### SPECIMEN REQUIREMENTS FOR MDS, CLL, ALL, AML, OTHERS

<table>
<thead>
<tr>
<th>Specimen</th>
<th>Minimum Volume</th>
<th>Maximum Volume</th>
<th>Container</th>
</tr>
</thead>
<tbody>
<tr>
<td>Whole blood</td>
<td>2 mL</td>
<td>10 mL</td>
<td>Lavender-top (EDTA) tube</td>
</tr>
<tr>
<td>Bone marrow</td>
<td>1 mL</td>
<td>2 mL</td>
<td>Green-top (heparin) tube</td>
</tr>
<tr>
<td>Leukemia</td>
<td>1 mL</td>
<td>2 mL</td>
<td>Lavender-top (EDTA) tube</td>
</tr>
<tr>
<td>Bone marrow</td>
<td>2 mL</td>
<td>4 mL</td>
<td>Yellow-top (ACD) tube</td>
</tr>
<tr>
<td>Bone marrow</td>
<td>1 mL</td>
<td>2 mL</td>
<td>Lavender-top (EDTA) tube</td>
</tr>
<tr>
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</tr>
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<td>1 mL</td>
<td>4 mL</td>
<td>Green-top (heparin) tube</td>
</tr>
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<td>Lavender-top (EDTA) tube</td>
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<td>Bone marrow</td>
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<td>2 mL</td>
<td>Green-top (heparin) tube</td>
</tr>
</tbody>
</table>

**NOTE:** 1-3 mL bone marrow in green-top (heparin) tube if MM FISH is also requested.

### SPECIMEN REQUIREMENTS FOR MM*

<table>
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<tr>
<th>Specimen</th>
<th>Minimum Volume</th>
<th>Maximum Volume</th>
<th>Container</th>
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<tbody>
<tr>
<td>Bone marrow</td>
<td>1 mL</td>
<td>2 mL</td>
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</tr>
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*If MM FISH is also requested, please provide 1-3 mL bone marrow in green-top (heparin) tube.

### REFERENCES


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www.integratedoncology.com
Myelodysplastic syndromes (MDS) and acute myeloid leukemia (AML)

**Reveal SNP Microarray**

A genome-wide array that utilizes single nucleotide polymorphism (SNP) and nonpolymorphic probes for high-resolution analysis in the detection of chromosomal copy-number variations (CNVs) and copy-neutral loss of heterozygosity (CN-LOH).

**Comparison of Chromosomal Abnormality Detection Technologies**

- Whole-genome SNP Microarray
- SNP Microarray whole-genome Virtual Karyotype
- High resolution; can detect small changes
- Can be used to detect disease-specific translocations
- Cytogenetics
- Low resolution limits detection
- Detects numerous small deletions and some cryptic rearrangements (CUX1, NFI, ETV6) not detected by standard cytogenetics
- Normal karyotype
- Does not detect CN-LOH
- Does not detect CN-LOH
- Leukemia
- Detects abnormalities in 74% of cases, as compared to 44% by cytogenetics alone.
- CN-LOH is detected by Reveal SNP Microarray
- CN-LOH is the loss of heterozygosity without the loss of copy number
- CN-LOH has been reported in MDS, CLL, ALL, and AML, involving a variety of chromosomes, including chromosomes 4, 7, 9, 13, 14, and 17.
- **Cytogenetics**
- Cytogenetics
- - Low-resolution karyotype
- - Detects structural abnormalities
- - Does not detect CN-LOH
- **Lesions by Comparison of Chromosomal Abnormality Detection Technologies**

**Identification of Additional Chromosomal Alterations has Prognostic Impact in MDS**

- **Results of metaphase cytogenetic analysis are an important component of the International Prognostic Scoring System (IPSS)**
- A recent study has shown that additional information provided from assays like Reveal SNP Microarray can impact prognostic classification of MDS patients.

**Detection of Copy Neutral Loss of Heterozygosity (CN-LOH)**

- CN-LOH is the loss of heterozygosity without the loss of copy number
- CN-LOH has been reported in MDS, CLL, ALL, AML, and ALL-involving a variety of chromosomes, including chromosomes 4, 7, 9, 13, 14, and 17.
- **Cytogenetics**
- Cytogenetics
- - Low-resolution karyotype
- - Detects structural abnormalities
- - Does not detect CN-LOH
- **Lesions by Comparison of Chromosomal Abnormality Detection Technologies**

**Chronic Lymphocytic Leukemia (CLL) and Acute Lymphocytic Leukemia (ALL)**

**Reveal SNP Microarray Identifies Abnormalities in CLL**

- Comparative studies of >450 cases tested by both FISH and Reveal SNP Microarray performed at LabCorp’s Center for Molecular Biology and Pathology showed that Reveal SNP Microarray increased detection of chromosomal abnormalities compared to FISH.
- Approximately 30% of FISH-normal CLL patients had an abnormality detected by Reveal SNP Microarray.
- Approximately 45% of patients with a 13q deletion had a deletion of the RB1 tumor-suppressor gene. Deletions of the RB1 gene may be associated with a more adverse prognosis.

**Reveal SNP Microarray is a Useful Prognostic Tool for Evaluating CLL**

- Studies have investigated the significance of acquired copy number changes (aCN) in both untreated and relapsed patients.
- Two or more aCN were shown to be present in 39% of cases (34% untreated, 56% relapsed).
- The detection of ≥2 aCN showed to be predictive of shortened time to first treatment (TTF) and overall survival (OS).

**Reveal SNP Array May Add Additional Prognostic Information in ALL**

- Detects abnormalities in 83% of patients with normal cytogenetics and detects additional abnormalities in 35% of patients with abnormal cytogenetics.
- Detects RUNX1 amplification, IKZF deletions, hypodiploid doubling, and some cryptic rearrangements.

<table>
<thead>
<tr>
<th>Prognostic Groups Based on MC and SNP</th>
<th>t-statistic</th>
<th>P*</th>
</tr>
</thead>
<tbody>
<tr>
<td>Favorable (t(12;21), t(4;11), del(17p))</td>
<td>t-statistic = 4.0</td>
<td>&lt; .0001</td>
</tr>
<tr>
<td>Intermediate-1</td>
<td>t-statistic = 3.4</td>
<td>&lt; .0001</td>
</tr>
<tr>
<td>Intermediate-2</td>
<td>t-statistic = 3.5</td>
<td>&lt; .0001</td>
</tr>
<tr>
<td>Unfavorable</td>
<td>t-statistic = 4.0</td>
<td>&lt; .0001</td>
</tr>
</tbody>
</table>

*Data sourced from studies performed at LabCorp’s Center for Molecular Biology and Pathology.
Reveal® SNP Microarray is a genome-wide array that utilizes single nucleotide polymorphism (SNP) and non-polymorphic probes for high-resolution analysis in the detection of chromosomal copy number variations (CNV) and copy-neutral loss of heterozygosity (CN-LOH).

Myelodysplastic syndromes (MDS), chronic lymphocytic leukemia (CLL), multiple myeloma (MM), acute myeloid leukemia (AML), and acute lymphoblastic leukemia (ALL) are especially suitable for Reveal SNP Microarray analysis because of the high incidence of dosage-related clinical changes that have been demonstrated to have an impact on patient outcomes.

### MYELODYSPLASTIC SYNDROMES (MDS) AND ACUTE MYELOID LEUKEMIA (AML)

**Reveal SNP Microarray Can Aid in the Diagnosis of MDS**

- Chromosomal abnormalities are shown to be detected by cytogenetics in ~50% of MDS.
- In a study of 430 patients, the SNP array in combination with cytogenetics was shown to detect abnormalities in 10% of cases, as compared to 48% by cytogenetics alone.
- **Reveal SNP Microarray has been shown to provide additional diagnostic and prognostic information for MDS patients with normal karyotypes.**

**Reveal SNP Microarray Identifies Abnormalities in CLL and MM**

- Approximately 30% of FISH-normal CLL patients had an abnormality detected by Reveal SNP Microarray.
- Approximately 45% of patients with a 13q deletion had a deletion of the Rb1 tumor-suppressor gene.
- Deletions of the Rb1 gene may be associated with a more adverse prognosis.

### CHRONIC LYMPHOCYTIC LEUKEMIA (CLL) AND ACUTE LYMPHOCYTIC LEUKEMIA (ALL)

**Reveal SNP Microarray Identifies Abnormalities in CLL**

- Comparative studies of ~500 cases tested by both FISH and Reveal SNP Microarray performed at LabCorp's Center for Molecular Biology and Pathology showed that Reveal SNP Microarray increased detection of chromosomal abnormalities compared to FISH.
- Approximately 30% of FISH-normal CLL patients had an abnormality detected by Reveal SNP Microarray.
- Approximately 45% of patients with a 13q deletion had a deletion of the Rb1 tumor-suppressor gene.
- Deletions of the Rb1 gene may be associated with a more adverse prognosis.

**Reveal SNP Microarray is a Useful Prognostic Tool for Evaluating ALL**

- Studies have investigated the significance of acquired copy number changes (aCN) in both untreated and relapsed patients.
- Two or more aCN were shown to be present in 39% of cases (35% untreated, 56% relapsed).
- The detection of ≥2 aCN showed to be predictive of shortened time to first treatment (TTFI) and overall survival (OS).

---

**Prognostic Groups Based on MC and SNP**

<table>
<thead>
<tr>
<th>Prognostic Group</th>
<th>Median EFS, mo</th>
<th>Median OS, mo</th>
</tr>
</thead>
<tbody>
<tr>
<td>Favorable</td>
<td>≥166</td>
<td>≥7</td>
</tr>
<tr>
<td>Intermediate-1</td>
<td>4-165</td>
<td>4-165</td>
</tr>
<tr>
<td>Intermediate-2</td>
<td>&lt;4-165</td>
<td>&lt;4-165</td>
</tr>
<tr>
<td>Unfavorable</td>
<td>&lt;2</td>
<td>&lt;2</td>
</tr>
</tbody>
</table>

**Comparison of Chromosomal Abnormality Detection Technologies**

<table>
<thead>
<tr>
<th>Class</th>
<th>Cytogenetics</th>
<th>Fluorescence In Situ Hybridization (FISH)</th>
<th>Whole-Genome SNP Microarray</th>
</tr>
</thead>
<tbody>
<tr>
<td>Normal karyotype</td>
<td>- Low resolution limits detection of aberrations</td>
<td>- Requires mitotic activity to detect clonal abnormalities</td>
<td>- Whole-genome perspective can detect CN-LOH</td>
</tr>
<tr>
<td>CN-LOH</td>
<td>- Whole-genome perspective</td>
<td>- Low resolution limits detection of aberrations</td>
<td>- Detects numerous small deletions and some cryptic rearrangements (CUX1, NF1, ETV6) not detected by standard cytogenetics</td>
</tr>
</tbody>
</table>
|CN-LOH (2009) has been reported in MDS, CML, MM, AML, and ALL, involving a variety of chromosomes, including chromosomes 4, 7, 9, 11, 13, 14, and 17.

**Detection of Copy Neutral Loss of Heterozygosity (CN-LOH)**

- CN-LOH is loss of heterozygosity without the loss of copy number.
- CN-LOH has been reported in MDS, CML, MM, AML, ALL, involving a variety of chromosomes, including chromosomes 4, 7, 9, 11, 13, 14, and 17.
- CN-LOH is detected by Reveal SNP Microarray but not detectable by standard cytogenetics.

**Reveal SNP Array May Add Additional Prognostic Information in AML**

- Detects abnormalities in 62% of patients with normal cytogenetics and detects additional abnormalities in 30% of patients with abnormal cytogenetics.
- Detects numerous small deletions and some cryptic rearrangements (CUX1, NF1, ETV6) not detected by standard cytogenetics.

---

*Data sourced from studies performed at LabCorp’s Center for Molecular Biology and Pathology.*
good
no
11.7
yes
0
median
2
47
very good
3.4
10
intermediate
30.4
3
new
that have been demonstrated to have an impact on patient outcomes.

acute myeloid leukemia (AML), and acute lymphocytic leukemia (ALL) are especially suitable for
myelodysplastic syndromes (MDS), chronic lymphocytic leukemia (CLL), multiple myeloma (MM),
and acute lymphocytic leukemia (ALL) are especially suitable for

Intermediate
30.4
3

Normal Karyotype

whole-genome SNP array

mitotic activity to

low resolution limits detection

only detects targeted genes

not detect CN-LOH

Fluorescence In Situ Hybridization (FISH)

whole-genome SNP array

Metaphase Cytogenetics (MC)

Can be used to detect disease- 

interstitial deletions

Oligonucleotide microarray

mitotic LOH: Mitotic

CN-LOH

Immunohistochemistry (IHC)

CN-LOH

Mitosis

comparison of chromosomal abnormality detection technologies

Comparison of Chromosomal Abnormality Detection Technologies

Negative

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®

SNP Microarray

CN-LOH

Rearrangeement

CN-LOH

Reverse-Transcribed Oligo-DNA

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**MULTIPLE MYELOMA (MM)**

*Reveal* Detects Abnormalities Unidentified by Classic Cytogenetic Studies

- Approximately 70% of MM patients have a normal karyotype and only 40% of MM patients have genetic alteration detected by FISH.
- Reveal has been shown to detect abnormalities in 50% of cases with normal cytogenetics and/or FISH.
- Reveal has also been shown to detect additional abnormalities in 85% of cases with abnormal cytogenetics and/or FISH. Each case either had additional abnormalities detected or the abnormalities were better-defined.* 

<table>
<thead>
<tr>
<th>Frequency Detected Genetic Abnormalities in Multiple Myeloma</th>
</tr>
</thead>
<tbody>
<tr>
<td>Abnormality</td>
</tr>
<tr>
<td>-------------</td>
</tr>
<tr>
<td>Chromothripsis</td>
</tr>
<tr>
<td>Heterozygosity of tumor suppressor gene</td>
</tr>
<tr>
<td>Amplification of 1q21</td>
</tr>
<tr>
<td>Homozygous loss of specific sub-chromosomal material</td>
</tr>
<tr>
<td>Copy-neutral loss of heterozygosity</td>
</tr>
<tr>
<td>Deletions of 1p, 6q, 8p, 12p, 14q, 16p, 19q, 20p, 22q</td>
</tr>
<tr>
<td>Amplification of 1q, 6p</td>
</tr>
<tr>
<td>12p deletions</td>
</tr>
<tr>
<td>13q deletions</td>
</tr>
<tr>
<td>16q deletions</td>
</tr>
<tr>
<td>20p deletions</td>
</tr>
</tbody>
</table>

**SPECIMEN REQUIREMENTS FOR MPS, CLL, ALL, AML, OTHERS**

**SPECIMEN REQUIREMENTS FOR MDS, CLL, ALL, AML, OTHERS**

**SPECIMEN REQUIREMENTS FOR MM**

**SPECIMEN REQUIREMENTS FOR MM**

<table>
<thead>
<tr>
<th>Abnormality</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Monosomy 13</td>
<td></td>
</tr>
<tr>
<td>Monosomy 17</td>
<td></td>
</tr>
<tr>
<td>Monosomy 18</td>
<td></td>
</tr>
<tr>
<td>Monosomy 21</td>
<td></td>
</tr>
</tbody>
</table>

**Turnaround Time:** 10-14 days

**References**


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Frequently Detected Genetic Abnormalities in Multiple Myeloma

<table>
<thead>
<tr>
<th>Abnormality</th>
<th>Description</th>
<th>% of Cases</th>
<th>Detected by SNP Array</th>
<th>Clinical Association</th>
</tr>
</thead>
<tbody>
<tr>
<td>t(11;14)</td>
<td>Chromosomal translocation involving IgH and cyclin D1 genes</td>
<td>3%</td>
<td>Yes</td>
<td>Frequently detected in 10% of myeloma cases</td>
</tr>
<tr>
<td>Del(17p)</td>
<td>Homogeneous deletion of chromosome 17p</td>
<td>5%</td>
<td>No</td>
<td>Suggests homozygous mutation in tumor suppressor gene</td>
</tr>
<tr>
<td>Del(17q)</td>
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<tr>
<td>Del(1p)</td>
<td>Homogeneous deletion of chromosome 1p</td>
<td>7%</td>
<td>No</td>
<td>Suggests homozygous mutation in tumor suppressor gene</td>
</tr>
<tr>
<td>Del(6q)</td>
<td>Homogeneous deletion of chromosome 6q</td>
<td>10%</td>
<td>No</td>
<td>Suggests homozygous mutation in tumor suppressor gene</td>
</tr>
<tr>
<td>Del(8p)</td>
<td>Homogeneous deletion of chromosome 8p</td>
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<tr>
<td>Del(16p)</td>
<td>Homogeneous deletion of chromosome 16p</td>
<td>2%</td>
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<tr>
<td>Del(20p)</td>
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<td>5%</td>
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<td>Ampl(1q)</td>
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