

Supplementary Materials

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Table S1. Study characteristics of the pan-cancer datasets

Cancer type	Cancer full name	Protein	RNA-Seq	miRNA-seq	Final	Age (mean±sd)	Gender (male/female)	Death proportion (%)
BRCA	Breast Invasive Carcinoma	116	120	101	94	60.82±13.87	0/94	2.13
COAD	Colon Adenocarcinoma	95	100	99	94	65.46±11.26	39/55	8.51
GBM	Glioblastoma	99	99	98	98	57.81±12.53	54/44	67.35
HNSC	Head and Neck Squamous Cell Carcinoma	70	110	109	68	61.21±9.48	61/7	14.71
KIRC	Clear Cell Renal Cell Carcinoma	160	110	110	110	60.55±12.18	80/30	10.91
LIHC	Hepatocellular Carcinoma	160	0	0	0	53.53±10.87	128/32	34
LUAD	Lung Adenocarcinoma	109	111	111	109	62.65±9.68	73/36	18.35
LUSC	Lung Squamous Cell Carcinoma	108	108	107	107	65.84±8.25	85/22	18.69
OV	Ovarian Serous Cystadenocarcinoma	100	101	101	97	59.63±10.11	0/97	7.22
PBT	Pediatric/AYA Brain Tumors	66	0	0	0	7.62±5.19	43/23	23
PDAC	Pancreatic Ductal Adenocarcinoma	137	140	140	137	64.14±11.15	71/66	63.5
UCEC	Uterine Corpus Endometrial Carcinoma	100	100	99	99	63.34±9.78	0/99	6.06
Total		1320	1099	1075	1013			

Table S2. Sample size of tumor-normal pairs in each cancer type

Cancer type	Cancer full name	Protein-tumor	Protein-normal	Final
BRCA	Breast Invasive Carcinoma	116	18	17
COAD	Colon Adenocarcinoma	95	100	94
GBM	Glioblastoma	99	10	0
HNSC	Head and Neck Squamous Cell Carcinoma	70	73	32
KIRC	Clear Cell Renal Cell Carcinoma	160	84	84
LIHC	Hepatocellular Carcinoma	160	160	160
LUAD	Lung Adenocarcinoma	109	102	100
LUSC	Lung Squamous Cell Carcinoma	108	100	100
OV	Ovarian Serous Cystadenocarcinoma	100	25	16
PBT	Pediatric/AYA Brain Tumors	66	77	9
PDAC	Pancreatic Ductal Adenocarcinoma	137	66	66
UCEC	Uterine Corpus Endometrial Carcinoma	100	30	30
Total		1320	845	708

Table S3. The descriptions of 30 m6A proteins enrolled in this study

Official symbol	Description	Category
METTL3	Methyltransferase like 3	Writer
METTL14	Methyltransferase like 14	Writer
METTL16	Methyltransferase like 16	Writer
METTL5	Methyltransferase like 5	Writer
WTAP	WT1 associated protein	Writer
VIRMA	Vir like m6A methyltransferase associated	Writer
RBM15	RNA binding motif protein 15	Writer
RBM15B	RNA binding motif protein 15B	Writer
ZC3H13	Zinc finger CCCH-type containing 13	Writer
CBLL1	Cbl proto-oncogene like 1	Writer
FTO	FTO alpha-ketoglutarate dependent dioxygenase	Eraser
ALKBH3	AlkB homolog 3, RNA demethylase	Eraser
ALKBH5	AlkB homolog 5, RNA demethylase	Eraser
YTHDF1	YTH N6-methyladenosine RNA binding protein 1	Reader
YTHDF2	YTH N6-methyladenosine RNA binding protein 2	Reader
YTHDF3	YTH N6-methyladenosine RNA binding protein 3	Reader
YTHDC1	YTH domain containing 1	Reader
YTHDC2	YTH domain containing 2	Reader
HNRNPA2B1	Heterogeneous nuclear ribonucleoprotein A2/B1	Reader
HNRNPC	Heterogeneous nuclear ribonucleoprotein C	Reader
FMR1	FMRP translational regulator 1	Reader
EIF3A	Eukaryotic translation initiation factor 3 subunit A	Reader
IGF2BP1	Insulin like growth factor 2 mRNA binding protein 1	Reader
IGF2BP2	Insulin like growth factor 2 mRNA binding protein 2	Reader
IGF2BP3	Insulin like growth factor 2 mRNA binding protein 3	Reader
ELAVL1	ELAV like RNA binding protein 1	Reader
G3BP1	G3BP stress granule assembly factor 1	Reader
G3BP2	G3BP stress granule assembly factor 2	Reader
PRRC2A	Proline rich coiled-coil 2A	Reader
RBMX	RNA binding motif protein X-linked	Reader

Table S4. The fold change of 30 m6A proteins in each cancer type

Protein	BRCA	COAD	HNSC	KIRC	LIHC	LUAD	LUSC	OV	PBT	PDAC	UCEC
ALKBH3	1.13	0.94	0.99	0.95	0.85	0.95	1.32	0.63	0.81	0.66	0.55
ALKBH5	1.97	1.35	1.67	1.65	1.12	1.13	1.28	0.97	1.26	0.96	0.82
CBLL1	1.10	1.35	1.36	1.46	1.31	1.25	1.17	1.11	1.41	0.71	0.91
EIF3A	1.57	1.29	1.45	1.39	1.13	1.16	1.08	1.09	0.86	0.72	0.79
ELAVL1	1.51	1.15	1.44	1.30	1.24	1.40	1.15	1.00	1.37	0.97	0.86
FMR1	1.98	1.19	1.43	1.26	1.47	1.39	0.84	1.08	1.14	1.21	1.28
FTO	0.98	1.10	0.97	1.13	1.00	0.93	1.38	0.64	0.70	0.87	0.79
G3BP1	1.39	1.46	1.67	1.58	1.42	1.66	1.27	1.55	1.55	0.96	1.11
G3BP2	2.24	1.49	1.51	1.50	1.15	1.13	0.97	1.28	1.90	1.03	1.11
HNRNPA2B1	1.20	1.20	1.10	1.16	1.27	1.46	1.02	1.10	1.81	0.99	0.92
HNRNPC	1.72	1.44	1.56	1.52	1.39	1.55	1.05	1.23	2.66	0.98	0.98
IGF2BP1	1.37	1.88	4.95	5.95	5.32	2.43	1.34	1.94	0.54	1.92	2.08
IGF2BP2	0.92	1.02	4.28	3.14	4.46	1.82	0.82	0.61	1.64	2.26	1.96
IGF2BP3	10.82	2.55	8.95	6.52	5.82	2.56	3.48	1.89	0.65	3.11	4.14
METTL14	1.62	1.24	1.00	1.11	1.33	0.90	1.09	0.91	0.83	0.93	0.85
METTL16	1.33	1.00	1.06	1.06	1.09	1.02	1.27	0.53	0.93	1.00	0.64
METTL3	1.14	1.11	1.09	1.12	1.42	0.99	1.13	0.91	1.17	0.98	0.87
METTL5	0.68	0.94	1.43	1.22	1.37	1.15	1.64	1.29	0.60	1.08	1.34
PRRC2A	1.97	1.38	1.62	1.67	1.49	1.35	1.07	1.13	1.97	0.92	0.98
RBM15	2.41	1.30	1.38	1.41	1.29	1.30	1.21	1.20	1.49	1.14	1.09
RBM15B	1.66	1.15	1.38	1.21	1.31	1.15	0.99	0.97	1.42	0.91	1.01
RBMX	1.24	1.42	1.36	1.38	1.59	1.58	1.18	1.20	2.21	1.20	1.13
VIRMA	1.47	1.12	1.49	1.40	1.26	1.28	1.17	1.23	0.64	1.09	0.98
WTAP	2.15	1.28	1.64	1.58	1.44	1.29	1.24	1.11	1.03	1.05	1.04
YTHDC1	2.07	1.39	1.67	1.63	1.37	1.52	1.11	0.98	1.32	1.18	1.08
YTHDC2	0.91	1.12	1.32	1.16	1.08	1.17	1.37	1.53	0.62	0.98	1.19
YTHDF1	2.39	1.63	1.66	1.77	1.56	1.63	1.09	1.26	1.16	0.94	1.15
YTHDF2	3.50	1.63	1.90	1.84	1.69	1.55	1.14	1.65	1.32	1.05	1.28
YTHDF3	2.43	1.59	1.65	1.63	1.63	1.42	1.11	1.11	1.23	0.92	1.08
ZC3H13	2.07	1.30	1.44	1.52	1.32	1.13	1.18	1.08	1.45	1.00	0.98

Table S5. Association of 30 m6A proteins and overall survival in pan-cancer

m6A proteins	HR	CI	CU	P	Category
METTL3	0.75	0.48	1.19	0.2240	Writer
METTL14	0.92	0.64	1.33	0.6577	Writer
METTL16	0.90	0.63	1.28	0.5432	Writer
METTL5	1.07	0.75	1.54	0.7031	Writer
RBM15	1.26	0.81	1.97	0.3033	Writer
RBM15B	1.28	0.83	1.99	0.2613	Writer
WTAP	1.25	0.85	1.85	0.2578	Writer
VIRMA	1.23	0.78	1.96	0.3773	Writer
ZC3H13	1.14	0.75	1.74	0.5377	Writer
CBLL1	1.01	0.64	1.61	0.9635	Writer
ALKBH5	1.51	1.07	2.14	0.0196	Eraser
ALKBH3	0.92	0.70	1.21	0.5459	Eraser
FTO	1.04	0.73	1.48	0.8226	Eraser
YTHDC1	1.06	0.71	1.57	0.7892	Reader
YTHDC2	0.81	0.54	1.22	0.3190	Reader
YTHDF1	2.34	1.46	3.75	0.0004	Reader
YTHDF2	1.89	1.29	2.77	0.0012	Reader
YTHDF3	1.66	1.13	2.44	0.0091	Reader
IGF2BP1	1.09	0.98	1.21	0.0963	Reader
IGF2BP2	1.22	1.08	1.38	0.0013	Reader
IGF2BP3	1.14	1.03	1.26	0.0081	Reader
HNRNPA2B1	1.14	0.66	1.96	0.6435	Reader
HNRNPC	1.51	0.97	2.36	0.0697	Reader
RBMX	1.28	0.86	1.89	0.2264	Reader
EIF3A	1.72	0.90	3.26	0.0982	Reader
FMR1	1.30	0.84	2.00	0.2361	Reader
ELAVL1	1.33	0.86	2.05	0.1950	Reader
G3BP1	1.82	1.13	2.94	0.0145	Reader
G3BP2	2.01	1.28	3.14	0.0022	Reader
PRRC2A	1.69	1.07	2.66	0.0232	Reader

Table S6. The Univariate Cox regression of m6Ascore in each cancer

Cancer type	Cutoff	HR	CI	CU	P
COAD	0.73	3.15	1.55	6.39	0.001497
GBM	-0.29	1.41	1.11	1.79	0.004411
HNSC	0.63	2.23	1.43	3.50	0.000431
KIRC	0.95	2.56	1.71	3.83	4.95E-06
LUAD	0.69	2.21	1.41	3.48	0.000603
LUSC	0.27	2.39	1.39	4.11	0.00169
OV	0.49	2.37	0.89	6.32	0.085013
PDAC	0.04	1.98	1.58	2.47	2.63E-09
UCEC	0.85	2.91	1.32	6.41	0.008017

Table S7. The association between m6Ascore and immune checkpoint

Immune check point	Beta	CI	CU	P
<i>PD-1</i>	0.08	0.03	0.13	0.003244
<i>PD-L1</i>	0.15	0.10	0.20	4.92E-08
<i>CTLA-4</i>	0.01	-0.06	0.07	0.855967
<i>PD-L2</i>	0.13	0.04	0.21	0.0034
<i>HAVCR2</i>	0.09	0.02	0.17	0.014211
<i>LAG3</i>	0.04	-0.04	0.12	0.308203
<i>VSIR</i>	-0.02	-0.08	0.05	0.621812
<i>B7-H3</i>	-0.06	-0.12	0.01	0.0889
<i>BTLA</i>	0.05	-0.01	0.12	0.112205
<i>TIGIT</i>	0.12	0.05	0.19	0.000742

Table S8. The association between m6Ascore and 28 immune pathways

Immune pathways	Beta	CI	CU	P
Activated B cell	0.006	-0.007	0.018	0.391824
Activated CD4 T cell	0.016	0.008	0.023	5.88E-05
Activated CD8 T cell	0.007	-0.001	0.015	0.092717
Activated dendritic cell	0.013	0.008	0.017	2.19E-08
CD56bright natural killer cell	0.004	0.001	0.006	0.004011
CD56dim natural killer cell	0.004	0.001	0.008	0.011631
Central memory CD4 T cell	0.011	0.008	0.013	1.09E-14
Central memory CD8 T cell	0.019	0.014	0.023	2.2E-16
Effector memory CD4 T cell	0.005	0.001	0.009	0.01253
Effector memory CD8 T cell	0.013	0.007	0.018	8.9E-06
Eosinophil	0.009	0.003	0.015	0.001992
Gamma delta T cell	0.013	0.010	0.017	6.16E-12
Immature B cell	0.010	0.000	0.020	0.051587
Immature dendritic cell	0.010	0.007	0.014	7.94E-11
Macrophage	0.022	0.015	0.028	3.63E-11
Mast cell	0.011	0.003	0.018	0.003942
MDSC	0.021	0.014	0.028	2.68E-08
Memory B cell	0.011	0.007	0.015	2.87E-08
Monocyte	0.005	0.002	0.009	0.003283
Natural killer cell	0.010	0.007	0.014	2.2E-08
Natural killer T cell	0.013	0.009	0.018	1.64E-09
Neutrophil	0.014	0.003	0.025	0.011214
Plasmacytoid dendritic cell	0.009	0.006	0.012	1.13E-10
Regulatory T cell	0.027	0.019	0.034	1.5E-12
T follicular helper cell	0.012	0.008	0.017	1.05E-07
Type 1 T helper cell	0.012	0.008	0.017	3.18E-07
Type 17 T helper cell	0.006	0.002	0.010	0.004461
Type 2 T helper cell	0.016	0.012	0.020	1.1E-14

Table S9. The fold change of 51 potential proteins in each cancer type

Potential protein	BRCA	COAD	HNSC	KIRC	LIHC	LUAD	LUSC	OV	PBT	PDAC	UCEC
CHORDC1	2.33	1.19	1.10	0.77	1.91	1.73	2.01	2.16	1.02	1.21	1.29
FAM114A1	0.62	0.69	1.94	1.22	0.91	1.56	1.15	1.47	1.05	0.98	0.53
BMP1	2.41	1.96	3.18	0.62	1.22	1.86	2.61	1.06	1.59	2.66	1.41
CALU	0.87	1.19	2.46	1.00	1.81	2.09	1.81	2.43	1.39	1.26	1.11
COLGALT1	1.50	1.63	3.92	0.72	1.42	1.17	1.47	0.91	1.00	1.99	1.61
ENY2	1.66	1.15	0.87	1.01	1.53	1.18	1.42	2.04	0.70	0.98	0.85
FKBP10	2.07	2.44	4.85	0.83	2.52	2.38	2.58	1.44	1.31	1.81	1.35
IFI35	1.58	1.14	2.75	0.79	1.19	1.36	1.45	1.78	0.82	1.41	1.25
MMP14	1.21	1.67	3.79	0.67	1.83	1.66	2.46	0.87	2.17	2.51	1.83
NFKB2	1.56	1.16	2.03	0.86	1.75	1.34	1.41	1.14	1.01	1.38	0.78
NUP98	1.23	1.44	1.20	0.92	1.42	1.23	1.41	1.28	1.05	0.97	0.92
P3H1	2.01	2.45	2.56	0.79	1.66	1.98	2.40	1.05	0.84	1.88	1.40
P3H4	3.12	1.98	2.06	0.73	1.92	2.59	3.12	0.68	1.04	2.21	1.27
PLOD1	2.10	1.99	3.23	0.66	1.67	1.72	2.24	1.19	1.24	2.17	1.67
RCN1	0.59	2.18	2.55	1.11	0.91	1.62	1.44	2.03	1.28	1.51	1.64
SPATS2	3.44	1.09	1.55	0.92	2.40	2.15	2.56	1.88	1.00	1.02	1.75
TIGAR	2.05	1.23	1.65	0.83	1.33	1.14	1.31	1.33	0.94	1.70	1.55
ANKHD1	1.64	1.30	1.34	1.01	1.42	1.33	1.23	1.01	1.16	0.81	1.14
ATF2	1.20	1.19	1.70	1.02	1.37	1.33	1.17	2.37	1.05	1.00	0.65
BOP1	2.32	2.11	1.59	0.83	1.82	1.45	1.99	1.45	0.81	0.97	1.17
BRIX1	2.35	1.95	2.79	0.83	1.73	1.72	2.08	0.95	0.43	1.47	1.55
C1orf174	2.72	1.09	1.17	0.95	1.07	1.38	1.27	2.06	1.16	0.74	1.08
CRTAP	1.35	2.03	2.20	0.77	2.12	2.02	2.22	0.72	1.39	1.98	1.17
CWC27	1.12	1.08	1.22	1.02	1.43	1.15	1.27	1.74	0.98	0.89	0.89
ERO1A	4.03	2.00	4.47	1.06	1.36	3.81	3.74	1.36	1.28	1.74	2.91
ETV6	1.16	1.18	1.64	1.18	1.06	1.55	1.77	1.32	1.32	1.59	1.76
IKBIP	1.73	2.05	5.68	0.69	2.15	1.81	1.81	1.29	1.36	1.96	1.35
JUNB	2.63	1.88	1.72	0.82	1.32	1.23	1.66	1.44	1.50	2.21	0.72
LOXL2	2.38	1.64	11.41	0.43	2.93	2.60	4.19	2.03	5.35	5.45	1.62
MICALL2	1.78	1.14	1.30	0.91	0.64	1.61	1.19	1.10	1.40	2.19	1.32
NMI	2.29	1.11	2.91	0.75	1.27	1.54	1.49	2.02	0.67	1.94	1.35
P4HA1	2.81	2.57	5.80	0.69	1.77	3.02	3.03	2.33	1.92	2.83	2.06
P4HA2	2.45	1.71	6.05	0.56	2.59	2.37	2.69	1.69	0.99	2.32	1.87
PKM	1.16	1.28	3.48	0.98	1.66	1.35	1.45	1.65	1.07	1.86	1.26
PLIN3	1.11	1.17	2.45	0.95	0.94	1.46	1.17	1.59	0.87	1.38	0.99
POLR2C	1.20	1.26	1.16	0.96	1.26	1.12	1.10	1.55	0.92	0.89	0.86
PPP1R18	2.75	1.10	2.41	0.84	1.15	1.14	1.07	1.56	1.00	1.82	0.73
RANBP2	2.03	1.55	1.09	0.88	1.47	1.40	1.56	1.44	1.03	0.93	1.08
RCOR1	1.93	1.32	1.19	1.00	1.41	1.44	1.69	2.05	1.09	1.04	1.31
RPRD2	1.17	1.30	1.02	1.00	1.81	1.40	1.41	1.00	0.97	0.98	0.99
RUNX1	0.81	1.26	2.16	0.88	0.85	1.16	1.36	1.24	1.23	1.82	1.71
SERPINH1	1.21	2.37	2.60	0.83	1.85	2.05	2.07	1.81	1.49	1.81	1.27
SNRPG	2.45	1.57	1.11	1.01	1.42	1.19	1.18	2.44	0.94	1.41	1.16
SUDS3	1.01	1.09	1.19	1.02	1.20	1.15	1.33	1.47	1.03	0.73	0.73
TCEA1	1.92	1.28	1.15	0.88	1.59	1.49	1.48	1.95	0.97	0.93	1.01
TCERG1	1.47	1.46	1.24	0.96	1.54	1.49	1.42	1.74	1.05	1.08	0.98
TRADD	0.80	0.73	2.67	1.07	0.84	1.19	1.01	1.33	2.61	1.33	0.90
U2SURP	2.79	1.62	1.03	0.91	1.65	1.35	1.85	1.41	0.86	1.07	1.31
WDR12	2.03	2.21	1.36	0.80	2.58	2.08	3.38	1.50	0.98	0.97	1.49
ZFR	1.69	1.35	1.03	0.89	1.38	1.41	1.71	1.02	0.98	1.01	0.95
ZMYND8	2.41	1.45	1.16	0.84	1.56	1.60	1.85	1.40	0.96	1.18	1.65

Table S10. The mutation frequency (%) of potential regulators across 10 cancer types

Potential regulators	BRCA	COAD	GBM	HNSC	KIRC	LUAD	LUSC	OV	PDAC	UCEC
RUNX1	3.57	3.03	4.04	0.93	0.00	2.75	0.93	2.08	0.72	3.00
RPRD2	0.89	3.03	1.01	1.85	4.59	3.67	0.93	2.08	0.00	6.00
RANBP2	0.00	6.06	1.01	1.85	2.75	1.83	4.63	2.08	0.72	7.00
NUP98	0.00	6.06	1.01	0.93	0.92	0.92	5.56	1.04	0.72	5.00
ZFR	0.00	4.04	1.01	1.85	1.83	1.83	2.78	1.04	0.72	3.00
ZMYND8	0.89	4.04	0.00	1.85	1.83	1.83	0.93	1.04	0.00	5.00
ETV6	0.89	4.04	0.00	0.93	0.00	0.92	0.93	0.00	0.72	2.00
MICALL2	0.89	1.01	0.00	2.78	0.00	0.92	0.00	1.04	0.72	3.00
P4HA2	0.00	2.02	1.01	0.93	0.92	0.00	2.78	2.08	0.00	3.00
PLOD1	0.89	2.02	0.00	0.00	0.92	0.00	2.78	1.04	0.00	3.00
TCERG1	0.00	9.09	0.00	0.00	0.00	1.83	0.93	2.08	0.72	7.00
P3H1	0.00	3.03	0.00	0.93	0.92	0.92	0.00	1.04	0.00	3.00
SPATS2	0.00	2.02	0.00	0.93	1.83	0.92	0.00	1.04	0.00	2.00
BOP1	0.00	2.02	0.00	1.85	0.92	0.00	1.85	1.04	0.00	2.00
COLGALT1	0.89	2.02	1.01	0.00	0.00	0.00	0.93	0.00	0.00	3.00
SUDS3	0.89	0.00	0.00	0.93	0.92	0.00	0.00	1.04	0.00	2.00
JUNB	0.00	1.01	0.00	1.85	0.00	0.00	2.78	0.00	0.72	1.00
PPP1R18	0.00	3.03	1.01	0.93	0.00	0.92	0.00	0.00	0.00	3.00
PLIN3	0.00	1.01	1.01	0.00	0.00	0.92	0.00	1.04	0.00	1.00
U2SURP	0.00	5.05	0.00	2.78	0.00	3.67	1.85	0.00	0.00	4.00
P4HA1	0.00	3.03	0.00	0.00	0.00	0.92	1.85	1.04	0.00	1.00
BMP1	0.00	4.04	0.00	0.93	0.00	0.92	0.93	0.00	0.00	5.00
CALU	1.79	0.00	0.00	0.00	0.00	0.00	0.93	1.04	0.00	1.00
RCN1	0.89	0.00	0.00	0.00	0.92	0.92	0.00	0.00	0.00	2.00
NFKB2	0.89	4.04	0.00	0.00	0.00	1.83	0.00	0.00	0.00	2.00
FKBP10	0.00	1.01	0.00	1.85	0.92	0.00	0.00	0.00	0.00	1.00
MMP14	0.00	3.03	1.01	0.00	0.00	0.92	0.00	1.04	0.00	0.00
SERPINH1	0.00	2.02	0.00	0.00	0.00	0.92	0.93	0.00	0.00	4.00
LOXL2	0.00	3.03	0.00	0.00	0.00	0.92	0.00	1.04	0.00	5.00
TRADD	0.00	2.02	0.00	0.00	0.00	1.83	1.85	1.04	0.00	0.00
RCOR1	0.00	3.03	0.00	0.00	0.00	2.75	1.85	1.04	0.00	0.00
BRIX1	0.00	1.01	0.00	0.93	0.00	0.92	0.00	1.04	0.00	0.00
ATF2	0.00	1.01	0.00	0.00	0.00	0.00	1.85	1.04	0.00	5.00
FAM114A1	0.00	1.01	0.00	0.93	0.00	0.00	0.00	1.04	0.00	3.00
TCEA1	0.00	1.01	0.00	0.00	0.92	0.00	2.78	0.00	0.00	4.00
IKBIP	0.00	0.00	1.01	0.00	0.00	0.92	0.00	1.04	0.00	1.00
CWC27	0.89	4.04	0.00	0.00	0.00	0.92	0.00	0.00	0.00	0.00
C1orf174	0.00	2.02	0.00	0.00	0.00	1.83	0.00	0.00	0.00	2.00
WDR12	0.00	1.01	0.00	0.93	0.00	0.00	0.00	0.00	0.00	1.00
CRTAP	0.00	0.00	0.00	0.93	0.00	0.00	0.93	0.00	0.00	1.00
P3H4	0.00	1.01	0.00	0.93	0.00	0.00	0.00	0.00	0.00	0.00
NMI	0.00	2.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.00
CHORDC1	0.00	2.02	0.00	0.00	0.00	0.00	0.00	0.00	0.72	0.00
PKM	0.00	2.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.00
POLR2C	0.00	0.00	0.00	0.00	0.92	0.00	0.00	0.00	0.00	2.00
ENY2	0.89	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
IFI35	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.00
ANKHD1	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.00
TIGAR	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
ERO1A	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
SNRPG	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Table S11. Comparison of ssGSEA enrichment score of the PI3K-AKT and mTOR pathways in high- and low-CHORDC1 group.

Pathways	Ctype	High CHORDC1 group	Low CHORDC1 group	P
MTOR_SIGNALING_PATHWAY	COAD	4.31	4.07	1.15E-42
PI3K_AKT_Pathway	COAD	3.59	3.37	1.16E-19
MTOR_SIGNALING_PATHWAY	HNSC	3.71	3.54	2.85E-10
PI3K_AKT_Pathway	HNSC	2.96	2.85	4.94E-05
MTOR_SIGNALING_PATHWAY	KIRC	2.94	2.71	1.52E-13
PI3K_AKT_Pathway	KIRC	2.25	2.1	4.05E-10
MTOR_SIGNALING_PATHWAY	LUSC	3.13	2.93	5.16E-26
PI3K_AKT_Pathway	LUSC	2.41	2.35	0.001784
MTOR_SIGNALING_PATHWAY	OV	3.27	3.13	4.79E-17
PI3K_AKT_Pathway	OV	2.57	2.49	0.000379
MTOR_SIGNALING_PATHWAY	UCEC	2.89	2.66	1.93E-38
PI3K_AKT_Pathway	UCEC	2.16	2	1.76E-14
PI3K_AKT_Pathway	HNSC	2.96	2.85	4.94E-05

Figure S1. Nine significant m6A prognostic proteins were correlation with PGR, ESR1 and ERBB3 in Breast cancer

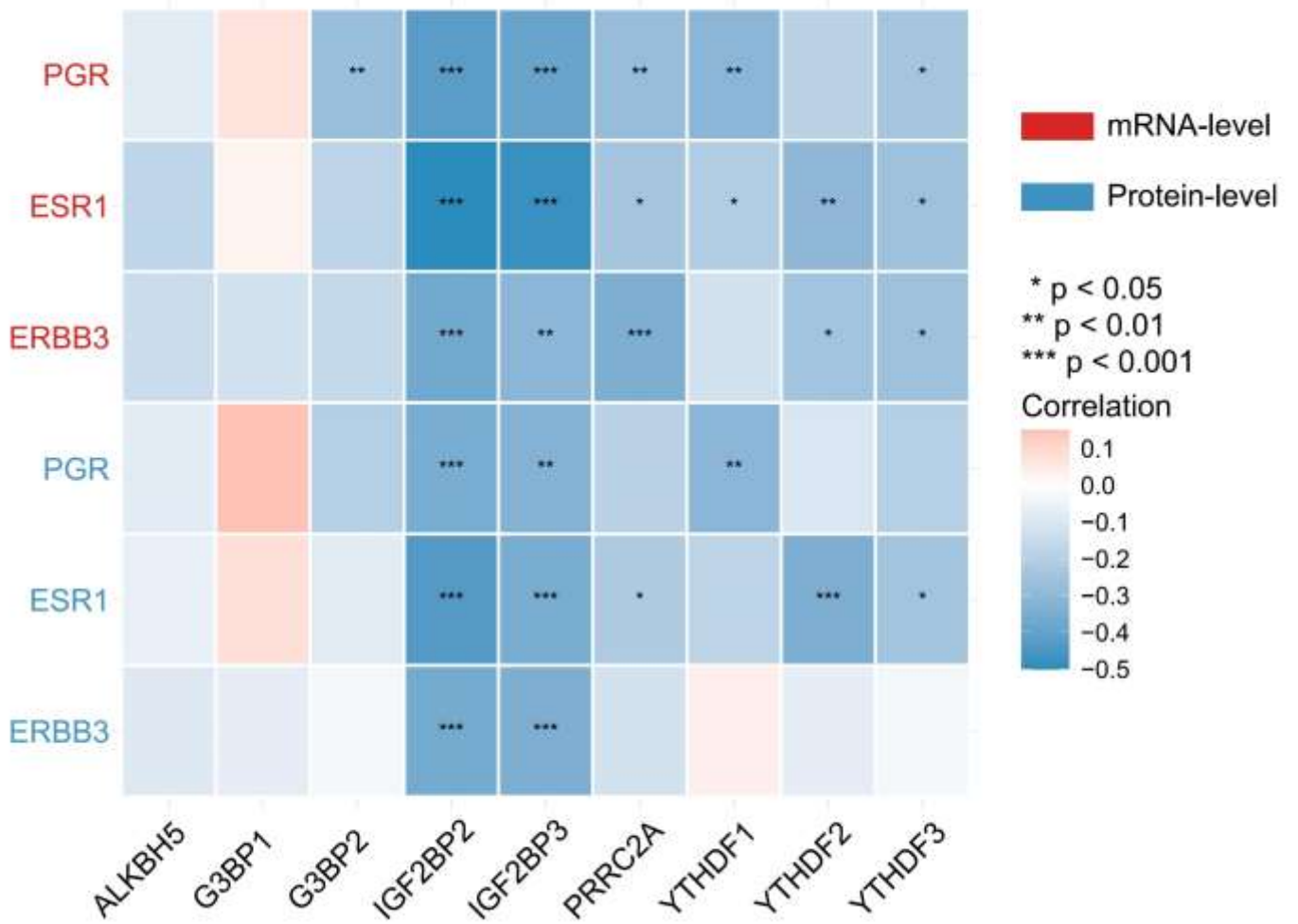


Figure S2. Nine significant m6A prognostic proteins differed in abundance between LUAD and LUSC.

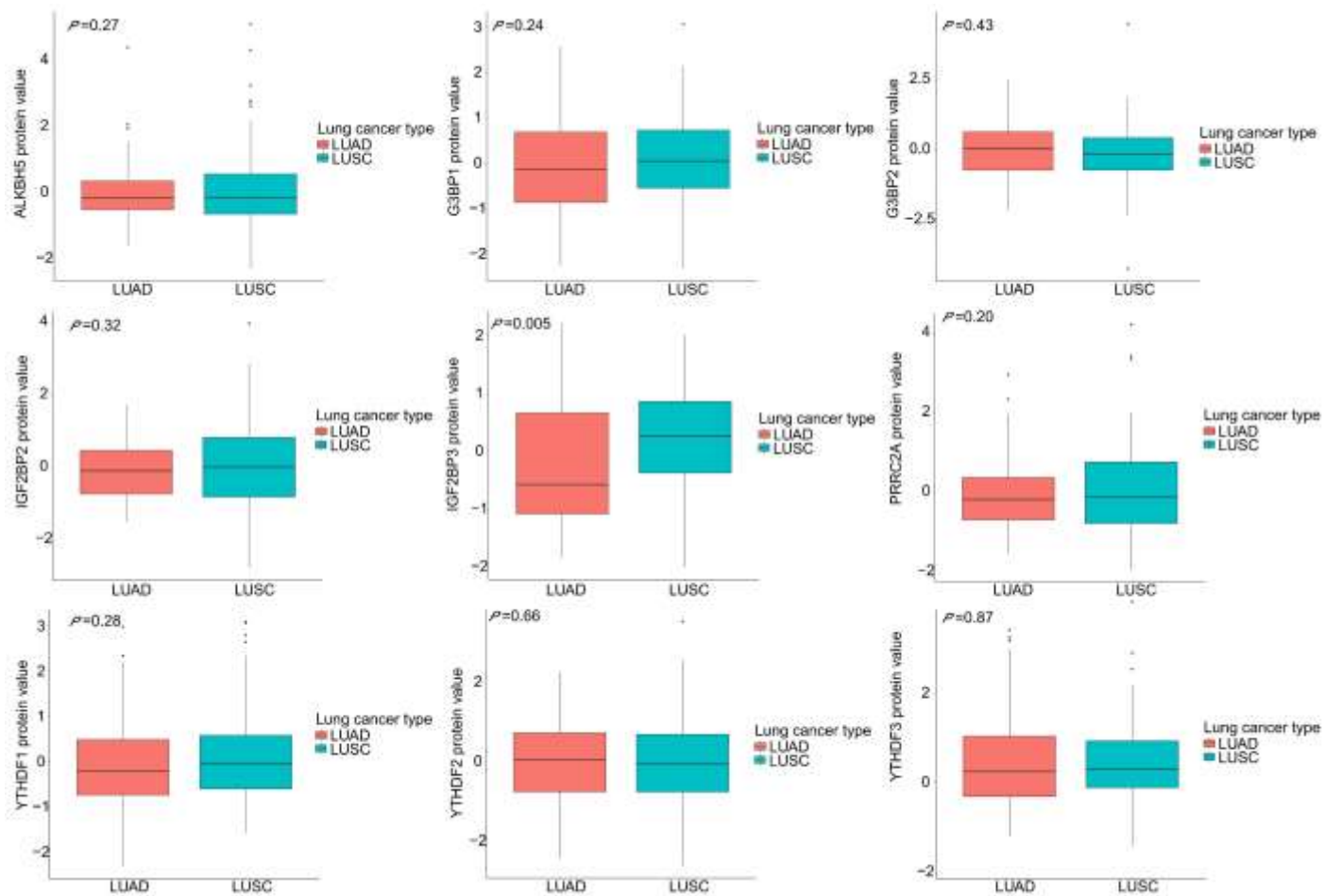


Figure S3. Kaplan-Meier survival analysis of *m6A*score in CPTAC project

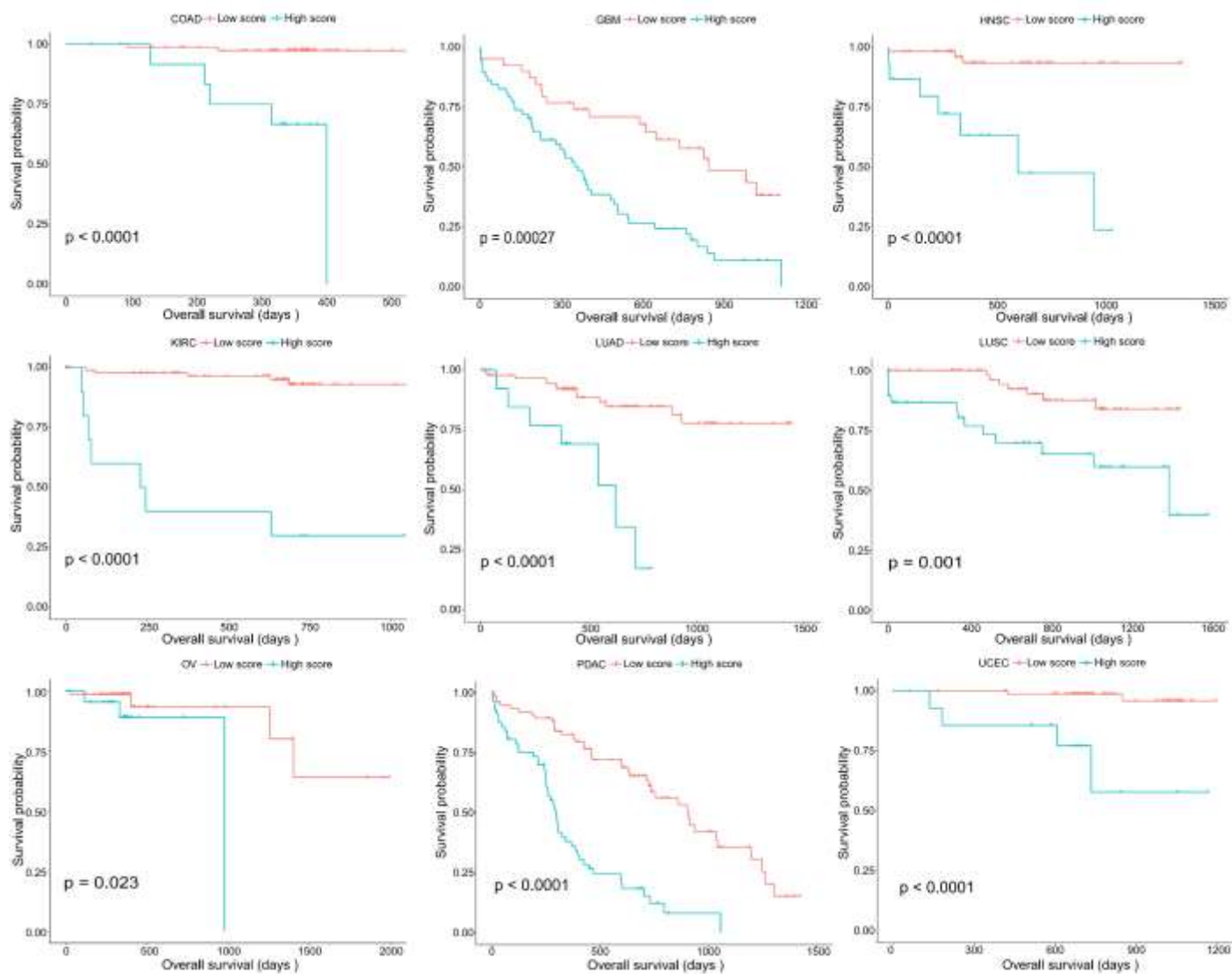


Figure S4. The OncoScore system to evaluate 51 potential proteins

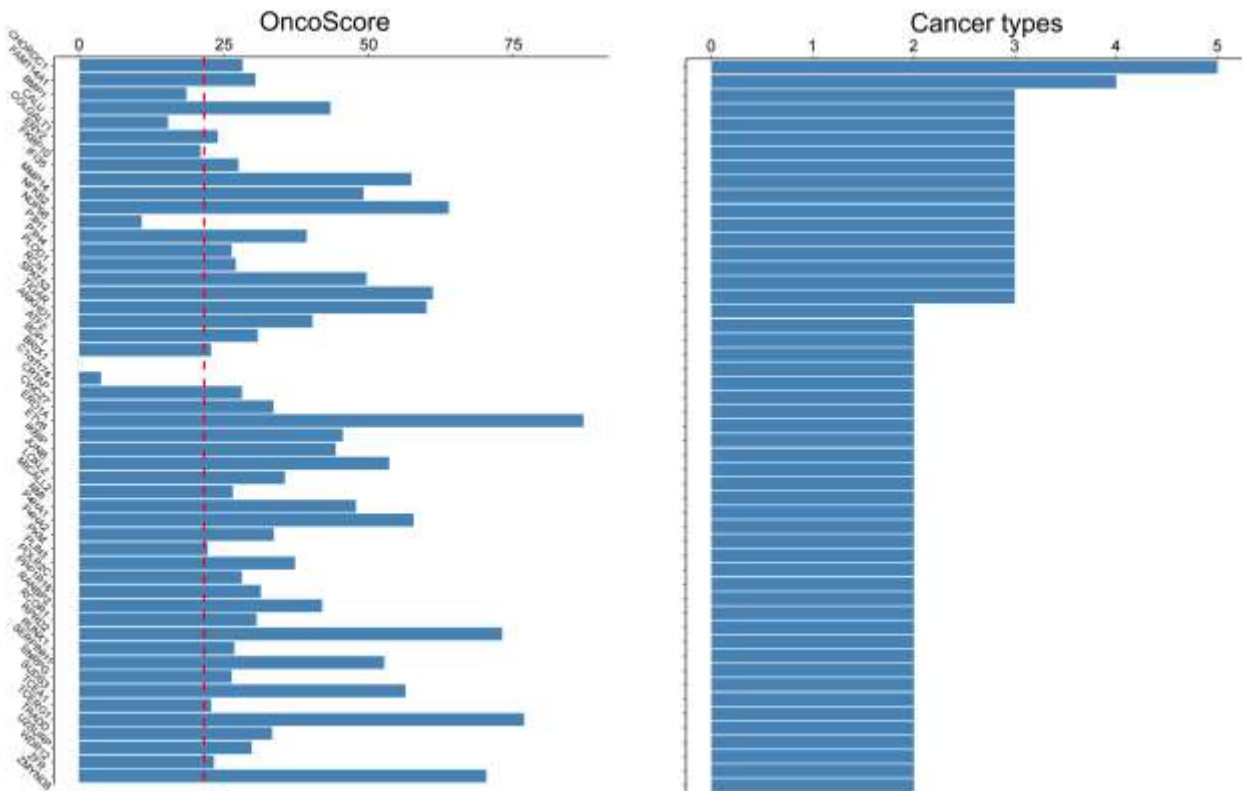


Figure S5. Somatic mutation frequency analysis of 51 potential regulators

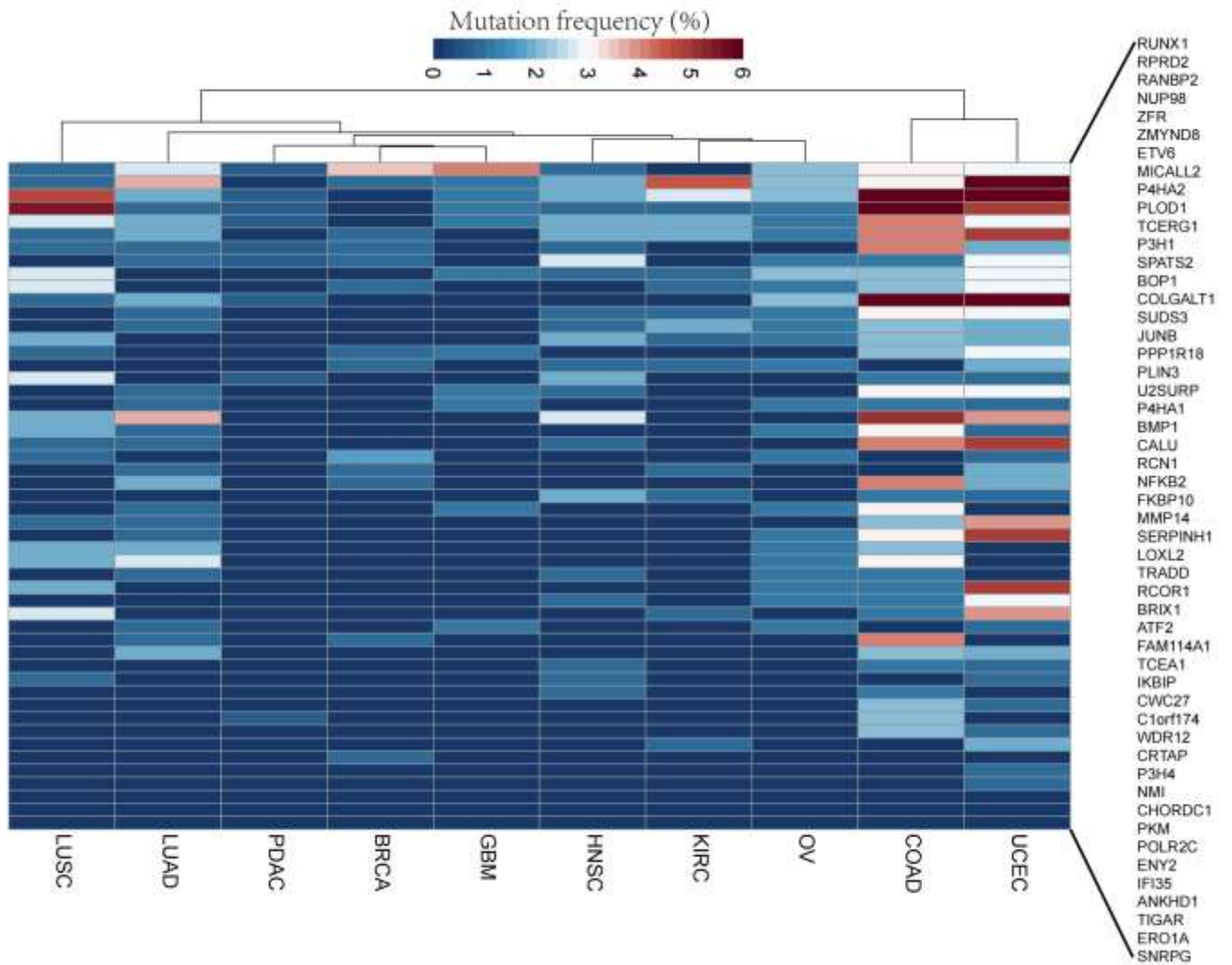


Figure S6. Kaplan-Meier survival analysis of CHORDC1 protein in CPTAC project

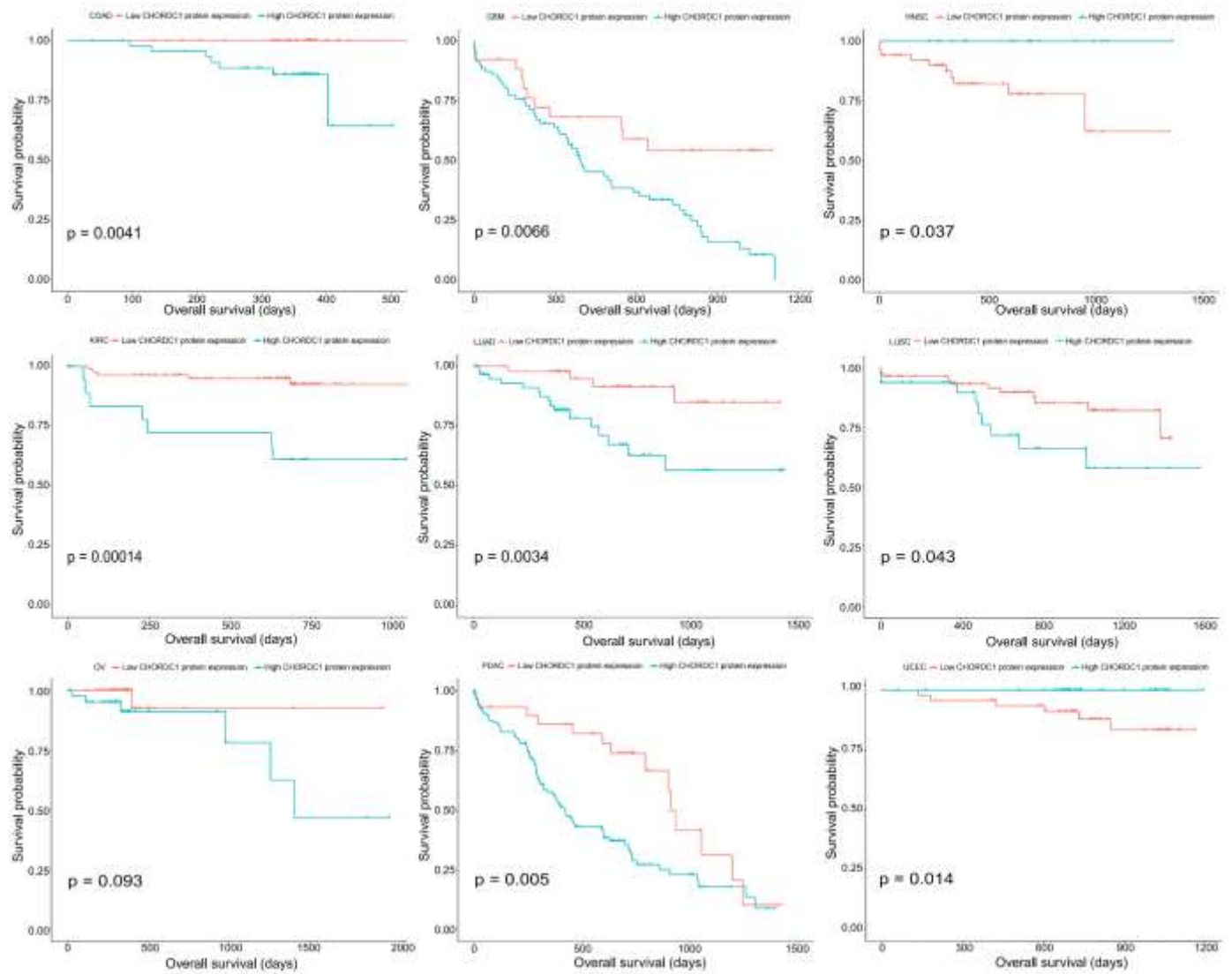


Figure S7. Meta-analysis of the associations of CHORDC1 protein expression and overall survival in CPTAC project

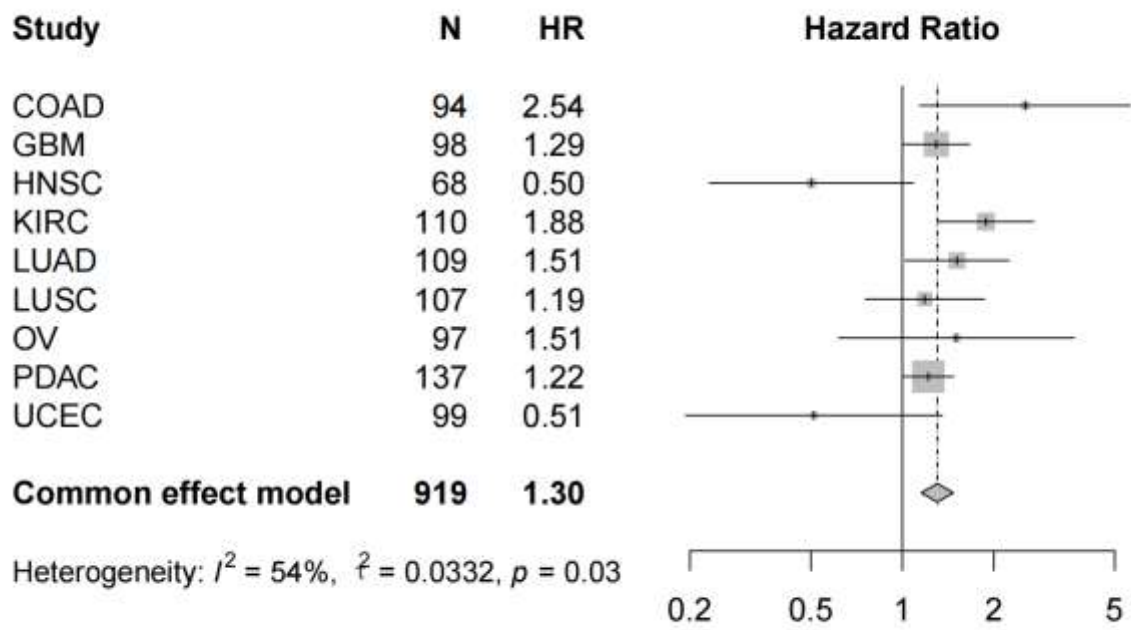


Figure S8. Correlation between ROCK1 protein expression and CHORDC1 protein expression

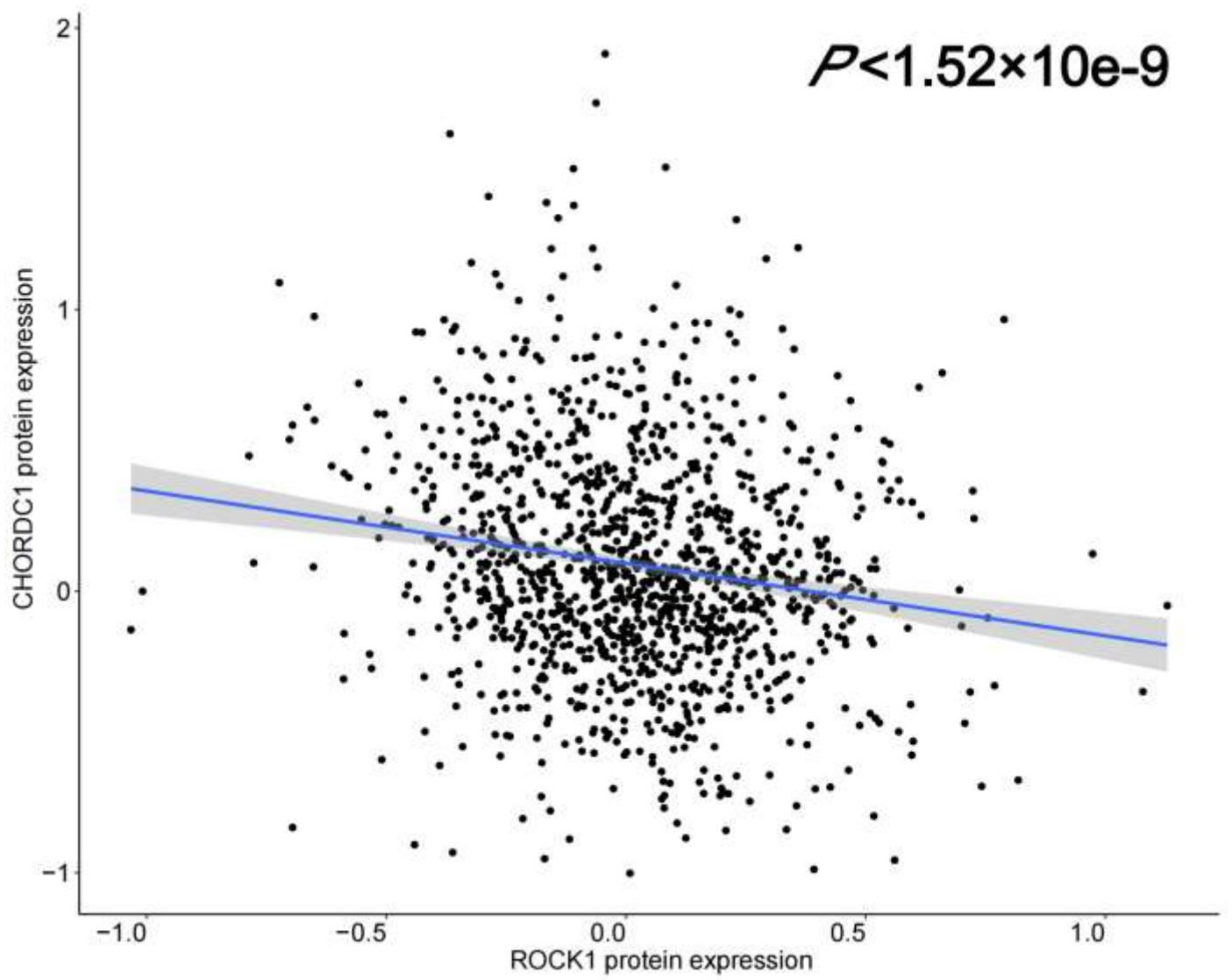


Figure S9. The 17 known biological pathways that are associated with the CHORDC1 protein expression

