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Supplementary Material

The *VvBAP1* gene is identified as a potential inhibitor of cell death in grape berries

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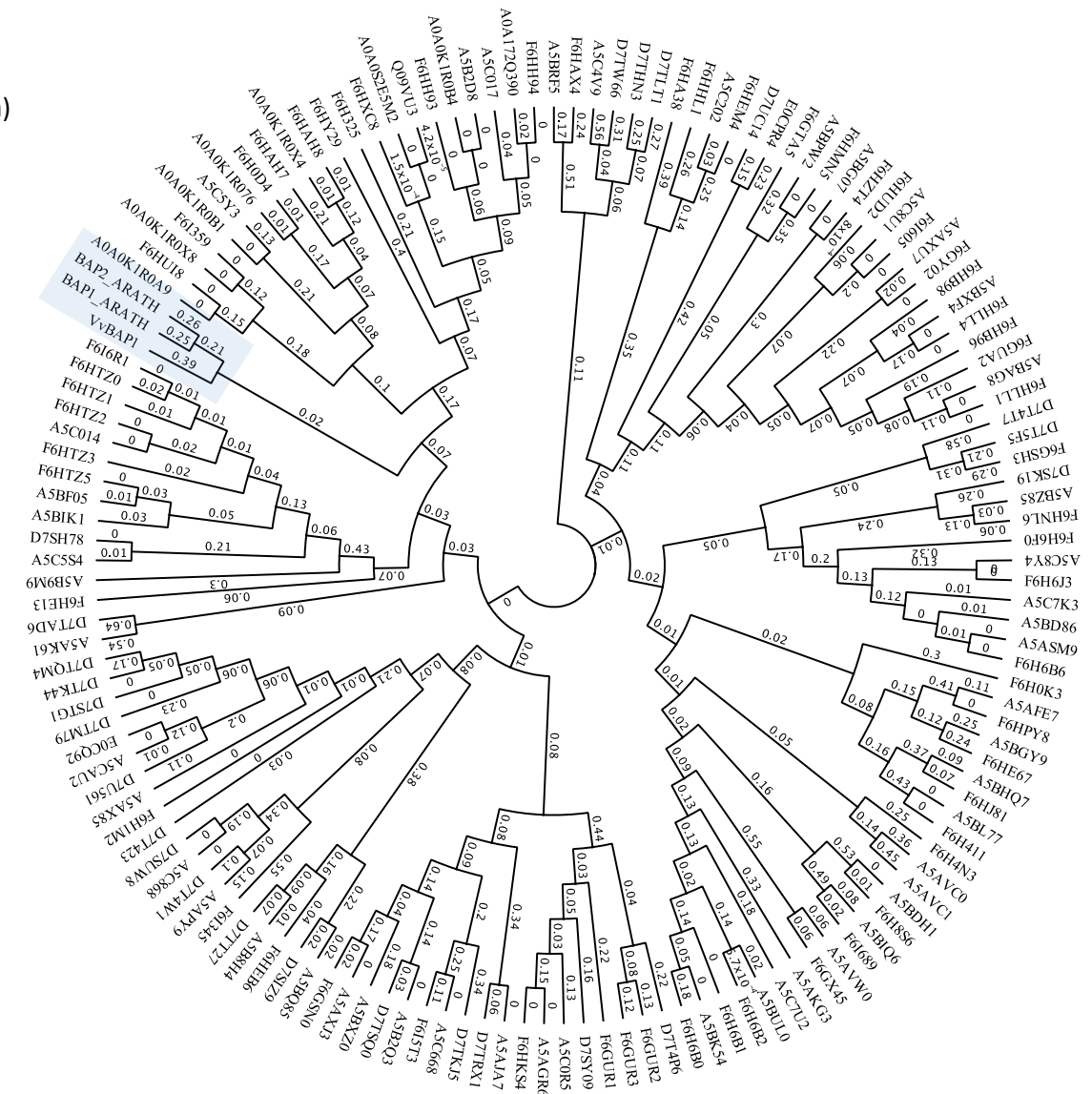
Table S1. List of primer sequences used in this work

Primer name	Sequence (5' - 3')	Purpose
VvBAP1-p1301-F	CATGCCATGGCCATGGAGGCCGCTTCA	Cloning
VvBAP1-p1301-R	GGACTAGTAACTTGA ACCGTCCGATACG	Cloning
VvBAP1-pESC-F	CGGAATTCATGGAGGCCGCTTCA	Cloning
VvBAP1-pESC-R	GGACTAGTGCAACTTGAACCGTCCG	Cloning
AtBAP1-pESC-F	CGGAATTCATGTCGTATT CAACATTCAAAG	Cloning
AtBAP1-pESC-R	GGACTAGTAGACGGC CGTTGATACG	Cloning
VvBAP1-RT-F	AGCTACTTGCATTTCTTG	qPCR/R T-PCR
VvBAP1-RT-R	TACGGACAGATTCACAAT	qPCR/R T-PCR
VvACT1-RT-F	CTTGCATCCCTCAGCACCTT	qPCR
VvACT1-RT-R	TCCTGTGGACAATGGATGGA	qPCR
VvEF1- α -RT-F	AACTGAAGTCAAGTCTGT	qPCR
VvEF1- α -RT-R	CACATTGAAGCCAACATT	qPCR
NbHSR203 J-RT-F	TCAACGATTACGCAGATT	qPCR/R T-PCR
NbHSR203 J-RT-R	CAACTTGGTGGACTATGT	qPCR/R T-PCR
NbACT-RT-F	CAACTTGGTGGACTATGT	qPCR/R T-PCR
NbACT-RT-R	CCACCACTGAGCACAATG	qPCR/R T-PCR
AtMSD1-RT-F	TCATCACCAGAAGCATCA	qPCR

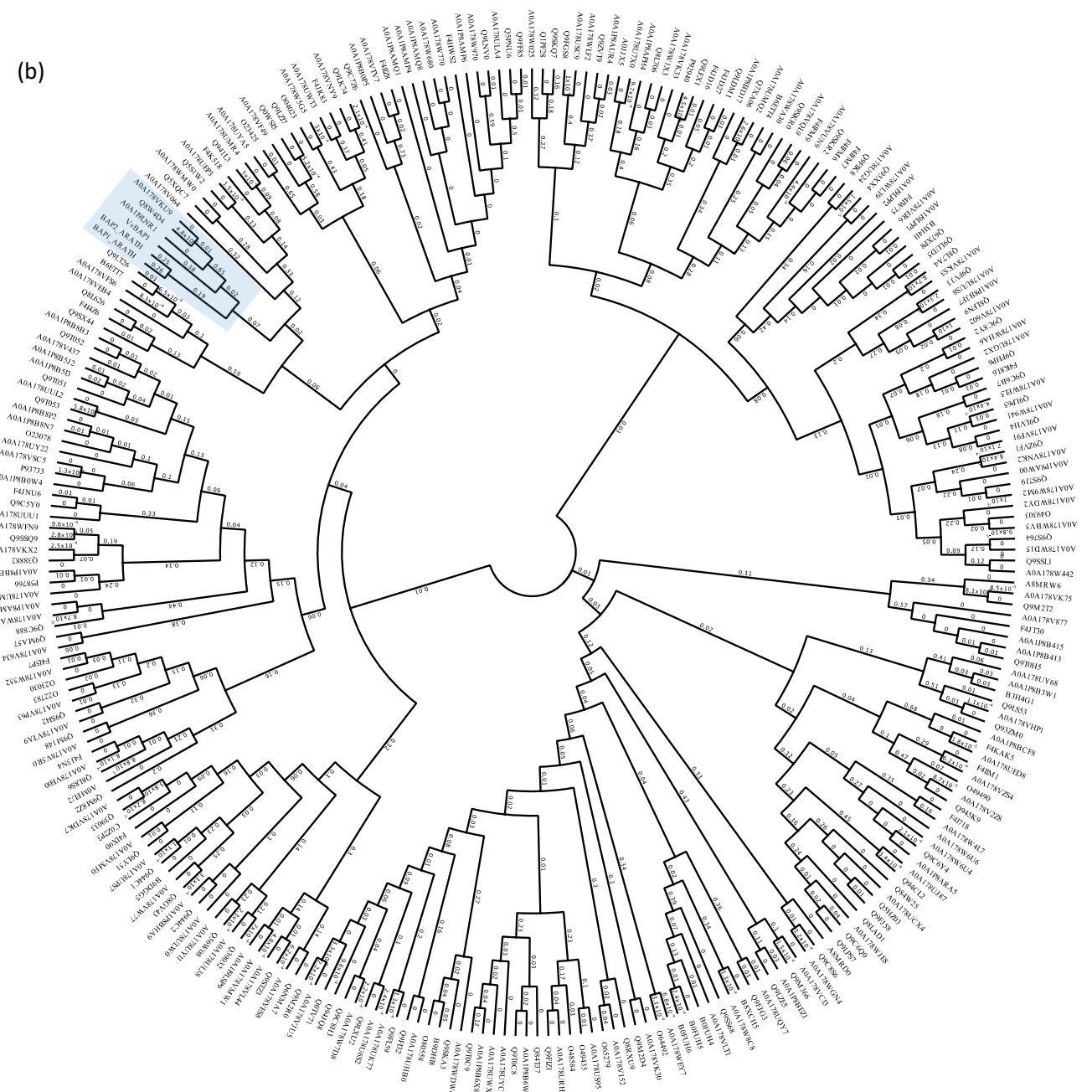
AtMSD1- RT-F	CAACAGTGGAAGCATCTC	qPCR
AtCAT1- RT-F	TATTCTTCGTCCGTGATG	qPCR
AtCAT1- RT-R	CAGTATCCTCCAGTTCTC	qPCR
AtAPX1- RT-F	AACTCTTACTTCAAGGAACTCT	qPCR
AtAPX1- RT-R	GGTCGTCCAATAGTGCTT	qPCR
AtGPX1- RT-F	TAATTCCTCAGCAACCTT	qPCR
AtGPX1- RT-R	GACGAGACTTGAAGAGAA	qPCR
AtPDR1.2- RT-F	CTTATCTTCGCTGCTCTTG	qPCR
AtPDR1.2- RT-R	CTTCTCGCACAACTTCTG	qPCR
AtPR1-RT- F	AGGTGTAACAATGGTGGAA	qPCR
AtPR1-RT- R	TTAGTATGGCTTCTCGTTCA	qPCR
AtRD29a- RT-F	CCAGAAGAAGTTGAACAT	qPCR
AtRD29a- RT-R	CTCGTCATCATCATCATC	qPCR
AtRD29b- RT-F	AGAAGAACCAATCAGAAT	qPCR
AtRD29b- RT-F	TCATACTCATCATCATCAT	qPCR
AtACT2- RT-F	TGAGCAAAGAAATCACAGCACT	qPCR/R T-PCR
AtACT2- RT-R	CCTGGACCTGCCTCATCATAC	qPCR/R T-PCR
VvBAP1- BD-F	AAAAGGCCAATCCGGCCATGGAGGCCGCTTCA	Y2H
VvBAP1- BD-R	CGCGGGCCTTAGAGGCCGCAACTTGAACCGTCCG	Y2H
VvBON1- AD-F	GGAGGCCAGTGAATTCATGGGAAATTGCTGCT	Y2H
VvBON1- AD-R	TCATCTGCAGCTCGAGGGAATTTGGAAGAATATTTTC	Y2H

VvBAP1- nY-F	CGGACTCAGATCTCGAGCTCAAATGGAGGCCG CTTCA	BiFC
VvBAP1- nY-R	GGGCCC GCGGTACCGTCGACAACTTGA ACCGTCCGATA	BiFC
VvBON1- cY-F	CGGACTCAGATCTCGAGCTCAAATGGGAAATTGCTG CT	BiFC
VvBON1- cY-R	GGGCCC GCGGTACCGTCGACGGAATTTGGAAGAATA TTTC	BiFC

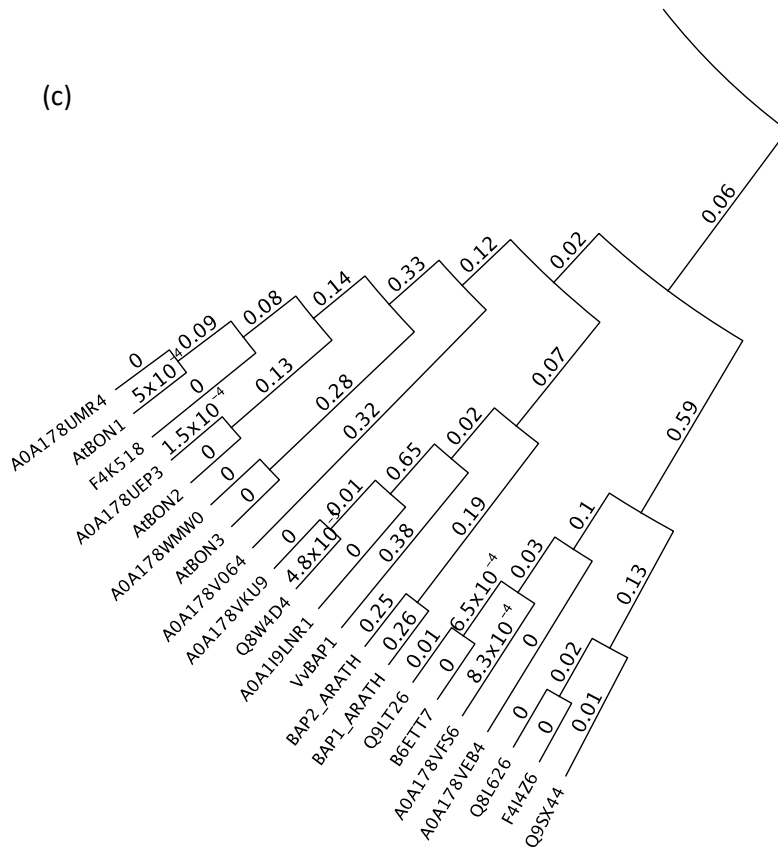
(a)



(b)



(c)



A0A178VKU9: At3g54070; Similar to BAG-associated GRAM protein 1; Length 594.

Q8W4D4: At3g59660; BAG-associated GRAM protein 1; Length 594.

A0A119LNR1: At3g59660; C2 domain-containing protein / GRAM domain-containing protein; Length 533.

Fig. S1. Consensus trees of C2 domain proteins in *Vitis vinifera* (a) and *Arabidopsis* (b, c) with VvBAP1 and AtBAP1 and AtBAP2 in each. The BAP proteins are present in the same clade in both consensus trees of the two species (high-lighted). For *Arabidopsis* the clade is reproduced in (c) and the proteins not identified as BAP homologs are identified above. Trees were constructed using Genus 9 with Blossum cost matrix and the Jukes Cantor genetic distance model. Protein sequences were obtained from EMBL IntPro (C2 domain IPR000008).

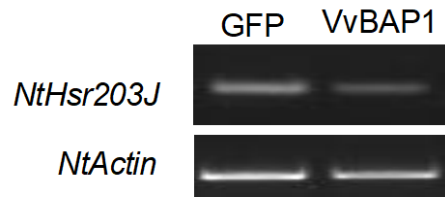


Fig. S2. Semi quantitative RT-PCR analysis of cell death marker gene Hsr203J expression in *N. benthamiana* leaves after 48 h of H₂O₂ treatment. Expression of the *N. benthamiana* Actin gene served as a control. Similar results were obtained from three independent experiments.

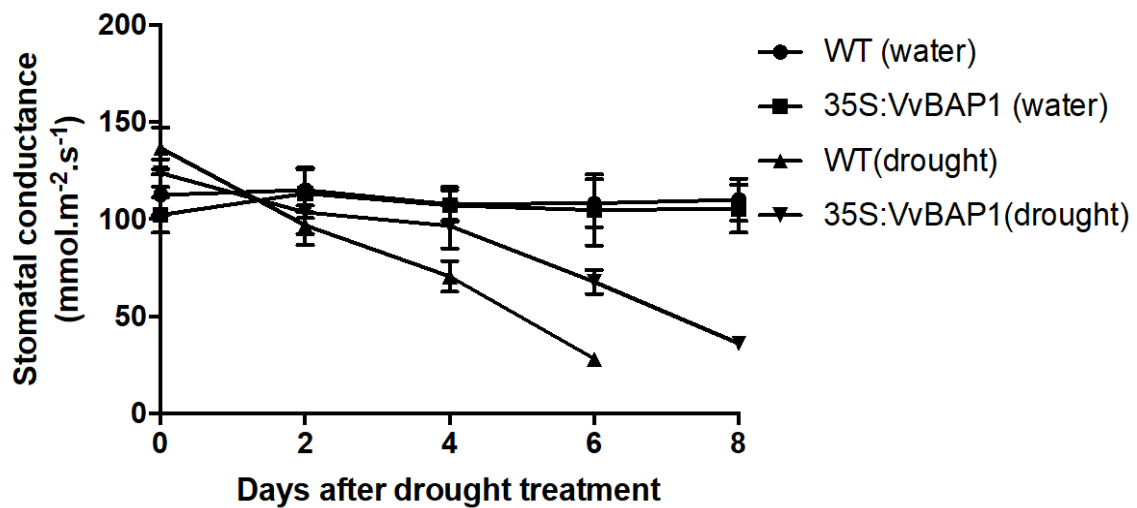


Fig. S3. Stomatal conductance of the leaves of wild-type or transgenic plants (T3) during drought stress. Four leaves from the third layer rosettes per plant were used to measure the stomatal conductance. Values are means \pm s.e.m. of ten biological repeats. (Note: WT plants under drought were too sick, and the measurement was stopped on day 6.)

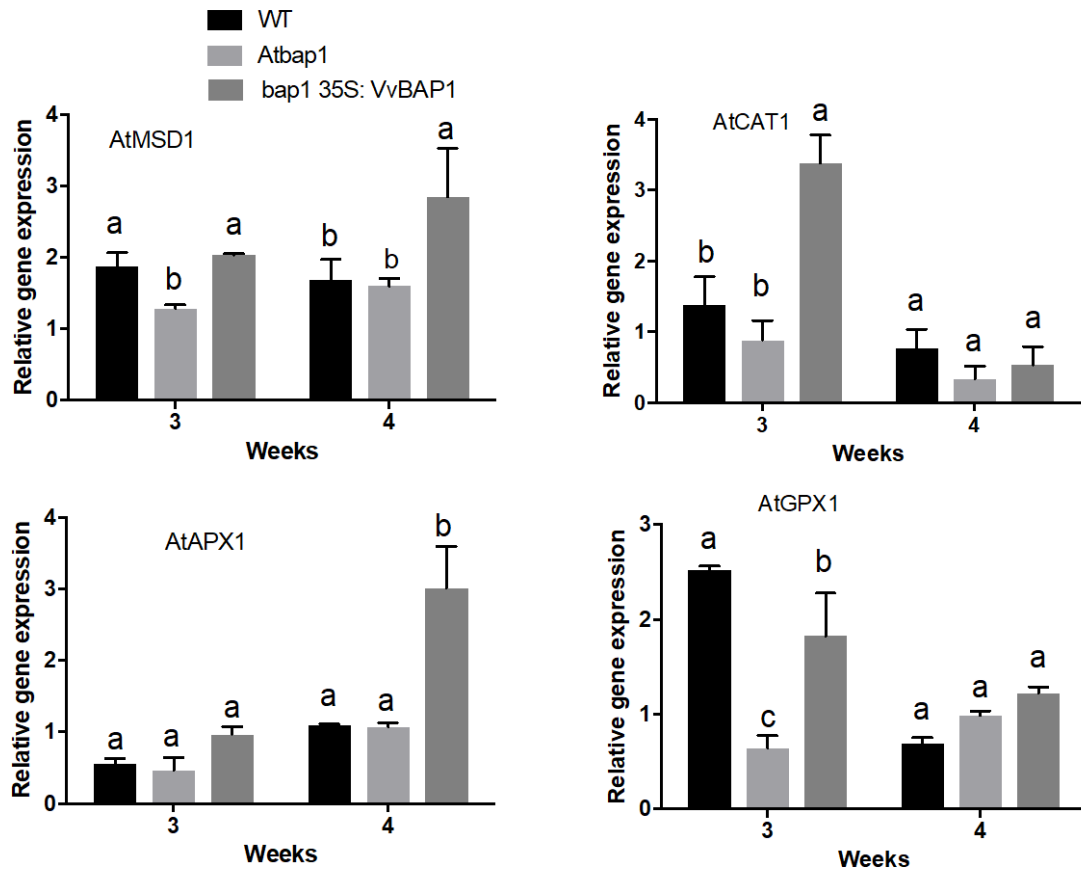


Fig. S4. Expression of *AtMSD1*, *AtCAT1*, *AtAPX1* and *AtGPX1* from *Arabidopsis* leaves from the *Arabidopsis bap1* mutant, WT and *VvBAP1* complemented line. Values are means \pm s.e.m. of three biological repeats. Different letters indicate statistically significant differences within a time cohort using one-way ANOVA (Tukey post-test) ($P < 0.05$).