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Mutational landscape analysis of prostate tumor

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Prostate cancer is a relatively common and homogenous form of cancer, ranking as the 5th most prevalent cancer in men in Korea. Despite its prevalence, prostate cancer in Korean patients has not been extensively analyzed. In this study, we aimed to characterize the molecular features of prostate cancer in the Korean population by reanalyzing targeted sequencing data from 140 samples collected as part of the K-master project. We have updated the original K-master project analysis pipeline to enhance variant prediction and sensitivity. The newly discovered variants have allowed us to provide a comprehensive genomic landscape of prostate cancer in the Korean cohort. These findings offer a comprehensive understanding of the genetic landscape of prostate cancer and may suggest potential therapeutic targets. Based on this analysis, we anticipate the development of treatments and the characterization of specific features of prostate tumor subtypes.