

Supplemental Table S5. Overview of important genetically modified ornamental plants.

plant	Biotic/abiotic stressresistance	Color	Senescence	Morphology	Perfume	Phenology	Transformation	promoter	terminator
<i>Amaranthus hypochondriacus</i>	Water deficit ^[1] , Salt ^[1] , Insect ^[2] , Aboitic stress ^[3] , Water ^[4]					Flowering ^[4]	<i>Agrobacterium tumefaciens</i> ^[1-4]	CaMV35S ^[1-4]	
<i>Ammopiptanthus nanus</i>	Drought ^[5,6] , Salt ^[6,7] , Cold ^[5,8] , Osmotic ^[9]						<i>Agrobacterium tumefaciens</i> ^[5-9]	CaMV35S ^[5-9]	Nos ^[5,6,9] , HSP ^[8] , OCS ^[7]
<i>Ananas comosus</i>						Flowering ^[10,11]	<i>Agrobacterium tumefaciens</i> ^[10,11]	CaMV35S ^[10,11]	Nos ^[10]
<i>Antirrhinum majus</i>				Asymmetry ^[12]		Flower development ^[13,14]	<i>Agrobacterium tumefaciens</i> ^[12-14]	CaMV35S ^[12-14]	CaMV poly(A) ^[13]
<i>Catharanthus roseus</i>				Abnormal morphology ^[15]			<i>Agrobacterium tumefaciens</i> ^[15]	CaMV35S ^[15]	
<i>Chimonanthus praecox</i>	Salt ^[16] , Heat ^[16] , Drought ^[17,18]				Perfume ^[19] ,	Flowering ^[20,21] , Flower development ^[20,22]	<i>Agrobacterium tumefaciens</i> ^[16-22]	CaMV35S ^[16-22]	Nos ^[17,19,20]
<i>Chrysanthemum nankingense</i>	Salt ^[23]						<i>Agrobacterium tumefaciens</i> ^[23]	CaMV35S ^[23]	
<i>Chrysanthemum seticuspe</i>						Flowering ^[24,25]	<i>Agrobacterium tumefaciens</i> ^[24,25]	CaMV35S ^[24,25]	
<i>Dendrobium officinale</i>	Salt ^[26-28] [26,27], Drought ^[27] , Osmotic ^[28] ,					Flower development ^[29]	<i>Agrobacterium tumefaciens</i> ^[26-29]	CaMV35S ^[26,28,29]	Nos ^[26,29] [26,29]
<i>Dianthus caryophyllus</i>			Senescence ^[30,31]	Phyllotaxis ^[32] , Stem ^[32] , Whole plant ^[32] , Petal number ^[33] , Stamen and carpel ^[33]			<i>Agrobacterium tumefaciens</i> ^[30-33]	CaMV35S ^[30-33]	Nos ^[30,32]
<i>Helianthus annuus</i>	Drought ^[34,35] , Disease ^[36,37]					Flower development ^[36,38,39] , flowering ^[40]	<i>Agrobacterium tumefaciens</i> ^[34-40]	CaMV35S ^[34-38,40] , FBPI ^[39]	Nos ^[38,39]
<i>Ipomoea nil</i>		Yellow ^[41] , Reddish-brown ^[42] , Purplish-gray ^[42] , Blue ^[43] , White ^[44]	Senescence ^[45,46]	Abnormal morphology ^[47]		Flower development ^[48,49] , flowering ^[49,50]	<i>Agrobacterium tumefaciens</i> ^[41-43,46-50] , CRISPR/Cas9 ^[44,45]	CaMV35S ^[41-43,46-50] , PcUbi -pro ^[45] , Ubiquitin4-2 ^[44,45] , U6 ^[45] , AtU6 ^[45]	Nos ^[41,42,47,49] , Pea3A ^[45] , CaMV35S ^[43]
<i>Lavandula angustifolia</i>					Perfume ^[51]	Flowering ^[52]	<i>Agrobacterium tumefaciens</i> ^[51,52]	CaMV35S ^[51,52]	
<i>Lupinus albus</i>	Disease ^[53] , Phosphorus deficiency ^[54]						<i>Agrobacterium tumefaciens</i> ^[53,54] , Biolistic ^[53]	CaMV35S ^[53]	Nos ^[53]
<i>Lupinus angustifolius</i>	Disease ^[55]	resistant to the herbicides ^[56]					<i>Agrobacterium tumefaciens</i> ^[55,56]	CaMV35S ^[55,56]	Nos ^[55]
<i>Malus baccata</i>	Drought ^[57-59] , Salt ^[60,61] , Cold ^[61]						<i>Agrobacterium tumefaciens</i> ^[57-61]	CaMV35S ^[57-61]	
<i>Nelumbo nucifera</i>	Drought ^[62,63] , Salt ^[63-65] , Heat ^[66,67]						<i>Agrobacterium tumefaciens</i> ^[62-67]	CaMV35S ^[62,64-67]	
<i>Osmanthus fragrans</i>					Perfume ^[68]		<i>Agrobacterium tumefaciens</i> ^[68]	CaMV35S ^[68]	

<i>Paeonia suffruticosa</i>	Salt ^[69] , Cold ^[70]	Acyanic ^[71] , Red ^[72] , Purple ^[73,74] , Color modification ^[75]	Senescence ^[76]			Flowering ^[77,78]	<i>Agrobacterium tumefaciens</i> ^[69-78]	CaMV35S ^[69-78]	Nos ^[71,74-76]
<i>Papaver somniferum</i>	Salt ^[79] , Disease ^[79]						<i>Agrobacterium tumefaciens</i> ^[79]	CaMV35S ^[79]	Nos ^[79]
<i>Petunia hybrida</i>	Disease ^[80] , Antioxidant ^[81]	Blue ^[82] , Purple ^[82,83] , Lilac ^[84]	Senescence ^[85]		Perfume ^[86-89]	Flowering ^[80,90,91] , Flower development ^[92,93]	<i>Agrobacterium tumefaciens</i> ^[80-93]	CaMV35S ^[80-92] , Ap3 ^[93]	Nos ^[80,82,84,85,91,93] , OCS ^[81,87,89]
<i>Phalaenopsis aphrodite</i>	Cold ^[94]			Floral organ maturation ^[95]		Flower development ^[96]	<i>Agrobacterium tumefaciens</i> ^[95,96] , PEG ^[94]	CaMV35S ^[94-96]	Nos ^[95]
<i>Phalaenopsis equestris</i>						Flower development ^[97-99]	<i>Agrobacterium tumefaciens</i> ^[97-99]	CaMV35S ^[97-99]	
<i>Prunus mume</i>	Cold ^[100-102] , Drought ^[100] , Antioxidant ^[101]	Red ^[103]				Flowering ^[104-107] , Endodormancy ^[102]	<i>Agrobacterium tumefaciens</i> ^[100-107]	CaMV35S ^[100-107]	CaMV35S ^[104] , OCS ^[105]
<i>Prunus persica</i>	Cold ^[108] , Salt ^[109]			Weep ^[110]		Flowering ^[111-113] , Flower Development ^[114,115] , dormancy ^[108]	<i>Agrobacterium tumefaciens</i> ^[108,109,111-115]	CaMV35S ^[108,109,111,112,114,115]	Nos ^[113]
<i>Punica granatum</i>						Flowering ^[116]	<i>Agrobacterium tumefaciens</i> ^[116]	CaMV35S ^[116]	
<i>Rosa chinensis</i>	Cold ^[117-119] , Drought ^[117] , Antioxidant ^[120,121] , Heat ^[121,122] , Osmotic ^[121]			Petal number ^[123]		Flowering ^[124]	<i>Agrobacterium tumefaciens</i> ^[117-124]	CaMV35S ^[117-124]	Nos ^[117]
<i>Rosa multiflora</i>	Cold ^[125] , Disease ^[126]					Flowering ^[127] , Flower development ^[127]	<i>Agrobacterium tumefaciens</i> ^[125-127]	CaMV35S ^[125-127]	
<i>Rosa rugosa</i>					Perfume ^[128-130]	Flower development ^[131,132]	<i>Agrobacterium tumefaciens</i> ^[128,129,131,132]	CaMV35S ^[128,131,132]	

1. Massange-Sanchez JA, Palmeros-Suarez PA, Espitia-Rangel E, Rodriguez-Arevalo I, Sanchez-Segura L, et al. 2016. Overexpression of grain amaranth (*Amaranthus hypochondriacus*) *AhERF* or *AhDOF* transcription factors in *Arabidopsis thaliana* increases water deficit-and salt-stress tolerance, respectively, via contrasting stress-amelioration mechanisms. *PLoS one* 11:e0164280
2. Massange-Sanchez JA, Palmeros-Suarez PA, Martinez-Gallardo NA, Castrillon-Arbelaez PA, Aviles-Arnaut H, et al. 2015. The novel and taxonomically restricted *Ah24* gene from grain amaranth (*Amaranthus hypochondriacus*) has a dual role in development and defense. *Frontiers in plant science* 6:602
3. Palmeros-Suárez PA, Massange-Sánchez JA, Sánchez-Segura L, Martínez-Gallardo NA, Rangel EE, et al. 2017. *AhDGR2*, an amaranth abiotic stress-induced DUF642 protein gene, modifies cell wall structure and composition and causes salt and ABA hyper-sensitivity in transgenic *Arabidopsis*. *Planta* 245:623-40
4. Palmeros-Suárez PA, Massange-Sánchez JA, Martínez-Gallardo NA, Montero-Vargas JM, Gómez-Leyva JF, Délano-Frier JP. 2015. The overexpression of an *Amaranthus hypochondriacus* *NF-YC* gene modifies growth and confers water deficit stress resistance in *Arabidopsis*. *Plant Science* 240:25-40
5. Liu Y, Zhang L, Hao W, Zhang L, Liu Y, Chen L. 2019. Expression of two α -type expansins from *Ammopiptanthus nanus* in *Arabidopsis thaliana* enhance tolerance to cold and drought stresses. *International journal of molecular sciences* 20:5255
6. Yu H-Q, Zhou X-Y, Wang Y-G, Zhou S-F, Fu F-L, Li W-C. 2017. A betaine aldehyde dehydrogenase gene from *Ammopiptanthus nanus* enhances tolerance of *Arabidopsis* to high salt and drought stresses. *Plant Growth Regulation* 83:265-76
7. Yu HQ, Yong TM, Li HJ, Liu YP, Zhou SF, et al. 2015. Overexpression of a phospholipase *Da* gene from *Ammopiptanthus nanus* enhances salt tolerance of phospholipase *Da*1-deficient *Arabidopsis* mutant. *Planta* 242:1495-509
8. Deng L-Q, Yu H-Q, Liu Y-P, Jiao P-P, Zhou S-F, et al. 2014. Heterologous expression of antifreeze protein gene *AnAFP* from *Ammopiptanthus nanus* enhances cold tolerance in *Escherichia coli* and tobacco. *Gene* 539:132-40
9. Yu HQ, Han N, Zhang YY, Tao Y, Chen L, et al. 2017. Cloning and characterization of vacuolar H⁺-pyrophosphatase gene (*AnVPI*) from *Ammopiptanthus nanus* and its heterologous expression enhances osmotic tolerance in yeast and *Arabidopsis thaliana*. *Plant Growth Regulation* 81:385-97
10. Lv L, Duan J, Xie J, Wei C, Liu Y, et al. 2012. Isolation and characterization of a *FLOWERING LOCUS T* homolog from pineapple (*Ananas comosus* (L.) Merr.). *Gene* 505:368-73
11. Trusov Y, Botella JR. 2006. Silencing of the ACC synthase gene *ACACS2* causes delayed flowering in pineapple [*Ananas comosus* (L.) Merr.]. *Journal of experimental botany* 57:3953-60

12. Baxter CE, Costa MMR, Coen ES. 2007. Diversification and co-option of *RAD*-like genes in the evolution of floral asymmetry. *The Plant Journal* 52:105-13
13. Jaffé FW, Tattersall A, Glover BJ. 2007. A truncated *MYB* transcription factor from *Antirrhinum majus* regulates epidermal cell outgrowth. *Journal of experimental botany* 58:1515-24
14. Perez-Rodriguez M, Jaffé FW, Butelli E, Glover BJ, Martin C. 2005. Development of three different cell types is associated with the activity of a specific *MYB* transcription factor in the ventral petal of *Antirrhinum majus* flowers.
15. Yang C-Y, Huang Y-H, Lin C-P, Lin Y-Y, Hsu H-C, et al. 2015. MicroRNA396-targeted *SHORT VEGETATIVE PHASE* is required to repress flowering and is related to the development of abnormal flower symptoms by the phyllody symptoms1 effector. *Plant Physiology* 168:1702-16
16. Li J, Yang J, Liu D, Huang R, Sui S, et al. 2017. Isolation and characterization of plant *TAF9*, an orthologous gene for TATA-binding protein-associated factor 9, from wintersweet (*Chimonanthus praecox*). *Canadian Journal of Plant Science* 97:1100-8
17. Zhang L, Liu M, Qiao G, Jiang J, Jiang Y, Zhuo R. 2013. Transgenic poplar “NL895” expressing *CpFATB* gene shows enhanced tolerance to drought stress. *Acta physiologiae plantarum* 35:603-13
18. Zhang L-H, Jia B, Zhuo R-Y, Liu J-L, Pan H-Y, et al. 2012. An acyl–acyl carrier protein thioesterase gene isolated from Wintersweet (*Chimonanthus praecox*), *CpFATB*, enhances drought tolerance in transgenic tobacco (*Nicotiana tabacum*). *Plant Molecular Biology Reporter* 30:433-42
19. Aslam MZ, Lin X, Li X, Yang N, Chen L. 2020. Molecular Cloning and Functional Characterization of *CpMYC2* and *CpBHLH13* Transcription Factors from Wintersweet (*Chimonanthus praecox* L.). *Plants* 9:785
20. Wang B-G, Zhang Q, Wang L-G, Duan K, Pan A-H, et al. 2011. The *AGL6*-like gene *CpAGL6*, a potential regulator of floral time and organ identity in wintersweet (*Chimonanthus praecox*). *Journal of plant growth regulation* 30:343-52
21. Huang R, Liu D, Huang M, Ma J, Li Z, et al. 2019. *CpWRKY71*, a *WRKY* transcription factor gene of Wintersweet (*Chimonanthus praecox*), promotes flowering and leaf senescence in *Arabidopsis*. *International journal of molecular sciences* 20:5325
22. Liu H, Huang R, Ma J, Sui S, Guo Y, et al. 2017. Two C3H type zinc finger protein genes, *CpCZF1* and *CpCZF2*, from *Chimonanthus praecox* affect stamen development in *Arabidopsis*. *Genes* 8:199
23. He M, Wang H, Liu Y, Gao W, Gao Y, et al. 2016. Cloning and characterization of *ChiMYB* in *Chrysanthemum indicum* with an emphasis on salinity stress tolerance. *Genet. Mol. Res* 15:1-17
24. Nakano Y, Takase T, Takahashi S, Sumitomo K, Higuchi Y, Hisamatsu T. 2019. *Chrysanthemum* requires short-day repeats for anthesis: Gradual *CsFTL3* induction through a feedback loop under short-day conditions. *Plant Science* 283:247-55
25. Oda A, Higuchi Y, Hisamatsu T. 2017. Photoperiod-insensitive floral transition in *chrysanthemum* induced by constitutive expression of chimeric repressor *CsLHY-SRDx*. *Plant Science* 259:86-93
26. He C, Yu Z, da Silva JAT, Zhang J, Liu X, et al. 2017. *DoGMP1* from *Dendrobium officinale* contributes to mannose content of water-soluble polysaccharides and plays a role in salt stress response. *Scientific reports* 7:1-13
27. Xu X, Wang C, Ma X, Pan Y, Ying Q, et al. 2015. Overexpression of *DnWRKY29* in tobacco impaired plants tolerance to salt and drought stresses. *Russian journal of plant physiology* 62:262-9
28. Yu Z, He C, da Silva JAT, Zhang G, Dong W, et al. 2017. Molecular cloning and functional analysis of *DoUGE* related to water-soluble polysaccharides from *Dendrobium officinale* with enhanced abiotic stress tolerance. *Plant Cell, Tissue and Organ Culture (PCTOC)* 131:579-99
29. Yu Z, Zhang G, da Silva JAT, Yang Z, Duan J. 2019. The β -1, 3-galactosyltransferase gene *DoGALT2* is essential for stigmatic mucilage production in *Dendrobium officinale*. *Plant Science* 287:110179
30. Kinouchi T, Endo R, Yamashita A, Satoh S. 2006. Transformation of carnation with genes related to ethylene production and perception: towards generation of potted carnations with a longer display time. *Plant cell, tissue and organ culture* 86:27-35
31. Satoh S. 2011. Ethylene production and petal wilting during senescence of cut carnation (*Dianthus caryophyllus*) flowers and prolonging their vase life by genetic transformation. *Journal of The Japanese Society for Horticultural Science* 80:127-35
32. Meng L-S, Song J-P, Sun S-B, Wang C-Y. 2009. The ectopic expression of *PttKNI* gene causes pleiotropic alternation of morphology in transgenic carnation (*Dianthus caryophyllus* L.). *Acta physiologiae plantarum* 31:1155-64
33. Wang Q, Dan N, Zhang X, Lin S, Bao M, Fu X. 2020. Identification, Characterization and Functional Analysis of C-Class Genes Associated with Double Flower Trait in Carnation (*Dianthus caryophyllus* L.). *Plants* 9:87
34. Cabello JV, Dezar CA, Manavella PA, Chan RL. 2007. The intron of the *Arabidopsis thaliana COX5 c* gene is able to improve the drought tolerance conferred by the sunflower *Hahb-4* transcription factor. *Planta* 226:1143-54
35. Manavella PA, Arce AL, Dezar CA, Bitton F, Renou JP, et al. 2006. Cross-talk between ethylene and drought signalling pathways is mediated by the sunflower *Hahb-4* transcription factor. *The Plant Journal* 48:125-37
36. Dezar CA, Giacomelli JI, Manavella PA, Ré DA, Alves-Ferreira M, et al. 2011. *HAHB10*, a sunflower *HD-Zip II* transcription factor, participates in the induction of flowering and in the control of phytohormone-mediated responses to biotic stress. *Journal of experimental botany* 62:1061-76
37. Singareddy V, Sheri VR, Muddanuru T, Tatineni R, Jain RK, et al. 2018. Genetic engineering of sunflower (*Helianthus annuus* L.) for resistance to necrosis disease through deployment of the TSV coat protein gene. *Plant Cell, Tissue and Organ Culture (PCTOC)* 135:263-77
38. Shchennikova A, Shulga O, Skryabin K. Ectopic Expression of the Homeotic MADS-Box Gene *HAM31* (*Helianthus annuus* L.) in Transgenic Plants *Nicotiana tabacum* L. Affects the Gynoecium Identity. *Proc. Doklady Biochemistry and Biophysics*, 2018, 483:363-8: Springer
39. Shulga O, Neskorođov YB, Shchennikova A, Gaponenko A, Skryabin K. Ectopic expression of the *HAM59* gene causes homeotic transformations of reproductive organs in sunflower (*Helianthus annuus* L.). *Proc. Doklady Biochemistry and Biophysics*, 2015, 461:110-3: Springer
40. Goloveshkina EN, Shchennikova AV, Kamionskaya AM, Skryabin KG, Shulga OA. 2012. Influence of ectopic expression of Asteraceae MADS box genes on plant ontogeny in tobacco. *Plant Cell, Tissue and Organ Culture (PCTOC)* 109:61-71
41. Hoshino A, Mizuno T, Shimizu K, Mori S, Fukada-Tanaka S, et al. 2019. Generation of yellow flowers of the Japanese morning glory by engineering its flavonoid biosynthetic pathway toward aurones. *Plant and Cell Physiology* 60:1871-9
42. Morita Y, Hoshino A, Kikuchi Y, Okuhara H, Ono E, et al. 2005. Japanese morning glory dusky mutants displaying reddish-brown or purplish-gray flowers are deficient in a novel glycosylation enzyme for anthocyanin biosynthesis, UDP-glucose:anthocyanidin 3-O-glucosyltransferase, due to 4-bp insertions in the gene. *The Plant Journal* 42:353-63
43. Takatori Y, Shimizu K, Ogata J, Endo H, Ishimaru K, et al. 2015. Cloning of the Flavonoid 3'-Hydroxylase Gene of *Eustoma grandiflorum* (Raf.) Shinn. (*EgF3'H*) and Complementation of an F3'H-deficient Mutant of *Ipomoea nil* (L.) Roth. by Heterologous Expression of *EgF3'H*. *The Horticulture Journal*:MI-029
44. Watanabe K, Kobayashi A, Endo M, Sage-Ono K, Toki S, Ono M. 2017. CRISPR/Cas9-mediated mutagenesis of the *dihydroflavonol-4-reductase-B* (*DFR-B*) locus in the Japanese morning glory *Ipomoea (Pharbitis) nil*. *Scientific reports* 7:1-9

45. Shibuya K, Watanabe K, Ono M. 2018. CRISPR/Cas9-mediated mutagenesis of the *EPHEMERALI* locus that regulates petal senescence in Japanese morning glory. *Plant Physiology and Biochemistry* 131:53-7
46. Shibuya K, Yamada T, Suzuki T, Shimizu K, Ichimura K. 2009. *InPSR26*, a putative membrane protein, regulates programmed cell death during petal senescence in Japanese morning glory. *Plant Physiology* 149:816-24
47. Ono M, Hiyama S, Higuchi Y, Kamada H, Nitasaka E, et al. 2012. Morphological changes in *Ipomoea nil* using chimeric repressors of *Arabidopsis TCP3* and *TCP5*. *Plant Biotechnology*:12.1010 a
48. Azuma M, Mitsuda N, Goto K, Oshima Y, Ohme-Takagi M, et al. 2016. The petal-specific *InMYB1* promoter functions by recognizing petaloid cells. *Plant and Cell Physiology* 57:580-7
49. Kikuchi R, Sage - Ono K, Kamada H, Handa H, Ono M. 2008. *PnMADS1*, encoding an *StMADS11* - clade protein, acts as a repressor of flowering in *Pharbitis nil*. *Physiologia plantarum* 133:786-93
50. Higuchi Y, Sage-Ono K, Sasaki R, Ohtsuki N, Hoshino A, et al. 2011. Constitutive expression of the *GIGANTEA* ortholog affects circadian rhythms and suppresses one-shot induction of flowering in *Pharbitis nil*, a typical short-day plant. *Plant and Cell Physiology* 52:638-50
51. Tsuru M, Asada S. 2014. Differential expression of limonene synthase gene affects production and composition of essential oils in leaf and floret of transgenic lavandin (*Lavandula × intermedia* Emeric ex Loisel.). *Plant biotechnology reports* 8:193-201
52. Wells RS, Adal AM, Bauer L, Najafianashrafi E, Mahmoud SS. 2020. Cloning and functional characterization of a floral repressor gene from *Lavandula angustifolia*. *Planta* 251:1-11
53. Oelofse D, Gazendam I, Veale A, Djami-Tchatchou A, Berger D, Dubery I. 2016. Functional characterization of a defense-related class-III chitinase promoter from *Lupinus albus*, active in legume and monocot tissues. *European journal of plant pathology* 146:923-36
54. Uhde - Stone C, Liu J, Zinn KE, Allan DL, Vance CP. 2005. Transgenic proteoid roots of white lupin: a vehicle for characterizing and silencing root genes involved in adaptation to P stress. *The Plant Journal* 44:840-53
55. Wijayanto T, Barker SJ, Wylie SJ, Gilchrist DG, Cowling WA. 2009. Significant reduction of fungal disease symptoms in transgenic lupin (*Lupinus angustifolius*) expressing the anti - apoptotic baculovirus gene *p35*. *Plant biotechnology journal* 7:778-90
56. Li H, Wylie S, Jones M. 2000. Transgenic yellow lupin (*Lupinus luteus*). *Plant Cell Reports* 19:634-7
57. Han D, Ding H, Chai L, Liu W, Zhang Z, et al. 2018. Isolation and characterization of *MbWRKY1*, a *WRKY* transcription factor gene from *Malus baccata* (L.) Borkh involved in drought tolerance. *Canadian Journal of Plant Science* 98:1023-34
58. Han D, Zhang Z, Ding H, Chai L, Liu W, et al. 2018. Isolation and characterization of *MbWRKY2* gene involved in enhanced drought tolerance in transgenic tobacco. *Journal of Plant Interactions* 13:163-72
59. Han D, Zhang Z, Ding H, Wang Y, Liu W, et al. 2018. Molecular cloning and functional analysis of *MbWRKY3* involved in improved drought tolerance in transformed tobacco. *Journal of Plant Interactions* 13:329-37
60. Han D, Du M, Zhou Z, Wang S, Li T, et al. 2020. An *NAC* transcription factor gene from *Malus baccata*, *MbNAC29*, increases cold and high salinity tolerance in *Arabidopsis*. *In Vitro Cellular & Developmental Biology-Plant* 56:588-99
61. Han D, Du M, Zhou Z, Wang S, Li T, et al. 2020. Overexpression of a *Malus baccata NAC* transcription factor gene *MbNAC25* increases cold and salinity tolerance in *Arabidopsis*. *International journal of molecular sciences* 21:1198
62. Cheng L, Yang J, Yin L, Hui L, Qian H, et al. 2017. Transcription factor *NnDREB1* from lotus improved drought tolerance in transgenic *Arabidopsis thaliana*. *Biologia plantarum* 61:651-8
63. Diao Y, Li G, Yu A, Zheng X, Xie K, et al. 2016. Cloning and characterization of the *UBC* gene from lotus (*Nelumbo nucifera*). *Genet Mol Res. <https://doi.org/10.4238/gmr.15038.341>*
64. Cheng L, Hui L, Yin L, Li S, Chen X, Li L. 2015. Overexpression of *NnDREB2*, isolated from lotus improves salt tolerance in transgenic *Arabidopsis thaliana*. *Acta physiologiae plantarum* 37:1-12
65. Cheng L, Li S, Hussain J, Xu X, Yin J, et al. 2013. Isolation and functional characterization of a salt responsive transcriptional factor, *LrbZIP* from lotus root (*Nelumbo nucifera* Gaertn). *Molecular biology reports* 40:4033-45
66. Chen Hh, Chu P, Zhou Yl, Ding Y, Li Y, et al. 2016. Ectopic expression of *NnPER1*, a *Nelumbo nucifera* 1 - cysteine peroxiredoxin antioxidant, enhances seed longevity and stress tolerance in *Arabidopsis*. *The Plant Journal* 88:608-19
67. Zhou Y, Chen H, Chu P, Li Y, Tan B, et al. 2012. *NnHSP17.5*, a cytosolic class II small heat shock protein gene from *Nelumbo nucifera*, contributes to seed germination vigor and seedling thermotolerance in transgenic *Arabidopsis*. *Plant cell reports* 31:379-89
68. Han Y, Wang H, Wang X, Li K, Dong M, et al. 2019. Mechanism of floral scent production in *Osmanthus fragrans* and the production and regulation of its key floral constituents, β -ionone and linalool. *Horticulture research* 6:1-12
69. Hao Q, Ren H, Zhu J, Wang L, Huang S, et al. 2017. Overexpression of *PSK1*, a *SKP1*-like gene homologue, from *Paeonia suffruticosa*, confers salinity tolerance in *Arabidopsis*. *Plant cell reports* 36:151-62
70. Zhang Y, Sun T, Liu S, Dong L, Liu C, et al. 2016. *MYC* cis-elements in *PsMPT* promoter is involved in chilling response of *Paeonia suffruticosa*. *PLoS One* 11:e0155780
71. Zhang Y, Cheng Y, Xu S, Ma H, Han J, Zhang Y. 2020. Tree peony variegated flowers show a small insertion in the *F3'H* gene of the acyanic flower parts. *BMC Plant Biol.* 20:1-13
72. Zhang Y, Xu S, Cheng Y, Wang J, Wang X, et al. 2020. Functional identification of *PsMYB57* involved in anthocyanin regulation of tree peony. *BMC genetics* 21:1-11
73. Du H, Wu J, Ji K-X, Zeng Q-Y, Bhuiya M-W, et al. 2015. Methylation mediated by an anthocyanin, O-methyltransferase, is involved in purple flower coloration in *Paeonia*. *Journal of Experimental Botany* 66:6563-77
74. Zhang X, Xu Z, Yu X, Zhao L, Zhao M, et al. 2019. Identification of two novel *R2R3-MYB* transcription factors, *PsMYB114L* and *PsMYB12L*, related to anthocyanin biosynthesis in *Paeonia suffruticosa*. *International journal of molecular sciences* 20:1055
75. Zhou L, Wang Y, Ren L, Shi Q, Zheng B, et al. 2014. Overexpression of *Ps-CH11*, a homologue of the chalcone isomerase gene from tree peony (*Paeonia suffruticosa*), reduces the intensity of flower pigmentation in transgenic tobacco. *Plant Cell, Tissue and Organ Culture (PCTOC)* 116:285-95
76. Zhou L, Zhang C, Fu J, Liu M, Zhang Y, et al. 2013. Molecular characterization and expression of ethylene biosynthetic genes during cut flower development in tree peony (*Paeonia suffruticosa*) in response to ethylene and functional analysis of *PsACSI* in *Arabidopsis thaliana*. *Journal of plant growth regulation* 32:362-75
77. Wang S, Beruto M, Xue J, Zhu F, Liu C, et al. 2015. Molecular cloning and potential function prediction of homologous *SOC1* genes in tree peony. *Plant Cell Reports* 34:1459-71
78. Zhou H, Cheng F-Y, Wu J, He C. 2015. Isolation and functional analysis of *flowering locus T* in Tree Peonies (*PsFT*). *Journal of the American Society for Horticultural Science* 140:265-71

79. Mishra S, Phukan UJ, Tripathi V, Singh DK, Luqman S, Shukla RK. 2015. *PsAP2* an *AP2/ERF* family transcription factor from *Papaver somniferum* enhances abiotic and biotic stress tolerance in transgenic tobacco. *Plant molecular biology* 89:173-86
80. Gargul JM, Mibus H, Serek M. 2015. Manipulation of *MKS 1* gene expression affects *Kalanchoë blossfeldiana* and *Petunia hybrida* phenotypes. *Plant biotechnology journal* 13:51-61
81. Wigoda N, Ben - Nissan G, Granot D, Schwartz A, Weiss D. 2006. The gibberellin - induced, cysteine - rich protein *GIP2* from *Petunia hybrida* exhibits in planta antioxidant activity. *The Plant Journal* 48:796-805
82. Mori S, Kobayashi H, Hoshi Y, Kondo M, Nakano M. 2004. Heterologous expression of the flavonoid 3', 5'-hydroxylase gene of *Vinca major* alters flower color in transgenic *Petunia hybrida*. *Plant cell reports* 22:415-21
83. Schwinn KE, Boase MR, Bradley JM, Lewis DH, Deroles SC, et al. 2014. *MYB* and *bHLH* transcription factor transgenes increase anthocyanin pigmentation in *petunia* and *lisianthus* plants, and the *petunia* phenotypes are strongly enhanced under field conditions. *Frontiers in plant science* 5:603
84. Seitz C, Vitten M, Steinbach P, Hartl S, Hirsche J, et al. 2007. Redirection of anthocyanin synthesis in *Osteospermum hybrida* by a two-enzyme manipulation strategy. *Phytochemistry* 68:824-33
85. Huang L-C, Lai U-L, Yang S-F, Chu M-J, Kuo C-I, et al. 2007. Delayed flower senescence of *Petunia hybrida* plants transformed with antisense broccoli ACC synthase and ACC oxidase genes. *Postharvest biology and technology* 46:47-53
86. Oliva M, Ovadia R, Perl A, Bar E, Lewinsohn E, et al. 2015. Enhanced formation of aromatic amino acids increases fragrance without affecting flower longevity or pigmentation in *Petunia* × *hybrida*. *Plant Biotechnology Journal* 13:125-36
87. Spitzer-Rimon B, Farhi M, Albo B, Cna'ani A, Ben Zvi MM, et al. 2012. The *R2R3-MYB*-like regulatory factor *EOBI*, acting downstream of *EOBII*, regulates scent production by activating *ODOI* and structural scent-related genes in *petunia*. *The Plant Cell* 24:5089-105
88. Underwood BA, Tieman DM, Shibuya K, Dexter RJ, Loucas HM, et al. 2005. Ethylene-regulated floral volatile synthesis in *petunia* corollas. *Plant physiology* 138:255-66
89. Verdonk JC, Haring MA, Van Tunen AJ, Schuurink RC. 2005. *ODORANT1* regulates fragrance biosynthesis in *petunia* flowers. *The Plant Cell* 17:1612-24
90. Ben - Nissan G, Lee JY, Borohov A, Weiss D. 2004. *GIP*, a *Petunia hybrida* GA - induced cysteine - rich protein: a possible role in shoot elongation and transition to flowering. *The Plant Journal* 37:229-38
91. Gargul J, Mibus H, Serek M. 2013. Constitutive overexpression of *Nicotiana GA 2 ox* leads to compact phenotypes and delayed flowering in *Kalanchoë blossfeldiana* and *Petunia hybrida*. *Plant Cell, Tissue and Organ Culture (PCTOC)* 115:407-18
92. Ruokolainen S, Ng YP, Albert VA, Elomaa P, Teeri TH. 2011. Over-expression of the *Gerbera hybrida At-SOC1*-like1 gene *Gh-SOC1* leads to floral organ identity deterioration. *Annals of botany* 107:1491-9
93. Verdonk JC, Shibuya K, Loucas HM, Colquhoun TA, Underwood BA, Clark DG. 2008. Flower - specific expression of the *Agrobacterium tumefaciens* isopentenyltransferase gene results in radial expansion of floral organs in *Petunia hybrida*. *Plant Biotechnology Journal* 6:694-701
94. Peng P-H, Lin C-H, Tsai H-W, Lin T-Y. 2014. Cold response in *Phalaenopsis aphrodite* and characterization of *PaCBF1* and *PaICE1*. *Plant and Cell Physiology* 55:1623-35
95. Koh KW, Lee S-H, Chen H-K, Chang C-Y, Chan M-T. 2018. *Phalaenopsis flowering locus VE* regulates floral organ maturation. *Plant cell reports* 37:467-82
96. Pan ZJ, Chen YY, Du JS, Chen YY, Chung MC, et al. 2014. Flower development of *Phalaenopsis* orchid involves functionally divergent *SEPALLATA* - like genes. *New Phytologist* 202:1024-42
97. Chen Y-Y, Lee P-F, Hsiao Y-Y, Wu W-L, Pan Z-J, et al. 2012. C-and D-class MADS-box genes from *Phalaenopsis equestris* (Orchidaceae) display functions in gynostemium and ovule development. *Plant and Cell Physiology* 53:1053-67
98. Lai P-H, Huang L-M, Pan Z-J, Jane W-N, Chung M-C, et al. 2020. *PeERF1*, a *SHINE*-Like Transcription Factor, Is Involved in Nanoridge Development on Lip Epidermis of *Phalaenopsis* Flowers. *Frontiers in plant science* 10:1709
99. Lin Y-F, Chen Y-Y, Hsiao Y-Y, Shen C-Y, Hsu J-L, et al. 2016. Genome-wide identification and characterization of TCP genes involved in ovule development of *Phalaenopsis equestris*. *Journal of experimental botany* 67:5051-66
100. Bao F, Du D, An Y, Yang W, Wang J, et al. 2017. Overexpression of *Prunus mume* dehydrin genes in tobacco enhances tolerance to cold and drought. *Frontiers in plant science* 8:151
101. Peng T, Guo C, Yang J, Xu M, Zuo J, et al. 2016. Overexpression of a Mei (*Prunus mume*) *CBF* gene confers tolerance to freezing and oxidative stress in *Arabidopsis*. *Plant Cell, Tissue and Organ Culture (PCTOC)* 126:373-85
102. Sasaki R, Yamane H, Ooka T, Jotatsu H, Kitamura Y, et al. 2011. Functional and expressional analyses of *PmDAM* genes associated with endodormancy in Japanese apricot. *Plant physiology* 157:485-97
103. Zhang Q, Hao R, Xu Z, Yang W, Wang J, et al. 2017. Isolation and functional characterization of a *R2R3-MYB* regulator of *Prunus mume* anthocyanin biosynthetic pathway. *Plant Cell, Tissue and Organ Culture (PCTOC)* 131:417-29
104. Esumi T, Kitamura Y, Hagihara C, Yamane H, Tao R. 2010. Identification of a *TFL1* ortholog in Japanese apricot (*Prunus mume* Sieb. et Zucc.). *Scientia horticultrae* 125:608-16
105. Lu J, Yang W, Zhang Q. 2015. Genome-wide Identification and Characterization of the *DELLA* Subfamily in *Prunus mume*. *Journal of the American Society for Horticultural Science* 140:223-32
106. Wang Y, Pijut PM. 2013. Isolation and characterization of a *TERMINAL FLOWER 1* homolog from *Prunus serotina* Ehrh. *Tree physiology* 33:855-65
107. Xing W, Wang Z, Wang X, Bao M, Ning G. 2014. Over-expression of an *FT* homolog from *Prunus mume* reduces juvenile phase and induces early flowering in *rugosa rose*. *Scientia Horticulturae* 172:68-72
108. Wisniewski M, Norelli J, Bassett C, Artlip T, Macarasin D. 2011. Ectopic expression of a novel peach (*Prunus persica*) *CBF* transcription factor in apple (*Malus* × *domestica*) results in short-day induced dormancy and increased cold hardiness. *Planta* 233:971-83
109. Li M-j, Wei Q-p, Peng F-t, Yu W, Luo J-j, Zhao Y-f. 2019. Identification and characterization of *ATP/ADP* Isopentenyltransferases (*ATP/ADP PpIPTs*) genes in peach. *Journal of Plant Growth Regulation* 38:416-30
110. Hollender CA, Pascal T, Tabb A, Hadiarto T, Srinivasan C, et al. 2018. Loss of a highly conserved sterile alpha motif domain gene (*WEEP*) results in pendulous branch growth in peach trees. *Proceedings of the National Academy of Sciences* 115:E4690-E9
111. Chen Y, Jiang P, Thammannagowda S, Liang H, Wilde HD. 2013. Characterization of peach *TFL1* and comparison with *FT/TFL1* gene families of the Rosaceae. *Journal of the American Society for Horticultural Science* 138:12-7
112. Xu Y, Zhang L, Ma R. 2008. Functional characterization and mapping of two MADS box genes from peach (*Prunus persica*). *Chinese Science Bulletin* 53:853-9
113. Wang Z, Yang R, Devisetty UK, Maloof JN, Zuo Y, et al. 2017. The divergence of flowering time modulated by *FT/TFL1* is independent to their interaction and binding activities. *Frontiers in plant science* 8:697
114. Li C, Xie H, Zhang L, Xu Y, Li Y-F, Ma R-C. 2012. Molecular characterization of the *PpMADS1* gene from peach. *Tree genetics & genomes* 8:831-40
115. Xu Y, Zhang L, Xie H, Zhang Y-Q, Oliveira MM, Ma R-C. 2008. Expression analysis and genetic mapping of three *SEPALLATA*-like genes from peach (*Prunus persica* (L.) Batsch). *Tree Genetics & Genomes* 4:693-703

116. Patil HB, Chaurasia AK, Azeez A, Krishna B, Subramaniam V, et al. 2018. Characterization of two *TERMINAL FLOWER1* homologs *PgTFL1* and *PgCENa* from pomegranate (*Punica granatum* L.). *Tree physiology* 38:772-84
117. Chen J-R, Chen Y-B, Ziemiańska M, Liu R, Deng Z-N, et al. 2016. Co-expression of *MtDREB1C* and *RcXET* enhances stress tolerance of transgenic China rose (*Rosa chinensis* Jacq.). *Journal of Plant Growth Regulation* 35:586-99
118. Chen J-R, Lü J-J, Liu R, Xiong X-Y, Wang T-x, et al. 2010. *DREB1C* from *Medicago truncatula* enhances freezing tolerance in transgenic *M. truncatula* and China Rose (*Rosa chinensis* Jacq.). *Plant Growth Regulation* 60:199-211
119. Li J, Zheng G, Li S, Tang Z, Sun J, Xin X. 2020. Characterization of *Rosa chinensis* *CBF* Genes and the Function of *RcCBF6* in Cold Tolerance. *Journal of Plant Biology* 63:267-78
120. Li Z, Chen W, Zhang C, Du C, Shao G, et al. 2019. *RcMYBPA2* of *Rosa chinensis* functions in proanthocyanidin biosynthesis and enhances abiotic stress tolerance in transgenic tobacco. *Plant Cell, Tissue and Organ Culture (PCTOC)* 137:441-54
121. Xu J, Zhang B, Jiang C, Ming F. 2011. *RceIF5A*, encoding an eukaryotic translation initiation factor 5A in *Rosa chinensis*, can enhance thermotolerance, oxidative and osmotic stress resistance of *Arabidopsis thaliana*. *Plant molecular biology* 75:167-78
122. Zhang X, Lu S, Jiang C, Wang Y, Lv B, et al. 2014. *RcLEA*, a late embryogenesis abundant protein gene isolated from *Rosa chinensis*, confers tolerance to *Escherichia coli* and *Arabidopsis thaliana* and stabilizes enzyme activity under diverse stresses. *Plant molecular biology* 85:333-47
123. Han Y, Tang A, Wan H, Zhang T, Cheng T, et al. 2018. An *APETALA2* Homolog, *RcAP2*, regulates the number of rose petals derived from stamens and response to temperature fluctuations. *Frontiers in plant science* 9:481
124. Lian L, Wang F, Zhang Y, Fang R, Liu Q. 2016. Isolation, identification and expression patterns of *RoLEAFY* in non-recurrent and recurrent flowering roses. *Eur J Hortic Sci* 81:122-32
125. Luo P, Li Z, Chen W, Xing W, Yang J, Cui Y. 2020. Overexpression of *RmICE1*, a *bHLH* transcription factor from *Rosa multiflora*, enhances cold tolerance via modulating *ROS* levels and activating the expression of stress-responsive genes. *Environmental and Experimental Botany* 178:104160
126. Qiu X, Wang Q, Zhang H, Jian H, Zhou N, et al. 2015. Antisense *RhMLO1* gene transformation enhances resistance to the powdery mildew pathogen in *Rosa multiflora*. *Plant molecular biology reporter* 33:1659-65
127. Otagaki S, Ogawa Y, Hibrand - Saint Oyant L, Foucher F, Kawamura K, et al. 2015. Genotype of *FLOWERING LOCUS T* homologue contributes to flowering time differences in wild and cultivated roses. *Plant Biology* 17:808-15
128. Sheng L, Zang S, Wang J, Wei T, Xu Y, Feng L. 2021. Overexpression of a *Rosa rugosa* Thunb. *NUDX* gene enhances biosynthesis of scent volatiles in *petunia*. *PeerJ* 9:e11098
129. Sheng L, Zeng Y, Wei T, Zhu M, Fang X, et al. 2018. Cloning and functional verification of genes related to 2-phenylethanol biosynthesis in *Rosa rugosa*. *Genes* 9:576
130. Sui X, Zhao M, Han X, Zhao L, Xu Z. 2019. *RrGT1*, a key gene associated with anthocyanin biosynthesis, was isolated from *Rosa rugosa* and identified via overexpression and VIGS. *Plant Physiology and Biochemistry* 135:19-29
131. Kitahara K, Hibino Y, Aida R, Matsumoto S. 2004. Ectopic expression of the rose *AGAMOUS*-like MADS-box genes '*MASAKO C1* and *DI*' causes similar homeotic transformation of sepal and petal in *Arabidopsis* and sepal in *Torenia*. *Plant Science* 166:1245-52
132. Hibino Y, Kitahara K, Hirai S, Matsumoto S. 2006. Structural and functional analysis of rose class B MADS-box genes '*MASAKO BP*, *euB3*, and *B3*': Paleo-type *AP3* homologue '*MASAKO B3*' association with petal development. *Plant Science* 170:778-85