKFDRDTFHIQFSSAG-
AT5G20480.1         SALEYLHVHCHDPVAHCDIKPSNILLDDDLTAHVSDFGLAQLLYKYDRESFLNQFSSAG-
AT5G39390.1         SALEYLHVYCHDPVAHCDIKPSNVLLDDDLTAHVSDFGLARLLYNFDEKTFLNQFSSAG-
AT2G24130.1         EGIAYLHHYSPVKVVHCDLKPSNILLDDEMTALVTDFGISRLVQGVEETVSTDDSVSFGS
AT5G46330.1         SGIDYLHSGYGFPIVHCDLKPANILLDSDRVAHVSDFGTARILGFREDGSTTASTSAFE- 1038
                    . : ***      :.***:**:*:**:.: .* *:*** ::::   :      .  :
                                     ↑

AT3G47090.1         ----VRGTIGYAAPEYGMGGQPSIHGDVYSFGVLVLEMFTGKRPT--NELFGGNFTLNSY
AT3G47580.1         ----VRGTIGYAAPEYGMGGQPSIHGDVYSFGVLLLEMFTGKRPT--DELFGGNLTLHSY
AT3G47570.1         ----VRGTIGYAAPEYGVGGQPSINGDVYSFGILLLEMFTGKRPT--NELFGGNFTLNSY
AT3G47110.1         ----VRGTIGYAAPEYGMGGHPSIMGDVYSFGIVLLEIFTGKRPT--NKLFVDGLTLHSF
AT5G20480.1         ----VRGTIGYAAPEYGMGGQPSIQGDVYSFGILLLEMFSGKKPT--DESFAGDYNLHSY
AT5G39390.1         ----VRGTIGYAAPEYGMGSKPSIQGDVYSFGVLLLEMFTGKKPT--DNSFGGGYNLHGY
AT2G24130.1         TDGLLCGSVGYIAPEYGMGKRASTHGDVYSFGVLLLEIVSGRRPT--DVLVNEGSSLHEF
AT5G46330.1         ------GTIGYLAPEFAYMRKVTTKADVFSFGIIMMELMTKQRPTSLNDEDSQDMTLRQL 1092
                          *::** ***:.   : :  .**:***:::*:.:  ::**  :     . .*.

AT3G47090.1         TKAALPER-VLDIADKSILHSGLRVGFPVLECLK-----GILDVGLRCCEESPLNRLATS
AT3G47580.1         TKLALPEK-VFEIADKAILHIGLRVGFRTAECLT-----LVLEVGLRCCEEYPTNRLATS
AT3G47570.1         TKSALPER-ILDIVDESILHIGLRVGFPVVECLT-----MVFEVGLRCCEESPMNRLATS
AT3G47110.1         TKSALQKRQALDITDETILRGAYAQHFNMVECLT-----LVFRVGVSCSEESPVNRISMA
AT5G20480.1         TKSILSGC------------TSSGGSNAIDEGLR-----LVLQVGIKCSEEYPRDRMRTD
AT5G39390.1         TKSVLSCS------------TSRGGRTMVDEWLR-----LVLEVGIKCSEEYPRDRMGMA
AT2G24130.1         MKSHYPDS-LEGIIEQALSRWKPQGKPEKCEKLWREVILEMIELGLVCTQYNPSTRPDML
AT5G46330.1         VEKSIGNGRKGMVRVLDMELGDSIVSLKQEEAIED-----FLKLCLFCTSSRPEDRPDMN 1147
                     :                            * :       .: : : * .  *  *

AT3G47090.1         EAAKELISIRERFFKTRRTARR----------------------
AT3G47580.1         EVAKELISIRERFFKTRRTPRR----------------------
AT3G47570.1         IVVKELISIRERFFKASRTTWR----------------------
AT3G47110.1         EAISKLVSIRESFFRDEET-------------------------
AT5G20480.1         EAVRELISIRSKFFSSKTTITESPRDAPQSSPQEWMLNTDMHTM
AT5G39390.1         EAVRELVSIKSKFFTSSR--------------------------
AT2G24130.1         DVAHEMGRLKEYLFACPSLLHFSSQETQGEASS-----------
AT5G46330.1         EILTHLMKLRGKANSFREDRNEDREV (1173 = end of FLS2)
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Supplemental Figure 6. Lack of conservation of FLS2 Ser-938 in related non-RD kinases. Sequence alignment of kinase domains of non-RD kinases from LRR-RLK subfamily XII in Arabidopsis (Shiu and Bleecker, 2001). Red arrow indicates phosphorylation site Ser-938 of FLS2, which resides in a 10 amino acid region that aligns only poorly with the closest related Arabidopsis kinases. Black arrow indicates the conserved D997 in kinase active site.

Shiu SH, and Bleecker AB, 2001. Receptor-like kinases from Arabidopsis form a monophyletic gene family related to animal receptor kinases. Proc Natl Acad Sci. 98: 10763-10768.