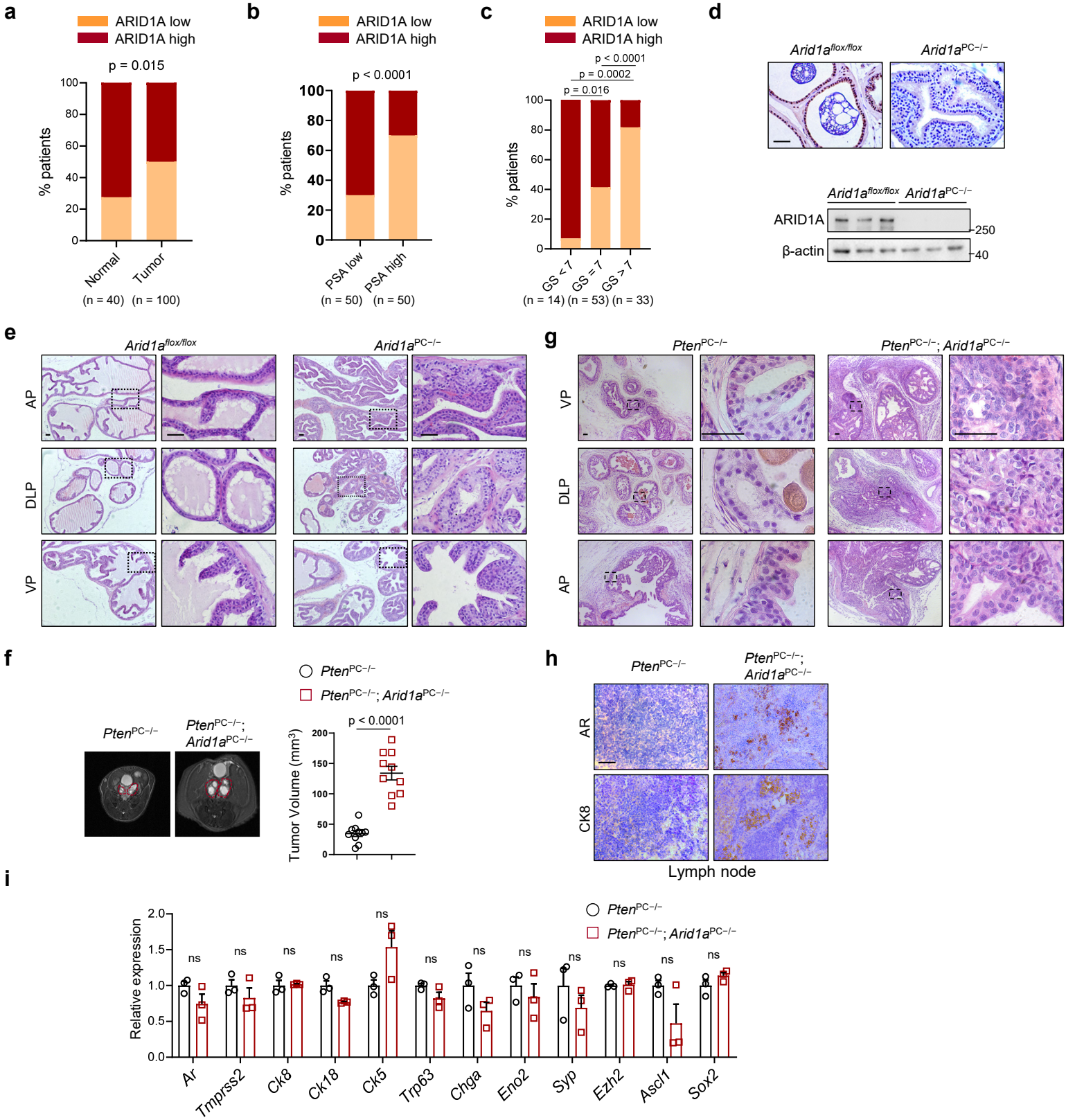
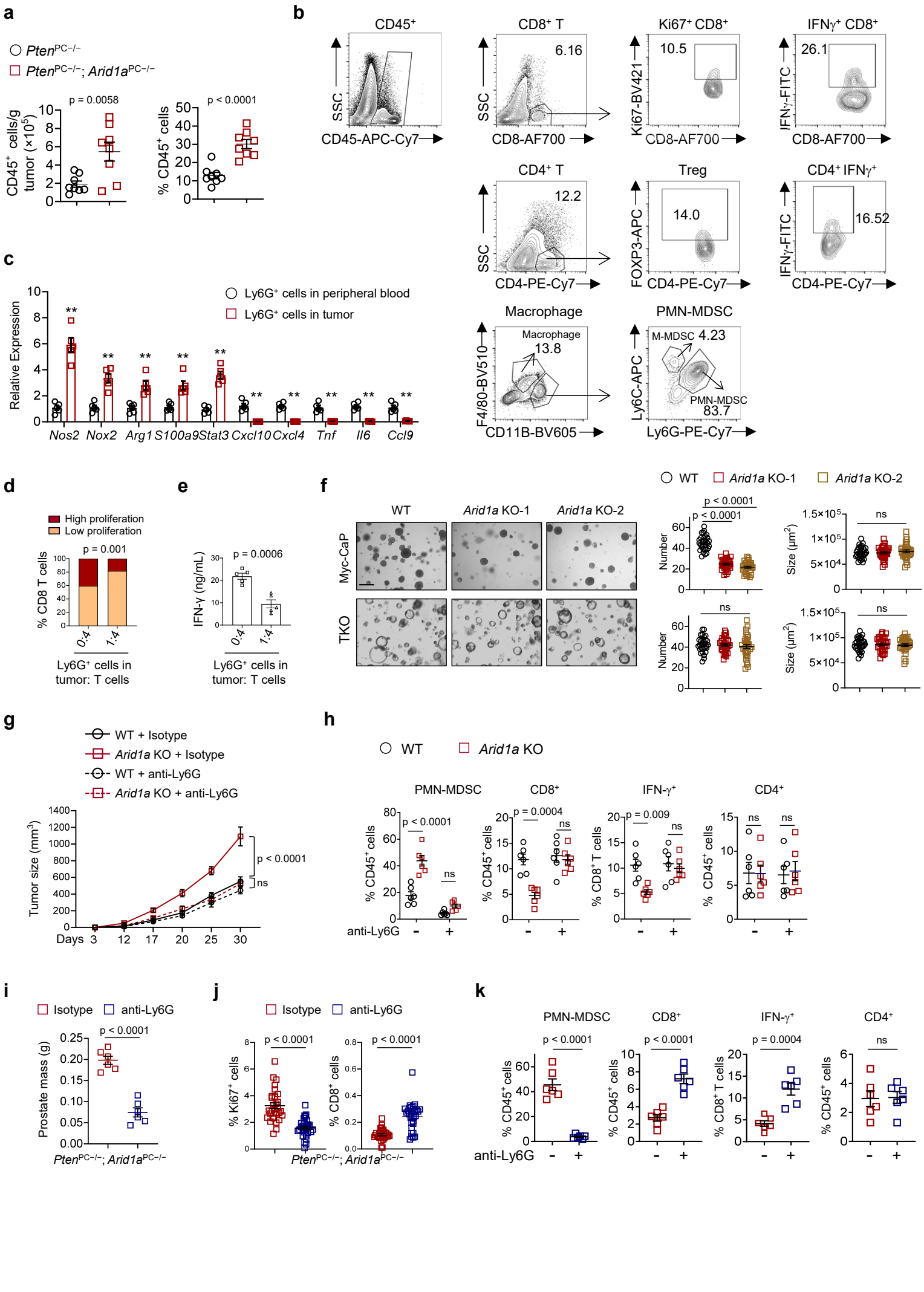
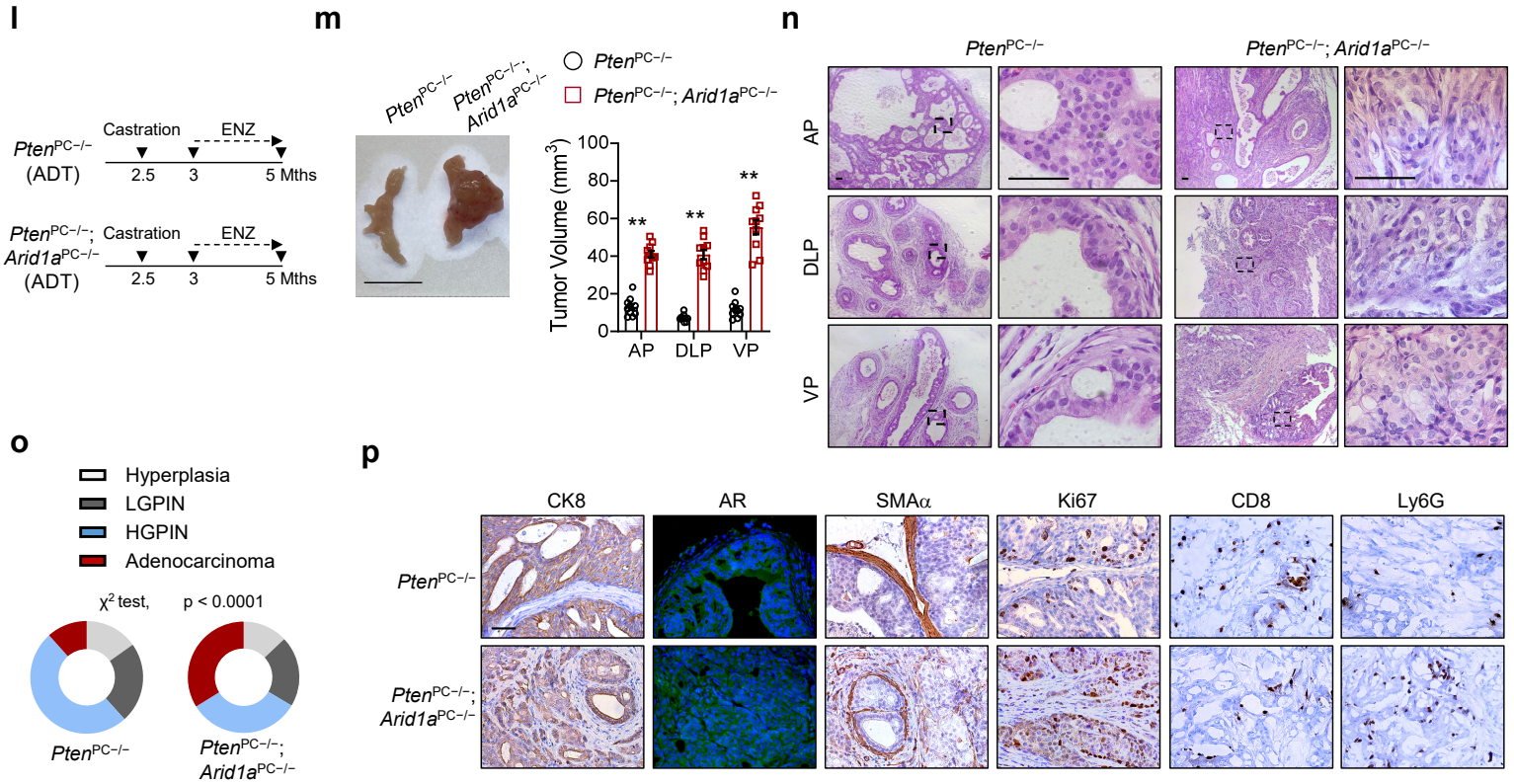


Supplementary Figure 1. *Arid1a* inactivation promotes prostate tumorigenesis.

a, ARID1A staining indexes using a 10-point quantification scale in cohorts of normal prostate tissues (n = 40) and tumors (n = 100). **b**, ARID1A expression levels stratified by PSA in TMA (n = 100). **c**, IHC score of ARID1A stratified by Gleason score (GS) in TMA (n = 100). **d**, ARID1A-stained sections of representative DLP and IB analysis of tissues from 6-month-old *Arid1a*$^{flox/flox}$ and *Arid1a*$^{PC-/-}$ mice (n = 3). Scale bar: 50 μm. **e**, H&E-stained sections of representative AP, DLP, and VP in mice at 12 months of ages (n =10, representative data are shown). Scale bar: 50 μm. **f**, MRI analysis and quantitation of 16-week-old *Pten*$^{PC-/-}$ and *Pten*$^{PC-/-}$; *Arid1a*$^{PC-/-}$ prostates (n = 10). **g**, H&E-stained sections of 12-week-old *Pten*$^{PC-/-}$ and *Pten*$^{PC-/-}$; *Arid1a*$^{PC-/-}$ mice (n = 15, representative data are shown). Scale bars, 50 μm. **h**, AR and CK8 staining of lymph nodes from 12-week-old mice. Scale bar, 50 μm. **i**, Relative expression of lineage markers in epithelium from 12-week-old mouse prostates (n = 3), ns, no significance.

f, **i**, Data represent the mean ± SEM. Statistical significance was determined by two-tailed χ^2 test (**a**, **b**, **c**) and two-tailed unpaired *t* test (**f**, **i**). Source data are provided as a Source Data file.

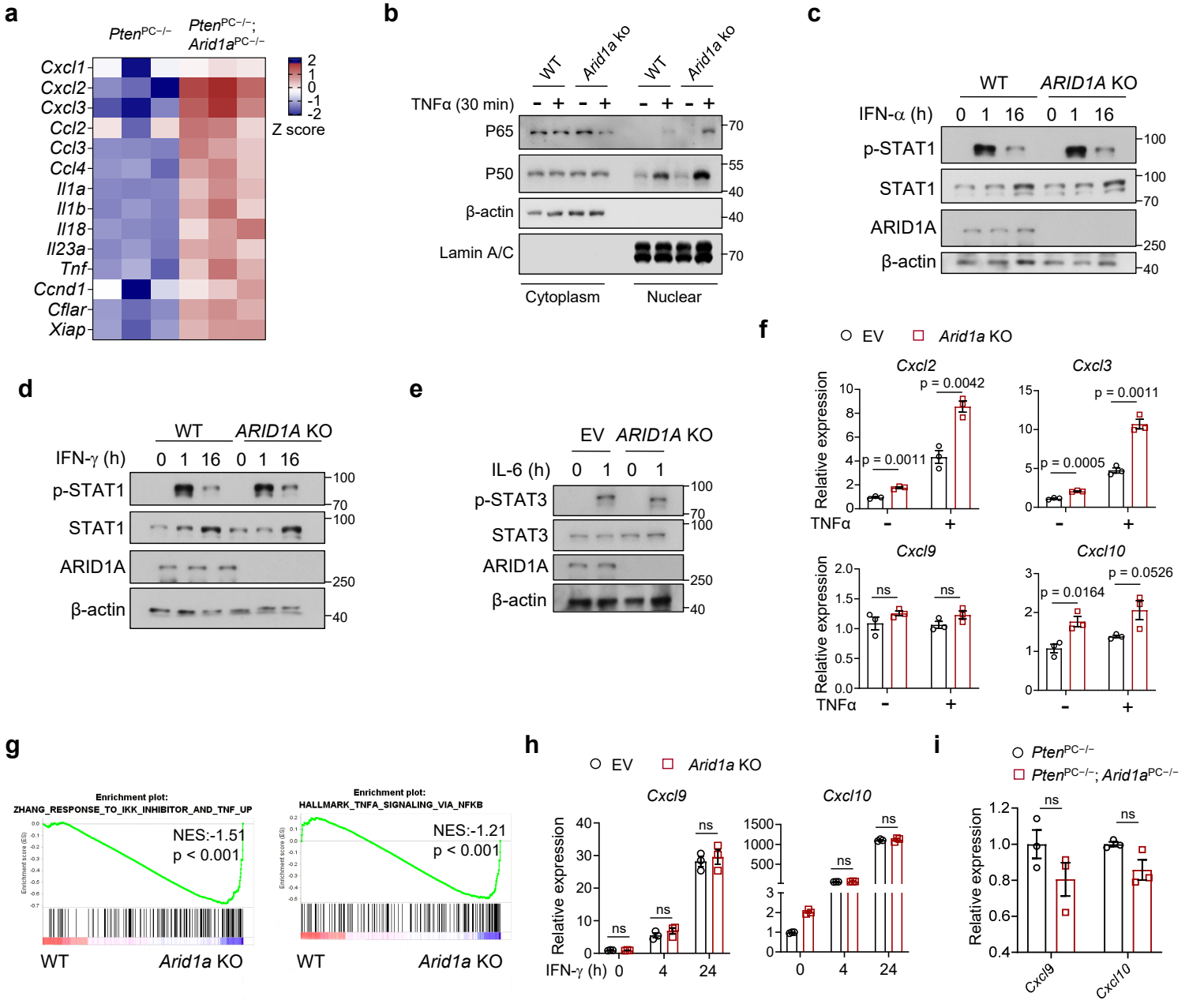

a
Pten PC−/−
Pten PC−/−; Arid1a PC−/−
p = 0.0058
CD45+ cells/g tumor (×10^5)
p < 0.0001
% CD45+ cells
b
CD45+
SSC
CD45-APC-Cy7
CD8+ T
6.16
CD8-AF700
Ki67+ CD8+
10.5
Ki67-BV421
IFNγ+ CD8+
26.1
IFNγ-FITC
CD4+ T
12.2
CD4-PE-Cy7
Treg
14.0
FOXP3-APC
CD4+ IFNγ+
16.52
Macrophage
13.8
F4/80-BV510
CD11B-BV605
PMN-MDSC
M-MDSC 4.23
PMN-MDSC 83.7
Ly6C-APC
Ly6G-PE-Cy7
c
Ly6G+ cells in peripheral blood
Ly6G+ cells in tumor
Relative Expression
Nos2 Nox2 Arg1 S100a9 Stat3 Cxcl10 Cxcl4 Tnf Il6 Ccl9
d
High proliferation
Low proliferation
p = 0.001
% CD8 T cells
0:4
1:4
Ly6G+ cells in tumor: T cells
e
p = 0.0006
IFN-γ (ng/mL)
Ly6G+ cells in tumor: T cells
f
WT
Arid1a KO-1
Arid1a KO-2
Myc-CaP
TKO
p < 0.0001
Number
Size (μm2)
ns
g
WT + Isotype
Arid1a KO + Isotype
WT + anti-Ly6G
Arid1a KO + anti-Ly6G
Tumor size (mm3)
Days
p < 0.0001
ns
h
WT
Arid1a KO
PMN-MDSC
CD8+
IFN-γ+
CD4+
% CD45+ cells
% CD8+ T cells
p < 0.0001
p = 0.0004
p = 0.009
ns
anti-Ly6G
i
Isotype
anti-Ly6G
p < 0.0001
Prostate mass (g)
PtenPC−/−; Arid1aPC−/−
j
Isotype
anti-Ly6G
p < 0.0001
% Ki67+ cells
% CD8+ cells
PtenPC−/−; Arid1aPC−/−
k
PMN-MDSC
CD8+
IFN-γ+
CD4+
p < 0.0001
p = 0.0004
ns
% CD45+ cells
% CD8+ T cells
anti-Ly6G



Supplementary Figure 2. PMN-MDSC enrichment promotes the progression of *Arid1a*-deleted tumors.

a, Percentage of CD45$^+$ immune cells in 3-month-old *Pten*$^{PC-/-}$ and *Pten*$^{PC-/-}$; *Arid1a*$^{PC-/-}$ prostate tumors (n = 8). **b**, Gating strategy for FACS analysis (Fig. 2c) is shown for tumor-infiltrating immune cells. The same strategy was used for the subsequent experiments. **c**, qRT-PCR analysis of Ly6G$^+$ cells from 3-month-old *Pten*$^{PC-/-}$; *Arid1a*$^{PC-/-}$ prostate tumors and peripheral blood of WT mice (n = 5). *p* values for the individual gene expression in Ly6G$^+$ cells of peripheral blood and tumor: *Nos2* ($p < 0.0001$), *Nox2* ($p = 0.0004$), *Arg1* ($p = 0.0017$), *S100a9* ($p = 0.0019$), *Stat3* ($p < 0.0001$), *Cxcl10* ($p = 0.0001$), *Cxcl4* ($p < 0.0001$), *Tnf* ($p = 0.0001$), *Il6* ($p < 0.0001$), *Ccl9* ($p = 0.0001$). **d**, Summary of T cell proliferation assessed by CFSE flow cytometry after 4 days of co-culture. High and low proliferation were defined as T cell division ≥ 2 and ≤ 1, respectively (n = 5). **e**, IFN-γ secretion by CD8$^+$ T cells measured by ELISA (n = 5). **f**, Representative images of organoids and quantification as indicated (n = 10 fields from 3 experiments per group). Scale bar, 500 μm. **g**, Volume of subcutaneous tumors derived from WT and *Arid1a* KO Myc-CaP cells with or without anti-Ly6G antibody treatment. WT + Isotype, WT + anti-Ly6G or *Arid1a* KO + anti-Ly6G (n = 12, each group); *Arid1a* KO + Isotype (n = 11). **h**, Quantification of tumor-infiltrating immune cells in WT and *Arid1a* KO Myc-CaP subcutaneous tumors with or without anti-Ly6G antibody treatment (n = 6). **i**, The prostate weights of *Pten*$^{PC-/-}$; *Arid1a*$^{PC-/-}$ mice with or without anti-Ly6G administration. The treatment was performed twice a week for 4 weeks when the mice were 10-week-old (n = 6). **j**, Quantification of Ki67$^+$ and CD8$^+$ in prostate sections. **k**, Flow cytometry analysis of PMN-MDSCs, CD8$^+$ T cells and IFNγ$^+$ CD8$^+$ T cells (n = 6). **l**, Graphical scheme describing the ADT strategy. **m**, Gross photographs and volume of prostates from the indicated mice with ADT (n = 10). Scale bar, 1 cm. *p* value for the prostatic volume: AP ($p < 0.0001$), DLP ($p < 0.0001$) and VP ($p < 0.0001$). **n**, H&E-stained sections in 5-month-old *Pten*$^{PC-/-}$ and *Pten*$^{PC-/-}$; *Arid1a*$^{PC-/-}$ prostates after ADT (n = 10, representative data are shown). Scale bars, 50 μm. **o**, Quantification of histological grade from the indicated mice with ADT (n = 10). **p**, Immunohistochemical analysis in castrated prostate sections. Scale bar, 50 μm.

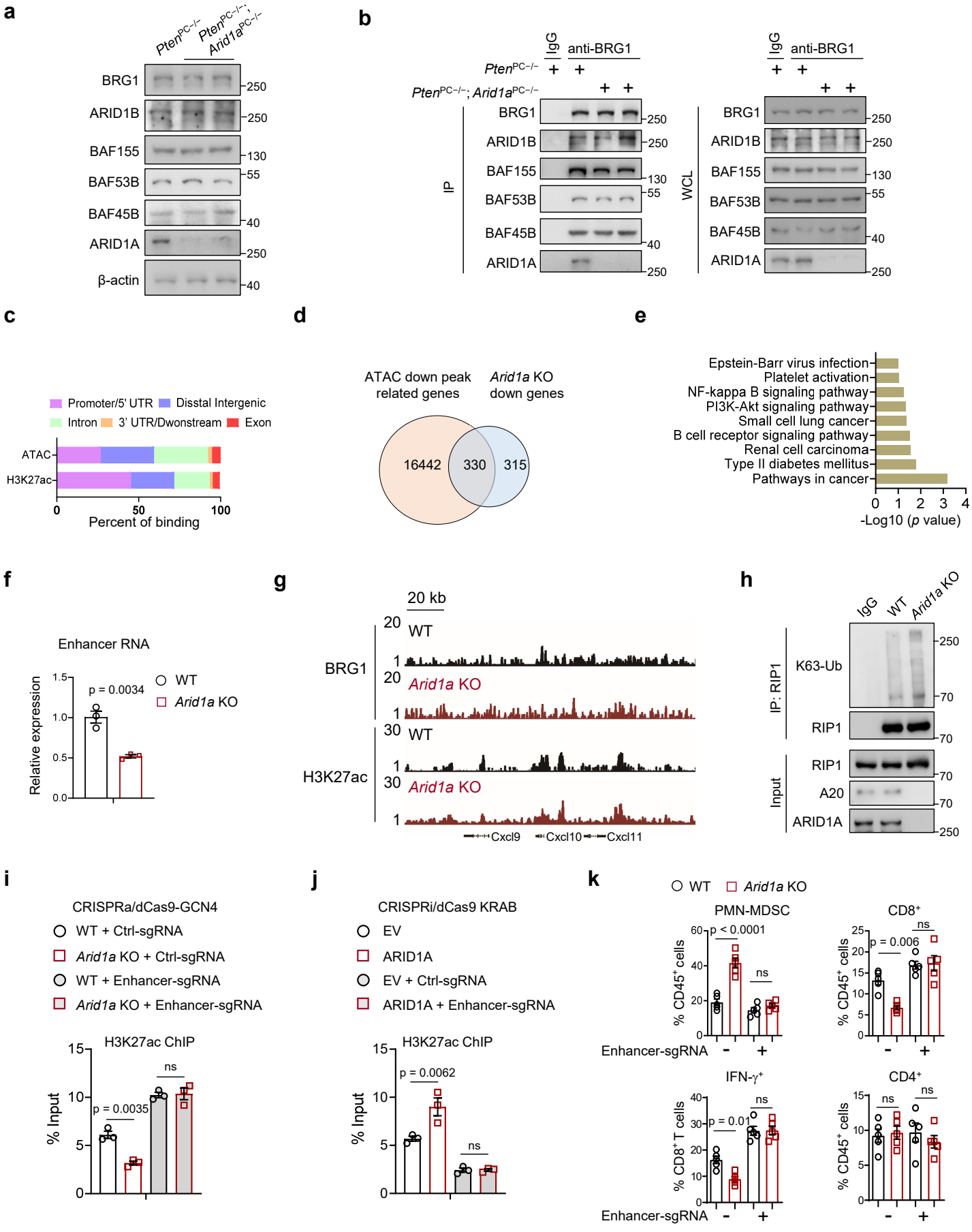
a, **c**, **e**-**k**, **m**, Data represent the mean ± SEM. Statistical significance was determined by two-tailed unpaired *t* test (**a**, **c**, **e**, **i**-**k**, **m**), Fisher's exact test (**d**), one-way ANOVA followed by multiple comparisons (**f**), two-way ANOVA followed by multiple comparison (**g**, **h**) and χ^2 test (**o**) . **p**, Representative data of triplicate experiments are shown. Source data are provided as a Source Data file. $^{**}p < 0.01$, ns, no significance.



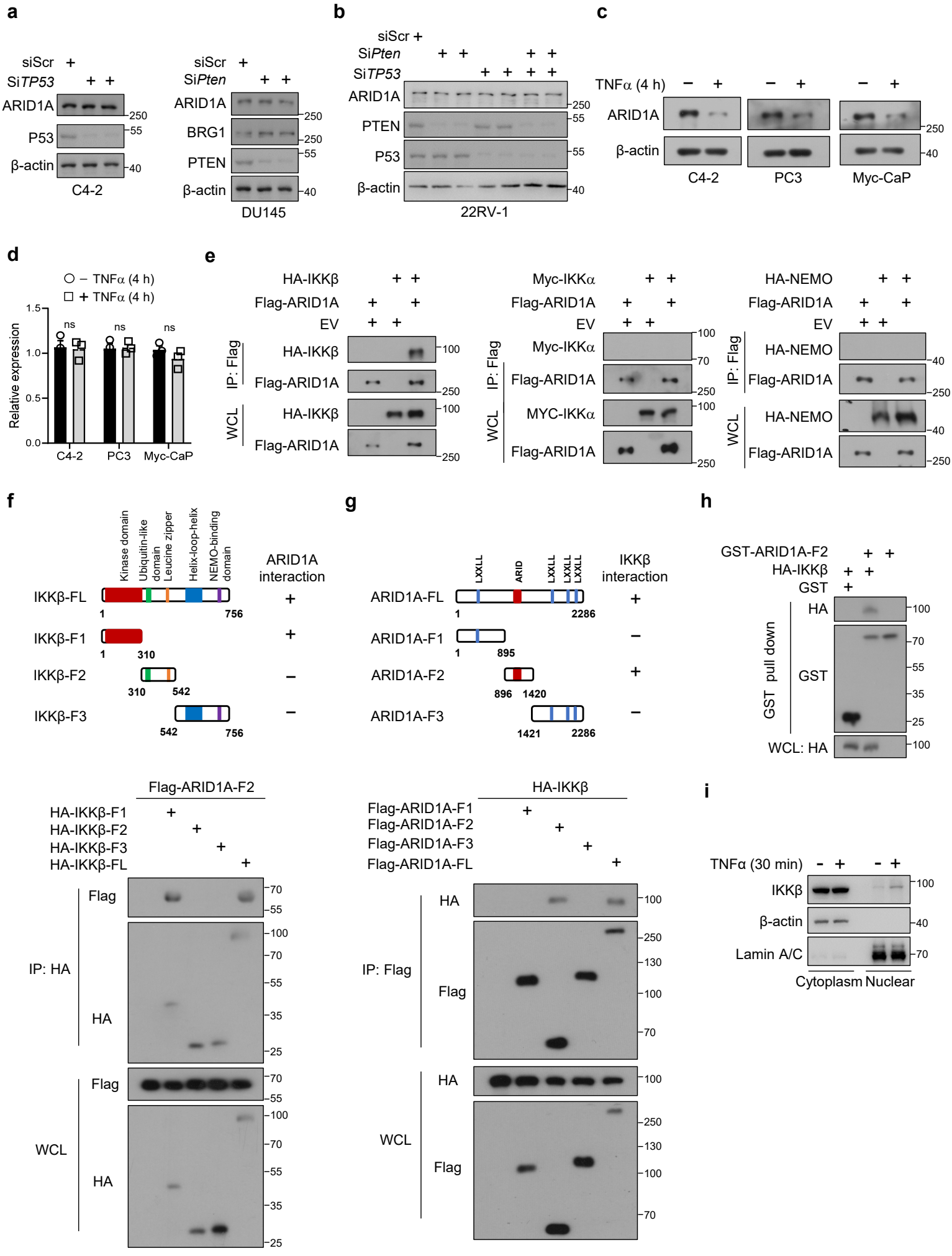
Supplementary Figure 3. ARID1A loss activates NF-κB signaling to enhance the recruitment of MDSCs.

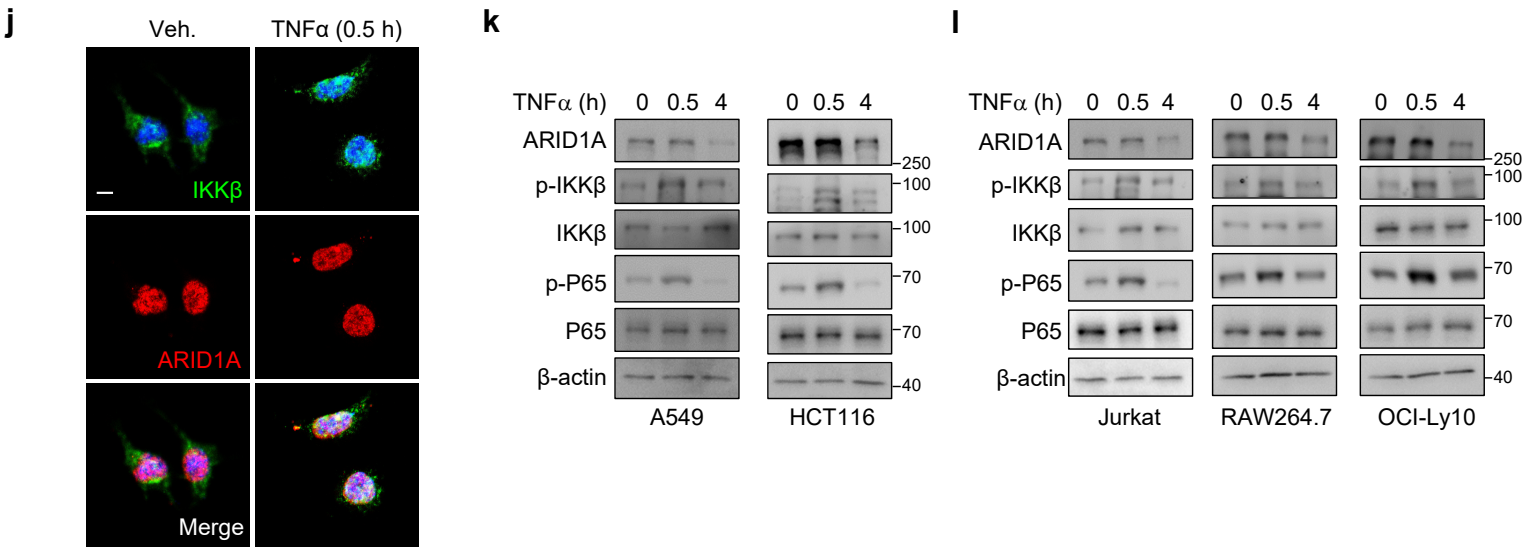
a, Heatmap summarizing the qRT-PCR results in epithelial cells of 3-month-old *Pten*$^{PC-/-}$ and *Pten*$^{PC-/-}$; *Arid1a*$^{PC-/-}$ mouse prostates (n = 3). **b**, IB analysis of the indicated proteins in cytoplasmic extracts and nuclear extracts from Myc-CaP cells stimulated with TNFα (30 min). **c-e**, IB analysis of WT and *Arid1a*-KO Myc-CaP cells with or without IFNα (**c**), IFNγ (**d**) and IL-6 (**e**) stimulation. **f**, The qRT-PCR results in WT and *Arid1a* KO Myc-CaP cells with or without TNFα stimulation (n =3). **g**, Hyperactivation of NF-κB in *Arid1a*-depleted Myc-CaP cells analyzed by GSEA. NES, normalized enrichment score. *p* value was determined by GSEA. **h**, *Cxcl9* and *Cxcl10* transcripts were quantified by real-time PCR in sg*Arid1a*- and vector-expressing Myc-CaP cells stimulated with IFNγ at the indicated time points (n = 3). **i**, *Cxcl9* and *Cxcl10* transcripts were quantified by real-time PCR in epithelial cells of 3-month-old *Pten*$^{PC-/-}$ and *Pten*$^{PC-/-}$; *Arid1a*$^{PC-/-}$ prostates (n = 3).

f, **h**, **i**, Data represent the mean ± SEM and statistical significance was determined by two-tailed unpaired *t* test. **b-e**, Data were evaluated in triplicate, and representative data are shown. Unprocessed immunoblots are shown as source data. ns, no significance.


a
Pten PC−/−
Pten PC−/−; Arid1a PC−/−
BRG1
ARID1B
BAF155
BAF53B
BAF45B
ARID1A
β-actin
250
250
130
55
40
250
40
b
IgG
anti-BRG1
Pten PC−/−
Pten PC−/−; Arid1a PC−/−
IP
WCL
BRG1
ARID1B
BAF155
BAF53B
BAF45B
ARID1A
250
250
130
55
40
250
c
Promoter/5' UTR
Disstal Intergenic
Intron
3' UTR/Dwonstream
Exon
ATAC
H3K27ac
0
50
100
Percent of binding
d
ATAC down peak related genes
Arid1a KO down genes
16442
330
315
e
Epstein-Barr virus infection
Platelet activation
NF-kappa B signaling pathway
PI3K-Akt signaling pathway
Small cell lung cancer
B cell receptor signaling pathway
Renal cell carcinoma
Type II diabetes mellitus
Pathways in cancer
0 1 2 3 4
-Log10 (p value)
f
Enhancer RNA
Relative expression
p = 0.0034
WT
Arid1a KO
1.5
1.0
0.5
0.0
g
20 kb
BRG1
H3K27ac
WT
Arid1a KO
Cxcl9
Cxcl10
Cxcl11
h
IgG
WT
Arid1a KO
IP: RIP1
K63-Ub
RIP1
Input
RIP1
A20
ARID1A
250
70
70
70
70
250
i
CRISPRa/dCas9-GCN4
WT + Ctrl-sgRNA
Arid1a KO + Ctrl-sgRNA
WT + Enhancer-sgRNA
Arid1a KO + Enhancer-sgRNA
H3K27ac ChIP
% Input
p = 0.0035
ns
15
10
5
0
j
CRISPRi/dCas9 KRAB
EV
ARID1A
EV + Ctrl-sgRNA
ARID1A + Enhancer-sgRNA
H3K27ac ChIP
% Input
p = 0.0062
ns
15
10
5
0
k
WT
Arid1a KO
PMN-MDSC
p < 0.0001
ns
% CD45+ cells
60
40
20
0
CD8+
p = 0.006
ns
ns
25
20
15
10
5
0
Enhancer-sgRNA
- +
IFN-γ+
p = 0.01
ns
% CD8+ T cells
40
30
20
10
0
CD4+
ns
ns
15
10
5
0
Enhancer-sgRNA
- +

Supplementary Figure 4. *Arid1a* ablation silences the enhancer of the A20 gene to stimulate NF-κB signaling. **a**, IB analysis of the indicated protein in 3-month-old *Pten*$^{PC-/-}$ and *Pten*$^{PC-/-}$; *Arid1a*$^{PC-/-}$ mouse prostates. **b**, IB analysis of the whole-cell lysate (WCL) from 12-week-old *Pten*$^{PC-/-}$ and *Pten*$^{PC-/-}$; *Arid1a*$^{PC-/-}$ prostates and anti-BRG1 immunoprecipitates as indicated. **c**, Bar charts revealing the distributions of ATAC-seq peaks and H3K27ac ChIP-seq peaks in vector-expressing Myc-CaP cells. **d**, Venn diagram of the genes showing the reduced accessibility and expression simultaneously in *Arid1a* KO Myc-CaP cells compared to WT cells. **e**, GO-BP enrichment of the overlapped 85 genes by DAVID, ranked according to *p* value. **f**, *A20* enhancer RNA were quantified by real-time PCR (n = 3). **g**, ChIP-seq tracks of BRG1 and H3K27ac signals in *Cxcl9*, *Cxcl10* and *Cxcl11* gene loci, as indicated. **h**, IB analyses of the WCL and anti-RIP1 immunoprecipitates of Myc-CaP cells. Cells were treated with 20 ng/ml TNFα for 30 min before harvesting. **i**, ChIP-qPCR assays of H3K27ac at the *A20* enhancer in WT and *Arid1a* KO Myc-CaP cells with or without *A20* enhancer activation (CRISPRa/dCas9-based induction, n = 3). **j**, ChIP-qPCR assays of H3K27ac at the *A20* enhancer in WT and ARID1A overexpressing Myc-CaP cells with or without A20 enhancer silencing (CRISPRi/dCas9-based suppression, n = 3). **k**, Quantification of tumor-infiltrating immune cells in WT and *Arid1a* KO tumors with or without A20 enhancer activation by FACS (n = 5). **f**, **i-k**, Data represent the mean ± SEM and statistical significance was determined by two-tailed unpaired *t* test. **a**, **b**, **h**, Experiments were repeated three times independently with similar results; data from one representative experiment are shown. Source data are provided as a Source Data file. ns, no significance.

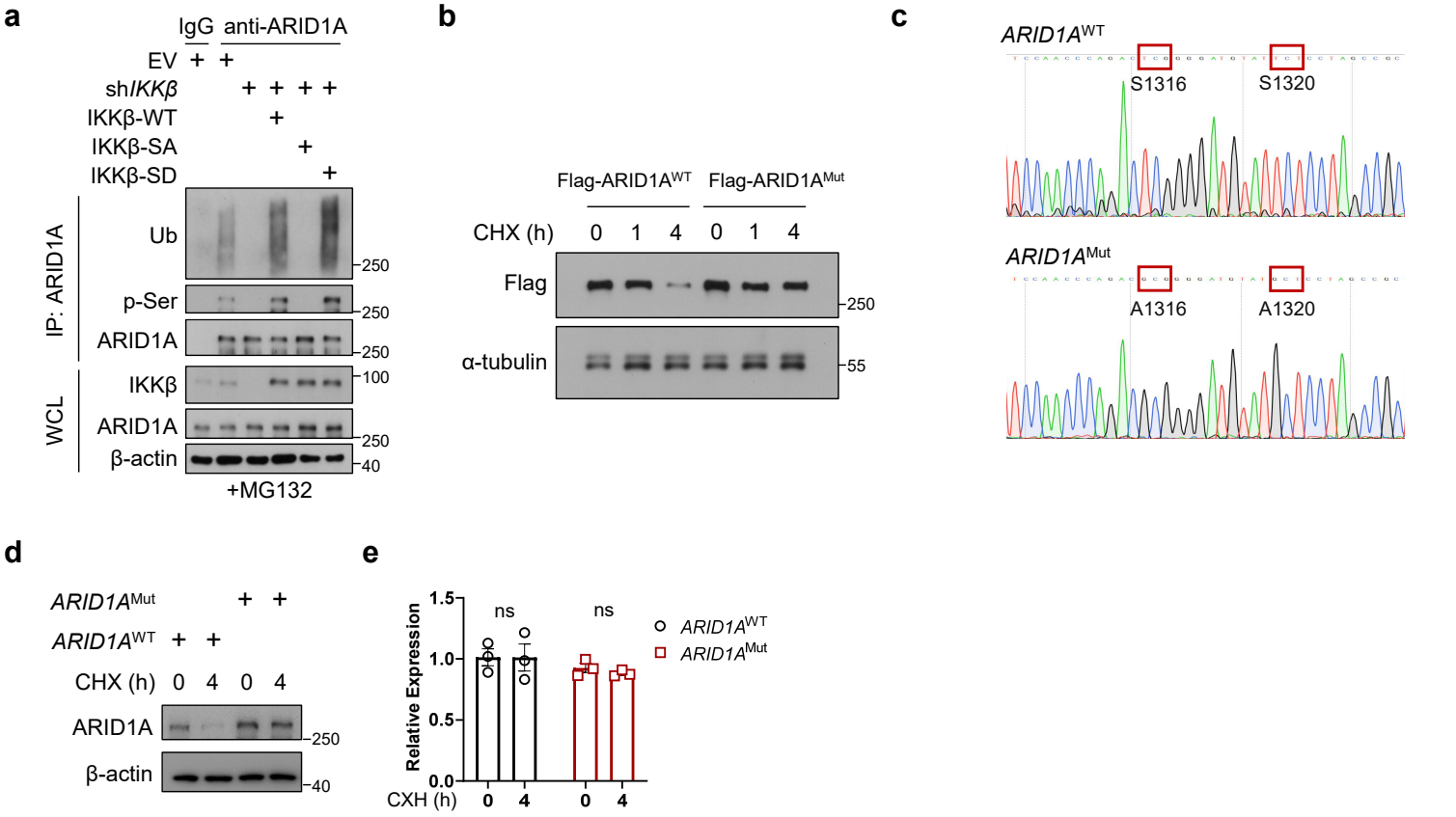

a
siScr
SiTP53
ARID1A
P53
β-actin
C4-2
siScr
SiPten
ARID1A
BRG1
PTEN
β-actin
DU145
b
siScr
SiPten
SiTP53
ARID1A
PTEN
P53
β-actin
22RV-1
c
TNFα (4 h)
ARID1A
β-actin
C4-2
PC3
Myc-CaP
d
○ – TNFα (4 h)
□ + TNFα (4 h)
Relative expression
ns
C4-2
PC3
Myc-CaP
e
HA-IKKβ
Flag-ARID1A
EV
IP: Flag
WCL
Myc-IKKα
MYC-IKKα
HA-NEMO
f
Kinase domain
Ubiquitin-like domain
Leucine zipper
Helix-loop-helix
NEMO-binding domain
ARID1A interaction
IKKβ-FL
IKKβ-F1
IKKβ-F2
IKKβ-F3
g
LXXLL
ARID
IKKβ interaction
ARID1A-FL
ARID1A-F1
ARID1A-F2
ARID1A-F3
h
GST-ARID1A-F2
HA-IKKβ
GST
GST pull down
HA
WCL: HA
Flag-ARID1A-F2
HA-IKKβ-F1
HA-IKKβ-F2
HA-IKKβ-F3
HA-IKKβ-FL
IP: HA
Flag
WCL
HA-IKKβ
Flag-ARID1A-F1
Flag-ARID1A-F2
Flag-ARID1A-F3
Flag-ARID1A-FL
IP: Flag
i
TNFα (30 min)
IKKβ
β-actin
Lamin A/C
Cytoplasm
Nuclear



Supplementary Figure 5. IKKβ promotes ARID1A reduction in PCa cells.

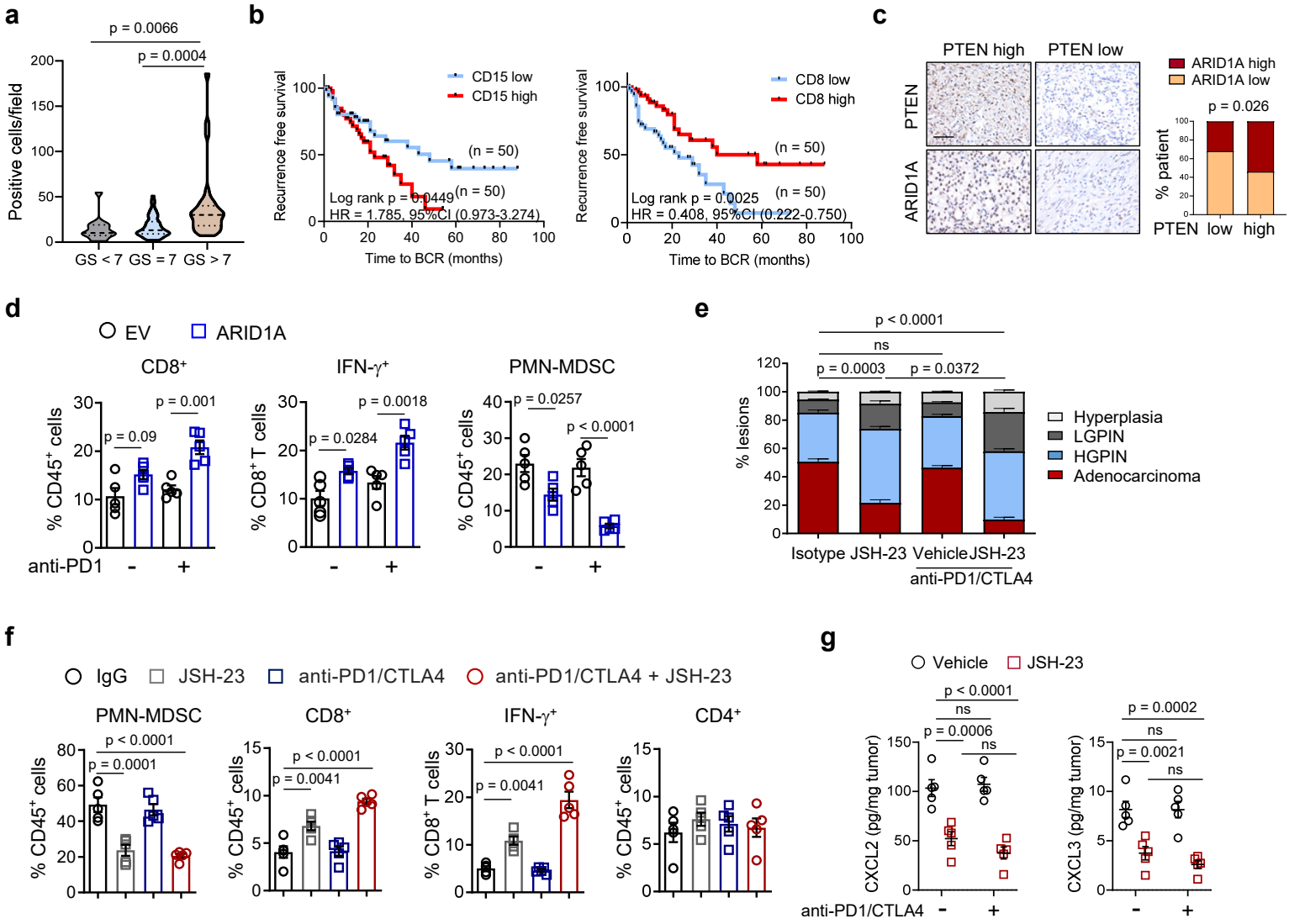
a, IB analysis of C4-2 and DU145 cells with *TP53* or *Pten* KD, respectively. **b**, IB analysis of 22RV-1 cells with *TP53* an/or *Pten* KD. **c**, IB analysis of C4-2, PC3 and Myc-CaP cells treated with TNFα for the indicated duration of time. **d**, *ARID1A* transcripts were quantified by real-time PCR in PCa cells with or without TNFα stimulation (n = 3), ns, no significance. **e**, IB analysis of the indicated protein in the WCL and immunoprecipitates from 293T cells transfected with Flag-ARID1A and HA-IKKβ, Myc-IKKα or HA-NEMO. **f**, Interaction between ARID1A and IKKβ. Flag-ARID1A-F2 and HA- IKKβ full-length (IKKβ-FL) and mutants (IKKβ-F1, IKKβ-F2, IKKβ-F3) were ectopically expressed in 293T cells, followed by anti-HA immunoprecipitation and immunoblotting with Flag and HA antibodies. **g**, HA-IKKβ and Flag-ARID1A full-length (ARID1A-FL) and mutants (ARID1A-F1, ARID1A-F2, ARID1A-F3) were ectopically expressed in 293T cells, followed by anti-Flag immunoprecipitation and immunoblotting. **h**, In vitro binding of ARID1A-F2 to IKKβ by GST pulldown analysis. **i**, IB analysis of the indicated proteins in cytoplasmic extracts and nuclear extracts from Myc-CaP cells stimulated with TNFα. **j**, IKKβ and ARID1A immunostaining as indicated in Myc-CaP cells. Scale bar, 100 μm. **k**, IB analysis of A549 and HCT116 cells treated with TNFα for the indicated duration of time. **l**, IB analysis of Jurkat, RAW264.7 and OCI-Ly10 cells treated with TNFα for the indicated duration of time.

d, Data represent the mean ± SEM and statistical significance was determined by two-tailed unpaired *t* test. All experiments were repeated three times independently with similar results; data from one representative experiment are shown. Source data are provided as a Source Data file.



Supplementary Figure 6. IKKβ phosphorylates ARID1A and promotes its β-TRCP-dependent degradation. **a**, IB analysis of the WCL and immunoprecipitates of the indicated proteins in C4-2 control and *IKKβ* KD cells with or without IKKβ-WT, IKKβ-SA or IKKβ-SD overexpression. **b**, IB analysis of 293T cells with WT or mutant ARID1A overexpression treated with TNFα for the indicated duration of time. **c**, Sequencing validations of the CRISPR ARID1A-SA knock-in allele in C4-2 cells. **d**, IB analysis of WT and *Arid1a*^{mut} Myc-CaP cells with or without CHX treatment for the indicated duration of time. **e**, *Arid1a* transcripts were quantified by real-time PCR. ns, no significance.

e, Data represent the mean ± SEM and statistical significance was determined by two-tailed unpaired *t* test. **a**, **b**, **d**, Experiments were repeated three times independently with similar results; data from one representative experiment are shown. Source data are provided as a Source Data file.



Supplementary Figure 7. Targeting ARID1A or its coordinated signals increase the sensitivity to ICB therapy.

a, CD15 expression levels stratified by GS in TMA (GS < 7, n = 14, GS = 7, n = 53, GS > 7, n = 33). **b**, Kaplan-Meier plot of recurrence after radical prostatectomy based on the proportions of $CD15^+$ and $CD8^+$ cells in patients (n = 50 for each group). **c**, IHC analysis for ARID1A and PTEN. Scale bars, 50 μm. The correlation between PTEN and ARID1A expression is shown as stacked columns (n = 100). **d**, Quantification of each tumor-infiltrating immune cell population in WT and ARID1A-overexpressing Myc-CaP xenografts with or without anti-PD-1 treatment (n = 5). **e**, Prostate tumor histology of $Pten^{PC-/-}$; $Arid1a^{PC-/-}$ mice with or without NF-κB inhibition (JSH-23) in combination with anti-PD1/CTLA-4 treatment (n = 10). **f**, Quantification of the indicated tumor-infiltrating immune cell population of $Pten^{PC-/-}$; $Arid1a^{PC-/-}$ mouse prostates with or without JSH-23 treatment in combination with anti-PD1/CTLA-4 therapy (n = 5). **g**, ELISA of CXCL2 and CXCL3 in prostate tumors of 4-month-old $Pten^{PC-/-}$; $Arid1a^{PC-/-}$ mice treated as indicated (n = 5).

d-g, Data represent the mean ± SEM. Statistical significance was determined by one-way ANOVA followed by multiple comparisons (**a**), log-rank test (**b**), χ^2 test (**c**, **e**) and two-way ANOVA followed by multiple comparisons (**d**, **f**, **g**). Source data are provided as a Source Data file. ns, no significance.

Supplementary Table 1. Clinical Summary of Tissue Microarray from PCa Patients, Related to Figure 1 and Figure 7

Variables	tumor	Benign Prostatic Hyperplasia
Numbers	100	40
Age at diagnosis, yr	50-82 (mean 67.8)	
Year of surgery	2012/8-2020/3	
PSA at diagnosis, ng/ml	0.48-157.9 (mean 25.4)	
Pathologic Gleason score, n (%)		
6	14 (14)	
7	53 (53)	
8	14 (14)	
9	18 (18)	
10	1 (1)	
No. of biochemical recurrence, n (%)	39 (39)	
Adverse pathologic events, n (%)		
Extra-prostaticextension	18 (18)	
Seminal vesicle invasion	15 (15)	
Positive surgical margins	2 (2)	

Supplementary Table 2. Clinical Summary of Tumor Tissue Specimens from Advanced PCa Patients, Related to Figure 7

Variables	Adenocarcinoma
Numbers	42
Age at diagnosis, yr	49-79 (mean 68)
PSA at diagnosis, ng/ml	0.07-359.87 (mean 58.25)
Pathologic Gleason score at initial diagnosis, n (%)	
8	10 (23.8)
9	28 (66.7)
10	4 (9.5)
Samples from body sites, n (%)	Prostate, 42 (100%)

Supplementary Table 3. Oligonucleotides

Oligonucleotides	
siP50-1	CGCCUGAAUCAUUCUCGAU
siP50-2	CCAGAGUUUACAUCUGAUG
siP52-1	ACAUUGAGGUUCGGUUCUA
siP52-2	GGACAUGACUGCCCAAUUU
siP65-1	CGGAUUGAGGAGAAACGUA
siP65-2	AUGGAUUCAUUACAGCUUA
siIKKα-1	GCAGAUGACGUAUGGGAUA
siIKKα-2	UAGGGUCUGGGAUUCGAUA
siIKKβ-1	CCAGCCAAGAAGAGUGAAG
siIKKβ-2	GCUGGUUCAUAUCUUGAAC
siNEMO-1	GAGGGAGUACAGCAAACUG
siNEMO-2	GCUCGAUCUGAAGAGGCAG
siPTEN-1	GCAGAUAAUGACAAGGAAUAUUA
siPTEN-2	GGUGAAGAUAUAUUCCUCCAAUA
siTRP53-1	GGAGTATTTGGATGACAG
siTRP53-2	AACCUCUUGGUGAACCUUAGUAC
Primers for shRNA	
ARID1A-shRNA-homo-1	F:CCGGGCCTGTGCAGTAGAGTGTAGACTCGAGTCTACACTCTACTGCACAGGCTTTTTG
	R:AATTCAAAAAGCCTGTGCAGTAGAGTGTAGACTCGAGTCTACACTCTACTGCACAGGC
ARID1A-shRNA-homo-2	F:CCGGGCTGCCACGTGTGTATATATACTCGAGTATATATACACACGTGGCAGCTTTTTG
	R:AATTCAAAAAGCTGCCACGTGTGTATATATACTCGAGTATATATACACACGTGGCAGC
ARID1A-shRNA-homo-3	F:CCGGGCGAGACACAGCTATTTAATCCTCGAGGATTAAATAGCTGTGTCTCGCTTTTTG
	R:AATTCAAAAAGCGAGACACAGCTATTTAATCCTCGAGGATTAAATAGCTGTGTCTCGC
IKKβ-shRNA-homo-1	F:CCGGGCTGATTGTGTGTGTGAAACACTCGAGTGTTTCACACACACAATCAGCTTTTTG
	R:AATTCAAAAAGCTGATTGTGTGTGTGAAACACTCGAGTGTTTCACACACACAATCAGC
IKKβ-shRNA-homo-2	F:CCGGGGACAGTGTCCAATTCAAATCCTCGAGGATTTGAATTGGACACTGTCCTTTTTG
	R:AATTCAAAAAGGACAGTGTCCAATTCAAATCCTCGAGGATTTGAATTGGACACTGTCC
IKKβ-shRNA-homo-3	F:CCGGGGATTCAGCTTCTCCTAAACACTCGAGTGTTTAGGAGAAGCTGAATCCTTTTTG
	R:AATTCAAAAAGGATTCAGCTTCTCCTAAACACTCGAGTGTTTAGGAGAAGCTGAATCC
Arid1a-shRNA-mus-1	F: CCGGCAGGCCCTATGGCCCTAATATCTCGAGATATTAGGGCCATAGGGCCTGTTTTTG
	R: AATTCAAAAACAGGCCCTATGGCCCTAATATCTCGAGATATTAGGGCCATAGGGCCTG
Arid1a-shRNA-mus-2	F: CCGGTGCCCAAGATCGAGGTTATATCTCGAGATATAACCTCGATCTTGGGCATTTTTG
	R: AATTCAAAAATGCCCAAGATCGAGGTTATATCTCGAGATATAACCTCGATCTTGGGCA
Primers for real-time RT-qPCR	
A20-mus	F: ACTGGAATGACGAATGGGACA R: CAGGGAATTGTACTGAAGTCCAC
Cxcl1-mus	F: ACTGCACCCAAACCGAAGTC R: TGGGGACACCTTTTAGCATCTT
Cxcl2-mus	F: CCAACCACCAGGCTACAGG R: GCGTCACACTCAAGCTCTG
Cxcl3-mus	F: GATTTTGAGACCATCCAGAGC R: CTCTTCAGTATCTTCTTGATG
Cxcl9-mus	F: GGAGTTCGAGGAACCCTAGTG R: GGGATTTGTAGTGGATCGTGC
Cxcl10-mus	F: CCAAGTGCTGCCGTCATTTTC R: GGCTCGCAGGGATGATTTCAA
Cxcl11-mus	F: GTAAACCAGTCAGCCTGAG R: GCTTTCTCCAGGTACTCTTG
Ccl2-mus	F: GGCCTGCTGTTCACAGTTG R: CTGCTGGTGATCCTCTTGTAG
Ccl3-mus	F: CTGCAACCAAGTCTTCTCAG R: GCCGGTTTCTCTTAGTCAGG
Ccl4-mus	F: CTTCTGTGCTCCAGGGTTCTC R: CTGTCTGCCTCTTTTGGTCAG
Ccl5-mus	F: GCTGCTTTGCCTACCTCTCC R: TCGAGTGACAAACACGACTGC
Arid1a-mus	F: CTTCCCCAACCACCAGTACAA R: CTGTGCGAAGGACGAAGAC
Arid1b-mus	F: GTTGTATGGGATGGGTACTCACC R: CTGGTTGTAGTATGGCTGCTG
Ar-mus	F: CTGGGAAGGGTCTACCCAC R: GGTGCTATGTTAGCGGCCTC
Tmprss2-mus	F: CAGTCTGAGCACATCTGTCCT R: CTCGGAGCATACTGAGGCA
Ck8-mus	F: TCCATCAGGGTGACTCAGAAA R: CCAGCTTCAAGGGGCTCAA
Ck18-mus	F: CAGCCAGCGTCTATGCAGG R: CTTTCTCGGTCTGGATTCCAC
Ck5-mus	F: TCTGCCATCACCCCATCTGT R: CCTCCGCCAGAACTGTAGGA
Trp63-mus	F: TACTGCCCCGACCCTTACAT R: GCTGAGGAACTCGCTTGTCTG
Ezh2-mus	F: AGTGACTTGGATTTTCCAGCAC R: AATTCTGTTGTAAGGGCGACC
Sox2-mus	F: GCGGAGTGGAAACTTTTGTCC R: CGGGAAGCGTGTACTTATCCTT
Ascl1-mus	F: GCAACCGGGTCAAGTTGGT R: GTCGTTGGAGTAGTTGGGGG
Brg1-mus	F: CAAAGACAAGCATATCCTAGCCA R: CACGTAGTGTGTGTTAAGGACC
Baf155-mus	F: AGCTAGATTCGGTGCGAGTCT R: CCACCAGTCCAGCTAGTGTTTT
Actl6a-mus	F: GTGTACGGCGGAGATGAAGTT R: GGGAAATCAACCTTAGGGCAGT
Actl6b-mus	F: GCGCTCGTCTTTGACATTGG R: ATTGGTGTCGATGTGGAAAATCT
Brm-mus	F: CTCCTGGACCAATTCTGGGG R: CATCGTTGACAGAGGATGTGAG
Dpf1-mus	F: GAGGCCATCGAGCACTGTC R: CGGGCGGGGTAAGTGTAGA
β-actin-mus	F: GGCTGTATTCCCCTCCATCG R: CCAGTTGGTAACAATGCCATGT
ARID1A-homo	F: CCTGAAGAACTCGAACGGGAA R: TCCGCCATGTTGTTGGTGG
Primers for sgRNA	
Arid1a-sgRNA-mus-1	F: CACCGGCAGCTGCGAAGATATCGGG R: AAACCCCGATATCTTCGCAGCTGCC
Arid1a-sgRNA-mus-2	F: CACCGTTCCGGTAAAGATCGTGCAG R: AAACCTGCACGATCTTTACCGGAAC
Primers for real-time Chip-qPCR	
A20-mus	F: CAAATCCCTCTACTTACAATCCC R: ACCGAAATCACCTCTGTATGTTC
Primers for enhancer RNA	
A20-eRNA-mus	F: TGGCAGGCATTCAGACTACAAAA R: AGAGCTTAAAGCAGGGTAGCAAA