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| --- | --- |
| Homo sapiens ABL proto-oncogene 1, non-receptor tyrosine kinase (ABL1) | |
| Transcript variant a, mRNA (NCBI Reference Sequence: NM\_005157.5) | Transcript variant b, mRNA (NCBI Reference Sequence: NM\_007313.2) |
| (a)  1 ttaacaggcg cgtcccggcc aggcggagac gcggccgcgg ccatgggcgg gcgcgggcgc  61 gcggggcggc ggtgagggcg gctggcgggg ccgg**gggcgc cgggggggcg cgcg**ggccga  121 gccgggcctg agccgggccc gcggaccgag ctgggagagg gg**t**tccggcc cccgacgtgc  181 tggcgcggga aaatgttgga gatctgcctg aagctggtgg gctgcaaatc caagaagggg  **Bieurnax (c,f) \*181** tggcgcggga aaatgttgga gatctgcctg aagctggtg**g gctgcaaatc** **caagaagggg**  **Bose (c,f) \*181** tggcgcggga aaatg**ttgga** **gatct*g*cctg** **aag**ctggtgg gctgcaaatc caagaagggg  **Song (c,f1.1) \*181** tggcgcggga aaatgttgga g**atctgcctg** **aagctggtgg** **gct**gcaaatc caagaagggg  **Ismail (c,f) \*181** tggcgcggga aaatgttgga gatctgcctg aagctggtgg g**ctgcaaatc** **caagaagggg**  241 ctgtcctcgt cctccagctg ttatctggaa gaagcccttc agcggccagt agcatctgac  **Bieurnax (c,f) \*241** **ctgt**cctcgt cctccagctg ttatctggaa gaagcccttc agcggccagt agcatctgac  **Song (c,f1.3) \*241** ctgtcctcgt cctccagctg ttatctggaa gaagccctt**c agcggccagt** **agcatctgac**  **Ismail (c,f) \*241** **ctg**tcctcgt cctccagctg ttatctggaa gaagcccttc agcggccagt agcatctgac  301 tttgagcctc agggtctgag tgaagccgct cgttggaact ccaaggaaaa ccttctcgct  **Song (c,f1.3) \*301** **t**ttgagcctc agggtctgag tgaagccgct cgttggaact ccaaggaaaa ccttctcgct  **Song (c,f2.1) \*301** tttgagcctc agggtctg**a*g* tgaagccgct cgttggaact** **ccaa**ggaaaa ccttctcgct  **Song (c,f2.2) \*301** tttga**gcctc** **agggtctgag tgaagccgct** **cgttg**gaact ccaaggaaaa ccttctcgct  **Uckun (m 2) \*301** tttgagcctc ag**ggtctgag** **tgaagccgct** **cg**ttggaact ccaaggaaaa ccttctcgct  **Kosik \*301** t**ttgagcctc** **agggtctgag tg**aagccgct cgttggaact ccaaggaaaa ccttctcgct  361 ggacccagtg aaaatgaccc caaccttttc gttgcactgt atgattttgt ggccagtgga  **Bieurnax (2) \*361** ggacccagtg aaaatgaccc caacctttt**c** **gttgcactgt** **atgattttgt** **ggcc**agtgga  **Ravetto (2) \*361** ggacccagtg aaaatgaccc caaccttttc gttgc**actgt atgattttgt** **ggccagtgga**  **Song (2.1) \*361** ggacccagtg aaaatgaccc caaccttttc gttgcac**tgt** **atgatttt*g*t** **ggcca*g*tgga**  **Boquett (1) \*361** ggacccagtg aaaatgaccc caaccttttc gttgcactgt atg**attttgt** **ggccagtgga**  **Boquett (2) \*361** ggacccagtg aaaatgaccc caaccttttc gttgca**ctgt** **atgattttgt ggccagtgga**  **Ismail (m 2) \*361** ggacccagtg aaaatgaccc caaccttttc gttgcact**gt atgattttgt ggcc**agtgga  421 gataacactc taagcataac **t**aaaggtgaa aagctccggg tcttaggcta taatcacaat  **Bieurnax (1) \*421** gataacactc taagcataac taaaggtgaa aag**ctccggg** **tcttaggcta** **ta*a*tcac*a***at  **Ravetto (1) \*421** gataacactc taagcataac taaaggtgaa aag**ctccggg** **tcttaggcta taatcaca**at  **Hsu (2) \*421** gataacactc taagcataac taaaggtgaa aagctccggg tct**taggcta** **taatcacaat**  **Song (1.1) \*421** gataacactc taagcataac taaaggtgaa aagc**tccggg** **tcttaggcta taatca**caat  **Song (2.1) \*421** **gat**aacactc taagcataac taaaggtgaa aagctccggg tcttaggcta taatcacaat  **Song (2.2) \*421** gataacactc taagcataac taaaggt**gaa** **aagctccggg tcttaggcta** **taatcaca**at  **Boquett (1) \*421 g**ataacactc taagcataac taaaggtgaa aagctccggg tcttaggcta taatcacaat  **Boquett (2) \*421 g**ataacactc taagcataac taaaggtgaa aagctccggg tcttaggcta taatcacaat  **Uckun (m 1) \*421** gataacactc taagcataac taaaggtgaa aag**ctccggg tcttaggcta** **taatcaca**at  481 ggggaatggt gtgaagccca aaccaaaaat ggccaaggct gggtcccaag caactacatc  **Bose (2) \*481** ggggaatggt gtgaagccca aaccaaaaat ggccaaggct gggtc**ccaag** **caactacatc**  **Hsu (1) \*481** gg**ggaatggt gtgaagccca aac**caaaaat ggccaaggct gggtcccaag caactacatc  **Hsu (2) \*481** **ggggaa**tggt gtgaagccca aaccaaaaat ggccaaggct gggtcccaag caactacatc  **le Coutre (2) \*481** ggggaatggt gtgaagccca aaccaaaaat ggccaaggct gggtc**ccaag** **caactacatc**  **Song (1.2) \*481** gg**ggaatggt gtgaagccca aaccaaaaat gg**ccaaggct gggtcccaag caactacatc  **Ismail (1) \*481** ggggaatggt gtgaagccca aaccaaaaat ggccaaggct gggtc**ccaag** **caactacatc**  **Ismail (2) \*481** **ggggaatggt gtgaa**gccca aaccaaaaat ggccaaggct gggtcccaag caactacatc  541 acgccagtca acagtctgga gaaacactcc 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ccgaggctgc cccaggccgg agcccagata cgggggctgt gactctgggc agggacccgg  5281 ggtctcctgg accttgacag agcagctaac tccgagagca gtgggcaggt ggccgcccct  5341 gaggcttcac gccgggagaa gccaccttcc caccccttca taccgcctcg tgccagcagc  5401 ctcgcacagg ccctagcttt acgctcatca cctaaacttg tactttattt ttctgataga  5461 aatggtttcc tctggatcgt tttatgcggt tcttacagca catcacctct ttgcccccga  5521 cggctgtgac gcagccggag ggaggcacta gtcaccgaca gcggccttga agacagagca  5581 aagcgcccac ccaggtcccc cgactgcctg tctccatgag gtactggtcc cttccttttg  5641 ttaacgtgat gtgccactat attttacacg tatctcttgg tatgcatctt ttatagacgc  5701 tcttttctaa gtggcgtgtg catagcgtcc tgccctgccc cctcgggggc ctgtggtggc  5761 tccccctctg cttctcgggg tccagtgcat tttgtttctg tatatgattc tctgtggttt  5821 tttttgaatc caaatctgtc ctctgtagta ttttttaaat aaatcagtgt ttacattaga  5881 a |
| Green highlighted sequence = sequence in exon 1a, i.e. the sequence that is different between variant a and b (1 – 271)  Blue highlighted sequence = sequence in exon 2 (272 – 445)  Grey highlighted sequence = sequence in exon 3 (446 – 741) | Green highlighted sequence = sequence in exon 1b, i.e. the sequence that is different between variant a and b (1 – 575)  *Note: all the other primers not involving exon 1b were shown in Figure 6(a).* |
| 1. = used in first run; **(2)** = used in second run; **(c,f)** = nucleotide sequence used as control, forward in the study; **(c,r)** = nucleotide sequence used as control, reverse in the study; **(m)** = used in m-BCR   ***Italic*** = different nucleotide sequence was 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 (**x** if frequency ≥1% (based on ExAC MAF)) [retrieved 18th - 28th November 2018 from NCBI  <https://www.ncbi.nlm.nih.gov/variation/view/?q=ABL1&filters=source%3Adbsnp&assm=GCF_000001405.26>.  Location of nucleotides in transcript in reference to coding DNA was cross-checked on 18th November 2018 from NCBI  <https://www.ncbi.nlm.nih.gov/projects/SNP/snp_ref.cgi?geneId=25&ctg=NT_008470.20&mrna=NM_005157.5&prot=NP_005148.2&orien=forward>] | |

Supplementary Figure 2. Primer sequence used in the studies in reference to the ABL1 sequence (a) transcript variant a NM\_005157.5 (retrieved 24th October 2018 from NCBI <https://www.ncbi.nlm.nih.gov/nuccore/NM_005157.5>), (b) transcript variant b NM\_007313.2 (retrieved 14th May 2018 from NCBI <https://www.ncbi.nlm.nih.gov/nuccore/NM_007313>)