

Supplemental Data. Bennett et al. (2010). Plant Cell 10.1105/tpc.109.07272.

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BRN1 -----MSSSNGGVPPGFRFHPTDEELLHYYLKKKKISYEKFEVEVIKEVDLNKIEPWLQDRCKIGSTPQNEWYFFSHKDRKYPTGS 81
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NST2 -----MNISVNGQSQVPPGFRFHPTDEELLKYYLRKKKISNIKIDLDVIRIDLNKLEPWLQEMCKIGTTPQNDWYFFSHKDKKYPTGT 84
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VND2 -----MESVDQSCSVPPGFRFHPTDEELVGYLRRKKVASQKIDLDVIRIDLYRIEPWDLQESCRIGYEEERNEWYFFSHKDKKYPTGT 83
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NST3 RTNRATVAGFWKATGRDKIICS-CVRRIGLRKTLVIFYKGRAPHGQKSDWIMHEYR-LDDTPMSNGYADVVTEDPM---SYNEEGWVVCRV 174
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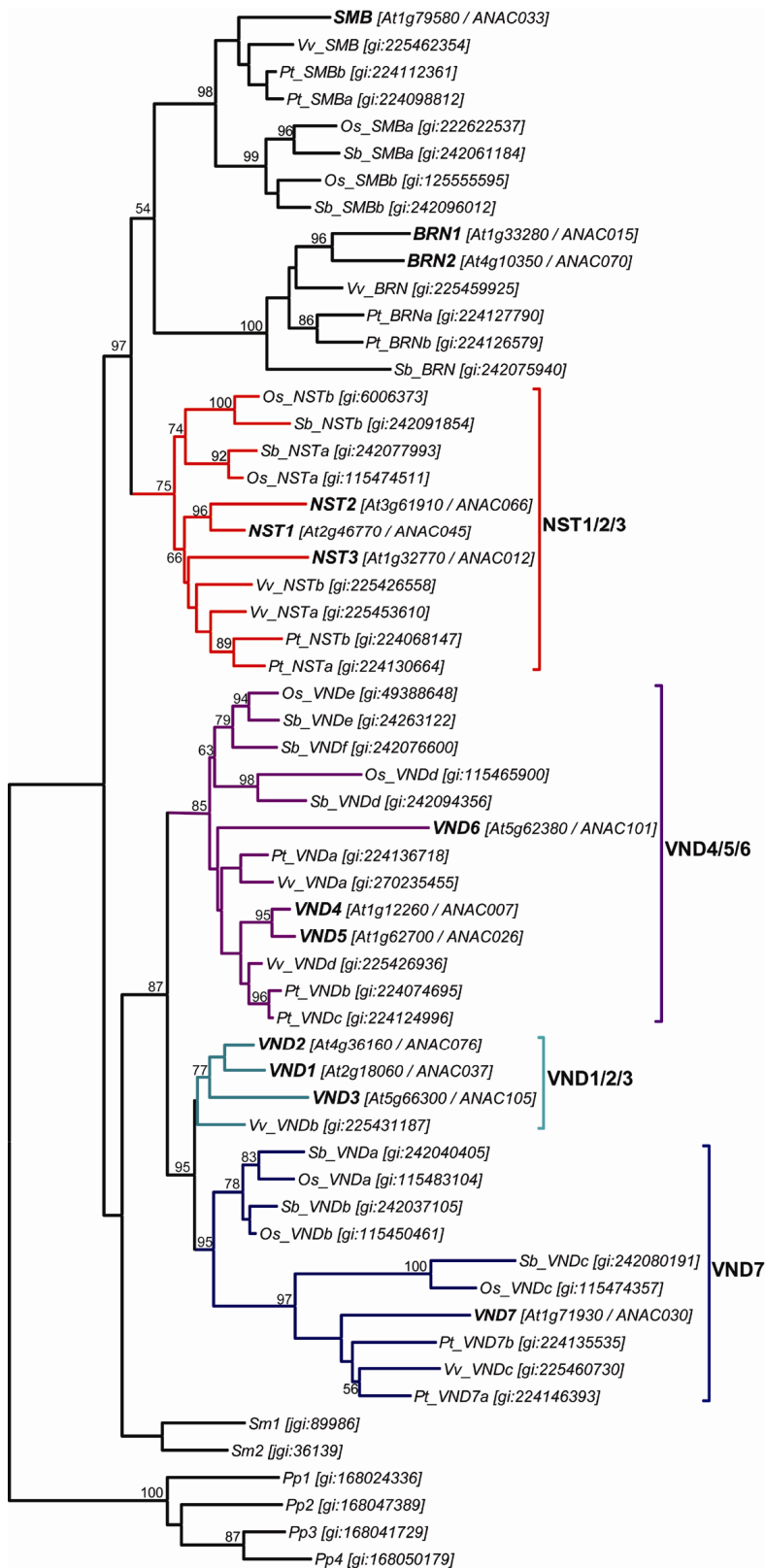
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NST2 FKKKNNLCKNMIS-----SSPASSVKTPS-----FNEETIEQL 204
NST3 FRKKKNYQKIDDCP-----KITLSSLPDDTEEEKGP-----TFHNTQNVDTGLDHV 218
VND1 FKKR-ATGQA-KNTETWSSS-----YFYDEVAP-----NGVNSVMDPIDYISKQOHNI-----FGKGLMCKQEQLEG 214
VND2 FKKKPMGTQA-KNTETWSSS-----YFYDELP-----SGVRSVTEPLNYVSKQKQNV-----FAQDLMFKQEQLEG 215
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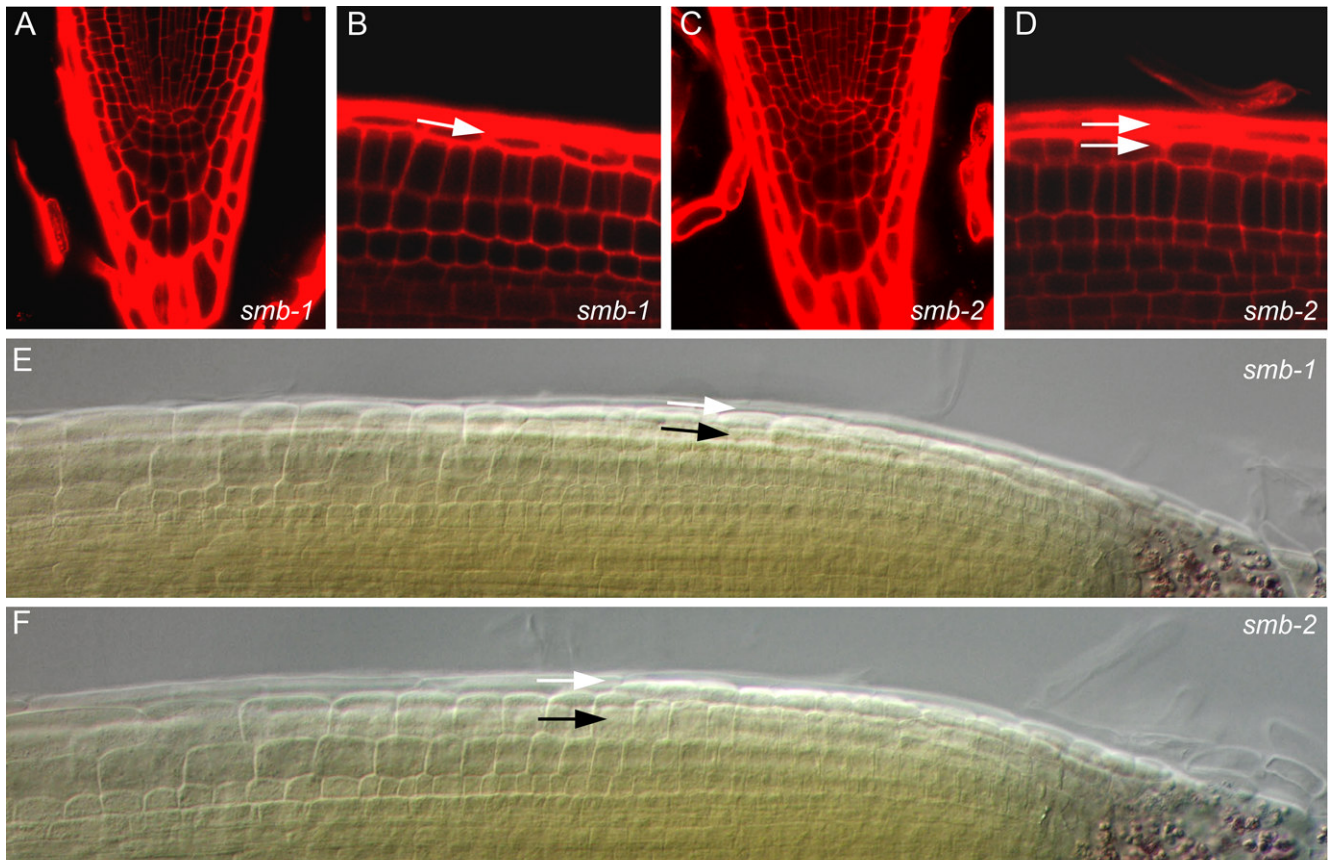
Supplemental Data. Bennett et al. (2010). Plant Cell 1 10.1105/tpc.109.072272.

BRN1	-----EARSFIRRESPTYQGISMFELNKPEEISVHQYPPMPFQPHHKPLSIGYDYSLALL-----	230
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SMB	DHHHHHHHIG-----RQIHMLPHEFANTLSHGSMHLPQLFSPDSAAA---AAAAAASAQPF-----	268
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NST2	LEVMGQS-CKGEI-----VLD-----PFLKLPNLECHNNTTITS-----	237
NST3	LLYMDRTGSNICMPESQ-----TTTQHQDDVLFMQLPSLETPKSESPVD-----	262
VND1	MVDGINYIQS-N-----QFIQLPQLQSPSLPLM-----	241
VND2	SDIGLNF IHC-D-----QFIQLPQLESPLPLT-----	242
VND3	FGSMYLCIDDD-----QFSQLPQLESPLPSE-----	248
VND4	LELHYNHLVQR---NHLLDESH-----LSFLQLPQLESFKIQODNS---NCNSLPYGT-SNIDNNSSHN	288
VND5	LELHYNQMVQHQQQNHHLRES-----MFLQLPQLESPTSNCN-----SDNNNTRNI	277
VND6	-----NYYHLPDLESPRMFQSSSSSSLSLHQNDQDPYGVVLSTIN	231
VND7	LMSNNHYNPNN-----TSSSMHQYGNIELPQLDSPSLSPSL-----	244
BRN1	-----PRESEYQQACQPSGVEVGTCKA-----VSEWIGIVNCNMVSHEDSS--RAMRFED-----	277
BRN2	-----RDSESAASEGLQYQQACEPGLDVGTCET---VASHN---HQQG-LGEWAMMDRLVTCHMGNEDESS--RGITYED--	310
SMB	-VSPINTTDIECSQN-LLRLTS-----NNN-----Y---GGDWSFLDKLLTTGNMNQQQQQQVQNHQAKCF	324
NST1	---CHVSSPDTNHNHIVSNVVDT-----SFVTSWAALDRLVASQLNGPTSYSITAVNESHVG	306
NST2	---YQWLIDDQVNNCHVSKVMDP-----SFITSWAALDRLVASQLNGPNSYSIPAVNETSQ-	290
NST3	---QSFLTPSKLDFSPVQEKITE-----RPVCSNWAASLDRLVAWQLNNGHHNPCHRKSFDEE-	316
VND1	-KRPSSSMSITSMNNYN-YKLPLADEE-----SFESFIR-GEDRRKKKKQVMVTGNWRELDKFVASQLMSQEDNGTSSF-----	313
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VND3	-ITPHSTTFSENSSRKDD-----MSSEKRITDWRVLDKFVASQFLMS-----	289
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VND5	SNLQKSSNISHEEQ- --QQGNQSF- --SLY--YDQGVQM---TTDWRVLDKFVASQLSND-----	329
VND6	ATPTTIMQRDDGHVITNDDDHMIMMNTSTGD-----HHQSGLLVNDHDNDQVMDWQTLDKFVASQLIMSQ-----	296
VND7	-----GTNK-----DQNESFEQE-EKSFNCVDWRTLDTLLETQVIHP-----	281
BRN1	-----DGNNTSSTVQ-----PPSNL-----LSLRGEN-GFLGLF-----	305
BRN2	-----GNNNSSSVVQ---PVPATNQ-----LTLRSEM-DFWGYSK-----	341
SMB	GDLS-----NNDNNDQ-----ADHLGNNN--GGSSSPVNQRFP-FHYLGND-LLKFKP-----	371
NST1	-----HDHLALPSVRSPYPSLNRAS-----YHAGLTQEY-TPEMELWNTTSSLSSS-----PGPFCHVSNVSG	365
NST2	-----SPYHGLNRSG-----CNTGLTPDYIPEIDLWNEADFARTT-----CHLLNGSG	334
NST3	-----EENGDTMMQRWD-----LHWNNDDNVDLWSSFTSSSS-----LDPLLHLSV---	358
VND1	----AGHH-----IVNEDKNNN--DVEMDSSMFL-SEREEENRFVSEFLST-----NSDYDIGICVFDN-----	365
VND2	----GGHHEEDNNKIGHYNNEESNNKG-SVETASSTLL-SDREEENRFISGLLCS-----NLDYDLYRDLHV-----	377
VND3	-----GED-----	292
VND4	-----E---AATASASIQNNAK-DTSNAEYQVDEE-----KDPKRASDMGEEYT---ASTSSSCQIDLWK-----	395
VND5	-----EEAAAVVSSSSHQNNVKIDTRNTGYHVIDEGINLPENDSERVVEMGEEYSNAHAASTSSSCQIDL-----	394
VND6	-----EEEEVNKDPDSSNETFHHL-EEQAATMVSMNAS-----SSSSPCSFYSWAQNTHT-----	348
VND7	-----HNPNIILMFETQSYNPA-----PSFSPMHQSYNEVEANIHHSLGCFPDS-----	324

Supplemental Figure 1 - Multiple sequence alignment of Class IIB NAC family. Fully conserved amino acids are indicated with black areas.



Supplemental Figure 2 - Extended phylogenetic tree of the SMB/NST/VND family
 Maximum likelihood phylogenetic tree inferred with RAXML and the WAG substitution model with gamma rate distribution. The numbers at the nodes indicate bootstrap support calculated by RAXML bootstrapping using 100 replicates. Only bootstrap values over 50% are indicated. We used the sequences from the moss *Physcomitrella patens* as an outgroup to root the tree.



Supplemental Figure 3 - Root cap phenotypes in *smb* alleles

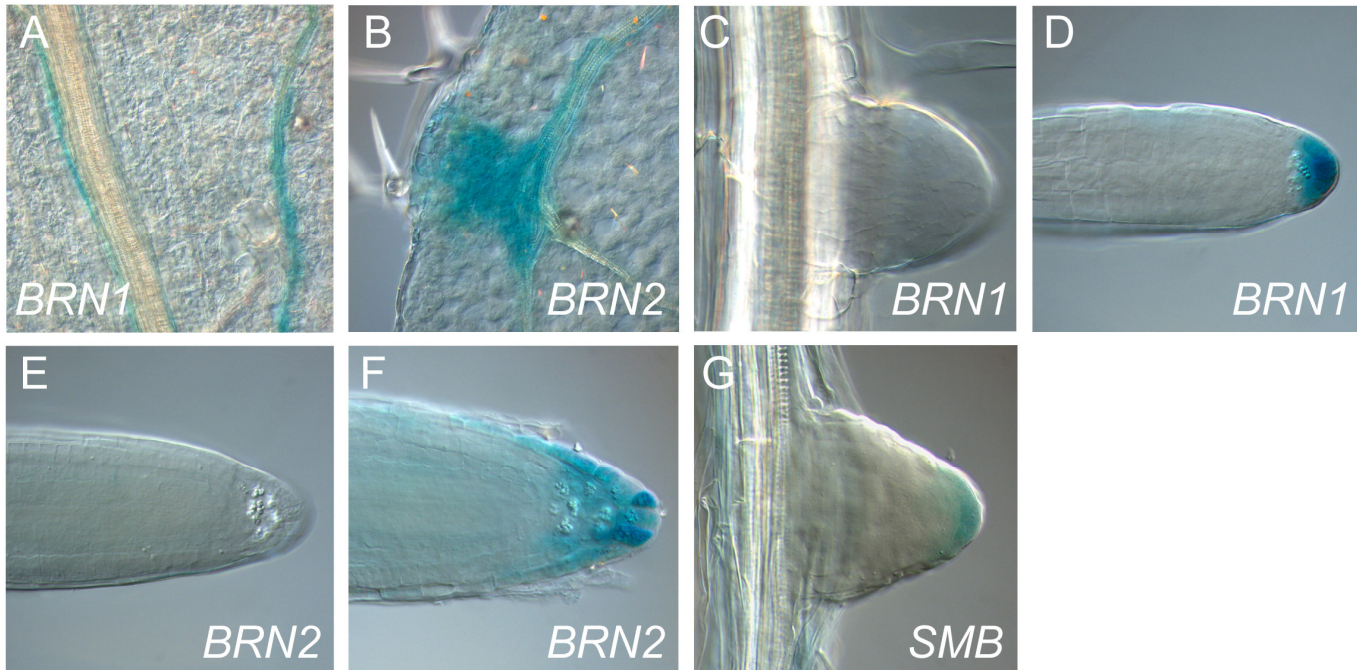
(A) Columella structure in *smb-1*

(B) LRC structure in the meristem zone of *smb-1*. White arrows indicates single LRC layer.

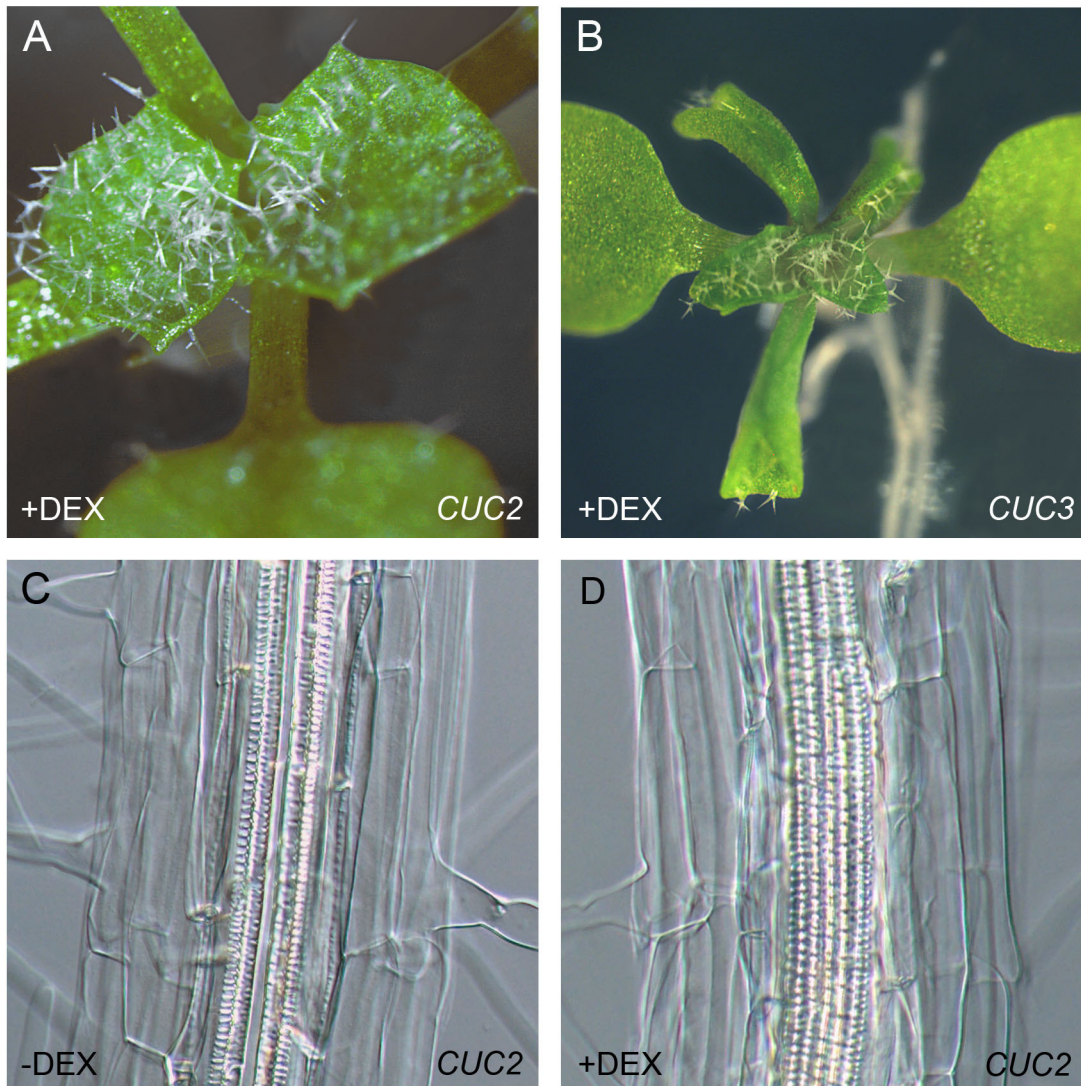
(C) Columella structure in *smb-2*

(D) LRC structure in the meristem zone of *smb-2*. White arrows indicate double LRC layer.

(E-F) Root meristem structure in *smb-1* and *smb-2*. White arrows indicate outer LRC layers, black arrows indicate epidermal layer.



Supplemental Figure 4 - SMB, BRN1 and BRN2 expression in vasculature and lateral roots.
(A) Staining for β -Glucuronidase activity in *BRN1_{pro}:GUS* in secondary vasculature in the first true leaf.
(B) Staining for β -Glucuronidase activity in *BRN2_{pro}:GUS* in hydathodes of the first true leaf.
(C-D) Staining for β -Glucuronidase activity in *BRN1_{pro}:GUS* in lateral roots.
(E-F) Staining for β -Glucuronidase activity in *BRN2_{pro}:GUS* in lateral roots.
(G) Staining for β -Glucuronidase activity in *SMB_{pro}:GUS* in lateral roots.



Supplemental Figure 5 - Overexpression phenotypes of *CUC2* and *CUC3*

(A) Shoot phenotype of *35S:CUC2-GR* treated with DEX.

(B) Shoot phenotype of *35S:CUC3-GR* treated with DEX.

(C-D) Phenotypes of *35S:CUC2-GR* in the DZ of the root, treated with or without DEX, as indicated.

Supplemental Table 1 - Sequences of oligonucleotide primers used in this study.

Primer Name	Purpose	Sequence 5'-3'
BRN1-SK-L	Genotyping <i>ber1-1</i> insertion	AAA TAT CCG ACA GGG TCA AGG
BRN1-SK-R		AAA CTC CGG CCA TAG TTT CAC
BRN2-SK-L	Genotyping <i>ber2-1</i> insertion	CAC TAG GGT TGG CTT GAG GAT
BRN2-SK-R		TAG TTG GAG ACA AGA GAA GGA A
LBb1.3	Genotyping SALK insertions	ATT TTG CCG ATT TCG GAA C
pSMB-F	Cloning SMB promoter	GAG GCC ATT GAC CTG AAA
pSMB-R		TAT CCT TAC TCT TCT TTA AGC
pBRN1-F	Cloning BER1 promoter	GGT CAA TTC TGG TTT CCG TTA GA
pBRN1-R		TGT TCG GTT AAT AAA TGA TCA
pBRN2-F	Cloning BER2 promoter	TTA GTA TAT GAC AAT ATG TGC TCA
pBRN2-R		TTC GAT TTA CGT TTT CCT TCT CT
pCEL5-F	Cloning CEL5 promoter	GT TCC AGA AAA GAA TCA TTG AT
pCEL5-R		TCT TGT TAT TGT GTT GGC TTG AGG GTA
cSMB-F	Cloning SMB cDNA	ATG GAG ATA GGG TCG TCA T
cSMB-R		CTT TGG GAA CTT GAG AAG AT
cBRN1-F	Cloning BER1 cDNA & expression analysis	ATG AGT TCG TCT AAC GGA GGT GT
cBRN1-R		AAA CAA CCC AAG AAA TCC ATT TTC A
cBRN2-F	Cloning BER2 cDNA & expression analysis	ATG GGT TCT TCG TCG AAC GGA
cBRN2-R		ATC CAT CTC ACT ACG CAA TGT T
cNST1-F	Cloning NST1 cDNA	ATG ATG TCA AAA TCT ATG AGC ATA
cNST1-R		TCC ACT ACC ATT CGA CAC GTG ACA AA
cVND6-F	Cloning VND6 cDNA	ATG GAA AGT CTC GCA CAC ATT
cVND6-R		CGT GTG TGT ATT TTG AGC CCA
cVND7-F	Cloning VND7 cDNA	ATG GAT AAT ATA ATG CAA TCG TCA AT
cVND7-R		CGA GTC AGG GAA GCA TCC AAG AGA AT
cCUC2-F	Cloning CUC2 cDNA	ATG GAC ATT CCG TAT TAC CA
cCUC2-R		GTA GTT CCA AAT ACA GTC AA
cCUC3-F	Cloning CUC3 cDNA	ATG ATG CTT GCG GTG GAA GAT
cCUC3-R		CAG CTG GAA TCC TAA AGG ACA T
CESA8-RT-F	Analysing expression of CESA8	GTG TAG TTT CCC GAT CTG CAA
CESA8-RT-R		GAG CCA AGA TGA TCA ACC GCA T
IRX9-RT-F	Analysing expression of IRX9	TGA GGC ACA TTG AAC ATC ACA A
IRX9-RT-R		ATC TTG TGC CGG AAG TCC CTT
4CL1-RT-F	Analysing expression of 4CL1	GAA TCC GTG CCA ATC CCT GAA
4CL1-RT-R		CTG CTT CCG TCA TTC CGT AT
XCPI-RT-F	Analysing expression of XCPI	CGA GTT TGC GGA TTT GAC CCA T
XCPI-RT-R		AGT CTC TTC CTG AAG CCT CAA
SND2-RT-F	Analysing expression of SND2	CCG ACG GAT CAA GAG GTC TT
SND2-RT-R		TGG CCG TGT TTT TCC TGT CTT
SND3-RT-F	Analysing expression of SND3	CCT TAT GCA TTT GGA GGC GAA
SND3-RT-R		CCA CCA TGC TCA TAC CCG AA

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CEL3-RT-F	Analysing expression of CEL3	ACT GCT CCT ACT CTG GTT ACA A
CEL3-RT-R		GGC GTA AGT TGT GAG CAA GAA
CEL5-RT-F	Analysing expression of CEL5	CAA TAC CGA GGC GCT TAC AGT A
CEL5-RT-R		TTT GGC GTA GGT GGT GAG CAA
QUA1-RT-F	Analysing expression of QUA1	GCA GAA TCA CAC TCA CAG CTT
QUA1-RT-R		CTC TTT AGC TTC AGC AAT CAC TT
ACT-RT-F	Analysing expression of ACTIN1	ATG GCT GAT GGT GAA GAC AT
ACT-RT-R		TGG AAG TGC ATA CCC CTC AT