

Supplementarymaterial2

SupplementaryTablesFor:Pan-Cancer Multi-Omics Analysis Uncovers CHD4 Driving Tumor Progression via Epigenetic Regulation of Genomic Stability and the Immune Microenvironment

Table S1: List of abbreviations

Full name	Abbreviations
Adrenocortical carcinoma	ACC
Bladder Urothelial Carcinoma	BLCA
Breast invasive carcinoma	BRCA
Cervical squamous cell carcinoma and endocervical adenocarcinoma	CESC
Cholangiocarcinoma	CHOL
Colon adenocarcinoma	COAD
Colon adenocarcinoma/Rectum adenocarcinoma Esophageal carcinoma	COADREAD
Lymphoid Neoplasm Diffuse Large B-cell Lymphoma	DLBC
Esophageal carcinoma	ESCA
FFPE Pilot Phase II	FPPP
Glioblastoma multiforme	GBM
Glioma	GBMLGG
Head and Neck squamous cell carcinoma	HNSC
Kidney Chromophobe	KICH
Pan-kidney cohort (KICH+KIRC+KIRP)	KIPAN
Kidney renal clear cell carcinoma	KIRC
Kidney renal papillary cell carcinoma	KIRP
Acute Myeloid Leukemia	LAML
Brain Lower Grade Glioma	LGG
Liver hepatocellular carcinoma	LIHC
Lung adenocarcinoma	LUAD
Lung squamous cell carcinoma	LUSC
Mesothelioma	MESO
Ovarian serous cystadenocarcinoma	OV
Pancreatic adenocarcinoma	PAAD
Pheochromocytoma and Paraganglioma	PCPG
Prostate adenocarcinoma	PRAD
Rectum adenocarcinoma	READ
Sarcoma	SARC
Stomach adenocarcinoma	STAD
Skin Cutaneous Melanoma	SKCM
Stomach and Esophageal carcinoma	STES
Testicular Germ Cell Tumors	TGCT
Thyroid carcinoma	THCA
Thymoma	THYM
Uterine Corpus Endometrial Carcinoma	UCEC
Uterine Carcinosarcoma	UCS
Uveal Melanoma	UVM
Osteosarcoma	OS
Acute Lymphoblastic Leukemia	ALL
Neuroblastoma	NB
High-Risk Wilms Tumor	WT
The Cancer Genome Atlas	TCGA
Genotype-Tissue Expression	GTEx
Cancer Cell Line Encyclopedia	CCLE
The University of Alabama at Birmingham Cancer data analysis Portal	UALCAN

Full name	Abbreviations
The Clinical Proteomic Tumor Analysis Consortium	CPTAC
The Human Protein Atlas	HPA
Immunohistochemistry	IHC
Receiver Operating characteristic Curves	ROC
Area Under the Curve	AUC
Overall Survival	OS
Disease-Specific Survival	DSS
Disease-Free Interval	DFI
Progression-Free Interval	PFI
Copy Number Variation	CNV
Single Nucleotide variant	SNV
Tumor Mutation Burden	TMB
Microsatellite Instability	MSI
Mutant-Allele Tumor Heterogeneity	MATH
Homologous Recombination Deficiency	HRD
Loss of Heterozygosity	LOH
Homologous Recombination Repair	HRR
Mismatch Repair	MMR
DNA Methyltransferases	DNMTs
RNA Stemness Score	RNAss
Epiregulin expression stemness score	EREG.EXPss
DNA Stemness Score	DNAss
EREG (Epiregulin) METHylation Stemness Score	EREG-METHss
Differentially Methylated Position stemness score	DMPss
ENHancer Stemness Score	ENHss
Cytotoxic Lymphocyte	CTL
N1-Methyladenosine	m1A
5-Methylcytidine	m5C
N6-Methyladenosine	m6A
Alternative Splicing	AS
Percent Spliced In	PSI
False Discovery Rate	FDR
Gene Set Enrichment Analysis	GSEA
Gene Set Variation Analysis	GSVA
Kyoto Encyclopedia of Genes and Genomes	KEGG
Gene Ontology	GO
Estimation of STromal and Immune cells in Malignant Tumor tissues using Expression data	ESTIMATE
Tumor Immune Estimation Resource	TIMER
Estimating the Proportions of Immune and Cancer cells	EPIC
Tumor Microenvironment	TME
Major Histocompatibility Complex	MHC
Half Maximal Inhibitory Concentration	IC50
Growth Inhibition of 50%	GI50
Mechanisms of Action	MoA

Table S2: CHD4 clinical-relevant AS events on OncoSplicing

Gene_Symbol	Splice_Type	Splice_Event	Project	Cancer_Type
CHD4	A3	alt_3prime_57936	SplAdder	UCEC/LIHC/UCS/UCEC/KIRC/KIRP/CHOL/LIHC
CHD4	A3	alt_3prime_57946	SplAdder	COAD
CHD4	A3	alt_3prime_57950	SplAdder	ACC/HNSC/MESO/ACC/SARC/DLBC/HNSC/OV/MESO
CHD4	A3	alt_3prime_57954	SplAdder	KIRC/LGG/ESCA
CHD4	A3	alt_3prime_57958	SplAdder	HNSC/TGCT
CHD4	A3	alt_3prime_57962	SplAdder	LUSC
CHD4	A3	alt_3prime_57964	SplAdder	BLCA/CHOL/THCA/SARC/READ/LUAD/TGCT
CHD4	A3	alt_3prime_57972	SplAdder	KICH/BRCA/PRAD
CHD4	A3	alt_3prime_57974	SplAdder	LGG/SLCM
CHD4	A3	alt_3prime_57978	SplAdder	THCA
CHD4	A3	alt_3prime_57979	SplAdder	THCA
CHD4	A3	alt_3prime_57980	SplAdder	UVM/MESO/SARC/BLCA/HNSC/DLBC/UVM
CHD4	A3	alt_3prime_57981	SplAdder	SKCM
CHD4	A5	alt_5prime_42649	SplAdder	OV
CHD4	A5	alt_5prime_42650	SplAdder	ACC/KIRP/ACC/LIHC/DLBC/LIHC/TGCT
CHD4	A5	alt_5prime_42651	SplAdder	KIRC/STAD/THYM/KIRC
CHD4	A5	alt_5prime_42655	SplAdder	UCS/BRCA
CHD4	ES	exon_skip_89532	SplAdder	LGG/LIHC/DLBC
CHD4	ES	exon_skip_89537	SplAdder	THYM
CHD4	IR	intron_retention_31528	SplAdder	LUSC/UVM/PRAD
CHD4	IR	intron_retention_31535	SplAdder	GBM/KIRP/OV/BLCA/KIRP/LIHC
CHD4	AA	CHD4_AA_19897	SpliceSeq	HNSC/SARC/GBM/MESO/KIRC/UVM/HNSC
CHD4	AA	CHD4_AA_19898	SpliceSeq	OV/THCA/BRCA
CHD4	ES	CHD4_ES_132940	SpliceSeq	COAD/LUSC/LUAD
CHD4	RI	CHD4_RI_19896	SpliceSeq	LUAD/LAML/UVM/READ

Table S3: Genes involved in oncogenic pathways

Chromatin modifiers	NRF2 pathway status	SWI/SNF complex status	HIPPO pathway status	WNT pathway status
CREBBP	NFE2L2	ACTB	MST1	WNT1
EHMT1	KEAP1	ACTL6A	MST2	WNT3A
EHMT2	HMOX1	ACTL6B	SAV1	FZD1
EP300	NQO1	ARID1A	LATS1	FZD7
EZH1	GCLC	ARID1B	LATS2	LRP5
EZH2	GCLM	ARID2	MOB1A	LRP6
KAT2A	MAFG	BCL11A	MOB1B	CTNNB1
KAT2B	MAFK	BCL11B	YAP1	APC
KDM1A		BCL6	WWTR1	AXIN1
KDM1B		BCL6B	TEAD1	AXIN2
KDM4A		BRD7	TEAD2	TCF7
KDM4B		BRD9	TEAD3	TCF7L2
KDM5A		DPF1	TEAD4	LEF1
KDM5B		DPF2	NF2	
KDM5C		DPF3		
KDM6A		PBRM1		
KDM6B		PHF10		
KMT2A		SMARCA2		
KMT2B		SMARCA4		
KMT2C		SMARCB1		
KMT2D		SMARCC1		
KMT2E		SMARCC2		
NSD1		SMARCD1		
SETD2		SMARCD2		
SMYD4		SMARCD3		
SRCAP		SMARCE1		

Table S4: GO pathways enriched by the top 100 CHD4 co-expressed genes identified on GEPIA2.0

ONTO LOGY	ID	Description	Gene Ratio	BgRatio	Pvalue	P.adjust	qvalue	Gene ID	Count
BP	GO:0008380	RNA splicing	32/93	434/18723	3.67319E-29	4.66128E-26	3.66546E-26	FUS/SF3B2/DHX9/DDX39B/SFPQ/KHDRBS1/RBM10/ZNF638/HNRNPM/SN RNP200/CD2BP2/HNRNPA1/TARDBP/HNRNPU/ACIN1/HNRNPA2B1/IK/S NW1/HNRNPC/PDCD7/HNRNPA1L2/NONO/HNRNPR/DHX8/SFSWAP/ME TTL16/HNRNPL/EFTUD2/SYF2/NCL/DDX47/SUGP1	32
BP	GO:1903311	regulation of mRNA etabolic process	19/93	288/18723	2.04156E-16	5.18147E-14	4.07452E-14	FUS/DHX9/SAFB/KHDRBS1/RBM10/HNRNPA0/HNRNPM/HNRNPA1/TAR DBP/HNRNPU/HNRNPD/RNF40/SNW1/HNRNPC/HNRNPR/SFSWAP/MET TL16/HNRNPL/NCL	19
BP	GO:0048255	mRNA stabilization	9/93	56/18723	7.74674E-12	1.22883E-09	9.66304E-10	FUS/DHX9/RBM10/HNRNPA0/TARDBP/HNRNPU/HNRNPD/HNRNPC/ME TTL16	9
BP	GO:0006325	chromatin organization	15/93	409/18723	1.5773E-09	1.251E-07	9.83737E-08	SMARCA4/SAFB/CHD8/SUPT16H/SMARCD1/HNRNPU/ DPF2/ALKBH4/HNRNPC/ACTR8/DAXX/HIRA/TPR/NAP1L4/BAHD1	15
BP	GO:0051052	regulation of DNA metabolic process	13/93	359/18723	2.48436E-08	1.43303E-06	1.12688E-06	FUS/DHX9/DDX39B/HNRNPA1/HNRNPU/HNRNPD/HNRNPA2B1/TP53BP 1/HNRNPC/XRCC1/MMS19/EHMT2/XRCC5	13
CC	GO:0005681	spliceosomal complex	18/96	191/19550	2.05414E-18	3.6769E-16	2.81092E-16	SF3B2/DDX39B/HNRNPM/SNRNP200/HNRNPA1/HNRNPU/HNRNPA2B1/I K/SNW1/HNRNPC/PDCD7/HNRNPA1L2/HNRNPR/DHX8/EFTUD2/SYF2/N CL/SUGP1	18
CC	GO:0016607	nuclear speck	21/96	412/19550	6.96669E-16	6.23519E-14	4.76668E-14	SF3B2/DDX39B/SFPQ/RBM10/ZNF638/PSPC1/GTF2H4/ CD2BP2/CHTOP/TARDBP/HNRNPU/NXF1/ACIN1/IK/SNW1/NONO/EP400/ TOE1/EFTUD2/EHMT2/SYF2	21
CC	GO:0071013	catalytic step 2 spliceosome	12/96	87/19550	1.26744E-14	7.56241E-13	5.78132E-13	SF3B2/HNRNPM/SNRNP200/HNRNPA1/HNRNPU/HNRNPA2B1/SNW1/HN RNP/HNRNPR/DHX8/EFTUD2/SYF2	12
CC	GO:0034399	nuclear eriphery	9/96	130/19550	1.53015E-08	6.84742E-07	5.23472E-07	DDX39B/SFPQ/PSPC1/HNRNPM/HNRNPU/HNRNPA2B1/ SNW1/NONO/TPR	9
CC	GO:0016363	nuclear matrix	8/96	111/19550	7.33013E-08	2.62419E-06	2.00614E-06	DDX39B/SFPQ/PSPC1/HNRNPM/HNRNPU/HNRNPA2B1/ SNW1/NONO	8
MF	GO:0004386	helicase activity	12/95	156/18368	2.73844E-11	5.75072E-09	4.00677E-09	DHX9/DDX39B/SMARCA4/CHD8/SNRNP200/DHX57/ DHX30/DHX8/EP400/SMARCA1/XRCC5/DDX47	12
MF	GO:0042162	telomeric DNA binding	6/95	36/18368	2.80364E-08	2.94382E-06	2.05108E-06	HNRNPA1/HNRNPD/HNRNPA2B1/TP53BP1/XRCC5/NCL	6
MF	GO:0003730	mRNA 3'-UTR binding	10/95	201/18368	8.86778E-08	6.20745E-06	4.32499E-06	FUS/ILF3/HNRNPA0/TARDBP/HNRNPU/HNRNPD/HNRNPA2B1/RNF40/H NRNPC/HNRNPR	10
MF	GO:0003724	RNA helicase activity	7/95	77/18368	1.41667E-07	7.11221E-06	4.95538E-06	DHX9/DDX39B/SNRNP200/DHX57/DHX30/DHX8/DDX47	7
MF	GO:0008186	ATP-dependent activity, acting on RNA	7/95	79/18368	1.69338E-07	7.11221E-06	4.95538E-06	DHX9/DDX39B/SNRNP200/DHX57/DHX30/DHX8/DDX47	7