Pan-cancer, checkpoint inhibitor (CPI) treated cohorts

Whole genome sequencing

Somatic mutations

Start-gain Frameshift in-del Stop-loss

5'UTR Coding sequence 3'UTR

Stop-loss (3'UTR neoORF)

PrimeCUTR

in-silico translation

1000 amino acids

Cumulative neoORF length

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HMF; n = 355

GEL; n = 364

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Start-gain (5'UTR) neoORFs are associated with response to checkpoint inhibitor treatment in pan-cancer datasets...

...and predict overall survival in a melanoma subset.

PrimeCUTR: Identifying clinically relevant neoantigens in the untranslated regions of cancer genomes.

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