

Comprehensive Genomic Profiling (CGP) & HRD Status

Sample Report — Case C

CANCER TYPE Serous Carcinoma	METHOD DNA Whole Exome Sequencing
QC STATUS PASS	SPECIMEN Peripheral blood
CGP COVERAGE 130.6x average depth	SEQUENCER Agilent SureSelect V6 + BGISEQ

Clinically Significant Gene Mutations

Genes tested: BRAF, BRCA1, BRCA2, BRIP1, CHEK1, CHEK2, PALB2, RAD51C, RAD51D, PIK3CA, TP53 — all negative. No clinically significant mutations detected.

Additional Likely / Non-Clinically Significant Findings (VUS)

GENE	MUTATION	VAF	SIGNIFICANCE
BAP1	c.1408G>A (p.G470R)	42.46% (heterozygous)	Uncertain significance
FLCN	c.1333G>A (p.A445T)	47.6% (heterozygous)	Uncertain significance

BAP1: BAP1 tumor predisposition syndrome (ClinVar Variation ID 133663 / dbSNP rs576538858).

FLCN: Birt-Hogg-Dube syndrome, colorectal cancer (ClinVar Variation ID 3370 / dbSNP rs41419545).

HRD Status

HRD FINAL STATUS

POSITIVE — GIS 51 / 100 (Threshold ≥ 42)

7

LOH

13

TAI

31

LST

Genomic Instability Score combines Loss of Heterozygosity (LOH) + Telomeric Allelic Imbalance (TAI) + Large-Scale state Transitions (LST). HRD-positive tumors combined with BRCA1/BRCA2 inactivation are susceptible to PARP inhibitors and platinum chemotherapy.

This is a de-identified sample of NCRO's report output, shared to illustrate report depth and format. All patient, ordering-physician and institution details have been removed. Variant classifications may change as scientific evidence evolves. This sample does not constitute a clinical report for any individual and should not be used for clinical decision-making.