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**Introduction & Objectives:** Current anti-angiogenic therapies for cancer therapy destroy tumor vessels by blocking VEGF, with the ultimate goal to starve cancer cells. Anti-VEGF therapy has been approved for various cancers, including metastatic colorectal cancer (CRC) and non-small cell lung cancer (NSCLC). However, VEGF-targeted therapy poses major problems and showed no effect in prostate cancer (PCA). Therefore there is an urgent need for alternative anti-angiogenic strategies, based on fundamentally different mechanisms. Therefore the aim of the ongoing clinical study is to isolate tumor endothelial cells (TECs) and normal endothelial cells (NECs) from PCA patients and to perform multi-omic profiling (including targeted metabolomics, transcriptomics) to identify new targets for anti-angiogenic therapies.

**Materials & Methods:** We isolated NECs and TECs from 50 radical prostatectomy specimens. After successful enrichment of NECs/TECs by culturing and CD31 magnetic bead purification we confirmed endothelial cell phenotype by immune-fluorescence and FACS analysis. Next we quantified cell proliferation using 3H-thymidine incorporation assay. Furthermore we collected NECs and TECs for unbiased RNA sequencing and untargeted lipidomics.

**Results:** NECs and TECs could be successfully isolated with an estimated success rate of 80%. Phenotypical investigations showed high CD31 positivity reflecting EC phenotype. Furthermore NECs and TECs differed from morphological aspects (cell size, cell nuclei and junctions formation). In addition TECs are hyper-proliferative compared to NECs reflecting are hyper-motile states. RNA-seq and lipidomics analysis are ongoing and will be presented at the meeting.

**Conclusions:** Here we show for the first time that human NECs and TECs can be isolated and cultured from fresh prostate tissue. First analysis of NECs and TECs show morphological and functional differences. Preliminary RNA-Seq analysis revealed difference in lipid metabolism between TEC and NEC, currently untargeted lipidomics analysis are ongoing and will be presented at the meeting.