Oxford Nanopore Technologies

Hereditary Cancer Panel

Targeted sequencing via adaptive sampling

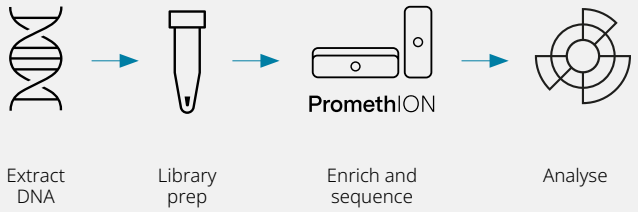
Comprehensive characterisation of hereditary cancer targets with Oxford Nanopore sequencing

The **Oxford Nanopore Hereditary Cancer Panel** is a comprehensive sequencing assay targeting 258 full-length genes — covering exons, introns, and promoters — linked to inherited cancer risk. The panel uses **adaptive sampling**: a fast and flexible on-sequencer target enrichment methodology. No lengthy library preparation, baits, or primers required.

Leveraging Oxford Nanopore reads of unrestricted length — from short to long — the Hereditary Cancer Panel can accurately resolve complex structural variants, single nucleotide variants, and insertions/deletions. It enables haplotype phasing and can resolve pseudogenes. Additionally, direct DNA sequencing captures methylation patterns, offering a multiomic view that enables the discovery of key biological insights such as gene silencing and parent-of-origin effects.

Hereditary Cancer Panel gene list

ABRAXAS1	*ACD*	*AIP*	*AKT1*	*ALK*	*ANKRD26*	*APC*	*ARID5B*	*ATG2B*	*ATM*	*ATR*	*AXIN2*	*BAP1*	*BARD1*	*BLM*
BMPR1A	*BRAF*	*BRCA1*	*BRCA2*	*BRIP1*	*BUB1B*	*CBL*	*CDC73*	*CDH1*	*CDK12*	*CDK4*	*CDKN1B*	*CDKN1C*	*CDKN2A*	*CEBPA*
CFTR	*CHEK2*	*COL7A1*	*CSF3R*	*CTC1*	*CTNNA1*	*CTR9*	*CYLD*	*DDB2*	*DDX41*	*DICER1*	*DIS3L2*	*DKC1*	*DNAH9*	*DNAJC21*
DOCK8	*DPYD*	*EFL1*	*EGFR*	*ELANE*	*ELP1*	*EPCAM*	*ERCC1*	*ERCC2*	*ERCC3*	*ERCC4*	*ERCC5*	*ERCC6L2*	*ETV6*	*EXT1*
EXT2	*FAAP100*	*FAN1*	*FANCA*	*FANCB*	*FANCC*	*FANCD2*	*FANCE*	*FANCF*	*FANCG*	*FANCI*	*FANCL*	*FANCM*	*FAS*	*FH*
FLCN	*G6PC3*	*GALNT12*	*GATA1*	*GATA2*	*GBA1*	*GFI1*	*GPC3*	*GPR161*	*GRB10*	*GREM1*	*GSKIP*	*H19*	*HAX1*	*HLA-A*
HLA-B	*HLA-C*	*HLA-DPA1*	*HLA-DQA1*	*HLA-DQB1*	*HLA-DRB1*	*HMBS*	*HOXB13*	*HRAS*	*IGF2*	*IKZF1*	*ITK*	*KCNQ1*	*KCNQ1OT1*	*KIF1B*
KIT	*KLLN*	*KRAS*	*L3MBTL1*	*LIG4*	*LZTR1*	*MAD2L2*	*MAP2K1*	*MAP2K2*	*MAX*	*MBD4*	*MC1R*	*MECOM*	*MEN1*	*MEST*
MET	*MITF*	*MLH1*	*MLH3*	*MPL*	*MRE11*	*MSH2*	*MSH3*	*MSH6*	*MTAP*	*MUTYH*	*NAF1*	*NAPRT*	*NBN*	*NF1*
NF2	*NHP2*	*NLRP2*	*NLRP5*	*NLRP7*	*NOP10*	*NPM1*	*NRAS*	*NSD1*	*NTHL1*	*PADI6*	*PALB2*	*PALLD*	*PARN*	*PAX5*
PAX6	*PDGFRA*	*PDGFRB*	*PHOX2B*	*PIK3CA*	*PMS2*	*PMS2CL*	*POLD1*	*POLE*	*POLH*	*POT1*	*PPM1D*	*PRF1*	*PRKAR1A*	*PRSS1*
PTCH1	*PTEN*	*PTPN11*	*RAD21*	*RAD50*	*RAD51*	*RAD51B*	*RAD51C*	*RAD51D*	*RAF1*	*RB1*	*RECQL4*	*REST*	*RET*	*RFWD3*
RHBDF2	*RINT1*	*RMRP*	*RNF43*	*RPA1*	*RPL11*	*RPL15*	*RPL23*	*RPL26*	*RPL27*	*RPL31*	*RPL35A*	*RPL36*	*RPL5*	*RPS10*
RPS17	*RPS19*	*RPS20*	*RPS24*	*RPS26*	*RPS27*	*RPS27A*	*RPS28*	*RPS29*	*RPS7*	*RTEL1*	*RUNX1*	*SAMD9*	*SAMD9L*	*SBDS*
SDHA	*SDHAF2*	*SDHB*	*SDHC*	*SDHD*	*SETBP1*	*SH2B3*	*SH2D1A*	*SHOC2*	*SLX4*	*SMAD4*	*SMARCA4*	*SMARCB1*	*SMARCE1*	*SOS1*
SPINK1	*SPRED1*	*SQSTM1*	*SRP72*	*SRY*	*STAT3*	*STK11*	*STN1*	*SUFU*	*TBXT*	*TERC*	*TERF2IP*	*TERT*	*TINF2*	*TMEM127*
TP53	*TRIM28*	*TRIM37*	*TRIP13*	*TSC1*	*TSC2*	*TSR2*	*UBE2T*	*UROD*	*VHL*	*WAS*	*WRAP53*	*WRN*	*WT1*	*XPA*
XPC	*XRCC2*	*ZCCHC8*												



Panel specifications

Enrichment method	Adaptive sampling
Genes	258
Reference genome	hg38
Recommended DNA input	1 µg
Sample type	Whole blood, DNA
Coverage uniformity (fold-80)	1.2
Samples per PromethION™ Flow Cell	3
Total assay time (hands-on time)	<5 days (<2 hours)

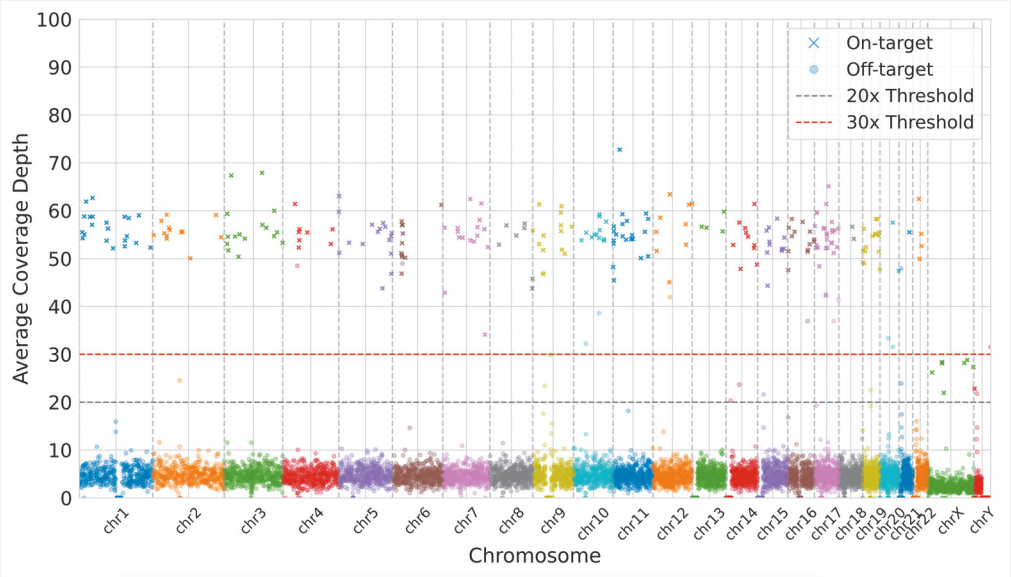


Figure 1. Sequencing coverage across the genome, depicting low-pass whole-genome coverage and >30x enrichment for target loci.

Figure 2. Representative large >1 kb deletion with long reads spanning the full deletion in *POLH*, a gene mutated in the hereditary disorder xeroderma pigmentosum, along with hypomethylation of the promoter region.

Find out more: nanoporetech.com/hereditary-cancer-panel

Oxford Nanopore Technologies

www.nanoporetech.com

phone +44 (0)845 034 7900

email support@nanoporetech.com

oxford-nanopore-technologies

@nanopore

@nanoporetech.com

FL_1291(EN)_V2_30Jul2025