



# Specimens:	Depot:		
Collect Date:	Time:	By:	ABN Signed: <input type="checkbox"/>
MR #:	A #:		

STAT

REQUIRED (PRINT OR PATIENT LABEL)

Name (Last, First, MI) _____

Date of Birth _____ Sex: (circle) M F

Street Address _____

Street Address 2 _____

City, State, Zip _____

Phone Number _____ Client Number _____

Indicate primary (1) and secondary (2) insurance

Blue Cross/Shield Child Health Plus MVP

Blue Choice Medicaid MVPG

Medicare Blue Choice Medicare Aetna

Other _____

1. Primary Contract #: _____

Subscriber's Name: _____

Relationship to Subscriber: _____

2. Secondary Contract # _____

Subscriber's Name: _____

Relationship to Subscriber: _____

Practice Name _____

Address _____

Address2 _____

City, State, Zip _____

Phone# _____

Ordering Provider _____

Phone Results to: _____ Fax Results to: _____

Ordering Provider's Signature _____

Date of Signature _____

Diagnosis Mandatory: Signs/Symptoms or ICD9 Codes
If ordered for screening, list test name here and write "SCREENING" after it

Send Additional Reports To: (Full Name/Address) _____

Compliance is Mandatory and Regulated. For the laboratory to bill properly and receive payment for tests ordered on Medicare Beneficiaries, specific ICD-9 code(s) or a descriptive diagnosis must be included on each patient for each test ordered. It is critical that the diagnosis provided to the lab is consistent with those recorded in the patient medical record on the date of service.

SPECIMEN TYPE SUBMITTED

<input type="checkbox"/> Blood	<input type="checkbox"/> Lymph Node Tissue
<input type="checkbox"/> Bone Marrow Aspirate	<input type="checkbox"/> Spleen Tissue
<input type="checkbox"/> Bone Marrow Core Biopsy	<input type="checkbox"/> Other Tissue (Type: _____)
<input type="checkbox"/> Fine Needle Aspirate	<input type="checkbox"/> Stem Cell Product
<input type="checkbox"/> Needle Core Biopsy. Other Tissue	

STUDIES REQUESTED

<p>Flow Cytometry</p> <p><input type="checkbox"/> (18240) Flow Cytometry for lymphoma/leukemia workup</p> <p><input type="checkbox"/> (28695) Lymphocyte subset testing (CD4/CD8)</p> <p><input type="checkbox"/> (29277) CD34 - Stem cell counts</p> <p><input type="checkbox"/> (18240) Paroxysmal Nocturnal Hemoglobinuria (PNH) Workup (GPI-linked protein studies)</p> <p>Cytogenetics</p> <p><input type="checkbox"/> (16807) Chromosome Analysis (Karyotype) Only</p> <p><input type="checkbox"/> (16807) Chromosome Analysis (Karyotype) and FISH</p> <p>_____</p> <p><input type="checkbox"/> (16807) FISH Only</p> <p>_____</p>	<p>Molecular Diagnostics</p> <p><input type="checkbox"/> (36680) IgKappa B cell gene rearrangement PCR</p> <p><input type="checkbox"/> (36680) IgH B cell gene rearrangement PCR</p> <p><input type="checkbox"/> (37343) T cell receptor gene rearrangement (TCRg)</p> <p><input type="checkbox"/> (22220) bcr-abl (major) RT-PCR t 9;22</p> <p><input type="checkbox"/> (42253) JAK2 V617F mutation</p> <p><input type="checkbox"/> (32206) FLT-3 mutation</p> <p><input type="checkbox"/> (24710) NPM1 (nucleophosmin)</p> <p><input type="checkbox"/> (CEBPA) CEBPA</p> <p><input type="checkbox"/> (REFLX) reflex if FLT-3 ITD and NPM1 are neg</p> <p>Reference Testing</p> <p><input type="checkbox"/> (BCRQL) bcr-abl (minor) RT-PCR</p> <p><input type="checkbox"/> (19815) t(115;17)(PML-RAR-X) RT-PCR</p>	<p><input type="checkbox"/> (CHIMR) Chimerism</p> <p><input type="checkbox"/> Pre Transplant</p> <p><input type="checkbox"/> Donor</p> <p><input type="checkbox"/> Recipient</p> <p><input type="checkbox"/> Post Transplant</p>
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RELEVANT CLINICAL HISTORY

(Check all that apply)

Previous bone marrow biopsies/aspirate, Date(s) _____

History of leukemia

History of lymphoma

History of myeloma (R/O Myeloma)

Recent history of growth factor treatment

Workup for myelodysplasia

Anemia

Neutropenia

Thrombocytopenia

Other Cytopenias

CBC Findings (Please enter relevant numbers):

Hemoglobin/Hematocrit: _____

Total WBC: _____

Plate Count: _____

Relevant Differential Findings (Blasts, Increased Basophils, Eosinophilia, etc.-Please specify):

Other relevant Information
(please write below):

284 Consent

Patient Name _____

Date of birth _____

Important Information about Genetic Testing

1. This test will look for changes in the DNA chromosomes, genes, or gene products which are known to be associated with the specific genetic condition in question.
2. This test may reveal that the individual tested is affected with the condition, carries the genetic pre-disposition for it, or that he/she does not. If a positive result is obtained, a medical and/or genetic counseling follow-up may be advised.
3. Genetic testing is ordinarily highly accurate, however, in some cases results may not be obtained or may be inconclusive. Also, accurate genetic testing depends upon an accurate diagnosis in affected family members. If the diagnosis in a family is not certain, results can be misleading. I have been able to discuss the expected accuracy of the testing in my particular case. Initial: _____
4. Some genetic testing may require comparison of samples from multiple family members with their consent, and in these cases, previous unknown non-paternity can be discovered.
5. Some genetic tests are only done by a few laboratories in the world. This sample may need to be sent out of state to laboratories that are not certified by the New York State Health Department. In these cases, approval for testing will be obtained from New York State.
6. Some types of genetic testing such as fluorescence in situ hybridization (FISH) are considered investigational by the New York State Health Department. Using DNA probes which bind to specific regions of the chromosomes, FISH is helpful in identifying the origin of unidentified "marker" chromosomes, unusual variations in chromosome structure or small chromosomal deletions which cannot be seen by standard chromosome testing. FISH may be used, if indicated on my sample. Initial : _____
7. Chromosome microarray CGH (Array CGH) test is considered to be investigational by the New York State Department of Health. Array CGH is helpful in detecting gains or losses of chromosomal material at the DNA level anywhere in the genome. The method uses cloned DNA probes 'on a chip' to detect deletions or duplications which cannot be seen by standard chromosome and FISH analysis. The purpose of this assay is to detect syndromic microdeletions/duplications and subtelomeric alterations. Copy number alterations of single loci may be false negative due to the limited resolution of the array CGH. Because array CGH is a new technology being used in clinical diagnosis, all abnormal array CGH findings will be confirmed by standard chromosome or FISH analysis. Parental studies and additional assays may be necessary to characterize and interpret the clinical significance of array CGH results. The array CGH is limited to the detection of copy number changes in the genome. It will not detect balanced translocations, inversions, low level mosaicism, point mutations and genomic regions not represented on the array.

Array CGH is used as an adjunct to chromosome analysis and all patients are required to have a chromosome analysis along with array CGH testing.

The patient or their legal counsel is required to sign an informed consent before the array CGH is performed. Due to the complexity of array CGH, the results will be reported directly to the ordering provider. Initial : _____

8. Records of this testing or test results will not be released to anyone other than me, my referring doctors and Strong Memorial Medical Records unless I specify otherwise. Initial: _____
9. No tests other than those authorized shall be performed on the biological sample and that the sample shall be destroyed at the end of the testing process or not more than sixty days after the sample was taken. Any part of the biological sample not used for specific genetic testing may be retained and used for medical research as long as names and other identifying information are not revealed. Initial : _____
10. I indicate my desire to opt out of participation in anonymized research studies using my DNA sample by checking this box: