

Table SI. Antibodies for western blotting.

Antibodies	Supplier	Cat. no.	Dilution
Rabbit monoclonal to Cdc25C	Abcam	ab32444	1:1,000
YTHDF1 antibody	Cell Signaling Technology, Inc.	86463	1:1,000
YTHDF2 Polyclonal antibody	Proteintech Group, Inc.	24744-1-AP	1:1,000
Anti-YTHDF3 antibody	Abcam	ab220161	1:1,000
Stat3 (124H6) Mouse mAb	Cell Signaling Technology, Inc.	9139	1:1,000
Phospho-Stat3 (Tyr705) (D3A7) XP® Rabbit mAb	Cell Signaling Technology, Inc.	9145	1:1,000
GAPDH (D16H11) XP® Rabbit mAb	Cell Signaling Technology, Inc.	92310	1:1,000
HRP-conjugated goat anti-rabbit secondary antibodies	Proteintech Group, Inc.	SA00001-2	1:10,000
HRP-conjugated goat anti-mouse secondary antibodies	Proteintech Group, Inc.	SA00001-1	1:10,000

Table III. Cytokinesis cyclin 25 homologous protein C expression in various cancer types from The Cancer Genome Atlas datasets.

Group 1	Group 2	Number	min	max	Median	IQR	Mean	SD	SE
BLCA	Normal	19	0.079429	3.6861	0.63673	1.3112	1.018	0.99285	0.22777
BLCA	Tumor	19	1.2761	4.5074	3.1384	0.93428	3.0088	0.81691	0.18741
BRCA	Normal	113	0.017637	2.9963	0.52296	0.57312	0.65782	0.52161	0.049069
BRCA	Tumor	113	0.46947	4.7867	2.8109	1.2133	2.6641	0.96337	0.090626
CESC	Normal	3	0.20902	1.0726	0.21537	0.43178	0.49899	0.49676	0.2868
CESC	Tumor	3	3.494	3.9909	3.9667	0.24847	3.8172	0.28017	0.16175
CHOL	Normal	8	0	0.30638	0.098181	0.077375	0.10117	0.094285	0.033335
CHOL	Tumor	8	1.4971	3.6613	2.6849	1.2232	2.7636	0.77096	0.27257
COAD	Normal	41	0.90904	3.06	2.253	0.47163	2.163	0.48219	0.075305
COAD	Tumor	41	1.6978	4.3845	3.4047	0.68574	3.3242	0.60071	0.093815
ESCA	Normal	8	0.15911	3.1959	1.0507	0.66338	1.2541	1.0006	0.35375
ESCA	Tumor	8	2.3011	4.4059	2.4628	0.58872	2.8694	0.79249	0.28019
HNSC	Normal	43	0.11876	2.0017	1.2183	0.75094	1.1676	0.55629	0.084833
HNSC	Tumor	43	1.058	3.5638	2.4184	0.92978	2.4068	0.6252	0.095342
KICH	Normal	24	0.017494	1.0533	0.11403	0.10536	0.1698	0.21883	0.044669
KICH	Tumor	24	0.043064	3.122	0.2642	0.4272	0.569	0.80329	0.16397
KIRC	Normal	72	0	1.7811	0.11989	0.13285	0.21021	0.33997	0.040066
KIRC	Tumor	72	0.23536	3.0187	0.95916	0.65825	1.0602	0.53511	0.063063
KIRP	Normal	32	0	0.37562	0.095249	0.12079	0.11603	0.092018	0.016267
KIRP	Tumor	32	0.047259	2.6377	0.78163	0.96064	0.86604	0.68724	0.12149
LIHC	Normal	50	0	0.78417	0.1119	0.13775	0.1556	0.16308	0.023063
LIHC	Tumor	50	0.1595	4.4704	1.75	1.3422	1.8801	1.0404	0.14713
LUAD	Normal	58	0.093425	1.2876	0.38874	0.27094	0.41427	0.22495	0.029537
LUAD	Tumor	58	0.23315	4.3277	2.2499	1.306	2.3275	1.0121	0.1329
LUSC	Normal	49	0.040822	1.3756	0.32826	0.21781	0.42684	0.32382	0.04626
LUSC	Tumor	49	0.24926	5.7717	2.7994	1.1709	2.8191	0.97736	0.13962
PAAD	Normal	4	0.70452	1.6658	0.85102	0.37839	1.0181	0.44373	0.22186
PAAD	Tumor	4	0.89437	2.1838	1.7585	0.67843	1.6488	0.57509	0.28754
PCPG	Normal	3	0.03492	0.094506	0.084473	0.029793	0.0713	0.031903	0.018419
PCPG	Tumor	3	0.089769	0.59206	0.4958	0.25115	0.39254	0.26659	0.15392
PRAD	Normal	52	0	2.3932	0.3251	0.33923	0.4147	0.40037	0.055522
PRAD	Tumor	52	0.14483	2.9432	0.86122	0.8101	1.0486	0.56792	0.078756
READ	Normal	9	1.6907	2.9438	2.2551	0.4175	2.2875	0.43031	0.14344
READ	Tumor	9	2.5503	3.631	2.8941	0.92304	3.0001	0.45253	0.15084
SARC	Normal	2	0.057138	0.62733	0.34223	0.28509	0.34223	0.40318	0.28509

SARC	Tumor	2	0.61843	2.9455	1.782	1.1635	1.782	1.6455	1.1635
SKCM	Normal	1	2.4172	2.4172	2.4172	0	2.4172		
SKCM	Tumor	1	2.8477	2.8477	2.8477	0	2.8477		
STAD	Normal	27	0.067088	2.4614	1.1868	0.98531	1.0948	0.70458	0.1356
STAD	Tumor	27	1.4488	4.7522	2.6109	1.2571	2.7599	0.82967	0.15967
THCA	Normal	59	0.036046	1.6636	0.22379	0.3038	0.36843	0.37888	0.049326
THCA	Tumor	59	0.048097	1.776	0.43627	0.42995	0.52628	0.35429	0.046125
THYM	Normal	2	2.2432	4.5593	3.4012	1.1581	3.4012	1.6378	1.1581
THYM	Tumor	2	4.7438	4.818	4.7809	0.037102	4.7809	0.05247	0.037102
UCEC	Normal	23	0.070252	1.5595	0.28155	0.36797	0.42699	0.38036	0.079311
UCEC	Tumor	23	1.7583	4.3048	3.2724	0.95498			

BLCA, bladder urothelial carcinoma; BRCA, breast invasive carcinoma; CESC, cervical squamous cell carcinoma and endocervical adenocarcinoma; CHOL, cholangiocarcinoma; COAD, colon adenocarcinoma; ESCA, esophageal carcinoma; HNSC, head and neck squamous cell carcinoma; KICH, kidney chromophobe; KIRC, kidney renal clear cell carcinoma; KIRP, kidney renal papillary cell carcinoma; LIHC, liver hepatocellular carcinoma; LUAD, lung adenocarcinoma; LUSC, lung squamous cell carcinoma; PAAD, pancreatic adenocarcinoma; PCPG, pheochromocytoma and paraganglioma; PRAD, prostate adenocarcinoma; READ, rectum adenocarcinoma; SARC, sarcoma; SKCM, skin cutaneous melanoma; STAD, stomach adenocarcinoma; THCA, thyroid carcinoma; THYM, thymoma; UCEC, uterine corpus endometrial carcinoma.

Table SIII. N6-methyladenosine modification site in cytokinesis cyclin 25 homologous protein C mRNA.

Position	Sequence context	Structural context	Score (binary)	Score (knn)	Score (spectrum)	Score (combined)	Decision m6A site
1	256	AUUCGAAGACCAUGUCUACGGAACUCUUCUCAUCCACAAGAGAGG	N/A 0.652	0.380	0.491	0.574	Moderate confidence
2	298	AGGAAGGAAGCUCUGGCUCAGGACCCAGUUUUAGGUCUAAUCAA	N/A 0.544	0.592	0.524	0.538	Low confidence
3	351	UUAACCUGCUCUCCUGGAGAGAGACACUCCUUUACCGUCUGUCCA	N/A 0.504	0.450	0.648	0.559	Moderate confidence
4	386	CGUCUGUCCAGAUGUCCCUAGAACUCCAGUGGGCAAUUUCUUGG	N/A 0.489	0.188	0.666	0.544	Low confidence
5	530	CACUUCUGCAGACCUUGAUGAAACUGGUCACCUGGAUUCUUCAGG	N/A 0.477	0.473	0.735	0.580	Moderate confidence
6	553	CUGGUCACCUGGAUUCUUCAGGACUUCAGGAAGUGCAUUUAGCUG	N/A 0.694	0.798	0.829	0.753	Very high confidence
7	588	CAUUUAGCUGGGAUGAAUCAUGACCAGCACCUAAUGAAAUGUAGC	N/A 0.372	0.253	0.844	0.555	Low confidence
8	648	UGUAGCACUCCGAAUGGUUUGGACCGUGGCCAUAGAAAGAGAGAU	N/A 0.556	0.575	0.785	0.648	High confidence
9	705	UCAUCUGCAAAUAAAGAAAAUGACAAUGGAAACUUGGUGGACAGU	N/A 0.472	0.602	0.777	0.600	High confidence
10	714	AAUAAAGAAAAUGACAAUGGAAACUUGGUGGACAGUGAAAUGAAA	N/A 0.468	0.265	0.759	0.574	Moderate confidence
11	723	AAUGACAAUGGAAACUUGGUGGACAGUGAAAUGAAAUAUUUGGC	N/A 0.670	0.467	0.730	0.684	Very high confidence
12	903	CGUCCCCGUCGAUGCCAGAGAACUUGAACAGGCCAAGACUGAAG	N/A 0.674	0.739	0.642	0.664	High confidence
13	909	CCGUCGAUGCCAGAGAACUUGAACAGGCCAAGACUGAAGCAGGUG	N/A 0.503	0.651	0.638	0.564	Moderate confidence
14	919	CAGAGAACUUGAACAGGCCAAGACUGAAGCAGGUGGAAAAAUUCA	N/A 0.677	0.576	0.626	0.652	High confidence
15	945	AAGCAGGUGGAAAAAUUCAAGGACAACACAAUACCAGAUAAAGUU	N/A 0.692	0.702	0.636	0.670	High confidence
16	1261	AUCCAUAUGAGUAUCUGGGAGGACACAUCAGGGAGCCUAAACU	N/A 0.537	0.474	0.646	0.577	Moderate confidence
17	1300	UAAACUUAUAUAGUCAGGAAGAACUGUUUAAACUUCUUCUGAAGA	N/A 0.677	0.677	0.544	0.624	High confidence
18	1341	AAGAAGCCAUCGUCCCUUUGGACACCCAGAAGAGAAUAAUCAUC	N/A 0.61	0.503	0.656	0.623	High confidence
19	1428	UGCCGCUGUCUGCGUGAAGAGGACAGGUCUCUGAACAGUAUCCU	N/A 0.555	0.640	0.693	0.614	High confidence
20	1497	AUCCUAAAGGCGGCUACAGAGACUUCUUCCAGAAUAUAUGGAA	N/A 0.659	0.646	0.706	0.677	Very high confidence
21	1519	ACUUCUUCCAGAAUAUAUGGAACUGUGUGAACACAGAGCUACU	N/A 0.662	0.689	0.731	0.691	Very high confidence
22	1560	UACUGCCCUAUGCAUCAUCAGGACCACAAGACUGAGUUGCUGAGG	N/A 0.562	0.493	0.762	0.638	High confidence
23	1568	UAUGCAUCAUCAGGACCACAAGACUGAGUUGCUGAGGUGUCGAAG	N/A 0.637	0.659	0.746	0.681	Very high confidence
24	1653	CAGAUUGCCCUUCUGGUGAAGGACAUGAGCCCAUGAUACAUCUCC	N/A 0.644	0.705	0.777	0.700	Very high confidence
25	1669	UGAAGGACAUGAGCCCAUGAUACAUCUCCAGCCACUGGCUGCUAA	N/A 0.756	0.477	0.743	0.737	Very high confidence
26	1706	GCUGCUAACAAGUCACCAAAAAGACACUGCAGAAACCCUGAGCAGA	N/A 0.579	0.611	0.696	0.628	High confidence

Table SIV. Differential peak analysis.

ensembl_gene_id	external_gene_name	class	fold_enrichment	diff. log2. fc
ENSG00000115415	STAT1	five_prime_utr	2.46	2.32
ENSG00000126561	STAT5A	three_prime_utr	21.3	0.193
ENSG00000173757	STAT5B	three_prime_utr	7.86	-0.322
ENSG00000166888	STAT6	five_prime_utr	-1.26	-1.26