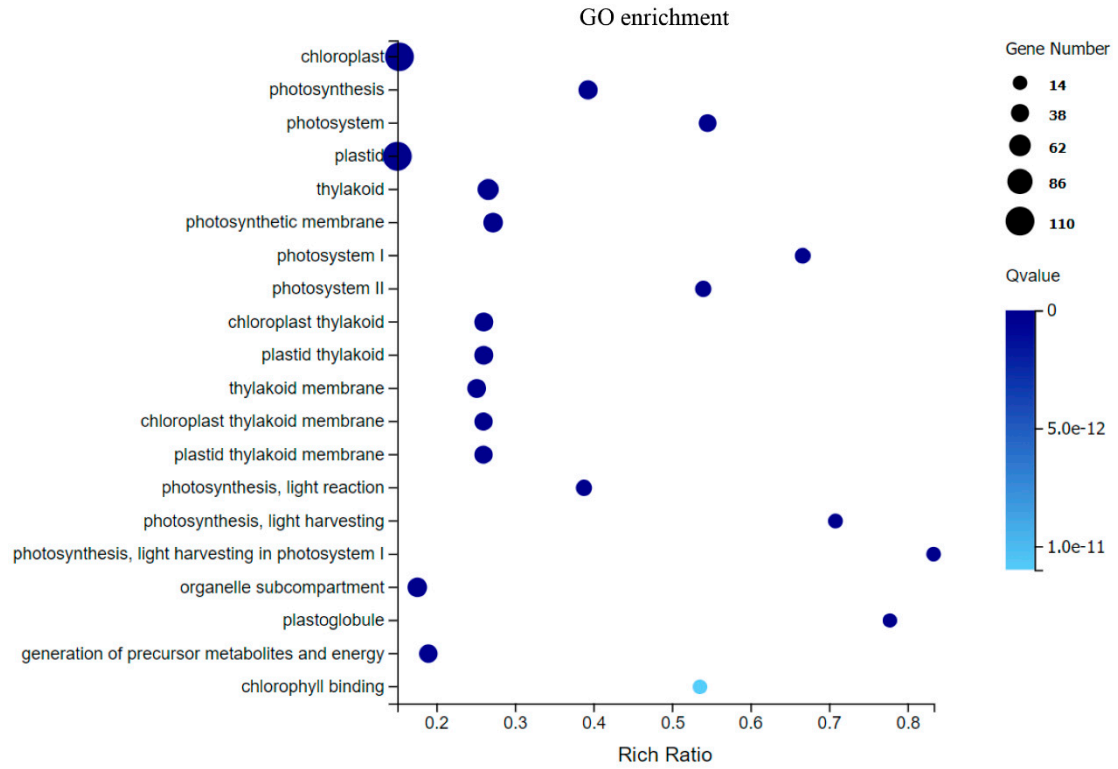**Figure S1.** Volcanic map of differences between groups of *se59* and WT. The X axis represents the difference multiple value after log2 conversion, and the Y axis represents the significant value after -log10 conversion. Red represents up-regulated DEGs, blue represents down-regulated DEGs, and gray represents non-DEGs.

Figure S2. The GO enrichment scatter plot of virescent leaf related genes in cucumber.

Table S1. Agronomic properties of wild type and mutant *se59* at different growth periods.

Growth Period	Material	Height (cm)	Leaf lengh (cm)	Leaf Width (cm)	Stem diameter (cm)	Petiole length (cm)	Petal length (cm)	Petal Width (cm)
Cotyledon stage	HB	2.3 ± 0.3	2.4 ± 0.12	1.4 ± 0.06	0.2 ± 0.1	-	-	-
	se59	3.4 ± 0.1**	2.4 ± 0.15	1.5 ± 0.12	0.2 ± 0.01	-	-	-
Seedling stage	HB	11.9 ± 3.1	11.1 ± 1.4	13.4 ± 2.1	0.9 ± 0.06	7.3 ± 0.3	-	-
	se59	10.7 ± 0.3	7.1 ± 0.6**	8.7 ± 1.0*	0.7 ± 0.1	6.5 ± 1.4	-	-
Vine stage	HB	102.3 ± 2.1	11.1 ± 0.75	13 ± 1.0	0.8 ± 0.03	5.3 ± 0.6	2.3 ± 4.4	1.7 ± 0.2
	se59	64.3 ± 2.1*	8.5 ± 0.8*	10.5 ± 0.9*	0.6 ± 0.1*	3.6 ± 0.7*	2.2 ± 0.1	1.4 ± 0. 1

Note: *: significant difference at $P < 0.05$ by *t*-test.

Table S2. The separation ratio of normal leaf color and virescent leaf traits of BC_1 and F_2 generations.

Offspring	Material	Virescent plant	green leaf plant	Total number	Actual ratio	Expected ratio	$\chi2$ value	p
BC_1	$F_1♀×se59♂$	76	80	156	1:1.1	1:1	0.1	0.75
F_2	$se59♀×HB♂$	46	143	189	1:3.1	1:3	0.044	0.83

（$\chi^2_{0.05,\ 1} = 3.84$）

Table S3. Candidate differentially expressed genes related to leaf color.

Gene ID	Gene description	FPKM (*se59*)	FPKM (HB)	Express trends
CsaV3_2G009680	Photosystem I reaction center subunit XI	1844.71	3143.97	-1299.26
CsaV3_2G010090	Photosystem I reaction center subunit IV	994.54	1761.63	-767.09
CsaV3_4G033870	NADPH-protochlorophyllide oxidoreductase	465.56	895.97	-430.41
CsaV3_3G005070	Reactive intermediate/imine deaminase	77.84	230.85	-153.01
CsaV3_1G032510	Chlorophyll a-b binding protein	42.89	85.42	-42.53
CsaV3_3G031580	Chlorophyll a-b binding protein	20.4	54.63	-34.23
CsaV3_6G001010	GDSL esterase/ lipaseGDSL	12.8	20.41	-7.61
CsaV3_1G011510	Protein DETOXIFICATION	1.66	4.33	-2.67
CsaV3_6G002540	pentatricopeptide repeat-containing protein At4g01400	10.6	10.63	-0.03
CsaV3_4G037030	Alpha-amylase	1.39	1.24	0.15
CsaV3_3G016180	pentatricopeptide repeat-containing protein At5g62370	4.36	3.62	0.74
CsaV3_6G002600	protein SET DOMAIN GROUP 41 isoform X1	7.96	6.5	1.46
CsaV3_3G016210	INVs/PMEIs	21.58	14.72	6.86

CsaV3_4G034720	Isoaspartyl peptidase/L-asparaginase	49.35	37.71	11.64
CsaV3_6G004820	HSP20-like chaperones superfamily protein	25.2	3.08	22.12
CsaV3_3G015240	Calmodulin	43.64	21.15	22.49
CsaV3_3G012890	Early light-induced protein	235.89	40.42	195.47

Table S4. Primers used in qRT-PCR.

Number	Gene ID	Primer sequence (5′-3′)
0	*CsAct3*	F: GAATCCAGCACGATACCA
		R: TCAACCCAAAGGCTAACA
1	*CsaV3_3G016180*	F: TAAGAAGTTCTATTTGACGATGA
		R: TGGAATACAATACAACATTAGGT
2	*CsaV3_3G016210*	F: GGATGATGACTGTTTATATGG
		R: TTAATTGGAGAATTAGTTGGA
3	*CsaV3_4G034720*	F: ATGCGTGGTGGTGGATAGCGAAG
		R: CCCGAGCCAATGTTCCTCTTATG
4	*CsaV3_6G002540*	F: TTACCCACATTTCTCTGTCATTC
		R: TCTCTTCTTACATCTTTCTTCAA
5	*CsaV3_6G002600*	F: ATTTAGTGGCTTTGAGTTCCGAA
		R: CCAGCAACAACCCAACAATTTGC
6	*CsaV3_1G032510*	F: TTCTCAGATTTTCAGCGAAGGTGGA
		R: CAGGAACAAAGTTGGTAGCGTAAGC
7	*CsaV3_3G031580*	F: GCTTGGGGCTCTAGGATGTGTATTC
		R: TTGACAGGATCAGCAAGATGGTCTG
8	*CsaV3_4G033870*	F: AGAGGACTCGCTGGAGGACTAAACG
		R: TCTCACTCAACTCCCACACTTTCCG
9	*CsaV3_3G012890*	F: ATCCCACCGTCACCTCCCAAACCAG
		R: AAGGCCAAGGCAACAAGGCCCAACA
10	*CsaV3_3G015240*	F: ATCCCACCGTCACCTCCCAAACCAG
		R: AAGGCCAAGGCAACAAGGCCCAACA
11	*CsaV3_6G004820*	F: TTTGCTTTTCTGCCGTTAGTGGAAC
		R: CACCCTCATCGTCGATGTCATTGTC
12	*CsaV3_3G005070*	F: CCATCACTCCCTCTGCCAGCACC
		R: ATCACTCTATCATAATCAGCCCC
13	*CsaV3_1G011510*	F: CTTCTTGCTCTCACCATTCTCCT
		R: TAATTCCTGTTTGTCATCCCAC
14	*CsaV3_6G001010*	F: AAGAAAGAGCTGGAGCGAGCAAGA
		R: AGGAAAAGGGAGGGTCAGAATAAG
15	*CsaV3_2G009680*	F: GACGCATCCCTACAAGAACACACT
		R: GGAGATACCACCGAAGAAAAACCC
16	*CsaV3_2G010090*	F: ATTCTTCATTCATCAGTTATTTG
		R: TAGGGGCAGGCTTAGGCTTGGGC
17	*CsaV3_4G037030*	F: CTCACGCACCCAGGGATACCAAC
		R: CTGCCACACTGCATATCTCCAGC