SUPPLEMENTAL FIGURE LEGENDS

Supplementary Fig. 1. Scheme of GA metabolic pathways.

Supplementary Fig. 2. Maximum likelihood phylogenetic tree based on comparison of *GA20ox*, *GA3ox* and *GA2ox* protein sequences from Arabidopsis and tomato. Branch lengths are proportional to sequence divergence. Bootstrap values above 50% are shown, whereas asterisks indicate statistical significance according to the weighted least-squares likelihood ration test (**, $P < 0.01$; *, $P < 0.05$). The five genes characterized in this study are shown in bold type. Accession numbers corresponding to the sequences in the tree are the following: AtGA20ox1, X83379; AtGA20ox2, X83380; AtGA20ox3, X83381; AtGA20ox4, NM104778; AtGA20ox5, DQ056484; AtGA3ox1, L37126; AtGA3ox2, AF070937; AtGA3ox3, NM118289; AtGA3ox4, NM106682; AtGA2ox1, AJ132435; AtGA2ox2, AJ132436; AtGA2ox3, AJ322437; AtGA2ox4, NM103695; AtGA2ox6, NM100121; AtGA2ox7, AC079284; AtGA2ox8, AL021960; SlGA20ox1, AF049898; SlGA20ox2, AF049899; SlGA20ox3, AF049900; SlGA3ox1, AB010991; SlGA3ox2, AB010992; SlGA2ox1, EF441351; SlGA2ox2, EF441352; SlGA2ox3, EF441353; SlGA2ox4, EF441354; SlGA2ox5, EF441355**.**

Supplementary Fig. 3. HPLC radioactivity traces of products of $[^{14}C]GA_{12}$, $[^{14}C]GA_9$, $[^{14}C]GA_4$, $[^{14}C]GA_{53}$, $[^{14}C]GA_{20}$, and $[^{14}C]GA_1$, incubated with heterologous expression products of *SlGA2ox1*, *-3*, *-4* and *-5* after 2 h incubation at 30ºC.

Supplementary Fig. 4. Alignment of amino acid sequences corresponding to GA 2-oxidases from groups I, II and III used to construct the phylogenetic tree of Fig. 5. ○, Fe^{2+} binding residues; ↑, 2-oxoglutarae binding residues; ●, amino acids conserved in groups I and II.