PGD | PLASMA*SELECT*-R™

PLASMA*SELECT*-R™ APPROACH

Plasma*Select*-R™ analyzes circulating tumor DNA for genetic alterations in cancer, eliminating the need for an invasive biopsy or tumor tissue. Plasma*Select*-R™ may also be used to evaluate sub-clonal mutations in tumor tissue, when available. Plasma*Select*-R™ evaluates a targeted panel of 63 well-characterized cancer genes. Cell-free DNA is extracted from plasma and prepared using proprietary methods that accommodate low abundance sample DNA. Samples are processed using a proprietary capture process and high coverage next-generation sequencing to allow tumor-specific (somatic) mutations, amplifications, and translocations to be identified with a high sensitivity and specificity. Analyses for sequence mutations or rearrangements can be performed together or separately, depending on the specific alterations of interest.

PLASMA*SELECT*-R™ HIGHLIGHTS

- Digital genomic sequencing combined with error correction methods enable discrimination of sequencing artifacts/errors from bona-fide somatic mutations with allele fractions as low as 0.10%
- DNA extraction and preparation methods that accommodate low abundance cell-free DNA samples
- Identification of mutated genes with biologic or clinical implications in human cancer
- Proprietary capture design and patented Digital Karyotyping analysis for high resolution analysis of copy number alterations with high sensitivity and specificity
- PARE (Personalized Analysis of Rearranged Ends) technology to identify structural changes in tumor-specific DNA, including translocations

PLASMA*SELECT*-R™ ANALYSIS DELIVERABLES

- Sequence alterations (single base and small indel alterations), amplifications and translocations
- Functional impact of mutations (predicted protein alterations and domain consequences)
- Altered genes and pathways with biological or clinical implications
- Data summary statistics (read data and depth distribution across target regions)
- Integrated Analysis Report (incidences and frequencies of mutations identified)

PLASMA*SELECT*-R™ SEQUENCING DELIVERABLES & ANALYSES

Analysis Metrics	Plasma*Select*-R™
Regions Analyzed	63 genes
Sample Prep and NGS Sequencing	✓
Sequence Mapping	✓
Somatic Mutation Analysis	✓
Amplification Analysis	✓
Translocation Analysis	✓
Integrated Project Analyses	✓

PLASMA*SELECT*-R™ SEQUENCING KEY METRICS

Regions Analyzed	Coding regions of 58 genes and/or selected regions of 10 genes
Sequencing Method	Illumina next generation sequencing
Bioinformatics	Patented PARE methods
Assay Sensitivity	>0.10% (>0.2% for amplifications)
Target Sequencing Coverage	20,000x
Turn-around Time	4 weeks
Sample Requirements	Blood or tumor tissue
Sample Types	Plasma or frozen tumor, FFPE, cell lines, and xenografts
Plasma Sample Input Required	10 ml (minimum 6 ml)
Tumor Sample Input Required	1 µg (minimum 50 ng)

PERSONAL GENOME DIAGNOSTICS | 2809 BOSTON STREET, SUITE 503 | BALTIMORE, MARYLAND 21224 | TEL (888) 571-2163

GENES EVALUATED IN PLASMA*SELECT*-R™

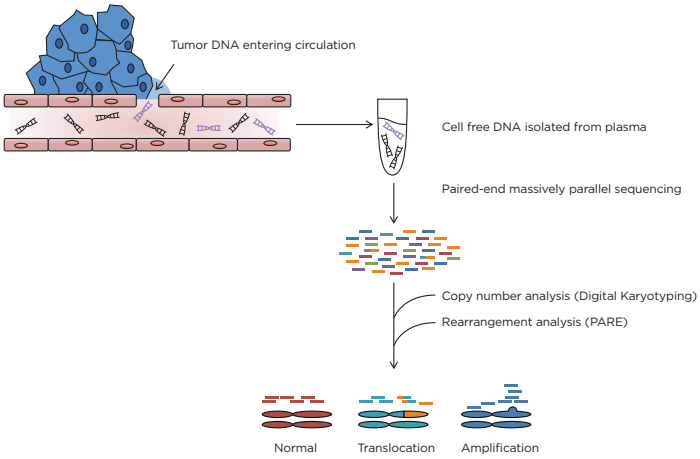
Full coding (*) and specific exon analyses for mutations in well-characterized cancer genes.
Amplification analyses are performed for 57 genes († excluded), with 6 genes (˚) evaluated using highly sensitive methods.

ABL1	BRAF*	CTNNB1	EZH2	GNA11	IDH2	MAP2K1	NRAS*	RB1	STK11*
AKT1	CDH1	DNMT3A	FBXW7	GNAQ	JAK2*	MET˚	PDGFRA*	RET	TERT
ALK*	CDK4*˚	EGFR*˚	FGFR1˚	GNAS	JAK3	MLH1	PIK3CA*	SMAD4	TP53*
APC	CDK6*˚	ERBB2˚	FGFR2	HNF1A	KDR	MPL	PIK3R1	SMARCB1	VHL
AR*	CDKN2A	ERBB4*	FGFR3	HRAS*	KIT*	MYC	PTEN*	SMO	
ATM	CSF1R	ESR1*	FLT3	IDH1	KRAS*	NPM1†	PTPN11	SRC	

Rearrangement analyses for selected regions of 10 well-characterized cancer genes.

ALK	BCR	BRAF	EGFR	NTRK1	PDGFRA	PGDFRB	RARA	RET	ROS1

FIGURE 1. SCHEMATIC FOR DETECTING CHROMOSOMAL ALTERATIONS FROM PATIENT PLASMA. The methods use next-generation paired-end sequencing of cell-free DNA isolated from plasma to identify chromosomal alterations characteristic of tumor DNA. Such alterations include rearrangements resulting from translocations. (from Leary et al, Sci Transl Med. 2012)



Related References

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