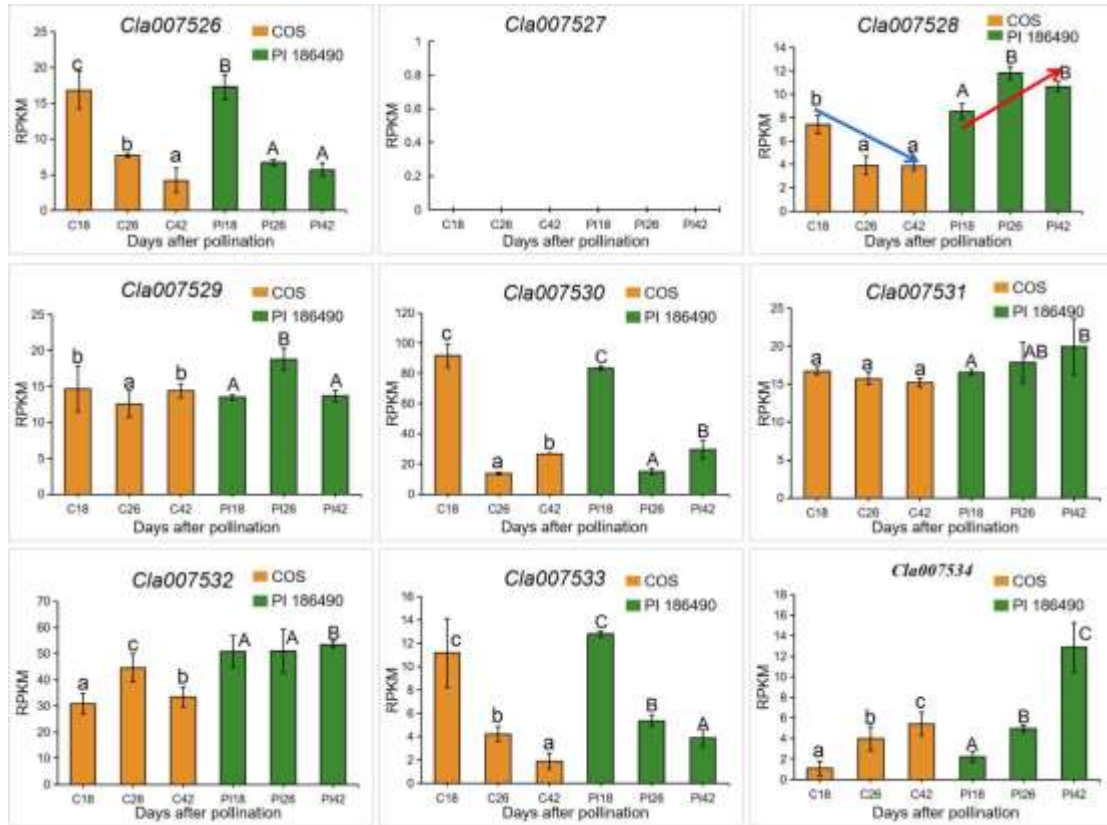


**Appendix A** The qRT-PCR primers in carotenoid pathway.

Gene ID	Symbol	Forward primer	Reverse primer
<i>Cla010898</i>	PDS	GTGTTGGCTCGGTCGCTTGT	GAGAGTGGTAGTTGTAGTGGCAGATT
<i>Cla003751</i>	ZDS	CGCTGTATGCTTACTATCTTCTCGTTGT	CCTCTGTCCGTGATATACTTCCTTATGG
<i>Cla017593</i>	CRTISO	CTTCTTCGGCTACTCGGTTGGTT	ACTATTGCGGCACGACGGATAT
<i>Cla005011</i>	LCYB	GAGCATTGAAGAGGATGAGCATTGTG	CGCTGCTAGAGTTCTTGCTACCATAT
<i>Cla009779</i>	NCED-1	CTGCTTCCCTCGCCTTAG	CTTCTTCCACTAGCGAGACCATCCT
<i>Cla005404</i>	NCED-7	CCAACCCACTTCACGAACCC	CGGCAAGCGTAACTAACACC
<i>Cla011420</i>	CHXE	TTCTGCTGTGGGCATGGAAT	AACCCTCGGCTTGTGATGAG
<i>Cla006149</i>	CHYB	CCATAATCAACGCTGTGCCG	GGCCATCCCAAAGACCGTAA
<i>Cla009122</i>	PSY1	CCCAAATTCCCGATTCTTCCAGATTCT	ACAGAGCCATATCCACCTTCACAGA
<i>Cla020175</i>	CLYLS8	AGAACGGCTTGTGGTCATTC	GAGGCCAACACTTCATCCAT

**Appendix B** Expression levels of 9 candidate gene in the fine mapping region obtained via RNA-seq.

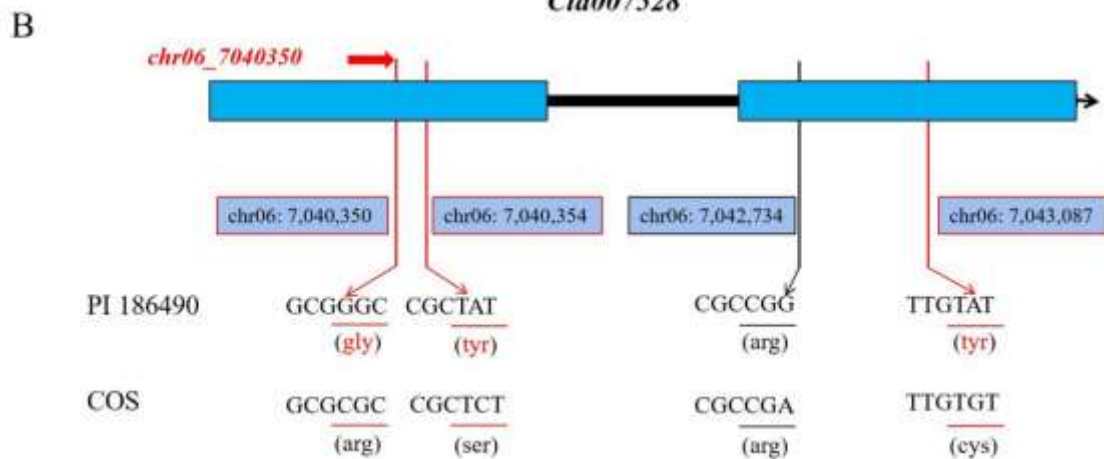


**Appendix C** Comparative analysis of the cloning sequence and amino acid sequence of *Cla007528*

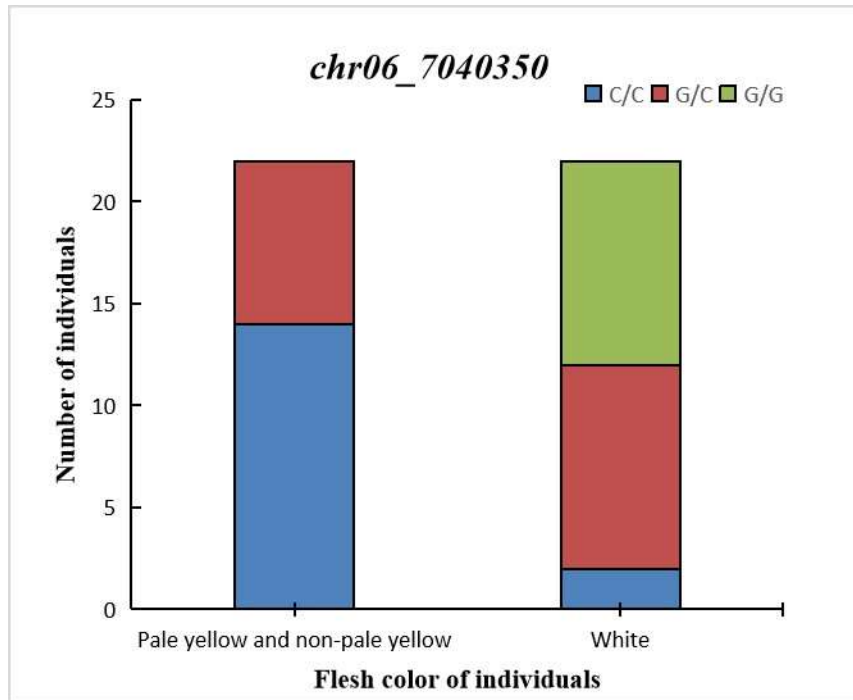
between COS and PI 186490. Cloning alignment of the *Cla007528* sequence in both parents and (B) gene structure of *Cla007528*, including two exons and one intron. The red color indicates that the change of SNP leads to the amino acid change.

**A**

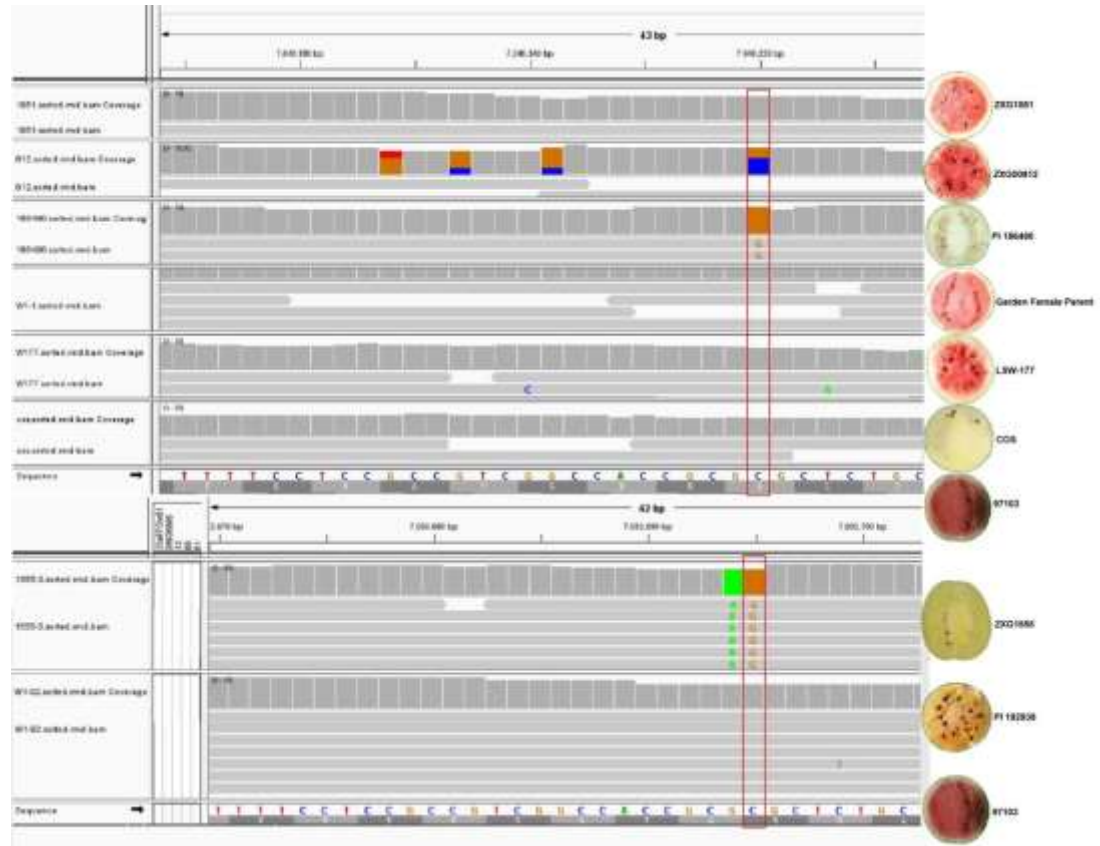
CDS-97103 (V1)	1	ATGGCTATGGCTACTGCTTCTTTTCTCCGCGCSTCGGOCACCGCGGCTCTCTCAAGTTTCG	60
CDS-F1186490	1	ATGGCTATGGCTACTGCTTCTTTTCTCCGCGCSTCGGOCACCGCGGCTCTCTCAAGTTTCG	60
CDS-COS	1	ATGGCTATGGCTACTGCTTCTTTTCTCCGCGCSTCGGOCACCGCGGCTCTCTCAAGTTTCG	60
CDS-97103 (V1)	61	TCCAATGCTTTCGAGATCGGAAAAATTCACGCGGTGCTTGAAAAGGTGAAATCGGCTGGA	120
CDS-F1186490	61	TCCAATGCTTTCGAGATCGGAAAAATTCACGCGGTGCTTGAAAAGGTGAAATCGGCTGGA	120
CDS-COS	61	TCCAATGCTTTCGAGATCGGAAAAATTCACGCGGTGCTTGAAAAGGTGAAATCGGCTGGA	120
CDS-97103 (V1)	121	TGTTGCTCATCTGGCCAAATTTCTTCCGCTCCTTCGCGGAGCCGCTGCTGATCGCCCGG	180
CDS-F1186490	121	TGTTGCTCATCTGGCCAAATTTCTTCCGCTCCTTCGCGGAGCCGCTGCTGATCGCCCGG	180
CDS-COS	121	TGTTGCTCATCTGGCCAAATTTCTTCCGCTCCTTCGCGGAGCCGCTGCTGATCGCCCGG	180
CDS-97103 (V1)	421	ATCAAAATAGCCCTCGCTGGCCACAGCCGGCGGCGCAAAACCTCCTTCGCTTTAGCCCAA	480
CDS-F1186490	421	ATCAAAATAGCCCTCGCTGGCCACAGCCGGCGGCGCAAAACCTCCTTCGCTTTAGCCCAA	480
CDS-COS	421	ATCAAAATAGCCCTCGCTGGCCACAGCCGGCGGCGCAAAACCTCCTTCGCTTTAGCCCAA	480
CDS-97103 (V1)	481	CAAAAATCCCCAAAATGTCAGCCCTAATCGGCTGATCCCGTGGACGAAACAGGGTCC	540
CDS-F1186490	481	CAAAAATCCCCAAAATGTCAGCCCTAATCGGCTGATCCCGTGGACGAAACAGGGTCC	540
CDS-COS	481	CAAAAATCCCCAAAATGTCAGCCCTAATCGGCTGATCCCGTGGACGAAACAGGGTCC	540
CDS-97103 (V1)	541	GGCAAGCAGAACCCATCCCCAGTCTGAAATACATCCCCCAATCCCTTGGATCTAGGGCTC	600
CDS-F1186490	541	GGCAAGCAGAACCCATCCCCAGTCTGAAATACATCCCCCAATCCCTTGGATCTAGGGCTC	600
CDS-COS	541	GGCAAGCAGAACCCATCCCCAGTCTGAAATACATCCCCCAATCCCTTGGATCTAGGGCTC	600
CDS-97103 (V1)	781	AGAGGGAGGCGAGCTACTGTTTCTTAAAAATGGGAACTCTAGAGCCGATGAGGAGG	840
CDS-F1186490	781	AGAGGGAGGCGAGCTACTGTTTCTTAAAAATGGGAACTCTAGAGCCGATGAGGAGG	840
CDS-COS	781	AGAGGGAGGCGAGCTACTGTTTCTTAAAAATGGGAACTCTAGAGCCGATGAGGAGG	840
CDS-97103 (V1)	841	TTTGTGGTGGGGCTGTGGTTGCGTTTTTGAAGGCTTATTTTATGATGGGAGAGAGGAGAT	900
CDS-F1186490	841	TTTGTGGTGGGGCTGTGGTTGCGTTTTTGAAGGCTTATTTTATGATGGGAGAGAGGAGAT	900
CDS-COS	841	TTTGTGGTGGGGCTGTGGTTGCGTTTTTGAAGGCTTATTTTATGATGGGAGAGAGGAGAT	900



**Appendix D** Genotyping for *Cla007528* by the LGC-KASP marker. LGC-KASP marker *chr06\_7040350* was designed on *Cla007528*, and genotyping for extreme phenotypic traits was carried out in the F<sub>2</sub> population. C/C, G/C and G/G represent the genotypes of COS, F<sub>1</sub> and PI 186490, respectively.



**Appendix E** SNP (*chr06\_7040350*) variation in the natural population. 9 watermelon lines :COS (pale yellow), PI 186490 (white), 97103 (red), Garden Female Parent (red), LSW-177 (red), ZXG00812 (red), ZXG01061 (red) ZXG1555 (green) and PI 192938 (orange) were used for the candidate gene alignment. Therein, ZXG1555 and PI 192938 were aligned with the reference genome 97103 V2, and other lines were aligned with the reference genome 97103 V1.



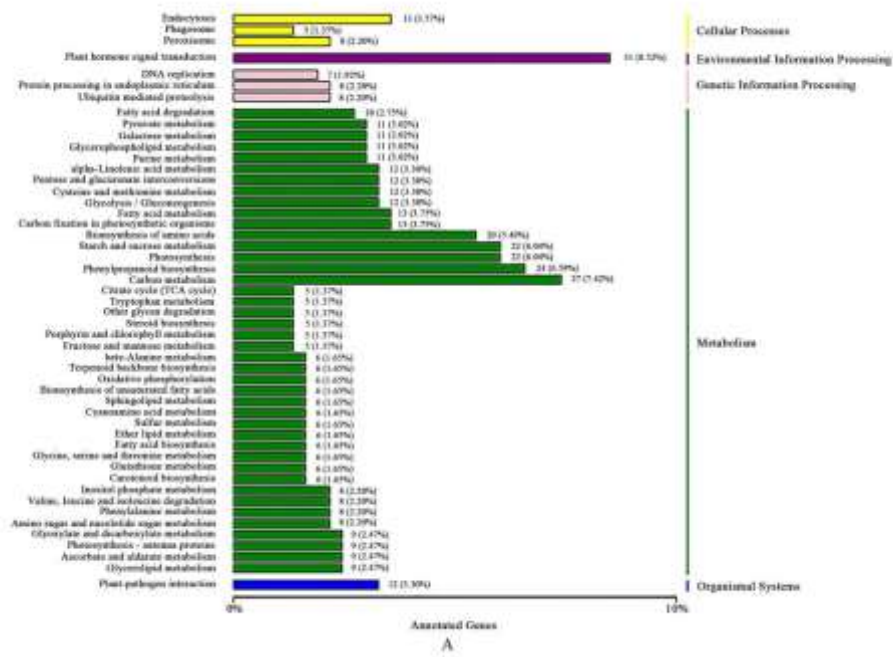
**Appendix F** The key KEGG pathways in COS at the 18nd day after pollination, 26nd day after pollination, and 42nd day after pollination. (A):

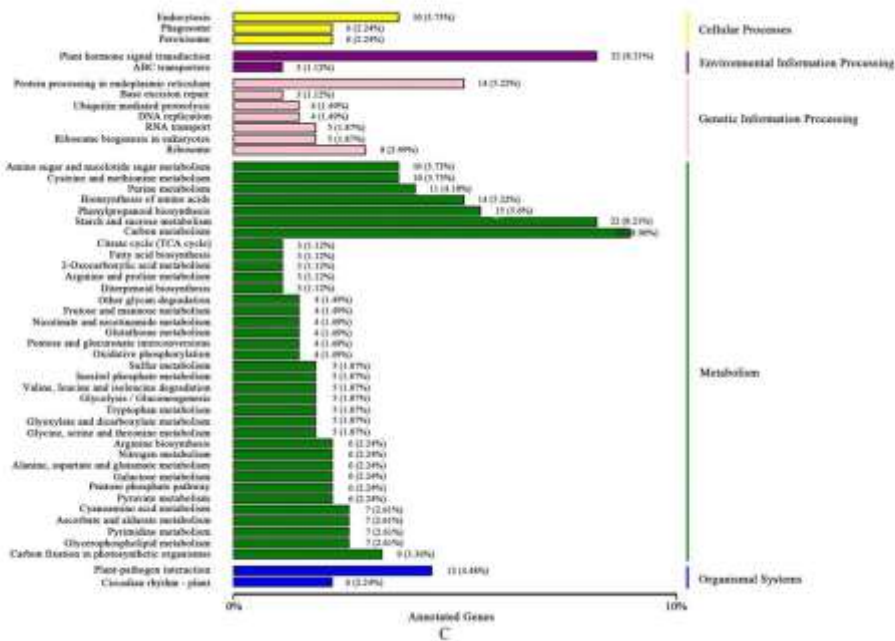
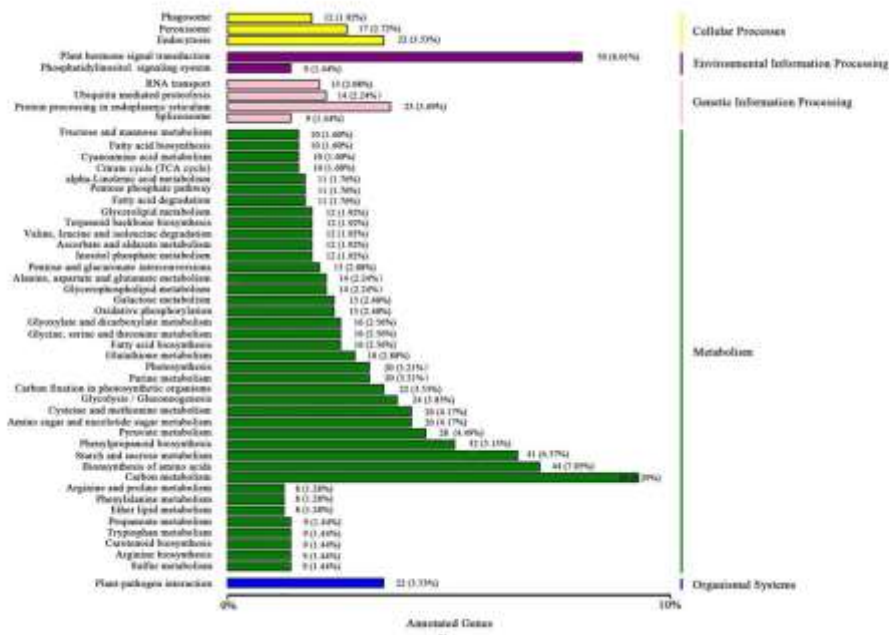
COS18-1\_COS18-2\_COS18-3\_vs\_COS26-1\_COS26-2\_COS26-3. KEGG\_classification

(B): COS18-1\_COS18-2\_COS18-3\_vs\_COS42-1\_COS42-2\_COS42-3. KEGG\_classification

(C): COS26-1\_COS26-2\_COS26-3\_vs\_COS42-1\_COS42-2\_COS42-3. KEGG\_classification

COS\_18-1, COS\_18-2, and COS\_18-3 represent the three replications of COS after 18 days of pollination; COS\_26-1, COS\_26-2, and COS\_26-3 represent the three replications of COS after 26 days of pollination; COS\_42-1, COS\_42-2, and COS\_42-3 represent the three replications of COS after 42 days of pollination.





**Appendix G** Comparative analysis of the cloning sequence and amino acid sequence of *Cla007528* between COS and PI 186490. (A) Cloning alignment of the *Cla007528* sequence in both parents and (B) gene structure of *Cla007528*, including two exons and one intron. The red color indicates that the change of SNP leads to the amino acid change.

***CINCED-1 (Cla009779)***

