

Fig. S1 (a) Phenotypic distribution for SCC. (b) Correlation analysis between SOC and SCC trait.

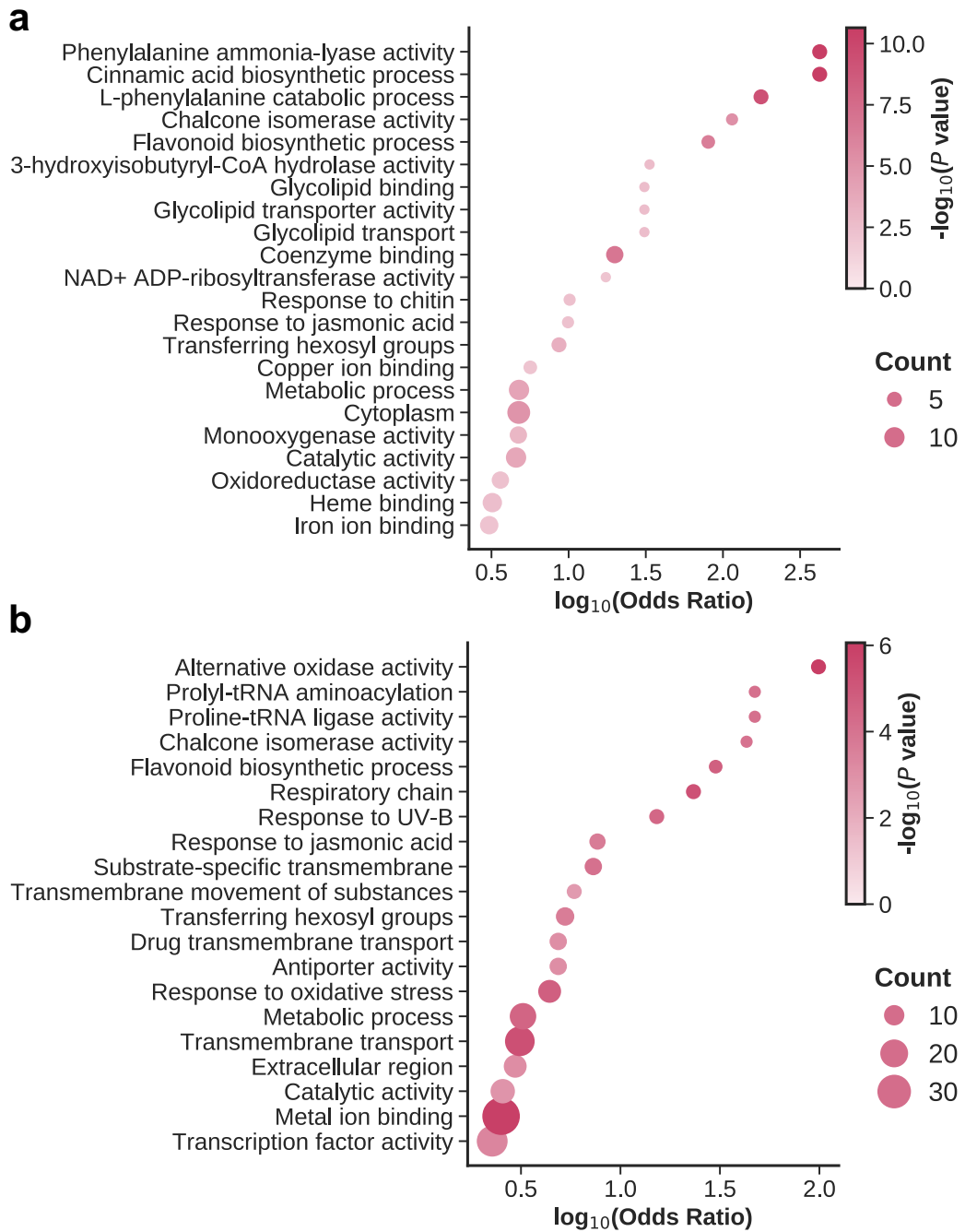


Fig. S2 (a) GO enrichment of TWAS significant genes for SCC at 20DAF. (b) GO enrichment of TWAS significant genes for SCC at 40DAF.

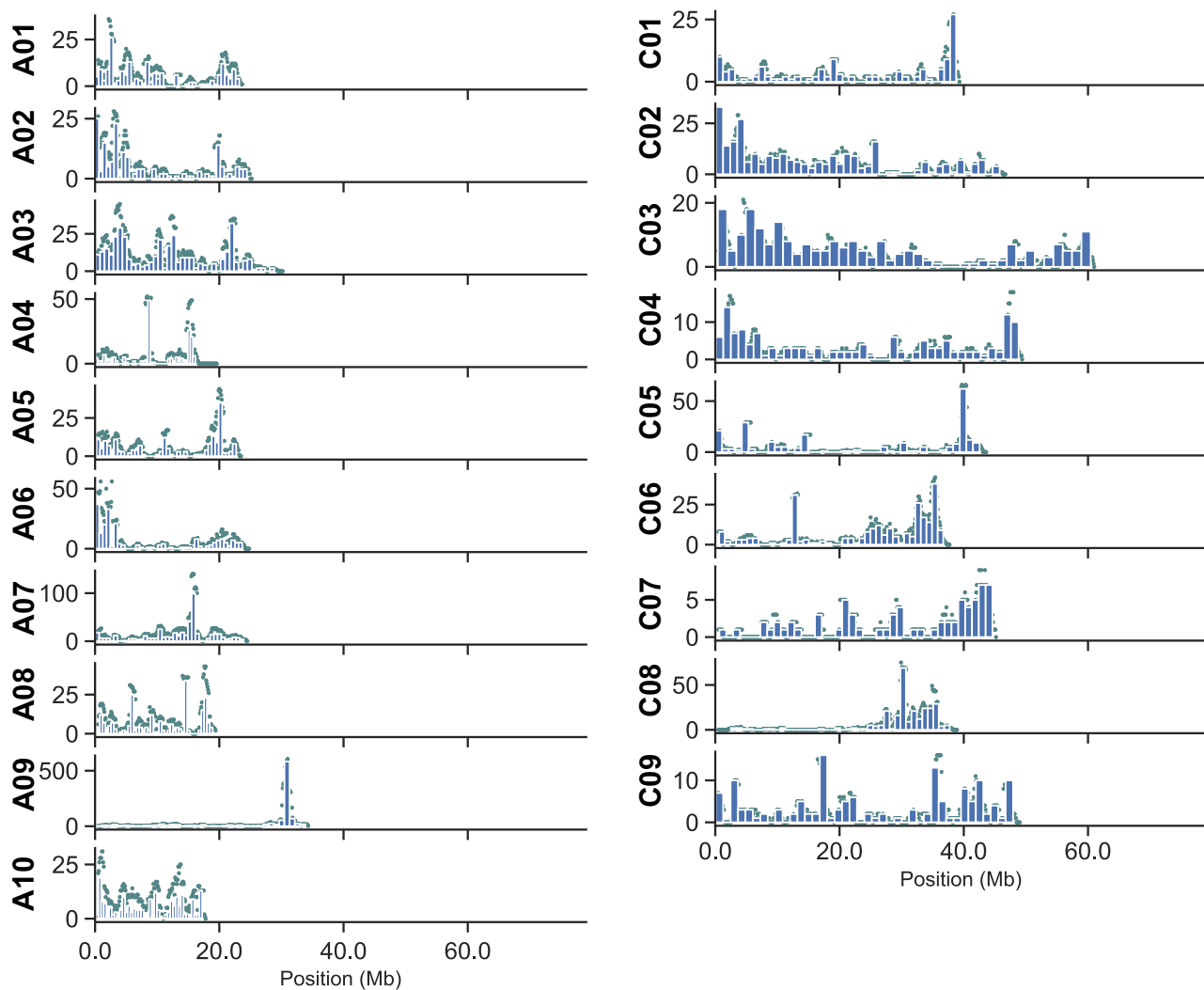


Fig. S3 The density plot and histogram of eQTL location for TWAS-SOC significant genes at 40 DAF.

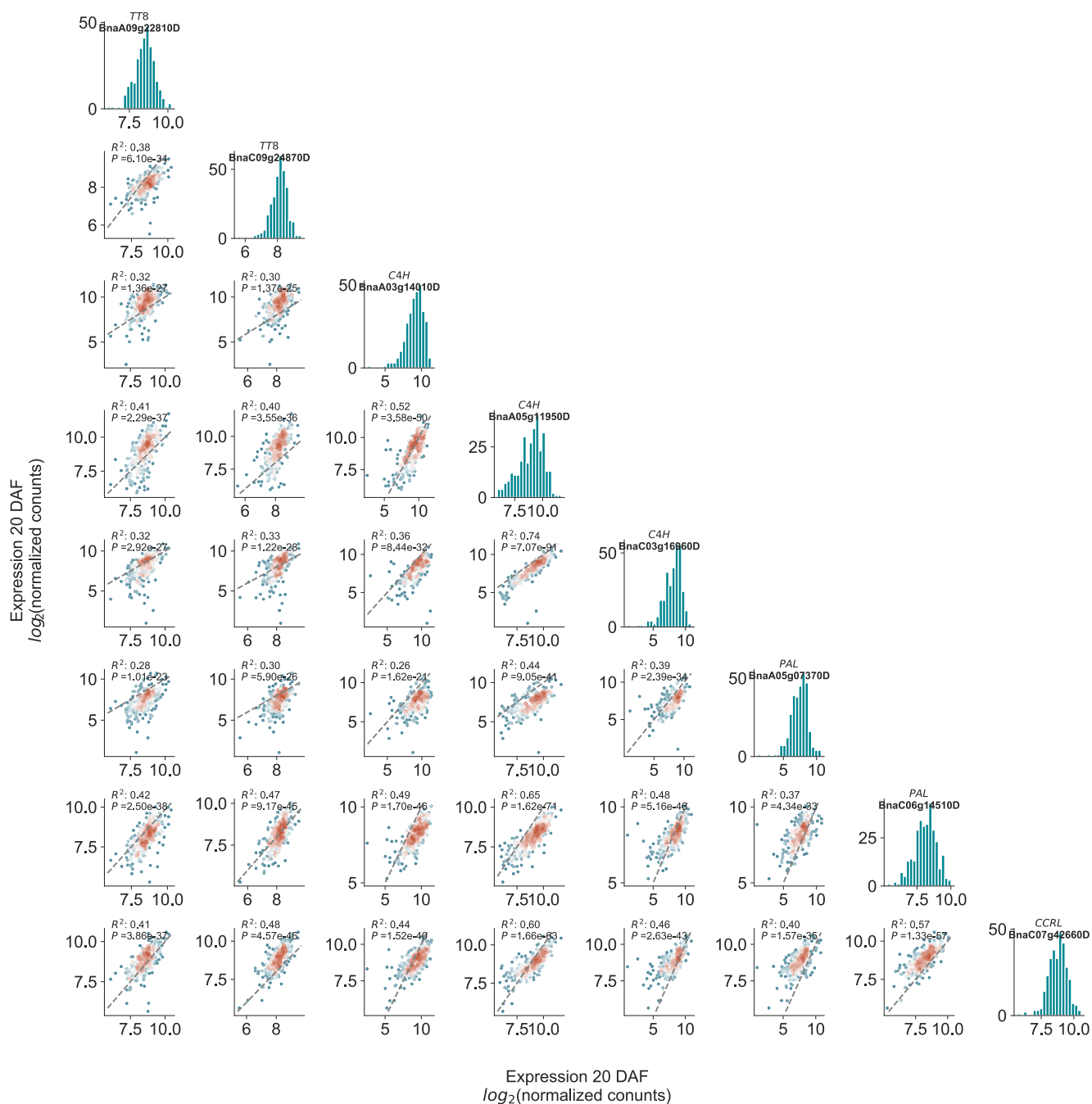


Fig. S4 Histogram of gene expression distribution and correlation coefficient between *BnaTT8s* and the expression of *PAL*, *C4H* and *CCRL* in 257 accessions at 20 DAF. R^2 is the square of Pearson correlation coefficient and the P -value is used for testing non-correlation.

Bna.A9-sgRNA1

L14: ATGGACATGATGAATCTAA-TGGAGGAAGGCGGA (WT)
L17: ATGGACATGATGAATCTAA-TGGAGGAAGGCGGA (WT)
L21: ATGGACATGATGAATCTAA-TGGAGGAAGGCGGA (WT)
L18: ATGGACATGATGAATCTAAATGGAGGAAGGCGGA (insertion)
L24: ATGGACATGATGAATCTAA---AGGAAGG-GGA (deletion)
L30: ATGGACATGATGAATCTAA--G-AGGAAGGCGGA (deletion)
Ref: ATGGACATGATGAATCTAA-TGGAGGAAGGCGGA

Bna.A9-sgRNA2

L14: TTGGTTCCATTTGTGA-----GATGGATAAAGTC (deletion)
L17: TTGGTTCCATTTGTGA-----GATGGATAAAGTC (deletion)
L21: TTGGTTCCATTTGTGA-----GATGGATAAAGTC (deletion)
L18: TTGGTTCCATTTG-----ATGGATAAAGTC (deletion)
L24: TTGGTTCCATTTGTGACC--GATGGATAAAGTC (deletion)
L30: TTGGTTCCATTTGTGAC-AAAG--GATAAAGTC (deletion and insertion)
Ref: TTGGTTCCATTTGTGACCAA-GATGGATAAAGTC

Bna.C9-sgRNA1

L14: ATGGACATGATGAATCTAAATGGAGGATAGCTAGCTA (insertion)
L17: ATGGACATGATGAATCTAA--GGAGGATAGCTAGCTA (deletion)
L21: ATGGACATGATGAATCTA-----GGTAGCTAGCTA (deletion)
L18: ATGGACATGATGAATCTAAATGGAGGATAGCTAGCTA (insertion)
L24: ATGGACATGATGAATCTAAATGGAGGATAGCTAGCTA (insertion)
L30: ATGGACATGATGAATCTAATGGAGGATAGCTAGCTA (insertion)
Ref: ATGGACATGATGAATCTAA-TGGAGGATAGCTAGCTA

Bna.C9-sgRNA2

L14: TTGGTTCCATTTGTGA---AGATGGATAAAGTCTCGA (deletion and insertion)
L17: TTGGTTCCATTTGTGA-----GATGGATAAAGTCTCGA (deletion)
L21: TTGGTTCCATTTGTGACCAAAGATGGATAAAGTCTCGA (insertion)
L18: TTGGTTCCATTTGTGACCAA-GATGGATAAAGTCTCGA (WT)
L24: TTGGTACATGTAGAGAGC-----CTCGA (deletion and insertion)
L30: TTGGTAGATGGAGAG-----A (deletion and insertion)
Ref: TTCAGTGCACGTGTGACCAA-GATGGGCATACGCTCGA

Fig. S6 Genotype of *BnaTT8-sgRNA* mutant lines in the T₀ generation. Nucleotides are shown with sgRNA target (red), PAM sequence (green) and mutation sites (blue) indicated.

BnaA09.TT8

L14:	FLHDNTKNKRLPREELNHVVAERRRREKLNERFITLRSLVPFV RWIKSRS	400
L17:	FLHDNTKNKRLPREELNHVVAERRRREKLNERFITLRSLVPFV RWIKSRS	400
L21:	FLHDNTKNKRLPREELNHVVAERRRREKLNERFITLRSLVPFV RWIKSRS	400
Ref:	FLHDNTKNKRLPREE LNHVVAERRRREKLNERFITLRSLVPFVTKMDKVS	400
<hr/>		
L14:	LETPLNT * 407	
L17:	LETPLNT * 407	
L21:	LETPLNT * 407	
Ref:	ILGDTIEY VNHLISKRIHELESTHHEPNQKRM RIGKGR TWEEVEVSIIESD	450
<hr/>		
L18:	SNQNLLSDFHIEATNSLDTHM DMMNL NGGRRKLFSDSINTSHVTTHKSSF	300
L24:	SNQNLLSDFHIEATNSLDTHM DMMNL KEGEIILRQYQHFSCHNPQVFFQI	300
L30:	SNQNLLSDFHIEATNSLDTHM DMMNL RGRKLFSDSINTSHVTTHKSSFR	300
Ref:	SNQNLLSDFHIEATNSLDTHM DMMNLMEEGGNYSQTVSTLLMSQPTSLLS	300
<hr/>		
L18:	RFSFHIFLRSIIVCLVES * 318	
L24:	QFPHLLTFNHRLSRGELRMSKSI SNISEWRKRRGHRRNGCSNT * 343	
L30:	FSFHIFLRSIIVCLVES * 317	
Ref:	DSVSTSSYVQSSFVSWRVENVKEHQYQ RVEKAAWSSSQWMLKHIILKVP	350
Ref:	FLHDNTKNKRLPREE LNHVVAERRRREKLNERFITLRSLVPFVTKMDKVS	400
Ref:	ILGDTIEY VNHLISKRIHELESTHHEPNQKRM RIGKGR TWEEVEVSIIESD	450

BnaC09.TT8

L14:	SNQNLLSDFHIEATNSLDTHM DMMNL IGGRRKLFSDSINTSHVTTHQSSF	300
L17:	SNQNLLSDFHIEATNSLDTHM DMMNL RRKAEIILRQYQHFSCHNPPVFFQ	300
L21:	SNQNLLSDFHIEATNSLDTHM DMMNL GRRKLFSDSINTSHVTTHQSSFRF	300
L18:	SNQNLLSDFHIEATNSLDTHM DMMNL IGGRRKLFSDSINTSHVTTHQSSF	300
L24:	SNQNLLSDFHIEATNSLDTHM DMMNL IGGRRKLFSDSINTSHVTTHQSSF	300
L30:	SNQNLLSDFHIEATNSLDTHM DMMNL SNGGRRKLFSDSINTSHVTTHQSSF	300
Ref:	SNQNLLSDFHIEATNSLDTHM DMMNLMEEGGNYSQTVSTLLMSQPTSLLS	300
<hr/>		
L14:	RFSFHIFLRSIIVYIVES * 318	
L17:	IQFPHLLTFNHRLYRGELRMSKSI SNISEWKKRRLRRRNGCSNT * 344	
L21:	SFHIFLRSIIVYIVES * 316	
L18:	RFSFHIFLRSIIVYIVES * 318	
L24:	RFSFHIFLRSIIVYIVES * 318	
L30:	RFSFHIFLRSIIVYIVES * 318	
Ref:	DSVSTSSYVQSSFISWRVENVKEHQYQ RVEKAASSSQWMLKHIILKVP	350
Ref:	FLHDNTKNKRLPREE LNHVVAERRRREKLNERFITLRSLVPFVTKMDKVS	400
Ref:	ILGDTIEY VNHLISKRIHELESTHHEPNQKRM RIGKGR TWEEVEVSIIESD	450

Fig. S7 Amino acid sequence alignment of the target sites derived from WT and *BnaTT8*-sgRNA lines.

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BnaA07g20090D_CCR2 .....
BnaC06g19540D_CCR2 .....
BnaA02g36250D_CCR2 .....MPADGKLLVCVVTGAGGYIASWIVKLLLLERGYTVRGTVR.NPADDPKNNHLRELQGAK
BnaC02g46610D_CCR2 .....MPADGKLLVCVVTGAGGYIASWIVKLLLLERGYTVRGTVR.NPADDPKNNHLRELQGAK
BnaA07g35280D_CCR2 .....MPADGKLLVCVVTGAGGYIASWIVKLLLLERGYTVRGTVR.NPADDPKNNHLRELQGAK
BnaC06g40190D_CCR2 .....MPADGKLLVCVVTGAGGYIASWIVKLLLLERGYTVRGTVR.NPADDPKNNHLRELQGAK
BnaA09g56490D_CCR1 MPVDESTAVGKTVCVVTGAGGYIASWIVKLLLLERGYTVKGTVR.NPDDPKNTHLRELLEGAK
BnaC08g38580D_CCR1 MPVDESTAVGKTVCVVTGAGGYIASWIVKLLLLERGYTVKGTVR.NPDDPKNTHLRELLEGAK
BnaA05g12180D_CCR1 MPVDESSPAGKTVCVVTGAGGYIASWIVKLLLLERGYTVKGTVR.NPDDPKNTHLRELLEGAK
BnaA06g10620D_CCR1 MPLAESSPAGKTVCVVTGAGGYIASWIVKLLLLERGYTVKGTVR.NPDDPKNTHLRELLEGAK
BnaC07g42660D_CCRL ..MDQEKSHSCCCVLDASTYVGFWILKLLSRGYSVHAAIRKNGDSEIEETIREMATE

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BnaA07g20090D_CCR2 .....
BnaC06g19540D_CCR2 .....
BnaA02g36250D_CCR2 ERLTLHSADLLDYEALCATIDGCDGVFHTASPMTDDPETMLEPAVNGAKFVIDAAAKAK..
BnaC02g46610D_CCR2 ERLTLHSADLLDYEALSATIDGCDGVFHTASPMTDDPETMLEPAVNGAKFVIDAAAKAK..
BnaA07g35280D_CCR2 ERLTLHSADLLDYEALCAIIDGCDGVFHTASPMTDDPETMLEPAVNGAKFVIDAAAKAK..
BnaC06g40190D_CCR2 ERLTLHSADLLDYEALCAIIDGCDGVFHTASPMTDDPETMLEPAVNGAKFVIDAAAKAE..
BnaA09g56490D_CCR1 ERLILCKADLDYDALKAAIDGCDGVFHTASPVTDDPEQMVPEAVNGAKFVINAAAEAK..
BnaC08g38580D_CCR1 ERLILCKADLDYDALKSAIDGCDGVFHTASPVTDDPEQMVPEAVNGAKFVINAAAEAK..
BnaA05g12180D_CCR1 ERLILCKADLDYDALKAAIDGCDGVFHTASPVTDDPEQMVPEAVNGAKFVINAAAEAK..
BnaA06g10620D_CCR1 ERLILCKADLDYDALKTAIDGCDGVFHTASPVTDDPEQMVPEAVNGAKFVINAAAEAK..
BnaC07g42660D_CCRL ERLIVYDQVLDYQSLVLSLKTCAVFCCLDSPEGYDEKEVDLEVRGAINVVEACGRTEES

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BnaA07g20090D_CCR2 .....110203040.....TQVKVGV
BnaC06g19540D_CCR2 .....MIGVGS
BnaA02g36250D_CCR2 VKRIVFTSSIGAVYMPNRDHQTIVDENCWSDLDFCKNTKNWYCYGKMVAEQSAWETAKV
BnaC02g46610D_CCR2 VKRIVFTSSIGAVYMPNRDPQTIVDES CWSDLDFCKNTKNWYCYGKMVAEQSAWETAKA
BnaA07g35280D_CCR2 VKRIVFTSSIGAVYMPNRDPQTIVNEDCWSDLDFCKNTKNWYCYGKMVAEQSAWETAKA
BnaC06g40190D_CCR2 VKRIVFTSSIGAVYMPNRHPQTIVNEDCWSDLDFCKNTKNWYCYGKMVAEQSAWETAKA
BnaA09g56490D_CCR1 VKRIVFTSSIGAVYMPNRDPEAVVDES CWSDLDFCKNTKNWYCYGKMVAEQSAWETAEE
BnaC08g38580D_CCR1 VKRIVFTSSIGAVYMPNRDPEAVVDES CWSDLDFCKNTKNWYCYGKMVAEQSAWETAEE
BnaA05g12180D_CCR1 VKRIVFTSSIGAVYMPNRDPEAVVDES CWSDLDFCKNTKNWYCYGKMVAEQSAWETAKE
BnaA06g10620D_CCR1 VKRIVFTSSIGAVYMPNRDPEAVVDES CWSDLDFCKNTKNWYCYGKMVAEQSAWETAKE
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BnaA07g20090D_CCR2 .....5060708090100.....GHV
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BnaA02g36250D_CCR2 KGVLDLVVLPN.VLVLGPPLOSAVNASLVHILKYLTSAGAKTYANLTQVYVVRDVAAGHV
BnaC02g46610D_CCR2 KGVLDLVVLPN.VLVLGPPLOSAVNASLVHILKYLTSAGAKTYANLTQVYVVRDVAAGHV
BnaA07g35280D_CCR2 KGVLDLVVLPN.VLVLGPPLOSAVNASLVHILKYLTSAGAKTYANLTQVYVVRDVAAGHV
BnaC06g40190D_CCR2 KGVLDLVVLPN.VLVLGPPLOSAVNASLVHILKYLTSAGAKTYANLTQVYVVRDVAAGHV
BnaA09g56490D_CCR1 KGVLDLVVLPN.VLVLGPPLOPTINASLFHVLKYLTSAGAKTYANLTQAYVVRDVAAGHV
BnaC08g38580D_CCR1 KGVLDLVVLPN.VLVLGPPLOPTINASLFHVLKYLTSAGAKTYANLTQAYVVRDVAAGHV
BnaA05g12180D_CCR1 KGVLDLVVLPN.VLVLGPPLOPTINASLFHVLKYLTSAGAKTYANLTQAYVVRDVAAGHV
BnaA06g10620D_CCR1 KGVLDLVVLPN.VLVLGPPLOPTINASLFHVLKYLTSAGAKTYANLTQAYVVRDVAAGHV
BnaC07g42660D_CCRL RRLNVMVSNP..GLIVGP...SVAQYNRPRTMSYLGAAQMYENGLVAYVDVKKFLADVHI

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BnaA07g20090D_CCR2 .....110.....
BnaC06g19540D_CCR2 MVEYDQRLRP LHLFQK.....
BnaA02g36250D_CCR2 MVEYDQRLRP LHLFQK.....
BnaC02g46610D_CCR2 MVEYDQRLRP LHLFQK.....
BnaA07g35280D_CCR2 MVEYDQRLRP LHLFQK.....
BnaC06g40190D_CCR2 MVEYDQRLRP LHLFQK.....
BnaA09g56490D_CCR1 MVEYDQRLRP LHLFQK.....
BnaC08g38580D_CCR1 MVEYDQRLRP LHLFQK.....
BnaA05g12180D_CCR1 MVEYDQRLRP LHLFQK.....
BnaA06g10620D_CCR1 MVEYDQRLRP LHLFQK.....
BnaC07g42660D_CCRL MVEYDQRLRP LHLFQK.....

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BnaA07g20090D_CCR2 .....
BnaC06g19540D_CCR2 .....
BnaA02g36250D_CCR2 DLGLL EFKPIKQSLYESVKS LQEKGHLP LPPQDSNQNVIIES.....
BnaC02g46610D_CCR2 DLGLL EFKPIKQSLYESVKS LQEKGHLP LPPQDSNQNVIIES.....
BnaA07g35280D_CCR2 DLGLL EFTPIKQSLYDSVKS LQEKGHLP LPPQDSNQNVIIES.....
BnaC06g40190D_CCR2 DLGLL EFTPIKQSLYDSVKS LQEKGHLP LPPQDSNQNVIIES.....
BnaA09g56490D_CCR1 DLGLL EFTSTKQSLYDTVKSLQEKGHLP LPPPPPPSTSEGSSONGIKIES
BnaC08g38580D_CCR1 DLGLL EFTSTKQSLYDTVKSLQEKGHLP LPPPPPPSTSEGSSONGIKIES
BnaA05g12180D_CCR1 DLGLL EFTSTKQSLYDTVKSLQEKGHLP LPPPPPPSTSEGSSONGIKIES
BnaA06g10620D_CCR1 DLGLL EFTSTKQSLYDTVKSLQEKGHLP LPPPPPPSTSEGSSONGIKIES
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Domain

Fig. S8. Protein sequence alignment analysis between CCRL and CCR in *B. napus*.

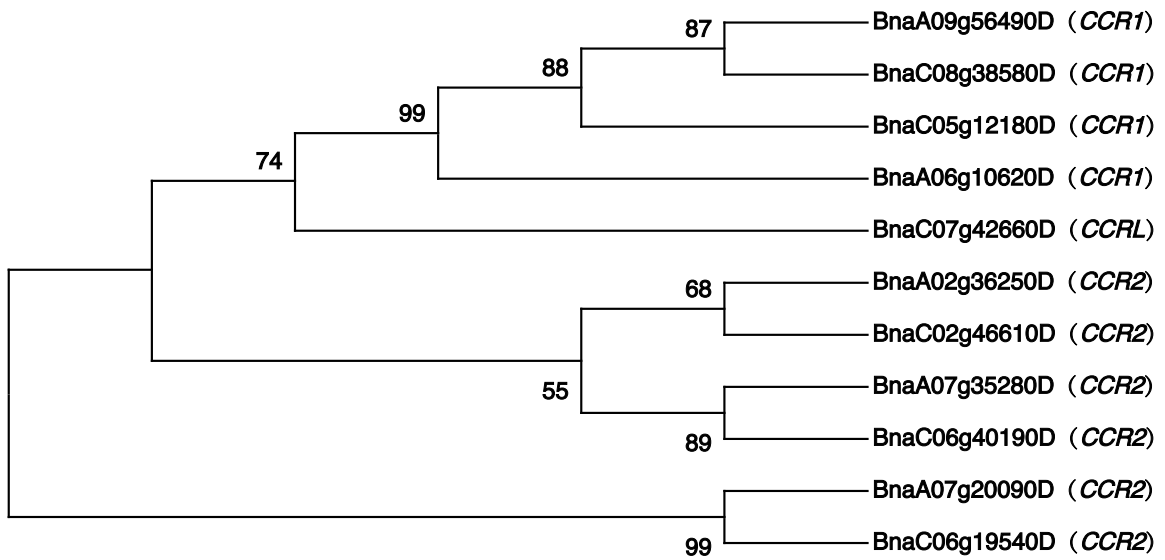


Fig. S9. Phylogenetic tree analysis of *CCRL* and *CCR* genes in *B. napus*.

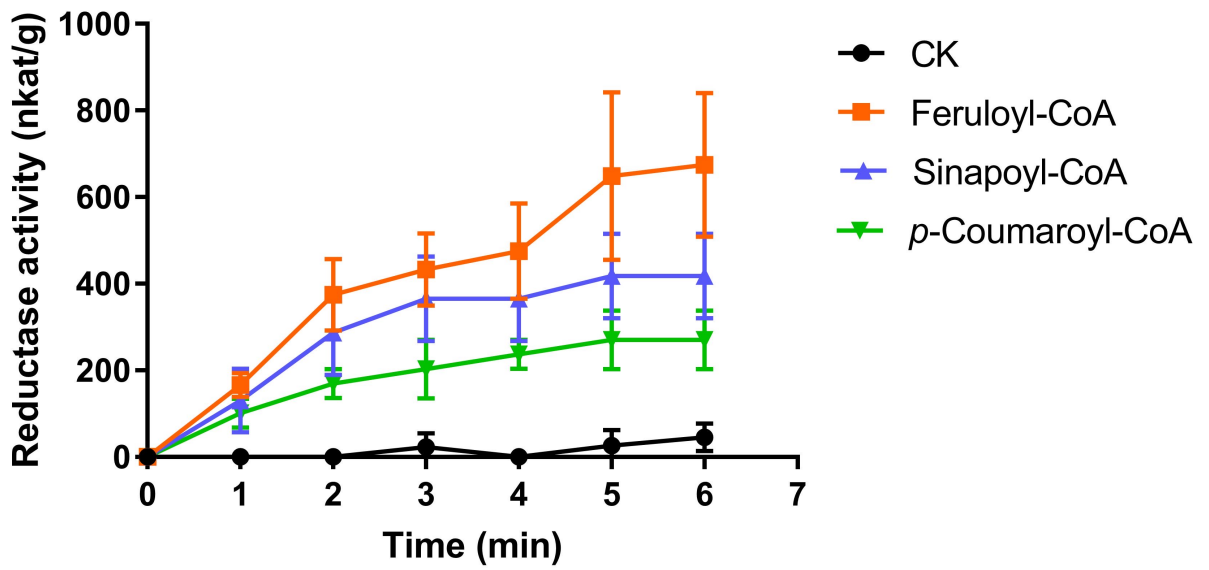


Fig. S10 The reductase activity of recombinant BnaCCRL.

BnaC07.CCRL-sgRNA1

L21:GGT**GAGAGGAGCTATCAATG**--**GTGGAAGCATG** (deletion)
L35:GGT**GAGAGGAGCTATCAATG****TGGTGG**AAGCATG (WT)
L43:GGT**GAGAGGAGCTATCAATG****TGGTGG**AAGCATG (insertion)
L48:GGT**GAGAGGAGCTATCAATG****TGGTGG**AAGCATG (insertion)
Ref:GGT**GAGAGGAGCTATCAATG****TGGTGG**AAGCATG

BnaC07.CCRL-sgRNA2

L21:GTCTC**CTTTGATACCTATGCCAACCGAGG**TACATT (insertion)
L35:GTCTC**CTTTGATACCTATGCCAACCGAGG**TACATT (insertion)
L43:GTCTC**CTTTGATACCTATGCCAACCGAGG**TACATT (insertion)
L48:GTCTC**CTTTGATACCTATGCCAACCGAGG**TACATT (insertion)
Ref:GTCTC**CTTTGATACCTATGCCAACCGAGG**TACATT

BnaA03.CCRL-sgRNA1

L21:GGT**GAGAGGAGCTATCAATGT****TGGTGG**AAGCATG (insertion)
L35:GGT**GAGAGGAGCTATCAATGT****TGGTGG**AAGCATG (insertion)
L43:GGT**GAGAGGAGCTATCAATGT****TGGTGG**AAGCATG (insertion)
L48:GGT**GAGAGGAGCTATCAATGT****TGGTGG**AAGCATG (insertion)
Ref:GGT**GAGAGGAGCTATCAATGT****TGGTGG**AAGCATG

BnaA03.CCRL-sgRNA2

L21:GTCTC**CTTTGATACCTATGCCAACCGAGG**TACATT (insertion)
L35:GTCTC**CTTTGATACCTATGCCAACCGAGG**TACATT (insertion)
L43:GTCTC**CTTTGATACCTATGCCAACCGAGG**TACATT (insertion)
L48:GTCTC**CTTTGATACCTATGTCCAACCGAGG**TACATT (insertion)
Ref:GTCTC**CTTTGATACCTATGCCAACCGAGG**TACATT

BnaC05.CCRL-sgRNA1

L21:GGT**GAGAGGAGCTATCAATGT****TGGTGG**AAGCATG (insertion)
L35:GGT**GAGAGGAGCTATCAATGT****TGGTGG**AAGCATG (WT)
L43:GGT**GAGAGGAGCTATCAATGT****TGGTGG**AAGCATG (insertion)
L48:GGT**GAGAGGAGCTATCAATGT****TGGTGG**AAGCATG (WT)
Ref:GGT**GAGAGGAGCTATCAATGT****TGGTGG**AAGCATG

Fig. S11 Genotype of *BnaCCRL-sgRNA* mutant lines in the T₀ generation. Nucleotides are shown with sgRNA target (red), PAM sequence (green) and mutation sites (blue) indicated.

BnaC07.CCRL

L21: LEVRGAINGGSMWKNREHREDCILFFFNSFNLERQHWHSEGEVLESRLLS 150
L35: LEVRGAINVVEACGRTESIEKIVFSSSLTASIWRDNIGTQKDVDEKCWSDQ 150
L43: LEVRGAINVVEACGRTESIEKIVFSSSLTASIWRDNIGTQKDVDEKCWSDQ 150
L48: LEVRGAINVVEACGRTESIEKIVFSSSLTASIWRDNIGTQKDVDEKCWSDQ 150
Ref: LEVRGAINVVEACGRTESIEKIVFSSSLTASIWRDNIGTQKDVDEKCWSDQ 150

L21: QQKVVARIGKDVVRESSLGTSHGPAQHGLYQSWSYRWTIGCTIPAHHVLP 200
L35: DFCRNKKLWHALAKMLSEKAAWALAMDRRLNMVSNPGLIVGPSVAQYNP 200
L43: DFCRNKKLWHALAKMLSEKAAWALAMDRRLNMVSNPGLIVGPSVAQYNP 200
L48: DFCRNKKLWHALAKMLSEKAAWALAMDRRLNMVSNPGLIVGPSVAQYNP 200
Ref: DFCRNKKLWHALAKMLSEKAAWALAMDRRLNMVSNPGLIVGPSVAQYNP 200

L21: RSCTNVEWSVGVRRIIFSGCSYSIRGCFSLWSIFLLQPNRHRSSQACR 250
L35: RPTMSYLKGAQMYENGLAYVDVKFLADVHIRAYEDVSACGRYFCFNQI 250
L43: RPTMSYLKGAQMYENGLAYVDVKFLADVHIRAYEDVSACGRYFCFNQI 250
L48: RPTMSYLKGAQMYENGLAYVDVKFLADVHIRAYEDVSACGRYFCFNQI 250
Ref: RPTMSYLKGAQMYENGLAYVDVKFLADVHIRAYEDVSACGRYFCFNQI 250

L21: EFVVSFDTYANRGMRVCKEAKFTKKDGTINASWWKLALLV* 289
L35: VNTEEEALKLVESLSPLIPMPTEVECNARKRSLRRKTEEQIEQAGGSWLC 300
L43: VNTEEEALKLVESLSPLIPMPTEVECNARKRSLRRKTEEQIEQAGGSWLC 300
L48: VNTEEEALKLVESLSPLIPMPTEVECNARKRSLRRKTEEQIEQAGGSWLC 300
Ref: VNTEEEALKLVESLSPLIPMPRYESVMQSEVYEERLRNNKLSKLVEAG 300

L35: LL* 302
L43: LL* 302
L48: LL* 302
Ref: SAC* 303

BnaA03.CCRL

L21: LEVRGAINVGGSMWKNREHREDCILFFFNSFNLERQHWNSEGEVLESRL 150
L35: LEVRGAINVGGSMWKNREHREDCILFFFNSFNLERQHWNSEGEVLESRL 150
L43: LEVRGAINVGGSMWKNREHREDCILFFFNSFNLERQHWNSEGEVLESRL 150
L48: LEVRGAINVGGSMWKNREHREDCILFFFNSFNLERQHWNSEGEVLESRL 150
Ref: LEVRGAINVVEACGRTESIEKIVFSSSLTASIWRDNIGTQKDVDEKCWSDQ 150

L21: SQQKVVARIGKDVVRESSLGTSHGPAQHGLYQSWSYRWTIGCTIPAHHV 200
L35: SQQKVVARIGKDVVRESSLGTSHGPAQHGLYQSWSYRWTIGCTIPAHHV 200
L43: SQQKVVARIGKDVVRESSLGTSHGPAQHGLYQSWSYRWTIGCTIPAHHV 200
L48: SQQKVVARIGKDVVRESSLGTSHGPAQHGLYQSWSYRWTIGCTIPAHHV 200
Ref: DFCRNKKLWHALAKMLSEKAAWALAMDRRLNMVSNPGLIVGPSVAQYNP 200

L21: PQRCTNVEWSVGVRRIIFSGCSYSIRGCFSLWSIFLLQPNRHRSSQA 250
L35: PQRCTNVEWSVGVRRIIFSGCSYSIRGCFSLWSIFLLQPNRHRSSQA 250
L43: PQRCTNVEWSVGVRRIIFSGCSYSIRGCFSLWSIFLLQPNRHRSSQA 250
L48: PQRCTNVEWSVGVRRIIFSGCSYSIRGCFSLWSIFLLQPNRHRSSQA 250
Ref: RPTMSYLKGAQMYENGLAYVDVKFLADVHIRAYEDVSACGRYFCFNQI 250

L21: CREFVSFDTYATEVECNARKRSLRRKTEEQIEQAGGSWLCCL* 292
L35: CREFVSFDTYATEVECNARKRSLRRKTEEQIEQAGGSWLCCL* 292
L43: CREFVSFDTYATEVECNARKRSLRRKTEEQIEQAGGSWLCCL* 292
L48: CREFVSFDTYATEVECNARKRSLRRKTEEQIEQAGGSWLCCL* 292
Ref: VNTEEEALKLVESLSPLIPMPRYESVMQSEVYEERLRNNKLSKLVEAG 300

Ref: SAC* 303

BnaC05.CCRL

L21:RGAINVGGSMKNREHRDCVLEFFFNFNFERQHWNSEGCEVLESRLLSQQ 100
L35:RGAINVVEACERTESIDKIVFSSSSLTASILRDNIGTQKDVDEKCWSDQD 100
L43:RGAINVVEACERTESIDKIVFSSSSLTASILRDNIGTQKDVDEKCWSDQD 100
L48:RGAINVVEACERTESIDKIVFSSSSLTASILRDNIGTQKDVDEKCWSDQD 100
Ref:RGAINVVEACERTESIDKIVFSSSSLTASILRDNIGTQKDVDEKCWSDQD 100

L21:KVCRRNGRVYWIAGGCERYLSYQRHDKCLCCLESREASNYCSTSKNCCE 150
L35:FCRNKKFAEGMVEFIGLLEVAVKKGTNLAIRDMMSDAYVALNLGKQVTI 150
L43:FCRNKKFAEGMVEFIGLLEVAVKKGTNLAIRDMMSDAYVALNLGKQVTI 150
L48:FCRNKKFAEGMVEFIGLLEVAVKKGTNLAIRDMMSDAYVALNLGKQVTI 150
Ref:FCRNKKFAEGMVEFIGLLEVAVKKGTNLAIRDMMSDAYVALNLGKQVTI 150

L21:LFEPGMESRTHAVCSQLWSCKTASVLYILCWHNGRSSTYPASDNICDGWV 200
L35:VHKLQKTVVNCNLNPVWNQELMLSVPDSYGPVKLQVYDYDTFSAGDIMGE 200
L43:VHKLQKTVVNCNLNPVWNQELMLSVPDSYGPVKLQVYDYDTFSAGDIMGE 200
L48:VHKLQKTVVNCNLNPVWNQELMLSVPDSYGPVKLQVYDYDTFSAGDIMGE 200
Ref:VHKLQKTVVNCNLNPVWNQELMLSVPDSYGPVKLQVYDYDTFSAGDIMGE 200

L21:GSRDVWGYADWEMAKVASANRQHHL* 225
L35:AQLDIQPLITSAMVFGDPEMFGDMQIGKWLKLHDNPPIDDSII* 243
L43:AQLDIQPLITSAMVFGDPEMFGDMQIGKWLKLHDNPPIDDSII* 243
L48:AQLDIQPLITSAMVFGDPEMFGDMQIGKWLKLHDNPPIDDSII* 243
Ref:AQLDIQPLITSAMVFGDPEMFGDMQIGKWLKLHDNPPIDDSII* 243

Fig. S12 Amino acid sequence alignment of the target sites derived from WT and *BnaCCRL-sgRNA* lines.

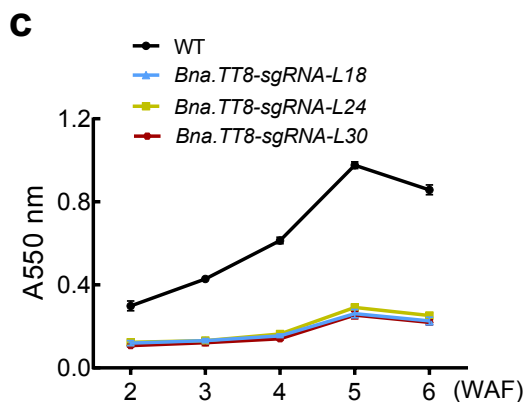
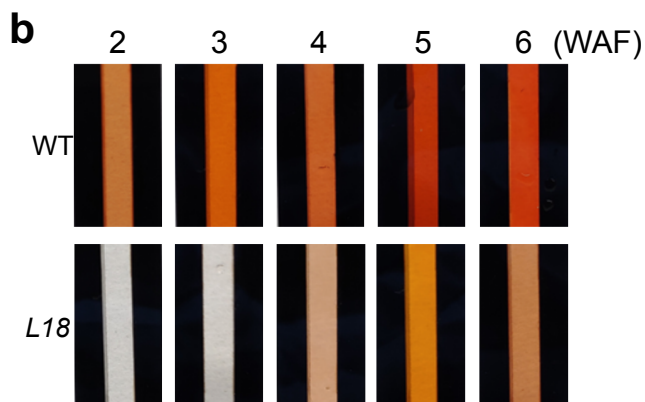
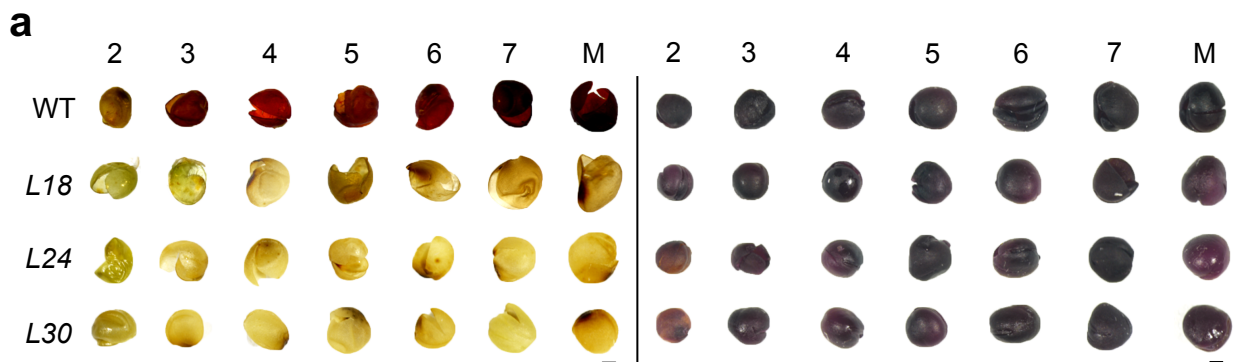


Fig. S13 Chemical staining of procyanidin in seed coats and embryos of the *BnaTT8* mutants (L18, L24 and L30) and the control at 2 weeks after flowering (WAF), 3 WAF, 4 WAF, 5 WAF, 6 WAF, 7 WAF and mature seed and estimation of insoluble procyanidin oligomers (PCs).

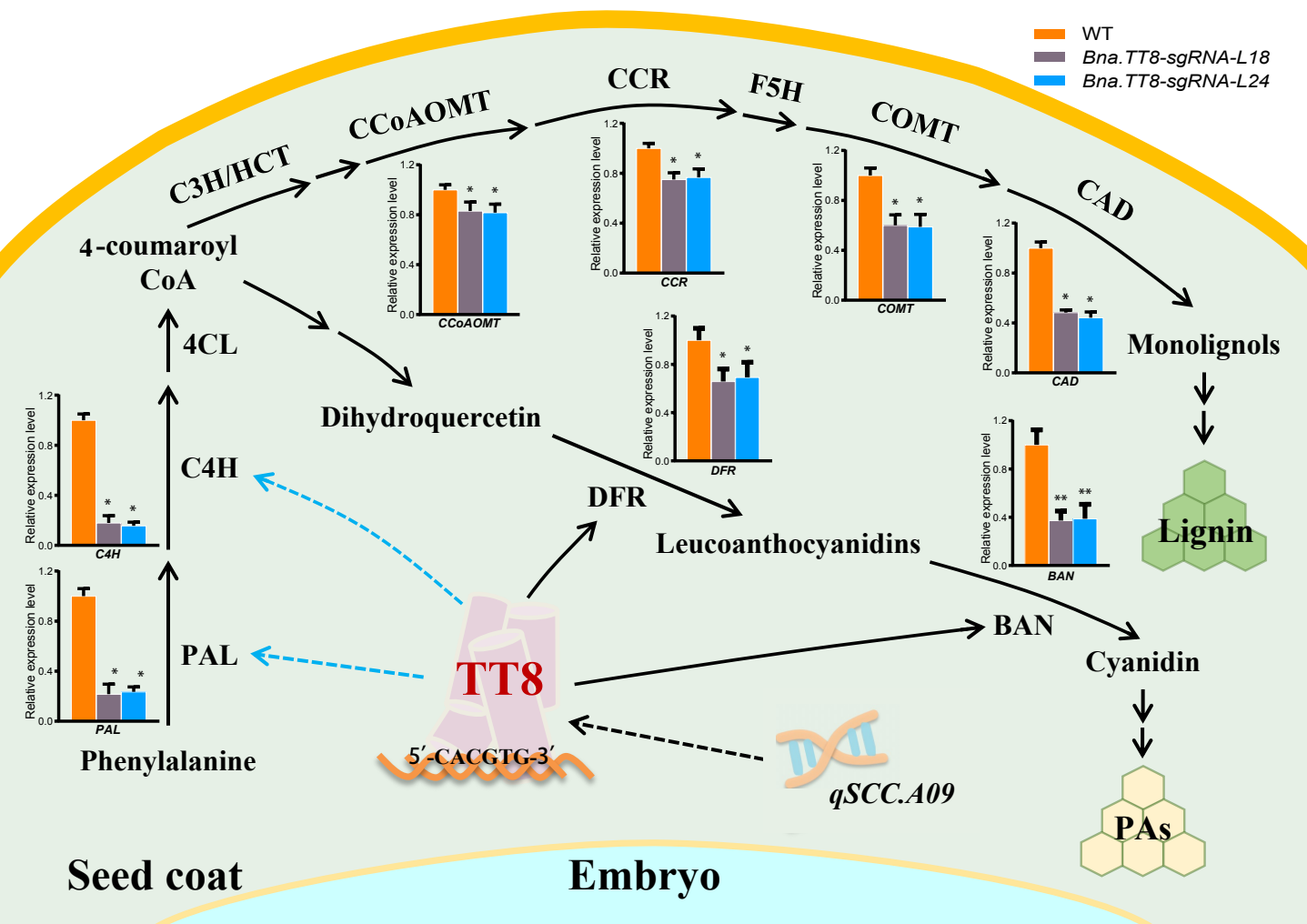


Fig. S14 A proposed working model of *BnaTT8* in the regulation of SCC. Expression levels of procyanidin and lignin biosynthesis genes determined by qRT-PCR in the phenylpropanoid pathway in the *BnaTT8* double knockout mutant seeds. Values are means \pm SE of three biological replicates (n = 3). Student's t-test was used for statistical analysis between the *BnaTT8-sgRNA* lines and WT (*, P < 0.05; **, P < 0.01). Blue dashed lines represent indirect regulation, black line represents direct regulation or known metabolic pathways. Black dashed line represents putative regulation. TT8, Transparent Testa 8; PAL, phenylalanine ammonia-lyase; C4H, cinnamate 4-hydroxylase; 4CL, 4-coumarate-CoA ligase; C3H, coumarate 3-hydroxylase; HCT, hydroxycinnamoyl-CoA shikimate/quinate hydroxycinnamoyl transferase; CCoAOMT, caffeoyl-CoA O-methyltransferase; CCR, cinnamoyl-CoA reductase; F5H, ferulate 5-hydroxylase; COMT, caffeic acid O-methyltransferase; CAD, cinnamyl alcohol dehydrogenase; DFR, dihydroflavonol-4-reductase; BAN, BANYULS.

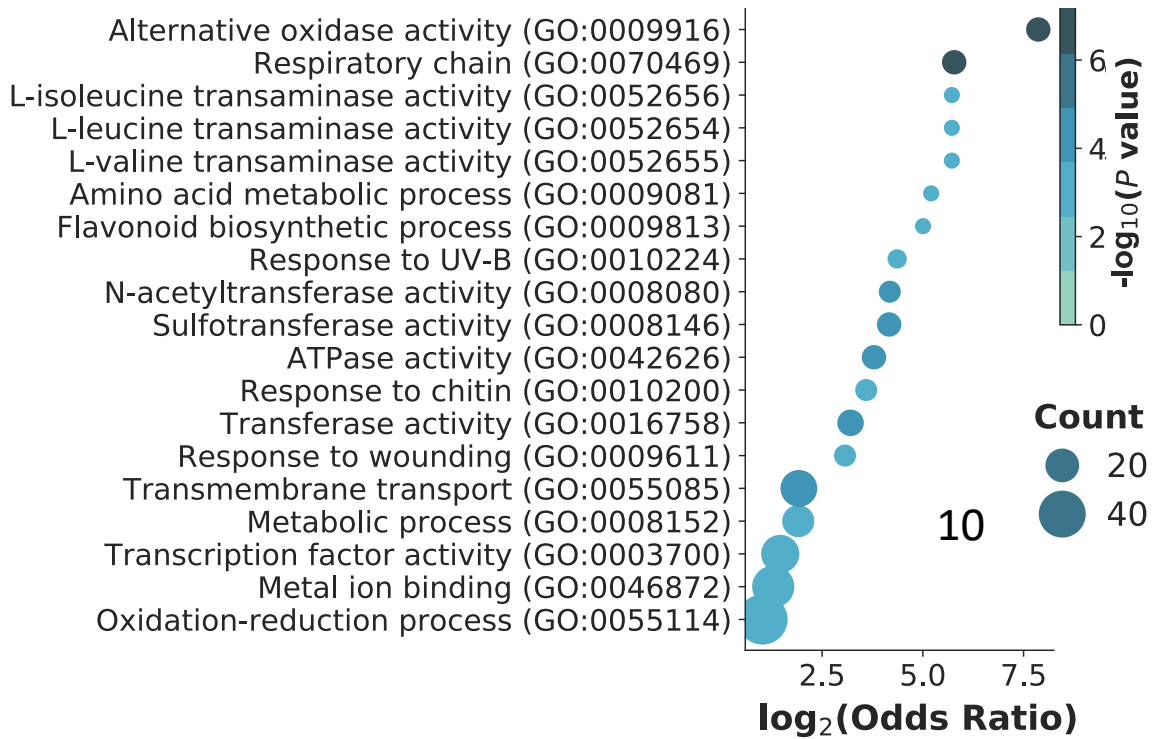


Fig. S15 GO enrichment analysis of overlapped significant genes identified by TWAS for SOC and SCC. The dot size and color indicate the gene number and the range of FDR values, respectively.

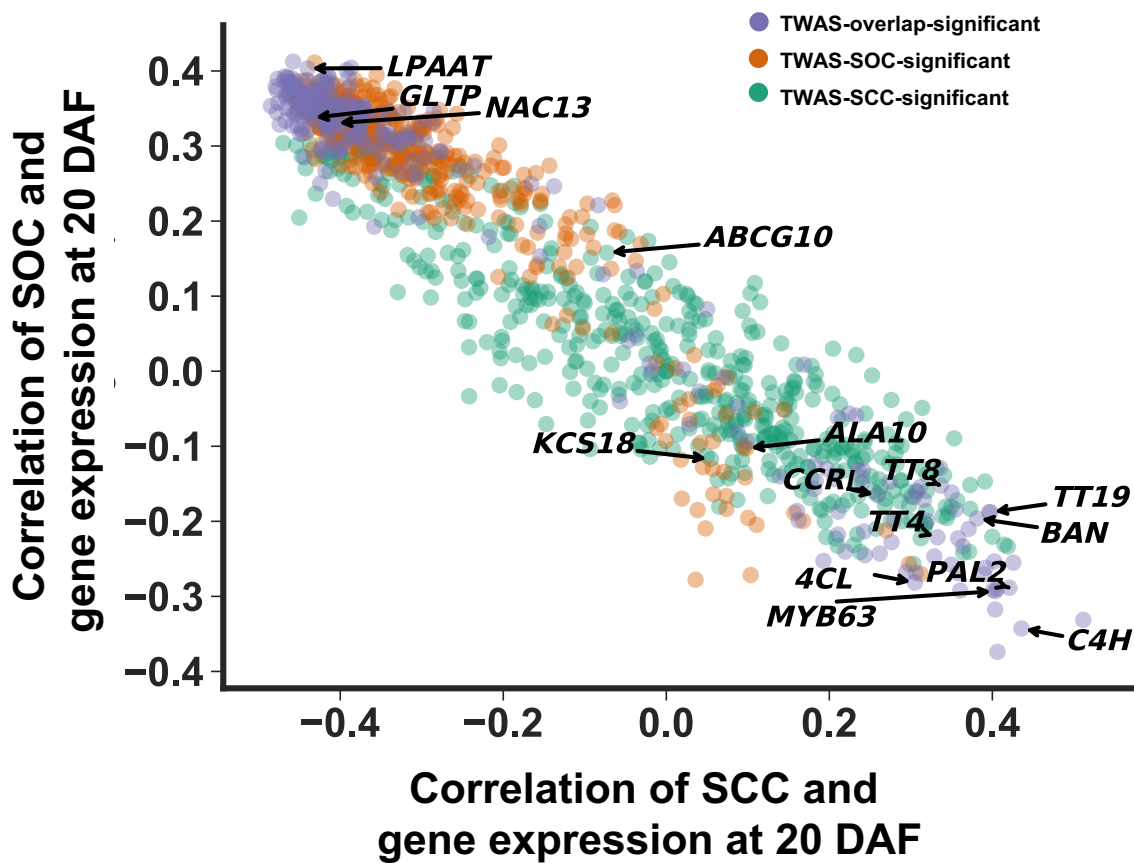


Fig. S16 Correlation analysis between TWAS significant gene expression and SOC trait or SCC trait at 20 DAF. Each dot represents a gene.

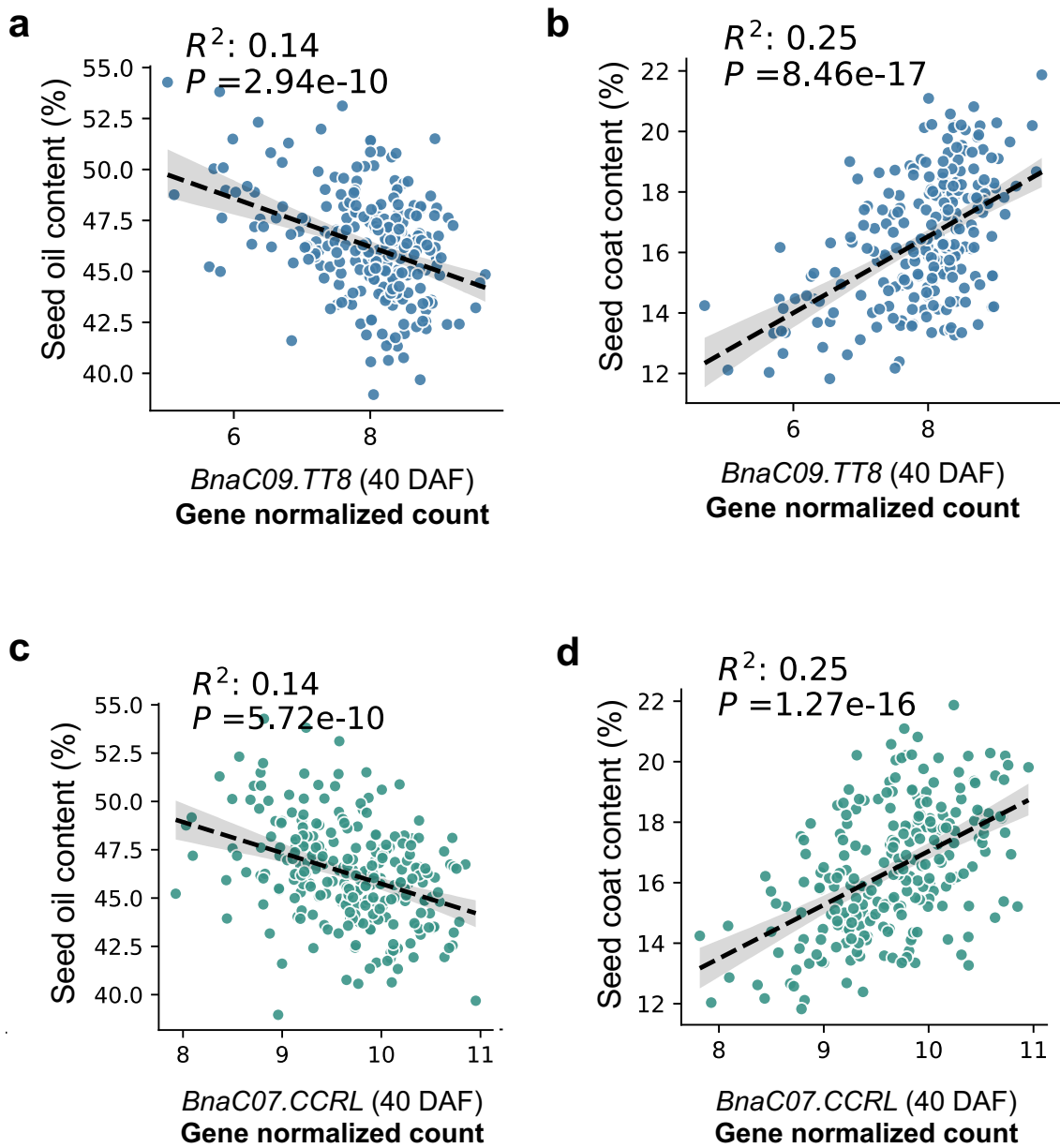


Fig. S17 Correlation between SOC and expression levels of *BnaC09.TT8* at 40 DAF (a), SCC and expression levels of *BnaC09.TT8* at 40 DAF (b), SOC and expression levels of *BnaC07.CCRL* at 40 DAF (c) and SCC and expression levels of *BnaC07.CCRL* at 40 DAF (d). Each point in a-d represents an accession. The normalized gene expression values are plotted on the X-axis and the SOC or SCC corresponding to the accessions is plotted on the Y-axis.

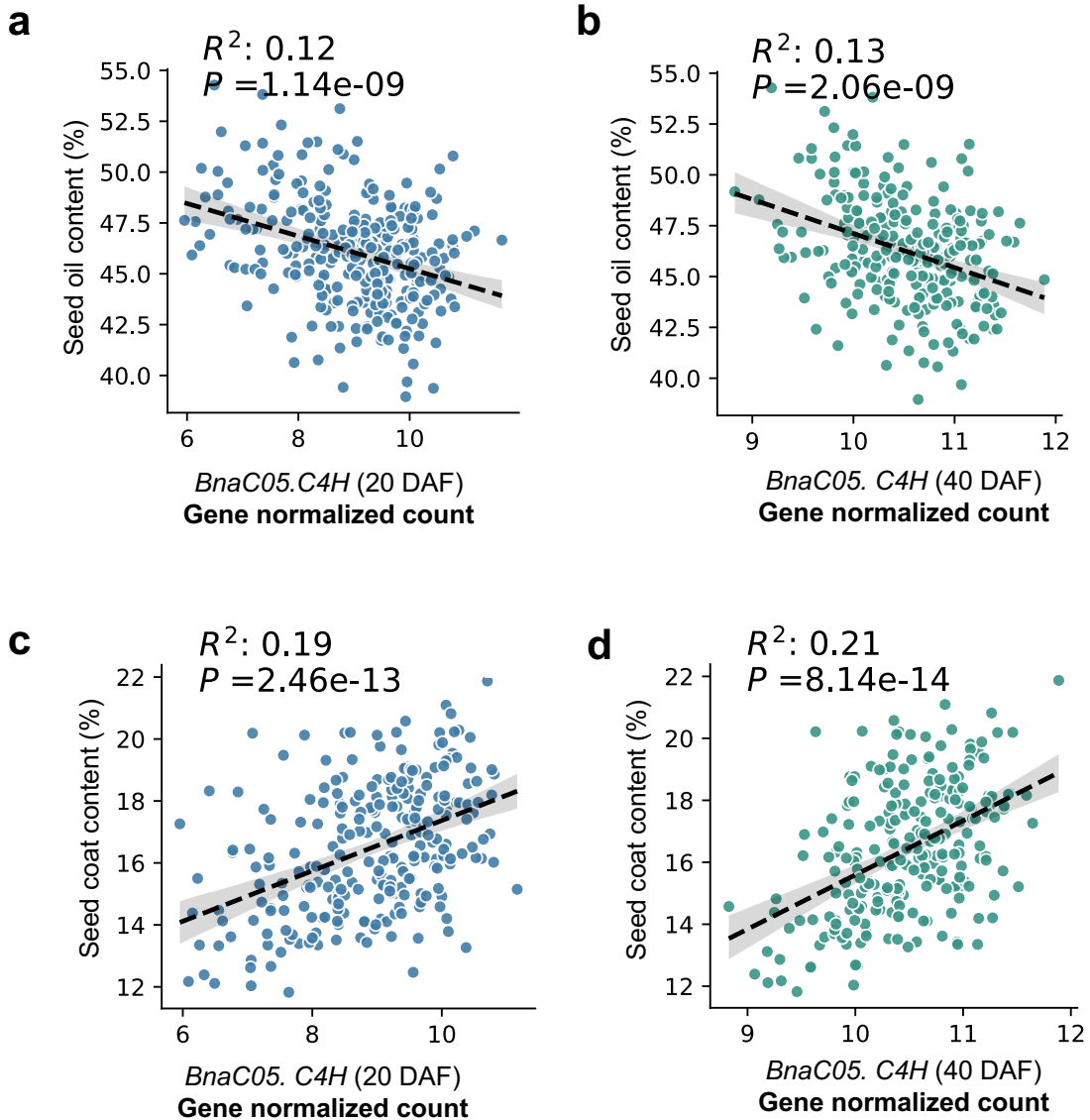


Fig. S18 Correlation between SOC and expression levels of *BnaC05.C4H* at 20 DAF (a), SOC and expression levels of *BnaC05.C4H* at 40 DAF (b), SCC and expression levels of *BnaC05.C4H* at 20 DAF (c) and SCC and expression levels of *BnaC05.C4H* at 40 DAF (d). Each point in a-d represents an accession. The normalized gene expression values are plotted on the X-axis and the SOC or SCC corresponding to the accessions is plotted on the Y-axis.

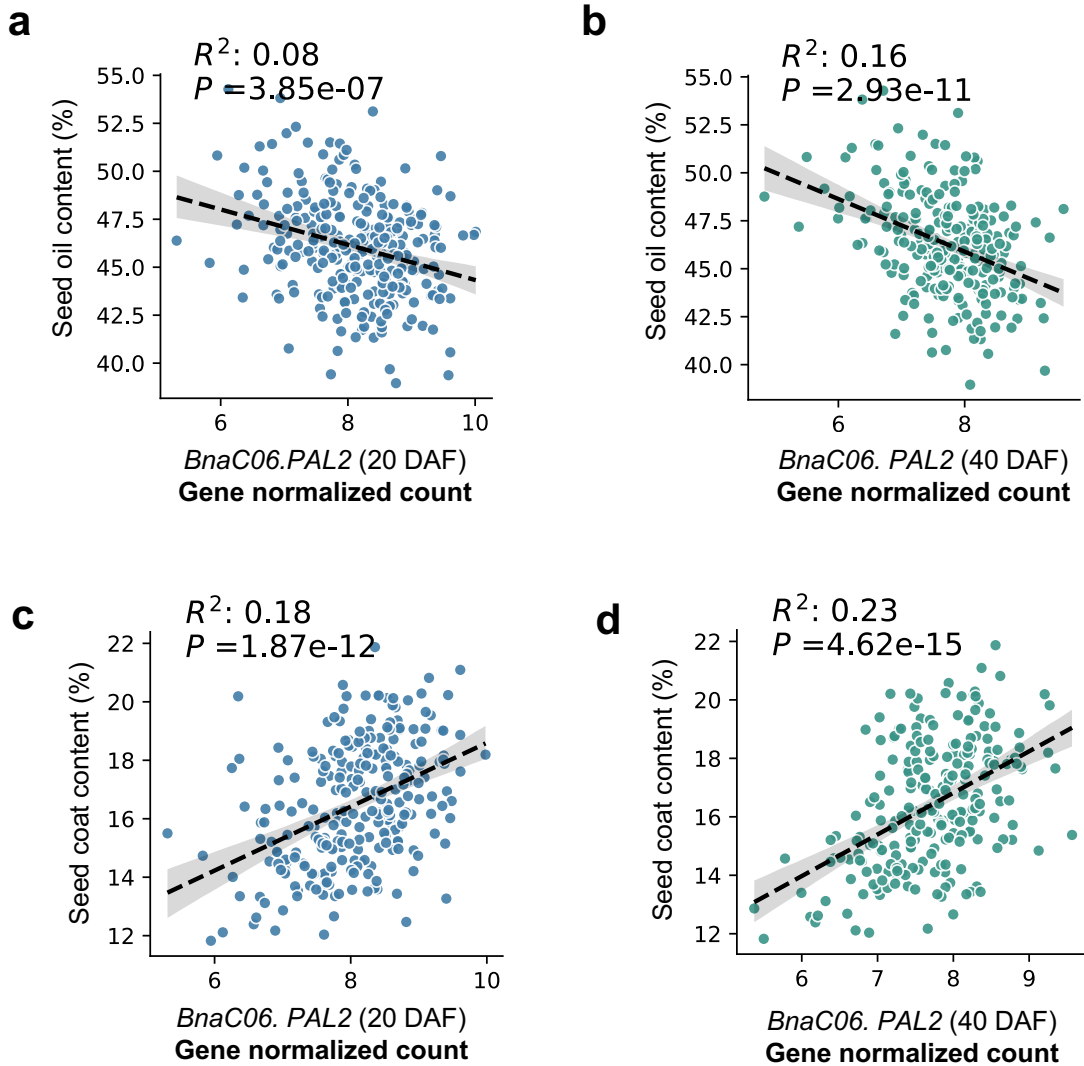


Fig. S19 Correlation between SOC and expression levels of *BnaC06.PAL2* at 20 DAF (a), SOC and expression levels of *BnaC06.PAL2* at 40 DAF (b), SCC and expression levels of *BnaC06.PAL2* at 20 DAF (c) and SCC and expression levels of *BnaC06.PAL2* at 40 DAF (d).

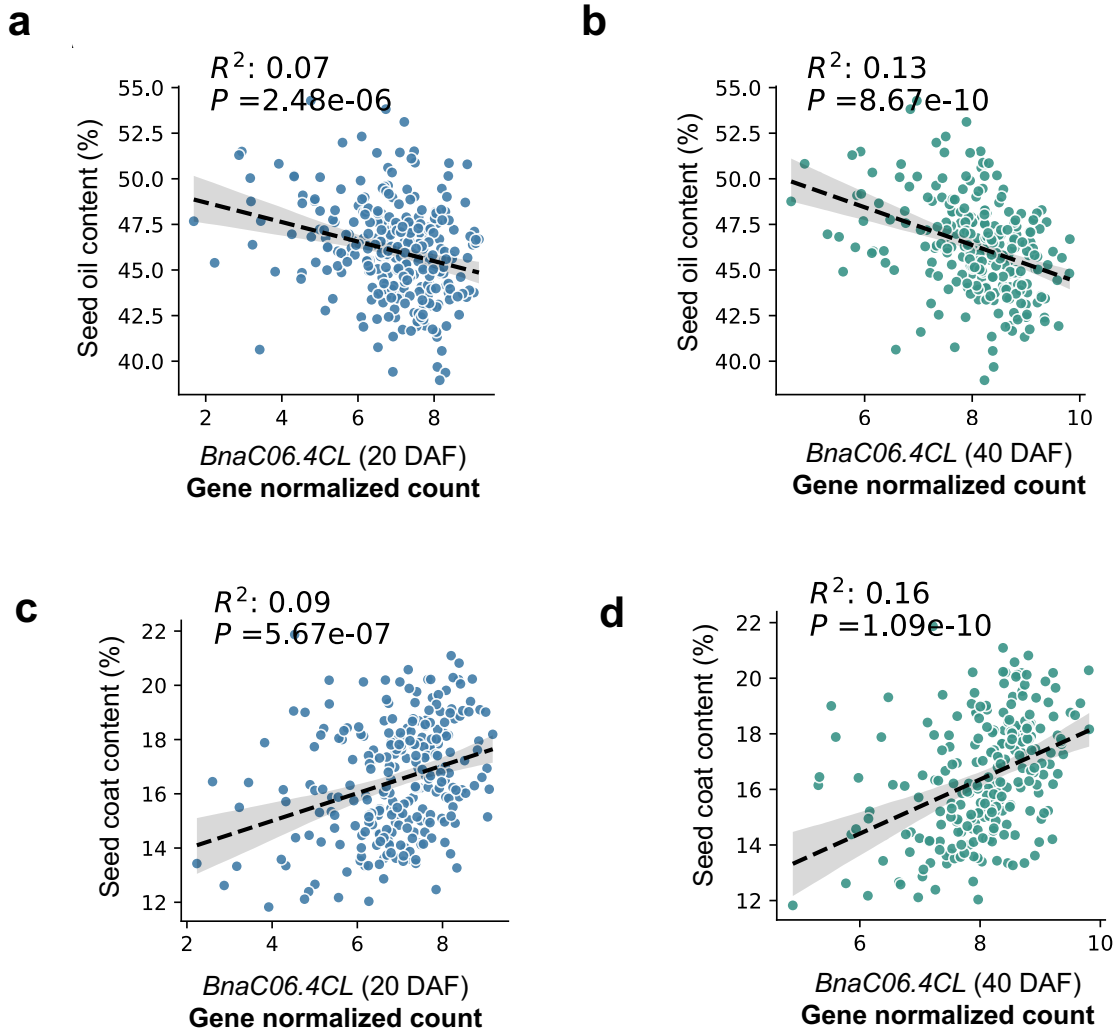


Fig. S20 Correlation between SOC and expression levels of *BnaC06.4CL* at 20 DAF (a), SOC and expression levels of *BnaC06.4CL* at 40 DAF (b), SCC and expression levels of *BnaC06.4CL* at 20 DAF (c) and SCC and expression levels of *BnaC06.4CL* at 40 DAF (d).