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| Homo sapiens BCR, RhoGEF and GTPase activating protein (BCR), transcript variant 1, mRNA (NCBI Reference Sequence: NM\_004327.3) |
| (a) 1 ggggggaggg tggcggctcg atgggggagc cgcctccagg gggccccccc gccctgtgcc 61 cacggcgcgg cccctttaag aggcccgcct ggctccgtca tccgcgccgc ggccacctcc 121 ccccggccct ccccttcctg cggcgcagag tgcgggccgg gcgggagtgc ggcgagagcc 181 ggctggctga gcttagcgtc cgaggaggcg gcggcggcgg cggcggcacg gcggcggcgg 241 ggctgtgggg cggtgcggaa gcgagaggcg aggagcgcgc gggccgtggc cagagtctgg 301 cggcggcctg gcggagcgga gagcagcgcc cgcgcctcgc cgtgcggagg agccccgcac 361 acaatagcgg cgcgcgcagc ccgcgccctt ccccccggcg cgccccgccc cgcgcgccga 421 gcgccccgct ccgcctcacc tgccaccagg gagtgggcgg gcattgttcg ccgccgccgc 481 cgccgcgcgg gccatggggg ccgcccggcg cccggggccg ggctggcgag gcgccgcgcc 541 gccgctgaga cgggccccgc gcgcagcccg gcggcgcagg taaggccggc cgcgccatgg 601 tggacccggt gggcttcgcg gaggcgtgga aggcgcagtt cccggactca gagcccccgc 661 gcatggagct gcgctcagtg ggcgacatcg agcaggagct ggagcgctgc aaggcctcca 721 ttcggcgcct ggagcaggag gtgaaccagg agcgcttccg catgatctac ctgcagacgt 781 tgctggccaa ggaaaagaag agctatgacc ggcagcgatg gggcttccgg cgcgcggcgc 841 aggcccccga 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tcgtt**c**ggaa caccacctgg atacggctgc gctgcagacc**Song (1.2) \*1861 tccat**ggaga cgcagatggc tcgttcggaa caccacctgg atacggctgc gctgcagacc**Song (2) \*1861 tccat**ggaga cgcagatggc tcgttcggaa caccacctgg atacggctgc gctgcagacc**Ismail (2) \*1861** tcc**atggaga** **cgcaga*t*g**gc tcgttcggaa caccacctgg atacggctgc gctgcagacc1921 gggcagagga gcagcgccgg caccaagatg ggctgcccta cattgatgac tggccctcct 1981 catcgcccca cctcagcagc aagggcaggg gcagccggga tgc**g**ctggtc tcgggagccc 2041 tggagtccac taaagcgagt gagctggact tggaaaaggg cttggagatg agaaaatggg 2101 tcctgtcggg aatcctggct agcgaggaga cttacctgag ccacctggag gcactgctgc 2161 tgcccatgaa gcctttgaaa gccgctgcca ccacctctca gccggtgctg acgagtcagc 2221 agatcgagac catcttcttc aaagtgcctg agctctacga gatccacaag gagttctatg 2281 atgggctctt cccccgcgtg cagcagtgga gccaccagca gcgggtgggc gacctcttcc 2341 agaagctggc cagccagctg ggtgtgtacc gggccttcgt ggacaactac ggagttgcca 2401 tggaaatggc tgagaagtgc tgtcaggcca atgctcagtt tgcagaaatc tccgagaacc 2461 tgagagccag aagcaacaaa gatgccaagg 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aagtttccac acggtcctgc aggaggagag 5881 gatgcagctg cccagaggga agcaggatca catttaagga agtgtgtggg gtccctggat 5941 gacaccagca cccagtgcgg ctctgtctgg cacccgctcc caaggtggga ggagtgggtg 6001 tcccctgtgt gtcagtgggc agctcctgct gaacccgcag ctcactaggg agcctgacag 6061 tggggccatg cgcctgacac tcctctctgc ttgtggacct ggcaaggcag ggagcagaaa 6121 acagccactt gaaggctttc tgtctgcgtc tgtgtgcagt gtggatttag ttgtgctttt 6181 ttcttgctgg gagagcacag ccaccattta caagcagtgt caccgtcgtg ggtggcgagg 6241 acagaacagg agcctctgct ctctgtacct atctgggccc ggtgggctcc cttgtcctgg 6301 cttccatctc tgtctcagcg accattcagc cctgcgcagg aacacgtgtt gcttagaaaa 6361 gccaaatcca gccttgtctc tgcctcctct ggtctcatga tgtgcatctg ttaccttgaa 6421 actggaaacc agtctatcaa tgtctgtgcc aattttttat tccctcccca acctccttcc 6481 ccatacgact ttttatttat gtaggatgtg tgctgtctaa tgatgggatg accacacttt 6541 tccatgttct aaaagtgctc ctctcccgca gggtcccagg gctggtggtt gctttgggtc 6601 tacagctacg tcttacccac ctcctgcctc aacagcctgt gtggtggcaa agccggtgtg 6661 gggctgggga acgcagcgtt ctccaggagg gggacctggc tctccttctg caatgcaggc 6721 gaaggcctag atgccagtgt gacctcccac aaggcgtggc ttccagactc cccggccgga 6781 agtgatgctt ttttgccttg ggccctgggt ttgaagcagc ctggctttct cttggtaagt 6841 ggctggtgtc ttagcagctg caatctgagc tcagccacct acacaccacc gtggccgaca 6901 ctttcattaa aaagtttcct gagacga |
| Green highlighted sequence = sequence in exon 12 (3123 – 3198)Blue highlighted sequence = sequence in exon 13 (3199 – 3303)Grey highlighted sequence = sequence in exon 14 (3304 – 3378) | Green highlighted sequence = sequence in exon 1 (1 – 1875)Blue highlighted sequence = sequence in exon 2 (1876 – 2057) |
| Yellow highlighted sequence = the sequence (in-frame exon) that is lacking in variant 21. = used in first run; **(2)** = used in second run

***Italic*** = different nucleotide sequence was used in the study; ***~~Italic~~*** = nucleotide sequence was not used in the studyt, c, a, g = single nucleotide variant (**t, c, a, g** if frequency ≥1% (based on ExAC MAF)); x = nucleotides with insertion / deletion polymorphism [retrieved 18th - 28th November 2018 from NCBI <https://www.ncbi.nlm.nih.gov/variation/view/?q=BCR&filters=source%3Adbsnp&assm=GCF_000001405.26>. Location of nucleotides in transcript in reference to coding DNA was cross-checked (done for transcript nucleotide 597 and onwards) on 18th November 2018 from NCBIhttps://www.ncbi.nlm.nih.gov/projects/SNP/snp\_ref.cgi?geneId=613] |

Supplementary Figure 1. BCR primer sequence used in the studies for (a) M-BCR, (b) m-BCR, in reference to the *BCR* sequence transcript variant 1 NM\_004327.3 (retrieved 12th May 2018 from NCBI <https://www.ncbi.nlm.nih.gov/nuccore/NM_004327.3?report=genbank&to=6927>)