8. ANEXOS

8.1. Anexo I.

Tabla Anexo I. Diseño del panel de genes dirigido a neoplasias mieloides hereditarias: genes incluidos en el panel e información sobre su localización, la condición patológica asociada y su NM. Información extraída de las bases de datos Gene, ClinVar y PubMed, del NCBI. Chr: *chromosome*, del inglés, cromosoma. ND: no disponible. NM: identificador de la secuencia de referencia.

GENES INCLUÍDOS EN EL PANEL DE GENES DIRIGIDO			
Gen	**RefSeq**	**Localización**	**Condición Patológica**
ABCB7	NM_004299.5	Chr X	*Anemia, sideroblastic, with ataxia*
ACD	NM_001082486.1	Chr 16	*Inherited bone marrow failure associated with germline mutation of ACD, the gene encoding telomere protein TPP1*
ADA	NM_000022.3	Chr 20	*Severe combined immunodeficiency due to adenosine deaminase deficiency*
AK2	NM_001625.3	Chr 1	*Human adenylate kinase 2 deficiency causes a profound hematopoietic defect associated with sensorineural deafness.*
AK7	ND	ND	ND
ALAS2	NM_000032.4	Chr X	*Anemia, sideroblastic, 1*
ANKRD26	NM_014915.2	Chr 10	*Thrombocytopenia 2*
AP3B1	NM_003664.4	Chr 5	*Hermansky-Pudlak syndrome 2; neutropenia gene*
ASXL1	NM_015338	Chr 20	*Myelodysplastic syndrome, somatic*
ATG2B	NM_018036.6	Chr 14	*A germline duplication of a region that includes this gene is associated with predisposition to myeloid malignancies; {Myeloproliferative neoplasms, familial, susceptibility to}*
ATM	NM_000051.3	Chr 11	*Lymphoma, B-cell non-Hodgkin, somatic; Lymphoma, mantle cell, somatic; T-cell prolymphocytic leukemia, somatic*
ATR	NM_001184	Chr 3	*Cutaneous telangiectasia and cancer syndrome, familial*
ATRX	NM_000489.4	Chr X	*Alpha-thalassemia/mental retardation syndrome*
BCOR	NM_001123383	Chr X	*BCOR and BCORL1 mutations in myelodysplastic syndromes (MDS). Correpresor BCL6*
BCORL1	NM_001184772 , NM_021946	Chr X	*BCOR and BCORL1 mutations in myelodysplastic syndromes (MDS). Correpresor BCL7*
BDKRB1	ND	Chr 14q32.2	ND
BDKRB2	ND	Chr 14q32.2	ND
BLM	NM_000057.3	Chr 15	*Bloom syndrome*

BPGM	NM_001724.4	Chr 7	*Erythrocytosis due to bisphosphoglycerate mutase deficiency*
BRCA1 (FANCS)	NM_007294.3	Chr 17	*Fanconi anemia, complementation group S*
BRIP1 (FANCJ)	NM_032043.2	Chr 17	*Fanconi anemia, complementation group J*
C15ORF41	NM_001130010.2	Chr 15	*Congenital dyserythropoietic anemia type Ib*
CALR	NM_004343	Chr 19	*Myelofibrosis, somatic; Thrombocythemia, somatic*
CBL	NM_005188.3	Chr 11	*Juvenile myelomonocytic leukemia; Noonan syndrome-like disorder with or without juvenile myelomonocytic leukemia*
CDAN1	NM_138477.3	Chr 15	*Congenital dyserythropoietic anemias.*
CDC25C	NM_001790.4	Chr 5	ND
CEBPA	NM_004364.4	Chr 19	*Familial Acute Myeloid Leukemia With Mutated CEBPA*
CHEK2 (CHK2)	NM_007194.3	Chr 22	*Loss of function germline mutation; Ubiquitous expression in bone marrow*
CSF3R	NM_156039.3	Chr 1	*Neutropenia, severe congenital, 7, autosomal recessive*
CSNK1A1	NM_001025105.2	Chr 5	*differentially expressed in the bone marrow microenvironment of osteoporotic patients, providing new ideas for finding therapeutic targets for osteoporosis.*
CTC1	NM_025099.5	Chr 17	*OMIM: Cerebroretinal microangiopathy with calcifications and cysts; Pubmed: Dyskeratosis congenita (DC)*
CUX1	NM_181552.3	Chr 3	*Pubmed involved in regulation of dendritogenesis and cortical synapse formation in layer II to IV cortical neurons.*
CXCR4	NM_003467.2	Chr 2	*Myelokathexis, isolated; WHIM syndrome*
DDX41	NM_016222.3	Chr 5	*{Myeloproliferative/lymphoproliferative neoplasms, familial (multiple types), susceptibility to}*
DKC1	NM_001363.4	Chr X	*Dyskeratosis congenita, X-linked*
DNAJC21	NM_194283.3	Chr 5	*Bone Marrow Failure Syndrome 3*
DNMT3A	NM_175629	Chr 2	*Acute myeloid leukemia, somatic (tambien Tatton-Brown-Rahman syndrome)*
EGLN1 (PHD2	NM_022051.2	Chr 1	*Erythrocytosis, familial*
ELANE	NM_001972.3	Chr 19	*Neutropenia, cyclic; Neutropenia, severe congenital 1, autosomal dominant*
EPAS1	NM_001430	Chr 2	*Mutations in this gene are associated with erythrocytosis familial type 4.*
EPCAM	NM_002354	Chr 2	*Colorectal cancer, hereditary nonpolyposis, type 8; Diarrhea 5, with tufting enteropathy, congenital*
EPO	NM_000799	Chr 7	*Diamond-Blackfan anemia-like; Erythrocytosis, familial, 5*
EPOR	NM_000121	Chr 19	*[Erythrocytosis, familial, 1]*

ETNK1	NM_018638	Chr 12	*Atypical chronic myeloid leukemia: Common cytogenetic features and mutations include trisomy 8, and mutations in SETBP1 and ETNK1*
ETV6	NM_001987.4	Chr 12	*Leukemia, acute myeloid, somatic; Thrombocytopenia 5*
EZH2	NM_004456	Chr 7	*Weaver syndrome. Remodelador de histonas (histona metil transferasa)*
FANCA	NM_000135.3	Chr 16	*Fanconi anemia, complementation group A*
FANCB	NM_152633.3	Chr X	*Fanconi anemia, complementation group B*
FANCC	NM_000136.2	Chr 9	*Fanconi anemia, complementation group C*
FANCD1/ BRCA2	NM_000059.3	Chr 13	*Fanconi anemia, complementation group D1*
FANCD2	NM_033084.4	Chr 3	*Fanconi anemia, complementation group D2*
FANCE	NM_021922.2	Chr 6	*Fanconi anemia, complementation group E*
FANCF	NM_022725.3	Chr 11	*Fanconi anemia, complementation group F*
FANCG	NM_004629.1	Chr 9	*Fanconi anemia, complementation group G*
FANCI	NM_001113378.1	Chr 15	*Fanconi anemia, complementation group I*
FANCL	NM_001114636.1	Chr 2	*Fanconi anemia, complementation group L*
FANCM	NM_020937.3	Chr 14	*A tumor suppressive DNA translocase; Premature ovarian failure 15; Spermatogenic failure 28*
FANCN/P ALB2	NM_024675.3	Chr 16	*Fanconi anemia, complementation group N*
FANCO/R AD51C	NM_058216.2	Chr 17	*Fanconi anemia, complementation group O*
FANCP/SL X4	NM_032444.3	Chr 16	*Fanconi anemia, complementation group P*
FANCQ/E RCC4	NM_005236.2	Chr 16	*Fanconi anemia, complementation group Q*
FLT3	NM_004119	Chr 13	*Leukemia, acute lymphoblastic, somatic; Leukemia, acute myeloid, reduced survival in, somatic; Leukemia, acute myeloid, somatic*
G6PC3	NM_138387.3	Chr 17	*Dursun syndrome; Neutropenia, severe congenital 4, autosomal recessive*
GATA1	NM_002049.3	Chr X	*Anemia, X-linked, with/without neutropenia and/or platelet abnormalities; Leukemia, megakaryoblastic, with or without Down syndrome, somatic; Thrombocytopenia with beta-thalassemia, X-linked; Thrombocytopenia, X-linked, with or without dyserythropoietic anemia*
GATA2	NM_032638.4	Chr 3	*"Emberger syndrome; Immunodeficiency 21, {Leukemia, acute myeloid, susceptibility to}; {Myelodysplastic syndrome, susceptibility to}*
GFI1	NM_001127216.2	Chr 1	*Neutropenia, nonimmune chronic idiopathic, of adults; Neutropenia, severe congenital 2, autosomal dominant*
GSKIP	NM_001271904.1	Chr 14	*Germline duplication of ATG2B and GSKIP predisposes to familial myeloid malignancies.*

HAX1	NM_006118.3	Chr 1	*Neutropenia, severe congenital 3, autosomal recessive*
EPAS1	NM_001430.4	Chr 2	*Erythrocytosis familial type 4*
HSPA9	NM_004134.6	Chr 5	*Congenital sideroblastic anemia*
IDH1	NM_00128238	Chr 2	*{Glioma, susceptibility to, somatic}*
IDH2	NM_002168	Chr 15	*D-2-hydroxyglutaric aciduria 2*
IKZF1	NM_006060.5	Chr 7	*Immunodeficiency, common variable, 13*
IL2RG	NM_000206.2	Chr X	*X-Linked Severe Combined Immunodeficiency*
JAGN1	NM_032492.3	Chr 3	*Severe Congenital Neutropenia*
JAK2	NM_001322194.1	Chr 9	*Primary Myelofibrosis*
KIF23	NM_138555.3	Chr 15	*Congenital Dyserythropoietic Anemia; Broad expression in bone marrow*
KIT	NM_000222	Chr 4	*Leukemia, acute myeloid*
KLF1	NM_006563	Chr 19	*"Dyserythropoietic anemia, congenital, type IV; Blood group--Lutheran inhibitor; [Hereditary persistence of fetal hemoglobin]*
KMT2A	NM_001197104	Chr 11	*"Leukemia, myeloid/lymphoid or mixed-lineage; Wiedemann-Steiner syndrome*
KRAS	NM_033360	Chr 12	*Leukemia, acute myeloid*
LAMTOR2	NM_014017.3	Chr 1	*Immunodeficiency due to defect in MAPBP-interacting protein*
LIG4	NM_001352598.1	Chr 13	*LIG4 syndrome; Severe combined immunodeficiency with sensitivity to ionizing radiation*
LYST	NM_000081.3	Chr 1	*Chediak-Higashi syndrome*
MAD2L2	NM_001127325.1	Chr 1	*Fanconi anemia; Broad expression in bone marrow*
MBD4	NM_003925	Chr 3	*Genomic profiling of 3 early-onset acute myeloid leukemias (AMLs) identified germ line loss of MBD4 as an initiator of 5mC-dependent hypermutation.*
MCFD2	NM_001171506	Chr 2	*Factor V and factor VIII, combined deficiency of*
MECOM	NM_001105077	Chr 3	*Radioulnar synostosis with amegakaryocytic thrombocytopenia 2*
MLH1	NM_000249.3	Chr 3	*"Mismatch repair cancer syndrome; Colorectal cancer, hereditary nonpolyposis, type 2; Muir-Torre syndrome*
MPL	NM_005373.2	Chr 1	*Myelofibrosis with myeloid metaplasia, somatic; Thrombocythemia 2; Thrombocytopenia, congenital amegakaryocytic*
MRE11A	NM_005591.3	Chr 11	*Ataxia-telangiectasia-like disorder 1*
MSH2	NM_000251.2	Chr 2	*Colorectal cancer, hereditary nonpolyposis, type 1; Mismatch repair cancer syndrome; Muir-Torre syndrome*
MSH6	NM_000179.2	Chr 2	*"Colorectal cancer, hereditary nonpolyposis, type 5, Endometrial cancer, familial; Mismatch repair cancer syndrome*

NAF1	NM_138386.2	Chr 4	*Multiple splicing variants of Naf1/ABIN-1 transcripts and their alterations in hematopoietic tumors.*
NBN (NBS1)	NM_002485.4	Chr 8	*"Aplastic anemia; Leukemia, acute lymphoblastic; Nijmegen breakage syndrome*
NCK1	NM_001291999	Chr 3	*Bcr-Abl is the transforming principle underlying chronic myelogenous leukaemia (CML). Here, we use a functional interaction proteomics approach to map pathways by which Bcr-Abl regulates defined cellular processes. The results show that Bcr-Abl regulates the actin cytoskeleton and non-apoptotic membrane blebbing via a GADS/Slp-76/Nck1 adaptor protein pathway.*
NF1	NM_001042492.2	Chr 17	*Neurofibromatosis, type 1; Juvenile myelomonocytic leukemia (JMML) is a unique clonal hematopoietic disorder of early childhood. It is classified as an overlap myeloproliferative/myelodysplastic neoplasm by the World Health Organization (WHO) and shares some features with chronic myelomonocytic leukemia in adults. JMML pathobiology is characterized by constitutive activation of the Ras signal transduction pathway. About 90% of patients harbor molecular alterations in one of five genes (PTPN11, NRAS, KRAS, NF1 or CBL) which define genetically and clinically distinct subtypes.*
NHP2	NM_017838.3	Chr 5	*Dyskeratosis congenita; Broad expression in bone marrow*
NOP10	NM_018648.3	Chr 15	*Dyskeratosis congenita, autosomal recessive 1*
NPM1	"NM_001355007, NM_002520 "	Chr 5	*Leukemia, acute myeloid, somatic; Coexisting and cooperating mutations in NPM1-mutated acute myeloid leukemia.*
NRAS	NM_002524	Chr 1	*RAS-associated autoimmune lymphoproliferative syndrome type IV, somatic*
PARN	NM_002582.3	Chr 16	*"Dyskeratosis congenita, autosomal recessive 6; Pulmonary fibrosis and/or bone marrow failure, telomere-related, 4*
PAX5	NM_016734.2	Chr 9	*{Leukemia, acute lymphoblastic, susceptibility to, 3}*
PHF6	"NM_001015877, NM_032458 "	Chr X	*Borjeson-Forssman-Lehmann syndrome*
PMS2	NM_000535.5	Chr 7	*"Mismatch repair cancer syndrome; Colorectal cancer, hereditary nonpolyposis, type 4*
POT1	NM_015450.2	Chr 7	*"PROTECTION OF TELOMERES 1; Germline variants in the POT1 gene have recently been*

			shown to be associated with risk of developing tumors in different tissues such as familial chronic lymphocytic leukemia; {Glioma susceptibility 9}; {Melanoma, cutaneous malignant, susceptibility to, 10}
PPM1D	NM_003620	Chr 17	*"development of clonal hematopoiesis; in the setting of chemotherapy treatment of solid tumors, hematopoietic mutations in TP53 and PPM1D appear to contribute to outgrowth of clones that may lead to subsequent malignancy.; Breast cancer, somatic; Intellectual developmental disorder with gastrointestinal difficulties and high pain threshold*
PTPN11	NM_002834.4	Chr 12	*Leukemia, juvenile myelomonocytic, somatic*
PUS1	NM_025215.5	Chr 12	*Myopathy, lactic acidosis, and sideroblastic anemia*
RAB27A	NM_183236.2	Chr 15	*disruption of exosome secretion in AML cells through targeting Rab27a, an important regulator involved in exosome release, significantly delayed leukemia development.; Griscelli syndrome, type 2*
RAC2	NM_002872.4	Chr 22	*Neutrophil immunodeficiency syndrome*
RAD21	NM_006265	Chr 8	*"Cohesin RAD21 Gene Promoter Methylation in Patients with Chronic Lymphocytic Leukemia.; early all NPM1-mutated AML patients showed concurrent mutations in genes involved in regulation of DNA methylation (DNMT3A, TET2, IDH1, IDH2), RNA splicing (SRSF2, SF3B1), or in the cohesin complex (RAD21, SMC1A, SMC3, STAG2); Mungan syndrome; Cornelia de Lange syndrome 4*
RAD50	NM_005732.3	Chr 5	*A-AML was characterized by increased genomic complexity based on exonic variants (an average of 26 somatic mutations per sample vs 15 for E-AML). The integration of exome, copy number, and gene expression data revealed alterations in genes involved in DNA repair (eg, SLX4IP, RINT1, HINT1, and ATR) and the cell cycle (eg, MCM2, MCM4, MCM5, MCM7, MCM8, MCM10, UBE2C, USP37, CK2, CK3, CK4, BUB1B, NUSAP1, and E2F) in A-AML, which was associated with a 3-gene signature defined by PLK1 and CDC20 upregulation and RAD50 downregulation and with structural or functional silencing of the p53 transcriptional program.; Nijmegen breakage syndrome-like disorder*
RAD51 (FANCR)	NM_133487.3	Chr 15	*Fanconi anemia, complementation group R*

RBBP6	NM_006910.4	Chr 16	*Growth factor independence 1B (Gfi-1B), a transcription factor essential for the development of hematopoietic cells and differentiation of erythroid and megakaryocytic lineages; transcripts within components of the signalling cascade of immune cells (PLD1, LAMP1, HSP90, IL6ST), of the tyrosine kinase pathway (TPR, RAC3) and of the transcription factors (RAC3, CEP290, JEM-1, ATR, MYC, SMC3, RARA, RBBP6) were found to be differentially expressed in Gfi-1B overexpressing cells compared to controls.*
RBM8A	NM_005105.4	Chr 1	*Thrombocytopenia-absent radius syndrome*
RGS2	NM_00292	Chr 1	*RGS2 is an important target gene of Flt3-ITD mutations in AML and functions in myeloid differentiation and leukemic transformation.*
RHAG	NM_000324	Chr 6	*Anemia, hemolytic, Rh-null, regulator type*
RMRP	NR_003051.3	Chr 9	*Anauxetic dysplasia 1; Cartilage-hair hypoplasia; Metaphyseal dysplasia without hypotrichosis; (Extended follow-up of the Finnish cartilage-hair hypoplasia cohort confirms high incidence of non-Hodgkin lymphoma and basal cell carcinoma.)*
RNF168	NM_152617.3	Chr 3	*RIDDLE syndrome*
RPL10	NM_001303624.1	Chr X	*"The pathogenic role of the recurrent R98S mutation in ribosomal protein L10 (RPL10 R98S) found in T-cell acute lymphoblastic leukemia (T-ALL); Mental retardation, X-linked, syndromic, 35; {Autism, susceptibility to, X-linked 5}*
RPL11	NM_000975.4	Chr 1	*Diamond-Blackfan anemia 7*
RPL15	NM_001253383.2	Chr 3	*Diamond-Blackfan anemia 12*
RPL26	NM_000987.4	Chr 17	*Diamond-Blackfan anemia 11*
RPL27	NM_001349922	Chr 17	*Diamond-Blackfan anemia 16*
RPL35A	NM_000996.3	Chr 3	*Diamond-Blackfan anemia 5*
RPL5	NM_000969.4	Chr 1	*Diamond-Blackfan anemia 6*
RPL9	"NM_000661, NM_001024921 "	Chr 4	ND
RPS10	NM_001203245.2	Chr 6	*"Diamond-Blackfan anemia 9*
RPS14	NM_001025071.1	Chr 5	*5q minus (5q-) syndrome is a type of bone marrow disorder called myelodysplastic syndrome (MDS)*
RPS17	NM_001021.5 *ribosome	Chr 15	*Diamond-Blackfan anemia 4*
RPS19	NM_001022.3	Chr 19	*Diamond-Blackfan anemia 1*
RPS24	NM_001142285.1	Chr 10	*Diamond-blackfan anemia 3*
RPS26	NM_001029.4	Chr 12	*Diamond-Blackfan anemia 10*
RPS27	"NM_001030 , NM_001349946, NM_001349947 "	Chr1	*Diamond-Blackfan anemia 17*

RPS29	NM_001030001.3	Chr 14	*Diamond-Blackfan anemia 13*
RPS7	NM_001011.3	Chr 2	*Diamond-Blackfan anemia 8*
RTEL1	NM_032957.4	Chr 20	*Germline mutations of regulator of telomere elongation helicase 1, RTEL1, in Dyskeratosis congenita.*
RUNX1	NM_001754.4	Chr 21	*Leukemia, acute myeloid; Platelet disorder, familial, with associated myeloid malignancy*
SAMD9	NM_001193307.1	Chr 7	*"MIRAGE syndrome; Tumoral calcinosis, familial, normophosphatemic*
SAMD9L	NM_152703.4	Chr 7	*"Ataxia-pancytopenia syndrome*
SBDS	NM_016038.3	Chr 7	*"{Aplastic anemia, susceptibility to}; Shwachman-Diamond syndrome*
SBF2	NM_030962.3	Chr 11	*Charcot-Marie-Tooth disease, type 4B2; The data presented indicate that B cells from patients with chronic lymphocytic leukemia (CLL) may produce suppressive factors capable of inhibiting T and B cell proliferation and Ig secretion. Two factors with the molecular weight 65-75 KDa (SBF1) and 15-25 KDa (SBF2) have been characterized. SBFs are primarily produced by B cells with a low flow density. There is a reverse dependence between the capacity of leukemic B cells for spontaneous Ig secretion and their ability for the production of suppressive factors.*
SETBP1	NM_015559	Chr 18	*"Mental retardation, autosomal dominant 29; Schinzel-Giedion midface retraction syndrome*
SF3B1	NM_012433	Chr 2	*Myelodysplastic syndrome, somatic*
SH2B3	NM_005475.2	Chr 12	*"Myelofibrosis, somatic; Thrombocythemia, somatic; Erythrocytosis, somatic*
SMC1A	NM_006306	Chr X	*"Hematologic;; Cornelia de Lange syndrome 2*
SMC3	NM_005445	Chr 10	*"Articles on SLC25A38;; Cornelia de Lange syndrome 3*
SMOH	NM_005631	Chr 7	*"Basal cell carcinoma, somatic; Curry-Jones syndrome, somatic mosaic*
SRP54	ND	ND	*Shwachman-Diamond syndrome (SDS) is a rare inherited disease mainly caused by mutations in the Shwachman-Bodian-Diamond Syndrome (SBDS) gene. However, it has recently been reported that other genes, including DnaJ heat shock protein family (Hsp40) member C21 (DNAJC21), elongation factor-like 1 (EFL1) and signal recognition particle 54 (SRP54) are also associated with an SDS-like phenotype.*
SRP72	NM_006947.3	Chr 4	*Bone marrow failure syndrome 1*
SRSF2	NM_003016	Chr 17	ND

STAG2	NM_001042749	Chr X	*NUCLEOPHOSMIN1 (NPM1) is the most frequently mutated gene in acute myeloid leukemia. Notably, NPM1 mutations are always accompanied by additional mutations such as those in cohesin genes RAD21, SMC1A, SMC3, STAG2*
TAZ	NM_000116.4	Chr X	*Barth syndrome*
TCIRG1	NM_006019.3	Chr 11	*Osteopetrosis, autosomal recessive 1; Severe Congenital Neutropenia ??; infantile malignant osteopetrosis (IMO). Genetic mutation in T-cell, immune regulator 1 (TCIRG1) was identified, confirming the diagnosis of IMO*
TCL1A	NM_021966	Chr 14	*Leukemia/lymphoma, T-cell*
TERC	NR_001566.1	Chr 3	*Dyskeratosis congenita, autosomal dominant 1; {Aplastic anemia}; {Pulmonary fibrosis, idiopathic, susceptibility to}*
TERF1	NM_017489.2	Chr 8	*TELOMERIC REPEAT-BINDING FACTOR 1*
TERF2	NM_005652.4	Chr 16	*TELOMERIC REPEAT-BINDING FACTOR 2*
TERT	NM_198253.2	Chr 5	*"{Leukemia, acute myeloid}; {Dyskeratosis congenita, autosomal dominant 2}; {Dyskeratosis congenita, autosomal recessive 4}; {Pulmonary fibrosis and/or bone marrow failure, telomere-related, 1}; {Melanoma, cutaneous malignant, 9}*
TET2	NM_001127208.2	Chr 4	*Myelodysplastic syndrome, somatic*
TINF2	NM_001099274.1	Chr 14	*TINF2 mutations result in very short telomeres: analysis of a large cohort of patients with dyskeratosis congenita and related bone marrow failure syndromes.*
TP53	NM_000546.5	Chr 17	*Bone marrow failure syndrome 5*
TRNT1	NM_182916.2	Chr 3	*Sideroblastic anemia with B-cell immunodeficiency, periodic fevers, and developmental delay*
TSR2	NM_058163.2	Chr X	*Diamond-Blackfan anemia 14 with mandibulofacial dysostosis*
U2AF1	NM_006758	Chr 21	*Clonal hematopoiesis is frequently present in otherwise healthy individuals and may persist for many years. Though largely asymptomatic, carrying these somatic mutations confers a small but significantly increased risk of leukemic transformation, affecting 0.5-1% carriers per year; although most genes confer an increased risk of transformation, mutations in TP53 and U2AF1 appear to carry a particularly high risk for transformation.*
UBE2T (FANCT)	NM_014176.3	Chr 1	*Fanconi anemia, complementation group T*

USB1 (C16orf57)	NM_024598.3	Chr 16	*Poikiloderma with neutropenia*
VHL	NM_000551.3	Chr 3	*Familial Erythrocytosis*
VPS13B	NM_017890.4	Chr 8	*Cohen syndrome;; Rearrangement of VPS13B, a causative gene of Cohen syndrome, in a case of RUNX1-RUNX1T1 leukemia with t(8;12;21).*
VPS45	NM_007259.4	Chr 1	*Neutropenia, severe congenital, 5, autosomal recessive*
WAS	NM_000377.2	Chr X	*"Neutropenia, severe congenital, X-linked; Thrombocytopenia, X-linked; Thrombocytopenia, X-linked, intermittent; Wiskott-Aldrich syndrome*

8.2. Anexo II.

Tabla Anexo II. Zonas de mejora del panel de genes dirigido. Se incluyen la localización cromosómica, las posiciones concretas iniciales y finales, el gen a que corresponde y el NM junto con el exón correspondiente. Chr: *chromosome*, del inglés, cromosoma. NM: identificador de la secuencia de referencia.

POSICIONES CROMOSÓMICAS MAL CUBIERTAS				
Localización	**Posición inicial**	**Posición final**	**Gen**	**NM con exón**
Chr 9	5077452	5077580	***JAK2***	NM_001322195.ex.14
Chr 7	6017218	6017388	***PMS2***	NM_001322004.ex.13
Chr 7	6018226	6018327	***PMS2***	NM_001322004.ex.12
Chr 7	6043320	6043423	***PMS2***	NM_001322004.ex.3
Chr 7	6043602	6043689	***PMS2***	NM_001322004.ex.2
Chr 17	8151321	8151413	***CTC1***	NM_025099.ex.1
Chr 3	10085167	10085276	***FANCD2***	NM_001319984.ex.13
Chr 3	10085512	10085548	***FANCD2***	NM_001319984.ex.14
Chr 3	10091057	10091189	***FANCD2***	NM_001319984.ex.17
Chr 3	10105475	10105595	***FANCD2***	NM_001319984.ex.21
Chr 3	10106039	10106113	***FANCD2***	NM_001319984.ex.22
Chr 3	10106412	10106559	***FANCD2***	NM_001319984.ex.23
Chr 3	10107547	10107663	***FANCD2***	NM_001319984.ex.25
Chr 16	14678605	14678648	***PARN***	NM_001242992.ex.14
Chr 16	14693760	14693817	***PARN***	NM_001242992.ex.11
Chr 16	14702137	14702176	***PARN***	NM_001242992.ex.8
Chr X	14871160	14871289	***FANCB***	NM_001018113.ex.6
Chr X	14875983	14876076	***FANCB***	NM_001018113.ex.5
Chr X	15833799	15834013	***ZRSR2***	NM_005089.ex.8
Chr 16	24557483	24557583	***RBBP6***	NM_032626.ex.2

Chr 10	27311486	27311616	***ANKRD26***	NM_014915.ex.29
Chr 10	27313375	27313488	***ANKRD26***	NM_014915.ex.28
Chr 10	27333085	27333119	***ANKRD26***	NM_014915.ex.19
Chr 10	27342248	27342319	***ANKRD26***	NM_014915.ex.16
Chr 10	27371731	27371762	***ANKRD26***	NM_014915.ex.6
Chr 22	29083730	29083974	***CHEK2***	NM_007194.ex.15
Chr 22	29085122	29085203	***CHEK2***	NM_007194.ex.14
Chr 22	29090019	29090105	***CHEK2***	NM_007194.ex.13
Chr 22	29091114	29091230	***CHEK2***	NM_007194.ex.12
Chr 22	29091697	29091861	***CHEK2***	NM_007194.ex.11
Chr 22	29105993	29106047	***CHEK2***	NM_007194.ex.7
Chr 22	29115382	29115473	***CHEK2***	NM_007194.ex.5
Chr 17	29541468	29541603	***NF1***	NM_001128147.ex.13
Chr 17	29548867	29549782	***NF1***	NM_001128147.ex.15
Chr 17	29557859	29557943	***NF1***	NM_001042492.ex.24
Chr 17	29579955	29580018	***NF1***	NM_001042492.ex.31
Chr 8	30925773	30925843	***WRN***	NM_000553.ex.7
Chr 8	30941214	30941295	***WRN***	NM_000553.ex.10
Chr 8	30942681	30942762	***WRN***	NM_000553.ex.11
Chr 8	30947980	30948048	***WRN***	NM_000553.ex.14
Chr 8	31000141	31000217	***WRN***	NM_000553.ex.27
Chr 13	32903579	32903629	***BRCA2***	NM_000059.ex.8
Chr 13	32918694	32918790	***BRCA2***	NM_000059.ex.12
Chr 13	32920963	32921033	***BRCA2***	NM_000059.ex.13
Chr 21	36265221	36265260	***RUNX1***	NM_001754.ex.3
Chr 3	37036320	37036444	***MLH1***	NM_001354619.ex.2
Chr 3	37083758	37083822	***MLH1***	NM_001354629.ex.14
Chr 15	40994003	40994124	***RAD51***	NM_133487.ex.4
Chr 17	41249260	41249306	***BRCA1***	NM_007298.ex.7
Chr 14	45624575	45624662	***FANCM***	NM_001308134.ex.8
Chr 14	45650632	45650727	***FANCM***	NM_001308133.ex.14
Chr 14	45650839	45650908	***FANCM***	NM_001308133.ex.15
Chr 14	45654419	45654576	***FANCM***	NM_001308133.ex.17
Chr 14	45656983	45657090	***FANCM***	NM_001308133.ex.18
Chr 2	47602372	47602438	***EPCAM***	NM_002354.ex.4
Chr 14	50050289	50050393	***RPS29***	NM_001032.ex.3
Chr 14	50050290	50050393	***RPS29***	NM_001351375.ex.3
Chr 4	57352490	57352563	***SRP72***	NM_006947.ex.11
Chr 4	57361522	57361560	***SRP72***	NM_006947.ex.17
Chr 7	66456123	66456288	***SBDS***	NM_016038.ex.4
Chr 7	66458203	66458404	***SBDS***	NM_016038.ex.3
Chr 7	66459198	66459328	***SBDS***	NM_016038.ex.2
Chr 8	73926129	73926225	***TERF1***	NM_017489.ex.2

Chr 8	73937056	73937206	***TERF1***	NM_017489.ex.5
Chr 8	73951350	73951454	***TERF1***	NM_017489.ex.9
Chr X	76872080	76872198	***ATRX***	NM_138270.ex.21
Chr X	76889053	76889200	***ATRX***	NM_138270.ex.17
Chr X	76907603	76907843	***ATRX***	NM_138270.ex.14
Chr X	76912049	76912143	***ATRX***	NM_138270.ex.12
Chr X	76940430	76940498	***ATRX***	NM_138270.ex.7
Chr X	76952064	76952192	***ATRX***	NM_138270.ex.5
Chr X	76954061	76954117	***ATRX***	NM_138270.ex.3
Chr 5	77396776	77396849	***AP3B1***	NM_001271769.ex.21
Chr 5	77461433	77461496	***AP3B1***	NM_001271769.ex.12
Chr 5	77521365	77521432	***AP3B1***	NM_001271769.ex.6
Chr 15	82821157	82821289	***RPS17***	NR_111943.ex.4
Chr 15	82822713	82822779	***RPS17***	NR_111943.ex.3
Chr 15	82823287	82823393	***RPS17***	NR_111943.ex.2
Chr 15	82824388	82824865	***RPS17***	NR_111943.ex.1
Chr 15	83205500	83205632	***RPS17***	NR_111943.ex.4
Chr 15	83207056	83207122	***RPS17***	NR_111943.ex.3
Chr 15	83207630	83207736	***RPS17***	NR_111943.ex.2
Chr 15	83208731	83209208	***RPS17***	NR_111943.ex.1
Chr 15	89816607	89816700	***FANCI***	NM_001113378.ex.11
Chr 8	90949253	90949303	***NBN***	NM_002485.ex.15
Chr 8	90960051	90960120	***NBN***	NM_002485.ex.12
Chr 15	91310139	91310253	***BLM***	NM_001287246.ex.11
Chr 14	96761818	96761897	***ATG2B***	NM_018036.ex.35
Chr 14	96777878	96777955	***ATG2B***	NM_018036.ex.27
Chr 14	96779665	96779772	***ATG2B***	NM_018036.ex.24
Chr 14	96810990	96811093	***ATG2B***	NM_018036.ex.4
Chr 9	98002930	98003025	***FANCC***	NM_001243743.ex.4
Chr 8	100146859	100146955	***VPS13B***	NM_017890.ex.9
Chr 15	83207630	83207736	***RPS17***	NR_111943.ex.2
Chr 15	83208731	83209208	***RPS17***	NR_111943.ex.1
Chr 15	89816607	89816700	***FANCI***	NM_001113378.ex.11
Chr 8	90949253	90949303	***NBN***	NM_002485.ex.15
Chr 8	90960051	90960120	***NBN***	NM_002485.ex.12
Chr 15	91310139	91310253	***BLM***	NM_001287246.ex.11
Chr 14	96761818	96761897	***ATG2B***	NM_018036.ex.35
Chr 14	96777878	96777955	***ATG2B***	NM_018036.ex.27
Chr 14	96779665	96779772	***ATG2B***	NM_018036.ex.24
Chr 14	96810990	96811093	***ATG2B***	NM_018036.ex.4
Chr 9	98002930	98003025	***FANCC***	NM_001243743.ex.4
Chr 8	100146859	100146955	***VPS13B***	NM_017890.ex.9
Chr 11	108159703	108159830	***ATM***	NM_001351834.ex.29

Chr 11	108204612	108204695	***ATM***	NM_001351834.ex.55
Chr 10	112361723	112361936	***SMC3***	NM_005445.ex.25
Chr X	123156380	123156521	***STAG2***	NM_001042750.ex.3
Chr X	123159689	123159768	***STAG2***	NM_001042750.ex.4
Chr X	123176418	123176495	***STAG2***	NM_001042750.ex.7
Chr X	123184970	123185069	***STAG2***	NM_001042750.ex.12
Chr X	123199725	123199796	***STAG2***	NM_001042750.ex.21
Chr X	123200024	123200112	***STAG2***	NM_001042750.ex.22
Chr X	123202413	123202506	***STAG2***	NM_001042750.ex.24
Chr X	123211806	123211908	***STAG2***	NM_001042750.ex.27
Chr 7	124537218	124537266	***POT1***	NR_003102.ex.5
Chr 5	131894975	131895059	***RAD50***	NM_005732.ex.2
Chr 5	131944306	131944417	***RAD50***	NM_005732.ex.17
Chr 5	131944808	131944901	***RAD50***	NM_005732.ex.18
Chr X	133512034	133512136	***PHF6***	NM_001015877.ex.3
Chr X	133527938	133527982	***PHF6***	NM_001015877.ex.5
Chr X	133549045	133549150	***PHF6***	NM_001015877.ex.8
Chr 3	136649316	136649436	***NCK1***	NM_001190796.ex.1
Chr 1	145510727	145510938	***GNRHR2***	NR_104033.ex.3
Chr 1	150115015	150115109	***VPS45***	NM_001279353.ex.13
Chr 7	152357785	152357867	***XRCC2***	NM_005431.ex.2
Chr 4	164066933	164067016	***NAF1***	NM_138386.ex.4
Chr 3	168825713	168825740	***MECOM***	NM_004991.ex.10
Chr 2	198283520	198285266	***SF3B1***	NM_001308824.ex.4
Chr 1	235875356	235875497	***LYST***	NM_001301365.ex.43
Chr 1	235963619	235963686	***LYST***	NM_001301365.ex.10