Supplementary Table 2. Other outcomes of the included studies

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| No | Article | Remarks |
| 1 | Biernaux C 1995[4] | * The relative amount of the *BCR-ABL*1 mRNA was ~5-20 copies/5 X 107 to 108 WBCs or greater. * **Validation results:** * **Direct sequencing:** likely only sequenced 1 sample as article stated:” (for 1 individual, this product was sequenced and shown a typical b3a2 junction)” * **Repeated in 2 independent labs:** unclear *(****Comments:*** *the result was not clear. Article did not report the no. of confirmed positive or negative of the no. of positive or negative sample send to each lab. Article just stated: “The results confirm the presence of bcr-ab1 RNA in 4 of 11 samples of normal adult individuals.”)* * **Types of transcript in positive subjects (after crosschecked with Biernaux 1996[10]):** b3a2 N=23, b2a2 N=2, b3a2 & b2a2 N=3 |
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| 2 | Bose S 1998[11] | * **Validation results (direct sequencing):** * **Types of transcript in M-BCR positive case:** all 4 had b2a2 &/or b3a2. 2 of 4 had additional co-expressed b4a2, b5a2 & e17a2. 3 of 4 co-expressed m-BCR. * **Types of transcript in m-BCR positive case** *(****Comments:*** *unsure article referred to subjects only or subjects & cell lines)***:** 74% of the transcripts had e1a2, but in 7 samples larger fragments were also observed, such as e2a2, e2a3, e1a3, e4a2, & e5a3 & fusions containing BCR &/or ABL intronic sequences in various rearrangements between e1 & a2. * **M-BCR positive subjects:** In 3 individuals, 2-3/10 cell aliquots yielded positive bands in >1/4 replicates. Another 1 subject had amplification products in 1/10 cell aliquots. |
| 3 | Uckun FM 1998[12] |  |
| 4 | Ravetto PF 2003[13] | * **Validation results (direct sequencing):** N=1, confirmed as m-BCR |
| 5 | Hsu H 2004[14] | * Amount of *BCR-ABL1* transcripts was 103 to 104 times less than those in the CML patients. |
| 6 | le Coutre P 2010[15] | * **Validation results (retested in different lab):** N=5, 1/5 was confirmed positive in another lab |
| 7 | Song J 2011[16] | * Frequency of PB cells containing M-BCR was approximately 10-4. * **Validation results (direct sequencing):** NR *(****Comments****: article only reported results for MLL PTD.)* |
| 8 | Zuna J 2011[17] |  |
| 9 | Boquett JA 2013[18] | * **Types of transcript in positive subjects:** both positive for b3a2 |
| 10 | Ismail SI 2014[19] | * **Types of transcript in M-BCR positive subjects** b3a2 N=10 & b2a2 N=9 * 3/4 children had the b2a2 transcripts, b3a2 transcripts were detected equally in males (N=5) & females (N=5), the b2a2 transcripts were detected in 7 males vs 2 females. |
| 11 | Kosik P 2017[22] | * **Validation results:**   Skorvaga M 2014[20]   * **Nested PCR:** NR * **Retested with BioRad CFX96:** N=15, 4/15 confirmed positive * **Retested in different lab:** positive sample N=18, 5/18 confirmed positive; negative sample N=2, 2/2 confirmed negative   Kosik P 2017[22]   * **Replicated qPCR verification run:** N=NR, just reported as 5% confirmed positive * **Direct sequencing:** unclear *(Comments: no. of sample for each fusion gene, TEL-AML1, MLL-AF4 & m-BCR NR. Total N=22. Article stated: “20 were found to contain he expected PFG sequence (i.e. sequence comprising the site of fusion gene), thus setting the sequencing validation rate to 20/22 (90.9%) (Supplementary Data 1). The remaining two probands could not be confirmed by sequencing due to the absence of PFG-specific sequences.”)* |

CB, umbilical cord blood; F, female; Hb, haemoglobin; M, male; mth, month(s); NB, newborn; NR, not reported; SD, standard deviation; TWC, total white cell count; yr, year(s)