**Supplementary Material 1**

1. Abbreviation list

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| RNA-sequencing | RNA-seq |
| Fragments Per Kilobase Million | FPKM |
| the Cancer Genome Atlas | TCGA |
| Least Absolute Shrinkage and Selection Operator | LASSO |
| risk score | RS |
| FC | Foldchange |
| ceRNA | competing endogenous RNA |
| Estimation of Stromal and Immune cells in malignant tumor tissues using Expression data | ESTIMATE |
| tumor microenvironment | TME |
| Tumor Immune Dysfunction and Exclusion | TIDE |
| tumor-associated macrophages | TAMs |
| myeloid-derived suppressor cells | MDSCs |
| cancer-associated fibroblasts | CAFs |
| Immune checkpoint inhibitor | ICI |

2. The datasets involved in this study

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| GSE22153 | https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE22153 |
| GSE65904 | https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE65904 |
| GSE19234 | https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE19234 |
| mRNA of TCGA-SKCM | https://xenabrowser.net/datapages/?dataset=TCGA-SKCM.htseq\_fpkm.tsv&host=https%3A%2F%2Fgdc.xenahubs.net&removeHub=https%3A%2F%2Fxena.treehouse.gi.ucsc.edu%3A443 |
| miRNA of TCGA-SKCM | https://xenabrowser.net/datapages/?dataset=TCGA-SKCM.mirna.tsv&host=https%3A%2F%2Fgdc.xenahubs.net&removeHub=https%3A%2F%2Fxena.treehouse.gi.ucsc.edu%3A443 |
| mutation of TCGA-SKCM | https://xenabrowser.net/datapages/?dataset=TCGA-SKCM.mutect2\_snv.tsv&host=https%3A%2F%2Fgdc.xenahubs.net&removeHub=https%3A%2F%2Fxena.treehouse.gi.ucsc.edu%3A443 |

3. Code to filter out key immune-related genes

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| rm(list=ls())options(stringsAsFactors = F)library(survival)library(survminer)dat=read.csv(file = 'dat.txt',sep = ',',header = T)rownames(dat)=dat$IDrt=dat[,-1]rt=rt[,-1]library(lars) library(glmnet) x=as.matrix(rt[,c(3:ncol(rt))])y=rt$eventmodel\_lasso <- glmnet(x, y, family="binomial", nlambda=50, alpha=1)print(model\_lasso)head(coef(model\_lasso, s=c(model\_lasso$lambda[29],0.009)))plot(model\_lasso, xvar = "norm", label = TRUE)plot(model\_lasso, xvar="lambda", label=TRUE)set.seed(2)cv\_fit <- cv.glmnet(x=x, y=y, alpha = 1, nlambda = 1000)plot(cv\_fit)c(cv\_fit$lambda.min,cv\_fit$lambda.1se) model\_lasso <- glmnet(x=x, y=y, alpha = 1, lambda=cv\_fit$lambda.1se)lasso.prob <- predict(cv\_fit, newx=x , s=c(cv\_fit$lambda.min,cv\_fit$lambda.1se) )re=cbind(y ,lasso.prob)dat=as.data.frame(re[,1:2])colnames(dat)=c('event','prob')dat$event=as.factor(dat$event)library(ggpubr) p <- ggboxplot(dat, x = "event", y = "prob", color = "event", palette = "jco", add = "jitter")p + stat\_compare\_means()library(ROCR)library(glmnet)library(caret)pred <- prediction(re[,2], re[,1])perf <- performance(pred,"tpr","fpr")performance(pred,"auc") # shows calculated AUC for modelplot(perf,colorize=FALSE, col="black") # plot ROC curvelines(c(0,1),c(0,1),col = "gray", lty = 4 )fit <- glmnet(x=x, y=y, alpha = 1, lambda=cv\_fit$lambda.1se)head(fit$beta)choose\_gene=rownames(fit$beta)[as.numeric(fit$beta)!=0]length(choose\_gene)myexpr=x[,choose\_gene]mysurv=rt[,c("time","event")]mysurv$time=as.numeric(mysurv$time)fit <- glmnet( myexpr, Surv(mysurv$time,mysurv$event),  family = "cox")plot(fit, xvar="lambda", label = TRUE)plot(fit, label = TRUE)e=x[,choose\_gene]d=rt[,1:2]dat=cbind(d,e)colnames(dat)s=Surv(time, event) ~ KIR2DL4+IFITM1+GPI+LIF+ADCYAP1R1+NTSmodel <- coxph(s, data = dat )summary(model,data=dat)options(scipen=1)ggforest(model, data =dat,  main = "Hazard ratio",  cpositions = c(0.10, 0.22, 0.4),  fontsize = 1.0,  refLabel = "1", noDigits = 4) |