

Summary Table

#Genes	#Samples
1283	89
1283	74
1283	105

About

Advanced Options

Methods for MetaPredict

Mean score

Max number of top scoring pairs (K)

10

Number of cores for parallel computing

1

Please select TWO labels to cluster

inv(16) t(8;21)

Please select studies for training

study1.csv study2.csv

Please select ONE study for testing

study3.csv

Train model

Number of top scoring pairs (K)

9

Predict

(1)

Gene pair table

GeneIndex1	GeneIndex2	Gene1	Gene2	Score_overall	Score_study1	Score_study2
238	1001	HCLS1	ITGB2	1.96	1.00	0.96
68	109	ITM2B	LAPTM5	1.90	0.97	0.93
182	209	HNRNPAB	LCP1	1.89	1.00	0.89
262	483	FAM101B	ADRM1	-1.89	-0.89	-1.00
181	198	TUBB4B	PLP2	1.87	0.94	0.93
878	958	CBFB	RASSF2	1.87	0.94	0.93
325	651	IL2RG	CFP	1.84	0.88	0.96
338	437	HCST	VAT1	-1.84	-0.91	-0.93
207	216	TYROBP	HLA-E	-1.83	-0.94	-0.89
716	1229	ABCC1	SASH3	1.83	0.94	0.89

(3)

Confusion Table

Original_inv(16)	Original_t(8;21)
26	4
2	36

(2)

K diagnostic plot

