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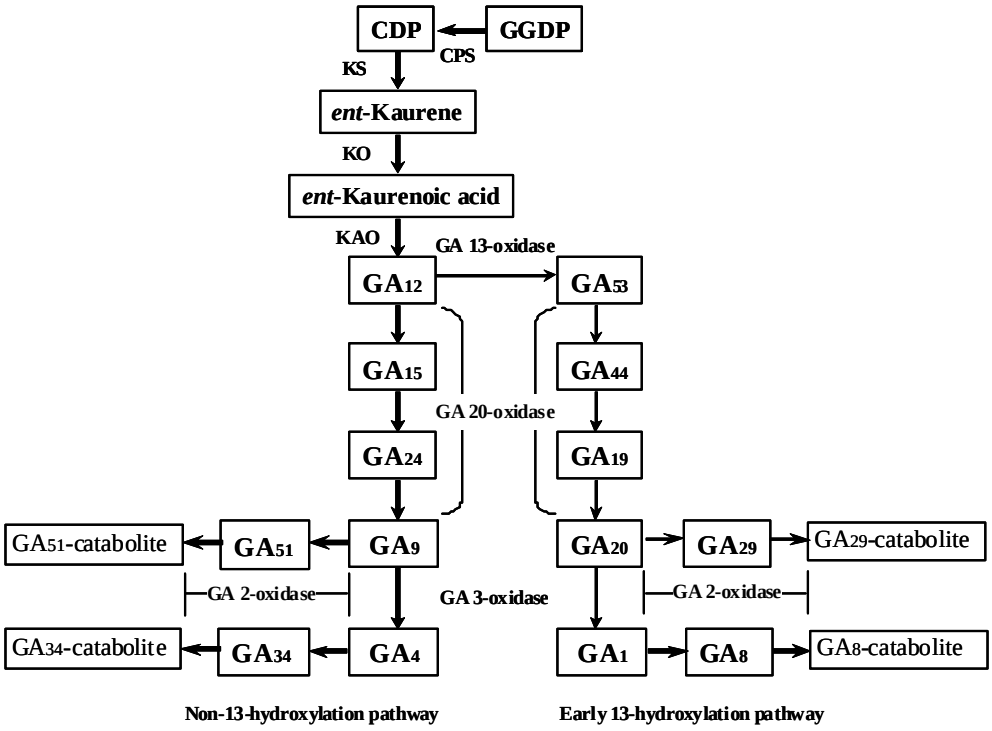
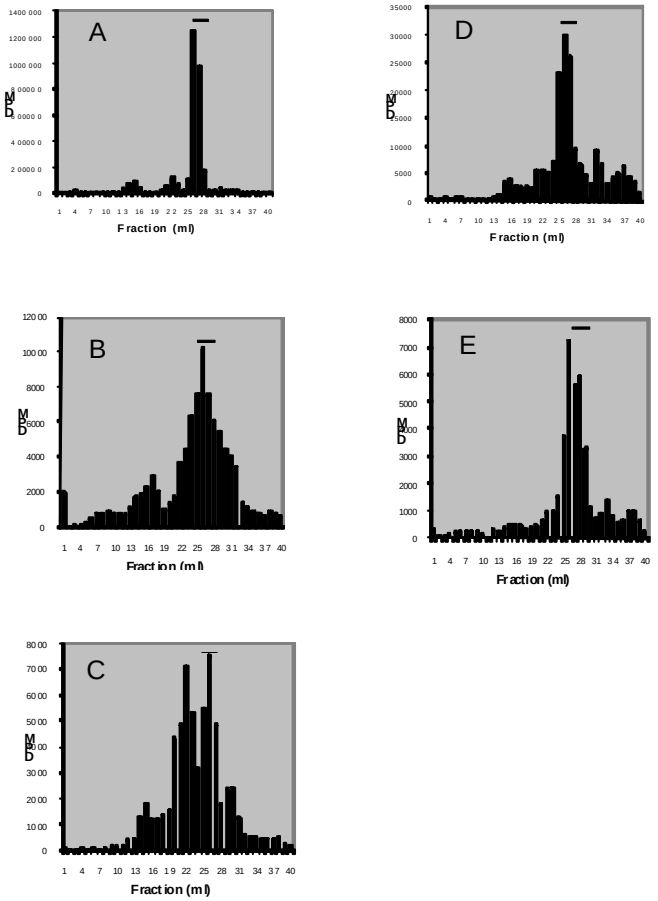
Supplemental Table I. Primer sequences used for quantitative RT-PCR analysis of genes from GA metabolism. *SlCPS* (AB015675), *SlGA20ox1* (AF049898), *SlGA20ox2* (AF049899), *SlGA20ox3* (AF049900), *SlGA20ox4* (EU652334), *SlGA3ox1* (AB010991), *SlGA3ox2* (AB010992), *SlGA2ox1*(EF441351), *SlGA2ox2* (EF441352), *SlGA2ox3* (EF441353), *SlGA2ox4* (EF441354), *SlGA2ox5* (EF441355),

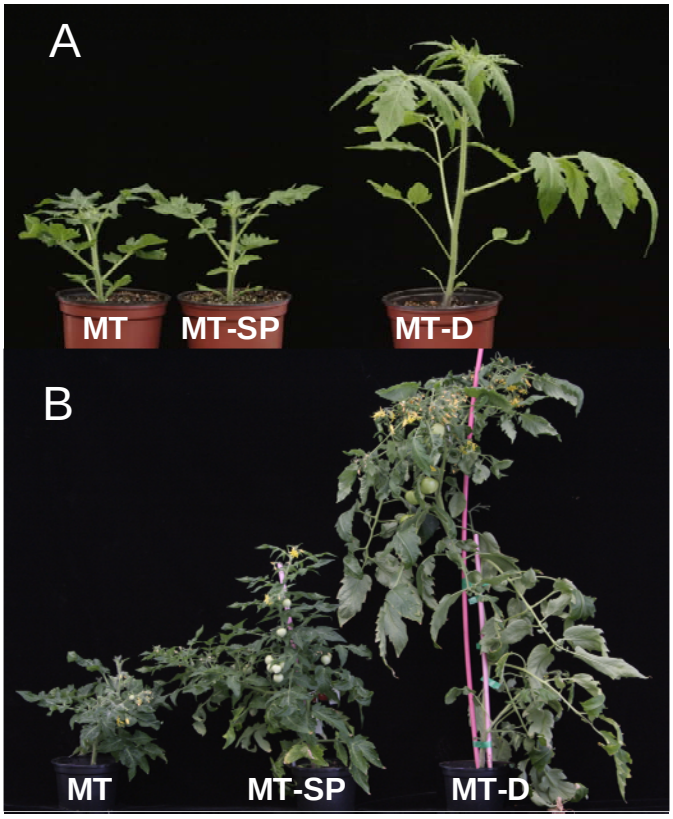
Gene	Sense	Antisense
SlCPS	5'-ATACCTAGAGCTAGCGAAATC-3'	5'-ACTGCCTAAATAGTACGTAACC-3'
SlGA20ox1	5'-CTCATTTCTAATGCTCATCGT-3'	5'-TGCAGATGATTCTTTCTTAGCG-3'
SlGA20ox2	5'-TTTCCATATTCTACCCTACAAG-3	5'-TCATCGCATTACAATACTCTT-3'
SlGA20ox3	5'-AGCCAAATTATGCTAGTGTTAC-3'	5'-TTTTATGAGATTTGTGTCAACC-3'
SlGA20ox4	5'-GATGATAAATGGCACTCTATTC-3'	5'-TGACTTCCTTGTTCTTCTACAG-3'
SlGA3ox1	5'-GGCATTAGTAGTTAATATAGGTGA-3'	5'-AAATAAGCTACAGAAAGTCGATA-3'
SlGA3ox2	5'-GATCATAAATTTGTCATGGATAC-3'	5'-TGTTTCCATATGGTTAAGTAATC-3'
SlGA2ox1	5'-GGCATGTAAGATATTAGAATTGA-3'	5'-TTAATCCGTAGTAGAGAATCAGA-3'
SlGA2ox2	5'-ATTAAGATCCAATAACACTTCG-3'	5'-TCTTGATTTCACACTATTTGC-3'
SlGA2ox3	5'-GACCCTTCTACTTTCAGCTC-3'	5'-AAATTGAATTGTCTTCTATCCA-3'
SlGA2ox4	5'-ATGGAAGGAAAAGACAGTTTA-3'	5'-CTTTTCTCAAATAGGACCAAC-3'
SlGA2ox5	5'-GATCACTTACCAATAATCAACAG-3'	5'-CGTCATGGTTTACGACTTTA-3'



Supplemental Fig. S1. Scheme of gibberellin metabolic pathway. GGDP, geranylgeranyl diphosphate; CPS, copalyldiphosphate; CPS, copalyldiphosphate synthase; KS, *ent*-kaurene synthase, KO, *ent*-kaurene oxidase; KAO, *ent*-kaurenoic acid oxidase.



Supplemental Fig. S2. HPLC profiles of applied [^{3}H]IAA and [^{3}H] radioactivity recovered in extracts from material collected 48 h after application of [^{3}H]IAA to the ovary or apex. (A) [^{3}H]IAA used in the experiments. (B) Extract from treated ovaries. (C) Extract from pedicels of treated ovaries. (D) Extract from treated apical shoots. (E) Extract from stem and young leaves below treated apices. The bars correspond to HPLC fractions with the same retention time as [^{3}H]IAA.



Supplemental Fig. S3. Pictures of representative MT, MT-SP and MT-D plants at six leaves (A) and at fruit ripening (B) stages. MT-SP and MT-D plants were obtained by introgressing into MT the wild type alleles *Sp* (from cv Moneymaker) and *D* (from cv Madrigal), respectively, according to the protocol described elsewhere (Zsögon et al., 2008). As expected, MT-SP plants had phenotype similar to MT plants until flowering (A), but were taller afterwards due to indeterminate growth (B). MT-D plants were taller than MT plants at all stages and their leaves were much larger and did not have the dark-green colour nor the wrinkle surface characteristic of brassinosteroid-deficient plants (Martí et al., 2006).