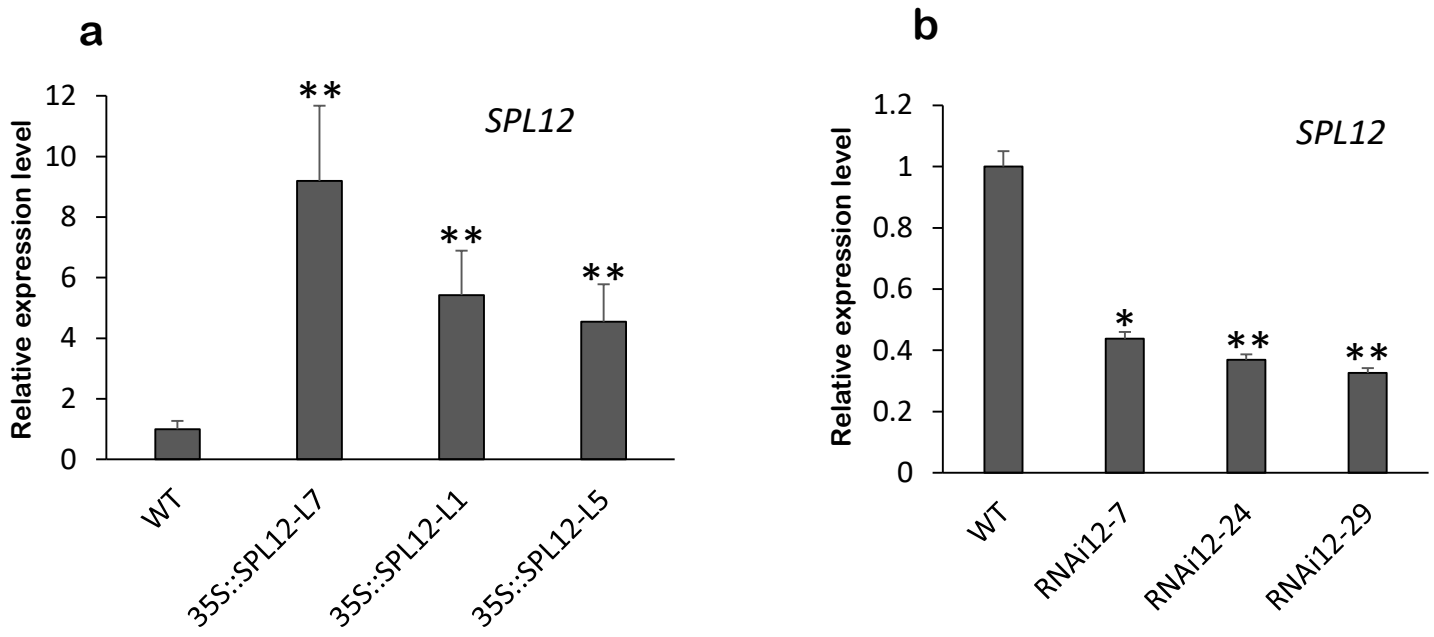
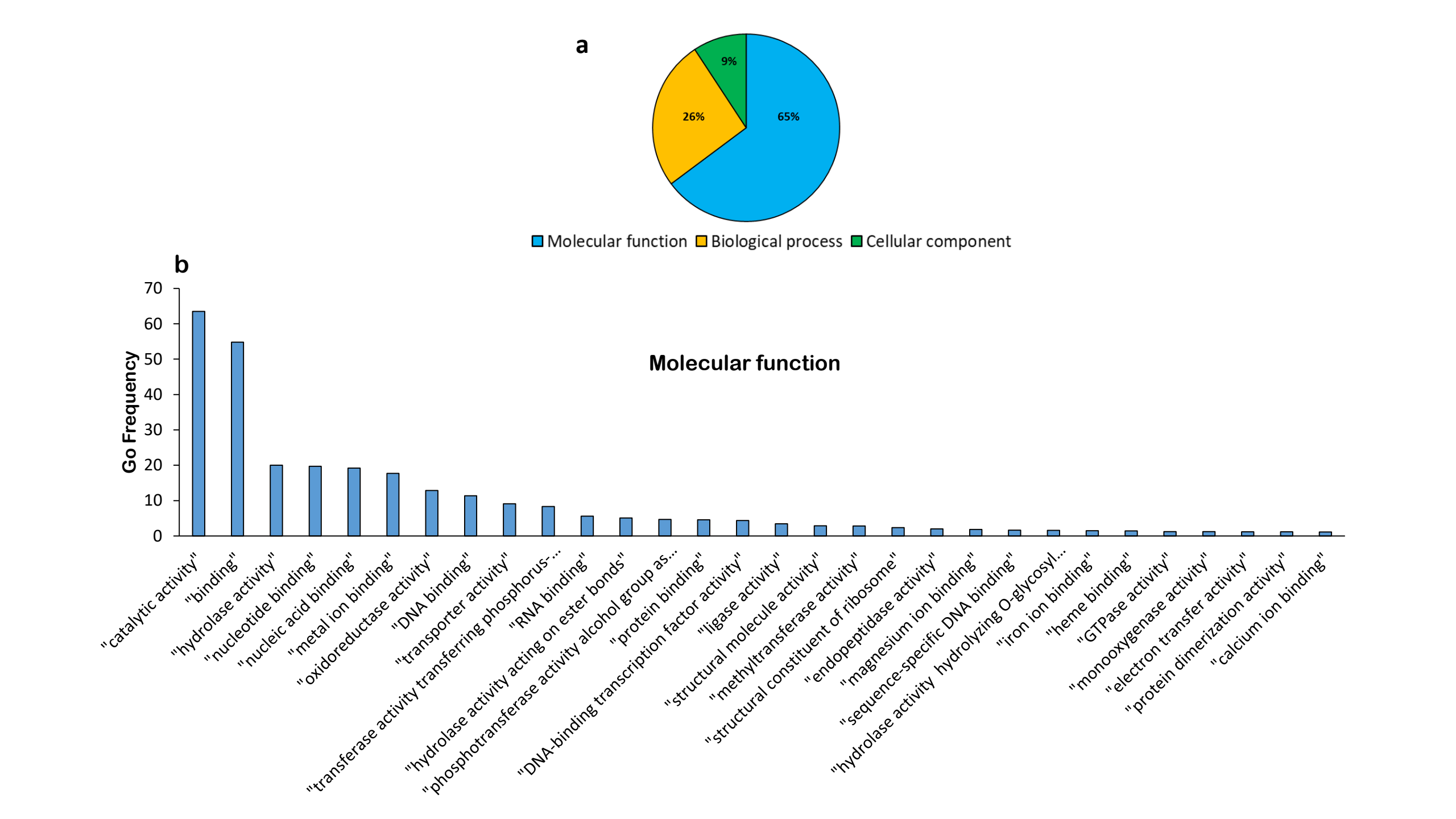


Fig. S1 Transcript analysis of *SPL12* gene in different alfalfa genotypes.

A) Relative *SPL12* transcript levels in *35S::SPL12* plants (n = 3). B) Relative *SPL12* transcript in *SPL12*-RNAi plants (n = 3). * and ** indicate significant differences relative to wild type using *t* test $p < 0.05$, $p < 0.01$, respectively. Error bar indicates standard deviation.


a
9%
26%
65%
Molecular function
Biological process
Cellular component
b
Molecular function
Go Frequency
70
60
50
40
30
20
10
0
"catalytic activity"
"binding"
"hydrolase activity"
"nucleotide binding"
"nucleic acid binding"
"metal ion binding"
"oxidoreductase activity"
"DNA binding"
"transporter activity"
"transferase activity transferring phosphorus-..."
"RNA binding"
"hydrolase activity acting on ester bonds"
"phosphotransferase activity alcohol group as..."
"protein binding"
"DNA-binding transcription factor activity"
"ligase activity"
"structural molecule activity"
"methyltransferase activity"
"structural constituent of ribosome"
"endopeptidase activity"
"magnesium ion binding"
"sequence-specific DNA binding"
"hydrolase activity hydrolyzing O-glycosyl..."
"iron ion binding"
"heme binding"
"GTPase activity"
"monooxygenase activity"
"electron transfer activity"
"protein dimerization activity"
"calcium ion binding"

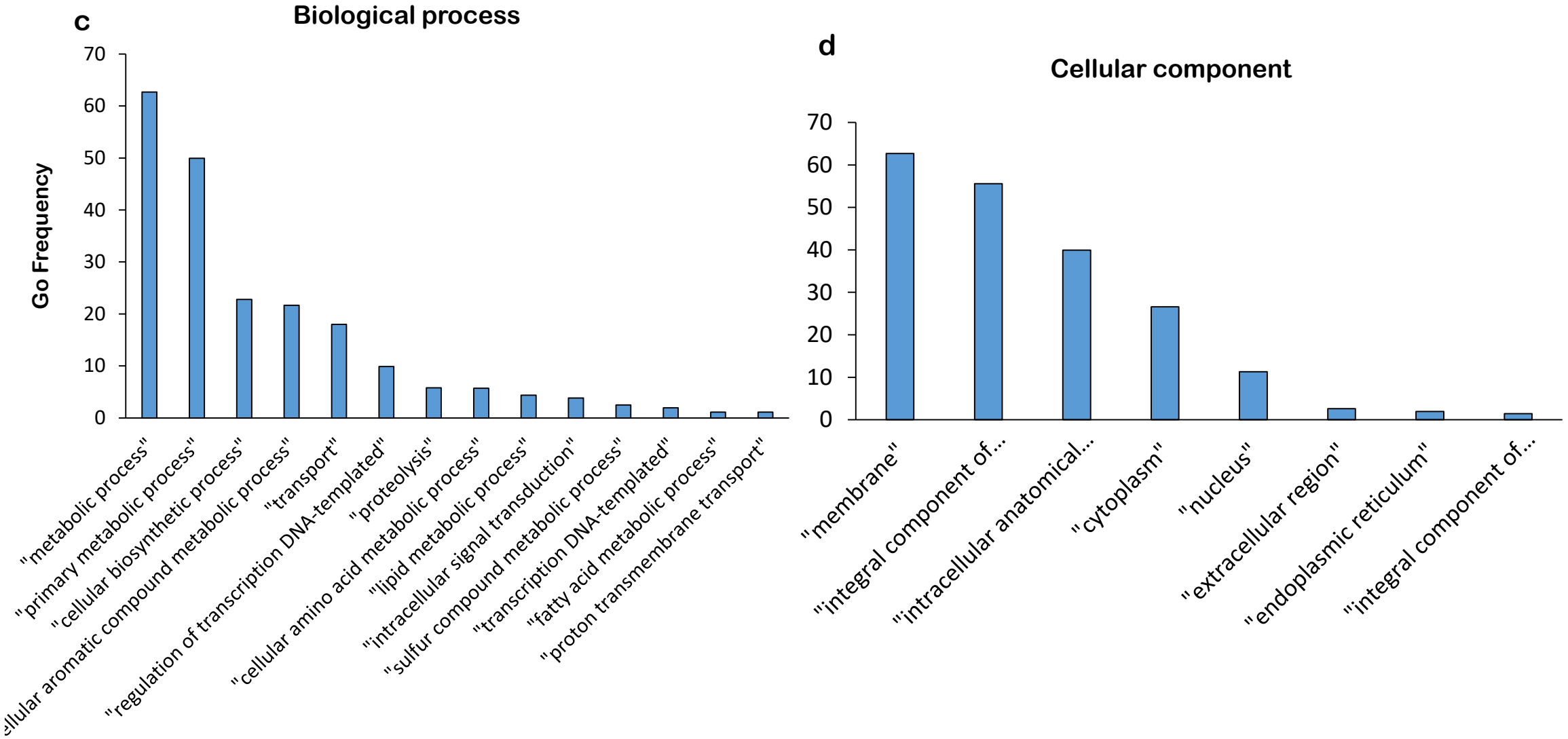

c
Biological process
Go Frequency
70
60
50
40
30
20
10
0
"metabolic process"
"primary metabolic process"
"cellular biosynthetic process"
"aromatic compound metabolic process"
"transport"
"regulation of transcription DNA-templated"
"proteolysis"
"lipid metabolic process"
"cellular amino acid metabolic process"
"intracellular signal transduction"
"sulfur compound metabolic process"
"transcription DNA-templated"
"fatty acid metabolic process"
"proton transmembrane transport"
d
Cellular component
70
60
50
40
30
20
10
0
"membrane"
"integral component of...
"intracellular anatomical...
"cytoplasm"
"nucleus"
"extracellular region"
"endoplasmic reticulum"
"integral component of...

Fig. S2 Gene Ontology (GO) enrichment analysis of DEGs between *SPL12*-RNAi and WT

A) Gene Ontology (GO-term) –based percent representation of DEGs between WT and *SPL12*-RNAi in alfalfa roots in cellular components, biological process, and molecular functions. Go frequency of B) molecular function, C) cellular component and D) biological process.

Fig. S3 Detection of SPL12m-GFP fusion protein in putative alfalfa transgenic plants using Western blotting.

CTTTCTGTGTTATGTGATGCTGAGGTTGCTCTTATCATTTTCTCCGGTCTTGGCAAGCTTTTTCAATACAGTACCACAGAGTGAGCAATTCATTTTCTTT
TAATATATATATCTTTAAGCAATTTTTTATCTCTTCGTTAGTTTTTTAAATACAAGCTTGGTCATAATTAAAAATATTCTAGGGGTTGTAAAATTATCTGTT
TAGCGCATTTTTGTTTGCCAAGAGAAATATCATAAGGTAAAAGCTACCGGCCGGTGGATTGGTCATTCATGAAGACAACTTGTTTGGCAAAGCACAA
CCACTTGATAGTTCTAGCAACATTCACTCATCATTTGACTAAGTTATTCCTTCTTGTCTTGGTTATAAGTAAACTAATTTCACACATTAAGAAATTCAGTA
AATATAATTAATCTTCTTGCAACAAAAAAAAATGGTACCCATCATAAAAATTTGTTTCATAAGAATGAAATGTCACTAAAAAAATAAAATATATATAAATTA
AAGAGTATTTTAGGATATGAGTCTTTATATCAAAAGTAGTCATATTAGCTTAATTATATTTTAAAAAAGTATGCACTTTTTTTTTTTTTTATCTTTATTTGA
GATTGGAATTAGGGGTGTCAATTTCATCTCTGAATGGGGATCTAAGCGGGTACCATCAAATTTGAAGTTACGTAGACGGAGAATTTTTTTCTATTGG
GGATGGGGGAGAAAGTATTCTCTGATAATAGTGCAGGGACACGATCATACCCCCCGATACATGGAGACTCGTCCCCGAGCAATTCAGTATAATATATT
TTATATTGGTATATACAAATATTTCCTATGTTATATTTATTTATCATTTTACGCAATTTTTTTATATGTAATGTTTACTGTAATGCCTTAATTATATTATATTTGT
TTTAATGTTAAATTTTAATTTTTTTAAAATAATATAAATTTAGTTATTTTTACATGCCGATGGATCTCTGTGGGACCGTGGTGATGTGCGGGGGTGAGG
ACAGGGAGGAAAAACTCTCCAAGACGGGGAATGGGGATGAGGGACAATTTAAGTGGCGGGAGAGGAAACATAGATGTACTCCTTGTCTCCTCCC
CACCCCATCCATTGACATCCCTGACTAGAATAGCTAGTAGAGTATTTTTTTTTTTTTTTGACAAAAAACAAGTAGAGTACGATAAAAAGGATTATTTTA
GTCATGGATTGAACTATAATATTCCAAGATAATTTGACCTTAATGAAGTTTTACTAACTACTTAAACTCAACCATTTAGTTAGACTTTAACATCAAAATG
TGTTTGAGTTGTGTAAGTTTGAGGTGGATTTGTGGGAGTAACTTGATAGCGGTTATAAAATTAAATTTGAGTTTCTTACAAATTTGTCATTGGAGATG
TTCTAAGGATCATACTAGCTTATATTCTAAGAGCACATGTTAAAGATTTTTACCAATAGTAATTATAATTGAAAAAAGTAATTTTCAACTTTTTGAAGAA
TGTACAAAGTTTTCAATAAGAAATTTCTATATTTAATGCACTAACAAGTGCCTTAACTATAAGGGTGCATTTTAACATTCCTCTTGTTGTAATACAAACA
ATGATGTTAGTTTTATTCAACGGGAGAGAATGTAGTTGTTAGTCCCTATATTTTTATAACGTATTATCTTTTTTTTTTTTGTTTCACGGTTTATTTCAATAAT
TTAACTCAAGTCAAAATTATATGGTACTAACCAATATAATTGATATACCTTGTTCATTCTGATCAGCTTGAACAAAATCATTGAGAAGTATCGTCAATGTT
GCTTCAACAATATGTCTGAGAATGGTGACTTAGGAGAACATGAGTCACAGG

Fig. S4 Promoter sequence of the alfalfa *AGL6* gene with putative SBD binding elements.

Nucleotides highlighted with yellow and blue colors represent putative SBD binding motifs with 'GTAC' core sequences and forward and reverse primer sequences used for ChIP-qPCR, respectively. The red text shows coding sequences of *AGL6*.