Table SI. The expression status of FABP5 and related proteins in prostate cells [the expression levels of FABP5, its related proteins (PPARγ1, PPARγ2, p-PPARγ1, p-PPARγ2), AR, ARV7 and VEGF in different cell types are summarized].

Cell type	**Expression level**							
	FABP5	**PPARγ1**	**PPARγ2**	**p-PPARγ1**	**p-PPARγ2**	**AR**	**ARV7**	**VEGF**
PNT2	Not detected	Strong	Strong	Not detected	Not detected	Not detected	Not detected	Lower
22RV1	Moderate	Moderate	Moderate	Moderate	Moderate	Present	Present	Higher
DU145	Very high	Slightly reduced	Slightly reduced	Very high	Very high	Not detected	Not detected	Higher
PC3M	Very high	Slightly reduced	Slightly reduced	Very high	Very high	Not detected	Not detected	Higher

FABP5, fatty acid-binding protein 5; pPPARγ, phosphorylated peroxisome proliferator-activated receptor-γ; AR, androgen receptor; ARV7, AR splicing variant 7.

Table SII. Summary of protein effects on prostate cancer cell lines after FABP5- or AR- knockout [the effect of FABP5- or AR- knockout, its related proteins (PPARγ1, PPARγ2, p-PPARγ1, p-PPARγ2), AR, ARV7 and VEGF in different cell types are summarized].

Cell Line	**Protein**	**Effect**
22RV1-FABP5-KO cells	ARFL	No change
	ARV7	Not detectable
	PPARγ-1	Increased by 75%
	PPARγ-2	Decreased by 68%
	p-PPARγ1	Decreased by 64%
	p-PPARγ2	Decreased by 88%
	VEGF	Reduced by 90%
22RV1-AR-KO cells	FABP5	Not detectable
	PPARγ-1	Reduced by 86%
	PPARγ-2	Reduced by 100%
	p-PPARγ1	Decreased by 100%
	p-PPARγ2	Decreased by 93%
	VEGF	Reduced by 95%
Du145-FABP5-KO cells	PPARγ-1	Completely inhibited
	PPARγ-2	Completely inhibited
	p-PPARγ1	Reduced by 85%
	p-PPARγ2	Reduced by 100%
	VEGF	Reduced by 90%
PC3M-FABP5-KO Cells	PPARγ-1	Reduced by 97.8%
	PPARγ-2	Reduced by 100%
	p-PPARγ1	Decreased by 50%

	p-PPARγ2	Decreased by 43%
	VEGF	Reduced by 58%

FABP5, fatty acid-binding protein 5; pPPARγ, phosphorylated peroxisome proliferator-activated receptor-γ; ARV7, AR splicing variant 7; KO, knockout.

Table SIII. The top 40 differentially expressed genes between 22RV1 and 22RV1-FABP5-KO cells.

Gene ID	**Gene name**	**log2Fold change**	**P-value**
ENSG00000171345	KRT19	-4.76503	$1.95\text{x}10^{-9}$
ENSG00000164647	STEAP1	-4.58614	$9.77\text{x}10^{-11}$
ENSG00000004776	HSPB6	-4.52465	$8.59\text{x}10^{-11}$
ENSG00000130164	LDLR	-4.05123	$6.01\text{x}10^{-12}$
ENSG00000196189	SEMA4A	-5.77535	$3.73\text{x}10^{-17}$
ENSG00000115648	MLPH	-6.85049	$2.48\text{x}10^{-36}$
ENSG00000166888	STAT6	-7.03778	$4.68\text{x}10^{-26}$
ENSG00000166840	GLYATL1	-9.07851	$4.27\text{x}10^{-9}$
ENSG00000127324	TSPAN8	-5.19101	$1.83\text{x}10^{-10}$
ENSG00000019991	HGF	-6.59939	$1.83\text{x}10^{-8}$
ENSG00000162458	FBLIM1	-5.75828	$5.97\text{x}10^{-8}$
ENSG00000196620	UGT2B15	-8.72938	$2.40\text{x}10^{-8}$
ENSG00000079112	CDH17	-7.72931	$1.88\text{x}10^{-6}$
ENSG00000196139	AKR1C3	-7.91328	$6.99\text{x}10^{-7}$
ENSG00000173702	MUC13	-7.62374	$2.46\text{x}10^{-6}$
ENSG00000007038	PRSS21	-7.43399	$5.13\text{x}10^{-6}$
ENSG00000163631	ALB	-4.91839	$2.25\text{x}10^{-6}$

ENSG00000006210	CX3CL1	-7.3886	6.02x10^{-6}
ENSG00000137648	TMPRSS4	-6.58036	0.00013
ENSG00000012504	NR1H4	-6.21572	0.000518
ENSG00000104332	SFRP1	7.918877	1.48x10^{-6}
ENSG00000090932	DLL3	7.051427	5.35x10^{-10}
ENSG00000119715	ESRRB	8.843079	1.52x10^{-7}
ENSG00000135074	ADAM19	8.656002	3.69x10^{-7}
ENSG00000113430	IRX4	9.309391	1.13x10^{-8}
ENSG00000187498	COL4A1	9.357618	8.34x10^{-9}
ENSG00000119698	PPP4R4	9.965597	4.78x10^{-10}
ENSG00000043039	BARX2	9.926337	4.91x10^{-10}
ENSG00000131620	ANO1	6.833901	1.86x10^{-10}
ENSG00000277586	NEFL	7.651159	1.82x10^{-16}
ENSG00000181031	RPH3AL	7.112501	9.85x10^{-12}
ENSG00000082397	EPB41L3	6.417703	2.01x10^{-14}
ENSG00000173320	STOX2	9.442916	6.22x10^{-10}
ENSG00000272636	DOC2B	9.415629	5.40x10^{-10}
ENSG00000101680	LAMA1	8.007561	6.76x10^{-21}
ENSG00000120833	SOCS2	7.073519	4.57x10^{-22}

ENSG00000079112	CDH17	-7.72931	1.88×10^{-6}
ENSG00000111249	CUX2	8.552648	2.88×10^{-38}
ENSG00000142173	COL6A2	6.638127	1.48×10^{-31}
ENSG00000130707	ASS1	8.848459	2.58×10^{-78}

FABP5, fatty acid-binding protein 5; KO, knockout.

Table SIV. The top 30 Gene Ontology enriched pathways connected with the differentially expressed genes between 22RV1 and 22RV1-FABP5-KO cells.

Enrichment FDR	**Fold enrichment**	**Pathway**
3.95×10^{-10}	20.85289	Response to fatty acid
4.10×10^{-8}	25.27623	Cellular response to fatty acid
4.05×10^{-5}	92.41622	Response to jasmonic acid
4.05×10^{-5}	92.41622	Cellular response to jasmonic acid stimulus
4.05×10^{-5}	92.41622	Response to prostaglandin D
4.05×10^{-5}	92.41622	Cellular response to prostaglandin D stimulus
1.68×10^{-7}	13.39365	Odontogenesis of dentin-containing tooth
2.64×10^{-5}	25.67117	Ammonium ion metabolic process.
5.65×10^{-7}	14.03791	Pancreas development
2.18×10^{-7}	12.9707	Positive regulation of neuron differentiation
0.000152	61.61081	Convergent extension involved in axon elongation
2.98×10^{-5}	16.80295	Exocrine system development
1.86×10^{-6}	12.05429	Artery development
2.13×10^{-12}	8.143958	Urogenital system development
3.75×10^{-8}	9.949572	Eye morphogenesis
5.17×10^{-9}	9.382357	Regulation of neuron differentiation
1.63×10^{-11}	8.293763	Renal system development
3.90×10^{-7}	10.34685	Camera-type eye morphogenesis
6.22×10^{-9}	9.241622	Multicellular organismal signaling
4.18×10^{-7}	10.26847	Odontogenesis
7.71×10^{-11}	8.13344	Kidney development
0.000167	27.38258	Progesterone metabolic process
0.000167	27.38258	Paraxial mesoderm development

0.000347	46.20811	Paraxial mesoderm formation
5.81×10^{-5}	14.78659	Positive regulation of epithelial to mesenchymal transition
2.30×10^{-5}	13.06896	Artery morphogenesis
9.56×10^{-10}	8.065415	Heart contraction
9.16×10^{-8}	9.153606	Response to corticosteroid
7.58×10^{-9}	8.249146	Regulation. of heart contraction
1.57×10^{-9}	7.782418	Heart process

FABP5, fatty acid-binding protein 5; KO, knockout.

Table SV. The top 40 differentially expressed genes between 22RV1 and 22RV1-AR-KO cells.

Gene ID	**Gene name**	**log2Fold change**	**P-value**
ENSG00000198804	MT-CO1	-2.83267	$2.10x10^{-6}$
ENSG00000198763	MT-ND2	-2.72373	$1.07x10^{-7}$
ENSG00000130164	LDLR	-4.52892	$5.40x10^{-14}$
ENSG00000228253	MT-ATP8	-2.54158	$1.35x10^{-7}$
ENSG00000198840	MT-ND3	-2.7471	$4.75x10^{-8}$
ENSG00000079459	FDFT1	-2.36796	$2.18x10^{-6}$
ENSG00000099194	SCD	-2.95305	$5.43x10^{-6}$
ENSG00000112972	HMGCS1	-3.05897	$1.14x10^{-7}$
ENSG00000169136	ATF5	-2.9933	$2.13x10^{-7}$
ENSG00000210191	MT-TL2	-2.82356	$6.33x10^{-6}$
ENSG00000196620	UGT2B15	-4.47231	$2.16x10^{-10}$
ENSG00000123201	GUCY1B2	-3.11183	$1.93x10^{-7}$
ENSG00000165816	VWA2	-3.47047	$7.10x10^{-5}$
ENSG00000185499	MUC1	-2.37316	0.000577
ENSG00000169857	AVEN	-3.17426	$7.45x10^{-6}$
ENSG00000163631	ALB	-3.66914	$1.29x10^{-5}$
ENSG00000102048	ASB9	-3.09574	0.0017
ENSG00000012504	NR1H4	-5.83903	0.000323
ENSG00000138115	CYP2C8	-5.71716	0.000638
ENSG00000066336	SPI1	-4.24645	0.001002
ENSG00000224825	RORB-AS1	4.911157	0.00167
ENSG00000109956	B3GAT1	7.906402	$7.39x10^{-6}$
ENSG00000169856	ONECUT1	4.772941	$7.69x10^{-5}$

ENSG00000109819	PPARGC1A	3.53184	0.00054
ENSG00000185483	ROR1	3.163251	1.35x10^{-5}
ENSG00000164741	DLC1	4.441879	5.59x10^{-5}
ENSG00000058335	ITPR1	4.817764	1.23x10^{-10}
ENSG00000111344	RASAL1	2.512553	0.000921
ENSG00000132692	BCAN	4.632247	4.54x10^{-7}
ENSG00000145040	UCN2	3.26252	5.12x10$_{-6}$
ENSG00000130707	ASS1	2.624126	0.000342
ENSG00000206503	HLA-A	4.722258	3.18x10$_{-9}$
ENSG00000186526	CYP4F8	4.63578	6.29x10^{-10}
ENSG00000180447	GAS1	10.8462	2.58x10^{-12}
ENSG00000105696	TMEM59L	4.920548	1.18x10^{-13}
ENSG00000198963	RORB	3.151807	1.03x10^{-5}
ENSG00000087258	GNAO1	3.95591	7.50x10^{-10}
ENSG00000074211	PPP2R2C	2.778014	9.65x10^{-5}
ENSG00000100292	HMOX1	7.007461	6.12x10^{-5}
ENSG00000100346	CACNA1I	4.142474	8.39x10^{-10}

AR, androgen receptor; KO, knockout.

Table SVI. The top 30 Gene Ontology enriched pathways connected with the differentially expressed genes between DU145 and DU145-FABP5-KO cells.

Enrichment FDR	**Fold enrichment**	**Pathway**
1.15×10^{-6}	11.44033	Positive regulation of lipid transport
3.12×10^{-6}	12.06138	Antibacterial humoral response
1.18×10^{-6}	9.735073	Positive regulation of lipid localization
0.00053	22.07311	Interleukin-27-mediated signaling pathway
4.16×10^{-6}	8.389575	Type I interferon signaling pathway
4.42×10^{-6}	8.321917	Cellular response to type I interferon
0.000763	19.74962	Positive regulation of eicosanoid secretion
0.00021	12.23618	Positive regulation of anion transport
5.46×10^{-5}	9.62161	Cellular response to virus
0.000109	10.59153	Negative regulation of viral genome replication
8.22×10^{-5}	9.041995	Peripheral nervous system development
0.001184	17.05649	Thyroid hormone generation
0.000769	12.67712	Positive regulation of insulin secretion involved in cellular response to glucose stimulus
0.001346	16.3149	Regulation of eicosanoid secretion
0.001346	16.3149	Positive regulation of fatty acid transport
8.44×10^{-6}	6.864198	Interferon-gamma-mediated signaling pathway
1.20×10^{-5}	6.621932	Regulation of lipid localization
0.001512	15.63512	Positive regulation of cholesterol efflux
0.001512	15.63512	Immunological memory process
5.07×10^{-5}	7.053436	Regulation of lipid transport
7.18×10^{-7}	5.69565	Positive regulation of T cell activation
0.002166	25.58474	Synaptic vesicle budding
5.06×10^{-7}	5.500302	Positive regulation of leukocyte cell-cell adhesion

0.001199	11.16794	Positive regulation of organic acid transport
0.002655	23.45267	MDA-5 signaling pathway
9.51×10^{-7}	5.211706	Adaptive immune response based on somatic recombination of immune receptors buil
0.000911	8.934352	Regulation of vasoconstriction
0.001412	10.66031	Response of progesterone
0.000735	7.547987	Positive regulation of chemokine production
1.18×10^{-6}	5.116947	Defense response to bacterium

FABP5, fatty acid-binding protein 5; KO, knockout.

Table SVII. The top 40 differentially expressed genes between Du145 and Du145-FABP5-KO cells.

Gene ID	**Gene name**	**log2Fold change**	**P-value**
ENSG00000113083	LOX	2.568477	$3.80\text{x}10^{-43}$
ENSG00000205364	MT1M	1.836739	0.011298
ENSG00000244242	IFITM10	2.114165	0.015518
ENSG00000176533	GNG7	2.065239	0.019687
ENSG00000125740	FOSB	3.057334	0.020109
ENSG00000120738	EGR1	1.313533	0.05133
ENSG00000163132	MSX1	2.474824	0.001865
ENSG00000132530	XAF1	5.107902	0.147392
ENSG00000130707	ASS1	1.740535	$1.72\text{x}10^{-5}$
ENSG00000123358	NR4A1	2.089559	0.008646
ENSG00000135625	EGR4	1.764551	0.02066
ENSG00000182809	CRIP2	1.553935	0.051683
ENSG00000104081	BMF	2.235654	$2.82\text{x}10^{-5}$
ENSG00000179388	EGR3	4.607518	0.007603
ENSG00000134107	BHLHE40	2.504767	$3.84\text{x}10^{-48}$
ENSG00000074181	NOTCH3	2.462673	$1.79\text{x}10^{-37}$
ENSG00000165025	SYK	2.018064	$1.72\text{x}10^{-7}$
ENSG00000122877	EGR2	2.442622	0.065936
ENSG00000153093	ACOXL	2.698124	0.006185
ENSG00000162496	DHRS3	2.41196	$1.56\text{x}10^{-25}$
ENSG00000105974	CAV1	-2.73978	0.010563
ENSG00000232192	KIF26B-AS1	-1.78448	0.02797
ENSG00000126010	GRPR	-4.20944	0.013582

ENSG00000115602	IL1RL1	-2.33115	0.001441
ENSG00000168497	CAVIN2	-2.37219	1.29×10^{-7}
ENSG00000165124	SVEP1	-1.78449	0.041951
ENSG00000185483	ROR1	-1.56502	4.73×10^{-5}
ENSG00000115365	LANCL1	-1.56907	0.04581
ENSG00000185697	MYBL1	-1.8815	2.71×10^{-5}
ENSG00000165672	PRDX3	-1.51662	0.045619
ENSG00000162894	FCMR	-2.18935	7.20×10^{-5}
ENSG00000144339	TMEFF2	-1.78211	0.031605
ENSG00000275126	HIST1H4L	-2.55737	0.090252
ENSG00000151655	ITIH2	-2.33497	0.017281
ENSG00000145337	PYURF	-2.11067	0.03719
ENSG00000030304	MUSK	-1.7563	0.026985
ENSG00000013297	CLDN11	-1.79274	0.000161
ENSG00000169330	KIAA1024	-3.04372	0.001224

FABP5, fatty acid-binding protein 5; KO, knockout.

Table SVIII. The top 30 Gene Ontology enriched pathways connected with the differentially expressed genes between Du145 and Du145-FABP5-KO cells.

Enrichment FDR	**Fold enrichment**	**Pathway**
$1.15\text{x}10^{-6}$	11.44033	Positive regulation of lipid transport
$3.12\text{x}10^{-6}$	12.06138	Antibacterial humoral response
$1.18\text{x}10^{-6}$	9.735073	Positive regulation. of lipid localization
0.00053	22.07311	Interleukin-27-mediated signaling pathway
$4.16\text{x}10^{-6}$	8.389575	Type I interferon signaling pathway
$4.42\text{x}10^{-6}$	8.321917	Cellular response to type I interferon
0.000763	19.74962	Positive regulation of icosanoid secretion
0.00021	12.23618	Positive regulation of anion transport
$5.46\text{x}10^{-5}$	9.62161	Cellular response to virus
0.000109	10.59153	Negative regulation of viral genome replication
$8.22\text{x}10^{-5}$	9.041995	Peripheral nervous system development
0.001184	17.05649	Thyroid hormone generation
0.000769	12.67712	Positive regulation of insulin secretion involved in cellular response to glucose stimulus
0.001346	16.3149	Regulation of icosanoid secretion
0.001346	16.3149	Positive regulation of fatty acid transport
$8.44\text{x}10^{-6}$	6.864198	Interferon-gamma-mediated signaling pathway
$1.20\text{x}10^{-5}$	6.621932	Regulation of lipid localization
0.001512	15.63512	Positive regulation of cholesterol efflux
0.001512	15.63512	Immunological memory process.
$5.07\text{x}10^{-5}$	7.053436	Regulation of lipid transport
$7.18\text{x}10^{-7}$	5.69565	Positive regulation of T cell activation
0.002166	25.58474	Synaptic vesicle budding
$5.06\text{x}10^{-7}$	5.500302	Positive regulation of leukocyte cell-cell adhesion

0.001199	11.16794	Positive regulation of organic acid transport
0.002655	23.45267	MDA-5 signaling pathway
$9.51\text{x}10^{-7}$	5.211706	Adaptive immune response based on somatic recombination of immune receptors buil
0.000911	8.934352	Regulation of vasoconstriction
0.001412	10.66031	Response to progesterone
0.000735	7.547987	Positive regulation of chemokine production
$1.18\text{x}10^{-6}$	5.116947	Defense response to bacterium

FABP5, fatty acid-binding protein 5; KO, knockout.

Table SIX. Summary of top 6 DEGs: Levels of changes and biological functions in FABP5- and AR-KO cells (the effect of FABP5 or AR-KO on the DEGs and biological effects in prostate cancer cells is summarized).

DEGs in FABP5- or AR-KO Cells	Expression changes in FABP5-KO cells	Expression changes in AR-KO cells	Expression changes in Du145-FABP5-KO cells	Biological effects	Pathways
CRIP2	Upregulated by 170%	Upregulated by 116%	Upregulated	Suppression of prostate cancer initiation and progression	Regulation of cellular response to type I interferon pathway
ERG3	Upregulated by 187%	Upregulated by 150%	Upregulated by 150%	Suppression of prostate cancer initiation and progression	Response to progesterone signaling pathway
FOSB	Upregulated by 110%	Upregulated by 100%	Upregulated by 100%	Suppression of prostate cancer initiation and progression	Peripheral nervous system development
GRPR	Downregulated by 96%	Downregulated by 98%	Downregulated by 96%	Suppression of prostate cancer initiation and progression	Fatty acid and lipid transport related pathways
CAV1	Downregulated by 80%	Downregulated by 85%	Downregulated by 85%	Suppression of prostate cancer initiation and progression	Steroid and cholesterol metabolic processes
NR1H4	Not expressed in KO cells	Not expressed in KO cells	Not expressed	Suppression of prostate cancer initiation and progression	Steroid and cholesterol metabolic processes

DEGs, differentially expressed genes; FABP5, fatty acid-binding protein 5; KO, knockout; AR, androgen receptor.