**Supplementary Table 3:** Role of the mutated genes

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| --- | --- |
| *ASXL1* | The *ASXL1* (additional sex combs like 1) gene is located in the chromosomal region 20q11. It is one of the most frequently mutated genes in malignant myeloid diseases, and it encodes for a protein involved in the chromatin remodeling. Somatic mutations in the *ASXL1* gene have been associated with acute myeloid leukemia, chronic myelomonocytic leukemia, and myelodysplastic syndrome. (1) |
| *SETBP1* | The *SETBP1* (SET binding protein 1) gene is located in the chromosomal region 18q12.3. It encodes for a DNA-binding protein responsible for the activation of gene expression through recruitment of a HCF1/KMT2A/PHF8 epigenetic complex. Mutations in this gene are responsible for SETBP1 protein accumulation and subsequent inhibition of the PP2A phosphatase oncosuppressor, and are associated with atypical chronic myeloid leukemia. (2, 3) |
| *TET2* | The *TET2* gene (Ten-Eleven Translocation-2) is located in the chromosomal region 4q24. It encodes for a methylcytosine dioxygenase that catalyzes the conversion of methylcytosine to 5-hydroxymethylcytosine, and is involved in myelopoiesis. Somatic *TET2* gene mutations are associated with myelodysplastic and myeloproliferative disorders. (4) |
| *RAS* | The *RAS* genes are a family of related genes: *HRAS*, located in the chromosomal region 11p15.5; *NRAS*, located in the chromosomal region 1p13.2; and *KRAS*, located in the chromosomal region 12p12.1. They encode for small GTPase which play important roles  in cell division, cell differentiation, and apoptosis. The *RAS* genes are the most common oncogenes in human cancer. Their mutations can lead to the production of permanently activated RAS proteins, causing unintended and overactive signaling inside the cell. (5) |
| *EZH2* | The *EZH2* gene (Enhancer of Zeste Homolog 2) is located in the chromosomal region 7q36.1. It encodes for a histone methyltransferase.  Mutations in this gene are associated with myelodysplastic and myeloproliferative disorders. (6) |
| *ETNK1* | The *ETNK1* gene (Ethanolamine Kinase 1) is located in the chromosomal region 12p12.1. It encodes for an ethanolamine kinase responsible for the first step of the phosphatidylethanolamine synthesis pathway. Mutations in this gene are associated with atypical chronic myeloid leukemia and systemic mastocytosis. (7) |
| *RUNX1* | The *RUNX1* gene (Runt-related transcription factor 1) is located in the chromosomal region 21q22.12. It encodes for a protein involved in the development of hematopoietic stem cells. Translocations and mutations involving this gene have been associated with acute lymphoblastic leukemia, chronic myelomonocytic leukemia, familial platelet disorder with predisposition to acute myeloid leukemia, and myelodysplastic syndromes. (8) |
| *SRSF2* | The *SRSF2* gene (Serine and Arginine Rich Splicing Factor 2) is located in the chromosomal region 17q25.2. It encodes for a protein belonging to the serine/arginine (SR)-rich family of pre-mRNA splicing factors, which constitute part of the spliceosome. Mutations in this gene are associated with Systemic Mastocytosis with associated hematologic neoplasm and chronic neutrophilic leukemia. (9) |
| *CBL* | The *CBL* gene (Casitas B-lineage Lymphoma) is located in the chromosomal region 11q23.3. It encodes for a RING finger E3 ubiquitin ligase which is required for targeting substrates for degradation by the proteasome. Mutations in this gene are associated with Juvenile Myelomonocytic Leukemia and acute myeloid leukemia. (10) |
| *CREBBP* | The *CREBBP* gene (CREB Binding Protein) is located in the chromosomal region 16p13.3. It encodes for a protein which plays an essential role in controlling cell growth and division. Translocations involving this gene are associated with acute myeloid leukemia chronic myeloid leukemia and myelodysplastic syndrome. Somatic mutations are associated with B-cell non-Hodgkin lymphoma. (11) |
| *CSF3R* | * The *CSF3R* gene (Colony Stimulating Factor 3 Receptor) is located in the chromosomal region 1p34.3. It encodes for a receptor for colony stimulating factor 3, a cytokine that controls the production, differentiation, and function of granulocytes. Mutation is this gene are associated with chronic neutrophilic leukemia. (12) |
| *KIT* | The *KIT* gene (Proto-Oncogene Tyrosine-Protein Kinase Kit) is located in the chromosomal region 4q12. It encodes for the human homolog of the proto-oncogene c-kit, and it is a member of a protein family called receptor tyrosine kinases. The signaling pathways stimulated by the KIT protein control many important cellular processes such as cell growth and division, survival, and migration. Somatic mutations in this gene are associated with acute myeloid leukemia, systemic mastocytosis, as well as gastrointestinal stromal tumors. (13) |

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