| | -Manin16g003910.1 |
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| 0.67 | -Manin03g008820.1 |
| CC | – ATPG59.AT3G57790 – Manin09g006660.1 |
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| 1.00 0.91 | ATPG55.AT3G61490 ATPG56.AT4G23500 |
| 0.53 | - Manin16g014550.1 - Manin04g001870.1 |
| | -Manin17g000810.1 |
| 0.86 | – Manin17g000810.2 – ATPG52.AT4G33440 |
| 0.70 | - Manin06g006140.1 - ATPG50.AT5G41870 |
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| 1.00 1.00 | -ATPG47.AT5G49215 |
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| | – Manin04g016040.2 – Manin05g011300.1 |
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| 1.00 1.00 | ATPG5.AT4G01890 ATPG6.AT1G48100 |
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| 0.97 | -Manin04g015430.1 -ATPG11.AT3G26610 |
| 0.70 1.00 | -Manin09g009540.1 |
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| | ATPG68.AT5G17200 ATPG60.AT5G44830 |
| 1.00 | -ATPG61.AT5G44840 |
| 0.86 | ATPG62.AT4G35670 ATPG63.AT5G27530 |
| 0.56 | - Manin05g011290.1 - ATPG66.AT4G32380 |
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| 0.62 0.95 | - ATPG16.AT3G07970 - Manin09g015600.1 |
| 0.79 | -Manin20g006090.1 -ATPG14.AT2G41850 |
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| | -Manin12g011700.1 |
| 0.97 | -Manin12g011710.1 -ATPG21.AT2G43880 |
| 0.57 | – ATPG20.AT2G43890 – ATPG18.AT1G05650 |
| 0.94 1.00 | - ATPG19.AT1G05660 |
| | -ATPG24.AT1G65570 -ATPG25.AT2G43860 |
| 0.60 | – ATPG22.At2g43870 – ATPG23.AT3G59850 |
| 0.71 | - Manin12g011680.1 - Manin12g011660.1 |
| 0.50 | -Manin12g011670.1 |
| 0.94 | – Manin12g011690.1 – Manin00g014940.1 |
| 1.00 | – Manin00g014950.1 – Manin12g011650.1 |
| 0.72 | - Manin02g006220.1 - Manin02g003470.1 |
| 0.97 | -Manin02g003450.1 |
| 0.99 | -Manin02g003460.1 -ATPG36.AT1G78400 |
| 0.71 | ATPG37.AT2G33160 ATPG35.AT1G17150 |
| 1.00 | -ATPG34.AT1G43080 |
| 0.92 1.00 | - ATPG32.AT1G43090 - ATPG33.AT1G43100 |
| 1:00 | ATPG30.AT2G40310 ATPG31.AT4G13760 |
| 0.36 | - ATPG29.AT2G26620 |
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| 0.52 | ATPG28.AT2G15470 ATPG44.AT4G18180 |
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| 0.52 | – Manin02g010300.1 – Manin04g016150.1 |
| | ATPG45.AT1G02790 Manin11g009310.1 |
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| 1.00 | - Manin00g002070.1 - ATPG40.AT3G07840 |
| 1.00 | -ATPG41.AT5G48140 |
| 0.50 | ATPG38.AT3G07820 ATPG39.AT3G07830 |
| | |

Supplementary Figure S2. Phylogenetic analysis of *Mangifera indica* L. and *Arabidopsis thaliana* polygalacturonases. The evolutionary history was inferred using the Neighbor-Joining method, while distances were computed using the Poisson correction method. The analysis involved 117 amino acid sequences, of which 48 sequences belong to mango (*MiPGs*). Taxa clustered together in the bootstrap test (2000 replicates). Evolutionary analyses were conducted in MEGA X.