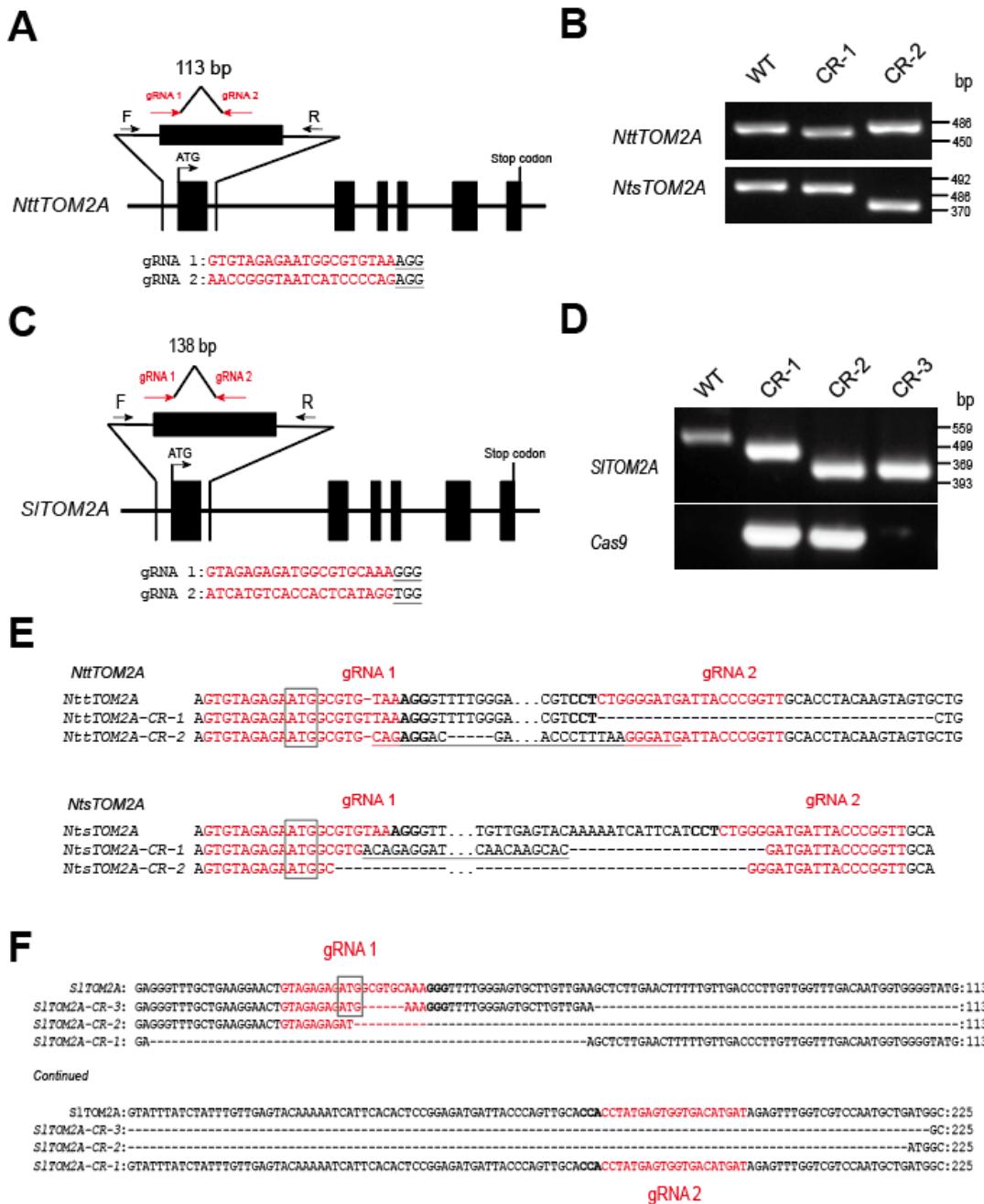
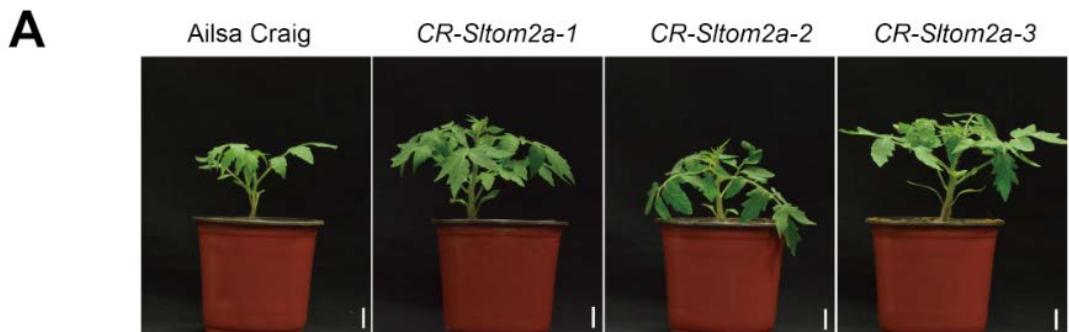


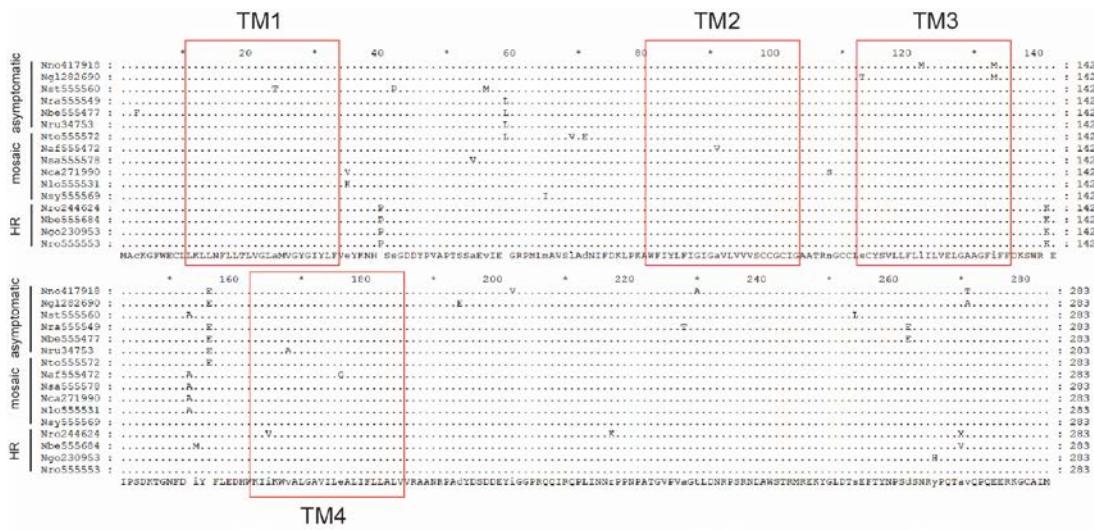
Supplemental Figure S1. Comparative sequence, expression and interaction analysis between TOM2A^{SR1} and TOM2A^{TI203}. (a) Amino acid sequence alignment of TOM2A from SR1 and TI203 mutant. Transmembrane domains are highlighted with green color. Conserved region are shaded with black color. (b) Relative expression analysis of TOM2A between SR1 and TI203. Gene expression was analyzed through RT-qPCR. *SlActin* gene was used as reference gene. The *TO2MA* transcript level in TI203 is significantly reduced when compared to that in SR1 (Student's t-test, $p < 0.01$). Three biological replicates were performed. The error bars represent mean \pm SD. (c) Protein interaction analysis of NtTOM1^{SR1} with TOM2A shortened proteins from TI203. Split-ubiquitin membrane-based yeast two-hybrid system was used for protein interaction analysis. TOM2A shortened proteins from TI203 failed to interact with NtsTOM1^{SR1}. pAT-Alg5, NtsTOM2A^{SR1} were used as positive control, pPR3-N was used as negative control.



Supplemental Figure S2. CRISPR/Cas9 engineering of TOM2A in tobacco (*Nicotiana tabacum*) and tomato (*Solanum lycopersicum*). Two gRNAs were developed in the first exon of each gene (a and c). The homozygosity at the TOM2A locus for each mutant was confirmed by PCR genotyping (b and d) and PCR products sequencing (e and f).

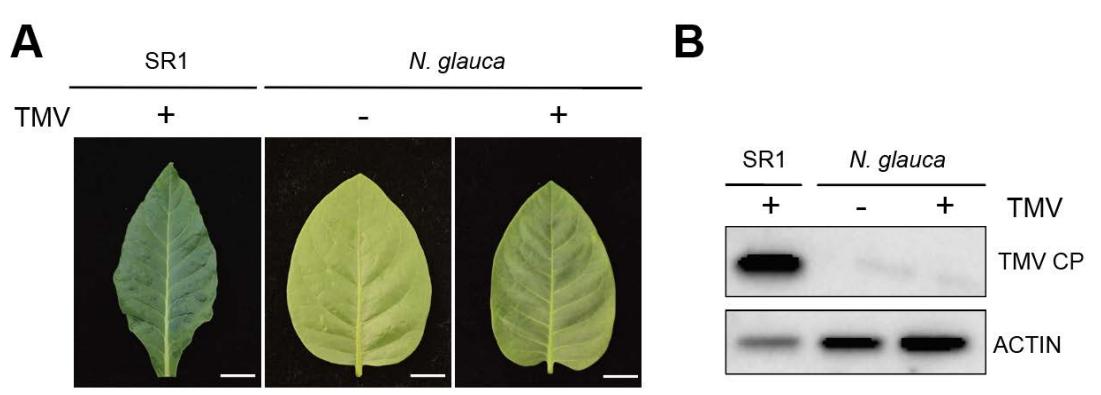


Supplemental Figure S3. Phenotype of *Sltom2a* CRISPR/Cas9 mutants. The *sltom2a* mutants show no obvious phenotype at early development stage (i.e., 30 days post sowing) compared with wild type (a) but show bent flower branch and main stem at flowering stage (b). The red arrow indicates the positions where bending was observed. Scale bar, 2 cm.

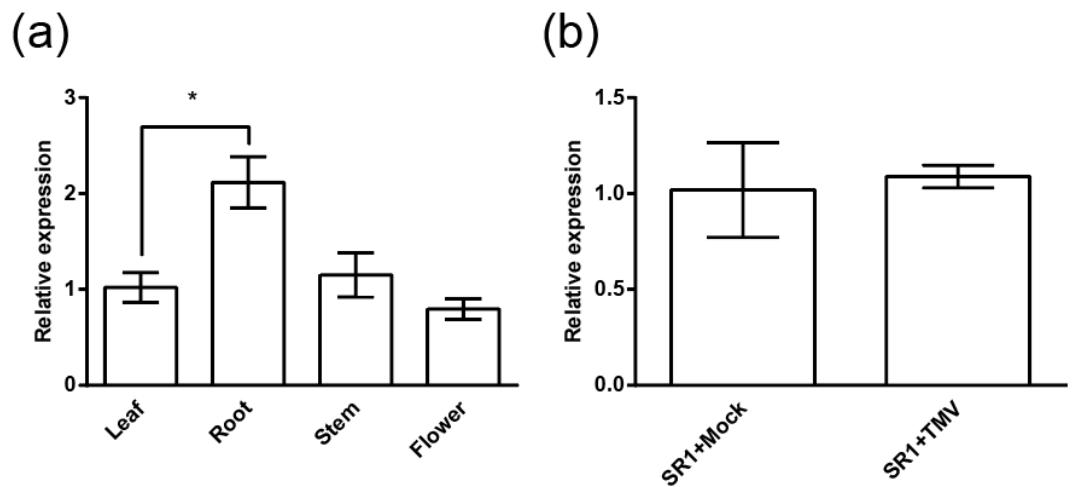


Supplemental Figure S4. Amino acid sequence alignment of *Nicotiana* TOM2As.

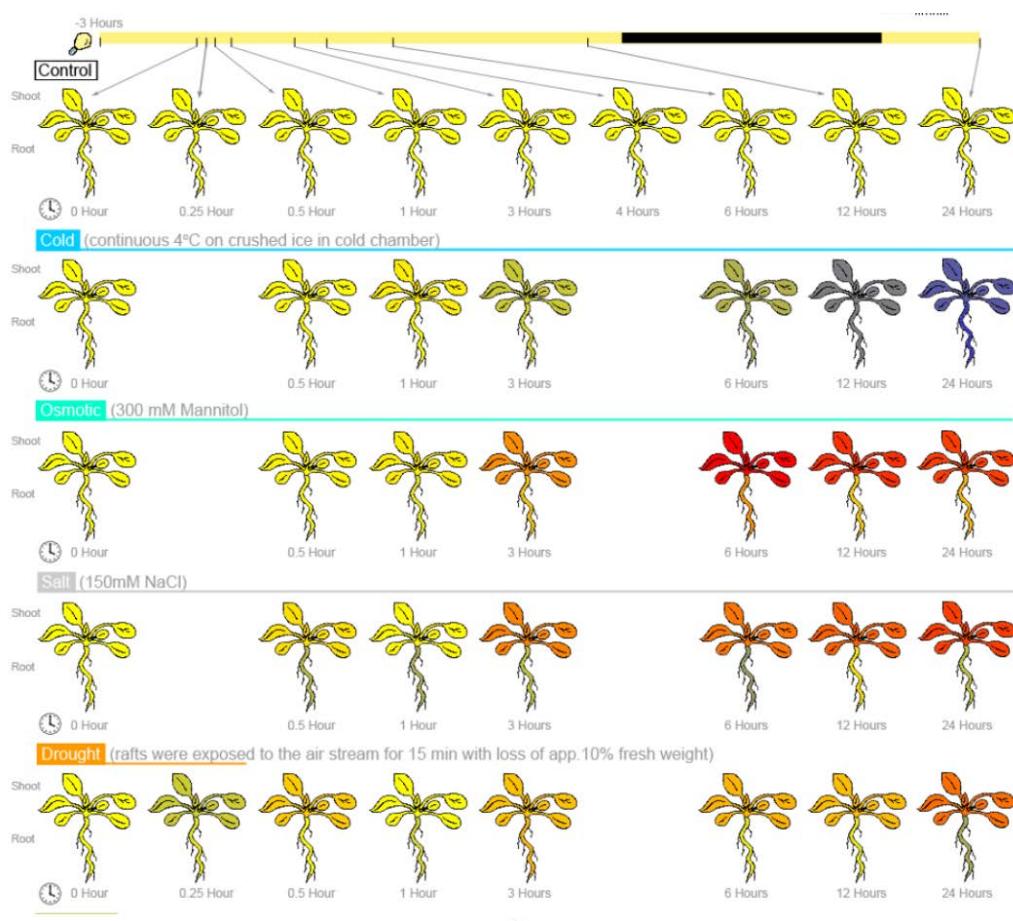
Amino acid residues that are the same among the TOM2A orthologs are shown as dots. The putative transmembrane domains are boxed in red.



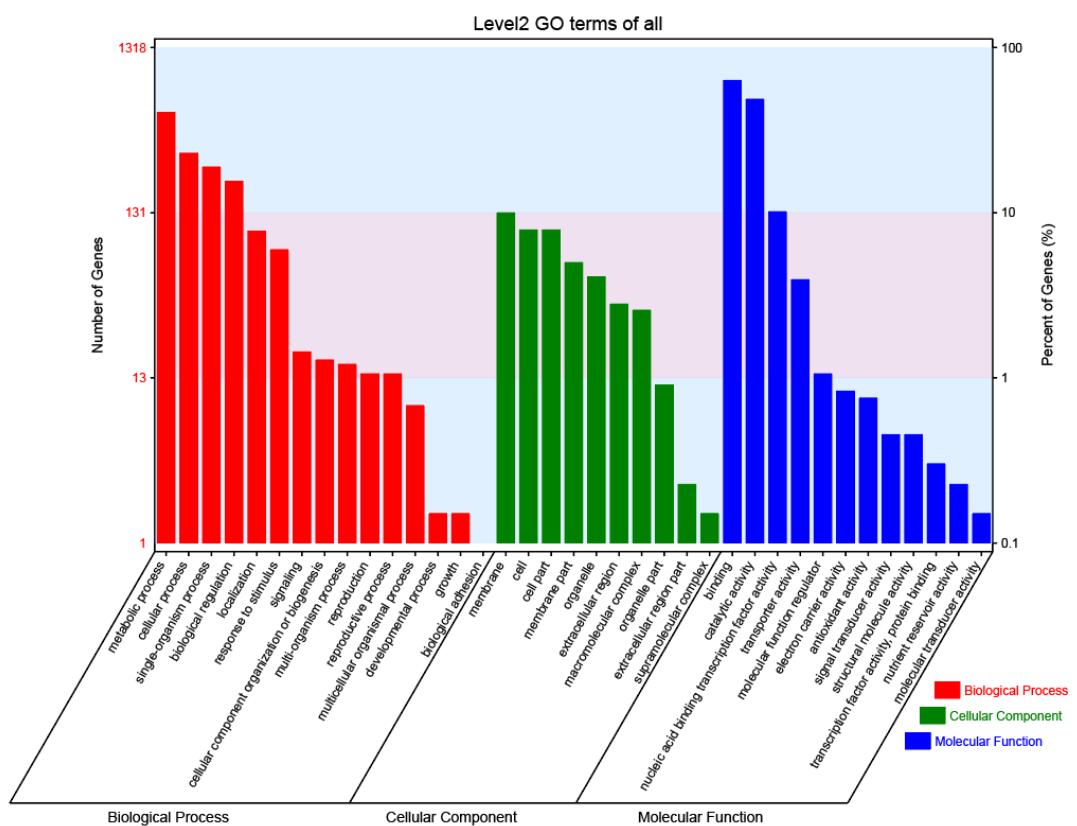
Supplemental Figure S5. Asymptomatic phenotype of *Nicotiana glauca* upon TMV inoculation. The upper systemic leaves from *N. glauca* show asymptomatic phenotype (a) and barely detectable TMV CP level (b) upon TMV inoculation. TMV CP level in the leaves were examined by western blot. ACTIN protein was used as loading control. Scale bar, 2 cm.



Supplemental Figure S6. Expression profile of *TOM2A* in tobacco. Relative expression level of *TOM2A* in leaf, root, stem, and flower (a) and after TMV inoculation (b) was quantified by RT-qPCR. Three biological replicates were performed. The error bars represent mean \pm SD. * means statistically significant at $p = 0.05$. Student's t-test was used to perform statistical test.



Supplemental Figure S7. Relative expression of *AtTOM2A*. These data were obtained using the Arabidopsis eFP browser (<http://www.bar.utoronto.ca>). Red indicates high levels of expression, orange indicates medium levels of expression, and yellow indicates undetectable levels of expression.



Supplemental Figure S8. GO term analysis of differentially expressed genes.

Supplemental Table S1. Genetic analysis of asymptomatic phenotype in F₂ and BC₁ population

Population	Number of individuals	Number of plants with mosaic phenotype	Number of plants with asymptomatic phenotype	Expected segregation ratio	Fitness test of expected segregation ratio	
					χ^2	p-value
F2	216	201	15	15:1	0.1778	0.6733
BC1	204	155	49	3:1	0.1049	0.7464

Supplemental Table S2. Genetic analysis of asymptomatic phenotype in BC₂ population

Population	Number of individuals	Number of plants with mosaic phenotype		Expected segregation ratio	Fitness test of expected segregation ratio		Predicted genotype of maternal plants
		plants with mosaic phenotype	plants with asymptomatic phenotype		χ^2	p-value	
BC2-01	162	85	77	1:1	0.40	0.5297	Aabb or aaBb
BC2-02	185	139	46	3:1	0	0.9661	AaBb
BC2-03	225	169	56	3:1	0	0.9693	AaBb
BC2-04	216	162	54	3:1	0	1.0000	AaBb
BC2-05	52	28	24	1:1	0.3077	0.5791	Aabb or aaBb
BC2-06	81	41	40	1:1	0.0123	0.9115	Aabb or aaBb

Supplemental Table S3. SNP allele frequency between the two RNA-sequencing bulks

SNP name	Allele in Ti203	Allele in SR1	Allele frequency in asymptomatic pool	Allele frequency in mosaic pool	ΔSNP
SNP1	C	T	1	0.7064	0.2936
SNP2	T	A	0.9944	0.4931	0.5013
SNP3	G	A	1	0.7500	0.2500
SNP4	A	T	1	0.7500	0.2500
SNP5	T	A	1	0.6400	0.3600
SNP6	C	T	1	0.5371	0.4629
SNP7	C	T	1	0.6818	0.3182

Supplemental Table S4. Genetic markers used for genetic mapping

Marker Name	Primer name	Forward primer (5'->3')	Comment
Genetic markers used for mapping <i>NttTOM2A</i>			
M1	M1-F1	ACTATGGTGGTGAACGCATG	CAPS, <i>BsuRI</i>
	M1-R1	AGAGTTGAAGAACAGTTGCACA	
M2	M2-F1	GCCTCCACTCTCATCTCAAGA	CAPS, <i>BsuRI</i>
	M2-R1	GGAACCTTAGCTCCTGAAACAC	
M3	M3-F1	CCAACCAAATCAATGTCTCTGGG	Dominant PCR marker
	M3-R1	CTGCGGAGTATTGTCTTGGAAAT	
M4	M4-F1	ACTGCTCTATCGCTGCTTGT	CAPS, <i>BsuRI</i>
	M4-R1	ATTATCTCCTATGGCGCGGG	
M5	M5-F1	GACATGTGGAGACCCCCAAAG	SNP marker
	M5-R1	TGTCGTATGTTACATAGCGTTGG	
M6	M6-F1	CGGACCTCCAAATCCACTTCTG	CAPS, <i>BsuRI</i>
	M6-R1	CCAAACCACCCCCAAAATTACACC	
M7	M7-F1	GAACCCCTGTGTGAACGTGG	SNP marker
	M7-R1	ATCCTAGCAGCAGCAGAGG	
M8	M8-F1	AGTCGCTACTCTCGAGGAGGC	CAPS, <i>BsuRI</i>
	M8-R1	CCCTTCACCACATACCAGCGG	
M9	M9-F1	GATCGGTTAACCTGTTCATGA	CAPS, <i>BsuRI</i>
	M9-R1	TGTT CCTATTCAATAAGTTGCGC	
M248	M248-F1	GTGATATGAGAAGTGGCACCTG	CAPS, <i>BsuRI</i>
	M248-R1	GCGGGTTACTTGACCGTTAG	
M254	M254-F1	GCCACTGGTTGATATCTGCTTC	CAPS, <i>Eco32I</i>
	M254-R1	AGGGTATACGTGGATGGTGTAC	
M265	M265-F1	AAGGTTGGATTGAATTCAAGG	CAPS, <i>BsuRI</i>
	M265-R1	CTCTAAAAGGCTGCATCATAACAC	
M350	M350-F1	CACCTTAACTATGACAGTACTCTGTG	Dominant PCR marker
	M350-R1	GGGAGATAGAGACATTATTGAGATTGG	
M421	M421-F1	TGCGCTTCTTTTTAGCAAGACT	SNP marker
	M421-R1	CGCTCGAGACGCTCTGATAA	
M424	M424-F1	GATGGGTATATTGGCCCTTCC	SNP marker
	M424-R1	CTTTGCTCATGTTCTCCGC	
Genetic Markers used for mapping <i>NtsTOM2A</i>			
M315	M315-F1	CTTGAACAAGTGCTACAAGCTTAT	CAPS, <i>BamHI</i>
	M315-R1	GATTAGCGCCAGTTAAACAAGG	
M373	M373-F1	GTTGAGTTGTACTTAGACTTTCGC	CAPS, <i>BsuRI</i>
	M373-R1	TGCTAGTACAAGTTGGGCATG	
M391	M391-F1	CACTCACTTAGATTTCGCC	CAPS, <i>BsuRI</i>
	M391-R1	GTGAAAGAAGTCCTGATAGCAAG	

M360	M360-F1	TTGTTTGTGGTGGGCCTC	CAPS, <i>Bsu</i> RI
	M360-R1	AACGTACACAAATACTCGGTATG	

Supplemental Table S5. Annotation of fifteen genes in the tomato mapping interval

No	Gene Locus	Chromosome	Start	Stop	Putative function
1	Solyc08g077090.2.1	SL2.40ch08	58184359	58189670	Eyes absent homolog 3
2	Solyc08g077100.2.1	SL2.40ch08	58192225	58194025	Baculoviral IAP repeat-containing protein 3
3	Solyc08g077110.2.1	SL2.40ch08	58200673	58202853	NAC domain protein
4	Solyc08g077120.2.1	SL2.40ch08	58211490	58212632	Pentatricopeptide repeat-containing protein
5	Solyc08g077130.2.1	SL2.40ch08	58212515	58213244	Unknown Protein
6	Solyc08g077140.1.1	SL2.40ch08	58212909	58213721	Pentatricopeptide repeat-containing protein
7	Solyc08g077150.2.1	SL2.40ch08	58214125	58220440	Protein phosphatase 2C containing protein
8	Solyc08g077160.1.1	SL2.40ch08	58232675	58233880	NAD(P)H-quinone oxidoreductase subunit 2 chloroplastic
10	Solyc08g077180.2.1	SL2.40ch08	58254085	58261125	Pyruvate kinase
11	Solyc08g077190.1.1	SL2.40ch08	58262559	58262858	Unknown Protein
12	Solyc08g077200.2.1	SL2.40ch08	58267856	58273524	Ribose-phosphate pyrophosphokinase
13	Solyc08g077210.2.1	SL2.40ch08	58274579	58279571	Inositol 1 4 5-trisphosphate 5-phosphatase
14	Solyc08g077220.2.1	SL2.40ch08	58295865	58302381	Tetraspanin family protein
15	Solyc08g077230.2.1	SL2.40ch08	58307194	58313022	Two-component response regulator ARR11

Supplemental Table S6. Genome-wide identification of *TOM2A* homologs in plants

Plant Species ¹	Family ²	Number of TOM2A homologs ³	Genome source ⁴	Reference ⁵
Eudicots				
<i>Glycine Max</i> ⁶	Fabaceae	8	PhytozomeV13	(Schmutz et al., 2010)
<i>Cucumis sativus</i> ⁶	Cucurbitaceae	3	PhytozomeV13	(Huang et al., 2009)
<i>Citrullus lanatus</i> ⁶	Cucurbitaceae	2	http://cucurbitgenomics.org/organism/1	(Guo et al., 2013)
<i>Malus domestica</i>	Rosaceae	9	PhytozomeV13	(Velasco et al., 2010)
<i>Populus trichocarpa</i> ⁶	Salicaceae	9	PhytozomeV13	(Tuskan et al., 2006)
<i>Arabidopsis thaliana</i> ⁶	Brassicaceae	4	PhytozomeV13	(Arabidopsis Genome, 2000)
<i>Citrus sinensis</i> ⁶	Rutaceae	8	PhytozomeV13	(Xu et al., 2013)
<i>Vitis vinifera</i>	Vitaceae	5	PhytozomeV13	(Canaguier et al., 2017)
<i>Nicotiana tabacum</i>	Solanaceae	8	www.solgenomics.net	(Edwards et al., 2017)
<i>Petunia axillaris</i>	Solanaceae	4	www.solgenomics.net	(Bombarely et al., 2016)
<i>Capsicum annuum</i>	Solanaceae	4	www.solgenomics.net	(Qin et al., 2014)
<i>Solanum melongena</i>	Solanaceae	3	www.solgenomics.net	(Hirakawa et al., 2014)
<i>Solanum lycopersicum</i> ⁶	Solanaceae	4	www.solgenomics.net	(Tomato Genome, 2012)
<i>Solanum tuberosum</i>	Solanaceae	4	www.solgenomics.net	(Potato Genome Sequencing et al., 2011)
<i>Coffea canephora</i>	Rubiaceae	4	http://www.coffee-genome.org/sites/coffee-genome.org/files/download/	(Denoeud et al., 2014)
<i>Lactuca sativa</i> ⁶	Compositae	5	https://lgr.genomecenter.ucdavis.edu/	(Reyes-Chin-Wo et al., 2017)

<i>Fragaria vesca</i> ⁶	Rosaceae	4	PhytozomeV13	(Shulaev et al., 2011)
Basal eudicots				
<i>Aquilegia coerulea</i>	Helleboraceae	2	PhytozomeV13	(Filiault et al., 2018)
Monocots				
<i>Zostera marina</i>	Zosteraceae	8	PhytozomeV13	(Olsen et al., 2016)
<i>Musa acuminata</i>	Musaceae	12	PhytozomeV13	(D'Hont et al., 2012)
<i>Brachypodium distachyon</i>	Seawrack	4	PhytozomeV13	(International Brachypodium, 2010)
<i>Zea mays</i> ⁶	Poaceae	6	PhytozomeV13	(Schnable et al., 2009)
<i>Oryza sativa</i> ⁶	Poaceae	4	PhytozomeV13	(Yu et al., 2002)
<i>Setaria italica</i>	Poaceae	4	PhytozomeV13	(Bennetzen et al., 2012)
<i>Sorghum bicolor</i>	Poaceae	4	PhytozomeV13	(Paterson et al., 2009)
Basal angiosperms				
<i>Amborella trichopoda</i> ⁶	Amborellaceae	4	PhytozomeV13	(Amborella Genome, 2013)
Gymnosperms				
<i>Picea abies</i> ⁶	Pinaceae	4	ftp://ftp.psb.ugent.be/pub/plaza/plaza_public_monocots_04/Fasta/	(Nystedt et al., 2013)
Lycopodiophyta				
<i>Selaginella moellendorffii</i> ⁶	Selaginellaceae	2	PhytozomeV13	(Banks et al., 2011)
Pteridophyta				
<i>Marchantia polymorpha</i>	Marchantiaceae	1	PhytozomeV13	(Bowman et al., 2017)
Bryophyta				
<i>Physcomitrium patens</i> ⁶	Funariaceae	5	PhytozomeV13	(Rensing et al., 2008)
<i>Sphagnum fallax</i>	Sphagnaceae	4	PhytozomeV13	Sphagnum fallax v0.5, DOE-JGI,

				http://phytozome.jgi.doe.gov/
Charophyte				
<i>Chara braunii</i> strain	NA ⁷	4	https://bioinformatics.psb.ugent.be/gdb/Chara_braunii/	(Nishiyama et al., 2018)
<i>Klebsormidium flaccidum</i>	NA ⁷	1	http://alga-pras.riken.jp/	(Hori et al., 2014)
<i>Klebsormidium nitens</i>	NA ⁷	1	ftp://ftp.uniprot.org/pub/databases/uniprot/current_release/knowledgebase/reference_proteomes/Eukaryota/	(Hori et al., 2014)
Chlorophyte				
<i>Ostreococcus tauri</i>	NA ⁷	1	https://genome.jgi.doe.gov/portal/pages/dynamicOrganismDownload.jsf?organism=Ostta4221_3	(Derelle et al., 2006)
<i>Coccomyxa subellipsoidea</i> ⁶	NA ⁷	1	https://genome.jgi.doe.gov/portal/Coc_C169_1/Coc_C169_1.download.ftp.html	(Blanc et al., 2012)
<i>Ostreococcus lucimarinus</i>	NA ⁷	1	Phytozome v13	(Palenik et al., 2007)
<i>Chlorella variabilis</i>	NA ⁷	1	https://genome.jgi.doe.gov/portal/ChlNC64A_1/download/	(Blanc et al., 2010)
<i>Bathycoccus prasinos</i>	NA ⁷	1	https://genome.jgi.doe.gov/ or Alga-PrAS	(Moreau et al., 2012)
<i>Volvox carteri</i>	NA ⁷	1	https://genome.jgi.doe.gov/portal/pages/dynamicOrganismDownload.jsf?organism=Phytozome#	(Prochnik et al., 2010)
<i>Monoraphidium neglectum</i>	NA ⁷	0	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCF/000/611/	(Bogen et al., 2013)
<i>Botryococcus braunii</i>	NA ⁷	0	Phytozome v13	(Browne et al., 2017)
<i>Chlamydomonas reihardtii</i>	NA ⁷	0	https://genome.jgi.doe.gov/portal/pages/dynamicOrganismDownload.jsf?organism=Phytozome#	(Merchant et al., 2007)
<i>Micromonas pusilla</i>	NA ⁷	0	Phytozome v13	(Worden et al., 2009)
<i>Micromonas sp. RCC299</i>	NA ⁷	0	Phytozome v13	(Worden et al., 2009)

<i>Dunaliella salina</i>	NA ⁷	0	Phytozome v13	(Polle et al., 2017)
<i>Chlorella protothecoides</i>	NA ⁷	0	ftp://ftp.ncbi.nlm.nih.gov/genomes/all/GCF/000/733/215/GCF_000733215.1_ASM73321v1/	(Gao et al., 2014)
Rhodophyta				
<i>Chondrus crispus</i>	NA ⁷	0		(Collen et al., 2013)
<i>Cyanidioschyzon merolae</i>	NA ⁷	0	http://merolae.biol.s.u-tokyo.ac.jp/download/cds.fasta	(Matsuzaki et al., 2004)
<i>Galdieria sulphuraria</i>	NA ⁷	0	ftp://ftp.ensemblgenomes.org/pub/plants/release-49/fasta/galdieria_sulphuraria/	(Schonknecht et al., 2013)
<i>porphyridium purpureum</i>	NA ⁷	0	http://cyanophora.rutgers.edu/porphyridium/	(Bhattacharya et al., 2013)
<i>Porphyra umbilicalis</i>	NA ⁷	0	Phytozome v13	(Brawley et al., 2017)
<i>Pyropia yezoensis</i>	NA ⁷	0	http://nrifs.fra.affrc.go.jp/cgi-bin/lime_download/lime.cgi?nori_FASTA_AminoAcid	(Wang et al., 2020)
Glaucophyte				
<i>Cyanophora paradoxa</i>	NA ⁷	0	http://cyanophora.rutgers.edu/cyanophora_v2018/	(Price et al., 2012)

¹ Species: binomial name of the species

² Family: family name to which corresponding species belongs

³ Number of TOM2A homologs: number of TOM2A homologs in this species by BLASTP analysis

⁴ Genome source: version of genome used for analysis in this study

⁵ References: original reference of the genome publication

⁶ TOM2A orthologs from these species were used for complementation test.

NA⁷: information for this part is not available

Supplemental Table S7. Primers used in this study

Primer Name	Primer sequence (5'-3')	Purpose
HQP541	GGCCTCTCCTGTACTAGCTCGG	Making NttTOM2A complementation construct
HQP542	ATGTTATCAAACCGCCAAGTCAA	Making NttTOM2A complementation construct
HQP543	GTGTCTGCCTGTGGAAGTGATATGT	Making NttTOM2A complementation construct
HQP544	GGTTTTCTGTACTAAAATAATGTTGGTTCT	Making NttTOM2A complementation construct
HQP545	CCAGGGCGCCCTCCTGCAGGATTGGCGGCCACCTGAACCTAACACTT	Making NttTOM2A complementation construct
HQP546	CGACCCGACGCCAGCAACGGTCATCACTTAAGTTATGT	Making NttTOM2A complementation construct
HQP547	CCTCCTGCAGGCCAGAAACATCTCAAATATTACTTGGAG	Making NttTOM2A complementation construct
HQP548	GGTGGCGGCCAATATATTATGCCATAA	Making NttTOM2A complementation construct
HQP549	TCGGTCCATAACTTCCCCGAA	Making NtsTOM2A complementation construct
HQP550	TGATTAGCAATAAAAGGAAGAAATGGTCT	Making NtsTOM2A complementation construct
HQP551	AATTGAGTGTCCCTAGGAGTAGAAGG	Making NtsTOM2A complementation construct
HQP552	CCAAAGTGTAGCTCCTCTCAACAA	Making NtsTOM2A complementation construct
HQP553	CCAGGGCGCCCTCCTGCAGGATAGGCGGCCCTTCGTCATAATATGG	Making NtsTOM2A complementation construct
HQP554	CGACCCGACGCCACCACATATGTCGATTTGACAATG	Making NtsTOM2A complementation construct
HQP555	CCTCCTGCAGGGCAAGTCTGTCAGCGCG	Making NtsTOM2A complementation construct
HQP556	AAAGGCGGCCATGTTATAATT	Making NtsTOM2A complementation construct
HQP713	CATTGGAGAGGACACGCTCGAGATGGCGTGTAAAGGGTTGGG	Making <i>NttTOM2A</i> -overexpression construct
HQP714	TCTCATTAAAGCAGGACTCTAGACAATCATGAGTCCTCCATAAGCCC	
HQP715	CATTGGAGAGGACACGCTCGAGATGGCGTGTAAAGGGTTCTGG	Making NtsTOM2A-overexpression construct
HQP716	TCTCATTAAAGCAGGACTCTAGACAATCACGAGTCCTCCATAAATTACAG	

HQP728	TCTCATTAAAGCAGGACTCTAGACCATCATTACATTATGGCACAAACCC	Making NglTOM2A-overexpression construct (together with HQP715)
HQP1019	CATTGGAGAGGACACGCTCGAGATGAGAACATCCGAAGTTTAGAGC	Making CsuTOM2A-overexpression construct
HQP1020	TCTCATTAAAGCAGGACTCTAGATCACATGACGGCACACCG	
HQP1013	CATTGGAGAGGACACGCTCGAGATGTCCTGCCAGGGATTCATC	
HQP1014	TCTCATTAAAGCAGGACTCTAGACTACATTATGATGCAACGACTCTGC	Making PpaTOM2A-overexpression construct
HQP1011	CATTGGAGAGGACACGCTCGAGATGGGCGCGTGTGCCAG	
HQP1012	TCTCATTAAAGCAGGACTCTAGATTACATGATCACACATCCTCTTCG	Making SmoTOM2A-overexpression construct
HQP1023	CATTGGAGAGGACACGCTCGAGATGGCTGCCGTTGGTTTG	
HQP1024	TCTCATTAAAGCAGGACTCTAGATTACATAATAGTCACCGACTCTTCT	Making PabTOM2A-overexpression construct
HQP1009	CATTGGAGAGGACACGCTCGAGATGGCTGCAAAGGCTTCTT	
HQP1010	TCTCATTAAAGCAGGACTCTAGATCACATGATGGTCACCTG	Making AtrTOM2A-overexpression construct
HQP721	CATTGGAGAGGACACGCTCGAGATCGTATGGCGTGCCG	
HQP722	TCTCATTAAAGCAGGACTCTAGATCACAGTATAACACAGCGGTTCC	Making OsaTOM2A-overexpression construct
HQP725	CATTGGAGAGGACACGCTCGAGGGAGGGAGGGCGGAGAT	
HQP726	TCTCATTAAAGCAGGACTCTAGAGGACGTCATGAAGAATTCTTCACA	Making ZmaTOM2A-overexpression construct
HQP723	CATTGGAGAGGACACGCTCGAGATGGCTGTAAAGGGTTTAGAGT	
HQP724	TCTCATTAAAGCAGGACTCTAGATCACATGATGATGCAACACC	Making LsaTOM2A-overexpression construct
HQP1066	CATTGGAGAGGACACGCTCGAGATGGCGTGCAAAGGGTTT	
HQP1065	TCTCATTAAAGCAGGACTCTAGACAGAACGACCATATCATCACATTATGG	Making SlyTOM2A-overexpression construct
HQP1017	CATTGGAGAGGACACGCTCGAGATGGCGTGTAAGGGATGCTTG	
HQP1018	TCTCATTAAAGCAGGACTCTAGATCACATGATGGTCACGAC	Making PtrTOM2A-overexpression construct
HQP731	CATTGGAGAGGACACGCTCGAGATGGCCTGTAGAGGGTGC	
HQP732	TCTCATTAAAGCAGGACTCTAGATCATTACATGATGGTCAGCG	Making CsiTOM2A-overexpression construct

HQP719	CATTGGAGAGGACACGCTCGAGATGGCTTAGAGGTTGTTGG	Making AthTOM2A-overexpression construct
HQP720	TCTCATTAAAGCAGGACTCTAGAGACTCACATGATGGTCATCG	
HQP737	CATTGGAGAGGACACGCTCGAGATGCCCTGCAGAGGGTG	Making FveTOM2A-overexpression construct
HQP738	TCTCATTAAAGCAGGACTCTAGATCACATGATGCTGCAGCG	
HQP757	CATTGGAGAGGACACGCTCGAGATGCCCTGCAGAGGGTG	Making CsaTOM2A-overexpression construct
HQP758	TCTCATTAAAGCAGGACTCTAGATATCACATGATTGTGCAGCG	
HQP717	CATTGGAGAGGACACGCTCGAGATGCCCTGCAGAGGGTG	Making ClaTOM2A-overexpression construct
HQP718	TCTCATTAAAGCAGGACTCTAGATTATCACATGATGGTCAGCG	
HQP735	CATTGGAGAGGACACGCTCGAGATGGCATGTAGGGGGTGCT	Making GmaTOM2A-overexpression construct
HQP736	TCTCATTAAAGCAGGACTCTAGACATGGAGTGATGCAGTACAGCAA	
QUNP064	GAATCTAACAGTGTAGTTGGTAGAGAGATGGCGTGCAAAGTTTAGAGCTAGAAATAG	Making CRISPR/Cas9 plasmid for SITOM2A
QUNP065	GCTATTCTAGCTCTAAACCCTATGAGTGGTGACATGATCAAACACTACACTGTTAGATT	Making CRISPR/Cas9 plasmid for SITOM2A
QUNP068	ATATATGGTCTCGATTGGTAGAGAGATGGCGTGTAAAGTT	Making CRISPR/Cas9 plasmid for NttTOM2A/NtsTOM2A
QUNP069	TGGTGTAGAGAATGGCGTGTAAAGTTAGAGCTAGAAATAGC	Making CRISPR/Cas9 plasmid for NttTOM2A/NtsTOM2A
QUNP070	AACCTGGGATGATTACCCGGTTCAATCTCTTAGTCGACTCTAC	Making CRISPR/Cas9 plasmid for NttTOM2A/NtsTOM2A
QUNP071	ATTATTGGTCTCGAAAC CTGGGGATGATTACCCGGTTCAA	Making CRISPR/Cas9 plasmid for NttTOM2A/NtsTOM2A
HQP1057	GGATTATGCACATATTGGATTGTG	Genotyping CR-SITOM2A mutants
QUNP156	AGAGCAAATACAGTCAGCAATACAAC	Genotyping CR-SITOM2A mutants

HQP1034	TGTGTCTTGGATAATTCTGAAGTATTG	Genotyping CR-NttTOM2A/NtsTOM2A mutants
HQP1035	GCAAATACAGCTTCCAGTATCACA	Genotyping CR-NttTOM2A mutants
HQP1036	AGCAAATACAGCTTCCAGTAGAAGTAA	Genotyping CR-NtsTOM2A mutants
HQP947	CCACACAGGTGTGATGGTTG	Tobacco actin primer for qRT-PCR
HQP948	GTGGCTAACACCATCACCAAG	Tobacco actin primer for qRT-PCR
HQP910	GGTGCTGCTGGTTTATATTCTTG	Tobacco NttTOM2A/NtsTOM2A primers for qRT-PCR
HQP911	TGATAATCTTCCAGTGGCCTCC	Tobacco NttTOM2A/NtsTOM2A primers for qRT-PCR
HQP741	ATGAAAAAGCCTGAACTCACCG	Hygromycin gene primers for selecting positive transgenic plants
HQP742	CTATTCCTTGCCCTCGGACG	Hygromycin gene primers for selecting positive transgenic plants
HQP743	ATGGCAATTACCTTATCCGCAAC	Kanamycin gene primers for selecting positive transgenic plants
HQP744	CAGAAGAACTCGTCAAGAAGGC	Kanamycin gene primers for selecting positive transgenic plants
CZFP166	GAACAGCGACAAGCTCATCG	Check for the presence of Cas9 gene in the CRISPR mutants
CZFP167	GAGCTGAGACAGGTCGATGC	Check for the presence of Cas9 gene in the CRISPR mutants

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