

Long non-coding RNA *TMPO-AS1* promotes aggressive triple-negative breast cancer by sponging hsa-let-7b-5p-mediated *AURKB* upregulation

Supplementary File

Table S1. AURKB gene ontology

Gene ontology	ID	Term
Biological process	GO: 0000022	Mitotic spindle elongation
	GO: 0000070	Mitotic sister chromatid segregation
	GO: 0000075	Cell cycle checkpoint
	GO: 0000226	Microtubule cytoskeleton organization
	GO: 0000723	Telomere maintenance
	GO: 0000819	Sister chromatid segregation
	GO: 0000910	Cytokinesis
	GO: 0001783	B cell apoptotic process
	GO: 0002902	Regulation of B cell apoptotic process
	GO: 0002903	Negative regulation of B cell apoptotic process
	GO: 0006278	RNA-dependent DNA biosynthetic process
	GO: 0007004	Telomere maintenance through telomerase
	GO: 0007051	Spindle organization
	GO: 0007052	Mitotic spindle organization
	GO: 0007059	Chromosome segregation
	GO: 0007062	Sister chromatid cohesion
	GO: 0007067	Mitotic nuclear division
	GO: 0007568	Aging
	GO: 0008608	Attachment of spindle microtubules to kinetochores
	GO: 0009314	Response to radiation
	GO: 0009411	Response to UV
	GO: 0009416	Response to light stimulus
	GO: 0009838	Abscission
	GO: 0010324	Membrane invagination
	GO: 0010498	Proteasomal protein catabolic process
	GO: 0010833	Telomere maintenance through telomere lengthening
	GO: 0010948	Negative regulation of cell cycle process
	GO: 0016233	Telomere capping
	GO: 0016570	Histone modification
	GO: 0016572	Histone phosphorylation
	GO: 0016925	Protein sumoylation
	GO: 0018105	Peptidyl-serine phosphorylation

(Cont'd...)

Table S1. (Continued)

Gene ontology	ID	Term
	GO: 0018205	Peptidyl-lysine modification
	GO: 0018209	Peptidyl-serine modification
	GO: 0031145	Anaphase-promoting complex-dependent catabolic
	GO: 0031577	Spindle checkpoint
	GO: 0032091	Negative regulation of protein binding
	GO: 0032200	Telomere organization
	GO: 0032204	Regulation of telomere maintenance
	GO: 0032206	Positive regulation of telomere maintenance
	GO: 0032210	Regulation of telomere maintenance through telomera
	GO: 0032212	Positive regulation of telomere maintenance through
	GO: 0032465	Regulation of cytokinesis
	GO: 0032466	Negative regulation of cytokinesis
	GO: 0032467	Positive regulation of cytokinesis
	GO: 0032506	Cytokinetic process
	GO: 0032844	Regulation of homeostatic process
	GO: 0032846	Positive regulation of homeostatic process
	GO: 0033044	Regulation of chromosome organization
	GO: 0034501	Protein localization to kinetochore
	GO: 0034502	Protein localization to chromosome
	GO: 0034644	Cellular response to UV
	GO: 0035404	Histone-serine phosphorylation
	GO: 0036089	Cleavage furrow formation
	GO: 0042787	Protein ubiquitination involved in ubiquitin-de
	GO: 0043161	Proteasome-mediated ubiquitin-dependent protein
	GO: 0043393	Regulation of protein binding
	GO: 0043988	Histone H3-S28 phosphorylation
	GO: 0045786	Negative regulation of cell cycle
	GO: 0045787	Positive regulation of cell cycle
	GO: 0046777	Protein autophosphorylation
	GO: 0051052	Regulation of DNA metabolic process
	GO: 0051054	Positive regulation of DNA metabolic process

(Cont'd...)

Table S1. (Continued)

Gene ontology	ID	Term
	GO: 0051098	Regulation of binding
	GO: 0051100	Negative regulation of binding
	GO: 0051225	Spindle assembly
	GO: 0051231	Spindle elongation
	GO: 0051255	Spindle midzone assembly
	GO: 0051256	Mitotic spindle midzone assembly
	GO: 0051302	Regulation of cell division
	GO: 0051781	Positive regulation of cell division
	GO: 0051782	Negative regulation of cell division
	GO: 0051972	Regulation of telomerase activity
	GO: 0051973	Positive regulation of telomerase activity
	GO: 0051983	Regulation of chromosome segregation
	GO: 0060249	Anatomical structure homeostasis
	GO: 0061640	Cytoskeleton-dependent cytokinesis
	GO: 0070227	Lymphocyte apoptotic process
	GO: 0070228	Regulation of lymphocyte apoptotic process
	GO: 0070229	Negative regulation of lymphocyte apoptotic pro
	GO: 0071214	Cellular response to abiotic stimulus
	GO: 0071459	Protein localization to chromosome, centromeric
	GO: 0071478	Cellular response to radiation
	GO: 0071482	Cellular response to light stimulus
	GO: 0071887	Leukocyte apoptotic process
	GO: 0071897	DNA biosynthetic process
	GO: 0072331	Signal transduction by p53 class mediator
	GO: 0090068	Positive regulation of cell cycle process
	GO: 0090307	Mitotic spindle assembly
	GO: 0098813	Nuclear chromosome segregation
	GO: 0099024	Plasma membrane invagination
	GO: 1901796	Regulation of signal transduction by p53 class
	GO: 1902850	Microtubule cytoskeleton organization involved
	GO: 1904353	Regulation of telomere capping
	GO: 1904355	Positive regulation of telomere capping
	GO: 1904356	Regulation of telomere maintenance through telomere
	GO: 1904358	Positive regulation of telomere maintenance through

(Cont'd...)

Table S1. (Continued)

Gene ontology	ID	Term
	GO: 2000106	Regulation of leukocyte apoptotic process
	GO: 2000107	Negative regulation of leukocyte apoptotic proc
	GO: 2000278	Regulation of DNA biosynthetic process
	GO: 2000573	Positive regulation of DNA biosynthetic process
	GO: 2001252	Positive regulation of chromosome organization
	GO: 2000573	Positive regulation of DNA biosynthetic process
	GO: 2001252	Positive regulation of chromosome organization
Molecular function	GO: 0004674	Protein serine/threonine kinase activity
	GO: 0004712	Protein serine/threonine/tyrosine kinase activity
	GO: 0035173	Histone kinase activity
Cellular component	GO: 0035174	Histone serine kinase activity
	GO: 0000775	Chromosome, centromeric region
	GO: 0000776	Kinetochore
	GO: 0000779	Condensed chromosome, centromeric region
	GO: 0000780	Condensed nuclear chromosome, centromeric region
	GO: 0000793	Condensed chromosome
	GO: 0000794	Condensed nuclear chromosome
	GO: 0000922	Spindle pole
	GO: 0005813	Centrosome
	GO: 0005819	Spindle
	GO: 0005874	Microtubule
	GO: 0005875	Microtubule-associated complex
	GO: 0005876	Spindle microtubule
	GO: 0010369	Chromocenter
	GO: 0030496	Midbody
	GO: 0031616	Spindle pole centrosome
	GO: 0032133	Chromosome passenger complex
	GO: 0044454	Nuclear chromosome part
	GO: 0045171	Intercellular bridge
	GO: 0051233	Spindle midzone
	GO: 0098687	Chromosomal region

Table S2. *AURKB*-enriched pathways

Name	<i>p</i> -value	Adjusted <i>p</i> -value	Odds ratio	Combined score
G2-M checkpoint	1.88×10 ⁻¹⁰	7.54×10 ⁻¹⁰	153.06	3,427.44
<i>E2F</i> targets	1.88×10 ⁻¹⁰	7.54×10 ⁻¹⁰	153.06	3,427.44
Mitotic spindle	0.0001106	0.0002949	43.28	394.28
mTORC1 signaling	0.004247	0.006796	24.99	136.48
<i>MYC</i> targets V1	0.004247	0.006796	24.99	136.48
<i>MYC</i> targets V2	0.02863	0.03817	38.86	138.07
Spermatogenesis	0.0655	0.07486	16.46	44.88
Estrogen response late	0.09564	0.09564	11.05	25.94

Table S3. Differential expression of *AURKB*-associated microRNAs

MicroRNA	Expression level in breast cancer	<i>p</i> -value
hsa-mir-24-3p	Downregulated	4.3×10 ⁻⁰¹
hsa-mir-214-3p	Downregulated	1.6×10 ⁻⁰²
hsa-mir-1-3p	Not expressed	NA
hsa-mir-130a-3p	Downregulated	1.6×10 ⁻¹²
hsa-mir-125b-3p (hsa-mir-125b-1)	Downregulated	<1×10 ⁻¹²
hsa-mir-16-5p	Upregulated	6.7×10 ⁻⁰¹
hsa-mir-106b-5p	Upregulated	1.6×10 ⁻¹²
hsa-mir-34a-5p	Downregulated	8.6×10 ⁻⁰²
hsa-let-7b-5p	Downregulated	4.6×10 ⁻⁰⁷
hsa-mir-155-5p	Upregulated	1.6×10 ⁻¹²
hsa-mir-378a-3p	Downregulated	6.6×10 ⁻¹²
hsa-mir-24-1	Downregulated	4.3×10 ⁻⁰¹
hsa-mir-27a-3p	Upregulated	1.1×10 ⁻¹⁰
hsa-let-7e-5p	Upregulated	3.8×10 ⁻⁰⁵

Table S4. Correlation between *AURKB* and downregulated microRNAs

MicroRNA	Correlation with <i>AURKB</i> (<i>r</i> value)	<i>p</i> -value
hsa-mir-214-3p	-0.080	8.5×10 ⁻⁰³
hsa-mir-130a-3p	0.199	3.6×10 ⁻¹¹
hsa-mir-125b-3p (hsa-mir-125b-1)	-0.058	5.7×10 ⁻⁰²
hsa-mir-34a-5p	0.064	3.3×10 ⁻⁰²
hsa-let-7b-5p	-0.338	4.6×10 ⁻⁰⁷
hsa-mir-378a-3p	0.328	1.2×10 ⁻²⁸

Table S5. Pan-cancer analysis of hsa-let-7b-5p

Cancer type	Fold change	Log ₂ fold change	Mean RPM (tumor)	Mean RPM (normal)	p-value	Adjusted p-value
Lung adenocarcinoma	-3.27	-1.71	15,765.4	51,536.4	1.14×10 ⁻²⁰	1.69×10 ⁻¹⁹
Pheochromocytoma and paraganglioma	-2.79	-1.48	5,553.68	15,491.32	0.00392	0.0382
Cervical squamous cell carcinoma and endocervical adenocarcinoma	-1.94	-0.96	17,404.89	33,843.83	0.0172	0.0568
Lung squamous cell carcinoma	-1.83	-0.87	16,297.65	29,783.76	1.47×10 ⁻¹⁷	7.23×10 ⁻¹⁷
Skin cutaneous melanoma	-1.79	-0.84	24,352.91	43,620.56	0.192	0.652
Uterine corpus endometrial carcinoma	-1.58	-0.66	16,997.1	26,893.93	1.02×10 ⁻⁰⁹	3.07×10 ⁻⁰⁹
Stomach adenocarcinoma	-1.55	-0.63	10,410.91	16,156.76	8.06×10 ⁻⁰⁶	2.44×10 ⁻⁰⁵
Stomach and esophageal carcinoma	-1.52	-0.6	10,349.3	15,704.5	3.03×10 ⁻⁰⁷	1.05×10 ⁻⁰⁶
Bladder urothelial carcinoma	-1.47	-0.55	10,460.37	15,330.69	4.28×10 ⁻⁰⁵	0.000114
Esophageal carcinoma	-1.39	-0.48	10,196.22	14,185.2	0.00933	0.0283
Head-and-neck squamous cell carcinoma	-1.38	-0.46	18,044.25	24,873.48	6.83×10 ⁻⁰⁶	1.54×10 ⁻⁰⁵
Thyroid carcinoma	-1.3	-0.37	10,040.22	13,014.25	2.16×10 ⁻⁰⁶	6.05×10 ⁻⁰⁶
Liver hepatocellular carcinoma	-1.29	-0.37	78,43.56	10,139.78	1.09×10 ⁻⁰⁷	3.14×10 ⁻⁰⁷
Breast invasive carcinoma	-1.26	-0.33	30,489.15	38,406.47	1.04×10 ⁻⁰⁹	2.12×10 ⁻⁰⁹
Kidney chromophobe	-1.23	-0.3	10,251.82	12,636.48	0.0297	0.0441
Kidney renal papillary cell carcinoma	-1.11	-0.14	7,285.97	8,054.57	0.0151	0.0205
Prostate adenocarcinoma	-1.1	-0.13	8,613.99	9,456.46	0.00212	0.00354
Thymoma	1.13	0.17	44,997.96	39,927.43	0.946	0.991
Pan-kidney cohort (KICH+KIRC+KIRP)	1.27	0.34	11,727.82	9,234.01	2.63×10 ⁻⁰⁶	4.24×10 ⁻⁰⁶
Cholangiocarcinoma	1.6	0.68	16,521.7	10,310.43	0.0759	0.14
Pancreatic adenocarcinoma	1.71	0.77	19,633.89	11,503.7	0.0105	0.217
Kidney renal clear cell carcinoma	1.78	0.83	14,848.28	8,346.26	4.36×10 ⁻²²	2.18×10 ⁻²¹

Abbreviations: KICH: Kidney chromophobe; KIRC: Kidney renal clear cell carcinoma; KIRP: Kidney renal papillary cell carcinoma; RPM: Reads per million microRNA.

Table S6. AURKB-associated long non-coding RNAs

Name	p-value	Adjusted p-value	Odds ratio	Combined score
PRC1-AS1	6.14×10 ⁻²⁴	5.40×10 ⁻²²	199,000	10,636,003.02
H2AZ1-DT	1.34×10 ⁻²⁰	3.94×10 ⁻¹⁹	1,968.03	90,049.77
DEPDC1-AS1	1.34×10 ⁻²⁰	3.94×10 ⁻¹⁹	1,968.03	90,049.77
CSRP3-AS1	1.31×10 ⁻¹⁷	2.88×10 ⁻¹⁶	865.13	33,631.66
APOBEC3B-AS1	7.48×10 ⁻¹⁵	7.31×10 ⁻¹⁴	499.21	16,237.8
RRM1-AS1	7.48×10 ⁻¹⁵	7.31×10 ⁻¹⁴	499.21	16,237.8
DDX11-AS1	7.48×10 ⁻¹⁵	7.31×10 ⁻¹⁴	499.21	16,237.8
LINC01775	7.48×10 ⁻¹⁵	7.31×10 ⁻¹⁴	499.21	16,237.8
HMMR-AS1	7.48×10 ⁻¹⁵	7.31×10 ⁻¹⁴	499.21	16,237.8
LINC00618	2.77×10 ⁻¹²	2.22×10 ⁻¹¹	317.49	8,448.82
LIX1L-AS1	2.77×10 ⁻¹²	2.22×10 ⁻¹¹	317.49	8,448.82
PRMT5-AS1	6.98×10 ⁻¹⁰	4.09×10 ⁻⁰⁹	209.42	4,415.27
SGO1-AS1	6.98×10 ⁻¹⁰	4.09×10 ⁻⁰⁹	209.42	4,415.27
TMPO-AS1	6.98×10 ⁻¹⁰	4.09×10 ⁻⁰⁹	209.42	4,415.27
EXOSC10-AS1	6.98×10 ⁻¹⁰	4.09×10 ⁻⁰⁹	209.42	4,415.27
LINC01224	1.21×10 ⁻⁰⁷	5.31×10 ⁻⁰⁷	138.15	2,200.74
MED8-AS1	1.21×10 ⁻⁰⁷	5.31×10 ⁻⁰⁷	138.15	2,200.74
LINC01096	1.21×10 ⁻⁰⁷	5.31×10 ⁻⁰⁷	138.15	2,200.74
LINC01842	1.21×10 ⁻⁰⁷	5.31×10 ⁻⁰⁷	138.15	2,200.74
UBL7-AS1	1.21×10 ⁻⁰⁷	5.31×10 ⁻⁰⁷	138.15	2,200.74

Table S7. Differential expression of long non-coding RNAs

Name	Expression level	p-value
PRC1-AS1	No difference	6.4×10 ⁻⁰³
H2AZ1-DT	Downregulated	7.0×10 ⁻⁰²
DEPDC1-AS1	Upregulated	5.2×10 ⁻⁴³
CSRP3-AS1	Upregulated	6.8×10 ⁻⁰³
APOBEC3B-AS1	Not expressed	4.7×10 ⁻⁰¹
RRM1-AS1	Upregulated	6.6×10 ⁻⁰⁸
DDX11-AS1	Upregulated	7.7×10 ⁻⁶⁵
LINC01775	Upregulated	1.3×10 ⁻⁶⁵
HMMR-AS1	Upregulated	2.3×10 ⁻¹⁶
LINC00618	Downregulated	3.1×10 ⁻⁰³
LIX1L-AS1	Downregulated	1.7×10 ⁻⁰²
PRMT5-AS1	Downregulated	5.6×10 ⁻⁰¹
SGO1-AS1	Not expressed	9.9×10 ⁻⁰¹
TMPO-AS1	Upregulated	9.0×10 ⁻¹⁰⁴
EXOSC10-AS1	Upregulated	3.8×10 ⁻⁰²
LINC01224	Upregulated	2.1×10 ⁻¹⁹
MED8-AS1	Downregulated	1.7×10 ⁻⁰⁵
LINC01096	Upregulated	1.2×10 ⁻²⁹
LINC01842	Upregulated	4.9×10 ⁻⁴⁶
UBL7-AS1	Downregulated	8.5×10 ⁻⁰⁶

Table S8. Correlation between *AURKB* and upregulated lncRNAs

Gene	lncRNA	r value	p-value
<i>AURKB</i>	<i>DEPDC1-AS1</i>	0.489	2.21×10^{-67}
	<i>CSRP3-AS1</i>	0.013	6.76×10^{-01}
	<i>RRM1-AS1</i>	0.12	6.51×10^{-05}
	<i>DDX11-AS1</i>	0.51	3.80×10^{-74}
	<i>LINC01775</i>	0.312	2.05×10^{-26}
	<i>HMMR-AS1</i>	0.222	8.73×10^{-14}
	<i>TMPO-AS1</i>	0.610	1.58×10^{-113}
	<i>LINC01224</i>	0.129	1.66×10^{-05}
	<i>LINC01096</i>	0.097	1.20×10^{-03}
	<i>LINC01842</i>	0.416	1.91×10^{-47}

Abbreviation: lncRNAs: Long non-coding RNAs.

Table S9. Transcriptome analysis of co-expressed genes

Symbol	Ensembl gene ID	Log fold change	Average expression	p-value	Adjusted p-value
<i>BIRC5</i>	ENSG00000089685	3.66157702	3.102300384	3.60×10^{-44}	1.43×10^{-42}
<i>CDC20</i>	ENSG00000117399	3.239156333	3.046024949	2.07×10^{-42}	7.04×10^{-41}
<i>CDC45</i>	ENSG00000093009	2.72550411	1.614201911	5.76×10^{-41}	1.73×10^{-39}
<i>CDCA5</i>	ENSG00000146670	2.812556548	2.983116166	1.09×10^{-42}	3.79×10^{-41}
<i>CDCA8</i>	ENSG00000134690	2.784368251	2.812120001	1.90×10^{-49}	1.48×10^{-47}
<i>KIF2C</i>	ENSG00000142945	3.110840135	2.827998895	8.97×10^{-46}	4.31×10^{-44}
<i>KIFC1</i>	ENSG00000237649	2.857644603	3.200502901	5.19×10^{-43}	1.85×10^{-41}
<i>PLK1</i>	ENSG00000166851	3.121461423	2.887775117	1.91×10^{-46}	9.93×10^{-45}
<i>RRM2</i>	ENSG00000171848	3.723321255	3.718685291	9.84×10^{-48}	6.15×10^{-46}
<i>TROAP</i>	ENSG00000135451	3.313451907	1.575374806	3.10×10^{-48}	2.07×10^{-46}
<i>AURKB</i>	ENSG00000178999	3.030904561	1.50169094	2.48×10^{-42}	8.36×10^{-41}
<i>MKI67</i>	ENSG00000148773	3.400262386	4.754181177	2.15×10^{-50}	1.94×10^{-48}
<i>E2F1</i>	ENSG00000101412	2.097473235	2.816446165	6.37×10^{-34}	1.03×10^{-32}

Table S10. Databases and tools used in the study

Database/tool	Function in the study	Data type	Statistical model/method
Broad Firehose GDAC	Accessing preprocessed, batch-corrected TCGA data	RNA-seq, clinical, mutation, and CNV data	Data generated through the standardized Firehose pipeline
TNMplot	Comparison of <i>AURKB</i> gene expression in tumor, normal, and metastatic tissues	RNA-seq (TCGA, GTEx, TARGET)	Mann–Whitney U test; ANOVA
GEPIA	Expression profiling and gene correlation analysis	TCGA and GTEx RNA-seq	$\log_2$ (TPM+1) normalization; Student's <i>t</i> -test
Bc-GenExMiner	Gene expression and prognostic analysis	Microarray and RNA-seq data	Kaplan–Meier survival analysis; Log-rank test; Cox proportional hazards models
Dependency Map	Gene dependency and clustered regularly interspaced short palindromic repeats/short hairpin RNA-based gene essentiality screens	Gene essentiality scores (e.g., CERES, DEMETER2), gene expression, copy number, and mutation data	CRISPR–Cas9 screens; RNA interference, correlation analysis to find co-dependencies
TACCO	Genomic and clinical landscape of tumors	Somatic copy number alterations, clinical data (survival), and gene expression	Statistical models for chromosomal instability (e.g., <i>FGA</i> score); survival analysis (Kaplan–Meier, Cox regression)
TISIDB	Integrate tumor-immune system interactions	RNA-seq and clinical data from TCGA, immune cell subtype data from public deconvolution algorithms	Correlation analysis (Spearman), survival analysis (Log-rank test), expression comparison (Wilcoxon rank-sum test)
TIMER2.0	Evaluation of immune infiltration and <i>AURKB</i> gene association in BRCA	TCGA RNA-seq and immune deconvolution data	CIBERSORT/TIMER deconvolution; correlation analysis

(Cont'd...)

Table S10. (Continued)

Database/tool	Function in the study	Data type	Statistical model/method
miRNet	Network construction of lncRNA–miRNA–mRNA interactions (ceRNA networks)	miRNA–lncRNA–mRNA interaction data	Network-based multi-database integration
ENCORI	Correlation and survival validation of ceRNA regulatory axes	CLIP-seq, RNA-seq	Pearson correlation; Kaplan–Meier estimator
UALCAN	Expression and subgroup-based comparison (e.g., tumor vs. normal, stage, gender)	TCGA transcriptomic data	Welch's <i>t</i> -test; log2 TPM normalization
Kaplan–Meier plotter	Survival analysis (Kaplan–Meier for overall survival, first-progression survival, post-progression survival by gene expression levels)	TCGA and GEO meta-analysis	Log-rank test; Cox proportional hazards model
CancerMIRNome	miRNA-level expression and survival analysis for let-7b-5p	TCGA/TARGET miRNA-seq and clinical data	Log-rank test; Cox regression; Receiver operating curve analysis
OncoDB	Cross-validation of gene expression and survival across cancers	TCGA and GTEx expression and mutation data	Welch's <i>t</i> -test; Kaplan–Meier estimator
CancerSEA	Functional annotation of the <i>AURKB</i> gene states at the single-cell level	Single-cell RNA-seq	AUCell-based functional state scoring
GSCA (Gene Set Cancer Analysis)	Multi-omics integration and drug sensitivity analysis	Genomic, transcriptomic, and pharmacogenomic data	Correlation analysis; GSEA; regression models
TCGAnalyzeR	Visualization of gene expression, survival, and mutation landscape	Genomic, transcriptomic, and survival data	DESeq2, Cox regression, Kaplan–Meier estimator
Enrichr	Functional and pathway enrichment analysis of DEGs and interactors	GO terms, pathway annotations	Fisher's exact test and <i>z</i> -score for the combined score
lncHUB	Identification of co-expression partners and functional associations of lncRNAs	RNA-seq-based co-expression networks	Pearson correlation and gene enrichment scoring

Abbreviations: BRCA: Breast cancer; CancerSEA: Cancer single-cell state atlas; CLIP: Cross-linking immunoprecipitation; ENCORI: Encyclopedia of RNA Interactomes; GDAC: Genome Data Analysis Center; lncRNA: Long non-coding RNA; GEPIA: Gene Expression Profiling Interactive Analysis; GO: Gene ontology; GTEx: Genotype-Tissue Expression; miRNA: MicroRNA; RNA-seq: RNA sequencing; TACCO: Transcriptome Alterations in Cancer Omnibus; TCGA: The Cancer Genome Atlas; TISIDB: Tumor-Immune System Interactions and Drug Bank; TIMER: Tumor Immune Estimation Resource; TPM: Transcripts per million; UALCAN: University of Alabama Cancer Database.

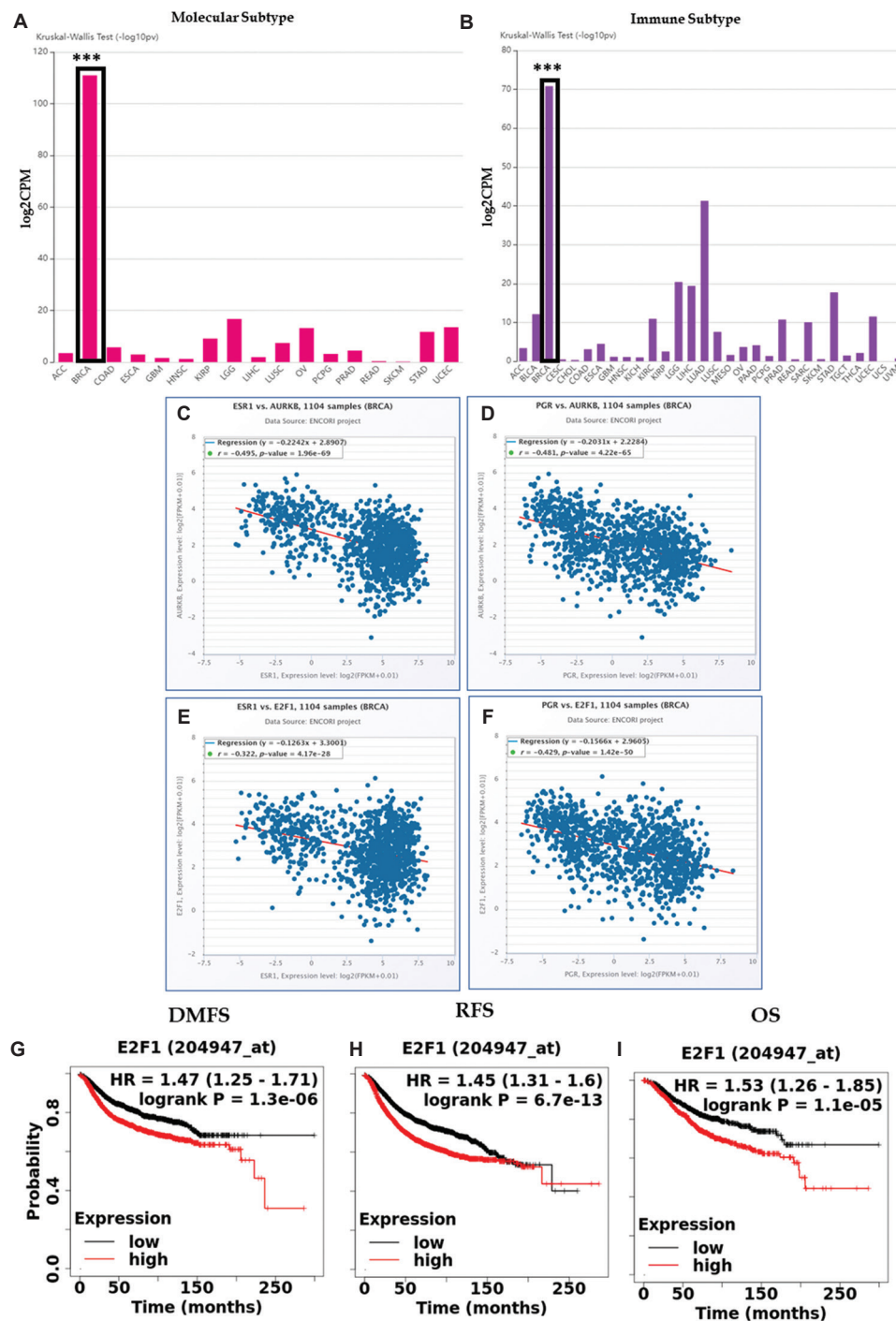
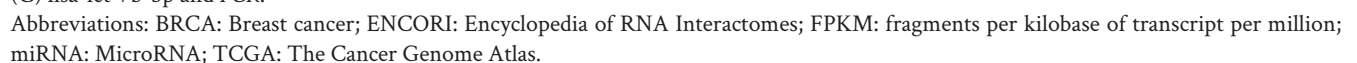


Figure S1. Pan-cancer analysis of *AURKB* expression using the TISIDB database in (A) the molecular subtype and (B) the immune subtype. Correlation analysis conducted using ENCORI to show relations between (C) *ESR1* and *AURKB*; (D) *PGR* and *AURKB*; (E) *ESR1* and *E2F1*; and (F) *PGR* and *E2F1*. Kaplan-Meier survival curves were plotted for (G) DMFS ($n = 2,765$), (H) RFS ($n = 4,929$), and (I) OS ($n = 1,879$) associated with *E2F1* expression. *** $p < 0.05$.

Abbreviations: BRCA: Breast cancer; CPM: Counts per million; DMFS: Distant-metastasis-free survival; ENCORI: Encyclopedia of RNA Interactomes; FPKM: fragments per kilobase of transcript per million; HR: Hazard ratio; OS: Overall survival; RFS: Relapse-free survival; TISIDB: Tumor-Immune System Interactions and Drug Bank.



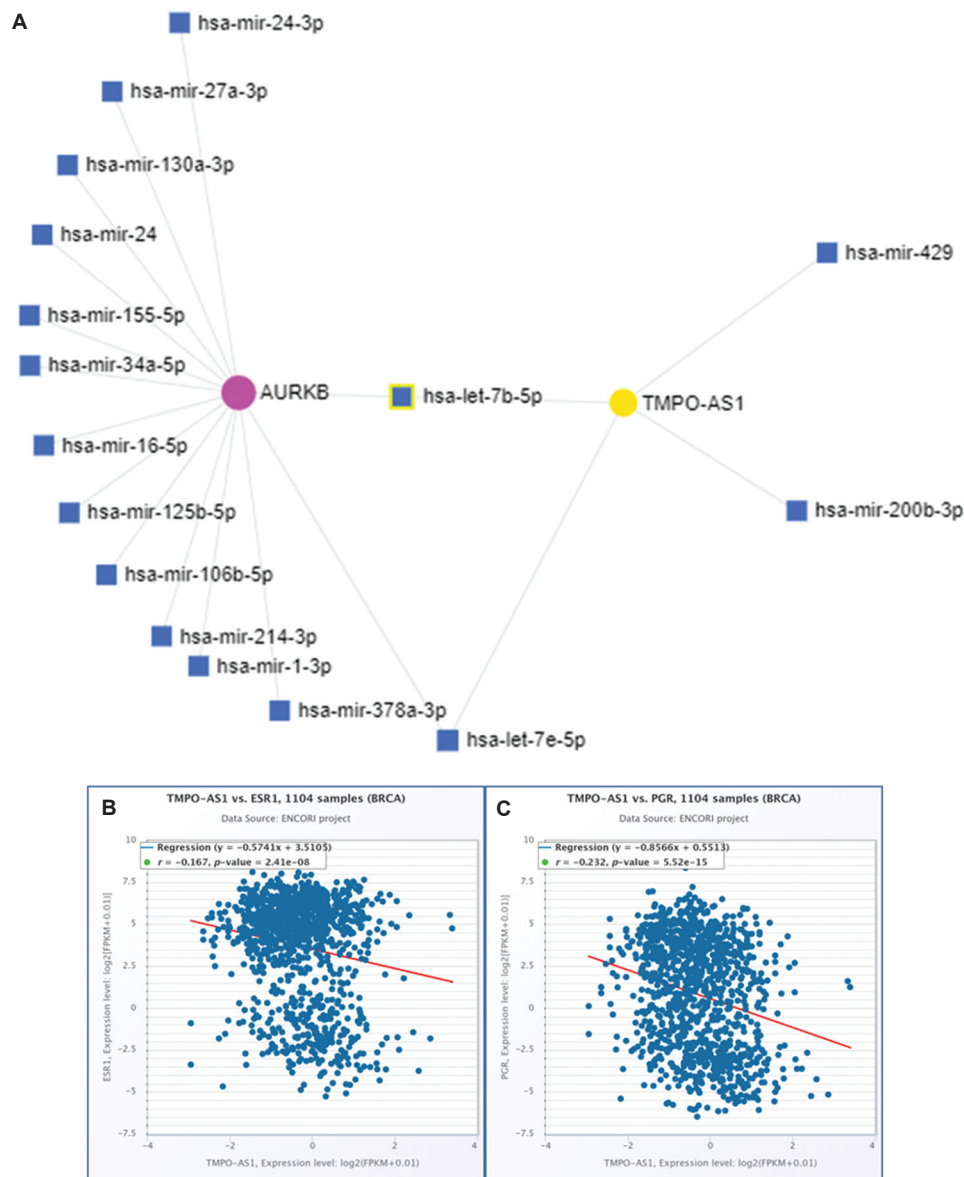


Figure S3. Network and correlation analysis of TMPO-AS1 in BRCA. (A) Network showing association between *AURKB*, *hsa-let-7b-5p*, and *TMPO-AS1* created using miRNet. Correlation analysis using ENCORI shows correlations between (B) *TMPO-AS1* and *ESR1*, and (C) *TMPO-AS1* and *PGR*.

Abbreviations: BRCA: Breast cancer; ENCORI: Encyclopedia of RNA Interactomes; FPKM: fragments per kilobase of transcript per million.