THE UNIVERSITY OF TEXAS MD Anderson Cancer Center
Making Cancer History®

The University of Texas MD Anderson Cancer Center
1515 Holcombe Blvd., Houston, TX 77030

Print Date: 12/18/2020 15:30 CST
Location: MN Molecular Diag
Ordering: GONZALEZ PA,CIPRIANO C

Name: XXXXXX
MRN: XXXXXX
DOB/Age/Sex: X/XX/XXXX 60 years Female

Molecular Diagnostics

MD-20-124975

Solid Tumor Genomic Assay-DNA Report

Accession: MD-XX-XXXXX
Collection Date: 05/05/2020
Received In-lab Date: 11/25/2020 2:13 PM
Specimen Type: FFPE Slides
Pathology Accession for Source Material: XXX-XXXXXX 5 Outside Accession: XXX-XXXX
Histologic Diagnosis for Source Material (refer to source accession for details): Salivary carcinoma with myoepithelial differentiation
Control Source: PB

NAME XXXXX MRN XXXXXX MDL XXXXXXX

Solid Tumor Genomic Assay 2018 - DNA

Clinical test requisition for mutation studies on the following genes was received: *AKT1*, *BRAF*, *CDKN2A*

A next generation sequencing (NGS)-based analysis for the detection of somatic mutations in the coding sequence of 134 genes and selected copy number variations (amplifications) in 47 genes (overlap: 146 genes total) was performed on the DNA extracted from the sample in our CLIA-certified molecular diagnostics laboratory. Interpretative findings are reported in the gene summary table(s) below followed by specific details of detected sequence and/or copy number variants.

Interpretation Key:

Circled/Bold:	Mutation and/or amplification detected
Underlined:	Testing requested (ordered gene)
Asterisk:	Additional confirmation studies in progress

GENE SUMMARY:

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AKT1	*BTK*	*CREBBP*	*FGF19*	*HRAS*	*MAPK1*	*NBN*	*PIK3CB*	*RAF1*	*SPOP*
AKT2	*CBL*	*CSF1R*	*FGF3*	*IDH1*	*MAX*	*NF1*	*PIK3R1*	*RB1*	*SRC*
AKT3	*CCND1*	*CTNNB1*	*FGFR1*	*IDH2*	*MDM2*	*NF2*	*PMS2*	*RET*	*STAT3*
ALK	*CCND2*	*DDR2*	*FGFR2*	*IGF1R*	*MDM4*	*NFE2L2*	*POLE*	*RHEB*	*STK11*
AR	*CCND3*	*EGFR*	*FGFR3*	*JAK1*	*MED12*	*NOTCH1*	*PPARG*	*RHOA*	*TERT*
ARAF	*CCNE1*	*ERBB2*	*FGFR4*	*JAK2*	*MET*	*NOTCH2*	*PPP2R1A*	*RICTOR*	*TOP1*
ARID1A	*CDK12*	*ERBB3*	*FLT3*	*JAK3*	*MLH1*	***NOTCH3***	*PTCH1*	*RNF43*	***TP53***
ATM	*CDK2*	*ERBB4*	*FOXL2*	*KDR*	*MRE11A*	*NRAS*	*PTEN*	*ROS1*	*TSC1*
ATR	*CDK4*	*ERCC2*	*GATA2*	*KIT*	*MSH2*	*NTRK1*	*PTPN11*	*SETD2*	*TSC2*
ATRX	*CDK6*	*ESR1*	*GNA11*	*KNSTRN*	*MSH6*	*NTRK2*	*RAC1*	*SF3B1*	*U2AF1*
AXL	*CDKN1B*	*EZH2*	*GNAQ*	*KRAS*	*MTOR*	*NTRK3*	*RAD50*	*SLX4*	*XPO1*
BAP1	*CDKN2A*	*FANCA*	*GNAS*	*MAGOH*	*MYC*	*PALB2*	*RAD51*	*SMAD4*	
BRAF	*CDKN2B*	*FANCD2*	*H3F3A*	*MAP2K1*	*MYCL*	*PDGFRA*	*RAD51B*	*SMARCA4*	
BRCA1	*CHEK1*	*FANCI*	*HIST1H3B*	*MAP2K2*	*MYCN*	*PDGFRB*	*RAD51C*	*SMARCB1*	
BRCA2	*CHEK2*	*FBXW7*	*HNF1A*	*MAP2K4*	*MYD88*	*PIK3CA*	*RAD51D*	*SMO*	

FINDINGS:

Copy Number Variations
None identified

Somatic Mutations***

Gene	Standardized Nomenclature (HGVS)	Location	DNA change	Protein change	COSMIC ID	VAF*
NOTCH3	NM_000435.2(NOTCH3):c.5086C>T p.P1696S	Exon 27	SNV	Missense		4.3%
TP53	NM_000546.5(TP53):c.702C>G p.Y234*	Exon 7	SNV	Nonsense	COSM44785	6%

*** These mutations are present at low allelic frequencies compared to estimated tumor cellularity. The assay was repeated twice.* VAF, variant allele frequency

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GUIDE TO STANDARDIZED NOMENCLATURE AND EXPLANATION OF CHANGES:

Mutations identified are described using an implementation of a standardized nomenclature developed by the Human Genome Variation Society (HGVS, <http://www.hgvs.org/mutnomen/>).

The normative Genbank gene reference sequence identifier and gene symbol in parentheses are provided, followed by the coding DNA sequence change (e.g., "c. 200A>G", which would mean that the position 200 adenine is changed to guanine), and then the inferred protein change (e.g., "p. V35C", which would mean that the amino acid at codon 35 is changed from valine to cysteine).

Additional explanations for the DNA and protein changes seen in the current specimen are shown in the following tables:

Explanation of DNA variant/mutation types seen in this specimen

DNA Change	
SNV	A single nucleotide difference (point mutation) has been identified in the patient sample relative to the reference wild-type gene sequence

Explanation of protein variant/mutation types seen in this specimen

Protein Change	
Missense	A single amino acid residue change in the patient sample relative to the reference wild-type protein sequence
Nonsense	A single nucleotide change resulting in a premature stop codon leading to a truncated protein product in the patient sample relative to the reference wild-type protein sequence

ADDITIONAL INFORMATION ON GENES WITH FINDINGS IDENTIFIED ON THIS ASSAY

NOTCH3	http://www.genenames.org/data/hgnc_data.php?hgnc_id=7883
TP53	http://www.genenames.org/data/hgnc_data.php?hgnc_id=11998

METHODOLOGY:

Test Platform: PCR-based sequencing is performed using a next generation sequencing (NGS) platform on genomic DNA to screen for mutations and copy number amplifications in the coding sequences of genes listed below. NGS sequencing analysis of these genes was further confirmed by other platforms during validation in our CLIA-certified molecular diagnostics laboratory. The genomic reference sequence used is GRCh37/hg19. Detailed information about

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the signal-processing, base calling, alignment, variant calling, and copy number calling algorithms are available upon request.

Analytical sensitivity and additional details: For this assay, sensitivity of detection is related in part to depth of coverage, tumor percentage, and allelic frequency for the mutation. Although the NGS platform is capable of achieving a much higher analytical sensitivity; for clinical purposes, we determined the effective lower limit of detection of this assay (analytical sensitivity) for single nucleotide variations to be in the range of 5% (one mutant allele in the background of nineteen wild type alleles) to 10% (one mutant allele in the background of nine wild type alleles) by taking into consideration the depth of coverage at a given base and the ability to confirm low level mutations using independent conventional platforms. Sensitivity for amplifications depends on both input tumor percentage and the amplitude of the gene amplification. We require a minimum of 20% tumor nuclei in the sample to reduce the potential for false-negative results. The analytic pipeline in this assay attempts to normalize for inter-amplicon performance differences and total sample loading, but does not attempt to correct for tumor percentage. A nominal threshold of 7 for the estimated copy number is used to restrict reporting to high-confidence amplification calls.

Details and limitations of the test:

- Matched non-tumor tissue from this patient has been tested and germline variants have been excluded.
- The primary purpose of this panel is to detect somatic mutations in genes involved in oncogenesis of this patient's tumor. This panel is not designed to detect germline variants for familial tumors, and the test or results thereof should not be used to detect germline variants for hereditary cancer syndromes.
- The assay is designed to detect point mutations, small insertion/deletions, and copy number gains (amplifications).
- Variants detected at very low allelic frequencies not deemed to be confirmable by independent, orthogonal methods and/or in significant discordance with the percentage of tumor in the tested sample may be excluded as the clinical significance and reliability of such low level variant calls is not clear.
- Copy number assessment by next generation sequencing can be affected by tumor percentage, amplitude of gene amplification, enrichment of tumor during pre-analytical phase, library preparation methods and analysis algorithms. False negative results can be obtained in cases with low tumor percentage, low amplicon coverage and/or borderline copy number gains. Correlation with traditional methods of copy number assessment such as fluorescent in situ hybridization (FISH) is recommended as applicable

Report annotation and generation software: A post-variant calling analysis and annotation tool, OncoSeek version 1.8.1.490, was used in the construction of this report.

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Sequencing coverage of the genes: The following table describes adequacy of coverage in this assay across the full set of covered genes, exons, and codons, for genes with exon-level sequencing on this assay. Adequately covered amplicons are defined as those having total coverage depth of greater than or equal to 250 reads, or for which an orthogonal mutation analysis testing has been performed. Presence of mutations outside the tested regions listed below cannot be ruled out.

Coverage by gene and codon(s) tested for adequate amplicons

Gene	Exons (codons) tested
AKT1 (NM_005163)	3 (16-56), 4 (59-96), 6 (146-149), 6-7 (177-195), 9 (235-274), 11 (320-380), 12 (391-411), 13 (450-455), 14 (459-481)
AKT2 (NM_001626)	3 (16-55), 4 (76-96), 6 (148-153), 7 (192-210), 8 (221-236), 10 (278-279), 11 (322-381), 12 (395-421), 14 (456-482)
AKT3 (NM_005465)	2 (16-28), 2 (48-58), 3 (66-95), 4 (123-143), 6 (188-209), 8 (233-267), 10 (317-367), 11 (388-399)
ALK (NM_004304)	20-28 (1096-1388)
AR (NM_000044)	1 (1-45), 1 (135-178), 1 (245-285), 1 (342-388), 3 (615-629), 4 (707-725), 6-7 (797-831), 8 (870-910)
ARAF (NM_001654)	7 (186-216)
ARID1A (NM_006015)	1 (28-73), 1 (106-151), 1-8 (161-838), 8-20 (861-2062), 20 (2081-2286)
ATM (NM_000051)	2-17 (1-865), 18-19 (880-974), 20-25 (1001-1249), 26 (1258-1283), 26-44 (1292-2136), 44-46 (2146-2262), 47-49 (2270-2389), 49-51 (2414-2542), 52-54 (2544-2667), 55 (2671-2711), 56-57 (2718-2806), 58-63 (2823-3028), 63 (3041-3057)
ATR (NM_001184)	1-5 (1-450), 6-8 (458-582), 8 (584-629), 9-13 (636-882), 13-15 (896-1052), 16-19 (1058-1237), 20 (1242-1262), 21-27 (1274-1618), 28-29 (1628-1692), 29-34 (1705-1965), 35-38 (1967-2184), 39-40 (2187-2296), 41-47 (2300-2645)
ATRX (NM_000489)	1-8 (1-221), 9-11 (257-1301), 12-16 (1315-1562), 17-18 (1567-1644), 19-21 (1653-1766), 21-28 (1785-2108), 29-35 (2117-2493)
AXL (NM_001699)	1 (1-29), 3 (103-137), 6 (223-261), 7 (288-332), 8 (351-378), 9 (386-429), 11 (473-497), 12 (516-536), 15 (593-633), 17 (670-686), 19 (769-782)
BAP1 (NM_004656)	1-17 (6-730)
BRAF (NM_004333)	11-18 (439-722)
BRCA1 (NM_007294)	2-7 (1-183), 8-23 (191-1864)
BRCA2 (NM_000059)	2-10 (1-280), 10-27 (294-3419)
BTK (NM_000061)	7 (174-196), 15 (457-498)
CBL (NM_005188)	8-9 (366-435), 9 (446-477)
CCND1 (NM_053056)	1 (1-10), 1-2 (14-81), 2 (91-138), 3 (142-192), 4-5 (199-291)
CCND2 (NM_001759)	1-2 (1-80), 2-3 (116-191), 4-5 (195-282)
CCND3 (NM_001760)	1-2 (53-122), 3 (139-180), 4 (192-237), 5 (250-293)
CCNE1 (NM_001238)	4-5 (39-92), 6-9 (127-258), 11-12 (348-411)
CDK12 (NM_016507)	1 (1-42), 1-14 (71-1491)

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CDK2 (NM_001798)	1-2 (1-45), 4 (106-153), 5-6 (163-228), 6-7 (252-297)
CDK4 (NM_000075)	2-3 (17-116), 4 (119-163), 5-6 (175-228), 7-8 (268-304)
CDK6 (NM_001259)	2 (7-75), 3 (78-86), 3 (104-123), 4 (136-179), 5 (183-216), 6 (221-233), 7-8 (236-287), 8 (315-327)
CDKN1B (NM_004064)	1-2 (1-199)
CDKN2A (NM_000077)	1-2 (1-90), 2 (98-140), 2-3 (143-157)
CDKN2B (NM_004936)	1-2 (1-139)
CHEK1 (NM_001274)	2-10 (1-334), 10-13 (363-477)
CHEK2 (NM_007194)	11 (366-420), 15 (515-544)
CREBBP (NM_004380)	1-3 (1-325), 4-5 (356-444), 6-31 (476-1933), 31 (1961-2443)
CSF1R (NM_005211)	7 (297-319), 11 (517-542), 22 (963-973)
CTNNB1 (NM_001904)	3 (5-67), 7 (327-361)
DDR2 (NM_006182)	5 (97-139), 8 (228-279), 13-18 (540-856)
EGFR (NM_005228)	3 (84-125), 7 (281-297), 12 (452-494), 15 (582-625), 18-20 (688-801), 20-24 (807-977)
ERBB2 (NM_004448)	8 (301-327), 17 (649-680), 18-24 (696-990)
ERBB3 (NM_001982)	2-3 (48-118), 6 (207-243), 7-8 (270-326), 9 (330-350), 23 (898-934)
ERBB4 (NM_005235)	12 (437-478), 17 (649-671), 18 (694-726), 20 (781-823), 28 (1194-1236)
ERCC2 (NM_000400)	3 (36-47), 5 (84-114), 8 (223-240), 15 (460-492), 21 (658-682)
ESR1 (NM_000125)	1 (1-42), 1 (53-99), 2 (184-215), 3 (232-254), 4 (268-340), 5 (367-412), 7 (457-518), 8 (532-574)
EZH2 (NM_004456)	16 (639-649), 18 (677-704)
FANCA (NM_000135)	1-43 (1-1456)
FANCD2 (NM_033084)	2-15 (1-409), 15-19 (423-589), 21-28 (610-904), 29 (906-927), 29-43 (948-1472)
FANCI (NM_018193)	2-37 (1-1269)
FBXW7 (NM_033632)	2-4 (1-242), 5-9 (255-473), 10 (478-509), 10-12 (522-708)
FGF19 (NM_005117)	1 (1-33), 2-3 (78-217)
FGF3 (NM_005247)	1-3 (1-217), 3 (229-240)
FGFR1 (NM_015850)	4 (120-148), 6 (217-247), 8 (311-355), 9 (408-426), 12 (516-553), 14 (642-657), 16 (709-727), 18 (786-821)
FGFR2 (NM_000141)	6 (209-235), 7 (250-273), 7-8 (277-350), 9 (362-399), 10 (453-480), 12 (521-558), 13 (589-621), 14-15 (631-686), 16 (699-730), 18 (768-804)
FGFR3 (NM_000142)	2 (1-37), 4 (127-133), 8 (329-359), 9 (368-412), 10 (423-439), 14 (633-653), 15-16 (659-719)
FGFR4 (NM_022963)	1 (1-31), 2 (72-116), 4 (163-199), 6 (243-283), 8 (359-392), 10-11 (467-535), 13 (609-632), 15 (683-713)
FLT3 (NM_004119)	3 (93-123), 6 (205-213), 8 (302-346), 10 (402-435), 12 (502-533), 15 (613-648), 18 (742-764), 20-21 (808-885), 24 (957-994)
FOXL2 (NM_023067)	1 (94-137)
GATA2 (NM_032638)	4 (291-330), 5 (341-379), 6 (452-481)
GNA11 (NM_002067)	4 (165-196), 5 (205-240)
GNAQ (NM_002072)	2 (60-100), 4-5 (163-224)

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GNAS (NM_000516)	8 (196-218), 9 (220-240)
H3F3A (NM_002107)	2 (1-36)
HIST1H3B (NM_003537)	1 (6-37), 1 (61-102)
HNF1A (NM_000545)	2 (109-116), 3 (196-238)
HRAS (NM_005343)	2 (6-34), 3 (44-87), 4 (97-150)
IDH1 (NM_005896)	4 (100-138)
IDH2 (NM_002168)	4 (125-155), 4 (162-178)
IGF1R (NM_000875)	1 (1-32), 2 (138-176), 4 (318-328), 6 (416-457), 8 (572-608), 10 (674-711), 12 (829-865), 14 (928-946), 17 (1063-1099), 20 (1196-1220)
JAK1 (NM_002227)	14 (634-663), 15-16 (668-743)
JAK2 (NM_004972)	14 (600-622)
JAK3 (NM_000215)	11-12 (502-563), 15 (639-683)
KDR (NM_002253)	11 (482-512), 16 (766-791), 23 (1026-1064), 24 (1082-1102)
KIT (NM_000222)	8 (411-445), 9 (487-514), 10-20 (516-934)
KNSTRN (NM_033286)	1 (1-28)
KRAS (NM_004985)	2-3 (1-93), 4-5 (97-189)
MAGOH (NM_002370)	5 (114-147)
MAP2K1 (NM_002755)	2 (27-96), 3 (98-135), 6 (190-227), 11 (357-394)
MAP2K2 (NM_030662)	3 (102-123)
MAP2K4 (NM_003010)	4 (132-154), 5 (178-208)
MAPK1 (NM_002745)	7 (300-322)
MAX (NM_002382)	3 (22-56), 4 (58-83)
MDM2 (NM_002392)	2 (22-33), 3 (51-58), 4 (79-103), 7 (160-175), 8 (198-228), 9 (236-267), 10 (289-306), 11 (340-373), 11 (406-439)
MDM4 (NM_002393)	2 (1-17), 3 (27-50), 5-6 (96-137), 7 (158-171), 8 (212-224), 9 (229-269), 11 (302-334), 11 (348-386), 11 (428-459)
MED12 (NM_005120)	2 (34-59), 26 (1199-1227)
MET (NM_001127500)	2 (151-192), 2 (217-257), 2 (287-331), 2 (344-384), 14 (981-989), 14-21 (1003-1367)
MLH1 (NM_000249)	1-19 (1-757)
MRE11A (NM_005590)	2 (1-7), 3-19 (20-681)
MSH2 (NM_000251)	1-4 (1-259), 5 (265-307), 6-10 (315-521), 11-15 (554-852), 16 (879-935)
MSH6 (NM_000179)	1-10 (1-1361)
MTOR (NM_004958)	29 (1418-1443), 30 (1452-1490), 31 (1509-1524), 39 (1789-1803), 40 (1876-1905), 43 (1971-1994), 43-44 (1999-2035), 47-48 (2187-2251), 53 (2394-2434), 56-57 (2483-2520)
MYC (NM_002467)	1-2 (1-87), 2 (98-131), 2 (140-185), 2 (196-226), 3 (268-278), 3 (297-340), 3 (352-395), 3 (413-453)
MYCL (NM_005376)	2 (60-96), 2 (163-237)
MYCN (NM_005378)	2 (1-125), 2-3 (229-349), 3 (371-450)
MYD88 (NM_002468)	3 (181-221), 5 (259-269)

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NBN (NM_002485)	1-5 (1-166), 6-16 (200-755)
NF1 (NM_001042492)	1-16 (1-596), 17-23 (616-1038), 25-58 (1071-2840)
NF2 (NM_000268)	1-10 (1-332), 11-16 (334-596)
NFE2L2 (NM_006164)	2 (23-59), 2 (74-104)
NOTCH1 (NM_017617)	2-27 (21-1680), 27 (1686-1723), 28-34 (1736-2116), 34 (2145-2556)
NOTCH2 (NM_024408)	1 (1-25), 3 (68-131), 4 (139-191), 4-34 (193-2472)
NOTCH3 (NM_000435)	1-2 (16-48), 3-18 (66-959), 18-24 (969-1292), 24 (1414-1449), 25-26 (1468-1631), 27-33 (1659-2153), 33 (2163-2322)
NRAS (NM_002524)	2 (1-22), 3 (49-89), 4 (110-150)
NTRK1 (NM_002529)	2 (71-92), 3 (106-120), 6 (192-227), 8 (321-393), 11 (418-446), 14 (553-599), 15 (658-682), 17 (747-790)
NTRK2 (NM_006180)	4 (1-43), 6 (96-120), 9 (197-239), 11 (294-366), 14 (433-466), 16 (490-531), 17 (580-588), 18 (601-641), 19 (674-723), 20 (725-756)
NTRK3 (NM_002530)	7 (155-161), 10 (303-318), 10 (377-402), 13 (432-456), 14 (472-518), 16 (576-630), 17 (662-711), 19 (808-826)
PALB2 (NM_024675)	1-3 (1-71), 4-6 (79-862), 7-13 (888-1187)
PDGFRA (NM_006206)	12-15 (552-719), 17-21 (775-960)
PDGFRB (NM_002609)	2 (1-14), 3 (99-122), 5 (211-235), 7 (333-370), 9 (450-456), 11 (527-545), 12-13 (587-638), 16 (753-782), 19 (881-900), 22 (969-1009), 23 (1093-1107)
PIK3CA (NM_006218)	2 (1-5), 2-3 (77-138), 5 (311-351), 8 (418-457), 10-11 (532-582), 14 (693-729), 21 (1015-1057)
PIK3CB (NM_006219)	1 (31-57), 3 (138-174), 5 (268-294), 7 (400-434), 10 (518-527), 11 (545-586), 14 (679-683), 16 (784-809), 20 (933-954), 22 (1026-1071)
PIK3R1 (NM_181523)	2-11 (1-437), 11-16 (440-725)
PMS2 (NM_000535)	1-2 (1-30), 2-5 (35-165), 6-11 (180-657), 12 (669-680), 12-13 (716-726), 15 (855-863)
POLE (NM_006231)	1-36 (1-1531), 36-46 (1540-2177), 47-49 (2217-2287)
PPARG (NM_015869)	1 (1-28), 2 (53-78), 3 (104-134), 3 (152-160), 4 (169-200), 5 (207-228), 5 (257-273), 6 (282-321), 6 (350-390), 7 (424-461)
PPP2R1A (NM_014225)	5 (172-199), 6 (220-263)
PTCH1 (NM_000264)	1-23 (6-1344), 23 (1374-1448)
PTEN (NM_000314)	1-9 (1-382)
PTPN11 (NM_002834)	3 (52-91), 13 (485-527)
RAC1 (NM_006908)	2 (18-36)
RAD50 (NM_005732)	1-5 (1-244), 6-9 (253-478), 10 (485-545), 11-12 (553-657), 13-16 (681-902), 17-19 (907-980), 19-23 (987-1206), 24-25 (1212-1313)
RAD51 (NM_002875)	2-4 (1-115), 5-10 (121-340)
RAD51B (NM_133509)	2-5 (1-113), 5-7 (142-245), 8-11 (253-374)
RAD51C (NM_002876)	1-2 (1-136)
RAD51D (NM_133629)	1-7 (1-217)
RAF1 (NM_002880)	7 (235-276), 12 (407-442)
RB1 (NM_000321)	1-2 (1-85), 3-4 (89-159), 5-6 (167-194), 6-15 (196-464), 16-18 (480-582), 18-21 (587-736), 22-27 (743-929)

THE UNIVERSITY OF TEXAS MD Anderson Cancer Center
Making Cancer History®

The University of Texas MD Anderson Cancer Center
1515 Holcombe Blvd., Houston, TX 77030

Print Date: 12/18/2020 15:30 CST
Location: MN Molecular Diag
Ordering: GONZALEZ PA,CIPRIANO C

Name: XXXXXX
MRN: XXXXXX
DOB/Age/Sex: X/XX/XXXX 60 years Female

Molecular Diagnostics

RET (NM_020975)	10-11 (609-654), 12-14 (713-869), 15-18 (875-1013)
RHEB (NM_005614)	2 (18-42)
RHOA (NM_001664)	2 (2-44)
RICTOR (NM_152756)	7 (153-175), 10 (291-297), 16 (462-467), 21 (658-684), 26 (834-863), 30 (981-1019), 31 (1210-1246), 32 (1382-1416), 35 (1588-1597), 38 (1690-1709)
RNF43 (NM_017763)	2-9 (1-442), 9-10 (455-784)
ROS1 (NM_002944)	36-38 (1926-2045), 39-40 (2050-2092), 40-42 (2106-2245)
SETD2 (NM_014159)	1-11 (1-1799), 12-21 (1809-2565)
SF3B1 (NM_012433)	14 (603-640), 14 (655-679), 15 (693-716), 15-16 (738-747)
SLX4 (NM_032444)	2-12 (1-1477), 12-15 (1493-1835)
SMAD4 (NM_005359)	9 (335-375), 10 (380-401), 12 (519-553)
SMARCA4 (NM_003072)	2-12 (1-644), 13-15 (648-756), 16-19 (759-936), 20-25 (954-1162), 26-35 (1183-1648)
SMARCB1 (NM_003073)	1-2 (1-72), 3-5 (78-206), 6-9 (210-386)
SMO (NM_005631)	3 (186-228), 4-5 (263-354), 6 (397-422), 9 (511-551), 11 (608-646)
SPOP (NM_003563)	5 (88-118), 6 (125-160)
SRC (NM_005417)	12 (374-418)
STAT3 (NM_139276)	13 (398-411), 20 (583-620), 21 (630-667)
STK11 (NM_000455)	1-8 (1-361), 9 (370-434)
TERT (NM_198253)	1 (1-18), 2 (267-310), 2 (394-425), 3 (553-585), 4 (626-650), 6 (718-762), 9 (823-852), 11 (920-948), 14 (1011-1043), 16 (1099-1133)
TOP1 (NM_003286)	20 (682-722)
TP53 (NM_000546)	2-11 (1-394)
TSC1 (NM_000368)	3-23 (1-1165)
TSC2 (NM_000548)	2-35 (1-1523), 37-39 (1555-1690), 40-42 (1706-1808)
U2AF1 (NM_006758)	2 (15-41), 6 (137-161)
XPO1 (NM_003400)	15 (563-575)

DISCLAIMER:

This test was developed and its performance characteristics determined by the Molecular Diagnostic Laboratory (MDL) at the M.D. Anderson Cancer Center. It has not been cleared by the U.S. Food and Drug Administration. However, such approval is not required for clinical implementation, and the test results on the ordered genes have been shown to be clinically useful. This laboratory is CAP accredited and CLIA certified to perform high complexity molecular testing for clinical purposes.

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Location: MN Molecular Diag
Ordering: GONZALEZ PA,CIPRIANO C

Name: XXXXXX
MRN: XXXXXX
DOB/Age/Sex: X/XX/XXXX 60 years Female

Molecular Diagnostics

Electronically Signed By: ASIF RASHID, MD - 10160 and reported on 12/18/20 15:30 PM

Test performed by:
The University of Texas MD Anderson Cancer Center Molecular Diagnostic Lab
6565 MD Anderson Blvd
Houston, TX 77030