Supplementary data: Dinant et al.,

Synchrotron FTIR and Raman spectroscopy provide unique spectral fingerprints for *Arabidopsis* floral stem vascular tissues

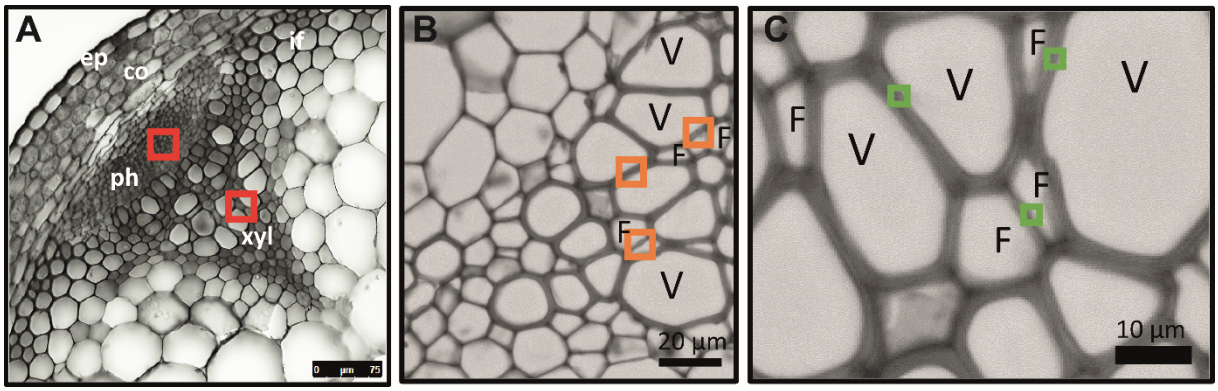

Fig. S1. Illustration of the different spatial resolutions offered by vibrational spectroscopy techniques.

(A-C) Transverse sections of an Arabidopsis floral stem showing different cell types. ep: epidermis, co: cortex, ph: phloem, F: xylem fibers, if: interfascicular fibers, V: xylem vessel, xyl: xylem. The square in each photograph represents the size of the acquisition zone for thermal source FTIR (A), SR-FTIR (B) and Raman spectroscopy (C). In classic FTIR, the 30x30 µm acquisition zone includes different cell types within the xylem tissue (A), while the 8x8 µm spatial resolution offered by SR-FITR enables the precise targeting of some cell-specific cell walls (B). The 2x2 µm spatial resolution offered by Raman spectroscopy is beneficial for studying cell walls (C). Bar represent 75 µm (A), 20 µm (B) or 10 µm (C).

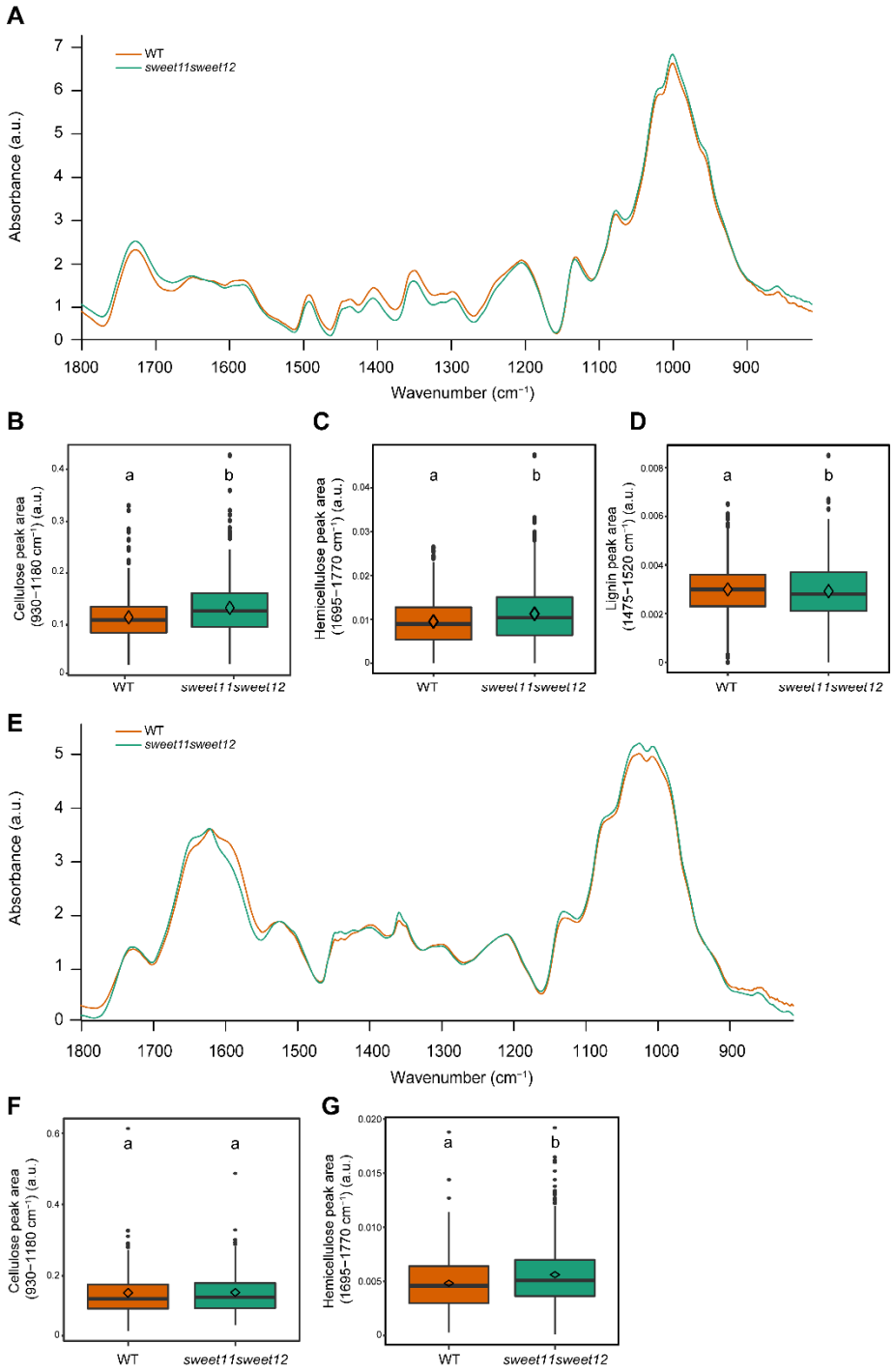

Fig. S2. Comparison of SR-FTIR average spectra and peak areas of cellulose, hemicellulose and lignin between WT and *sweet11-1sweet12-1* xylem or phloem tissues.

(A) Average spectra of WT and *sweet11-1sweet12-1* xylem tissue. Spectra were baseline-corrected and area-normalized in the range of 1800-850 cm^{-1}.

(B-D) Boxplot representations of the cellulose (B), hemicellulose (C) and lignin (D) composition of xylem spectra. The box and whisker plots represent the values of 521 and 494 individual spectra of wild-type (WT) and *sweet11-1sweet12-1* lines.

(E) Average spectra of WT and *sweet11-1sweet12-1* phloem tissue. Spectra were baseline-corrected and area-normalized in the range of 1800-850 cm^{-1}.

(F-G) Boxplot representations of the cellulose (F) and hemicellulose (G) composition of phloem spectra. The box and whisker plots represent the values of 314 and 311 individual spectra of wild-type and *sweet11-1sweet12-1* lines. The diamonds represent mean values, lines represent median values, the tops and bottoms of the boxes represent the first and third quartiles, respectively, and whisker extremities represent maximum and minimum data points. The black dots are the outliers. Letters above the boxes indicate groups with significant differences as determined by an approximate Fisher-Pitman permutation test and a pairwise comparison test ($P < 0.05$). a.u.: arbitrary unit.

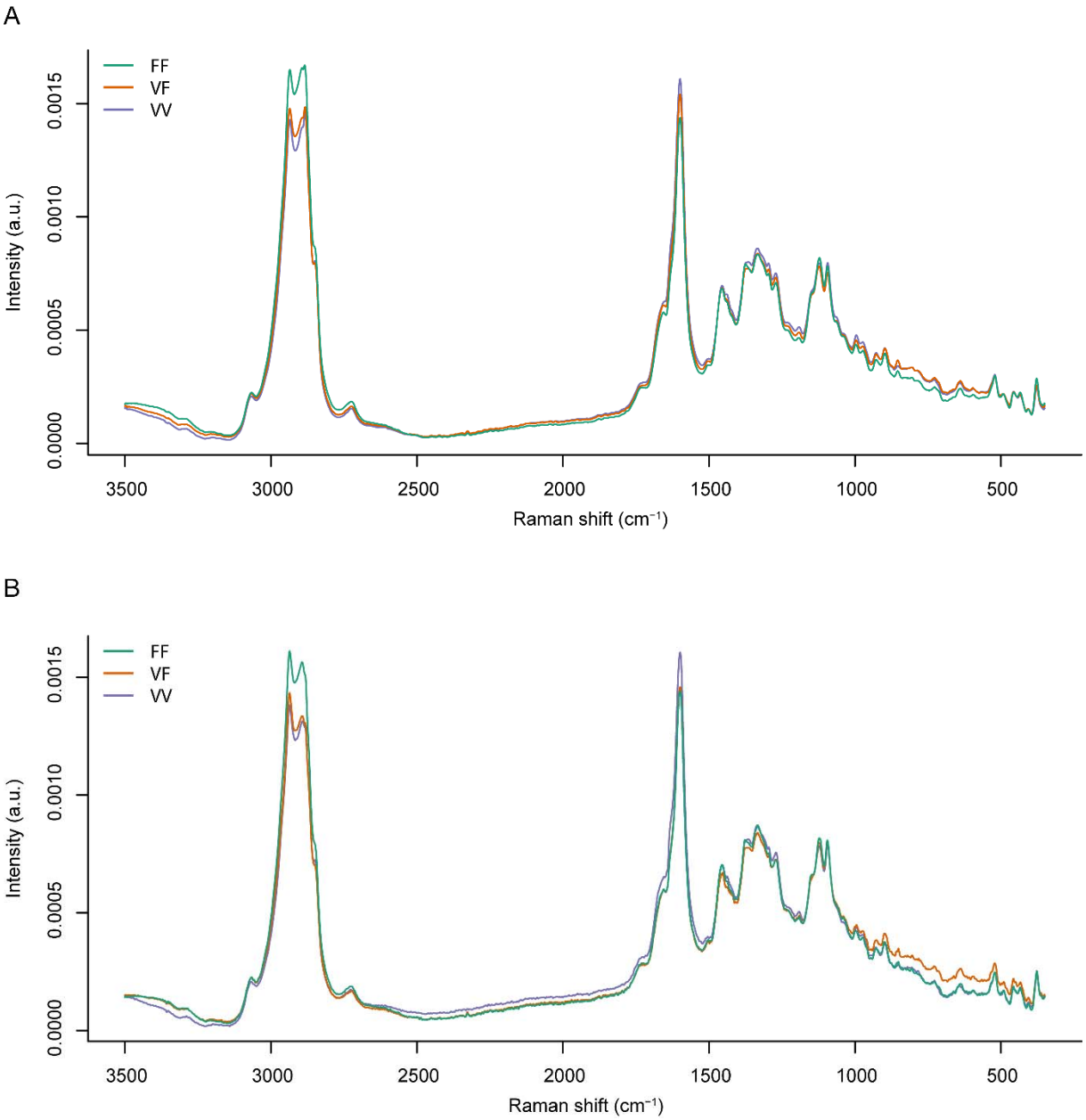

Fig. S3. Average Raman spectra of the different xylem cell types in wild-type and *sweet11-1sweet12-1* lines.

Average Raman spectra of the wild-type (A) or *sweet11-1sweet12-1* line (B) cell walls between xylem vessels (VV), xylem vessels and fibers (VF) or xylem fibers (FF). Spectra were baseline-corrected and area-normalized in the 3500-350 cm^{-1} range. For the wild-type, 51, 139 and 119 individual spectra of VV, VF and FF, respectively, were used to generate the respective average spectra. For *sweet11-1sweet12-1* line, 65, 131 and 71 individual spectra of VV, VF and FF, respectively, were used to generate the respective average spectra. a.u.: arbitrary unit.