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*      20      *      40      *      60
0025396 : ME-RDRDPLVGRVIGDVLNPFTKSISLTVSYNNR-EINNGCEIKPSQIVNQPRVDIGGDDL : 61
LcFT1  : ME-RDRDPLVGRVIGDVLNPFTKSISLTVSYNNR-EINNGCEIKPSQIVNQPRVDIGGDDL : 61
DlFT1  : ME-RDRDPLVGRVIGDVLDPFTKSISLTVSYNNR-EINNGCEIKPSQIVNQPRVDVGGDDL : 61
LcFT2  : ME-RDRDPLVGRVIGDVLDPFTKSISLTVSYNNR-EINNGCEIKPSQIVNQPRVDVGGDDL : 61
DlFT2  : MS-RNRDPLAVGRVIGDVLDPFTRSISLTVSYNNR-AINNGYELKPSQIVNQPRVDIGGDDL : 61
MdFT1  : ME-RDRDPLVGRVVGVDLDPFTRSVSLRVTYGK-EVNNGCEIKPSEVVQPRADIGGDDL : 61
VvFT1  : ME-RERDPLVGRVVGVDLDPFTRSILRVTYNNR-EVANGCEFRPSQLVSOQPRVDIGGDDL : 61
AtFT   : MSINIRDPLVSRVVGVDLDPFTRSILKVTYQGR-EVINGLDLRPSQVQNKPRVEIGGDDL : 62
CuFT   : MSSRERDPLVGRVVGVDLDPFTRTIEMRITYSNK-DVNNGREIKPSEVLNQPRVEIGGDDL : 62
PtFT   : MS-RDRDPLVGRVIGDVLDPFTKSILRVTYNSR-EVNNGCEIKPSQIVNQPRVDIGGDDL : 61
GmFT   : ME-RSTDPLVIGGVIGDVLDPFTSSVSMGIVYNNCPQVINCCEIKPSKILLNRPRVEIGGDDL : 62

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*      80      *      100     *      120
0025396 : TFYTLVMVDPDAPSPSEERLREYLHWLVDIPATTGATFGQEVVVCYESPRPTSGIHRFIVVLF : 124
LcFT1  : TFYTLVMVDPDAPSPSEERLREYLHWLVDIPATTGATFGQEVVVCYESPRPTSGIHRFIVVLF : 124
DlFT1  : ACYTLVMVDPDAPSPSEERLREYLHWLVDIPATTGATFGQEVVVCYESPRPTAGIHRFIVVLF : 124
LcFT2  : TCYTLVMVDPDAPSPSEERLREYLHWLVDIPATTGATFGQEVVVCYESPRPTVGIHRFIVVLF : 124
DlFT2  : TFYTLVMVDPDAPSPSEERLREYLHWLVDIPATTGATFGQEVVVCYESPRPTVGIHRFIVVLF : 124
MdFT1  : TFYTLVMVDPDAPSPSDENLKEYLHWLVDIPATTAASFGQEVVVCYESPRPTVGIHRFIVVLF : 124
VvFT1  : TFYTLVMVDPDAPSPSEERLREYLHWLVDIPATTGATFGQEVVVCYESPRPTAGIHRFIVVLF : 124
AtFT   : NFYTLVMVDPDAPSPSEERLREYLHWLVDIPATTGATFGQEVVVCYESPRPTAGIHRFIVVLF : 125
CuFT   : TFYTLVMVDPDAPSPSEERLREYLHWLVDIPATTGATFGQEVVVCYESPRPTMGIHRFIVVLF : 125
PtFT   : TFYTLVMVDPDAPSPSEERLREYLHWLVDIPATTGATFGQEVVVCYESPRPTMGIHRFIVVLF : 124
GmFT   : TFYTLVMVDPDAPSPSEERLREYLHWLVDIPATTGATFGQEVVVCYESPRPTVGIHRFIVVLF : 125

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*      140     *      160     *
0025396 : RQLGROTYYAPGWRQNFNTKFAELYNLGSPVAAVYFNCQRESC-SGGRRR-- : 174
LcFT1  : RQLGROTYYAPGWRQNFNTKFAELYNLGSPVAAVYFNCQRESC-SGGRRR-- : 174
DlFT1  : QCPSTOTMYAPGWRQNFNTKFAELYNLGSPVAAVYFNCQRESC-SGGRRR-- : 174
LcFT2  : RCPSTOTMYAPGWRQNFNTKFAELYNLGSPVAAVYFNCQRESC-SGGRRR-- : 174
DlFT2  : RQCGROTYYAPGWRQNFNTKFAELYNLGSPVAAVYFNCQREII-SGGSRR-- : 174
MdFT1  : RQLGROTYYAPGWRQNFNTKFAELYNLGSPVAAVYFNCQREGG-SGGRRR-- : 174
VvFT1  : RQLGROTYYAPGWRQNFNTKFAELYNLGSPVAAVYFNCQREGG-SGGRRS-- : 174
AtFT   : RQLGROTYYAPGWRQNFNTKFAELYNLGSPVAAVYFNCQRESC-CGGRRL-- : 175
CuFT   : RQLGROTYYAPGWRQNFNTKFAELYNLGSPVAAVYFNCQRESC-SGGRPVRR : 177
PtFT   : RQLGROTYYAPGWRQNFNTKFAELYNLGSPVAAVYFNCQRESC-SGGRRR-- : 174
GmFT   : RQLRRTLQPPGWRQNFNTKFAELYNLGSPVAAVYFNCQRENDQSSGRRR-- : 176

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**Additional file 15. Analysis of FT homologous transcripts in litchi.**

(A) Alignment of the FT homologues proteins. (B) Phylogenetic relationship between Unigene0025396 and other FT proteins from higher plant species. The accession numbers of the sequences used for the alignment are: LcFT1 [*Litchi chinensis*, AEU08960.1], LcFT2 [*Litchi chinensis*, AEU08961.1], DIFT1 [*Dimocarpus longan*, AEZ63949.1], DIFT2 [*Dimocarpus longan*, AEZ63950.1], MdFT1 [*Malus x domestica*, BAD08340.1], VvFT1 [*Vitis vinifera*, ABL98120.1], AtFT [*Arabidopsis thaliana*, BAA77838], CuFT [*Citrus unshiu*, BAF96644.1], PtFT [*Populus tomentosa*, AFU08239.1] and GmFT [*Glycine max*, BAJ33489.1].