

Table S1 Primary antibodies used in this study

| Antigens | Application | Host | Manufacturer | Cat. number |
|-------------------|-------------------|--------|----------------|-------------|
| β -actin | 1:5000 | Mouse | Zen BioScience | 250132 |
| ADPGK | 1:500 – 1:3000 | Rabbit | Abcam | ab228633 |
| CCND1 | 1:500 – 1:2000 | Rabbit | Zen BioScience | 382442 |
| β -tubulin | 1:500 – 1:2000 | Rabbit | Zen BioScience | 380628 |
| ALDOC | 1:500 – 1:2000 | Rabbit | Zen BioScience | 611464 |
| GAPDH | 1:5000 – 1:20,000 | Mouse | Zen BioScience | 200306-7E4 |
| AMPK α 2 | 1:1000 | Rabbit | Zen BioScience | R23464 |
| p-AMPK α 2 | 1:500 – 1:2000 | Rabbit | Zen BioScience | 381164 |
| His-tag | 1:5000 | Rabbit | Abcam | ab213204 |
| ALDOC | 1:5000 | Mouse | Proteintech | 66120-1-Ig |

ADPGK ADP-dependent glucokinase, *CCND1* cyclin D1, *ALDOC* aldolase C, *AMPK* AMP-activated protein kinase

Table S2 siRNA sequences

| siRNA number | Sequence (5' – 3') |
|--------------|---------------------|
| siADPGK #1 | GGAACGGTGTTCCTGATGT |
| siADPGK #2 | TGAGCAGCATTGTCCATCA |
| siADPGK #3 | GCAGCCAACTCAGATTTAA |
| siALDOC #1 | GCAGCACAGTCACTCTACA |
| siALDOC #2 | CCTCAAACGTTGTCAGTAT |
| siALDOC #3 | GAACGCTGTGCCCAATACA |

ADPGK ADP-dependent glucokinase, *ALDOC* aldolase C

Table S3 sgRNAs sequences

| Gene name | Forward primer (5' – 3') | Reverse primer (5' – 3') |
|-----------|--------------------------|--------------------------|
| sgADPGK#2 | caccgGTCAATGCATGTGTTGATG | aaacCATCAACACATGCATTGACc |
| sgADPGK#3 | caccgTCTCTCAGACCTCTCCAA | aaacTTGGAGAGGTCGTGAGAGAc |
| sgADPGK#4 | caccgTGCTTGATACTCTAAAATG | aaacCATTTTAGAGTATCAAGCAc |

ADPGK ADP-dependent glucokinase

Table S4 Primers used in this study

| Gene name | Forward primer (5' – 3') | Reverse primer (5' – 3') |
|--------------|--------------------------|--------------------------|
| <i>ADPGK</i> | CGTGGCAGTGGGAGTCAAT | TGAATGCAGAATGCTGTGATCT |
| <i>ACTB</i> | CATGTACGTTGCTATCCAGGC | CTCCTTAATGTCACGCACGAT |

ADPGK ADP-dependent glucokinase, *ACTB* β -actin

Table S5 Univariate Cox regression analysis

| Variables | BCR | |
|--|------------------------|-------|
| | HR (95%CI) | P |
| Age (≥ 65 years vs. < 65 years) | 1.155 (0.361 – 3.692) | 0.808 |
| Baseline PSA (≥ 20 ng/ml vs. < 20 ng/ml) | 2.854 (0.893 – 9.121) | 0.077 |
| BMI (≥ 25 kg/m ² vs. < 25 kg/m ²) | 0.976 (0.326 – 2.925) | 0.966 |
| Neoadjuvant ADT (yes vs. no) | 5.070 (1.717 – 14.975) | 0.003 |
| ADPGK expression (high vs. low) | 3.785 (1.048 – 13.673) | 0.042 |
| pT stage (\geq pT3 vs. $<$ pT3) | 2.591 (0.811 – 8.281) | 0.108 |
| GS (≥ 8 vs. < 8) | 3.110 (1.039 – 9.310) | 0.043 |
| EPE (+ vs. -) | 2.591 (0.811 – 8.281) | 0.108 |
| SVI (+ vs. -) | 4.284 (1.475 – 12.446) | 0.007 |
| PNI (+ vs. -) | 3.168 (0.707 – 14.201) | 0.132 |
| PSM (+ vs. -) | 2.310 (0.517 – 10.327) | 0.273 |
| ADT (yes vs. no) | 6.202 (1.385 – 27.764) | 0.017 |
| Adjuvant radiotherapy (yes vs. no) | 1.910 (0.668 – 5.465) | 0.228 |
| Post RARP 3-month PSA | | 0.093 |
| < 0.003 ng/ml | Ref. | |
| 0.003 – 0.200 ng/ml | 0.823 (0.206 – 3.293) | 0.783 |
| > 0.200 ng/ml | 2.989 (0.704 – 12.680) | 0.138 |

BCR biochemical recurrence, *HR* hazard ratio, *CI* confidence interval, *PSA* prostate specific antigen, *BMI* body mass index, *ADT* androgen deprivation therapy, *pT* pathologic T, *GS* Gleason score, *EPE* extraprostatic extension, *SVI* seminal vesicle invasion, *PNI* perineural invasion, *PSM* positive surgical margin, *RARP* robot-assisted laparoscopic radical prostatectomy, *ADPGK* ADP-dependent glucokinase, *Ref.* reference

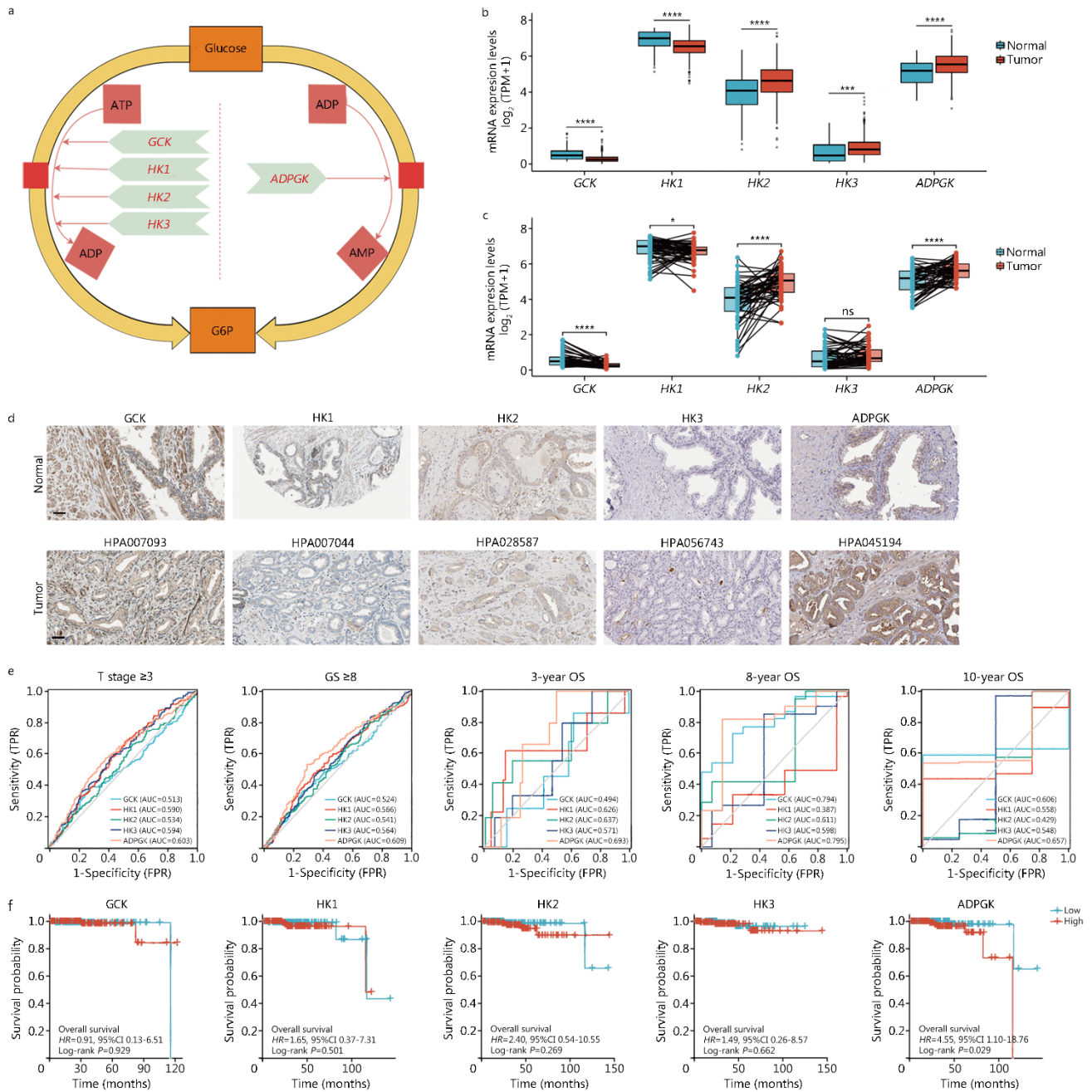


Fig. S1 Function and expression of genes involved in the oxidative phosphorylation of glucose and their associations with clinical outcomes. **a** Five genes including *GSK*, *HK1*, *HK2*, *HK3* and *ADPGK* were involved in the conversion of glucose to glucose-6-phosphate (G6P). mRNA expressions of *GSK*, *HK1*, *HK2*, *HK3* and *ADPGK* in TCGA-PRAD samples compared with normal tissues (**b**, $n = 553$) or paired normal tissues (**c**, $n = 104$) were showed. **d** Immunohistochemistry results from the Human Protein Atlas showed the protein expression of *GSK*, *HK1*, *HK2*, *HK3* and *ADPGK* in normal and PCa tissues. Scale bar = 50 μ m. **e** Sensitivities and specificities of *GSK*, *HK1*, *HK2*, *HK3* and *ADPGK* in predicting high T stage (≥ 3), high Gleason score (GS; ≥ 8), and 3-, 8- and 10-year OS were showed in ROC curves ($n = 496$). **f** Survival curves of *GSK*, *HK1*, *HK2*, *HK3* and *ADPGK* in predicting PCa OS were exhibited ($n = 496$). * $P < 0.05$, *** $P < 0.001$, **** $P < 0.0001$. ns non-significant, TCGA The Cancer Genome

Atlas, PRAD prostate adenocarcinoma, ATP adenosine triphosphate, ADP adenosine diphosphate, AMP adenosine monophosphate, GCK glucokinase, HK hexokinase, ADPGK ADP-dependent glucokinase, OS overall survival, *HR* hazard ratio, TPR true positive rate, FPR false positive rate

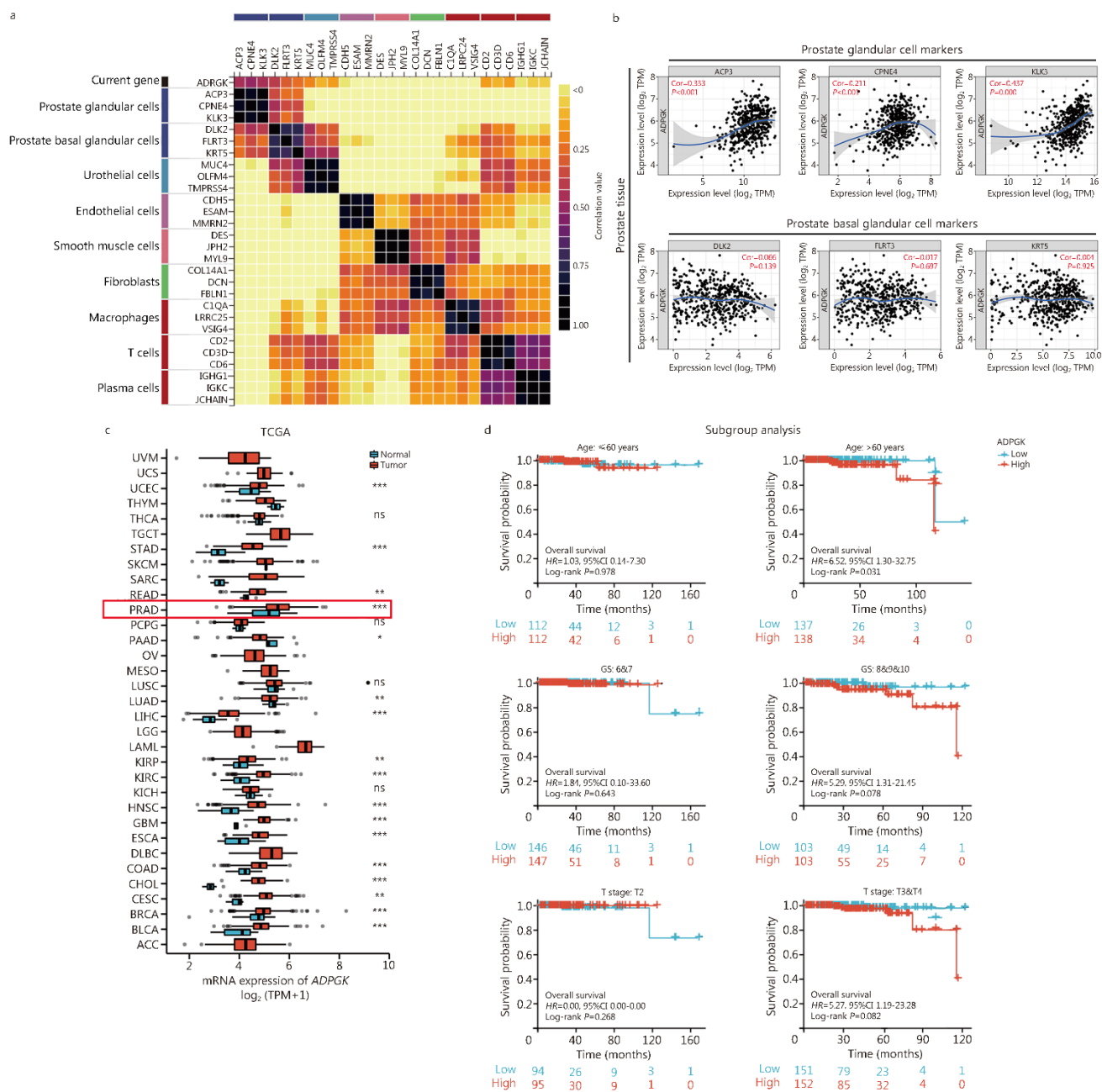


Fig. S2 Cell type enrichment and prognosis of PRAD subgroups based on ADPGK expression. **a** ADPGK was significantly correlated with prostate glandular cell markers (ACP3, CPNE4, KLK3, DLK2, FLRT3, and KRT5). **b** In PCa, ADPGK was significantly positively correlated with ACP3 (also known as ACP3), CPNE4, and KLK3. **c** ADPGK mRNA expression differences were analyzed in pan-cancer analysis. **d** Subgroup analyses were conducted according to PRAD patients' age, Gleason score (GS) and T stage. * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$. ns non-significant. ADPGK ADP-dependent glucokinase, TCGA The Cancer Genome Atlas, PRAD prostate adenocarcinoma, HR hazard ratio, ACP3 prostatic acid phosphatase, CPNE4 copine 4, KLK3 kallikrein-3, DLK2 delta-like 2, FLRT3 fibronectin leucine rich transmembrane protein 3, KRT5 keratin 5, MUC4 mucin 4, OLFM4 olfactomedin 4, TMPRSS4 transmembrane protease serine 4, CDH5 cadherin 5, ESAM endothelial cell-specific adhesion molecule, MMRN2 multimerin-2, DES desmin, JPH2 junctophilin-2, MYL9 myosin light chain 9,

COL14A1 collagen, type XIV, alpha 1, DCN decorin, FBLN1 fibulin 1, C1QA complement component 1, q subcomponent, A chain, LRRC25 leucine rich repeat containing 25, VSIG4 V-set and immunoglobulin domain containing 4, IGHG1 immunoglobulin heavy constant gamma 1, IGKC immunoglobulin kappa constant, JCHAIN joining chain of multimeric IgA and IgM, UVM uveal melanoma, UCS uterine carcinosarcoma, UCEC uterine corpus endometrial carcinoma, THYM thymoma, THCA thyroid carcinoma, TGCT testicular germ cell tumors, STAD stomach adenocarcinoma, SKCM skin cutaneous melanoma, SARC sarcoma, READ rectum adenocarcinoma, PCPG pheochromocytoma and paraganglioma, PAAD pancreatic adenocarcinoma, OV ovarian serous cystadenocarcinoma, MESO mesothelioma, LUSC lung squamous cell carcinoma, LUAD lung adenocarcinoma, LIHC liver hepatocellular carcinoma, LGG brain lower grade glioma, LAML acute myeloid leukemia, KIRP kidney renal papillary cell carcinoma, KIRC kidney renal clear cell carcinoma, KICH kidney chromophobe, HNSC head and neck squamous cell carcinoma, GBM glioblastoma multiforme, ESCA esophageal carcinoma, DLBC lymphoid neoplasm diffuse large B-cell lymphoma, COAD colon adenocarcinoma, CHOL cholangiocarcinoma, CESC cervical squamous cell carcinoma and endocervical adenocarcinoma, BRCA breast invasive carcinoma, BLCA bladder urothelial carcinoma, ACC adrenocortical carcinoma

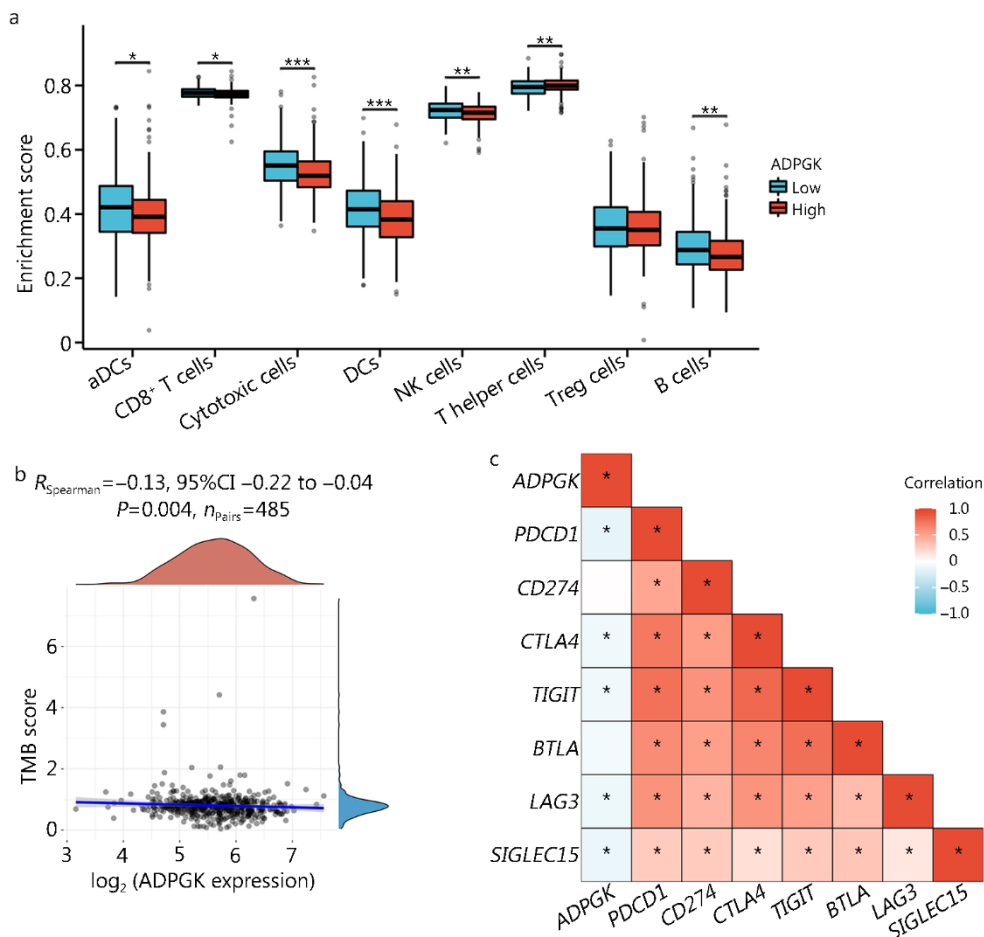


Fig. S3 Association between ADPGK and PCa immune status. **a** Immune cell infiltration comparison between ADPGK high and low groups in PCa were analyzed with ssGSEA algorithm using R package “GSVA”. **b** Correlation analysis between ADPGK expression and TMB in PCa was performed using Spearman’s method. **c** Correlation analysis between ADPGK and immune checkpoint genes expression was performed using Spearman’s method with R package “ggplot2”. * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$. ADPGK ADP-dependent glucokinase, PCa prostate cancer, DC dendritic cell, NK natural killer, Treg regulatory T, GSEA Gene Set Enrichment Analysis, TMB tumor mutational burden

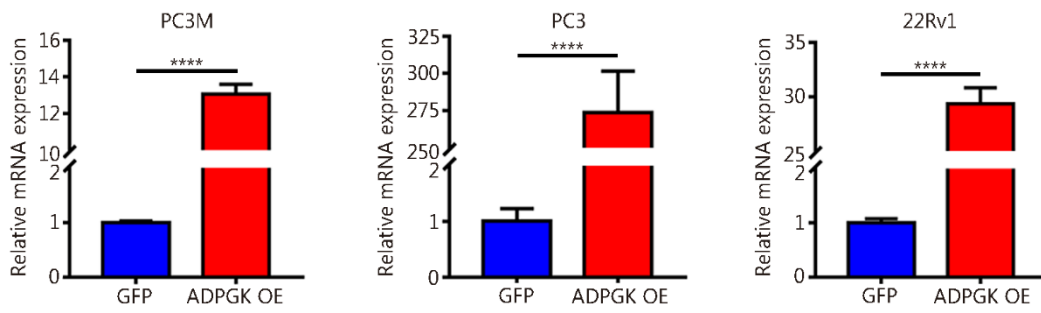


Fig. S4 qPCR results showed the stable overexpression of ADPGK in PCa cell lines after lentivirus transfection. Data were presented as the mean \pm SD ($n = 3$). *** $P < 0.001$, **** $P < 0.0001$. qPCR quantitative polymerase chain reaction, ADPGK ADP-dependent glucokinase, OE overexpression

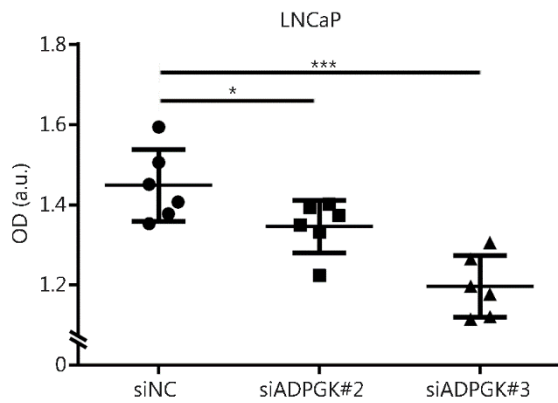


Fig. S5 The impact of *ADPGK* knockdown on LNCaP cell viability was assessed in CCK-8 assay. * $P < 0.05$, *** $P < 0.001$. OD optical density, NC negative control, ADPGK ADP-dependent glucokinase, a.u. artificial unit

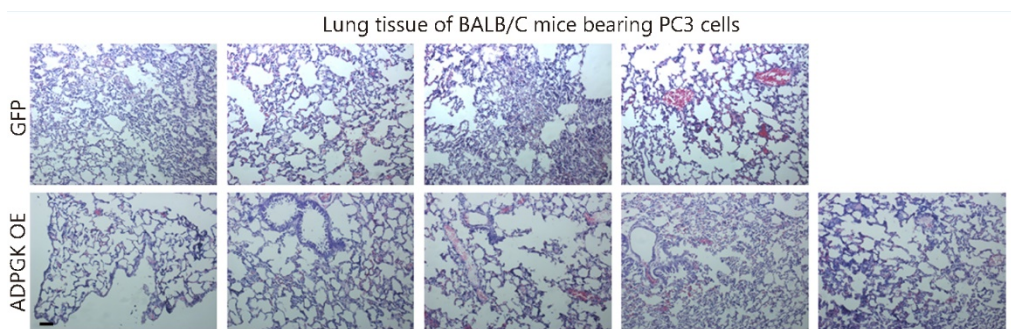


Fig. S6 Hematoxylin and eosin (HE) staining of lung tissues of mice bearing PC3 cells. Scale bar = 50 μ m. ADPGK ADP-dependent glucokinase, OE overexpression