Supplementary file 1

In-silico analysis of CEP55/E2F1/hsa-let-7b-5p/TMPO-AS1 axis-based ceRNA network promoting poor prognosis in lung adenocarcinoma smokers

Prerna Vats, Sakshi Nirmal, Gurpreet Bamrah, Saurabh Srivastava, Rajeev Nema*

Department of Biosciences, Manipal University Jaipur, Dehmi Kalan, Jaipur-Ajmer Expressway, Jaipur, Rajasthan, 303007, India

Table S1: CEP55 associated Long non-coding RNA analysis

Index	Name	Upregulated/Downregulated	P-value
1	PRC1-AS1	Upregulated	1.16e-19
2	SGO1-AS1	Downregulated	3.91e-03
3	DEPDC1-AS1	Upregulated	6.23e-27
4	HMMR-AS1	Downregulated	2.09e-13
5	CSRP3-AS1	Downregulated	7.74e-02
6	H2AZ1-DT	Upregulated	7.78e-08
7	LINC01775	Upregulated	3.60e-36
8	TMPO-AS1	Upregulated	6.31e-53
9	DIAPH3-AS1	Downregulated	N/A
10	RRM1-AS1	Downregulated	1.42e-04

Table S2: CEP55 associated Long non-coding RNA Correlation analysis

S.No.	Gene Name	lncRNA Name	Correlation Value
1	CEP55	PRC1-AS1	0.133
2		DEPDC1-AS1	0.512
3		H2AZ1-DT	No Value Found
4		LINC01775	0.481
5		TMPO-AS1	0.587

Table S3: Survival Index of Lung Cancer Patients: TMPO-AS1

S.NO.	lncRNA	Index	Patient Number	Hazard Ratio	CI	Log(P)	High expression cohort (months)	Low expression cohort (months)
1	TMPO-AS1	OS	1411	1.5	1.29-1.74	7.2e-08	52.97	99.43
		FP	874	1.9	1.52-2.38	8.1e-09	13	41.4
		PPS	242	1.77	1.32-2.39	0.00013	8	16.34
2		OS+LUAD	1161	2.16	1.69-2.76	4.1e-10	63	133.57
		FP+LUAD	906	1.67	1.24-2.25	0.00069	21	43
		PPS+LUAD	376	1.32	0.87-2	0.2	11	20
3		OS+LUSC	780	0.87	0.7-1.1	0.25	65.57	52
		FP+LUSC	220	1.28	0.85-1.93	0.24	12.55	13
		PPS+LUSC	51	1	0.56-1.81	0.99	7.1	10
4		OS+LUAD+ Smoker	546	2.34	1.41-3.88	0.00066	-	-
5		OS+LUAD+Smoker +Male	319	2.33	1.28-4.25	0.0046	-	-
6		OS+LUAD+Smoker +Female	227	3.13	1.18-8.29	0.016	-	-

Table S4: Lung cancer Patients Survival Index

S.NO.	Gene	Index	Patient Number	Hazard Ratio	CI	Log(P)	Low expression cohort (months)	High expression cohort (months)
1	E2F1	OS	2166	1.45	1.28-1.63	1.1e-09	89	52.97
		FP	1252	2.1	1.76-2.5	<1e-16	33.13	10.28
		PPS	477	1.15	0.93-1.41	0.2	15.7	11
2	E2F2	OS	2166	1.12	0.99-1.26	0.065	73	67
		FP	1252	1.18	1-1.4	0.054	164	75
		PPS	477	1.1	0.89-1.35	0.39	13.6	13
3	E2F3	OS	2166	0.91	0.81-1.02	0.12	69	72
		FP	1252	0.97	0.82-1.14	0.7	94	93
		PPS	477	1.12	0.91-1.38	0.29	15.62	11
4	E2F4	OS	2166	1.31	1.16-1.48	8.4e-06	80.03	59.53
		FP	1252	1.69	1.42-2	1.6e-09	25.73	11.83
		PPS	477	0.95	0.77-1.17	0.65	12.32	14.98
5	E2F5	OS	2166	0.92	0.82-1.04	0.18	68	71
		FP	1252	1.1	0.93-1.3	0.27	93	81
		PPS	477	1.03	0.84-1.27	0.78	14.98	12
6	E2F6	OS	2166	0.96	0.86-1.09	0.55	69	71
		FP	1252	0.94	0.8-1.12	0.49	79	102
		PPS	477	1.02	0.83-1.25	0.87	13.57	13.2
7	E2F7	OS	2166	1.6	1.38-1.86	4e-10	107	53
		FP	1252	1.81	1.45-2.26	1.1e-07	34.9	15.43
		PPS	477	1.24	0.92-1.66	0.15	15	9
8	E2F8	OS	2166	1.39	1.24-1.57	4.4e-08	85	51
		FP	1252	1.58	1.33-1.87	1.2e-07	26	12.13
		PPS	477	1.24	1-1.52	0.045	16.94	10.87

Table S5: Overall survivality based on Histology of Lung Cancer

S.NO.	Gene	Index		Patient Number	Hazard Ratio	CI	Log(P)	Low expression cohort (months)	High expression cohort (months)
1	E2F1	Histology	Adenocarcinoma	1161	1.53	1.29-1.81	1.1e-06	108	64
			Squamous cell Carcinoma	780	1.06	0.87-1.28	0.56	56	54.57
2	E2F4	Histology	Adenocarcinoma	1161	1.55	1.3-1.84	5.5e-07	107	68
			Squamous cell Carcinoma	780	1.12	0.92-1.36	0.26	57	54
3	E2F7	Histology	Adenocarcinoma	1161	1.15	0.9-1.46	0.25	110.27	90
			Squamous cell Carcinoma	780	0.81	0.64-1.02	0.068	51.27	65
4	E2F8	Histology	Adenocarcinoma	1161	1.26	1.07-1.5	0.0073	96	74
			Squamous cell Carcinoma	780	0.98	0.81-1.19	0.83	59.53	54

Table S6: Overall survival of Lung Adenocarcinoma patients based on Stages

S.NO.	Gene	Index		Patient Number	Hazard Ratio	CI	Log(P)	Low expression cohort (months)	High expression cohort (months)
1	E2F1	Stage	1	370	2.11	1.41-3.15	0.00019	76	40.97
		Stage	2	136	2.07	1.27-3.37	0.0031	88.7	32.95
		Stage	3	24	0.6	0.21-1.71	0.33	15	52
2	E2F4	Stage	1	370	1.3	0.88-1.92	0.18	56.5	47.63
		Stage	2	136	1.45	0.9-2.34	0.13	68.67	44.83
		Stage	3	24	2.08	0.75-5.78	0.15	40.77	15
3	E2F8	Stage	1	370	1.54	1.03-2.29	0.033	72	47.63
		Stage	2	136	0.69	0.42-1.11	0.13	48	68
		Stage	3	24	2.1	0.72-6.09	0.16	52	26.09

Table S7: Overall Survival of Lung adenocarcinoma patients based on Gender

S.NO.	Gene	Index		Patient Number	Hazard Ratio	CI	Log(P)	Low expression cohort (months)	High expression cohort (months)
1	E2F1	Gender	Male	566	1.34	1.06-1.7	0.013	95.07	64
		Gender	Female	537	1.89	1.43-2.49	4.2e-06	116	71
2	E2F8	Gender	Male	566	1.23	0.98-1.56	0.078	79	62
		Gender	Female	537	1.28	0.97-1.68	0.078	96.2	96

Table S8: Overall Survivality of Lung adenocarcinoma patients based on Smoking History

S.NO.	Gene	Index		Patient Number	Hazard Ratio	CI	Log(P)	Low expression cohort (months)	High expression cohort (months)
1	E2F1	Smoking History	Smoker	546	1.63	1.25-2.12	0.00026	116	65
		Smoking History	Non-Smoker	192	2.35	1.26-4.38	0.0054	NA	NA

Supplementary Figure 1

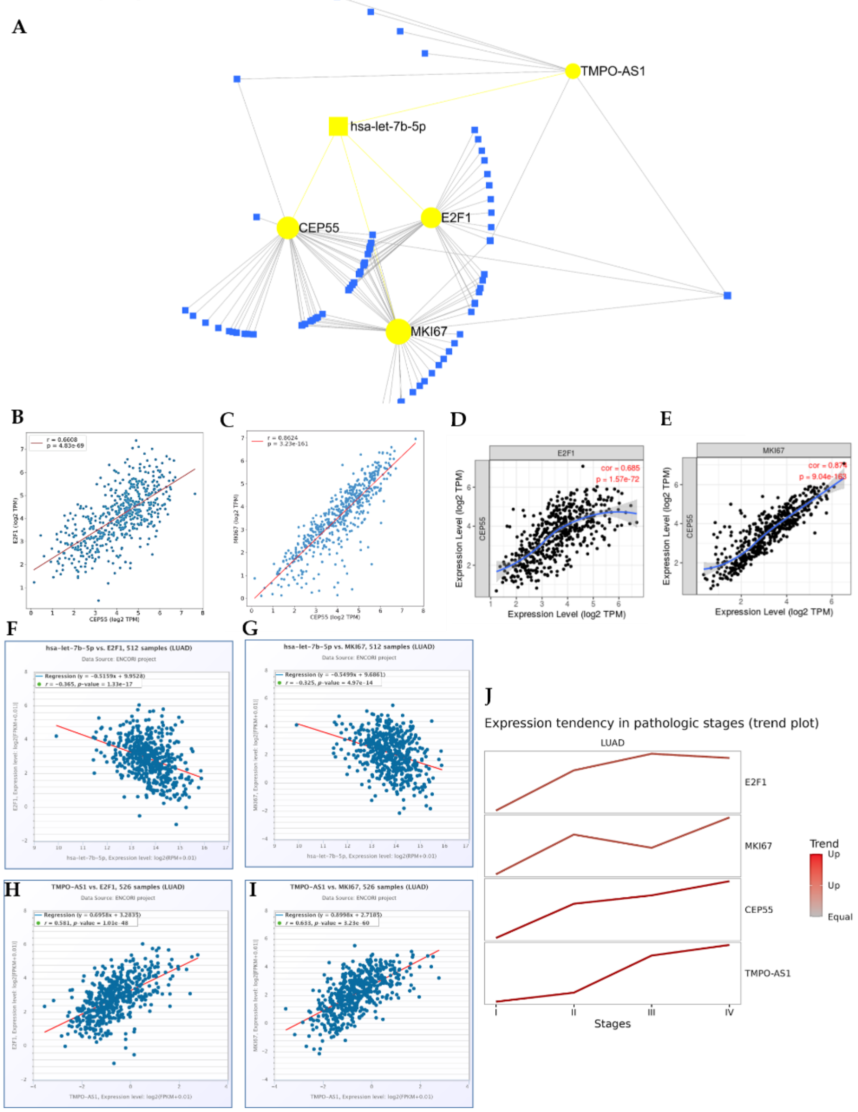

Figure S1. Using the miRNet database to create a network analysis between the TMPO-AS1/hsa-let-7b-5p/E2F1/CEP55 axis. Correlation between E2F1/CEP55 and MKI67/CEP55, using **(B-C)** OncoDB and **(D-E)** TIMER2.0, respectively. Correlation between **(F)** hsa-let-7b-5p/E2F1 and **(G)** hsa-let-7b-5p/MKI67 **(H)** TMPO-AS1/E2F1 and **(I)** TMPO-AS1/MKI67 in LUAD, using the ENCORI database. **(J)** Using the GSCA database for CEP55/E2F1/TMPO-AS1/MKI67 expression based on pathological stages.

Supplementary Figure 2

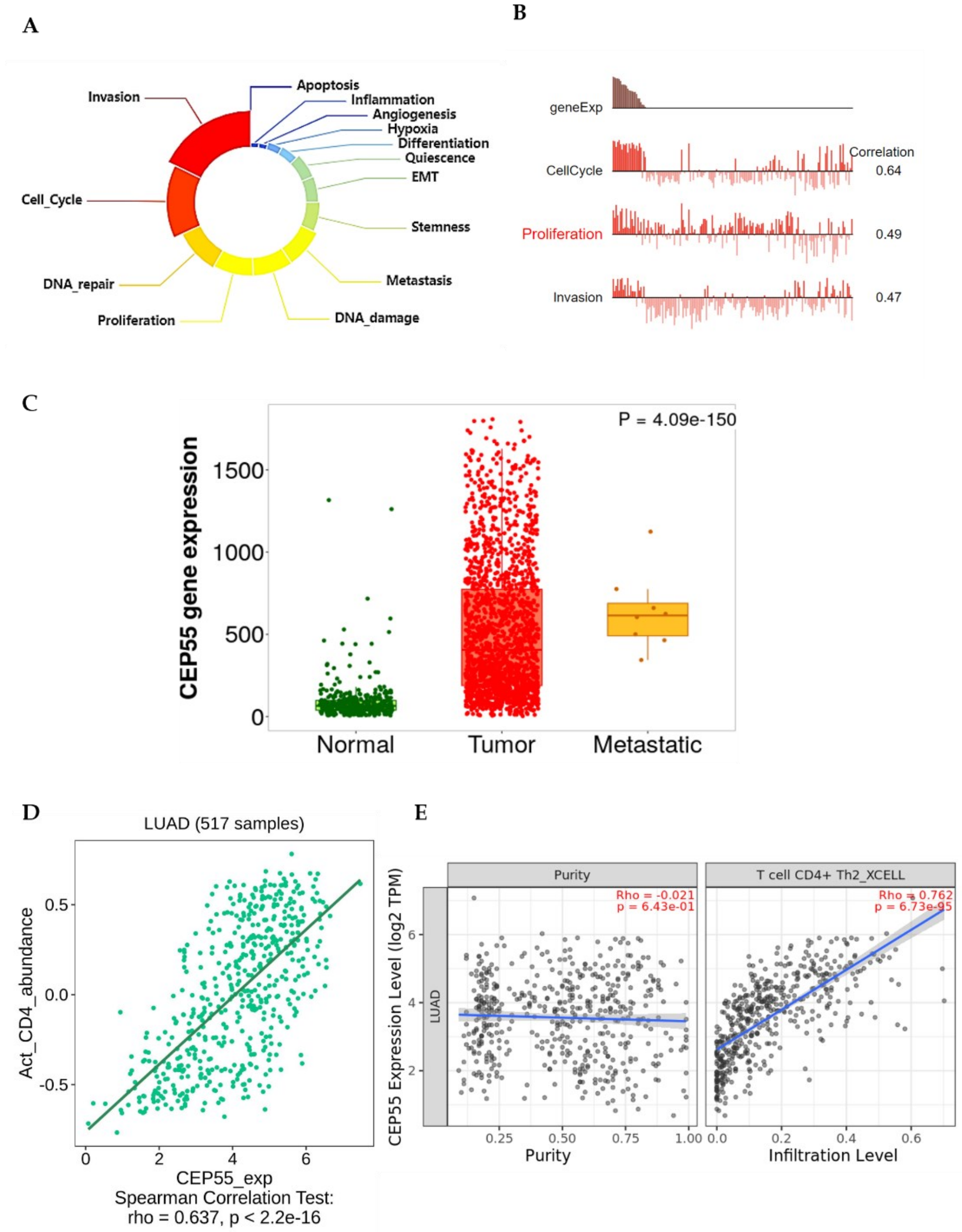

Figure S2. Biological Processes and Proliferation Mechanism Analysis. **(A)** Using the CellTracer database to find out the role of CEP55 in various biological processes and validated by using **(B)** CancerSEA. (**C)** Expression of CEP55 by TNMplot database, tumors compared with matched normal and metastatic samples. Correlation analysis between CD4 and CEP55 by using **(D)** TISIDB and **(E)** TIMER2.0 databases.