Sequence retrieved from hg38 database from UCSC:

>hg38\_dna range=chr16:68744022-68745681 5'pad=0 3'pad=0 strand=+ repeatMasking=none

GTAAAGAGAGAAAGTAGAGAGAATATTTTCAACAGTAGTTGATATTTCTTAGGGACACAGTAAACTCTCAATGTTATTTTGAGCAAATGAATGAACACATGAATAAATCGCTATCTTGGCCAATATTTTTCCCTCTCAAACTCTATGGACTTGGTCCAGCCCTTAAGGTTGATTGTAAATGGGCGGGGAAGAATTTGGTGGGTTAGAACCTTCCATTATGCTCTGTGTGTGCTGGGGATACTGTGTTCATAGCTTCCCTCTGAACAGCTGTGCAGGGCAGGCAGGGAGATCTCAAACCTGAGTCTGGAAATGGGAGGGCATATAGCCATTTTTAAGTGTTTTCCACCTTTGGTCAAATAAAAAGAAATCTGTGGTGCATGCTCACTCTTTCTCTCTCTATCCCCATCTCTAGCCATCTCCCTTTCTTTCTCTCTTCCTCTTTGTTAATGTAAGTTTCCCTAGGCCAGGGATCTCAGTGTCCCAGCTTGTTCTTGTTACTCTTGGGGGACTGGGGTTTAGGCCTCCTCCCTTTCTGCACTTTTCATCTTCCTCCTTCCTTCCTCTTACCTGCCTCCAATCCTCCACTTCTGCCCAAGATTTGGGTGGCATCTTCCCCAAATTCAGAAGGTTCTTGAATCAGACTGCCTAGATTTCAATCCAGACAATGTCACTTCCCAGCCTAGGGATGTCAGCCAAGGACTTAGTTTCCCTCTCTGTAAAATGAGCATAATAGCATGGAGACATCATAGGATGGTATGTCAAGCGTTCAGTGAATATGAAATATTAGAGCCCCAGGAGGACTTGGTGCTGTCTGTTTGAAAGTCTCCCATGTTTTACGTTTGGTTCAAAAGATCCCCTGCGCTCCCTCTCACCCAGCAAACCAGCCAAACCAGTTTCTTCACCCTGCCTGCTTCTGTGTTAAGCAAACAGTGCACTGCAAACAGTGACTAAGCCTAGTGCCTTGTTAGGAAGAAACTGGCGTTTTTTTGCTTGCCACTGTGCAGGGTGCTCAGGGTGGACCGGAACGGGTTTGTTGTGGCTTAGGAAAGGGGACCTGCTCGTGGAGGTTGTGTAGAACTGGAGTGGGAGGAGTGGGGCAAGGCGCAGCTAGGGCCGGGGGAGTCGGGATGATCTTGAACTTGTCAGCTTCTGCTTGGCTTTTAAAAGTTATCCAGGCCAGATAGATGCTGTGGCTCACACCTGTAATCCCAGTGCTTTGGGAGGCCAAGGCCGCAGGATTACTTGAGCCCAGGAGTTTGAGACCAGCCTGGGCAACGTGGCGAGACCCCCATCTCTACAAAGATTAAAAAAAAAATTTAGCCAGGTATGGTGGCGTGCACCTGTGGTACTAGCATCAAAAAAATGCAAAAATTTGCTGGGCGTGGTGGCATGTGCATGTAGTCCCAACTACTCAGGAGGCTGAGGTGGGGGGATTGCGTGAAGCCCGGGAGGTCGAGGCTGCAGTAAGCCATGATTGCACCACGGCACTCCAGCTGATAGAGATCCTGTCTCAAAAAAAAAAAAAAAAATATATATATATATGTATATATATATGTATGTGTAATATATGTGTATATATATGTATGTGTATATATATATATATATGTATATATATTTCATGATGCACATGCCTAAGAATACCTGTCTGTTCTCCTGCTGC

We designed a Primer Reverse to amply the sequence highlighted in yellow (intronic region of CDH1): 5´AGGCTGGTCTCAAACTCCTG’3

We tried IN SILICO PCR but there was no match, we then used BLAST and there is no match again. Following, we increased the primer sequence in 21 bp (GGGGGTCTCGCCACGTTGCCCAGGCTGGTCTCAAACTCCTG) and it had a match both IN SILICO PCR and BLAST. We then trimmed the sequence until there was no match again: (GGGGGTCTCGCCACGTTGCCCAGGCTGGTCTCAAACTCCTG)

Why does this happen?

Thank you.