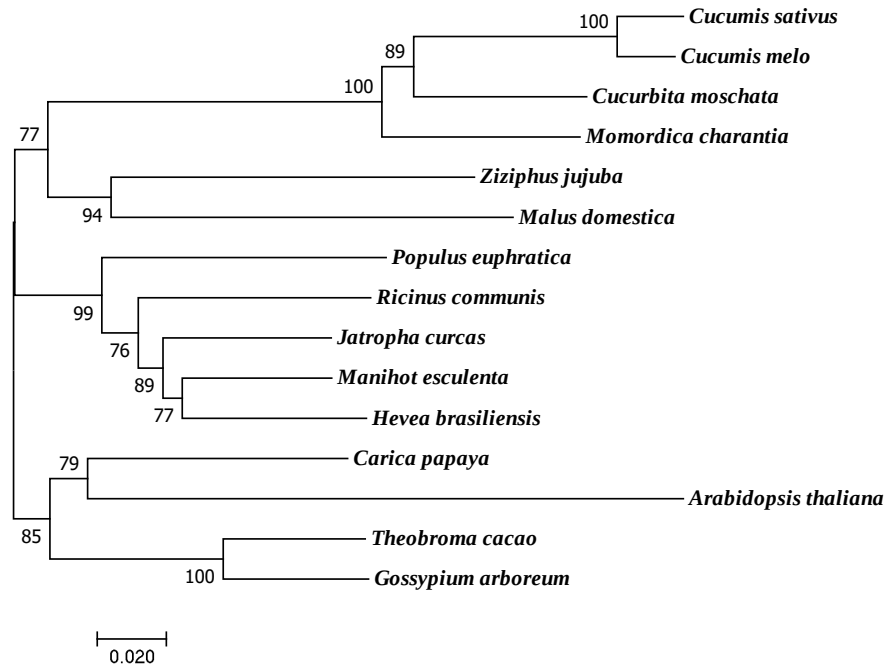


Supplementary Material

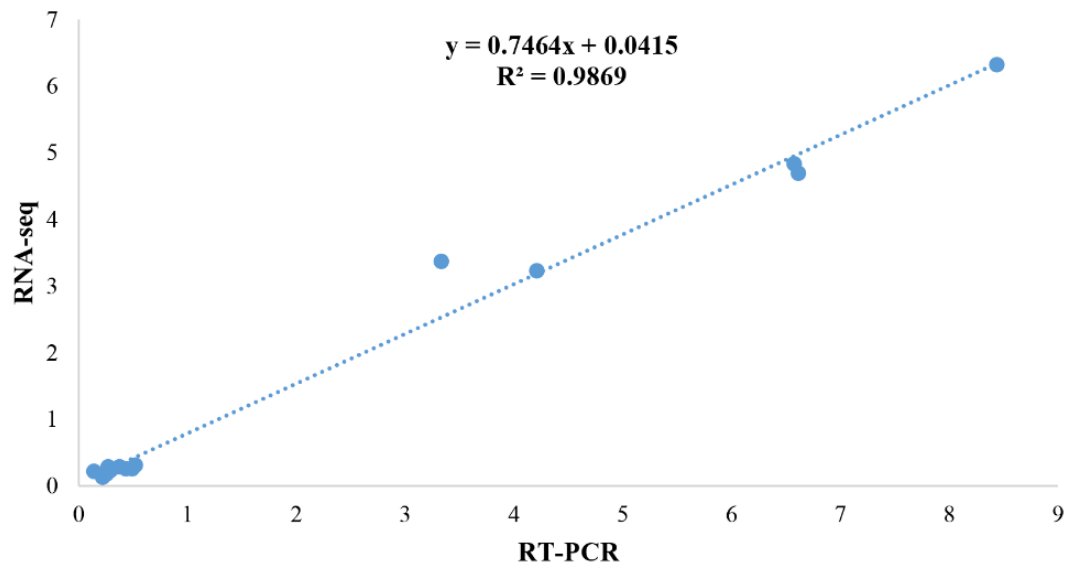
1 Supplementary Figures

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LFCCEGFGTSGIAVVAARCRHLRVLDLIASDVGDDEVDWISCFPEKETCLES LIFECVEWPI
NFEALERLVS RSPSLKKLG VNRHVSIAQLYQLMIRAPRLTHLGTGSFNTLEAVIHGESEPDY
ASVFAACNSLVCLSGFKDVL PDYLPCIYPVCANLTTLNLSYANITPEQLKPAIRHCHKLQTF
WALDSICDEGLQAVASTCKELREL RVFPFDARE DVEGPIS EVGFQAI SEGCRKLQYILYFCQ
RMTNAAVVAMSQNCQDLVVFR L CIMGRHQPDHKTGDP MDEGF GAIVINCKKLTRLAISG
LLTDRAFSYIGKYGKLVRTL S VAFAGNSDLGLKYVLEGCHRLQKLEIRDSPFGDIALHSGL
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LLYMYRSLEGPRDDAPEFRGSDEGSGC(R/K)AALKALITSESLVIHRIKIELE NVGDLIN YK
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ALNEKLRLCFLV*

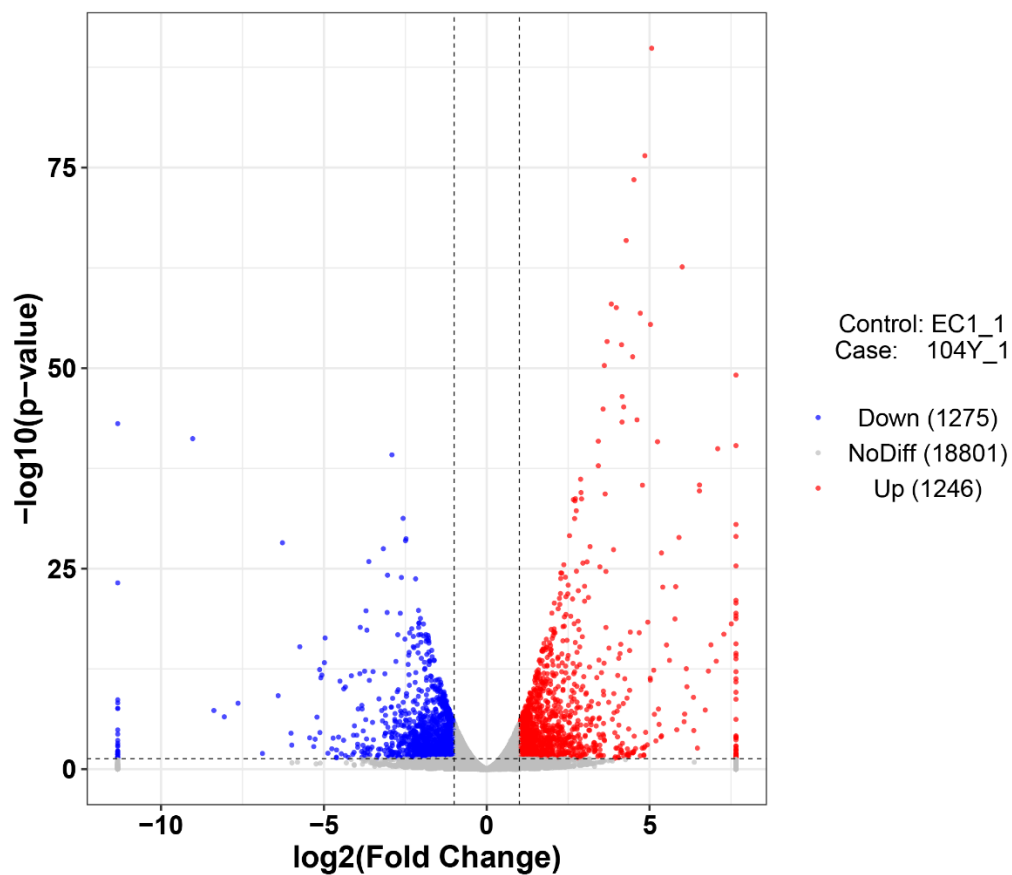
Supplementary Figure 1. The 632th amino acid substitution in the *Csa3G890020* protein. R is the arginine (the normal amino acid), K is lysine (the mutant amino acid).



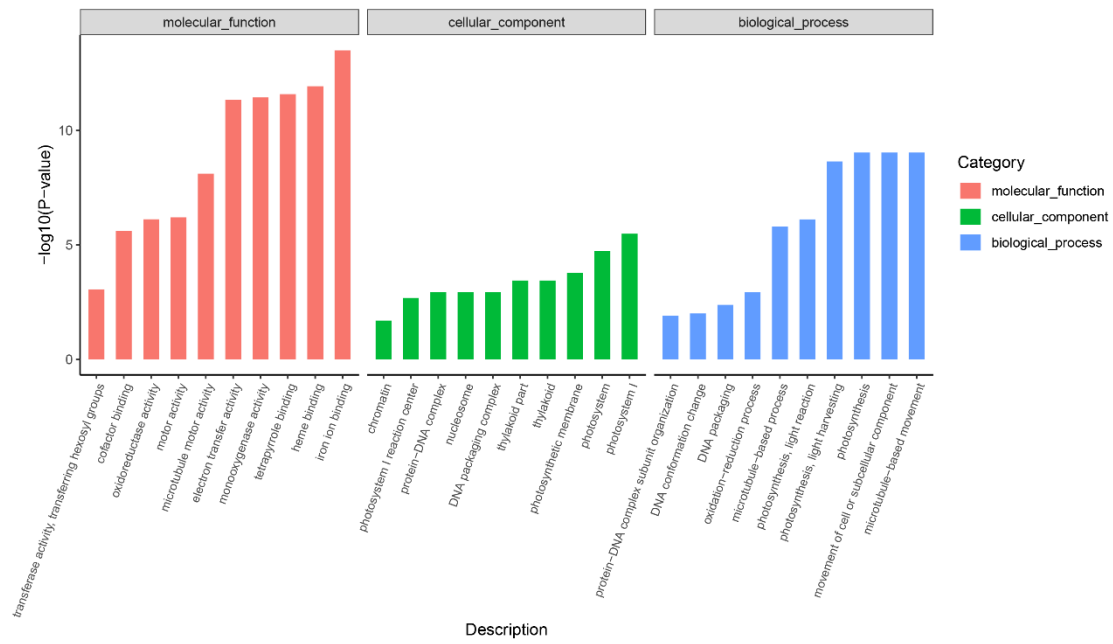
Supplementary Figure 2. Phylogenetic tree of closely related homologs of Auxin F-box proteins in cucumber and other species. The phylogenetic tree was constructed using the neighbor-joining method built in MEGA 7.0. The numbers indicate the percentage of replicate trees in which the associated taxa clustered together according to the bootstrap test (1000 replicates).



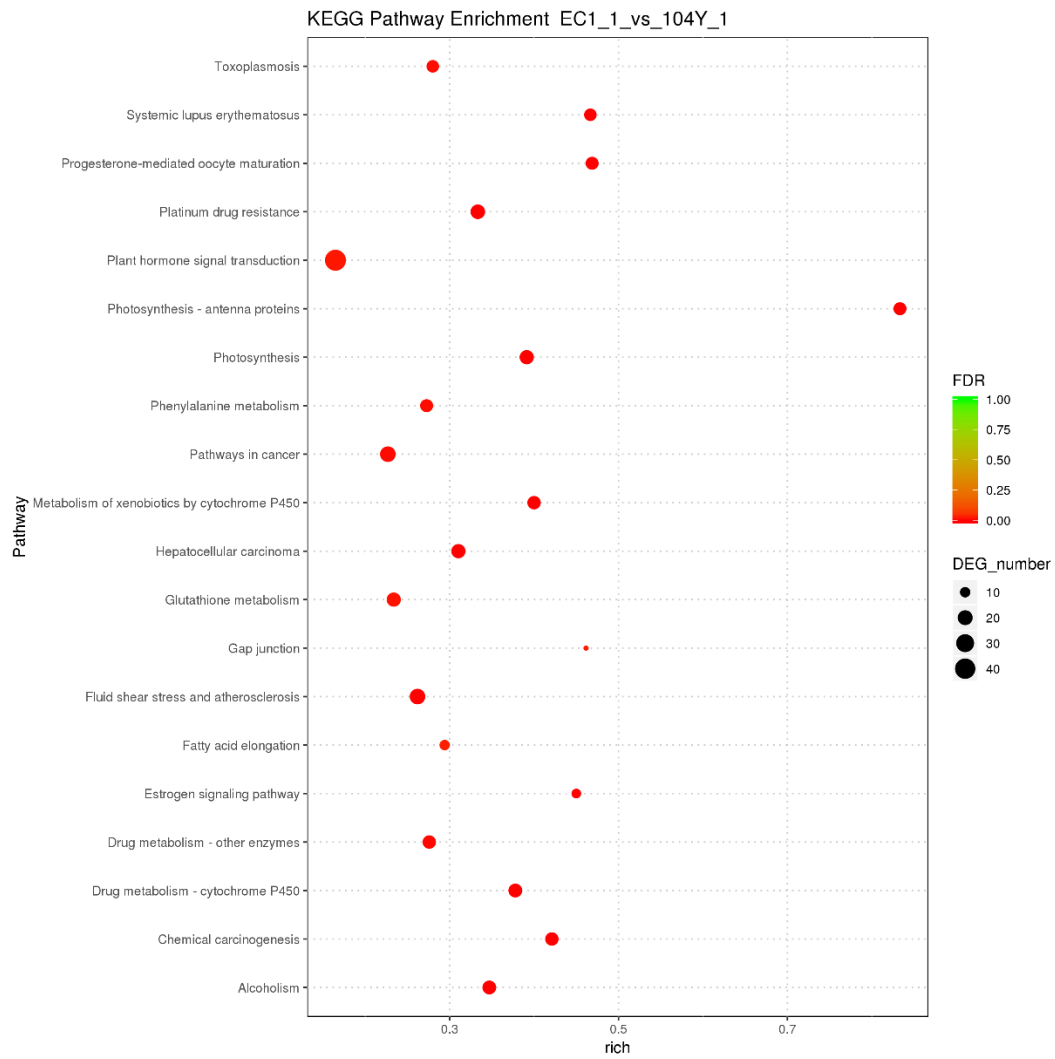
Supplementary Figure 3. Verification of the expression profiles of 15 genes obtained in RNA-seq analysis by qPCR. The RNA-seq Fold-change value of 104Y/EC1 (y-axis) was plotted against the value from the RT-PCR (x-axis).



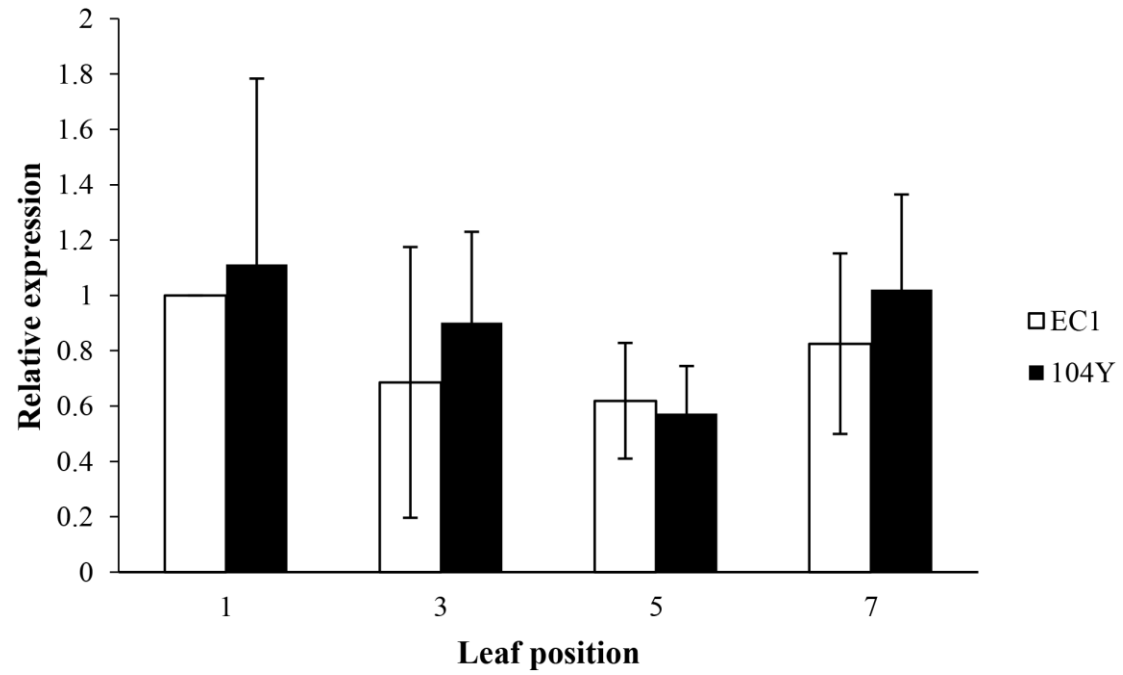
Supplementary Figure 4. The differentially expressed genes (DEGs) between the first true leaves of 104Y and EC1.



Supplementary Figure 5. GO annotations and functional classifications of the DEGs between 104Y and EC1.



Supplementary Figure 6. KEGG pathway enrichment analysis of the DEGs between 104Y and EC1.



Supplementary Figure 7. Relative expression levels of Csa3G890020 gene in the first, third, fifth and seventh true leaves of EC1 and 104Y by qRT-PCR analysis. Data were displayed using the *CsActin* gene as an internal control with three biological and three technical replicates. Values are the mean $\pm$ SD.

2 Supplementary Tables

Supplementary Table 1. The information of SNP mutation in the v-2 locus based on BSA-seq analysis.

Chr	Pos	Ref	Alt	EC1_	EC1_	104Y_	104Y_	Green_	Green	Virescent	Virescent_	Region	Gene	Feature
				genotype	ref_alt_depth	genotype	ref_alt_depth	bulk_	bulk_ref_alt_depth	bulk_	bulk_ref_alt_depth			
				genotype	ref_alt_depth	genotype	ref_alt_depth	genotype	ref_alt_depth	genotype	ref_alt_depth			
Chr3	37935558	T	C	0@0	26 0	1@1	0 32	0@1	17 5	1@1	0 30	intergenic	Csa3G889990	-
													(dist=2167),	
													Csa3G890000	
Chr3	37941105	A	G	0@0	18 0	1@1	0 40	0@1	22 11	1@1	0 22	downstream	Csa3G890000	-
													(dist=4894)	
													Csa3G890010	
Chr3	37954130	A	T	0@0	24 0	1@1	0 40	0@1	18 4	1@1	0 19	intergenic	Csa3G890020	-
													(dist=6917),	
													Csa3G890020	
Chr3	37958774	C	T	0@0	18 0	1@1	0 37	0@1	20 9	1@1	0 24	exonic	Csa3G890020	nonsynonymous
													SNV	
Chr3	38008661	C	G	0@0	20 0	1@1	0 25	0@1	28 11	1@1	0 34	intronic	Csa3G890070	-

Supplementary Table 2. List of primers used in quantitative RT-PCR for the 8 genes located in v-2 locus.

Gene ID	Forward primer 5' to 3'	Reverse primer 5' to 3'
Csa3G890000	GTTGTGCGAGAGTGGAGGTTA	GCGACTTGGGTGATGAGCAA
Csa3G890010	GAACGCGGCTTCACTTGTTT	GCGACGTAACCTCTACGAGGG
Csa3G890020	TCGTGGTATCGTGTTGAGGC	CTCGACTAAACCGCGACGTA
Csa3G890030	TGGAGGACTTCGCCTTTCAC	GCATCTGCAAACCATAGGCG
Csa3G890040	GGCGCATCGTATCCTCCATT	AGACCTCGGTGAGTTCGGAT
Csa3G890050	CTTGGGATGAAGCCCGATACT	CGGCTCTGCAATCTTTGTCC
Csa3G890060	TCGACAACCCGACTCCGATA	TGTCATCGTCGGTAGCATCG
Csa3G890070	CATGGCATATGTGCACGCAA	ACGGGTACGTTTCTTGACC

Supplementary Table 3. List of primers used in quantitative RT-PCR for validation of RNA-seq analysis.

Gene ID	Forward primer 5' to 3'	Reverse primer 5' to 3'
<i>Csa1G126040</i>	ATATGAAGCGTCAAACCGCA	TAGCGTTCGTTAAGCAGACC
<i>Csa1G153560</i>	TCGGGATATTAGGGACTGGAA	TACTATCCCGCCGATCGTT
<i>Csa3G099680</i>	GAGTTAAGTACTTGGGGCCG	ACCTTCCGTGGATTACCTCA
<i>Csa3G145780</i>	CATTCTGTCAACCACCGCTA	TGATGGAATCGCTTGCTCTC
<i>Csa3G826660</i>	CACAATACCACAAGCCATGC	GACAAACGGCTTTGTTTCCA
<i>Csa4G152270</i>	GAAGTGTTAGAAAGGCTGCG	CGGTTGTTGTGAGGAGGATTA
<i>Csa5G153020</i>	ATGATCTTCGCCCTCGTCTA	TACTGCTCTTGTGAGGGACA
<i>Csa5G623470</i>	CCAACCATTTTCAACGACCG	CTGCCATGCTGATGTTTGTG
<i>Csa6G076800</i>	AATGGCGCTCTCTCTCCTAT	CCAAGACGATGTGGAGACTG
<i>Csa6G139750</i>	ACCCCCATCCTATCTTACCG	GCCCATCTCGAGTGGATTAC
<i>Csa6G157120</i>	GAACCGGTTGTCATCAGGAA	AGATTTGTTTCGACCCAGCAG
<i>Csa6G423360</i>	ATTCTATGGGACCCACCAA	TACCAAAAGCACTGCCCATT
<i>Csa6G505950</i>	GACTCATCTGCCACCGATTT	AGCTTCCGATCGTAATCAGC
<i>Csa6G522690</i>	CCAAGAACCGTGAGTTGGAA	TCACACCATTGCGAGACAAA
<i>Csa7G351890</i>	TTTAATGGAGGTGGGTTGGC	CAGAATGTTTGGTTGTTCGGC

Supplementary Table 4. The FPKM values of the 8 genes located in v-2 locus based on RNA-seq analysis.

Gene ID	104Y_1_1	104Y_1_2	104Y_1_3	EC1_1_1	EC1_1_2	EC1_1_3
<i>Csa3G890000</i>	7.6387987	6.6341431	8.2346802	6.3649471	7.1188034	5.1002666
<i>Csa3G890010</i>	13.524667	14.525304	15.730124	18.800003	19.978988	18.742411
<i>Csa3G890020</i>	9.4083245	8.5075366	9.644823	12.249818	11.159044	9.4676353
<i>Csa3G890030</i>	3.7960014	3.3385003	3.2211876	2.370509	2.4131446	2.1350157
<i>Csa3G890040</i>	37.337254	34.668195	36.612307	39.262073	36.772474	30.671381
<i>Csa3G890050</i>	5.2156447	4.0054429	4.674527	4.3022805	3.1570973	4.3262344
<i>Csa3G890060</i>	3.7424076	3.9554284	4.128211	5.6899056	4.2430888	4.4389873
<i>Csa3G890070</i>	6.79787	8.6410627	8.7266949	11.714972	7.7295704	8.068231