SUPPLEMENTARY TABLES

Supplementary Table 1. Number of mutations and differentially expressed genes in each patient

Patient N° (this study)	N° of passed mutations	N° of moderate mutations	N° of high mutations	N° of DEGs (FC > 2; adj p -value < 0.01)
1	86	34	9	1982
2	105	39	5	3170
3	71	29	7	2808
4	68	21	5	2652
5	49	20	6	4029
6	53	18	6	1034
7	87	31	8	2889
8	77	31	6	1439
9	83	27	3	3528
10	55	21	1	2159
11	83	31	11	1215
12	114	43	16	3438
13	89	27	6	1797
14	63	21	2	3563
15	68	24	2	2453

Patient samples that complied with the histological selection criteria for homogeneity and tumor cellularity were renumbered from 1 to 15. Mutations were classified as defined by Ensembl. Duplicate RNA-seq of tumor and patient-matched normal tissue was used to define differentially expressed genes (DEGs) by counting the reads with Genomic Alignments (1.17.3) and then using DESeq2 (1.17.3) with R (3.5.0). The results have been obtained following the general guidelines given in the DESeq2 tool. We used a Log2FC of -1/+1 (+2/-2) and a cutoff for the adjusted p-value (Q-value) < 0.01. All main figures have been generated using the high, moderate and modifier mutations specified in Supplementary Data File 1.

Supplementary Table 2. Novel mutations previously not reported for prostate cancer patients

Patient 1		Total number of somatic mutations: 86	
Gene	**Type of Variant**	**New Mutation**	**Function**
OR10H1	Missense	T57M	olfactory receptor
CDHR5	Splicing mut	Splice donor exon 6	member of the cadherin superfamily; enriched in colorectal cancer, liver cancer, pancreatic cancer, renal cancer, stomach cancer
HSD17B6	Missense	R52Q	17 Beta-hydroxysteroid dehydrogenase type 6; involved in intra-tumoral synthesis of DHT
TRMT10A	Missense	R275Q	tRNA (Guanine-1)-methyltransferase
BANP	Missense	R246H	forms complex with p53 & negatively regulates p53 transcription, tumor suppressor and cell cycle regulator
DGAT2	Missense	L91R	Diacylglycerol O-Acyltransferase 2
CASD1	Missense	I755S	O-acetyltransferase
TTC28	Frameshift	L1164LLTC…..	During mitosis, may be involved in the condensation of spindle midzone microtubules, leading to the formation of midbody
ITGB7	Frameshift & splice region	PCERHR644PGLCR…..	Integrin Subunit Beta 7 (ECM signaling)
FEZ1	Stop gain	E65*	leucine-zipper protein, its expression is altered in multiple human tumors; candidate tumor suppressor
TINAGL1	Missense	A424V	Inhibits TNBC progression and metastasis; prognostic marker in renal cancer (favourable) and thyroid cancer (favourable)
ZFR2	Missense	Q632H	Zinc-finger RNA binding protein
SLC35B2	Missense	S218F	Predicted membrane protein Transporter; Prognostic marker in liver (unfavorable), prostate (favorable) & breast cancer (unfavorable)
PPP2R5D	Missense	L183Q,	protein phosphatase 2 regulatory subunit B Delta isoform
WDFY1	Missense	L149P	phosphatidylinositol 3-phosphate binding protein (signaling)

Patient 2		Total number of somatic mutations: 105	
Gene	**Type of Variant**	**New Mutation**	**Function**
NBR1	Missense	V96I	Autophagy cargo receptor
RHPN2	Missense	V73M	Rhophilin-Like Rho-GTPase Binding Protein
SH3PXD2A	Missense	T847P	Adapter protein adhesion
MUC2	Missense	T2305A	Member of mucin family
CHN2	Missense	R47W	Role in cell proliferation and migration
CCDC169	Missense	R197T	Coiled-Coil Domain-Containing Protein 169
SPTLC2	Frameshift Ins	P467SSS…,	Serine palmitoyltransferase
TRIM49C	Missense	K363E	Uncharacterized
BRF1	Missense	K282Q	RNA Polymerase III Transcription Initiation Factor Subunit
HIST1H3J	Missense	H114Y	AR signaling
ZBTB42	Missense	F82C	Transcriptional repressor
LRRCC1	Missense	E525K	Leucine Rich Repeat & Coiled-Coil Centrosomal Protein 1
ZNF44	Missense	E348A	Uncharacterized
PPP1R26	Missense	C186F	Phosphatase

Patient 3		Total number of somatic mutations: 71	
Gene	**Type of Variant**	**New Mutation**	**Function**
GSG1L2	Missense	V72L	Germ Cell-Specific Gene 1-Like Protein 2-Like, Uncharacterized
ASB15	Missense	V358I	Participate in the ubiquitin-proteasome system for the degradation of proteins in the cell cycle and signal transduction pathways
SH3PXD2A	Missense	T847P	Role in cell migration

TOPAZ1	Missense	R85H	Required for progression to the post-meiotic stages of spermatocyte development
ZNF280A	Missense	R457Q	Uncharacterized
OTOG	Missense	R2294C	Component of the acellular membranes of the inner ear
LTK	Missense	R221H	Tyrosine kinase
LRRTM4	Missense	Q87K	Development and maintenance of the vertebrate nervous system
JAK2	Missense	P121L	Tyrosine kinase
RGPD2	Missense	L12V	RNA transport
KRT5	in-frame del	GGGLGGGLA517G	Member of keratin gene family
TEAD4	Missense	I242L	Hippo signaling, EMT
TTC34	Missense	G538S	Uncharacterized
CCDC71L	Missense	G28V	Uncharacterized
DUOXA1	Missense	F130L	Involved in hydrogen peroxide production necessary for thyroid hormonogenesis
VWCE	Missense	A58V	Regulatory element in the beta-catenin signaling pathway

Patient 4		Total number of somatic mutations: 68	
Gene	**Type of Variant**	**New Mutation**	**Function**
DERL3	Missense	V106I	Degrades misfolded glycoproteins in the ER
PDGFB	Missense	R217W	catalytic receptors with intracellular tyrosine kinase activity. Regulate embryonic development, angiogenesis, cell proliferation and differentiation.
TEKT4	Missense & Stop gain	L366V	Contributes to sperm motility
TET3	Missense	L1035M	Methylcytosine Dioxygenase
PRH2	Missense	I42L	Inhibitor of calcium phosphates
TAS1R3	Missense	G314D	G-protein coupled receptor
KRTAP3-2	Frameshift del	A16APP…	Keratin associated protein
DRG2	Missense	A135T	GTP binding protein
NPFF	Missense	R21H	Morphine modulating peptide

Patient 5		Total number of somatic mutations: 49	
Gene	**Type of Variant**	**New Mutation**	**Function**
SCCPDH	Missense & splice region	Y102C	Oxidoreductase
WRN	Missense	V1155L	Helicase
ZBED5	Missense & Stop gain	Q329*	Not well characterized
HDAC1	Missense	R77S	Histone deacetylase
TPSB2	Missense	R22P	Serine protease
ZNF777	Missense	P158A	Not well characterized
IL15	Start lost	M1L	Cytokine activity
FEZ2	Missense	K278E	Involved in axonal outgrowth
FKBP9	Missense	H620Q	Calcium ion binding
IFITM2	frameshift del	R86RRW	Cytokine signaling
PIM3	in-frame del	AT226	Ser/thr kinase

Patient 6		Total number of somatic mutations: 53	
Gene	**Type of Variant**	**New Mutation**	**Function**
ZP1	Missense	Y271S	Structural component of zona pellucida
FASTKD3	Missense	R216H	Kinase
MAST3	Missense	M786V	Kinase

TGFB3	Missense & splice region	E119K	TGF beta/Smad signaling network
DLL1	Stop gain	C44*	Notch ligand
ZBED8	Missense	A523S	Uncharacterized

Patient 7		Total number of somatic mutations: 87	
Gene	**Type of Variant**	**New Mutation**	**Function**
COLCA2	Missense & splice region	T34N	Colorectal Cancer Associated 2
FASTKD3	Missense	R216H	Kinase
ATG101	Missense	T133K	Autophagy
HTATIP2	Missense	R49S	Oxidoreductase required for tumor suppression
ALDH2	Missense	R338Q	Oxidoreductase
TTC29	Frameshift	N499K*	Uncharacterized
ARHGAP45	Missense	L371Q	GTPase activator
EMC9	Missense	F30Y	ER membrane protein
CCDC168	Missense	D5448G	Uncharacterized
HLA-DRB1	Missense	D31G	Antigen presentation
SLC5A9	Missense	A386V	Glucose transport
LRRC18	Missense	A217T	Sperm maturation
SHROOM2	Missense	A1406V	Endothelial cell morphology

Patient 8		Total number of somatic mutations: 77	
Gene	**Type of Variant**	**New Mutation**	**Function**
ZNF354C	Missense	V176I	Transcriptional repressor
ZMYM6	Missense	S300C	Regulates cell morphology
RABGGTB	Frameshift & stop gain	R65RMN….	RAB GTPase Binding
ALDH2	Missense	R338Q	Oxidoreductase
SCRN1	Missense	R50W	Peptidase
RASSF8	Missense	R208H	Tumor suppressor
ITPRIPL2	Missense	P171A	Intracellular calcium signaling
ZBTB14	Missense	H355Q	Not well characterized
CYB5A	Missense	F63V	Cytochrome C oxidase
EFNA1	Missense	E55A	Receptor tyrosine kinase
SLC11A1	Missense	A505S	Fe and Mn transporter
OR5M9	Missense	A298P	Signaling by GPCR

Patient 9		Total number of somatic mutations: 83	
Gene	**Type of Variant**	**New Mutation**	**Function**
METTL4	Missense	Y79F	Probable methyltransferase
ROGDI	Missense	V244M	Uncharacterized
ZIC2	Missense & in-frame del	S422C	Transcription repressor/activator
MAPK7	Missense	R400H	Role in proliferation
AMIGO3	Missense	R293W	May regulate cell-cell interaction
GABPB2	Missense	R117Q	May function as TF for purine rich repeats
OLFM3	Missense	N251S	Uncharacterized
OR5AP2	Missense	I220T	Olfactory receptor
DBR1	in-frame del	DD541D	RNA lariat debranching enzyme that hydrolyzes 2'-5' prime branched phosphodiester bonds

GAK	Missense & splice region	D1016Y	Cyclin G associated kinase
GOPC	Missense	A203V	Protein trafficking

Patient 10		Total number of somatic mutations: 55	
Gene	**Type of Variant**	**New Mutation**	**Function**
ACSM4	Missense	R325W	Fatty acid beta-oxidation
RAB29	Missense	P131A	Rab GTPase
PPP1R10	Missense & in-frame del	H896Q	Phosphatase
TBL2	Missense	H400Y	Beta transducin
EHD3	Missense	F18L	Membrane re-organization
PMEL	Missense	T419K	Melanosome biogenesis
DNAH12	Missense	A1501T	Dynein

Patient 11		Total number of somatic mutations: 83	
Gene	**Type of Variant**	**New Mutation**	**Function**
TMEM132C	Missense	V51G	Protein phosphatase
SRM	Missense	V112M	Spermidine biosynthesis
WHRN	Missense	S175T	Actin cytoskeletal assembly
ADAMTS4	Missense	R447H	Metalloproteinase
SIGLEC12	Missense	P198L	Protein carbohydrate interaction
ANXA1	Frameshift del	aa315*	Tumor suppressor. Inhibits phospholipase A2; anti-inflammatory
STEAP1	Frameshift del	aa244*	Cell surface antigen expressed at cell-cell junctions
OR4E2	Frameshift del	aa147*	Olfactory receptor
ZFP30	Missense	E159G	Not well characterized
ISM1	Missense	D181N	Uncharacterized
SLC6A18	Missense	G33E	Sodium transporter
RNH1	Missense	D436N	Ribonuclease inhibitor
UBE2R2	Missense	D232N	Beta-catenin degradation
RHOBTB1	Missense	V580I	Rho GTPase
MMP15	Missense	P575Q	Matrix Metallopeptidase
SLC6A13	Splice donor & intron	Splice site	GABA transporter

Patient 12		Total number of somatic mutations: 114	
Gene	**Type of Variant**	**New Mutation**	**Function**
KCMF1	Missense	Y82C	E3 Ub Ligase function
SH3PXD2A	Missense	T847P	Adapter protein podosome formation
HOXB7	Missense	T173M	Homeobox transcription factor
CCDC168	Stop gain	S4604*	Uncharacterized
WNK2	Missense	R874W	Mitogen-Activated Protein Kinase Kinase Kinase
KRTAP19-8	Stop gain	R50*	Keratin associated protein
FAM198A	Missense	P42Q	Uncharacterized
KIR3DL2	Missense, frame-shift ins & del	N239S	Killer cell immunoglobulin-like receptor
SEC11A	Missense	M156I	Peptidase
ANKRD31	Stop gain	L276*	Uncharacterized
COPB1	Missense	K450Q	Vesicle transport
TEAD4	Missense	I242L	Transcription factor, hippo pathway, EMT
SKOR2	Missense	F947S	Transcriptional repressor
DENND5B	frameshift	AKRTG461VWLW…,	Guanine nucleotide exchange factor

MUC2	Missense	S1943R	Member of the mucin family

Patient 13		Total number of somatic mutations: 89	
Gene	**Type of Variant**	**New Mutation**	**Function**
CYP24A1	Missense	Y145H	Cytochrome p 450
MRPL46	Missense	R7W	Mitochondrial ribosomal protein
RIBC2	Missense	R112C	Uncharacterized
INF2	Missense	P1163H	(de)polymerization of actin filaments
OR10V1	Missense	R15C	Olfactory receptor
NKAPL	Missense	M266I	Transcriptional repressor of Notch signaling
CAMK2G	Missense	I45T	Calmodulin dependent protein kinase
TANC1	Missense	D1438N	Not well characterized

Patient 14		Total number of somatic mutations: 63	
Gene	**Type of Variant**	**New Mutation**	**Function**
UBE2J1	Missense & splice region	Y227H	Ubiquitin conjugating enzyme
TET2	Stop gain	S774*	Methylcytosine Dioxygenase
SLC39A11	Missense	S153R	Metal ion transporter
SPATA21	Missense	R227C	Differentiation of haploid spermatids
PRR36	Missense	P832H	Uncharacterized
GOLGA8K	Missense	L311V	Uncharacterized
TAAR1	Missense	K188N	G-Protein coupled receptor
OR2W1	Missense	I256L	Olfactory receptor
HMCN2	Missense	G3327S	Calcium ion binding

Patient 15		Total number of somatic mutations: 68	
Gene	**Type of Variant**	**New Mutation**	**Function**
ATP1A4	Missense	V287A	Cation transport ATPase
SCLT1	Missense	T468M	Sodium channel regulator
MCEMP1	Missense	T159M	Not well characterized
MARCH11	Missense	R311C	Membrane-bound E3 ubiquitin ligases
CASP5	Missense	R24H	Aspartate protease (caspase)
ZRANB3	Missense	M162L	DNA annealing helicase and endonuclease
C5orf30	Missense	K108E	Putative role in protein trafficking *via* interaction with UNC119 and UNC119B cargo adapters
P2RX7	Missense	G27V	Ligand gated ion channel, receptor for ATP
LRRC45	Stop gain	E564*	Centrosome linker required for cohesion
CHRNG	Missense	C450Y	Muscle-type acetylcholine receptor

Red, mutations considered to have important cell biological effects.

Supplementary Table 3. Annotated differentially expressed (>2-fold) lncRNAs and miRs in each patient.

Patient	Differentially expressed lncRNAs	Differentially expressed miRs
1	HOTTIP, SCHLAP1, NEAT1, PCA3, DANCR, MEG3, ARLNC1	MIR205HG, MIR4300HG, MIR4458HG, MIR646HG, MIR9-3HG, MIR99AHG
2	SCHLAP1, NEAT1, PCAT1, PCA3, DANCR, MEG3	MIR1-1HG-AS1, MIR205HG, MIR222HG, MIR23A, MIR27A, MIR5687, MIR5704
3	PCAT1, PCA3, DANCR, ARLNC1	MIR181A1HG, MIR205HG, MIR22HG, MIR27A, MIR3142HG, MIR4458HG, MIR5687, MIR5704, MIR9-3HG
4	HOTTIP, HOTAIRM1, NKILA, SCHLAP1, PCAT1, PCA3, ARLNC1	MIR1-1HG-AS1, MIR2052HG, MIR222HG, MIR3142HG, MIR3189, MIR34AHG, MIR3648-2, MIR3687-2, MIR4300HG, MIR4435-2HG, MIR4500HG, MIR4796, MIR5704, MIR578, MIR646HG, MIRLET7BHG
5	HOTTIP, NKILA	MIR100HG, MIR222HG, MIR3189, MIR4453HG, MIR4458HG, MIR5704
6	HOTTIP, NEAT1, ARLNC1	MIR205HG, MIR3142HG, MIR4429, MIR4435-2HG, MIR561
7	HOTTIP, NKILA, SCHLAP1, NEAT1, PCAT1, PCA3, DANCR, MEG3	MIR1-1HG-AS1, MIR205HG, MIR222HG, MIR22HG, MIR23A, MIR27A, MIR3142HG, MIR5687, MIR5704
8	HOTTIP, SCHLAP1, PCAT1, PCA3, DANCR, MEG3	MIR1-1HG-AS1, MIR205HG, MIR222HG
9	HOTTIP, NEAT1, PCAT1, PCA3, DANCR, ARLNC1	MIR100HG, MIR1-1HG-AS1, MIR155HG, MIR193BHG, MIR2052HG, MIR205HG, MIR222HG, MIR3648-2, MIR5704, MIR5706, MIR99AHG, MIRLET7BHG
10	HOTTIP, SCHLAP1, NEAT1, PCAT1, PCA3, MEG3, ARLNC1	MIR1-1HG-AS1, MIR222HG, MIR22HG, MIR34AHG, MIR5687, MIR5704
11	SCHLAP1, PCAT, ARLNC1	MIR1251, MIR137HG, MIR22HG, MIR23A, MIR27A, MIR3648-2, MIR578, MIR646HG
12	HOTTIP, HOTAIRM1, SCHLAP1, NEAT1, PCAT1, PCA3, DANCR, MEG3, ARLNC1	MIR100HG, MIR1-1HG-AS1, MIR17HG, MIR200CHG, MIR205HG, MIR222HG, MIR25, MIR3142HG, MIR4429, MIR4697HG, MIR503HG, MIR5706, MIR635, MIR646HG, MIR99AHG
13	NKILA, SCHLAP1, PCAT1, MEG3	MIR1-1HG-AS1, MIR205HG, MIR22HG, MIR34AHG, MIR4697HG
14	SCHLAP1, PCAT1, PCA3, MEG3, ARLNC1	MIR100HG, MIR1-1HG, MIR1-1HG-AS1, MIR1255A, MIR193BHG, MIR205HG, MIR222HG, MIR27B, MIR4697HG, MIR5687, MIR99AHG
15	NKILA, SCHLAP1, PCAT1, PCA3, MEG3, ARLNC1	MIR205HG, MIR3189, MIR34AHG, MIR4664, MIR4697HG, MIR5687, MIR646HG, MIR99AHG

Functionally relevant annotated miRs and lncRNAs were taken from[1-9]. Red, upregulated in tumors; black, downregulated in tumors relative to the patient-matched normal prostate tissue. All patient-specific deregulated miRs and lncRNAs can be found in Supplementary Data File 2.

Supplementary Table 4. Sequencing statistics for RNA-seq and EXOME-seq

Normal	RNA-SEQ		EXOME-SEQ			Tumor	RNA-SEQ		EXOME-SEQ		
	Reads	Align %	Reads	Align %	Duplicate reads %		Reads	Align %	Reads	Align %	Duplicate reads %
1N_rep1 1N_rep2	36603682 38501720	92.26 92.64	42475200	96.07	9.12	1T_rep1 1T_rep2	49485994 52252504	91.34 91.78	55706200	96.12	9.12
2N_rep1 2N_rep2	35578814 63894243	90.50 91.60	56298000	96.51	11.09	2T_rep1 2T_rep2	34340289 53856558	86.04 91.50	44136000	96.09	10.30
3N_rep1 3N_rep2	33037647 38061308	88.49 87.49	45167400	95.96	11.62	3T_rep1 3T_rep2	39206644 44685255	83.38 87.41	45636400	95.90	9.85
4N_rep1 4N_rep2	39635442 54890556	87.12 92.23	45418800	96.31	8.21	4T_rep1 4T_rep2	47273179 53502497	84.77 91.40	49255300	96.06	8.41
5N_rep1 5N_rep2	40283379 46638779	91.73 90.20	49694100	96.43	7.78	5T_rep1 5T_rep2	64602422 47515766	94.25 91.17	43400000	96.26	13.96
6N_rep1 6N_rep2	46031895 55861482	86.04 91.92	34157000	96.06	9.98	6T_rep1 6T_rep2	33455857 76033143	87.00 92.16	45420600	96.29	8.19
7N_rep1 7N_rep2	31882647 42675237	87.96 87.76	43500400	96.04	11.28	7T_rep1 7T_rep2	47721526 38438256	86.91 93.03	47714500	96.02	11.74
8N_rep1 8N_rep2	35333114 80370444	83.44 94.85	54276700	96.33	9.09	8T_rep1 8T_rep2	74598149 44121100	88.50 91.54	48035100	96.09	14.18
9N_rep1 9N_rep2	80833193 41562421	88.13 94.28	46282300	95.93	10.72	9T_rep1 9T_rep2	39677083 38703772	90.05 93.42	48773100	96.04	7.44
10N_rep1 10N_rep2	53431330 51151259	85.30 91.93	53645600	96.29	8.11	10T_rep1 10T_rep2	42928847 54227448	86.65 91.26	55294500	96.26	8.08
11N_rep1 11N_rep2	42821733 56544524	83.82 92.71	51965800	96.32	9.47	11T_rep1 11T_rep2	48657860 53899463	82.43 92.03	57373400	96.42	11.73
12N_rep1 12N_rep2	37996964 40528066	91.08 91.61	55279200	96.12	16.20	12T_rep1 12T_rep2	44233768 47182837	91.96 92.44	52977500	96.37	8.51
13N_rep1 13N_rep2	48075036 44318278	87.48 93.21	49494300	95.97	5.36	13T_rep1 13T_rep2	51068154 48949742	87.50 91.89	60609000	96.16	11.58
14N_rep1 14N_rep2	36167783 45548318	86.15 90.53	46894500	96.11	9.67	14T_rep1 14T_rep2	45615157 35440307	85.63 89.91	56130300	96.08	14.89
15N_rep1 15N_rep2	46655594 43936010	88.21 90.63	53319000	96.06	12.62	15T_rep1 15T_rep2	43724856 66277516	85.14 91.99	49329900	96.03	11.78

Strand specific paired-end RNA sequencing (Illumina Hiseq 2500, 125/150bp) of Ribo-depleted total RNA from biological duplicates (adjacent tissues sections). Quality of sequencing was assessed using FastQC tool. Exome sequencing was performed using Exome capture kit (Agilent) and subsequently sequenced on Hiseq2500 for 125 bp paired-end.

Supplementary Table 5. Number of target genes co-deregulated with the indicated cognate transcription factor in each prostate cancer sample.

P No	Total DEGs	ERG	FOXA1	HOXB13	MAZ	MYB	MYC	NKX2-1	PAX5
1	1982	462						191	
2	3170	756					1038	340	
3	2808	596					952		
4	2652	516				591	797		234
5	4029	910		291		947			
6	1034	174							69
7	2889	586			556		892	324	
8	1439	292					444		97
9	3528	762				759	1083	388	
10	2159	379		151			606		
11	1215	200				242			
12	3438	781			696		1105	377	232
13	1797	367							
14	3563	755	2337	245		736	1130		
15	2453	452	1602		480		759		

REFERENCES

[1] Arun G, Diermeier SD and Spector DL. Therapeutic Targeting of Long Non-Coding RNAs in Cancer. Trends in Molecular Medicine 2018; 24: 257-277.

[2] Schmitt AM and Chang HY. Long Noncoding RNAs in Cancer Pathways. Cancer Cell 2016; 29: 452-463.

[3] Campbell JD, Yau C, Bowlby R, Liu Y, Brennan K, Fan H, Taylor AM, Wang C, Walter V, Akbani R, Byers LA, Creighton CJ, Coarfa C, Shih J, Cherniack AD, Gevaert O, Prunello M, Shen H, Anur P, Chen J, Cheng H, Hayes DN, Bullman S, Pedamallu CS, Ojesina AI, Sadeghi S, Mungall KL, Robertson AG, Benz C, Schultz A, Kanchi RS, Gay CM, Hegde A, Diao L, Wang J, Ma W, Sumazin P, Chiu HS, Chen TW, Gunaratne P, Donehower L, Rader JS, Zuna R, Al-Ahmadie H, Lazar AJ, Flores ER, Tsai KY, Zhou JH, Rustgi AK, Drill E, Shen R, Wong CK, Stuart JM, Laird PW, Hoadley KA, Weinstein JN, Peto M, Pickering CR, Chen Z and Van Waes C. Genomic, Pathway Network, and Immunologic Features Distinguishing Squamous Carcinomas. Cell Rep 2018; 23: 194-212.e196.

[4] Di Agostino S, Valenti F, Sacconi A, Fontemaggi G, Pallocca M, Pulito C, Ganci F, Muti P, Strano S and Blandino G. Long Non-coding MIR205HG Depletes Hsa-miR-590-3p Leading to Unrestrained Proliferation in Head and Neck Squamous Cell Carcinoma. Theranostics 2018; 8: 1850-1868.

[5] Larzabal L, de Aberasturi AL, Redrado M, Rueda P, Rodriguez MJ, Bodegas ME, Montuenga LM and Calvo A. TMPRSS4 regulates levels of integrin α5 in NSCLC through miR-205 activity to promote metastasis. Br J Cancer 2014; 110: 764-774.

[6] Pipan V, Zorc M and Kunej T. MicroRNA Polymorphisms in Cancer: A Literature Analysis. Cancers (Basel) 2015; 7: 1806-1814.

[7] Sárközy M, Kahán Z and Csont T. A myriad of roles of miR-25 in health and disease. Oncotarget 2018; 9: 21580-21612.

[8] Wan X, Huang W, Yang S, Zhang Y, Zhang P, Kong Z, Li T, Wu H, Jing F and Li Y. Androgen-induced miR-27A acted as a tumor suppressor by targeting MAP2K4 and mediated prostate cancer progression. Int J Biochem Cell Biol 2016; 79: 249-260.

[9] Wang C, Wang X, Su Z, Fei H, Liu X and Pan Q. MiR-25 promotes hepatocellular carcinoma cell growth, migration and invasion by inhibiting RhoGDI1. Oncotarget 2015; 6: 36231-36244.