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Array Comparative Genomic Hybridization (array CGH) Analysis for Hematological Malignancies

*See link for *Array CGH Clinical Testing for Hematological Malignancies Handout using the Agilent 4x180k aCGH+SNP array*

Description	Turn Around	CPT codes
This test utilizes the Agilent 4x180k aCGH+SNP array, which contains ~110,000 oligo probes for the detection of genomic copy number changes, and ~60,000 SNP probes for the detection of copy-neutral loss of heterozygosity (cn-LOH). This array contains genome-wide coverage with an average probe spacing of ~25 kb. It is designed to detect copy number changes with a minimum size of ~50 kb across the genome. This test will detect genomic copy number changes associated with unbalanced chromosomal rearrangements. It will detect aneuploidies, deletions, duplications, amplifications, and unbalanced translocations/insertions of the regions represented on the array, as well as cn-LOH. It has a greater resolution than both routine chromosome analysis and FISH analysis in detecting submicroscopic aberrations.	~2 weeks	81229x1

Specimen requirements: Bone marrow (BM) aspirate in a BM transport medium tube (4-5cc)One EDTA tube (purple top) tube and one sodium heparin (green top) tube

OR

Peripheral blood (PB) in one EDTA (Purple top) tube AND one sodium heparin (Green top) tube, 4-5 cc per tube

****At least 30% involvement of the BM or PB by the malignant process is required**