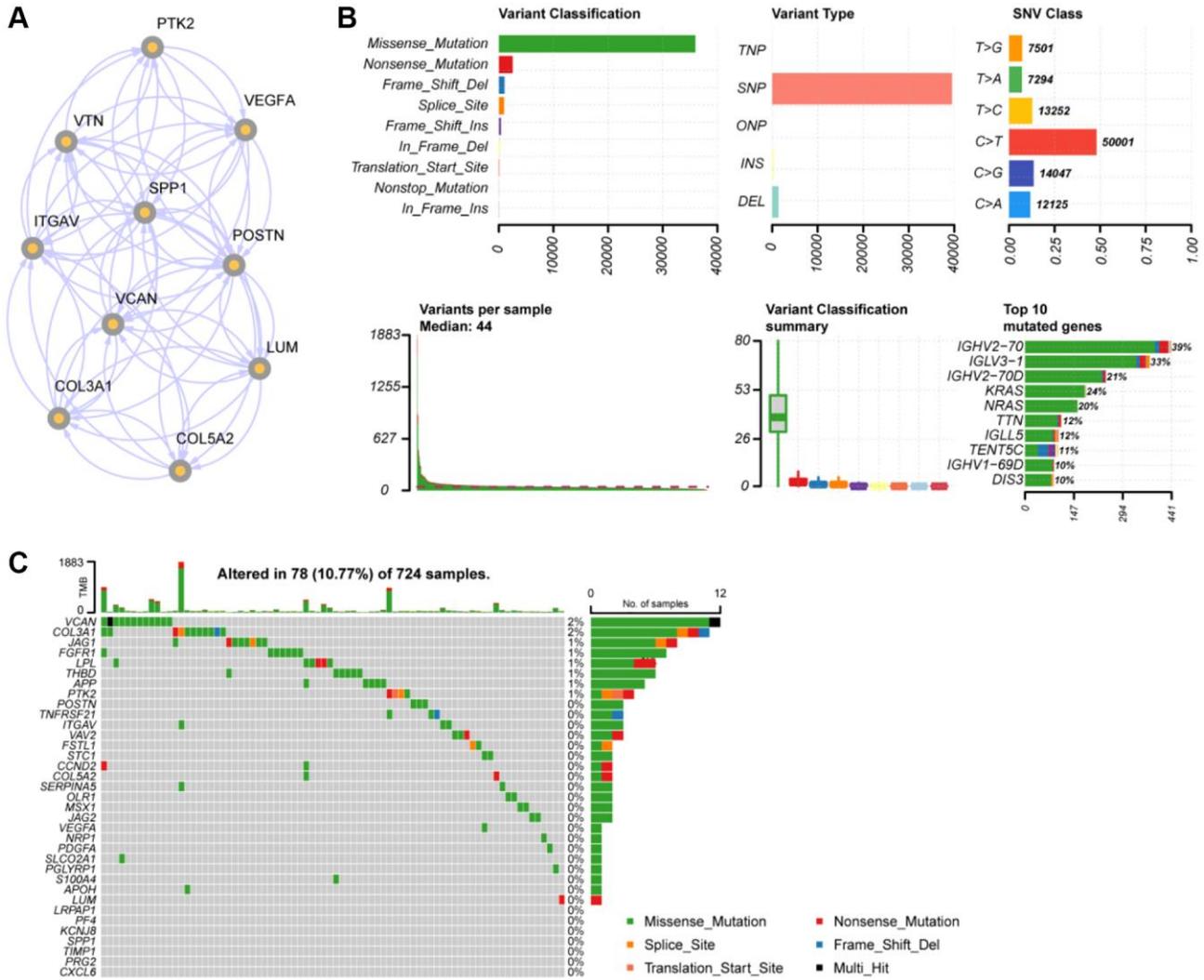
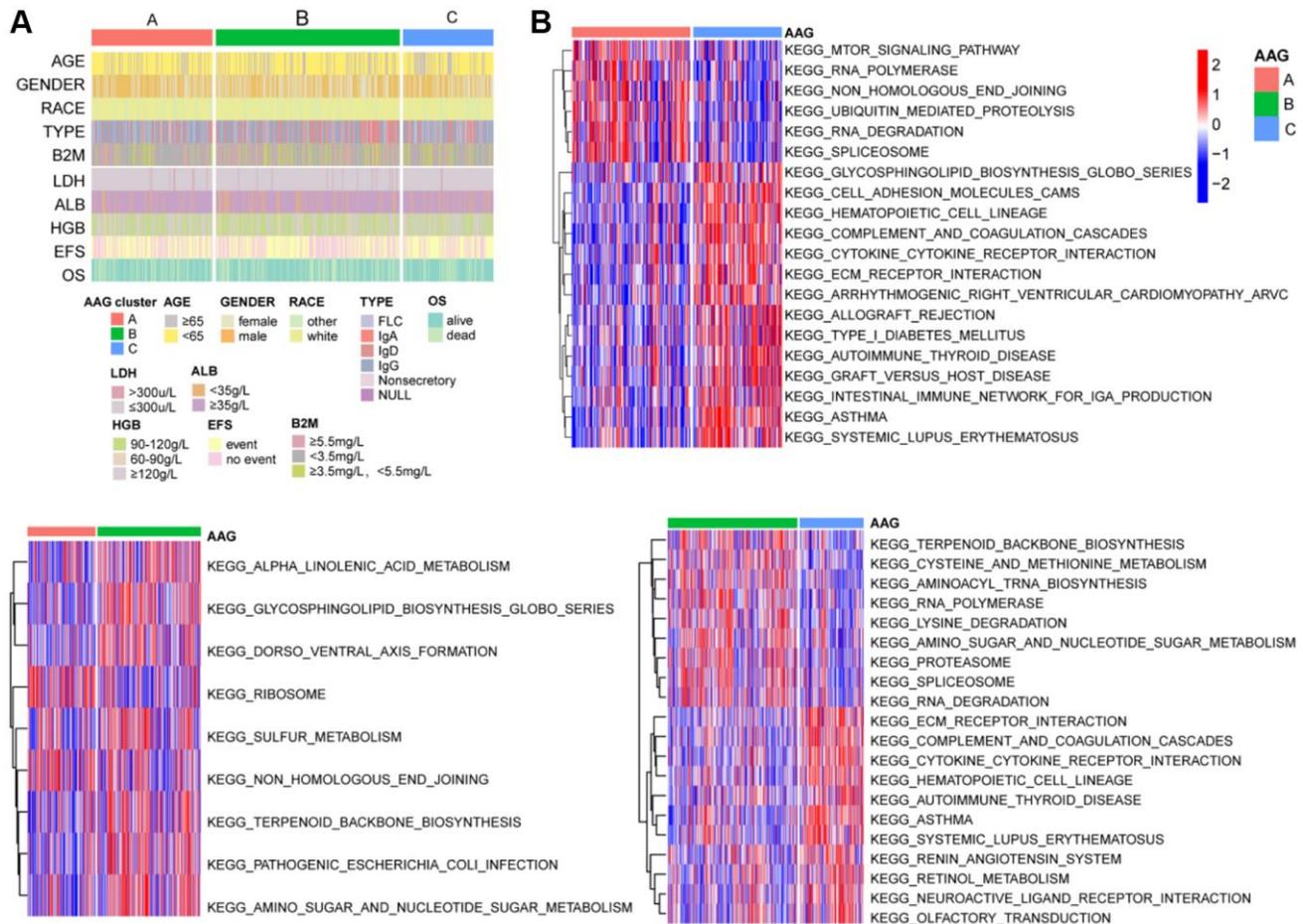


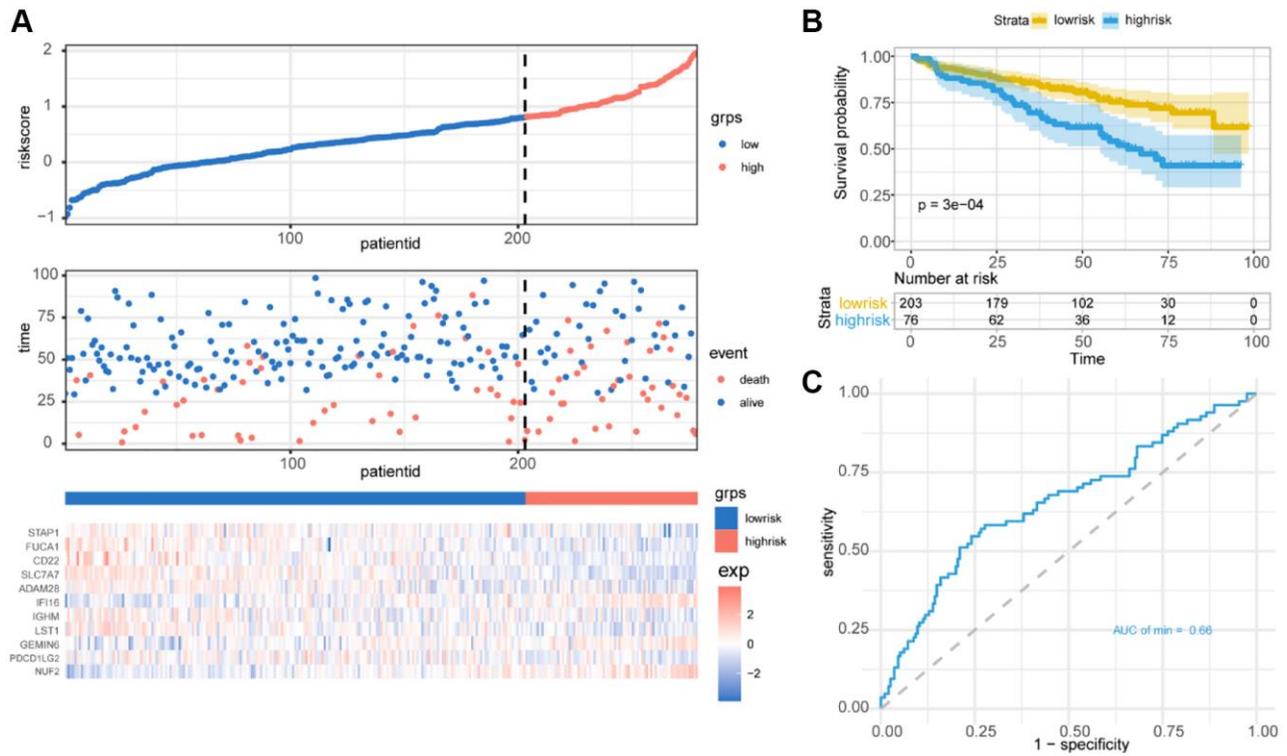
**SUPPLEMENTARY FIGURES**



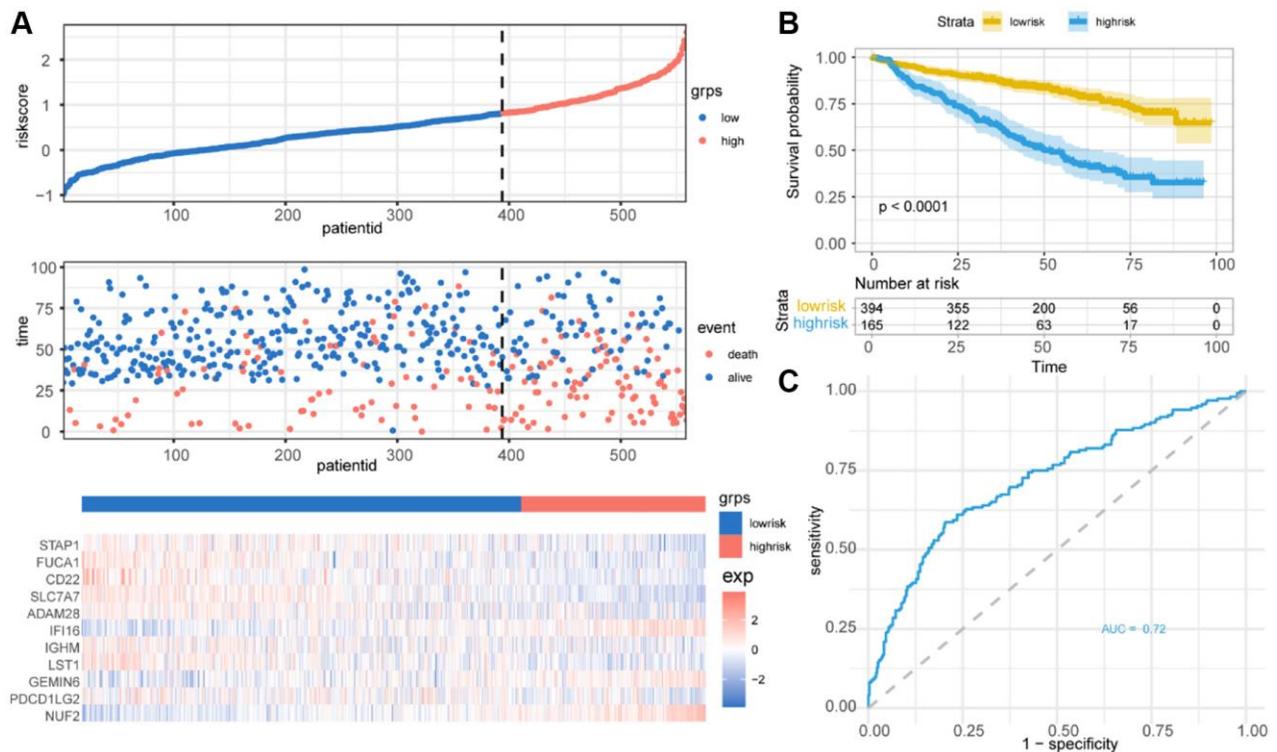
**Supplementary Figure 1. PPI network and mutational landscape of AAGs.** (A) Construction of PPI network of hub genes using the MCODE plugin in Cytoscape. (B) Variant classifications of mutations in MM. (C) Genetic alteration on a query of AAGs.



**Supplementary Figure 2. Clinical characteristics and GSEA of key pathways among three AAG\_clusters. (A) Cluster diagram of clinical characteristics among the three AAG\_clusters. (B) GSEA of biological activities among three distinct subgroups.**



**Supplementary Figure 3. Validation of AAG\_score in the test cohort.** (A) Percentage of deaths in high and low-risk groups as AAG\_score values increased. Expression patterns of 11 selected molecules in different risk groups. (B) Overall survival analysis of risk groups using Kaplan-Meier curves. (C) The predictive value of AAG\_score for predicting the OS of MM patients.



**Supplementary Figure 4. Validation of AAG\_score in the entire cohort.** (A) Percentage of deaths in high and low-risk groups as AAG\_score values increased. Expression patterns of 11 selected molecules in different risk groups. (B) Overall survival analysis of risk groups using Kaplan-Meier curves. (C) The predictive value of AAG\_score for predicting the OS of MM patients.