

Florina 01.01.2024

Dear Colleague,

We report the results from the analysis on patient (**ID-XXXX**) **XXXXXX** . The sample we received for analysis was a **XX ml** of whole blood that contained EDTA-Ca as anti-coagulant and packed with an ice pack. Upon arrival there were performed:

- Malignant cell isolation and then positive and negative selection using multiple cell markers.
- DNA extraction from the above cells and evaluation of the above with molecular-based assays as well with spectrophotometry.
- CGH experiments using commercial reference genomic DNA samples.

The results after process are presented below:

Chromosome/ Size	Start- Stop Position (bp)	Genes	Outcome
AMP 11p15.4/ 753 Kb	5529738- 6282871	UBQLN3 (OMIM), TRIM6 (OMIM), TRIM34 (OMIM), TRIM5 (OMIM), TRIM22 (OMIM), FAM160A2 (OMIM), CNGA4 (OMIM), CCKBR (OMIM), UBQLNL, OLFM5P, OR52H1, OR52B6, TRIM6-TRIM34, OR56B1, OR52N4, OR52N5, OR52N1, OR52N2, OR52E6, OR52E8, OR52E4, OR52E5, OR56A3, OR56A5, OR52L1, OR56A4, OR56A1, OR56B4, OR52B2, OR52W1, C11orf42	PATHOGENIC TRIM Family → Contribute to tumorigenesis, cancer development and drug resistance TRIM6 → Overexpressed in colorectal and breast cancer TRIM22 → Downregulated in gastric cancer. Overexpressed in glioblastoma.



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Appendix:

DEL: Deletion

AMP: Amplification

CNP: Copy Number Polymorphic-Normal variation in DNA which are common and widely distributed in human genome

Conclusion: The aberrations that have been detected are more compatible with breast carcinoma and less for colorectal.

Sincerely,

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