GENOMIC® TESTING COOPERATIVE

25371 Commercentre Drive, Lake Forest, CA 92630
Tel: 1-866-484-8870 www.genomictestingcooperative.com
CLIA #: 05D2111917 CAP #: 9441574

Hematology Profile Plus

Patient Name:		Ordering Physician:	
Date of Birth:		Physician ID:	
Gender (M/F):		Accession #:	
Client:		Specimen Type:	BONE MARROW
Case #:		Specimen ID:	
Body Site:	NOT SPECIFIED		

MRN:				Indication for Testing:	C90.0 Multiple myeloma
Collected Date:		Time:		Tumor Type:	Myeloma
Received Date:	04/17/2025	Time:	10:18 AM		

Detected Genomic Alterations				
FANCA	U2AF1	RAF1	KRAS (2 mutations)	RET
TET2	SMC1A	RAD51D	EZH2	LFNG (?Germline, VUS)
SP1	Autosomal chromosomal structural analysis shows: 3q+, +5, +7, 8p-, +9, +11 (low-level), 14q-, +15, +19, 20p-	B cell clonality: Detected (IGHV3-21 / IGKV1-5)	T cell clonality: Not detected	

Results Summary

- **-Somatic mutations in FANCA, U2AF1, RAF1, KRAS (2 mutations), RET, TET2, SMC1A, RAD51D, EZH2, and SP1 genes.**
  -Possible germline mutation in LFNG gene, heterozygous.
  -Autosomal chromosomal structural analysis shows: 3q+, +5, +7, 8p-, +9, +11 (low-level), 14q-, +15, +19, 20p-
  -B cell clonality: Detected (IGHV3-21 / IGKV1-5)
  -T cell clonality: Not detected
  -Plasma cell markers (CD138, BCMA): Increased
  -Low level CCND1, MAF, MAFB, MYC, NSD2 mRNA
  -EBV viral RNA: Not detected
  -HPV viral RNA: Not detected
  -TTV viral RNA: Not detected
  -HLA Genotyping:
  -HLA-A: A*23:17-A*74:01
  -HLA-B: B*08:01-B*15:03
  -HLA-C: C*07:02-C*02:10

  -These findings are consistent with multiple myeloma with hyperdiploidy.

-The LFNG mutation is detected at high level, raising the possibility of a germline mutation. This mutation leads to early termination (loss of function). However, there is no data on its clinical relevance and should be classified as of "uncertain significance" at this time.

See chromosomal abnormality graph and expression plots at the end of the report.

Heterogeneity
There are dominant abnormal clones with FANCA, U2AF1, RAF1, and KRAS (p.Gln61Pro) mutations. The RET, KRAS (p.Ala59Glu), TET2, SMC1A, RAD51D, EZH2, and SP1 mutations are detected in subclones. The LFNG mutation is detected at a high level, possible germline abnormality.

Expression	
Plasma cell markers (CD138, BCMA): Increased	Low level CCND1, MAF, MAFB, MYC, NSD2 mRNA

Diagnostic Implications	
FANCA, U2AF1, RAF1, KRAS (2 mutations), RET, TET2, SMC1A, RAD51D, EZH2, LFNG, SP1	-These findings are consistent with multiple myeloma. -The LFNG mutation is likely a germline variant.

Therapeutic Implications	
FANCA	DNA cross-linking agents such as diepoxybutane (DEB) and mitomycin C (MMC)
U2AF1	Spliceosome modifiers
RAF1	RAF inhibitors
KRAS	MEK inhibitors
RET	RET inhibitors
TET2	DNA methyltransferase inhibitors
SMC1A	PARP inhibitors
RAD51D	PARP inhibitors
EZH2	EZH2 inhibitors

Prognostic Implications	
FANCA, SMC1A, SP1	Unknown
U2AF1, RAF1, KRAS (2 mutations), RET, RAD51D, EZH2	Poor
TET2	Neutral

Relevant Genes with NO Alteration

No evidence of mutation in FLT3, NPM1, IDH1, or IDH2

Biological relevance of detected Alterations

- FANCA. The Fanconi anemia complementation group (FANC) currently includes FANCA, FANCB, FANCC, FANCD1 (also called BRCA2), FANCD2 FANCE, FANCF, FANCG, FANCI, FANCJ (also called BRIP1), FANCL, FANCM and FANCN (also called PALB2). The previously defined group FANCH is the same as FANCA. Fanconi anemia is a genetically heterogeneous recessive disorder characterized by cytogenetic instability, hypersensitivity to DNA crosslinking agents, increased chromosomal breakage, and defective DNA repair. The members of the Fanconi anemia complementation group do not share sequence similarity; they are related by their assembly into a common nuclear protein complex. This gene encodes the protein for complementation group A. Alternative splicing results in multiple transcript variants encoding different isoforms. Mutations in this gene are the most common cause of Fanconi anemia. [provided by RefSeq, Jul 2008]

- U2AF1. This gene belongs to the splicing factor SR family of genes. U2 auxiliary factor, comprising a large and a small subunit, is a non-snRNP protein required for the binding of U2 snRNP to the pre-mRNA branch site. This gene encodes the small subunit which plays a critical role in both constitutive and enhancer-dependent RNA splicing by directly mediating interactions between the large subunit and proteins bound to the enhancers. Alternatively spliced transcript variants encoding different isoforms have been identified. [provided by RefSeq, Jul 2008]

- RAF1. This gene is the cellular homolog of viral raf gene (v-raf). The encoded protein is a MAP kinase kinase kinase (MAP3K), which functions downstream of the Ras family of membrane associated GTPases to which it binds directly. Once activated, the cellular RAF1 protein can phosphorylate to activate the dual specificity protein kinases MEK1 and MEK2, which in turn phosphorylate to activate the serine/threonine specific protein kinases, ERK1 and ERK2. Activated ERKs are pleiotropic effectors of cell physiology and play an important role in the control of gene expression involved in the cell division cycle, apoptosis, cell differentiation and cell migration. Mutations in this gene are associated with Noonan syndrome 5 and LEOPARD syndrome 2. [provided by RefSeq, Jul 2008]

- KRAS. This gene, a Kirsten ras oncogene homolog from the mammalian ras gene family, encodes a protein that is a member of the small GTPase superfamily. A single amino acid substitution is responsible for an activating mutation. The transforming protein that results is implicated in various malignancies, including lung adenocarcinoma, mucinous adenoma, ductal carcinoma of the pancreas and colorectal carcinoma. Alternative splicing leads to variants encoding two isoforms that differ in the C-terminal region. [provided by RefSeq, Jul 2008]

- RET. This gene encodes a transmembrane receptor and member of the tyrosine protein kinase family of proteins. Binding of ligands such as GDNF (glial cell-line derived neurotrophic factor) and other related proteins to the encoded receptor stimulates receptor dimerization and activation of downstream signaling pathways that play a role in cell differentiation, growth, migration and survival. The encoded receptor is important in development of the nervous system, and the development of organs and tissues derived from the neural crest. This proto-oncogene can undergo oncogenic activation through both cytogenetic rearrangement and activating point mutations. Mutations in this gene are associated with Hirschsprung disease and central hypoventilation syndrome and have been identified in patients with renal agenesis. [provided by RefSeq, Sep 2017]

- TET2. The protein encoded by this gene is a methylcytosine dioxygenase that catalyzes the conversion of methylcytosine to 5-hydroxymethylcytosine. The encoded protein is involved in myelopoiesis, and defects in this gene have been associated with several myeloproliferative disorders. Two variants encoding different isoforms have been found for this gene. [provided by RefSeq, Mar 2011]

- SMC1A. Proper cohesion of sister chromatids is a prerequisite

multiprotein complex is required for sister chromatid cohesion. This complex is composed partly of two structural maintenance of chromosomes (SMC) proteins, SMC3 and either SMC1B or the protein encoded by this gene. Most of the cohesin complexes dissociate from the chromosomes before mitosis, although those complexes at the kinetochore remain. Therefore, the encoded protein is thought to be an important part of functional kinetochores. In addition, this protein interacts with BRCA1 and is phosphorylated by ATM, indicating a potential role for this protein in DNA repair. This gene, which belongs to the SMC gene family, is located in an area of the X-chromosome that escapes X inactivation. Mutations in this gene result in Cornelia de Lange syndrome. Alternative splicing results in multiple transcript variants encoding different isoforms. [provided by RefSeq, Jul 2013]

- RAD51D. The protein encoded by this gene is a member of the RAD51 protein family. RAD51 family members are highly similar to bacterial RecA and Saccharomyces cerevisiae Rad51, which are known to be involved in the homologous recombination and repair of DNA. This protein forms a complex with several other members of the RAD51 family, including RAD51L1, RAD51L2, and XRCC2. The protein complex formed with this protein has been shown to catalyze homologous pairing between single- and double-stranded DNA, and is thought to play a role in the early stage of recombinational repair of DNA. Alternative splicing results in multiple transcript variants. Read-through transcription also exists between this gene and the downstream ring finger and FYVE-like domain containing 1 (RFFL) gene. [provided by RefSeq, Jan 2011]

- EZH2. This gene encodes a member of the Polycomb-group (PcG) family. PcG family members form multimeric protein complexes, which are involved in maintaining the transcriptional repressive state of genes over successive cell generations. This protein associates with the embryonic ectoderm development protein, the VAV1 oncoprotein, and the X-linked nuclear protein. This protein may play a role in the hematopoietic and central nervous systems. Multiple alternatively splcied transcript variants encoding distinct isoforms have been identified for this gene. [provided by RefSeq, Feb 2011]

- LFNG. This gene is a member of the glycosyltransferase 31 gene family. Members of this gene family, which also includes the MFNG (GeneID: 4242) and RFNG (GeneID: 5986) genes, encode evolutionarily conserved glycosyltransferases that act in the Notch signaling pathway to define boundaries during embryonic development. While their genomic structure is distinct from other glycosyltransferases, these proteins have a fucose-specific beta-1,3-N-acetylglucosaminyltransferase activity that leads to elongation of O-linked fucose residues on Notch, which alters Notch signaling. The protein encoded by this gene is predicted to be a single-pass type II Golgi membrane protein but it may also be secreted and proteolytically processed like the related proteins in mouse and Drosophila (PMID: 9187150). Mutations in this gene have been associated with autosomal recessive spondylocostal dysostosis 3. [provided by RefSeq, May 2018]

- SP1. The protein encoded by this gene is a zinc finger transcription factor that binds to GC-rich motifs of many promoters. The encoded protein is involved in many cellular processes, including cell differentiation, cell growth, apoptosis, immune responses, response to DNA damage, and chromatin remodeling. Post-translational modifications such as phosphorylation, acetylation, glycosylation, and proteolytic processing significantly affect the activity of this protein, which can be an activator or a repressor. Three transcript variants encoding different isoforms have been found for this gene. [provided by RefSeq, Nov 2014]

Drug Information

H3B-8800

H3B-8800 is a spliceosome inhibitor. H3B-8800 preferentially targets cells with spliceosome complexes containing mutant splicing factor 3B1 (SF3B1) protein, modulating intron splicing leading to increased death in cancer cells while having little effect on the viability cells with wild-type SF3B1. Both normal and aberrant mature mRNA are suppressed in mutant and wild-type cells, the selectivity of the lethal effect is thought to be due to the presence of mutant SF3B1 and its implications rather than a change in mechanism or potency of effect on the mutant protein over the wild-type. H3B-8800 was granted orphan drug status by the FDA in August 2017 and is in clinical trials for the treatment of acute myelogenous leukemia and chronic myelomonocytic leukemia.

Sorafenib

Sorafenib is a small molecular inhibitor of Raf kinase, PDGF (platelet-derived growth factor), VEGF receptor 2 & 3 kinases and c Kit the receptor for Stem cell factor. A growing number of drugs target most of these pathways. The originality of Sorafenib lays in its simultaneous targeting of the Raf/Mek/Erk pathway.

Sorafenib interacts with multiple intracellular (CRAF, BRAF and mutant BRAF) and cell surface kinases (KIT, FLT3, VEGFR-2, VEGFR-3, and PDGFRB). Several of these kinases are thought to be involved in angiogenesis, thus sorafenib reduces blood flow to the tumor. Sorafenib is unique in targeting the Raf/Mek/Erk pathway. By inhibiting these kinases, genetic transcription involving cell proliferation and angiogenesis is inhibited.

Sorafenib is indicated for the treatment of unresectable hepatocellular carcinoma and advanced renal cell carcinoma.

Dabrafenib

Dabrafenib mesylate (Tafinlar) is a reversible ATP-competitive kinase inhibitor and targets the MAPK pathway.

Dabrafenib is an orally bioavailable inhibitor of B-raf (BRAF) protein with antineoplastic activity. Dabrafenib selectively binds to and inhibits the activity of B-raf, which may inhibit the proliferation of tumor cells which contain a mutated BRAF gene.

Dabrafenib causes an inhibition of phosphorylated extracellular signal-regulated kinase (ERK). This indicates a decrease in cell proliferation.

Furthermore, within 24 hours of administration, downstream mediators of the MAPK pathway are inhibited. BRAF belongs to the raf/mil family of serine/threonine protein kinases and plays a role in regulating the MAP kinase/Extracellular Signal-regulated Kinases signaling pathway, which may be constitutively activated due to BRAF gene mutations.

Binimetinib

Binimetinib is an orally available inhibitor of mitogen-activated protein kinase kinase 1 and 2 (MEK1/2) with potential antineoplastic activity. Binimetinib, noncompetitive with ATP, binds to and inhibits the activity of MEK1/2. Inhibition of MEK1/2 prevents the activation of MEK1/2-dependent effector proteins and transcription factors, which may result in the inhibition of growth factor-mediated cell signaling. This may eventually lead to an inhibition of tumor cell proliferation and an inhibition in production of various inflammatory cytokines including interleukin-1, -6 and tumor necrosis factor. MEK1/2 are dual-specificity threonine/tyrosine kinases that play key roles in the activation of the RAS/RAF/MEK/ERK pathway and are often upregulated in a variety of tumor cell types.

Potential Clinical Trials

Trial URL	Status	Title	Disease	Drug	Sites
https://clinicaltrials.gov/study/NCT05972135	Recruiting	Outpatient Administration of Teclistamab or Talquetamab for Multiple Myeloma	Multiple Myeloma	Teclistamab, Talquetamab, Tocilizumab	Oncology Associates of Oregon, Eugene, Oregon 97401 Arizona Oncology Associates, Tucson, Arizona 85711 Colorado Blood Cancer Institute, Denver, Colorado 80218
https://clinicaltrials.gov/study/NCT05002816	Recruiting	Novel Combination of Belantamab Mafodotin and Elotuzumab to Enhance Therapeutic Efficacy in Multiple Myeloma	Multiple Myeloma	Elotuzumab, Belantamab mafodotin	Yale New Haven Hospital, New Haven, Connecticut 06512
https://clinicaltrials.gov/study/NCT04680468	Recruiting	Phase 2 Study of Belantamab Mafodotin as Pre- and Post-autologous Stem Cell Transplant Consolidation and Maintenance for Multiple Myeloma	Multiple Myeloma	Belantamab mafodotin	University of Pennsylvania, Philadelphia, Pennsylvania 19104
https://clinicaltrials.gov/study/NCT03909412	Recruiting	Phase I Study of Carfilzomib-based Chemotherapy Mobilization for Autologous Stem Cell Transplantation in Multiple Myeloma	Multiple Myeloma	Carfilzomib, Cyclophosphamide, Dexamethasone, Granulocyte Colony-Stimulating Factor	Hackensack Meridian Health - John Theurer Cancer Center, Hackensack, New Jersey 07601

Detailed Results

Single Nucleotide Variant (SNV) and Insertions-Deletions (INDELS)								
Gene name	Hgvsp	Hgvsc	Amino acids	Codons	Consequence	Allele frequency	Read depth	Predicted effect on protein
FANCA	NP_000126.2:p.Asn213Thr	NM_000135.2:c.638A>C	N/T	aAt/aCt	missense_variant	25.84	623	deleterious
U2AF1	NP_001020374.1:p.Gln157Pro	NM_001025203.1:c.470A>C	Q/P	cAg/cCg	missense_variant	24.24	854	deleterious
RAF1	NP_002871.1:p.Ser257Leu	NM_002880.3:c.770C>T	S/L	tCg/tTg	missense_variant	23.99	521	deleterious

KRAS	NP_203524.1:p.Gln61Pro	NM_033360.2:c.182A>C	Q/P	cAa/cCa	missense_variant	19.54	394	deleterious
RET	NP_065681.1:p.Glu713Asp	NM_020630.4:c.2139G>T	E/D	gaG/gaT	"missense_variant,splice_region_variant"	3.8	658	tolerated
TET2	NP_001120680.1:p.Tyr1337Ter	NM_001127208.2:c.4011T>A	Y/*	taT/taA	stop_gained	2.24	581	0
KRAS	NP_203524.1:p.Ala59Glu	NM_033360.2:c.176C>A	A/E	gCa/gAa	missense_variant	2.21	408	deleterious
SMC1A	NP_001268392.1:p.Ile957Met	NM_001281463.1:c.2871T>G	I/M	atT/atG	missense_variant	2.17	506	tolerated
RAD51D	NP_001136043.1:p.Asn95His	NM_001142571.1:c.283A>C	N/H	Aat/Cat	missense_variant	1.52	461	tolerated
EZH2	NP_004447.2:p.Lys515Arg	NM_004456.4:c.1544A>G	K/R	aAg/aGg	"missense_variant,splice_region_variant"	1.48	474	tolerated
LFNG (RNA)	NP_001159827.1:p.Glu56GlyfsTer2	NM_001166355.1:c.163_166dup	-/DX	-/GATG	frameshift_variant	61.19	67	0
SP1 (RNA)	NP_612482.2:p.Gln631Ter	NM_138473.2:c.1891C>T	Q/*	Caa/Taa	stop_gained	14.63	82	0

Methodology and Test Background

This is a next generation sequencing (NGS) test that analyzes DNA of 302 genes and RNA of >1600 genes for abnormalities that are reported in various types of hematologic neoplasms. The assay also detects several viruses that are important in oncology, including EBV, HPV and TTV. TTV (torque teno virus) was first discovered in a patient with non-A-E hepatitis and is now regarded as a part of the human virome. In general, TTV does not cause pathology in immunocompetent individuals. TTV is considered as a marker of immune competence in patients with immunological impairment and inflammatory disorders. High TTV load is associated with increased risk of infection. In patients with organ transplant, low TTV load is associated with an increased risk of rejection.

Nucleic acid is isolated from fresh cells, peripheral blood cells, bone marrow, body fluid, or paraffin-embedded tissue. For optimal results, neoplastic cells should be >30% of the analyzed cells. For fresh bone marrow specimens with the clinical indication of myeloma, enrichment for CD138-positive cells may be performed using immunomagnetic positive selection and both the CD138-positive and CD138-negative cell fractions extracted for NGS testing and the findings integrated within the final report. Testing is performed using massive parallel sequencing of the coding DNA of the listed genes. This includes sequencing of all the exons as well as approximately 50 nucleotides at the 5' and 3' ends of each coding exon to detect splice site abnormalities. The TERT promoter region, including the hotspots at -124 and -146 bp, is also covered. Our DNA sequencing method has a sensitivity of 1% for detecting single nucleotide variants (SNVs) and small (<60 bp) insertions/ deletions (indels). Significant gene amplification and deletion (copy number variants) are also reported. In addition, fragment length analysis is performed for CALR, FLT3, and NPM1 to enhance the detection of large indels and has a sensitivity of 2%-5% for detecting CALR, FLT3-ITD, and NPM1 indels in wildtype background. For cases with indication of acute myeloid leukemia, preliminary FLT3-ITD results based on fragment analysis will be reported. Targeted RNA NGS is performed by hybrid capture and duplicates are excluded for levels measurements. The Universal Human Reference (UHR) RNA is used as control. All detected fusion transcripts are reported. While the major focus of the RNA analysis is the detection of fusion mRNA, mutations in the expressed RNA of the analyzed genes, B- and T-cell clonality, HLA class I genotyping, and Epstein-Barr virus (EBV), human papillomavirus (HPV) and torque teno virus (TTV) viral RNA are also analyzed and reported. In cases of suspected chronic lymphocytic leukemia (CLL), IgVH mutation rate will also be reported. The sensitivity of this assay for detecting fusion mRNA is between 5% and 10%. This test specifically detects translocations that lead to the expression of fusion RNA. Translocations that lead to deregulation of expression can be addressed by this test if compared to the proper normal expression control. Since the clinical relevance of the RNA expression level of most of the genes is not well-characterized at this time, only a small subset of the genes may be described based on the suspected disease, including but not limited to MYC, BCL2, CD274, CD19, CD22, CD34, and CD138. CRLF2 mRNA levels

are reported in acute lymphoblastic leukemia. CD274 (PD-L1) mRNA levels are reported when they are significantly elevated. Performance of the assay may vary dependent on the quantity and quality of nucleic acid, sample preparation, and sample age. Decalcified specimens have not been validated. Decalcification with strong acids is not recommended and may lead to poor nucleic acid quality and suboptimal results.

Based on our validation study, the following exonic regions of the genes listed below are not covered appropriately <100 X coverage and sequencing by NGS may not be reliable in these regions. The poor coverage is primarily due to the inherent difficulty in obtaining adequate sequencing coverage in regions with high GC content. No well-characterized hotspots are present in these regions. RAD51 NM_133487 chr15:40994004-40994124, BRCA1 NM_007300 chr17:41231351-41231416, FUBP1 NM_003902 chr1:78435609-78435699, CBLB NM_170662 chr3:105420938-105421303, TERT NM_198253 chr5:1295183-1295250, ARID1B NM_017519 chr6:157098715-157100605, CUX1 NM_001202543 chr7:101740644-101740781, KMT2C NM_170606 chr7:151891314-151891346 and 151935792-151935911, GALNT12 NM_024642 chr9:101569952-101570351, ATM NM_000051 chr11:108164040-108164204, CDK17 NM_001170464 chr12:96679880-96679926, RB1 NM_000321 chr13:48954189-48954220, SETBP1 NM_015559 chr18:42643044-42643692, KMT2B NM_014727 chr19:36208921-36209283, AR NM_000044 chrX:66764889-66766604, STAG2 NM_001042749 chrX:123200025-123200112.

The table below may contain a partial list of the tested DNA genes. For a complete list, please go to: https://genomictestingcooperative.com/genomic-tests/gtc-hematology-profile-plus/ *(click the DNA tab)*

The table below contains a partial list of the tested RNA genes (Fusions/Expression). For a complete list, please go to: https://genomictestingcooperative.com/genomic-tests/gtc-hematology-profile-plus/ *(click the RNA tab)*

Tested genes

Genes Tested for Abnormalities in Coding Sequence												
ABL1	B2M	CCNE1	CUX1	ETNK1	GALNT12	IL7R	MCL1	NFE2L2	PIM1	RB1	SMO	TRAF3
ABRAXAS1	BAP1	CD274	CXCR4	ETV6	GATA1	INHBA	MDM2	NFKBIA	PLCG1	RET	SOCS1	TSC1
ACVR1B	BARD1	CD79A	CYLD	EXO1	GATA2	IRF4	MDM4	NKX2-1	PMS1	RHEB	SOX2	TSC2
AKT1	BCL2	CD79B	DAXX	EZH2	GATA3	JAK1	MED12	NOTCH1	PMS2	RHOA	SOX9	TSHR
AKT2	BCL2L1	CDC73	DDR2	FANCA	GEN1	JAK2	MEF2B	NOTCH2	POLD1	RIT1	SPOP	U2AF1
AKT3	BCL6	CDH1	DDX41	FANCC	GNA11	JAK3	MEN1	NOTCH3	POLE	RNF43	SRC	U2AF2
ALK	BCOR	CDK12	DICER1	FANCD2	GNAQ	KAT6A	MET	NPM1	POT1	ROS1	SRSF2	UBA1
AMER1	BCORL1	CDK4	DNM2	FANCE	GNAS	KDM5C	MITF	NRAS	PPM1D	RUNX1	STAG2	VHL
ANKRD26	BCR	CDK6	DNMT3A	FANCF	GNB1	KDM6A	MLH1	NSD1	PPP2R1A	SAMD9	STAT3	WT1
APC	BIRC3	CDKN1B	DOT1L	FANCG	GREM1	KDR	MPL	NSD2 (WHSC1)	PRDM1	SAMD9L	STAT5B	XPO1
AR	BLM	CDKN2A	EED	FAS	GRIN2A	KEAP1	MRE11	NTHL1	PRKAR1A	SDHA	STK11	XRCC2
ARAF	BMPR1A	CDKN2B	EGFR	FBXW7	H3-3A (H3F3A)	KIT	MSH2	NTRK1	PRKDC	SDHAF2	SUFU	XRCC3
ARID1A	BRAF	CDKN2C	EGLN1	FGF4	H3C2 (HIST1H3B)	KMT2A	MSH3	NTRK2	PRPF8	SDHB	SUZ12	ZNF217
ARID1B	BRCA1	CEBPA	ELANE	FGF6	HGF	KMT2B	MSH6	NTRK3	PRSS1	SDHC	TAL1	ZRSR2
ARID2	BRCA2	CHEK1	EP300	FGFR1	HNF1A	KMT2C	MTOR	PAK3	PTCH1	SDHD	TCF3	-
ASXL1	BRIP1	CHEK2	EPAS1	FGFR2	HOXB13	KMT2D	MUTYH	PALB2	PTEN	SETBP1	TENT5C (FAM46C)	-
ATM	BTK	CIC	EPCAM	FGFR3	HRAS	KRAS	MYC	PAX5	PTPN11	SETD2	TERC	-
ATR	CALR	CREBBP	EPHA3	FGFR4	HSP90AA1	LRP1B	MYCL	PBRM1	RAC1	SF3B1	TERT	-
ATRX	CARD11	CRLF2	EPHA5	FH	ID3	MAP2K1	MYCN	PDGFRA	RAD21	SMAD2	TET2	-
AURKA	CBL	CSF1R	ERBB2	FLCN	IDH1	MAP2K2	MYD88	PDGFRB	RAD50	SMAD4	TGFBR2	-
AURKB	CBLB	CSF3R	ERBB3	FLT3	IDH2	MAP2K4	NBN	PHF6	RAD51	SMARCA4	TMEM127	-
AURKC	CBLC	CTCF	ERBB4	FLT4	IGF1R	MAP3K1	NF1	PIK3CA	RAD51C	SMARCB1	TNFAIP3	-
AXIN1	CCND1	CTNNA1	ERG	FOXL2	IKZF1	MAP3K14	NF2	PIK3R1	RAD51D	SMC1A	TNFRSF14	-
AXIN2	CCND3	CTNNB1	ESR1	FUBP1	IKZF3	MAPK1	NFE2	PIK3R2	RAF1	SMC3	TP53	-

RNA Fusions/Expression

Fusion/Expression															
ABL1	BCL2	CCND1	CREBBP	EGFR	ETV4	FGFR2	FOXO1	IKZF3	MAP3K1	MYH9	NTRK3	PAX5	PDGFRB	PTK2B	ROS1	TAL1
ABL2	BCL6	CD274 (PD-L1)	CRLF2	EPOR	ETV5	FGFR3	FUS	JAK2	MECOM	NOTCH1	NUP214	PBX1	PICALM	RARA	RUNX1	TCF3
AKT3	BRAF	CBL	CSF1R	ERG	ETV6	FIP1L1	GLI1	KMT2A	MRTFA	NTRK1	NUP98	PCM1	PIGA	RET	RUNX1T1	TFG
ALK	CBFB	CIC	DUSP22	ETV1	FGFR1	FLT3	HLF	LYN	MYC	NTRK2	P2RY8	PDGFRA	PML	RHOA	STAT6	TYK2

Reference

1. Multiple myeloma: signaling pathways and targeted therapy. Lu Q, Yang D, Li H, Niu T, Tong A. Mol Biomed. 2024 Jul 4;5(1):25. doi: 10.1186/s43556-024-00188-w. PMID: 38961036.

2. Multiple myeloma: 2024 update on diagnosis, risk-stratification, and management. Rajkumar SV. Am J Hematol. 2024 Sep;99(9):1802-1824. doi: 10.1002/ajh.27422. Epub 2024 Jun 28. PMID: 38943315.

3. Immunotherapy for the treatment of multiple myeloma. Boussi LS, Avigan ZM, Rosenblatt J. Front Immunol. 2022 Oct 28;13:1027385. doi: 10.3389/fimmu.2022.1027385. eCollection 2022. PMID: 36389674.

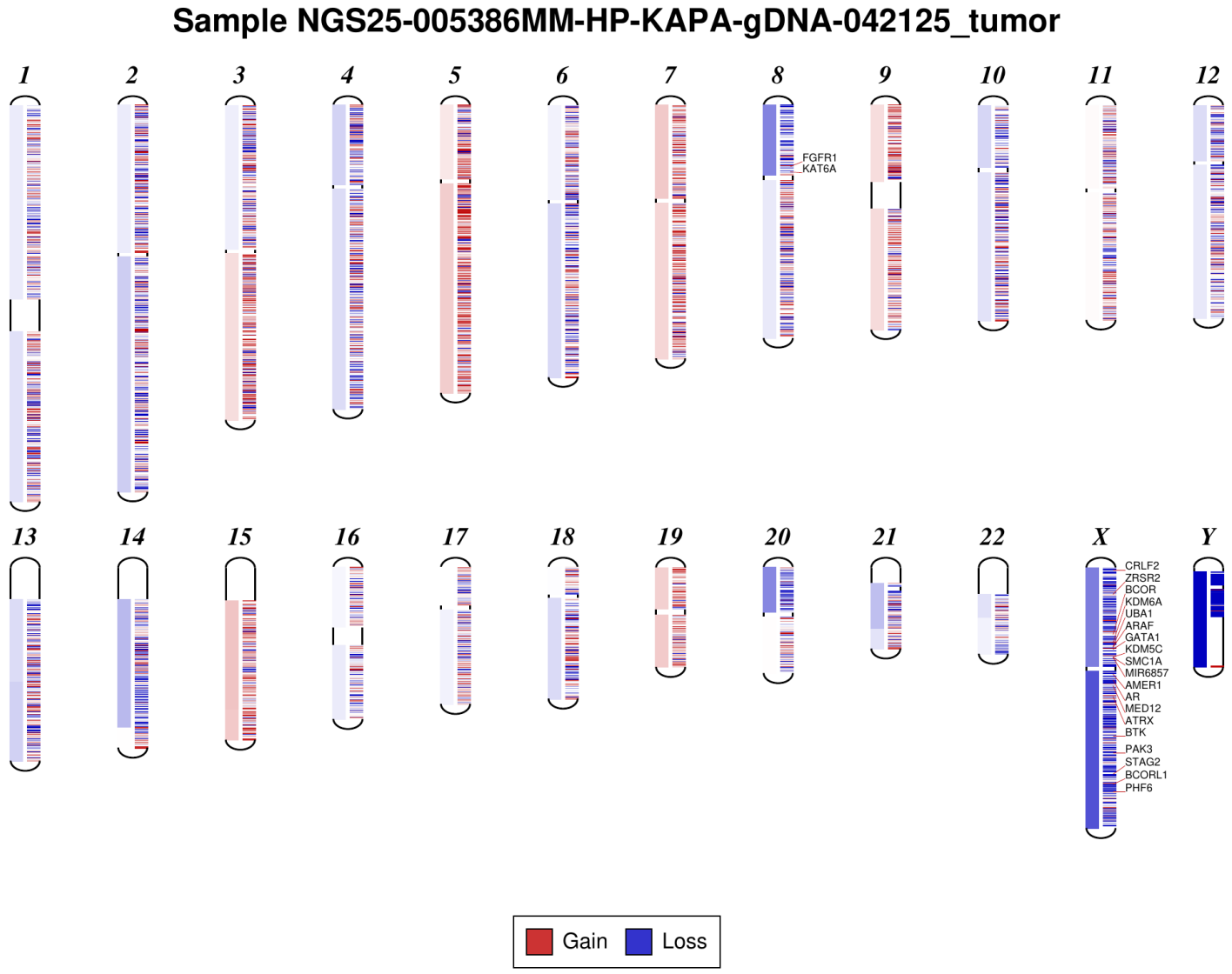
4. Diagnosis and Management of Multiple Myeloma: A Review. Cowan AJ, Green DJ, Kwok M, Lee S, Coffey DG, Holmberg LA, Tuazon S, Gopal AK Libby EN. JAMA. 2022 Feb 1;327(5):464-477. doi: 10.1001/jama.2022.0003. PMID: 35103762.

Electronic Signature

The test (sample processing, sequencing and data generation) was performed at Genomic Testing Cooperative, LCA, 25371 Commercentre Drive Lake Forest, CA 92630. Medical Director Maher Albitar, M.D. Analysis of the data was performed by Genomic Testing Cooperative, LCA, 25371 Commercentre Drive, Lake Forest, CA 92630. Medical Director: Maher Albitar, M.D.

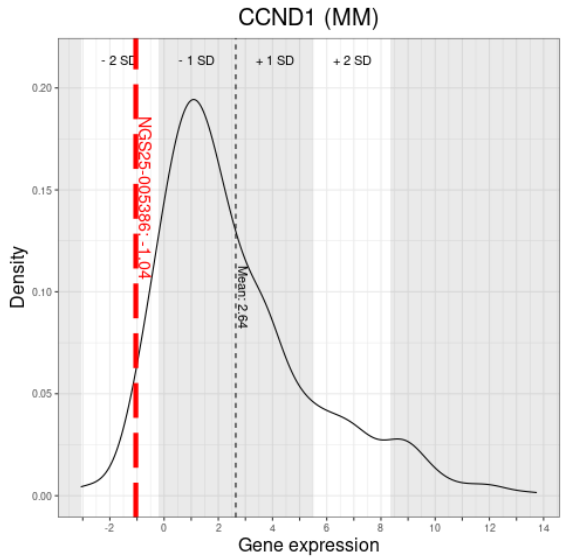
The test was developed and its performance characteristics have been determined by Genomic Testing Cooperative, LCA. This test has not been approved by the FDA. The FDA has determined such clearance or approval is not necessary. This laboratory is CLIA certified to perform high complexity clinical testing.

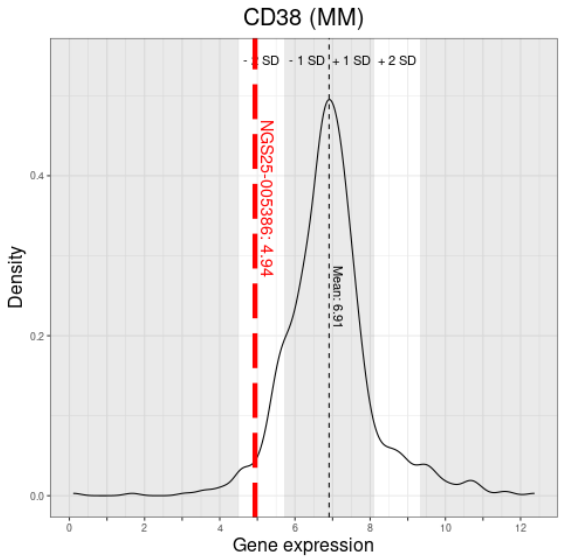
Additional Report Information

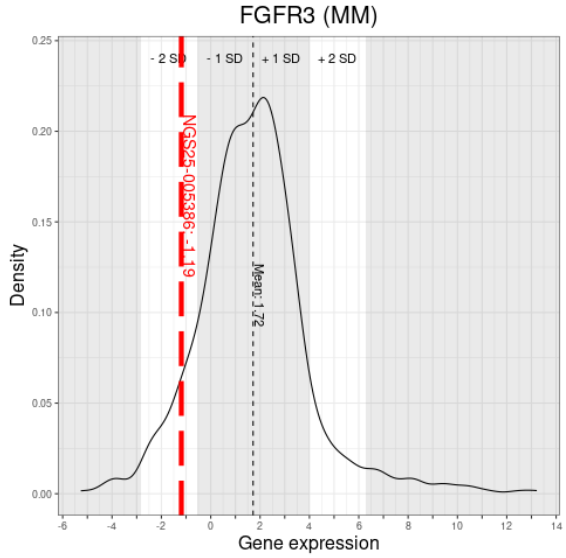


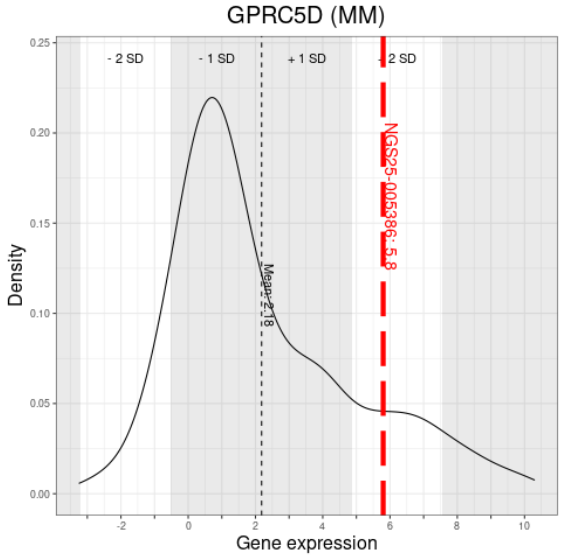
Additional Report Information

These plots represent the distribution of the expression in log2 transformed TPM (transcript per million) for each gene across GTC's history for the specified disease. The mean for each distribution is denoted by the black dotted line, while the alternating shaded areas depict the standard deviation. The expression for the current patient is marked by the red dotted line.









Additional Report Information