

Supplementary Materials

Prognostic Significance of Gene Expression and DNA Methylation Markers in Circulating Tumor Cells and Paired Plasma Derived Exosomes in Metastatic Castration Resistant Prostate Cancer

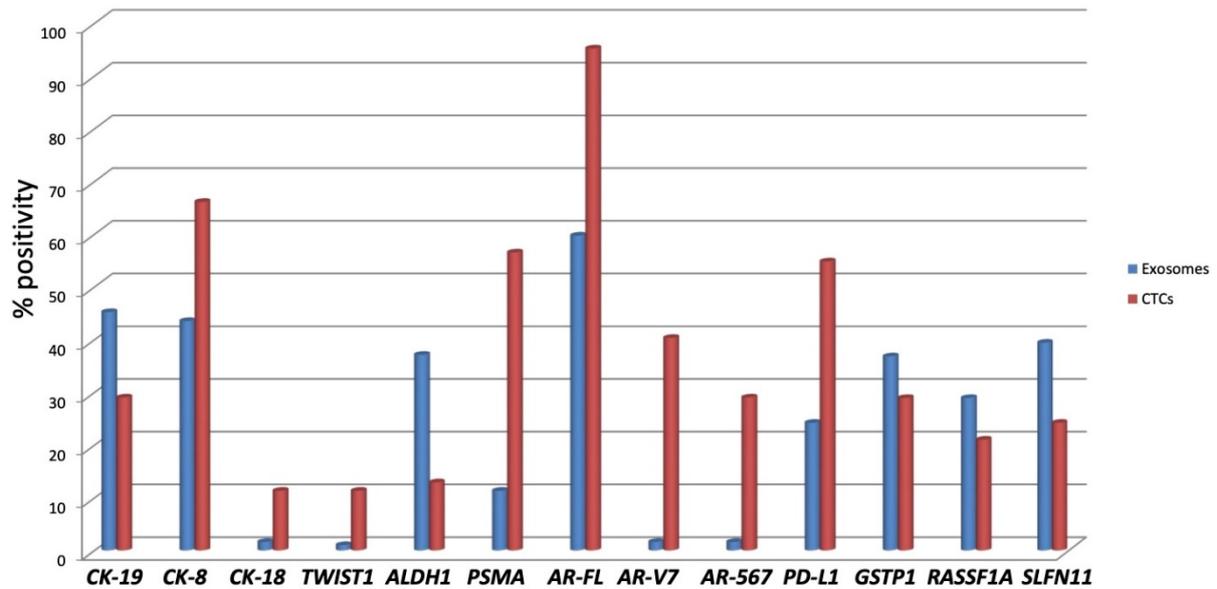


Figure S1. % Positivity of gene expression and DNA methylation markers in EpCAM positive CTCs in comparison to plasma-derived exosomes

Table S1. Clinical characteristics of mCRPC patients ($n = 62$)

Variable	mCRPC patients ($n = 62$)	
Age	<74	24(38.7%)
	\geq 74	24(38.7%)
	Unknown	14 (22.6%)
Gleason score	<8	16(25.8%)
	\geq 8	36(58.1%)
	Unknown	10(16.1%)
PSA	<50	26(41.9%)
	\geq 50	24(38.7%)
	Unknown	12(19.4%)
Therapy	Chemo	22(35.5%)
	NHA	20(32.3%)
	Unknown	10(16.1%)

Table S2. Direct comparison study of gene expression and DNA methylation markers in CTCs and exosomes derived from identical blood draws in mCRPC patients.

Exosomes	CTCs		Concordance (p , Fisher's Exact test)
Gene expression markers (RT-qPCR)			
<i>CK-19</i>	<i>CK-19</i> Negative Positive		
Negative	29	5	Concordance: 42/62, 68% ($p = 0.011$)
Positive	15	13	
<i>CK-8</i>	<i>CK-8</i> Negative Positive		
Negative	14	20	Concordance: 35/62, 57% ($p = 0.281$)
Positive	7	21	
<i>CK-18</i>	<i>CK-18</i> Negative Positive		
Negative	55	6	Concordance: 56/62, 90% ($p = 0.113$)
Positive	0	1	
<i>TWIST1</i>	<i>TWIST1</i> Negative Positive		
Negative	52	5	Concordance: 54/62, 87% ($p = 0.093$)
Positive	3	2	

<i>ALDH1</i>	<i>ALDH1</i> Negative Positive		
Negative	35	4	Concordance: 39/62, 63% (<i>p</i> = 0.454)
Positive	19	4	
<i>PSMA</i>	<i>PSMA</i> Negative Positive		
Negative	26	29	Concordance: 32/62, 52% (<i>p</i> = 0.126)
Positive	1	6	
<i>AR-FL</i>	<i>AR-FL</i> Negative Positive		
Negative	1	25	Concordance:35/62, 57% (<i>p</i> = 1)
Positive	2	34	
<i>AR-V7</i>	<i>AR-V7</i> Negative Positive		
Negative	37	24	Concordance: 38/62, 61% (<i>p</i> = 0.403)
Positive	0	1	
<i>AR-567</i>	<i>AR-567</i> Negative Positive		
Negative	43	18	Concordance: 43/62, 69% (<i>p</i> = 1)
Positive	1	0	
<i>PD-L1</i>	<i>PD-L1</i> Negative Positive		
Negative	24	23	Concordance: 35/62, 57% (<i>p</i> = 0.139)
Positive	4	11	
DNA Methylation markers (MSP)			
<i>GSTP1</i>	<i>GSTP1</i> Unmethylated Methylated		
Unmethylated	21	3	Concordance: 28/38, 74% (<i>p</i> = 0.021)
Methylated	7	7	
<i>RASSF1A</i>	<i>RASSF1A</i> Unmethylated Methylated		
Unmethylated	25	3	Concordance:30/38, 79% (<i>p</i> = 0.019)
Methylated	5	5	
<i>SLFN11</i>	<i>SLFN11</i> Unmethylated Methylated		
Unmethylated	18	5	Concordance:25/38, 66% (<i>p</i> = 0.157)
Methylated	8	7	