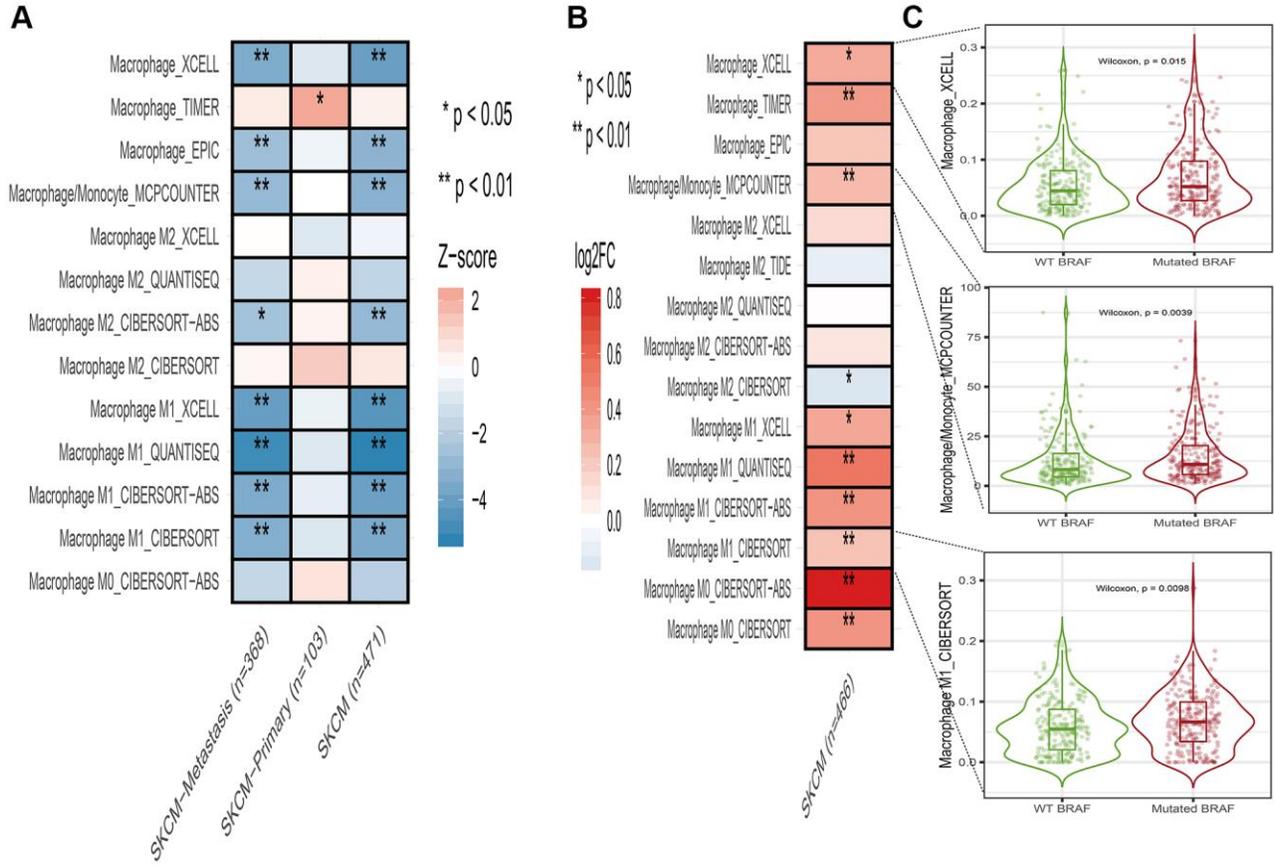
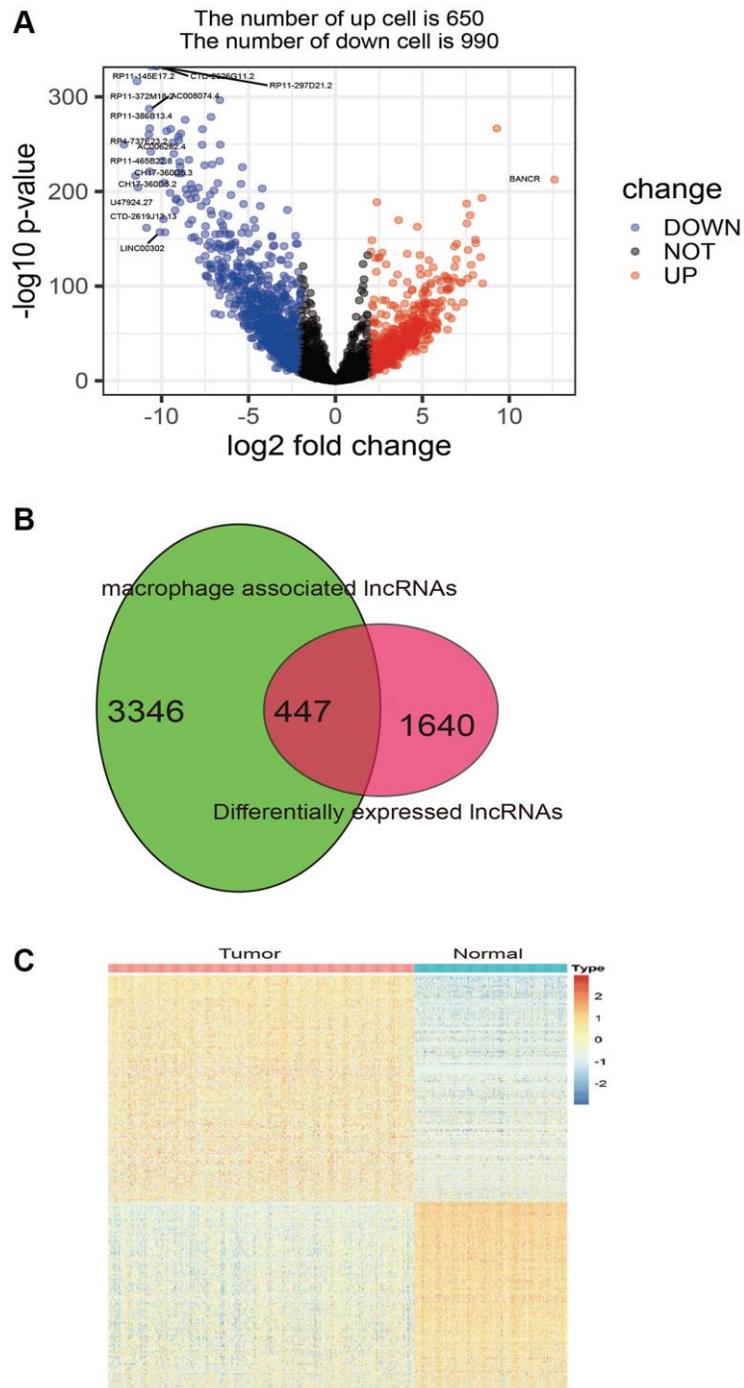


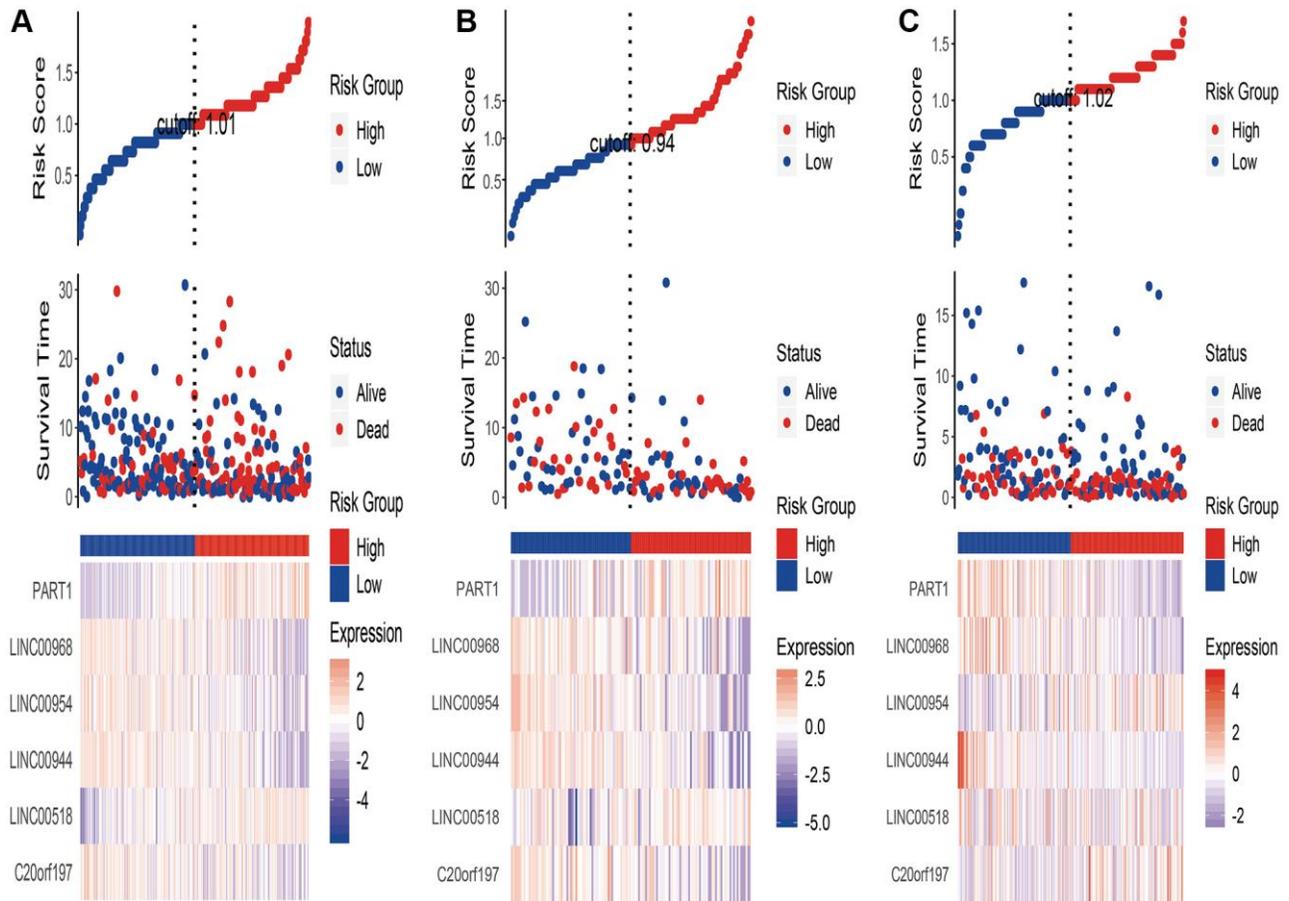
SUPPLEMENTARY FIGURES



Supplementary Figure 1. The prognostic value of macrophage in TCGA-SKCM by multiple immune deconvolution methods. (A) Heatmap of multivariable Cox proportional hazard model for macrophage in TCGA-SKCM datasets. (B) Heatmap of correlation between macrophage and BRAF mutant. (C) Boxplot of macrophage between BRAF mutant and BRAF wildtype.



Supplementary Figure 2. Selection of macrophage associated differentially expressed lncRNAs (DEMlncRNAs). (A) Volcano plot of differentially expressed lncRNAs between normal and melanoma. The highly differentially expressed lncRNAs were labeled ($|\text{Log}_2\text{FC}| > 10$). (B) The Venn plot of macrophage associated differentially expressed lncRNAs (DEMlncRNAs). (C) Heat map of the DEMlncRNAs in TCGA-SKCM dataset.



Supplementary Figure 3. Risk score model. (A) The risk model in train dataset: the distribution of risk score which are arranged in ascending order from left to right; Overall survival (OS) time and life status; The prognostic lncRNA expression patterns. (B) The risk model in validation dataset: the distribution of risk score which are arranged in ascending order from left to right; Overall survival (OS) time and life status; The prognostic lncRNA expression patterns. (C) The risk model in GSE65904 dataset: the distribution of risk score which are arranged in ascending order from left to right; Overall survival (OS) time and life status; The prognostic lncRNA expression patterns.