**SMARCA2 ENSG00000080503**

**4773 nt**

ATGTCCACGCCCACAGACCCTGGTGCGATGCCCCACCCAGGGCCTTCGCCGGGGCCTGGGCCTTCCCCTGGGCCAATTCTTGGGCCTAGTCCAGGACCAGGACCATCCCCAGGTTCCGTCCACAGCATGATGGGGCCAAGTCCTGGACCTCCAAGTGTCTCCCATCCTATGCCGACGATGGGGTCCACAGACTTCCCACAGGAAGGCATGCATCAAATGCATAAGCCCATCGATGGTATACATGACAAGGGGATTGTAGAAGACATCCATTGTGGATCCATGAAGGGCACTGGTATGCGACCACCTCACCCAGGCATGGGCCCTCCCCAGAGTCCAATGGATCAACACAGCCAAGGTTATATGTCACCACACCCATCTCCATTAGGAGCCCCAGAGCACGTCTCCAGCCCTATGTCTGGAGGAGGCCCAACTCCACCTCAGATGCCACCAAGCCAGCCGGGGGCCCTCATCCCAGGTGATCCGCAGGCCATGAGCCAGCCCAACAGAGGTCCCTCACCTTTCAGTCCTGTCCAGCTGCATCAGCTTCGAGCTCAGATTTTAGCTTATAAAATGCTGGCCCGAGGCCAGCCCCTCCCCGAAACGCTGCAGCTTGCAGTCCAGGGGAAAAGGACGTTGCCTGGCTTGCAGCAACAACAGCAGCAGCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAACAGCAGCCGCAGCAGCAGCCGCCGCAACCACAGACGCAGCAACAACAGCAGCCGGCCCTTGTTAACTACAACAGACCATCTGGCCCGGGGCCGGAGCTGAGCGGCCCGAGCACCCCGCAGAAGCTGCCGGTGCCCGCGCCCGGCGGCCGGCCCTCGCCCGCGCCCCCCGCAGCCGCGCAGCCGCCCGCGGCCGCAGTGCCCGGGCCCTCAGTGCCGCAGCCGGCCCCGGGGCAGCCCTCGCCCGTCCTCCAGCTGCAGCAGAAGCAGAGCCGCATCAGCCCCATCCAGAAACCGCAAGGCCTGGACCCCGTGGAAATTCTGCAAGAGCGGGAATACAGACTTCAGGCCCGCATAGCTCATAGGATACAAGAACTGGAAAATCTGCCTGGCTCTTTGCCACCAGATTTAAGAACCAAAGCAACCGTGGAACTAAAAGCACTTCGGTTACTCAATTTCCAGCGTCAGCTGAGACAGGAGGTGGTGGCCTGCATGCGCAGGGACACGACCCTGGAGACGGCTCTCAACTCCAAAGCATACAAACGGAGCAAGCGCCAGACTCTGAGAGAAGCTCGCATGACCGAGAAGCTGGAGAAGCAGCAGAAGATTGAGCAGGAGAGGAAACGCCGTCAGAAACACCAGGAATACCTGAACAGTATTTTGCAACATGCAAAAGATTTTAAGGAATATCATCGGTCTGTGGCCGGAAAGATCCAGAAGCTCTCCAAAGCAGTGGCAACTTGGCATGCCAACACTGAAAGAGAGCAGAAGAAGGAGACAGAGCGGATTGAAAAGGAGAGAATGCGGCGACTGATGGCTGAAGATGAGGAGGGTTATAGAAAACTGATTGATCAAAAGAAAGACAGGCGTTTAGCTTACCTTTTGCAGCAGACCGATGAGTATGTAGCCAATCTGACCAATCTGGTTTGGGAGCACAAGCAAGCCCAGGCAGCCAAAGAGAAGAAGAAGAGGAGGAGGAGGAAGAAGAAGGCTGAGGAGAATGCAGAGGGTGGGGAGTCTGCCCTGGGACCGGATGGAGAGCCCATAGATGAGAGCAGCCAGATGAGTGACCTCCCTGTCAAAGTGACTCACACAGAAACCGGCAAGGTTCTGTTCGGACCAGAAGCACCCAAAGCAAGTCAGCTGGACGCCTGGCTGGAAATGAATCCTGGTTATGAAGTTGCCCCTAGATCTGACAGTGAAGAGAGTGATTCTGATTATGAGGAAGAGGATGAGGAAGAAGAGTCCAGTAGGCAGGAAACCGAAGAGAAAATACTCCTGGATCCAAATAGCGAAGAAGTTTCTGAGAAGGATGCTAAGCAGATCATTGAGACAGCTAAGCAAGACGTGGATGATGAATACAGCATGCAGTACAGTGCCAGGGGCTCCCAGTCCTACTACACCGTGGCTCATGCCATCTCGGAGAGGGTGGAGAAACAGTCTGCCCTCCTAATTAATGGGACCCTAAAGCATTACCAGCTCCAGGGCCTGGAATGGATGGTTTCCCTGTATAATAACAACTTGAACGGAATCTTAGCCGATGAAATGGGGCTTGGAAAGACCATACAGACCATTGCACTCATCACTTATCTGATGGAGCACAAAAGACTCAATGGCCCCTATCTCATCATTGTTCCCCTTTCGACTCTATCTAACTGGACATATGAATTTGACAAATGGGCTCCTTCTGTGGTGAAGATTTCTTACAAGGGTACTCCTGCCATGCGTCGCTCCCTTGTCCCCCAGCTACGGAGTGGCAAATTCAATGTCCTCTTGACTACTTATGAGTATATTATAAAAGACAAGCACATTCTTGCAAAGATTCGGTGGAAATACATGATAGTGGACGAAGGCCACCGAATGAAGAATCACCACTGCAAGCTGACTCAGGTCTTGAACACTCACTATGTGGCCCCCAGAAGGATCCTCTTGACTGGGACCCCGCTGCAGAATAAGCTCCCTGAACTCTGGGCCCTCCTCAACTTCCTCCTCCCAACAATTTTTAAGAGCTGCAGCACATTTGAACAATGGTTCAATGCTCCATTTGCCATGACTGGTGAAAGGGTGGACTTAAATGAAGAAGAAACTATATTGATCATCAGGCGTCTACATAAGGTGTTAAGACCATTTTTACTAAGGAGACTGAAGAAAGAAGTTGAATCCCAGCTTCCCGAAAAAGTGGAATATGTGATCAAGTGTGACATGTCAGCTCTGCAGAAGATTCTGTATCGCCATATGCAAGCCAAGGGGATCCTTCTCACAGATGGTTCTGAGAAAGATAAGAAGGGGAAAGGAGGTGCTAAGACACTTATGAACACTATTATGCAGTTGAGAAAAATCTGCAACCACCCATATATGTTTCAGCACATTGAGGAATCCTTTGCTGAACACCTAGGCTATTCAAATGGGGTCATCAATGGGGCTGAACTGTATCGGGCCTCAGGGAAGTTTGAGCTGCTTGATCGTATTCTGCCAAAATTGAGAGCGACTAATCACCGAGTGCTGCTTTTCTGCCAGATGACATCTCTCATGACCATCATGGAGGATTATTTTGCTTTTCGGAACTTCCTTTACCTACGCCTTGATGGCACCACCAAGTCTGAAGATCGTGCTGCTTTGCTGAAGAAATTCAATGAACCTGGATCCCAGTATTTCATTTTCTTGCTGAGCACAAGAGCTGGTGGCCTGGGCTTAAATCTTCAGGCAGCTGATACAGTGGTCATCTTTGACAGCGACTGGAATCCTCATCAGGATCTGCAGGCCCAAGACCGAGCTCACCGCATCGGGCAGCAGAACGAGGTCCGGGTACTGAGGCTCTGTACCGTGAACAGCGTGGAGGAAAAGATCCTCGCGGCCGCAAAATACAAGCTGAACGTGGATCAGAAAGTGATCCAGGCGGGCATGTTTGACCAAAAGTCTTCAAGCCACGAGCGGAGGGCATTCCTGCAGGCCATCTTGGAGCATGAGGAGGAAAATGAGGAAGAAGATGAAGTACCGGACGATGAGACTCTGAACCAAATGATTGCTCGACGAGAAGAAGAATTTGACCTTTTTATGCGGATGGACATGGACCGGCGGAGGGAAGATGCCCGGAACCCGAAACGGAAGCCCCGTTTAATGGAGGAGGATGAGCTGCCCTCCTGGATCATTAAGGATGACGCTGAAGTAGAAAGGCTCACCTGTGAAGAAGAGGAGGAGAAAATATTTGGGAGGGGGTCCCGCCAGCGCCGTGACGTGGACTACAGTGACGCCCTCACGGAGAAGCAGTGGCTAAGGGCCATCGAAGACGGCAATTTGGAGGAAATGGAAGAGGAAGTACGGCTTAAGAAGCGAAAAAGACGAAGAAATGTGGATAAAGATCCTGCAAAAGAAGATGTGGAAAAAGCTAAGAAGAGAAGAGGCCGCCCTCCCGCTGAGAAACTGTCACCAAATCCCCCCAAACTGACAAAGCAGATGAACGCTATCATCGATACTGTGATAAACTACAAAGATAGGTGTAACGTGGAGAAGGTGCCCAGTAATTCTCAGTTGGAAATAGAAGGAAACAGTTCAGGGCGACAGCTCAGTGAAGTCTTCATTCAGTTACCTTCAAGGAAAGAATTACCAGAATACTATGAATTAATTAGGAAGCCAGTGGATTTCAAAAAAATAAAGGAAAGGATTCGTAATCATAAGTACCGGAGCCTAGGCGACCTGGAGAAGGATGTCATGCTTCTCTGTCACAACGCTCAGACGTTCAACCTGGAGGGATCCCAGATCTATGAAGACTCCATCGTCTTACAGTCAGTGTTTAAGAGTGCCCGGCAGAAAATTGCCAAAGAGGAAGAGAGTGAGGATGAAAGCAATGAAGAGGAGGAAGAGGAAGATGAAGAAGAGTCAGAGTCCGAGGCAAAATCAGTCAAGGTGAAAATTAAGCTCAATAAAAAAGATGACAAAGGCCGGGACAAAGGGAAAGGCAAGAAAAGGCCAAATCGAGGAAAAGCCAAACCTGTAGTGAGCGATTTTGACAGCGATGAGGAGCAGGATGAACGTGAACAGTCAGAAGGAAGTGGGACGGATGATGAGTGA

Forward (3426-3446: 20 bp) Tm: 59.98

CATCTTTGACAGCGACTGGA

Reverse（3569-3589: 20 bp）Tm: 59.98

TCTGATCCACGTTCAGCTTG

Product: 164 bp

produced by Primer3 (version 0.4.0)

GRCh38.p13 (Ensemble Genome Browser: release 100)