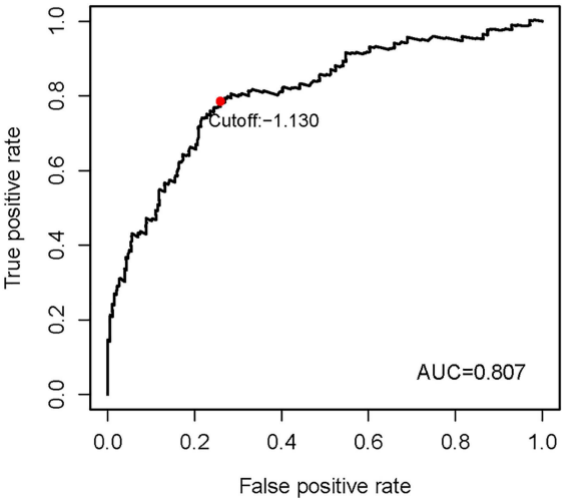
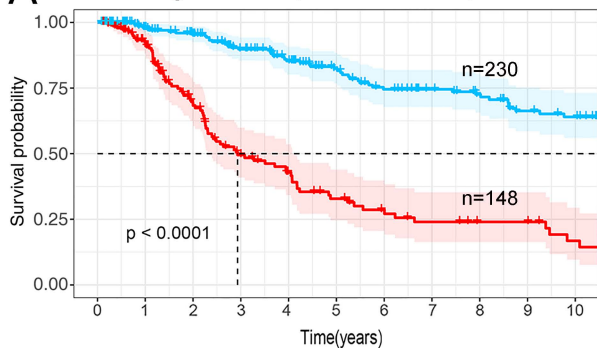


Fig 1

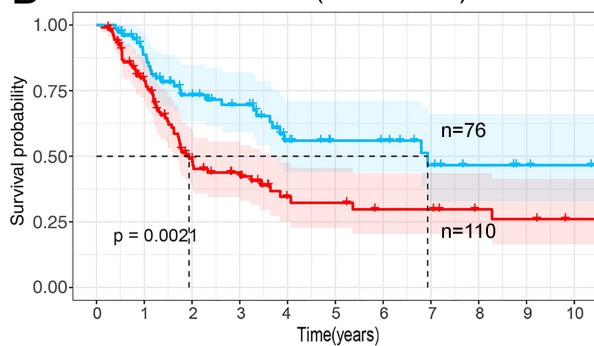


A Training dataset (TCGA-SKCM) n=378



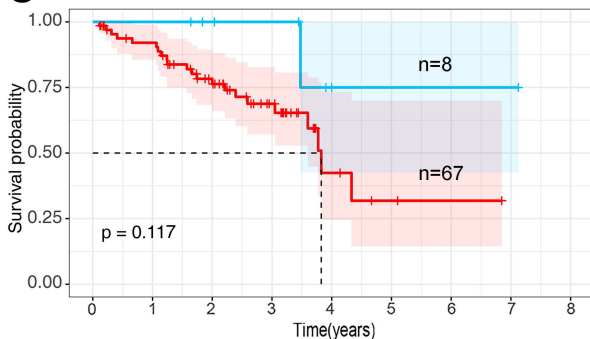
High risk	148	116	73	47	35	25	19	15	12	12	7
Low risk	230	194	177	152	130	107	92	80	72	60	56

B Validation dataset (GSE65904) n=186



High risk	110	75	39	29	15	14	11	11	8	7	5
Low risk	76	60	43	35	21	16	15	10	7	5	4

C Validation dataset (TCGA-UVM) n=75



High risk	67	56	39	21	5	2	1	0	0
Low risk	8	8	6	5	1	1	1	1	0

High risk Low risk

Fig 2

A Training dataset (TCGA-SKCM) n=378

Univariate analyses

	P-value	HR(95%CI)
Age	0.005	1.023(1.007-1.039)
Gender	0.328	1.297(0.770-2.185)
Stage	<0.001	1.538(1.205-1.962)
T_stage	<0.001	1.828(1.431-2.337)
N_stage	<0.001	1.546(1.212-1.973)
Clark_level	0.006	1.506(1.128-2.011)
RiskScore	<0.001	3.831(2.726-5.383)

Multivariate analyses

	P-value	HR(95%CI)
Age	0.129	1.012(0.997-1.028)
Gender	0.697	1.115(0.645-1.926)
Stage	0.630	1.210(0.557-2.625)
T_stage	0.145	1.428(0.885-2.305)
N_stage	0.923	0.970(0.526-1.791)
Clark_level	0.293	0.819(0.565-1.188)
RiskScore	<0.001	3.453(2.392-4.985)

B Validation dataset (GSE65904) n=186

Univariate analyses

	P-value	HR(95%CI)
Gender	0.249	1.302(0.832-2.039)
Age	0.713	0.997(0.982-1.012)
Stage	<0.001	1.405(1.167-1.692)
RiskScore	0.002	1.723(1.226-2.423)

Multivariate analyses

	P-value	HR(95%CI)
Gender	0.233	1.316(0.838-2.065)
Age	0.986	1.000(0.985-1.015)
Stage	<0.001	1.457(1.211-1.754)
RiskScore	<0.001	1.902(1.319-2.744)

C Validation dataset (TCGA-UVM) n=75

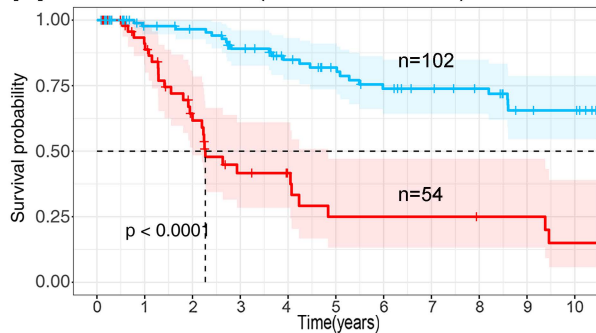
Univariate analyses

	P-value	HR(95%CI)
Age	0.019	1.046(1.008-1.085)
Gender	0.325	1.542(0.651-3.652)
Stage	0.234	1.311(0.839-2.048)
T stage	0.195	1.941(0.712-5.294)
RiskScore	0.004	5.213(1.686-16.120)

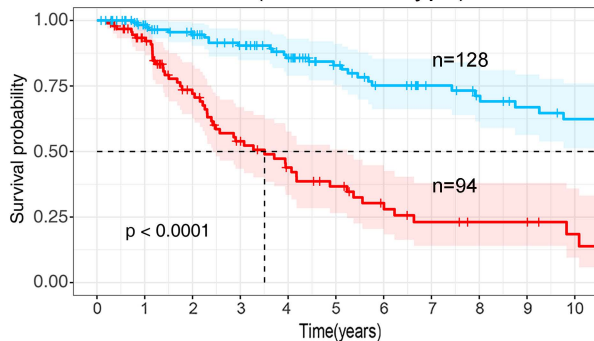
Multivariate analyses

	P-value	HR(95%CI)
Age	0.010	1.051(1.012-1.092)
Gender	0.484	1.376(0.563-3.366)
Stage	0.176	1.392(0.862-2.246)
T stage	0.443	1.506(0.529-4.291)
RiskScore	0.002	7.645(2.054-28.452)

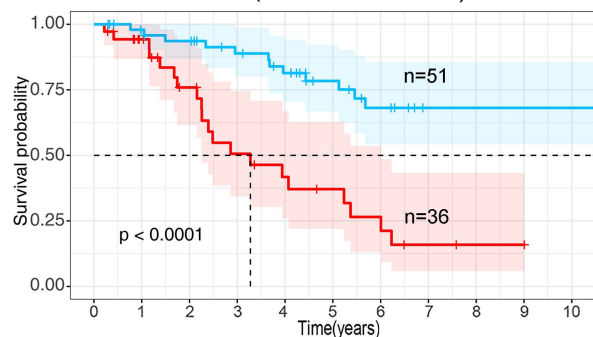
Fig 3

A TCGA-SKCM (*BRAF*-mutated) n=156

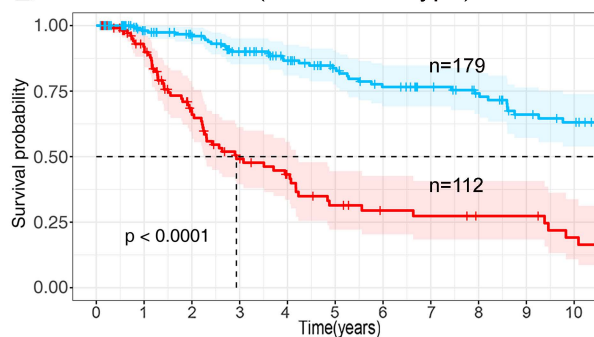
High risk	54	40	24	13	10	6	6	6	5	5	3
Low risk	102	84	80	68	51	45	41	38	30	29	

B TCGA-SKCM (*BRAF*-wild-type) n=222

High risk	94	76	49	34	25	19	13	9	7	7	4
Low risk	128	110	97	84	72	56	47	39	34	30	27

C TCGA-SKCM (*NRAS*-mutated) n=87

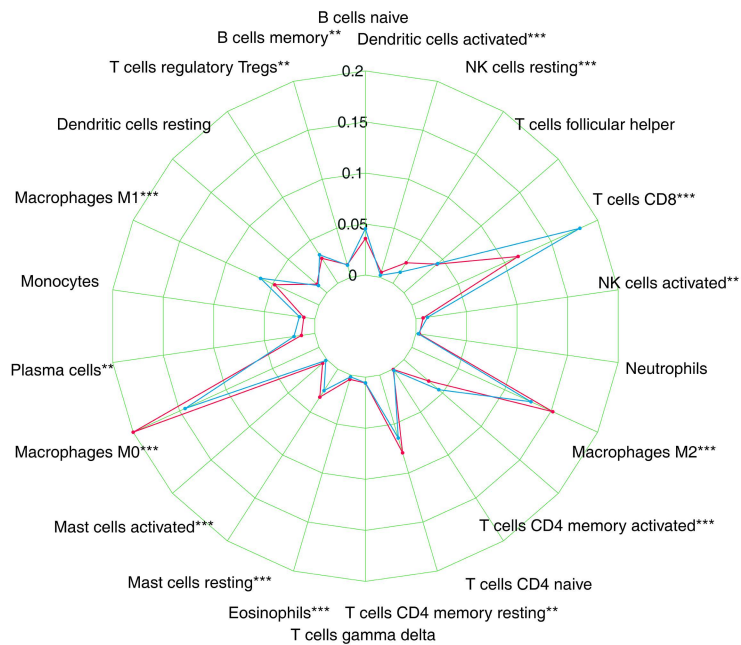
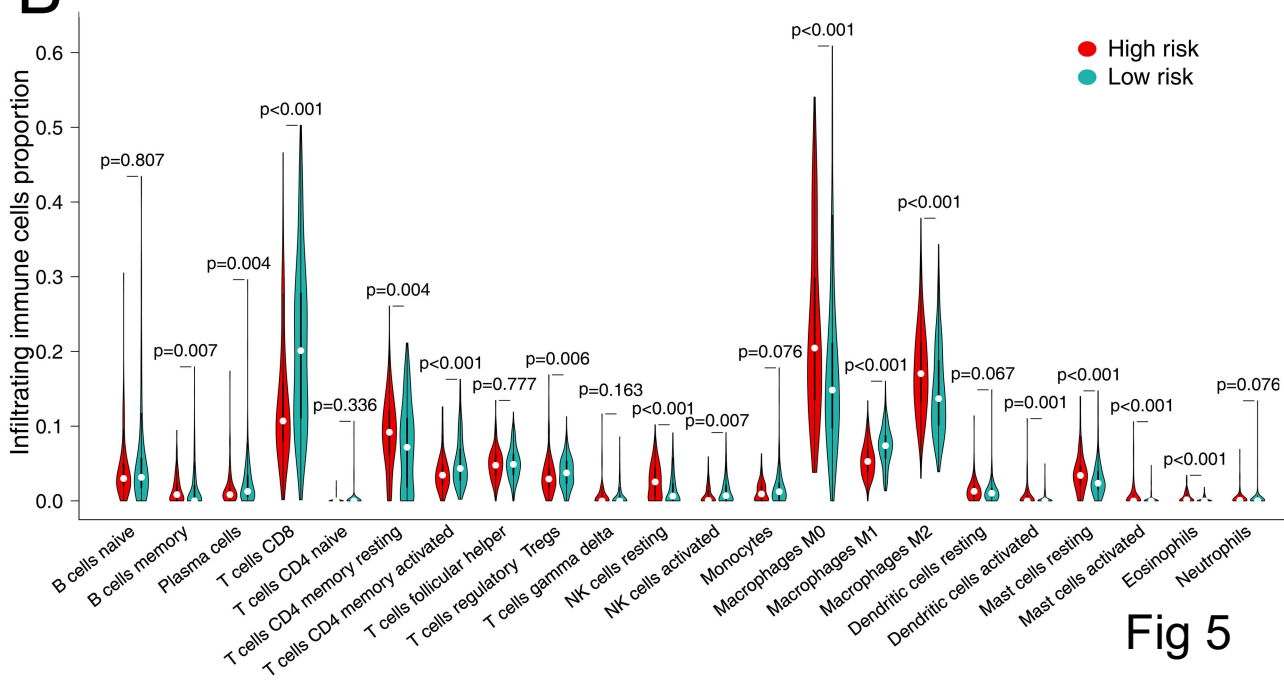
High risk	36	28	19	12	9	7	5	2	1	1	0
Low risk	51	46	43	37	32	24	19	14	14	14	14

D TCGA-SKCM (*NRAS*-wild-type) n=291

High risk	112	88	54	35	26	18	14	13	11	11	7
Low risk	179	148	134	115	98	83	73	66	58	46	42

High risk Low risk

Fig 4

A**B****Fig 5**

Enrichment KEGG Pathways

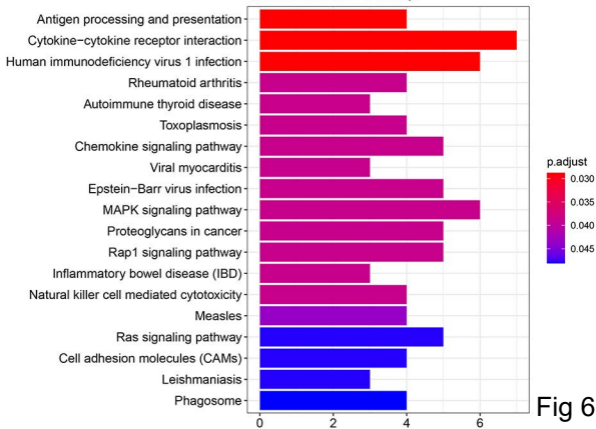
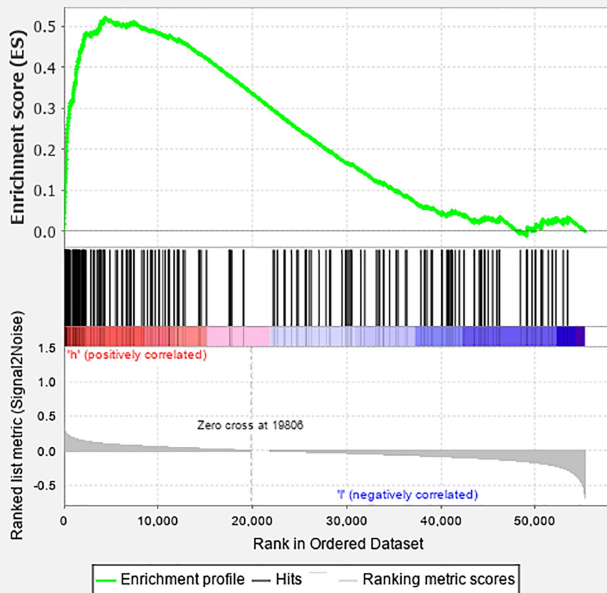
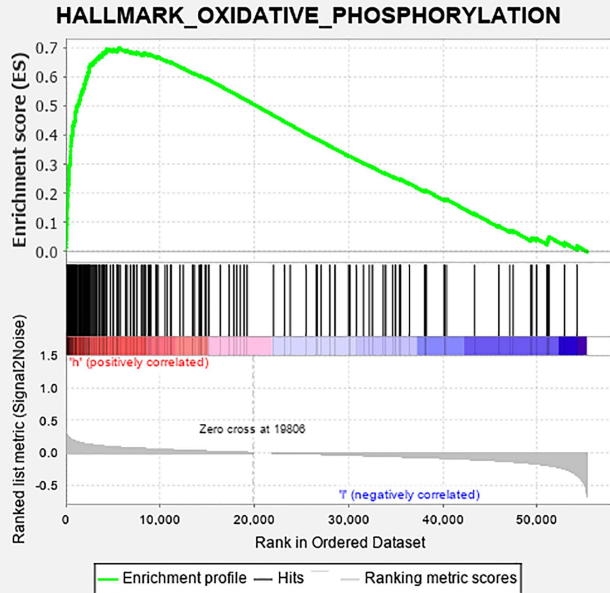


Fig 6

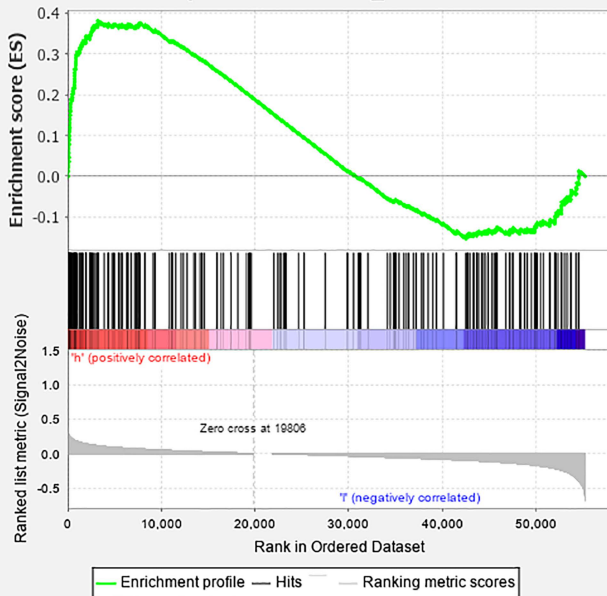
Enrichment plot: HALLMARK_MYC_TARGETS_V1



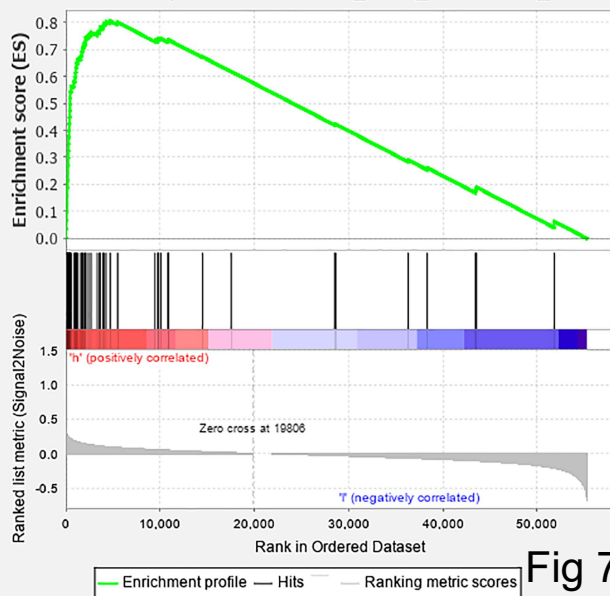
Enrichment plot: HALLMARK_OXIDATIVE_PHOSPHORYLATION



Enrichment plot: HALLMARK_ADIPOGENESIS

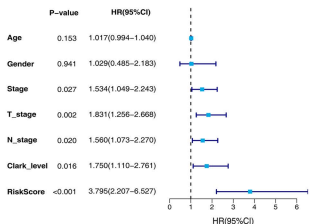


Enrichment plot: HALLMARK_MYC_TARGETS_V2

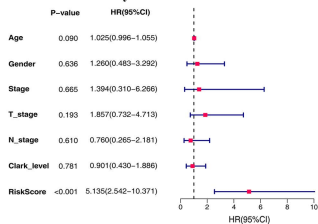


A TCGA-SKCM (*BRAF*-mutated) n=156

Univariate analyses

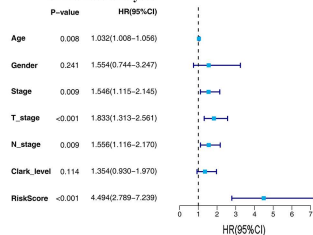


Multivariate analyses

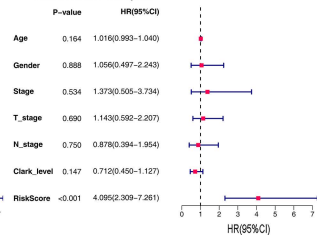


B TCGA-SKCM (*BRAF*-wild-type) n=222

Univariate analyses

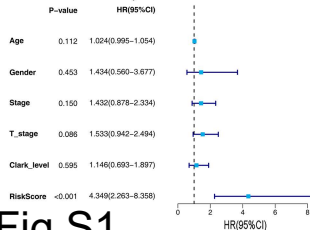


Multivariate analyses

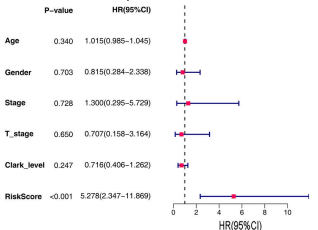


C TCGA-SKCM (*NRAS*-mutated) n=87

Univariate analyses

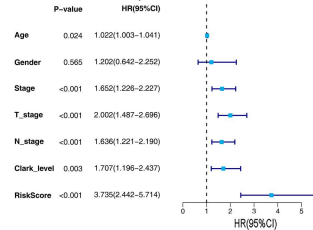


Multivariate analyses



D TCGA-SKCM (*NRAS*-wild-type) n=291

Univariate analyses



Multivariate analyses

