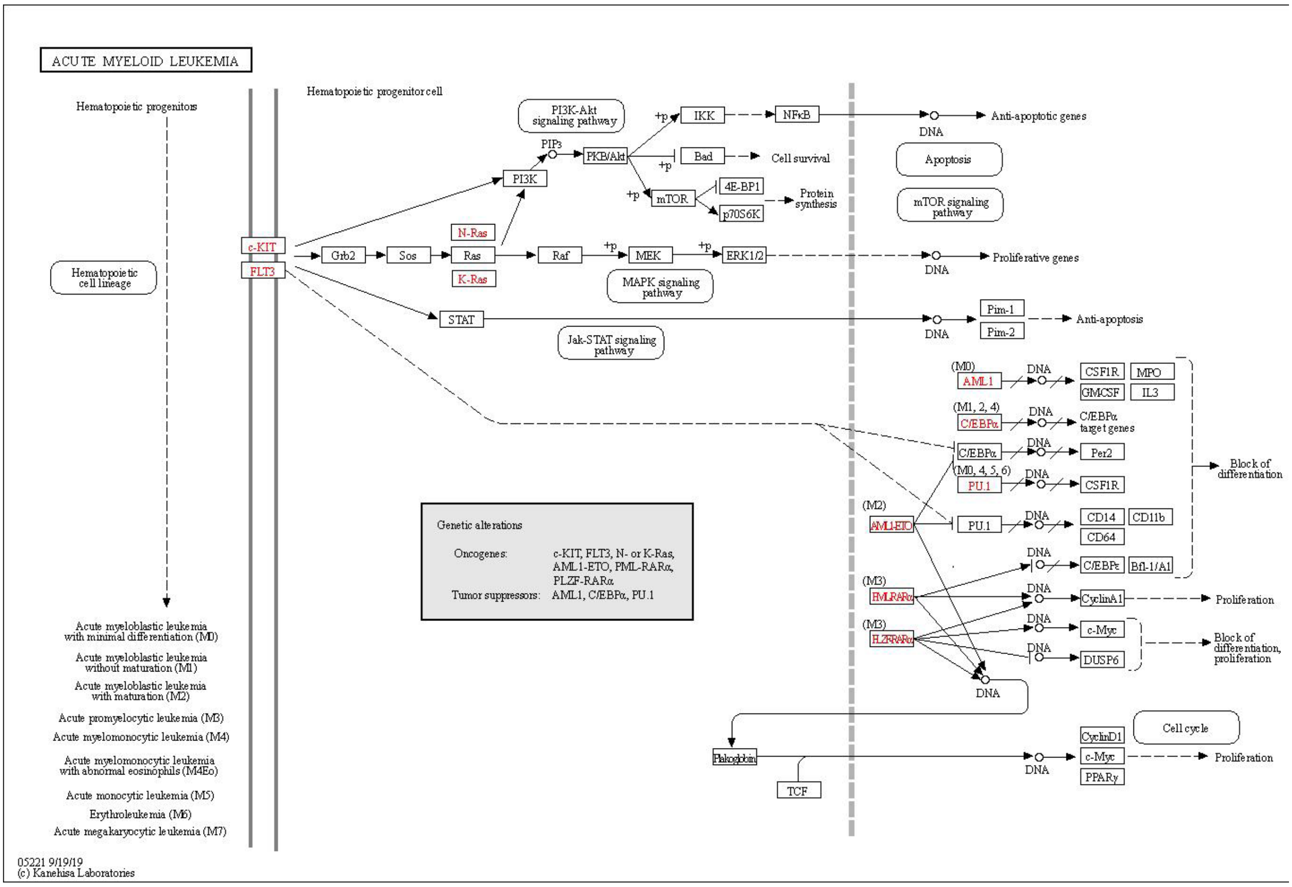

Supplementary Figure 1. KEGG pathway: map05221. Source: https://www.genome.jp/entry/pathway+map05221#:~:text=KEGG%20PATHWAY%3A%20map05221&text=Acute%20myeloid%20leukemia%20(AML)%20is,with%20an%20impaired%20differentiation%20program

61 Genes in KEGG Pathway: Map05221

PIK3CA, PIK3CB, PIK3CD, BAD, BCL2A1, NFKB1, TCF7, PER2, PIK3R1, PIK3R2, PIK3R3, HRAS, SOS, GRB2, BRAF, RAF1, MAP2K1, MAP2K2, ERK, MYC, CD14, AKT, IKBKA, TCF7L1, TCF7L2, LEF1, CCND1, NR1C2, RPS6KB, STAT3, PIM1, RELA, IL3, CSF1R, KIT, FLT3, CSF2, ITGAM, FCGR1A, CCNA, MTOR, EIF4EBP1, IKBKB, IKBKG, KRAS, NRAS, RUNX1, RARA, PIM2, ARAF, CEBPA, SPI1, CEBPE, RUNX1T1, PML, ZBTB16, JUP, MPO, STAT5A , STAT5B, DUSP6.

3 Genes in the Best Model

PIK3CA: PIK3CA is the most recurrently mutated gene in breast cancer and has been found to be important in a number of cancer types. An integral part of the PI3K pathway, PIK3CA has long been described as an oncogene, with two main hotspots for activating mutations, the 542/545 region of the helical domain, and the 1047 region of the kinase domain. PIK3CA, and its interaction with the AKT and mTOR pathways, is the subject of an immense amount of research and development, and PI3K inhibition has seen some limited success in recent clinical trials. This gene has been found to be oncogenic and has been implicated in cervical cancers. A pseudogene of this gene has been defined on chromosome 22. Source: https://www.genecards.org/cgi-bin/carddisp.pl?gene=PIK3CA

PIM1: The protein encoded by this gene belongs to the Ser/Thr protein kinase family, and PIM subfamily. This gene is expressed primarily in B-lymphoid and myeloid cell lines and is overexpressed in hematopoietic malignancies and in prostate cancer. It plays a role in signal transduction in blood cells, contributing to both cell proliferation and survival, and thus provides a selective advantage in tumorigenesis. Both the human and orthologous mouse genes have been reported to encode two isoforms (with preferential cellular localization) resulting from the use of alternative in-frame translation initiation codons, the upstream non-AUG (CUG) and downstream AUG codons (PMIDs:16186805, 1825810). Source: https://www.genecards.org/cgi-bin/carddisp.pl?gene=PIM1&keywords=PIM1

MPO: Myeloperoxidase is a heme protein synthesized during myeloid differentiation that constitutes the major component of neutrophil azurophilic granules. Produced as a single chain precursor, myeloperoxidase is subsequently cleaved into a light and heavy chain. The mature myeloperoxidase is a tetramer composed of 2 light chains and 2 heavy chains. This enzyme produces hypohalous acids central to the microbicidal activity of neutrophils. Source: https://www.genecards.org/cgi-bin/carddisp.pl?gene=MPO&keywords=MPO