Q014

CHROMOSOME ANALYSIS, SOLID TUMOUR

Name	**: DUMMY**			**Collected:**
				Received:
Lab No.	**: 135091313**	**Age : 28 Years**	**Gender: Male**	**Reported:**
A/c Status	**: P**	**Ref by : DUMMY**		**Report Status: Final**

Interpretation

Specimen received

Specimen type: Solid Tumor (Retroperitoneal Mass)

Reason for referral: Neoplasm of Retroperitoneum, Low-grade lipomatous tumor, MDM2 Amplification Negative

Test performed: Chromosome Analysis

Laboratory analysis
Number of cells counted: 20
Number of cells analyzed: 20
Number of cells karyotyped: 20
ISCN Band level: 375
Banding Method: G-Banding

Chromosome results:
46,XY,t(3;11)(p13;p14),add(8)(q11.2)[cp19]/46,XY[1]

Diagnostic Impression:
An abnormal male cell line was detected in multiple cultures from this patient. It showed the following clonal aberrations in 19/20 (95%) cells:
- a translocation between the short arms of chromosomes 3 and 11;
- added material resulting in a loss in long arm of chromosome 8.

There was some variation from cell to cell with the abnormalities present; therefore a composite (cp) of all the abnormalities is listed in the nomenclature.

The remaining 1/20 (5%) cells showed a normal male chromosome complement. These findings are consistent with a neoplastic process. Please correlate this result with clinical and other laboratory findings.

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Further analysis by cytogenomic SNP microarray analysis may prove informative. Cytogenomic microarray technology can be useful for characterizing uncertain genomic material detected by karyotype, as well as for detection of copy number alterations below the level of resolution of metaphase cytogenetics and copy neutral loss-of-heterozygosity (LOH), which may be helpful for diagnosis, prognosis and therapeutic decisions, as well as monitoring disease progression and response to therapy. Balanced rearrangements including translocations and inversions cannot be detected by this technology. Depending on the specimen type(s) available, LPL has several genomic microarray testing options.