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Isolation of prostate cancer-derived urinary EV subpopulation leads to the identification of novel prostate cancer biomarkers

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ABSTRACT

Extracellular Vesicles (EVs) are considered potent tools for cancer biomarker discovery and diagnostics. Nevertheless, cancer-derived EVs in bio fluids are diluted to various degrees with a plethora of EVs from different sources of origin, which limits their current applications. Here we used 3-valent anti-STEAP1, STEAP2, and PSMA dynabeads to overcome this obstacle by enriching Prostate Cancer (PC)-derived extracellular vesicles from urine samples of 16 patients with PC and Benign Prostatic Hyperplasia (BPH). RNA sequencing of the EV content revealed the majority of reads being mapped to mRNA fragments, followed by lncRNAs, rRNA pseudogenes, and miRNAs. Comparing EVs from PC vs BPH patients revealed 45 differentially expressed miRNAs, 298 differentially expressed mRNA fragments, and 26 differentially expressed lncRNA fragments (LogFC>1 or <-1; adj P<0.05). Seven of these miRNAs were also found to be deregulated in the same direction in PC vs adjacent normal tissues (LogFC>1 or <-1; adj P<0.05). A selected set of miRNA candidates are currently being validated in urinary 3-valent EVs from the same patients as well as in independent BPH and longitudinal PC cohorts. So far, our data suggest that EVs isolated by 3-val beads are a rich source of PC biomarkers.

Key words: prostate tumour, biomarkers, malignant.

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