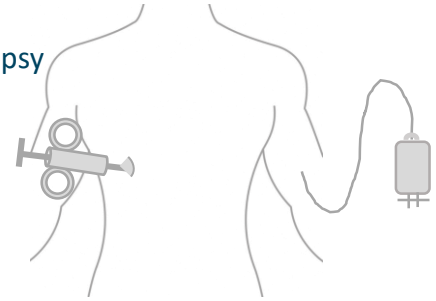
exosomics

The challenge:

Traditional biopsies are invasive and do not represent tumour heterogeneity. Liquid biopsies instead are minimally invasive, they capture the whole tumour picture but tumour-derived material is scarce and its detection in the bloodstream is challenging

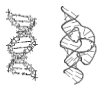
1.Traditional Biopsy

-Invasive.
-Time consuming.
-Does not represent the whole tumour.
-Cannot be used for monitoring.
-Risk associated.



2. Liquid Biopsy

-Minimally invasive.
-Cheaper.
-Tumour heterogeneity detectable -> better treatment indications
-Can be easily obtained and repeated -> ideal for screening, staging, profiling and monitoring.
-Preferred approach for unresectable tumours.



Circulating free nucleic acids (cfDNA & cfRNA)

-Come mostly from dead cells.
-Tumour causing mutation is barely detectable because of the confounding background noise: Needle in a haystack problem.
-Free circulating RNA is usually degraded, not good if looking for fusions.

Circulating Tumour Cells (CTCs)

-Cancers may shed cells into the bloodstream.
-Very rare.
-Requirement of very expensive instrumentation for detection.

Exosomes

-Exosomes (40-100nm) are released into the bloodstream especially from tumour cells.
-They contain and protect from degradation DNA, RNA and proteins, multi-analyte analysis possible.

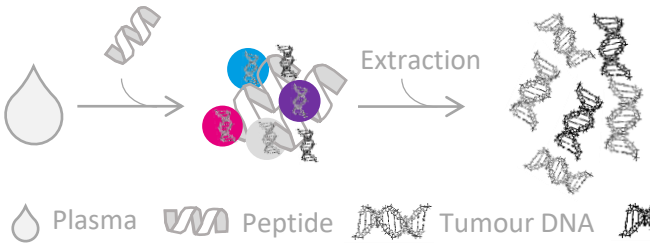
The solution:

Exosomics has a range of pre-analytical solutions to selectively isolate tumour-derived exosomes from biofluids and extract their tumour-derived content. This allows easier detection of tumour-causing mutations from liquid biopsies and enables the next generation of tumour screening, staging, profiling and monitoring tests.

Tumour-derived Exosomes

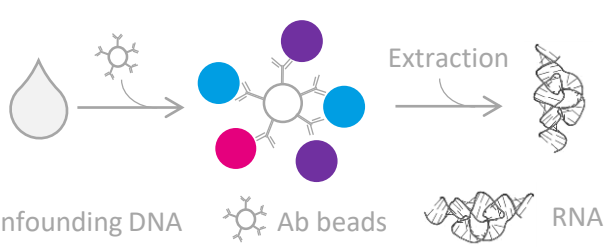
-Exosomics solutions allow selective isolation of tumour-derived exosomes and extraction of DNA or RNA through peptide-affinity or antibody-affinity methods, respectively.
-This allows better performance of any downstream analytical assay such as qPCR, ddPCR, hybridisation and NGS.

SeleCTEV™ Enrichment Kit (RUO)



-Peptide affinity purification
-Exosome isolation and DNA extraction workflows combined.
-Peptide pulls down tumour-derived exosomes and circulating DNA
-Best pre-analytical method to harvest as much as possible DNA from biofluids.
-It's easy, does not require complex ultracentrifugation or chromatography steps
-Enables better downstream analytical performance

SoRTEV ™ Enrichment Kit (RUO)



-Antibody coated beads pull down tumour-derived exosomes selectively.
-Best pre-analytical method to harvest the purest tumour-derived RNA from biofluids.
It's easy, does not require complex ultracentrifugation or chromatography steps.
-Enables the next generation of RNA-based tumour diagnostics assays.

Plasma

exosomics

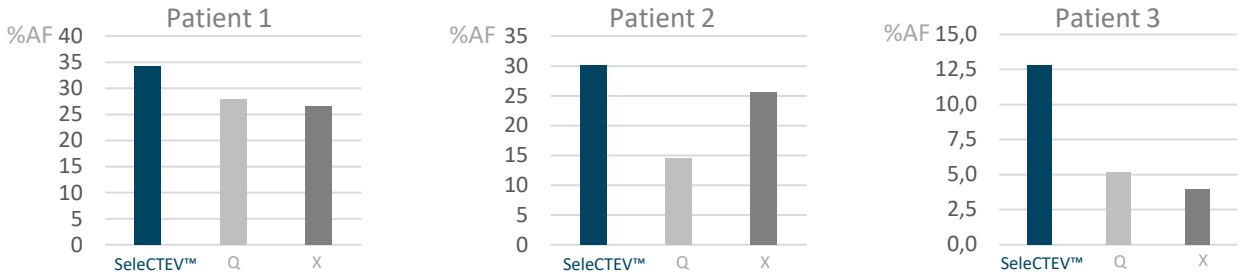
Tumour-derived material enrichment

qPCR
ddPCR
Hybridization
NGS
Your Analytical Assay

Lower % AF detectable
Improved stratification
More accurate staging
Earlier detection
Better Patient Outcomes

Case study #1: SeleCTEV™ – Metastatic Melanoma Patients, *BRAF* V600E detection

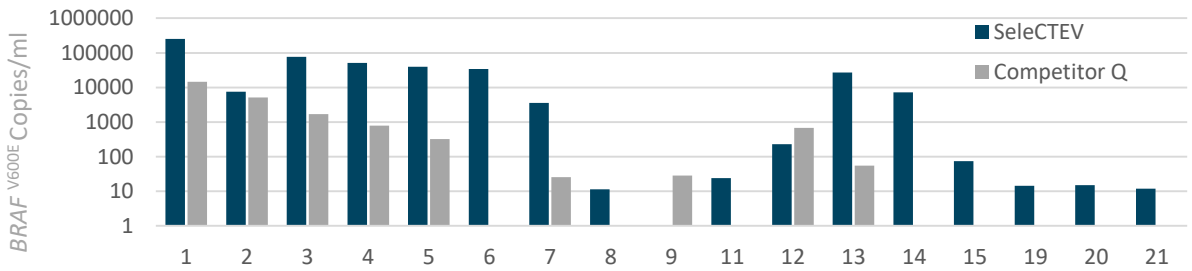
Plasma from three metastatic melanoma patients with *BRAF* V600E mutation was processed with either SeleCTEV™, Company X or Competitor Q to obtain DNA. Such DNA was then tested for *BRAF* V600E by ddPCR (BioRad®).



The bar represents the % of allelic frequency (%AF) of *BRAF* V600E detected. For all three patients the use of SeleCTEV™ as the pre-analytical step yielded tumour-enriched DNA as shown by a higher allelic frequency. Note that the lower is the allelic frequency in the patient the bigger is the difference between SeleCTEV™ and the competitors. This suggests the SeleCTEV™ performs better by increasing the signal to noise ratio especially in cases when the copy number of mutated DNA molecules is low and confounding background is high. Data generated by Company X, Belgium

Case study #2: SeleCTEV™ Metastatic Melanoma Patients, *BRAF* V600E detection

Plasma from twenty-one metastatic melanoma patients was processed with either SeleCTEV™ or Competitor Q to obtain DNA. Such DNA was then tested for *BRAF* V600E by ddPCR (Thermo®).

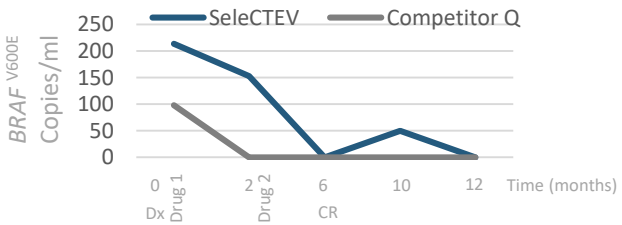


The bar represents the number of copies of *BRAF* V600E DNA detected. For almost all but 2 patients, the use of SeleCTEV™ as the pre-analytical step yielded a higher number of *BRAF* V600E - mutated gene copies. In seven cases SeleCTEV™ could detect the mutation whilst the competitor did not. Data generated by University of Brescia, Italy, manuscript in preparation.

Case study #3: SeleCTEV™

BRAF V600E Monitoring

Plasma from a single patient was withdrawn every two months from diagnosis and then processed with either SeleCTEV™ or Competitor Q to obtain DNA. Such DNA was then tested for *BRAF* V600E by ddPCR (Thermo®).

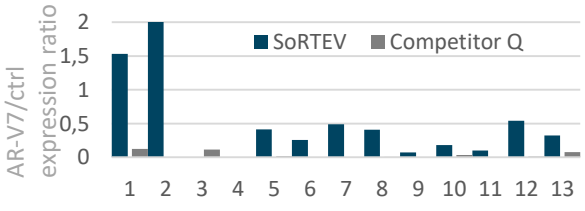


The lines represent the number of mutated DNA copies detected every two months from diagnosis. The use of SeleCTEV™ as the pre-analytical step yielded a higher number of copies of DNA mutated for *BRAF* V600E than the competitor Q. Data generated by University of Brescia, Italy, manuscript in preparation.

Case study #4: SoRTEV™

Androgen Receptor V7 (AR-V7) Detection

Plasma was withdrawn from thirteen prostate cancer patients and then processed with either SoRTEV™ or Competitor Q to obtain RNA. The ratio between AR-V7 and a control (ctrl) mRNA was tested by RT-ddPCR (Thermo®).



AR-V7 mRNA can be detected when SoRTEV™ is used as the pre-analytical step whilst it is not or barely detectable when Competitor Q is used. High levels of AR-V7 correlate with poor response to first and second line novel hormonal therapy in castration-resistant prostate cancer. Data generated by University of Brescia, Italy.

info@exosomics.eu