Table S5. Gene expression for genes flanking insertion 1 in 'HoneySweet' was compared to that of 'Stanley' to determine if changes in expression was detected.

| Tree n° | Scaffold1234 (121,739) | Scaffold1235 (115,945) | Scaffold1332 (85,887) | Scaffold1429 (102,615) | Scaffold1650 (95,093) |
|---------|------------------------|------------------------|------------------------|------------------------|------------------------|
| Leaf    |                        |                        |                        |                        |                        |
| HS      | 83                     | 0.1 0.5               | 0 0 0 0 0.3936         | 0.1 8.5                | 0.4 7.0                |
| ST Inf  | 29                     | 0.3                     | 0.4 0.1 6.0 0.1       | 0.1 31 0.2            |
| ST      | 51                     | 0.1 0.1               | 0.5 0.4 4.9           | 0.7 1.7               |
| Fruit   |                        |                        |                        |                        |                        |
| HS      | 51                     | 0.0                     | 0.0 0 0.2349 0.84     | 0.1 0.3               | 0.0 0.9 0.2           |
| ST Inf  | 47                     | 0.1                     | 0.5 0.4 0.1           | 0.4 1.2               |
| ST      | 107                    | 0.0                     | 0.0 0 0.6474 0.35     | 0.4 1.2               |

- Scaffolds that have sequence matching the plum border sequence of insert 1 are named here with the total nucleotides that cover the 5-7 flanking genes in common with the other scaffolds.
- Tree number represents individual trees from which a leaf and a fruit leaf was made from RNA and sequenced.
- 'HoneySweet'
- 'Stanley' infected with Plum pox virus
- Scale that color codes the ranges of TPMs from 0 to 15.
- A line indicates the position of the insertion.