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No.3341-LTSF2      MPVKVAKRKHQFQTENGFSQSEQQMEKQRIPPIIQIQPYNEAKKVDLESRKKANILKCQQQ 60
sy2-LTSF2          MPVKVAKRKHQFQTENGFSQSEQQMEKQRIPPIIQIQPYNEAKKVDLESRKKANILKCQQQ 60
No.3341-LTSF1      MPVKVAKRKHQFQTENGFSQSEQQMEKQRIPPIIQIQPYNEAKKVDLESRKKANILKCQH 60
sy-2-LTSF1         MPVKVAKRKHQFQTENGFSQSEQQMEKQRIPPIIQIQPYNEAKKVDLESRKKANILKCQH 60
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No.3341-LTSF2      GKKKLLKKKSVPHGQIRKGRVVKIDYDQQAIHFQEQLVDILSRLPLRSLRKFCA 120
sy2-LTSF2          GKKKLLKKKSVPHGQIRKGRVVKIDYDQQAIHFQEQLVDILSRLPLRSLRKFCA 120
No.3341-LTSF1      GKKKLLKKKSVPHGQIRKGRVVKIDYDQQAIHFQEQLVDILSRLPLRSLRKFCA 120
sy-2-LTSF1         GKKKLLKKKSVPHGQIRKGRVVKIDYDQQAIHFQEQLVDILSRLPLRSLRKFCA 120
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No.3341-LTSF2      TWEALISDPYFHKMIMKKQRQSPDSTSQKLLIRKMFSDTAPSRKFYSSSLSTFEDVQQL 180
sy2-LTSF2          TWEALISDPYFHKMIMKKQRQSPDSTSQKLLIRKMFSDTAPSRKFYSSSLSTFEDVQQL 180
No.3341-LTSF1      TWEALISDPYFHKMIMKKQRQSPDSTSQKLLIRKMFSDTAPSRKFYSSSLSTFEDVQQL 180
sy-2-LTSF1         TWEALISDPYFHKMIMKKQRQSPDSTSQKLLIRKMFSDTAPSRKFYSSSLSTFEDVQQL 180
*****
No.3341-LTSF2      DPPLTHYVDRYHIFSSFQDGLALLAADTQLFLWNPLTRTETALLPHTEFAMCTCFVLGYDD 240
sy2-LTSF2          DPPLTHYVDRYHIFSSFQDGLALLAADTQLFLWNPLTRTETALLPHTEFAMCTCFVLGYDD 240
No.3341-LTSF1      DPPLTHYVDRYHIFSSFQDGLALLAADTQLFLWNPLTRTETALLPHTEFAMCTCFVLGYDD 240
sy-2-LTSF1         DPPLTHYVDRYHIFSSFQDGLALLAADTQLFLWNPLTRTETALLPHTEFAMCTCFVLGYDD 240
*****
No.3341-LTSF2      ATDGYKILKFVMRLQSSMEILTLKTGLWRKICNYPTAVCPTTGHEMIIIPRPSKNIPMEP 300
sy2-LTSF2          ATDGYKILKFVMRLQSSMEILTLKTGLWRKICNYPTAVCPTTGHEMIIIPRPSKNIPMEP 300
No.3341-LTSF1      ATDGYKILKFVMRLQSSMEILTLKTGLWRKICNYPTAVCPTTGHEMIIIPRPSKNIPMEP 300
sy-2-LTSF1         ATDGYKILKFVMRLQSSMEILTLKTGLWRKICNYPTAVCPTTGHEMIIIPRPSKNIPMEP 300
*****
No.3341-LTSF2      LVCVHGAFHWLGDLDVSGKFYVVSFISNEVYGDVPLLEEMGKKVNYRPFGLSLLDGML 360
sy2-LTSF2          LVCVHGAFHWLGDLDVSGKFYVVSFISNEVYGDVPLLEEMGKKVNYRPFGLSLLDGML 360
No.3341-LTSF1      LVCVHGAFHWLGDLDVSGKFYVVSFISNEVYGDVPLLEEMGKKVNYRPFGLSLLDGML 360
sy-2-LTSF1         LVCVHGAFHWLGDLDVSGKFYVVSFISNEVYGDVPLLEEMGKKVNYRPFGLSLLDGML 360
*****
No.3341-LTSF2      CYYTTTNDGSLGSFKLWAMKDYGVKESWIVLCTLQFNGLVIAKPRYRFPDGGLLLYAPGE 420
sy2-LTSF2          CYYTTTNDGSLGSFKLWAMKDYGVKESWIVLCTLQFNGLVIAKPRYRFPDGGLLLYAPGE 420
No.3341-LTSF1      CYYTTTNDGSLGSFKLWAMKDYGVKESWIVLCTLQFNGLVIAKPRYRFPDGTFAPAIKCR 420
sy-2-LTSF1         CYYTTTNDGSLGSFKLWAMKDYGVKESWIVLCTLQFNGLVIAKPRYRFPDGTFAPAIKCR 420
*****
No.3341-LTSF2      FPHQCGVPSCFTF-----QTFKGKFGFWPERGGTFEKGIYVRESLISPKLVI 467
sy2-LTSF2          FPHQCGVPSCFTF-----QTFKGKFGFWPERGGTFEKGIYVRESLISPKLVI 467
No.3341-LTSF1      PLVLSVACKFSFTEVACVFYALASYLWLW----- 450
sy-2-LTSF1         PLVLSVACKFSFTEVACVFYALASYLWLW----- 450
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Figure S1. Multiple sequence alignment of the LTSF1 and LTSF2 proteins from ‘No.3341’ and ‘sy-2’.

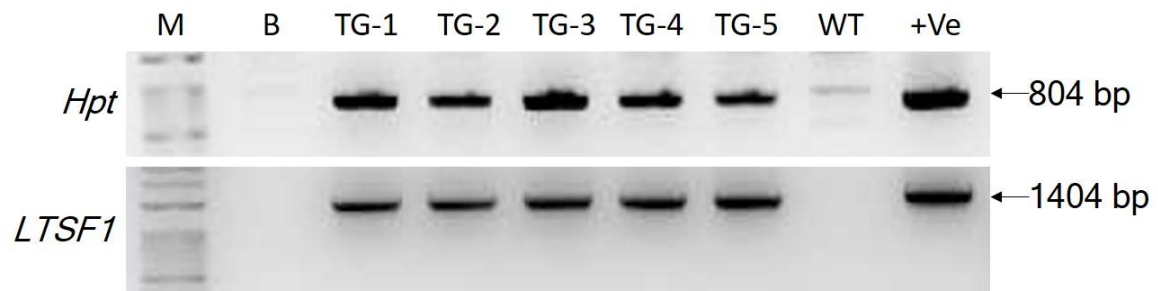


Figure S2. RT-PCR analysis of *N. benthamiana* transgenic plants. TG-1 to TG5: *LTSF1* *N. benthamiana* transgenic plants; *Hpt*, hygromycin phosphotransferase gene; M, molecular weight marker; WT, wild type *N. benthamiana* plant, Ve+, pMDC83-*LTSF1*:GFP vector.

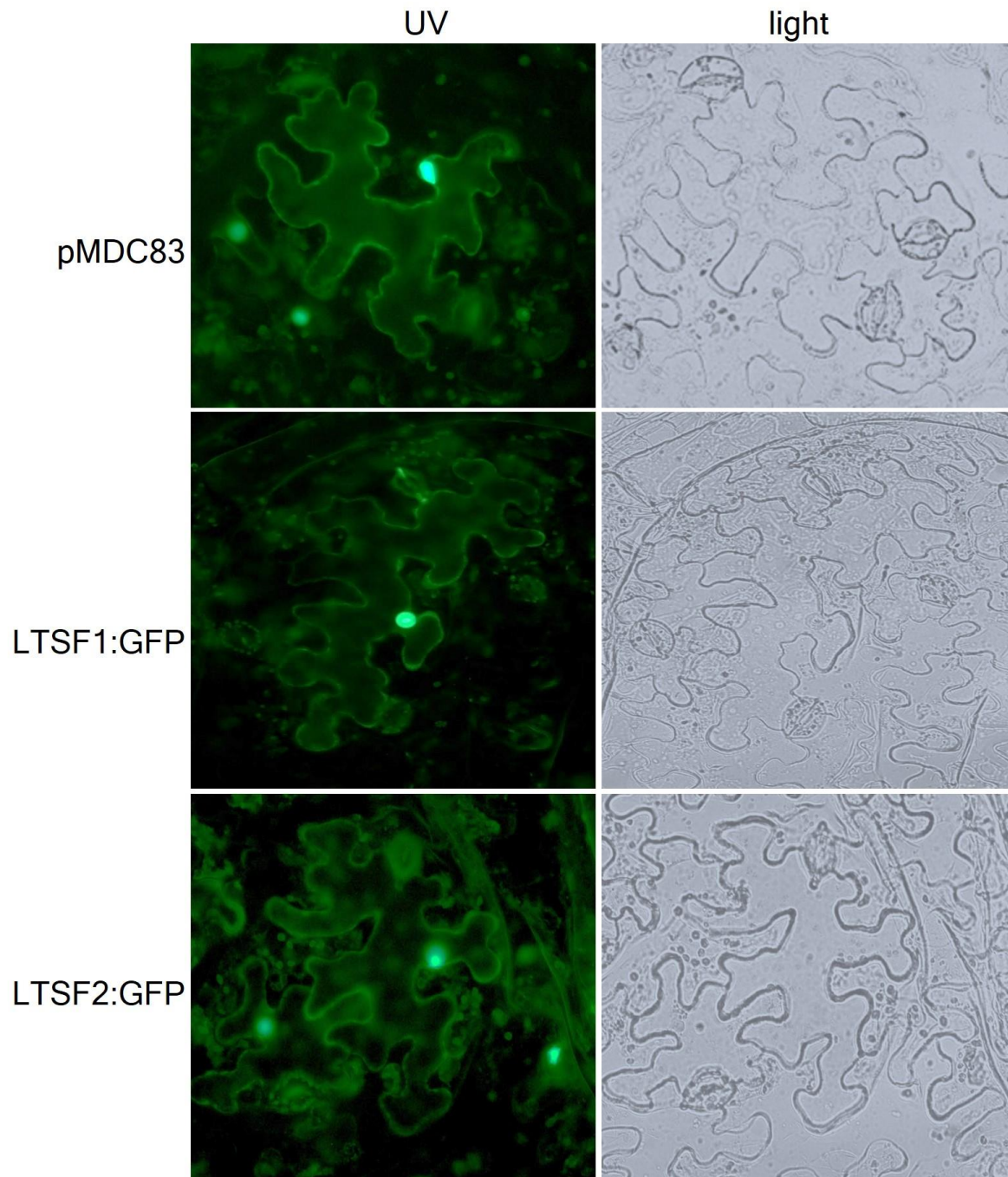


Figure S3. Subcellular localization of the LTsf1 and LTsf2 proteins. In *N. benthamiana* leaves transiently expressing 35S::LTsf1-GFP or 35S::LTsf2-GFP, the GFP signal was observed in the nucleus, cytoplasm, and cell membrane. pMDC83, empty GFP vector.