Supplemental Information

Flexible and digestible wood caused by

viral-induced alteration of cell wall composition

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Figure S1 Symptom distribution in ARWV-infected branches and cell wall composition. Related to Figure 1. (A) Uninfected (UN) and ARW-infected (ARW) apple tree grafts. The ARW graft has been bent to demonstrate the stem flexibility. (B) 4 year old symptomatic branch from ARW-infected apple tree grafts growing unaided (left hand side) and bent to demonstrate the stem flexibility (right hand side) (C) Representative apple xylem cross-sections stained with 0.05% Toluidine blue taken from uninfected branches and ARWV-infected branches exhibiting variable or severe symptoms. Asymptomatic regions of infected material resemble the uninfected, while cell walls of symptomatic fibres stain a purple colour. Arrow indicates the growth ring. While year 1 growth exhibits clear symptoms, symptoms are only apparent at the end of year 2 and absent from year 3. Scale bars = 50 µm (D) Transmission electron microscopy of apple xylem. Scale bars = 5 µm (left panel) and 3 µm (right panel). Fibres (f), ray cells (r), vessels (v), secondary cell wall (scw), mid lamellae (m) and cell lumen (l) are indicated. (E) Monosaccharide composition of xylem from uninfected (white bars) and symptomatic xylem (grey bars). (F) Normalized spectra of solid-state $^{13}$C NMR analysis from uninfected (black) and symptomatic (blue) cell walls.
Figure S2 Expression of lignin biosynthetic genes and proteins in apple xylem. Related to Table 1. Each square represents the expression of a different gene (regular font) or protein (bold). Log fold change (FC) in gene expression and FC in protein abundance is expressed in terms of symptomatic xylem relative to uninfected xylem. All genes exhibit significantly altered expression with an FDR-adjusted p-value ≤ 0.01 and logFC ± 2. All proteins exhibit significantly altered abundance with a p-value ≤ 0.05 and FC ± 2.
Figure S3 Disruption in the late stages of lignin biosynthesis in symptomatic xylem. Related to Figure 2. Arrows represent enzymatic steps during the late stages of lignin biosynthesis. Dashed arrows indicate steps that are uncharacterised. Graphs show mean metabolites abundance. Asterisks indicate significance based on a T-test (*, p ≤ 0.05, **, p ≤ 0.01). Table shows metabolites that have a fold-change with a p-value < 0.05. Abbreviations: CCR = cinnamoyl-CoA reductase, CAD = cinnamyl alcohol dehydrogenase, FSH = ferulate 5-hydroxylase and COMT = caffeic acid 3-O-methyltransferase.

| Metabolite ID | Putative name                        | Type | FC  | UN   | SYM  |
|---------------|-------------------------------------|------|-----|------|------|
| 2.74_359.0981m/z | syringic acid 4-O-hexoside         | P    | 0.57| 1907.56 | 1093.77 |
| 3.52_359.0980m/z | syringoyl hexose                  | P    | 0.37| 469.20  | 171.49  |
| 9.99_207.0666m/z | sinapaldehyde                      | P    | 0.06| 48.06   | 2.83   |
Table S3 Differentially abundant phenolic metabolites in symptomatic xylem. Related to Figure 2. Fold change (FC) is expressed in terms of symptomatic xylem (SYM) relative to uninfected (UN) xylem. Compounds in bold are annotated with high confidence based on MS/MS spectral library identity matching, and compounds not in bold are putative structures based on MS/MS spectral similarity to library spectra and structural elucidation. The upper table shows metabolites that have a greater than two-fold change in abundance and a minimum abundance of 100 in either symptomatic or uninfected xylem with a p-value ≤ 0.001, while in the lower table the metabolites have a p-value < 0.01. Abbreviations: P = phenylpropanoid, F = flavonoids, O = oligolignols and U = unassigned.
| sRNA sequence                          | ARW-1 | ARW-2 | ARW-3 | ARW-4 | Total |
|---------------------------------------|-------|-------|-------|-------|-------|
| CTCTGACTGGTCTCTCACAATG                | 1718  | 2008  | 710   | 170   | 4606  |
| ATAGTCTACCTGCACGATTAA                | 290   | 616   | 485   | 175   | 1566  |
| CATCACCATCTTTCTCTACAAA              | 260   | 473   | 243   | 89    | 1065  |
| CCACCCGGTTCTTTGCATTCTT               | 137   | 632   | 196   | 37    | 1002  |
| ATAGTCTACCTGCACGATTAA               | 142   | 359   | 222   | 77    | 800   |
| CTCATGGCTGAAGGAAATTTTC            | 187   | 386   | 191   | 36    | 800   |
| CTAGAGGGAACATCGAGAGG                  | 73    | 360   | 152   | 47    | 632   |
| CCACCCGGTTCTTTGCATTCTT                | 95    | 387   | 126   | 22    | 630   |
| GCCACCCGGTTCTTTGCATTCTT               | 140   | 192   | 104   | 51    | 487   |
| GCTTGTGGCCACCCGGTTTTG                  | 58    | 234   | 141   | 52    | 485   |
| CTTAACATGTCAGGATCGCAA                  | 180   | 168   | 117   | 11    | 476   |
| CATCACAGCTTGTTGGCCACCG                 | 111   | 182   | 124   | 21    | 438   |
| TAGAGGGAACATCGAGAGGA                 | 39    | 273   | 92    | 26    | 430   |
| TCATCACCATCTTTCTCTAACA                 | 70    | 181   | 112   | 63    | 426   |
| CCTGGCATCTAACTCAACTT                  | 92    | 235   | 50    | 19    | 396   |
| ACGACTATAGAAAAACTGCAAT                 | 123   | 151   | 88    | 11    | 373   |
| CTTAACATGTCAGGATCGCAA                  | 107   | 124   | 91    | 28    | 350   |
| GCCACCCGGTTCTTTGCATTCTT                | 67    | 160   | 81    | 34    | 342   |
| CACCGGTTCCTTGCACTTCTAG                | 61    | 205   | 48    | 18    | 332   |
| CTTTGCAGAGAGTGCGATTAG                  | 96    | 155   | 49    | 12    | 312   |
| CATCACCATCTTTCTCTATTGAAAC              | 49    | 153   | 57    | 50    | 309   |
| TCATCACATCTTTTCATAACCAA                | 42    | 133   | 55    | 64    | 294   |
| TCATGCCTAGGATCTGAAG                    | 74    | 121   | 56    | 11    | 262   |
| CAGCTGTGGGCGACCGGGTTTCT               | 26    | 95    | 85    | 18    | 224   |
| TCACGCATGCTGGTCTCACAAC                 | 36    | 112   | 46    | 11    | 205   |
| TTTCGTGCAACTACTTCAAAGC                 | 47    | 73    | 56    | 18    | 194   |
| CTGTTGCCACCGGGTTCTTGC                 | 26    | 85    | 62    | 18    | 191   |
| TAGAGGGAACATCTCGAGAGGA                 | 14    | 110   | 33    | 13    | 170   |
| TCAAGATAAGTAGCGAGCTTA                | 31    | 82    | 42    | 11    | 166   |
| TTGGCCCACGGCTTCTGGATT                  | 22    | 70    | 49    | 25    | 166   |
| TCACCATCTTTCTCTAACACA                   | 43    | 67    | 15    | 28    | 153   |
| GAAGTTAAGCCACCGAGATTAA                | 25    | 66    | 33    | 19    | 143   |
| GGGGATTCTCTGAGACGACTA                  | 32    | 80    | 19    | 12    | 143   |
| CTTAACATGCAGGAGTGACCA                  | 27    | 70    | 30    | 14    | 141   |
| TTCAGCCTGAGGGATCTGCC                   | 29    | 57    | 40    | 11    | 137   |
| ATGCTTTTCTACCCTTCTTTC                 | 21    | 45    | 46    | 23    | 135   |
| CATCACATCTTTTCATAACAA                 | 44    | 35    | 37    | 10    | 126   |
| TTAATCGATTAGAGTAGGACG                  | 17    | 61    | 28    | 10    | 116   |
| GCAATTTGACTGTGCAGAGT                   | 32    | 35    | 36    | 12    | 115   |
| AGCTTGTGGCCACCGGTTCTTG                | 24    | 51    | 19    | 20    | 114   |
| TAAGTCATGAGTCGCAA                      | 19    | 61    | 20    | 12    | 112   |
| sRNA sequence                              | ARW-1 | ARW-2 | ARW-3 | ARW-4 | Total |
|-------------------------------------------|-------|-------|-------|-------|-------|
| GCAATTCAGGTAGTGCAGAGTG                   | 18    | 56    | 18    | 14    | 106   |
| TCAACCATCTTTTCTAACA                      | 23    | 32    | 19    | 26    | 100   |
| TTCATCACCATCTTTCTAACAAA                  | 13    | 45    | 18    | 12    | 88    |
| TTCATCACCATCTTTCTAACA                    | 10    | 38    | 17    | 20    | 85    |
| TTCATCACCATCTTTCTAACA                    | 16    | 23    | 29    | 14    | 82    |
| TTCATCACCATCTTTCTAACA                    | 21    | 26    | 16    | 10    | 73    |
| CTGGGCAACCCGATTTCCTGCA                   | 10    | 31    | 15    | 12    | 68    |
| TTCATCACCATCTTTCTAAC                     | 11    | 15    | 13    | 16    | 55    |
| TAATCAAGATAAGTGGCAGC                     | 11    | 21    | 10    | 10    | 52    |

Table S4 sRNAs mapping to the ARWV. Related to Table 2. All sRNA sequences were found in each ARWV-infected wood sample with more than 10 reads per samples. No reads were detected in UN samples.