**BRWD1 ENSG00000185658**

**6600 nt**

ATGGCGGAGCCGTCGTCCGCCCGACGCCCGGTGCCTCTCATCGAGTCGGAGCTGTACTTCCTTATCGCCCGGTACCTATCGGCGGGCCCGTGTCGGAGAGCGGCCCAGGTGCTGGTGCAGGAGCTGGAGCAGTACCAGTTGTTGCCGAAGAGATTGGACTGGGAGGGCAACGAGCACAACAGGAGCTACGAGGAGTTGGTCTTGTCCAATAAGCATGTGGCTCCTGATCATCTTTTGCAAATCTGCCAGCGCATCGGTCCTATGTTGGATAAAGAAATTCCACCCAGTATTTCAAGAGTCACTTCTTTACTTGGTGCAGGAAGGCAGTCTTTGCTACGTACAGCAAAAGACTGCAGGCACACAGTTTGGAAGGGCTCTGCCTTTGCTGCTCTTCATAGAGGAAGACCTCCTGAAATGCCAGTGAATTATGGTTCCCCACCAAATCTTGTGGAGATACATCGAGGAAAACAACTCACAGGGTGTTCCACTTTTAGTACAGCATTTCCAGGAACTATGTATCAGCATATAAAAATGCACAGAAGGATTCTCGGACATCTATCTGCTGTTTACTGTGTAGCATTTGATAGGACAGGACATAGAATCTTTACAGGTTCAGATGACTGTTTGGTAAAGATTTGGTCAACACATAATGGCCGCTTGTTATCTACATTAAGAGGTCATTCTGCAGAAATTTCAGATATGGCAGTAAACTATGAGAATACAATGATTGCTGCGGGGAGCTGTGATAAAATTATTAGAGTGTGGTGCTTGAGAACTTGTGCCCCAGTTGCTGTGCTCCAAGGACACACAGGATCAATTACATCTTTACAGTTTAGCCCGATGGCCAAAGGCTCTCAAAGATACATGGTTTCCACTGGTGCTGATGGGACAGTTTGCTTTTGGCAATGGGATTTAGAATCCTTAAAATTTAGCCCACGTCCCCTGAAGTTCACTGAAAAGCCTAGGCCAGGCGTTCAAATGCTTTGTTCTTCTTTTAGTGTTGGTGGTATGTTTTTAGCCACAGGTAGTACTGATCATGTAATCAGAATGTATTTTTTGGGTTTTGAAGCACCCGAAAAAATCGCAGAACTTGAAAGCCACACTGATAAAGTAGATAGTATCCAATTTTGTAACAATGGTGATCGGTTCCTAAGTGGTAGCAGAGATGGAACAGCACGGATTTGGAGATTTGAGCAGTTAGAATGGAGGAGCATTTTATTGGATATGGCTACCAGAATCTCAGGGGACTTATCTTCCGAAGAGGAAAGGTTTATGAAACCTAAAGTAACAATGATAGCTTGGAATCAAAATGATAGCATTGTTGTCACAGCTGTGAATGATCATGTCCTCAAAGTGTGGAATTCTTACACTGGACAACTGCTTCATAACTTAATGGGACATGCTGATGAAGTATTTGTTCTGGAGACACATCCCTTTGATTCCAGAATTATGTTATCTGCAGGACATGATGGCAGCATATTTATATGGGATATTACAAAAGGTACCAAGATGAAACATTATTTTAATATGATTGAAGGACAAGGACATGGAGCTGTGTTTGACTGTAAGTTTTCACAGGATGGACAGCATTTTGCCTGTACAGATTCTCATGGGCACCTTCTGATATTTGGTTTTGGATGCAGCAAACCATATGAAAAGATTCCTGATCAGATGTTCTTCCATACTGACTATCGACCACTTATTAGAGATTCTAATAATTATGTCTTAGATGAGCAAACTCAGCAGGCTCCTCATCTTATGCCTCCACCATTCTTGGTAGATGTAGATGGAAATCCTCATCCAACCAAGTATCAGAGATTAGTACCAGGCCGAGAAAATTCTGCAGATGAACATTTGATTCCACAGCTGGGCTATGTGGCAACAAGTGATGGAGAGGTGATTGAACAAATTATAAGCCTGCAAACCAATGATAATGATGAACGCAGCCCAGAATCGAGTATTCTTGATGGAATGATAAGACAGTTGCAGCAGCAGCAAGATCAGAGAATGGGAGCAGATCAGGATACTATTCCAAGAGGACTTTCAAATGGTGAAGAAACACCCCGGAGAGGTTTTAGAAGGCTGAGCTTAGACATTCAGTCCCCTCCAAATATTGGTCTGCGTCGTAGTGGACAAGTTGAAGGTGTTCGTCAGATGCATCAAAACGCTCCACGCAGTCAGATTGCTACAGAACGTGACCTGCAGGCTTGGAAACGAAGAGTGGTTGTACCAGAGGTACCACTAGGCATATTTAGGAAGCTGGAAGACTTCCGATTAGAGAAAGGTGAAGAGGAAAGAAATCTTTATATAATAGGAAGAAAAAGAAAGACTCTTCAGCTCTCACATAAGTCGGATTCAGTGGTTTTGGTATCACAGTCTAGACAAAGGACATGTAGGCGTAAATATCCAAATTATGGTAGAAGAAATCGTAGCTGGCGTGAGTTATCTTCTGGAAATGAGTCTTCAAGCTCTGTAAGACATGAGACTTCCTGTGATCAGAGTGAAGGTTCTGGTTCTTCAGAAGAGGATGAATGGAGAAGTGACAGAAAAAGTGAGAGTTACAGCGAAAGTTCAAGTGACTCTTCATCTAGATATTCCGATTGGACAGCTGATGCGGGCATCAATTTGCAGCCTCCTTTAAGAACATCATGTCGTCGACGAATTACTCGATTTTGTAGTAGTTCAGAAGATGAAATATCTACTGAGAATTTATCTCCTCCAAAAAGAAGACGAAAGAGAAAGAAAGAAAATAAGCCTAAGAAGGAGAATTTGCGGAGGATGACTCCAGCAGAGCTTGCAAATATGGAGCATTTATATGAATTTCACCCTCCAGTTTGGATTACTGACACCACACTTAGAAAATCTCCTTTTGTTCCTCAAATGGGTGATGAGGTAATATATTTTCGACAGGGTCATGAAGCTTATATTGAGGCTGTAAGAAGAAATAATATTTATGAACTGAACCCTAATAAGGAGCCATGGAGAAAAATGGATCTTAGGGATCAAGAATTGGTTAAAATAGTTGGAATACGATATGAAGTTGGGCCCCCTACACTCTGTTGCCTAAAACTAGCATTTATAGATCCAGCAACTGGAAAACTTATGGACAAATCTTTCTCTATTAGATATCATGATATGCCAGATGTTATTGACTTTCTTGTATTGCGTCAATTTTATGATGAAGCAAGACAGAGGAATTGGCAGTCTTGTGACAGATTCCGCTCTATTATTGATGATGCTTGGTGGTTTGGAACAGTGTTAAGTCAAGAGCCATATCAACCACAGTATCCTGATAGTCATTTCCAGTGTTATATTGTTAGGTGGGATAATACTGAAATTGAAAAACTTAGCCCATGGGACATGGAACCAATTCCTGATAATGTTGATCCACCTGAAGAATTAGGAGCTAGTATTTCTGTCACAACAGATGAGCTAGAGAAATTGCTCTATAAACCACAAGCTGGTGAATGGGGTCAGAAATCAAGAGATGAAGAATGTGATAGAATTATCAGTGGTATAGATCAACTTTTGAATCTTGATATAGCAGCAGCTTTTGCAGGCCCTGTTGATTTGTGTACATACCCGAAGTACTGTACTGTAGTAGCTTATCCAACCGATCTTTACACAATTCGAATGAGACTTGTTAATCGATTTTACAGGAGGCTGTCTGCGTTAGTTTGGGAAGTCAGATATATAGAACATAATGCCAGAACATTTAACGAACCTGAGAGTGTAATTGCAAGATCAGCTAAAAAGATAACTGACCAACTTTTAAAATTTATCAAGAATCAACACTGTACAAATATCTCAGAACTTTCTAACACATCTGAAAATGATGAGCAAAATGCTGAGGATTTGGATGATAGTGATCTTCCTAAAACATCTTCTGGAAGGAGGAGAGTCCATGATGGGAAAAAAAGCATCAGAGCTACGAACTATGTTGAAAGCAACTGGAAGAAACAGTGTAAGGAACTAGTGAACTTAATTTTTCAGTGTGAAGATTCTGAACCATTTAGACAACCTGTTGATTTGGTTGAATATCCAGACTACAGAGATATTATAGATACCCCAATGGATTTTGGAACAGTAAGGGAAACTCTAGATGCGGGAAATTATGACAGCCCTTTGGAGTTTTGCAAAGACATCCGGCTGATATTTAGCAATGCAAAAGCGTATACACCAAACAAAAGATCAAAGATTTATAGTATGACCTTGAGATTATCTGCCTTATTTGAAGAAAAAATGAAGAAAATCTCTTCTGATTTTAAAATTGGTCAAAAATTCAATGAAAAACTTCGAAGAAGCCAGAGGTTCAAGCAACGGCAAAATTGTAAAGGTGACAGTCAGCCTAACAAAAGTATCAGAAACCTCAAGCCGAAGAGGTTAAAATCTCAGACAAAAATAATTCCTGAGTTGGTAGGTTCTCCTACCCAGTCTACCTCAAGTAGGACAGCTTATCTTGGAACCCACAAGACAAGTGCTGGTATCTCTTCAGGTGTTACTTCTGGTGACTCTTCAGATTCAGCAGAATCATCAGAAAGGAGGAAAAGAAATAGACCTATAACAAATGGTTCTACATTATCTGAAAGTGAAGTGGAAGATTCTTTAGCTACCTCTTTGTCATCGTCAGCTTCCAGTAGTTCTGAGGAAAGCAAAGAGAGTTCCAGAGCTCGTGAATCCTCCTCACGCAGTGGGCTATCCAGAAGCAGCAATCTCAGGGTAACCAGAACTAGAGCTGCTCAAAGAAAAACTGGTCCCGTTTCATTAGCAAATGGATGTGGCAGAAAAGCCACTCGAAAGAGAGTCTATTTAAGTGATTCTGATAACAATTCATTGGAGACTGGTGAAATTCTAAAAGCCAGAGCTGGAAATAACCGAAAAGTCTTAAGGAAGTGTGCTGCTGTGGCTGCCAATAAAATAAAGCTAATGAGTGATGTAGAAGAGAATTCTAGCTCTGAAAGTGTCTGTTCTGGTCGGAAGCTGCCTCACCGCAATGCTTCTGCTGTAGCTAGAAAAAAGTTATTACATAATTCTGAAGATGAACAGAGCTTAAAGTCAGAAATTGAAGAAGAGGAGCTAAAAGATGAAAATCAACTATTACCAGTGTCCAGTTCTCACACTGCCCAGAGCAATGTTGATGAATCTGAAAACAGAGACTCAGAGTCAGAAAGTGATTTGCGGGTAGCCCGGAAAAATTGGCATGCTAATGGTTACAAGTCCCATACTCCAGCACCTTCAAAGACAAAATTTCTTAAAATAGAGTCTTCTGAGGAAGACTCTAAAAGTCATGATTCAGATCATGCATGTAACAGAACTGCTGGCCCATCAACGTCTGTGCAGAAACTTAAGGCAGAGAGCATCTCAGAGGAAGCAGATTCTGAACCAGGAAGATCTGGTGGTAGGAAATACAATACATTTCACAAGAATGCGAGTTTCTTTAAAAAAACCAAGATTCTGAGTGACTCAGAAGACTCTGAATCTGAAGAGCAAGATAGAGAAGATGGGAAATGTCATAAAATGGAAATGAACCCAATTTCAGGAAATCTGAACTGTGACCCTATTGCTATGTCCCAGTGTTCCTCAGATCATGGATGTGAAACTGATTTAGATTCAGATGATGACAAAATAGAAAAACCAAACAATTTTATGAAAGATTCTGCATCACAAGACAATGGACTAAGCAGAAAAATTTCCAGGAAAAGGGTCTGTTCCAGTGACTCAGACAGTAGTTTACAGGTGGTTAAGAAATCATCAAAAGCCAGAACAGGTCTCCTGAGGATTACTCGAAGATGTGCAGCTACGGCTGCCAATAAGATCAAGCTCATGAGTGATGTAGAAGATGTCAGTTTAGAAAATGTGCACACTAGAAGCAAAAATGGAAGGAAAAAACCTCTCCATCTTGCTTGTACTACAGCTAAGAAGAAATTGAGTGATTGTGAAGGAAGTGTACATTGTGAAGTACCAAGTGAACAGTATGCCTGTGAAGGCAAGCCACCTGATCCTGACTCCGAAGGTAGTACAAAAGTGCTTAGTCAGGCTCTAAATGGAGACTCAGACTCTGAAGATATGTTGAATTCAGAACACAAGCACAGGCATACCAATATTCACAAAATAGATGCACCTTCTAAAAGAAAAAGTTCCTCTGTTACATCTTCAGGAGAAGATTCAAAAAGTCATATTCCAGGGAGTGAGACTGATAGGACATTTTCTTCAGAGTCAACCTTGGCACAAAAAGCTACTGCAGAGAATAATTTTGAAGTGGAACTGAATTATGGGCTGCGCAGGTGGAATGGCAGAAGACTCAGGACCTATGGAAAGGCTCCTTTTAGTAAGACAAAAGTGATTCATGATTCACAGGAAACAGCAGAGAAGGAAGTAAAAAGGAAGAGATCGCATCCTGAATTGGAAAATGTGAAAATCTCTGAAACAACTGGGAATTCAAAGTTTAGACCTGATACTAGTTCCAAATCATCAGATTTGGGATCTGTAACTGAATCAGATATTGACTGTACTGATAATACAAAAACCAAAAGGAGGAAAACGAAAGGAAAAGCAAAAGTAGTTAGAAAAGACAAAACCTTTTCTCCTGTGTATCTTTGA

Forward (42-62: 20 bp) Tm: 60.01

CGAGTCGGAGCTGTACTTCC

Reverse（179-199: 20 bp）Tm: 60.01

CCAACTCCTCGTAGCTCCTG

Product: 158 bp

produced by Primer3 (version 0.4.0)

GRCh38.p13 (Ensemble Genome Browser: release 100)