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At_FT       1 MSINIRDPLIVSRVVGDVLDPFNRSITLKVTYGQREVTNGLDLRPSQVQNKPRVEIGGED
Cm_FTL1     1 MPRN-RDPLVVGRVIGDVVDSFSRSISIRVVYDSREVNNGCELKPSQAVNKPRVEIGGTD
Cm_FTL2     1 MPRD-RDPLVVGRVIGDVIDSFTKSISIRATYNNREISNGCELKPSQVVNQPRVEIGGTD
Cmo_FTL1    1 MPRD-RDPLVVGRVIGDVIDSFSRSISIRVAYNSRKVKNGCELKPCQVINKPRVEIGGTD
Cmo_FTL2    1 MPRD-RDPLVIGRVIGDVIDSFTRSISIRATYNNREISNGCELKPSQVVNQPRVEIGGTD

At_FT      61 LRNFYTLVMVDPDVPSPSNPHLREYLHWLVTDIPATTGTTFGNEIVCYENPSPTAGIHRV
Cm_FTL1    60 LRTFFTLVMVDPDAPSPSDPNLREYLHWLVTDIPATTEATFGQEIVCYENPRPTVGIHRF
Cm_FTL2    60 LRTFFTLVMVDPDAPSPSDPNLREYLHWLVTDIPATTGANFGQEIVCYESPRPTVGIHRL
Cmo_FTL1   60 LRTFFTLVMVDPDAPSPSDPNLREYLHWLVTDIPATTEATFGQEIVCYENPRPTAGIHRF
Cmo_FTL2   60 LRTFFTLVMVDPDAPSPSDPNLREYLHWLVTDIPATTGATFGQEIVCYESPRPTVGIHRL

At_FT     121 VFILFRQLGRQTVYAPGWRQNFNTREFAEIYNLGLPVAAVFYNCQRESGCGGRRL------ 175
Cm_FTL1   120 VLVLFRQLGRQTVYAPGWRQNFNTRHFAELYNLGSPVAAVYFNCQRENGSGGRRRAGDECS 180
Cm_FTL2   120 VLVLFRQLGRQTVYAPGWRQNFNTRDFAELYNLGLPVAAVYFNCQRESGSGGRRRTQDDF- 179
Cmo_FTL1  120 VLVLFRQLGRQTVYAPGWRQNFNTRHFAELYNLGSPVAAVYFNCQRENGSGGRRRAGDECS 180
Cmo_FTL2  120 VLVLFRQLGRQTVYAPGWRQNFNTRDFAELYNLGLPVAAVYFNCQRESGSGGRRRSQDDF- 179
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Supplemental Figure 1: Comparison of *Arabidopsis* FT, Cm_FTL1, Cm_FTL2, Cmo_FTL1 and Cmo_FTL2 conceptual amino acid sequences. Cm_FTL1 (GenBank accession number DQ865290), Cm_FTL2 (GenBank accession number DQ865291), Cmo_FTL1 (GenBank accession number EF462211) and Cmo_FTL2 (GenBank accession number EF462212) encode proteins of 20.3, 20.2, 20.3 and 20.2 kDa, respectively. Yellow boxes indicate identity.