

### Survival analysis result using only gene expression

Cancer Type	Average of Low-Level Scores	Average of High-Level Scores
Brca_hypo	0.36	0.494
Lusc_hypo	0.347	0.487
Coad_hypo	0.374	0.563
Kirc_hypo	0.401	0.515
Brca_hyper	0.365	0.497
Lusc_hyper	0.335	0.4819
Coad_hyper	0.374	0.567
Kirc_hyper	0.394	0.509

Cancer Type	Gene Name	Prognostic Score Level	Hazard Rate	P-value	Number of patients at score level	Number of deaths
Lusc_hypo	ADGRD1	low	1.6715	0.0129	102	46

### Survival analysis result using only DNA methylation

Cancer Type	Average of Low-Level Scores	Average of High-Level Scores
Brca_hypo	0.247	0.648
Lusc_hypo	0.287	0.618
Coad_hypo	0.224	0.567
Kirc_hypo	0.187	0.476
Brca_hyper	0.364	0.765
Lusc_hyper	0.325	0.700
Coad_hyper	0.362	0.750
Kirc_hyper	0.488	0.846

Cancer Type	Gene Name	Prognostic Score Level	Hazard Rate	P-value	Number of patients at score level	Number of deaths
Coad_hypo	CPQ	High	3.280e-01	0.0456	44	4
Lusc_hypo	LPCAT1	high	2.1294	0.00439	40	20
	IMMP2L	low	1.7847	0.032	44	19
	IMMP2L	high	1.7056	0.0112	97	42

### Survival analysis result using only mutation status

Cancer Type	Gene Name	Hazard Rate	P-value	Number of patients with the mutation	Number of deaths
Brca_hypo	ADGRD1	41.302	0.001	5	1
Coad_hyper	SLC9A3	3.791	0.009	9	5
	BRIP1	3.096	0.069	7	3