

**Table S3: Modular Cloning Level 0 modules**

All plasmids carry a Spectinomycin resistance gene as selection marker. Module type refers to the 4 bp overhangs created by *Bsal* excision as according to Engler et al. 2014 [1].

plasmid name	module type	description	plate pos.
<b>Promoter modules: Pro, Pro+5U and Pro+5U(f)</b>			
pTEI036 <sup>GB</sup>	Pro+5U	Fusion of LexA operator and 35S minimal promoter; inducible by the synthetic TF XVE (Estradiol-inducible) [2]	B3
pTEI042 <sup>GB</sup>	Pro+5U	Fusion of GAL4 <sub>UAS</sub> and 35S minimal promoter; inducible by the synthetic TF GVG (Dex-inducible) [3]	B4
pJOG644 <sup>GB</sup>	Pro+5U(f)		B5
pTEI038 <sup>GB</sup>	Pro+5U	Promoter G10-90 (strong, constitutive in Arabidopsis) [4]	B6
pJOG640 <sup>GB</sup>	Pro+5U(f)	~ 1300 bp fragment of the 35S promoter (Cauliflower mosaic virus) and 5'UTR Ω (Tobacco Mosaic Virus) [5-7]	B7
pJOG684* <sup>GB</sup>	Pro+5U	~ 800 bp fragment upstream of Arabidopsis <i>UBQ10</i> (At4g05320) (strong, constitutive promoter) [8]	B8
pJOG603	Pro+5U	~ 1700 bp upstream of Arabidopsis <i>RPS5a</i> (At3g11940) (strong, constitutive promoter in Arabidopsis) [9]	B9
pTEI044	Pro+5U(f)		B10
pJOG301	Pro+5U	~ 1000 bp upstream of Arabidopsis <i>DD45/EC1.2</i> (At2g21740) (egg cell-specific promoter) [10, 11]	B11
pAGM28521 <sup>GB</sup>	Pro+5U	Egg cell-specific promoter: Fusion of the <i>EC1.2</i> enhancer with <i>EC1.1</i> promoter ( <i>EC1.2en-EC1.1p</i> ) [11]	B12
pJOG299	Pro+5U	~ 1400 bp upstream of Arabidopsis <i>AP1</i> (At1g69120) (flower mersitem-specific promoter) [12]	C1
pJOG298 <sup>GB</sup>	Pro+5U	~ 600 bp fragment upstream of Arabidopsis <i>ICU2</i> (At5g67100) (dividing cell-specific promoter) [13]	C2
pJOG295* <sup>GB</sup>	Pro+5U	~ 2100 bp fragment upstream of Arabidopsis <i>GILT</i> (At4g12960)	C3
pJOG300* <sup>GB</sup>	Pro+5U	~ 350 bp fragment upstream of Arabidopsis At1g66850	C4
pJOG025	Pro+5U	~ 1000 bp fragment upstream of Arabidopsis <i>EDS1</i> (At3g48090) [14]	C5
pJOG123	Pro+5U(f)		C6
pJOG026	Pro+5U	~ 1200 bp fragment upstream of Arabidopsis <i>PAD4</i> (At3g52430) [15,	C7
pJOG124	Pro+5U(f)	16]	C8
pJOG466 <sup>GB</sup>	Pro+5U	~ 1000 bp fragment upstream of Arabidopsis <i>SAG101</i> (At5g14920) [17]	C9
pJOG467 <sup>GB</sup>	Pro+5U(f)		C10
pJOG010 <sup>GB</sup>	Pro+5U	~ 1200 bp fragment upstream of Arabidopsis <i>PR1</i> (At2g14610) (pathogen-responsive promoter) [18]	C11
pJOG648	Pro+5U	~ 550 bp fragment upstream of Arabidopsis <i>SESA3/AtS2S3</i> (At4g27160) (seed-specific promoter) [19]	C12
pTEI067* <sup>GB</sup>	Pro+5U	~ 1500 bp fragment upstream of Arabidopsis <i>CER6</i> (At1g68530) (epidermis-specific promoter) [20]	D1
pTEI068* <sup>GB</sup>	Pro+5U	~ 2000 bp fragment upstream of Arabidopsis <i>CUE1</i> (At5g33320) (mesophyll-specific promoter) [21]	D2
pTEI069 <sup>GB</sup>	Pro+5U	~ 1000 bp fragment upstream of Arabidopsis <i>BODYGUARD1</i> (At1g64670) (epidermis-specific promoter) [22]	D3
pTEI070 <sup>GB</sup>	Pro+5U	~ 1000 bp fragment upstream of Arabidopsis At1g22690 ("pGC1") (guard cell-specific promoter) [23]	D4
pTEI071 <sup>GB</sup>	Pro+5U	~ 1000 bp fragment upstream of Arabidopsis <i>CAB3</i> (At1g29910) (mesophyll-specific promoter) [24]	D5
pTEI073* <sup>GB</sup>	Pro+5U	~ 2000 bp fragment upstream of Arabidopsis <i>ALMT12</i> (At4tg17585) (guard cell-specific promoter) [25]	D6
pCK019* <sup>GB</sup>	Pro+5U	~ 750 bp fragment upstream of Arabidopsis <i>EXP7</i> (At1g12560) (root hair-specific promoter) [26, 27]	D7
pCK020*	Pro+5U	~ 2300 bp fragment upstream of Arabidopsis <i>WOX5</i> (At3g11260) (root stem cell niche / quiescent center-specific promoter) [28]	D8

plasmid name	module type	description	plate pos.
<b>Promoter modules: Pro, Pro+5U and Pro+5U(f) [continued]</b>			
pCK021* <sup>GB</sup>	Pro+5U	~ 3300 bp fragment upstream of Arabidopsis <i>SOMBRERO</i> (At1g79580) (root cap-specific promoter) [29, 30]	D9
pAGM1761 <sup>GB</sup>	Pro	~ 3000 bp fragment upstream of Arabidopsis <i>AtDMC1</i> (At3G22880) (meiosis-specific promoter) [31]	D10
pJOG020 <sup>GB</sup>	Pro+5U	~ 1000 bp fragment upstream of parsley <i>Ubi4-2</i> [32]	D11
pJOG575 <sup>GB</sup>	Pro+5U(f)		D12
pJOG022 <sup>GB</sup>	Pro+5U	~ 1500 bp fragment of the <i>Zea mays</i> Ubiquitin promoter + UTR [33]	E1
pJOG213 <sup>GB</sup>	Pro+5U	~ 1200 bp fragment upstream of <i>S/EDS1</i> (Solyc060g071280)	E2
pJOG004 <sup>GB</sup>	Pro+5U(f)		E3
pJOG535 <sup>GB</sup>	Pro+5U	~ 1000 bp fragment of the <i>CaBs3</i> promoter (TALE = AvrBs3-inducible promoter) [34]	E4
pJOG577 <sup>GB</sup>	Pro+5U(f)		E5
pJOG638 <sup>GB</sup>	Pro+5U	~ 1000 bp fragment of the <i>CaBs3</i> promoter (TALE = AvrBs3-inducible promoter); weaker variant; mutation in TALE-binding site	E6
pJOG639 <sup>GB</sup>	Pro+5U(f)		E7

plasmid name	module type	description	plate pos.
<b>Tag modules: NT1 and CT</b>			
pJOG170 <sup>GB</sup>	NT1	CDS of mEGFP variant of GFP ( <i>Aequorea victoria</i> ) [35, 36]	E8
pJOG176 <sup>GB</sup>	CT		E9
pJOG169 <sup>GB</sup>	NT1	CDS of mTRQ variant of GFP ( <i>Aequorea victoria</i> ) [35, 37]	E10
pJOG175 <sup>GB</sup>	CT		E11
pJOG168 <sup>GB</sup>	NT1	CDS of mVenus variant of GFP ( <i>Aequorea victoria</i> ) [35, 38]	E12
pJOG174 <sup>GB</sup>	CT		F1
pJOG142 <sup>GB</sup>	CT	mYFP-NES; CDS of mYFP fused to the PKI nuclear export signal [39, 40]	F2
pJOG143 <sup>GB</sup>	CT	mYFP-NLS; CDS of mYFP fused to SV40 nuclear localization signal [40, 41]	F3
pJOG140 <sup>GB</sup>	NT1	NES; PKI nuclear export signal [39]	F4
pJOG141 <sup>GB</sup>	NT1	NLS; SV40 nuclear localization signal [41]	F5
pJOG824 <sup>GB</sup>	CT		F6
pAGM16456 <sup>GB</sup>	NT1	6xHis-NES(Rev); fusion of 6xHis tag with nuclear export signal (NES from Rev, HIV-1) [39]	F7
pAGM16467 <sup>GB</sup>	NT1	6xHis-NES(PKI); fusion of 6xHis tag with nuclear export signal (NES from PKI) [39]	F8
pAGM16418* <sup>GB</sup>	NT1	6xHis-NES(Rev)-GFP; fusion of 6xHis tag with NES (Rev) and GFP	F9
pAGM16429* <sup>GB</sup>	NT1	6xHis-NES(PKI)-GFP ; fusion of 6xHis tag with NES (PKI) and GFP	F10
pJOG642 <sup>GB</sup>	NT1	3 x HA tag fused to the tagRFP-T CDS [42]	F11
pJOG317 <sup>GB</sup>	CT	4 x myc tag fused to Twin-Strep tag [43]	F12
pJOG331 <sup>GB</sup>	CT	6 x HA tag fused to Twin-Strep tag [43]	G1
pJOG658 <sup>GB</sup>	NT1	3 x HA tag fused to firefly ( <i>Photinus pyralis</i> ) Luciferase CDS [44]	G2
pJOG659 <sup>GB</sup>	CT	Renilla ( <i>Renilla reniformis</i> ) luciferase CDS fused to a 3 x HA tag [45]	G3
pJOG643 <sup>GB</sup>	NT1	Hormone-binding domain of the rat glucocorticoid receptor [3, 46]	G4
pCK032 <sup>GB</sup>	CT		G5
pTEI037* <sup>GB</sup>	NT1	Hormone-binding domain of the rat glucocorticoid receptor fused to mEGFP [3, 36]	G6
pTEI041	NT1	Hormone-binding domain and regulatory sequences of the human estrogen receptor [2, 47]	G7
pCK025	CT		G8

plasmid name	module type	description	plate pos.
<b>STOP module: CT -&gt; 3U+ter</b>			
pAGM16841 <sup>GB</sup>	CT-3Uter	STOP codon and <i>nos</i> terminator; to fuse a STOP codon to CDS1ns modules while simultaneously adding a <i>nos</i> terminator	G9

plasmid name	module type	description	plate pos.
<b>CDS modules: CDS1, CDS1ns and CDS2</b>			
pJOG173 <sup>GB</sup>	CDS1	CDS of mEGFP variant of GFP ( <i>Aequorea victoria</i> ) [35, 36]	G10
pJOG172 <sup>GB</sup>	CDS1	CDS of mTRQ variant of GFP ( <i>Aequorea victoria</i> ) [35, 37]	G11
pJOG171 <sup>GB</sup>	CDS1	CDS of mVenus variant of GFP ( <i>Aequorea victoria</i> ) [35, 38]	G12
pJOG021	CDS1	Hygromycin phosphotransferase (hpt) CDS ( <i>Escherichia coli</i> ) [48]	H1
pJOG351 <sup>GB</sup>	CDS1	Neomycin phosphotransferase (nptII) CDS ( <i>Escherichia coli</i> ) [48]	H2
pJOG031	CDS1	AvrRps4 ( <i>Pseudomonas syringae</i> pv. <i>pisi</i> ) [49]	H3
pJOG536*	CDS1	“Nuclear targeting factor” [RanGAP1(WPP)-GFP-BLRP] of the INTACT system [50]	H4
pJOG545	CDS1	AvrBs3 ( <i>Xanthomonas campestris</i> pv. <i>vesicatoria</i> ) [51]	H5
pCK039* <sup>GB</sup>	CDS1	dTALE binding to Bs3 promoter ( <i>Capsicum annuum</i> ) as transactivator	H6
pCK038* <sup>GB</sup>	CDS1ns		H7
pJOG641 <sup>GB</sup>	CDS1	GVG synthetic TF: GAL4-VP16-GR (inducible expression, dexamethasone) [3]	H8
pTEI039	CDS1	XVE synthetic TF: LexA-VP16-ER (inducible expression, estradiol) [2]	H9
pCK026 <sup>GB</sup>	CDS1	Bs3 gene (encodes an FMO enzyme) from <i>Capsicum annuum</i> [34]	H10
pJOG822 <sup>GB</sup>	CDS1	Yellow Fluorescent Protein (YFP) fused with SV40 NLS	H11
pJOG587 <sup>GB</sup>	CDS2	β-glucuronidase ( <i>Escherichia coli</i> ) CDS with two introns, no ATG-START codon [1]	H12

\* module not experimentally validated

<sup>GB</sup> compatible with GoldenBraid system (no *BsmBI* sites)

	1	2	3	4	5	6	7	8	9	10	11	12
A	pJOG130 CDS1 GG-GW shuttle	pJOG131 CDS1ns GG-GW shuttle	pJOG387 CDS1 GW destination	pJOG267 CDS1ns GW destination	pJOG562 Pro+CDS1ns GW destination	pJOG417 CDS1 Y2H-AD	pJOG418 CDS1 Y2H-BD	pCK011 CDS1ns Y2H-AD	pCK012 CDS1ns Y2H-BD	pCK013 CDS1 Bacterial secretion AvrRps4	pCK014 CDS1ns Bacterial secretion AvrRps4	pCK015 CDS1 Bacterial secretion AvrRpt2
B	pCK016 CDS1ns Bacterial secretion AvrRpt2	pTRV2-GG VIGS GG-TRV2	pTEI036 Pro+5U min35S:LexA Estradiol inducible	pTEI042 Pro+5U min35S: GAL4 <sub>UAS</sub> DEX- inducible	pJOG644 Pro+5U(f) min35S: GAL4 <sub>UAS</sub> DEX- inducible	pTEI038 Pro+5U pG10-90	pJOG640 Pro+5U(f) 35S:+5'UTR of TMV	pJOG684 Pro+5U p(At)UBQ10	pJOG603 Pro+5U p(At)RPS5a	pTEI044 Pro+5U(f) p(At)RPS5a	pJOG301 Pro+5U p(At)DD45/ EC1.2	pAGM28521 Pro+5U fusion p(At)EC1.2en +EC1.1
C	pJOG299 Pro+5U p(At)AP1	pJOG298 Pro+5U p(At)ICU2	pJOG295 Pro+5U p(At)GILT	pJOG300 Pro+5U pAt1G66850	pJOG025 Pro+5U p(At)EDS1	pJOG123 Pro+5U(f) p(At)EDS1	pJOG026 Pro+5U p(At)PAD4	pJOG124 Pro+5U(f) p(At)PAD4	pJOG466 Pro+5U p(At)SAG101	pJOG467 Pro+5U(f) p(At)SAG101	pJOG010 Pro+5U p(At)PR1	pJOG648 Pro+5U p(At)SESA3
D	pTEI067 Pro+5U p(At)CER6	pTEI068 Pro+5U p(At)CUE1	pTEI069 Pro+5U p(At)BODY- GUARD1	pTEI70 Pro+5U p(At)GC1	pTEI071 Pro+5U p(At)CAB3	pTEI073 Pro+5U p(At)ALMT12	pCK019 Pro+5U p(At)EXP7	pCK020 Pro+5U p(At)WOX5	pCK021 Pro+5U p(At)SOM- BRERO	pAGM1761 Pro p(At)DMC1	pJOG020 Pro+5U p(Pc)Ubi4-2	pJOG575 Pro+5U(f) p(Pc)Ubi4-2
E	pJOG022 Pro+5U p(Zm)Ubi	pJOG213 Pro+5U p(S)EDS1	pJOG004 Pro+5U(f) p(S)EDS1	pJOG535 Pro+5U p(Ca)Bs3	pJOG577 Pro+5U(f) p(Ca)Bs3	pJOG638 Pro+5U p(Ca)Bs3 weaker	pJOG639 Pro+5U(f) p(Ca)Bs3 weaker	pJOG170 NT1 CDS of mEGFP	pJOG176 CT CDS of mEGFP	pJOG169 NT1 CDS of mTRQ	pJOG175 CT CDS of mTRQ	pJOG168 NT1 CDS of mVenus
F	pJOG174 CT CDS of mVenus	pJOG142 CT mYFP-NES	pJOG143 CT mYFP-NLS	pJOG140 NT1 NES	pJOG141 NT1 NLS	pJOG824 CT NLS	pAGM16456 NT1 6xHis-NES (Rev)	pAGM16467 NT1 6xHis-NES (PKI)	pAGM16418 NT1 6xHis- NES(PKI)- GFP	pAGM16429 NT1 6xHis- NES(PKI)- GFP	pJOG642 NT1 3xHA- tagRFP-T	pJOG317 CT 4 x Myc- 2Strep
G	pJOG331 CT 6xHA- 2Strep	pJOG658 NT1 3xHA-LUC	pJOG659 CT REN-3xHA	pJOG643 NT1 GR (rat)	pCK032 CT GR (rat)	pTEI037 NT1 GR-mEGFP	pTEI041 NT1 ER (human)	pCK025 CT ER (human)	pAGM16841 CT-3U+ter STOP+nos terminator	pJOG173 CDS1 mEGFP	pJOG172 CDS1 mTRQ	pJOG171 CDS1 mVenus
H	pJOG021 CDS1 hpt	pJOG351 CDS1 nptII	pJOG031 CDS1 AvrRps4	pJOG536 CDS1 NTF from INTACT	pJOG545 CDS1 AvrBs3	pCK039 CDS1ns dTALE	pCK038 CDS1ns dTALE	pJOG641 CDS1 GVG synthetic TF	pTEI039 CDS1 XVE synthetic TF	pCK026 CDS1 Bs3	pJOG822 CDS1 YFP-NLS	pJOG587 CDS2 GUS-ATG

▲ contains *ccdB/cat* cassette. Propagation of empty plasmid requires *ccdB* survival/DB3.1 cells, and additional Chloramphenicol selection is advised.

▲ contains *lacZ* fragment for blue/white selection

■ bacterial selection: Kanamycin

■ bacterial selection: Spectinomycin

■ bacterial selection: Ampicillin / Carbenicillin

■ bacterial selection: Gentamicin

## References

1. Engler, C., M. Youles, R. Gruetzner, T.M. Ehnert, S. Werner, J.D. Jones, N.J. Patron, and S. Marillonnet, *A Golden Gate Modular Cloning Toolbox for Plants*. ACS Synth Biol, 2014.
2. Zuo, J., Q.W. Niu, and N.H. Chua, *An estrogen receptor-based transactivator XVE mediates highly inducible gene expression in transgenic plants*. Plant J, 2000. **24**(2): p. 265-73.
3. Aoyama, T. and N.H. Chua, *A glucocorticoid-mediated transcriptional induction system in transgenic plants*. Plant J, 1997. **11**(3): p. 605-12.
4. Ishige, F., M. Takaichi, R. Foster, N.H. Chua, and K. Oeda, *A G-box motif (GCCACGTGCC) tetramer confers high-level constitutive expression in dicot and monocot plants*. Plant J, 1999. **18**(4): p. 443-448.
5. Gallie, D.R., D.E. Sleat, J.W. Watts, P.C. Turner, and T.M. Wilson, *The 5'-leader sequence of tobacco mosaic virus RNA enhances the expression of foreign gene transcripts in vitro and in vivo*. Nucleic Acids Res, 1987. **15**(8): p. 3257-73.
6. Ow, D.W., J.D. Jacobs, and S.H. Howell, *Functional regions of the cauliflower mosaic virus 35S RNA promoter determined by use of the firefly luciferase gene as a reporter of promoter activity*. PNAS, 1987. **84**(14): p. 4870-4.
7. Guille, H., R.K. Dudley, G. Jonard, E. Balazs, and K.E. Richards, *Transcription of Cauliflower mosaic virus DNA: detection of promoter sequences, and characterization of transcripts*. Cell, 1982. **30**(3): p. 763-73.
8. Grefen, C., N. Donald, K. Hashimoto, J. Kudla, K. Schumacher, and M.R. Blatt, *A ubiquitin-10 promoter-based vector set for fluorescent protein tagging facilitates temporal stability and native protein distribution in transient and stable expression studies*. Plant J, 2010. **64**(2): p. 355-65.
9. Tsutsui, H. and T. Higashiyama, *pKAMA-ITACHI Vectors for Highly Efficient CRISPR/Cas9-Mediated Gene Knockout in Arabidopsis thaliana*. Plant Cell Physiol, 2017. **58**(1): p. 46-56.
10. Steffen, J.G., I.H. Kang, J. Macfarlane, and G.N. Drews, *Identification of genes expressed in the Arabidopsis female gametophyte*. Plant J, 2007. **51**(2): p. 281-92.
11. Wang, Z.P., H.L. Xing, L. Dong, H.Y. Zhang, C.Y. Han, X.C. Wang, and Q.J. Chen, *Egg cell-specific promoter-controlled CRISPR/Cas9 efficiently generates homozygous mutants for multiple target genes in Arabidopsis in a single generation*. Genome Biol, 2015. **16**: p. 144.
12. Gao, Y., Y. Zhang, D. Zhang, X. Dai, M. Estelle, and Y. Zhao, *Auxin binding protein 1 (ABP1) is not required for either auxin signaling or Arabidopsis development*. PNAS, 2015. **112**(7): p. 2275-80.
13. Hyun, Y., J. Kim, S.W. Cho, Y. Choi, J.S. Kim, and G. Coupland, *Site-directed mutagenesis in Arabidopsis thaliana using dividing tissue-targeted RGEN of the CRISPR/Cas system to generate heritable null alleles*. Planta, 2015. **241**(1): p. 271-84.
14. Wagner, S., J. Stuttmann, S. Rietz, R. Guerois, E. Brunstein, J. Bautor, K. Niefind, and J.E. Parker, *Structural basis for signaling by exclusive EDS1 heteromeric complexes with SAG101 or PAD4 in plant innate immunity*. Cell Host Microbe, 2013. **14**(6): p. 619-30.
15. Feys, B.J., L.J. Moisan, M.A. Newman, and J.E. Parker, *Direct interaction between the Arabidopsis disease resistance signaling proteins, EDS1 and PAD4*. EMBO Journal, 2001. **20**(19): p. 5400-5411.
16. Jirage, D., T.L. Tootle, T.L. Reuber, L.N. Frost, B.J. Feys, J.E. Parker, F.M. Ausubel, and J. Glazebrook, *Arabidopsis thaliana PAD4 encodes a lipase-like gene that is important for salicylic acid signaling*. PNAS, 1999. **96**(23): p. 13583-8.
17. Feys, B.J., M. Wiermer, R.A. Bhat, L.J. Moisan, N. Medina-Escobar, C. Neu, A. Cabral, and J.E. Parker, *Arabidopsis SENESCENCE-ASSOCIATED GENE101 stabilizes and signals within an ENHANCED DISEASE SUSCEPTIBILITY1 complex in plant innate immunity*. Plant Cell, 2005. **17**(9): p. 2601-13.
18. van Loon, L.C., M. Rep, and C.M. Pieterse, *Significance of inducible defense-related proteins in infected plants*. Annu Rev Phytopathol, 2006. **44**: p. 135-62.
19. Kroj, T., G. Savino, C. Valon, J. Giraudat, and F. Parcy, *Regulation of storage protein gene expression in Arabidopsis*. Development, 2003. **130**(24): p. 6065-73.

20. Hooker, T.S., A.A. Millar, and L. Kunst, *Significance of the expression of the CER6 condensing enzyme for cuticular wax production in Arabidopsis*. Plant Phys, 2002. **129**(4): p. 1568-80.
21. Li, H., K. Culligan, R.A. Dixon, and J. Chory, *CUE1: A Mesophyll Cell-Specific Positive Regulator of Light-Controlled Gene Expression in Arabidopsis*. Plant Cell, 1995. **7**(10): p. 1599-1610.
22. Kurdyukov, S., A. Faust, C. Nawrath, S. Bar, D. Voisin, N. Efremova, R. Franke, L. Schreiber, H. Saedler, J.P. Metraux, and A. Yephremov, *The epidermis-specific extracellular BODYGUARD controls cuticle development and morphogenesis in Arabidopsis*. Plant Cell, 2006. **18**(2): p. 321-39.
23. Yang, Y., A. Costa, N. Leonhardt, R.S. Siegel, and J.I. Schroeder, *Isolation of a strong Arabidopsis guard cell promoter and its potential as a research tool*. Plant Methods, 2008. **4**: p. 6.
24. Susek, R.E., F.M. Ausubel, and J. Chory, *Signal transduction mutants of Arabidopsis uncouple nuclear CAB and RBCS gene expression from chloroplast development*. Cell, 1993. **74**(5): p. 787-99.
25. Meyer, S., P. Mumm, D. Imes, A. Endler, B. Weder, K.A. Al-Rasheid, D. Geiger, I. Marten, E. Martinoia, and R. Hedrich, *AtALMT12 represents an R-type anion channel required for stomatal movement in Arabidopsis guard cells*. Plant J, 2010. **63**(6): p. 1054-62.
26. Stenzel, I., T. Ischebeck, S. Konig, A. Holubowska, M. Sporysz, B. Hause, and I. Heilmann, *The type B phosphatidylinositol-4-phosphate 5-kinase 3 is essential for root hair formation in Arabidopsis thaliana*. Plant Cell, 2008. **20**(1): p. 124-41.
27. Cho, H.T. and D.J. Cosgrove, *Regulation of root hair initiation and expansin gene expression in Arabidopsis*. Plant Cell, 2002. **14**(12): p. 3237-53.
28. Sarkar, A.K., M. Luijten, S. Miyashima, M. Lenhard, T. Hashimoto, K. Nakajima, B. Scheres, R. Heidstra, and T. Laux, *Conserved factors regulate signalling in Arabidopsis thaliana shoot and root stem cell organizers*. Nature, 2007. **446**(7137): p. 811-4.
29. Bennett, T., A. van den Toorn, G.F. Sanchez-Perez, A. Campilho, V. Willemse, B. Snel, and B. Scheres, *SOMBRERO, BEARSKIN1, and BEARSKIN2 regulate root cap maturation in Arabidopsis*. Plant Cell, 2010. **22**(3): p. 640-54.
30. Willemse, V., M. Bauch, T. Bennett, A. Campilho, H. Wolkenfelt, J. Xu, J. Haseloff, and B. Scheres, *The NAC domain transcription factors FEZ and SOMBRERO control the orientation of cell division plane in Arabidopsis root stem cells*. Dev Cell, 2008. **15**(6): p. 913-22.
31. Klimyuk, V.I. and J.D. Jones, *AtDMC1, the Arabidopsis homologue of the yeast DMC1 gene: characterization, transposon-induced allelic variation and meiosis-associated expression*. Plant J, 1997. **11**(1): p. 1-14.
32. Fauser, F., S. Schiml, and H. Puchta, *Both CRISPR/Cas-based nucleases and nickases can be used efficiently for genome engineering in Arabidopsis thaliana*. Plant J, 2014. **79**(2): p. 348-59.
33. Christensen, A.H., R.A. Sharrock, and P.H. Quail, *Maize polyubiquitin genes: structure, thermal perturbation of expression and transcript splicing, and promoter activity following transfer to protoplasts by electroporation*. Plant Mol Biol, 1992. **18**(4): p. 675-89.
34. Romer, P., S. Hahn, T. Jordan, T. Strauss, U. Bonas, and T. Lahaye, *Plant pathogen recognition mediated by promoter activation of the pepper Bs3 resistance gene*. Science, 2007. **318**(5850): p. 645-8.
35. Hecker, A., N. Wallmeroth, S. Peter, M.R. Blatt, K. Harter, and C. Grefen, *Binary 2in1 Vectors Improve in Planta (Co)localization and Dynamic Protein Interaction Studies*. Plant Phys, 2015. **168**(3): p. 776-87.
36. Yang, T.T., L. Cheng, and S.R. Kain, *Optimized codon usage and chromophore mutations provide enhanced sensitivity with the green fluorescent protein*. Nucleic Acids Res, 1996. **24**(22): p. 4592-3.
37. Goedhart, J., D. von Stetten, M. Noirclerc-Savoye, M. Lelimousin, L. Joosen, M.A. Hink, L. van Weeren, T.W. Gadella, Jr., and A. Royant, *Structure-guided evolution of cyan fluorescent proteins towards a quantum yield of 93%*. Nat Commun, 2012. **3**: p. 751.

38. Nagai, T., K. Ibata, E.S. Park, M. Kubota, K. Mikoshiba, and A. Miyawaki, *A variant of yellow fluorescent protein with fast and efficient maturation for cell-biological applications*. Nature Biotechnology, 2002. **20**(1): p. 87-90.
39. Wen, W., J.L. Meinkoth, R.Y. Tsien, and S.S. Taylor, *Identification of a signal for rapid export of proteins from the nucleus*. Cell, 1995. **82**(3): p. 463-73.
40. Garcia, A.V., S. Blanvillain-Baufume, R.P. Huibers, M. Wiermer, G. Li, E. Gobbato, S. Rietz, and J.E. Parker, *Balanced nuclear and cytoplasmic activities of EDS1 are required for a complete plant innate immune response*. PLoS Pathog, 2010. **6**: p. e1000970.
41. Lange, A., R.E. Mills, C.J. Lange, M. Stewart, S.E. Devine, and A.H. Corbett, *Classical nuclear localization signals: definition, function, and interaction with importin alpha*. J Biol Chem, 2007. **282**(8): p. 5101-5.
42. Shaner, N.C., M.Z. Lin, M.R. McKeown, P.A. Steinbach, K.L. Hazelwood, M.W. Davidson, and R.Y. Tsien, *Improving the photostability of bright monomeric orange and red fluorescent proteins*. Nat Methods, 2008. **5**(6): p. 545-51.
43. Schmidt, T.G., L. Batz, L. Bonet, U. Carl, G. Holzapfel, K. Kiem, K. Matulewicz, D. Niermeier, I. Schuchardt, and K. Stanar, *Development of the Twin-Strep-tag(R) and its application for purification of recombinant proteins from cell culture supernatants*. Protein Expr Purif, 2013. **92**(1): p. 54-61.
44. Gould, S.J. and S. Subramani, *Firefly luciferase as a tool in molecular and cell biology*. Anal Biochem, 1988. **175**(1): p. 5-13.
45. Lorenz, W.W., M.J. Cormier, D.J. O'Kane, D. Hua, A.A. Escher, and A.A. Szalay, *Expression of the Renilla reniformis luciferase gene in mammalian cells*. J Biolumin Chemilumin, 1996. **11**(1): p. 31-7.
46. Picard, D., *Steroid-binding domains for regulating the functions of heterologous proteins in cis*. Trends Cell Biol, 1993. **3**(8): p. 278-80.
47. Greene, G.L., P. Gilna, M. Waterfield, A. Baker, Y. Hort, and J. Shine, *Sequence and expression of human estrogen receptor complementary DNA*. Science, 1986. **231**(4742): p. 1150-4.
48. Sundar, I.K. and N. Sakthivel, *Advances in selectable marker genes for plant transformation*. J Plant Phys, 2008. **165**(16): p. 1698-716.
49. Hinsch, M. and B. Staskawicz, *Identification of a new Arabidopsis disease resistance locus, RPS4, and cloning of the corresponding avirulence gene,avrRps4, from Pseudomonas syringae pv. pisi*. Mol Plant Microbe Interact, 1996. **9**(1): p. 55-61.
50. Deal, R.B. and S. Henikoff, *A simple method for gene expression and chromatin profiling of individual cell types within a tissue*. Dev Cell, 2010. **18**(6): p. 1030-40.
51. Boch, J. and U. Bonas, *Xanthomonas AvrBs3 family-type III effectors: discovery and function*. Annu Rev Phytopathol, 2010. **48**: p. 419-36.