Supplementary Figure S1. BrSR45a promoter sequences with marked region of potential promoter motifs

GACCAAGATAAAGTTTGCATCACAAAACGAGTTGGAGATGGGTATTATTATTATTATTACCAACCTTTTTGACTCCATAA

CTTGTGCCCGCTGTTCTGGGATCTTATCAGCTTCACTCGCTGTATAGCTAAAACATGATTCAATATAAAATATATTAACA

AAGCCTTAAACTTTTTATGCTTCACATTCCAAAAACCTTATTGTTGACAAACCTAGAGGGATGAGCAGAAGGAGGGAC

GAGAGGAGCATAAGCGGTTTCTCTTTCAGCAGCTGTCTGCTGAGCTTTCTGAAACTCTTTCAACACAGCTTGAAAGTC

CTTTGCAAGCTTAGCATCTGCAATCTTCTTACTTGGCTACAACAAACATTTAACAAACCATCATCATCAAACTCCAACAA

AACCAAAGAAGAAAAGATTGTGACTTTTACATTGACACCGCTTCGATGATCAGTTTCACTAGCTTCTTTAAGCTTAGCA

GAAGTATCCTTCACAAGCTGTCCTATATGCAACCTTGTCTTGTGCCTATAACGCAAATCAACCATTAGAGTCAATTCTG

AGCAGCTACAAAAAAAATAAAATGATTTTTAAATTTCAATCTTACAGCTTCTCACGGAGCTCGGGCGTGTCTTTGGGAGT

ACCGAGCGTGTTAACGAGCCGCTGAAACGTGGAGACTCCGGTATTGATCTGGAAGATACCGGAAGCGACGGCTTGC

GTCGAATCTTGGCGACCACCACCACCGCCATTGATCTTCCTCGATCTTCCTTTCCCAGCTTCCAAATCTTGAAAACTCA

TCTTCTCTCTTTCGTGCCTATCTCTCTCTCTCCAACGATGAACGATTTGGTTTGAGAAGGGAAAATGATGAATGAGG

GGTCAAGGCGTGAATCGTGGAGACAGATAGACAGAACTTGAAAAGCGTTTTTTTTCTTATAACTGATTAGAAGAGATG

MBS

AAAGGCGAGATCAATTTTTGTTTCTTTCTGGTCCTTTCATTTCTATTTACTTACTAATGTCTCCTTATTTTATTGTTTAGT

GTAGGTTTGCATACTTTTGGCGTTTTAAGGTATAGAAAATTTAATAGTTTGTGTTTGATTTGGTGTGCATTAGGAGTGG

ABRE

GACAGAAATCAACCTGAACTGAACCAAATTCTGACCAAACCAAAATATATATCCAAGAACATTTGATTGATATTTTTAAC

AACTTGAATAGTTTGTTTTTTTTTTGTTCGGTTTAAAACCGAACTGAACCAAAACCAATATATTTAGTAGTTAGCTTAAAT

AATATATTCATGATATTAAGATATTACCATCCTTTGATATAAACTCAACTTTTTAGCATTGATGATCAAAAGTGATGTTTG

TTTTCTTTTATGTTGTGTAGATTGCTTTTAAGTGAATTACACCAAATCCAAGCCAATATTAATTCGATATAAACCAAACTC

AACATAAATCAAACCGAATACAAATTAAACATAATCAAAATGGAATCAACCCAAAATTGAACCAAAATGGTCATGCCTA

ATTTATATACACAAAATCAGTTTCAGTAAACATTTAGTTGTAGTTTATTTTGGTTGTTCTCCATCTATTTAAAGTTACGGA

GCAGTCACAGTTTAACTATTCATAAATCGGCCGGGGGGTTAATTTATAATTAAGATATTCAGTGATGAGGTTACTTTAC

AAGTGGCCGTCCGACGTGGATGATTGTAATTGGTGGATAAAGTGATTATGTCACGTCTAAAATAATAAAGTATATGTTA

CAT-Box CCGTCC-Box

TTATTTAATTAAATGGAATCGTTCCCGACAAAGCAAAAGCTCTACGCACGACAACCTTCTCTGTCCCTTCACACGTATA

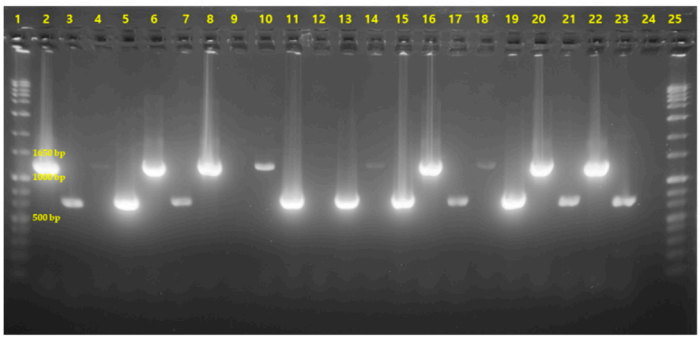
AAGTCGCCGGCGAGAGAAGAAGTTTCCGGACAGTCACGCGTGCCATTTTCTCAATATAAATAGAATTCACATTTTTGT

TTCTCACACCATCAAAAATTTTCTTTCTTCAAATTCGTTCTTCGCTGGTAAAAGAGAAAATCTTCCGTTACATCAGATTT

HSE

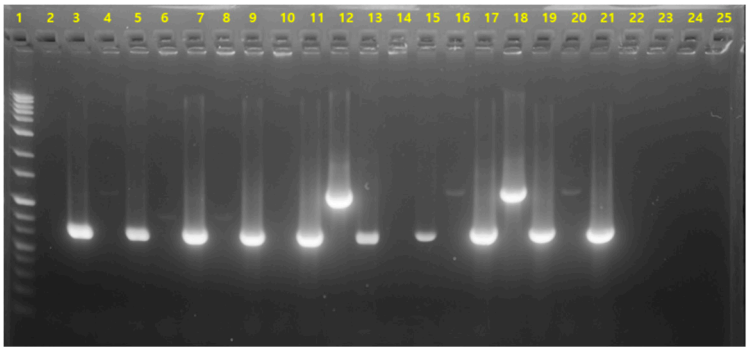
CTAAGAGTTTCTCAGCAATG

Supplementary Figure S**2.** PCR based genotyping for selection of homozygous SR45a mutants from SALK_052345 seedlings



1-1 kb plus DNA ladder
2-W12 Heterozygous
3-T12
4-W2 Homozygous
5-T2
6-W3 Heterozygous
7-T3
8-W4 Wild
9-T4
10-W5 *
11-T5
12-W6 Homozygous
13-T6
14-W8 Homozygous
15-T8
16-W9 Heterozygous
17-T9
18-W10 Homozygous
19-T10
20-W11 Heterozygous
21-T11
22-W13 Heterozygous
23-T13
24-Negative control
25-1 kb plus DNA ladder

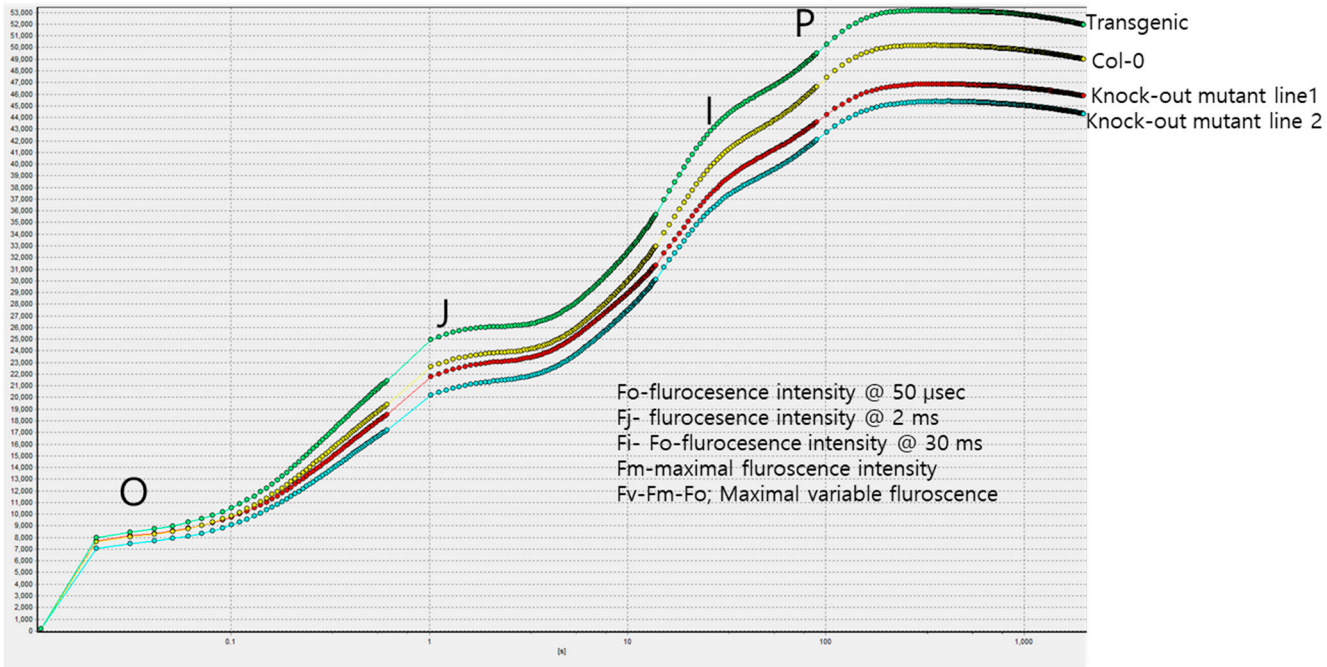
Confirmatory analysis



To select homozygous mutant through PCR based genotyping (A two-step PCR genotyping assay) for further studies, the following primers were designed.

1. SR45F TCAAGCACTGAGAACAACGG
2. SR45R TGAACATGCTAAATCGAACCAC
Product size: 1239 bp
3. T-DNA LB ATTTTGCCGATTTCGGAAC
Product size: 602-902 bp

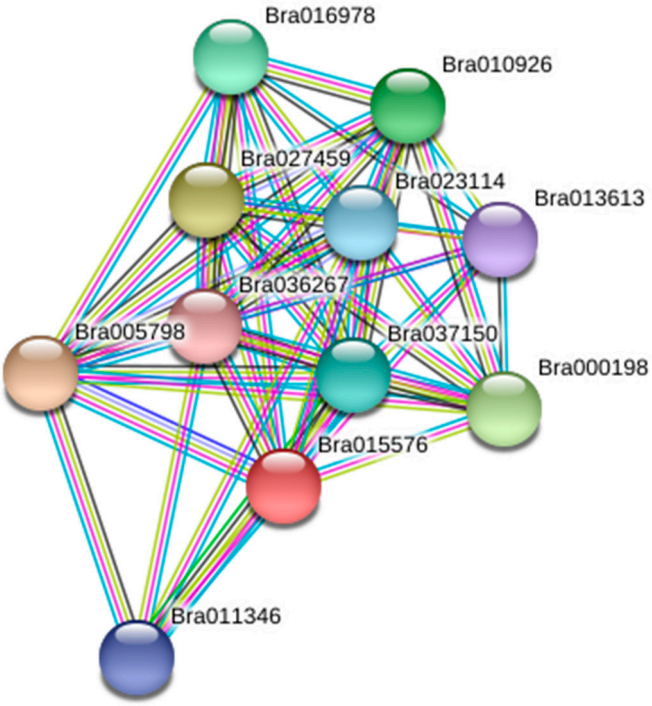
Supplementary Figure S3. Chlorophyll a fluorescence transients (OJIP curves) in dark adopted leaves of Arabidopsis seedlings BrSR45a overexpressors, Col-0, *SR45a* knock-out mutants (Knock-out mutant line 1 and 2) subjected to drought stress (15 DAS)



Supplementary Table S1. List of primers and their annealing temperature used in this study

Primer Name	Sequence (5'->3')	Annealing Temp.	Product Size
UPF1-FP	ACTGTGGGTGTCGGAATGTC	57°C/50 sec	1326 bp
UPF1-RP	ACAACCGAAGATCAGCAGCA		
DCP5-FP	ATGGCGGCTGATAATACGGG	58°C/50 sec	712 bp
DCP5-RP	ATGAAGAGGGTGCTTCTGGC		
ABI4-FP	AATCCGATTCCACCACCGAC	58°C/50 sec	976 bp
ABI-RP	TCCAATGCTCTTGACCGACC		
DREB2B-FP	GCAAAGTTCCTGCGAAAGGG	57°C/50 sec	626 bp
DREB2B-RP	AGGCCAACCGTAATCTGCAA		
NCED2-FP	ATATCCGTAACGGCGCGAAT	57°C/50 sec	1027 bp
NCED2-RP	ATAGCCAAAAACGCGAACCG		
RD29A-FP	CCACCAGGGACAAAGGTGTT	58°C/50 sec	881
RD29A-RP	CCGTCAGATTCCGGCGAATA		
MKK3-FP	GGAGCTATAGGAAGCGGAGC	57°C/50 sec	1164
MKK3-RP	AAGCCCTTCTGCTTGGACTC		
SQE-FP	AGCAGGAGAGGAACAAACCG	57°C/50 sec	798
SQE-RP	CCATAAACCGCAACCGCAAA		
GTL1-FP	TCAGGCTAACATTGCGGGTT	59°C/50 sec	873
GTL1-RP	CTAGAACCACCGCCACTACC		
GOLS1-FP	AGACAGCGATCGAGCTTACG	58°C/50 sec	1058
GOLS1-RP	TATGTGTGGTTGTCGACCCG		
AKR-FP	TACCTTGCGTCGGTCTAGGA	57°C/50 sec	727
AKR-RP	TGAAGACCTTGTTGCTGCCA		
U4/U6.U5-FP	TGAAAGCCAGCAAGAAACGC	57°C/50 sec	525
U4/U6.U5-RP	ACACCTTCTCCCCTTCTGGT		
SR34-FP	AGGCTTGCCTTCATCTGCTT	57°C/50 sec	907
SR34-RP	AAGCAGACGTCTCCAGACAAG		
U2AF-FP	ACTCGCGAACAAAGCAAACC	57°C/50 sec	906
U2AF-RP	TTGAACCGTCCCTCTCTTGC		
PPI-FP	CGCATGCGTCTGCATTCTAC	56°C/50 sec	1357
PPI-RP	ACCCAATTGCAGAGAGTTGAAA		
MYB117-FP	ACGGAAAAACAAGTGTGGATGG	58°C/50 sec	831
MYB117-RP	TAGGCTACCTTGAAAGCAATGG		
SDR-FP	ATGGCTTCCTCAGTCTCCTCT	59°C/50 sec	773
SDR-RP	TTGCTGATTCTTGTGTCACCAC		

Supplementary Figure S4. BrSR45a interaction with other proteins predicted by string-db online tools



Bra013613.1=PREDICTED: U4/U6.U5 tri-snRNP-associated protein 2-like isoform X2 [Brassica rapa]

Bra005798.1-P=PREDICTED: glycine-rich RNA-binding protein RZ1C isoform X1

Bra036267.1-P=PREDICTED: serine/arginine-rich-splicing factor SR34 [Brassica rapa]

Bra037150.1-P=unnamed protein product [Brassica rapa],Sequence ID: VDC59016.1; 62% coverage with PREDICTED: ATP-dependent DNA helicase DDM1-like [Brassica rapa]

Bra000198.1-P=PREDICTED: pre-mRNA-splicing factor 38 [Brassica rapa]

Bra015576.1-P=PREDICTED: serine/arginine-rich splicing factor SR45a [Brassica rapa]

Bra011346.1-P=PREDICTED: peptidyl-prolyl cis-trans isomerase CYP95 isoform X1 [Brassica rapa]

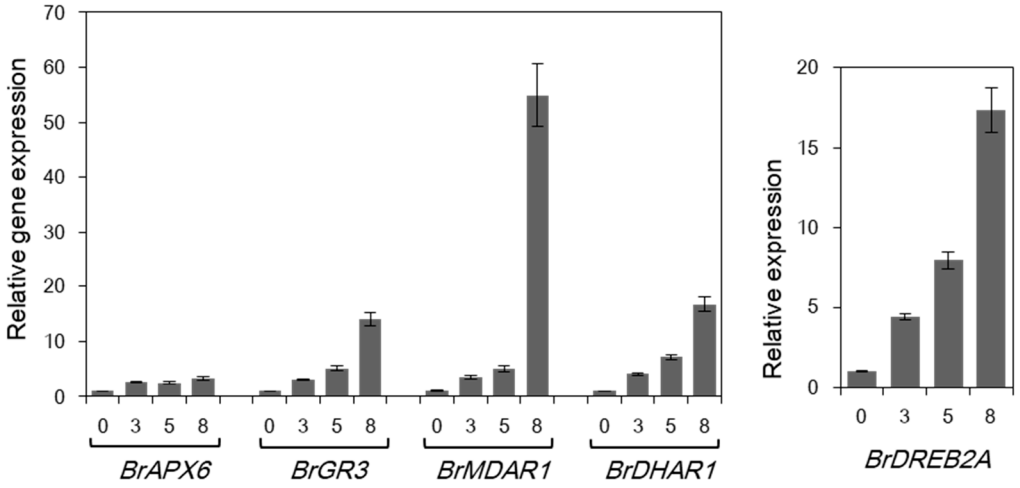
Bra016978.1-P=Pre-mRNA splicing factor-38 like

Bra010926.1-P=splicing factor U2af small subunit

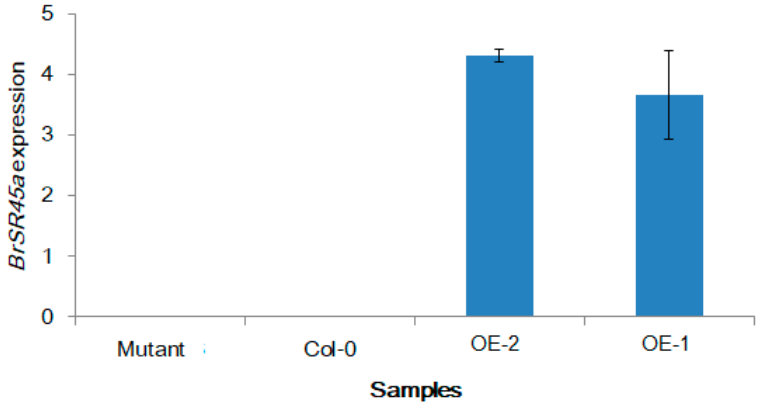
Bra027459.1-P=splicing factor U2af small subunit B

Bra023114.1-P=serine/arginine-rich splicing factor RS2Z33

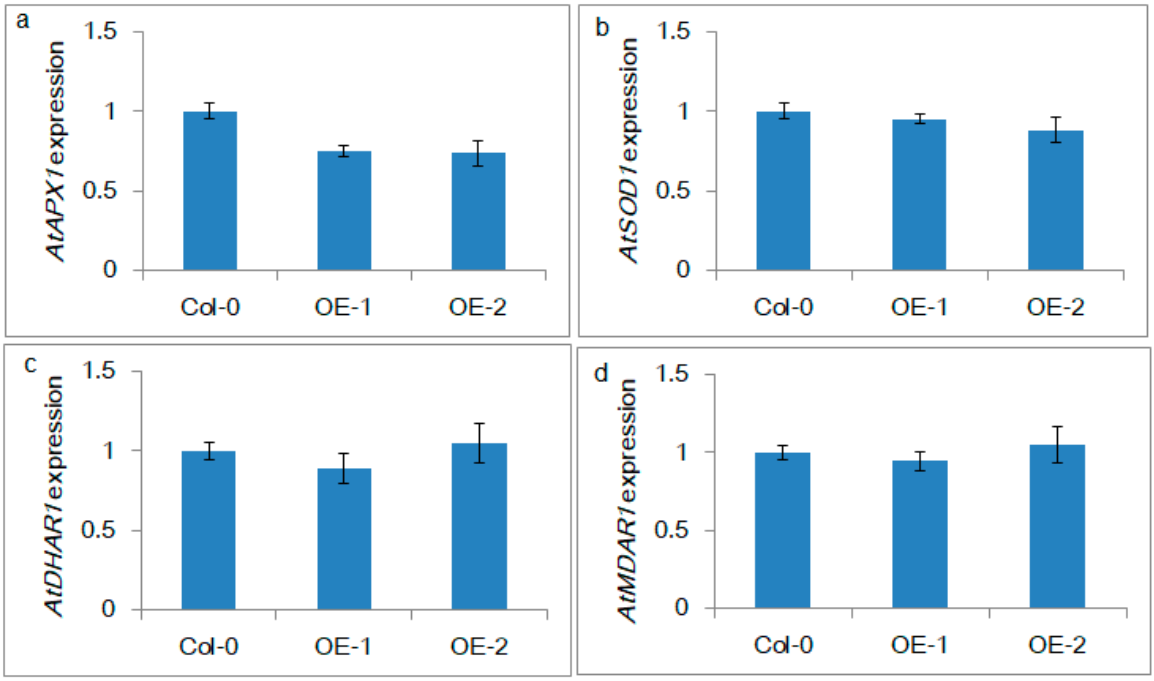
Supplementary Figure S5. Expression of stress markers under different time interval (0, 3rd, 5th and 8th days) of progressive drought stress



Supplementary Figure S6. *BrSR45a* expression pattern in selected transgenic lines (OE-2,OE-1), mutants (SR45a knock-out) and Col-0.



Supplementary Figure S7. The expression pattern of antioxidative enzyme genes in selected transgenic lines (OE-2,OE-1) and control (Col-0).



Supplementary Figure S8. Measurement of Superoxide dismutase (SOD) enzyme activity during different times of drought stress (d-0,5,7) in in selected transgenic lines (OE-2,OE-1), and control (Col-0) Arabidopsis plants.