



RBCK1 (NM_031229.4) - cDNA - 2026-07-12

ACTTTCACTT TCTCTTCCGC CGAAGCCGCT CCCCTTGCGA AGAACTGGGG -410 [c.ex1_ex4del](#)
CCTCCCGGGA GGAGAGAGGG CTTTGCCTTG AAACCCGGGA CGCCAGGGGC -360
GCTCCCGCAA GTGGGGGTCC TCCGGGACTT GGAACGCCCC GGCTGGGTGG -310
TGTCCGGGCG TCCTTTCCCC GCTTCTTCCC ACCTCGGCTG GTCCCGTTTC -260
CTCCTGCGCC CAGTGC GGAC CTGTCTCGGC GCCCGCTGCC CTCTCACCGC -210
CCCACGCAGG ATCCCGGCCT GGTCAACGGG CAGTGTGATG CTTCCCGACT -160
GCCGCGGGGA CAGCGAGGCA CACACAGGGC TTGGGCGCG CCGGAGGCCA -110
CACGGCCTGG CTGAGTTGCT CCTGGTCTCC CGCCTCTCCC AGGCGACCCG -60
GAGGTAGCAT TTCCAGGAG GCACGGTCCC CCCAGGGGG ATGGGCACAG -10
CCACGCCAGA **TGGACGAGAA** GACCAAGAAA GCAGAGGAAA TGGCCCTGAG 41
CCTCACCCGA GCAGTGGCGG GCGGGGATGA ACAGGTGGCA ATGAAGTGTG 91 [c.52G>C](#)
CCATCTGGCT GGCAGAGCAA CGGGTGCCC TGAGTGTGCA ACTGAAGCCT 141 [L41fsX7](#)
GAGGTCTCCC CAACGCAGGA CATCAGGCTG TGGGTGAGCG TGGAGGATGC 191
TCAGATGCAC ACCGTCACCA TCTGGCTCAC AGTGCGCCCT GATATGACAG 241
TGGCGTCTCT CAAGGACATG GTTTTTCTGG ACTATGGCTT CCCACCAGTC 291
TTGCAGCAGT GGGTGATTGG GCAGCGGCTG GCACGAGACC AGGAGACCCT 341
GCAC'TCCCAT GGGGTGCGGC AGAATGGGA CAGTGCCCTAC CTCTATCTGC 391 [N122H](#)
TGTCAGCCCG CAACACCTCC CTCAACCCTC AGGAGCTGCA GCGGGAGCGG 441
CAGCTGCGGA TGCTGGAAGA TCTGGGCTTC AAGGACCTCA CGCTGCAGCC 491 [c.456+1G>C](#)
GCGGGGCCCT CTGGAGCCAG GCCCCCCAAA GCCCGGGGTC CCCAGGAAC 541 [c.494delG](#)
CCGGACGGGG GCAGCCAGAT GCAGTGCCTG AGCCCCCACC GGTGGGCTGG 591 [Q185X](#)
CAGTGCCCGG GGTGCACCTT CATCAACAAG CCCACGCGGC CTGGCTGTGA 641

GATGTGCTGC CGGGCGCGCC CCGAGGCCCTA CCAGGTCCCC GCCTCATAC 691 [Q231sfs*45](#)
AGCCCGACGA GGAGGAGCGA GCGCGCCTGG CGGGCGAGGA GGAGGCGCTG 741 [P190fs](#) [c.722del](#) [c.727_728insGGCG](#) [c.727G>T](#)
CGTCAGTACC AGCAGCGGAA GCAGCAGCAG CAGGAGGGGA ACTACCTGCA 791 [Q222X](#)
GCACGTCCAG CTGGACCAGA GGAGCCTGGT GCTGAACACG GAGCCCGCCG 841 [Q267*](#) [L273Pfs*27](#)
AGTGCCCCGT GTGCTACTCG GTGCTGGCGC CCGGCGAGGC CGTTGGTGCTG 891 [V295L](#)
CGTGAGTGTC TGCACACCTT CTGCAGGGAG TGCCTGCAGG GCACCATCCG 941 [c.896_899del](#) [C305F](#)
CAACAGCCAG GAGGCGGAGG TCTCCTGCCC CTTTATTGAC AACACCTACT 991 [A319V](#)
CGTGCTCGGG CAAGCTGCTG GAGAGGGAGA TCAAGGCGCT CCTGACCCCT 1041
GAGGATTACC AGCGATTTCT AGACCTGGGC ATCTCCATTG CTGAAAACCG 1091 [c.1054C>T](#)
CAGTGCC TTC AGCTACCATT GCAAGACCCC AGATTGCAAG GGATGGTGCT 1141
TCTTTGAGGA TGATGTCAAT GAGTTCACCT GCCCTGTGTG TTTCCACGTC 1191 [c.1160A>G](#)
AACTGCCTGC TCTGCAAGGC CATCCATGAG CAGATGAACT GCAAGGAGTA 1241
TCAGGAGGAC CTGGCCCTGC GGGCTCAGAA CGATGTGGCT GCCCGGCAGA 1291
CGACAGAGAT GCTGAAGGTG ATGCTGCAGC AGGGCGAGGC CATGCGCTGC 1341
CCCCAGTGCC AGATCGTGGT ACAGAAGAAG GACGGCTGCG ACTGGATCCG 1391
CTGCACCGTC TGCCACACCG AGATCTGCTG GGTACCAAG GGCCCACGCT 1441 [T470S](#) [E471K](#)
GGGGCCCTGG GGGCCCAGGA GACACCAGCG GGGGCTGCCG CTGCAGGGTA 1491 [T489Pfs*9](#)
AATGGGATTC CTTGCCACCC AAGCTGTGAG AACTGCCACT GAGCTAAAGA *8 [N508Pfs*4](#)
TGGTGGGGCC ACATGCTGAC CCAGCCCCAC ATCCACATTC TGTTAGAATG *58
TAGCTCAGGG AGCTTCGTGG ACGGCCTTGC TTGCTGTAGC GTTGTAGGGG *108
CCCTGCCTGC ACTGCGTTG TCCACGGTCA CATCTGCCCC AGTGCCTTTG *158
TCCTTCCCTT GGGGCTTGCC GGCCAGACTT CTCTCCCCTG CGGCTCCAC *208
CTCTGCCTGA CCCCAGCCTT AAACATAGCC CCTGGCCAGA GGCCTTGCTG *258
GGTGGAGCCT CTGTGTGACT CCATACTCCT CCCACCACAA CACTCATCTG *308
TCAAACACCA AGCACTCTCA GCCTCCCCGC CTTTCTGCTG CAGCTTTCTG *358
GGGCTAACTT CTCTGCCTTT GTGGTTGGAG GCCTGAGGCC TCTTGGAAGT *408
CTTGCTAACC TGTTTCTGAGC CAGGAAGGAG ACTGCACAGT TTTGAAAGCA *458
CAGCCCGTCA GGTCCGGCTC TCGTCTCCC TCTCTGCAGC CTGTGTAAGC *508

TATTATAATT AAAATGGTTT TCCGGGAAGG GATGAGTGTG ATGTCCTTGA *558
GAGGAAATGA ATGTCCTGGC CTGGGACTCT ACACACAGGC AGGATCCTGA *608
GGTCTCTGGG AACTGCATCA GAAAGTTGAC TTGTCAGTCC ATCTGTGGTA *658
GAATGAGGCT GTGACTGAGC ACTGGGACCT TTCTACCAGA TGTGGACCCC *708
ATGCCCAGCC TCAGGGGCAA GGATGCTCTT GGGTCACCGT CAGCCAGGAC *758
AGGTGGAGTG TGCAGTGTGT CAAGTCTGCA GAGAAGGATG GGCTTAGGGG *808
CGGGAGGGGA AGTCTTGCCA CTCCCTGCTCC CTTTTGACCT CTCAGCAGGC *858
ATCTAGGGTT GGCAGGTAGA TAGTTCAAGA AGGAACGAAG CTGCTGCAGT *908
TGAGGGGTGG GGTGTGCCAT CCTATTTTCT CGTCTCAAGC AAGATGGCAC *958
AGTATCGATT CAGCAGTATT TACTAGAACC CACTCTGTGC TGGTCGGAGG *1008
TTACTAAGAC AGGGTCCTGG GATGTTTATT CTCTAAGTCT TTCCTCCGCT *1058
CTGTGACCCA CCCTCCTTCC CCTTTTGAGA TCTGGTATTT GATGCCCAAC *1108
ACATTGTCCA CGCTGTGACG TGACCATCAT CATAGCAGGC AGAGGGCGCC *1158
TCTGCTGCTG AAGGCCTGTG ATTTTGTGGG GAAGGGCCTG TTCTAGCAAC *1208
TGAAAAGGCA CTGCCACCTG CCGTTGGATG CCAGGACTCA AGAGCTGGCC *1258
CCAGTCACTG TGCAGCAGAGC TGCTTGAGAA TGTGTGAGTG GACTGGGTCC *1308
TTCGGCACTG CCTGCATTGG CTCAGGGCAG TCAACCGTCG CAGAGGATGA *1358
GGGGCACACT CAGGCAGCCT CCCC GGCCCT GGAGGCAGAA AGGCCCAGGC *1408
AGAACCCTG ACTGGGAGGA AACAGAAAAA GCAGAGGAGA GCCAGGCTGC *1458
AGGCGTGTGG ATGGGACCAG CTCAGGCAGA CGCTGTCTCA TACCCACTCT *1508
CCCCCTCTTT GCCAGGGCCT GGCCCTGGTGT CTCTCAGGAG CCTGGGCATG *1558
AGACAAAAGC AGAGATTGTT CTCTTGTGGT ACCACAGGCT GTAACCAGTC *1608
CACCCAGTGT TGTTTTAGAA ATTTAAATCG GTTGCCCATC TTTTAAATT *1658
GGCAACATCG TTTACCACAT TAAAATCTAG ATGCCCTGCT TCTCTTGAAA *1708

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