Table S2. Enrichment analysis for the differentially expressed filtered gene lists of genes within a certain Gene Ontology term, Related to Figure 5A

GO.ID	Term	Annotated	Significant	Expected	P.Value
GO:0010469	regulation of receptor activity	202	15	1.44	9.20E-12
GO:0006954	inflammatory response	290	17	2.07	1.40E-11
GO:0032101	regulation of response to external stimulus	339	18	2.42	1.70E-11
GO:0097529	myeloid leukocyte migration	70	10	0.5	5.30E-11
GO:0051240	positive regulation of multicellular organismal process	850	26	6.07	6.70E-11
GO:0045765	regulation of angiogenesis	131	12	0.93	1.20E-10
GO:0030334	regulation of cell migration	439	19	3.13	1.50E-10
GO:0048514	blood vessel morphogenesis	292	16	2.08	1.70E-10
GO:0007155	cell adhesion	748	24	5.34	1.70E-10
GO:0001525	angiogenesis	248	15	1.77	1.70E-10
GO:0022610	biological adhesion	752	24	5.37	1.90E-10
GO:0030595	leukocyte chemotaxis	81	10	0.58	2.30E-10
GO:0016477	cell migration	763	24	5.45	2.60E-10
GO:0040012	regulation of locomotion	514	20	3.67	2.90E-10
GO:0050920	regulation of chemotaxis	83	10	0.59	3.00E-10
GO:0001568	blood vessel development	352	17	2.51	3.00E-10
GO:0050921	positive regulation of chemotaxis	60	9	0.43	3.30E-10
GO:1901342	regulation of vasculature development	144	12	1.03	3.50E-10
GO:0050900	leukocyte migration	181	13	1.29	3.90E-10
GO:0032501	multicellular organismal process	3942	55	28.13	4.60E-10

Table S3. The number of PubMed citations for specific keywords, Related to Figure 5A

ID	Mean RPKM Enza I	Mean RPKM Enza II	FC	FDR	Number of PubMed citations (Gene + PCa)	(Gene + cancer)	Gene +EMT / +PCa	Gene +NE / +PCa	Gene +Migration / +PCa	Gene +Invasion / +PCa	Gene +Inflammation /+PCa	Gene +Glycolysis / +PCa	Gene +Lipid / + PCa	Gene +Cholesterol / +PCa	Gene +Steroid / +PCa	Gene +Androgen /+Pca	Gene +Angiogenesis / +PCa	Gene +Proliferation / +PCa	Gene +Apopto-sis / +PCa
TOP 10 up regulated																			
ICAM1	2.6	29.4	8.5	0.000	57	2133	43/0	12/0	2033/8	472/9	6769/14	14/0	876/1	604/0	118/0	23/8	485/7	1735/14	1377/12
THBS1	32.5	163.4	4.9	0.000	10	271	11/0	3/1	67/0	44/0	73 /0	3/0	17/0	4/0	5/0	1/1	106/2	119/2	87/0
SCNN1A	3.6	24.3	5.5	0.000	0	22	3	1	4	4	8	0	5	2	8	0	0	12	4
PLOD2	2.6	14.9	4.4	0.000	0	82	8	0	35	28	11	0	0	0	0	0	5	30	5
CCL2	12.4	71.9	5.4	0.000	136	2206	97/10	17/0	2165/43	463/39	7893/33	27/0	845/0	614/0	87/1	46/23	758/16	1642/46	1183/25
HSPA6	5.3	25.8	4.3	0.000	1	52	1/0	0	17/0	8/0	12/0	2/0	5/0	0	2/0	1/1	1/0	18/0	25/1
KLK3	58.1	195.0	3.3	0.000	223	257	3/3	4/3	12/11	18/15	11/5	1/1	2/2	3/1	16/14	99/86	21/17	38/31	12/8
AKAP12	14.4	48.8	3.2	0.000	15	113	3/0	2/0	32/3	23/6	25/0	0	5/1	2/0	1/0	2/2	18/2	51/6	28/2
TMEFF2	20.9	72.3	3.3	0.000	26	107	2/0	1/1	9/2	10/3	3/0	0	0	0	1/0	7/7	0	24/6	11/3
OR51E2	2.3	11.5	3.7	0.000	26	32	1/1	1/1	4/3	4/4	4/1	0	0	0	0	5/5	0	10/7	0
TOP 10 down regulated																			
NOV/CCN3	25.9	8.10	-3.0	0.000	12	88	6/1	0	70/2	26/0	45/0	3/0	7/0	3/0	4/0	5/5	49/1	108/3	29/0
NTM/ neurotrimin	8.5	3.17	-2.3	0.000	0	4	1	0	4	0	0	0	1	1	1	0	0	5	3
DSC3	58.3	27.99	-2.0	0.000	1	50	3/1	1/0	9/1	5/1	1/0	0	2/0	2/0	1/0	1/0	0	14/1	4/1
EPHB4	51.8	26.33	-1.9	0.000	14	249	4/0	0	113/8	59/8	28/0	1/0	6/1	0	2/0	1/1	183/3	145/4	72/3
MCC gene	43.6	21.96	-1.9	0.000	1	33	0	0	2/0	0	2/0	0	1/0	1/0	0	0	0	4/0	3/0
LINC00940	6.9	3.21	-1.9	0.000	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
DPP4	8.3	2.50	-2.7	0.020	15	356	22/0	9/0	85/2	41/2	445/0	2/0	263/0	176/0	16/0	12/3	57/0	229/3	196/1
TRPM8	148.6	84.41	-1.8	0.000	80	198	3/0	6/1	41/17	20/5	140/1	0	47/4	9/0	11/5	29/23	7/1	73/26	48/21
GLI3	3.1	1.36	-1.7	0.000	12	192	11/0	3/0	42/1	23/0	9/0	2/0	9/0	6/0	7/1	7/3	11/0	177/5	70/0
PLEKHN1	7.8	3.99	-1.8	0.000	0	3	0	0	0	0	0	0	4	0	0	0	0	0	2

Table S4. Real-Time Quantitative RT–PCR Primer Sequences, Related to STAR Methods

	RT-qPCR primer sequence	
Human gene	Forward	Reverse
AR-FL	CTTACACGTGGACGACCAGA	GCTGTACATCCGGGACTTGT
AR-V1	CCATCTTGTCGTCTTCGGAAATGTTATGAAGC	CTGTTGTGGATGAGCAGCTGAGAGTCT
AR-V7	CCATCTTGTCGTCTTCGGAAATGTTATGAAGC	TTTGAATGAGGCAAGTCAGCCTTTCT
L19	AGGCACATGGGCATAGGTAA	CCATGAGAATCCGCTTGTTT

Mouse gene	Forward	Reverse
Cyp11a1	AGATCCCTTCCCCTGGCGACAATG	CGCATGAGAAGAGTATCGACGCATC
Cyp17a1	CAAGCCAAGATGAATGCAGA	AGGATTGTGCACCAGGAAAG
Hsd3b1	CAGGAGCAGGAGGGTTTGTG	GTGGCCATTCAGGACGAT
Hsd3b2	CAGTTGTTGGTGCAAGAGGA	CCTGGGAATGACACCTGTGA
Hsd17b3	GTCGGACACTGGAAAAGCTAC	CGGAAGTGCTCAGGAAATGG
Hsd17b6	TTTGGAGGATTCTACAGTTGCTC	TCACCCCGAAATCTTGAACCT
L19	GGACAGAGTCTTGATGATCTC	CTGAAGGTCAAAGGGAATGTG
Srd5a1	CCCTGCTGTTCACCTTTGTC	ATCACCATGCCCACTAACCA
Srd5a2	TTACCTGGTTTATTGCGCGG	TGGCTCCAGACACATACGTA

Full names of human genes: androgen receptor, androgen receptor splice variant-1, androgen receptor splice variant-7, ribosomal protein L19

Full names of mouse genes: cytochrome P450, family 11, subfamily a, polypeptide 1; cytochrome P450, family 17, subfamily a, polypeptide 1; hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 1, hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 2, hydroxysteroid (17-beta) dehydrogenase 3, hydroxysteroid (17-beta) dehydrogenase 6, ribosomal protein L19, steroid 5 alpha-reductase 1, steroid 5 alpha-reductase 2, steroid 5 alpha-reductase 3