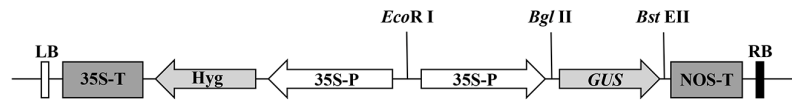


Supporting Information

Overexpression of *AtMYB2* promotes tolerance to salt stress and accumulations of tanshinones and phenolic acid in *Salvia miltiorrhiza*

A: pCambia1301



B: p35S::AtMYB2

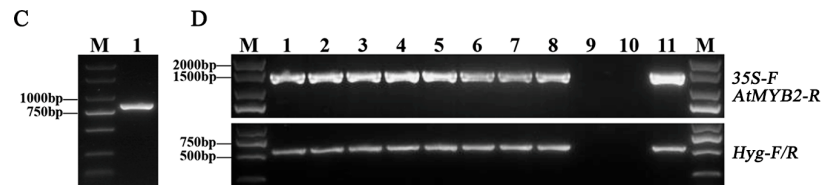
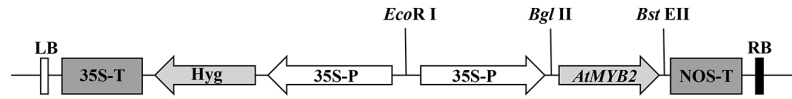


Figure S1. Construction of the *AtMYB2* overexpression vector. A: The schematic diagram of the T-DNA region structure in the pCambia1301 vector; B: The schematic diagram of the T-DNA region structure in the *pCambia1301-AtMYB2* overexpression vector; C: Amplification of the full-length CDS region of the *AtMYB2* gene, M, DL2000 Marker; D: PCR verification of *pCambia1301-AtMYB2* colonies, M, DL2000 Marker, lanes 1-8 represent positive colonies identified by PCR analysis, lane 9, negative control, lane 11, plasmid positive control.

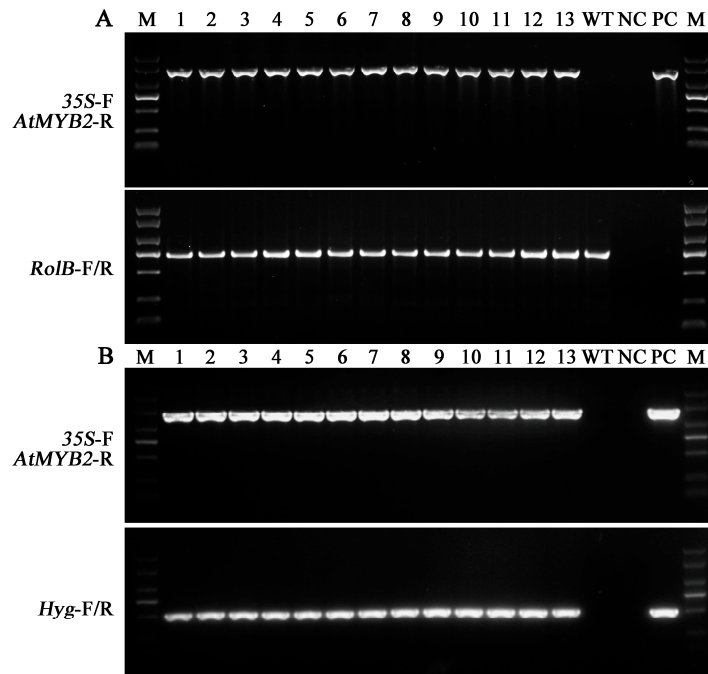


Figure S2. Identification of *AtMYB2* transgenic hairy roots and transgenic plants by PCR. *35S-F*, *AtMYB2-R* primers and *Hyg-F/R* primers were used to identify transgenic positive clones. The *rolB* gene was used to prove that the hairy roots were infected with *Agrobacterium*. WT, wild type; NC, negative control; PC, positive control; M, DL2000 DNA Marker.

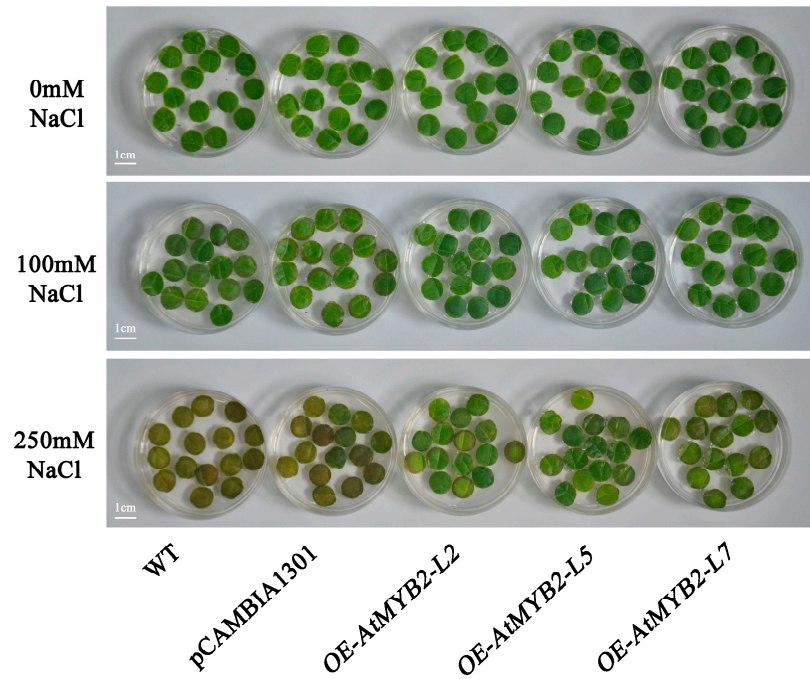


Figure S3. Phenotypic observation of detached leaf discs after treatment with 0 mM, 100 mM and 250 mM NaCl. WT, wild type; pCAMBIA1301, empty vector control pCAMBIA1301 line; *OE-AtMYB2-L2/L5/L7*, pCAMBIA1301-*AtMYB2* transgenic line 2/5/7. Images were taken at 4 DAT (days after treatment).

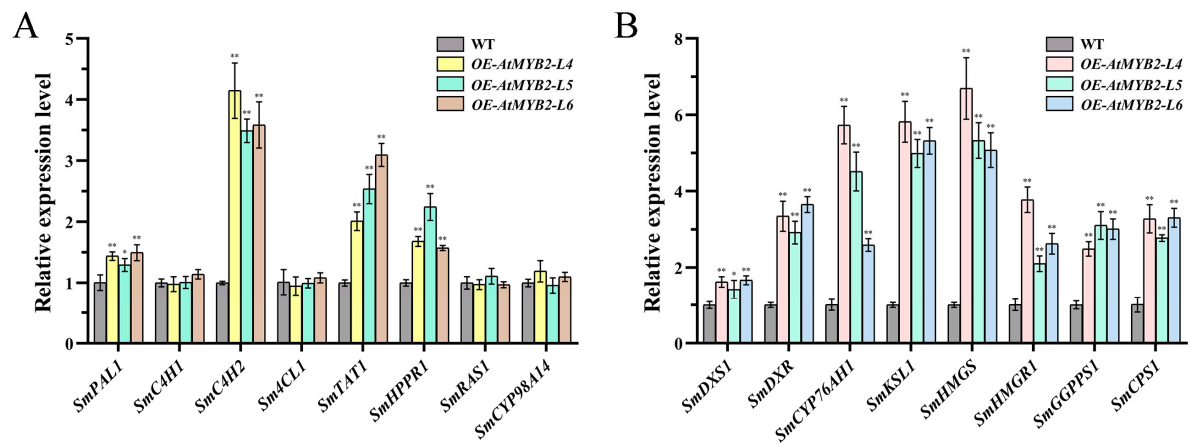


Figure S4. Transcript level of salvianolic acid biosynthesis pathway genes (A) and tanshinone biosynthesis pathway genes (B) in *S. miltiorrhiza* transgenic hairy roots. * and ** represent significant differences at $p < 0.05$ and $p < 0.01$.

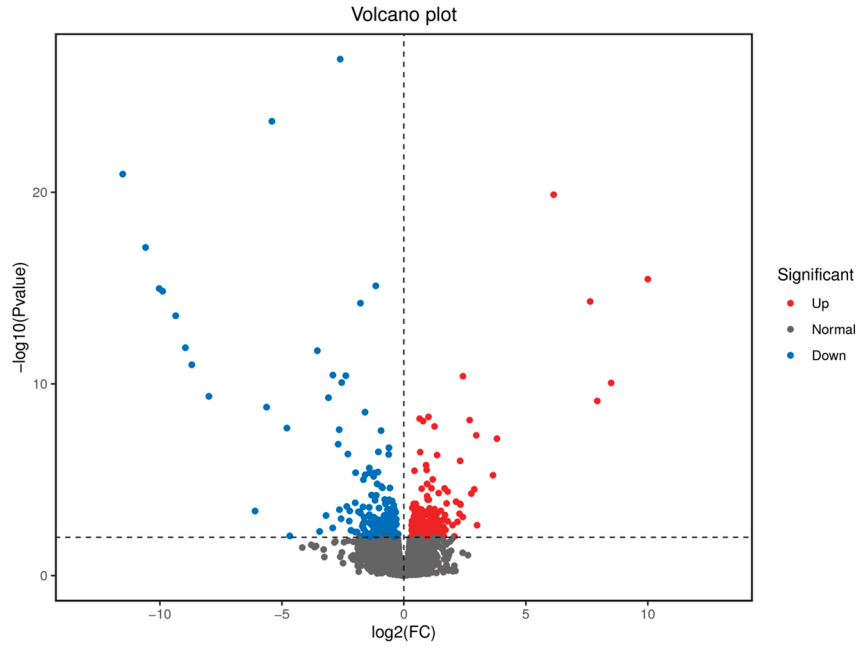


Figure S5. Volcano plot of DEGs of *AtMYB2* transgenic lines versus those of WT plants. Note: in the volcano plot, each dot represents a gene. X-axis: \log_2 FC of expression; Y-axis: $-\log_{10}$ (FDR) or $-\log_{10}$ (P-value). Blue dots are down-regulated genes, while red dots are up-regulated ones and black dots are genes without significant differences.

Table S1. Statistics of sequencing data of *AtMYB2* transgenic *S. miltiorrhiza*.

Samples	Clean reads	Clean bases	GC Content	% \geq Q30
MYB2-1	20,579,033	6,139,823,990	49.86%	94.00%
MYB2-2	25,998,774	7,769,656,646	50.00%	93.64%
MYB2-3	24,657,193	7,364,060,990	49.19%	94.16%
p1301-1	21,309,595	6,365,646,636	49.66%	93.63%
p1301-2	25,825,132	7,717,456,100	49.38%	94.05%
p1301-3	23,376,367	6,973,266,094	50.92%	94.28%

Table S2. Primers used in this study

Primers	Sequence (5' to 3')
<i>AtMYB2-F</i>	ACTCTTGACCATGGT <u>AGATCT</u> ATGGAAGATTACGAGCGAATAA
<i>AtMYB2-R</i>	GGGGAAATTCGAGCT <u>GGTCACCT</u> TAAATTATACGAATACGATGTCG
<i>35S-F</i>	AACAGAACTCGCCGTAAAG
<i>Hyg-F</i>	TACACAGCCATCGGTCCAGACG
<i>Hyg-R</i>	TCGGTCAATACACTACATGGCG
<i>rolB-F</i>	GCTCTTGCAGTGCTAGATTT
<i>rolB-R</i>	GAAGGTGCAAGCTACCTCTC
<i>q-AtMYB2-F</i>	CGAATCAACGCCCAATCATTACC
<i>q-AtMYB2-R</i>	ATCATAACCTGACCCGTTACCA
<i>SmPAL1-QF</i>	ACCCCGTCACCAACCACGTGCAGAG
<i>SmPAL1-QR</i>	CGCCCATTTGTGAGAGTTTCGTTT
<i>SmPAL2-QF</i>	CAGGATCAAGGGGAGCAGATCGTAT
<i>SmPAL2-QR</i>	CACCATTCCATTCCCTGAGACAG
<i>SmPAL3-QF</i>	CGAGCTCGAGGTGCTCCTC
<i>SmPAL3-QR</i>	CGGCTCTCCATTCCACGATTC
<i>SmC4H1-QF</i>	CCAGGAGTCCAAATAACAGAGC
<i>SmC4H1-QR</i>	GCCACCAAGCGTTCACCAAGAT
<i>SmC4H2-QF</i>	TGGACCATTGCGGAACTCATC
<i>SmC4H2-QR</i>	ATGGAACCACCATTCTACGACG
<i>Sm4CL1-QF</i>	ATTCGCATTTCGCATTTCTCGG
<i>Sm4CL1-QR</i>	GCGGCGTAGTGCTTCACCTTT
<i>Sm4CL2-QF</i>	AGCTCTTCATCGTGGACCGA
<i>Sm4CL2-QR</i>	CACGACGAAAGCAACTGGGA
<i>Sm4CL3-QF</i>	GTCGACGCGGACAACCCTAA
<i>Sm4CL3-QR</i>	AGCAGCGAGCCGATCTCAA
<i>SmTAT1-QF</i>	CAACTGCTGGTCTTCCACAAAC
<i>SmTAT1-QR</i>	GCGAGCCAAAACGGACA
<i>SmTAT2-QF</i>	CGCTGACCCAGCAACCTTTAT
<i>SmTAT2-QR</i>	TGTCATCCTCAATGCCTTCG
<i>SmHPPR1-QF</i>	TGACTCCAGAAACAACCCACATT
<i>SmHPPR1-QR</i>	CCCAGACGACCCTTCACAAG
<i>SmHPPR2-QF</i>	AATGTGGGAGTGATGATGACCAC
<i>SmHPPR2-QR</i>	GCTTGAAGAGTGTGAAGCGC
<i>SmHPPR3-QF</i>	GCGCTACCGCTCCTTGAGAT
<i>SmHPPR3-QR</i>	CACAAATCCGCCGCGAAGTC
<i>SmRAS1-QF</i>	CGAGATCGCCTACTCCAAGTTCAAG
<i>SmRAS1-QR</i>	AGATGGCGTTACCGAAGTATCCCTG
<i>SmRAS-Like-QF</i>	ACCTTGAGTCTAAGCCTGCGTG
<i>SmRAS-Like-QR</i>	CGTCACCCAACTCGTTATCCC
<i>SmCYP98A14-QF</i>	GGTCTGTACCGTCGTCCTCTTCTCC
<i>SmCYP98A14-QR</i>	CCTTTTCCCAAATACCAGCCTTGT
<i>SmDXS1-QF</i>	GGAAGAAGAGACAGGATGCCGAGTT

<i>SmDXS1-QR</i>	AGTCCAGGTAGCCAGCATTGTTTCAT
<i>SmDXR-QF</i>	CGACGAGAAAATCGGATACCTGG
<i>SmDXR-QR</i>	CATACAAGAGCAGGACTCAAACCG
<i>SmMCT-QF</i>	AGGTTCTGAAGGATGGCAAGCGAAT
<i>SmMCT-QR</i>	CCATAGCGTCTTCCTGTCCAGTGTT
<i>SmCMK-QF</i>	TACACCAACGCCACTCTTCCTCAA
<i>SmCMK-QR</i>	GCCGTCGCTCTGATAAGATGGATTG
<i>SmMDS-QF</i>	GAGCACGGTTGGAGCAGAGACT
<i>SmMDS-QR</i>	TGAGGAATATTGATGCCGCCGATAATG
<i>SmHDS1-QF</i>	GTTTGGTAGTCTCTTTGCGTG GTG
<i>SmHDS1-QR</i>	AACTGGGAAGTCGAGCGAGTTCTC
<i>SmHDR-QF</i>	TGAAGCTAGAAGACAGTTCCCCTC
<i>SmHDR-QR</i>	GTATTCCAAACCTTAGACACCCATG
<i>SmIDI-QF</i>	GCAACGATCCACAATAAGGT
<i>SmIDI-QR</i>	ATGCCGAGTTCATCCAACAG
<i>SmGPPS-QF</i>	CACTTTCGCAATCCTATTCAGTC
<i>SmGPPS-QR</i>	GGGAACCTCCGCAACTACCAT
<i>SmGGPPS-QF</i>	AGGTGGAAGCAGCGATCAAAT
<i>SmGGPPS-QR</i>	CCAGCCGTCTTTCCCAACTC
<i>SmCPS1-QF</i>	GATCGCCTCGTCAATACCAT
<i>SmCPS1-QR</i>	TTCGAACCCACAAGTCATGT
<i>SmKSL1-QF</i>	GTGTGACCCTTCTGCTAGCA
<i>SmKSL1-QR</i>	TGCATTGTCTTG GGAAGATG
<i>SmCYP76AH1-QF</i>	TCCATCTCGGCAGCCTCTACAC
<i>SmCYP76AH1-QR</i>	GAGAAGACCTGCCCCGTGCCT
<i>SmAACT1-QF</i>	GGAGAGGACGACCATCCACCATTG
<i>SmAACT1-QR</i>	GGCATGAGCGGCATCAGCATATCC
<i>SmHMGR1-QF</i>	TCGTTTTCAATAAGTCGAGTAGA
<i>SmHMGR1-QR</i>	ATTCTGAAGGAAGTCCAAAACAT
<i>SmHMGS-QF</i>	GATGAGCATGACAGCGGTTACTT
<i>SmHMGS-QR</i>	GGATTTGCTCTTGTCGAGTACGGT
<i>SmMK-QF</i>	CTGGGATAGACAATACAGTAAGCAC
<i>SmMK-QR</i>	ACGAGCATCTTCAAAGGCATA
<i>SmPMK-QF</i>	GCTTGCCATTGACCTCGGAATCT
<i>SmPMK-QR</i>	ACCACTGAACTCTGAAGGAAGACTGA
<i>SmMDC-QF</i>	AAGCACTGGGATGACCTCGTTAT
<i>SmMDC-QR</i>	ATGGAACTGATTACTATCGGCACAAG
<i>SmFPPS-QF</i>	GTGGACTGATGGTTCTCGTCAATGG
<i>SmFPPS-QR</i>	CACACCAGCCAAGAGCACTAGC
<i>SmActin-QF</i>	AGCACCGAGCAGCATGAAGATT
<i>SmActin-QR</i>	AGCAAAGCAGCGAACGAAGAGT
