

PredicineRNA™

88-Gene cfRNA Liquid Biopsy Assay

cfRNA panel for detection of RNA-level fusions and splicing variants

88

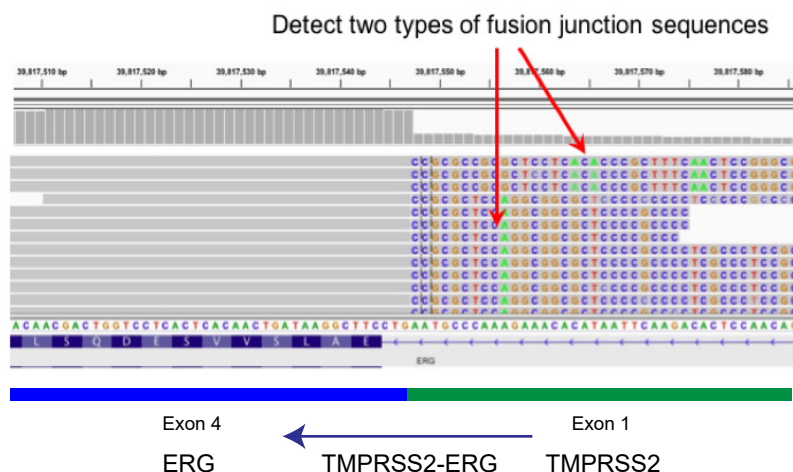
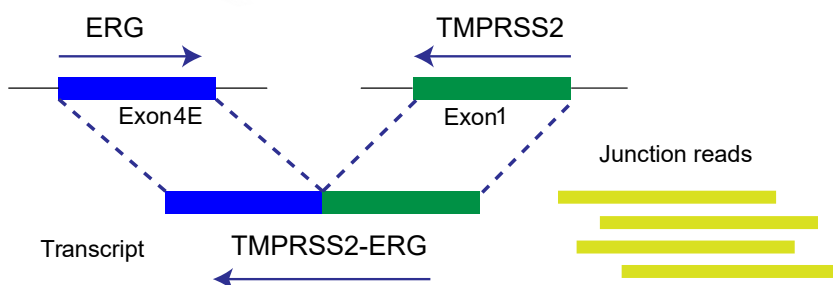
Fusion genes and splicing variants interrogated

1 tube

cfDNA+cfRNA co-extraction

10ng

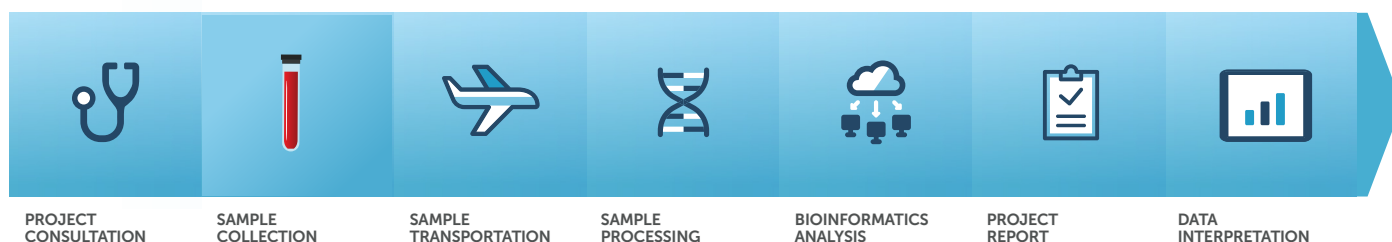
cfRNA Recommend input (down to 1ng)



Methods and Reporting

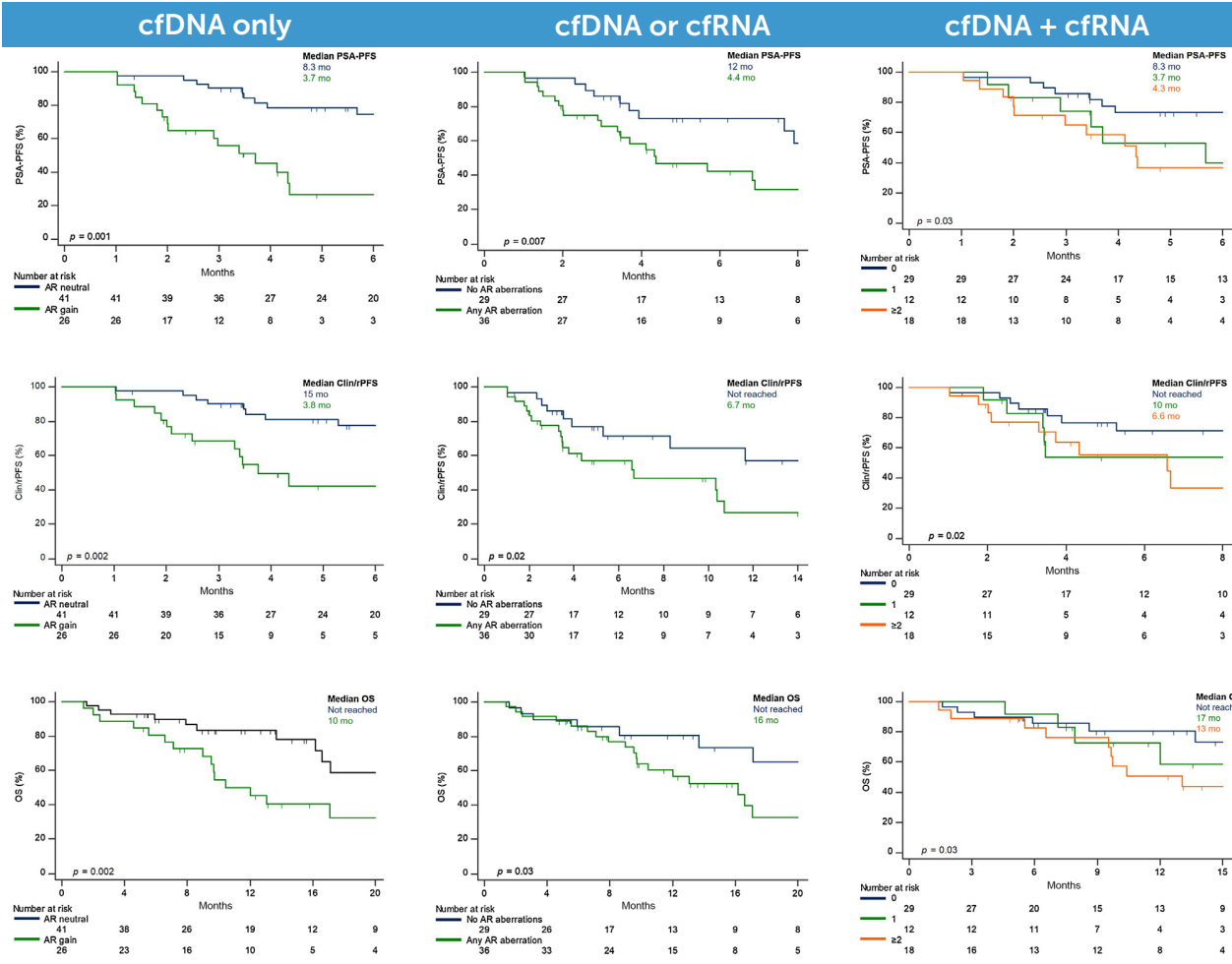
- Reports RNA-based fusions and splicing variants
- Improves overall fusion detection rate by detecting both known and novel fusion variants
- Co-extraction enables cfRNA and ctDNA analysis from a single sample from blood or plasma
- Uses a proprietary hybrid capture-based NGS methodology combined with in-house bioinformatics platform that enable accurate and sensitive detection of cancer variants
- Research Use Only (RUO)

Workflow



PERFORMANCE SPECIFICATIONS	
Specimen Type and Requirement	2-5 mL plasma 4-10 mL blood
Turnaround Time	14 days
Regions Analyzed	88 genes
Panel Size	53 kb
Sequencing	Illumina NGS

Case Study: Integrated cfDNA and cfRNA profiling of AR status in mCRPC patients*



Kaplan-Meier analysis of PSA-PFS (top), clinical or radiographic PFS (middle), and overall survival (bottom), according to AR copy number status (left), the presence of at least one of AR gain, AR splice variant, or AR somatic mutation (centre), and the total number of AR aberrations (0, 1, 2) present (right). Two and eight patients were excluded from analysis for any AR aberration and total AR aberrations, respectively, due to insufficient information on AR-V expression. AR = androgen receptor; AR-V = AR splice variant; Clin/rPFS = clinical/radiographic progression-free survival; OS = overall survival; PFS = progression-free survival; PSA = prostate-specific antigen.

Conclusions

- The data suggest that combined cfDNA and cfRNA sequencing may provide insights into prognosis and drug resistance mechanisms in metastatic castration-resistant prostate cancer (mCRPC).
- Using PredicineRNA assay in two independent cohorts, the authors identified a novel poor prognosis subgroup harbouring concurrent AR gain and expression of the AR-V splice variant.

*Fettke, et al. European Urology. 2020; 78(2): 173-180.