Liquid Precision Panel- 1000 Genes

Test Description

Liquid 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: Mr. Mahaveer
Sex: Male
Date of Birth/Age: 46 years
Disease: Lung Adenocarcinoma

Clinician

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

Specimen

Booking ID: 012401240051
Sample Type: Blood
Tumor Content Percentage: NA
Date of Collection: 24-01-2024
Date of Booking: : 24-01-2024

CLINICAL SYNOPSIS

Mahaveer, is a known case of lung adenocarcinoma. He has been evaluated for pathogenic variations in the genes listed in Appendix 2.

RESULT SUMMARY

Potential clinically significant alteration was observed in ***MAP3K1*** (p.Ser941Tyrfs*62, VAF=02%).
MAP3K1 mutations may induce dysregulation in JNK signaling pathway that result in defective apoptosis, leading to unresponsiveness to environmental and genotoxic stresses. However, its mutation effects in lung cancer still warrants further clinical investigations.

Variant of Unknown Significance (VUS) detected:

ATM mutation (p.Ile2683Thr, VAF= 48%) is present in the given sample.
Although not clinically relevant in the current scenario, future reclassifications may need to be carefully monitored through a genomic counsellor.

Other Markers

Major immunotherapy markers (MSI and TMB) are low while PD-L1 is Positive in **1 CTC/1.5 mL.** The overall HRD score is low.
PD-L1-positive CTCs are prone to evasion from the innate immune system. Although therapeutic responses to Immunotherapy agents have not yet been established through PD- L1 positivity on CTCs, clinical correlation is advised.

RESULTS

Potential clinically significant alteration was observed in *MAP3K1*.

Gene	Variant	Allele Frequency	Variant Effect	*Relevant Therapies (In this cancer type)	*Relevant Therapies (In other cancer type)	Tier
MAPK3K1	p.Ser941Tyrfs*62	02%	Insertion Frameshift	None	None	IId

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

VARIANT OF UNKNOWN SIGNIFICANCE (VUS)

ATM p.Ile2683Thr, VAF=48%, Tier III.

IMMUNO-ONCOLOGY FINDINGS

MSI/MMR Status NGS Based	TMB (Tissue / Blood)	PDL-1 IHC on tissue (TBx), Dako clone 22C3 or CTC (LBx)
2.35% Low	3.66 Muts/Mb Low	**PD-L1 Positive in 1 CTC/ 1.5 mL**

HOMOLOGOUS RECOMBINANT DEFICIENCY (HRD) FINDINGS

Overall HRD Scoring	HRR Gene	LOH (Loss of Heterozygosity)	TAI & LST (Telomeric Allelic Instability & Large State Transitions)
36% Low	*ATM*	10% Low	TAI: 21% LST: 05%

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

OTHER BIOMARKERS

Gene	Findings	Gene	Findings
ALK	None detected	*NTRK1*	None detected
BRAF	None detected	*NTRK2*	None detected
EGFR	None detected	*NTRK3*	None detected
ERBB2	None detected	*RET*	None detected
KRAS	None detected	*ROS1*	None detected
MET	None detected		

LONGITUDINAL MONITORING MARKERS

Circulating Tumor Cells (CTC)	CTC Cluster	Highest Mutant Allele Frequency	ct DNA Tumor Fraction (%)
1 CTC/1.5mL	0 CTC Cluster/1.5mL	None	100

Note: 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

MAP3K1 **p.Ser941Tyrfs*62**

Gene description: *MAP3K1*, mitogen-activated protein kinase kinase kinase 1, is a E3 ubiquitin protein ligase and serine/threonine kinase that regulates JNK and ERK signaling and the full length Map3k1 protein functions in cell migration and cell survival, while the caspase-cleaved C-terminal Map3k1 fragment acts to promote apoptosis[1]. *MAP3K1* mutations have been

identified in breast cancer[2-4]. MAP3K1 activates the JNK pathway by selectively phosphorylating and activating MAP2K4[5,6]. Deficiency in the JNK signaling pathway results in defective apoptosis, leading to unresponsiveness to environmental and genotoxic stresses[7]. According to AACR genie studies, MAP3K1 is altered in 3.24% of all cancers with breast invasive ductal carcinoma, lung adenocarcinoma, colon adenocarcinoma, endometrial endometrioid adenocarcinoma, and invasive breast carcinoma having the greatest prevalence of alterations.

REFERENCES

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5. Yan M. et al. Activation of stress-activated protein kinase by MEKK1 phosphorylation of its activator SEK1. Nature. 1994, 372:798–800.
6. Fanger G.R. et al. MEK kinases are regulated by EGF and selectively interact with Rac/Cdc42. The EMBO Journal. 1997, 16: 4961-4972.
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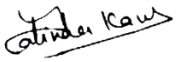
RECOMMENDATIONS

- 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

Circulating cell-free total nucleic acid (cfTNA) 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 (≥10 Muts/Mb), or TMB-Low (<10 Muts/Mb).

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.

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*	*PCLO*	*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*	*SMARCAL1*	*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*
APLNR	*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*
ARHGEF10	*CD74*	*DUSP22*	*FGFR1*	*HLA-DMA*	*KLF5*	*MYC*	*PIK3R2*	*RGPD3*	*SPEN*	*UNCX*
ARHGEF12	*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	*CENPA*	*ELANE*	*FOXO3*	*HMGA2*	*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*

Liquid Precision Panel- 1000 Genes

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*	*PRKAR1A*	*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*	*ERRFI1*	*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*	*EZHIP*	*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*	*MLLT10*	*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*	