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Hereditary Plus
OncoKit DX

Analysis of predisposition to hereditary cancer.

For diagnostic use.
Format: 48 rx / Technology: NGS / Reference: IMG-399

> Characteristics

- Panel for the study of 101 genes related to some of the most frequent hereditary cancer types: breast, ovarian, colorectal, uterine, melanoma, kidney, prostate, pancreatic, multiple endocrine neoplasia (MEN), pheochromocytoma, paraganglioma, and retinoblastoma.
- Detection of SNVs, indels, ALUs, and CNVs.
- Bioinformatic analysis using the software Datagenomics.
- It can include STID (integrated sample identification system for traceability).
- Coverage: 99% of bases covered at 50X minimum depth.
- Uniformity: 98.8% of bases covered at >20% mean coverage.
- Specificity: > 99 %
- Sensitivity: > 99 %
- Repeatability: > 99 %
- Reproducibility: > 99 %

> Added value

- Technical support from first protocol implementation, both online and on-site. All protocols will be fine-tuned in collaboration with laboratory personnel.
- Clinical support or genetic counseling, with clinical geneticists available to answer any clinical questions.
- Possibility of externalizing 10% of the samples to our laboratory at the same price during periods of excess laboratory workload or urgent deadlines.

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> Specifications

- **Compatible sequencers:** Illumina MiSeq and NextSeq.
- **Number of reactions:** 48.
- **Number of samples per run:**
  - MiSeq V2 300 cycles: 16 samples.
  - NextSeq Mid Output v2.5 kit (300 cycles): 32 samples.
- **Sequencing:** Paired-end (2 x 150 cycles)
- **Sample type:** DNA from peripheral blood and saliva.
- **Amount of input DNA:** 50 ng
- **Mean coverage:** >350X
- Fully automated panel for Magnis NGS Prep System Dx equipment.
- **Target genes:**

ABRAXAS1 (FAM175A)	*BRCA2*	*FANCC*	*MAX*	*NTHL1*	*RAD51C*	*SMARCB1*
ACD	*BRIP1*	*FANCG*	*MC1R*	*PALB2*	*RAD51D*	*SMARCE1*
AIP	*CDC73*	*FANCM*	*MEN1*	*PHOX2B*	*RB1*	*SPRED1*
AKT1	*CDH1*	*FH*	*MET*	*PIK3CA*	*RECQL4*	*STK11*
ALK	*CDK4*	*FLCN*	*MITF*	*PMS2*	*RET*	*SUFU*
APC (incl. 5' UTR)	*CDKN1B*	*GALNT12*	*MLH1*	*POLD1*	*RINT1*	*TERF2IP*
ATM	*CDKN1C*	*GALNT14*	*MLH3*	*POLE*	*SDHA*	*TERT*
ATR	*CDKN2A*	*GDNF*	*MRE11A*	*POT1*	*SDHAF2*	*TMEM127*
AXIN2	*CHEK2*	*GEN1*	*MSH2*	*PRKAR1A*	*SDHB*	*TP53*
BAP1	*CTNNA1*	*GREM1*	*MSH3*	*PRSS1*	*SDHC*	*TSC1*
BARD1	*CYLD*	*HABP2*	*MSH6*	*PTCH1*	*SDHD*	*TSC2*
BLM	*DICER1*	*HOXB13*	*MUTYH*	*PTEN*	*SEC23B*	*VHL*
BMPR1A	*EPCAM (incl. 3' UTR)*	*KIF1B*	*NBN*	*RAD50*	*SLX4*	*WT1*
BRCA1		*KLLN*	*NF1*	*RAD51*	*SMAD4*	*XRCC2*
		LZTR1	*NF2*	*RAD51B*	*SMARCA4*	

- Moreover, other **intergenic regions of interest** for the calculation of CNVs in genes *EPCAM* (3' UTR) and *MSH2* (5' UTR) have been included, as well as **50 intronic regions to cover hotspots** described in genes *APC, ATM, ATR, BRCA1, BRCA2, CHEK2, FH, LZTR1, MET, MLH1, MSH2, NF1, PMS2, PTEN, RB1, RET, SDHB, STK11* and *TERT*.
- CE/IVD and analysis software labeling.

Contact our oncology team for clinical counseling on this product:
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