

Table S7. Co-detected genes in DEGs and DEPs of each group.

Spot ID ¹	Accession no. ²	Protein name ³	Group ⁴	Ss 0 d vs. Ss 1 d	Ss 0 d vs. Ss 3 d	Rs 0 d vs. Rs 1 d	Rs 0 d vs. Rs 1 d
A2	Cla97C09G162960	Auxin-binding protein ABP19a-like	Hormone metabolism	-	-	+	+
B2	Cla97C04G076580	Enolase	Carbon metabolism	+	-	-	-
B4	Cla97C09G167000	S-adenosylmethionine synthetase isoform 4	Amino acid synthesis	-	-	+	+
B5	Cla97C05G088280	Galactokinase	Carbon metabolism	-	-	-	+
B9	Cla97C04G071440	Triosephosphate isomerase, cytosolic-like	Carbon metabolism	+	-	-	-
B10	Cla97C02G037100	Triosephosphate isomerase chloroplastic-like	Photosynthesis	-	-	-	+
B11	Cla97C07G134850	Ribulose biphosphate carboxylase large chain-like	Photosynthesis	-	-	-	+
C2	Cla97C09G177130	L-arabinofuranosidase 2	Carbon metabolism	-	+	-	+
C4	Cla97C10G192810	Heat shock 70 kDa protein	Stress defense	+	-	-	-
C6	Cla97C05G086890	Glutamine synthetase leaf isozyme	Amino acid synthesis	-	-	+	-
C7	Cla97C05G107870	Glutamate-glyoxylate aminotransferase	Amino acid synthesis	-	+	-	-
C10	Cla97C03G065070	20 kDa chaperonin, chloroplastic-like	Stress defense	+	-	+	-
C12	Cla97C02G027850	Cytochrome b6-f complex iron-sulfur subunit, chloroplastic-like	Photosynthesis	-	-	+	-
C13	Cla97C03G051890	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit 2, partial	Photosynthesis	-	-	-	+

¹ Spot number in Figure 5.² Accession number in the watermelon genome database.³ Description of the matched protein.⁴ Functional classification.

“-” indicates absent, “+” indicates present.