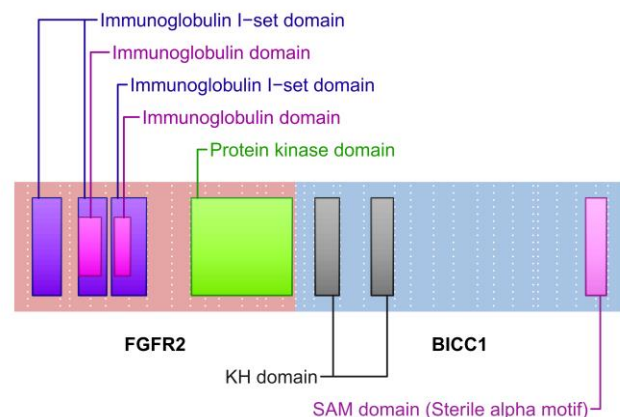
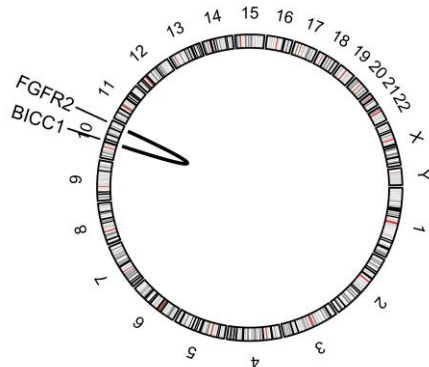


Material:	Block 12345/6789
Clinical Details:	Request for DNA based NGS FGFR2 fusion analysis
Histopathology:	Cholangiocarcinoma

Report:

Identified Fusion

5' Translocation Partner	3'Translocation Partner	Translocation Supporting Reads	Ratio Translocation Reads
<i>FGFR2 intron 17</i> Break point: chr10:123243212 GRCh37 - hg19	<i>BICC1 intron 2</i> Break point: chr10:60461834 GRCh37 - hg19	4321	49 %



Comments – Interpretation:

In the present material, an FGFR2::BICC1 translocation with breakpoints in FGFR2 intron 17 and BICC1 intron 2 was detected at the DNA level, consistent in principle with a fusion of FGFR2 exon 17 (NM_000141.4) and BICC1 exon 3 (NM_001080512.1). The predicted fusion transcript results in the loss of the negative regulatory C-terminal region of FGFR2, while the kinase domain remains complete and intact. Further, a respective fusion protein would contain domains facilitating polymerization (KH and SAM) contributed by BICC1. The scientific literature describes both aspects as recurrent oncogenic mechanisms in cholangiocarcinoma (PMID: #####).

Additional information:

Pre-analytics

<i>DNA input quantity:</i>	80 ng	<i>Mapped Fragments:</i>	2000000
<i>Tumor cell content:</i>	70 %	<i>Unique mapped Fragments:</i>	999999

Performed analytics

Fusion analysis was performed on the morphologically confirmed and enriched tumor tissue (70% tumor cell content) using next-generation sequencing technology (**SEQUENCING SYSTEM**) using a hybrid capture based assay (**ASSAY**), that allows the identification of fusion transcripts without the need to know the fusion partner. A list of the fusion genes analyzed is given below.

Investigated fusion genes in alphabetical order			
Gene A	Gene B	FGFR2 intron 17, exon 17-18	Gene Z