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PATIENT	DOB	DISEASE	MRN	REPORT DATE	REPORT STATUS
J D	05/15/1953	Non-small cell lung cancer	12		Final

REPORT SUMMARY

Executive Summary

[Please add your summary for this case.]

Other Biomarkers

TMB	
MSI	

Genomic Findings

IA		IB		IIC		IID	
BRAF	p.V600E c.1799T>A	*TP53*	p.P72R c.215C>G	*TP53*	p.V274F c.820G>T	*PDGFRA*	p.G79D c.236G>A

CLINICALLY RELEVANT RESULTS

Tier I - Strong Clinical Significance

VARIANT	CLINICAL IMPACT
BRAF p.V600E c.1799T>A A NM_004333.4 VAF % 32 DEPTH 197	**May benefit from** — Vemurafenib, Pembrolizumab, Ipilimumab + Nivolumab, Dabrafenib, Durvalumab + Tremelimumab-actl, Cemiplimab-rwlc, Dabrafenib + Trametinib, Binimetinib + Encorafenib, or Atezolizumab *in Non-small cell lung cancer* INTERPRETATION BRAF is a proto-oncogene, downstream of RAS which activates the RAF-MEK-ERK signaling pathway, and regulates cell division and differentiation (RefSeq, Aug 2017). Dabrafenib in combination with trametinib is FDA (Dabrafenib, 202806s010lbl; Trametinib, 204114Orig1s009lbl) and EMA (Dabrafenib, Revision 18; Trametinib, Revision 16) approved and NCCN (NSCLC, 3.2019), ASCO (PMID: 28806116, 2017; PMID: 29401004, 2018) and ESMO (PMID: 30285222, 2018) guideline recommended for use in non-small cell lung cancer harboring BRAF p.(Val600Glu), as a first-line therapy or as subsequent therapy following disease progression. Per EMA, dabrafenib in combination with trametinib is approved for adults with advanced non-small cell lung cancer with a BRAF Val600 mutation. The safety and efficacy of dabrafenib in the pediatric population has not been established. Dabrafenib is NCCN (NSCLC, 3.2019) and ASCO (PMID: 28806116, 2017; PMID: 29401004, 2018) guideline recommended for use in non-small cell lung cancer harboring BRAF p.(Val600Glu), as a single agent therapy if the combination of dabrafenib and trametinib is not tolerated, or as subsequent therapy following disease progression. Vemurafenib is NCCN (NSCLC, 3.2019) guideline recommended for use in non-small cell lung cancer harboring BRAF p.(Val600Glu) as a single agent therapy if the combination of dabrafenib and trametinib is not tolerated, or as subsequent therapy following disease progression. The following associations with this genomic finding are from other tumor type contexts: Binimetinib in combination with encorafenib is ESMO (PMID: 26314774, 2015) guideline recommended for use in metastatic melanoma harboring a BRAF Val600 mutation, as first-line and second-line therapy. Binimetinib in combination with encorafenib is NCCN (Cutaneous Melanoma, 1.2019) guideline recommended for use in metastatic or unresectable cutaneous melanoma harboring a BRAF Val600 activating mutation, as first-line therapy and as second-line or subsequent

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INTERPRETATION

therapy for disease progression. Binimetinib in combination with encorafenib is NCCN (Cutaneous Melanoma, 1.2019) guideline recommended for use in metastatic or unresectable cutaneous melanoma harboring a BRAF Val600 activating mutation, as first-line therapy and as second-line or subsequent therapy for disease progression. Cetuximab in combination with vemurafenib is NCCN (Colon Cancer, 4.2018; Rectal Cancer, 3.2018) guideline recommended for use in unresectable metastatic colorectal cancer harboring BRAF p.(Val600Glu), as a primary treatment or as a subsequent therapy following disease progression. Cobimetinib in combination with vemurafenib is NCCN (Cutaneous Melanoma, 1.2019) guideline recommended for use in metastatic or unresectable cutaneous melanoma harboring a BRAF Val600 activating mutation, as first-line therapy and as second-line or subsequent therapy for disease progression. Cobimetinib in combination with vemurafenib is NCCN (Cutaneous Melanoma, 1.2019) guideline recommended for use in metastatic or unresectable cutaneous melanoma harboring a BRAF Val600 activating mutation, as first-line therapy and as second-line or subsequent therapy for disease progression. Dabrafenib in combination with trametinib is ESMO (PMID: 26314774, 2015) guideline recommended for use in metastatic melanoma harboring a BRAF Val600 mutation, as first-line and second-line therapy. Dabrafenib in combination with trametinib is NCCN (Cutaneous Melanoma, 1.2019) guideline recommended for use in metastatic or unresectable cutaneous melanoma harboring a BRAF Val600 activating mutation, as first-line therapy and as second-line or subsequent therapy for disease progression. Dabrafenib in combination with trametinib is NCCN (Cutaneous Melanoma, 1.2019) guideline recommended for use in metastatic or unresectable cutaneous melanoma harboring a BRAF Val600 activating mutation, as first-line therapy and as second-line or subsequent therapy for disease progression. Panitumumab in combination with vemurafenib is NCCN (Colon Cancer, 4.2018; Rectal Cancer, 3.2018) guideline recommended for use in unresectable metastatic colorectal cancer harboring BRAF p.(Val600Glu), as a primary treatment or as a subsequent therapy following disease progression. Cobimetinib in combination with vemurafenib is EMA (Cobimetinib, Revision 6) approved and ESMO (PMID: 26314774, 2015) guideline recommended for use in unresectable or metastatic melanoma harboring a BRAF Val600 mutation. Per EMA, this combination is approved for adults with unresectable or metastatic melanoma harboring a BRAF Val600 mutation. The safety and efficacy of cobimetinib in the pediatric population and in non-Caucasians has not been established. Dabrafenib in combination with trametinib is FDA (Dabrafenib, 202806s010lbl; Trametinib, 204114Orig1s009lbl) approved and NCCN (Thyroid Carcinoma, 3.2018) guideline recommended for use in locally advanced or metastatic anaplastic thyroid carcinoma harboring BRAF p.(Val600Glu). Binimetinib in combination with encorafenib is FDA (Binimetinib, 210498s001lbl; Encorafenib, 210496s001lbl) and EMA (Binimetinib, Revision 1) approved and ESMO (PMID: 26314774, 2015) guideline recommended for use in unresectable or metastatic melanoma harboring a BRAF Val600 mutation. Per EMA, this combination is approved for adults with unresectable or metastatic melanoma harboring a BRAF Val600 mutation. The safety and efficacy of binimetinib and encorafenib in the pediatric population has not been established. Cobimetinib in combination with vemurafenib is FDA (Cobimetinib, 206192s002lbl) and EMA (Cobimetinib, Revision 6) approved and ESMO (PMID: 26314774, 2015) guideline recommended for use in unresectable or metastatic melanoma harboring a BRAF Val600 mutation. Per EMA, this combination is approved for adults with unresectable or metastatic melanoma harboring a BRAF Val600 mutation. The safety and efficacy of cobimetinib in the pediatric population and in non-Caucasians has not been established. Dabrafenib in combination with trametinib is FDA (Dabrafenib, 202806s010lbl; Trametinib, 204114Orig1s009lbl) and EMA (Dabrafenib, Revision 18; Trametinib, Revision 16) approved and ESMO (PMID: 26314774, 2015) guideline recommended for use in use in unresectable or metastatic melanoma harboring a BRAF Val600 mutation. Per EMA, this combination

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is approved for adults with unresectable or metastatic melanoma harboring a BRAF Val600 mutation. The safety and efficacy of dabrafenib and trametinib in the pediatric population and in non-Caucasians has not been established. Dabrafenib is NCCN (Cutaneous Melanoma, 1.2019) guideline recommended as a monotherapy for use in metastatic or unresectable cutaneous melanoma harboring a BRAF Val600 activating mutation, if BRAF/MEK inhibitor combination therapy is contraindicated. Dabrafenib is NCCN (Cutaneous Melanoma, 1.2019) guideline recommended as a monotherapy for use in metastatic or unresectable cutaneous melanoma harboring a BRAF Val600 activating mutation, if BRAF/MEK inhibitor combination therapy is contraindicated. Dabrafenib is FDA (Dabrafenib, 202806s010lbl) and EMA (Dabrafenib, Revision 18) approved for use in unresectable or metastatic melanoma harboring a BRAF Val600 mutation. Per EMA, dabrafenib is approved for adults with unresectable or metastatic melanoma harboring a BRAF Val600 mutation. The safety and efficacy of dabrafenib in the pediatric population and in non-Caucasians has not been established. Trametinib is FDA (Trametinib, 204114Orig1s009lbl) and EMA (Trametinib, Revision 16) approved as monotherapy for use in unresectable or metastatic melanoma harboring a BRAF Val600 mutation. Per EMA, trametinib is approved for adults with unresectable or metastatic melanoma harboring a BRAF Val600 mutation. The safety and efficacy of trametinib in the pediatric population and in non-Caucasians has not been established. However, per NCCN (Cutaneous Melanoma, 1.2019), trametinib monotherapy is no longer a recommended treatment option due to relatively poor efficacy compared with BRAF inhibitor monotherapy and BRAF/MEK inhibitor combination therapy. Vemurafenib is NCCN (Cutaneous Melanoma, 1.2019) guideline recommended as a monotherapy for use in metastatic or unresectable cutaneous melanoma harboring a BRAF Val600 activating mutation, if BRAF/MEK inhibitor combination therapy is contraindicated. Vemurafenib is NCCN (Cutaneous Melanoma, 1.2019) guideline recommended as monotherapy for use in metastatic or unresectable cutaneous melanoma harboring a BRAF Val600 activating mutation, if BRAF/MEK inhibitor combination therapy is contraindicated. Vemurafenib is FDA (Vemurafenib, 202429s016lbl) and EMA (Vemurafenib, Revision 18) approved as a monotherapy for use in unresectable or metastatic melanoma harboring a BRAF Val600 mutation. Per EMA, vemurafenib is approved for adults with unresectable or metastatic melanoma harboring a BRAF Val600 mutation. The safety and efficacy of vemurafenib in the pediatric population and in non-Caucasians has not been established. Colorectal cancer harboring BRAF p.(Val600Glu) is deemed unlikely to respond to cetuximab given as a single agent or in combination with cytotoxic chemotherapy per NCCN (Colon Cancer, 4.2018; Rectal Cancer, 3.2018) guidelines. Colorectal cancer harboring BRAF p.(Val600Glu) is deemed unlikely to respond to panitumumab given as a single agent or in combination with cytotoxic chemotherapy per NCCN (Colon Cancer, 4.2018; Rectal Cancer, 3.2018) guidelines. BRAF p.(Val600Glu) is deemed an unfavorable prognostic marker in colorectal cancer per NCCN (Colon Cancer, 4.2018; Rectal Cancer, 3.2018) and ASCO (PMID: 28165299, 2017) guidelines. BRAF p.(Val600Glu) is associated with an unfavorable prognosis in papillary thyroid carcinoma per NCCN (Thyroid Carcinoma, 3.2018) guidelines.

TP53

p.P72R
c.215C>G

B

NM_001126114.2
VAF % 99.1

INTERPRETATION

TP53 is a tumor suppressor and regulates expression of target genes, by inducing cell cycle arrest, apoptosis, senescence, DNA repair, or changes in metabolism (PMID- 20182602).

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VARIANT	CLINICAL IMPACT
DEPTH 213	INTERPRETATION
	A missense alteration in *TP53*, P72R, is identified. Codon 72 lies in exon 4 within the CCAR2, HRMT1L2, and WWOX-interacting region of the TP53 protein (UniProt.org). This variant is predicted to be 'Tolerated' by SIFT and 'Possibly Damaging' by Polyphen2Hdiv and 'Benign' by Polyphen2Hvar prediction algorithms. The *TP53*, P72R has been reported to induce apoptosis in vitro (PMID-12567188, 2003). In ClinVar, the clinical significance of germline *TP53* P72R is 'Benign and **having drug response**'; 'Benign' in the context of hereditary cancer-predisposing syndrome and Li-Fraumeni syndrome; 'drug response' was mentioned in the context of the following conditions: antineoplastic agents response, cisplatin response, cyclophosphamide response, fluorouracil response and paclitaxel response (Variation ID: 12351). *TP53* P72R has been reported in multiple neoplasms including carcinoma of bile duct (COSMIC, October 2018). The clinical significance of *TP53* P72R in poorly differentiated carcinoma involving hepatic parenchyma is not known. The P72R polymorphism of p53 predisposes to obesity and metabolic dysfunction (PMID: 26947067; 2016). A study of patients with plasma cell myeloma (PCM) reported that P72R polymorphisms may be associated with an increased PCM risk and significantly affect overall survival (OS) of PCM patients (PMID- 29333597). Acute myeloid leukemia (AML) patients with SNP P72R showed a possible trend towards worse OS (PMID- 24641375). Currently, there are no clinical trials recruiting cholangiocarcinoma or solid tumor patients harboring *TP53* P72R alteration.

Tier II - Potential Clinical Significance

VARIANT	CLINICAL IMPACT
TP53 p.V274F c.820G>T C NM_001126114.2 **VAF** % 100 **DEPTH** 191	**Unfavorable Prognosis in** — Essential thrombocythemia, Medulloblastoma, Myelosclerosis with myeloid metaplasia, Myeloproliferative disorder, or Myeloproliferative neoplasm INTERPRETATION TP53 is a tumor suppressor and regulates expression of target genes by inducing cell cycle arrest, apoptosis, senescence, DNA repair, or changes in metabolism (PMID: 22294769, 2012; 20182602, 2010). Some evidence suggests that adenocarcinoma of lung harboring a TP53 mutation may be associated with an unfavorable prognosis based on: a) overall survival in a study of 225 participants following resection (PMID: 30885352, 2019); and b) a retrospective study of 363 Brazilian participants (PMID: 37031678, 2023).

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VARIANT	CLINICAL IMPACT
PDGFRA p.G79D c.236G>A D NM_006206.4 VAF % 38.9 DEPTH 193	INTERPRETATION A non-synonymous *PDGFRA* p.G79D variant is detected that has been previously described in dbSNP (rs36035373) with a minor allele frequency of 0.007 but up to 1.8% in one cohort. This variant has been previously detected in non-small cell lung cancer but is not thought to be activating (PMID: 19755855). Overall, the clinical significance, if any, is not known.

Other Biomarkers

BIOMARKER	CLINICAL IMPACT
TMB 11.6 muts/Mb	INTERPRETATION
MSI 0.0% Unstable Sites	INTERPRETATION

Clinical Trials

Clinical Trials associated with this patient's genomic profile and tumor type as displayed below.

TITLE	TRIAL IDENTIFIER	PHASE	VARIANT
A Study of Multiple Therapies in Biomarker-Selected Patients With Resectable Stages IB-III Non-Small Cell Lung Cancer	NCT04302025	II	**BRAF** p.V600E c.1799T>A
Pilot Trial of Molecular Profiling and Targeted Therapy for Advanced Non-Small Cell Lung Cancer, Small Cell Lung Cancer, and Thymic Malignancies	NCT01306045	II	**PDGFRA** p.G79D c.236G>A
A Study to Characterize the Safety, Tolerability, and Preliminary Efficacy of CFT1946 as Monotherapy and in Combination With Trametinib in Subjects With BRAF V600 Mutant Solid Tumors	NCT05668585	I/II	**BRAF** p.V600E c.1799T>A

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TITLE	TRIAL IDENTIFIER	PHASE	VARIANT
A Pilot Study of Nintedanib in Molecularly Selected Patients With Advanced Non-Small Cell Lung Cancer (NSCLC)	NCT02299141	I	**PDGFRA** p.G79D c.236G>A **TP53** p.V274F c.820G>T **TP53** p.P72R c.215C>G
A Pilot Study of Pazopanib in Molecularly Selected Patients With Advanced Non-Small Cell Lung Cancer (NSCLC)	NCT02193152	I	**TP53** p.V274F c.820G>T **TP53** p.P72R c.215C>G

TIER III - VARIANTS OF UNCERTAIN SIGNIFICANCE

No variants were reported for this classification tier.

CLASSIFICATION AND LEVELS OF EVIDENCE

The variant classification system used in this report is based on joint consensus recommendations of the Association for Molecular Pathology, American Society of Clinical Oncology, and the College of American Pathologists (J Mol Diagn 2017, 19:4-23). Tiers IA, IB, IIC, IID, III and IV describe variant categories of descending clinical significance in the patient. Variants in Tier IV are not reported in accordance with the consensus recommendations.

IA	IB	IIC	IID
Variant of strong clinical significance, Level A evidence (FDA approved therapy or practice guideline in patient's tumor type)	Variant of strong clinical significance, Level B Evidence (consensus in the field based on well-powered studies in patient's tumor type)	Variant of potential clinical significance, Level C evidence (FDA approved therapy or practice guideline in other tumor type(s), evidence from multiple small published studies, or based on availability of investigational therapies)	Variant of potential clinical significance, Level D evidence (case reports or preclinical studies)

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III	Variant of uncertain clinical significance
IV	Benign or likely benign variant

TEST DETAILS

REPORTED GENES

A total of 523 genes were subjected to targeted next generation sequencing analysis. Details available upon request.

CGW VERSION

CGW_v6.27

DATABASE DETAILS

The versions, releases, builds, dates of the following databases were used to generate this report.

- Genomic Build: GRCh37.p13
- Genomic Annotation Sources: NCBI RefSeq v105
- gnomAD: r2.1
- dbSNP: 149
- ExAC: v1.0
- dbNSFP: 4.4c
- ClinVar: 20230930
- NHLBI ESP: v.0.0.30
- COSMIC: v98

CODING EXON COVERAGE METRICS

Level 2: 100x coverage for > 50% of positions was not achieved for the targeted exon regions listed below:

Gene Transcript ID (Exon/Intron('))					
BRD4 NM_058243.2 (14)	***FAM175A*** NM_139076.2 (7)	***FAM175A*** NM_139076.2 (4)	***FAM175A*** NM_139076.2 (3)	***GATA6*** NM_005257.4 (2)	***GATA6*** NM_005257.4 (3)
IGF1 NM_000618.3 (1)	***POLE*** NM_006231.2 (1)	***TAF1*** NM_138923.2 (1)	***TAF1*** NM_138923.2 (2)	***TAF1*** NM_138923.2 (4)	***TAF1*** NM_138923.2 (7)
TAF1 NM_138923.2 (9)	***TAF1*** NM_138923.2 (10)	***TAF1*** NM_138923.2 (11)	***TAF1*** NM_138923.2 (12)	***TAF1*** NM_138923.2 (13)	***TAF1*** NM_138923.2 (14)
TAF1 NM_138923.2 (15)	***TAF1*** NM_138923.2 (16)	***TAF1*** NM_138923.2 (17)	***TAF1*** NM_138923.2 (18)	***TAF1*** NM_138923.2 (19)	***TAF1*** NM_138923.2 (20)
TAF1 NM_138923.2 (21)	***TAF1*** NM_138923.2 (22)	***TAF1*** NM_138923.2 (24)	***TAF1*** NM_138923.2 (25)	***TAF1*** NM_138923.2 (26)	***TAF1*** NM_138923.2 (27)

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TAF1 NM_138923.2 (28)	*TAF1* NM_138923.2 (29)	*TAF1* NM_138923.2 (30)	*TAF1* NM_138923.2 (31)	*TAF1* NM_138923.2 (33)	*TAF1* NM_138923.2 (34)
GEN1 NM_182625.3 (3)	*GEN1* NM_182625.3 (8)	*GEN1* NM_182625.3 (9)	*GEN1* NM_182625.3 (10)	*GEN1* NM_182625.3 (11)	*GEN1* NM_182625.3 (12)
GEN1 NM_182625.3 (13)	*NPM1* NM_002520.6 (2)	*NPM1* NM_002520.6 (5)	*NPM1* NM_002520.6 (6)	*NPM1* NM_002520.6 (7)	*NPM1* NM_002520.6 (9)
NPM1 NM_002520.6 (11)	*RUNX1* NM_001754.4 (3)	*CYLD* NM_015247.2 (6)	*CYLD* NM_015247.2 (9)	*CYLD* NM_015247.2 (13)	*CYLD* NM_015247.2 (14)
CYLD NM_015247.2 (15)	*CYLD* NM_015247.2 (17)	*FANCA* NM_000135.2 (5)	*FANCA* NM_000135.2 (1)	*GID4* NM_024052.4 (1)	*MAP3K4* NM_005922.2 (1)
MAP3K4 NM_005922.2 (19)	*TCEB1* NM_001204857.1 (2)	*ACVR1B* NM_004302.4 (1)	*BTK* NM_000061.2 (19)	*BTK* NM_000061.2 (18)	*BTK* NM_000061.2 (17)
BTK NM_000061.2 (16)	*BTK* NM_000061.2 (15)	*BTK* NM_000061.2 (14)	*BTK* NM_000061.2 (12)	*BTK* NM_000061.2 (10)	*BTK* NM_000061.2 (9)
BTK NM_000061.2 (8)	*BTK* NM_000061.2 (6)	*BTK* NM_000061.2 (5)	*BTK* NM_000061.2 (4)	*BTK* NM_000061.2 (3)	*BTK* NM_000061.2 (2)
FANCC NM_000136.2 (5)	*FANCC* NM_000136.2 (4)	*MAPK1* NM_002745.4 (1)	*NRG1* NM_013956.3 (4)	*NRG1* NM_013956.3 (8)	*NRG1* NM_013956.3 (5)
PPP2R1A NM_014225.5 (1)	*TCF3* NM_003200.3 (15)	*TCF3* NM_003200.3 (14)	*TCF3* NM_003200.3 (12)	*TCF3* NM_003200.3 (11)	*TCF3* NM_003200.3 (10)
TCF3 NM_003200.3 (9)	*TCF3* NM_003200.3 (8)	*TCF3* NM_003200.3 (7)	*TCF3* NM_003200.3 (6)	*TCF3* NM_003200.3 (3)	*DCUN1D1* NM_020640.2 (6)
DCUN1D1 NM_020640.2 (5)	*DCUN1D1* NM_020640.2 (1)	*FANCD2* NM_033084.3 (3)	*FANCD2* NM_033084.3 (7)	*FANCD2* NM_033084.3 (13)	*FANCD2* NM_033084.3 (14)
FANCD2 NM_033084.3 (20)	*GNA11* NM_002067.2 (1)	*MAPK3* NM_002746.2 (1)	*NSD1* NM_022455.4 (8)	*PPP2R2A* NM_002717.3 (3)	*PPP2R2A* NM_002717.3 (5)
PPP2R2A NM_002717.3 (6)	*SDHA* NM_004168.2 (1)	*SDHA* NM_004168.2 (14)	*TCF7L2* NM_030756.4 (12)	*FANCE* NM_021922.2 (1)	*GNA13* NM_006572.4 (3)
MAX NM_002382.4 (2)	*PPP6C* NM_001123355.1 (2)	*AKT3* NM_005465.4 (12)	*GNAQ* NM_002072.3 (3)	*GNAQ* NM_002072.3 (1)	*NTRK2* NM_006180.3 (12)

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NTRK2 NM_006180.3 (15)	***SDHB*** NM_003000.2 (1)	***TERT*** TERT_Promoter (0')	***NTRK3*** NM_001012338.2 (18)	***PREX2*** NM_024870.2 (4)	***PREX2*** NM_024870.2 (13)
PREX2 NM_024870.2 (17)	***SDHC*** NM_003001.3 (6)	***DICER1*** NM_030621.3 (8)	***FANCI*** NM_001113378.1 (6)	***FANCI*** NM_001113378.1 (7)	***FANCI*** NM_001113378.1 (14)
FANCI NM_001113378.1 (22)	***FANCI*** NM_001113378.1 (28)	***GPR124*** NM_032777.9 (1)	***MDM2*** NM_002392.5 (4)	***MDM2*** NM_002392.5 (5)	***NUP93*** NM_014669.4 (16)
SDHD NM_003002.3 (4)	***ANKRD11*** NM_001256183.1 (13)	***DIS3*** NM_014953.3 (1)	***FANCL*** NM_001114636.1 (14)	***FANCL*** NM_001114636.1 (13)	
FANCL NM_001114636.1 (12)	***FANCL*** NM_001114636.1 (11)	***FANCL*** NM_001114636.1 (10)	***FANCL*** NM_001114636.1 (4)	***FANCL*** NM_001114636.1 (3)	
FANCL NM_001114636.1 (2)	***INPP4A*** NM_004027.2 (4)	***INPP4A*** NM_004027.2 (6)	***PRKCI*** NM_002740.5 (4)	***PRKCI*** NM_002740.5 (8)	***PRKCI*** NM_002740.5 (12)
PRKCI NM_002740.5 (13)	***PRKCI*** NM_002740.5 (15)	***TFE3*** NM_006521.4 (9)	***TFE3*** NM_006521.4 (8)	***TFE3*** NM_006521.4 (7)	***TFE3*** NM_006521.4 (2)
TFE3 NM_006521.4 (1)	***ANKRD26*** NM_001256053.1 (34)	***ANKRD26*** NM_001256053.1 (33)	***ANKRD26*** NM_001256053.1 (31)	***ANKRD26*** NM_001256053.1 (29)	
ANKRD26 NM_001256053.1 (28)	***ANKRD26*** NM_001256053.1 (22)	***ANKRD26*** NM_001256053.1 (19)	***ANKRD26*** NM_001256053.1 (16)	***ANKRD26*** NM_001256053.1 (15)	
ANKRD26 NM_001256053.1 (14)	***ANKRD26*** NM_001256053.1 (11)	***ANKRD26*** NM_001256053.1 (10)	***ANKRD26*** NM_001256053.1 (6)	***ANKRD26*** NM_001256053.1 (5)	
FAS NM_000043.4 (8)	***INPP4B*** NM_001101669.1 (24)	***INPP4B*** NM_001101669.1 (23)	***INPP4B*** NM_001101669.1 (14)	***INPP4B*** NM_001101669.1 (12)	
INPP4B NM_001101669.1 (11)	***INPP4B*** NM_001101669.1 (5)	***MED12*** NM_005120.2 (17)	***MED12*** NM_005120.2 (18)	***MED12*** NM_005120.2 (20)	***MED12*** NM_005120.2 (28)
MED12 NM_005120.2 (32)	***MED12*** NM_005120.2 (33)	***MED12*** NM_005120.2 (40)	***MED12*** NM_005120.2 (42)	***MED12*** NM_005120.2 (43)	***MED12*** NM_005120.2 (45)
PRKDC NM_006904.6 (39)	***PRKDC*** NM_006904.6 (23)	***PRKDC*** NM_006904.6 (14)	***PRKDC*** NM_006904.6 (9)	***PRKDC*** NM_006904.6 (5)	***PRKDC*** NM_006904.6 (3)
PRKDC NM_006904.6 (1)	***SETD2*** NM_014159.6 (13)	***SETD2*** NM_014159.6 (4)	***SETD2*** NM_014159.6 (2)	***TFRC*** NM_001128148.1 (7)	***TFRC*** NM_001128148.1 (2)

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APC NM_000038.5 (3)	*APC* NM_000038.5 (5)	*APC* NM_000038.5 (14)	*APC* NM_000038.5 (15)	*DNMT1* NM_001379.2 (40)	*DNMT1* NM_001379.2 (39)
DNMT1 NM_001379.2 (38)	*DNMT1* NM_001379.2 (37)	*DNMT1* NM_001379.2 (17)	*DNMT1* NM_001379.2 (14)	*DNMT1* NM_001379.2 (13)	*DNMT1* NM_001379.2 (12)
DNMT1 NM_001379.2 (11)	*DNMT1* NM_001379.2 (9)	*DNMT1* NM_001379.2 (8)	*DNMT1* NM_001379.2 (7)	*DNMT1* NM_001379.2 (5)	*DNMT1* NM_001379.2 (3)
DNMT1 NM_001379.2 (2)	*DNMT1* NM_001379.2 (1)	*FAT1* NM_005245.3 (4)	*INSR* NM_000208.2 (1)	*MEF2B* NM_001145785.1 (9)	*PAK3* NM_001128166.1 (4)
PAK3 NM_001128166.1 (5)	*PAK3* NM_001128166.1 (6)	*PAK3* NM_001128166.1 (7)	*PAK3* NM_001128166.1 (8)	*PAK3* NM_001128166.1 (9)	
PAK3 NM_001128166.1 (10)	*PAK3* NM_001128166.1 (11)	*PAK3* NM_001128166.1 (12)	*PAK3* NM_001128166.1 (13)	*PAK3* NM_001128166.1 (14)	
PAK3 NM_001128166.1 (15)	*PAK3* NM_001128166.1 (16)	*PRSS8* NM_002773.3 (2)	*PRSS8* NM_002773.3 (1)	*SF3B1* NM_012433.2 (11)	*TGFBR1* NM_004612.2 (1)
AR NM_000044.3 (3)	*AR* NM_000044.3 (7)	*DNMT3A* NM_175629.2 (2)	*FBXW7* NM_033632.3 (3)	*IRF2* NM_002199.3 (5)	*PTCH1* NM_000264.3 (1)
SH2B3 NM_005475.2 (2)	*ARAF* NM_001256196.1 (2)	*ARAF* NM_001256196.1 (7)	*ARAF* NM_001256196.1 (11)	*ARAF* NM_001256196.1 (12)	
CCNE1 NM_001238.2 (2)	*CCNE1* NM_001238.2 (7)	*PTEN* NM_000314.4 (2)	*PTEN* NM_000314.4 (3)	*PTEN* NM_000314.4 (4)	*PTEN* NM_000314.4 (8)
PTEN NM_000314.4 (9)	*SH2D1A* NM_002351.4 (2)	*SH2D1A* NM_002351.4 (4)	*SH2D1A* NM_002351.4 (3)	*CD274* NM_014143.3 (2)	*CD274* NM_014143.3 (7)
DOT1L NM_032482.2 (12)	*DOT1L* NM_032482.2 (13)	*H3F3A* NM_002107.4 (2)	*H3F3A* NM_002107.4 (4)	*PARK2* NM_004562.2 (1)	*PTPN11* NM_002834.3 (1)
SHQ1 NM_018130.2 (8)	*TMPRSS2* NM_005656.3 (14)	*TMPRSS2* NM_005656.3 (2)	*ARID1A* NM_006015.4 (1)	*MITF* NM_000248.3 (1)	*PTPRD* NM_002839.3 (19)
PTPRD NM_002839.3 (17)	*PTPRD* NM_002839.3 (16)	*PTPRD* NM_002839.3 (26)	*SLIT2* NM_004787.1 (2)	*SLIT2* NM_004787.1 (5)	*SLIT2* NM_004787.1 (7)
SLIT2 NM_004787.1 (10)	*SLIT2* NM_004787.1 (15)	*SLIT2* NM_004787.1 (17)	*SLIT2* NM_004787.1 (19)	*SLIT2* NM_004787.1 (22)	*SLIT2* NM_004787.1 (25)

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ARID1B NM_017519.2 (1)	*EED* NM_003797.3 (8)	*EED* NM_003797.3 (9)	*EED* NM_003797.3 (11)	*FGF19* NM_005117.2 (1)	*JAK1* NM_002227.2 (2)
MLH1 NM_000249.3 (7)	*PTPRS* NM_002850.3 (24)	*PTPRS* NM_002850.3 (18)	*PTPRS* NM_002850.3 (15)	*PTPRS* NM_002850.3 (9)	*ARID2* NM_152641.2 (5)
ARID2 NM_152641.2 (6)	*ARID2* NM_152641.2 (7)	*ARID2* NM_152641.2 (9)	*ARID2* NM_152641.2 (20)	*CD79A* NM_001783.3 (4)	*FGF2* NM_002006.4 (1)
HGF NM_000601.4 (12)	*HGF* NM_000601.4 (2)	*JAK2* NM_004972.3 (8)	*JAK2* NM_004972.3 (12)	*JAK2* NM_004972.3 (15)	*JAK2* NM_004972.3 (21)
KMT2A NM_005933.3 (1)	*PAX5* NM_016734.2 (1)	*PTPRT* NM_133170.3 (16)	*PTPRT* NM_133170.3 (13)	*PTPRT* NM_133170.3 (1)	*PTPRT* NM_133170.3 (14)
TOP1 NM_003286.2 (1)	*TOP1* NM_003286.2 (2)	*TOP1* NM_003286.2 (7)	*TOP1* NM_003286.2 (8)	*ARID5B* NM_032199.2 (7)	*EGFR* NM_005228.3 (1)
MLLT3 NM_004529.2 (3)	*TOP2A* NM_001067.3 (32)	*TOP2A* NM_001067.3 (13)	*ASXL1* NM_015338.5 (1)	*ASXL1* NM_015338.5 (3)	*CDC73* NM_024529.4 (5)
CDC73 NM_024529.4 (17)	*EIF1AX* NM_001412.3 (7)	*EIF1AX* NM_001412.3 (6)	*EIF1AX* NM_001412.3 (5)	*EIF1AX* NM_001412.3 (4)	*EIF1AX* NM_001412.3 (3)
EIF1AX NM_001412.3 (2)	*EIF1AX* NM_001412.3 (1)	*FGF3* NM_005247.2 (1)	*RAB35* NM_006861.6 (1)	*SMAD4* NM_005359.5 (4)	*SMAD4* NM_005359.5 (8)
ASXL2 NM_018263.4 (2)	*CDH1* NM_004360.3 (1)	*FGF4* NM_002007.2 (1)	*KAT6A* NM_006766.3 (10)	*MRE11A* NM_005591.3 (20)	*MRE11A* NM_005591.3 (17)
MRE11A NM_005591.3 (14)	*MRE11A* NM_005591.3 (7)	*MRE11A* NM_005591.3 (3)	*PBRM1* NM_018313.4 (18)	*PBRM1* NM_018313.4 (9)	*RAC1* NM_018890.3 (1)
ATM NM_000051.3 (3)	*ATM* NM_000051.3 (5)	*ATM* NM_000051.3 (8)	*ATM* NM_000051.3 (12)	*ATM* NM_000051.3 (16)	*ATM* NM_000051.3 (21)
ATM NM_000051.3 (24)	*ATM* NM_000051.3 (25)	*ATM* NM_000051.3 (27)	*ATM* NM_000051.3 (28)	*ATM* NM_000051.3 (29)	*ATM* NM_000051.3 (31)
ATM NM_000051.3 (40)	*ATM* NM_000051.3 (44)	*ATM* NM_000051.3 (54)	*ATM* NM_000051.3 (59)	*EIF4E* NM_001130678.1 (7)	*EIF4E* NM_001130678.1 (6)
EIF4E NM_001130678.1 (4)	*FGF5* NM_004464.3 (2)	*KDM5A* NM_001042603.1 (22)	*MSH2* NM_000251.2 (2)	*MSH2* NM_000251.2 (8)	*MSH2* NM_000251.2 (11)

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MSH2 NM_000251.2 (16)	*ATR* NM_001184.3 (41)	*ATR* NM_001184.3 (39)	*ATR* NM_001184.3 (20)	*ATR* NM_001184.3 (15)	*ATR* NM_001184.3 (9)
ATR NM_001184.3 (2)	*EML4* NM_019063.3 (6)	*EML4* NM_019063.3 (20)	*KDM5C* NM_004187.3 (22)	*KDM5C* NM_004187.3 (18)	*KDM5C* NM_004187.3 (17)
KDM5C NM_004187.3 (14)	*KDM5C* NM_004187.3 (11)	*KDM5C* NM_004187.3 (6)	*KDM5C* NM_004187.3 (4)	*MSH3* NM_002439.4 (11)	*MSH3* NM_002439.4 (12)
MSH3 NM_002439.4 (15)	*MSH3* NM_002439.4 (16)	*MSH3* NM_002439.4 (19)	*PDCD1LG2* NM_025239.3 (7)	*RAD50* NM_005732.3 (2)	*RAD50* NM_005732.3 (6)
RAD50 NM_005732.3 (9)	*RAD50* NM_005732.3 (11)	*RAD50* NM_005732.3 (17)	*RAD50* NM_005732.3 (18)	*RAD50* NM_005732.3 (19)	*RAD50* NM_005732.3 (20)
RAD50 NM_005732.3 (21)	*RAD50* NM_005732.3 (22)	*SMARCD1* NM_003076.4 (1)	*ATRX* NM_000489.3 (35)	*ATRX* NM_000489.3 (34)	*ATRX* NM_000489.3 (33)
ATRX NM_000489.3 (32)	*ATRX* NM_000489.3 (31)	*ATRX* NM_000489.3 (30)	*ATRX* NM_000489.3 (29)	*ATRX* NM_000489.3 (28)	*ATRX* NM_000489.3 (27)
ATRX NM_000489.3 (26)	*ATRX* NM_000489.3 (25)	*ATRX* NM_000489.3 (24)	*ATRX* NM_000489.3 (23)	*ATRX* NM_000489.3 (22)	*ATRX* NM_000489.3 (21)
ATRX NM_000489.3 (20)	*ATRX* NM_000489.3 (19)	*ATRX* NM_000489.3 (18)	*ATRX* NM_000489.3 (17)	*ATRX* NM_000489.3 (16)	*ATRX* NM_000489.3 (15)
ATRX NM_000489.3 (14)	*ATRX* NM_000489.3 (13)	*ATRX* NM_000489.3 (12)	*ATRX* NM_000489.3 (11)	*ATRX* NM_000489.3 (10)	*ATRX* NM_000489.3 (9)
ATRX NM_000489.3 (8)	*ATRX* NM_000489.3 (7)	*ATRX* NM_000489.3 (6)	*ATRX* NM_000489.3 (5)	*ATRX* NM_000489.3 (4)	*ATRX* NM_000489.3 (3)
ATRX NM_000489.3 (2)	*ATRX* NM_000489.3 (1)	*CDK6* NM_001259.6 (6)	*EP300* NM_001429.3 (21)	*EP300* NM_001429.3 (26)	*EP300* NM_001429.3 (27)
KDM6A NM_021140.2 (1)	*KDM6A* NM_021140.2 (2)	*KDM6A* NM_021140.2 (3)	*KDM6A* NM_021140.2 (4)	*KDM6A* NM_021140.2 (5)	*KDM6A* NM_021140.2 (6)
KDM6A NM_021140.2 (7)	*KDM6A* NM_021140.2 (8)	*KDM6A* NM_021140.2 (9)	*KDM6A* NM_021140.2 (10)	*KDM6A* NM_021140.2 (11)	*KDM6A* NM_021140.2 (12)
KDM6A NM_021140.2 (13)	*KDM6A* NM_021140.2 (14)	*KDM6A* NM_021140.2 (15)	*KDM6A* NM_021140.2 (18)	*KDM6A* NM_021140.2 (19)	*KDM6A* NM_021140.2 (20)

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KDM6A NM_021140.2 (21)	*KDM6A* NM_021140.2 (22)	*KDM6A* NM_021140.2 (23)	*KDM6A* NM_021140.2 (24)	*KDM6A* NM_021140.2 (25)	*KDM6A* NM_021140.2 (26)
KDM6A NM_021140.2 (27)	*KDM6A* NM_021140.2 (28)	*KDM6A* NM_021140.2 (29)	*MSH6* NM_000179.2 (1)	*MSH6* NM_000179.2 (7)	*MSH6* NM_000179.2 (8)
MSH6 NM_000179.2 (10)	*SMC1A* NM_006306.3 (23)	*SMC1A* NM_006306.3 (20)	*SMC1A* NM_006306.3 (16)	*SMC1A* NM_006306.3 (8)	*TSC1* NM_000368.4 (16)
AURKA NM_198435.1 (4)	*AURKA* NM_198435.1 (2)	*CDK8* NM_001260.1 (2)	*CDK8* NM_001260.1 (8)	*CDK8* NM_001260.1 (9)	*EPCAM* NM_002354.2 (1)
EPCAM NM_002354.2 (6)	*EPCAM* NM_002354.2 (9)	*MST1* NM_020998.3 (14)	*MST1* NM_020998.3 (7)	*RAD51B* NM_133509.3 (11)	*SMC3* NM_005445.3 (3)
SMC3 NM_005445.3 (5)	*SMC3* NM_005445.3 (14)	*SMC3* NM_005445.3 (23)	*SMC3* NM_005445.3 (27)	*SMC3* NM_005445.3 (28)	*EPHA3* NM_005233.5 (12)
KEAP1 NM_203500.1 (5)	*KEAP1* NM_203500.1 (4)	*PDK1* NM_001278549.1 (1)	*PDK1* NM_001278549.1 (7)	*SMO* NM_005631.4 (1)	*TSHR* NM_000369.2 (2)
TSHR NM_000369.2 (5)	*TSHR* NM_000369.2 (8)	*EPHA5* NM_004439.5 (12)	*PDPK1* NM_002613.4 (1)	*PDPK1* NM_002613.4 (2)	*PDPK1* NM_002613.4 (7)
SNCAIP NM_005460.2 (2)	*SNCAIP* NM_005460.2 (11)	*EPHA7* NM_004440.3 (12)	*EPHA7* NM_004440.3 (9)	*EPHA7* NM_004440.3 (2)	*KIF5B* NM_004521.2 (20)
KIF5B NM_004521.2 (11)	*KIF5B* NM_004521.2 (8)	*KIF5B* NM_004521.2 (6)	*KIF5B* NM_004521.2 (5)	*KIF5B* NM_004521.2 (4)	*KIF5B* NM_004521.2 (3)
PGR NM_000926.4 (5)	*SOCS1* NM_003745.1 (2)	*FGFR3* NM_001163213.1 (2)	*PHF6* NM_001015877.1 (2)	*PHF6* NM_001015877.1 (3)	*PHF6* NM_001015877.1 (4)
PHF6 NM_001015877.1 (5)	*PHF6* NM_001015877.1 (6)	*PHF6* NM_001015877.1 (8)	*PHF6* NM_001015877.1 (9)	*PHF6* NM_001015877.1 (10)	
B2M NM_004048.2 (3)	*RAF1* NM_002880.3 (13)	*SOX17* NM_022454.3 (2)	*CEBPA* NM_004364.3 (1)	*MYCL* NM_001033082.2 (1)	*RANBP2* NM_006267.4 (1)
RANBP2 NM_006267.4 (2)	*RANBP2* NM_006267.4 (3)	*RANBP2* NM_006267.4 (4)	*RANBP2* NM_006267.4 (5)	*RANBP2* NM_006267.4 (6)	*RANBP2* NM_006267.4 (9)
RANBP2 NM_006267.4 (10)	*RANBP2* NM_006267.4 (11)	*RANBP2* NM_006267.4 (12)	*RANBP2* NM_006267.4 (14)	*RANBP2* NM_006267.4 (15)	*RANBP2* NM_006267.4 (16)

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RANBP2 NM_006267.4 (18)	***RANBP2*** NM_006267.4 (19)	***RANBP2*** NM_006267.4 (22)	***RANBP2*** NM_006267.4 (23)	***WISP3*** NM_198239.1 (4)	***BARD1*** NM_000465.2 (5)
BARD1 NM_000465.2 (2)	***BARD1*** NM_000465.2 (1)	***CENPA*** NM_001809.3 (1)	***KMT2B*** NM_014727.1 (1)	***KMT2B*** NM_014727.1 (16)	***MYCN*** NM_005378.4 (2)
PIK3C2G NM_004570.4 (4)	***PIK3C2G*** NM_004570.4 (5)	***PIK3C2G*** NM_004570.4 (7)	***PIK3C2G*** NM_004570.4 (8)	***PIK3C2G*** NM_004570.4 (9)	***PIK3C2G*** NM_004570.4 (10)
PIK3C2G NM_004570.4 (19)	***PIK3C2G*** NM_004570.4 (20)	***PIK3C2G*** NM_004570.4 (28)	***PIK3C2G*** NM_004570.4 (29)	***WT1*** NM_024426.4 (3)	***WT1*** NM_024426.4 (1)
BBC3 NM_014417.4 (3)	***BBC3*** NM_014417.4 (2)	***CHD2*** NM_001271.3 (11)	***CHD2*** NM_001271.3 (15)	***CHD2*** NM_001271.3 (27)	***CHD2*** NM_001271.3 (36)
KMT2C NM_170606.2 (30)	***KMT2C*** NM_170606.2 (28)	***KMT2C*** NM_170606.2 (24)	***KMT2C*** NM_170606.2 (23)	***KMT2C*** NM_170606.2 (22)	***KMT2C*** NM_170606.2 (21)
KMT2C NM_170606.2 (20)	***KMT2C*** NM_170606.2 (17)	***PIK3C3*** NM_002647.2 (5)	***PIK3C3*** NM_002647.2 (6)	***PIK3C3*** NM_002647.2 (7)	***PIK3C3*** NM_002647.2 (9)
PIK3C3 NM_002647.2 (11)	***PIK3C3*** NM_002647.2 (13)	***PIK3C3*** NM_002647.2 (18)	***PIK3C3*** NM_002647.2 (23)	***PIK3C3*** NM_002647.2 (25)	***RASA1*** NM_002890.2 (4)
RASA1 NM_002890.2 (5)	***RASA1*** NM_002890.2 (6)	***RASA1*** NM_002890.2 (7)	***RASA1*** NM_002890.2 (9)	***RASA1*** NM_002890.2 (10)	***RASA1*** NM_002890.2 (12)
RASA1 NM_002890.2 (14)	***RASA1*** NM_002890.2 (15)	***RASA1*** NM_002890.2 (19)	***RASA1*** NM_002890.2 (21)	***XIAP*** NM_001204401.1 (3)	***XIAP*** NM_001204401.1 (4)
XIAP NM_001204401.1 (5)	***XIAP*** NM_001204401.1 (6)	***XIAP*** NM_001204401.1 (7)	***ERCC2*** NM_000400.3 (10)	***ERCC2*** NM_000400.3 (1)	***FLT1*** NM_001160030.1 (1)
KMT2D NM_003482.3 (42)	***PIK3CA*** NM_006218.2 (12)	***PIK3CA*** NM_006218.2 (13)	***PIK3CA*** NM_006218.2 (14)	***PIK3CA*** NM_006218.2 (20)	***RB1*** NM_000321.2 (1)
RB1 NM_000321.2 (4)	***RB1*** NM_000321.2 (5)	***RB1*** NM_000321.2 (6)	***RB1*** NM_000321.2 (9)	***RB1*** NM_000321.2 (10)	***RB1*** NM_000321.2 (12)
RB1 NM_000321.2 (15)	***RB1*** NM_000321.2 (21)	***RB1*** NM_000321.2 (22)	***RB1*** NM_000321.2 (24)	***XPO1*** NM_003400.3 (13)	***XPO1*** NM_003400.3 (11)
XPO1 NM_003400.3 (8)	***XPO1*** NM_003400.3 (6)	***XPO1*** NM_003400.3 (4)	***CHEK1*** NM_001114121.2 (3)	***CHEK1*** NM_001114121.2 (5)	***CHEK1*** NM_001114121.2 (12)

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ERCC3 NM_000122.1 (1)	*FLT3* NM_004119.2 (1)	*HLA-A* NM_002116.7 (4)	*KRAS* NM_033360.2 (5)	*PIK3CB* NM_006219.2 (16)	*PIK3CB* NM_006219.2 (6)
RBM10 NM_001204467.1 (6)	*RBM10* NM_001204467.1 (9)	*RBM10* NM_001204467.1 (11)	*RBM10* NM_001204467.1 (12)	*RBM10* NM_001204467.1 (18)	
RBM10 NM_001204467.1 (4)	*SPTA1* NM_003126.2 (49)	*SPTA1* NM_003126.2 (47)	*SPTA1* NM_003126.2 (1)	*CHEK2* NM_001005735.1 (15)	*CHEK2* NM_001005735.1 (13)
CHEK2 NM_001005735.1 (9)	*CHEK2* NM_001005735.1 (8)	*CHEK2* NM_001005735.1 (6)	*ERCC4* NM_005236.2 (2)	*FLT4* NM_182925.4 (20)	*FLT4* NM_182925.4 (1)
LAMP1 NM_005561.3 (1)	*NBN* NM_002485.4 (16)	*NBN* NM_002485.4 (6)	*PIK3CD* NM_005026.3 (16)	*RECQL4* NM_004260.3 (3)	*RECQL4* NM_004260.3 (2)
RECQL4 NM_004260.3 (1)	*SRC* NM_005417.4 (4)	*CIC* NM_015125.3 (1)	*CIC* NM_015125.3 (20)	*NCOA3* NM_001174087.1 (16)	*NCOA3* NM_001174087.1 (23)
REL NM_002908.2 (1)	*REL* NM_002908.2 (4)	*REL* NM_002908.2 (6)	*REL* NM_002908.2 (8)	*YES1* NM_005433.3 (8)	*YES1* NM_005433.3 (5)
YES1 NM_005433.3 (3)	*CREBBP* NM_004380.2 (21)	*CREBBP* NM_004380.2 (11)	*ERG* NM_182918.3 (9)	*ERG* NM_182918.3 (8)	*ERG* NM_182918.3 (1)
FOXL2 NM_023067.3 (1)	*NCOR1* NM_006311.3 (15)	*NCOR1* NM_006311.3 (9)	*NCOR1* NM_006311.3 (8)	*NCOR1* NM_006311.3 (7)	*PIK3R1* NM_181523.2 (10)
PIK3R1 NM_181523.2 (11)	*PIK3R1* NM_181523.2 (7)	*RET* NM_020975.4 (1)	*STAG1* NM_005862.2 (34)	*STAG1* NM_005862.2 (20)	*STAG1* NM_005862.2 (12)
STAG1 NM_005862.2 (9)	*STAG1* NM_005862.2 (6)	*STAG1* NM_005862.2 (2)	*FOXO1* NM_002015.3 (1)	*HNRNPK* NM_002140.3 (17)	*HNRNPK* NM_002140.3 (14)
HNRNPK NM_002140.3 (7)	*LMO1* NM_002315.2 (1)	*PIK3R2* NM_005027.3 (2)	*PIK3R2* NM_005027.3 (4)	*PIK3R2* NM_005027.3 (6)	*RFWD2* NM_022457.5 (20)
RFWD2 NM_022457.5 (6)	*RFWD2* NM_022457.5 (1)	*STAG2* NM_001042749.1 (3)	*STAG2* NM_001042749.1 (4)	*STAG2* NM_001042749.1 (5)	*STAG2* NM_001042749.1 (6)
STAG2 NM_001042749.1 (7)	*STAG2* NM_001042749.1 (8)	*STAG2* NM_001042749.1 (9)	*STAG2* NM_001042749.1 (10)	*STAG2* NM_001042749.1 (11)	
STAG2 NM_001042749.1 (12)	*STAG2* NM_001042749.1 (13)	*STAG2* NM_001042749.1 (14)	*STAG2* NM_001042749.1 (15)	*STAG2* NM_001042749.1 (16)	

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STAG2 NM_001042749.1 (17)	*STAG2* NM_001042749.1 (18)	*STAG2* NM_001042749.1 (19)	*STAG2* NM_001042749.1 (20)	*STAG2* NM_001042749.1 (21)
STAG2 NM_001042749.1 (22)	*STAG2* NM_001042749.1 (23)	*STAG2* NM_001042749.1 (24)	*STAG2* NM_001042749.1 (25)	*STAG2* NM_001042749.1 (26)
STAG2 NM_001042749.1 (27)	*STAG2* NM_001042749.1 (28)	*STAG2* NM_001042749.1 (29)	*STAG2* NM_001042749.1 (30)	*STAG2* NM_001042749.1 (31)
STAG2 NM_001042749.1 (32)	*STAG2* NM_001042749.1 (33)	*STAG2* NM_001042749.1 (34)	*STAG2* NM_001042749.1 (35)	*BCOR* NM_001123385.1 (14)
BCOR NM_001123385.1 (13)	*BCOR* NM_001123385.1 (12)	*BCOR* NM_001123385.1 (6)	*BCOR* NM_001123385.1 (5)	*BCOR* NM_001123385.1 (3)
BCOR NM_001123385.1 (2)	*FOXP1* NM_032682.5 (16)	*LRP1B* NM_018557.2 (91)	*LRP1B* NM_018557.2 (88)	*LRP1B* NM_018557.2 (81)	*LRP1B* NM_018557.2 (77)
LRP1B NM_018557.2 (76)	*LRP1B* NM_018557.2 (75)	*LRP1B* NM_018557.2 (70)	*LRP1B* NM_018557.2 (58)	*LRP1B* NM_018557.2 (24)	*LRP1B* NM_018557.2 (17)
LRP1B NM_018557.2 (16)	*LRP1B* NM_018557.2 (15)	*LRP1B* NM_018557.2 (14)	*LRP1B* NM_018557.2 (13)	*LRP1B* NM_018557.2 (12)	*LRP1B* NM_018557.2 (11)
LRP1B NM_018557.2 (10)	*LRP1B* NM_018557.2 (9)	*LRP1B* NM_018557.2 (8)	*LRP1B* NM_018557.2 (7)	*LRP1B* NM_018557.2 (6)	*LRP1B* NM_018557.2 (5)
LRP1B NM_018557.2 (4)	*NF1* NM_001042492.2 (1)	*NF1* NM_001042492.2 (2)	*NF1* NM_001042492.2 (3)	*NF1* NM_001042492.2 (5)
NF1 NM_001042492.2 (7)	*NF1* NM_001042492.2 (11)	*NF1* NM_001042492.2 (13)	*NF1* NM_001042492.2 (15)	*NF1* NM_001042492.2 (16)
NF1 NM_001042492.2 (20)	*NF1* NM_001042492.2 (22)	*NF1* NM_001042492.2 (23)	*NF1* NM_001042492.2 (24)	*NF1* NM_001042492.2 (36)
NF1 NM_001042492.2 (31)	*PIK3R3* NM_001114172.1 (6)	*RHEB* NM_005614.3 (6)	*RHEB* NM_005614.3 (5)	*BCORL1* NM_021946.4 (7)	*NF2* NM_000268.3 (16)
STAT4 NM_001243835.1 (24)	*STAT4* NM_001243835.1 (19)	*STAT4* NM_001243835.1 (14)	*STAT4* NM_001243835.1 (12)	*STAT4* NM_001243835.1 (11)
ZNF217 NM_006526.2 (4)	*ZNF217* NM_006526.2 (2)	*BCR* NM_004327.3 (7)	*BCR* NM_004327.3 (18)	*BCR* NM_004327.3 (20)	*CSF3R* NM_156039.3 (7)

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FUBP1 NM_003902.3 (20)	*FUBP1* NM_003902.3 (7)	*FUBP1* NM_003902.3 (5)	*FUBP1* NM_003902.3 (4)	*FUBP1* NM_003902.3 (3)	*FUBP1* NM_003902.3 (2)
LZTR1 NM_006767.3 (14)	*NFE2L2* NM_006164.4 (1)	*RICTOR* NM_152756.3 (11)	*RICTOR* NM_152756.3 (9)	*RICTOR* NM_152756.3 (2)	*STAT5A* NM_003152.3 (8)
STAT5A NM_003152.3 (9)	*BIRC3* NM_001165.4 (5)	*BIRC3* NM_001165.4 (8)	*CSNK1A1* NM_001025105.2 (8)	*MAGI2* NM_012301.3 (22)	*MAGI2* NM_012301.3 (21)
MAGI2 NM_012301.3 (20)	*MAGI2* NM_012301.3 (18)	*MAGI2* NM_012301.3 (14)	*MAGI2* NM_012301.3 (13)	*MAGI2* NM_012301.3 (11)	*MAGI2* NM_012301.3 (7)
MAGI2 NM_012301.3 (6)	*MAGI2* NM_012301.3 (5)	*MAGI2* NM_012301.3 (4)	*STAT5B* NM_012448.3 (8)	*STAT5B* NM_012448.3 (7)	*STAT5B* NM_012448.3 (6)
ZRSR2 NM_005089.3 (1)	*ZRSR2* NM_005089.3 (2)	*ZRSR2* NM_005089.3 (3)	*ZRSR2* NM_005089.3 (4)	*ZRSR2* NM_005089.3 (5)	*ZRSR2* NM_005089.3 (6)
ZRSR2 NM_005089.3 (7)	*ZRSR2* NM_005089.3 (9)	*ZRSR2* NM_005089.3 (11)	*BLM* NM_000057.2 (4)	*BLM* NM_000057.2 (6)	*BLM* NM_000057.2 (10)
BLM NM_000057.2 (13)	*BLM* NM_000057.2 (16)	*BLM* NM_000057.2 (17)	*GABRA6* NM_000811.2 (6)	*ICOSLG* NM_015259.4 (1)	*MALT1* NM_006785.3 (1)
MALT1 NM_006785.3 (7)	*MALT1* NM_006785.3 (8)	*MALT1* NM_006785.3 (9)	*MALT1* NM_006785.3 (11)	*MALT1* NM_006785.3 (13)	*MALT1* NM_006785.3 (15)
NKX2-1 NM_001079668.2 (3)	*PMAIP1* NM_021127.2 (1)	*STK11* NM_000455.4 (3)	*STK11* NM_000455.4 (5)	*STK11* NM_000455.4 (7)	*BMPR1A* NM_004329.2 (7)
BMPR1A NM_004329.2 (9)	*BMPR1A* NM_004329.2 (10)	*BMPR1A* NM_004329.2 (11)	*GATA1* NM_002049.3 (2)	*GATA1* NM_002049.3 (6)	*NKX3-1* NM_006167.3 (1)
PMS1 NM_000534.4 (5)	*PMS1* NM_000534.4 (8)	*PMS1* NM_000534.4 (9)	*PMS1* NM_000534.4 (11)	*PMS1* NM_000534.4 (12)	*ROS1* NM_002944.2 (34)
ROS1 NM_002944.2 (28)	*ROS1* NM_002944.2 (22)	*ROS1* NM_002944.2 (3)	*BRAF* NM_004333.4 (1)	*IDH1* NM_005896.2 (10)	*NOTCH1* NM_017617.3 (1)
PMS2 NM_000535.5 (13)	*PMS2* NM_000535.5 (3)	*RPS6KA4* NM_003942.2 (16)	*RPS6KA4* NM_003942.2 (17)	*SUFU* NM_016169.3 (1)	*BRCA1* NM_007300.3 (19)
BRCA1 NM_007300.3 (8)	*BRCA1* NM_007300.3 (4)	*BRCA1* NM_007300.3 (3)	*IDH2* NM_002168.2 (1)	*MAP2K4* NM_001281435.1 (1)	*MAP2K4* NM_001281435.1 (2)

PATIENT	DOB	DISEASE	MRN	REPORT DATE	REPORT STATUS
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MAP2K4 NM_001281435.1 (6)	*MAP2K4* NM_001281435.1 (7)	*MAP2K4* NM_001281435.1 (11)	*RPS6KB1* NM_003161.3 (6)	*RPS6KB1* NM_003161.3 (13)	*SUZ12* NM_015355.2 (2)
SUZ12 NM_015355.2 (4)	*SUZ12* NM_015355.2 (5)	*SUZ12* NM_015355.2 (6)	*SUZ12* NM_015355.2 (9)	*SUZ12* NM_015355.2 (11)	*SUZ12* NM_015355.2 (15)
BRCA2 NM_000059.3 (5)	*BRCA2* NM_000059.3 (8)	*BRCA2* NM_000059.3 (12)	*CUL3* NM_003590.4 (9)	*GATA4* NM_002052.3 (2)	*IFNGR1* NM_000416.2 (6)
IFNGR1 NM_000416.2 (5)	*IFNGR1* NM_000416.2 (3)	*MAP3K1* NM_005921.1 (1)	*MAP3K1* NM_005921.1 (5)	*MAP3K1* NM_005921.1 (8)	*NOTCH3* NM_000435.2 (24)
NOTCH3 NM_000435.2 (1)	*RPS6KB2* NM_003952.2 (1)				

METHODOLOGY

Sample Assessment: A tissue block, stained cytology slide, or blood sample was used to assess adequacy and then the technical component of the testing passed all established laboratory QC metrics.
Assay Methods: This test uses the TruSight™ Oncology 500 (TSO500) targeted hybrid-capture based next generation sequencing assay that utilizes UMIs to enable detection of variants present in tumor samples at low VAFs with a high degree of sensitivity and specificity. TSO500 is designed to detect multiple classes of mutations including single-nucleotide variants (SNVs), multi-nucleotide variants (<3bp), small Insertions (1-18bp) /Deletions (1-27bp), and is also capable of assessing both microsatellite instability (MSI) and tumor mutational burden (TMB). In parallel, fusions and splice variants can also be detected in certain targeted genes from the same sample, using extracted RNA and an integrated TruSight Tumor 170 RNA workflow. DNA and RNA extracted from the appropriate sample and were prepared into sheared DNA and cDNA. The regions of interest for DNA and RNA were hybridized to biotinylated probes using the Trusight Oncology 500 (Illumina, Inc) and Trusight Tumor 170 (Illumina, Inc) library prep kits, respectively. The probes with the hybridized DNA and cDNA were magnetically pulled down with streptavidin-coated beads and eluted to enrich the library pool. Libraries were normalized, then pooled and sequenced on an Illumina NextSeq 500 instrument.
Secondary Analysis Methods: DNA and RNA Data were analyzed using the Illumina TSO500 Local App Software v1.3.1 and TST170 Local App Software v1.0.1, respectively, and a customized analysis pipeline within the Clinical Genomics Workspace software platform from PierianDx.
Variant Calling: Variants are reported according to HGVS nomenclature (www.hgvs.org/mutnomen) and classified as per the AMP classification system into tiers IA, IB, IIC, IID, III and IV. These tiers are stratified by clinical utility and previously reported data in the medical literature. Variations found in gnomAD (https://gnomad.broadinstitute.org/) that have ≥1% minor allele frequency (except those that are also in Clinvar denoted as clinically relevant, used in a clinical diagnostic assay, or reported as a mutation in a publication) are classified as known polymorphisms.
TMB and MSI: Both TMB and MSI were comprehensively validated by Illumina Inc.
Gene Fusions and Splice Variants: Illumina's TST170 secondary analysis pipeline reports high confidence fusions and splice variants. Several reference standards and clinical samples containing known fusions and splice variants were evaluated using the TruSight Tumor 170 assay and secondary analysis software. 100% concordance of expected fusion and splice variants was observed.

DISCLAIMER

This Report was generated using the materials and methods described above, which required the use of various reagents, protocols, instruments, software, databases, and other items.
The Report has been created based on, or incorporates references 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. PierianDx 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 of information. If any 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. PierianDx is not obligated to notify you of any impact that future scientific or medical research 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 to a patient or developing and implementing a plan of care for a patient. The manifestation 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 (or that are otherwise unknown). This Report is based on a next generation sequencing assay which does not distinguish between somatic and germline variants. If a germline variant is in question, further testing may be recommended. As such, the relevance of the Report should be interpreted in the context of a patient's clinical manifestations. The Report provided by PierianDx is provided on an "AS IS" basis. PierianDx makes no representation or warranty of any kind, expressed or implied, regarding the Report. In no event shall PierianDx 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 annotation is constantly updated and reflects the current knowledge at the time.

The test performance characteristics were determined by the Molecular Diagnostic Laboratory at Pi. The test performance characteristics were determined by the PierianDx Molecular Laboratory. The Report was generated by the PierianDx Molecular 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 U.S. Food and Drug Administration (FDA). The FDA has determined that such clearance or approval is not necessary. The test results have been shown to be clinically useful. This laboratory is CLIA certified to perform high complexity testing.

PATIENT AND ORDER DETAILS

PATIENT

SAMPLE ID

DATE OF BIRTH
05/15/1953

SEX

ETHNICITY

RACE

PHYSICIAN

ORDERING PHYSICIAN
Dr Dr

FACILITY
Research Genetic Cancer Centre International GmbH (RGCC)

SPECIMEN

SPECIMEN TYPE
Formalin-fixed paraffin-embedded tissue specimen

EXT. SPECIMEN ID

DATE COLLECTED
11/08/2022

DATE RECEIVED
04/07/2024

% TUMOR IN SELECTED AREA

CASE

REVIEW STATUS
Final

DATE ACCESSIONED
04/08/2024 10:50

DATE REPORTED

ACCESSION NUMBER
RGCC_Panel_Update_UR