

**Disease:** Endometrioid carcinoma

### Test Description

Precision panel is a comprehensive cancer genomic NGS assay to accurately and rapidly identify key actionable biomarkers and provide precision treatment options including Chemotherapy, Targeted Therapy and Immunotherapy. This assay screens both exonic and selected intronic regions of >1000 genes with known genomic alterations with high coverage depth. The assay can detect all classes of genomic alterations, including SNVs, small Indels, CNVs and selected translocations. In addition, TMB, MSI and HRD are analyzed to help guide immunotherapy decisions.

### Patient Demographic

**Name:** Ms. Nidhi Gulati  
**Sex:** Female  
**Date of Birth/Age:** 53 years

### Clinician

**Clinician Name:** Dr Amit Verma  
**Medical Facility:** Dr AV Institute of Personalized Cancer Therapy and Research  
**Pathologist:** Not Provided

### Specimen

**Booking ID:** 012406080159  
**Sample Type:** FFPE Block No. H-10863/24  
**Specimen Site:** Intramural fibroid and serosa  
**Tumor Content Percentage:** NA  
**Date of Collection:** 08-06-2024  
**Date of Booking:** : 08-06-2024

## CLINICAL SYNOPSIS

Nidhi Gulati, is a known case of endometrioid carcinoma. She has been evaluated for pathogenic variations in the genes listed in Appendix 2.

## RESULT SUMMARY

### Potential clinically significant alteration.

Tier I mutations in the *PTEN* (p.X70\_splice) and Tier II mutations in the *FGFR2* (p.Ser252Trp), *ARID1A* (p.Asp1850Glyfs\*4 and p.Gln546Argfs\*73), *CTNNB1* (p.Thr41Ile) and *AXIN2* (p.Asn666Glnfs\*41), *AXIN1*(p.Gly508Valfs\*197), genes were observed.

*PTEN mutations instigates dysregulation of key downstream pathways, including PI3K/AKT/MTOR pathway promoting tumorigenesis. Thus, mTOR inhibitors may show sensitivity in this case.*

*FGFR2 alterations instigate constitutive activation of key downstream pathways, including FGF/FGFR, thereby fostering carcinogenesis. Thus, FGFR inhibitors may show sensitivity in solid cancers.*

*Moreover, PTEN mutation and ARID1A mutations indicates aberration in the HRR pathway and may lead to genomic instability and thus indicates a potential response to PARP inhibitors.*

*Mutations in CTNNB1 gene and loss of function mutations in AXIN1 and AXIN2 promotes cellular proliferation by modulating WNT/B-catenin signaling pathway, fostering carcinogenesis. Additionally, it is documented that elevated levels of CTNNB1 expression are correlated with unfavorable clinical outcomes and prognoses across a spectrum of cancers.*

### Other Markers

Immunotherapy markers: **TMB is high** and **MSI is intermediate**, while PD-L1 is negative (CPS <1%). The overall HRD score is low.

*High TMB and intermediate MSI indicate aberration of mismatch repair pathway and potential response to immunotherapy.*

## RESULTS

**Potential clinically significant alterations were observed in *PTEN*, *FGFR2*, *ARID1A*, *CTNNB1*, *AXIN1* and *AXIN2*.**

Gene (Transcript ID)	Variant	Allele Frequency	Exon	Mutation Effect	Variant Effect	Tier
<i>PTEN</i> (NM_000314.8)	c.210-1G>A p.X70_splice	32%	-	Likely Loss-of-function	Splice acceptor	Ib
<i>FGFR2</i> (NM_000141.5)	c.755C>G p.Ser252Trp	20%	7	Gain-of-function	Missense	IIC
<i>ARID1A</i> (NM_006015.6)	c.5548dup p.Asp1850Glyfs*4	06%	20	Likely Loss-of-function	Frameshift	IIC
<i>ARID1A</i> (NM_006015.6)	c.1636del p.Gln546Argfs*73	02%	3	Likely Loss-of-function	Frameshift	IIC
<i>CTNNB1</i> (NM_001904.4)	c.122C>T p.Thr41Ile	24%	3	Unknown	Missense	IIC
<i>AXIN1</i> (NM_003502.4)	c.1523del p.Gly508Valfs*197	23%	6	Likely Loss-of-function	Frameshift	IId
<i>AXIN2</i> (NM_004655.4)	c.1994dup p.Asn666Glnfs*41	07%	8	Likely Loss-of-function	Frameshift	IId

As per guidelines of the ACMG/AMP/ASCO/CAP

## VARIANT OF UNKNOWN SIGNIFICANCE (VUS)

None

## IMMUNO-ONCOLOGY FINDINGS

<b>MSI/MMR Status</b> NGS Based <b>18.96%</b> Intermediate	<b>TMB</b> (Tissue / Blood) <b>10 Muts/Mb</b> High	<b>PDL-1</b> IHC on tissue (TBx), Dako clone 22C3 or CTC (LBx) PD-L1 Negative on Tissue (CPS <1%)
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## HOMOLOGOUS RECOMBINANT DEFICIENCY (HRD) FINDINGS

Overall HRD Scoring	HRR Gene	LOH (Loss of Heterozygosity)	TAI & LST (Telomeric Allelic Instability & Large State Transitions)
29% Low	<i>PTEN, ARID1A</i>	09% Low	TAI: 17% LST: 03%

Note: LOH score is calculated based on the genome wide LOH markers present in gene panel.

## OTHER BIOMARKERS

Gene	Findings
<i>ALK</i>	None detected
<i>BRAF</i>	None detected
<i>RET</i>	None detected
<i>NTRK</i>	None detected
<i>MMR genes</i>	None detected

**LONGITUDINAL MONITORING MARKERS**

Circulating Tumor Cells (CTC)	CTC Cluster	Highest Mutant Allele Frequency	Tumor DNA Fraction (%)
NA	NA	PTEN: p.X70_splice (VAF: 32%)	28

Note: EDTA blood sample for CTS is not provided.

AI-powered probabilistic model is used to calculate the tumor fraction, enabling the simultaneous segmentation of the genome and accurate prediction of large-scale copy number variations. The model takes into consideration variations in clonality and copy number at each locus, ensuring a comprehensive analysis.

**CLINICAL CORRELATION AND VARIANT INTERPRETATION**

**PTEN p.X70\_splice**

**Gene description:** PTEN, phosphatidylinositol 3,4,5-trisphosphate 3-phosphatase and dual-specificity protein phosphatase PTEN, is a tumor suppressor (Wang, Li-Hui et al. 2018) with roles in the cell cycle, growth, DNA repair, cell survival and regulation of the Akt-Mtor pathway (Hopkins, Benjamin D et al. 2014; Naderali, Elahe et al. 2018). *PTEN* somatic alterations resulting in loss of function have been found in many types of cancer including, mainly endometrial (Liang, Xiaohuan et al. 2018), melanoma and prostate (Chalhoub, Nader, and Suzanne J Baker. 2009; Gao, Song et al. 2018). According to AACR GENIE cases, *PTEN* is altered in 7.24% of all cancers with endometrial endometrioid adenocarcinoma, conventional glioblastoma multiforme, prostate adenocarcinoma, breast invasive ductal carcinoma and colon adenocarcinoma.

**Variant description:** The intronic variant, **p.X70\_splice** occurs within a consensus splice junction and is predicted to result in abnormal mRNA splicing of either an out-of-frame exon or an in-frame exon necessary for protein stability and/or normal function. This nucleotide position is highly conserved in available vertebrate species. *In silico* splice site analysis predicts that this alteration will weaken the native splice acceptor site and may result in the creation or strengthening of a novel splice acceptor site.

**Potential relevance:** PTEN is involved in the regulation of the Akt-mTOR pathway, PTEN mutated tumors are predicted to be sensitive to mTOR inhibitors. Standard guidelines have recommended mTOR inhibitors in combination with hormonal therapy in recurrent disease of endometrioid histology. Furthermore, PTEN is involved in the repair of DSBs via HR by regulating RAD51 expression (Pei, Xile et al. 2020). Moreover, efficacy of PARP inhibitors in PTEN mutated cancers is under clinical investigation.

**FGFR2 p.Ser252Trp**

**Gene description:** FGFR2, fibroblast growth factor receptor 2, is a receptor tyrosine kinase activated upon binding of the FGF ligand, which activates RAS-MAPK and PI3K-AKT pathways (Tenhagen, M et al. 2012). Altered function of FGFR2 through activating mutations, fusions and amplification increases cell proliferation and tumorigenesis (Tenhagen, M et al. 2012) and is observed in prostate (Wang C et al. 2019), breast, lung, uterine and ovarian cancers (Lei H et al. 2017). *FGFR2* is altered in 2.02% of all cancers with endometrial endometrioid adenocarcinoma, breast invasive ductal carcinoma, cutaneous melanoma, colon adenocarcinoma and lung adenocarcinoma having the greatest prevalence of alterations. Recent studies show that *FGFR2* mutations are associated with poor outcomes in endometrioid endometrial cancer (Jeske, Yvette W et al. 2017; Byron, Sara A et al. 2012).

**Variant description:** The variant *FGFR2* **Ser252Trp** is located in a mutational hot spot and/or well-established functional domain in which established pathogenic variants have been reported. Missense changes are a common disease-causing mechanism. Computational prediction analysis indicated that this variant is deleterious/damaging.

**Potential relevance:** Several FGFR tyrosine kinase inhibitors (TKIs) such as Erdafitinib, Futibatinib, and Pemigatinib demonstrate their therapeutic effectiveness on cancer cells both *in vitro* and *in vivo* (Takeda, Masayuki et al. 2007; Gavine, Paul R et al. 2012, Zhu, Dong-Li et al. 2020). These inhibitors have been approved for use in other cancer indications and are currently being tested in clinical trials (NCT04083976).

**ARID1A p.Asp1850Glyfs\*4 and p.Gln546Argfs\*73**

**Gene description:** ARID1A, AT-rich interaction domain 1A, is a member of the cBaF subunit (Mittal, Priya and Charles W M Roberts.2020) of the SWI/SNF chromatin remodeling complex and is involved in cell-cycle activation (Sun, Xuxu et al.2017). ARID1A has been reported to influence PI3K/AKT pathways (Wu, Ren-Chin et al. 2014) and loss of function is commonly found in ovarian clear cell carcinoma (Kuroda, Takafumi, and Takashi Kohno.2020; Li, Jing et al.2020), gastric, colorectal (Kim, Young-Sik et al. 2017) and bladder cancers (Pietzak, Eugene J et al.2017), while in liver cancer, ARID1A has a context-dependent role (Sun, Xuxu et al. 2017) and *ARID1A* promoter hypermethylation has been observed in squamous cell carcinoma (Luo, Qingyu et al.2020).

**Variant description:** According to AACR Genie cases, *ARID1A* is altered in 8.77% of all cancers with endometrial endometrioid adenocarcinoma, lung adenocarcinoma, colon adenocarcinoma, bladder urothelial carcinoma, and breast invasive ductal carcinoma.

**Potential relevance:** A study demonstrated that mutated or downregulated ARID1A compromises the HRR of DNA DSBs through stimulation of the PI3K-Akt1 pathway. Attenuation of DNA HRR in ARID1A-mut tumor cells sensitizes them to PARPi and PARPi/IR combination by a mechanism of synthetic lethality (Yakovlev, Vasily A et al.2023). The use of PARP Inhibitors in non-BRCA mutation carrier patients can be expanded to sporadic cancers that display “BRCAness” (cancers that have defective HR without germline BRCA1 and 2 mutations) (Mekonnen, Negesse et al.2022).

### **CTNNB1 p.Thr41Ile**

**Gene description:** CTNNB1, catenin beta 1, is a member of the Wnt signaling pathway, component of cadherin-based adherens junctions and is also a tumor antigen recognized by T-cells in melanoma (Durgeau, Aurélie et al. 2018). CTNNB1 imbalance is implicated in cancer progression and metastasis (Valenta, Tomas et al. 2012) and exon 3 mutations are common in endometrioid endometrial carcinoma and melanoma (Gao, Chao et al. 2017). According to AACR Genie cases, *CTNNB1* is altered in 3.10% of all cancers with endometrial endometrioid adenocarcinoma, lung adenocarcinoma, colon adenocarcinoma, prostate adenocarcinoma and hepatocellular carcinoma.

**Variant description:** *CTNNB1 Thr41Ile* lies within a Gsk3b phosphorylation site of the Ctnnb1 protein (UniProt.org). Thr41Ile is predicted to confer a gain of function to the Ctnnb1 protein as demonstrated by nuclear accumulation of Ctnnb1 in culture (Garcia-Rostan, G et al. 1999).

**Potential relevance:** This oncogene usually exhibits gain of function mutational effect resulting in aberrant accumulation of the  $\beta$ -catenin protein and are prevalent in a wide range of solid tumors. These mutations alter the spatial characteristics of the  $\beta$ -catenin protein, leading to drastic reprogramming of the nuclear transcriptional network.  $\beta$ -catenin mutations may lead to constitutive activation of the Wnt/ $\beta$ -catenin signaling pathway and reprogramming of downstream nuclear transcriptional networks and is associated with poor prognosis across a spectrum of cancers.

### **AXIN1 p.Gly508Valfs\*197**

**Gene description:** AXIN1, axin 1, axis inhibition protein 1 is a scaffold protein that regulates the Wnt signaling pathway and also Tp53, Myc, TGF beta and Jun pathways (Harnoř, Jakub et al. 2018).

**Variant description:** Germline variations in *AXIN1* have been associated with ovarian (Zhang, Yan et al. 2019), bladder (Li, Qin et al. 2019), kidney (Pu, Yan et al. 2017) and colorectal cancers (Mazzoni, Serina M, and Eric R Fearon. 2014) and loss of Axin1 function leads to increased cellular beta-catenin (CTNNB1), potentially promoting cell proliferation (Satoh, S et al. 2000).

**Potential relevance:** According to AACR GENIE cases, AXIN1 is altered in 1.58% of all cancers with colon adenocarcinoma, lung adenocarcinoma, breast invasive ductal carcinoma, cutaneous melanoma and prostate adenocarcinoma.

### **AXIN2 p.Asn666Glnfs\*41**

**Gene description:** AXIN2, axin 2, a homologue of Axin, is a gene that encodes a protein that functions in the regulation of the stability of beta-catenin in the WNT signaling pathway. (Behrens, J et al. 1998). *AXIN2* mutations have been identified in colorectal, ovarian, endometrial, and liver cancers. (Salahshor, S and J R Woodgett. 2005).

**Variant description:** Frameshift variant **p.Asn666Glnfs\*41** is predicted to result in protein truncation or nonsense mediated decay in a gene for which loss of function is not an established mechanism of disease.

**Potential relevance:** According to AACR GENIE cases, *AXIN2* is altered in 2.40% of all cancers with colon adenocarcinoma, breast invasive ductal carcinoma, lung adenocarcinoma, endometrial endometrioid adenocarcinoma and invasive breast carcinoma. Moreover, missense mutations, nonsense mutations, silent mutations and frameshift deletions and insertions, are observed in cancers such as endometrial cancer, intestinal cancer and stomach cancer.

## DESCRIPTION OF PERTINENT BIOMARKERS

**Tumor mutational burden (TMB)** is defined as the number of somatic mutations per megabase of the coding region in the genome. TMB is a clinical biomarker associated with response to immune checkpoint inhibitors in various cancers, including NSCLC, bladder cancer, and melanoma (Rizvi, Naiyer A., et al. 2015; Carbone, David P et al. 2017; Hellmann, Matthew D et al. 2018; Kowanz, Marcin, et al. 2017; Rizvi, Hira et al. 2018). High tumor mutational burden (TMB-H) is defined by >10 mutations/megabase [mut/Mb] can be seen frequently in cancers linked to mutagens, such as exposure to ultraviolet light in melanoma and smoking in non-small-cell lung cancer. Other tumor forms, such as mesothelioma, sarcomas and prostate cancers have been reported to have a TMB-H prevalence of less than 5% (Shao C, Li G, Huang L, et al. 2020). TMB is also affected by mutations in the proofreading domains of DNA polymerases encoded by the *POLE* and *POLD1* genes and microsatellite instability (MSI). (Cancer Genome Atlas Research Network et al. 2013; Briggs, Sarah and Ian Tomlinson.2013; Heitzer, Ellen and Ian Tomlinson.2014; Cancer Genome Atlas Network.2012; Roberts, Steven A. and Dmitry A. Gordenin. 2014).

**Microsatellite instability (MSI)** is a condition of genetic hypermutability that generates excessive amounts of short insertion/deletion mutations in the genome; it generally occurs at microsatellite DNA sequences and is caused by a deficiency in DNA mismatch repair (MMR) in the tumor (Kocarnik, Jonathan M et al. 2015). Particularly, defective MMR and as a result MSI occur when one of the MMR pathway proteins, primarily MLH1, MSH2, MSH6 or PMS2 is genetically or epigenetically inactivated (Kocarnik, Jonathan M et al. 2015; You, J-F et al.2010; Bairwa, Narendra K., et al. 2014). DNA mismatch repair failure, which leads to the accumulation of many mutations at repeating DNA sequence stretches (microsatellites) and is known as high-level microsatellite instability (MSI-H), is a significant molecular mechanism of genetic instability in cancer (Warth, Arne et al. 2016). MSI-H tumors to respond to anti-PD-1 immune checkpoint inhibitors (Gatalica, Zoran et al. 2014; Kroemer, Guido et al. 2015; Lal, Neeraj et al. 2015) including approved therapies nivolumab and pembrolizumab (Michael J. Overman 2016; Le, Dung T et al. 2015).

Pembrolizumab is a monoclonal antibody that binds to the PD-1 receptor and disrupts its interaction with PD-L1 and PD-L2, resulting in PD-1 pathway-mediated immune response suppression, including antitumor immunity. Antibodies to PD-1 or its ligands have been used to block this pathway in patients with a variety of cancers, including melanomas, non-small-cell lung cancer, renal cell carcinoma, bladder cancer and Hodgkin lymphoma. (Marcus, Leigh et al. 2019). The FDA approved for the treatment of adult and pediatric patients with unresectable or metastatic tumor mutational burden-high solid tumors and for patients with unresectable or metastatic, MSI-H/dMMR solid tumors with progression on prior treatment with no satisfactory alternative treatment options. FDA granted the approval based on a clinically important overall response rate (29%; 95% confidence interval, 21-39) and duration of response (57% of responses lasting  $\geq$  12 months) in the subset of patients with TMB-H solid tumors (n = 102) spanning nine different tumor types enrolled in a multicenter single-arm trial (KEYNOTE- 158, Marcus, Leigh et al. 2021).

This was the FDA's first tissue/site agnostic approval and was based on the combined results of five multi-cohort, single-arm clinical trials evaluating pembrolizumab in patients with metastatic or unresectable solid tumors who had received a median of two prior lines of therapy. Moreover, KEYNOTE-158 was a non-randomized, open-label, multicenter, multi-cohort phase II study evaluating pembrolizumab in a variety of tumor types including a specific cohort of non-colorectal MSI-H/dMMR solid tumors previously treated with standard therapy. Clinical evidence from the KEYNOTE-158 trial in patients with MSI-H/dMMR solid cancers (n=233) reported sensitivity to pembrolizumab demonstrating overall response rate ORR of 34.4% while, the response rate in the subset of patients with MSI-H/dMMR pancreatic cancers (n=22) was not as robust, demonstrated overall response rate (ORR) of 18.2% and overall survival of 4 months.

Additionally, another humanized monoclonal antibody, dostarlimab, directed against the negative immunoregulatory human cell surface receptor programmed cell death 1 (PD-1; programmed death-1), with potential immune checkpoint inhibitory and



antineoplastic activities. This drug is approved for adult patients with mismatch repair deficient (dMMR) recurrent or advanced solid tumors, as determined by an FDA-approved test, that have progressed on or following prior treatment and who have no satisfactory alternative treatment options (fda.gov.2022). The efficacy of dostarlimab was evaluated in the GARNET Trial (NCT02715284), a non-randomized, multicenter, open-label, multi-cohort trial. The drug demonstrated durable antitumor activity in patients with dMMR solid tumors, with consistent antitumor activity seen across solid tumor types.

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## RECOMMENDATIONS

- A follow-up liquid biopsy after 3 months may be recommended to explore markers for immunotherapy.
- Validation of the variant(s) by Sanger sequencing is recommended to rule out false positives.
- Genetic counselling is advised for interpretation on the consequences of the variant(s).
- If results obtained do not match the clinical findings, additional testing should be considered as per referring clinician's recommendations.



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**APPENDIX 1: TEST METHODOLOGY**

**Test Description & Methodology**

Nucleic acids were isolated from samples and after quality check was directly loaded on Next Generation Sequencer and subjected to automated library preparation and template preparation followed by sequencing.

Analysis is done and the data is visualized on Integrative Genomics Viewer (IGV) and analyzed. The final report is generated using curated knowledgebase reporter. The assay has been optimized to enable rapid and accurate detection of true somatic alterations by effective sequencing of both tissue and ctDNA based blood samples with high sensitivity and specificity for supporting reliable treatment decisions. The assay can detect all classes of genomic alterations, including Single Nucleotide Variants (SNVs), Small Insertions and Deletions (Indels), Copy Number Alterations (Amplifications) and selected translocations with minimal amounts of routine clinical samples (including core or fine-needle biopsies). In addition, all samples are simultaneously profiled for Tumor Mutation Burden (TMB), Microsatellite Instability (MSI) status and Homologous Recombination Deficiency (HRD) to help guide immunotherapy decisions. MSI status is reported as MSI-High, MSI-Intermediate or MSI-Stable (MSS). TMB status is reported for all cancer types as TMB-High ( $\geq 10$  Muts/Mb), or TMB-Low ( $< 10$  Muts/Mb).

**AMP/ASCO/CAP Classification**

<b>Tier I:</b> Variants of Strong Clinical Significance	1A	Biomarkers that predict response or resistance to US FDA-approved therapies for a specific type of tumor or have been included in <b>professional guidelines</b> as <b>therapeutic, diagnostic, and/or prognostic biomarkers</b> for specific types of tumors.
	1B	Biomarkers that predict response or resistance to a therapy based on well-powered studies with consensus from experts in the field, or have diagnostic and/or prognostic significance of certain diseases based on <b>well- powered studies with expert consensus</b> .
<b>Tier II:</b> Variants of Potential Clinical Significance	2C	Biomarkers that predict response or resistance to therapies approved by FDA or professional <b>societies for a different tumor type (ie, off-label use of a drug)</b> , serve as inclusion criteria for clinical trials, or have diagnostic and/or prognostic significance based on the results of multiple small studies.
	2D	Biomarkers that show plausible therapeutic significance based on preclinical studies, or may assist disease diagnosis and/or prognosis themselves or along with other biomarkers based on <b>small studies or multiple case reports with no consensus</b> .
<b>Tier III:</b> Variants of Unknown Clinical Significance		Not observed at a significant allele frequency in the general or specific subpopulation databases, or pan-cancer or tumor-specific variant databases No convincing published evidence of cancer association.
<b>Tier IV:</b> Benign or Likely Benign Variants		Observed at significant allele frequency in the general or specific subpopulation databases.

**DISCLAIMER**

- This report was generated using the materials and methods as recommended which required the use of quality reagents, protocols, instruments, software, databases and other items, some of which were provided or made accessible by third parties. A defect or malfunction in any such reagents, protocols, instruments, software, databases and/or other items may compromise the quality or accuracy of the report.
- The report has been created based on, or incorporated inferences to, various scientific manuscripts, references, and other sources of information, including without limitation manuscripts, references, and other sources of information that were prepared by third parties that describe correlations between certain genetic mutations and particular diseases (and/or certain therapeutics that may be useful in ameliorating the effects of such diseases). Such information and correlations are subject to change over time in response to future scientific and medical findings. MolQ Laboratory makes no representation or warranty of any kind, expressed or implied, regarding the accuracy of the information provided by or contained in such manuscripts, references, and other sources is later determined to be inaccurate, the accuracy and quality of the Report may be adversely impacted. MolQ Laboratory is not obligated to notify you of any of the impact that future scientific or medical findings may have on the report.
- The report must always be interpreted and considered within the clinical context, and a physician should always consider the report along with all other pertinent information and data that a physician would prudently consider prior to providing a diagnosis or developing and implementing a plan of care for the patient. The report should never be considered or relied upon alone in making any diagnosis or prognosis. The manifestations of many diseases are caused by more than one gene

variant, a single gene variant may be relevant to more than one disease, and certain relevant gene variants may not have been considered in the report. In addition, many diseases are caused or influenced by modifier genes, epigenetic factors, environmental factors, and other variables that are not addressed by the report. This report is based on a Next Generation Assay which does not distinguish between a somatic and a germline variant. If germline variant is in question, further testing is recommended. The report provided by MolQ Laboratory is on a "as is" basis. MolQ Laboratory makes no representation or warranty of any kind, expressed or implied, regarding the report. In no event will MolQ Laboratory be liable for any actual damages, indirect damages, and/or special or consequential damages arising out of or in any way connected with the Report, your use of the report, your reliance on the report, or any defect or inaccurate information included within the report.

- Medical knowledge and annotation are constantly updated and reflects the current knowledge at the time.
- Due to inherent technology limitations of the assay, not all bases of the exome can be covered by this test. Accordingly, variants in regions of insufficient coverage may not be identified and/or interpreted. Therefore, it is possible that certain variants are present in one or more of the genes analyzed, but have not been detected. The variants not detected by the assay that was performed may/ may not impact the phenotype.
- It is also possible that a pathogenic variant is present in a gene that was not selected for analysis and/or interpretation in cases where insufficient phenotypic information is available.
- The report shall be generated within turnaround time (TAT), however, such TAT may vary depending upon the complexity of test(s) requested. MolQ Laboratory under no circumstances will be liable for any delay beyond afore mentioned TAT.
- It is hereby clarified that the report(s) generated from the test(s) do not provide any diagnosis or opinion or recommends any cure in any manner. MolQ Laboratory hereby recommends the patient and/or the guardians of the patients, as the case may be, to take assistance of the clinician or a certified physician or doctor, to interpret the report(s) thus generated. MolQ Laboratory hereby disclaims all liability arising in connection with the report(s).
- In a very few cases genetic test may not show the correct results, e.g. because of the quality of the material provided to MolQ Laboratory. In case where any test provided by MolQ Laboratory fails for unforeseeable or unknown reasons that cannot be influenced by MolQ Laboratory in advance, MolQ Laboratory shall not be responsible for the incomplete, potentially misleading or even wrong result of any testing if such could not be recognized by MolQ Laboratory in advance.
- This is a laboratory developed test and the development and the performance characteristics of this test was determined by reference laboratory as required by the CLIA 1988 regulations. The report, and the tests used to generate the Report have not been cleared or approved by the US Food and Drug Administration (FDA). The FDA has determined that such clearance or approval is not necessary. The test results have scientifically shown to be clinically useful.

APPENDIX 2: GENE LIST WITH COVERAGE

DNA Hotspots										
ABCB1	CARD11	CYP19A1	FANCA	H2BC12	IRS2	MIB1	PAX3	QKI	SHQ1	TNFAIP3
ABL1	CARM1	CYP2D6	FANCB	H2BC17	IRS4	MIDEAS	PAX5	RAB35	SIN3A	TNFRSF11A
ABL2	CASP8	CYSLTR2	FANCC	H2BC4	ITGAM	MIR142	PAX7	RABEP1	SIRPA	TNFRSF14
ABRAXAS1	CBFA2T3	DACH1	FANCD2	H2BC5	ITK	MITF	PAX8	RAC1	SLC26A3	TNFRSF17
ACTA2	CBFB	DAXX	FANCE	H3-3A	ITPKB	MKI67	PAXIP1	RAC2	SLC34A2	TNFRSF18
ACTB	CBL	DAZAP1	FANCF	H3-3B	JAK1	MKNK1	PBRM1	RAD21	SLFN11	TNFRSF4
ACVR1	CBLB	DCSTAMP	FANCG	H3-4	JAK2	MLH1	PC	RAD50	SLIT2	TNFRSF9
ACVR1B	CBLC	DCUN1D1	FANCI	H3-5	JAK3	MLH3	PCBP1	RAD51	SLX4	TOP1
ACVR2A	CBWD3	DDB2	FANCL	H3C1	JARID2	MLLT1	PLO	RAD51B	SMAD2	TOP2A
ADGRA2	CCDC6	DDR1	FANCM	H3C10	JAZF1	MLLT10	PDCD1	RAD51C	SMAD3	TP53
ADGRB1	CCL2	DDR2	FAS	H3C11	JUN	MLLT3	PDCD11	RAD51D	SMAD4	TP53BP1
AGO1	CCN6	DDX3X	FASLG	H3C12	KANSL1	MPL	PDCD1LG2	RAD52	SMARCA1	TP63
AGO2	CCNB3	DDX41	FAT1	H3C13	KAT6A	MR1	PDGFB	RAD54B	SMARCA2	TPMT
AJUBA	CCND1	DEK	FBXO11	H3C14	KAT6B	MRE11	PDGFRA	RAD54L	SMARCA4	TPTE2
AKT1	CCND2	DHX9	FBXO31	H3C15	KBTBD4	MRTFA	PDGFRB	RAF1	SMARCA1	TRAF2
AKT2	CCND3	DIAPH2	FBXW7	H3C2	KDM2B	MRTFB	PDK1	RANBP17	SMARCB1	TRAF3
AKT3	CCNE1	DICER1	FCGR2A	H3C3	KDM4C	MSH2	PDPK1	RANBP2	SMARCD1	TRAF5
ALB	CCR2	DIS3	FCGR3A	H3C4	KDM5A	MSH3	PDS5B	RARA	SMARCE1	TRAF7
ALK	CCR4	DIS3L2	FGF1	H3C6	KDM5C	MSH6	PGBD5	RASA1	SMC1A	TRIP13
ALOX12B	CCR5	DKC1	FGF10	H3C7	KDM6A	MSI2	PGR	RASGEF1A	SMC3	TRPA1
AMER1	CCT6B	DKK4	FGF12	H3C8	KDM6B	MSMB	PHF6	RB1	SMO	TSC1
ANKRD11	CD19	DMD	FGF14	HAVCR2	KDR	MST1	PHOX2B	RBM10	SMYD3	TSC2
ANKRD26	CD22	DNAJB1	FGF19	HDAC1	KEAP1	MST1R	PICALM	RBM15	SNCAIP	TSHR
APC	CD27	DNM2	FGF2	HDAC2	KEL	MT1JP	PIGA	RBM38	SOCS1	TSLP
APH1A	CD274	DNMT1	FGF23	HDAC4	KIF1A	MTAP	PIK3C2B	RECQL	SOCS2	TUSC3
APLN	CD276	DNMT3A	FGF3	HDAC7	KIF1B	MTOR	PIK3C2G	RECQL4	SOCS3	TXNIP
APOB	CD28	DNMT3B	FGF4	HDAC9	KIF5B	MUC17	PIK3C3	REL	SOS1	TYK2
AR	CD33	DOCK8	FGF5	HGF	KIR3DL1	MUC6	PIK3CA	RELA	SOX10	TYRO3
ARAF	CD36	DOT1L	FGF6	HIF1A	KIT	MUSK	PIK3CB	RELN	SOX17	U2AF1
ARFRP1	CD40	DROSHA	FGF7	HLA-A	KLF2	MUTYH	PIK3CD	REST	SOX2	U2AF2
ARHGAP26	CD58	DTX1	FGF8	HLA-B	KLF3	MYB	PIK3CG	RET	SOX9	UBE2T
ARHGAP35	CD70	DUSP2	FGF9	HLA-C	KLF4	MYBL1	PIK3R1	RFC1	SP140	UBR5
ARHGFEF10	CD74	DUSP22	FGFR1	HLA-DMA	KLF5	MYC	PIK3R2	RGPD3	SPEN	UNCX
ARHGFEF12	CD79A	DUSP4	FGFR2	HLA-DMB	KLHL6	MYCL	PIK3R3	RHEB	SPOP	USP6
ARID1A	CD79B	DUSP9	FGFR3	HLA-DOA	KLLN	MYCN	PIM1	RHOA	SPRED1	USP8
ARID1B	CD80	E2F3	FGFR4	HLA-DOB	KMT2A	MYD88	PKN1	RHOB	SPRTN	USP9X
ARID2	CDC73	EBF1	FGR	HLA-DPA1	KMT2B	MYH11	PLAG1	RHPN2	SPTA1	VAV1
ARID3A	CDH1	ECT2L	FH	HLA-DPB1	KMT2C	MYH9	PLCB4	RICTOR	SPTAN1	VEGFA
ARID4B	CDH10	EED	FHIT	HLA-DPB2	KMT2D	MYO18A	PLCG1	RINT1	SRC	VHL
ARID5B	CDH4	EEF1A1	FLCN	HLA-DQA1	KNSTRN	MYOD1	PLCG2	RIT1	SRP72	VTCN1
ASMTL	CDK12	EEF2	FLI1	HLA-DQA2	KRAS	NADK	PLK2	RNF111	SRSF2	WAS
ASXL1	CDK4	EGFL7	FLNA	HLA-DQB1	KRT222	NBN	PLXNB2	RNF139	SS18	WDR90
ASXL2	CDK6	EGFR	FLT1	HLA-DQB2	LAG3	NCOA2	PMAIP1	RNF43	SSBP2	WEE1
ATF7IP	CDK8	EGLN1	FLT3	HLA-DRA	LATS1	NCOA3	PML	ROBO1	STAG1	WIF1
ATM	CDKN1A	EGR1	FLT4	HLA-DRB1	LATS2	NCOR1	PMS1	ROS1	STAG2	WNK2
ATP6AP1	CDKN1B	EGR2	FLYWCH1	HLA-DRB5	LCK	NCOR2	PMS2	RPA1	STAT1	WRN
ATP6V1B2	CDKN1C	EGR3	FOXA1	HLA-DRB6	LDB1	NCSTN	PNRC1	RPL10	STAT2	WT1
ATR	CDKN2A	EIF1AX	FOXA2	HLA-E	LEF1	NECTIN4	POLD1	RPL22	STAT3	WWTR1
ATRX	CDKN2B	EIF3E	FOXD4L1	HLA-F	LEMD2	NEGR1	POLE	RPL5	STAT4	XBP1
ATXN3	CDKN2C	EIF4A2	FOXL2	HLA-G	LIFR	NEIL2	POLH	RPS15	STAT5A	XIAP
ATXN7	CEBPA	EIF4E	FOXO1	HLTF	LMO1	NF1	POLQ	RPS20	STAT5B	XPA
AURKA	CEBPA	ELANE	FOXO3	HMG2	LRP1B	NF2	POLR2A	RPS3A	STAT6	XPC
AURKB	CFTR	ELF3	FOXP1	HNF1A	LRP5	NFATC2	POLRMT	RPS6KA3	STK11	XPO1
AXIN1	CHD2	ELOC	FOXQ1	HNRNPK	LRP6	NFE2	POT1	RPS6KA4	STK19	XRCC1
AXIN2	CHD3	ELP2	FRK	HOXA11	LRRK2	NFE2L2	POU2F2	RPS6KB1	STK40	XRCC2
AXL	CHD4	EML4	FRS2	HOXB13	LTB	NFKBIA	PPARG	RPS6KB2	SUFU	XRCC3

B2M	CHD7	EMSY	FUBP1	HRAS	LTK	NFKBIE	PPM1D	RPTOR	SUSD2	YAP1
BABAM1	CHD8	ENG	FUS	HSD3B1	LUC7L2	NIPBL	PPP2R1A	RRAGC	SUZ12	YEATS4
BAP1	CHEK1	EP300	FYN	HSP90AA1	LYN	NKX2-1	PPP2R2A	RRAS	SYK	YES1
BARD1	CHEK2	EPAS1	GAB1	HSP90AB1	LZTR1	NKX3-1	PPP4R2	RRAS2	TAF1	YWHAE
BBC3	CIC	EPC1	GAB2	HUWE1	MACF1	NOD1	PPP6C	RSPO2	TAF15	YY1AP1
BCL10	CIITA	EPCAM	GABRA6	ICOS	MAD2L2	NOTCH1	PRDM1	RSPO3	TAL1	ZBTB2
BCL11B	CILK1	EPHA2	GADD45B	ICOSLG	MAF	NOTCH2	PRDM14	RTEL1	TAP1	ZBTB20
BCL2	CKS1B	EPHA3	GALNT12	ID3	MAFB	NOTCH3	PREX2	RUNX1	TAP2	ZBTB7B
BCL2L1	CLIP1	EPHA5	GATA1	IDH1	MAGED1	NOTCH4	PRF1	RUNX1T1	TAPBP	ZC3H12A
BCL2L11	CMTR2	EPHA7	GATA2	IDH2	MAGI2	NPM1	PRKACA	RXRA	TBL1XR1	ZCCHC12
BCL2L12	CNBD1	EPHB1	GATA3	IDO1	MALT1	NPRL2	PRKARIA	RYBP	TBX3	ZFHX3
BCL2L2	CNOT9	EPHB4	GATA4	IFNAR1	MAML2	NR4A3	PRKCA	S1PR2	TCF12	ZFP36L1
BCL6	COL1A1	EGP1	GATA6	IFNGR1	MAMLD1	NRAS	PRKCB	SALL4	TCF3	ZFP36L2
BCL7A	COL5A1	ERBB2	GEM	IFNGR2	MAP2K1	NRG1	PRKCD	SAMD9	TCF7L2	ZMYM2
BCL9	COL7A1	ERBB3	GEN1	IGF1	MAP2K2	NSD1	PRKCI	SAMD9L	TCL1A	ZMYM3
BCLAF1	COP1	ERBB4	GID4	IGF1R	MAP2K4	NSD2	PRKD1	SAMHD1	TCL1B	ZNF133
BCOR	CPS1	ERCC1	GLI1	IGF2	MAP3K1	NSD3	PRKDC	SBDS	TDG	ZNF217
BCORL1	CRBN	ERCC2	GLI2	IKBKE	MAP3K13	NT5C2	PRKN	SCAF4	TEK	ZNF24
BCR	CREB3L3	ERCC3	GLIS2	IKZF1	MAP3K14	NT5E	PRPF40B	SCG5	TENT5C	ZNF384
BIRC3	CREBBP	ERCC4	GNA11	IKZF2	MAP3K4	NTHL1	PRPF8	SDC4	TENT5D	ZNF703
BLM	CRKL	ERCC5	GNA12	IKZF3	MAP3K6	NTRK1	PRPS1	SDHA	TERC	ZNF750
BMPR1A	CRLF1	ERCC6	GNA13	IL10	MAP3K7	NTRK2	PRSS1	SDHAF2	TERF1	ZNRF3
BRAF	CRLF2	ERF	GNAI2	IL2	MAPK1	NTRK3	PRSS8	SDHB	TERT	ZRANB3
BRCA1	CRTC1	ERG	GNAQ	IL2RB	MAPK3	NUDT15	PSIP1	SDHC	TET1	ZRSR2
BRCA2	CSDE1	ERRF1	GNAS	IL2RG	MAST1	NUF2	PSMB5	SDHD	TET2	
BRCC3	CSF1R	ESR1	GNB1	IL3	MAST2	NUMBL	PTCH1	SERP2	TET3	
BRD3	CSF3R	ESRRA	GPC3	IL4R	MAX	NUP133	PTCH2	SERPINA1	TFE3	
BRD4	CSNK1A1	ETNK1	GPS2	IL6ST	MBD4	NUP214	PTEN	SERPINB3	TFEB	
BRD7	CTC1	ETS1	GREM1	IL7R	MC1R	NUP93	PTK2	SERPINB4	TFG	
BRINP3	CTCF	ETV1	GRIN2A	ING1	MCL1	NUP98	PTK2B	SESN2	TGFBR1	
BRIP1	CTDNEP1	ETV4	GRIN2D	INHA	MDC1	NUTM1	PTMA	SESN3	TGFBR2	
BRSK1	CTLA4	ETV5	GRM3	INHBA	MDM2	P2RY8	PTP4A1	SETBP1	TGIF1	
BTG1	CTNNA1	ETV6	GSK3B	INO80	MDM4	PABPC1	PTPDC1	SETD1B	THADA	
BTG2	CTNNB1	EWSR1	GTF2I	INPP4A	MEAF6	PAG1	PTPN1	SETD2	THRAP3	
BTK	CTNND1	EXO1	GTSE1	INPP4B	MECOM	PAK1	PTPN11	SETDB1	TIPARP	
BTLA	CTR9	EXOSC6	H1-2	INPP5D	MED12	PAK3	PTPN13	SETDB2	TLL2	
BUB1B	CUL1	EXT1	H1-3	INPPL1	MEF2B	PAK5	PTPN14	SF1	TLR4	
C3orf70	CUL3	EXT2	H1-4	INSR	MEF2C	PALB2	PTPN2	SF3A1	TLR9	
C8orf34	CUL4A	EZH1	H19	IRF1	MEF2D	PARP1	PTPN6	SF3B1	TLX3	
CACNA1A	CUL4B	EZH2	H2AC11	IRF2	MEN1	PARP2	PTPRC	SGK1	TMEM127	
CACNA1D	CUX1	EZH1P	H2AC16	IRF4	MERTK	PARP3	PTPRD	SH2B3	TMEM30A	
CAD	CXCR4	EZR	H2AC17	IRF6	MET	PARP4	PTPRO	SH2D1A	TMPRSS2	
CALR	CYLD	FAF1	H2AC6	IRF8	MGA	PARPBP	PTPRS	SHH	TMSB4X	
CAMTA1	CYP17A1	FAM135B	H2BC11	IRS1	MGMT	PASK	PTPRT	SHOC2	TMSB4XP8	

## Fusions/ Translocations

ABL1	BCL6	CIITA	DUSP22	FLI1	JAK2	MLL10	NTRK3	RBM15	TCF3	TYK2
ABL2	BRAF	CREBBP	EPOR	FOXP1	KMT2A	MYC	PDGFB	RET	TCL1A	
ALK	CBFB	CRLF2	FGFR1	GATA1	MAF	NRG1	PDGFRA	ROS1	TCL1B	
BCL10	CCND1	CSF1R	FGFR2	IL3	MAFB	NTRK1	PDGFRB	RUNX1	TLX3	
BCL2	CCND3	DEK	FGFR3	IRF4	MALT1	NTRK2	RARA	TAL1	TP63	