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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  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**Song (2) \*1801** ccaccatcgt gggcgtccgc aagaccgggc agatctggcc caacg**atggc** **gagggcgcct**  **Kosik \*1801** ccaccatcgt gggcgtccgc aagaccgggc agat**ctggcc** **caacgatggc** **ga**gggcgcct  1861 tccatggaga cgcagatggc 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 gctgcagacc  1921 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 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| 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 2   1. = 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 study  t, 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 NCBI  https://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>)