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Differentially expressed genes associated with TMPRSS2-ERG molecular subtype of prostate cancer

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- Prostate cancer (PC) is one of the most common and socially significant oncological diseases in men.
- There are seven subtypes of PC, the most common is TMPRSS2-ERG
- TMPRSS2-ERG is the result of translocation between exon 1 of TMPRSS2 gene and exon 4 of ERG gene
- The presence of the TMPRSS2-ERG transcript is most often considered an important predictor of unfavorable prognosis

The aim of our study is to investigate the characteristics of the transcriptome profile of this molecular subtype, which can serve as a basis for understanding the mechanisms of progression in prostate cancer and help in the search for informative prognostic markers.

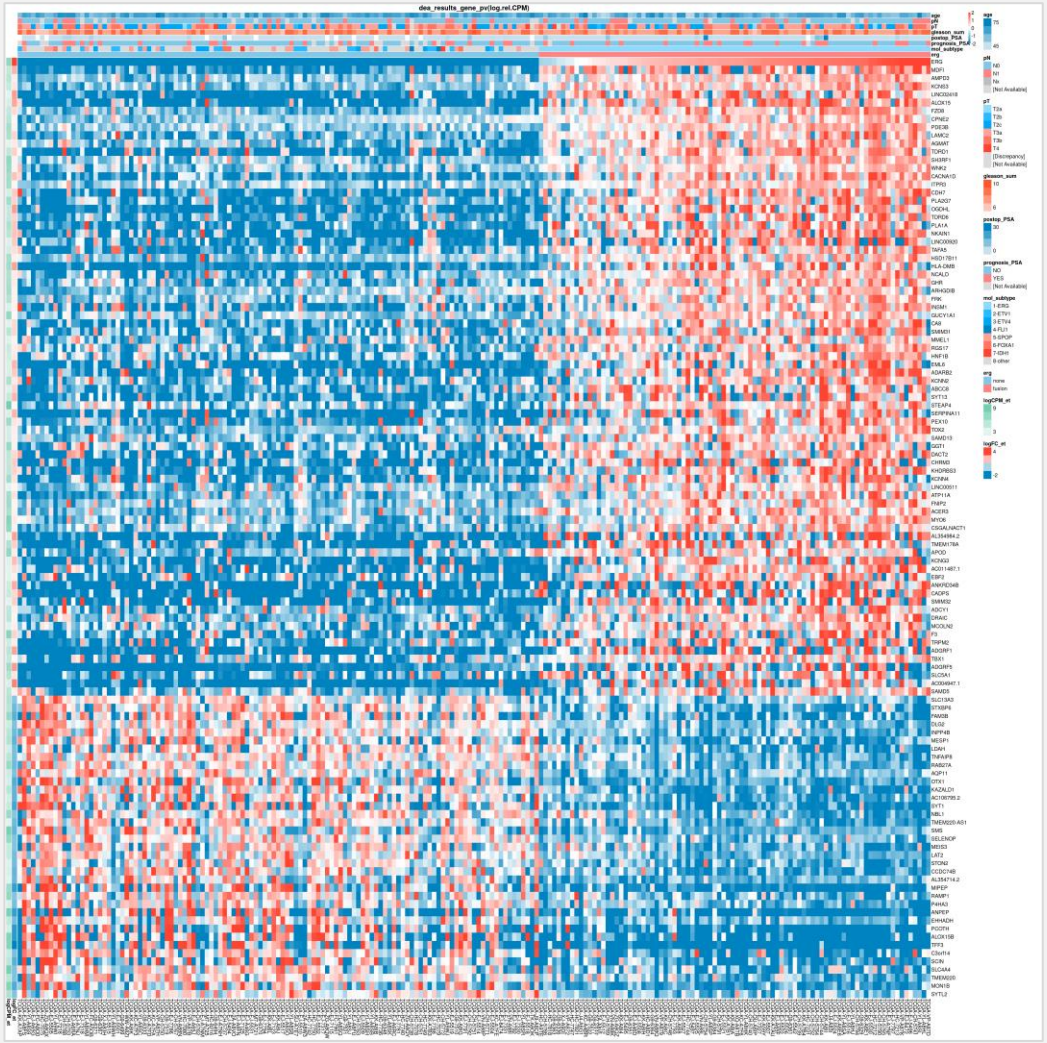
Materials and Methods

- PC samples RNA-Seq data of TCGA project. Two groups: tumors with TMPRSS2-ERG fusion transcript (88 cases) and TMPRSS2-ERG-free tumors (117 cases)
- Differential expression analysis in statistical environment R using the EdgeR. The Mann-Whitney test, Exact test and quasi-likelihood method (QLF) as statistical tests with FDR control
- Enrichment pathways analysis by clusterProfiler and ReactomePA packages

Results

We found out at list 115 DEGs. Among those next genes are of most interest with fold-expression level more than 4 for TMPRSS2-ERG-positive group: ALOX15, CACNA1D, EML6, HLA-DMB, NKAIN1, OGDHL, PLA1A, SYT13.

Figure.1 – Differentially expressed genes of TMPRSS2-ERG molecular subtype PC



Results

According to the results of enrichment pathways analysis, these genes are participants in the following cancer-significant pathways in the KEGG database associated with the progression: Arachidonic acid metabolism (hsa00590), Focal adhesion (hsa04510), Mucin type O-glycan biosynthesis (hsa00512), Notch signaling pathway (hsa04330), PI3K-Akt signaling pathway (hsa04151), Prostate cancer (hsa05215), Sphingolipid metabolism (hsa00600).

Thus, the results underscore the potential association with an unfavorable prognosis in the group of samples belonging to the molecular subtype TMPRSS2-ERG

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References

Arora K., Barbieri C.E. (2018) Molecular Subtypes of Prostate Cancer. Curr Oncol Rep. 20(8):58. doi: 10.1007/s11912-018-0707-9.

Cancer Genome Atlas Research Network. (2015) The molecular taxonomy of primary prostate cancer. Cell. 163(4):1011-25. doi: 10.1016/j.cell. 2015.10.02.

Krumbholz M., Agaimy A., Stoehr R., Burger M., Wach S., Taubert H., Wullich B., Hartmann A., Metzler M. (2019) Molecular Composition of Genomic TMPRSS2-ERG Rearrangements in Prostate Cancer. Dis Markers. 2019:5085373. doi: 10.1155/2019/5085373.

Wang Z., Wang Y., Zhang J., Hu Q., Zhi F., Zhang S., Mao D., Zhang Y., Liang H. (2017) Significance of the TMPRSS2:ERG gene fusion in prostate cancer. Mol Med Rep. 16(4):5450-5458. doi: 10.3892/mmr.2017.7281.