

Appendix 1 All Rscripts of this manuscript

```

####downloading the TCGA data R script
library(GDCRNATools)
library(edgeR)

# seting up parameters
project <- „TCGA-SARC“

work_dir <- „E:/SARC/4.14/tablefigure/supplementary10-R script/supplementary10.1-downloadR“
setwd(work_dir)
rmdir <- paste(project, „RNAseq“, sep=‘/‘)
#1.downloading the RNAseq data
#####
gdcRNADownload(project.id = project,
               data.type = „RNAseq“,
               write.manifest = FALSE,
               method = „gdc-client“,
               directory = rmdir)

# acquiring the meta informations of the RNAseq data
metaMatrix.RNA <- gdcParseMetadata(project.id = project,
                                  data.type = „RNAseq“,
                                  write.meta = FALSE)

# filtering the repeating data
metaMatrix.RNA <- gdcFilterDuplicate(metaMatrix.RNA)

# saving the tumor (code:01) and normal(code:11) samples
metaMatrix.RNA <- gdcFilterSampleType(metaMatrix.RNA)

# merging the clinical and RNAseq data.
rnaCounts <- gdcRNAMerge(metadata = metaMatrix.RNA,
                        path = rmdir,
                        organized = FALSE,
                        data.type = „RNAseq“)
View(rnaCounts)

```

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# saving the results
RAN_count_file <- paste0(work_dir, "/RNA_Counts.txt")
write.table(rnaCounts, file=RAN_count_file, quote=FALSE, row.names=T, sep="\t")

##### 2.lncRNA preprocessing
expr_file <- „E:/SARC/4.14/tablefigure/supplementary10-R script/supplementary10.1-downloadR/RNA_Counts.txt“
data_expr = read.table(expr_file,header=T,row.names=1,comment.char = „,“,check.names=F)
lncRNA_info_file <- „E:/SARC/4.14/tablefigure/supplementary10-R script/supplementary10.1-downloadR/lncRNA_info.
txt“
### downloading from https://www.gencodegenes.org/human/release_22.html

# extracting lncRNA matrix expression
lncRNA_info = read.table(lncRNA_info_file,header = 1)
cat(„Total LncRNA annotation:“, dim(lncRNA_info)[1])
lncRNA_selected <- row.names(data_expr) %in% lncRNA_info$Gene_id
lncRNA_expr <- data_expr[lncRNA_selected,]
cat(„Total LncRNA Selected:“, dim(lncRNA_expr)[1])

# filtering the repeating lncRNA
uniq_gene_name <- unique(row.names(lncRNA_expr))
lncRNA_expr <- lncRNA_expr[uniq_gene_name,]

# transposing the data
datExpr <- t(lncRNA_expr)
# saving the 12 bits barcode
rownames(datExpr) <- substr(rownames(datExpr), 1, 12)
datExpr <- as.data.frame(datExpr)
datExpr$bcr_patient_barcode <- row.names(datExpr)
write.table(datExpr, file = „lncRNAcount.txt“,sep="\t“, row.names = T, quote = F)

###selecting the data
# reading the expression of the data
#####
expr_file <- „E:/SARC/4.14/tablefigure/supplementary10-R script/supplementary10.1-downloadR/lncRNAcount1.txt“
datExpr = read.table(expr_file,header=T,row.names=1,comment.char = „,“,check.names=F)
##### filtering the low expression data(express counts >0 and appears in at least 50% of the total samples )

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```

rem <- function(x){
  x <- as.matrix(x)
  x <- t(apply(x,1,as.numeric))
  r <- as.numeric(apply(x,1,function(i) sum(0<i)))
  remove <- which(r > dim(x)[2]*0.5)
  return(remove)
}

selected<- rem(datExpr)
datExpr<- datExpr[selected,] +1
dim(datExpr)

# normalizing
norExpr <- DGEList(counts=datExpr)
norExpr <- calcNormFactors(norExpr)
norExpr_cpm <- cpm(norExpr,prior.count=2, log=TRUE)###(log2-transformed)
#### filtering the low expression data(express level >0 and appears in at least 50% of the total samples )
k <- rowSums(norExpr_cpm>=1) > 130
norExpr <- norExpr[k,]
norExpr_cpm <- norExpr_cpm[k,]
dim(norExpr_cpm)
norExpr_cpm=t(norExpr_cpm)
write.table(norExpr_cpm, file = „lncRNA .txt“,sep=“\t“, row.names =T, quote = F)

#####3.mRNA preprocessing
expr_file <- „E:/SARC/4.14/tablefigure/supplementary10-R script/supplementary10.1-downloadR/RNA_Counts.txt“
data_expr = read.table(expr_file,header=T,row.names=1,comment.char = „“,check.names=F)
gene_info_file <- „E:/SARC/4.14/tablefigure/supplementary10-R script/supplementary10.1-downloadR/gene_info.txt“
##extracting mRNA matrix expression

gene_info = read.table(gene_info_file,header = 1)

cat(„Total Gene annotation:“, dim(gene_info)[1])

gene_selected <- row.names(data_expr) %in% gene_info$Gene_id

gene_expr <- data_expr[gene_selected,]

```

```

cat(„Total Gene Selected:“, dim(gene_expr)[1])

# filtering the repeating lncRNA
uniq_gene_name <- unique(rownames(gene_expr))
gene_expr <- gene_expr[uniq_gene_name,]

# transposing the data
datExpr <- t(gene_expr)

# saving the 12 bits barcode
rownames(datExpr) <- substr(rownames(datExpr), 1, 12)
datExpr <- as.data.frame(datExpr)
datExpr$bcr_patient_barcode <- row.names(datExpr)
datExpr=t(datExpr)
write.table(datExpr, file = „mRNAcount.txt“,sep=“\t“, row.names =T, quote = F)

###selecting the data
# reading the expression of the data
#####
expr_file <- „E:/SARC/4.14/tablefigure/supplementary10-R script/supplementary10.1-downloadR/mRNAcount1.txt“
datExpr = read.table(expr_file,header=T,row.names=1,comment.char = „“,check.names=F)
# filtering the low expression data(express counts >0 and appears in at least 50% of the total samples )
rem <- function(x){
  x <- as.matrix(x)
  x <- t(apply(x,1,as.numeric))
  r <-as.numeric(apply(x,1,function(i) sum(0<i)))
  remove <- which(r >dim(x)[2]*0.5)
  return(remove)
}

selected<- rem(datExpr)
datExpr<- datExpr[selected,] +1
dim(datExpr)

# normalizing
norExpr <- DGEList(counts=datExpr)
norExpr <- calcNormFactors(norExpr)

```

```

norExpr_cpm <- cpm(norExpr,prior.count=2, log=TRUE)
### ## filtering the low expression data(express level >0 and appears in at least 50% of the total samples )
k <- rowSums(norExpr_cpm>=1) > 130
norExpr <- norExpr[k,]
norExpr_cpm <- norExpr_cpm[k,]
dim(norExpr_cpm)
norExpr_cpm=t(norExpr_cpm)
write.table(norExpr_cpm, file = „mRNA .txt“,sep=“\t“, row.names =T, quote = F)

### Cox proportional hazards model R script
library(dplyr)
library(„plyr“)
library(survival)
library(rbsurv)
library(edgeR)
expr_file <- „E:/SARC/4.14/tablefigure/supplementary10-R script/supplementary10.1-downloadR/lncRNAcount1.txt“
work_dir <- „E:/SARC/4.14/tablefigure/supplementary10-R script/supplementary10.2-cox regressionR“
p_cutoff <- 0.05
top_n_select <- 20
setwd(work_dir)

#####

#####

###reading data
#####
datExpr = read.table(expr_file,header=T,row.names=1,comment.char = „“,check.names=F)
dim(datExpr)

rownames(datExpr) <- gsub(„-“,“_“,rownames(datExpr))

rem <- function(x){
  x <- as.matrix(x)
  x <- t(apply(x,1,as.numeric))
  r <-as.numeric(apply(x,1,function(i) sum(0<i)))
  remove <- which(r >dim(x)[2]*0.5)

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return(remove)
}

selected<- rem(datExpr)
datExpr<- datExpr[selected,] +1
dim(datExpr)

norExpr <- DGEList(counts=datExpr)
norExpr <- calcNormFactors(norExpr)
norExpr_cpm <- cpm(norExpr,prior.count=2, log=TRUE)

k <- rowSums(norExpr_cpm>=1) > 130
norExpr <- norExpr[k,]
norExpr_cpm <- norExpr_cpm[k,]
dim(norExpr_cpm)
gene_names <- row.names(norExpr_cpm)

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#####
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train=read.table(„train.txt“,header = T,sep=“\t“)
testing=read.table(„test.txt“,header = T,sep=“\t“)
exprSet=read.table(„exprSet.txt“,header = T,sep=“\t“)
dim(train)
dim(testing)

```

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#####
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###part1
###Univariable Cox regression analysis
#####
mysurv <- Surv(train$time, train$status)

```

```

Unicox <- function(x){
  fml <- as.formula(paste0(„mysurv~“, x))

```

```

gcox <- coxph(fml, train)
cox_sum <- summary(gcox)
HR <- round(cox_sum$coefficients[,2],2)
PValue <- round(cox_sum$coefficients[,5],6)
CI <- paste0(round(cox_sum$conf.int[,3:4],2),collapse='-')
Uni_cox <- data.frame(,Characteristics' = x,
                    ,Hazard Ratio' = HR,
                    ,CI95' = CI,
                    ,P value' = PValue)
return(Uni_cox)
}

test_var = colnames(train)[4]
Unicox(test_var)

VarNames <- gene_names
Univar <- lapply(VarNames, Unicox)

Univar <- ldply(Univar, data.frame)

uni_topN <- top_n(Univar,-top_n_select)
topN_names <- uni_topN$Characteristics
topN_expr <- t(train[,topN_names])
write.table(uni_topN, file = „top20uni .txt“,sep=“\t“, row.names =T, quote = F)

length(Univar$Characteristics[Univar$P.value < p_cutoff])
sign_gene_id <- as.character(Univar$Characteristics[Univar$P.value < p_cutoff])
uni=subset(Univar,P.value< 0.05)
write.table(uni, file = „uni .txt“,sep=“\t“, row.names =T, quote = F)

#####
#part2
###Robust analysis

```

```
#####
sign_gene_expr <- t(exprSet[sign_gene_id])
dim(sign_gene_expr)

rust_test <- matrix(as.numeric(unlist(sign_gene_expr)), nrow = nrow(sign_gene_expr))
row.names(rust_test) <- row.names(sign_gene_expr)
time <- exprSet$time
status <- exprSet$status

fit <- rbsurv(time = time, status = status, x = rust_test, method = "efron", max.n.genes = 21, n.iter = 1000, n.fold = 3, gene.ID = row.names(rust_test))

fit$model
fit <- rbsurv(time = time, status = status, x = rust_test, method = "efron", max.n.genes = 21, n.iter = 1000, n.fold = 3, gene.ID = row.names(rust_test))

#####
# part3
### Multivariable Cox regression analysis
#####

multi_var <- paste0(sign_rbsurv_gene_names, collapse = ',+')
fml <- as.formula(paste0('mysurv~', multi_var))

Multi_cox <- coxph(fml, data = train)

Multi_sum <- summary(Multi_cox)
Multi_sum

#####
# select lncRNA
```



```

multit_pvalue <- 0.18
multi_var_coefs <- Multi_sum$coefficients
multi_var_sign <- multi_var_coefs[, 'Pr(>|z|)'] < multit_pvalue
multi_sign_coefs <- multi_var_coefs[multi_var_sign,]

multi_sign_gene <- rownames(multi_sign_coefs)
multi_sign_coef <- multi_sign_coefs[, 'coef']
length(multi_sign_gene)

multi_var2 <- paste0(multi_sign_gene, collapse = ,+)
fml2 <- as.formula(paste0(mysurv~', multi_var2))
Multi_cox2 <- coxph(fml2, data=train)
Multi_cox2

Multi_sum2 <- summary(Multi_cox2)
Multi_sum2

#####
# ggforest(Multi_cox2, data = train)

#####
#PH test
zphmodel <- cox.zph(Multi_cox2)
zphmodel
plot(zphmodel)

#### DEmRNA R script
setwd(„E:/SARC/4.14/tablefigure/supplementary10-R script/supplementary10.3-DEmRNAR“)
###merging clinical data and lncRNA expression.
data1 = read.table(„mRNA.txt“, header=TRUE, sep=„\t“)
data2 = read.table(„low.txt“, header=TRUE, sep=„\t“)
data3 = data2[data2$bcr_patient_barcode %in% data1$bcr_patient_barcode,]
data4 = merge(data3, data1, by.x=„bcr_patient_barcode“, by.y=„bcr_patient_barcode“)
write.table(data4, file = „, lowgene.txt“, sep=„\t“, row.names = T, quote = F)
data2 = read.table(„high.txt“, header=TRUE, sep=„\t“)
data3 = data2[data2$bcr_patient_barcode %in% data1$bcr_patient_barcode,]

```

```
data4=merge(data3,data1,by.x="bcr_patient_barcode",by.y="bcr_patient_barcode")
write.table(data4, file = „ highgene.txt“,sep="\t“, row.names =T, quote = F)
```

```
library(limma)
rt<-read.table(„SARCgenedata.txt“,header=T,sep="\t“,row.names="Gene_id")
#differential
class<-c(rep(„low“,126),rep(„high“,133))
design<-model.matrix(~factor(class))
colnames(design)<-c(„low“,“high“)
fit<-lmFit(rt,design)
fit2<-eBayes(fit)
allDiff=topTable(fit2,adjust='fdr',coef=2,number=200000)
write.table(allDiff,file="limmaTab.xls“,sep="\t“,quote=F)
```

```
#write table
diffLab<-allDiff[with(allDiff, ((logFC>2 |logFC<(-2)) & adj.P.Val<0.05)),]
write.table(diffLab,file="diffExp.txt“,sep="\t“,quote=F)
```

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####
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```
my1=read.table(„diffExp1.txt“,header=TRUE,sep="\t“)
my2=read.table(„gene_info.txt“,header=TRUE,sep="\t“)###downloading from https://www.encodegenes.org/human/
release\_22.html
my3=my2[my2$Gene_id %in% my1$Gene_id,]
my4=merge(my3,my1,by.x="Gene_id",by.y="Gene_id")
write.table(my4, file = „ diffgene.txt“,sep="\t“, row.names =T, quote = F)
```

```
####
```

```
ht1=read.table(„SARCgenedata.txt“,header=T,sep="\t“)
ht2=my4
ht3 <- ht2[ht2$Gene_id %in% ht1$Gene_id,]
ht4<-merge(ht3,ht1,by.x="Gene_id",by.y="Gene_id")
write.table(ht4, file = „ diffgeneExp1.txt“,sep="\t“, row.names =T, quote = F)
```

```
###heatmap
```

```
library(pheatmap)
rt=read.table(„heatmapdata1.txt“,sep="\t“,header=T,row.names=1)
tiff(filename = „figure4.tif“,width = 10000,height = 6000,compression="none“,bg="white“,res=1000)
```

```
annotation=read.table(„group1.txt“,sep=“\t“,header=T,row.names=1)
ann_colors=list(group=c(High=“#EE7942“,Low=“#548B54“),type = c(LMS = „#FF6A6A“, DDLPS = „#00FF7F“,FBS=“#EE
82EE“,UDS=“#00BFFF“,SS=“#FFFF00“,MFH=“#8B5742“,MPNST=“#436EEE“,PS=“#7A67EE“,GCS=“#FFA500“))
pheatmap(rt, annotation=annotation, cluster_rows =F,cluster_cols = FALSE, annotation_colors = ann_colors,color = colorRa
mpPalette(c(„#548B54“,“#1C1C1C“, „#EE7942“))(50))
dev.off()
###heatmap
```

```
###heatmap
setwd(„E:/SARC/4.14/geneEXp“)
library(pheatmap)
rt=read.table(„heatmapdata.txt“,sep=“\t“,header=T,row.names=1)
annotation=read.table(„group.txt“,sep=“\t“,header=T,row.names=1)
ann_colors=list(group=c(High=“#EE7942“,Low=“#548B54“),type = c(LMS = „#FF6A6A“, DDLPS = „#00FF7F“,FBS=“#EE
82EE“,UDS=“#00BFFF“,SS=“#FFFF00“,MFH=“#8B5742“,MPNST=“#436EEE“,PS=“#7A67EE“,GCS=“#FFA500“))
pheatmap(rt, annotation=annotation, cluster_rows =F,cluster_cols = FALSE, annotation_colors = ann_colors,color = colorRa
mpPalette(c(„#548B54“,“#1C1C1C“, „#EE7942“))(50))
```

Table S1 412 lncRNAs selected from univariable Cox regression analysis

Ensemble ID	Hazard ratio	95% CI	P value
ENSG00000163597	1.5	1.1-2.06	0.011133
ENSG00000174171	0.79	0.62-1	0.049249
ENSG00000175746	1.31	1.02-1.69	0.037321
ENSG00000177133	0.83	0.71-0.98	0.030768
ENSG00000177640	0.72	0.55-0.94	0.0179
ENSG00000178977	0.72	0.55-0.93	0.011578
ENSG00000179082	0.69	0.5-0.95	0.02388
ENSG00000179219	1.42	1-2.02	0.04838
ENSG00000184274	1.3	1.02-1.64	0.03215
ENSG00000197670	1.32	1.03-1.69	0.028331
ENSG00000198590	1.54	1.01-2.35	0.044929
ENSG00000203497	0.69	0.5-0.95	0.021573
ENSG00000203585	1.21	1.02-1.44	0.032017
ENSG00000203930	1.26	1.07-1.49	0.006071
ENSG00000204261	0.79	0.65-0.97	0.022737
ENSG00000204971	0.64	0.42-0.97	0.033417
ENSG00000206337	0.74	0.61-0.91	0.003367
ENSG00000206573	1.7	1.04-2.77	0.034171
ENSG00000214184	1.74	1.24-2.45	0.001333
ENSG00000214999	1.53	1.1-2.11	0.01036
ENSG00000215424	1.64	1.14-2.35	0.007022
ENSG00000215533	1.22	1.05-1.41	0.008552
ENSG00000221817	0.73	0.53-1	0.049515
ENSG00000221949	0.67	0.49-0.92	0.012369
ENSG00000222012	1.26	1.07-1.49	0.005338
ENSG00000222032	1.26	1.1-1.45	0.001016
ENSG00000223768	1.48	1.07-2.03	0.016938
ENSG00000223930	1.23	1.04-1.46	0.015791
ENSG00000223991	1.28	1.04-1.57	0.017546
ENSG00000224050	1.42	1.08-1.85	0.011289
ENSG00000224093	1.5	1.09-2.06	0.013884
ENSG00000224137	0.73	0.57-0.93	0.011876
ENSG00000224184	1.25	1.08-1.45	0.002321
ENSG00000224195	0.63	0.44-0.92	0.015078
ENSG00000224413	1.18	1.01-1.38	0.0373
ENSG00000224513	0.79	0.64-0.98	0.034663
ENSG00000224533	0.57	0.36-0.89	0.013325
ENSG00000224536	0.73	0.55-0.95	0.020196
ENSG00000224635	1.39	1.02-1.89	0.035915
ENSG00000224666	0.67	0.49-0.92	0.013716
ENSG00000224745	1.67	1.07-2.62	0.023343
ENSG00000225163	2	1.29-3.11	0.002006
ENSG00000225173	1.34	1.02-1.75	0.034068
ENSG00000225218	1.88	1.22-2.91	0.004178
ENSG00000225235	0.48	0.27-0.87	0.01525
ENSG00000225399	1.2	1.02-1.42	0.031642
ENSG00000225493	1.61	1.01-2.56	0.0435
ENSG00000225511	0.84	0.73-0.97	0.01606
ENSG00000225649	1.17	1.02-1.33	0.023452
ENSG00000225721	2.06	1.36-3.13	0.00069
ENSG00000225806	1.5	1.13-1.98	0.005172
ENSG00000225969	0.67	0.51-0.89	0.005714
ENSG00000226419	1.63	1.05-2.53	0.030626
ENSG00000226659	0.73	0.54-0.99	0.040912
ENSG00000226849	1.52	1.03-2.24	0.033765
ENSG00000226935	1.42	1.02-1.99	0.038762
ENSG00000226950	1.37	1.01-1.85	0.04219
ENSG00000227484	1.87	1-3.48	0.049765
ENSG00000227486	0.78	0.62-1	0.047813
ENSG00000227495	0.67	0.46-0.99	0.043401
ENSG00000227517	1.37	1.03-1.83	0.028768
ENSG00000227542	1.47	1.14-1.89	0.002909
ENSG00000227744	1.21	1.02-1.44	0.026439
ENSG00000228060	1.58	1.05-2.37	0.026729
ENSG00000228107	1.64	1.19-2.26	0.002288
ENSG00000228137	1.86	1.2-2.88	0.005689
ENSG00000228288	1.29	1.06-1.57	0.010537
ENSG00000228427	0.81	0.66-1	0.04554
ENSG00000228459	1.43	1.12-1.82	0.004376
ENSG00000228677	1.83	1.19-2.8	0.005788
ENSG00000228686	1.49	1.06-2.11	0.023451
ENSG00000228801	1.58	1.05-2.39	0.028364
ENSG00000228817	1.52	1.06-2.2	0.023948
ENSG00000229191	1.53	1.13-2.09	0.006434
ENSG00000229214	0.79	0.65-0.98	0.027991
ENSG00000229588	0.74	0.57-0.96	0.025714
ENSG00000229688	1.5	1.08-2.09	0.014892
ENSG00000229896	1.52	1.09-2.12	0.014587
ENSG00000230074	0.78	0.63-0.98	0.035119
ENSG00000230102	0.72	0.53-0.97	0.032859
ENSG00000230107	0.54	0.36-0.83	0.004716
ENSG00000230176	1.66	1.04-2.64	0.033796
ENSG00000230366	2.2	1.41-3.42	0.00047
ENSG00000230433	2.18	1.35-3.52	0.001364
ENSG00000230536	0.46	0.22-0.95	0.036084
ENSG00000230695	1.58	1-2.5	0.04966
ENSG00000230699	1.15	1-1.33	0.045134
ENSG00000230899	2	1.28-3.12	0.002206
ENSG00000231010	0.72	0.52-0.99	0.041036
ENSG00000231050	1.31	1.03-1.67	0.026489
ENSG00000231073	1.54	1.01-2.36	0.046948
ENSG00000231074	1.59	1.02-2.5	0.042115
ENSG00000231113	1.72	1.05-2.82	0.031104
ENSG00000231185	1.22	1.01-1.49	0.040758
ENSG00000231290	1.14	1.02-1.27	0.017395
ENSG00000231426	0.68	0.47-0.98	0.040892
ENSG00000231842	1.54	1.06-2.25	0.024024
ENSG00000231881	2.19	1.59-3	1.00E-06
ENSG00000232053	1.24	1-1.52	0.046953
ENSG00000232118	1.52	1.02-2.27	0.038907
ENSG00000232811	1.44	1.06-1.96	0.019918
ENSG00000232934	0.65	0.43-0.98	0.039616
ENSG00000233143	1.34	1.03-1.74	0.029505
ENSG00000233175	0.75	0.56-0.99	0.044083
ENSG00000233242	1.83	1.04-3.22	0.03572
ENSG00000233532	1.22	1.06-1.41	0.005907
ENSG00000233593	1.25	1.04-1.5	0.017551
ENSG00000234142	0.57	0.36-0.89	0.013934
ENSG00000234155	1.36	1.09-1.69	0.005592
ENSG00000234161	1.72	1.13-2.63	0.012279
ENSG00000234215	1.46	1.07-1.99	0.016723
ENSG00000234222	1.51	1.01-2.27	0.04385
ENSG00000234290	0.76	0.59-0.98	0.032019
ENSG00000234630	1.34	1.02-1.76	0.032663
ENSG00000234848	2.37	1.08-5.18	0.031333
ENSG00000235023	1.53	1.22-1.93	0.000268
ENSG00000235051	1.3	1.02-1.65	0.032525
ENSG00000235419	0.57	0.33-0.99	0.045491
ENSG00000235423	1.35	1.02-1.79	0.038707
ENSG00000235480	0.57	0.35-0.92	0.021063
ENSG00000235488	2.11	1.41-3.15	0.000265
ENSG00000235529	1.47	1.08-2	0.014593
ENSG00000235530	1.4	1-1.96	0.047626
ENSG00000235576	0.79	0.65-0.97	0.021903
ENSG00000235884	1.15	1-1.33	0.047579
ENSG00000235933	0.68	0.46-1	0.049374
ENSG00000236008	0.57	0.37-0.88	0.011497
ENSG00000236304	1.24	1.02-1.51	0.031208
ENSG00000236333	1.14	1.03-1.25	0.008915
ENSG00000236345	1.28	1.08-1.5	0.003797
ENSG00000236528	1.91	1.08-3.37	0.026204
ENSG00000236546	0.68	0.46-0.98	0.04058
ENSG00000236682	0.72	0.56-0.93	0.012079
ENSG00000236711	1.55	1.03-2.31	0.033969
ENSG00000236756	0.62	0.39-0.98	0.042642
ENSG00000236824	1.17	1.01-1.35	0.031462
ENSG00000236935	0.7	0.52-0.95	0.020753

Table S1 (continued)

Table S1 (continued)

Ensemble ID	Hazard ratio	95% CI	P value
ENSG00000237372	0.74	0.56-0.98	0.034056
ENSG00000237413	1.24	1.02-1.51	0.033183
ENSG00000237870	1.31	1.08-1.6	0.006959
ENSG00000237903	1.44	1.01-2.06	0.046181
ENSG00000238141	2.35	1.41-3.93	0.00112
ENSG00000238280	1.74	1.07-2.83	0.024676
ENSG00000239322	1.47	1.1-1.97	0.009489
ENSG00000239415	1.32	1.07-1.63	0.010009
ENSG00000240050	1.4	1.02-1.92	0.036238
ENSG00000240086	1.16	1.02-1.33	0.023653
ENSG00000240207	0.68	0.53-0.88	0.003356
ENSG00000240687	0.74	0.57-0.98	0.036277
ENSG00000240990	1.15	1.01-1.31	0.039068
ENSG00000241954	1.72	1.17-2.54	0.00555
ENSG00000242474	1.83	1.27-2.66	0.001375
ENSG00000242540	1.29	1.05-1.59	0.014818
ENSG00000242553	1.68	1.18-2.39	0.004006
ENSG00000242797	1.31	1.04-1.66	0.019886
ENSG00000242861	0.71	0.52-0.97	0.030312
ENSG00000243155	1.62	1.2-2.2	0.001626
ENSG00000243415	1.42	1.05-1.91	0.021868
ENSG00000243766	1.19	1.01-1.41	0.038403
ENSG00000243961	1.44	1.15-1.81	0.001286
ENSG00000244578	1.22	1.04-1.43	0.012858
ENSG00000244586	1.2	1.01-1.42	0.040495
ENSG00000245017	0.71	0.53-0.97	0.029944
ENSG00000245060	0.73	0.54-0.99	0.042944
ENSG00000245156	1.52	1.01-2.29	0.043982
ENSG00000245468	0.79	0.63-0.99	0.039414
ENSG00000245556	0.66	0.44-0.99	0.047221
ENSG00000245571	0.6	0.41-0.89	0.01111
ENSG00000245910	1.37	1.02-1.86	0.03941
ENSG00000246174	1.35	1.04-1.76	0.025513
ENSG00000247121	0.59	0.39-0.9	0.015395
ENSG00000247828	0.71	0.5-1	0.049145
ENSG00000248318	1.58	1.01-2.46	0.045089
ENSG00000248371	1.24	1.03-1.5	0.024151
ENSG00000248576	0.82	0.68-0.99	0.040904
ENSG00000248698	1.21	1.06-1.38	0.004409
ENSG00000248719	2.01	1.33-3.05	0.000988
ENSG00000248734	0.63	0.46-0.85	0.003044
ENSG00000248773	1.61	1.05-2.47	0.030285
ENSG00000249328	1.34	1.08-1.67	0.007239
ENSG00000249375	1.43	1.01-2.03	0.042492
ENSG00000249406	1.29	1.01-1.65	0.041999
ENSG00000249451	1.85	1.05-3.26	0.033098
ENSG00000249572	1.41	1.03-1.92	0.029968
ENSG00000249592	1.51	1.06-2.15	0.022618
ENSG00000249628	1.36	1.16-1.59	0.000176
ENSG00000249700	0.49	0.33-0.72	0.000276
ENSG00000249786	1.65	1.06-2.58	0.027486
ENSG00000249816	1.21	1.01-1.45	0.040618
ENSG00000250057	0.48	0.25-0.91	0.023988
ENSG00000250131	0.65	0.44-0.95	0.027371
ENSG00000250432	0.65	0.46-0.94	0.020295
ENSG00000250634	1.7	1.08-2.67	0.021346
ENSG00000250748	1.26	1.09-1.44	0.001237
ENSG00000250906	1.48	1.04-2.1	0.029688
ENSG00000250917	1.51	1.12-2.04	0.007517
ENSG00000251095	1.67	1.27-2.21	0.000305
ENSG00000251141	0.75	0.57-1	0.046501
ENSG00000251330	0.52	0.31-0.86	0.010373
ENSG00000251533	0.83	0.7-0.97	0.020285
ENSG00000251615	0.72	0.53-0.98	0.037115
ENSG00000253163	1.28	1.05-1.55	0.012242
ENSG00000253284	1.28	1.02-1.61	0.032851
ENSG00000253438	1.45	1.12-1.88	0.004775
ENSG00000253508	1.26	1.02-1.55	0.031171
ENSG00000253553	1.33	1.02-1.73	0.038069
ENSG00000253			

Table S1 (continued)

Ensemble ID	Hazard ratio	95% CI	P value
ENSG00000261286	1.61	1.04-2.51	0.034422
ENSG00000261359	0.6	0.38-0.93	0.021178
ENSG00000261404	1.4	1.05-1.88	0.023507
ENSG00000261416	0.71	0.54-0.95	0.0203
ENSG00000261550	0.68	0.47-0.99	0.042551
ENSG00000261567	1.8	1.27-2.54	0.000994
ENSG00000261625	0.76	0.65-0.9	0.001072
ENSG00000261670	1.54	1.08-2.2	0.017022
ENSG00000261707	0.68	0.49-0.94	0.020126
ENSG00000261786	1.12	1.01-1.25	0.035224
ENSG00000261889	0.71	0.51-0.98	0.036277
ENSG00000262039	2.13	1.29-3.5	0.00306
ENSG00000262133	0.69	0.49-0.97	0.032913
ENSG00000262172	1.41	1.05-1.9	0.023135
ENSG00000262185	0.81	0.67-0.98	0.033593
ENSG00000262227	1.35	1.02-1.78	0.03422
ENSG00000262370	0.77	0.63-0.96	0.019105
ENSG00000262420	0.68	0.46-0.99	0.045729
ENSG00000262678	1.59	1.06-2.38	0.024354
ENSG00000263069	1.43	1.05-1.94	0.022917
ENSG00000263335	0.57	0.41-0.78	0.000489
ENSG00000263393	1.55	1.05-2.3	0.028469
ENSG00000263612	1.44	1.09-1.89	0.009325
ENSG00000263766	1.77	1.06-2.95	0.028637
ENSG00000263823	1.36	1.01-1.83	0.04206
ENSG00000264263	1.5	1.07-2.11	0.019126
ENSG00000264513	1.49	1.01-2.18	0.043351
ENSG00000264808	1.94	1.38-2.74	0.00014
ENSG00000265533	1.47	1.02-2.12	0.037294
ENSG00000265579	1.21	1.06-1.39	0.004812
ENSG00000266402	1.36	1.06-1.76	0.017258
ENSG00000266441	1.31	1.03-1.66	0.027011
ENSG00000266680	0.73	0.57-0.94	0.014165
ENSG00000266821	0.53	0.28-0.98	0.041976
ENSG00000266846	0.61	0.38-0.96	0.034476
ENSG00000267024	0.48	0.29-0.8	0.004761
ENSG00000267069	0.81	0.67-0.98	0.028307
ENSG00000267130	1.31	1.01-1.69	0.041977
ENSG00000267131	1.31	1.03-1.66	0.025849
ENSG00000267141	1.81	1.11-2.94	0.016618
ENSG00000267191	1.34	1.01-1.76	0.040617
ENSG00000267249	0.53	0.34-0.85	0.007964
ENSG00000267275	0.58	0.36-0.92	0.019742
ENSG00000267280	1.46	1.15-1.84	0.001533
ENSG00000267288	0.76	0.6-0.97	0.026795
ENSG00000267316	0.51	0.28-0.94	0.030168
ENSG00000267416	1.66	1.17-2.36	0.0049
ENSG00000267532	0.82	0.71-0.95	0.007175
ENSG00000267667	1.47	1.16-1.86	0.001467
ENSG00000267778	1.54	1.14-2.09	0.005391
ENSG00000267783	1.46	1.02-2.07	0.03714
ENSG00000267886	1.21	1.01-1.46	0.036562
ENSG00000268288	0.57	0.34-0.95	0.030948
ENSG00000268583	2.17	1.34-3.53	0.001733
ENSG00000268592	0.74	0.57-0.96	0.0212
ENSG00000268947	1.48	1.12-1.96	0.006597
ENSG00000269842	1.51	1.1-2.07	0.010283
ENSG00000269902	1.47	1.09-1.99	0.011949
ENSG00000269983	1.84	1.04-3.26	0.035509
ENSG00000270068	2.15	1.12-4.11	0.020793
ENSG00000270077	0.63	0.41-0.96	0.03323
ENSG00000270177	0.65	0.47-0.89	0.008147
ENSG00000270179	0.77	0.61-0.97	0.028319
ENSG00000270182	2.07	1.3-3.28	0.002057
ENSG00000270959	0.64	0.44-0.93	0.01895
ENSG00000271009	0.78	0.61-0.99	0.044115
ENSG00000271147	1.52	1.01-2.27	0.043101
ENSG00000271218	1.34	1.04-1.72	0.021601
ENSG00000271344	0.68	0.51-0.91	0.009712
ENSG00000271646	0.75	0.56-1	0.048241
ENSG00000271824	1.19	1.02-1.38	0.024556
ENSG00000271849	0.71	0.54-0.95	0.018929
ENSG00000271882	0.71	0.51-0.97	0.031559
ENSG00000271888	1.63	1.19-2.23	0.002192
ENSG00000271926	0.66	0.46-0.94	0.019872
ENSG00000271970	0.73	0.54-1	0.048392
ENSG00000271978	1.36	1.04-1.77	0.025536
ENSG00000272056	0.63	0.45-0.88	0.007047
ENSG00000272100	1.7	1.19-2.42	0.003666
ENSG00000272121	1.18	1.03-1.36	0.020592
ENSG00000272323	0.79	0.63-0.98	0.035321
ENSG00000272356	1.7	1.13-2.56	0.01026
ENSG00000272389	0.64	0.44-0.94	0.021323
ENSG00000272411	0.69	0.49-0.96	0.029431
ENSG00000272502	1.27	1.04-1.54	0.018815
ENSG00000272589	0.57	0.34-0.96	0.034835
ENSG00000272610	1.37	1.02-1.85	0.037737
ENSG00000272727	1.37	1.09-1.73	0.006505
ENSG00000272902	0.63	0.44-0.9	0.011908
ENSG00000272915	1.44	1.01-2.04	0.041703
ENSG00000273014	0.6	0.41-0.89	0.010761
ENSG00000273058	0.71	0.52-0.96	0.024144
ENSG00000273342	1.42	1.02-1.98	0.040582
ENSG00000273447	0.74	0.56-0.99	0.039853
ENSG00000273584	1.46	1.05-2.03	0.022602
ENSG00000273733	0.8	0.64-1	0.047417
ENSG00000273972	0.52	0.32-0.84	0.007917
ENSG00000274021	1.4	1.11-1.76	0.00439
ENSG00000274029	0.66	0.5-0.87	0.00339
ENSG00000274372	1.37	1.09-1.73	0.007876
ENSG00000274422	1.37	1.03-1.82	0.032776
ENSG00000274695	0.54	0.32-0.93	0.024934
ENSG00000274767	0.71	0.55-0.92	0.00933
ENSG00000274859	1.86	1.03-3.35	0.038481
ENSG00000274943	1.38	1.07-1.78	0.013444
ENSG00000275040	0.56	0.33-0.93	0.026495
ENSG00000275179	0.64	0.42-0.98	0.04083
ENSG00000275343	0.58	0.35-0.95	0.028918
ENSG00000275846	1.67	1.07-2.61	0.025019
ENSG00000275963	0.67	0.48-0.93	0.017413
ENSG00000276337	1.36	1.01-1.82	0.041248
ENSG00000276533	0.7	0.53-0.91	0.00815
ENSG00000276718	0.6	0.44-0.82	0.001446
ENSG00000276768	1.55	1-2.39	0.047815
ENSG00000276900	1.39	1.01-1.93	0.044473
ENSG00000276995	0.7	0.5-0.98	0.039128
ENSG00000277873	0.67	0.46-0.98	0.037256
ENSG00000277954	0.79	0.66-0.94	0.009326
ENSG00000278058	0.65	0.49-0.85	0.001775
ENSG00000278200	1.36	1.08-1.7	0.008115
ENSG00000278638	1.68	1.03-2.74	0.036278
ENSG00000278703	0.72	0.53-0.98	0.037778
ENSG00000278719	1.84	1.16-2.9	0.008998
ENSG00000278743	1.42	1.06-1.91	0.019866
ENSG00000279038	1.56	1.07-2.26	0.019458
ENSG00000280156	1.34	1.08-1.68	0.009338
ENSG00000280279	1.33	1.02-1.74	0.037285
ENSG00000280303	1.38	1.04-1.85	0.027548
ENSG00000280370	1.52	1.01-2.28	0.042778
ENSG00000280434	1.24	1-1.52	0.048919
ENSG00000280543	1.45	1.03-2.06	0.033643
ENSG00000280953	1.38	1.14-1.67	0.001137
ENSG00000281016	1.49	1.06-2.09	0.021985
ENSG00000281332	0.65	0.45-0.92	0.014219
ENSG00000281376	1.31	1.03-1.67	0.030052
ENSG00000281591	0.73	0.55-0.97	0.028232
ENSG00000281852	0.79	0.65-0.97	0.022503
ENSG00000281881	1.45	1.12-1.88	0.004861

Table S2 Proportional hazards assumption of Cox proportional hazards model

lncRNA	Ensembl ID	rho	chisq	P
<i>AC018645.2</i>	ENSG00000273014	-0.0191	0.0198	0.888
<i>LINC02454</i>	ENSG00000256268	-0.0549	0.1387	0.71
<i>ERICD</i>	ENSG00000280303	0.2012	1.7156	0.19
<i>DSCR9</i>	ENSG00000230366	0.0489	0.1056	0.745
<i>AL031770.1</i>	ENSG00000230433	0.0178	0.0166	0.898
<i>GLOBAL</i>		NA	2.2682	0.811

Table S3 44 DEmRNAs between the high-risk group and the low-risk group

Ensemble ID	gene_name	logFC	P value	adj.P.Val
ENSG00000054938	CHRD2	3.250918	3.18E-11	5.52E-09
ENSG00000055118	KCNH2	2.970302	1.34E-11	2.9E-09
ENSG00000065534	MYLK	2.51435	4.78E-11	7.46E-09
ENSG00000069535	MAOB	2.304127	7.71E-09	3.7E-07
ENSG00000072952	MRVI1	2.339071	1.14E-14	2.81E-11
ENSG00000077157	PPP1R12B	2.549512	1.39E-14	2.87E-11
ENSG00000077274	CAPN6	2.312172	0.0000093	0.000096
ENSG00000095637	SORBS1	2.289595	2.21E-11	4.02E-09
ENSG00000100628	ASB2	2.52334	2.61E-09	1.62E-07
ENSG00000103710	RASL12	2.213783	2.27E-12	9.01E-10
ENSG00000106772	PRUNE2	2.185523	1.19E-11	2.76E-09
ENSG00000109339	MAPK10	2.133807	4.34E-10	4.25E-08
ENSG00000112183	RBM24	2.155162	0.00000021	4.77E-06
ENSG00000121577	POPDC2	2.071798	1.71E-15	7.03E-12
ENSG00000130176	CNN1	3.052829	1.34E-11	2.9E-09
ENSG00000131471	AOC3	2.112268	1.2E-13	1.06E-10
ENSG00000133392	MYH11	4.11097	1.52E-13	1.25E-10
ENSG00000136842	TMOD1	2.148349	1.6E-09	1.11E-07
ENSG00000137558	PI15	2.165601	0.000000023	8.96E-07
ENSG00000140285	FGF7	2.079786	4.65E-09	2.5E-07
ENSG00000145936	KCNMB1	2.565684	5.4E-11	8.02E-09
ENSG00000146477	SLC22A3	2.342808	4.64E-10	4.4E-08
ENSG00000148357	HMCN2	2.589182	1.07E-10	1.41E-08
ENSG00000149591	TAGLN	2.059747	1.23E-08	5.4E-07
ENSG00000149596	JPH2	2.361934	3.61E-08	1.25E-06
ENSG00000154330	PGM5	2.57784	2.52E-14	4.17E-11
ENSG00000163017	ACTG2	3.038325	1.01E-09	7.94E-08
ENSG00000163431	LMOD1	2.973749	3.01E-12	1.02E-09
ENSG00000163531	NFASC	2.087288	7.79E-10	6.62E-08
ENSG00000164107	HAND2	2.237149	2.67E-08	9.96E-07
ENSG00000164764	SBSPON	2.777236	1.79E-12	7.87E-10
ENSG00000166825	ANPEP	-2.00357	1.34E-09	9.87E-08
ENSG00000167641	PPP1R14A	2.067059	1.85E-11	3.57E-09
ENSG00000167676	PLIN4	2.78314	1.52E-12	7.65E-10
ENSG00000169083	AR	2.316037	5.97E-12	1.71E-09
ENSG00000170500	LONRF2	2.885893	6.76E-12	1.85E-09
ENSG00000172061	LRRC15	-2.19654	0.00000509	0.0000594
ENSG00000172403	SYNPO2	2.768896	5.24E-14	5.88E-11
ENSG00000173175	ADCY5	2.418178	5.83E-11	8.45E-09
ENSG00000175084	DES	3.193704	0.000000144	3.58E-06
ENSG00000185052	SLC24A3	2.266278	2.75E-09	1.67E-07
ENSG00000185274	WBSCR17	2.288665	4.66E-08	1.52E-06
ENSG00000198523	PLN	2.304658	0.000000232	5.14E-06
ENSG00000198848	CES1	2.146793	0.0000121	0.0001194

lncRNA, long non-coding RNA; DEmRNA, differentially expressed messenger RNA.