Taipei Veterans General Hospital

Department of Pathology and Laboratory Medicine
No.201, Sec. 2, Shipai Rd., Beitou District, Taipei City, Taiwan
11217, R.O.C.
Tel: 02-2875-7449

Sample Information

Patient Name: 莊佳敏
Gender: Female
ID No.: T222376968
History No.: 44623236
Age: 41

Ordering Doctor: DOC1878G 沈佳儀
Ordering REQ.: 0ALXFRD
Signing in Date: 2019/11/05

Path No.: S108-98788
MP No.: TM1901
Assay: Oncomine Tumor Mutation Load Assay
Sample Type: FFPE
Block No.: S108-47840C
Percentage of tumor cells: 80%
Note:

Sample Cancer Type: Non-Small Cell Lung Cancer

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Report Highlights

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Clinically Significant Biomarkers

Indicated Contraindicated

Genomic Alteration	Relevant Therapies (In this cancer type)	Relevant Therapies (In other cancer type)	Clinical Trials
EGFR exon 20 insertion epidermal growth factor receptor Tier: IA Allele Frequency: 76.08%	osimertinib gefitinib [2]	None	58
Tumor Mutational Burden 4.17 Mut/Mb measured	ipilimumab + nivolumab nivolumab	None	11

Sources included in relevant therapies: FDA1, NCCN, EMA2, ESMO

Prevalent cancer biomarkers without clinical significance based on included data sources
RECQL4 splice site mutation

Tier Criteria Met

Genomic Alteration	Tier Classification for Non-Small Cell Lung Cancer
EGFR exon 20 insertion Tier: IA	IA: Biomarker predicts response or resistance to FDA or EMA approved therapies in this cancer type IA: Biomarker is included in NCCN or ESMO guidelines that predict response or resistance to therapies in this cancer type IIC: Biomarker is an inclusion criteria for clinical trials

Reference: Li et al. *Standards and Guidelines for the Interpretation and Reporting of Sequence Variants in Cancer: A Joint Consensus Recommendation of the Association for Molecular Pathology, American Society of Clinical Oncology, and College of American Pathologists.* J Mol Diagn. 2017 Jan;19(1):4-23.

Variant Details

DNA Sequence Variants

Gene	Amino Acid Change	Coding	Variant ID	Locus	Allele Frequency	Transcript	Variant Effect	Coverage
EGFR	p.(M766_A767insASV)	c.2308_2309insCCAGCGTGG	COSM12376	chr7:55248998	76.08%	NM_005228.4	nonframeshift Insertion	1990
RECQL4			.	chr8:145738767	100.00%	NM_004260.3		1956
TNFRSF14	p.(K17R)	c.50A>G	.	chr1:2488153	36.05%	NM_003820.3	missense	1373
MTOR	p.(=)	c.4731G>A	.	chr1:11205058	100.00%	NM_004958.3	synonymous	1302
MTOR	p.(=)	c.2997C>T	.	chr1:11288758	99.88%	NM_004958.3	synonymous	1708
MTOR	p.(=)	c.1437T>C	.	chr1:11301714	100.00%	NM_004958.3	synonymous	1998
SDHB	p.(=)	c.18C>A	.	chr1:17380497	99.40%	NM_003000.2	synonymous	2000
PAX7	p.(=)	c.279C>T	.	chr1:18960990	38.32%	NM_002584.2	synonymous	1746
MYCL	p.(T392S)	c.1175C>G	.	chr1:40363054	99.77%	NM_001033082.2	missense	1327
MPL	p.(L265F)	c.793C>T	.	chr1:43805737	57.99%	NM_005373.2	missense	1690
TAL1	p.(=)	c.933A>G	.	chr1:47685455	99.91%	NM_003189.5	synonymous	1074
CDKN2C	p.(=)	c.342C>T	.	chr1:51439777	42.39%	NM_078626.2	synonymous	1517
JAK1	p.(=)	c.2199A>G	.	chr1:65310489	49.25%	NM_002227.3	synonymous	1998
LOC64662(			.	chr1:85741921	100.00%	NR_045484.1		1656
LOC646626			.	chr1:85741968	48.25%	NR_045484.1		1745
DPYD	p.(R29C)	c.85C>T	.	chr1:98348885	99.79%	NM_000110.3	missense	1418
TRIM33	p.(I840T)	c.2519T>C	.	chr1:114948281	49.82%	NM_015906.3	missense	1084
PDE4DIP	p.(=)	c.6771G>A	.	chr1:144855782	8.20%	NM_001198834.3	synonymous	61
PDE4DIP	p.(=)	c.6687T>C	.	chr1:144855866	4.90%	NM_001198834.3	synonymous	2000
PDE4DIP	p.(D1910E)	c.5730C>A	.	chr1:144865850	47.60%	NM_001198834.3	missense	1998
PDE4DIP	p.(R1867C)	c.5599C>T	.	chr1:144866643	40.51%	NM_001198834.3	missense	1997

Variant Details (continued)

DNA Sequence Variants (continued)

Gene	Amino Acid Change	Coding	Variant ID	Locus	Allele Frequency	Transcript	Variant Effect	Coverage
PDE4DIP	p.(=)	c.5580A>G	.	chr1:144866662	84.93%	NM_001198834.3	synonymous	1998
PDE4DIP	p.(=)	c.4848A>G	.	chr1:144874760	33.93%	NM_001198834.3	synonymous	1998
PDE4DIP	p.(H1598R)	c.4793A>G	.	chr1:144874815	29.03%	NM_001198834.3	missense	627
PDE4DIP	p.(=)	c.4701C>G	.	chr1:144875979	36.30%	NM_001198834.3	synonymous	2000
PDE4DIP	p.(K1454E)	c.4360A>G	.	chr1:144879090	20.65%	NM_001198834.3	missense	2000
PDE4DIP	p.(=)	c.3438T>C	.	chr1:144882581	47.50%	NM_001198834.3	synonymous	2000
PDE4DIP	p.(A1066T)	c.3196G>A	.	chr1:144882823	43.48%	NM_001198834.3	missense	1757
PDE4DIP	p.(F1013I)	c.3037T>A	.	chr1:144886197	42.74%	NM_001198834.3	missense	1996
PDE4DIP	p.(=)	c.2232C>T	.	chr1:144909956	17.51%	NM_001198834.3	synonymous	1999
PDE4DIP	p.(R681H)	c.2042G>A	.	chr1:144912233	45.05%	NM_001198834.3	missense	2000
PDE4DIP	p.(S536T)	c.1607G>C	.	chr1:144916748	45.57%	NM_001198834.3	missense	1997
PDE4DIP	p.(=)	c.1558T>C	.	chr1:144917546	47.02%	NM_001198834.3	synonymous	1999
PDE4DIP	p.(E410V)	c.1229A>T	.	chr1:144918957	44.17%	NM_001198834.3	missense	1999
PDE4DIP	p.(S275L)	c.824C>T	.	chr1:144922583	43.70%	NM_001198834.3	missense	2000
PDE4DIP	p.(R25L)	c.74G>T	.	chr1:144994658	44.91%	NM_001198834.3	missense	1995
ITGA10	p.(=)	c.1002T>C	.	chr1:145532549	99.14%	NM_003637.4	synonymous	1863
ARNT	p.(=)	c.567G>C	.	chr1:150808889	73.29%	NM_001668.3	synonymous	1730
DDR2	p.(=)	c.1260C>G	.	chr1:162737116	71.56%	NM_006182.2	synonymous	1579
PBX1	p.(G21S)	c.61G>A	.	chr1:164529120	98.95%	NM_002585.3	missense	475
RNASEL	p.(D541E)	c.1623T>G	.	chr1:182551337	33.01%	NM_021133.3	missense	1557
MIR1278			.	chr1:193104778	73.91%	NR_031691.1		598
PIK3C2B	p.(=)	c.2295C>T	.	chr1:204418364	26.29%	NM_002646.3	synonymous	1750
PIK3C2B	p.(=)	c.1899C>T	.	chr1:204425028	67.59%	NM_002646.3	synonymous	108
PIK3C2B	p.(=)	c.597G>A	.	chr1:204438334	74.84%	NM_002646.3	synonymous	1999
PIK3C2B	p.(=)	c.288C>A	.	chr1:204438643	72.37%	NM_002646.3	synonymous	1998
IKBKE	p.(=)	c.156A>G	.	chr1:206647742	99.45%	NM_014002.3	synonymous	1999
MIR6769B			.	chr1:206647742	99.45%	NR_106919.1		1999
IKBKE	p.(=)	c.201T>C	.	chr1:206647787	99.56%	NM_014002.3	synonymous	1574
MIR6769B			.	chr1:206647787	99.56%	NR_106919.1		1574
IKBKE	p.(=)	c.717G>A	.	chr1:206651107	99.00%	NM_014002.3	synonymous	1999

Variant Details (continued)

DNA Sequence Variants (continued)

Gene	Amino Acid Change	Coding	Variant ID	Locus	Allele Frequency	Transcript	Variant Effect	Coverage
IKBKE	p.(P713L)	c.2138C>T	.	chr1:206669465	69.83%	NM_014002.3	missense	1999
PARP1	p.(=)	c.1056A>G	.	chr1:226570840	96.48%	NM_001618.3	synonymous	1989
MTR	p.(=)	c.3144A>G	.	chr1:237054569	75.60%	NM_000254.2	synonymous	2000
MTR	p.(=)	c.3492C>A	.	chr1:237058744	68.99%	NM_000254.2	synonymous	1996
MTR	p.(=)	c.3496C>T	.	chr1:237058748	29.20%	NM_000254.2	synonymous	2000
MTR	p.(=)	c.3576C>T	.	chr1:237058828	72.74%	NM_000254.2	synonymous	1999
FH	p.(P26L)	c.77C>T	.	chr1:241682946	24.35%	NM_000143.3	missense	1433
NCOA1	p.(=)	c.462G>C	.	chr2:24905927	100.00%	NM_003743.4	synonymous	1329
NCOA1	p.(=)	c.1512A>T	.	chr2:24929851	46.88%	NM_003743.4	synonymous	1538
NCOA1	p.(=)	c.3801T>G	.	chr2:24974945	99.90%	NM_003743.4	synonymous	1997
ALK	p.(D1529E)	c.4587C>G	.	chr2:29416366	99.95%	NM_004304.4	missense	1998
ALK	p.(K1491R)	c.4472A>G	.	chr2:29416481	99.60%	NM_004304.4	missense	1982
ALK	p.(I1461V)	c.4381A>G	.	chr2:29416572	99.90%	NM_004304.4	missense	1999
ALK	p.(=)	c.3375C>A	.	chr2:29445458	100.00%	NM_004304.4	synonymous	1997
ALK	p.(=)	c.1500A>G	.	chr2:29543663	99.80%	NM_004304.4	synonymous	1995
ALK	p.(=)	c.702T>A	.	chr2:29940529	96.60%	NM_004304.4	synonymous	589
ALK	p.(=)	c.27C>G	.	chr2:30143499	99.80%	NM_004304.4	synonymous	1998
EML4	p.(K283E)	c.847A>G	.	chr2:42510018	99.12%	NM_019063.4	missense	1707
EML4	p.(I382V)	c.1144A>G	.	chr2:42515388	99.88%	NM_019063.4	missense	852
MSH6	p.(G39E)	c.116G>A	.	chr2:48010488	41.94%	NM_000179.2	missense	1545
MSH6	p.(=)	c.3306T>A	.	chr2:48030692	49.40%	NM_000179.2	synonymous	1994
BCL11A	p.(=)	c.2088T>C	.	chr2:60687959	99.54%	NM_022893.3	synonymous	1961
AFF3	p.(S383N)	c.1148G>A	.	chr2:100343557	99.90%	NM_001025108.1	missense	1003
LRP1B	p.(=)	c.13047G>A	.	chr2:141032088	99.58%	NM_018557.2	synonymous	959
LRP1B	p.(=)	c.8526T>C	.	chr2:141260668	100.00%	NM_018557.2	synonymous	1021
LRP1B	p.(=)	c.5256A>G	.	chr2:141571329	100.00%	NM_018557.2	synonymous	802
LRP1B	p.(=)	c.2616C>T	.	chr2:141751592	58.25%	NM_018557.2	synonymous	1145
SF3B1	p.(=)	c.3657A>G	.	chr2:198257795	71.43%	NM_012433.3	synonymous	1995
SF3B1	p.(=)	c.2631T>C	.	chr2:198265526	67.15%	NM_012433.3	synonymous	1108
SF3B1	p.(=)	c.423A>G	.	chr2:198283305	71.07%	NM_012433.3	synonymous	1310

Variant Details (continued)

DNA Sequence Variants (continued)

Gene	Amino Acid Change	Coding	Variant ID	Locus	Allele Frequency	Transcript	Variant Effect	Coverage
ERBB4	p.(=)	c.3195A>G	.	chr2:212251864	99.94%	NM_005235.2	synonymous	1659
FN1	p.(V2261I)	c.6781G>A	.	chr2:216235089	100.00%	NM_212482.2	missense	1593
FN1	p.(=)	c.5691A>T	.	chr2:216242917	99.77%	NM_212482.2	synonymous	853
FN1	p.(=)	c.4725G>A	.	chr2:216249587	99.94%	NM_212482.2	synonymous	1730
FN1	p.(T817P)	c.2449A>C	.	chr2:216272900	100.00%	NM_212482.2	missense	1999
FN1	p.(Q15L)	c.44A>T	.	chr2:216300482	100.00%	NM_212482.2	missense	1305
STK36	p.(=)	c.2328G>A	.	chr2:219558698	15.83%	NM_015690.4	synonymous	1409
STK36	p.(=)	c.3237C>T	.	chr2:219563504	82.79%	NM_015690.4	synonymous	1778
PAX3	p.(?)	c.1451+3GCGTA>AAAGAC	.	chr2:223066128	6.57%	NM_181459.3	unknown	1980
PAX3	p.(=)	c.129T>C	.	chr2:223161889	99.92%	NM_181459.3	synonymous	1262
CCDC140	p.(?)	c.-6733A>G	.	chr2:223161889	99.92%	NM_153038.1	unknown	1262
UGT1A8	p.(P361L)	c.1082C>T	.	chr2:234676872	81.17%	NM_019076.4	missense	1689
UGT1A10	p.(P361L)	c.1082C>T	.	chr2:234676872	81.17%	NM_019075.2	missense	1689
UGT1A9	p.(P361L)	c.1082C>T	.	chr2:234676872	81.17%	NM_021027.2	missense	1689
UGT1A7	p.(P361L)	c.1082C>T	.	chr2:234676872	81.17%	NM_019077.2	missense	1689
UGT1A6	p.(P96L)	c.287C>T	.	chr2:234676872	81.17%	NM_205862.1	missense	1689
UGT1A5	p.(P365L)	c.1094C>T	.	chr2:234676872	81.17%	NM_019078.1	missense	1689
UGT1A4	p.(P365L)	c.1094C>T	.	chr2:234676872	81.17%	NM_007120.2	missense	1689
UGT1A3	p.(P365L)	c.1094C>T	.	chr2:234676872	81.17%	NM_019093.2	missense	1689
UGT1A1	p.(P364L)	c.1091C>T	.	chr2:234676872	81.17%	NM_000463.2	missense	1689
CRBN	p.(=)	c.735T>C	.	chr3:3197918	26.04%	NM_016302.3	synonymous	937
XPC	p.(Q939K)	c.2815C>A	.	chr3:14187449	100.00%	NM_004628.4	missense	1001
XPC	p.(=)	c.1881T>A	.	chr3:14197987	100.00%	NM_004628.4	synonymous	1390
XPC	p.(A499V)	c.1496C>T	.	chr3:14199887	23.86%	NM_004628.4	missense	1999
XPC	p.(L16V)	c.46C>G	.	chr3:14220023	75.86%	NM_004628.4	missense	1628
LSM3	p.(?)	c.-338G>C	.	chr3:14220023	75.86%	NM_014463.2	unknown	1628
TGFBR2	p.(=)	c.1242C>T	.	chr3:30713842	25.16%	NM_001024847.2	synonymous	1228
MLH1	p.(R217C)	c.649C>T	.	chr3:37053562	20.27%	NM_000249.3	missense	587
ITGA9	p.(G507E)	c.1520G>A	.	chr3:37574951	99.73%	NM_002207.2	missense	1507

Variant Details (continued)

DNA Sequence Variants (continued)

Gene	Amino Acid Change	Coding	Variant ID	Locus	Allele Frequency	Transcript	Variant Effect	Coverage
LTF	p.(=)	c.1894T>C	.	chr3:46480801	77.69%	NM_002343.5	synonymous	1067
LTF	p.(E579D)	c.1737G>C	.	chr3:46480958	26.16%	NM_002343.5	missense	1827
LTF	p.(=)	c.1623C>T	.	chr3:46484964	99.89%	NM_002343.5	synonymous	1744
LTF	p.(K47R)	c.140A>G	.	chr3:46501213	99.37%	NM_002343.5	missense	1279
LTF	p.(A29T)	c.85G>A	.	chr3:46501268	74.65%	NM_002343.5	missense	359
LTF	p.(R23dup)	c.68_69insAAG	.	chr3:46501284	100.00%	NM_002343.5	nonframeshift Insertion	358
SETD2	p.(P1962L)	c.5885C>T	.	chr3:47125385	99.51%	NM_014159.6	missense	1017
SETD2	p.(=)	c.3465T>C	.	chr3:47162661	100.00%	NM_014159.6	synonymous	813
PBRM1	p.(=)	c.4335A>G	.	chr3:52584787	99.64%	NM_018313.4	synonymous	1374
PBRM1	p.(=)	c.3522A>T	.	chr3:52610651	99.62%	NM_018313.4	synonymous	1039
PBRM1	p.(=)	c.2211A>G	.	chr3:52643685	99.85%	NM_018313.4	synonymous	1334
GATA2	p.(=)	c.15C>G	.	chr3:128205860	99.70%	NM_032638.4	synonymous	1320
EPHB1	p.(=)	c.435C>T	.	chr3:134670524	34.07%	NM_004441.4	synonymous	1996
EPHB1	p.(=)	c.1800C>T	.	chr3:134898742	99.92%	NM_004441.4	synonymous	1229
ATR	p.(=)	c.7875G>A	.	chr3:142168331	99.57%	NM_001184.3	synonymous	1395
ATR	p.(=)	c.5208T>C	.	chr3:142222284	32.55%	NM_001184.3	synonymous	1155
ATR	p.(=)	c.1815T>C	.	chr3:142277536	35.77%	NM_001184.3	synonymous	1339
ATR	p.(=)	c.1776T>A	.	chr3:142277575	20.19%	NM_001184.3	synonymous	644
ATR	p.(M211T)	c.632T>C	.	chr3:142281612	37.13%	NM_001184.3	missense	1080
BCL6	p.(=)	c.1161C>T	.	chr3:187447032	99.80%	NM_001706.4	synonymous	2000
LPP	p.(=)	c.942C>T	.	chr3:188327461	66.37%	NM_005578.4	synonymous	1998
TNK2	p.(=)	c.273T>C	.	chr3:195615376	63.31%	NM_001010938.1	synonymous	1998
FGFR3	p.(=)	c.990C>T	.	chr4:1805478	98.34%	NM_000142.4	synonymous	963
FGFR3	p.(=)	c.1953G>A	.	chr4:1807894	99.91%	NM_000142.4	synonymous	1144
PDGFRA	p.(=)	c.1701A>G	.	chr4:55141055	99.71%	NM_006206.5	synonymous	1732
PDGFRA	p.(=)	c.3222T>C	.	chr4:55161391	99.93%	NM_006206.5	synonymous	1538
KDR	p.(Q472H)	c.1416A>T	.	chr4:55972974	47.66%	NM_002253.2	missense	749
ADGRL3	p.(=)	c.612C>T	.	chr4:62598689	99.84%	NM_015236.5	synonymous	1287
ADGRL3	p.(=)	c.2079T>C	.	chr4:62800728	50.21%	NM_015236.5	synonymous	932

Variant Details (continued)

DNA Sequence Variants (continued)

Gene	Amino Acid Change	Coding	Variant ID	Locus	Allele Frequency	Transcript	Variant Effect	Coverage
ADGRL3	p.(=)	c.2709G>C	.	chr4:62845388	49.44%	NM_015236.5	synonymous	1962
NFKB1	p.(=)	c.1143T>C	.	chr4:103514658	99.80%	NM_003998.3	synonymous	1020
TET2	p.(I1762V)	c.5284A>G	.	chr4:106196951	99.94%	NM_001127208.2	missense	1743
IL2	p.(=)	c.114G>T	.	chr4:123377482	100.00%	NM_000586.3	synonymous	268
SDHA	p.(Y55H)	c.163T>C	.	chr5:224487	49.65%	NM_004168.3	missense	1138
SDHA	p.(=)	c.891T>C	.	chr5:231111	47.43%	NM_004168.3	synonymous	1849
MTRR	p.(S284T)	c.850T>A	.	chr5:7878424	53.39%	NM_024010.2	missense	1208
MTRR	p.(=)	c.1236G>A	.	chr5:7889216	54.17%	NM_024010.2	synonymous	1198
MTRR	p.(R442C)	c.1324C>T	.	chr5:7889304	53.63%	NM_024010.2	missense	1613
IL7R	p.(I66T)	c.197T>C	.	chr5:35861068	48.30%	NM_002185.4	missense	1236
IL7R	p.(V138I)	c.412G>A	.	chr5:35871190	42.08%	NM_002185.4	missense	1925
IL7R	p.(I356V)	c.1066A>G	.	chr5:35876274	48.65%	NM_002185.4	missense	2000
IL7R	p.(D389Y)	c.1165G>T	.	chr5:35876373	26.59%	NM_002185.4	missense	1463
APC	p.(=)	c.1458T>C	.	chr5:112162854	42.42%	NM_000038.5	synonymous	1589
APC	p.(=)	c.4479G>A	.	chr5:112175770	99.20%	NM_000038.5	synonymous	1253
APC	p.(=)	c.5034G>A	.	chr5:112176325	99.46%	NM_000038.5	synonymous	1114
APC	p.(=)	c.5268T>G	.	chr5:112176559	99.47%	NM_000038.5	synonymous	937
APC	p.(=)	c.5880G>A	.	chr5:112177171	100.00%	NM_000038.5	synonymous	735
RAD50	p.(?)	c.-38G>A	.	chr5:131892979	99.71%	NM_005732.3	unknown	1723
CSF1R	p.(R748W)	c.2242C>T	.	chr5:149436927	74.57%	NM_005211.3	missense	1998
CSF1R	p.(=)	c.726C>T	.	chr5:149457678	70.76%	NM_005211.3	synonymous	1997
PDGFRB	p.(=)	c.3252A>G	.	chr5:149495395	99.93%	NM_002609.3	synonymous	1394
PDGFRB	p.(=)	c.2601A>G	.	chr5:149499672	98.14%	NM_002609.3	synonymous	1989
FGFR4	p.(V10I)	c.28G>A	.	chr5:176516631	98.60%	NM_213647.2	missense	1999
FGFR4	p.(=)	c.162T>G	.	chr5:176517461	100.00%	NM_213647.2	synonymous	1998
FGFR4	p.(P136L)	c.407C>T	.	chr5:176517797	98.80%	NM_213647.2	missense	1997
FGFR4	p.(=)	c.702C>T	.	chr5:176518784	99.85%	NM_213647.2	synonymous	1995
NSD1	p.(=)	c.1482C>T	.	chr5:176636882	39.18%	NM_022455.4	synonymous	1654
NSD1	p.(=)	c.1749G>A	.	chr5:176637149	42.74%	NM_022455.4	synonymous	1996
NSD1	p.(S726P)	c.2176T>C	.	chr5:176637576	41.98%	NM_022455.4	missense	1584

Variant Details (continued)

DNA Sequence Variants (continued)

Gene	Amino Acid Change	Coding	Variant ID	Locus	Allele Frequency	Transcript	Variant Effect	Coverage
NSD1	p.(=)	c.6829T>C	.	chr5:176721198	59.00%	NM_022455.4	synonymous	1995
DEK	p.(=)	c.849G>A	.	chr6:18237661	100.00%	NM_003472.3	synonymous	655
DEK	p.(=)	c.9C>T	.	chr6:18264210	99.36%	NM_003472.3	synonymous	939
POU5F1	p.(=)	c.63G>A	.	chr6:31138335	53.55%	NM_002701.5	synonymous	338
NOTCH4	p.(=)	c.2967A>C	.	chr6:32172065	100.00%	NM_004557.3	synonymous	1994
NOTCH4	p.(K117Q)	c.349A>C	.	chr6:32190390	60.70%	NM_004557.3	missense	2000
NOTCH4	p.(=)	c.333T>C	.	chr6:32190406	61.33%	NM_004557.3	synonymous	1999
NOTCH4	p.(L13_L16del)	c.36_47delGCTGCTGCTGCT	.	chr6:32191658	45.74%	NM_004557.3	nonframeshift Deletion	
DAXX	p.(=)	c.1173T>C	.	chr6:33288271	62.64%	NM_001141970.1	synonymous	1997
PKHD1	p.(Q3899R)	c.11696A>G	.	chr6:51491884	48.75%	NM_138694.3	missense	1282
PKHD1	p.(=)	c.10521C>T	.	chr6:51524403	49.84%	NM_138694.3	synonymous	1603
PKHD1	p.(=)	c.9237G>A	.	chr6:51613177	99.69%	NM_138694.3	synonymous	1965
PKHD1	p.(=)	c.7764A>G	.	chr6:51720838	99.62%	NM_138694.3	synonymous	793
PKHD1	p.(L1870V)	c.5608T>G	.	chr6:51875250	99.85%	NM_138694.3	missense	1297
PKHD1	p.(V836A)	c.2507T>C	.	chr6:51910887	50.00%	NM_138694.3	missense	1882
PKHD1	p.(K626R)	c.1877A>G	.	chr6:51918923	50.45%	NM_138694.3	missense	1433
PKHD1	p.(Y617H)	c.1849T>C	.	chr6:51918951	49.02%	NM_138694.3	missense	1424
PKHD1	p.(=)	c.1185T>C	.	chr6:51924774	99.92%	NM_138694.3	synonymous	1248
PKHD1	p.(=)	c.234C>T	.	chr6:51947237	99.68%	NM_138694.3	synonymous	1546
ICK	p.(=)	c.975A>G	.	chr6:52878637	56.64%	NM_014920.3	synonymous	761
DST	p.(L4874V)	c.14620C>G	.	chr6:56351972	47.38%	NM_001144769.2	missense	1315
DST	p.(R4599H)	c.13796G>A	.	chr6:56362247	47.31%	NM_001144769.2	missense	1655
DST	p.(=)	c.10041G>A	.	chr6:56417192	50.59%	NM_001144769.2	synonymous	1194
DST	p.(M3317I)	c.9951G>A	.	chr6:56417282	100.00%	NM_001144769.2	missense	1029
DST	p.(T3230A)	c.9688A>G	.	chr6:56417545	51.68%	NM_001144769.2	missense	1341
DST	p.(R2795H)	c.8384G>A	.	chr6:56420538	50.37%	NM_001144769.2	missense	1868
DST	p.(=)	c.8184A>G	.	chr6:56422216	48.31%	NM_001144769.2	synonymous	1571
ADGRB3	p.(N503S)	c.1508A>G	.	chr6:69666684	99.77%	NM_001704.2	missense	436
ADGRB3	p.(=)	c.4008G>A	.	chr6:70071173	99.89%	NM_001704.2	synonymous	888

Variant Details (continued)

DNA Sequence Variants (continued)

Gene	Amino Acid Change	Coding	Variant ID	Locus	Allele Frequency	Transcript	Variant Effect	Coverage
EPHA7	p.(=)	c.2076G>A	.	chr6:93967851	26.49%	NM_004440.3	synonymous	721
EPHA7	p.(=)	c.1341T>C	.	chr6:93982124	24.29%	NM_004440.3	synonymous	1128
EPHA7	p.(=)	c.981G>A	.	chr6:94067981	100.00%	NM_004440.3	synonymous	900
PRDM1	p.(G74S)	c.220G>A	.	chr6:106536253	21.36%	NM_001198.3	missense	1175
ROS1	p.(T145P)	c.433A>C	.	chr6:117725448	23.90%	NM_002944.2	missense	1071
ROS1	p.(=)	c.303A>T	.	chr6:117725578	100.00%	NM_002944.2	synonymous	1254
SGK1	p.(=)	c.633A>G	.	chr6:134494481	17.16%	NM_001143676.1	synonymous	1055
ESR1	p.(=)	c.30T>C	.	chr6:152129077	17.89%	NM_001122740.1	synonymous	1627
ESR1	p.(=)	c.729T>C	.	chr6:152201875	99.81%	NM_001122740.1	synonymous	1029
ESR1	p.(=)	c.975G>C	.	chr6:152265522	17.34%	NM_001122740.1	synonymous	1995
ESR1	p.(=)	c.1782G>A	.	chr6:152420095	16.80%	NM_001122740.1	synonymous	1762
SYNE1	p.(L8741M)	c.26221C>A	.	chr6:152443744	18.62%	NM_182961.3	missense	1676
SYNE1	p.(=)	c.25038T>C	.	chr6:152464839	99.51%	NM_182961.3	synonymous	1422
SYNE1	p.(F7302V)	c.21904T>G	.	chr6:152540278	97.99%	NM_182961.3	missense	1093
SYNE1	p.(T5426M)	c.16277C>T	.	chr6:152640110	16.93%	NM_182961.3	missense	1453
SYNE1	p.(=)	c.15597C>G	.	chr6:152646279	15.59%	NM_182961.3	synonymous	1649
SYNE1	p.(L5015M)	c.15043T>A	.	chr6:152647681	16.13%	NM_182961.3	missense	1147
SYNE1	p.(=)	c.14163C>T	.	chr6:152651657	82.78%	NM_182961.3	synonymous	1690
SYNE1	p.(S4596T)	c.13786T>A	.	chr6:152652034	17.29%	NM_182961.3	missense	827
SYNE1	p.(K4121R)	c.12362A>G	.	chr6:152658142	18.05%	NM_182961.3	missense	1014
SYNE1	p.(E4060D)	c.12180G>T	.	chr6:152665261	18.74%	NM_182961.3	missense	1724
SYNE1	p.(=)	c.10866T>C	.	chr6:152675854	19.41%	NM_182961.3	synonymous	1556
SYNE1	p.(=)	c.10191C>A	.	chr6:152683413	15.59%	NM_182961.3	synonymous	802
SYNE1	p.(=)	c.9495A>G	.	chr6:152694184	16.59%	NM_182961.3	synonymous	916
SYNE1	p.(V1035A)	c.3104T>C	.	chr6:152772264	100.00%	NM_182961.3	missense	150
IGF2R	p.(L252V)	c.754C>G	.	chr6:160448324	82.30%	NM_000876.3	missense	1774
IGF2R	p.(=)	c.1050A>G	.	chr6:160453978	100.00%	NM_000876.3	synonymous	432
IGF2R	p.(=)	c.1590G>A	.	chr6:160464289	99.34%	NM_000876.3	synonymous	1956
IGF2R	p.(=)	c.2139A>G	.	chr6:160468278	15.89%	NM_000876.3	synonymous	1429
IGF2R	p.(R1619G)	c.4855A>G	.	chr6:160494409	16.45%	NM_000876.3	missense	1884

Variant Details (continued)

DNA Sequence Variants (continued)

Gene	Amino Acid Change	Coding	Variant ID	Locus	Allele Frequency	Transcript	Variant Effect	Coverage
IGF2R	p.(=)	c.6051C>G	.	chr6:160505199	100.00%	NM_000876.3	synonymous	1996
RPS6KA2	p.(=)	c.2221C>T	.	chr6:166826255	17.11%	NM_001006932.2	synonymous	1216
RPS6KA2	p.(=)	c.2172A>G	.	chr6:166826304	16.83%	NM_001006932.2	synonymous	1224
RPS6KA2	p.(=)	c.132C>T	.	chr6:166952264	99.76%	NM_001006932.2	synonymous	1681
CARD11	p.(=)	c.3276A>G	.	chr7:2946461	100.00%	NM_032415.5	synonymous	518
CARD11	p.(=)	c.2344C>T	.	chr7:2959172	52.13%	NM_032415.5	synonymous	1999
CARD11	p.(=)	c.2244G>C	.	chr7:2962293	63.98%	NM_032415.5	synonymous	1999
PMS2	p.(K541E)	c.1621A>G	.	chr7:6026775	99.25%	NM_000535.6	missense	1999
PMS2	p.(T485K)	c.1454C>A	.	chr7:6026942	52.60%	NM_000535.6	missense	1998
PMS2	p.(P470S)	c.1408C>T	.	chr7:6026988	46.65%	NM_000535.6	missense	2000
PMS2	p.(=)	c.780C>G	.	chr7:6036980	99.85%	NM_000535.6	synonymous	1996
PMS2	p.(=)	c.288C>T	.	chr7:6043386	54.19%	NM_000535.6	synonymous	1910
ETV1	p.(S100G)	c.298A>G	.	chr7:13978809	49.94%	NM_001163147.1	missense	847
EGFR	p.(R521K)	c.1562G>A	.	chr7:55229255	98.80%	NM_005228.4	missense	1999
EGFR	p.(=)	c.1887T>A	.	chr7:55238874	85.84%	NM_005228.4	synonymous	1992
EGFR	p.(=)	c.2361G>A	.	chr7:55249063	87.63%	NM_005228.4	synonymous	1996
EGFR	p.(=)	c.2709T>C	.	chr7:55266417	99.80%	NM_005228.4	synonymous	1982
AKAP9	p.(M463I)	c.1389G>T	.	chr7:91630620	28.28%	NM_005751.4	missense	1478
AKAP9	p.(=)	c.3075C>T	.	chr7:91632306	99.60%	NM_005751.4	synonymous	1513
AKAP9	p.(=)	c.3504A>G	.	chr7:91641928	55.43%	NM_005751.4	synonymous	1999
AKAP9	p.(N2792S)	c.8375A>G	.	chr7:91712698	55.74%	NM_005751.4	missense	1507
AKAP9	p.(=)	c.8665C>T	.	chr7:91713972	54.11%	NM_005751.4	synonymous	1508
AKAP9	p.(P2979S)	c.8935C>T	.	chr7:91714911	99.59%	NM_005751.4	missense	1234
AKAP9	p.(=)	c.9145C>T	.	chr7:91715662	60.56%	NM_005751.4	synonymous	1942
AKAP9	p.(=)	c.10426A>C	.	chr7:91726927	55.28%	NM_005751.4	synonymous	1402
SAMD9	p.(=)	c.1860A>G	.	chr7:92733551	47.18%	NM_001193307.1	synonymous	1509
SAMD9	p.(=)	c.960T>C	.	chr7:92734451	99.69%	NM_001193307.1	synonymous	1297
EPHB4	p.(=)	c.1752A>G	.	chr7:100411278	99.70%	NM_004444.4	synonymous	1995
EPHB4	p.(=)	c.1314T>C	.	chr7:100416250	99.90%	NM_004444.4	synonymous	2000
PIK3CG	p.(=)	c.972A>G	.	chr7:106508978	99.75%	NM_002649.3	synonymous	1999

Variant Details (continued)

DNA Sequence Variants (continued)

Gene	Amino Acid Change	Coding	Variant ID	Locus	Allele Frequency	Transcript	Variant Effect	Coverage
PIK3CG	p.(=)	c.981T>C	.	chr7:106508987	99.90%	NM_002649.3	synonymous	1999
PIK3CG	p.(=)	c.2025C>T	.	chr7:106513011	49.73%	NM_002649.3	synonymous	1878
MET	p.(=)	c.3912C>T	.	chr7:116435768	50.55%	NM_001127500.2	synonymous	2000
MET	p.(=)	c.4071G>A	.	chr7:116436022	26.15%	NM_001127500.2	synonymous	1893
MET	p.(=)	c.4146G>A	.	chr7:116436097	50.73%	NM_001127500.2	synonymous	1999
SMO	p.(=)	c.1164G>C	.	chr7:128846328	99.75%	NM_005631.4	synonymous	1994
WRN	p.(=)	c.513C>T	.	chr8:30924557	99.87%	NM_000553.4	synonymous	793
WRN	p.(=)	c.2361G>T	.	chr8:30973957	27.34%	NM_000553.4	synonymous	545
WRN	p.(L1074F)	c.3222G>T	.	chr8:30999280	23.50%	NM_000553.4	missense	583
WRN	p.(=)	c.4083C>T	.	chr8:31024638	73.51%	NM_000553.4	synonymous	653
NCOA2	p.(M1282I)	c.3846G>C	.	chr8:71039118	54.37%	NM_006540.3	missense	1865
NBN	p.(=)	c.2016A>G	.	chr8:90958422	35.40%	NM_002485.4	synonymous	2000
NBN	p.(=)	c.1197T>C	.	chr8:90967711	99.73%	NM_002485.4	synonymous	1486
NBN	p.(=)	c.102G>A	.	chr8:90995019	32.90%	NM_002485.4	synonymous	2000
CSMD3	p.(=)	c.6204T>C	.	chr8:113364696	35.55%	NM_198123.1	synonymous	1626
CSMD3	p.(=)	c.2121T>C	.	chr8:113702131	36.71%	NM_198123.1	synonymous	1204
CSMD3	p.(I219M)	c.657A>G	.	chr8:114186003	66.92%	NM_198123.1	missense	1998
JAK2	p.(=)	c.2490G>A	.	chr9:5081780	23.39%	NM_004972.3	synonymous	667
PTPRD	p.(E1639D)	c.4917G>T	.	chr9:8341723	28.55%	NM_002839.3	missense	774
PTPRD	p.(=)	c.4254G>C	.	chr9:8389364	74.30%	NM_002839.3	synonymous	747
PTPRD	p.(R995C)	c.2983C>T	.	chr9:8485834	26.15%	NM_002839.3	missense	1602
PTPRD	p.(Q447E)	c.1339C>G	.	chr9:8518052	72.47%	NM_002839.3	missense	1006
TAF1L	p.(G1659R)	c.4975G>C	.	chr9:32630603	41.59%	NM_153809.2	missense	1998
TAF1L	p.(A1229T)	c.3685G>A	.	chr9:32631893	14.52%	NM_153809.2	missense	1997
PAX5	p.(=)	c.1110C>T	.	chr9:36840623	66.24%	NM_016734.2	synonymous	1783
PTCH1	p.(P1315L)	c.3944C>T	.	chr9:98209594	20.30%	NM_000264.3	missense	2000
PTCH1	p.(=)	c.1686C>T	.	chr9:98238358	75.00%	NM_000264.3	synonymous	1644
XPA	p.(?)	c.-4A>G	.	chr9:100459578	18.76%	NM_000380.3	unknown	986
ABL1	p.(=)	c.3324A>G	.	chr9:133761001	100.00%	NM_005157.5	synonymous	1999
NUP214	p.(P574S)	c.1720C>T	.	chr9:134020092	99.10%	NM_005085.3	missense	1218

Variant Details (continued)

DNA Sequence Variants (continued)

Gene	Amino Acid Change	Coding	Variant ID	Locus	Allele Frequency	Transcript	Variant Effect	Coverage
TSC1	p.(=)	c.1335A>G	.	chr9:135782221	66.24%	NM_000368.4	synonymous	1004
TSC1	p.(M322T)	c.965T>C	.	chr9:135786904	63.80%	NM_000368.4	missense	1232
BRD3	p.(=)	c.1284C>T	.	chr9:136907005	98.99%	NM_007371.3	synonymous	1589
BRD3	p.(=)	c.936A>G	.	chr9:136913355	99.85%	NM_007371.3	synonymous	1997
NOTCH1	p.(=)	c.6555C>T	.	chr9:139391636	99.74%	NM_017617.4	synonymous	1535
NOTCH1	p.(=)	c.5094C>T	.	chr9:139397707	99.78%	NM_017617.4	synonymous	1791
NOTCH1	p.(=)	c.2265T>C	.	chr9:139407932	100.00%	NM_017617.4	synonymous	1997
NOTCH1	p.(?)	c.1441+7C>T	.	chr9:139412197	100.00%	NM_017617.4	unknown	1617
NOTCH1	p.(=)	c.312T>C	.	chr9:139418260	99.65%	NM_017617.4	synonymous	1720
GATA3	p.(P236A)	c.706C>G	.	chr10:8100732	48.90%	NM_001002295.1	missense	1996
RET	p.(=)	c.135A>G	.	chr10:43595968	52.83%	NM_020975.4	synonymous	1999
RET	p.(=)	c.1296A>G	.	chr10:43606687	99.75%	NM_020975.4	synonymous	1999
RET	p.(=)	c.2307G>T	.	chr10:43613843	50.85%	NM_020975.4	synonymous	1237
NCOA4	p.(F8V)	c.22T>G	.	chr10:51568378	99.58%	NM_001145260.1	missense	1430
NCOA4	p.(=)	c.717C>T	.	chr10:51582894	49.62%	NM_001145260.1	synonymous	1707
NCOA4	p.(Q629P)	c.1886A>C	.	chr10:51586410	54.20%	NM_001145260.1	missense	1107
TET1	p.(?)	c.-30C>T	.	chr10:70332066	50.38%	NM_030625.2	unknown	1320
TET1	p.(D162G)	c.485A>G	.	chr10:70332580	50.82%	NM_030625.2	missense	1285
TET1	p.(I1123M)	c.3369A>G	.	chr10:70405855	53.17%	NM_030625.2	missense	756
KAT6B	p.(E1364D)	c.4092G>C	.	chr10:76788674	27.04%	NM_012330.3	missense	995
FAS	p.(=)	c.642T>C	.	chr10:90771829	99.76%	NM_000043.5	synonymous	831
CYP2C19	p.(=)	c.99T>C	.	chr10:96522561	51.62%	NM_000769.2	synonymous	1515
CYP2C19	p.(W212*)	c.636G>A	.	chr10:96540410	45.56%	NM_000769.2	nonsense	1420
CYP2C19	p.(=)	c.681G>A	.	chr10:96541616	45.40%	NM_000769.2	synonymous	663
CYP2C19	p.(=)	c.990C>T	.	chr10:96602622	50.75%	NM_000769.2	synonymous	1734
CYP2C19	p.(=)	c.1251A>C	.	chr10:96609775	50.25%	NM_000769.2	synonymous	804
BLNK	p.(=)	c.171T>C	.	chr10:97990583	45.26%	NM_013314.3	synonymous	897
NFKB2	p.(=)	c.1269A>G	.	chr10:104159196	99.83%	NM_001077494.3	synonymous	572
NFKB2	p.(=)	c.1821A>G	.	chr10:104160434	99.83%	NM_001077494.3	synonymous	1165
FGFR2	p.(=)	c.696A>G	.	chr10:123298158	100.00%	NM_000141.4	synonymous	1661

Variant Details (continued)

DNA Sequence Variants (continued)

Gene	Amino Acid Change	Coding	Variant ID	Locus	Allele Frequency	Transcript	Variant Effect	Coverage
RRM1	p.(=)	c.2232G>A	.	chr11:4159466	38.69%	NM_001033.4	synonymous	654
FANCF	p.(=)	c.786A>G	.	chr11:22646571	45.06%	NM_022725.3	synonymous	1305
FANCF	p.(?)	c.-10C>T	.	chr11:22647366	56.25%	NM_022725.3	unknown	1321
DDB2	p.(=)	c.378T>C	.	chr11:47238522	99.95%	NM_000107.2	synonymous	1999
MEN1	p.(T546A)	c.1636A>G	.	chr11:64572018	49.22%	NM_000244.3	missense	1999
MEN1	p.(=)	c.1314T>C	.	chr11:64572557	99.95%	NM_000244.3	synonymous	1999
MEN1	p.(=)	c.1269C>T	.	chr11:64572602	51.65%	NM_000244.3	synonymous	1998
CCND1	p.(=)	c.723G>A	.	chr11:69462910	53.35%	NM_053056.2	synonymous	1700
NUMA1	p.(=)	c.2337G>A	.	chr11:71726212	46.85%	NM_006185.3	synonymous	1998
BIRC3	p.(=)	c.1200G>A	.	chr11:102201848	51.16%	NM_182962.2	synonymous	258
ATM	p.(N1983S)	c.5948A>G	.	chr11:108183167	100.00%	NM_000051.3	missense	761
KMT2A	p.(P3032A)	c.9094C>G	.	chr11:118375701	34.82%	NM_001197104.1	missense	1999
CHEK1	p.(I471V)	c.1411A>G	.	chr11:125525195	99.90%	NM_001274.5	missense	1920
ETS1	p.(=)	c.1143A>G	.	chr11:128333503	99.86%	NM_001143820.1	synonymous	1437
FLI1	p.(=)	c.279C>T	.	chr11:128638061	51.95%	NM_002017.4	synonymous	2000
FLI1	p.(=)	c.630A>G	.	chr11:128651893	46.52%	NM_002017.4	synonymous	1610
FLI1	p.(=)	c.687T>A	.	chr11:128675292	52.60%	NM_002017.4	synonymous	886
KRAS	p.(=)	c.483G>A	.	chr12:25368462	99.56%	NM_033360.3	synonymous	1124
ADAMTS20	p.(=)	c.1296T>C	.	chr12:43860526	99.69%	NM_025003.4	synonymous	321
ARID2	p.(Y1299C)	c.3896A>G	.	chr12:46245802	51.06%	NM_152641.3	missense	995
KMT2D	p.(=)	c.13689C>T	.	chr12:49424534	48.21%	NM_003482.3	synonymous	809
KMT2D	p.(=)	c.7479G>T	.	chr12:49434074	44.19%	NM_003482.3	synonymous	1247
ATF1	p.(=)	c.327C>T	.	chr12:51203371	50.79%	NM_005171.4	synonymous	1144
DDIT3	p.(=)	c.99C>T	.	chr12:57911160	47.99%	NM_001195055.1	synonymous	1567
HNF1A	p.(S574G)	c.1720A>G	.	chr12:121437382	99.93%	NM_000545.6	missense	1414
EP400	p.(=)	c.4758A>G	.	chr12:132508389	52.88%	NM_015409.4	synonymous	1999
EP400	p.(A3094T)	c.9280G>A	.	chr12:132562126	51.06%	NM_015409.4	missense	1835
FLT3	p.(=)	c.288C>T	.	chr13:28636084	99.92%	NM_004119.2	synonymous	1295
FLT1	p.(=)	c.3639C>T	.	chr13:28883061	100.00%	NM_002019.4	synonymous	399
FLT1	p.(=)	c.2901G>A	.	chr13:28896979	24.95%	NM_002019.4	synonymous	1912

Variant Details (continued)

DNA Sequence Variants (continued)

Gene	Amino Acid Change	Coding	Variant ID	Locus	Allele Frequency	Transcript	Variant Effect	Coverage
FLT1	p.(=)	c.1704G>A	.	chr13:28964198	26.27%	NM_002019.4	synonymous	491
FLT1	p.(?)	c.-59C>T	.	chr13:29069039	24.85%	NM_002019.4	unknown	837
BIVM-ERCC5	p.(=)	c.1500T>C	.	chr13:103504517	31.48%	NM_001204425.1	synonymous	702
ERCC5	p.(=)	c.138T>C	.	chr13:103504517	31.48%	NM_000123.3	synonymous	702
BIVM-ERCC5	p.(G1507R)	c.4519G>C	.	chr13:103527849	99.85%	NM_001204425.1	missense	679
ERCC5	p.(G1053R)	c.3157G>C	.	chr13:103527849	99.85%	NM_000123.3	missense	679
BIVM-ERCC5	p.(G1534R)	c.4600G>C	.	chr13:103527930	99.85%	NM_001204425.1	missense	686
ERCC5	p.(G1080R)	c.3238G>C	.	chr13:103527930	99.85%	NM_000123.3	missense	686
BIVM-ERCC5	p.(D1558H)	c.4672G>C	.	chr13:103528002	66.27%	NM_001204425.1	missense	759
ERCC5	p.(D1104H)	c.3310G>C	.	chr13:103528002	66.27%	NM_000123.3	missense	759
IRS2	p.(G1057D)	c.3170G>A	.	chr13:110435231	38.81%	NM_003749.2	missense	371
IRS2	p.(=)	c.3099A>G	.	chr13:110435302	64.13%	NM_003749.2	synonymous	446
IRS2	p.(=)	c.2673G>C	.	chr13:110435728	68.70%	NM_003749.2	synonymous	591
IRS2	p.(=)	c.2448T>C	.	chr13:110435953	99.94%	NM_003749.2	synonymous	1634
IRS2	p.(=)	c.2169C>T	.	chr13:110436232	100.00%	NM_003749.2	synonymous	52
LAMP1	p.(=)	c.556C>A	.	chr13:113965176	100.00%	NM_005561.3	synonymous	1126
BCL2L2-PABPN1	p.(=)	c.123G>A	.	chr14:23777099	99.94%	NM_001199864.1	synonymous	1706
BCL2L2	p.(=)	c.123G>A	.	chr14:23777099	99.94%	NM_001199839.1	synonymous	1706
BCL2L2-PABPN1	p.(Q133R)	c.398A>G	.	chr14:23777374	100.00%	NM_001199864.1	missense	2000
BCL2L2	p.(Q133R)	c.398A>G	.	chr14:23777374	100.00%	NM_001199839.1	missense	2000
NIN	p.(=)	c.5637G>A	.	chr14:51204996	100.00%	NM_020921.3	synonymous	1442
NIN	p.(G1320E)	c.3959G>A	.	chr14:51223789	58.22%	NM_020921.3	missense	1673
NIN	p.(Q1125P)	c.3374A>C	.	chr14:51224374	63.28%	NM_020921.3	missense	1999
NIN	p.(P1111A)	c.3331C>G	.	chr14:51224417	65.23%	NM_020921.3	missense	1714
NIN	p.(=)	c.1128T>C	.	chr14:51237701	40.00%	NM_020921.3	synonymous	2000
NIN	p.(=)	c.933G>C	.	chr14:51239067	99.85%	NM_020921.3	synonymous	1999
HIF1A	p.(P582S)	c.1744C>T	.	chr14:62207557	62.60%	NM_001530.3	missense	1441

Variant Details (continued)

DNA Sequence Variants (continued)

Gene	Amino Acid Change	Coding	Variant ID	Locus	Allele Frequency	Transcript	Variant Effect	Coverage
TSHR	p.(E727D)	c.2181G>C	.	chr14:81610583	60.63%	NM_000369.2	missense	1999
HSP90AA1	p.(=)	c.1446C>T	.	chr14:102550803	100.00%	NM_001017963.2	synonymous	725
HSP90AA1	p.(=)	c.282C>T	.	chr14:102568296	99.44%	NM_001017963.2	synonymous	360
HSP90AA1	p.(M71L)	c.211A>T	.	chr14:102568367	100.00%	NM_001017963.2	missense	1692
AKT1	p.(=)	c.726G>A	.	chr14:105239894	33.62%	NM_001014431.1	synonymous	1047
THBS1	p.(=)	c.1290G>A	.	chr15:39879717	18.85%	NM_003246.3	synonymous	2000
THBS1	p.(=)	c.1410C>T	.	chr15:39880358	18.49%	NM_003246.3	synonymous	1314
THBS1	p.(T523A)	c.1567A>G	.	chr15:39880822	22.26%	NM_003246.3	missense	1999
KNL1	p.(R43T)	c.128G>C	.	chr15:40898643	19.41%	NM_144508.4	missense	608
KNL1	p.(A460S)	c.1378G>T	.	chr15:40913840	22.88%	NM_144508.4	missense	883
KNL1	p.(R910G)	c.2728A>G	.	chr15:40915190	22.62%	NM_144508.4	missense	526
KNL1	p.(K1259E)	c.3775A>G	.	chr15:40916237	23.04%	NM_144508.4	missense	881
TGM7	p.(=)	c.1992C>T	.	chr15:43568794	84.35%	NM_052955.2	synonymous	1796
TGM7	p.(=)	c.1764G>C	.	chr15:43571390	84.08%	NM_052955.2	synonymous	1998
TGM7	p.(V515L)	c.1543G>T	.	chr15:43571958	84.75%	NM_052955.2	missense	2000
TGM7	p.(=)	c.777T>C	.	chr15:43579566	83.91%	NM_052955.2	synonymous	1585
TGM7	p.(G241E)	c.722G>A	.	chr15:43579621	81.55%	NM_052955.2	missense	1740
TCF12	p.(=)	c.135A>G	.	chr15:57213283	85.17%	NM_207037.1	synonymous	1234
PML	p.(L217V)	c.649C>G	.	chr15:74315215	16.56%	NM_033238.2	missense	1999
NTRK3	p.(=)	c.678C>T	.	chr15:88679785	100.00%	NM_001012338.2	synonymous	1999
NTRK3	p.(=)	c.573C>T	.	chr15:88680684	68.13%	NM_001012338.2	synonymous	1999
IGF1R	p.(=)	c.2298C>T	.	chr15:99465473	74.76%	NM_000875.4	synonymous	1997
IGF1R	p.(=)	c.3129G>A	.	chr15:99478225	71.55%	NM_000875.4	synonymous	2000
TSC2	p.(R1268H)	c.3803G>A	.	chr16:2131788	78.54%	NM_000548.4	missense	1421
CREBBP	p.(=)	c.6711C>T	.	chr16:3778337	19.10%	NM_004380.2	synonymous	513
CREBBP	p.(=)	c.3900C>A	.	chr16:3795292	21.89%	NM_004380.2	synonymous	1448
ERCC4	p.(?)	c.-30T>A	.	chr16:14013993	80.26%	NM_005236.2	unknown	1140
MYH11	p.(A1241T)	c.3721G>A	.	chr16:15820863	99.85%	NM_001040114.1	missense	1998
MYH11	p.(=)	c.2493C>T	.	chr16:15839034	99.75%	NM_001040114.1	synonymous	1997
MYH11	p.(=)	c.1764T>C	.	chr16:15850204	99.55%	NM_001040114.1	synonymous	1997

Variant Details (continued)

DNA Sequence Variants (continued)

Gene	Amino Acid Change	Coding	Variant ID	Locus	Allele Frequency	Transcript	Variant Effect	Coverage
MYH11	p.(=)	c.417C>T	.	chr16:15917197	14.25%	NM_001040114.1	synonymous	2000
MMP2	p.(=)	c.750C>T	.	chr16:55519607	57.78%	NM_004530.5	synonymous	1999
MMP2	p.(=)	c.1149T>C	.	chr16:55523705	99.90%	NM_004530.5	synonymous	1999
MMP2	p.(=)	c.1380G>A	.	chr16:55527113	55.22%	NM_004530.5	synonymous	1724
CDH11	p.(S373A)	c.1117T>G	.	chr16:65016087	99.85%	NM_001797.3	missense	1994
CDH11	p.(M275I)	c.825G>A	.	chr16:65022234	99.68%	NM_001797.3	missense	1549
CDH5	p.(=)	c.384C>T	.	chr16:66420885	99.90%	NM_001795.4	synonymous	1989
CDH5	p.(I517T)	c.1550_1551delTCinsCT	.	chr16:66432423	99.90%	NM_001795.4	missense	1975
CDH1	p.(=)	c.2076T>C	.	chr16:68857441	67.43%	NM_004360.4	synonymous	1977
FANCA	p.(=)	c.3807G>C	.	chr16:89807233	15.30%	NM_000135.3	synonymous	1144
FANCA	p.(=)	c.2901C>T	.	chr16:89825065	16.50%	NM_000135.3	synonymous	2000
FANCA	p.(G809D)	c.2426G>A	.	chr16:89836323	99.15%	NM_000135.3	missense	1999
FANCA	p.(G501S)	c.1501G>A	.	chr16:89849480	99.53%	NM_000135.3	missense	1715
FANCA	p.(A412V)	c.1235C>T	.	chr16:89857935	25.93%	NM_000135.3	missense	1697
FANCA	p.(=)	c.1143G>T	.	chr16:89858417	16.38%	NM_000135.3	synonymous	1996
FANCA	p.(T266A)	c.796A>G	.	chr16:89866043	99.69%	NM_000135.3	missense	982
FANCA	p.(=)	c.115A>C	.	chr16:89882359	82.21%	NM_000135.3	synonymous	1647
NLRP1	p.(=)	c.4389C>T	.	chr17:5418107	99.72%	NM_033004.3	synonymous	1432
NLRP1	p.(R1366C)	c.4096C>T	.	chr17:5418799	99.74%	NM_033004.3	missense	1543
NLRP1	p.(=)	c.3741C>T	.	chr17:5424886	98.62%	NM_033004.3	synonymous	1381
NLRP1	p.(M1184V)	c.3550A>G	.	chr17:5425077	99.74%	NM_033004.3	missense	1135
NLRP1	p.(=)	c.2934A>G	.	chr17:5440197	99.65%	NM_033004.3	synonymous	1991
NLRP1	p.(=)	c.114G>C	.	chr17:5487164	76.52%	NM_033004.3	synonymous	1516
TP53	p.(C277F)	c.830G>T	.	chr17:7577108	58.90%	NM_000546.5	missense	2000
TP53	p.(P72R)	c.215C>G	.	chr17:7579472	73.82%	NM_000546.5	missense	1975
PER1	p.(A962P)	c.2884G>C	.	chr17:8046772	16.57%	NM_002616.2	missense	1949
PER1	p.(=)	c.639A>C	.	chr17:8053085	18.63%	NM_002616.2	synonymous	1444
AURKB	p.(M298T)	c.893T>C	.	chr17:8108331	20.69%	NM_004217.3	missense	1498
AURKB	p.(=)	c.885C>T	.	chr17:8108339	20.37%	NM_004217.3	synonymous	1507

Variant Details (continued)

DNA Sequence Variants (continued)

Gene	Amino Acid Change	Coding	Variant ID	Locus	Allele Frequency	Transcript	Variant Effect	Coverage
ITGB3	p.(=)	c.882T>C	.	chr17:45364540	53.86%	NM_000212.2	synonymous	1530
ITGB3	p.(=)	c.1143A>C	.	chr17:45368337	44.85%	NM_000212.2	synonymous	1496
ITGB3	p.(=)	c.1143A>T	.	chr17:45368337	54.95%	NM_000212.2	synonymous	1496
ITGB3	p.(=)	c.1533A>G	.	chr17:45369777	46.20%	NM_000212.2	synonymous	2000
ITGB3	p.(=)	c.1545G>A	.	chr17:45369789	45.64%	NM_000212.2	synonymous	1994
COL1A1	p.(T1075A)	c.3223A>G	.	chr17:48265495	99.90%	NM_000088.3	missense	1996
COL1A1	p.(=)	c.2298T>C	.	chr17:48268223	99.94%	NM_000088.3	synonymous	1740
COL1A1	p.(G130C)	c.388G>T	.	chr17:48276670	38.20%	NM_000088.3	missense	1979
HLF	p.(?)	c.-50G>GTTTC	.	chr17:53342796	16.41%	NM_002126.4	unknown	
BRIP1	p.(=)	c.2637A>G	.	chr17:59763465	53.24%	NM_032043.2	synonymous	958
CD79B	p.(=)	c.369T>C	.	chr17:62007498	48.45%	NM_001039933.2	synonymous	1994
SEPT9	p.(M576V)	c.1726A>G	.	chr17:75494705	100.00%	NM_001113491.1	missense	1609
BIRC5	p.(?)	c.-31G>C	.	chr17:76210367	47.56%	NM_001012271.1	unknown	1659
BIRC5	p.(E152K)	c.454G>A	.	chr17:76219591	50.75%	NM_001012271.1	missense	2000
RNF213	p.(N1045D)	c.3133A>G	.	chr17:78298938	99.65%	NM_001256071.2	missense	2000
RNF213	p.(=)	c.10470G>A	.	chr17:78327358	45.51%	NM_001256071.2	synonymous	1903
ZNF521	p.(=)	c.3597G>A	.	chr18:22775185	47.01%	NM_015461.2	synonymous	502
CDH2	p.(=)	c.2091T>C	.	chr18:25565082	100.00%	NM_001792.4	synonymous	1034
CDH2	p.(=)	c.1431C>G	.	chr18:25570228	97.82%	NM_001792.4	synonymous	641
CDH2	p.(A118T)	c.352G>A	.	chr18:25593694	45.56%	NM_001792.4	missense	1475
CDH2	p.(=)	c.333C>G	.	chr18:25593713	45.55%	NM_001792.4	synonymous	1473
MBD1	p.(P401A)	c.1201C>G	.	chr18:47800179	49.48%	NM_001204136.1	missense	1334
MBD1	p.(=)	c.240G>A	.	chr18:47803354	51.04%	NM_001204136.1	synonymous	1542
DCC	p.(F23L)	c.67T>C	.	chr18:49867224	99.84%	NM_005215.3	missense	1234
DCC	p.(R201G)	c.601C>G	.	chr18:50432602	98.08%	NM_005215.3	missense	1984
DCC	p.(=)	c.2724A>G	.	chr18:50923713	49.76%	NM_005215.3	synonymous	822
DCC	p.(=)	c.3108T>C	.	chr18:50936994	99.90%	NM_005215.3	synonymous	1037
CDH20	p.(?)	c.-23T>C	.	chr18:59157764	99.43%	NM_031891.3	unknown	529
CDH20	p.(=)	c.369C>T	.	chr18:59166541	49.06%	NM_031891.3	synonymous	1800
CDH20	p.(=)	c.780C>G	.	chr18:59170304	100.00%	NM_031891.3	synonymous	631

Variant Details (continued)

DNA Sequence Variants (continued)

Gene	Amino Acid Change	Coding	Variant ID	Locus	Allele Frequency	Transcript	Variant Effect	Coverage
TCF3	p.(=)	c.1302A>G	.	chr19:1619339	99.91%	NM_001136139.3	synonymous	1095
KEAP1	p.(=)	c.1611C>T	.	chr19:10599965	62.12%	NM_203500.1	synonymous	1930
KEAP1	p.(=)	c.1413C>G	.	chr19:10600442	99.77%	NM_203500.1	synonymous	1738
PIK3R2	p.(S313P)	c.937T>C	.	chr19:18273047	99.90%	NM_005027.3	missense	1997
PIK3R2	p.(=)	c.1911T>C	.	chr19:18279638	100.00%	NM_005027.3	synonymous	1996
CCNE1	p.(Q180K)	c.538C>A	.	chr19:30311684	63.58%	NM_001238.3	missense	755
CCNE1	p.(=)	c.1215C>T	.	chr19:30314666	66.25%	NM_001238.3	synonymous	1997
AXL	p.(N266D)	c.796A>G	.	chr19:41743861	99.45%	NM_021913.4	missense	1649
MARK4	p.(=)	c.1683T>C	.	chr19:45801018	100.00%	NM_001199867.1	synonymous	1998
ERCC2	p.(=)	c.468A>C	.	chr19:45868309	65.88%	NM_000400.3	synonymous	1826
ERCC1	p.(=)	c.354T>C	.	chr19:45923653	99.88%	NM_001983.3	synonymous	1673
ASXL1	p.(L815P)	c.2444T>C	.	chr20:31022959	99.66%	NM_015338.5	missense	1747
ASXL1	p.(=)	c.3759T>C	.	chr20:31024274	100.00%	NM_015338.5	synonymous	1819
SRC	p.(=)	c.1218G>C	.	chr20:36030939	99.58%	NM_198291.2	synonymous	1918
PLCG1	p.(I813T)	c.2438T>C	.	chr20:39797465	57.51%	NM_002660.2	missense	1998
MIR6871			.	chr20:39797465	57.51%	NR_106931.1		1998
PTPRT	p.(=)	c.2904C>T	.	chr20:40757394	28.10%	NM_133170.3	synonymous	2000
PTPRT	p.(E808G)	c.2423A>G	.	chr20:40828005	15.01%	NM_133170.3	missense	1999
AURKA	p.(I57V)	c.169A>G	.	chr20:54961463	55.06%	NM_003600.3	missense	1998
GNAS	p.(=)	c.393C>T	.	chr20:57478807	99.80%	NM_000516.5	synonymous	1999
ERG	p.(?)	c.-6C>T	.	chr21:39870310	99.88%	NM_182918.3	unknown	844
ITGB2	p.(=)	c.1323T>C	.	chr21:46311813	99.80%	NM_000211.4	synonymous	1999
ITGB2	p.(Q354H)	c.1062A>T	.	chr21:46314907	99.58%	NM_000211.4	missense	1660
TIMP3	p.(=)	c.249T>C	.	chr22:33253280	56.88%	NM_000362.4	synonymous	1591
MYH9	p.(I1626V)	c.4876A>G	.	chr22:36684354	99.75%	NM_002473.5	missense	1611
MYH9	p.(=)	c.4872G>T	.	chr22:36684358	99.75%	NM_002473.5	synonymous	1613
MYH9	p.(=)	c.3429T>G	.	chr22:36691607	99.93%	NM_002473.5	synonymous	1381
EP300	p.(=)	c.3183T>A	.	chr22:41551039	98.48%	NM_001429.3	synonymous	985
CYP2D6	p.(C296R)	c.886T>C	.	chr22:42523943	99.85%	NM_000106.5	missense	1998
CYP2D6	p.(P34S)	c.100C>T	.	chr22:42526694	99.10%	NM_000106.5	missense	2000

Variant Details (continued)

DNA Sequence Variants (continued)

Gene	Amino Acid Change	Coding	Variant ID	Locus	Allele Frequency	Transcript	Variant Effect	Coverage
KDM6A	p.(T726K)	c.2177C>A	.	chrX:44929077	100.00%	NM_021140.3	missense	1368
TAF1	p.(R1193Q)	c.3578G>A	.	chrX:70617214	48.71%	NM_004606.4	missense	657
ATRX	p.(Q929E)	c.2785C>G	.	chrX:76937963	36.79%	NM_000489.4	missense	723
MAGEA1	p.(=)	c.813C>T	.	chrX:152482198	20.00%	NM_004988.4	synonymous	1640
MAGEA1	p.(T32A)	c.94A>G	.	chrX:152482917	18.74%	NM_004988.4	missense	1473

Relevant Therapy Summary

● In this cancer type ○ In other cancer type ◑ In this cancer type and other cancer types ⊘ Contraindicated ⚠ Both for use and contraindicated ✖ No evidence

EGFR exon 20 insertion

Relevant Therapy	FDA	NCCN	EMA	ESMO	Clinical Trials*
osimertinib	✖	●	✖	✖	● (II)
gefitinib	✖	✖	⊘	✖	● (III)
apatinib + erlotinib, apatinib + gefitinib, apatinib + icotinib hydrochloride	✖	✖	✖	✖	● (IV)
apatinib + gefitinib	✖	✖	✖	✖	● (IV)
erlotinib + natural product, erlotinib + placebo, gefitinib + natural product, gefitinib + placebo, icotinib hydrochloride + natural product, icotinib hydrochloride + placebo	✖	✖	✖	✖	● (IV)
gefitinib, radiation therapy	✖	✖	✖	✖	● (IV)
icotinib hydrochloride, radiation therapy	✖	✖	✖	✖	● (IV)
atezolizumab, bevacizumab, chemotherapy	✖	✖	✖	✖	● (III)
bevacizumab + chemotherapy, bevacizumab (Shanghai Hengrui Pharmaceutical) + chemotherapy	✖	✖	✖	✖	● (III)
chemotherapy, nivolumab	✖	✖	✖	✖	● (III)
erlotinib, gefitinib	✖	✖	✖	✖	● (III)
afatinib + bevacizumab	✖	✖	✖	✖	● (II)
afatinib + chemotherapy + radiation therapy + surgical intervention	✖	✖	✖	✖	● (II)

* Most advanced phase (IV, III, II/III, II, I/II, I) is shown and multiple clinical trials may be available.

Relevant Therapy Summary (continued)

● In this cancer type ○ In other cancer type ◑ In this cancer type and other cancer types ⊘ Contraindicated ⚠ Both for use and contraindicated ✖ No evidence

EGFR exon 20 insertion (continued)

Relevant Therapy	FDA	NCCN	EMA	ESMO	Clinical Trials*
anlotinib hydrochloride + sintilimab	✖	✖	✖	✖	● (II)
apatinib + chemotherapy	✖	✖	✖	✖	● (II)
bevacizumab, osimertinib	✖	✖	✖	✖	● (II)
chemotherapy, ramucirumab	✖	✖	✖	✖	● (II)
erlotinib	✖	✖	✖	✖	● (II)
erlotinib + chemotherapy	✖	✖	✖	✖	● (II)
erlotinib + radiation therapy	✖	✖	✖	✖	● (II)
gefitinib + chemotherapy	✖	✖	✖	✖	● (II)
icotinib hydrochloride	✖	✖	✖	✖	● (II)
ipilimumab, nivolumab	✖	✖	✖	✖	● (II)
KN046	✖	✖	✖	✖	● (II)
poziotinib	✖	✖	✖	✖	● (II)
radiation therapy, tyrosine kinase inhibitors	✖	✖	✖	✖	● (II)
sintilimab	✖	✖	✖	✖	● (II)
sunitinib	✖	✖	✖	✖	● (II)
targeted therapy, targeted therapy + chemotherapy	✖	✖	✖	✖	● (II)
tarloxotinib	✖	✖	✖	✖	● (II)
afatinib + necitumumab	✖	✖	✖	✖	● (I/II)
bevacizumab + erlotinib + chemotherapy	✖	✖	✖	✖	● (I/II)
cetuximab, cetuximab + natural killer cell therapy	✖	✖	✖	✖	● (I/II)
EMB01	✖	✖	✖	✖	● (I/II)
gefitinib + ningetinib	✖	✖	✖	✖	● (I/II)
icotinib hydrochloride + chemotherapy + radiation therapy	✖	✖	✖	✖	● (I/II)
oleclumab + osimertinib	✖	✖	✖	✖	● (I/II)
TAK788	✖	✖	✖	✖	● (I/II)

* Most advanced phase (IV, III, II/III, II, I/II, I) is shown and multiple clinical trials may be available.

Relevant Therapy Summary (continued)

● In this cancer type ○ In other cancer type ◑ In this cancer type and other cancer types ⊘ Contraindicated ⚠ Both for use and contraindicated ✖ No evidence

EGFR exon 20 insertion (continued)

Relevant Therapy	FDA	NCCN	EMA	ESMO	Clinical Trials*
cetuximab + FATE-NK100	✖	✖	✖	✖	● (I)
durvalumab + oleclumab, oleclumab	✖	✖	✖	✖	● (I)
erlotinib + ixazomib	✖	✖	✖	✖	● (I)
everolimus + neratinib, neratinib + palbociclib, neratinib + trametinib	✖	✖	✖	✖	● (I)
JNJ-61186372	✖	✖	✖	✖	● (I)
necitumumab, osimertinib	✖	✖	✖	✖	● (I)
osimertinib, osimertinib + radiation therapy	✖	✖	✖	✖	● (I)
pirotinib	✖	✖	✖	✖	● (I)
TP-0903	✖	✖	✖	✖	● (I)
tyrosine kinase inhibitors, tyrosine kinase inhibitors + chemotherapy	✖	✖	✖	✖	● (I)

Tumor Mutational Burden

Relevant Therapy	FDA	NCCN	EMA	ESMO	Clinical Trials*
ipilimumab + nivolumab	✖	●	✖	●	✖
nivolumab	✖	●	✖	✖	✖
atezolizumab	✖	✖	✖	✖	● (II/III)
durvalumab + tremelimumab	✖	✖	✖	✖	● (II)
ipilimumab + nivolumab, nivolumab	✖	✖	✖	✖	● (II)
ipilimumab + nivolumab, pembrolizumab	✖	✖	✖	✖	● (II)
ipilimumab, nivolumab	✖	✖	✖	✖	● (II)
lenvatinib, MK-1308, MK-4280, pembrolizumab	✖	✖	✖	✖	● (II)
pembrolizumab, pembrolizumab + chemotherapy	✖	✖	✖	✖	● (II)
sintilimab	✖	✖	✖	✖	● (I/II)
KN046	✖	✖	✖	✖	● (I)

* Most advanced phase (IV, III, II/III, II, I/II, I) is shown and multiple clinical trials may be available.

Relevant Therapy Details

Current NCCN Information

In this cancer type | In other cancer type | In this cancer type and other cancer types | Contraindicated | Not recommended | Resistance

NCCN information is current as of 2019-05-15. For the most up-to-date information, search www.nccn.org.
For NCCN International Adaptations & Translations, search www.nccn.org/global/international_adaptations.aspx.

EGFR exon 20 insertion

osimertinib

Cancer type: Non-Small Cell Lung Cancer **Variant class:** EGFR mutation

NCCN Recommendation category: 2A

Population segment (Line of therapy):
- Non-Small Cell Lung Cancer; Brain metastases; Newly diagnosed (Not specified)
- Non-Small Cell Lung Cancer; Leptomeningeal and Spine metastases (Not specified)

Reference: NCCN Guidelines® - NCCN-Central Nervous System Cancers [Version 1.2019]

pembrolizumab

Cancer type: Non-Small Cell Lung Cancer **Variant class:** EGFR mutation

Other criteria: CD274 overexpression

Summary:
NCCN Guidelines® include the following supporting statement(s):
- "A small study suggests that single-agent pembrolizumab is not effective as first-line therapy in patients with metastatic NSCLC and EGFR mutations, even those with PD-L1 levels more than 50%."

Reference: NCCN Guidelines® - NCCN-Non-Small Cell Lung Cancer [Version 5.2019]

EGFR tyrosine kinase inhibitor

Cancer type: Non-Small Cell Lung Cancer **Variant class:** EGFR exon 20 insertion

Summary:
NCCN Guidelines® include the following supporting statement(s):
- "Patients with EGFR exon 20 insertion mutations are usually resistant to TKIs, although there are rare exceptions."

Reference: NCCN Guidelines® - NCCN-Non-Small Cell Lung Cancer [Version 5.2019]

Tumor Mutational Burden

ipilimumab + nivolumab

Cancer type: Non-Small Cell Lung Cancer **Variant class:** Tumor Mutational Burden

NCCN Recommendation category: 2A

Population segment (Line of therapy):
- Non-Small Cell Lung Cancer; Emerging targeted agents

Reference: NCCN Guidelines® - NCCN-Non-Small Cell Lung Cancer [Version 5.2019]

nivolumab

Cancer type: Non-Small Cell Lung Cancer **Variant class:** Tumor Mutational Burden

NCCN Recommendation category: 2A

Population segment (Line of therapy):
- Non-Small Cell Lung Cancer; Emerging targeted agents

Reference: NCCN Guidelines® - NCCN-Non-Small Cell Lung Cancer [Version 5.2019]

Current EMA Information

● In this cancer type ○ In other cancer type ◑ In this cancer type and other cancer types ⊘ Contraindicated 👎 Not recommended 🛡 Resistance

EMA information is current as of 2019-08-23. For the most up-to-date information, search www.ema.europa.eu/ema.

EGFR exon 20 insertion

⊘ gefitinib

Cancer type: Non-Small Cell Lung Cancer **Label as of:** 2019-05-28 **Variant class:** EGFR exon 20 insertion

Reference:

https://www.ema.europa.eu/en/documents/product-information/iressa-epar-product-information_en.pdf

Current ESMO Information

● In this cancer type ○ In other cancer type ◑ In this cancer type and other cancer types ⊘ Contraindicated 👎 Not recommended 🛡 Resistance

ESMO information is current as of 2019-05-15. For the most up-to-date information, search www.esmo.org.

Tumor Mutational Burden

● ipilimumab + nivolumab

Cancer type: Non-Small Cell Lung Cancer **Variant class:** Tumor Mutational Burden

ESMO Level of Evidence/Grade of Recommendation: I / A

Population segment (Line of therapy):
- Stage IV Squamous and Non-squamous Non-Small Cell Lung Cancer (First-line therapy)

Reference: ESMO Clinical Practice Guidelines - ESMO-Metastatic Non-Small-Cell Lung Cancer [Ann Oncol (2018) 29 (suppl 4): iv192–iv237. (Corrigendum: 30 January 2019)]

Signatures

Testing Personnel: Shin-Ying Lin 2019.11.14 13:24:30 +08'00'

Laboratory Supervisor: 2019.11.14 13:26:51 +08'00'

Pathologist: Yi-Chu Yeh 2019.11.14 13:28:18 +08'00'