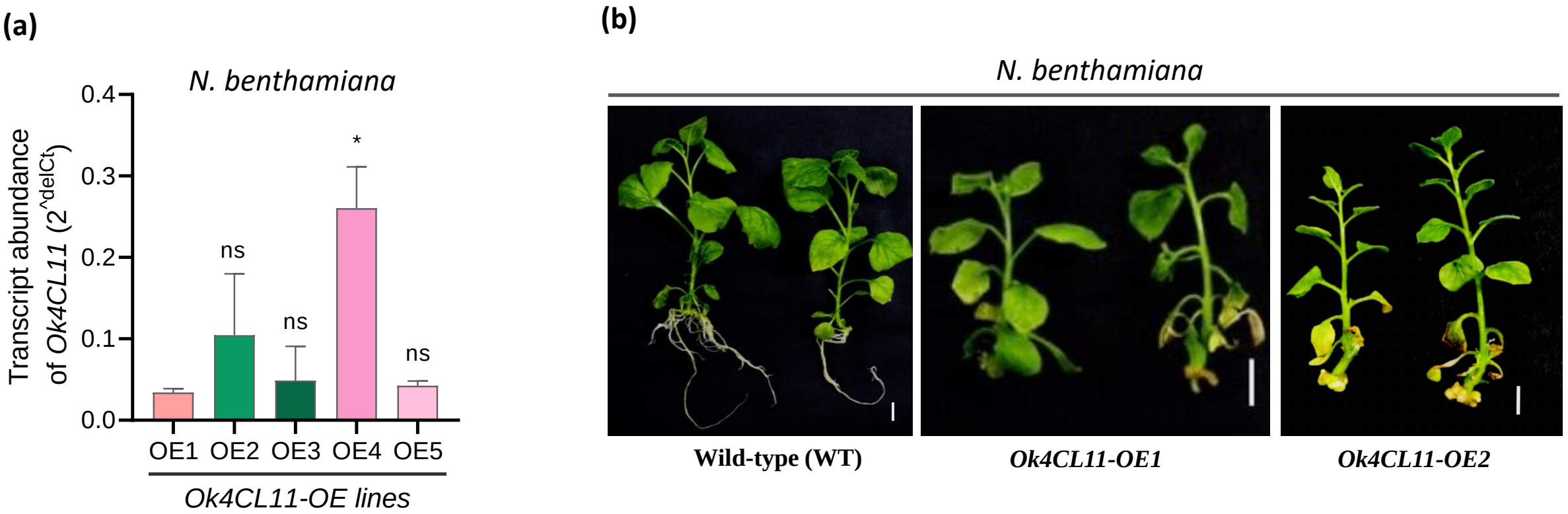
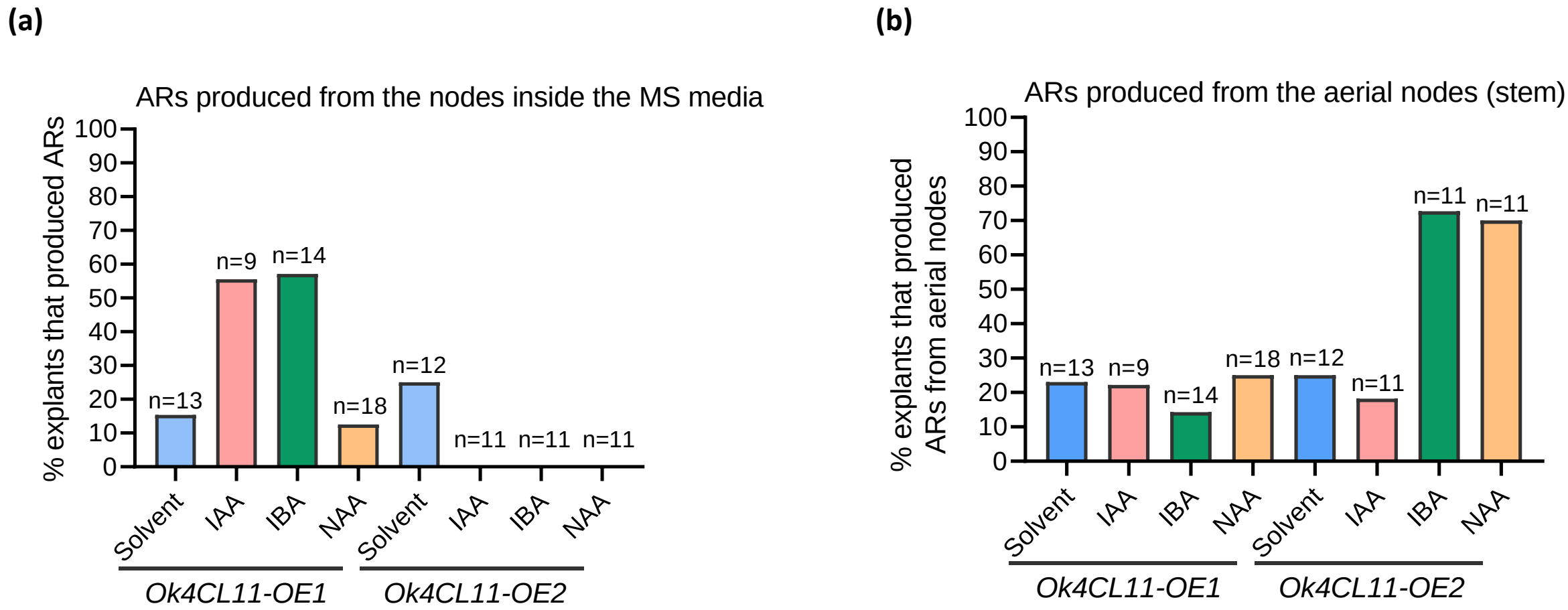
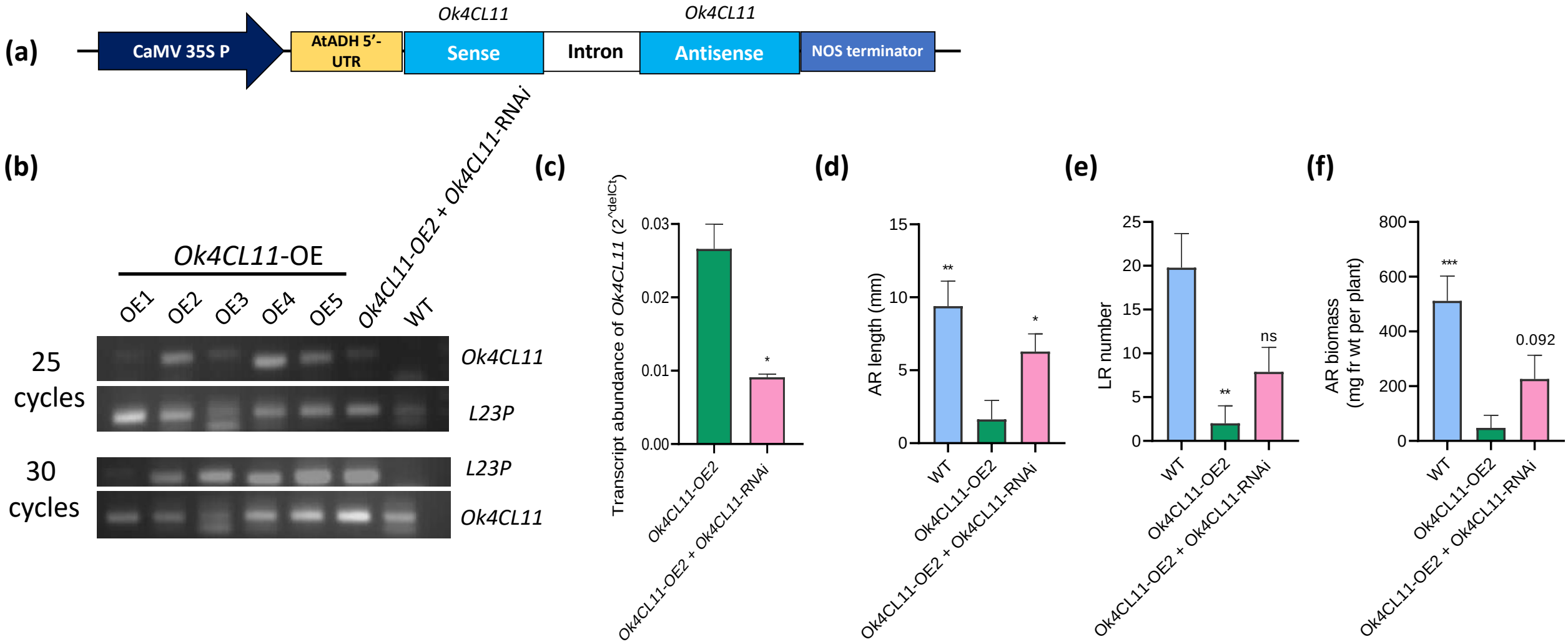


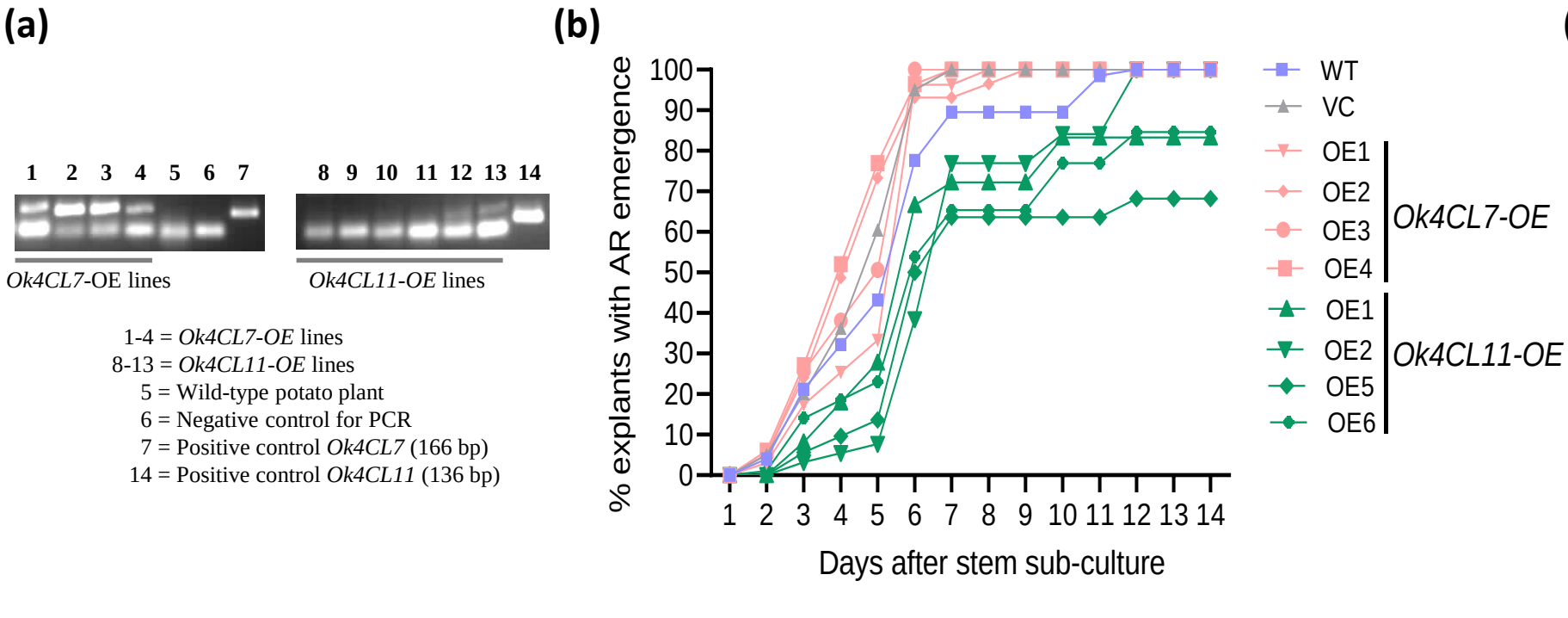
Supplementary Fig. 1 Transgenic line screening and the phenotypes of *Ok4CL11-OE N. benthamiana* lines after two months of stem sub-culture. RT-qPCR analysis was performed to check the levels of *Ok4CL11* overexpression in five independent transgenic *N. benthamiana* lines expressing *Ok4CL11* gene (a). To calculate the statistical significance, the transcript level in OE1 was considered as 1.0. Student's t-test was used to check the level of significance with one asterisk indicating $p<0.05$. ns= not significant. Error bars represent ± standard error of means from three biological replicates. Images of *in vitro* grown *N. benthamiana* plants of wild-type (WT) and two *Ok4CL11-OE* lines (b). Two months after stem sub-culture, WT plants show normal root growth, whereas *Ok4CL11-OE* lines (OE1 and OE2) exhibited a rootless phenotype. Two representative plants of WT and both *Ok4CL11-OE* lines are shown. Scale bar= 1 cm.



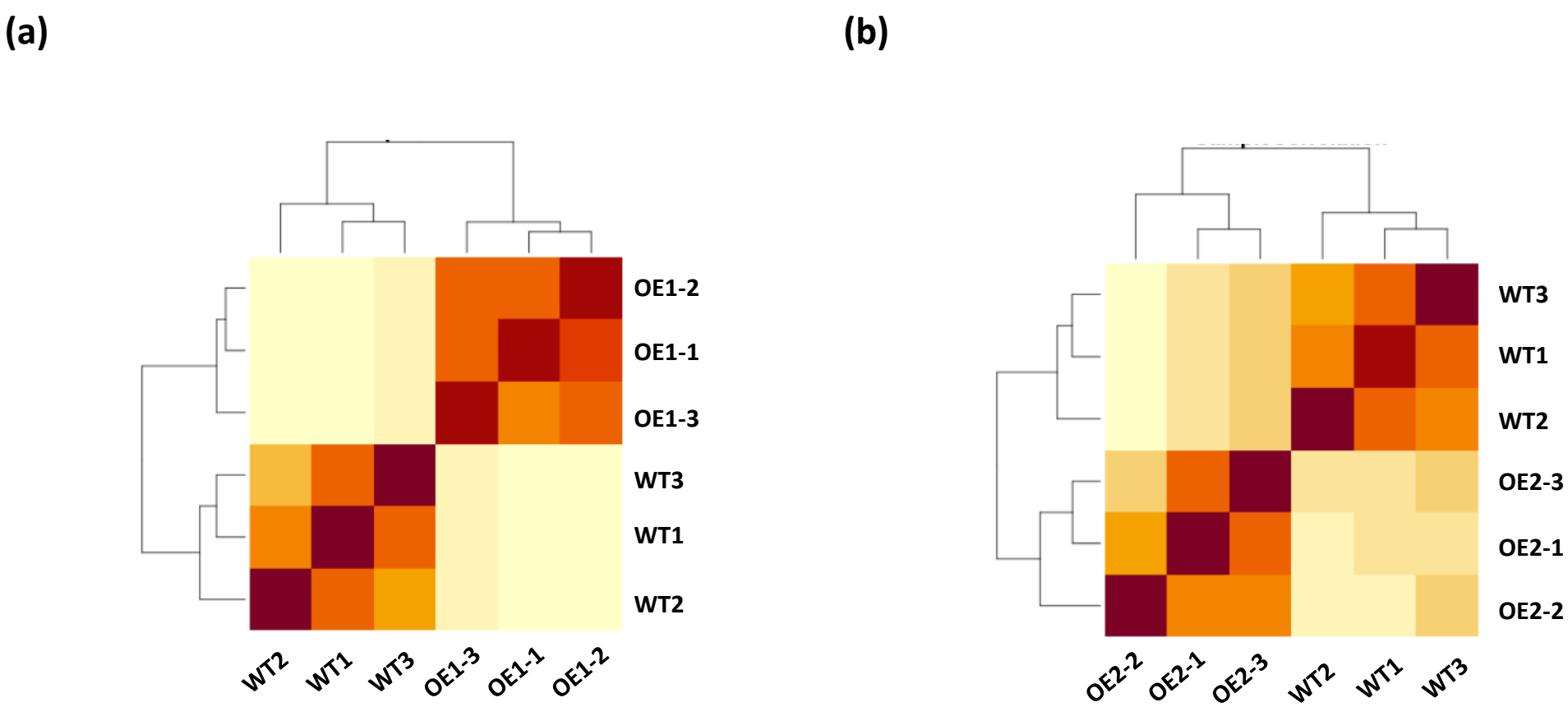
Supplementary Fig. 2 Effect of supplementing various auxins to stem explants of *Ok4CL11-OE* lines of *N. benthamiana*. Stem explants of two *Ok4CL11-OE* lines of *N. benthamiana* (OE1 and OE2) were grown on MS media with and without auxins (IAA, IBA and NAA) under *in vitro* conditions. All three phytohormones were used at 0.1 mg/L concentration. The explants were observed for the AR emergence from the node (stem) inside media (a) and the explants that produced ARs from the aerial stem nodes (b) were recorded after 1 month of hormone supplementation. The number of biological replicates (n) used are shown above each bar in the graph.



Supplementary Fig. 3 Molecular screening of the *Ok4CL11*-RNA*i* line of *N. benthamiana* and associated AR phenotypes. *Ok4CL11*-RNA*i* construct (a) was transformed in *Ok4CL11-OE2* line background. Semi-quantitative PCR (25 and 30 cycles for both reference gene *L23P* from *N. benthamiana* (amplicon: 110 bp) and *Ok4CL11* (amplicon: 136 bp) (b), and RT-qPCR analysis confirmed 66% silencing of *Ok4CL11* in the *Ok4CL11-OE2+Ok4CL11-RNAi* line (biological replicates= 3) (c). An unique sequence of *Ok4CL11* gene spanning ~350 bp were used to generate *Ok4CL11*-RNA*i* construct. The root growth phenotypes- AR length (d), LR number (e) and the AR biomass (measured as milligram fresh weight; mg fr wt) (f) were represented. For panels D-F, Student's t-test was used to check the level of significance with one, two and three asterisks indicating p-values of <0.05, <0.01, and <0.001, respectively. ns= not significant at p<0.05. Error bars represent ± standard error of means. n= 9, 8 and 9 for WT, *Ok4CL11-OE2* and the *Ok4CL11-OE2 + Ok4CL11-RNAi* line, respectively.



Supplementary Fig. 4 *Ok4CL11*-OE lines of potato (*S. tuberosum* cv. Désirée) exhibited a reduced AR emergence rate, whereas *Ok4CL7-OE* showed normal AR growth. RT-PCR based confirmation of *Ok4CL7* and *-11* overexpression potato lines (a). AR emergence rate (b) and the number of ARs per plant (c) in transgenic potato lines is compared to wild-type (WT) or vector control (VC) plants. Number of stem sub-cultured explants per line (n) in panel (b) were: WT= 65, VC= 63, *4CL11-OE1*= 18, *4CL11-OE2*= 13, *4CL11-OE3*= 22, *4CL11-OE4*= 26, *4CL7-OE1*= 27, *4CL7-OE2*= 29, *4CL7-OE3*= 32, *4CL7-OE4*= 27. Percentage of the total explants showing the AR emergence was scored daily up to 2 weeks. The number of ARs and biomass was measured at 14 days after stem sub-culture. For panel C, Student's t-test was used to check the level of significance with four asterisks indicating p-value <0.001. ns= not significant at p<0.05. Error bars represent ± standard error of means.

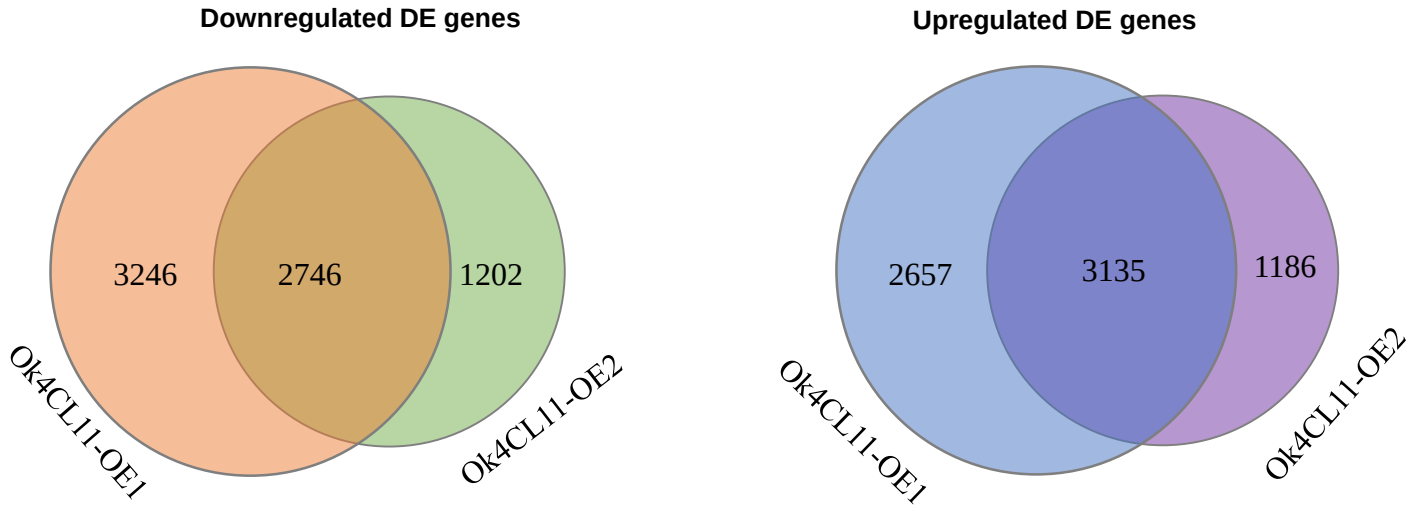


Supplementary Fig. 5 Heat map representing the correlations between the RNA-sequencing samples. The overall similarity across the samples (between the biological replicates and lines) using the variance stabilizing transformed values. Comparison is shown between (a) WT and *Ok4CL11-OE1*, and (b) WT and *Ok4CL11-OE2*.

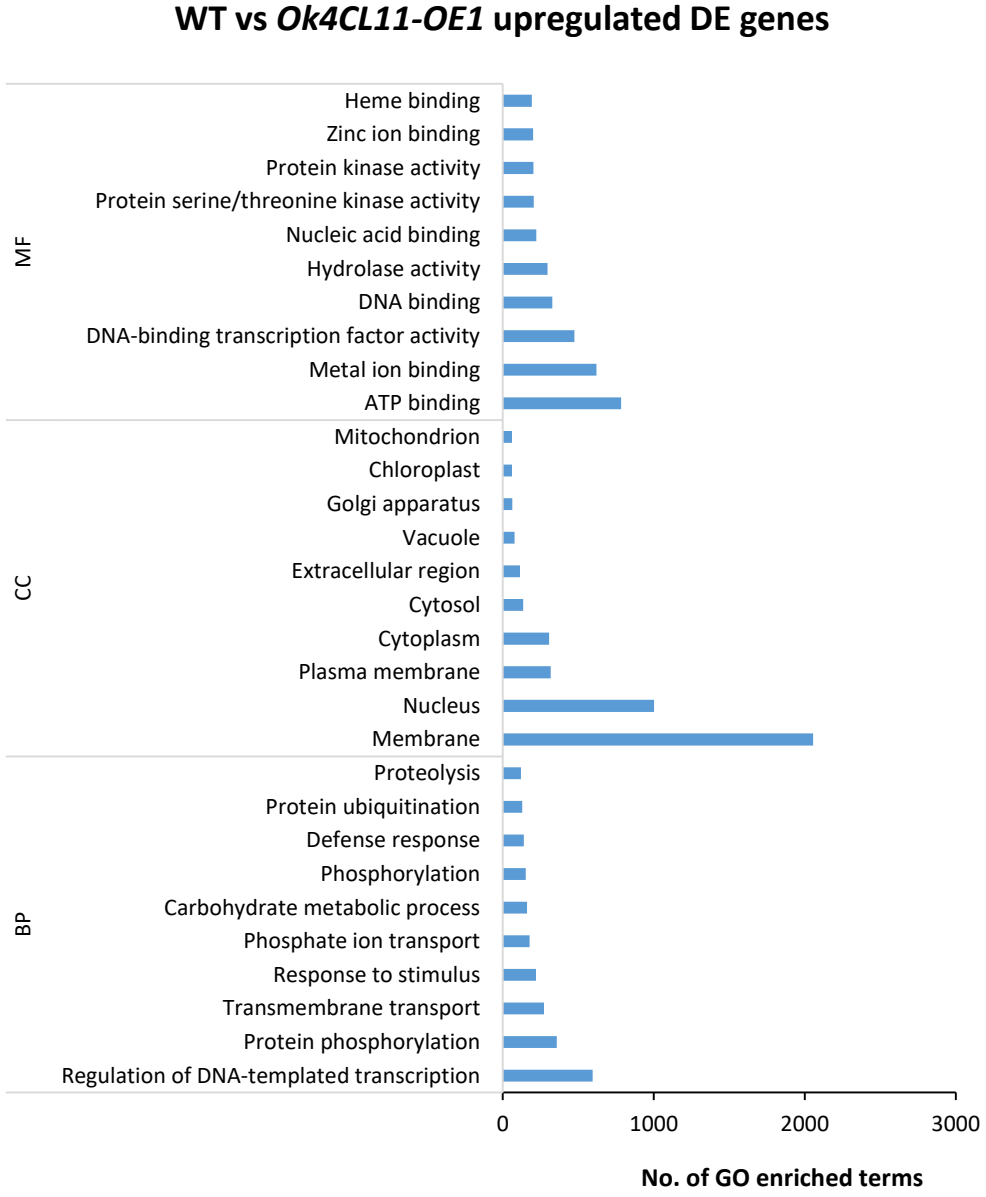
(a)

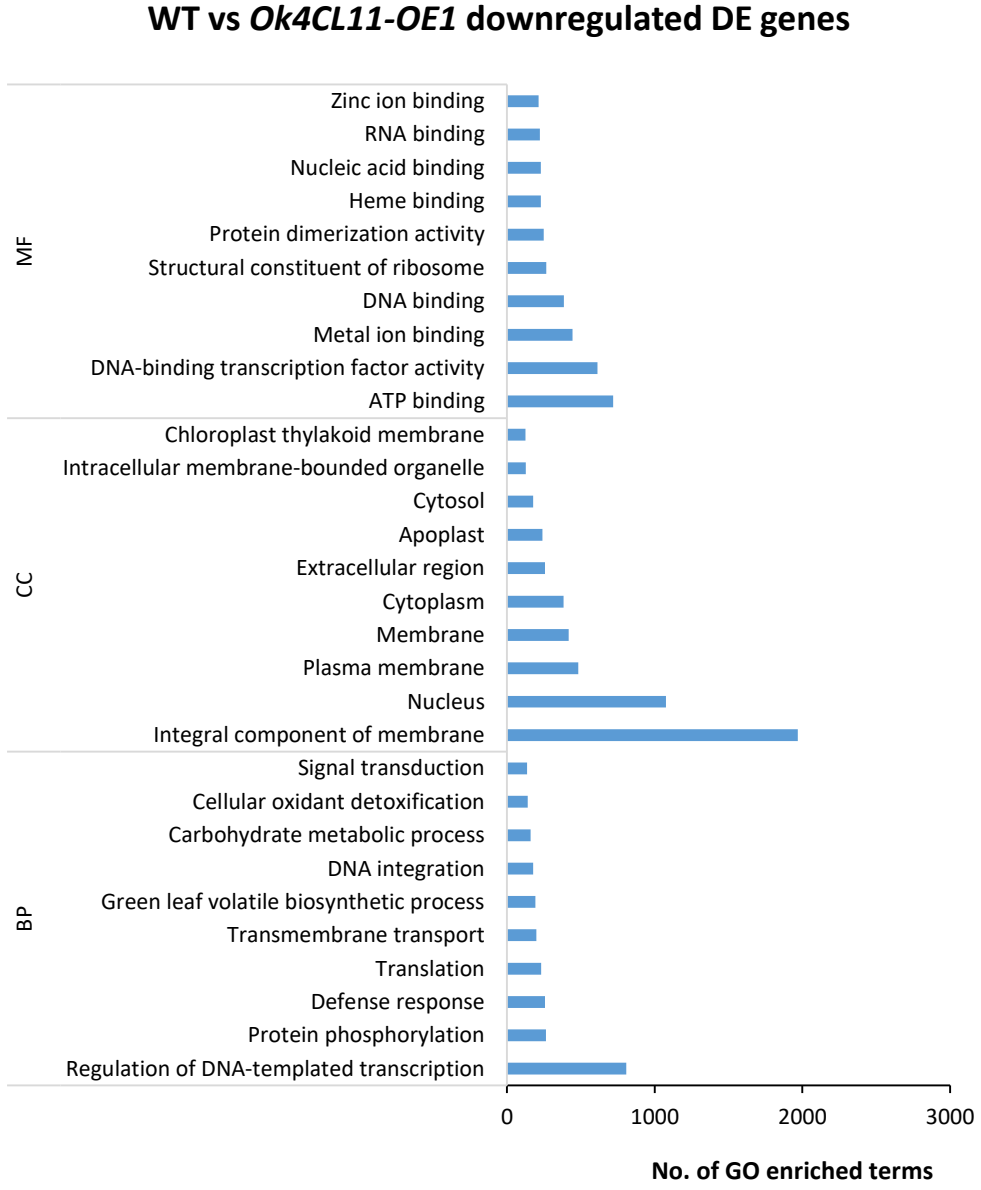
Comparison	Total number of DE genes	Gene expression pattern	Number of DE genes
WT vs *Ok4CL11-OE1*	11784	Upregulated	5792
		Downregulated	5992
WT vs *Ok4CL11-OE2*	8269	Upregulated	4321
		Downregulated	3948

(b)

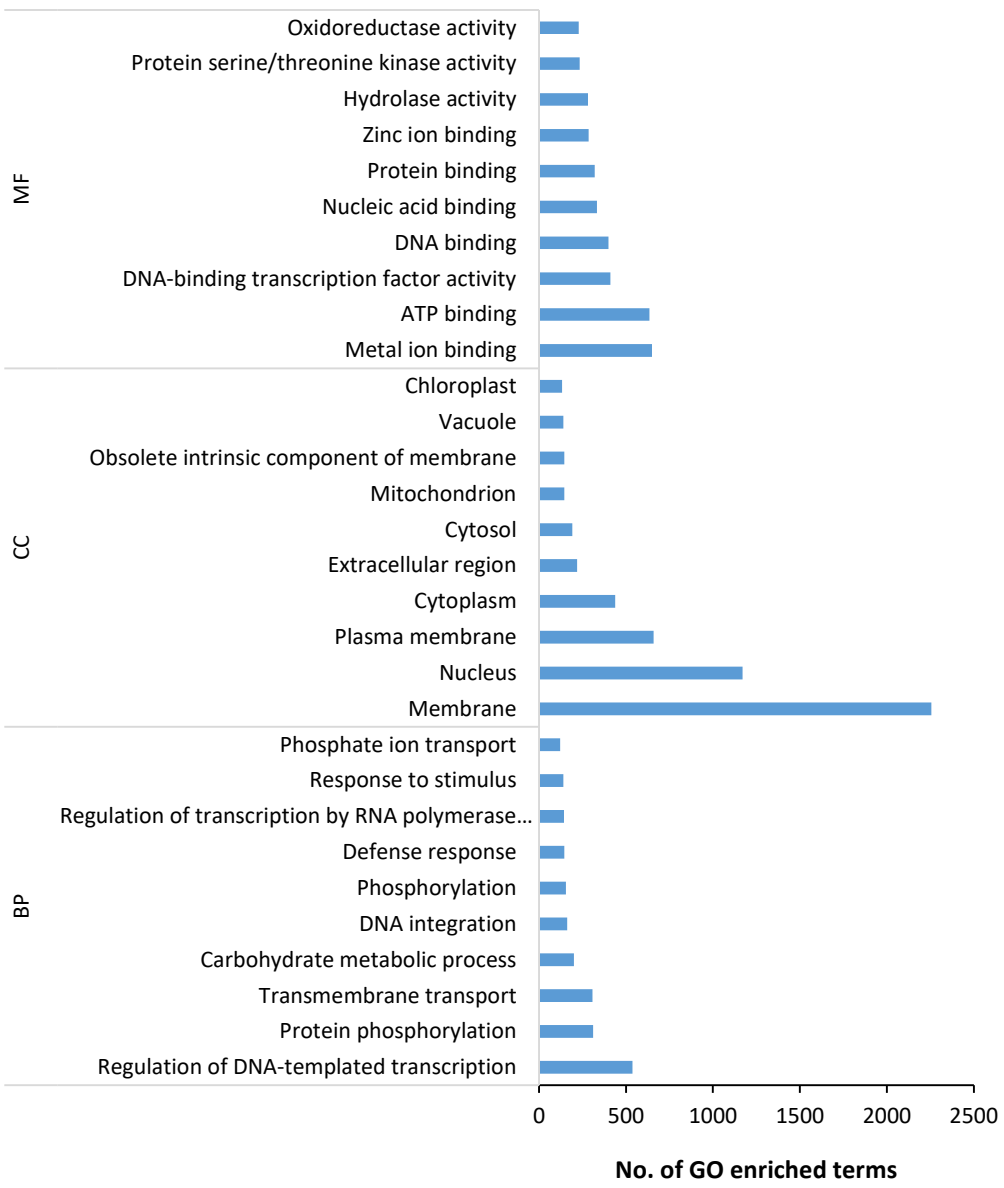


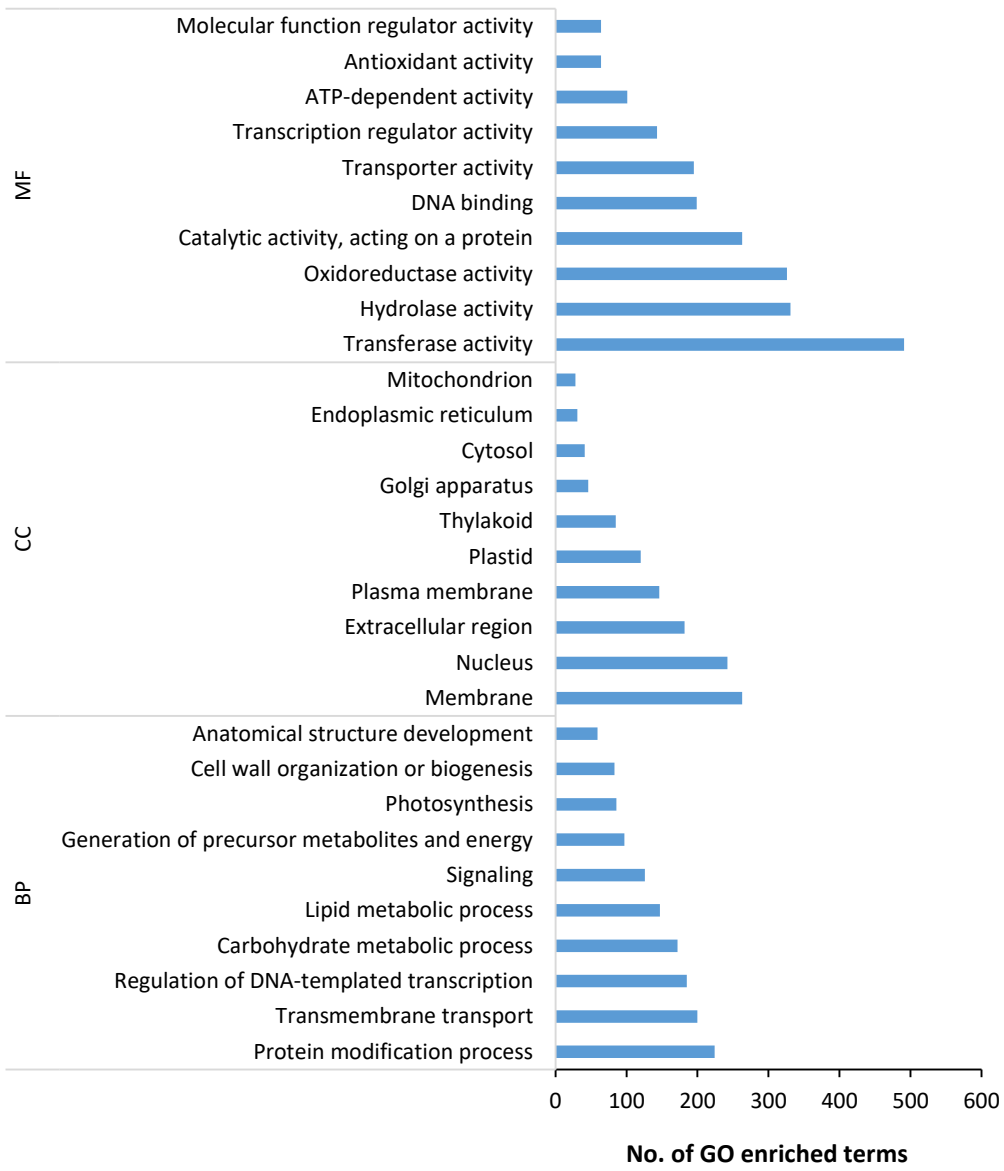
Supplementary Fig. 6 Summary of DE genes from the RNA-sequencing analysis. (a) RNA-sequencing data summarizing Table of DE genes for WT vs *Ok4CL11-OE1* and WT vs *Ok4CL11-OE2* comparisons. (b) Venn diagrams for DE genes.



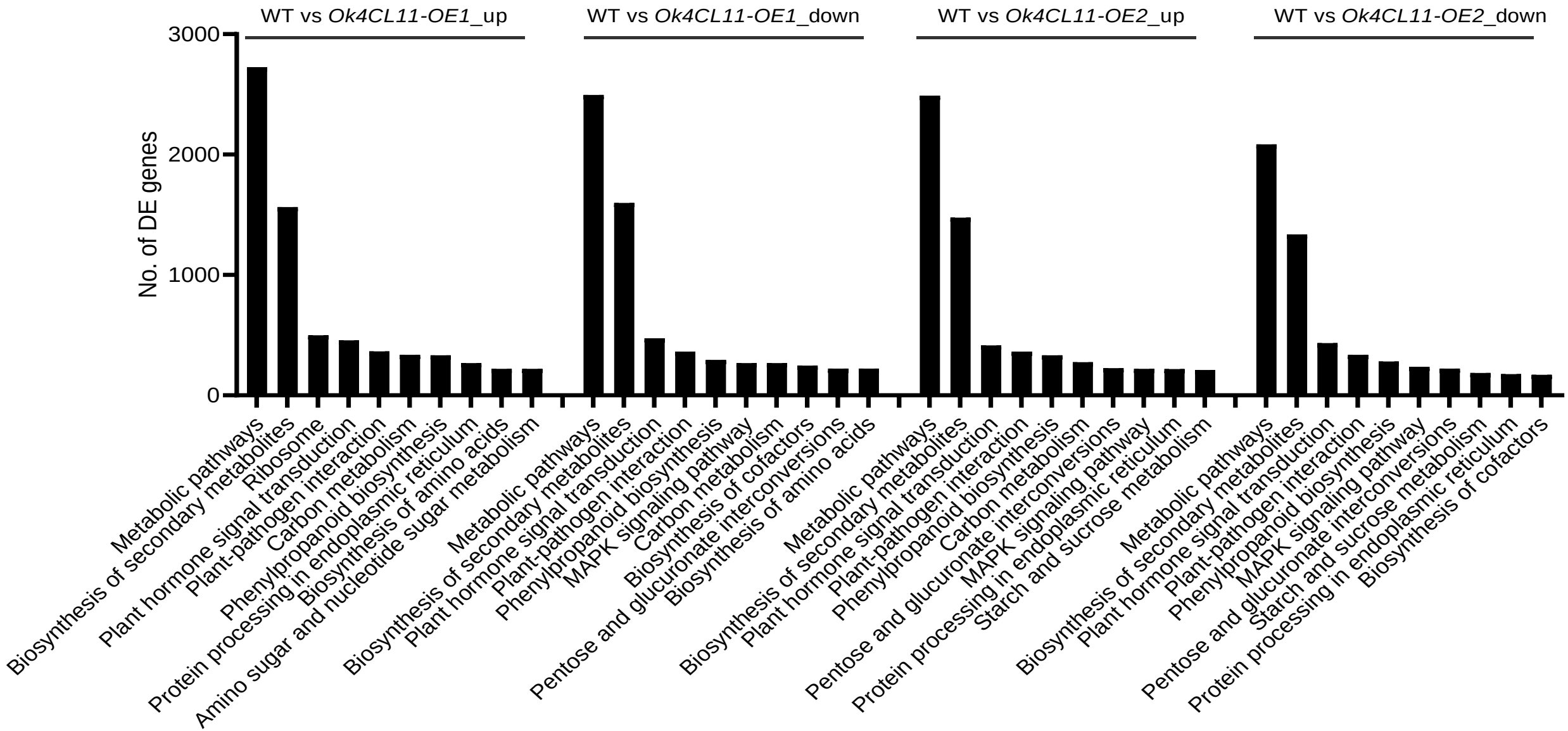


Supplementary Fig. 7 Gene Ontology (GO) analysis for DE genes of WT vs *Ok4CL11-OE1* line. Top 10 enriched GO terms are shown.

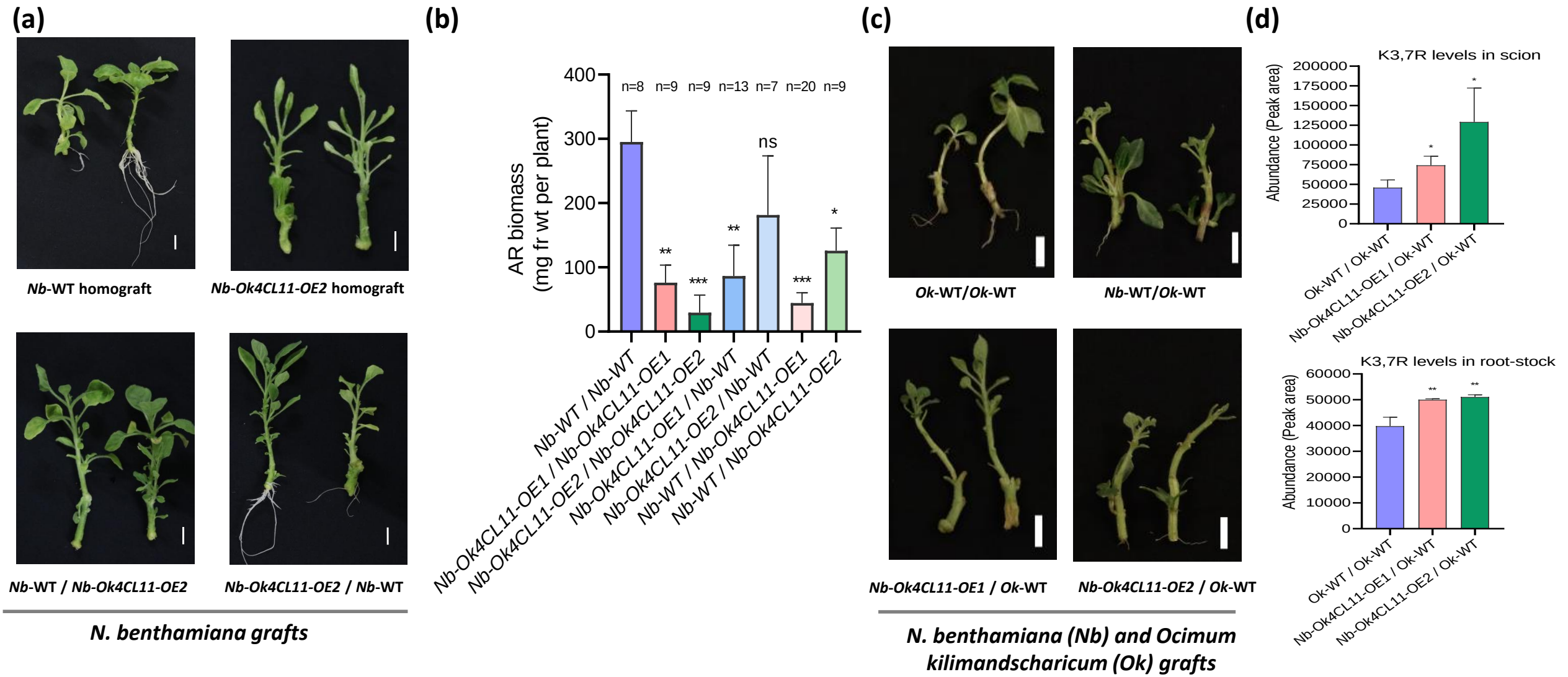




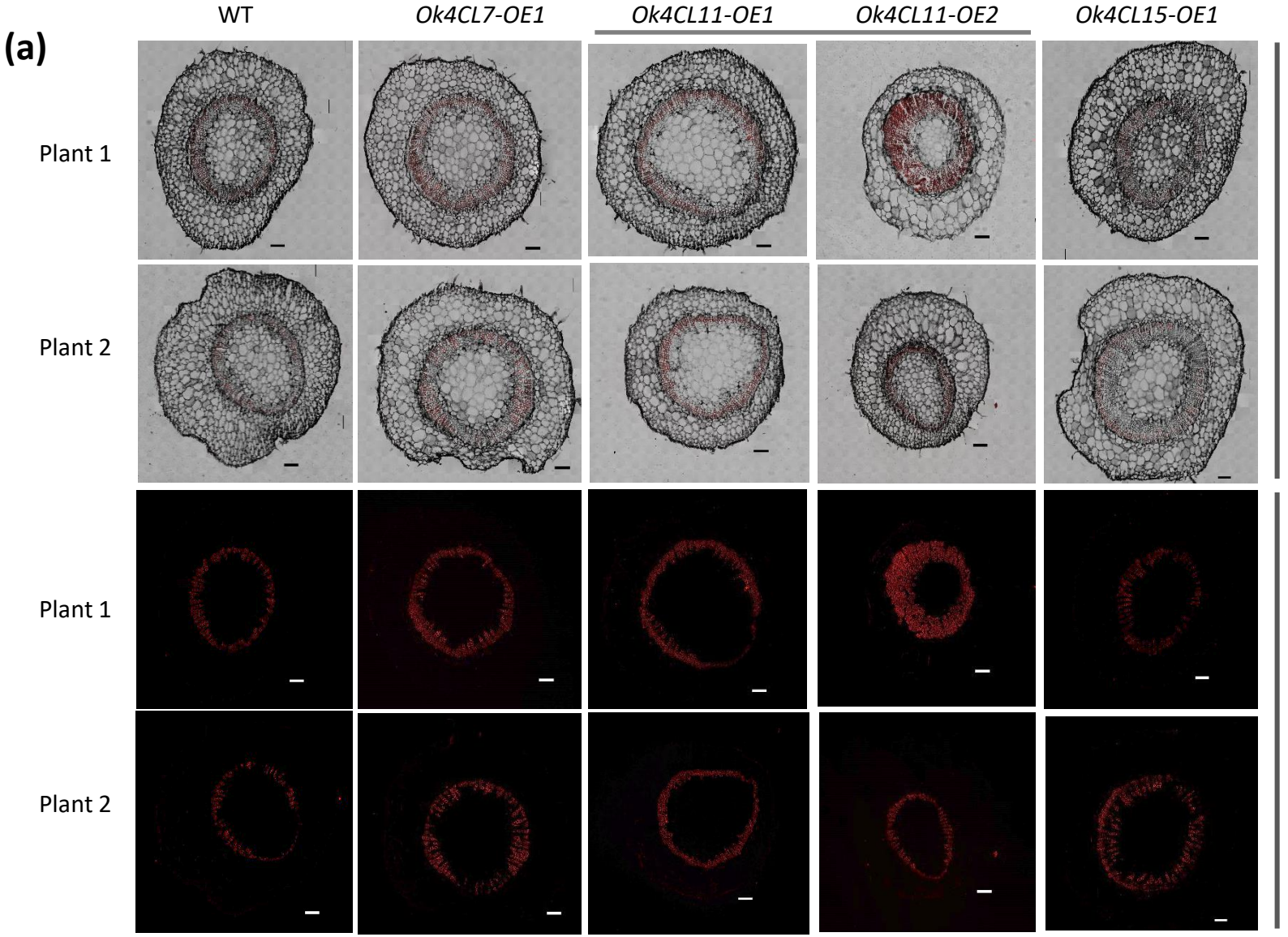
Supplementary Fig. 8 Gene Ontology (GO) analysis for DE genes of WT vs *Ok4CL11-OE2* line. Top 10 enriched GO terms are shown.

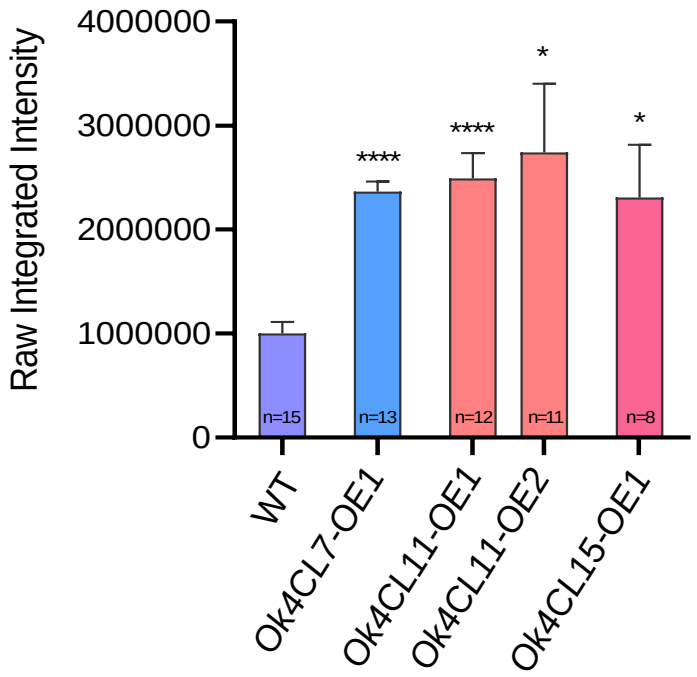


Supplementary Fig. 9 KEGG pathway enrichment for DE genes of WT vs *Ok4CL11-OE* lines comparison. Top 10 enriched pathways are represented for both types of comparisons- upregulated (up) or downregulated (down) genes in comparisons (WT vs *Ok4CL11-OE1* and WT vs *Ok4CL11-OE2*).

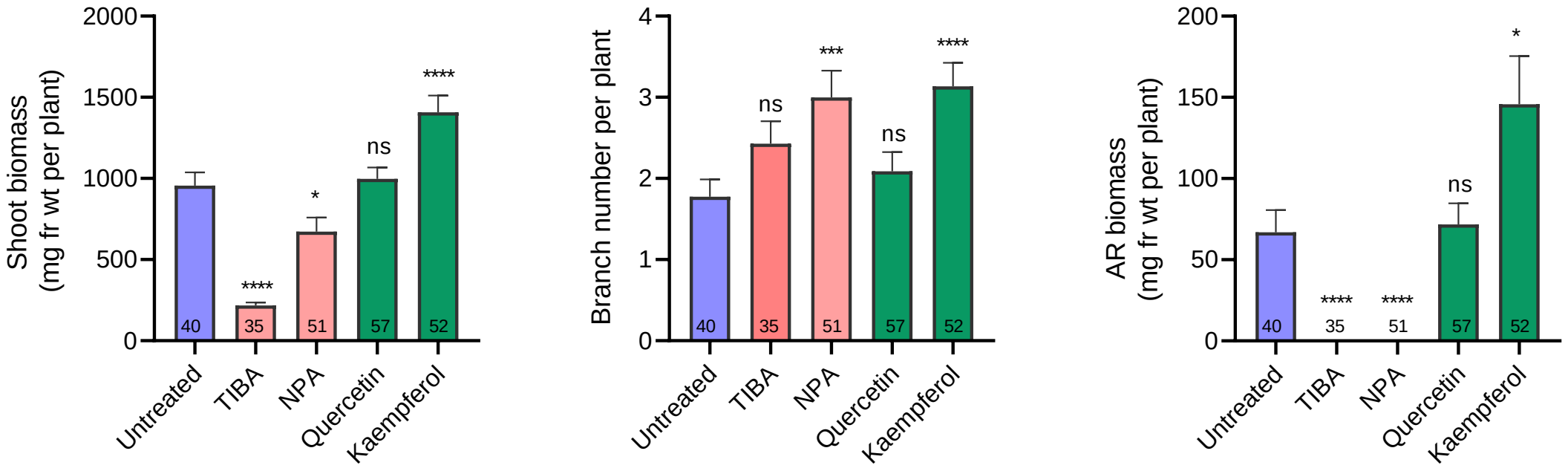


Supplementary Fig. 10 Effect of grafting on the AR biomass and accumulation of K3,7R in the scion and root-stock of homo or hetero-grafts. Images of grafts *between N. benthamiana* (WT) as scion and *Ok4CL11-OE N. benthamiana* line 2 (OE2) as root-stock and their reverse hetero-grafts along with respective line homo-grafts of *N. benthamiana* (WT) or *Ok4CL11-OE* line 2 (a), and AR biomass (miligram fresh weight; mg fr wt) from the root-stocks of these grafts (b). Number of grafts (n) used for biomass measurements for each type is shown at the bottom of each bar in the graph. Images of grafts between *N. benthamiana* (WT), *Ok4CL11-OE N. benthamiana* lines (OE1 and OE2) as scion onto the *Ocimum kilimandscharicum* (WT) root-stock (c). Accumulation of K3,7R in the scion and root-stock after 2-weeks of transferring grafts to MS solid media (d). For the panels (b) and (d), student's t-test was used to check the level of significance with one, two and three asterisks indicating p-values of <0.05, <0.01, and <0.005, respectively. ns= not significant at p<0.05. Error bars represent ± standard error of means. For the panel (d), n= 3. In each graft type, the label before a forward slash (/) represents scion, whereas the label after a forward slash indicates the respective root-stock. WT= Wild-type; *Nb= N. benthamiana, Ok= Ocimum kilimandscharicum*.

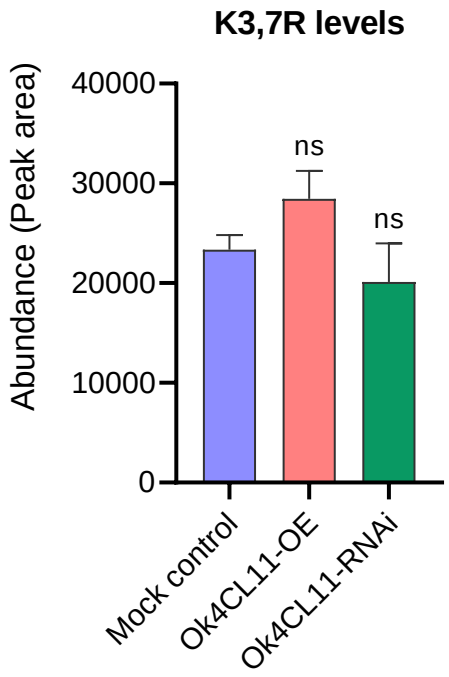




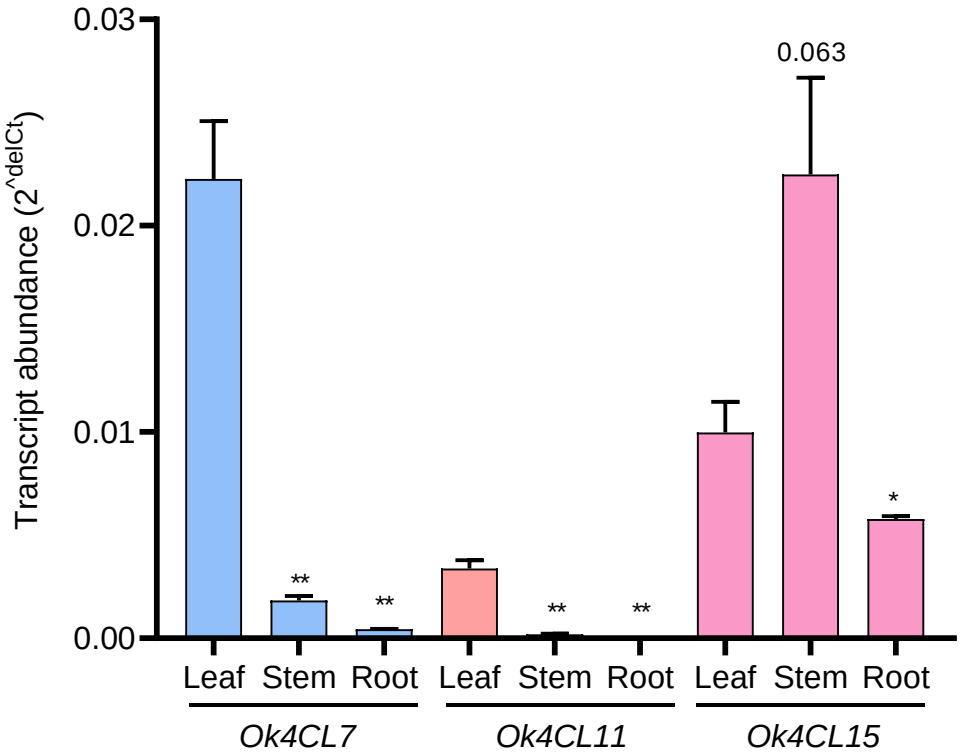
Supplementary Fig. 11 Histology of stem tissues and staining for cell wall lignin accumulation. (a) Merged images of stem cross-sections acquired under Confocal microscope showing lignin accumulation (red color) and the acquisition of the red part of the safranin spectra for lignin (excitation, 561 nm; emission, 570–600 nm). (b) Quantification of lignin accumulation. The protocol reported in Baldacci-Cresp et al.[92] was followed for lignin estimation. Stem cross-sections of *Ok4CL7-OE1*, *Ok4CL11-OE1/2, Ok4CL15-OE1* lines and *N. benthamiana* WT plants were stained using safranin and imaged under Confocal microscope. One month old *in vitro* plants were used. In the panel (a), images of two independent plants per line are represented. Scale bar= 200 µm. In the panel (b), the number of sections (n) for each line are mentioned at the base of each bar. Errors bars= SEM. Student's t-test was used to check the level of significance with one and four asterisks indicating p-values of <0.05 and <0.001, respectively. ns= not significant at p<0.05.



Supplementary Fig. 12 Effect of aglycon flavonoids (kaempferol and quercetin) and auxin inhibitors (TIBA and NPA) on WT *N. benthamiana* plants to mimic the reduced AR growth phenotype observed in *Ok4CL11-OE* lines. None of the explants grown on either TIBA or NPA showed AR emergence. Supplementation of quercetin had no effect on AR formation, whereas kaempferol treatment produced more number of ARs. Number of plants used for scoring the observations (n) are shown at the bottom of each bar in the graphs. Student's t-test was used to check the level of significance with one, three and four asterisks indicating p-values of <0.05, <0.005, and <0.001, respectively. ns= not significant at p<0.05. Error bars represent ± standard error of means.



Supplementary Fig. 13 Accumulation of K3,7R in leaves of *O. kilimandscharicum* Agroinfiltrated with empty vector (mock control), *Ok4CL11-OE* and *Ok4CL11-RNAi* gene constructs. Leaf samples 48 hrs post *Agro*-infiltration were used for quantifying the relative accumulation of K3,7R. Four plants with two Agroinfiltrated leaves pooled from each plant (n=4) were used for quantification of K3,7R levels (plotted as peak area).



Supplementary Fig. 14 Tissue-specific gene expression of *Ok4CL7*, *-11* and *-15* in *O. kilimandscharicum* plants. Tissues used include leaf, stem (internode) and roots of *in vitro* grown *O. kilimandscharicum* plants post 1 month of shoot-apex sub-culture. Biological replicates (n)= 3. *Tubulin* was used as a reference gene for normalization of data. Student's t-test was used to check the level of significance with one and two asterisks indicating p-values of <0.05 and <0.01, respectively. Error bars represent ± standard error of means. The respective expression of *Ok4CL7*, *-11* or *-15* in leaf was considered as 1.0 to perform the statistical analysis for stem and root tissues. For better representation, all three genes are plotted on the same graph.