



Figure S1. Anthocyanins pigmented organs in rice. From left to right: hull, apiculus, pericarp, awn, pistil, culm, leaf sheath, leaf blade.

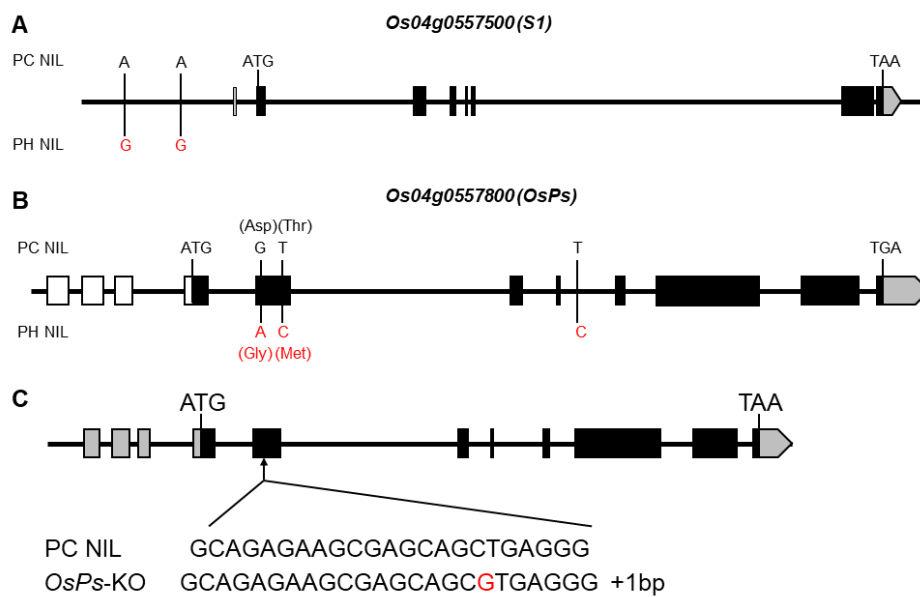


Figure S2. Schematic diagrams of gene structure. *S1* (A) and *OsPs* (B) show differences between PC NIL and PH NIL. (C) Knockout of *OsPs* by CRISPR/Cas9 system. A 'G' insertion in the second exon of the gene caused frame shift.

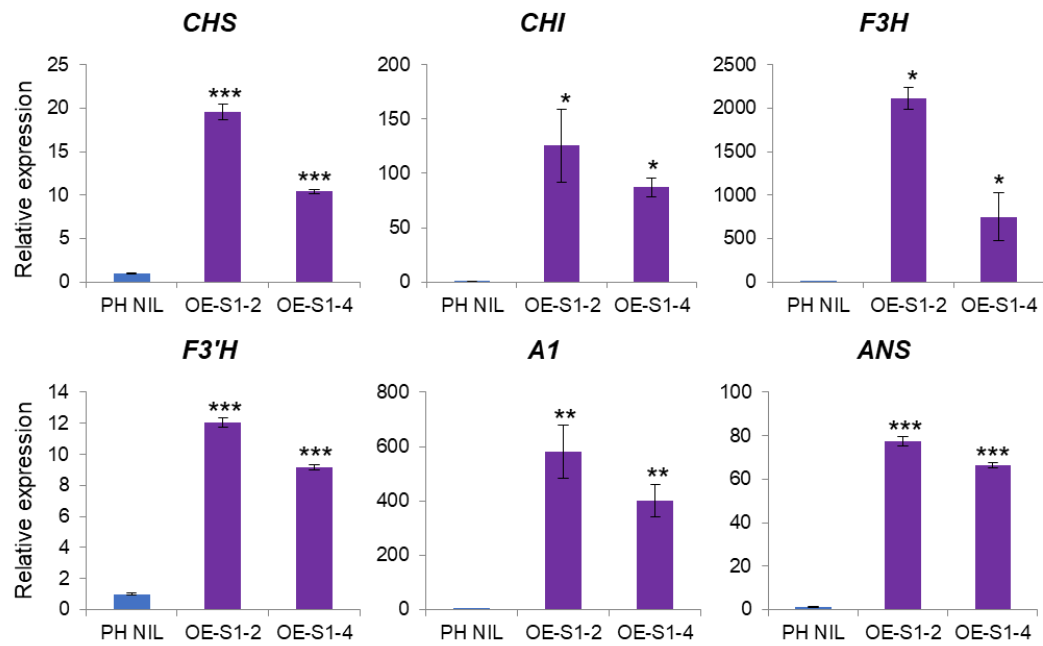


Figure S3. Expression of biosynthesis genes in *S1* overexpressed transgenic lines (OE-S1-2 and OE-S1-4). Data represent means \pm s.e.m (n=3 biological replicates). The asterisks indicate statistical significance by two-tailed Student's *t*-tests (**P*<0.05, ***P*<0.01, ****P*<0.001).

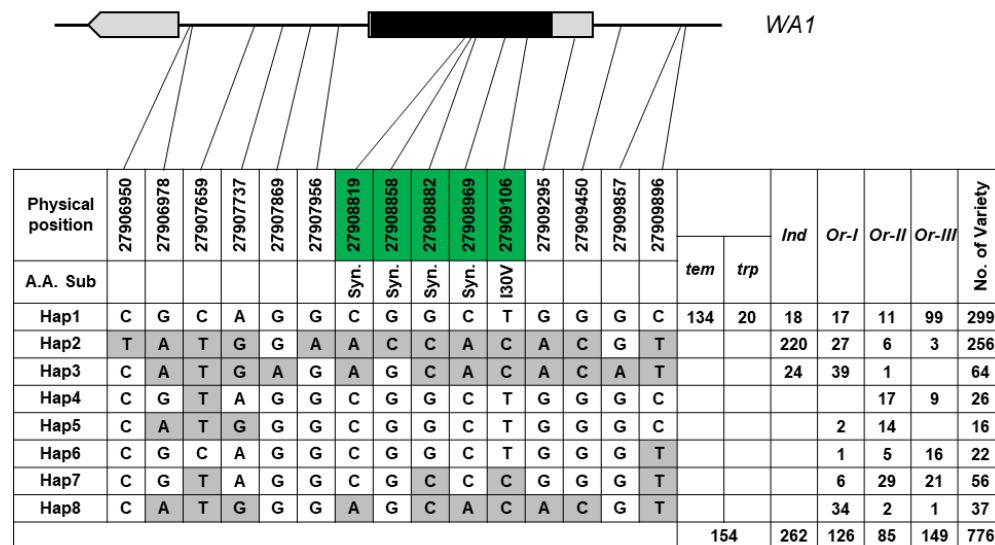


Figure S4. Haplotype of *WA1*. Syn., synonymous mutation.

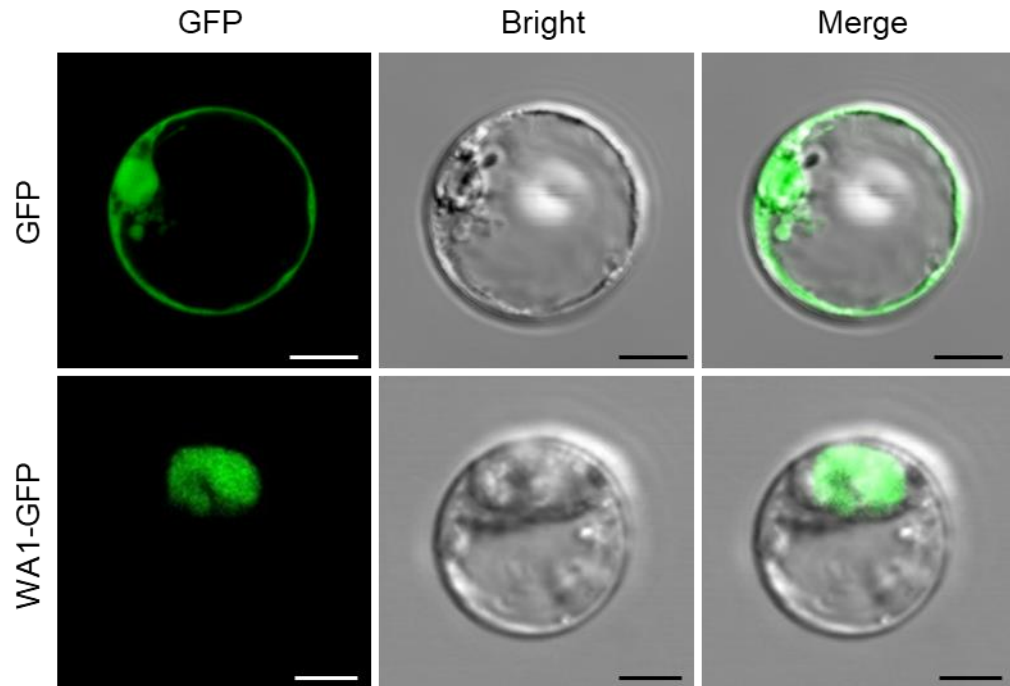


Figure S5. Sub-cellular localization of WA1 in rice protoplast. Bar=5 μ m.

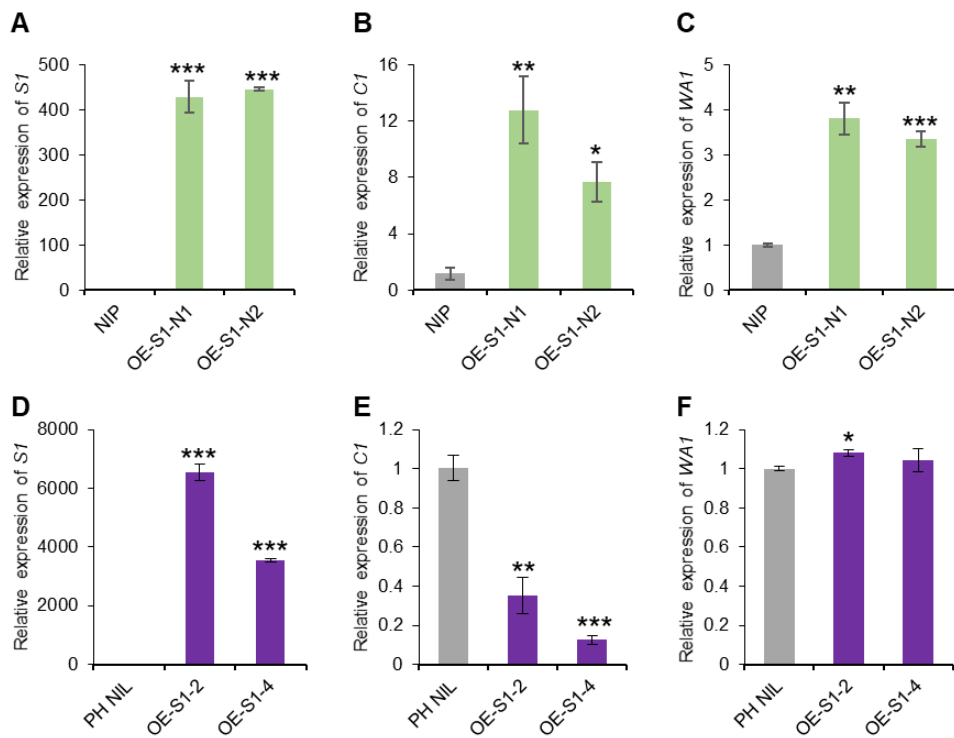


Figure S6. Expression of *S1*, *C1* and *WAI* in *S1* overexpressed transgenic lines. (A-C) *S1* overexpressed in Nipponbare. (D-F) *S1* overexpressed in PH NIL. Data represent means \pm s.e.m (n=3 biological replicates). The asterisks indicate statistical significance by two-tailed Student's *t*-tests (* P <0.05, ** P <0.01, *** P <0.001).

Promoters	C1 binding motif	S1 binding motif (CANNTG)
<i>proCHS</i> (Os11g0530600)	CCAACC(-171)	CACGTG(-262;-300)
<i>proCHI</i> (Os03g0819600)	CCAACC(-948)	CACTTG(-900)
<i>proF3H</i> (Os04g0662600)	CCTACC(-339)	CAGGTG(-692)
<i>proF3'H</i> (Os10g0320100)	CCTACC(-126)	CAGGTG(-228)
<i>proA1</i> (Os01g0633500)	CCTACC(-470,-2017)	CACGTG(-2031) /CAGGTG(-484)
<i>proANS</i> (Os01g0372500)	CCTACC(-568)	CACGTG(-212)

Figure S7. Predicted binding sites of C1 and S1 in the promoter of structural genes.