

**Appendix 1**

```

library(survival)

# ----- 1) Define coefficients (fill with your final model) -----
coef <- c(
  PANX1=0.4449, GPR107=0.4443, MTFR1=0.2276, FKBP5=-0.1919,
  CD24=0.1577, CRISP3=0.0647, NPY1R=-0.0753, ADIRF=-0.0578
)

genes <- names(coef)

# ----- 2) Preprocess expression -----
# RNA-seq: expr_fpkms is a matrix (rows=genes, cols=samples) or data.frame
fpkm_to_tpm <- function(fpkm_mat){
  # columns sum to 1e6
  tpm <- sweep(fpkm_mat, 2, colSums(fpkm_mat), "/") * 1e6
  return(tpm)
}

log2_tpm1 <- function(tpm_mat){
  log2(tpm_mat + 1)
}

# Microarray: assume already log2 normalized. Ensure gene symbols and collapse probes beforehand.

# ----- 3) Compute CRPRG score -----
compute_score <- function(expr_mat_log2, coef){
  # expr_mat_log2: matrix with gene symbols as rownames, samples as columns
  expr_sub <- expr_mat_log2[names(coef), , drop=FALSE]
  score <- as.numeric(crossprod(coef, expr_sub)) # 1 x n
  names(score) <- colnames(expr_sub)
  score
}

# ----- 4) (Recommended) Center score using training mean -----
center_score <- function(score, train_mean){
  score - train_mean
}

# ----- 5) Fit Cox model on training set -----
# dat_train must contain: time, status (1=event), and sample_id matching score names.
fit_cox <- function(dat_train, score_centered){
  dat_train$CRPRG <- score_centered[dat_train$sample_id]
  coxph(Surv(time, status) ~ CRPRG, data=dat_train, x=TRUE)
}

```

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# ----- 6) Extract baseline survival at 1/3/5 years -----
get_baseline_S0 <- function(fit, times_days=c(365, 1095, 1825)){
  # baseline at CRPRG=0 (i.e., centered reference)
  sf0 <- survfit(fit, newdata=data.frame(CRPRG=0))
  s <- summary(sf0, times=times_days)$surv
  out <- data.frame(time=times_days, S0=s)
  out
}

# ----- 7) Predict survival for a single sample -----
predict_survival <- function(fit, crprg_value, times_days=c(365,1095,1825)){
  sf <- survfit(fit, newdata=data.frame(CRPRG=crprg_value))
  data.frame(time=times_days, S=summary(sf, times=times_days)$surv)
}

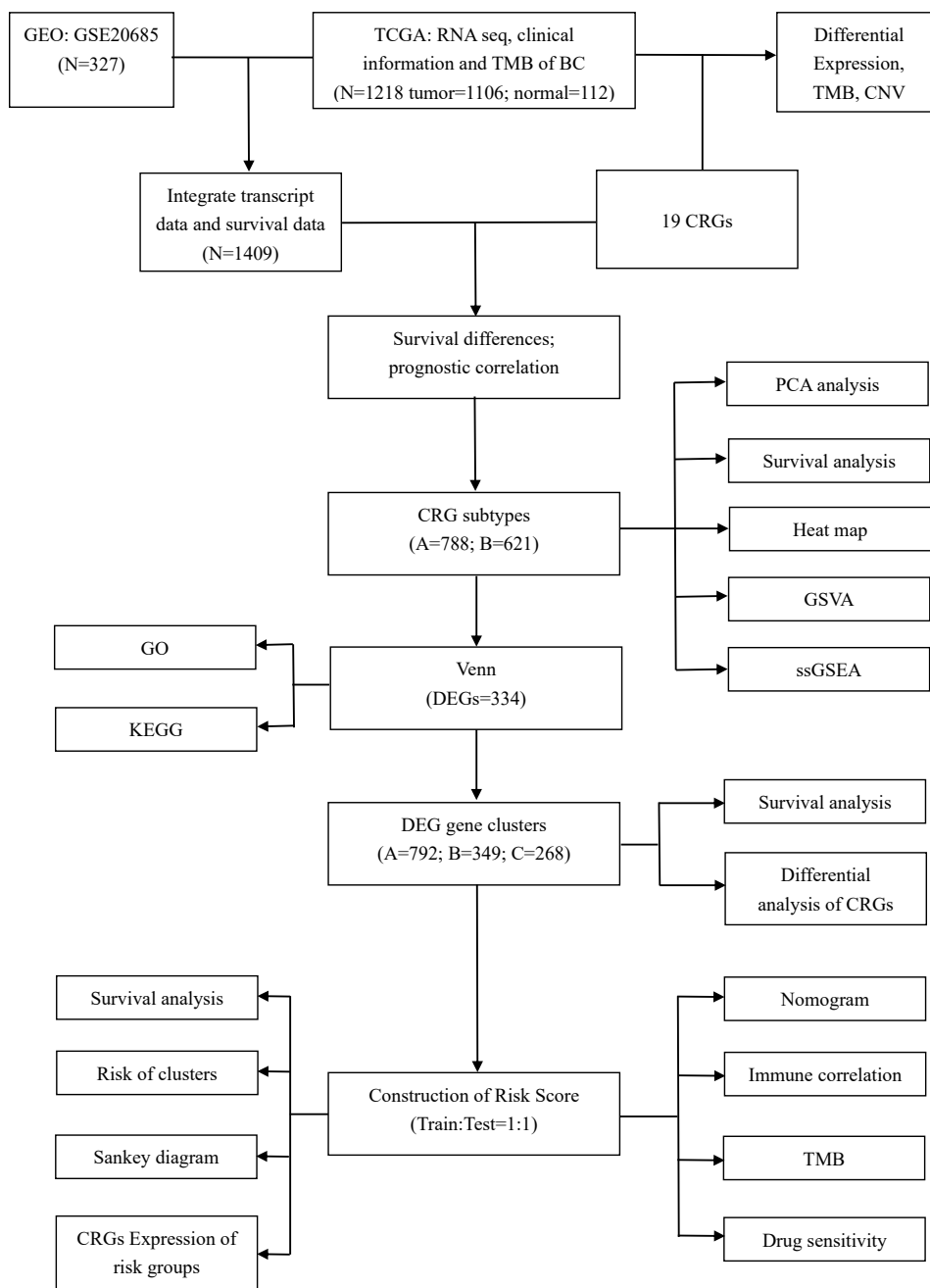
# ===== Example workflow (YOU fill real objects) =====
# expr_fpk_train <- ... # genes x samples
# tpm_train <- fpkm_to_tpm(expr_fpk_train)
# expr_log2_train <- log2_tpm1(tpm_train)

# score_train_raw <- compute_score(expr_log2_train, coef)
# train_mean <- mean(score_train_raw, na.rm=TRUE) # report this in Table Sx
# score_train <- center_score(score_train_raw, train_mean)

# fit <- fit_cox(dat_train, score_train)
# baseline_table <- get_baseline_S0(fit) # put into Table Sx (1/3/5y)

## External cohort:
# expr_log2_ext <- ... # after platform-specific preprocessing
# score_ext_raw <- compute_score(expr_log2_ext, coef)
# score_ext <- center_score(score_ext_raw, train_mean)
# pred_one <- predict_survival(fit, crprg_value=score_ext["SAMPLE_A"])

```

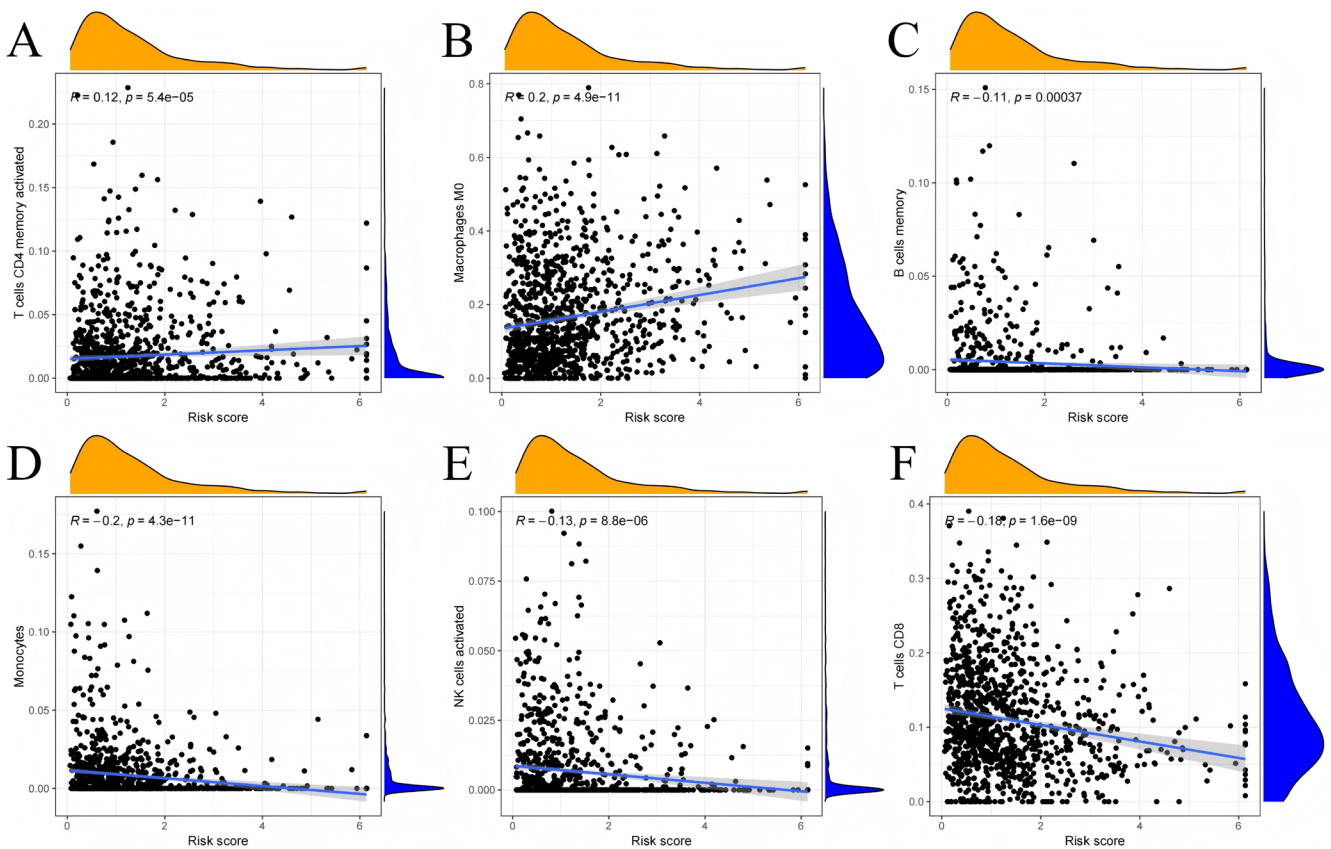


**Figure S1** Flow diagram of this study.

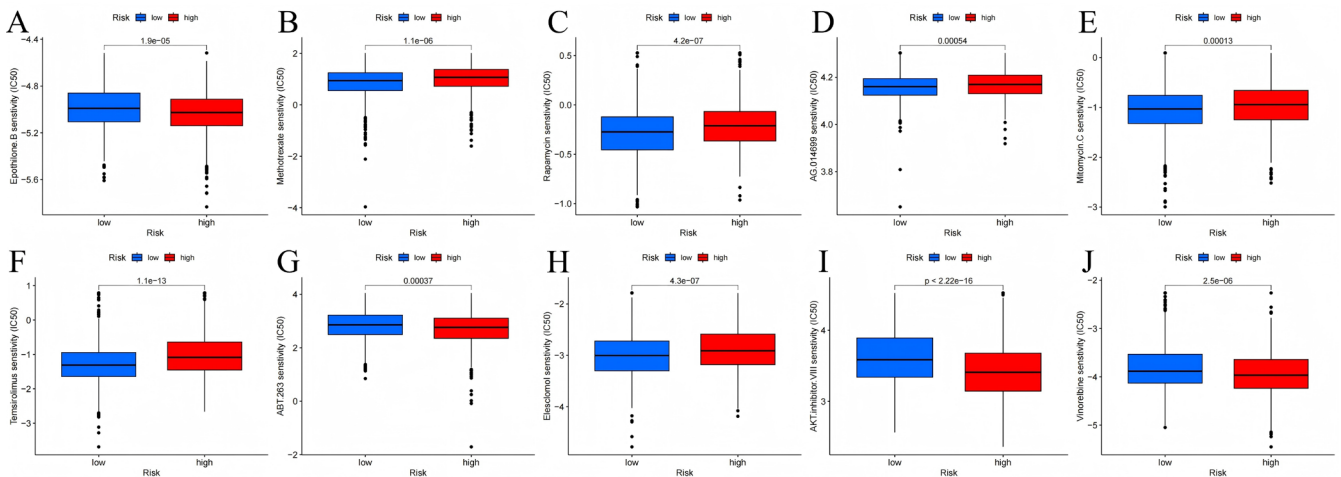
**Table S1** Clinical characteristics of the cohort

Characteristics	Classification	Training set (n=705)	Testing set (n=704)	P value
Age		55.88±13.34	56.04±13.51	0.82
OS (years)		3.13 (1.43-7.00)	3.12 (1.50-6.59)	0.58
Status				0.56
	0	594 (84.3%)	584 (83.0%)	
	1	111 (15.7%)	120 (17.0%)	
Stage				0.58
	1	116 (16.5%)	134 (19.0%)	
	2	384 (54.5%)	373 (53.0%)	
	3	180 (25.5%)	166 (23.6%)	
	4	12 (1.7%)	13 (1.8%)	
	Unknown	13 (1.8%)	18 (2.6%)	
T Stage				0.42
	1	174 (24.7%)	204 (29.0%)	
	2	417 (59.1%)	392 (55.7%)	
	3	81 (11.5%)	81 (11.5%)	
	4	28 (4.0%)	22 (3.1%)	
	Unknown	5 (0.7%)	5 (0.7%)	
N Stage				0.73
	0	332 (47.1%)	314 (44.6%)	
	1	211 (29.9%)	230 (32.7%)	
	2	88 (12.5%)	93 (13.2%)	
	3	61 (8.7%)	53 (7.5%)	
	Unknown	13 (1.8%)	14 (2.0%)	

Age is tested by Welch t; OS was tested by Mann-Whitney U; The Chi-squared test was used for categorical variables (Fisher's exact test if necessary).



**Figure S2** Relationship between CRPRG score and immune cells. The correlation between CRPRG and (A) Activated CD4 memory T cells, (B) M0 macrophages, (C) B memory cells, (D) Monocytes, (E) Activated NK cells, (F) CD8<sup>+</sup> T cells.



**Figure S3** Relationships between CRPRG score and drug sensitivity. The 50% inhibitory concentration of (A) epothilone-B, (B) methotrexate, (C) rapamycin, (D) AG014699, (E) mitomycin-C, (F) temsirolimus, (G) ABT-263, (H) elesclomol, (I) AKT-inhibitor-VIII, (J) vinorelbine in the high-risk and low-risk groups.