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| **Supplementary Table 1. Primer sequences and concentrations for quantitative PCR.** | | |
| **Gene1** | **Sequence** | **Concentration** |
| *BCL2* | FW: ATGTGTGTGGAGAGCGTCAA  RV: ACAGTTCCACAAAGGCATCC | 300 nM |
| *BCL2L1* | FW: CTTGGATGGCCACTTACCTGAA  RV: GCTGCTGCATTGTTCCCATA | 300 nM |
| *BCL2L2* | FW: GCGGAGTTCACAGCTCTATAC  RV: AAAAGGCCCCTACAGTTACCA | 300 nM |
| *MCL1* | FW: GTAATAACACCAGTACGGACGG  RV: TCCCGAAGGTACCGAGAGAT | 300 nM |
| *BCL2A1* | FW: TTACAGGCTGGCTCAGGACT  RV: AGCACTCTGGACGTTTTGCT | 300 nM |
| *BCL2L10* | FW: GCCTTCATTTATCTCTGGACAC  RV: AAGGTGCTTTCCCTCAGTTC | 300 nM |
| *BAX* | FW: GAGCTGCAGAGGATGATTGC  RV: CAGCTGCCACTCGGAAAA | 300 nM |
| *BAK1* | FW: TGAGTACTTCACCAAGATTGCCA  RV: AGTCAGGCCATGCTGGTAGAC | 300 nM |
| *BOK* | FW: GCGATGAGCTGGAGATGATCC  RV: CTGCAGAGAAGATGTGGCCA | 300 nM |
| *BID* | FW: ATGGACCGTAGCATCCCTCC  RV: GTAGGTGCGTAGGTTCTGGT | 300 nM |
| *BCL2L11* | FW: ATGTCTGACTCTGACTCTCG  RV: CCTTGTGGCTCTGTCTGTAG | 300 nM |
| *BBC3* | FW: GACCTCAACGCACAGTACGAG  RV: AGGAGTCCCATGATGAGATTGT | 300 nM |
| *PMAIP1* | FW: CGCGCAAGAACGCTCAACC  RV: CACACTCGACTTCCAGCTCTGCT | 300 nM |
| *BIK* | FW: TCTGAAGAGGACCTGGACCCT  RV: GGCTCACGTCCATCTCGTC | 300 nM |
| *BAD* | FW: CACCAGCAGGAGCAGCCAAC  RV: CGACTCCGGATCTCCACAGC | 300 nM |
| *BMF* | FW: CCTCCTTCCCAATCGAGTCTG  RV: TCCATCTCTCCTGGGTGACT | 300 nM |
| *BNIP3* | FW: ATATGGGATTGGTCAAGTCGG  RV: CGCTCGTGTTCCTCATGCT | 300 nM |
| *BNIP3L* | FW: ACACCAGCAGGGACCATAGC  RV: TTTCTTCAAAGCCTCGACTTCC | 300 nM |
| *BECN1* | FW: TCTGAAGAGGACCTGGACCCT  RV: GGCTCACGTCCATCTCGTC | 300 nM |
| *HPRT1* | FW: GAACGTCTTGCTCGAGATGTGA  RV: TCCAGCAGGTCAGCAAAGAAT | 150 nM |
| *ACTB* | FW: AGGCCAACCGCGAGAAG  RV: ACAGCCTGGATAGCAACGTACA | 150 nM |

1Genes are reported according Human Genome Organisation (HUGO) Gene Nomenclature Committee (HGNC).

Abbreviations: FW, forward; RV, reverse.

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| **Supplementary Table 2. Expression of BCL2-related genes in AML cell lines1.** | | | | | | | | |
| Genes2 | **MOLM13 cells** | | **MV-4-11 cells** | | **Kasumi 1 cells** | | **OCI-AML3 cells** | |
| Mean | SD | Mean | SD | Mean | SD | Mean | SD |
| *BCL2* | 0.99 | 0.12 | 1.90 | 0.15 | 0.43 | 0.03 | 1.25 | 0.15 |
| *BCL2L1* | 0.45 | 0.06 | 0.79 | 0.08 | 2.60 | 0.53 | 1.09 | 0.09 |
| *BCL2L2* | 0.65 | 0.09 | 1.14 | 0.24 | 1.05 | 0.13 | 1.32 | 0.08 |
| *MCL1* | 0.74 | 0.05 | 0.91 | 0.04 | 0.94 | 0.06 | 1.60 | 0.28 |
| *BCL2A1* | 2.54 | 0.41 | 0.50 | 0.28 | 0.98 | 0.12 | 0.93 | 0.05 |
| *BCL2L10* | 0.47 | 0.24 | 3.81 | 0.80 | 0.72 | 0.23 | 0.88 | 0.23 |
| *BAX* | 1.09 | 0.11 | 1.78 | 0.01 | 0.75 | 0.15 | 0.70 | 0.05 |
| *BAK1* | 1.10 | 0.06 | 0.84 | 0.07 | 1.12 | 0.26 | 0.99 | 0.03 |
| *BOK* | 0.46 | 0.15 | 0.76 | 0.30 | 4.11 | 0.81 | 0.78 | 0.03 |
| *BID* | 0.95 | 0.11 | 0.76 | 0.03 | 0.87 | 0.12 | 1.61 | 0.17 |
| *BCL2L11* | 1.32 | 0.09 | 0.58 | 0.02 | 0.50 | 0.04 | 2.62 | 0.06 |
| *BBC3* | 2.24 | 0.12 | 2.69 | 0.28 | 0.11 | 0.01 | 1.56 | 0.09 |
| *PMAIP1* | 0.62 | 0.06 | 0.89 | 0.04 | 1.93 | 0.14 | 0.95 | 0.05 |
| *BIK* | 1.87 | 0.15 | 1.14 | 0.02 | 1.17 | 0.25 | 0.41 | 0.03 |
| *BAD* | 0.68 | 0.00 | 1.00 | 0.18 | 1.69 | 0.38 | 0.89 | 0.08 |
| *BMF* | 1.48 | 0.37 | 4.53 | 0.89 | 0.37 | 0.29 | 0.60 | 0.42 |
| *BNIP3* | 0.83 | 0.07 | 0.43 | 0.10 | 2.07 | 0.24 | 1.39 | 0.07 |
| *BNIP3L* | 0.85 | 0.12 | 0.93 | 0.11 | 0.62 | 0.08 | 2.06 | 0.10 |
| *BECN1* | 0.74 | 0.04 | 0.97 | 0.02 | 1.11 | 0.09 | 1.27 | 0.13 |

1*HPRT1* and *ACTB* were used as reference genes. Relative quantification values were calculated using the 2-ΔΔCT equation and the median of ΔCT from all cell lines was used as calibrator for each gene.

2Genes are reported according Human Genome Organisation (HUGO) Gene Nomenclature Committee (HGNC).

Abbreviations: SD. Standard deviation.