

Patient		Sample		Physician	
Name	Jane Jones	Specimen Type	Blood	Ordering Physician	John Smith
Date of Birth (Age)	11/27/1940 (82 yrs)	Collection Date	06/01/2023	Medical Facility	BillionToOne Inc
Assigned Sex at Birth	Female	Receipt Date	06/05/2023	Address	1035 O'Brien Drive Suite 112 Menlo Park, California 94025
Diagnosis	Rectal adenocarcinoma	Accession ID	V010900AA001-1	Phone	(833) 537-1819
Medical Record #	ID400231	Report Date	07/05/2023	Fax	(833) 874-0918
Internal Patient ID	10000090	Test Number	1		

## Northstar Select Results

**9** informative genomic alterations identified

### Summary of Informative Genomic Alterations

Detected Genomic Findings <sup>§</sup>	Associated FDA-Approved Therapies			Clinical Trials <sup>§§</sup>	% cfDNA / Copy number	
	✔ Approved in indication	⊕ Approved in other indication	⊗ Associated with resistance			
<b>MSI-High</b>	<ul style="list-style-type: none"> <li>dostarlimab</li> <li>ipilimumab/nivolumab</li> <li>nivolumab</li> <li>pembrolizumab</li> </ul>			10	Detected	
<b>KRAS G12V</b>		<ul style="list-style-type: none"> <li>binimetinib</li> <li>selumetinib</li> </ul>	<ul style="list-style-type: none"> <li>cobimetinib</li> <li>trametinib</li> </ul>	<ul style="list-style-type: none"> <li>cetuximab</li> <li>panitumumab</li> </ul>	1	51%
<b>ATM N619fs*3</b>		<ul style="list-style-type: none"> <li>olaparib</li> </ul>			4	21%
<b>CHEK2 K373E</b>		<ul style="list-style-type: none"> <li>olaparib</li> </ul>			2	2.81%
<b>BRIP1 K606*</b>		<ul style="list-style-type: none"> <li>olaparib</li> </ul>			1	2.38%
<b>CHEK2 c.319+1G&gt;T</b>		<ul style="list-style-type: none"> <li>olaparib</li> </ul>			2	0.42%
<b>BRCA2 T3033fs*29</b>		<ul style="list-style-type: none"> <li>bevacizumab/olaparib</li> <li>niraparib</li> <li>rucaparib</li> </ul>	<ul style="list-style-type: none"> <li>olaparib</li> <li>talazoparib</li> </ul>		2	0.09%
<b>FBXW7 R393*</b>					0	24%
<b>APC Y1075*</b>					0	0.73%

<sup>§</sup> For additional variant information, please see the Variant Details section of the report. Variants of Unknown Significance (VUS) are reported after the Variant Details section of the report.

<sup>§§</sup> Clinical trials are matched within 500 miles of the ordering physician, based on detected genomic alterations and provided patient demographics. For additional options, please visit [www.clinicaltrials.gov](http://www.clinicaltrials.gov).

### Microsatellite Instability Status

Microsatellite Instability Status (MSI) is reported here based upon mutation detection at curated genome-wide MSI sites and subsequent bioinformatic algorithm calculation.

Stable **High**

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## Clinical Trial Availability

Clinical trial matches are displayed based upon somatic variant detection and patient demographic and diagnostic information provided on the test requisition form. Trials are matched within 500 miles of the ordering provider's location. This list is neither comprehensive nor a guarantee of eligibility, as many other requirements must be met prior to enrollment.

For further details on eligibility, please visit [www.clinicaltrials.gov](http://www.clinicaltrials.gov) and enter the NCT#.

<b>Phase 3</b> NCT02997228	Colorectal Cancer Metastatic dMMR/MSI-H Immuno-Therapy (COMMIT) Study: A Randomized Phase III Study of mFOLFOX6/Bevacizumab/Atezolizumab Combination Versus Single Agent Atezolizumab in the First-Line Treatment of Patients With Deficient DNA Mismatch Repair (dMMR)/Microsatellite Instability-High (MSI-H) Metastatic Colorectal Cancer  <span style="border: 1px solid black; border-radius: 10px; padding: 2px;">MSI-High</span>	<b>Berkeley, California (94704)</b> Alta Bates Summit Medical Center-Herrick Campus
<b>Phase 3</b> NCT04008030	A Phase 3 Randomized Clinical Trial of Nivolumab Alone, Nivolumab in Combination With Ipilimumab, or Investigator's Choice Chemotherapy in Participants With Microsatellite Instability High (MSI-H) or Mismatch Repair Deficient (dMMR) Metastatic Colorectal Cancer  <span style="border: 1px solid black; border-radius: 10px; padding: 2px;">MSI-High</span>	<b>Los Angeles, California (90033)</b> USC/Norris Comprehensive Cancer Center
<b>Phase 2</b> NCT03767348	An Open-Label, Multicenter, Phase 1/2 Study of RP1 as a Single Agent and in Combination With PD1 Blockade in Patients With Solid Tumors  <span style="border: 1px solid black; border-radius: 10px; padding: 2px;">MSI-High</span>	<b>San Francisco, California (94115)</b> University of California - San Francisco
<b>Phase 2</b> NCT05608044	A Randomized, Open-Label, Phase 2 Study of Botensilimab (AGEN1181) as Monotherapy and in Combination With Balstilimab (AGEN2034) or Investigator's Choice Standard of Care (Regorafenib or Trifluridine and Tipiracil) for the Treatment of Refractory Metastatic Colorectal Cancer  <span style="border: 1px solid black; border-radius: 10px; padding: 2px;">MSI-High</span>	<b>Duarte, California (91010)</b> City of Hope National Medical Center
<b>Phase 2</b> NCT05221320	A Phase 2 Basket Trial of Ulixertinib (BVD-523) in Combination With Hydroxychloroquine in Patients With Advanced GI Malignancies Harboring Mitogen-activated Protein Kinase (MAPK) Pathway Mutations (BVD-523-HCQ)  <span style="border: 1px solid black; border-radius: 10px; padding: 2px;">MSI-High</span>	<b>San Francisco, California (94143)</b> University of California San Francisco
<b>Phase 2</b> NCT02628067	A Clinical Trial of Pembrolizumab (MK-3475) Evaluating Predictive Biomarkers in Subjects With Advanced Solid Tumors (KEYNOTE 158)  <span style="border: 1px solid black; border-radius: 10px; padding: 2px;">MSI-High</span>	<b>Los Angeles, California (90048)</b> Call for Information (Investigational Site 0017)
<b>Phase 2</b> NCT02693535	Targeted Agent and Profiling Utilization Registry (TAPUR) Study  <span style="border: 1px solid black; border-radius: 10px; padding: 2px;">MSI-High</span> <span style="border: 1px solid black; border-radius: 10px; padding: 2px;">ATM N619fs*3</span> <span style="border: 1px solid black; border-radius: 10px; padding: 2px;">CHEK2 K373E</span> <span style="border: 1px solid black; border-radius: 10px; padding: 2px;">CHEK2 c.319+1G&gt;T</span> <span style="border: 1px solid black; border-radius: 10px; padding: 2px;">BRCA2 T3033fs*29</span>	<b>Palo Alto, California (94301)</b> Sutter Palo Alto Medical Foundation: Palo Alto
<b>Phase 2</b> NCT05593328	A Phase 2, Randomized, Open-label Study of Onvansertib in Combination With FOLFIRI and Bevacizumab Versus FOLFIRI and Bevacizumab for Second Line Treatment of Metastatic Colorectal Cancer in Patients With a KRAS or NRAS Mutation  <span style="border: 1px solid black; border-radius: 10px; padding: 2px;">KRAS G12V</span>	<b>Bakersfield, California (93309)</b> Comprehensive Blood and Cancer Center - Bakersfield
<b>Phase 2</b> NCT04564027	A Modular Phase 2a Multicentre Open-Label Study to Investigate DNA-damage Response Agents (or Combinations) in Patients With Advanced Cancer Whose Tumours Contain Molecular Alterations (PLANETTE)  <span style="border: 1px solid black; border-radius: 10px; padding: 2px;">ATM N619fs*3</span>	<b>San Francisco, California (94115)</b> Research Site

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**Phase 2**  
NCT04123366

A Phase 2 Study of Olaparib in Combination With Pembrolizumab in Participants With Previously Treated, Homologous Recombination Repair Mutation (HRRm) and/or Homologous Recombination Deficiency (HRD)-Positive Advanced Cancer

**San Francisco, California (94158)**  
University of California San Francisco (Site 0015)

ATM N619fs\*3 CHEK2 K373E BRIP1 K606\* CHEK2 c.319+1G>T BRCA2 T3033fs\*29

**Phase 2**  
NCT03682289

Phase II Trial of Ceralasertib (AZD6738) Alone and in Combination With Olaparib or Durvalumab in Patients With Selected Solid Tumor Malignancies

**San Francisco, California (94143)**  
University of California, San Francisco

ATM N619fs\*3

**Phase 1/Phase 2**  
NCT04521413

A First-In-Human, Phase 1/2 Study Of CFI-402411, a Hematopoietic Progenitor Kinase-1 (HPK1) Inhibitor, as a Single Agent and in Combination With Pembrolizumab in Subjects With Advanced Solid Malignancies

**Los Angeles, California (90025)**  
The Angeles Clinic

MSI-High

**Phase 1/Phase 2**  
NCT04041310

A Phase I/II, Multicenter, Open-Label Study of Nous-209 Genetic Vaccine for the Treatment of Microsatellite Unstable Solid Tumors

**Duarte, California (91010)**  
City of Hope Comprehensive Cancer Center

MSI-High

**Phase 1/Phase 2**  
NCT04381650

A Phase 1b/2 Study of TAK-981 Plus Pembrolizumab to Evaluate the Safety, Tolerability, and Antitumor Activity of the Combination in Patients With Select Advanced or Metastatic Solid Tumors

**Stanford, California (94305)**  
Stanford Cancer Institute (SCI)

MSI-High

## Variant Details

### Microsatellite Instability-High (MSI-H)

Tumors exhibiting microsatellite instability (MSI) have a higher mutational burden than microsatellite stable (MSS) tumors and express higher levels of immune checkpoint receptors [1, 2, 3, 4, 5]. Thus, checkpoint inhibitors, several of which have received agency approval for certain indications, may be clinically relevant for tumors exhibiting MSI [6, 7, 8, 9, 10, 11]. In fact, pembrolizumab has been FDA-approved as a second or later line of therapy for the treatment of pediatric and adult solid tumors with high microsatellite instability (MSI-H) or that are deficient in mismatch repair (dMMR), as a front-line therapy for colorectal carcinoma patients with MSI-H or dMMR, and endometrial carcinoma patients with MSI-H or dMMR, who are not eligible for curative surgery or radiation, following progression on systemic therapy [12, 10]. In addition, nivolumab and the combination of nivolumab and ipilimumab have been FDA-approved for the treatment of MSI-H or dMMR colorectal carcinoma [13, 14]. In contrast, the combination of lenvatinib and pembrolizumab has been FDA-approved for the treatment of advanced endometrial cancer patients with unresectable tumors lacking markers for MSI-H and dMMR following disease progression on systemic therapy [15].

MSI has been associated with proximal colon location, mucinous histology, lower tumor grade, age at diagnosis of less than 50 years old, and the presence of BRAF mutation in colorectal carcinoma studies [16, 17, 18, 19, 20]. In addition, increased frequency of PD-L1 expression has been reported in colorectal carcinoma cases with MSI-H as compared with MSS/MSI-L cases [21, 22, 23, 24, 25]. Several studies have reported MSI-high status to be associated with better prognosis in colorectal carcinoma patients compared with patients lacking MSI-high [26, 27, 28, 29]. Adjuvant 5-FU may not benefit colorectal cancer patients with stage II/III MSI-H tumors when given as monotherapy [30, 31, 32].

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## KRAS

KRAS encodes the signaling protein K-Ras, a member of the Ras family; activating KRAS alterations may result in activation of downstream signaling pathways, including the Raf/MEK/ERK pathway [35, 36]. Clinical studies have suggested limited efficacy of MEK inhibitors in KRAS mutant tumors; however, combinations of MEK inhibitors with other targeted therapies may still be relevant [37, 38, 39, 40, 41, 42, 43, 44]. Other clinical approaches are also under investigation in the context of KRAS-mutant tumors, including FAK and Shp-2 inhibitors [45, 46, 47, 48, 49, 50]. In addition, inhibitors specifically targeting KRAS G12C and cell-based therapies targeting KRAS G12V and G12D are being investigated clinically and preclinically [51, 52, 53, 54]. Sotorasib and adagrasib have been FDA-approved in patients with locally advanced or metastatic non-small cell lung carcinoma harboring a KRAS G12C mutation, as determined by an FDA-approved test, following treatment with at least one prior systemic therapy [55, 56]. In addition, the combination of adagrasib with cetuximab has been reported to provide clinical benefit in colorectal carcinoma patients with KRAS G12C mutation and has been granted "breakthrough" designation by the FDA for accelerated review [57].

### KRAS G12V

Gene **KRAS**  
 Nucleotide **NM\_004985.5: c.35G>T**  
 Amino Acid **p.G12V**  
 Exon **2**  
 Biomarker Type **activating**

The KRAS G12V mutation lies within the first "G box" domain of the K-Ras protein, one of several conserved regions responsible for GTP binding and hydrolysis; disruption of this region creates a protein that is defective for GTP hydrolysis and is therefore constitutively active [58, 35, 59, 60]. KRAS G12V has been shown to induce hyperplastic lesions and metastatic tumor formation in mice, and is one of the more common KRAS mutations cited in colorectal cancer, where it has been associated with metastatic and aggressive tumors [61, 62, 63, 64, 65, 66].

## ATM

ATM encodes the serine/threonine protein kinase Ataxia telangiectasia mutated (Atm), which is a member of the PI3K/PI4K family [67]. Based on preclinical and clinical evidence, ATM-deficient tumors may be sensitive to poly(ADP-ribose) polymerase (PARP) inhibitors, Atr inhibitors, and DNA-PKcs inhibitors, which are under investigation in clinical trials [68, 69, 70, 71, 72, 73, 74]. The PARP inhibitors olaparib, rucaparib, and talazoparib have been approved for certain indications in the context of BRCA1 or BRCA2 mutation, or alteration in one or more homologous recombination repair genes, including ATM mutation [75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85].

### ATM N619fs\*3

Gene **ATM**  
 Nucleotide **NM\_000051.4: c.1856dupA**  
 Amino Acid **p.N619fs\*3**  
 Exon **12**  
 Biomarker Type **inactivating**

The ATM frameshift alteration reported here is expected to effectively truncate the 3056-amino acid Atm protein prior to the FAT, kinase, and FATC domains (UniProt). The FAT and FATC domains are involved in activation, and the FATC and kinase domains are critical to the function of Atm in DNA damage response [86, 87, 88, 89, 90, 91]. In addition, this alteration is likely to elicit nonsense-mediated decay [92, 93, 94, 95]. Therefore, this alteration is expected to be inactivating.

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## CHEK2

CHEK2 encodes the tumor suppressor, checkpoint kinase 2 (Chk2), a serine/threonine kinase that plays an important role in cell cycle arrest in response to DNA damage [96, 97, 98, 99]. Depletion of CHEK2 has been reported to increase sensitivity to PARP inhibitors in preclinical models and PARP inhibitors are in clinical trials in cancers with DNA repair deficiencies, including CHEK2 alterations [100]. The PARP inhibitors olaparib, rucaparib, and talazoparib have been approved for certain indications in the context of BRCA1 or BRCA2 mutation, or alteration in one or more homologous recombination repair genes, including CHEK2 mutation [75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85].

### CHEK2 K373E

Gene **CHEK2**  
 Nucleotide **NM\_007194.4: c.1116\_1117delinsTG**  
 Amino Acid **p.K373E**  
 Exon **11**  
 Biomarker Type **inactivating**

CHEK2 K373E is a missense alteration that occurs in the kinase domain of the Chk2 protein, specifically in the activation loop (UniProt). K373E has been reported to impair Chk2 autophosphorylation and kinase activity and to result in increased cell survival after ionizing radiation [101]. Therefore, this alteration is predicted to be inactivating.

### CHEK2 c.319+1G>T

Gene **CHEK2**  
 Nucleotide **NM\_007194.4: c.319+1G>T**  
 Amino Acid **p.?**  
 Exon **2**  
 Biomarker Type **unknown - predicted inactivating**

CHEK2 splice site 319+1G>T occurs in a conserved splice donor site at the junction of transcribed exons 2 and 3, corresponding to amino acid 107 of 543 in the Chk2 protein (IGV). Splice site mutations may lead to exon skipping or protein truncation. Exon skipping or protein truncation near this location would result in the loss of the majority of the Chk2 protein, including the entire kinase domain (UniProt). Therefore, although this alteration has not been functionally characterized, it may lead to a loss of protein function.

## BRIP1

BRIP1, also known as BACH1, encodes the Fanconi anemia group J protein (FancJ). Inactivating BRIP1 mutations may result in impaired DNA damage repair; germline BRIP1 mutations have been associated with Fanconi anemia complementation group J (FA-J) and some forms of familial cancer [102, 103, 104, 105, 106, 107]. Inactivation of the FA/BRCA pathway, including FancJ deficiency, has been reported to sensitize cells to mitomycin C and cisplatin [108, 109, 110, 111, 112]. In addition, inactivation of FancJ may sensitize cells to inhibition of poly(ADP-ribose) polymerase (PARP) [113, 114]. PARP inhibitors are currently under investigation in both preclinical and clinical studies. The PARP inhibitors olaparib, rucaparib, and talazoparib have been approved for certain indications in the context of BRCA1 or BRCA2 mutation, or alteration in one or more homologous recombination repair genes, including BRIP1 mutation [75, 76, 77, 78, 79, 80, 81, 82, 83, 84].

### BRIP1 K606\*

Gene **BRIP1**  
 Nucleotide **NM\_032043.3: c.1816A>T**  
 Amino Acid **p.K606\***  
 Exon **13**  
 Biomarker Type **inactivating**

The nonsense alteration reported here is expected to truncate the 1249 amino acid FancJ protein, resulting in the loss of the region involved in the interaction with Brca1, as well as several C-terminal phosphoserine residues (UniProt). The C-terminus of FancJ interacts with Brca1, and this interaction is important for double-strand break repair functions in cells [115]. In addition, a germline BRIP1 mutation resulting in a frameshift at K998 has been reported in a breast cancer patient with a family history of multiple cancers; this alteration was reported to lead to reduced protein stability and decreased Brca1 binding in vitro [116]. This alteration is also likely to elicit nonsense-mediated decay [92, 93, 94, 95]. Therefore, this alteration is predicted to be inactivating.

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## BRCA2

BRCA2 inactivation may impair the DNA damage repair process and result in a loss of cell cycle checkpoint control leading to tumorigenesis [117, 118]. Inactivating BRCA2 alterations have been reported to predict sensitivity to platinum-based chemotherapy and PARP inhibitors, including olaparib, rucaparib, niraparib, and talazoparib, which are FDA-approved in specific indications [84, 119, 76, 77, 120, 82]. In addition, talazoparib in combination with enzalutamide has been FDA-approved for the treatment of metastatic castration-resistant prostate cancer patients with tumors harboring germline or somatic alteration in one or more homologous recombination repair genes, including BRCA2 [85].

### BRCA2 T3033fs\*29

Gene	<b>BRCA2</b>
Nucleotide	<b>NM_000059.4: c.9097delA</b>
Amino Acid	<b>p.T3033fs*29</b>
Exon	<b>23</b>
Biomarker Type	<b>inactivating</b>

The alteration reported here is expected to effectively truncate the 3418-amino acid Brca2 protein prior to the C-terminal Rad51 binding domain and three nuclear localization signals crucial to Brca2 protein function; truncating mutations including T3195\* and Y3308\* have been reported to result in Brca2 inactivation [121, 122, 123, 124, 125]. In addition, this alteration is likely to elicit nonsense-mediated decay [92, 93, 94, 95]. Therefore, this alteration is expected to be inactivating.

## FBXW7

FBXW7 encodes the F-box/WD repeat-containing protein 7, Fbxw7, which is a subunit of the SCF ubiquitin ligase complex responsible for recruitment of substrates for targeted degradation by the proteasome [126]. Loss of Fbxw7 function may result in the stabilization of some oncoproteins, including mTOR, Notch1, Myc, Jun, and Cyclin E1, all of which are substrates for Fbxw7-targeted degradation by the proteasome [127, 128, 129]. Preclinical studies have reported that inactivation of Fbxw7 results in stabilization of mTOR; however, FBXW7 alterations have been shown not to be predictive of response to everolimus or temsirolimus in clinical studies [127, 130, 131]. Other agents that target mTOR, including dual mTORC1/mTORC2 inhibitors and dual PI3K/mTOR inhibitors, are currently in preclinical and clinical development [132, 133, 134].

### FBXW7 R393\*

Gene	<b>FBXW7</b>
Nucleotide	<b>NM_033632.3: c.1177C&gt;T</b>
Amino Acid	<b>p.R393*</b>
Exon	<b>8</b>
Biomarker Type	<b>unknown - predicted inactivating</b>

The FBXW7 nonsense alteration reported here is expected to truncate the 707-amino acid Fbxw7 protein, resulting in a protein that retains the conserved F-box domain but lacks all or a portion of the WD40 repeat region (UniProt). The WD40 repeat region is responsible for substrate recognition; therefore, this mutation is predicted to result in a failure to target substrates for degradation, thus enhancing the stability of known oncogene substrates including Cyclin E, Notch1, Myc, Jun, and mTOR [128, 127]. Therefore, this mutation is expected to be inactivating.

## APC

Inactivation of Apc results in the deregulation of Wnt signaling through beta-catenin [135]. There are currently no approved drugs targeted to APC defects in cancer. However, several potential approaches, including downstream Wnt pathway, Cox-2 inhibitors, and tankyrase 1/2 inhibitors are under investigation [136, 137, 138, 139, 140].

### APC Y1075\*

Gene	<b>APC</b>
Nucleotide	<b>NM_000038.6: c.3225T&gt;A</b>
Amino Acid	<b>p.Y1075*</b>
Exon	<b>16</b>
Biomarker Type	<b>inactivating</b>

The nonsense alteration reported here is expected to truncate the 2843-amino acid Apc protein within the beta-catenin binding domain, and is therefore likely to result in a disruption of the ability of the Apc protein to bind to beta-catenin, which in turn may upregulate Wnt signaling [141, 142, 143].

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## Variants of Unknown Significance (VUS)

The clinical relevance of these variants is currently unknown. Therefore, the functional impact of targeting these variants cannot be determined at this time.

RAD51C c.506T>C (p.V169A), 52%	BRCA2 c.5023T>C (p.C1675R), 24%	TP53 c.697C>T (p.H233Y), 24%
CDK12 c.3230A>C (p.E1077A), 23%	RHOA c.101A>G (p.Y34C), 22%	AR c.173A>T (p.Q58L), 15%
CHEK2 c.1604G>A (p.R535H), 14%	ERBB2 c.1059delG (p.R354fs*77), 10%	MAP2K2 c.158G>A (p.R53Q), 3.85%
APC c.1394C>A (p.A465E), 0.92%	APC c.6471A>C (p.K2157N), 0.87%	EGFR c.2538A>C (p.K846N), 0.48%
PALB2 c.1940A>G (p.H647R), 0.3%	FGFR3 c.2387delC (p.P796fs*?), 0.21%	APC c.4844A>G (p.Y1615C), 0.18%
FANCA c.2057C>T (p.A686V), 0.17%	AR c.1951A>T (p.S651C), 0.12%	APC c.7973G>T (p.W2658L), 0.11%
CDK12 c.4382dupG (p.T1463fs*?), 0.08%	BRAF c.1177+1857G>C (p.?), 0.07%	

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## Interpretation

Genomic alterations (SNVs/indels/fusions) were detected in the cell-free DNA (cfDNA) isolated from the patient's blood specimen. The variant frequency of the mutations, reported as %cfDNA, is calculated and reported for detected SNVs and indels. These alterations may be informative to cancer treatment response and/or clinical trial eligibility. While somatic actionability is of primary concern when determining report inclusion, some variants may be included without matched actionable outcomes. These variants may be critical to carcinogenesis in the patient's tumor.

The cell-free DNA (cfDNA) isolated from the patient's blood specimen was identified as Microsatellite instability-High (MSI-H). Microsatellite instability is linked to deficient DNA mismatch repair (dMMR), caused by inactivating mutations in one or more mismatch repair (MMR) genes (MLH1, MSH2, MSH6, and PMS2) or by somatic MLH1 promoter hypermethylation. As a result of MMR deficiency, most MSI-high tumors are marked by elevated tumor mutational burdens, with an abundance of low allele frequency insertion/deletion mutations. The reported somatic alterations should be interpreted in this context of MSI-H.

The KRAS G12V mutation included in this report was observed at an allele fraction suspicious for potential germline origin. Northstar Select™ is validated for the detection of somatic variants, and was not developed to distinguish germline variants, which may predispose the patient to certain types of cancer, from detected somatic variants. Discussion with a qualified professional as well as additional investigation with a test validated for calling germline mutations is recommended.

## Methods and Limitations

Northstar Select™ is a next generation sequencing (NGS)-based in vitro diagnostic test for detection of substitutions (SNVs), small insertion and deletion alterations (indels), selected genes' copy number alterations (CNAs, including amplifications and deletions) and selected gene-rearrangements in a total of 84 genes (Table 1), as well as microsatellite instability status. Cell-free DNA (cfDNA) is extracted from plasma, and the targeted regions, encompassing >250kb, are amplified and sequenced. The sensitivity of the test is 100% (95% CI: [99.84%,100.00%]) for SNVs and indels for variant allele fraction (VAF) ≥0.5% and fusions examined in the assay analytical validation, and 100% (95% CI: [76.84%,100.00%]) for CNAs. The limit of detection for the assay is 0.13-0.16% (VAF) for SNVs and indels. However, key actionable variants may be reported at lower VAFs where technically feasible. The overall base-wise specificity of the Northstar Select™ test is >99.99%, leading to high confidence in true positive reporting for variants with VAF >0.2%, despite the expansive genomic loci targeted and assayed. For CNAs, the LOD for gene amplifications is 2.125-2.16 copies and for loss is 1.78 copies. CNA LOD is subject to aneuploidy noise, with less aneuploid samples having a superior LOD. MSI score is calculated using a count of somatic indel mutations in targeted microsatellite sites; based upon meeting threshold, MSI-H status is reported when detected. The sensitivity of the MSI component is 100% (95% CI: [97.72%,100.00%]) for MSI-H at a tumor fraction of ≥0.5%, and the limit of detection of the assay for MSI-H is 0.07-0.4% tumor fraction. An MSI-Indeterminate result is an inconclusive result as it does not suggest the presence or absence of MSI-H in the patient. For certain cfDNA sample or variant characteristics, such as low cfDNA input or high level of cancer-associated chromosomal copy abnormality, the analytical sensitivity may be reduced.

Variants detected in the cfDNA are aligned to the hg19 reference genome. Informative genomic alterations are potentially actionable or biologically relevant variants based on evidence from medical and scientific literature. Variants of unknown significance (VUS) are genomic alterations that do not have sufficient evidence to determine biological/clinical significance.

Reported treatments and trials should be comprehensively evaluated by the medical provider, as inclusion in the report is neither a guarantee of treatment/trial match, nor intended to be fully comprehensive. Treatments and trials are reported based upon the information provided at the time of test requisition, including diagnosis, sex, age, and location, and may not account for all elements of the patient's medical history. Certain treatments may have specifications surrounding other clinical factors, such as HR/HER2-status or germline mutation origin. The ordering provider should consult official FDA-approval information for full approval specifications. Inclusion in Northstar Select™ does not guarantee that reported treatments or trials will have an impact on clinical outcome.

This assay is validated for the detection of somatic variants, but was not developed to distinguish germline variants, which may predispose the patient to certain types of cancer, from detected somatic variants. For variants with a VAF reported between 40-60% cfDNA, separate germline testing may be recommended to identify and characterize such variants that may have hereditary implications.

**Table 1: Genes on the Northstar Select™ panel**

Northstar Select™ reports single nucleotide variants, insertion and deletion variants (indels), and splice site mutations for clinically relevant exons in 82 genes, copy number amplifications in 19 genes, and copy number loss in 5 genes, and fusion events in 9 genes, as detailed in the table below.

AKT1, AKT2, ALK<sup>^</sup>, APC, AR<sup>+</sup>, ARAF, ARID1A, ATM<sup>-</sup>, BRAF<sup>^+</sup>, BRCA1<sup>-</sup>, BRCA2<sup>-</sup>, BRIP1, CCND1, CCND2, CCNE1<sup>+</sup>, CD274<sup>+</sup>, CDH1, CDK12, CDK4<sup>+</sup>, CDK6<sup>+</sup>, CDKN2A<sup>-</sup>, CDKN2B, CHEK2, CTNNB1, DDR2, EGFR<sup>+</sup>, ERBB2<sup>+</sup>, ESR1<sup>+</sup>, EZH2, FANCA, FBXW7, FGFR1<sup>+</sup>, FGFR2<sup>^+</sup>, FGFR3<sup>^</sup>, FGFR4, GATA3, GNA11, GNAQ, GNAS, HRAS, IDH1, IDH2, JAK2, JAK3, KIT<sup>+</sup>, KRAS<sup>+</sup>, MAP2K1, MAP2K2, MET<sup>+</sup>, MLH1, MPL, MSH2, MSH6, MTOR, MYC<sup>+</sup>, NF1, NOTCH1, NPM1, NRAS, NTRK1<sup>^</sup>, NTRK2<sup>^^</sup>, NTRK3<sup>^^</sup>, PALB2, PDGFRA<sup>+</sup>, PIK3CA<sup>+</sup>, PMS2, PTEN<sup>-</sup>, PTPN11, RAD51C, RAD51D, RAF1<sup>+</sup>, RB1, RET<sup>^+</sup>, RHOA, RIT1, ROS1<sup>^</sup>, SF3B1, SMAD4, SMO, STK11, TERT, TP53, TSC1, VHL

<sup>^</sup> Northstar Select™ also reports fusion events for this gene

<sup>^^</sup> Northstar Select™ reports only reports only fusion events for these genes, no SNVs and indels will be reported; NTRK3 is limited to NTRK3-ETV6 fusions only

<sup>+</sup> Northstar Select™ also reports copy number amplifications of this gene

<sup>-</sup> Northstar Select™ also reports copy number deletions of this gene



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Patient Name	<b>Jane Jones</b>	Date of Birth (Age)	<b>11/27/1940 (82 yrs)</b>	Assigned Sex at Birth	<b>Female</b>
Diagnosis	<b>Rectal adenocarcinoma</b>	Internal Patient ID	<b>1000090</b>	Report Date	<b>07/05/2023</b>

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Patient Name	<b>Jane Jones</b>	Date of Birth (Age)	<b>11/27/1940 (82 yrs)</b>	Assigned Sex at Birth	<b>Female</b>
Diagnosis	<b>Rectal adenocarcinoma</b>	Internal Patient ID	<b>10000090</b>	Report Date	<b>07/05/2023</b>

This NGS-based assay was developed and its performance characteristics determined by BillionToOne, Inc. It has not been cleared or approved by the U.S. Food and Drug Administration. BillionToOne, Inc. is regulated under CLIA. This test is used for clinical purposes. It should not be regarded as investigational or for research. This test was performed using BillionToOne's patented technology ([www.billiontoone.com/patents](http://www.billiontoone.com/patents)).

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