blat on YourSeq

Upstream Seq

GENCODE V49 (2 items filtered out)

RPS29

RefSeq genes from NCBI

RefSeq Curated

Alignment of Upstream (5') Sequence

TTGTTTCCGTCAGTACGCGAAGGATATCGGTTTCTAAGTTGGACTAAATGCTTTCCTTCAGAGGATTATCCGGGCATCTACTCAATGAAAAACCATGATAATTCTTTGTATATAAAATAAACATTTGAAAAAACCAAAAAAAAAAAAAAA

1   150

AAAATTACTCTCCCATCCCCTACCATACCAACCCATTTTCATTTACGCCCTCCATCACAACCCTATCTTTCCCCCTTTAGGGCTACGGCTGACCGTTTTTTGTGGTGTACTCCGTGCCATCATGTCCGTCCTGACGCCGCCGCTGCTGCTGC

151   300

GGGGCTTGACAGGCTCAGCCCGGCGGCTCCAGTGCCGCGCGCCAAGATCCATTCGTTACTGCCGCCGGAGGGGAAGCTTGGGATCATGGAATTGGCCGTTGGGCCTTACCTCCTGCTTCGTGACCTTCCTGCCTGTAGGCTGGATCCTGTC

301   450

ACACCTGGAGACCTACAGGAGGCCAGAGTGAAGGGGTCCGTTCTGTCCCTCACCATCACTGTGACCTGACCAGCCCACCAGCCCATCCTGATGTTCTTGTTACTTGTGGCCGGCCTCCCCTGGATCATGTCATTCATAATTCCAGTC

451   600

ACCTCTTCTGCAATCATGACCTCTGATGTCTCCATGGTGACCTCACTGGGGTCACTGACCCTGCTTGGTGGGGTCCCCCTTGTAACAATAAAAATCTTATTTAATTAAAAAAAAAAAAAATTCCC

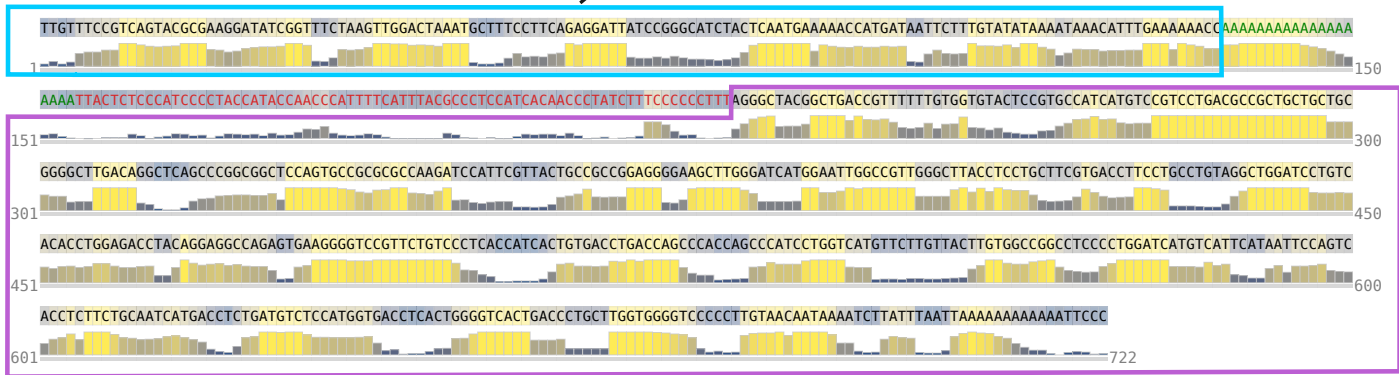601   722

Alignment of Downstream (3') Sequence

blat on YourSeq

Downstream Seq

GENCODE V49

ENSG00000256100

COX8A

RefSeq genes from NCBI

RefSeq Curated

Base quality (Q score)

50

40

30

20

10