Comprehensive Panel- 500 Genes

Test Description

The MolQ Comprehensive Panel includes 500+ key solid tumor genes (for SNV, CNV, TMB, MSI and fusions) that are well characterized in the published literature and associated with oncology drugs that are FDA approved, part of NCCN guidelines, or in clinical trials.

Patient Demographic

Name: Mr. Jai Prakash Naraian Pandeya
Sex: Male
Date of Birth/Age: 75 years
Disease: Hepatocellular Carcinoma

Clinician

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

Specimen

Booking ID: 012402260212
Sample Type: FFPE Block ID- 701/24-A
Tumor Content Percentage: 15%
Date of Collection: 26-02-2024
Date of Booking: 26-02-2024

CLINICAL SYNOPSIS

J P N Pandeya is a known case of hepatocellular carcinoma. He has been evaluated for pathogenic variations in the genes listed in Appendix 2.

RESULTS

No clinically relevant alteration was detected.

Tumor Mutation Burden is 2.85 Mut/Mb.

Microsatellite Instability (MSI) is stable.

VARIANT DETECTED AS PER NCCN GUIDELINES

No clinically relevant alteration detected.

OTHER VARIANTS DETECTED

Mutation in *ACVRB1* (p.Asn387Metfs*6, VAF= 7.41%) and *PARP4* (c.3285_3285+5delinsAGT, VAF= 100%) are present in the given sample.

"Important disclaimer: As a standard of care, our case selection criteria for NGS run is ≥20% tumor content. The run was performed in this case after receiving informed consent from the clinician."

Note: Average Base Coverage Depth achieved was 3406 in this sample.

RELEVANT HEPATOCELLUALR CARCINOMA FINDINGS

Gene	Findings	Gene	Findings
NTRK1	None detected	*NTRK3*	None detected
NTRK2	None detected	*RET*	None detected

RELEVANT BIOMARKERS

Gene/ Transcript (Locus)	Variant ID	Variant/ Exon/ Variant Effect	Allele Frequency/ Coverage	*Relevant Therapies (In this cancer type)	*Relevant Therapies (In other cancer type)	Tier[1]
PARP4 (chr13:25021149)	-	c.3285_3285+5delinsAGT (p.?) Exon 26 *Frameshift Deletion*	100% / 18	None	None	IIc

*Public data sources included in relevant therapies: FDA[i], NCCN, EMA[ii], ESMO

[1]Li et al. Standards and Guidelines for the Interpretation and Reporting of Sequence Variants in Cancer: A Joint Consensus Recommendation of the Association for Molecular Pathology, American Society of Clinical Oncology, and College of American Pathologists. J Mol Diagn. 2017 Jan;19(1):4-23.

HRR DETAILS

Gene/Genome Alterations	Findings
Not Detected	Not Applicable

Homologous recombination repair (HRR) genes were defined from published evidence in relevant therapies, clinical guidelines, as well as clinical trials, and include - *BRCA1, BRCA2, ATM, BARD1, BRIP1, CDK12, CHEK1, CHEK2, FANCL, PALB2, RAD51B, RAD51C, RAD51D* and *RAD54L*.

VARIANT OF UNKNOWN SIGNIFICANCE (VUS)

Not present

PREVALENT CANCER BIOMARKERS WITHOUT RELEVANT EVIDENCE BASED ON INCLUDED DATA SOURCES

Gene/ (Locus)	Variant	Variant Effect/ Variant ID	Variant Allele Frequency	Location	Coverage	#ClinVar
ACVR1B (chr12:52379028)	c.1160delA (p.Asn387Metfs*6)	Frameshift Deletion	7.41%	Exon 7	162	-

#Based on Clinvar version 20220709

CLINICAL CORRELATION AND VARIANT INTERPRETATION

PARP4 **c.3285_3285+5delinsAGT** **Coverage Frequency 18**

Gene description: The *PARP4* gene encodes the poly(ADP-ribose) polymerase 4 protein[1]. PARP4 belongs to the large PARP protein family that also includes PARP1, PARP2, and PARP3[2]. PARP enzymes are responsible for the transfer of ADP-ribose, known as poly(ADPribosyl)ation or PARylation, to a variety of protein targets resulting in the recruitment of proteins involved in DNA repair, DNA synthesis, nucleic acid metabolism, and regulation of chromatin structure[2,3]. PARP enzymes are involved in several DNA repair pathways[2,3]. Although the functional role of PARP4 is not well understood, PARP4 has been predicted to function in base excision repair (BER) due to its BRCA1 C Terminus (BRCT) domain which is found in other DNA repair pathway proteins[4].

Alterations and prevalence: Somatic mutations in *PARP4* are observed in 9% of skin cutaneous melanoma, 8% of uterine corpus endometrial carcinoma, 5% of bladder urothelial carcinoma, 4% of stomach adenocarcinoma, and 3% of lung squamous cell carcinoma[5,6]. Biallelic deletions in *PARP4* are observed in 2% of diffuse large B-cell lymphoma (DLBCL)[5,6].

Potential relevance: Currently, no therapies are approved for *PARP4* aberrations. However, PARP inhibition is known to induce synthetic lethality in certain cancer types that are homologous recombination repair (HRR) deficient (HRD) due to mutations in

the HRR pathway. This is achieved from PARP inhibitors (PARPi) by promoting the accumulation of DNA damage in cells with HRD, consequently resulting in cell death[7,8]. Although not indicated for specific alterations in PARP4, several PARPis including olaparib, rucaparib, talazoparib, and niraparib have been approved in various cancer types with HRD. Olaparib[9] (2014) was the first PARPi to be approved by the FDA for BRCA1/2 aberrations. Originally approved for the treatment of germline variants, olaparib is now indicated (2018) for the maintenance treatment of both germline BRCA1/2-mutated (gBRCAm) and somatic BRCA1/2-mutated (sBRCAm) epithelial ovarian, fallopian tube, or primary peritoneal cancers that are responsive to platinum-based chemotherapy. Olaparib is also indicated for the treatment of patients with gBRCAm HER2-negative metastatic breast cancer and metastatic pancreatic adenocarcinoma. Additionally, olaparib[9] is approved (2020) for metastatic castration-resistant prostate cancer (mCRPC) with deleterious or suspected deleterious, germline or somatic mutations in HRR genes that includes BRCA1. Rucaparib[10] (2016) was the first PARPi approved for the treatment of patients with either gBRCAm or sBRCAm epithelial ovarian, fallopian tube, or primary peritoneal cancers and is also approved (2020) for deleterious gBRCAm or sBRCAm mCRPC. Talazoparib[11] (2018) is indicated for the treatment of gBRCAm HER2-negative locally advanced or metastatic breast cancer. Niraparib[12] (2017) is another PARPi approved for the treatment of epithelial ovarian, fallopian tube, or primary peritoneal cancers with a deleterious or suspected deleterious BRCA mutation.

REFERENCES

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ACVR1B **p.Asn387Metfs*6** **Coverage Frequency 162**

Gene description: The *ACVR1B* gene encodes the activin A type 1B receptor protein, a transmembrane serine-threonine kinase receptor and member of the bone morphogenic protein (BMP)/transforming growth factor-beta (TGFβ) receptor family[1,2]. ACVR1B is a type I receptor that forms a heterotetrametric complex with at least two type I receptors (including ACVR1) and two type II receptors (including BMPR2, ACVR2A, and ACVR2B)[2,3]. When ligands, such as activin A or BMPs, dimerize and bind to the heterotetrametric complex, type II receptors transphosphorylate and activate type I receptors leading to phosphorylation of SMAD proteins and downstream signaling[2,3]. Loss of function mutations and homozygous deletion in *ACVR1B* has been observed in pancreatic cancer and is associated with increased cell growth, colony formation, and tumorigenicity[4,5].

Alterations and prevalence: Somatic mutations of *ACVR1B* are observed in 5% of uterine corpus endometrial carcinoma, 4% of colorectal adenocarcinoma, 3% of stomach adenocarcinoma, 2% of lung adenocarcinoma, skin cutaneous melanoma, lung squamous cell carcinoma, uterine carcinosarcoma, esophageal adenocarcinoma, and kidney chromophobe, and 1% of head and neck squamous cell carcinoma, kidney renal clear cell carcinoma, breast invasive carcinoma, brain lower grade glioma, ovarian serous cystadenocarcinoma, pancreatic adenocarcinoma, liver hepatocellular carcinoma, and acute myeloid leukemia[6,7]. Biallelic deletion of ACRV1B is observed in 1% of stomach adenocarcinoma, brain lower grade glioma, and pancreatic adenocarcinoma[6,7].

Potential relevance: Currently, no therapies are approved for *ACVR1B* aberrations.

REFERENCES

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RECOMMENDATIONS

- Genetic counselling is advised for interpretation on the consequences of the variant(s).

Jatinder Kaur, PhD
Head, Molecular Biology & Genomics

Dr. Gulshan Yadav, MD
Head, Pathology

APPENDIX 1: TEST METHODOLOGY

METHOD

Pathology Assessment

The FFPE block is reviewed for presence of tumor cells and tumor percentage by histopathologists through screening of H & E staining slides.

Assay Methods

The test was performed using the Oncomine Comprehensive Assay Plus targeted, amplicon based next-generation sequencing assay that analyses 500+ unique genes for SNV, CNV, TMB, MSI and fusions. The minimum of 20ng of DNA isolated by Qiagen nucleic acid isolation kit is amplified using Oncomine Comprehensive assay plus as per the instruction manual. The amplicon libraries are prepared from 4 pools of primer which includes 2 pools of DNA based targets. The amplified primer pools are enzyme fragmented and Ion adapter barcodes are added. Amplified library is purified followed by quantitation using Ion Library TaqManTM Quantitation Kit. The quality of amplified libraries having 150-200bp sizes are confirmed by Agilent TapeStation. The quantified pooled library is loaded on Ion 550 Chip using Ion Chef and sequencing is performed on the Ion GeneStudio S5 prime system. For the current report RNA was not included.

Secondary Analysis Methods

The sequence data is processed using Ion Torrent server and the Ion reporter software 5.20.2.0. TMB is reported as High (>10 mutations/Mb), Intermediate (>3 to 10 mutations/Mb) and Low (<3 mutations/Mb). All the reported alterations are manually curated using Integrative Genomics Viewer (IGV). The Final report is generated using oncomine knowledgebase which includes contextual investigations of sample-specific variants with respect to labels, guidelines (AMP, ASCO, CAP), current clinical trials and peer-reviewed literature which is frequently updated.

Genes Assayed

The panel covers 1.50M bases of DNA region, including 1.06M bases of exonic regions. It includes a total of 500+ genes covering 165 hotspot genes, 333 genes with focal CNV gains and loss, 227 genes with full coding sequence (CDS), >1 Mb exonic regions for TMB evaluation and 76 MSI markers for Microsatellite Instability (MSI) and Microsatellite stable (MSS). It also covers 46 genes (SNVs, Indels, CNVs) for homologous recombination deficiency (HRD) including *BRCA1* and *BRCA2*. A subset of these (20 genes) were assessed for determining Loss of Heterozygosity (LOH) at gene level. Details available on request.

AMP/ASCO/CAP Classification

Tier I: 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 **professional guidelines** as **therapeutic, diagnostic, and/or prognostic biomarkers** 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 **well- powered studies with expert consensus**.
Tier II: Variants of Potential Clinical Significance	2C	Biomarkers that predict response or resistance to therapies approved by FDA or professional **societies for a different tumor type (ie, off-label use of a drug)**, 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 **small studies or multiple case reports** with no consensus.
Tier III: 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.
Tier IV: 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.

LIMITATIONS

- Testing has been performed assuming that the sample received belongs to the above-named individual(s) and any stated relationships between individuals are accepted as true.
- Due to inherent technology limitations, coverage is not uniform across all regions. Hence pathogenic variants present in areas of insufficient coverage may not be analyzed/ reported.
- Variants with very low allele frequency (<5%) present in the given specimen or lower copy number variation might not be detected. Similarly fusion variants with less read may not be detected. Variant detection is also based on tumor percentage and affected by tumor heterogeneity. The FFPE fixation issues and the age of the block also widely affects the genomic findings.

- The classification and interpretation of all the variants in this assay reflects the current state of scientific understanding at the time this report was issued. In some instances, the classification and interpretation of such variants may change as new scientific information comes to light.
- Test results should be interpreted in context of clinical findings, tumor sampling, histopathology, and other laboratory data.
- If results obtained do not match other clinical laboratory findings, please contact the laboratory for possible. Misinterpretation of results may occur if the information provided is inaccurate or incomplete.
- Genetic testing is highly accurate. Rarely, inaccurate results may occur for various reasons. These reasons include, but are not limited to mislabelled samples, inaccurate reporting of clinical/medical information, rare technical errors or unusual circumstances such as bone marrow transplantation, blood transfusion; or the presence of change(s) in such a small percentage of cells that may not be detectable by the test (mosaicism).

APPENDIX 2: GENE LIST

Gene	Gene	Gene	Gene	Gene	Gene	Gene
ABL1	*CDKN2A*	*FANCF*	*HIST3H3*	*MEN1*	*PIK3R3*	*SMAD3*
ABL2	*CDKN2B*	*FANCG*	*HLA-A*	*MET*	*PIM1*	*SMAD4*
ACVR1	*CDKN2C*	*FANCI*	*HLA-B*	*MGA*	*PLCG2*	*SMARCA4*
ACVR1B	*CEBPA*	*FANCL*	*HLA-C*	*MITF*	*PLK2*	*SMARCB1*
AKT1	*CENPA*	*FAS*	*HNF1A*	*MLH1*	*PMAIP1*	*SMARCD1*
AKT2	*CHD2*	*FAT1*	*HNRNPK*	*MLL*	*PMS1*	*SMC1A*
AKT3	*CHD4*	*FBXW7*	*HOXB13*	*MLLT3*	*PMS2*	*SMC3*
ALK	*CHEK1*	*FGF1*	*HRAS*	*MPL*	*PNRC1*	*SMO*
ALOX12B	*CHEK2*	*FGF10*	*HSD3B1*	*MRE11A*	*POLD1*	*SNCAIP*
ANKRD11	*CIC*	*FGF14*	*HSP90AA1*	*MSH2*	*POLE*	*SOCS1*
ANKRD26	*CREBBP*	*FGF19*	*ICOSLG*	*MSH3*	*PPARG*	*SOX10*
APC	*CRKL*	*FGF2*	*ID3*	*MSH6*	*PPM1D*	*SOX17*
AR	*CRLF2*	*FGF23*	*IDH1*	*MST1*	*PPP2R1A*	*SOX2*
ARAF	*CSF1R*	*FGF3*	*IDH2*	*MST1R*	*PPP2R2A*	*SOX9*
ARFRP1	*CSF3R*	*FGF4*	*IFNGR1*	*MTOR*	*PPP6C*	*SPEN*
ARID1A	*CSNK1A1*	*FGF5*	*IGF1*	*MUTYH*	*PRDM1*	*SPOP*
ARID1B	*CTCF*	*FGF6*	*IGF1R*	*MYB*	*PREX2*	*SPTA1*
ARID2	*CTLA4*	*FGF7*	*IGF2*	*MYC*	*PRKAR1A*	*SRC*
ARID5B	*CTNNA1*	*FGF8*	*IKBKE*	*MYCL1*	*PRKCI*	*SRSF2*
ASXL1	*CTNNB1*	*FGF9*	*IKZF1*	*MYCN*	*PRKDC*	*STAG1*
ASXL2	*CUL3*	*FGFR1*	*IL10*	*MYD88*	*PRSS8*	*STAG2*
ATM	*CUX1*	*FGFR2*	*IL7R*	*MYOD1*	*PTCH1*	*STAT3*
ATR	*CXCR4*	*FGFR3*	*INHA*	*NAB2*	*PTEN*	*STAT4*
ATRX	*CYLD*	*FGFR4*	*INHBA*	*NBN*	*PTPN11*	*STAT5A*
AURKA	*DAXX*	*FH*	*INPP4A*	*NCOA3*	*PTPRD*	*STAT5B*
AURKB	*DCUN1D1*	*FLCN*	*INPP4B*	*NCOR1*	*PTPRS*	*STK11*
AXIN1	*DDR2*	*FLI1*	*INSR*	*NEGR1*	*PTPRT*	*STK40*
AXIN2	*DDX41*	*FLT1*	*IRF2*	*NF1*	*QKI*	*SUFU*
AXL	*DHX15*	*FLT3*	*IRF4*	*NF2*	*RAB35*	*SUZ12*
B2M	*DICER1*	*FLT4*	*IRS1*	*NFE2L2*	*RAC1*	*SYK*
BAP1	*DIS3*	*FOXA1*	*IRS2*	*NFKBIA*	*RAD21*	*TAF1*
BARD1	*DNAJB1*	*FOXL2*	*JAK1*	*NKX2-1*	*RAD50*	*TBX3*
BBC3	*DNMT1*	*FOXO1*	*JAK2*	*NKX3-1*	*RAD51*	*TCEB1*
BCL10	*DNMT3A*	*FOXP1*	*JAK3*	*NOTCH1*	*RAD51B*	*TCF3*
BCL2	*DNMT3B*	*FRS2*	*JUN*	*NOTCH2*	*RAD51C*	*TCF7L2*
BCL2L1	*DOT1L*	*FUBP1*	*KAT6A*	*NOTCH3*	*RAD51D*	*TERC*
BCL2L11	*E2F3*	*FYN*	*KDM5A*	*NOTCH4*	*RAD52*	*TERT*
BCL2L2	*EED*	*GABRA6*	*KDM5C*	*NPM1*	*RAD54L*	*TET1*
BCL6	*EGFL7*	*GATA1*	*KDM6A*	*NRAS*	*RAF1*	*TET2*
BCOR	*EGFR*	*GATA2*	*KDR*	*NRG1*	*RANBP2*	*TFE3*
BCORL1	*EIF1AX*	*GATA3*	*KEAP1*	*NSD1*	*RARA*	*TFRC*
BCR	*EIF4A2*	*GATA4*	*KEL*	*NTRK1*	*RASA1*	*TGFBR1*
BIRC3	*EIF4E*	*GATA6*	*KIF5B*	*NTRK2*	*RB1*	*TGFBR2*
BLM	*EML4*	*GEN1*	*KIT*	*NTRK3*	*RBM10*	*TMEM127*
BMPR1A	*EP300*	*GID4*	*KLF4*	*NUP93*	*RECQL4*	*TMPRSS2*
BRAF	*EPCAM*	*GLI1*	*KLHL6*	*NUTM1*	*REL*	*TNFAIP3*

Comprehensive Panel- 500 Genes

BRCA1	*EPHA3*	*GNA11*	*KMT2B*	*PAK1*	*RET*	*TNFRSF14*
BRCA2	*EPHA5*	*GNA13*	*KMT2C*	*PAK3*	*RFWD2*	*TOP1*
BRD4	*EPHA7*	*GNAQ*	*KMT2D*	*PAK7*	*RHEB*	*TOP2A*
BRIP1	*EPHB1*	*GNAS*	*KRAS*	*PALB2*	*RHOA*	*TP53*
BTG1	*ERBB2*	*GPR124*	*LAMP1*	*PARK2*	*RICTOR*	*TP63*
BTK	*ERBB3*	*GPS2*	*LATS1*	*PARP1*	*RIT1*	*TRAF2*
C11orf30	*ERBB4*	*GREM1*	*LATS2*	*PAX3*	*RNF43*	*TRAF7*
CALR	*ERCC1*	*GRIN2A*	*LMO1*	*PAX5*	*ROS1*	*TSC1*
CARD11	*ERCC2*	*GRM3*	*LRP1B*	*PAX7*	*RPS6KA4*	*TSC2*
CASP8	*ERCC3*	*GSK3B*	*LYN*	*PAX8*	*RPS6KB1*	*TSHR*
CBFB	*ERCC4*	*H3F3A*	*LZTR1*	*PBRM1*	*RPS6KB2*	*U2AF1*
CBL	*ERCC5*	*H3F3B*	*MAGI2*	*PDCD1*	*RPTOR*	*VEGFA*
CCND1	*ERG*	*H3F3C*	*MALT1*	*PDCD1LG2*	*RUNX1*	*VHL*
CCND2	*ERRFI1*	*HGF*	*MAP2K1*	*PDGFRA*	*RUNX1T1*	*VTCN1*
CCND3	*ESR1*	*HIST1H1C*	*MAP2K2*	*PDGFRB*	*RYBP*	*WISP3*
CCNE1	*ETS1*	*HIST1H2BD*	*MAP2K4*	*PDK1*	*SDHA*	*WT1*
CD274	*ETV1*	*HIST1H3A*	*MAP3K1*	*PDPK1*	*SDHAF2*	*XIAP*
CD276	*ETV4*	*HIST1H3B*	*MAP3K13*	*PGR*	*SDHB*	*XPO1*
CD74	*ETV5*	*HIST1H3C*	*MAP3K14*	*PHF6*	*SDHC*	*XRCC2*
CD79A	*ETV6*	*HIST1H3D*	*MAP3K4*	*PHOX2B*	*SDHD*	*YAP1*
CD79B	*EWSR1*	*HIST1H3E*	*MAPK1*	*PIK3C2B*	*SETBP1*	*YES1*
CDC73	*EZH2*	*HIST1H3F*	*MAPK3*	*PIK3C2G*	*SETD2*	*ZBTB2*
CDH1	*FAM123B*	*HIST1H3G*	*MAX*	*PIK3C3*	*SF3B1*	*ZBTB7A*
CDK12	*FAM175A*	*HIST1H3H*	*MCL1*	*PIK3CA*	*SH2B3*	*ZFHX3*
CDK4	*FAM46C*	*HIST1H3I*	*MDC1*	*PIK3CB*	*SH2D1A*	*ZNF217*
CDK6	*FANCA*	*HIST1H3J*	*MDM2*	*PIK3CD*	*SHQ1*	*ZNF703*
CDK8	*FANCC*	*HIST2H3A*	*MDM4*	*PIK3CG*	*SLIT2*	*ZRSR2*
CDKN1A	*FANCD2*	*HIST2H3C*	*MED12*	*PIK3R1*	*SLX4*	
CDKN1B	*FANCE*	*HIST2H3D*	*MEF2B*	*PIK3R2*	*SMAD2*	