**Supplementary material**

**Table S1** Olive SRBs accession numbers and qRT-PCR primers.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Genbank accession | Gene | Description | Primer sequence (5' – 3') | Size (bp) |
| KF953476 | *OeMO1* | Monooxygenase 1 | GATAAATGAAGTTGGAGAAGCAATTG | 171 |
|  |  |  | ACCAACTGGATCACGAAACAGAATG |  |
| KF953477 | *OeCCX1* | Cation calcium exchanger 1 | CTTCATTTTTAGGGCTCACGGTACTAGC | 169 |
|  |  |  | AAGAGTGACAATCCCAAACCCACC |  |
| KF953478 | *OeSTO* | Salt tolerance protein | CGGAATTCAGGTTGCTTTAAACTCC | 163 |
|  |  |  | TTGAAGCAAATCGTCGATAGCCC |  |
| KF953479 | *OePMP3* | Proteolipid membrane potential modulator | GATATGGCTGCAAGGTTGAATTTTGG ATCAACACCATCCAGCAAGAAAGG | 182 |
| KF953480 | *OeUSP2* | Universal stress protein | ATAGTCAAGGATCCAGATTTTCACAAGC | 177 |
|  |  |  | CAACACCGTAACCAGAAACAATTCATCT |  |
| KF953481 | *OeAP-4* | Adaptor protein complex 4 medium mu4 subunit | GAAGCTAACGTTTCCACAGGAGTTGC CACCCAACGATATGGGTTGTAAGC | 160 |
| KF953482 | *OeWRKY1* | WRKY1 transcription factor | CGTCCATGCAAGCACCATCG | 178 |
|  |  |  | ACATTGCATCCAGCATGTGTGC |  |
| KF953483 | *OeKT2* | Potassium transporter 2 | GAATCTGAACTCATTAGTAGACTGGCGG | 170 |
|  |  |  | AATGCAGGTAAGCCAGAGAATGTC |  |
| - |  | Actin 1 | TTAATAGGAATGGAATCTGCAGGAATCC | 167 |
|  |  |  | CAAGAGCTGTAATTTCCTTACTCATGCG |  |

**Table S2** GO terms associated with olive SRBs.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | Protein | GO | Term | Type\* |
| 1 | OeMO1 | GO:0005783GO:0009617 | Endoplasmic reticulum Response to bacterium | CP |
| 2 | OeCCX1 | GO:0005432GO:0010260GO:0046482GO:0035725GO:0016021 | Calcium:sodium antiporter activityOrgan senescencePara-aminobenzoic acid metabolic process Sodium ion transmembrane transport Integral to membrane | FPPPC |
| 3 | OeSTO | GO:0016301GO:0016310GO:0005622GO:0008270 | Kinase activityPhosphorylationIntracellularZinc ion binding | FPCF |
| 4 | OePMP3 | GO:0016023GO:0016021 | Cytoplasmic membrane-bounded vesicleIntegral to membrane | CC |
| 5 | OeUSP2 | GO:0009506GO:0005886GO:0006950 | PlasmodesmaPlasma membraneResponse to stress | CCP |
| 6 | OeAP-4 | GO:0006623GO:0030125GO:0016192GO:0005829GO:0030131GO:0005515 | Protein targeting to vacuoleClathrin vesicle coatVesicle-mediated transport Cytosol Clathrin adaptor complex Protein binding | PCPCCF |
| 7 | OeWRKY1 | GO:0003700GO:0006355GO:0043565 | Sequence-specific DNA binding transcription factor activityRegulation of transcription, DNA-dependent Sequence-specific DNA binding | FPF |
| 8 | OeKT2 | GO:0015079GO:0071805GO:0016020 | Potassium ion transmembrane transporter activityPotassium ion transmembrane transportMembrane | FPC |

\* C = cellular component, F = molecular function and P = biological process. ± SE.

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**Fig. S1** Phylogeny of OeMO1 and homologs from related plant species based on parsimony method. Accession numbers are indicated left to scientific names. Branching points showing bootstrap values.



**Fig. S2** Phylogeny of OeSTO and homologs from related plant species based on parsimony method. Accession numbers are indicated left to scientific names. Branching points showing bootstrap values.

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**Fig. S3** Phylogeny of OePMP3 and homologs from related plant species based on parsimony method. Accession numbers are indicated left to scientific names. Branching points showing bootstrap values.

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**Fig. S4** Phylogeny of OeUSP2 and homologs from related plant species based on parsimony method. Accession numbers are indicated left to scientific names. Branching points showing bootstrap values.



**Fig. S5** Phylogeny of OeAP-4 and homologs from related plant species based on parsimony method. Accession numbers are indicated left to scientific names. Branching points showing bootstrap values.



**Fig. S6** Phylogeny of OeKT2 and homologs from related plant species based on parsimony method. Accession numbers are indicated left to scientific names. Branching points showing bootstrap values.