HEVA pro

Hereditary and somatic variants profiling in Breast and Ovary Cancer

HEVA pro

4bases HEVA pro is kit for the identification of mutations in genes related to Breast and Ovary cancer, Familial adenomatous polyposis (FAP) and hereditary nonpolyposis colorectal cancer (HNPCC) , two syndromes of colorectal cancer predisposition, inherited in an autosomal dominant fashion.

HEVA pro allows the search for variants linked to a defect in homologous recombination repair (HRD), similarly to pathogenic variants in *BRCA1 or BRCA2*. The defect in HR causes error-prone DNA repair pathways in the cell, resulting in increased genomic instability, which may be responsible for susceptibility to poly- (ADP) -ribose polymerase (PARPis) inhibitors.

HEVA pro is a kit for the analysis of 50 genes through a molecular protocol based on Next Generation Sequencing (NGS) technologies. The kit is validated for germline and somatic analysis (SNPs, indels, CNVs) of DNA extracted from blood or body tissues (fresh, frozen, FFPE, FNA) samples. HEVA pro kit contains all reagents required for the preparation of the capture of specifically designed probes and for the NGS analysis using Thermofisher sequencers.

Table 1: List of genes in **HEVA pro**

ATM	MSH6	FAM175A	LZTR1
APC	MUTYH	MRE11	CTNNB1
BARD1	NBN	PIK3CA	KRAS
BRCA1	PALB2	PMS2CL	ERBB2
BRCA2	PMS2	XRCC2	ALK
BRIP1	PTEN	NF1	EGFR
CDH1	RAD50	SPRED1	RB1
CHEK2	RAD51C	MEN1	CDKN2A
EPCAM	RAD51D	RET	CDK4
MLH1	STK11	SMARCB1	FLCN
MSH2	TP53	NF2	RUNX1
XPC	WRN	PTCH1	CDKN1C
SMAD4	HRAS		

TECHNOLOGY

The HEVA pro kit is part of a DNA-to-variant solution that offers streamlined content, easy-to-perform library preparation, push-button sequencing systems, and simplified data analysis.

WORKFLOW

Library preparation follows a straightforward, capture-based protocol that can be completed in as little as 36 hours, with < 3 hours hands-on time. Resulting libraries can be normalized, pooled, and then loaded on to a chip for sequencing. Prepared libraries are sequenced on any compatible Thermofisher sequencers.

VALIDATION

To demonstrate assay capabilities, clinical samples were run in a clinical setting. DNA quality and quantity of the libraries prepared were verified using Qubit and Agilent Bioanalyzer.

Profile of the prepared libraries in Figure .

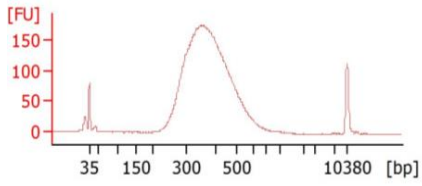

Figure 1. HEVA PRO Bioanalyzer library profile

SAMPLE PER RUN

Instrument	Samples per run*	
	Germline	Somatic
Ion 316™ Chip/Ion 510™ Chip	8	0
Ion 318™ Chip/Ion 520™ Chip	16	0
Ion 530™ Chip	48	0
Ion PI™ Chip/Ion 540™ Chip	160	8
Ion 550™ Chip	480	16

**the estimated maximum number of samples per chip assumes a reading depth of 300x for the germline and 5000x for the somatic. The optimal number of samples can be empirically estimated on the local setup.*

The volume present in the kit is calculated to allow the subdivision into multiples of 8 analysis sessions. Dividing the kit in different ways decrease the total number of tests that can be performed.

ORDERING INFORMATION

Product	REF
HEVA pro	RC3040Y-16 (16 test)
HEVA pro	RC3040Y-96 (96 test)
Adapter	
Y ADAPTER	R9001-16 (16 test)
Y ADAPTER	R9001-96 (96 test)