Client: Example Client ABC123
123 Test Drive
Salt Lake City, UT 84108
UNITED STATES

Physician: Doctor, Example

Patient: Patient, Example

DOB	1/20/1972
Sex:	Male
Patient Identifiers:	01234567890ABCD, 012345
Visit Number (FIN):	01234567890ABCD
Collection Date:	00/00/0000 00:00

Hereditary Cancer Panel, Sequencing and Deletion/Duplication

ARUP test code 2012032

Cancer Panel, Hereditary, Spcm	Whole Blood
Cancer Panel, Hereditary, Interp	Negative

RESULT
No pathogenic variants were detected in any of the genes tested.

INTERPRETATION
No pathogenic variants were detected in any of the genes tested. This result decreases the likelihood of, but does not exclude, a hereditary cause of cancer. Please refer to the background information included in this report for a list of the genes analyzed, methodology, and limitations of this test.

RECOMMENDATIONS
Medical screening and management should rely on clinical findings and family history. If this individual has a family history, determination of a causative familial variant in an affected family member is necessary for optimal interpretation of this negative result. Further testing may be warranted if there is a familial variant that is not detectable by this assay. Genetic consultation is recommended.

COMMENTS
Likely benign and benign variants are not reported.
Variants in the following region(s) may not be detected by NGS with sufficient confidence in this sample due to technical limitations: None

This result has been reviewed and approved by [redacted]

BACKGROUND INFORMATION: Hereditary Cancer Panel, Sequencing and Deletion/Duplication
CHARACTERISTICS: Pathogenic variants in multiple genes have been implicated in hereditary cancer, often characterized by early age of cancer onset (typically before age 50) and multiple, multifocal, and/or related cancers in an individual or in closely related family member(s). Pathogenic variants in the genes analyzed by this panel cause variable phenotypes and cancer risks.

EPIDEMIOLOGY: Approximately 5-10 percent of cancer is associated with a hereditary cause.

CAUSE: Pathogenic germline variants in genes associated with hereditary cancer.

INHERITANCE: Varies depending on the gene and specific variant.

H=High, L=Low, *=Abnormal, C=Critical

GENES TESTED: ALK; APC*; ATM; AXIN2; BAP1; BARD1; BMPR1A*; BRCA1*; BRCA2; BRIP1; CDC73; CDH1*; CDK4; CDKN1B; CDKN2A*; CHEK2*; CTNNA1*; DICER1; EGFR; EPCAM**; FH; FLCN*; HOXB13; HRAS; KIT; LZTR1; MAX; MC1R; MEN1*; MET; MITF*; MLH1; MLH3*; MSH2; MSH3; MSH6; MUTYH; NBN; NF1; NF2; NTHL1; PALB2; PDGFRA*; PMS2***; POLD1; POLE; POT1; PRKAR1A; PTCH1; PTEN*; RAD51C; RAD51D; RB1*; RECQL*; RET; SDHA*; SDHAF2; SDHB; SDHC*; SDHD*; SMAD4; SMARCA4; SMARCB1; SMARCE1*; STK11; SUFU; TERT; TMEM127; TP53; TSC1; TSC2; VHL*; WT1
* - One or more exons are not covered by sequencing and/or deletion/duplication analysis for the indicated gene; see limitations section below.
** - Deletion/duplication analysis of EPCAM (NM_002354) exon 9 only, sequencing is not available for this gene.
*** Deletions/duplications in exons 12-15 may not be distinguishable from the PMS2CL pseudogene and may be reported as inconclusive.

METHODOLOGY: Probe hybridization-based capture of all coding exons and exon-intron junctions of the targeted genes (including selected PTEN promoter variants), followed by massively parallel sequencing. Sanger sequencing was performed as necessary to fill in regions of low coverage and to confirm reported variants that do not meet acceptable quality metrics. A proprietary bioinformatic algorithm was used to detect large (single exon-level or larger) deletions or duplications in the indicated genes. Large deletions/duplications confirmed using an orthogonal exon-level microarray. Human genome build 19 (Hg 19) was used for data analysis. Testing of selected exons (and exon/intron boundaries) of PMS2, PTEN and MSH2 was performed by bidirectional Sanger sequencing. Deletion/duplication testing of PMS2 was performed by multiplex ligation-dependent probe amplification (MLPA).

ANALYTICAL SENSITIVITY: The analytical sensitivity is approximately 99 percent for single nucleotide variants (SNVs) and greater than 93 percent for insertions/duplications/deletions (indels) from 1-10 base pairs in size. Indels greater than 10 base pairs may be detected, but the analytical sensitivity may be reduced. Deletions of 2 exons or larger are detected with sensitivity greater than 97 percent; single exon deletions are detected with 62 percent sensitivity. Duplications of 3 exons or larger are detected at greater than 83 percent sensitivity. Specificity is greater than 99.9 percent for all variant classes. The analytical sensitivity for MLPA is greater than 99 percent.

LIMITATIONS: A negative result does not exclude a heritable form of cancer. This test only detects variants within the coding regions and intron-exon boundaries of the targeted genes. Deletions/duplications/insertions of any size may not be detected by massively parallel sequencing. Regulatory region variants and deep intronic variants will not be identified. Precise breakpoints for large deletions or duplications are not determined in this assay and single exon deletions/duplications may not be detected based on the breakpoints of the rearrangement. The actual breakpoints for the deletion or duplication may extend beyond or be within the exon(s) reported. This test is not intended to detect duplications of 2 or fewer exons in size, though these may be identified. Single exon deletions are reported but called at a lower sensitivity. Diagnostic errors can occur due to rare sequence variations. In some cases, variants may not be identified due to technical limitations caused by the presence of pseudogenes, repetitive, or homologous regions. This test is not intended to detect low-level mosaic or somatic variants, gene conversion events, complex inversions, translocations, mitochondrial DNA (mtDNA) variants, or repeat expansions. Interpretation of this test result may be impacted if this patient has had an allogeneic stem cell transplantation. Noncoding transcripts were not

analyzed.

The following regions may have reduced sequencing sensitivity due to technical limitations of the assay:
RB1 (NM_000321) exon 22
SUFU (NM_016169, NM_001178133) exon 1

The following regions are not sequenced due to technical limitations of the assay:
APC (NM_001354896) exon 12
APC (NM_001354898, NM_001354904) exon 2
APC (NM_001354900) exon 11
BRCA1 (NM_007300) exon 13
CHEK2 (NM_001005735) exon 3
CHEK2 (NM_001349956) exon 4
FLCN (NM_001353229) exon 7
MEN1 (NM_001370251) exon 8
MITF (NM_001354607) exon 2
PDGFRA (NM_001347827) exon 17
PDGFRA (NM_001347828) exon 2
PDGFRA (NM_001347830) exon 1
RECQL (NM_002907) exons 14,15
RECQL (NM_032941) exons 15,16
SDHA (NM_004168) exon 14
SDHA (NM_001294332) exon 13
SDHA (NM_001330758) exon 12
SDHC (NM_001035511) partial exon 5 (Chr1:161332225-161332330)
SDHC (NM_001278172) partial exon 4 (Chr1:161332225-161332330)
SDHD (NM_001276506) exon 4
VHL (NM_001354723) exon 2

Deletions/duplications will not be called for the following exons:
APC (NM_001354896) 12; APC (NM_001354898, NM_001354904) 2; APC (NM_001354900) 11; BMPR1A (NM_004329) 12-13; BRCA1 (NM_007294, NM_007299, NM_007300) 2; BRCA1 (NM_007298) 1; CDH1 (NM_001317185) 10; CDKN2A (NM_000077, NM_001195132, NM_001363763, NM_058195) 2; CHEK2 (NM_007194) 11-15; CHEK2 (NM_001005735) 3,12-16; CHEK2 (NM_001257387) 12-16; CHEK2 (NM_001349956) 4,10-14; CHEK2 (NM_145862) 10-14; CTNNA1 (NM_001290307) 19; CTNNA1 (NM_001324002, NM_001324004) 13; CTNNA1 (NM_001324003) 15; CTNNA1 (NM_001324005) 16; FLCN (NM_001353229) 7; MEN1 (NM_001370251) 8; MITF (NM_001354607) 2; MLH3 (NM_001040108) 7-8; MLH3 (NM_014381) 7; PDGFRA (NM_001347827) 17; PDGFRA (NM_001347828) 2; PDGFRA (NM_001347830) 1; PTEN (NM_000314, NM_001304718) 9; PTEN (NM_001304717) 1,10; RB1 (NM_000321) 22; RECQL (NM_002907) 14-15; RECQL (NM_032941) 15-16; SDHA (NM_004168) 1,10-15; SDHA (NM_001294332) 1,9-14; SDHA (NM_001330758) 1,10-13; SDHD (NM_001276506) 4; SMARCE1 (NM_003079) 7,10-11; VHL (NM_001354723) 2

This test was developed and its performance characteristics determined by ARUP Laboratories. It has not been cleared or approved by the U.S. Food and Drug Administration. This test was performed in a CLIA-certified laboratory and is intended for clinical purposes.

Counseling and informed consent are recommended for genetic testing. Consent forms are available online.

VERIFIED/REPORTED DATES

Procedure	Accession	Collected	Received	Verified/Reported
Cancer Panel, Hereditary, Spcm	26-092-401093	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00

H=High, L=Low, *=Abnormal, C=Critical

Cancer Panel, Hereditary, Interp	26-092-401093	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00

END OF CHART

H=High, L=Low, *=Abnormal, C=Critical