**PCF11 ENSG00000165494**

**4668 nt**

ATGTCAGAGCAGACGCCGGCCGAGGCCGGTGCTGCGGGGGCCCGGGAGGACGCCTGTCGGGATTATCAGTCATCGCTCGAAGACCTGACCTTCAATAGCAAGCCGCACATCAATATGCTGACCATTCTAGCCGAGGAGAACCTGCCCTTCGCCAAGGAGATCGTCTCTCTCATCGAGGCCCAAACCGCCAAGGCTCCTTCCTCAGAGAAGCTTCCTGTTATGTACCTTATGGATTCTATTGTGAAAAACGTTGGAAGAGAGTATCTCACTGCCTTTACTAAAAATCTAGTTGCAACATTTATTTGTGTGTTTGAAAAGGTGGATGAAAATACTAGGAAAAGTTTATTTAAGTTACGTTCTACATGGGATGAAATATTCCCTTTGAAGAAACTTTATGCCCTGGATGTCAGAGTCAATTCATTAGATCCTGCTTGGCCTATTAAACCTCTACCCCCCAATGTGAATACGTCTAGCATCCATGTGAATCCTAAATTTTTAAATAAATCGCCCGAGGAGCCTTCAACACCTGGTACAGTGGTCAGTTCCCCTAGCATCTCCACTCCTCCAATTGTTCCTGATATACAAAAGAATCTTACACAAGAACAACTAATAAGGCAGCAGTTACTGGCAAAGCAAAAACAGTTGTTAGAACTTCAGCAGAAAAAGCTGGAGCTTGAGCTAGAGCAAGCTAAGGCACAGTTGGCAGTTTCTCTTAGTGTTCAGCAGGAAACATCCAATTTAGGTCCTGGATCTGCACCATCCAAATTACATGTTTCACAGATTCCCCCTATGGCAGTTAAAGCTCCTCATCAGGTTCCTGTGCAATCTGAGAAAAGCCGTCCAGGACCATCCTTACAAATTCAGGATTTAAAAGGAACTAACCGGGATCCTCGTCTGAACAGGATAAGCCAACATTCTCATGGAAAAGATCAGAGTCACAGGAAAGAATTTCTAATGAACACATTAAACCAGTCTGATACTAAGACAAGTAAAACTATACCCTCTGAAAAACTAAATTCATCCAAGCAAGAAAAAAGTAAATCAGGTGAAAAAATAACCAAGAAAGAACTTGACCAATTAGATTCTAAATCGAAATCGAAATCGAAATCACCCTCACCTTTGAAAAACAAATTATCTCACACAAAAGACTTGAAAAATCAAGAATCGGAAAGTATGAGGTTGTCTGATATGAACAAGAGAGATCCAAGATTAAAAAAACATCTTCAGGATAAGACCGATGGCAAAGATGATGATGTGAAAGAGAAGAGAAAAACTGCAGAAAAAAAGGATAAAGATGAGCACATGAAGTCATCCGAACACAGACTGGCTGGAAGTAGAAATAAAATCATAAATGGCATTGTACAAAAACAGGATACAATAACAGAAGAGTCAGAAAAACAGGGGACAAAACCAGGGAGATCGAGTACTAGAAAGCGATCAAGATCTCGATCACCCAAGTCTAGGTCACCAATTATACATTCCCCAAAGAGAAGAGATAGGCGGTCACCCAAACGAAGGCAAAGAAGTATGTCTCCAACATCGACACCTAAAGCTGGAAAGATTCGCCAATCTGGAGCTAAGCAGTCACATATGGAAGAGTTTACACCACCTTCTAGGGAAGACAGAAATGCTAAGAGAAGTACTAAACAGGATATTCGGGATCCAAGGCGAATGAAAAAGACTGAAGAGGAGCGACCACAAGAAACTACAAATCAGCATTCTACAAAGTCAGGCACTGAACCAAAGGAGAATGTAGAAAACTGGCAAAGTTCCAAGTCTGCCAAAAGATGGAAATCTGGTTGGGAAGAAAATAAAAGCTTACAACAGGTTGATGAACATAGTAAACCTCCTCATCTGAGGCATAGGGAGAGCTGGTCAAGCACTAAAGGAATTTTATCACCTCGAGCCCCAAAGCAGCAACAGCATCGATTAAGTGTAGATGCCAATCTTCAGATTCCTAAAGAGTTAACTCTTGCAAGCAAAAGAGAATTACTTCAAAAGACGAGTGAACGTTTAGCATCTGGTGAAATTACACAGGATGACTTCCTTGTTGTTGTGCATCAAATTCGACAGCTATTTCAGTATCAAGAAGGTGTGCGAGAAGAGCAGAGATCTCCATTCAATGATCGTTTTCCACTTAAGCGACCTCGATATGAAGATTCAGATAAACCATTTGTAGATAGTCCAGCATCAAGATTCGCCGGCCTGGATACAAATCAGCGACTTACAGCTTTAGCTGAAGACAGACCGTTATTTGATGGACCTAGTAGGCCATCAGTAGCAAGAGATGGCCCAACGAAGATGATTTTTGAAGGACCCAATAAATTAAGCCCTCGAATTGATGGACCTCCCACACCAGCTTCTCTTCGGTTTGATGGGTCACCAGGACAAATGGGGGGAGGAGGCCCTTTGAGATTTGAGGGGCCACAAGGTCAGCTAGGAGGTGGGTGTCCTTTGAGATTTGAAGGTCCTCCAGGACCAGTGGGGACACCTCTGCGGTTTGAGGGCCCAATTGGTCAAGCAGGAGGAGGTGGTTTTCGGTTTGAAGGTTCCCCTGGTCTGAGGTTTGAGGGATCTCCAGGTGGTTTGAGATTTGAGGGACCAGGAGGCCAGCCTGTGGGTGGTCTGAGGTTTGAGGGACATCGTGGTCAACCTGTGGGTGGTCTAAGGTTTGAGGGACCTCATGGTCAGCCTGTGGGTGGACTTAGATTTGATAATCCCCGAGGTCAGCCTGTAGGTGGACTTAGATTTGAGGGGGGTCATGGTCCATCAGGGGCTGCGATTAGGTTTGATGGACCTCATGGTCAGCCAGGAGGTGGAATCAGATTTGAGGGCCCTTTGCTACAGCAAGGGGTTGGAATGAGGTTTGAGGGCCCCCATGGTCAGTCAGTAGCTGGTCTGAGATTTGAGGGACAACATAATCAACTTGGTGGGAACCTTAGGTTTGAGGGTCCACATGGTCAGCCAGGGGTTGGTATCAGGTTTGAAGGCCCTTTAGTCCAACAAGGAGGTGGAATGAGGTTTGAGGGTCCTTCTGTACCAGGAGGTGGCCTGAGAATTGAAGGGCCTCTGGGTCAAGGTGGTCCAAGATTTGAAGGTTGTCATGCTTTAAGGTTTGATGGGCAGCCAGGTCAGCCGTCACTCTTGCCAAGATTTGATGGATTACATGGTCAGCCAGGTCCTAGATTTGAAAGGACTCCTGGTCAGCCAGGCCCTCAGAGGTTTGATGGACCACCTGGACAGCAGGTTCAACCCAGATTTGACGGTGTACCTCAAAGATTTGATGGTCCACAACATCAGCAAGCATCAAGGTTTGATATTCCTCTTGGTCTTCAAGGCACAAGATTTGACAATCATCCTTCACAAAGGCTTGAATCAGTATCTTTCAATCAGACTGGTCCATATAATGATCCACCTGGCAATGCTTTTAATGCCCCATCCCAAGGACTACAGTTCCAAAGACATGAACAAATATTTGATTCACCTCAAGGACCAAATTTTAATGGACCACATGGCCCTGGAAACCAGAGTTTCTCTAATCCACTTAACAGAGCTTCTGGACACTATTTTGATGAAAAAAATCTTCAGAGTTCTCAATTTGGAAACTTTGGCAATATACCTGCTCCAATGACAGTAGGAAATATTCAGGCATCTCAACAGGTTCTGAGTGGTGTTGCTCAGCCAGTAGCTTTTGGTCAAGGACAACAGTTTTTACCAGTTCATCCACAAAATCCTGGATTTGTTCAGAATCCTTCAGGAGCCCTCCCTAAGGCATATCCTGATAATCATCTCAGTCAGGTGGATGTAAATGAATTGTTTTCAAAATTGCTAAAAACAGGAATTCTCAAATTGTCCCAAACTGATTCAGCTACAACACAAGTAAGTGAAGTAACTGCTCAGCCTCCCCCTGAAGAGGAGGAAGATCAAAATGAAGATCAAGATGTTCCAGATCTTACTAATTTTACAGTTGAAGAATTGAAACAACGTTATGACAGTGTTATAAATCGACTGTACACTGGTATTCAGTGTTACTCTTGTGGAATGAGGTTTACAACATCACAGACAGATGTTTATGCAGATCATTTGGACTGGCATTATCGGCAAAATAGAACTGAAAAGGATGTTAGCCGAAAAGTCACTCATAGACGTTGGTACTACAGTTTAACAGACTGGATAGAATTTGAGGAGATAGCTGATCTGGAAGAACGGGCAAAGAGCCAGTTTTTTGAAAAGGTGCATGAAGAAGTTGTGCTCAAAACTCAAGAGGCTGCTAAAGAAAAAGAGTTCCAAAGTGTACCTGCTGGACCAGCTGGAGCAGTTGAGAGTTGTGAAATCTGTCAAGAACAATTTGAACAATACTGGGATGAAGAAGAGGAGGAATGGCATTTGAAAAATGCTATTAGAGTAGATGGAAAGATTTATCATCCATCATGTTATGAAGATTATCAAAATACATCTTCATTTGATTGTACACCATCTCCCAGCAAGACACCAGTTGAAAACCCCTTGAATATTATGTTGAACATTGTCAAAAACGAATTGCAGGAACCCTGTGACAGTCCCAAAGTTAAGGAAGAACGAATTGATACACCACCAGCTTGTACAGAGGAAAGCATAGCAACACCCTCTGAAATTAAAACAGAAAATGACACAGTCGAGTCAGTTTAA

Forward (1236-1256: 20 bp) Tm: 60.03

CGATGGCAAAGATGATGATG

Reverse（1403-1423: 20 bp）Tm: 60.05

TCGATCTCCCTGGTTTTGTC

Product: 188 bp

produced by Primer3 (version 0.4.0)

GRCh38.p13 (Ensemble Genome Browser: release 100)