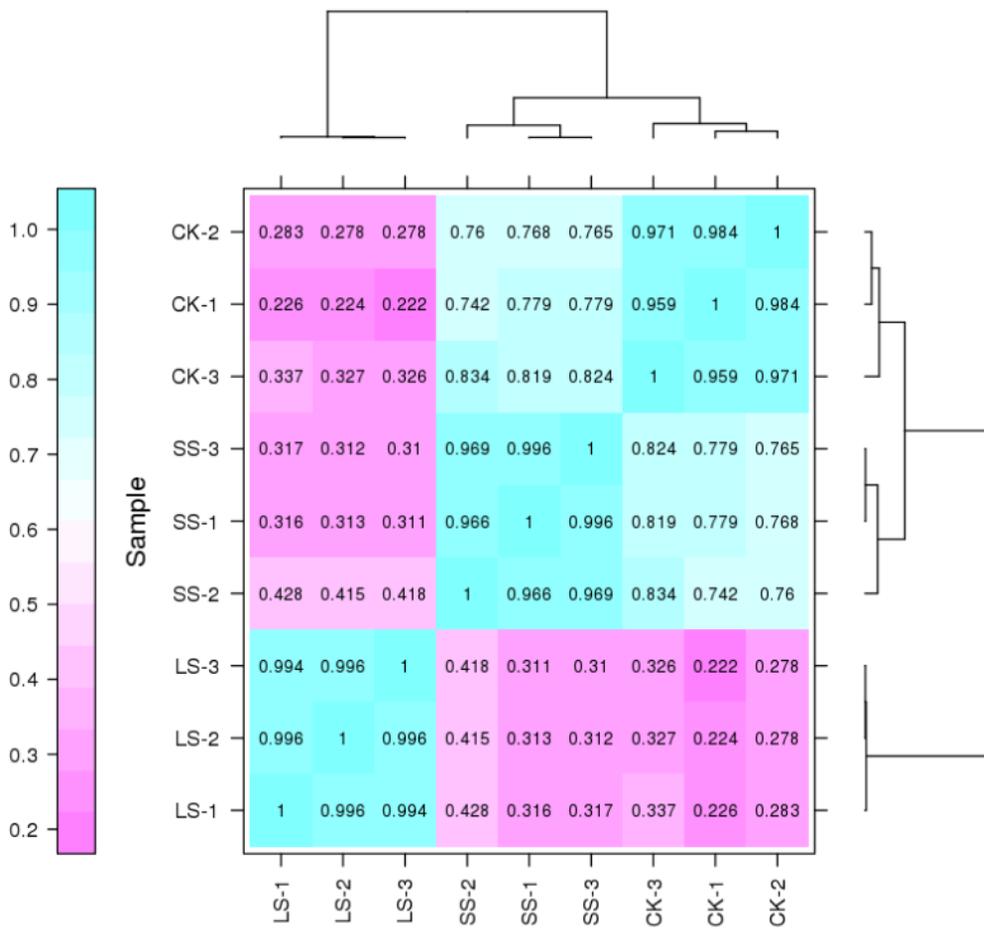
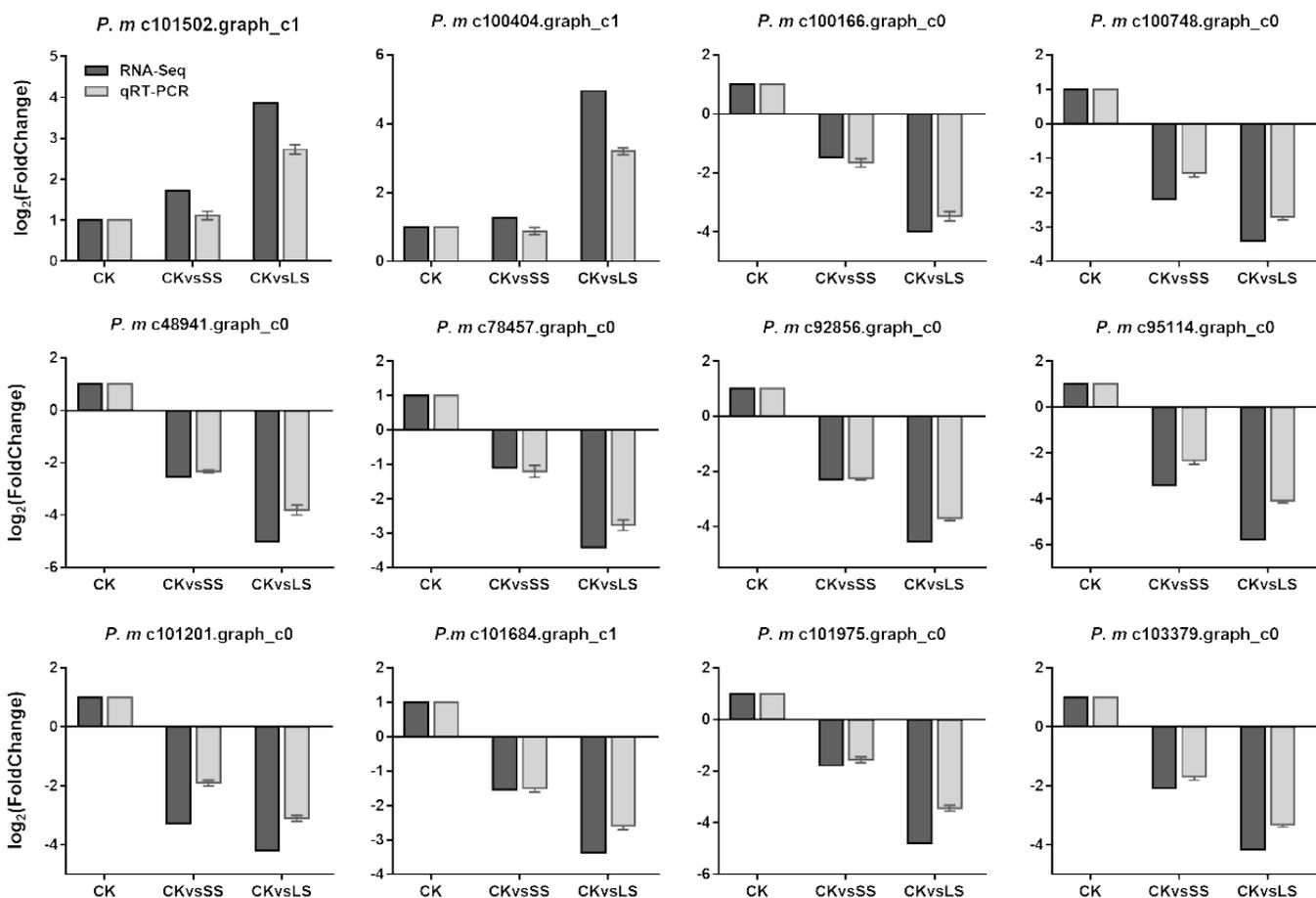


Supplementary Figure 1. Distribution of the different lengths of unigenes in the *de novo* assembled transcriptome of *P. macrophyllus*.

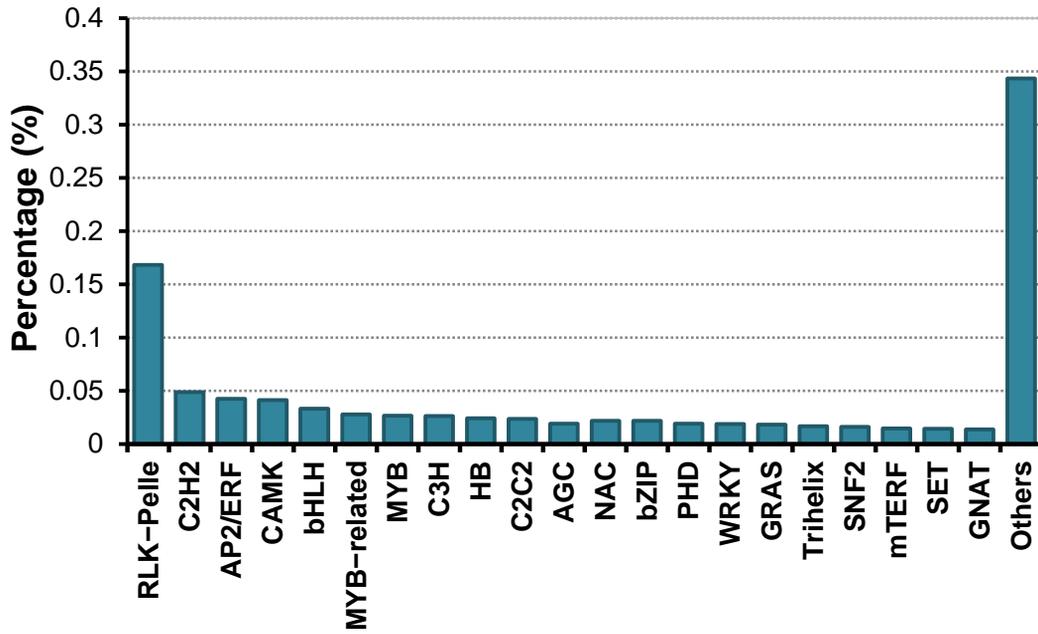


Supplementary Figure 2. Heatmap and Pearson correlation coefficients for RNA-seq replicates of *P. macrophyllus* under SS and LS salt stress and control. Three biological replicates are shown.

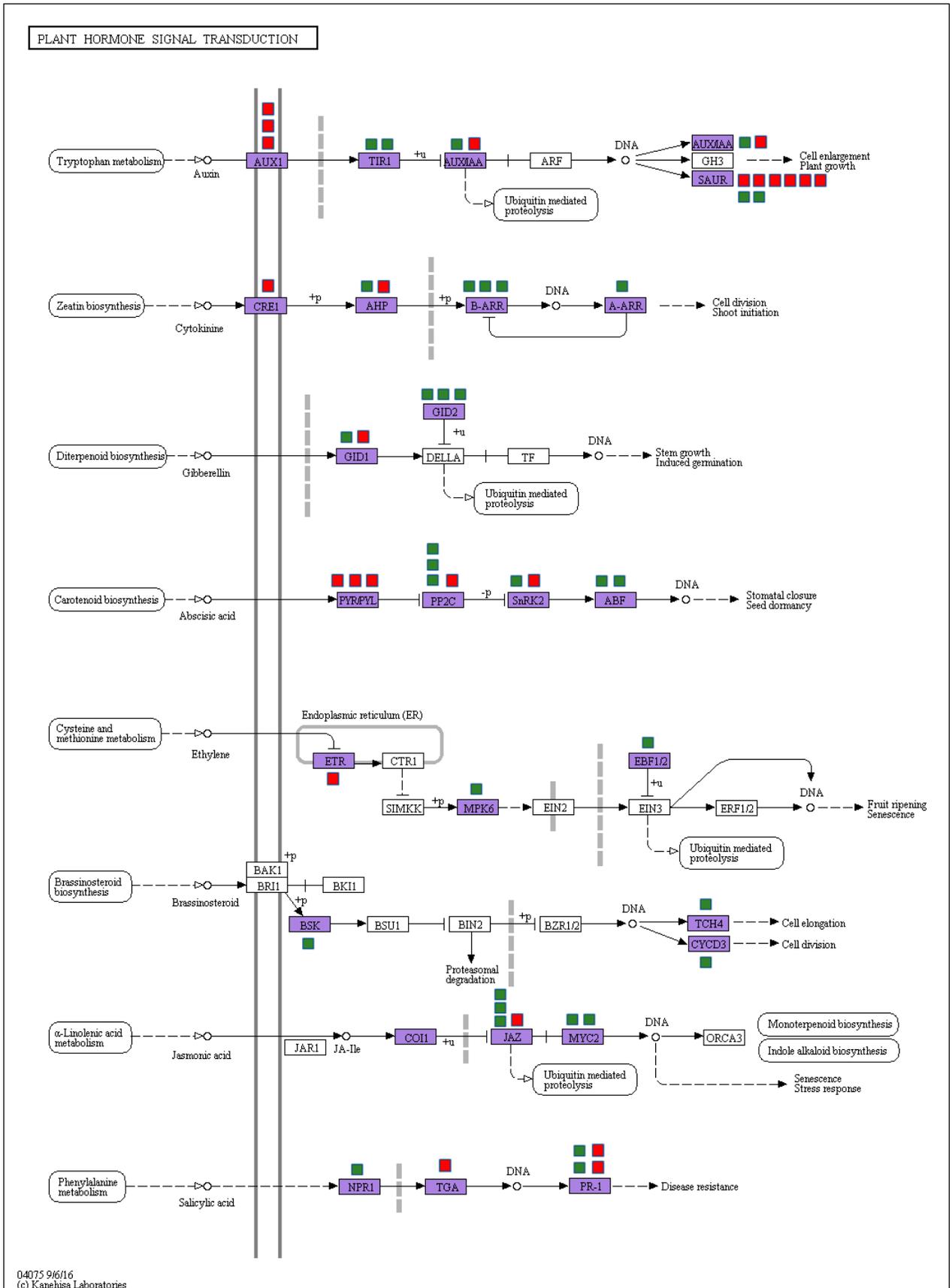


Supplementary Figure 3. Analysis of the fold changes of the 12 candidate DEGs in *P. macrophyllus* determined by RNA-seq and qRT-PCR. The x-axis represents the comparisons between salt stress and CK, the y-axis represents the log₂(fold change).

Transcription factors



Supplementary Figure 4. Percentage of different families of transcription factors that identified in the assembly transcriptome of *P. macrophyllus*.



Supplementary Figure 5. The genes involved in phytohormones transport or synthesis in the DEGs of *P. macrophyllus* under salt stress.

Supplementary Table 1. Information of RNA-seq data of *P. macrophyllus*.

Samples	Replicate	Clean Reads	Base Number	Mapped reads	Mapped Ratio	GC Content	% \geq Q30
Control	1	22,977,316	6,883,571,484	19,466,660	84.72%	45.68%	94.56%
Control	2	23,184,133	6,940,680,172	19,736,403	85.13%	45.36%	94.48%
Control	3	25,143,716	7,536,426,190	21,795,599	86.68%	45.50%	94.49%
Salt-3h	1	25,018,533	7,490,966,990	21,334,701	85.28%	45.35%	94.27%
Salt-3h	2	22,717,951	6,804,419,372	19,333,906	85.10%	45.55%	94.86%
Salt-3h	3	24,819,231	7,429,970,482	21,250,331	85.62%	45.54%	95.02%
Salt-14d	1	23,264,042	6,968,409,636	19,269,476	82.83%	45.80%	94.42%
Salt-14d	2	25,203,205	7,544,301,178	20,621,413	81.82%	46.00%	94.49%
Salt-14d	3	25,253,988	7,566,205,914	20,523,535	81.27%	45.91%	94.40%

Supplementary Table 2. Primers used for qRT-PCR in *P. macrophyllus*.

Primers name	Sequences (5'-3')
<i>P.m</i> c100166.graph_c0-F	ATCTCGGTCGGGATAGGA
<i>P.m</i> c100166.graph_c0-R	TATTCAAAGACGAAGGTGGT
<i>P.m</i> c95114.graph_c0-F	GTATGGCAGTATGATCGTGTT
<i>P.m</i> c95114.graph_c0-R	GAGCGAATTGCTTGGTCT
<i>P.m</i> c100748.graph_c0-F	AGCCAAAGAAGCCCAAGA
<i>P.m</i> c100748.graph_c0-R	CAAATCAAACGCAAACCTC
<i>P.m</i> c101201.graph_c0-F	CCCCAACACTAACAGGATG
<i>P.m</i> c101201.graph_c0-R	CGGTGACAGTACCCAAGC
<i>P.m</i> c101684.graph_c0-F	TGCGTGTTGGATTGTAGC
<i>P.m</i> c101684.graph_c0-R	AATGGCAAACCTCGTTATGG
<i>P.m</i> c101975.graph_c0-F	GGGTAAGAGTATTAAGCCACA
<i>P.m</i> c101975.graph_c0-R	AATAAAGATTGCTGGAAACAG
<i>P.m</i> c103379.graph_c0-F	CGCCTACACCATAACTTAG
<i>P.m</i> c103379.graph_c0-R	AGCAGCCTCACTCCTCTG
<i>P.m</i> c48941.graph_c0-F	TCGGGAAGGGCAACCA
<i>P.m</i> c48941.graph_c0-R	CACCGCCACGACGATAT
<i>P.m</i> c78457.graph_c0-F	GTTGAAATTCATGGGCAATA
<i>P.m</i> c78457.graph_c0-R	TCCTCCTCCCTTACCACC
<i>P.m</i> c92856.graph_c0-F	AGAGGCACGAATGAAAGTC
<i>P.m</i> c92856.graph_c0-R	ATAAGCGTCAGTAACAAACATG
<i>P.m</i> c100404.graph_c1-F	AAATAGTTTCCCTCCTTGATTT
<i>P.m</i> c100404.graph_c1-R	GTGAATTGCCGTCCCTCT
<i>P.m</i> c101502.graph_c1-F	ACGCTCATCCACCTTACAAC
<i>P.m</i> c101502.graph_c1-R	GAGCTCTGATCCTTCTCCC
Actin-F	TTGCTCCAGAAGAACATC
Actin-R	ATGGCAACATACATAGCAGG