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HLID#: **PATIENT NAME:** .
PATIENT ID#: **DOB :** **SEX:**
NPI: **ORDERING PHYSICIAN:**
SPECIMEN TYPE: Bone Marrow Aspirate
COLLECTION DATE: **RECEIPT DATE:**
REPORT DATE: **ICD-9:** **UNITS:** 1 Microarray

CLINIC ID#:
ACCOUNT: CPT:

Patient Name HLID#

Specimen Type: Bone Marrow Aspirate

Clinical History/Indications: A xx year old male with a listed clinical history of myelodysplastic syndrome (MDS). Previous flow cytometry results revealed abnormal myeloid antigen expression and abnormal myeloblasts in 1.2% of the bone marrow, **FISH and cytogenetic studies were negative** (see separate reports).

aCGH/SNP Microarray : ABNORMAL

Positive for gain of 8q24.13-q24.21 (4 Mb) [including c-MYC]

Interpretation:

- **These findings reveal the presence of an aberrant cell population harboring a 4 Mb gain at 8q24.**
- **Amplification of the c-MYC gene (located at 8q24) has been reported in MDS and AML** *[Storlazzi et al. 2006 Hum Mole Gene 15/6]*.
- **Clinical and histological correlation required for definitive diagnosis.**

The presence of chromosome aberrations and LOH/UPD** below the detection sensitivity of this analysis (20% for gains and losses; 1 Mb in length for gains or losses and 20 Mb for LOH/UPD) cannot be completely ruled out.*

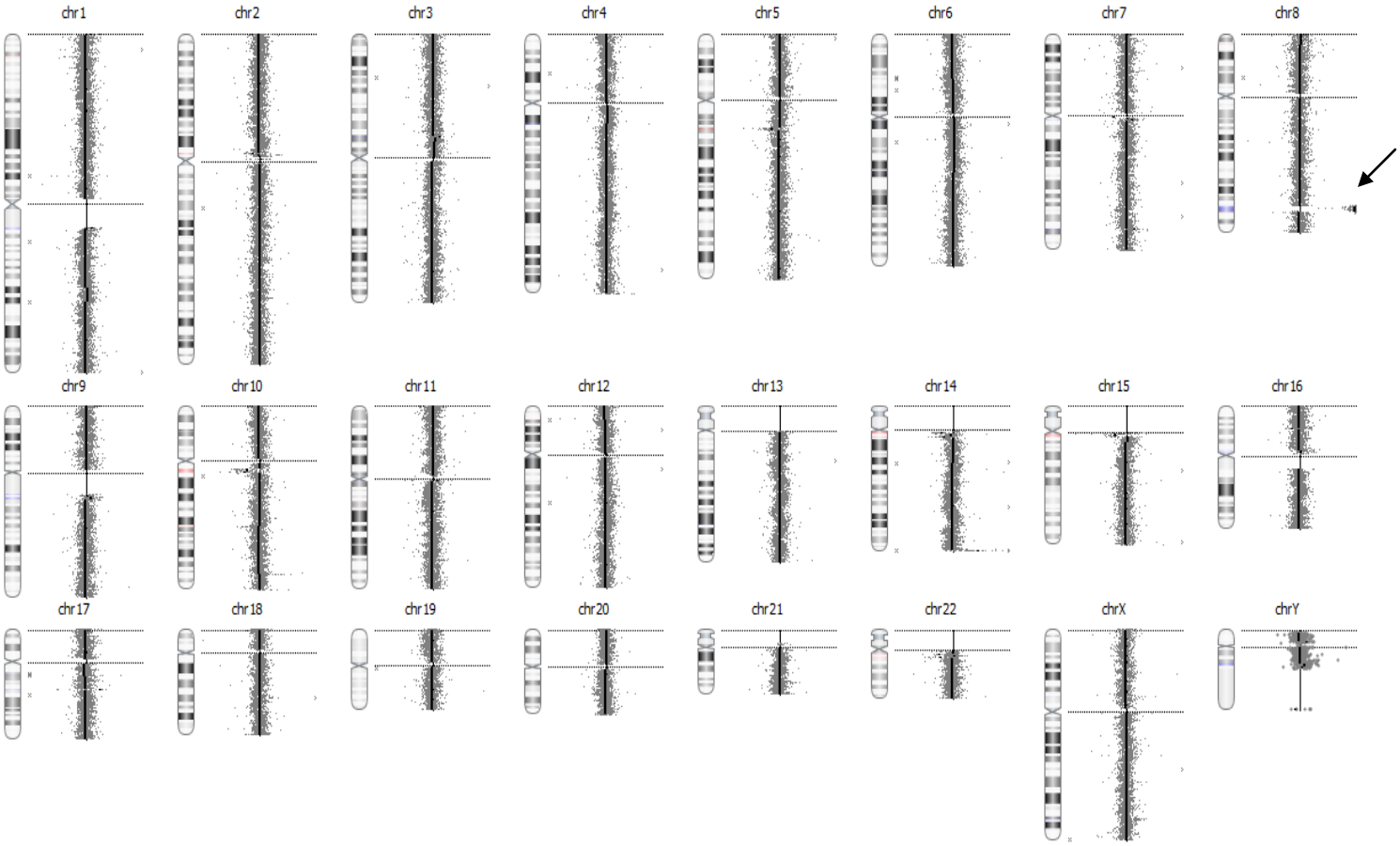
***Loss of heterozygosity (LOH)** is defined as consecutive homozygous SNP tracts exceeding 1Mb in length. LOH can result from deletion of all copies of one homolog or from **uniparental disomy** (UPD)** in which both copies, or region, of a chromosome pair have the same parental origin. Regions of UPD are continuous stretches of homozygous SNP calls (LOH) *without copy number loss.* Both LOH and UPD play known roles in tumorigenesis.

Method: Genomic DNA was isolated from the whole bone marrow aspirate. Oligonucleotide array-based comparative genomic hybridization (array CGH) and SNP (single nucleotide polymorphism) analysis of 180,000 genomic loci, including ~20,000 cancer-associated CGH as well as ~60,000 SNP probes, was performed on the extracted DNA sample and referenced to a normal male DNA sample.

PATIENT NAME:

HLID#: **UNITS:** 1 **DOB :** **SEX:**

SPECIMEN TYPE: **Bone Marrow Aspirate** **COLLECTION DATE:** **CLINIC ID#:**



Electronically signed by: Barbara K. Zehentner, Ph.D., HCLD (ABB), Director of Molecular Analysis and Denise A. Wells, MD, Medical Director

This test was developed and its performance characteristics determined by HematoLogics, Inc. It has not been cleared or approved by the US Food and Drug Administration