For i = 1 to 10 splits do

Split D into D_i^{train}, D_i^{test} for ith split

For n = 20, 30, 40, …, 500 do

For j = 1 to 10 splits do

Split D_i^{train} into $SubD_j^{train}$, $SubD_j^{test}$

$Index_n$ <- mrmr ($SubD_j^{train}$, n)

$Sub_n_ D_j^{train}$ <- $SubD_j^{train}(Index_n)$

$Sub_n_ D_j^{test}$ <- $SubD_j^{test}(Index_n)$

$Predict_j$ <- simpleMKL ($Sub_n_ D_j^{train}$, $Sub_n_ D_j^{test}$)

Auc_j <- auc ($Predict_j$)

End

Auc_n <- mean(Auc_j)

End

[best_Auc, best_N] = max(Auc_n)
$Index_N$ <- mrmr (D_i^{train}, best_N)
$Sub_N_ D_i^{train}$ <- $D_i^{train}(Index_N)$

$Sub_N_ D_i^{test}$ <- $D_i^{test}(Index_N)$

$Predict_i$ <- simpleMKL ($Sub_N_ D_i^{train}$, $Sub_N_ D_i^{test}$)

AUC_i <- auc ($Predict_i$)

End

AUC <- mean(AUC_i)

Figure S1. 10-fold Nested Cross-Validation with Omics_MKL

Note**:** a. D represents all omics data. n is the number of selected features.

b. mrmr is a filter method of feature selection.

(mrmr: Minimum Redundancy and Maximum Relevance)

c: simpleMKL: is a classifier.

(MKL: multiple kernel learning)