Supplemental Data

Transcription factors BBX11 and HY5 interdependently regulate the molecular and metabolic responses to UV-B

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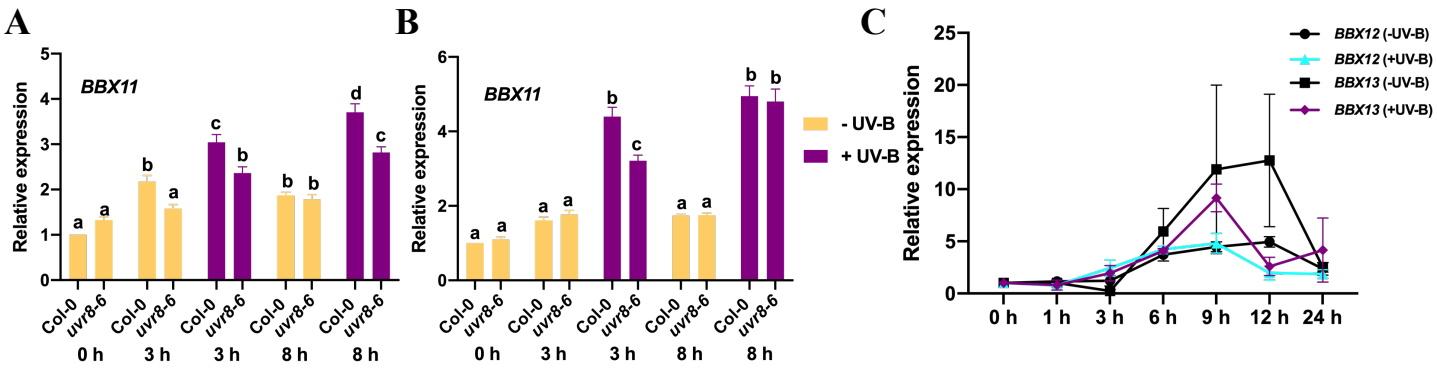
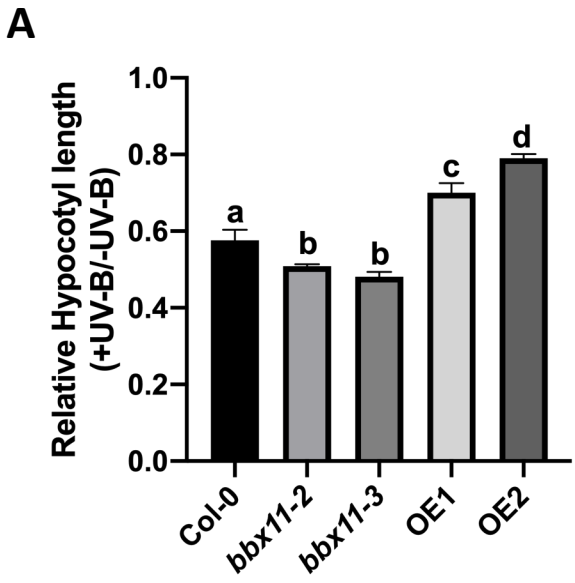
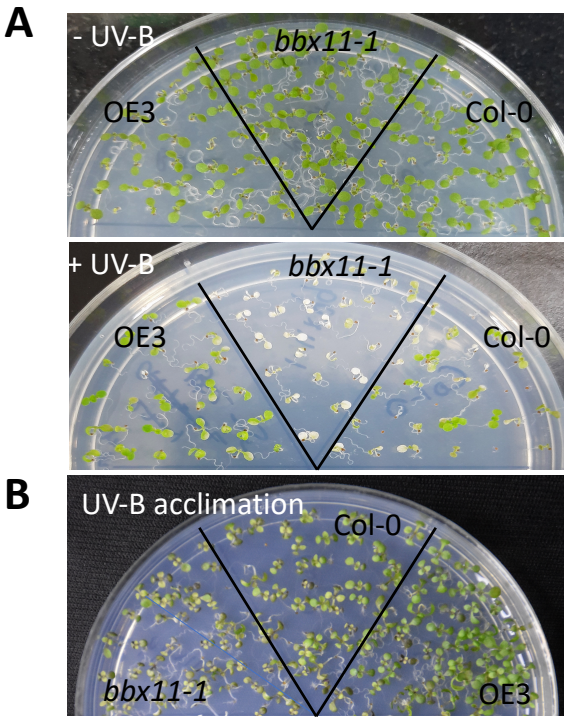


Supplemental Figure S1. *BBX12* and *BBX13* mRNA expression is not induced by UV-B and the UV-B mediated induction of *BBX11* is partially dependant on UVR8.
qRT-PCR analysis of BBX11 expression in 5-d-old Col-0 and *uvr8-6* seedlings grown in constant white light and exposed to supplemental UV-B 1 (A) and UV-B 2 (B) (+) or not (-) for 3h and 8 h. GAPDH was used as internal control. Error bars represent SEM, n=3. Statistical groups indicated by letters were determined by two-way ANOVA, with Tukey's test, $P \leq 0.05$. (A) RT-qPCR analysis of *BBX12* and *BBX13* expression in 5-d-old Col-0 seedlings grown in constant white light and exposed to supplemental UV-B 2 (+) or not (-) for the indicated time period. GAPDH was used as internal control. Error bars represent SEM, n=3.

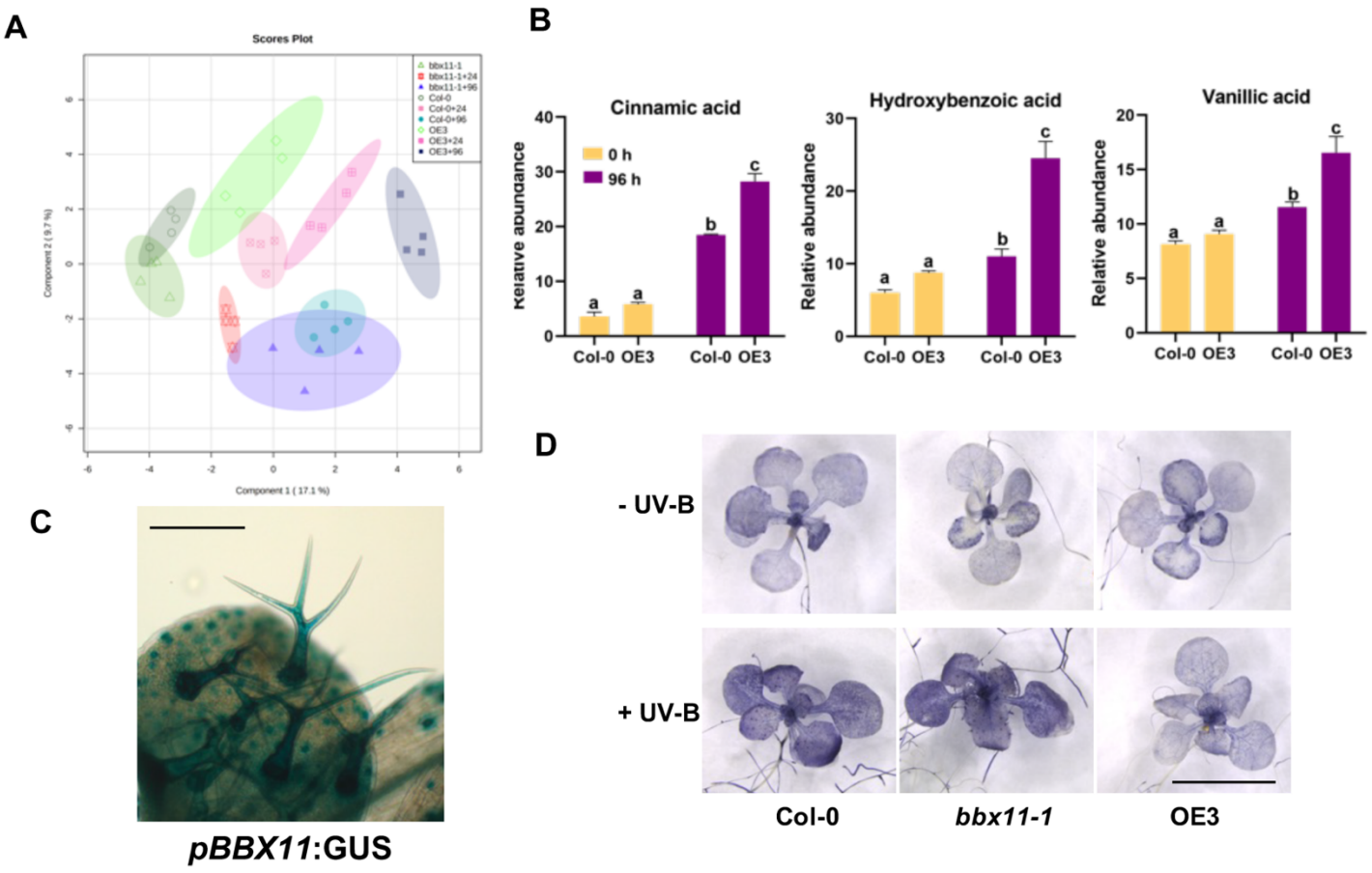


Supplemental Figure S2. Relative hypocotyl length of loss and gain of function mutants of *BBX11* under UV-B

(A) Relative hypocotyl length of 5-d-old seedlings of the indicated genotypes grown under constant white light supplemented with UV-B 1 (+) or not (-). Error bar represents SEM, n=3, Statistical groups indicated by letters were determined by one-way ANOVA, with Tukey's test, $P \leq 0.05$

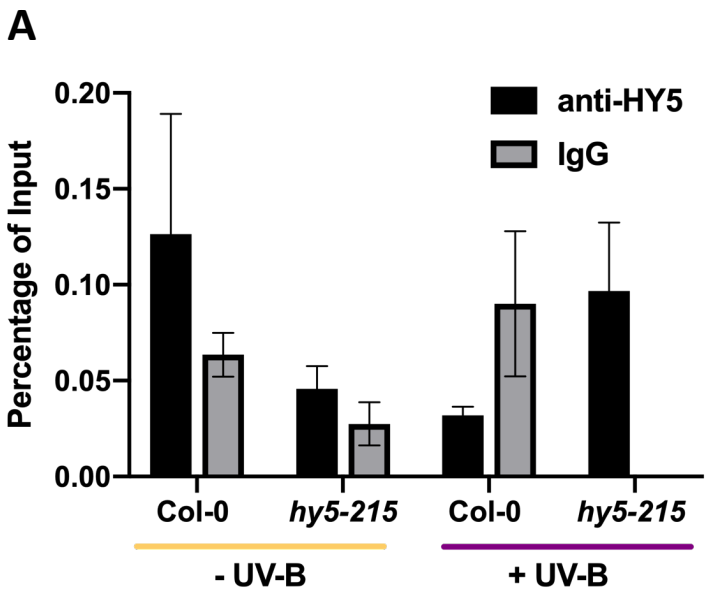


Supplemental Figure S3. Over expression of *BBX11* enhances protection against UV-B stress
(A) 4 d-old seedlings of the indicated genotypes grown under constant white light and exposed to supplemental UV-B 3 (+UV-B) or not (-UV-B) for 20 h and allowed to recover under white light for 1 d before imaging. (B) For UV-B acclimation experiment, seedlings of the indicated genotypes grown under constant white light supplemented with UV-B 1 for 5 days and irradiated with UV-B 3 for another 24 hrs allowed to recover under white light for 1 d before imaging.

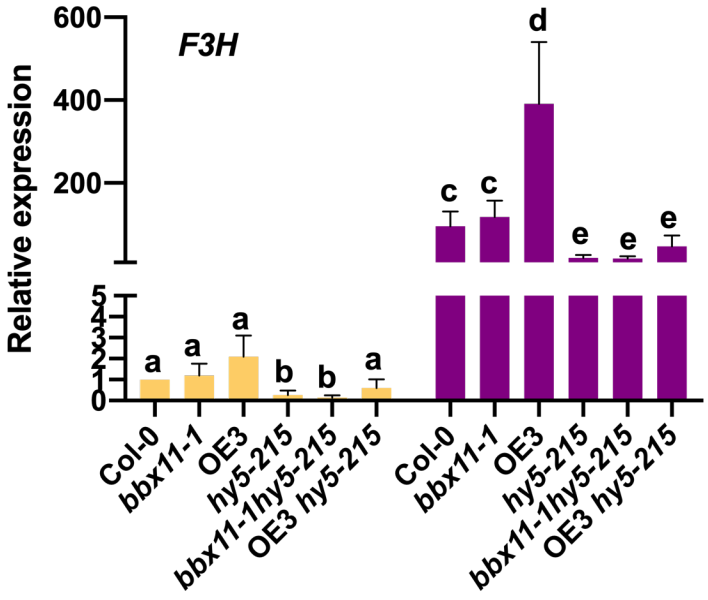


Supplemental Figure S4. BBX11 modulates accumulation of photoprotective secondary metabolites

(A) Multivariate analyses using Partial least squares-discriminant analysis (PLS-DA) showing that Col-0, *bbx11-1,* and *OE3* alter their metabolome differently after 24 h and 96 h of UV-B irradiation. In PLS-DA, components one and component two plots represent variation in x and y axes, respectively. Ovals covering the replicates represents a 90% confidence interval of metabolome under the given treatment. (B) Relative abundance of the indicated phenolics after in Col-0, *bbx11-1* and *OE3* after 96 h of UV-B 3 treatment. Error bars represent SEM, n=3. Statistical groups indicated by letters were determined by one-way ANOVA, with Tukey's test, $P \leq 0.05$. (C) histochemical staining of *promBBX11*:GUS seedlings grown for 10 d in constant white light indicating that *BBX11* is expressed in the trichomes. Scale bar- 200 µm (D) Representative images of NBT stained seedlings of Col-0, *bbx11-1* and *OE3* grown under constant white light for 14 days before treating with supplemental UV-B 3 or not for 2 d and allowed to recover for another 2 d before staining with NBT. Scale bar- 5mm

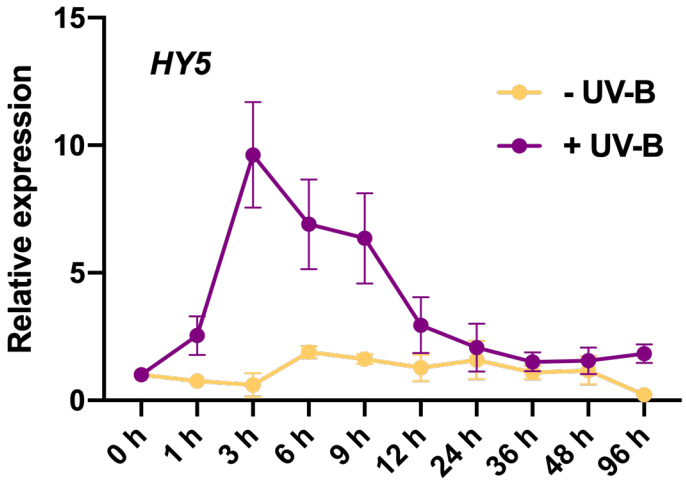


Supplemental Figure S5. HY5 directly binds to the promoter of *BBX11*
(A) ChIP-qPCR analyses of HY5 binding to the *BBX11* promoter in vivo. 14-d-old Col-0 and *hy5-215* seedlings grown in constant white light and exposed to supplemental UV-B 3 (+) or not (-) for 3 h before crosslinking. DNA-protein complexes were immunoprecipitated using antibodies against HY5 (anti-HY5) and rabbit IgG (negative control). ChIP DNA was quantified by qPCR with primers specific to the previously known HY5 binding site. Error bar represents SEM, n=3



Supplemental Figure S6. Expression of *F3H* is upregulated in *OE3* seedlings overexpressing *BBX11*

RT-qPCR analysis of *F3H* (A) in 5-d-old seedlings grown in constant white light and exposed to supplemental UV- B 2 (+) or not (-) for the 4 h. GAPDH was used as internal control. Error bars represent SEM, n=3. Statistical groups indicated by letters were determined by one-way ANOVA, with Tukey's test, $P \leq 0.05$.



Supplemental Figure S7.
***HY5* is an early UV-B inducible gene**
RT-qPCR analysis of *HY5* expression in 5-d-old Col-0 seedlings grown in constant white light and exposed to supplemental UV-B 2 (+) or not (-) for the indicated time period. GAPDH was used as internal control. Error bars represent SEM, n=3

Supplemental Table S1. List of primers used in this study

Primer name	Primer sequence (5'- 3')
BBX11 RT-qPCR FW	GCGGGTCGGGTACTCATAAC
BBX11 RT-qPCR RV	CTGGATAGTCCACGGAGCTG
promBBX11 ChiP HY5 binding site FW qPCR	CAAAGTCCTTTTTTTCGTTTG
promBBX11 ChiP HY5 binding site RV qPCR	GTAAATAAGATCATAACTAATGAAGG
promBBX11 ChiP 3' UTR FW qPCR	GAGCAAGAAGGGCTTGATG
promBBX11 ChiP 3' UTR RV qPCR	AGAGTGAAAGCTGCGACG
BBX12 RT-qPCR FW	TGCTGCCATTCACTCGCATA
BBX12 RT-qPCR RV	ATCAGCATTCGTTACCGCCA
BBX13 RT-qPCR FW	TGAGGAGATCAATGGTGGCG
BBX13 RT-qPCR RV	ACTCGTATCCTCAGGTCCCC
ELIP1 RT-qPCR FW	GAAGTCACCATCTCCTCCTCCTC
ELIP1 RT-qPCR RV	CCAACGCCGCAACGAATCC
ELIP2 RT-qPCR FW	GGATCAACGGGAGACTAGCA
ELIP2 RT-qPCR RV	CCTTTTGACTTTGCCTCTGC
UVR2 RT-qPCR FW	TAAAGGGTTTGCGTCAGCTT
UVR2 RT-qPCR RV	CATCTTTACAACGCCGGATT
CHS RT-qPCR FW	TCGGTCAGGCTCTTTTCAGT
CHS RT-qPCR RV	GGAGATGGAAGGTGAGACCA
CHI RT-qPCR FW	CATCGATCCTCTTCGCTCTC
CHI RT-qPCR RV	AGGTGACACACCGTTCTTCC
F3H RT-qPCR FW	ATGGCTTCCAGGAACTTTGACTGAGCTA
F3H RT-qPCR RV	GATCTGACGGCAGATCAC
SOD1 RT-qPCR FW	GGTTCCATGTCCATGCTCT
SOD1 RT-qPCR RV	ATTGTGAAGGTGGCAGTTCC
UVR3 RT-qPCR FW	GACAACCCGGCTCTTGAATA
UVR3 RT-qPCR RV	AAAGCAACCGTGAACC
CAT2 RT-qPCR FW	AAGTATCCAACTCCGCCTGCTG
CAT2 RT-qPCR RV	TGGATGAATCGTTCTTGCCTCTC
RUP1 RT-qPCR FW	CTCTCTTTCCGCCGTTGTTTC
RUP1 RT-qPCR RV	CGTCACGTGACTCTAACAAAGAG
RUP2 RT-qPCR FW	CTGAATTCGATCCCACTGATAACA
RUP2 RT-qPCR RV	CAGATGTAATATTCGCAGGCG
GAPDH RT-qPCR FW	TTGGTGACAACAGGTCAAGCA
GAPDH RT-qPCR RV	AAACTTGTCGCTCAATGCAATC
HY5 RT-qPCR FW	AAGAGAACAAGCGGCTGAAGAGG
HY5 RT-qPCR FW	TTCTCGTTCTGAAGAGTAGAGAGTCGC