Clinical Features and Molecular Genetics:
The familial occurrence of myelodysplastic syndrome (MDS) and/or acute leukemia (AL) is rare and heterogeneous. Some families inherit purely AL, and others inherit purely MDS or both disorders within the same pedigree. Many cases of familial MDS/AL also arise in those with particular genetic syndromes with additional clinical findings. Patients with familial MDS/AL are usually younger at presentation than individuals with sporadic disease and are recognized by an unusual family history of more than one first-degree relative with MDS/AL. Most of the families show a pattern of inheritance consistent with a single gene mutation, inherited in an autosomal dominant manner [1, 2].

Our Comprehensive Familial Myelodysplastic Syndrome/Acute Leukemia includes sequence and deletion/duplication analysis of the 30 genes listed below, and deletion/duplication analysis only for the 2 genes listed below in bold.

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<tr>
<th>Tier 1: Familial MDS/AL Panel</th>
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<td>GATA2</td>
<td>GSKIP</td>
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<td>ATM</td>
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**Tier 1: Familial Myelodysplastic Syndrome/Acute Leukemia Panel (Pure familial MDS/AL)**

Pure familial MDS/AL is characterized by multiple cases of MDS and/or AL without bone marrow failure or other phenotypic features in one family. It is due to inheritance of a single abnormal copy of a gene encoding a transcription factor that is critical for hematopoiesis [1]. Mutation carriers can have additional findings in addition to the clinical features than MDS/AL, but these may be subtle or absent [1].

<table>
<thead>
<tr>
<th>Gene</th>
<th>Inheritance</th>
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</tr>
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<tbody>
<tr>
<td>ANKRD26</td>
<td>AD</td>
<td>Mutations in the 5’UTR and protein coding regions of ANKRD26 were reported to cause an autosomal-dominant form of inherited thrombocytopenia, THC2. It has been reported that among 105 people with confirmed or suspected ANKRD26 mutations, 10 developed hematologic malignancies, including seven with acute leukemias. The overall incidence of development of hematologic malignancies was 240 out of 100,000, and of acute leukemia was 167 out of 100,000, both elevated over expected levels [3-5].</td>
</tr>
<tr>
<td>ATG2B/ GSKIP</td>
<td>AD</td>
<td>Germline duplication of ATG2B and GSKIP predisposes to familial myeloid malignancies, including myeloproliferative neoplasms, frequently progressing to leukemia [6].</td>
</tr>
<tr>
<td>CEBPA</td>
<td>AD</td>
<td>Mutations in the CEBPA gene are associated with familial acute myeloid leukemia (AML). Typically the first mutation present in the germline within the 5’ end of the gene, and a second 3’ mutation is acquired within the leukemia. Though germline 3’ CEBPA mutations have also been identified. CEBPA mutations confer a relatively favorable prognosis. Patients found to have biallelic CEBPA mutations within their leukemic cells should be tested for germline mutations [7].</td>
</tr>
<tr>
<td>DDX41</td>
<td>AD</td>
<td>Recurrent mutations in the DEAD/H-box RNA helicase gene DDX41 have been reported in patients with familial and acquired myelodysplasia and acute myeloid leukemia [8].</td>
</tr>
<tr>
<td>ETV6</td>
<td>AD</td>
<td>Germline mutations in ETV6 are associated with thrombocytopenia, red cell macrocytosis and predisposition to hematological malignancies [9-11].</td>
</tr>
</tbody>
</table>
| GATA2 | AD | Germline mutations in GATA2 have been described in association with familial MDS/AML, as well as with several heterogeneous clinical syndromes, including Emberger syndrome and the
MonoMAC syndrome which show an overall increased risk of developing MDS/AML [7, 12]. Although the incidence of MDS/AL appears very high, there is incomplete penetrance, with some individuals living into late adulthood without developing malignancy or demonstrating hematologic or infectious abnormalities [1].

IKZF1  AD  A germline IKZF1 mutation can cause an autosomal dominant form of common variable immunodeficiency that is associated with a striking decrease in B-cell numbers, and is a predisposition to B-cell precursor acute lymphoblastic leukemia, pancytopenia and autoimmune diseases [13, 14].

PAX5  AD  PAX5 is a member of the PAX family of transcription factors and is required for normal B cell development. Germline mutations in PAX5 are associated with susceptibility to B cell precursor acute lymphoblastic leukemia (B-ALL) [15, 16].

RTEL1  AD/AR  Both dominant and recessive mutations in the RTEL1 gene have been associated with Hoyeraaal Heidarrsson syndrome, a clinically severe variant of DC with cerebellar hypoplasia, severe immunodeficiency, enteropathy, and intrauterine growth retardation [17]. Anticipation has been described in one family where two affected males inherited a heterozygous mutation from a clinically unaffected female with short telomeres [17]. Heterozygous mutations in RTEL1 have been reported in patients with bone marrow failure and myelodysplastic syndromes [18, 19].

RUNX1  AD  Germline mutations of RUNX1 can cause familial platelet disorder with propensity to myeloid malignancy (FPD/AML). The clinical presentation is highly variable, but typically includes a lifelong mild to moderate bleeding tendency due to quantitative and/or functional platelet defects. The incidence of MDS/AL in individuals with germline RUNX1 mutations is over 40% [2, 20]. Patients may present with MDS/AL at any age, with a median age of onset of 33 years and a range of 6 – 76 years [1]. Different FPD/AL families have varying risks of progressing to myeloid malignancy due to different mutations [7].

SAMD9  AD  Mutations in SAMD9 cause a multisystem disorder including myelodysplasia, infection, restriction of growth, adrenal hypoplasia, genital phenotypes, and enteropathy. Patients carrying a SAMD9 mutation can develop MDS that was accompanied by loss of the chromosome 7 [21, 22].

SAMD9L  AD  Mutations in SAMD9L cause ataxia-pancytopenia syndrome which is characterized by cerebellar ataxia, variable hematologic cytopenias, and predisposition to marrow failure, myelodysplastic syndrome and myeloid leukemia, sometimes associated with monosomy 7. Hematopoietic revertant mosaicism has been reported and was associated with milder disease [23, 24].

SRP72  AD  SRP72 encodes one of six protein subunits of the signal recognition particle (SRP), part of the cellular apparatus responsible for nascent protein processing and trafficking. To date, only a small number of families have been identified with SRP72 mutations and aplastic anemia/MDS [7].

TERC  AD  TERC mutations cause autosomal dominant dyskeratosis congenita which often presents later in life without classic mucocutaneous symptoms. TERC mutations are associated with anticipation, with progressively shorter telomeres passed down through generations [25]. Members of earlier generations often demonstrate mild disease, whereas those of younger generations experience more severe disease manifestations, such as aplastic anemia or MDS/AML [7, 26-28].

TERT  AD  Heterozygous mutations in the TERT gene are associated with autosomal dominant dyskeratosis congenita. Penetration of these mutations appears to be reduced, with some individuals being asymptomatic [29]. Variable expressivity has also been described, with some individuals being mildly affected [29]. More severe disease manifestations may include aplastic anemia or MDS/AML [7, 26-28].

TP53  AD  Li-Fraumeni syndrome, caused by an inherited germline mutation in the TP53 tumor suppressor genes, presents with an increased risk of nearly all malignancies, including leukemias [2, 30].

Tier 2: Familial Myelodysplastic Syndrome/Acute Leukemia Panel

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<td>ATM</td>
<td>AR</td>
<td>Approximately 10% of patients with ataxia telangiectasia due to biallelic ATM mutations develop cancer, mostly of the lymphoid malignancies including Hodgkin’s lymphoma, non-Hodgkin’s lymphoma, and several forms of leukemia [31, 32]. AML has also been reported in patients with AT [33, 34].</td>
</tr>
<tr>
<td>BLM</td>
<td>AR</td>
<td>Mutations in the gene encoding DNA helicase RecQ protein-like-3 (BLM) cause Bloom syndrome. A 13%-25% lifetime risk of MDS/AML has been reported in patients with Bloom syndrome [20, 30].</td>
</tr>
<tr>
<td>BRCA1</td>
<td>AD</td>
<td>Germline mutations in BRCA1 increase the risks of breast or ovary cancer and many other types of cancer, including myeloid leukemia [35-37].</td>
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<tr>
<td>BRCA2</td>
<td>AD</td>
<td>Germline mutations in BRCA2 predispose individual to a number of different cancers, including leukemia [35-37].</td>
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<tr>
<td>CBL</td>
<td>AD</td>
<td>Germline mutations of the CBL gene are associated with CBL syndrome with predisposition to juvenile myelomonocytic leukemia [38].</td>
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<tr>
<td>Gene</td>
<td>Mutation Type</td>
<td>Description</td>
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<tr>
<td>CHEK2 (CHK2)</td>
<td>AD</td>
<td>Li-Fraumeni syndrome, which can be caused by an inherited germline mutation in the CHEK2 tumor suppressor gene, presents with an increased risk of nearly all malignancies, including leukemias [2, 30].</td>
</tr>
<tr>
<td>MLH1</td>
<td>AR/AD</td>
<td>Heterozygous mutations in MLH1, MSH2, MSH6 and PMS2 are associated with hereditary nonpolyposis colon cancer (HNPCC), which is associated with an increased risk of certain cancers, particularly colon and ovarian cancers. Homozygous or compound heterozygous mutations in these genes lead to a mismatch repair deficiency that can result in a mutator phenotype characterized by early onset gastrointestinal tumors, leukemia and/or lymphoma and features of neurofibromatosis type 1. These features can be summarized with the acronym CoLoN' (Colon tumors or/and Leukemia/Lymphoma or/and Neurofibromatosis features) [39-41].</td>
</tr>
<tr>
<td>NBN (NBS1)</td>
<td>AR</td>
<td>Biallelic mutations in the NBS1 gene are responsible for the Nijmegen breakage syndrome which display an elevated risk to lymphoblastic leukemia [40].</td>
</tr>
<tr>
<td>NF1</td>
<td>AD</td>
<td>NF1 microdeletions are associated with a more severe neurofibromatosis 1 (NF1) phenotype and increased risk for developing malignant tumors, including leukemias (especially juvenile myelomonocytic leukemia, with a risk of progression toward AML) [42, 43].</td>
</tr>
<tr>
<td>PTPN11</td>
<td>AD</td>
<td>PTPN11 mutations are the most common cause of Noonan syndrome, and cause 90% of LEOPARD syndrome cases [44]. Patients with Noonan syndrome and LEOPARD syndrome have a predisposition for leukemia and certain solid tumors [45-47]. Noonan syndrome and a pathogenic PTPN11 mutation represents a 3.5 times increased risk of developing a cancer compared with the general population [47].</td>
</tr>
</tbody>
</table>

**Testing Options**

**Comprehensive Familial Myelodysplastic Syndrome/Acute Leukemia Panel (sequencing and deletion/duplication analysis of 28 genes, deletion/duplication analysis only of two additional genes)**

- **Sample specifications:** 2 T-25 flasks of cultured skin fibroblasts, or DNA extracted from fibroblasts. NOTE: Peripheral blood samples are not accepted for patients with a history of MDS/leukemia.
- **Cost:** $4000
- **CPT codes:** 81406, 81407
- **Turn-around time:** 4-6 weeks

**Note:** We cannot bill insurance for this test.

**Tier 1: Familial Myelodysplastic Syndrome/Acute Leukemia Panel (sequencing and deletion/duplication analysis of 15 genes, deletion/duplication analysis only of two additional genes)**

- **Sample specifications:** 2 T-25 flasks of cultured skin fibroblasts, or DNA extracted from fibroblasts. NOTE: Peripheral blood samples are not accepted for patients with a history of MDS/leukemia.
- **Cost:** $3500
- **CPT codes:** 81406, 81407
- **Turn-around time:** 4-6 weeks

**Note:** We cannot bill insurance for this test.

**Tier 2: Familial Myelodysplastic Syndrome/Acute Leukemia Panel (sequence and deletion/duplication analysis of 13 genes)**

- **Sample specifications:** 2 T-25 flasks of cultured skin fibroblasts, or DNA extracted from fibroblasts. NOTE: Peripheral blood samples are not accepted for patients with a history of MDS/leukemia.
- **Cost:** $2000
- **CPT codes:** 81406, 81407
- **Turn-around time:** 4-6 weeks

**Note:** We cannot bill insurance for this test.

**Test methods:**

Comprehensive sequence coverage of the coding regions and splice junctions of all genes in this panel is performed. Targets of interests are enriched and prepared for sequencing using the Agilent SureSelect system. Sequencing is performed using Illumina technology and reads are aligned to the reference sequence. Variants are identified and evaluated using a custom collection of bioinformatic tools and comprehensively interpreted by our team of directors and genetic counselors. All pathogenic and likely pathogenic variants are confirmed by Sanger sequencing. The technical sensitivity of this test is estimated to be >99% for single nucleotide changes and insertions and deletions of less than 20 bp. Deletion/duplication analysis of the panel genes is performed by oligonucleotide array-CGH. Partial exonic copy number changes and rearrangements of less than 400 bp may not be detected by array-CGH. Array-CGH will not detect low-level mosaicism, balanced translocations, inversions, or point mutations that may be responsible for the clinical phenotype. The sensitivity of this assay may be reduced when DNA is extracted by an outside laboratory.
**Results:**
Results, along with an interpretive report, are faxed to the referring physician as soon as they are completed. One report will be issued for the entire panel. All abnormal results are reported by telephone.

*For more information about our testing options, please visit our website at dnatesting.uchicago.edu or contact us at 773-834-0555.*

**References:**


