Supplemental methods:

Expression Plasmids and sgRNA. The full-length human BRG1, FBXW7, GSK3β and PTEN cDNA was cloned into pMSCV-puro/neo (Clontech), pcDNA5 (Flag tag) (Invitrogen), and pcDNA3.1 (Myc or HA tag) (Invitrogen) to generate expression plasmids. To generate BRG1-SA and BRG1-SD mutated PC3 cells, a DNA template in which serine (S) in BRG1 1417/1421 sites were substituted by alanine acid (A) or aspartic acid (D) and flanked by 500 bp homology arms was used. By CRISPR-Cas9 induced homology directed repair, the template was incorporated into the native locus resulting in endogenous SA or SD mutation in PC3 cells. The shRNA, sgRNA and siRNA sequences are listed in Supplemental Table 4.

Immunohistochemical and Western Blotting Antibodies. The antibodies used for western blot analysis and immunohistochemistry were pAKT Ser473 (Cell Signaling Technology; 4060, 1:1000 dilution), PTEN (Cell Signaling Technology; 9556, 1:1000 dilution), AKT (Cell Signaling Technology; 4691, 1:1000 dilution), pERK Thr202/Tyr204 (Cell Signaling Technology; 4370, 1:1000 dilution), FBXW7 (Bethyl, A301-721; 1:1000 dilution), pGSK3β-S9 (Cell Signaling Technology; 9323, 1:1000 dilution), GSK3β (Cell Signaling Technology; 5558, 1:1000 dilution), AR N-20 (Santa Cruz Biotechnology; SC-816, 1:1000 dilution), SMAα (Sigma; A2547, 1:5000 dilution), P63 (Santa Cruz Biotechnology; SC-8431, 1:1000 dilution), c-Myc (Abcam; ab32072, 1:1000 dilution), and β-actin (Santa Cruz Biotechnology; SC-47778, 1:10000 dilution). Antibody specific to p-BRG1-1417/1421 was prepared commercially from immunizing rabbits at Shanghai Genomic Inc. (with 1:500 working dilution). Biotinylated secondary antibodies were purchased from Jackson Immunology. Staining was visualized with ABC Kit Vectastain Elite (Vector Laboratories) and DAB substrate (Vector Laboratories).

RNA isolation and real-time PCR. Total RNA was extracted using TRIzol followed by RNeasy Mini kit (Qiagen) clean up. First strand cDNA was synthesized using Superscript II (Invitrogen) and 2 μg of total RNA was used in each cDNA synthesis reaction. SYBR green Universal Master Mix reagents (Roche) and primer mixtures (Supplemental Table 4) were used for the RT-qPCR assay.

Immunoprecipitation and western blotting. Cells were lysed in 0.3% Nonidet P40 buffer (150 mM NaCl, 50 mM Tris-HCl, pH7.5) containing inhibitors (1 mM phenylmethylsulphonyl fluoride, 1μg/ml of aprotinin, 1 μg/ml of leupeptin, 1 μg/ml of pepstatin, 1 mM Na3VO4, and 1 mM NaF, all in their final concentrations). Cell debris were removed by centrifuging at 4 °C, 13,000 r.p.m. for 15 min, and lysates were incubated for 6 h at 4 °C with anti-Flag M2 agarose (Sigma). The immunoprecipitates were washed three times with 0.3% Nonidet P40 buffer before boiled and analyzed by western blotting according to the standard methods. The following primary antibodies were commercially obtained: Flag (Sigma, ab1162, 1:10,000 working dilution), BRG1(Abcam, ab110641, 1;2000), HA (cell signaling, 3724, 1:1,000), FBXW7 (Bethyl, A301-721, 1:500), AKT (Cell signaling, 4691, 1:1,000), PTEN (Cell signaling, 9556, with 1:1,000 working dilution), c-Myc (Abcam, ab32072, 1:2,000), Phospho-ERK (Cell signaling, 4370, 1:1,000) and Ub (Cell signaling, 3933, 1:1,000).

Mass spectrometry analysis. To identify BRG1 phosphorylation sites, 293T cells stably expressing Flag-BRG1 with or without GSK3β overexpression. Cell lysates were collected to perform Flag-IP and the band corresponding to Flag-BRG1 was excised and sent for mass spectrometry analysis by National Facility for Protein Science in Shanghai, China.

In vitro ubiquitination assay. The procedure for in vitro ubiquitination assay was conducted according to the manufacturer's instructions. Flag-tagged BRG1, BRG1-SA, BRG1-SD and Flag-FBXW7 immunocomplexes were purified from 293 cells using Flag M2 beads (Sigma), and then eluted by incubating with a molar excess of Flag peptide. The FBXW7 immunocomplex was mixed with BRG1 substrate, and this mixture was added to a ubiquitin ligation reaction (Enzo Life Sciences). After the reactions, and the samples were submitted to immunoblotting with the anti-Ub antibody to examine ubiquitin ladder formation.

In vitro Kinase Assay. GSK3β was purchased from Abcam (ab63193). Briefly, 1 μg of purified Flag tagged proteins were incubated with GSK3β in the presence of 5 μCi [γ-32P] ATP and 200 μM cold ATP in the reaction buffer for 15–30 min. The reaction was stopped by the addition of

SDS-containing lysis buffer and detected by autoradiography.

GST pull-down assay. BRG1 truncated protein was obtained from in-vitro translation (Promega). BL21 E. coli transformed with pGEX-GST-GSK3β plasmid was induced (or not induced) by isopropyl-β-D-thiogalactoside (0.1 mM) at 20 °C for 12 h. Protein was then purified through GST antibody-conjugated beads, and incubated with BRG1 protein. Beads were subsequently harvested through centrifugation and washed four times by 0.2% NP40 buffer before boiled by 1 × SDS–polyacrylamide gel electrophoresis loading buffer and subjected to western blotting.

Chromatin-immunoprecipitation assays. The ChIP assays were performed using Magnetic ChIP kit (Millipore). The procedure was as described in the kit provided by the manufacturer. BRG1 (Abcam, ab110641), H3K27ac (Cell signaling, 9733), H3K27me3 (Abcam, ab6002) were then used for immunoprecipitation. After reverse-crosslinking, the precipitated DNA was amplified by primers and quantified by the Step One Plus real-time-PCR machine. Primer sequences can be found in the Supplemental Table 4.

A

PTEN-WT 22RV-1

Symbol	log2 beta score (Day 0 vs Day 45)	p value
BRD8	0.61494	0.001106
DAXX	0.8287	0.002277
DDX23	0.7485	0.004962
DDX27	0.72716	0.006304
DDX51	1.0182	0.000494
DHX16	0.79607	0.00305
DIDO1	0.81236	0.002674
HDAC3	0.74673	0.005059
INTS6	0.87064	0.001611
LSM7	0.75212	0.004801
RAD54L	0.77266	0.003888
SETD1A	0.87651	0.001536
TERF2	0.90433	0.001257
TPR	0.76217	0.004339
ANKRD36	1.0025	0.000537
BANF1	0.77831	0.003695
CHAF1A	0.82799	0.002288
CHAF1B	1.0918	0.000226
CHD4	0.6883	0.009322
CHMP6	0.90345	0.001257
DDX41	0.7632	0.004318
DDX42	0.72112	0.006713
DDX49	1.2246	0.000118
EIF4A3	0.85503	0.001858
EP400	0.74755	0.005005

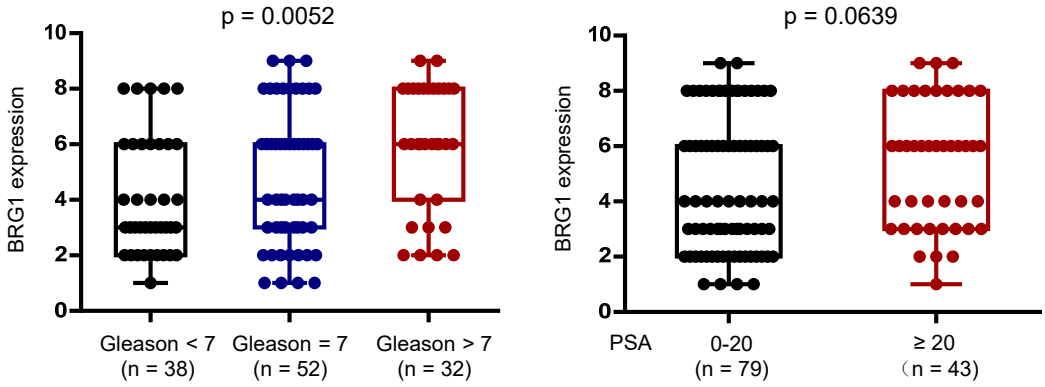
Symbol	log2 beta score (Day 0 vs Day 45)	p value
H3F3A	0.85445	0.001869
HIST2H2AC	0.70635	0.007765
INTS4	0.85057	0.001933
KAT8	0.72222	0.00668
KTI12	0.90983	0.001171
LSM2	1.1627	0.00014
MCM4	0.80682	0.002792
NCAPD3	0.73538	0.005735
PRMT5	0.72195	0.00668
RFC2	0.69224	0.009043
RUVBL1	0.95215	0.000752
RUVBL2	1.0464	0.000354
SMG6	0.89365	0.001343
SNRNP200	1.3751	6.44E-05
SNRPB	1.4705	5.37E-05
SNRPD2	0.95652	0.000709
SNRPE	0.96633	0.000666
SNRPG	0.89621	0.0013
TCP1	0.93805	0.000827
TERF1	0.78264	0.003609
TINF2	0.77808	0.003705
XRCC6	1.1658	0.00014

PTEN-KD (shPTEN) 22RV-1

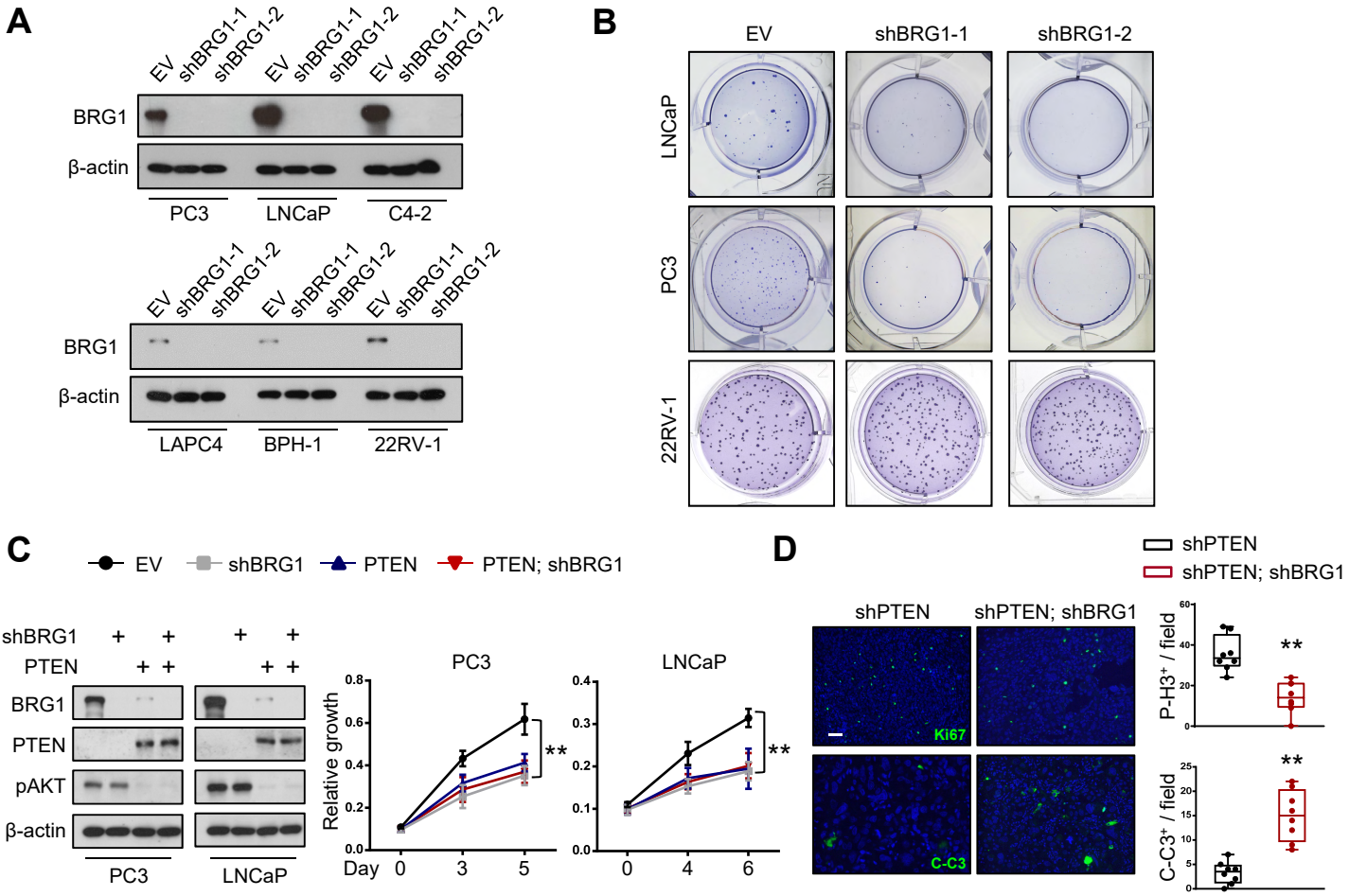
Symbol	log2 beta score (Day 0 vs Day 45)	p value
ACTL6A	0.72582	0.008839
CENPT	0.71975	0.009269
DDX11	0.76006	0.00653
DDX18	0.83743	0.003233
DDX24	0.8656	0.00246
DDX47	0.83538	0.003276
DDX55	0.94985	0.001149
DHX37	0.93767	0.001278
ELP3	0.85423	0.002792
EP300	0.80391	0.004457
HIST1H2AH	0.823	0.00377
HIST1H2AI	0.7758	0.005703
HUWE1	0.77828	0.005574
JMJD6	0.61851	0.003952
LSM12	0.87185	0.00232
LSM6	0.74705	0.007282
PHF5A	1.1137	0.000279
RBBP5	0.73854	0.007829
RTF1	0.71355	0.009945
SAP18	1.33	7.52E-05
SF3B1	1.1258	0.000258
SKIV2L2	0.91178	0.001568
SMARCA4	1.048	0.000473
SMARCA5	0.86202	0.002545
SMARCB1	1.2251	0.000172
SMARCE1	0.88691	0.00203
SMC3	1.052	0.000462
SNRPF	0.98523	0.000784
SUZ12	0.83128	0.003383
TADA2B	0.89269	0.001923
UPF1	0.96248	0.000999
YEATS4	0.713	0.009956

Symbol	log2 beta score (Day 0 vs Day 45)	p value
ANKRD36	0.84749	0.002943
BANF1	0.90995	0.001622
CHAF1A	0.77751	0.005617
CHAF1B	1.422	6.44E-05
CHD4	0.84712	0.002964
CHMP6	0.89407	0.001923
DDX41	0.97964	0.000827
DDX42	0.80198	0.004543
DDX49	1.1413	0.000247
EIF4A3	0.97152	0.00087
EP400	0.96808	0.000902
H3F3A	1.0506	0.000462
HIST2H2AC	0.73011	0.008474
INTS4	0.82212	0.00377
KAT8	0.72206	0.009118
KTI12	2.0273	2.15E-05
LSM2	1.3152	8.59E-05
MCM4	1.0127	0.000677
NCAPD3	0.85276	0.002835
PRMT5	0.80299	0.004479
RFC2	0.99659	0.000698
RUVBL1	1.1518	0.000226
RUVBL2	1.2143	0.000172
SMG6	0.73655	0.007991
SNRNP200	1.3738	7.52E-05
SNRPB	1.2148	0.000172
SNRPD2	1.0812	0.000344
SNRPE	1.192	0.000183
SNRPG	1.1927	0.000183
TCP1	0.75983	0.006541
TERF1	1.1181	0.000269
TINF2	0.97171	0.00087
XRCC6	0.94623	0.001181

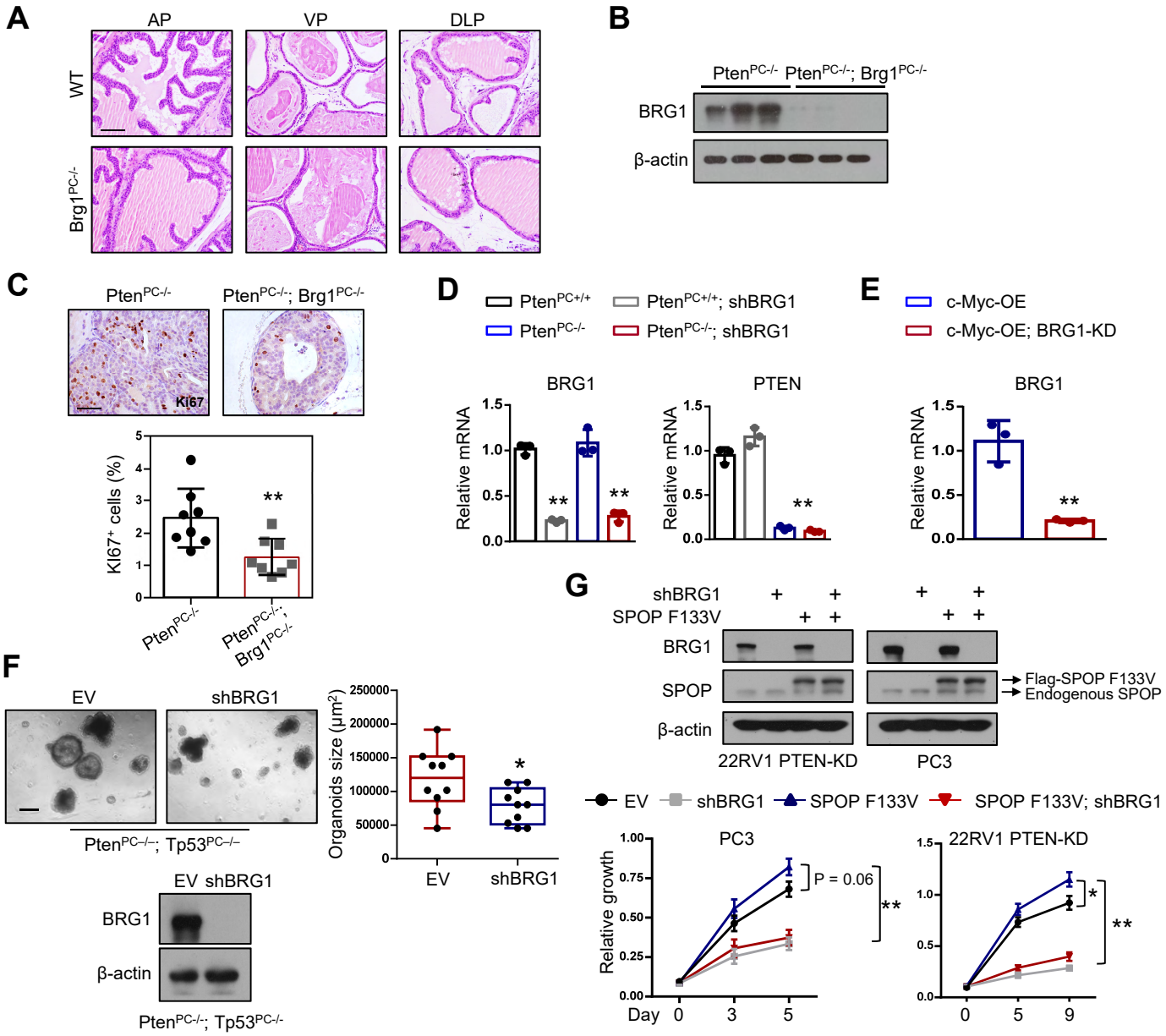
B



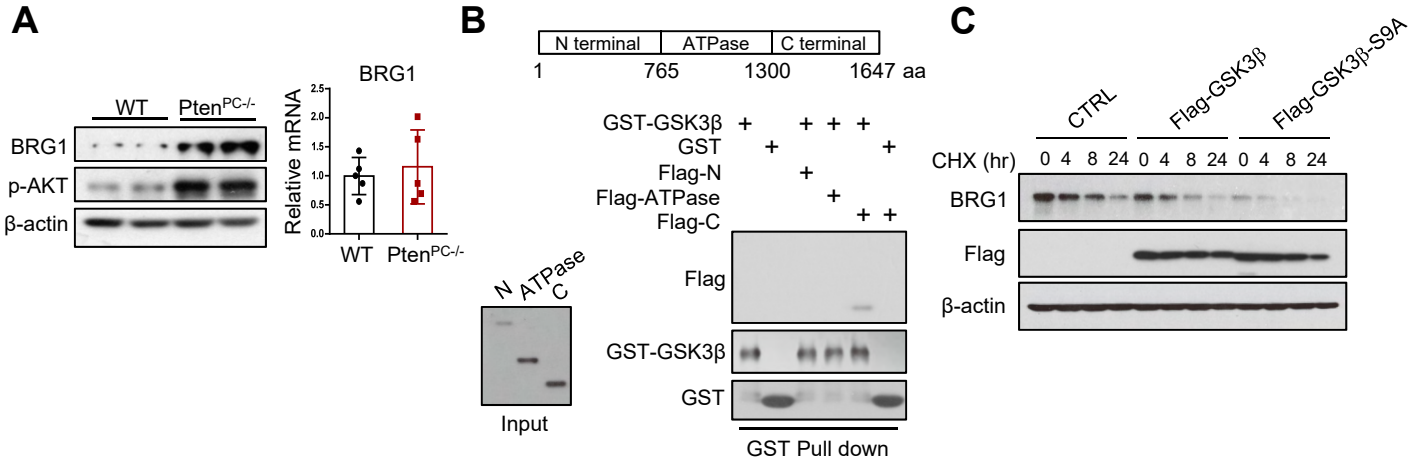
Supplemental Figure 1. An epigenome-wide based CRISPR-Cas9 screen identifies BRG1 as a synthetic lethal target in PTEN-deficient PCa cells. (**A**) Summary of the gene list showing the decreased sgRNA abundance in PTEN-WT and PTEN-KD (shPTEN) 22RV-1 cells. Genes in red denotes that their abundances are only decreased in PTEN knockdown cells. (**B**) The correlation between BRG1 expression and Gleason score or PSA levels in patients. Wilcoxon rank sum test was used to determine statistical significance (Asian radical prostatectomy cohort).



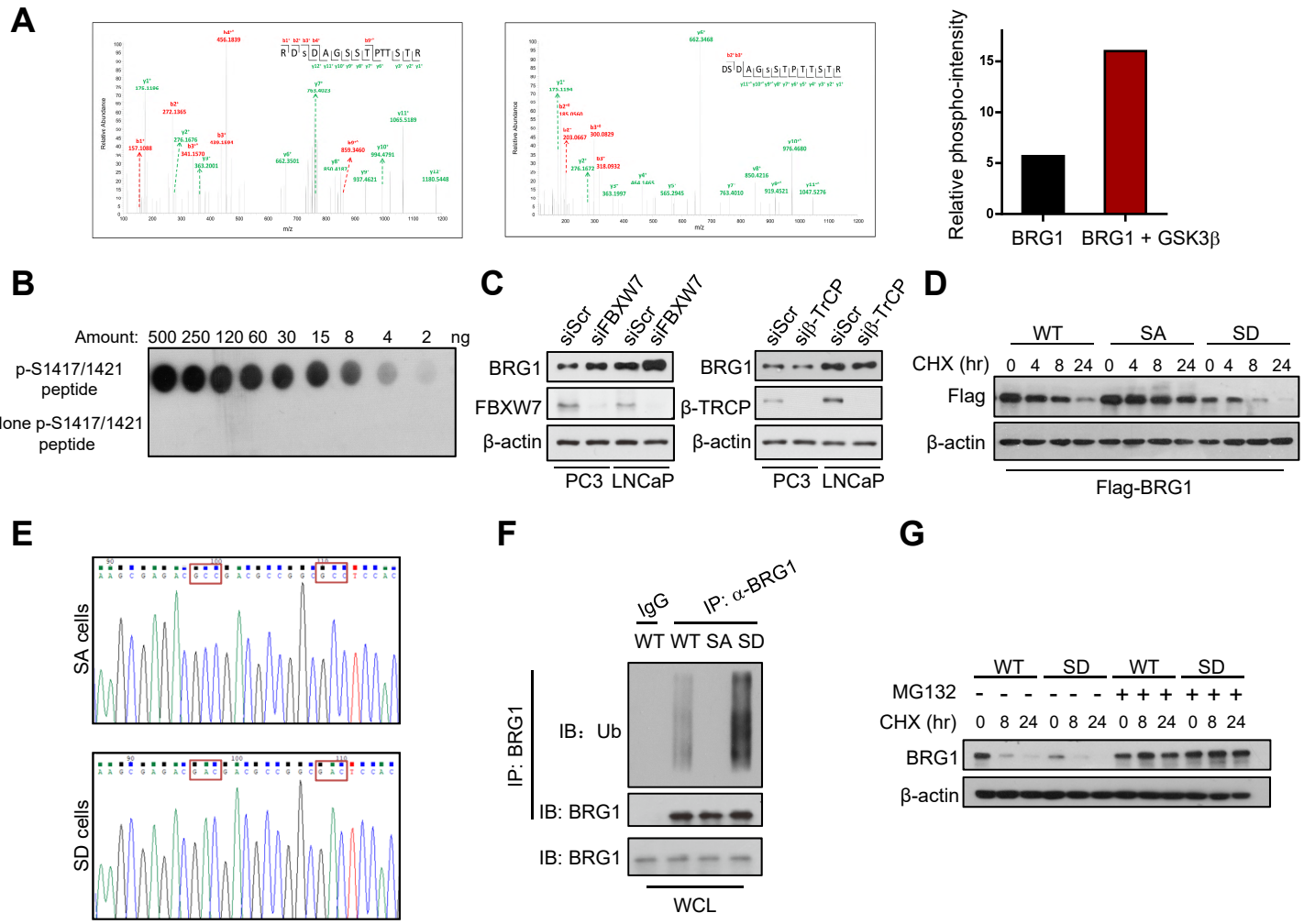
Supplemental Figure 2. BRG1 is important for PTEN-null PCa cells. (**A**) IB analysis of BRG1 knockdown efficiency in PCa cells as indicated. (**B**) Soft agar assays in parental and BRG1-KD cells. **(C)** IB of lysates (left) and cell growth measurements (right) in control and BRG1-KD (shBRG1) PC3 and LNCaP cells with or without PTEN overexpression (quantitative results shown are representative of 3 experiments, 2-way ANOVA followed by Tukey's multiple comparisons test). (**D**) Ki67 and C-Caspase 3 (C-C3) staining from xenografts derived from PTEN-KD and PTEN/BRG-KD 22RV-1 cells, and the quantitative results are shown in the right panel (n = 8, two-tailed Student's t-test). Scale bar: 100 μm. **p < 0.01.



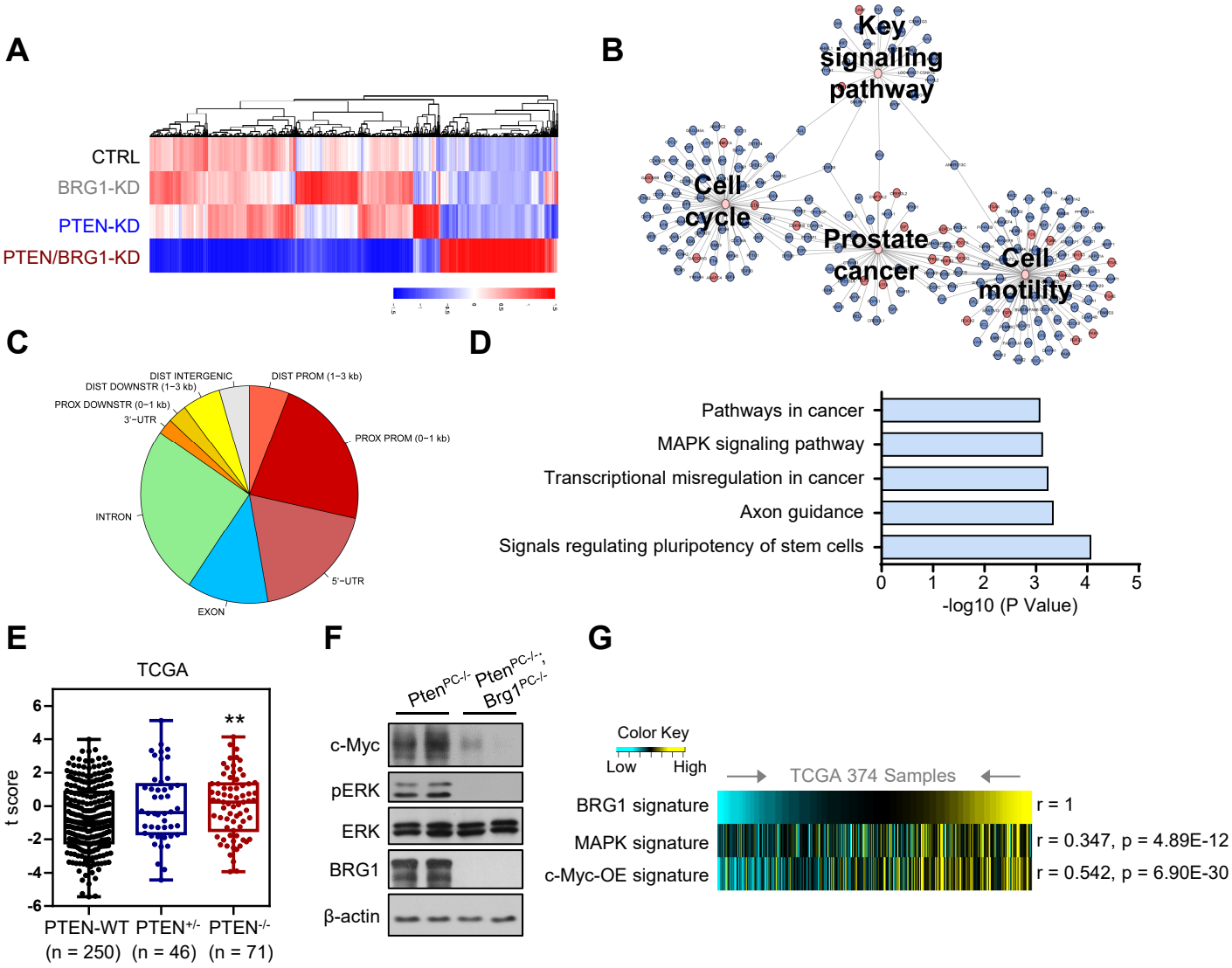
Supplemental Figure 3. BRG1 loss inhibits prostate tumorigenesis elicited by Pten loss. (**A**) H&E-stained sections of representative anterior prostate (AP), dorsal-lateral prostate (DLP) and ventral prostate (VP) of 6-month-old control and Brg1$^{PC-/-}$ mice. Scale bar: 100 μm. (**B**) IB analysis of BRG1 protein in the prostatic lysates from Pten$^{PC-/-}$ and Pten$^{PC-/-}$; Brg1$^{PC-/-}$ mice. (**C**) Ki67 staining of prostate section from Pten$^{PC-/-}$ and Pten$^{PC-/-}$; Brg1$^{PC-/-}$ mice, and the quantitative results are shown in the lower panel (n = 8, two-tailed Student's t-test). Scale bar: 50 μm. (**D**) RT-qPCR analysis of BRG1 and PTEN in the organoids derived from wild-type, Pen-null mice as indicated (two-tailed Student's t-test). (**E**) BRG1 knockdown efficiency in c-Myc overexpressed (Hi-Myc) organoids (two-tailed student's t-test). **(F)** Representative images and quantitation of organoid sizes from Pten; Tp53 null prostates (Pten$^{PC-/-}$; Tp53$^{PC-/-}$) with or without BRG1 KD. BRG1 KD efficiency is shown on the bottom (two-tailed student's t-test). Scale bar: 400 μm. **(G)** IB of lysates (top) and cell growth measurements (low) in control and BRG1-KD PC3 and 22RV-1 (shPTEN) cells with or without SPOP (F133V) overexpression (2-way ANOVA followed by Tukey's multiple comparisons test). *p < 0.01, **p < 0.01. Data represents mean ± S.E.M of 3 independent experiments (**D-G**).



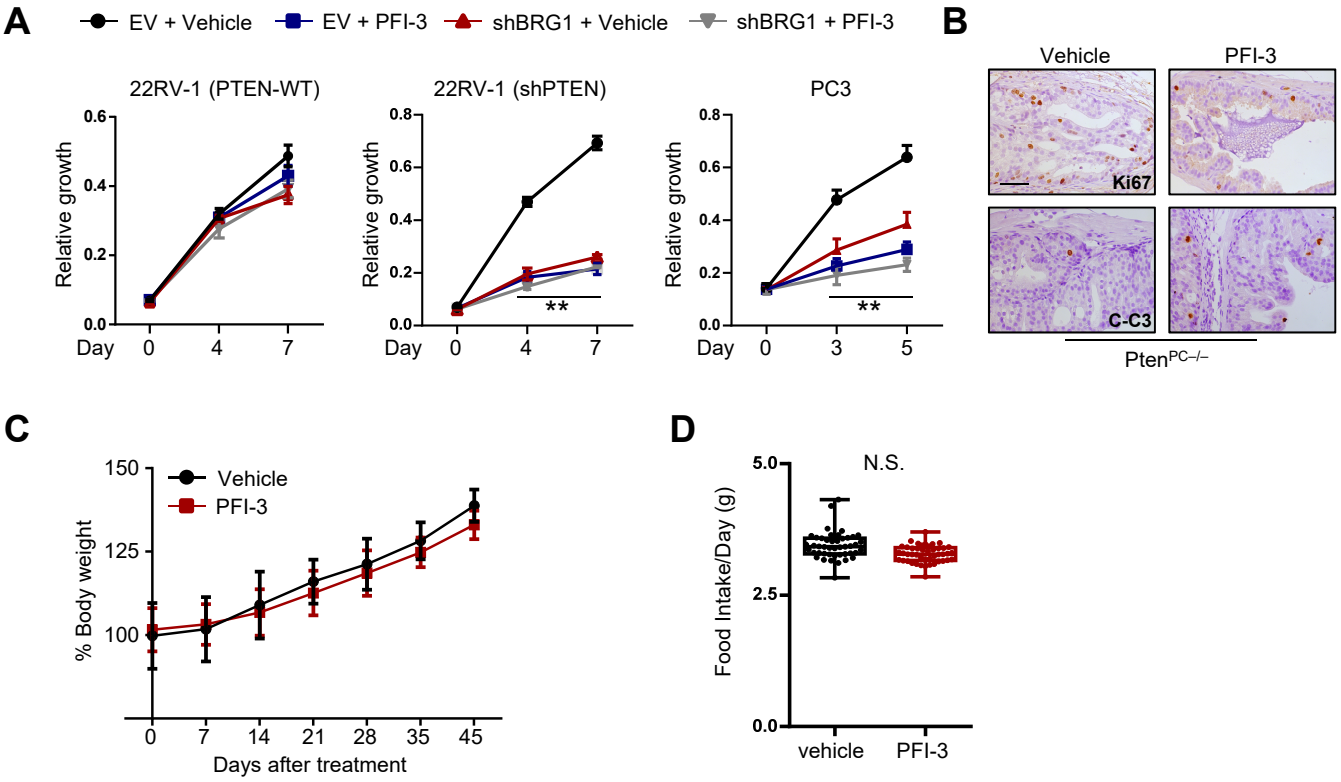
Supplemental Figure 4. PTEN loss stabilizes BRG1 in PCa cells. (**A**) IB analysis of BRG1 protein in the prostatic lysates from wild type and Pten$^{PC-/-}$ mice. Quantitative results shown are representative of 3 experiments, two-tailed student's t-test. (**B**) GST-pull down analysis to map the region in BRG1 responsible for the interaction with GSK3β. (**C**) IB analysis of BRG1 stability in 293 cells with Flag tagged GSK3β or GSK3β-S9A overexpression.



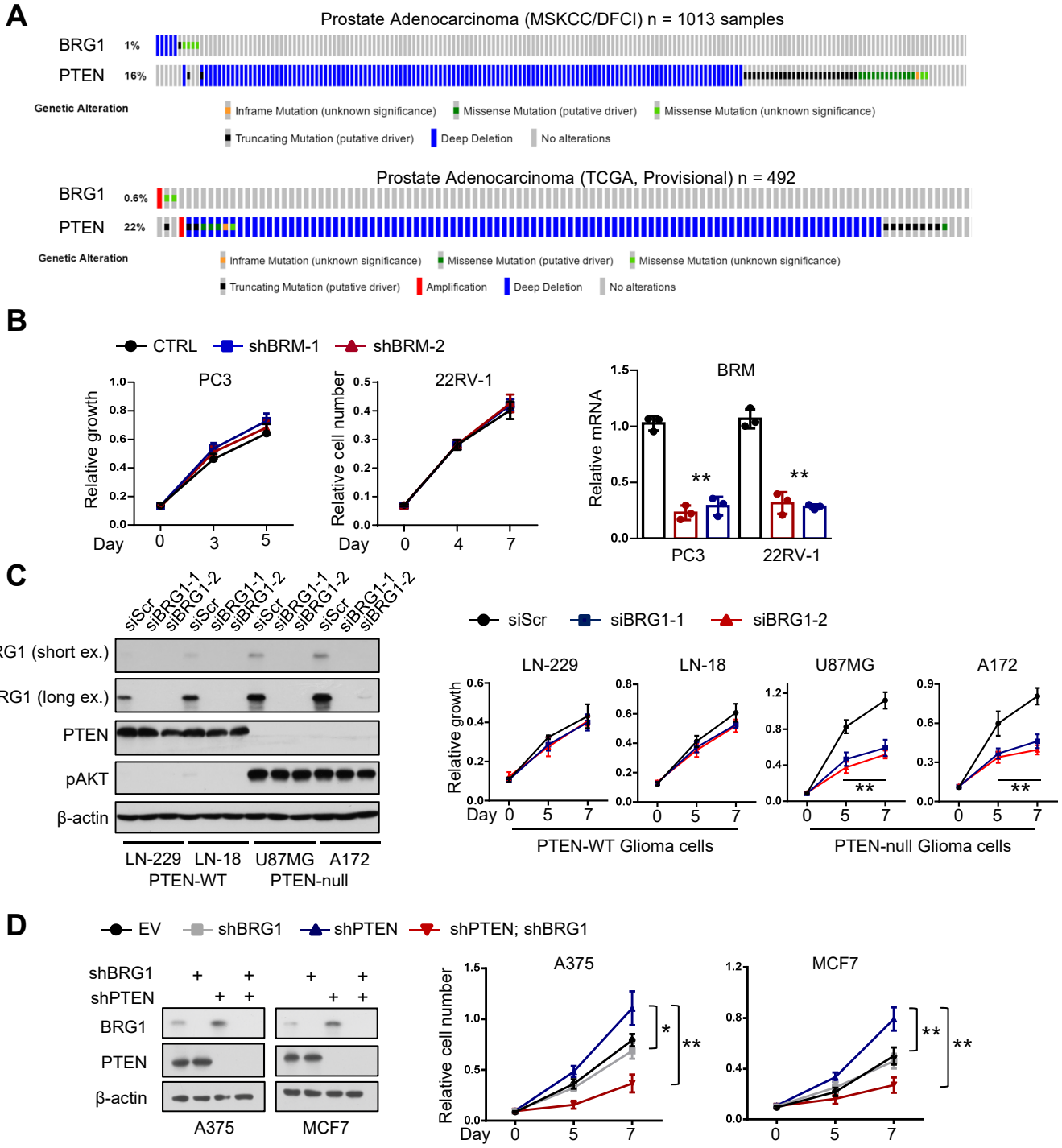
Supplemental Figure 5. The phosphorylation of BRG1 in Serine 1417 and 1421 facilities FBXW7 binding and subsequent BRG1 degradation. (**A**) Spectrum results of peptide containing BRG1 S1417 and S1421 phosphorylation. The phosphorylation signal is stimulated upon GSK3β overexpression in 293 cells. (**B**) Specificity of phospho-S1417/1421-BRG1 antibody is determined by dot blot assay. PVDF membrane was spotted with indicated amounts of phospho-S1417/1421 or none phosphorylated peptide, and probed with p-S1417/1421-BRG1 antibody. (**C**) IB analysis of BRG1 in PC3 and LNCaP cell transfected with scramble or FBXW7, β-TrCP oligonucleotides. (**D**) Examination of exogenously expressed Flag tagged wild type, SA and SD BRG1 protein in 293 cells. (**E**) Sequencing validations of CRISPR BRG1-SA and BRG1-SD knock-in allele in PC3 cells. (**F**) WT, SA and SD cell lysates were subjected to IP with anti-BRG1 antibody and IB with anti-ubiquitin (anti-Ub). (**G**) Wild-type or SD PC3 cells were treated with 100 μg/ml cycloheximide (CHX), and IB analysis of WCL at indicated time points.



Supplemental Figure 6. BRG1 modulated chromatin configurations in PTEN-deficient PCa cells to initiate pro-tumorigenic transcriptome. (**A**) Unsupervised cluster analysis of differentially expressed genes in control, BRG1-KD, PTEN-KD and PTEN; BRG1-KD 22RV-1 cells. (**B**) KEGG-DEGs relationship network between PTEN-KD and PTEN; BRG1-KD cells. (**C**) The genomic distribution of BRG1 intervals in PTEN-KD 22RV-1 cells. (**D**) KEGG pathway enrichment analysis of the overlapping genes (PTEN-dependent BRG1 signature), which harbor BRG1 peaks and the changes of DEGs and OCRs. (**E**) The activity of PTEN-dependent BRG1 signature in PTEN-WT and PTEN-deleted PCa tumors (TCGA dataset, 1-way ANOVA followed by Tukey's multiple comparisons test). (**F**) IB analysis of c-Myc and p-ERK in the prostatic lysates from $Pten^{PC-/-}$, and $Pten^{PC-/-}$; $Brg1^{PC-/-}$ mice. Blots images are derived from replicate samples run on parallel gels. (**G**) Correlations (by Pearson's) between the BRG1 transcriptome (GSE115619), MAPK signature (GSE4739), and Myc overexpressed signature (GSE10954) within PCa specimens (TCGA, n = 374) are shown. Yellow, high-signature scoring in prostate tumor specimens; blue, low-signature scoring. **$p < 0.01$.



Supplemental Figure 7. Treatment of PFI-3 specifically inhibits the growth of PTEN-deficient PCa cells. (**A**) MTT analysis of effect for PFI-3 treatment (500 nM) in wild-type 22RV-1 (left), PTEN-KD (shPTEN) 22RV-1 (middle) or PC3 (right) cells with or without BRG1 knockdown (shBRG1) (data from 3 independent experiments, two-way ANOVA followed by Tukey's multiple comparisons test). (**B**) Ki67 and C-C3 staining of mice prostatic sections from vehicle and PFI-3 treated $Pten^{PC-/-}$ mice. Scale bar: 50 μm. **(C-D)** Body weight changes (**C**) and daily food intake (**D**) in $Pten^{PC-/-}$ mice treated with vehicle or PFI-3 as indicated (n = 5, two-tailed Student's t-test). **p < 0.01.



Supplemental Figure 8. Analysis of BRG1 and PTEN in PCa patients and the other tumor type of cancer cells. (**A**) Genomic alterations of BRG1 and PTEN genes in prostate cancer datasets. (**B**) MTT analysis of control and BRM-depleted PC3 and 22RV-1 cell. BRM knockdown efficiency is verified by RT-qPCR analysis (right, 1-way ANOVA followed by Tukey's multiple comparisons test). **(C)** MTT analysis of glioma cells with or without BRG1 KD (shBRG1) as indicated (right,). BRG1 KD efficiency is shown by western blotting (left). **(D)** IB of lysates (left) and cell growth measurements (right) in control and BRG1-KD (shBRG1) melanoma (A375) and breast cancer cells (MCF7) with or without PTEN KD (shPTEN). n = 3 independent experiments, 2-way ANOVA followed by Tukey's multiple comparisons test (**B** left, **C** and **D**). *p < 0.05, **p < 0.01.

Supplemental Table 1. The gene list of chromatin regulators library.

ACD	CCDC67	DDX6	H1FOO	JMJD6	MYSM1	PRMT8	SKIV2L2	TNIP2
ACIN1	CCDC96	DDX60	H2AFB1	JMY	N6AMT1	PYGO1	SMARCA1	TNKS
ACTL6A	CDYL	DFFB	H2AFV	KAT2A	N6AMT2	PYGO2	SMARCA2	TNKS2
ACTL6B	CDYL2	DHX15	H3F3A	KAT2B	NAP1L1	RABGAP1L	SMARCA4	TOX4
AEBP2	CENPA	DHX16	HAT1	KAT5	NAP1L2	RAD18	SMARCA5	TPR
AICDA	CENPE	DHX29	HDAC1	KAT6B	NAP1L3	RAD50	SMARCAD1	TRAF5
AKAP8	CENPT	DHX30	HDAC10	KAT7	NAP1L5	RAD54B	SMARCAL1	TRAF7
ALKBH8	CEP63	DHX32	HDAC11	KAT8	NAT10	RAD54L	SMARCB1	TRDMT1
ANKRD26	CEP72	DHX35	HDAC2	KDM1A	NCAPD2	RAD54L2	SMARCC1	TRIM27
ANKRD36	CETN2	DHX37	HDAC3	KDM1B	NCAPD3	RAG1	SMARCC2	TRMT11
APITD1	CHAF1A	DHX38	HDAC4	KDM2A	NCOA1	RAG2	SMARCD1	TROVE2
AQR	CHAF1B	DHX40	HDAC5	KDM3A	NCOR1	RAI1	SMARCD2	TSPYL2
ARID1A	CHD1	DHX57	HDAC6	KDM3B	NINL	RBBP5	SMARCD3	TSPYL4
ARID1B	CHD1L	DHX9	HDAC7	KDM4A	NOVA2	RBBP7	SMARCE1	TTF2
ARID2	CHD2	DICER1	HDAC8	KDM4C	NPM2	RBX1	SMC1B	UBE2A
ARID3C	CHD3	DIDO1	HDAC9	KDM4D	NSD1	RCBTB1	SMC3	UBE2B
ARID4A	CHD4	DNA2	HELB	KDM5B	NSMCE1	RECQL	SMC5	UBR2
ASCC3	CHD5	DNAJC18	HELQ	KDM5C	NUMA1	RECQL5	SMC6	UHRF2
ASH1L	CHD6	DNAJC2	HELZ	KDM6A	ODF2L	RFC1	SMG6	UPF1
ASH2L	CHD7	DNMT3A	HFM1	KDM8	OFD1	RFC2	SMYD1	USP22
ASXL3	CHD8	DNMT3B	HIF1AN	KLHDC3	PARP1	RILPL1	SMYD2	UTP3
ATG14	CHD9	DNMT3L	HIST1H1A	KTI12	PBRM1	RING1	SMYD3	UTY
ATRX	CHMP2A	DOT1L	HIST1H1B	L3MBTL1	PCGF1	RNF168	SMYD4	WDR11
ATXN2	CHMP2B	DPF1	HIST1H1D	L3MBTL2	PCGF2	RNF2	SMYD5	WDR5
ATXN7L2	CHMP4B	DPF2	HIST1H1E	LIN28B	PCGF3	RNF20	SNRNP200	WHSC1
BAG6	CHMP4C	DPF3	HIST1H1T	LMNA	PCGF5	RNF40	SNRPB	WRN
BANF1	CHMP5	DQX1	HIST1H2AA	LMNB1	PCGF6	RNF6	SNRPD2	WRNIP1
BAP1	CHMP6	DZIP3	HIST1H2AB	LMNB2	PCNT	RNF8	SNRPD3	XRCC5
BAZ2A	CHRAC1	EDC3	HIST1H2AC	LRRC45	PHC1	RPTOR	SNRPE	XRCC6
BAZ2B	CNBP	EHMT1	HIST1H2AD	LRRFIP2	PHF1	RSF1	SNRPF	YEATS4
BICD1	COQ5	EHMT2	HIST1H2AG	LSM1	PHF11	RTEL1	SNRPG	YLPM1
BLM	CREBBP	EIF4A3	HIST1H2AH	LSM12	PHF12	RTF1	SNX29	YTHDC2
BLOC1S1	DAXX	ELP3	HIST1H2AI	LSM14A	PHF13	RUVBL1	SPAST	ZCCHC11
BMI1	DCLRE1C	EP300	HIST1H2AK	LSM2	PHF14	RUVBL2	SPOP	ZCCHC4
BRCA1	DDX1	EP400	HIST2H2AC	LSM6	PHF2	SAP18	SUDS3	ZMYND11
BRCC3	DDX10	EPC2	HIST3H2A	LSM7	PHF20L1	SBNO1	SUPT7L	ZMYND8
BRD1	DDX11	ERCC1	HLCS	LUZP2	PHF21B	SET	SUPV3L1	ZRANB3
BRD8	DDX18	ERCC2	HMGA2	MBD1	PHF23	SETD1A	SUV39H1	
BRIP1	DDX19A	ERCC3	HMGB3	MBD3	PHF3	SETD1B	SUV39H2	
BRPF1	DDX19B	ERCC4	HMGN2	MCM4	PHF5A	SETD2	SUV420H1	
BRPF3	DDX20	ERCC6	HMGN5	MECP2	PHF6	SETD3	SUV420H2	
BRWD1	DDX23	ERCC6L	HP1BP3	MEN1	PHF7	SETD5	SUZ12	
BRWD3	DDX24	EXOSC10	HR	METTL5	PHF8	SETD7	SVEP1	
CALCOCO1	DDX25	EZH1	HUWE1	MGMT	PHLDB1	SETD8	SYCE1	
CARM1	DDX26B	EZH2	IFT74	MIER2	PHLDB3	SETDB1	TADA2A	
CASC4	DDX27	FAM117A	IGHMBP2	MKRN1	PHRF1	SETDB2	TADA2B	
CBX1	DDX28	FAM81A	IKBKG	MLH3	PIBF1	SETMAR	TAF3	
CBX2	DDX3Y	FANCG	ING1	MORF4L1	PIF1	SETX	TCP1	
CBX4	DDX4	FANCL	ING2	MORF4L2	PINX1	SF3B1	TDG	
CBX6	DDX41	FANCM	ING3	MOV10	PLA2G4B	SHPRH	TDRD3	
CBX7	DDX42	G3BP1	ING4	MOV10L1	PLEKHA5	SHROOM4	TDRD9	
CBX8	DDX46	GATAD1	ING5	MPHOSPH8	PLEKHA7	SIPA1	TERF1	
CCDC122	DDX47	GATAD2A	INO80	MSL3	POC5	SIRT1	TERF2	
CCDC125	DDX49	GATAD2B	INTS12	MTA1	POLQ	SIRT2	TERF2IP	
CCDC146	DDX51	GCC2	INTS4	MTA2	PRDM9	SIRT3	TERT	
CCDC151	DDX52	GMCL1	INTS6	MTA3	PRMT1	SIRT4	TES	
CCDC160	DDX54	GMNN	IQCE	MTF2	PRMT3	SIRT5	TET1	
CCDC39	DDX55	GRIPAP1	JAKMIP2	MYEOV2	PRMT5	SIRT6	TFPT	
CCDC40	DDX58	GTF3C4	JARID2	MYOCD	PRMT6	SIRT7	TINF2	
CCDC6	DDX59	H1F0	JMJD4	MYPOP	PRMT7	SKIV2L	TMEM38B	

Supplemental Table 2. The clinical information of Asian radical prostate cohort.

Variables	All patients
Numbers	128
Age at diagnosis, yr.	61 - 71
Year of surgery	2006 - 2010
No. of biochemical recurrence, n(%)	47 (39.8)
Preoperative PSA, ng/mL	16.0 (10.4-31.6)
Pathologic Gleason score, n (%)	
≤6	29 (24.6)
7	53 (44.9)
8	21 (17.8)
≥9	15 (12.7)
Adverse pathologic events, n (%)	
Seminal vesicle invasion	13 (11.0)
Lymph node invasion	4 (3.4)
Positive surgical margins	6 (5.1)

Supplemental Table 3. Summary of the clinical information of GSE21032 and TCGA.

Variables	GSE21032	TCGA
Numbers	179	426
Normal sample	29	52
Tumor sample	150	374
Samples with clinical follow up, n	140	366
No. of biochemical recurrence, n (%)	36 (25.7%)	60 (16.4%)
Preoperative PSA, ng/mL	12.1 (1.15 - 506)	
Pathologic Gleason score, n	≤6 78 (55.7%)	
	7 49 (35.0%)	
	≥8 13 (9.3%)	
Seminal vesicle invasion	20 (14.3%)	
Lymph node invasion	12 (8.6%)	

Supplemental Table 4. Oligonucleotides. The RT-qPCR, ChIP-qPCR, shRNA , sgRNA and siRNA primer sequences are listed.

qRT-PCR		
BRG1	AGCGATGACGTCTCTGAGGT	GTACAGGGACACCAGCCACT
PTEN	TTGGCGGTGTCATAATGTCT	GCAGAAAGACTTGAAGGCGTA
ETV1	CTGAACCCTGTAACTCCTTTCC	AGACATCTGGCGTTGGTACATA
NCOA2	GCAGTGCTTCGCTGTCTCT	TTCATGGGAACTCTTCTTGCC
WEE1	GACGAAGATGATTGGGCATCC	TGGACTGGAGATCCTTGTTACA
ERBB2	TGGCCTGTGCCCACTATAAG	AGGAGAGGTCAGGTTTCACAC
FGFR3	CCCAAATGGGAGCTGTCTCG	CCCGGTCCTTGTCAATGCC
KRAS	ACAGAGAGTGGAGGATGCTTT	TTTCACACAGCCAGGAGTCTT
DOT1L	CGTGTATTGTTCGTTACCTGGA	TTCAGTAGTGGTCTGGTCTTGT
BMI1	CTGCCGGTCTACGATAAACATC	AGCTTGAGATCCGGGATTTCT
SIN3a	GGTGGAGGATGCGCTATCTTA	GGGTGTCGATGCTCTGAGATTT
c-Myc	TCCCTCCACTCGGAAGGAC	CTGGTGCATTTTCGGTTGTTG
ChIP-qPCR		
c-Myc	AACCAGGTAAGCACCGAAGTCCA	TTCATAAGGCAGAAATCTCGAAAGG
ETV1	ACAGCAACTTTAATGAGGCAAGA	TAACAGATAAGGCAGTCAGGAAT
KRAS	AGCCTTGCTTCTGCTCTGCGGGTTT	CCAGCCTTCCCTGCTGCATTTGG
BMI1	AGATCGGGGCGAGACAATGGGGATG	GACGCCGCTGTCAATGGGCAACC
shRNA		
shBRG1-3'UTR-1	CCGGCCATATTTATACAGCAGAGAACTCGAGTTCTCTGCTGTATAAATATGGTTTTTG AATTCAAAAACCATATTTATACAGCAGAGAACTCGAGTTCTCTGCTGTATAAATATGG	
shBRG1-3'UTR-2	CCGGGGCATAGGCCTTAGCAGTAACCTCGAGGTTACTGCTAAGGCCTATGCCTTTTTG AATTCAAAAAGGCATAGGCCTTAGCAGTAACCTCGAGGTTACTGCTAAGGCCTATGCC	
shGSK3β-1	CCGGGATGAATTACGGGACCCAAATCTCGAGATTTGGGTCCCGTAATTCATCTTTTTG AATTCAAAAAGATGAATTACGGGACCCAAATCTCGAGATTTGGGTCCCGTAATTCATC	
shGSK3β-2	CCGGCCAATGTTTCGTATATCTGTTCTCGAGAACAGATATACGAAACATTGGTTTTTG AATTCAAAAACCAATGTTTCGTATATCTGTTCTCGAGAACAGATATACGAAACATTGG	
shFBXW7-1	CCGGGGCAACAACGACGCCGAATTACTCGAGTAATTCGGCGTCGTTGTTGCCTTTTTG AATTCAAAAAGGCAACAACGACGCCGAATTACTCGAGTAATTCGGCGTCGTTGTTGCC	
shFBXW7-2	CCGGGGCATACTAATAGAGTCTATTCTCGAGAATAGACTCTATTAGTATGCCTTTTTG AATTCAAAAAGGCATACTAATAGAGTCTATTCTCGAGAATAGACTCTATTAGTATGCC	
shPTEN-1	CCGGGCAGATAATGACAAGGAATATTACTCGAGTAATATTCCTTGTCATTATCTGCTTTTTG AATTCAAAAAGCAGATAATGACAAGGAATATTACTCGAGTAATATTCCTTGTCATTATCTGC	
shPTEN-2	CCGGGGTGAAGATATATTCCTCCAATACTCGAGTATTGGAGGAATATATCTTCACCTTTTTG AATTCAAAAAGGTGAAGATATATTCCTCCAATACTCGAGTATTGGAGGAATATATCTTCACC	
sgRNA		
BRG1-sgRNA	CACCGCACGCTGGAGGAGATCGAAG	
BRG1-mutant-Template	AGTTCAAGACTGCAGTGAGCTATGAT	
siRNA		
siAKT-1	GCUAUUGUGAAGGAGGGUUTT	
siAKT-2	GGCCCAACACCUUCAUCAUTT	
siPTEN-1	GCAGAUAAUGACAAGGAAUAUUATT	
siPTEN-2	GGUGAAGAUAUAUUCCUCCAAUATT	
siBRG1-1	UCUCCGUCAGUGAGUCGCUdTdT	
siBRG1-2	UCUCUAGGUCGUUGAGGCUdTdT	
siFBXW7-1	GGGCAUACUAAUAGAGUCUAUUCAUTT	
siFBXW7-2	AGUUGGCACUCUAUGUGCUUUCAUUTT	
siβ-TRCP-1	GCGUUGUAUUCGAUUUGAUAATT	
siβ-TRCP-2	ACUUGCCCAGGACCCAUUAAATT	