Supplementary Figure 1 Prognostic value of risk models from the GSE65904, GSE19234, and GSE78220 datasets for melanoma. A-C: Survival analysis of autophagy-related lncRNA in data sets GSE65904, GSE19234, and GSE78220; D-F: Survival analysis of melanoma risk models from the
GSE65904, GSE19234, and GSE78220 datasets; G: The GSE65904 data set representative risk curve showing samples' risk scores; H: Scatter diagram of survival state of GSE65904. Green dots: Alive; Red dots: dead; I: A representative heat map of GSE65904 shows the expression of specific lncRNAs in different groups. Green and red represent low expression and high expression, respectively; J: The GSE78220 data set representative risk curve showing samples' risk scores; K: Scatter diagram of survival state of GSE78220. Green dots: Alive; Red dots: dead; L: A representative heat map of GSE78220 shows the expression of specific lncRNAs in different groups. Green and red represent low expression and high expression.
Supplementary Figure 2 Melanoma risk model evaluation of the GSE78220 dataset. A and B: Univariate and multivariate Cox regression analyses for prognostic risk scores and different clinical features; C: ROC curves for risk scores and different clinical characteristics (age, gender and stage).