|  |
| --- |
| **Supplementary Table 1. Primer sequences and concentrations for quantitative PCR.** |
| **Gene1** | **Sequence** | **Concentration** |
| *BCL2* | FW: ATGTGTGTGGAGAGCGTCAARV: ACAGTTCCACAAAGGCATCC | 300 nM |
| *BCL2L1* | FW: CTTGGATGGCCACTTACCTGAARV: GCTGCTGCATTGTTCCCATA | 300 nM |
| *BCL2L2* | FW: GCGGAGTTCACAGCTCTATACRV: AAAAGGCCCCTACAGTTACCA | 300 nM |
| *MCL1* | FW: GTAATAACACCAGTACGGACGGRV: TCCCGAAGGTACCGAGAGAT | 300 nM |
| *BCL2A1* | FW: TTACAGGCTGGCTCAGGACTRV: AGCACTCTGGACGTTTTGCT | 300 nM |
| *BCL2L10* | FW: GCCTTCATTTATCTCTGGACACRV: AAGGTGCTTTCCCTCAGTTC | 300 nM |
| *BAX* | FW: GAGCTGCAGAGGATGATTGCRV: CAGCTGCCACTCGGAAAA | 300 nM |
| *BAK1* | FW: TGAGTACTTCACCAAGATTGCCARV: AGTCAGGCCATGCTGGTAGAC | 300 nM |
| *BOK* | FW: GCGATGAGCTGGAGATGATCCRV: CTGCAGAGAAGATGTGGCCA | 300 nM |
| *BID* | FW: ATGGACCGTAGCATCCCTCCRV: GTAGGTGCGTAGGTTCTGGT | 300 nM |
| *BCL2L11* | FW: ATGTCTGACTCTGACTCTCGRV: CCTTGTGGCTCTGTCTGTAG | 300 nM |
| *BBC3* | FW: GACCTCAACGCACAGTACGAGRV: AGGAGTCCCATGATGAGATTGT | 300 nM |
| *PMAIP1* | FW: CGCGCAAGAACGCTCAACCRV: CACACTCGACTTCCAGCTCTGCT | 300 nM |
| *BIK* | FW: TCTGAAGAGGACCTGGACCCTRV: GGCTCACGTCCATCTCGTC | 300 nM |
| *BAD* | FW: CACCAGCAGGAGCAGCCAACRV: CGACTCCGGATCTCCACAGC | 300 nM |
| *BMF* | FW: CCTCCTTCCCAATCGAGTCTGRV: TCCATCTCTCCTGGGTGACT | 300 nM |
| *BNIP3* | FW: ATATGGGATTGGTCAAGTCGGRV: CGCTCGTGTTCCTCATGCT | 300 nM |
| *BNIP3L* | FW: ACACCAGCAGGGACCATAGCRV: TTTCTTCAAAGCCTCGACTTCC | 300 nM |
| *BECN1* | FW: TCTGAAGAGGACCTGGACCCTRV: GGCTCACGTCCATCTCGTC | 300 nM |
| *HPRT1* | FW: GAACGTCTTGCTCGAGATGTGARV: TCCAGCAGGTCAGCAAAGAAT | 150 nM |
| *ACTB* | FW: AGGCCAACCGCGAGAAGRV: ACAGCCTGGATAGCAACGTACA | 150 nM |

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

Abbreviations: FW, forward; RV, reverse.

|  |
| --- |
| **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.