Use of 144 stem-cuttings containing 3 nodes
(16 plants per treatment and per sampling time)

Dipping bottom node (node # 12) for 18 h at 25°C in either water ('control'),
50 ppm GA_3 ('GA_3') or 5 ppm PB ('PB')

Planting into pots with washed sand

1 week (1W) sampling
(16 plants X 3)

- Total of four plants used for root development parameters (including image capture and root architecture analysis by WinRHIZO*).

- Total of 12 plants used for root fresh weight, root anatomy (six to eight plants) and RNA extraction.

2 week (2W) sampling
(16 plants X 3)

- Total of four plants used for root development parameters (including image capture and root architecture analysis by WinRHIZO*).

- Total of 12 plants used for root fresh weight, gibberellin and starch analyses, root anatomy (six to eight plants) and RNA extraction.

5 week (5W) sampling
(16 plants X 3)

- Total of four plants used for root development parameters (including image capture and root architecture analysis by WinRHIZO*).

- Total of 12 plants used for root fresh weight, starch analysis, root anatomy (six to eight plants) and RNA extraction.

For all 16 plants, stem length was measured at 3W, 4W, 5W, and storage roots counted and analyzed at 5W.

SUPPLEMENTARY FIGURE S1. Schematic representation of the experimental setup. Details are given in Materials and methods section. *Root development parameters included adventitious root number and cumulative length; lateral root number and cumulative length, lateral root density, root volume and root surface area. For anatomy, roots were sampled in FAA. For RNA extraction, roots were immediately frozen at -80°C.
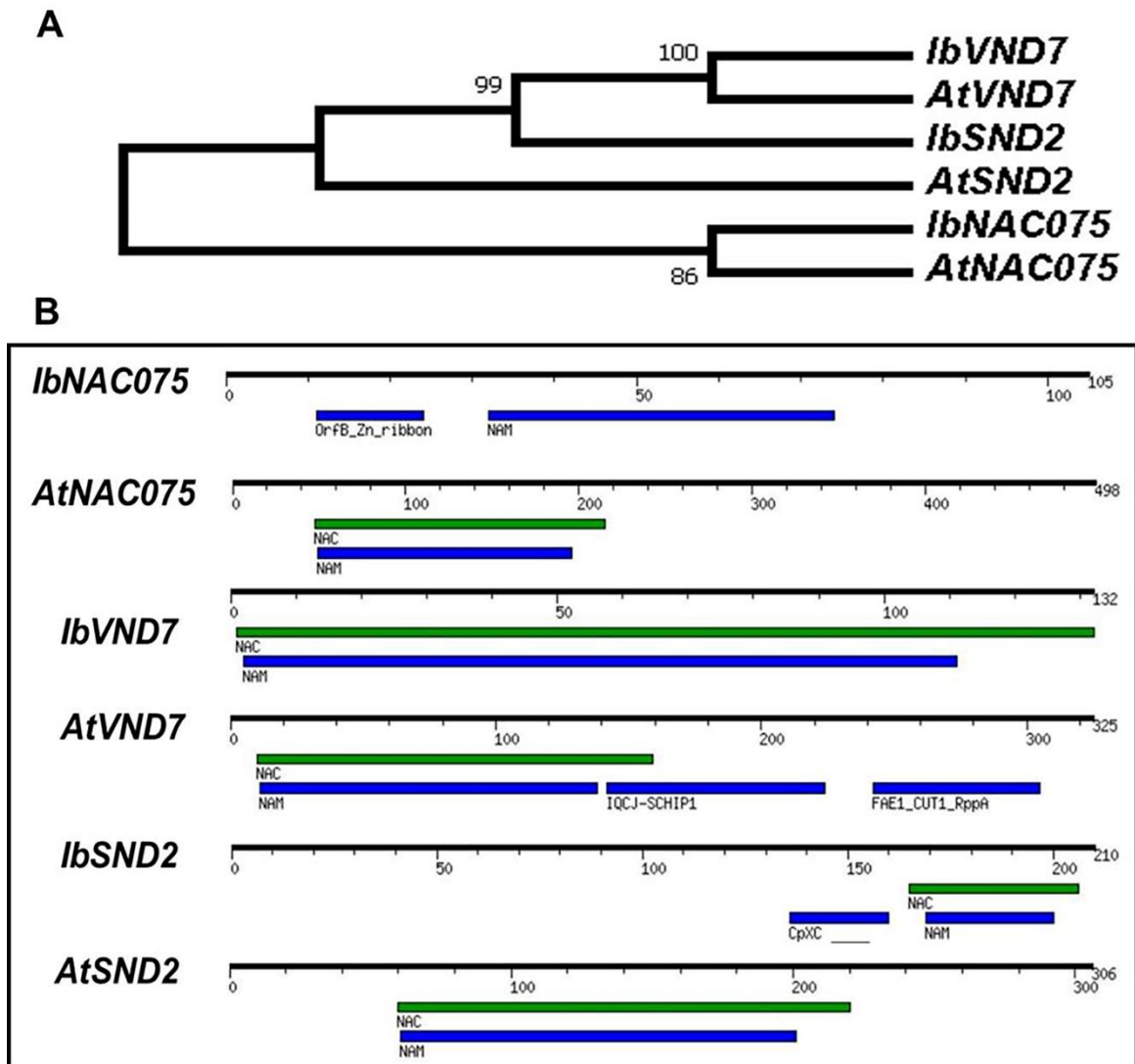
SUPPLEMENTARY FIGURE S2. Identification of potential sweetpotato orthologues of *Arabidopsis* vascular development regulators. Phylogenetic tree showing homology of sweetpotao orthologues/genes to their corresponding *Arabidopsis* genes (A). Phylogenetic tree was constructed using MEGA by neighbor-joining method with 1000 bootstrap replicates. Each gene showing conserved NAC and NAM domains (B). Identification of NAC and NAM domains was done by motif search analysis using MOTIF: Searching Protein Sequence Motifs- GenomeNet (https://www.genome.jp/tools/motif/).
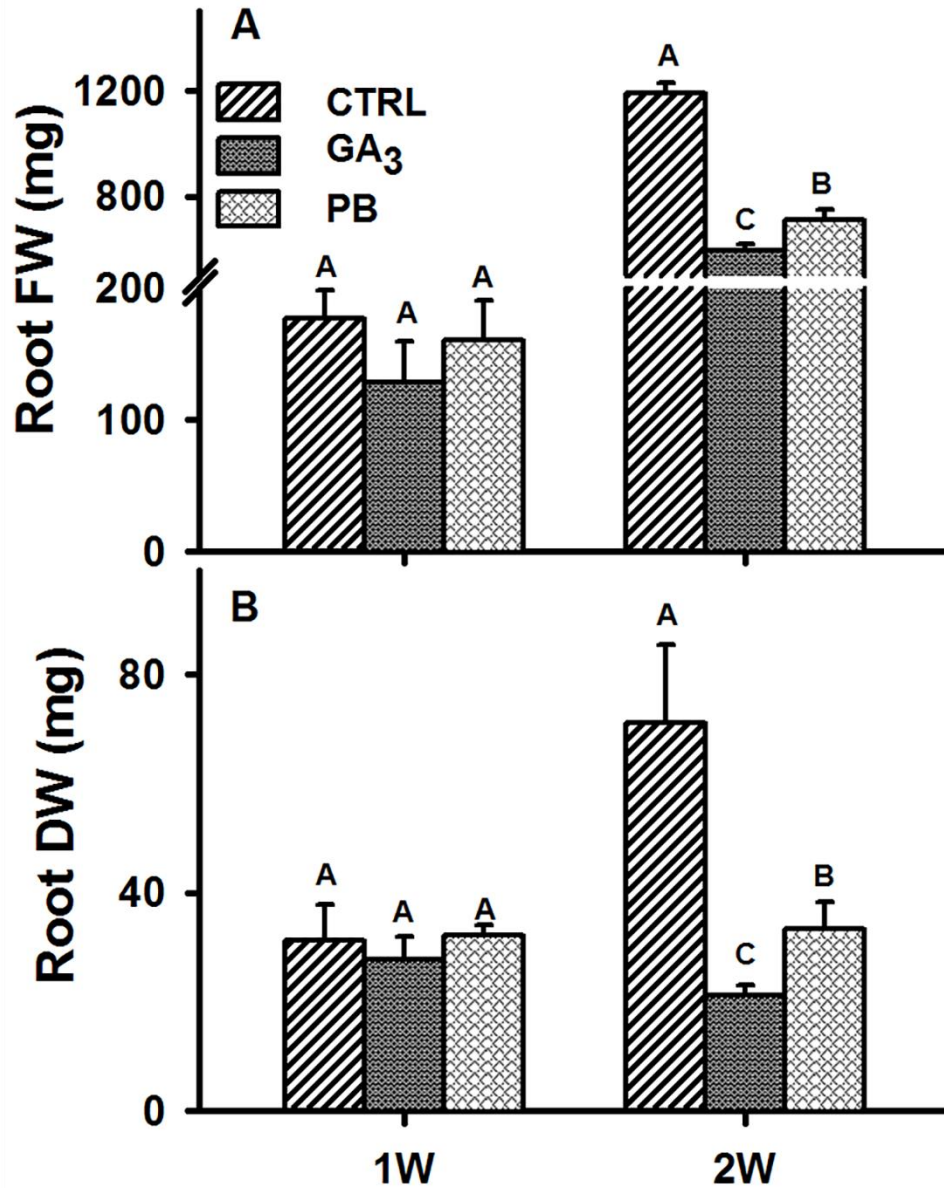
SUPPLEMENTARY FIGURE S3. Effect of GA$_3$ application on sweetpotato "*Georgia Jet*" root fresh weight (FW; **A**) and dry weight (DW; **B**). Root system weight per plant was recorded at one and two weeks (1W and 2W, respectively) after planting. Bars represent mean of 16 (FW) or 4 (DW) independent biological replicates (plants) ± SE. Significance analysis was performed by using student's t-test ($P \leq 0.05$), where unlike letters represent significant differences between treatments within a sampling group. CTRL, Control (treated with water); GA$_3$, application of 50 ppm gibberellic acid 3 for two weeks; PB, application of 5 ppm paclobutrazol for two weeks.
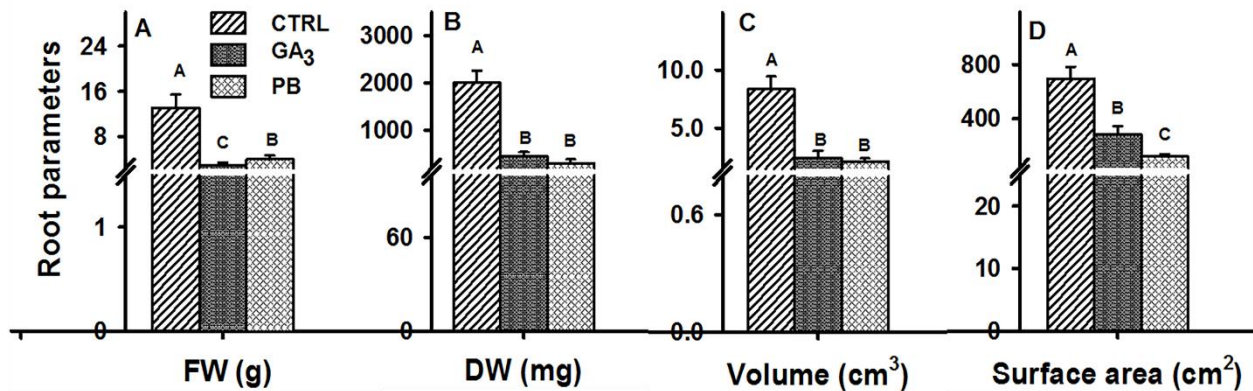
SUPPLEMENTARY FIGURE S4. Effect of GA3 application on sweetpotato "*Georgia Jet*" root system parameters at the time when storage-root formation was observed. Root system fresh weight (FW; **A**), dry weight (DW; **B**), volume (**C**), and surface area (**D**) per plant were recorded at five weeks after planting. The measured values included all root types present at the time of sampling (adventitious roots; lateral roots and storage-roots). Bars represent mean of four independent biological replicates (plants) ± SE. Significance analysis was performed by using student's t-test $(P \leq 0.05)$, where unlike letters represent significant differences between treatments within a sampling group. CTRL, Control (treated with water); GA3 , application of 50 ppm gibberellic acid 3 for two weeks; PB, application of 5 ppm paclobutrazol for two weeks.
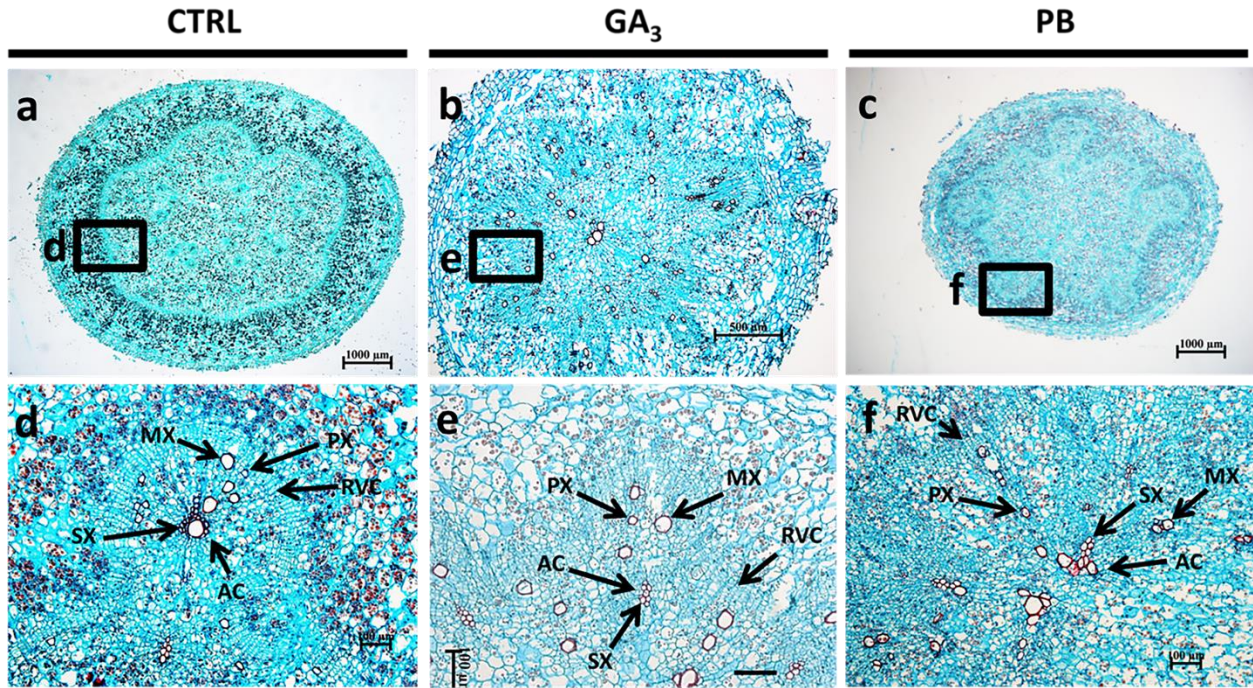
SUPPLEMENTARY FIGURE S5. Effect of GA_3 application on sweetpotato "*Georgia Jet*" storage-root anatomy. Representative cross-sections of SRs sampled at 5 weeks (5W) after planting from control plants (CTRL, treated with water; **a**, **d**), plants treated with 50 ppm gibberellic acid 3 for two weeks (GA_3; **b**, **e**) and plants treated with 5 ppm paclobutrazol for two weeks (PB; **c**, **f**). Sections were stained with safranin and fast green and represent six to eight roots sampled from individual plants. Areas marked by black rectangle (in **a**, **b**, **c**) were enlarged and are presented in **d**, **e** and **f**, respectively. Scale bar = 1000 µm (**a**, **c**), 500 µm (**b**) and 100 µm (**d**, **e**, **f**).