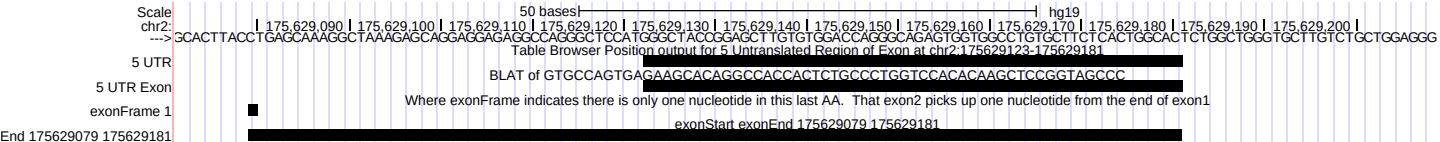
Scale
chr2:
50 bases
hg19
175,629,090 175,629,100 175,629,110 175,629,120 175,629,130 175,629,140 175,629,150 175,629,160 175,629,170 175,629,180 175,629,190 175,629,200
GCACTTACCTGAGCAAAGGCTAAAGAGCAGGAGGAGAGGCCAGGGCTCCATGGGCTACCGGAGCTTGTGTGGACCAGGGCAGAGTGGTGGCCTGTGCTTCTCACTGGCACTCTGGCTGGGTGCTTGTCTGCTGGAGGG
Table Browser Position output for 5 Untranslated Region of Exon at chr2:175629123-175629181
5 UTR
5 UTR Exon
BLAT of GTGCCAGTGAGAAGCACAGGCCACCACTCTGCCCTGGTCCACACAAGCTCCGGTAGCCC
Where exonFrame indicates there is only one nucleotide in this last AA. That exon2 picks up one nucleotide from the end of exon1
exonFrame 1
exonStart exonEnd 175629079 175629181
End 175629079 175629181