

Table S1. TCGA gene expression data sets used.

TCGA Code*	Entity/Study Name* (n = 23)	Primary Tumors (n = 8137)
ACC	Adrenocortical carcinoma	79
BLCA	Bladder – Urothelial carcinoma	408
BRCA	Breast – Invasive carcinoma	1094
CESC	Cervical squamous cell carcinoma and endocervical adenocarcinoma	304
COAD	Colon adenocarcinoma	457
DLBC	Diffuse large cell lymphoma	28
GBM	Glioblastoma multiforme	153
HNSC	Head and neck squamous cell carcinoma	520
KICH	Kidney - Chromophobe carcinoma	66
KIRC	Kidney – renal clear cell carcinoma	533
KIRP	Kidney – renal papillary carcinoma	290
LAML	Acute myeloid leucemia	173
LGG	Lower grade glioma	516
LIHC	Liver – Hepatocellular carcinoma	371
LUAD	Lung – Adenocarcinoma	515
LUSC	Lung – Squamous cell carcinoma	501
OV	Ovarian – Serous cystadenocarcinoma	261
PRAD (= pPCa)	Primary prostate cancer	496
READ	Rectum – Adenocarcinoma	166
SKCM	Skin – Cutaneous Melanoma	103
THCA	Thyroid carcinoma	501
UCEC	Uterine corpus endometrial carcinoma	545
UCS	Uterine carcinosarcoma	57

Overview of TCGA data regarding tumor entities and primary tumor samples included in the transcriptome analysis (* as given by the TCGA code tables, <https://tcga-data.nci.nih.gov/datareports/codeTablesReport.htm>).

Table S2. Mediator complex subunits*.

Gene Symbol	Gene name (alternative Name)	Module
MED6	Mediator complex subunit 6	Head
MED8	Mediator complex subunit 8	Head
MED11	Mediator complex subunit 11	Head
MED17	Mediator complex subunit 17 (TRAP80)	Head
MED18	Mediator complex subunit 18 (p28b)	Head
MED19	Mediator complex subunit 19 (LCMR1)	Head
MED20	Mediator complex subunit 20 (TRFP)	Head
MED22	Mediator complex subunit 22 (MED24)	Head
MED28	Mediator complex subunit 28 (Magicin)	Head
MED30	Mediator complex subunit 30 (TRAP25)	Head
MED4	Mediator complex subunit 4 (TRAP36)	Middle
MED7	Mediator complex subunit 7 (CRSP9)	Middle
MED9	Mediator complex subunit 9 (MED25)	Middle
MED10	Mediator complex subunit 10 (Nut2)	Middle
MED21	Mediator complex subunit 21 (Srb7)	Middle
MED31	Mediator complex subunit 31 (Soh1)	Middle
MED1	Mediator complex subunit 1 (TRAP220, CRSP200)	Tail
MED14	Mediator complex subunit 14 (TRAP170, Rgr1)	Tail
MED15	Mediator complex subunit 15 (ARC105)	Tail
MED16	Mediator complex subunit 16 (TRAP95)	Tail
MED23	Mediator complex subunit 23 (Sur2)	Tail
MED24	Mediator complex subunit 24 (TRAP100)	Tail
MED25	Mediator complex subunit 25	Tail
MED26	Mediator complex subunit 26	Tail
MED27	Mediator complex subunit 27 (TRAP37)	Tail
MED29	Mediator complex subunit 29 (IXL, Intersex)	Tail
CDK19	Cyclin-dependent kinase 19 (Cdc216, CDK11-like)	Kinase
CDK8	Cyclin-dependent kinase 8 (K35)	Kinase
MED12	Mediator complex subunit 12 (TRAP230)	Kinase
MED12L	Mediator complex subunit 12-like (TRALP)	Kinase
MED13	Mediator complex subunit 13 (TRAP240)	Kinase
MED13L	Mediator complex subunit 13-like (TRAP240L)	Kinase
CCNC	Cyclin C (CycC)	Kinase

Overview of Mediator complex subunits including official gene symbol, full gene names following

current nomenclature and corresponding module. For clarification purposes alternative names for the genes used in older articles are given where available. These aliases usually predate the knowledge about involvement of a gene in the Mediator complex. (Information obtained from www.ncbi.nlm.nih.gov/gene and Sato et al. Mol Cell 2004).

Table S3. Cohorts used for immunohistochemical analysis.

Tissue type	Samples (n = 622)	ERG Rearrangement			ERG protein expression			Ki-67 Index (Positive cells)			
		WT	ERG Rear.	NA	Neg.	Pos.	NA	0 %	1 – 10%	> 10%	NA
Benign prostate	102	3	1	98	3	2	97	4	0	0	98
Primary prostate cancer (pPCa)	410	65	69	276	168	149	93	102	43	0	262
Lymphnode metastasis (LNPC)	76	24	32	20	0	0	76	5	48	5	18
Metastatic Castration-resistant prostate cancer (CRPC)	34	23	9	2	19	9	6	0	18	16	0

Overview of samples included in the immunohistochemical staining analysis for nuclear CDK19 and CDK8 expression and known molecular characteristics from prior studies (NA = not available, WT = wild-type).