Supplementary Table 1. Clinical characteristics of the 9 mCRPC included in the global gene expression array.

Code	**Age**	**ECOG**	**Gleason score at diagnosis**	**Lymph node metastasis**	**Metastasis site**	**Nº previous treatments**	**Baseline PSA (ng/dl)**	**Number CTCs***	**PFS (months)**
Patient 2	64	1	-	yes	Bone and lung	3	196	55	7
Patient 5	80	1	-	yes	Bone	2	139	0	9
Patient 6	65	1	-	yes	Bone	2	1.929	59	6
Patient 9	52	1	-	no	Bone	3	409	78	4
Patient 11	73	0	-	no	Bone	3	233	12	10
Patient 13	79	1	9	no	Bone	4	715	12	6
Patient 17	71	1	8	no	Bone	2	3.115	199	9
Patient 21	68	1	9	yes	Bone	2	347	239	11
Patient 24	74	1	7	yes	Bone	1	279	21	6

Supplementary Table 2. Taqman assays employed for the RT-qPCR.

Gene	**TaqMan assay**
PTPRC (CD45)	Hs00894734_m1
HOXB13	Hs00197189_m1
MAOA	Hs00165140_m1
ARL4	Hs01932504_s1
FGD4	Hs01030780_m1
MOSPD1	Hs00219613_m1
QKI	Hs00916678_m1
SDK1	Hs01010140_m1

Supplementary Table 3. List of genes specifically expressed in CTCs from 9 mCRPC patients identified after the gene expression array.

GENE SYMBOL	*GENE SYMBOL*
TP53TG5	*HARBI1*
ENST00000372194	*TRIM15*
XM_001716578	*WHAMML1*
THBS4	*NKAIN4*
ROM1	*ENST00000412934*
MOSPD1	*C14orf72*
ARL4A	*AL050203*
QKI	*LEAP2*
MAOA	*PPIL6*
BIRC5	*DEFA4*
FOSL1	*FGD4*
PAGE2B	*ENST00000381747*
CREM	***EPCAM***
LOC100130700	*NUMBL*
A_33_P3215252	*LOC286058*
KLK3	*THPO*
ZMYM2	*C9orf71*
ZBTB49	*NBL1*
NGEF	*CCDC19*
TMTC1	*SDK1*
HOXB13	*CCNL2*
HOXA3	*NLRP4*
TULP2	*CLTB*
ENST00000409758	*C18orf25*
CADM4	*TMCC2*
ENST00000409646	*GHRL*
EFNA1	
BIK	

Supplementary Table 4. Main functions associated with the list of genes characterizing the CTC population of mCRPC patients after IPA analyses.

Molecules in the network	**Score**	**Top functions**
ACKR2, Akt, ALDH3A2, ANGPT4, ARL4A, BIRC5, CCDC169, CCND1, CCRL2, CLEC4A, CRYBG1, DEFA4, EFNA1, EPCAM, ERK1/2, FCHSD2, FFAR2, FOSL1, GHRL, GIMAP2, HOXB13, IAPP, KLK3, MC4R, mir637, MOSPD2, PACSIN2, PHIP, SLC9B2, SMARCA4, TCF, TGM2, THPO, TMEM204, TRIM15	22	Cellular Growth and Proliferation, Connective Tissue Development and Function, Tissue Development
ARMC10, BIK, CACTIN, CARD6, CCL5, CCNL2, CDKN1A, CDX2, CLTB, CREM, CTBP1-DT, DLX1, FOS, HOXA3, LINC00475, MBNL2, miR-515-3p (and other miRNAs w/seed AGUGCCU), NFkB (complex), NLRP4, NUMBL, POU5F1, PYHIN1, QKI, RELA, SDK1, SLC2A5, SLC52A1, SQLE, TP53, TPMT, TRIM39, TRIM6, USP42, ZBTB49, ZMYM2	22	Cell Cycle, Cellular Development, Cellular Growth and Proliferation

	HOXB13 **(mean)**	***MAOA*** **(mean)**	***ARL4*** **(mean)**	***FGD4*** **(mean)**	***MOSPD1*** **(mean)**	***QKI*** **(mean)**	***SDK1*** **(mean)**
ECOG							
0 (n=7)	-12.4397	-5.8801	2.0841	0.0971	-4.7007	0.4113	-7.9844
1-2 (n=21)	-7.5485	-5.7213	1.9537	-1.2609	-6.4775	-0.5055	-5.9864
Gleason score at diagnosis							
>7 (n=11)	-9.0773	-6.6863	1.8232	-1.4539	-6.1044	-0.5670	-7.5554
≤7 (n=14)	-8.3200	-5.1727	2.8895	0.0082	-6.5697	0.1633	-4.8440

Supplementary Table 5. Correlation between baseline characteristics and CTCs profile.

Prior hormone treatments							
1-2 (n=14)	-6.5583 *	-5.4231	2.4769	-1.1000	-5,5539	-,1317	-5,6247
> 2 (n=14)	-10.9844	-6.0989	1.4957	-0.7428	-6,5128	-,4209	-7,3471
PSA at baseline (ng/dl)							
<300 (n=21)	-8.9581	-6.4077	2.0555	-0.9752	-6.3134	-0.4308	-6.9219
≥300 (n=7)	-8.2109	-3.8210	1.7787	-0.7599	-5.1931	0.1871	-5.1779
LDH baseline (UI/L)							
<411 (n=6)	-11.5457	-10.9247*	1.4370	-0.6217	-6.6417	-0.1882	-8.4593
≥411 (n=7)	-6.2251	-3.8639	0.6679	-0.1847	-5.5033	0.1127	-4.2346
PA baseline (UI/L)							
<225 (n=6)	-10.9027	-9.4790	2.1310	-2.6233	-9.1682 *	-1.7557	-9.1160
≥225 (n=19)	-8.3609	-5.1302	1.7909	-0.4806	-5.3323	0.1279	-5.3262

*p<0.05 according to Mann Whitney U test.