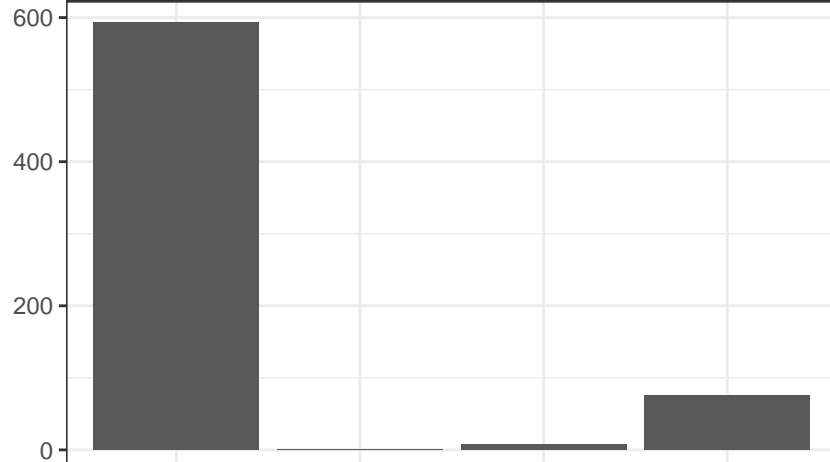


count

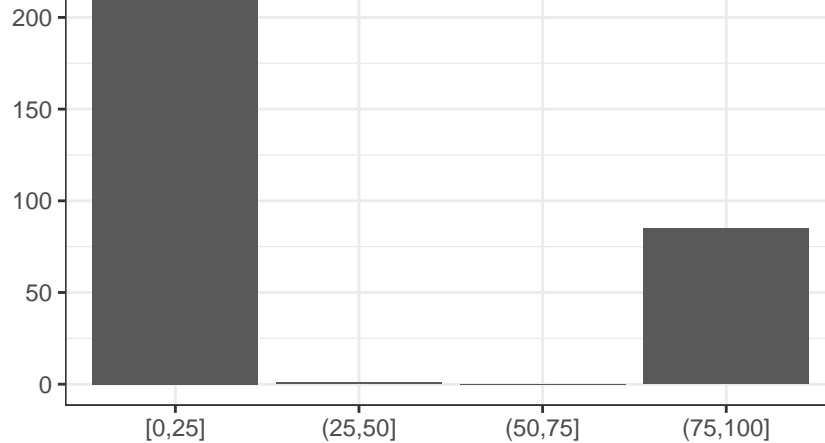
3' UTR



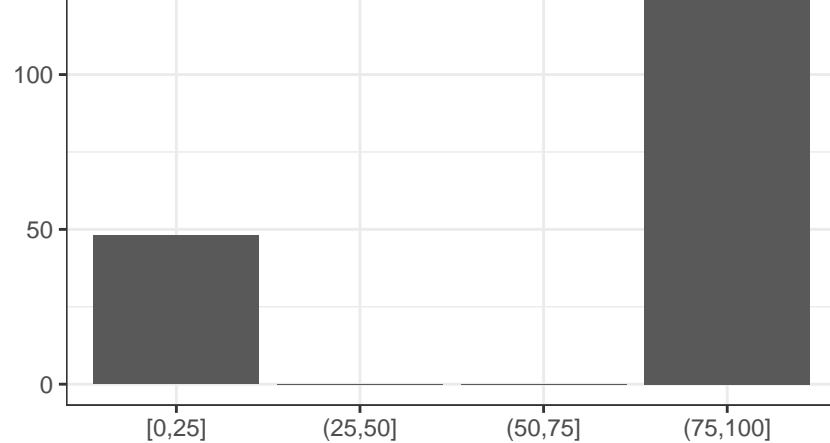
5' UTR



intergenic



internal



overlap with TUs relative to prediction length [%]