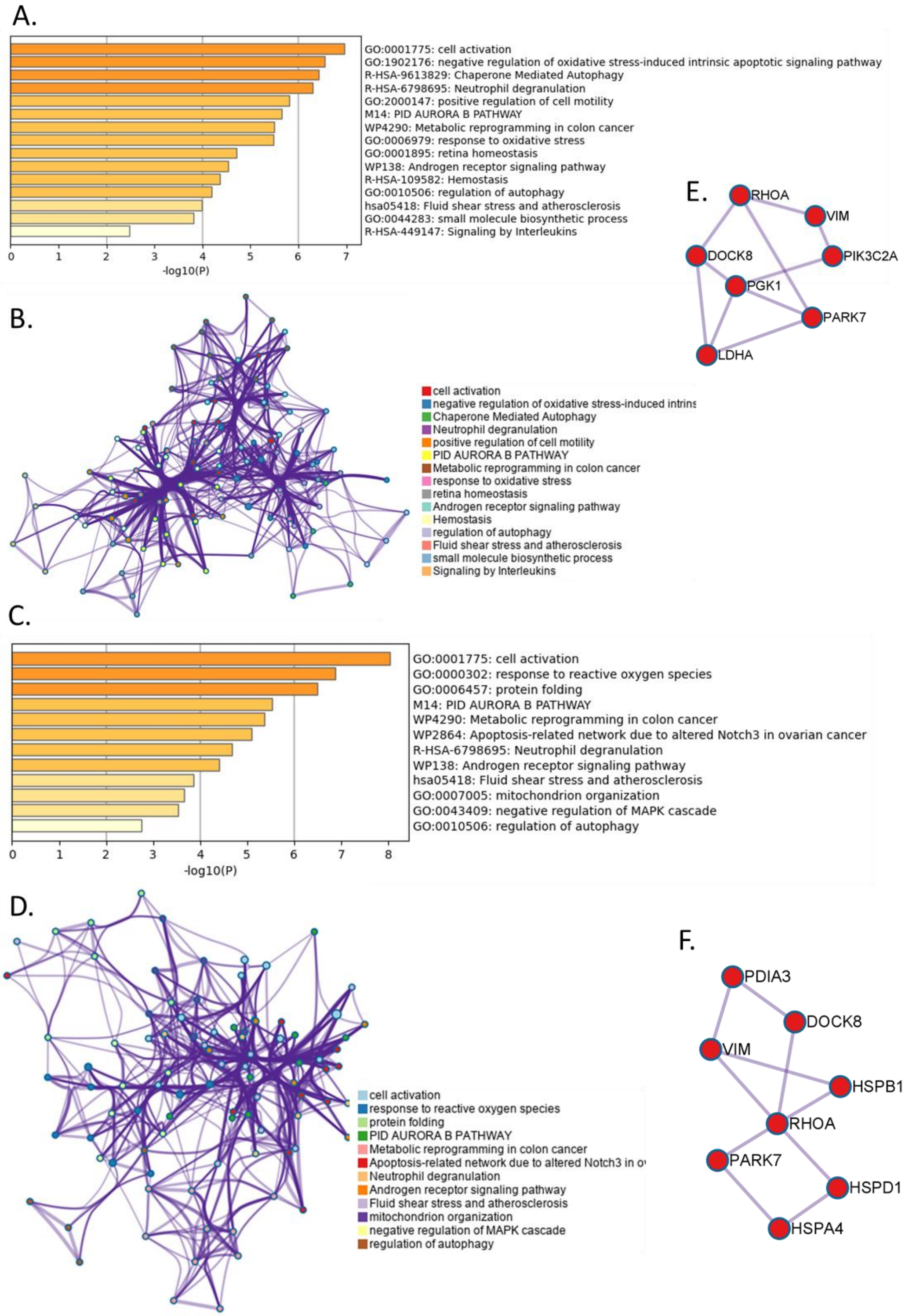

Figure S1: **Gene enrichment analysis of the identified allergy-related genes following DAT. A)** Gene enrichment of the identified allergy-related genes following ${}_{\mathrm{Allg}}\mathrm{DAT}_{\mathrm{A\beta1\text{-}6}}$ predicted by Metascape. Herein, Log10(P)" is the p-value in log base 10. **B**) Network of enriched terms for the identified allergy-related genes following ${}_{\mathrm{Allg}}\mathrm{DAT}_{\mathrm{A\beta1\text{-}6}}$ predicted by Metascape. Herein, each term is represented by a circle node, where its size is proportional to the number of input genes fall under that term, and its color represent its cluster identity (i.e., nodes of the same color belong to the same cluster). Terms with a similarity score > 0.3 are linked by an edge (the thickness of the edge represents the similarity score). **C)** Gene enrichment of the identified allergy-related genes following ${}_{\mathrm{Allg}}\mathrm{DAT}_{\mathrm{A\beta17\text{-}23}}$ predicted by Metascape. **D**) Network of enriched terms for the identified allergy-related genes following ${}_{\mathrm{Allg}}\mathrm{DAT}_{\mathrm{A\beta1\text{-}6}}$ predicted by Metascape. **E**) Protein-protein interaction MCODE components for the identified allergy-related gene sets following ${}_{\mathrm{Allg}}\mathrm{DAT}_{\mathrm{A\beta1\text{-}6}}$. MCODE components were identified from the merged network. **F**) Protein-protein interaction MCODE components for the identified allergy-related gene sets following ${}_{\mathrm{Allg}}\mathrm{DAT}_{\mathrm{A\beta17\text{-}23}}$. All the protein-protein interaction network was edited using the Cytoscape software v3.9.0.

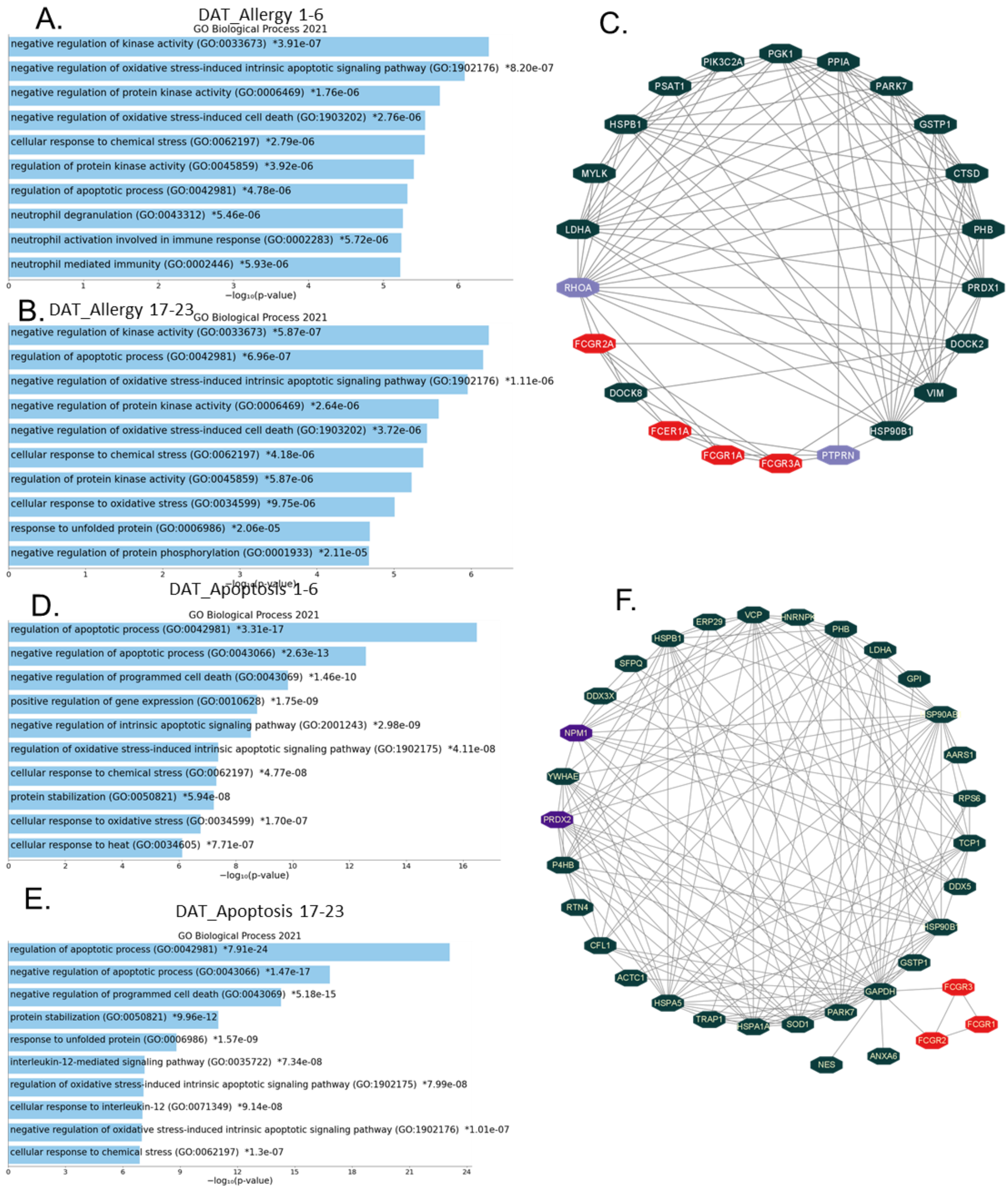

Figure S2: Gene enrichment analysis of the identified allergy-and apoptosis-related genes following DAT. A) Gene enrichment of the identified allergy-related genes following ${}_{\text{Allg}}\text{DAT}_{\text{A}\beta1\text{-}6}$ predicted by ModEnrichr. Herein, Log10(P)" is the *p*-value in log base 10. **B)** Gene enrichment of the identified allergy-related genes following ${}_{\text{Allg}}\text{DAT}_{\text{A}\beta17\text{-}23}$ predicted by ModEnrichr **C)** Protein-protein interaction analysis of the identified allergy-related genes with the FcγR1, FcγR2, FcγR3, FcεR1A (red color). Purple color indicates the high interaction with other proteins. Protein-protein interaction was performed using the STRING v11.5 database and the data was edited using the Cytoscape v3.9.0 software. **D**) Gene enrichment of the identified apoptosis-related genes following ${}_{Apop}DAT_{A\beta 1\text{-}6}$ predicted by ModEnrichr. **E**) Gene enrichment of the identified apoptosis-related genes following ${}_{Apop}DAT_{A\beta 17\text{-}23}$ predicted by ModEnrichr **F**) Protein-protein interaction analysis of the identified apoptosis-related genes with FcγR1, FcγR2, FcγR3, and FcεR1A (red color).

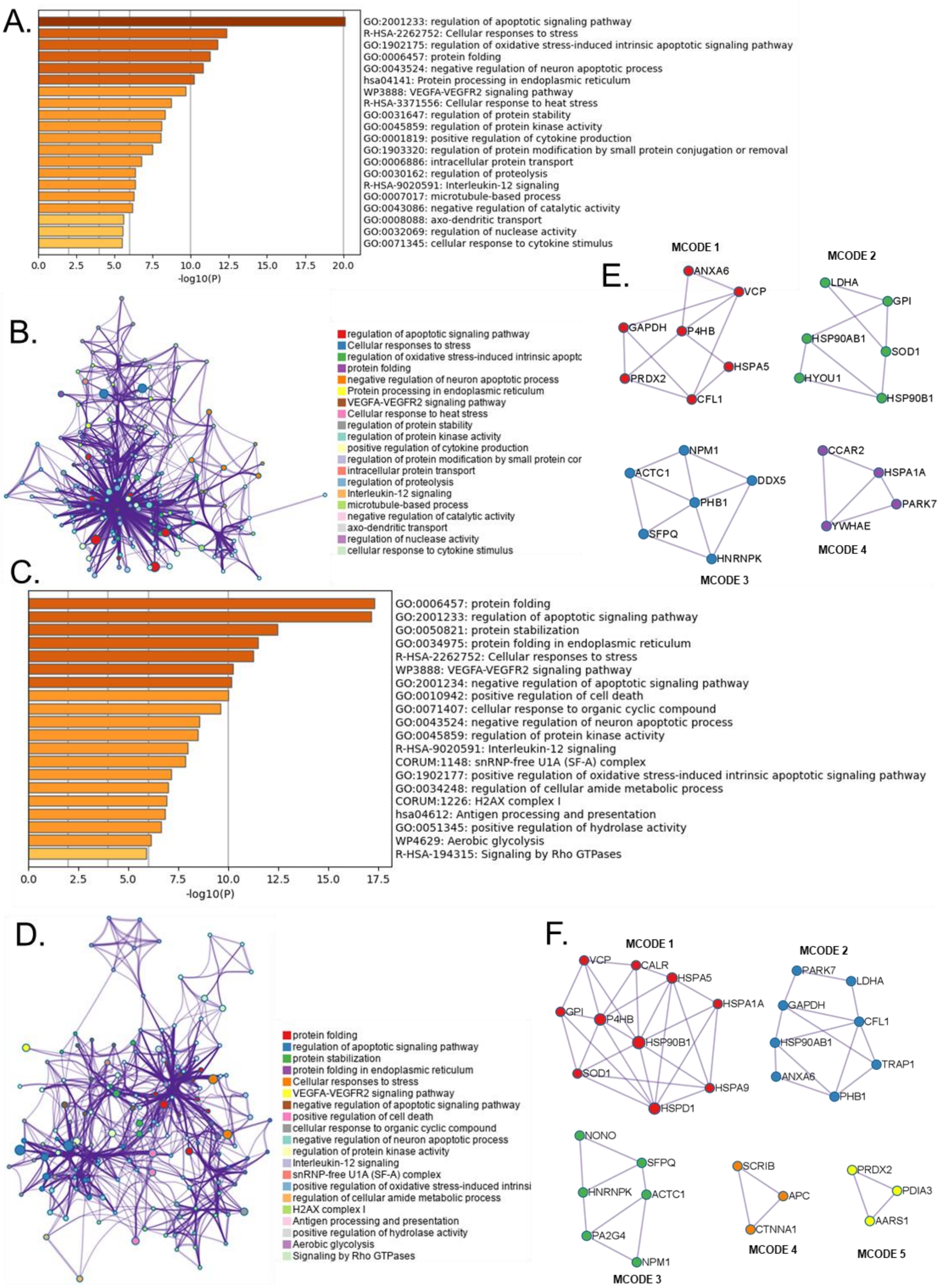

Figure S3: Gene enrichment analysis of the identified apoptosis-related genes following DAT. A) Gene enrichment of the identified apoptosis-related genes following $_{\text{Apop}}\text{DAT}_{\text{A}\beta 1\text{-}6}$ predicted by Metascape. Herein, Log10(P)" is the p-value in log base 10. **B**) Network of enriched terms for the identified apoptosis-related genes following $_{\text{Apop}}\text{DAT}_{\text{A}\beta 1\text{-}6}$ predicted by Metascape. Herein, each term is represented by a circle node, where its size is proportional to the number of input genes fall under that term, and its color represent its cluster identity (i.e., nodes of the same color belong to the same cluster). Terms with a similarity score > 0.3 are linked by an edge (the thickness of the edge represents the similarity score). **C**) Gene enrichment of the identified apoptosis-related genes following ${}_{\mathrm{Apop}}\mathrm{DAT}_{\mathrm{A\beta 17\text{-}23}}$ predicted by Metascape. **D**) Network of enriched terms for the identified apoptosis-related genes following ${}_{\mathrm{Apop}}\mathrm{DAT}_{\mathrm{A\beta 1\text{-}6}}$ predicted by Metascape. **E**) Protein-protein interaction MCODE components for the identified apoptosis-related gene sets following ${}_{\mathrm{Apop}}\mathrm{DAT}_{\mathrm{A\beta 1\text{-}6}}$. MCODE components were identified from the merged network. **F**) Protein-protein interaction MCODE components for the identified apoptosis-related gene sets following ${}_{\mathrm{Apop}}\mathrm{DAT}_{\mathrm{A\beta 17\text{-}23}}$. All the protein-protein interaction network was edited using the Cytoscape software v3.9.0.

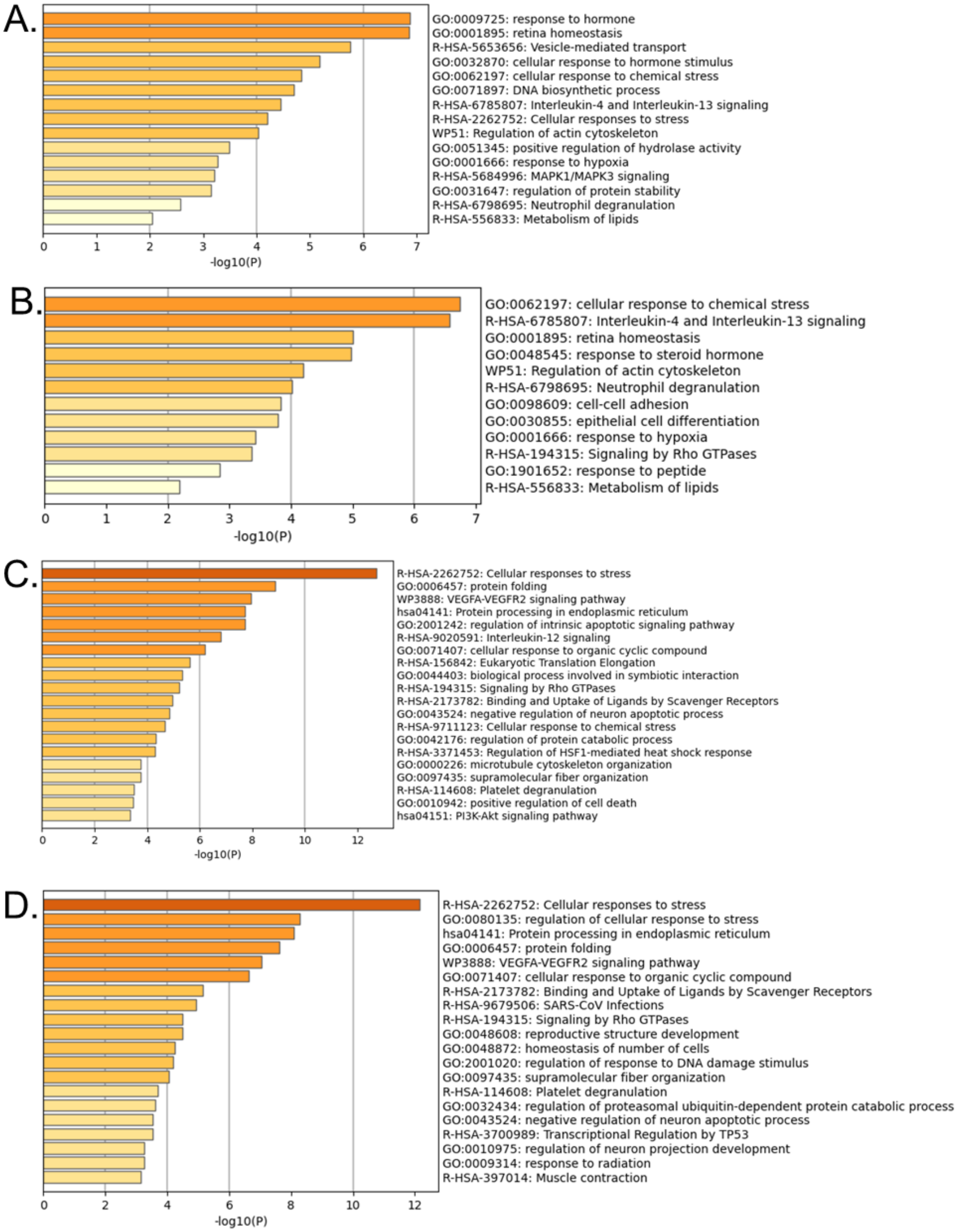

Figure S4: Gene enrichment analysis of the identified allergy- and apoptosis-related genes following DMT by Metascape. A) Gene enrichment of the identified allergy-related genes following ${}_{\mathrm{Allg}}\mathrm{DMT}_{\mathrm{A\beta 1\text{-}6}}$ of HSC predicted by Metascape. **B)** Gene enrichment of the identified allergy-related genes following ${}_{\mathrm{Allg}}\mathrm{DMT}_{\mathrm{A\beta 17\text{-}23}}$ predicted by Metascape. **C)** Gene enrichment of the identified apoptosis-related genes following ${}_{\mathrm{Apop}}\mathrm{DMT}_{\mathrm{A\beta 1\text{-}6}}$ predicted by Metascape. **D)** Gene enrichment of the identified apoptosis-related genes following ${}_{\mathrm{Apop}}\mathrm{DMT}_{\mathrm{A\beta 17\text{-}23}}$ predicted by Metascape. Herein, Log10(P)" is the p-value in log base 10.

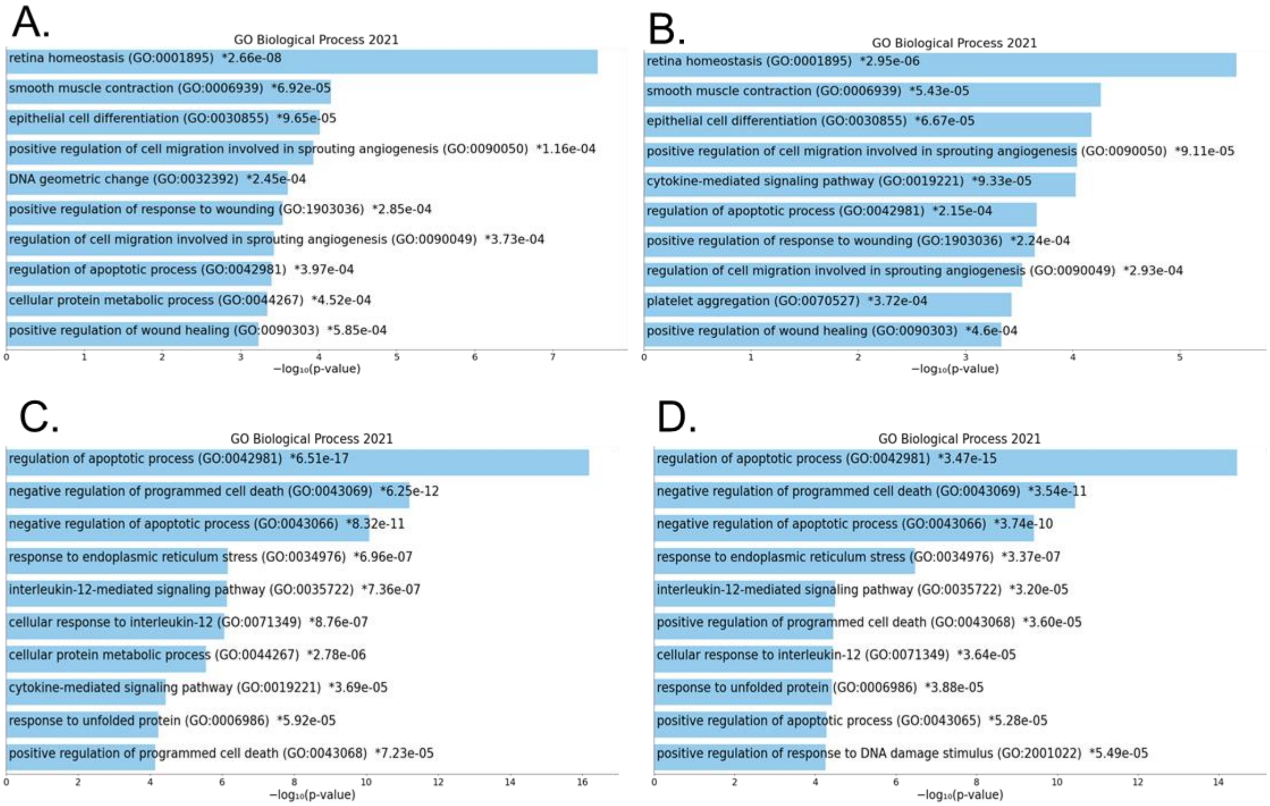

Figure S5: Gene enrichment analysis of the identified allergy- and apoptosis-related genes following DMT by ModEnrichr. A) Gene enrichment of the identified allergy-related genes following ${}_{Allg}DMT_{A\beta 1-6}$ of HSC predicted by ModEnrichr. **B)** Gene enrichment of the identified allergy-related genes following ${}_{Allg}DMT_{A\beta 17-23}$ predicted by ModEnrichr. **C)** Gene enrichment of the identified apoptosis-related genes following ${}_{Apop}DMT_{A\beta 1-6}$ predicted by ModEnrichr. **D)** Gene enrichment of the identified apoptosis-related genes following ${}_{Apop}DMT_{A\beta 17-23}$ predicted by ModEnrichr. Herein, Log10(P)" is the p-value in log base 10.

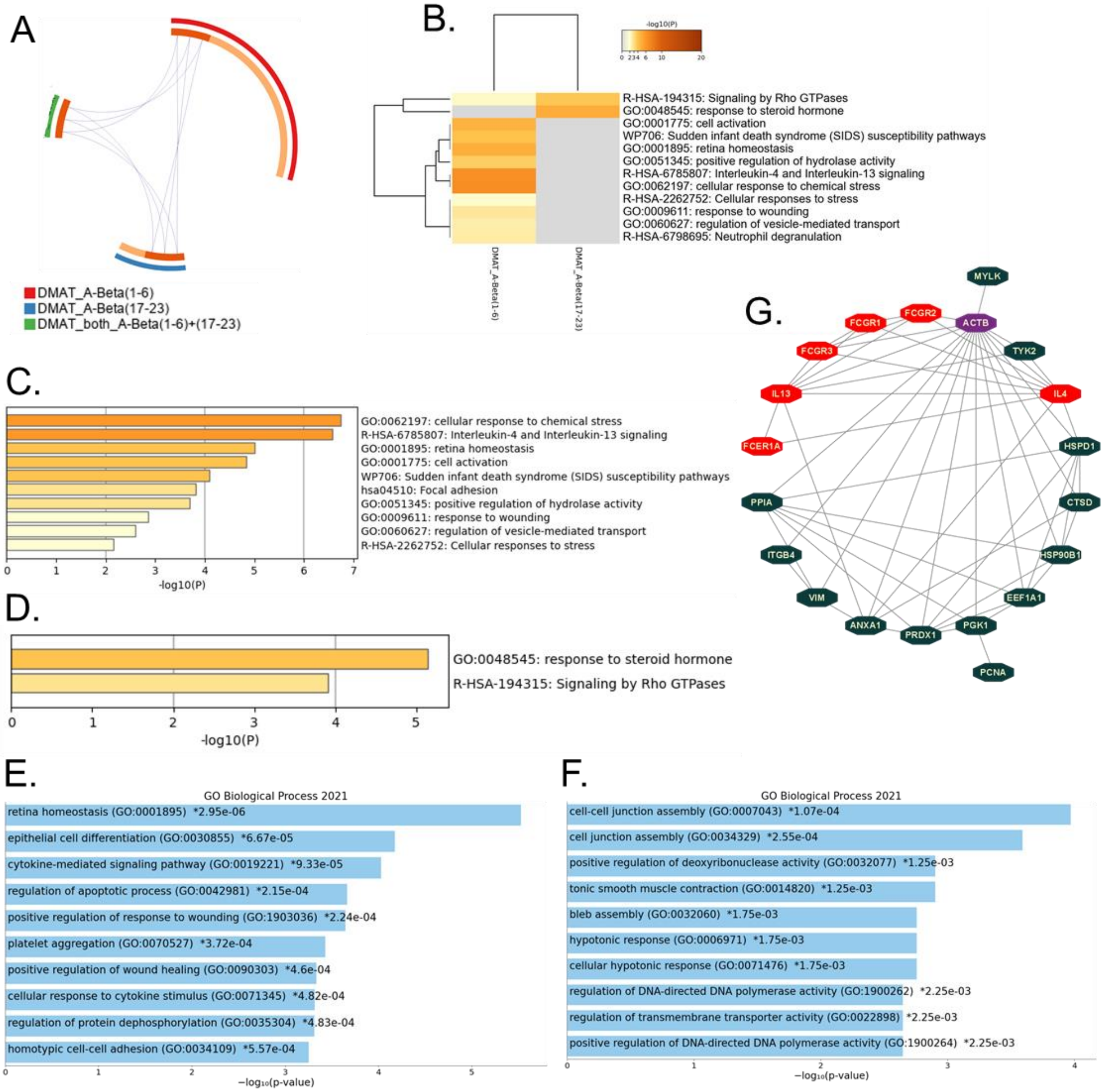

Figure S6: Gene enrichment analysis of the identified allergy-related proteins following DMAT. A) Gene overlap analysis for the identified allergy-related genes following ${}_{\text{allg}}\text{DMAT}_{\text{A}\beta1\text{-}6}$ and ${}_{\text{Allg}}\text{DMAT}_{\text{A}\beta17\text{-}23}$ predicted by Metascape. On the outside, each arc represents the identity of each gene list, using the same color code. On the inside, each arc represents a gene list, where each gene member of that list is assigned a spot on the arc. Dark orange color represents the genes that are shared by multiple lists and light orange color represents genes that are unique to that gene list. **B**) Heat map of the gene enriched term for the identified allergy-related genes following ${}_{\text{Allg}}\text{DMAT}_{\text{A}\beta1\text{-}6}$ and ${}_{\text{Allg}}\text{DMAT}_{\text{A}\beta17\text{-}23}$. Herein, Log10(P)" is the *p*-value in log base 10. The heatmap cells are colored by their *p*-values, white cells indicate the lack of enrichment for that term in the corresponding gene list. **C)** Gene enrichment of the identified allergy-related genes following ${}_{\text{Allg}}\text{DMAT}_{\text{A}\beta1\text{-}6}$ predicted by Metascape. **D**) Gene enrichment of the identified allergy-related genes following ${}_{\text{Allg}}\text{DMAT}_{\text{A}\beta17\text{-}23}$ predicted by Metascape. **E**) Gene enrichment of the identified allergy-related genes following ${}_{\text{Allg}}\text{DMAT}_{\text{A}\beta1\text{-}6}$ predicted by ModEnrichr. **F)** Gene enrichment of the identified allergy-related genes following ${}_{\mathrm{Allg}}\mathrm{DMAT}_{\mathrm{A\beta17\text{-}23}}$ predicted by ModEnrichr. **G**) Protein-protein interaction analysis of the identified allergy-related genes following DMAT with FcγR1, FcγR2, FcγR3, FcεR1A, IL-4, and IL-13 (red color). Purple color indicates the high interaction with other proteins. Protein-protein interaction was performed using the STRING v11.5 database and the data was edited using the Cytoscape v3.9.0 software.

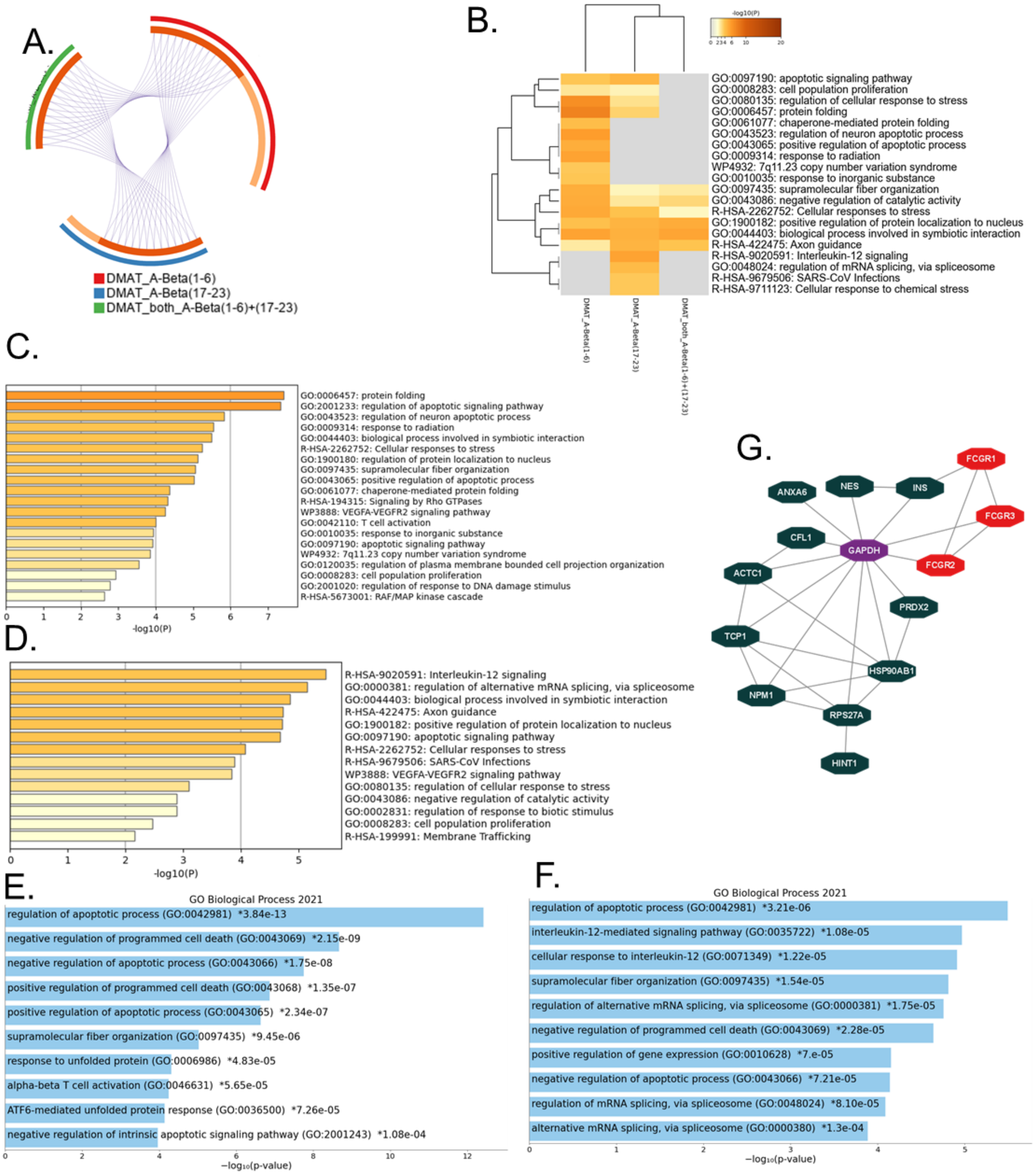

Figure S7: Gene enrichment analysis of the identified apoptosis-related proteins following DMAT. A) Gene overlap analysis for the identified apoptosis-related genes following $_{\text{apop}}$DMAT$_{\text{A}\beta\text{1-6}}$ and $_{\text{Apop}}$DMAT$_{\text{A}\beta\text{17-23}}$ predicted by Metascape. On the outside, each arc represents the identity of each gene list, using the same color code. On the inside, each arc represents a gene list, where each gene member of that list is assigned a spot on the arc. Dark orange color represents the genes that are shared by multiple lists and light orange color represents genes that are unique to that gene list. **B**) Heat map of the gene enriched term for the identified apoptosis-related genes following $_{\text{apop}}$DMAT$_{\text{A}\beta\text{1-6}}$ and $_{\text{Apop}}$DMAT$_{\text{A}\beta\text{17-23}}$. Herein, Log10(P)" is the *p*-value in log base 10. The heatmap cells are colored by their *p*-values, white cells indicate the lack of enrichment for that term in the corresponding gene list. **c**) Gene enrichment of the identified apoptosis-related genes following $_{\text{Apop}}\text{DMAT}_{\text{A}\beta 1\text{-}6}$ predicted by Metascape. **D**) Gene enrichment of the identified apoptosis-related genes following $_{\text{Apop}}\text{DMT}_{\text{A}\beta 17\text{-}23}$ predicted by Metascape. **E**) Gene enrichment of the identified apoptosis-related genes following $_{\text{Apop}}\text{DMAT}_{\text{A}\beta 1\text{-}6}$ predicted by ModEnrichr. **F)** Gene enrichment of the identified apoptosis-related genes following $_{\text{Apop}}\text{DMAT}_{\text{A}\beta 17\text{-}23}$ predicted by ModEnrichr. **G**) Protein-protein interaction analysis of the identified apoptosis-related genes following DMAT with FcγR1, FcγR2, FcγR3, and FcεR1A (red color). Purple color indicates the high interaction with other proteins. Protein-protein interaction was performed using the STRING v11.5 database and the data was edited using the Cytoscape v3.9.0 software.