BioChain®
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Data Sheet

Product Name: CancerSeq AMS Paraffin Tissue Curl

Catalog No.: T2235152-AC **Lot No.: C201066**

Species: ■Human □ Mouse □ Rat □ Monkey (Rh) □ Guinea Pig □ Porcine
□ Bovine □ Hamster □ Dog □ Monkey (Cy) □ Rabbit □ Plant

Tissue Type: □ Normal ■ Adult □ Fetal ■ Tumor □Disease □ Cell line

Tissue Name: Lung

Donor Information:

Male: 47 year(s) old
Female: _____ year(s) old

Pathological Diagnosis: Adenocarcinoma

Tumor Size: diameter 5 cm

Location: right middle lobe

Components:
1. **5 curls per package**
2. **Certificate of Analysis**

FOR IN VITRO RESEARCH USE ONLY **APPROVED BY:** _____

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35 Genes Targeted

AKT1	FGFR2	MAP2K1
ALK	FGFR3	MAP2K2
AR	GNA11	MET
BRAF	GNAQ	MTOR
CDK4	HRAS	NRAS
CTNNB1	IDH1	PDGFRA
DDR2	IDH2	PIK3CA
EGFR	JAK1	RAF1
ERBB2	JAK2	RET
ERBB3	JAK3	ROS1
ERBB4	KIT	SMO
ESR1	KRAS	

Details of Variants

Column Header	Definition
Gene ID	The Gene symbol for the gene located at this position
Chrom	The chromosome where the target region is located
Position	The genomic position of the variant in the build of the genome database
Ref	The reference allele of the variation
Variant	The alternate allele of the variation
Allele Call	The type of variation, either heterozygous or homozygous
Frequency	The percentage of reads for the sample that includes the variant
Quality	The quality score of the variant
Type	The variant type, which can be SNP, MNP, Ins, Del, and Complex
Allele Source	Listed as Hotspot for alleles found within the hotspots sequencing file and Novel for all other alleles
Coverage	The number of reads that cover the region
Allele Name	The allele name that is defined within the hotspots sequencing file (if Novel allele, then there is no name)

C201066

Gene ID	Chrom	Position	Ref	Variant	Allele Call	Frequency	Quality	Type	Allele Source	Coverage	Allele Name
ALK	chr2	29416366	G	C	Heterozygous	77.6	25231	SNP	Novel	2486	---
ALK	chr2	29416572	T	C	Homozygous	100	33005	SNP	Novel	2069	---
ALK	chr2	29445458	G	T	Heterozygous	75.5	38833	SNP	Novel	3991	---
PIK3CA	chr3	178922274	C	A	Heterozygous	92.4	5922	SNP	Novel	435	---
FGFR3	chr4	1807894	G	A	Homozygous	100	63830	SNP	Novel	3991	---
FGFR3	chr4	1809317	G	A	Heterozygous	3.1	16	SNP	Novel	1717	---
FGFR3	chr4	1809321	G	A	Heterozygous	2.9	10	SNP	Novel	1733	---
PDGFRA	chr4	55097802	C	T	Heterozygous	3	10	SNP	Novel	1295	---
PDGFRA	chr4	55141055	A	G	Homozygous	100	22074	SNP	Novel	1381	---
KIT	chr4	55566266	G	A	Heterozygous	45.4	1759	SNP	Novel	416	---
RET	chr10	43613843	G	T	Heterozygous	51.9	21321	SNP	Novel	3963	---
RET	chr10	43615594	G	A	Heterozygous	3	12	SNP	Novel	1611	---
KRAS	chr12	25386063	C	A	Heterozygous	60.9	6488	SNP	Novel	939	---
KRAS	chr12	25391239	G	C	Heterozygous	56.2	8396	SNP	Novel	1376	---
KRAS	chr12	25400206	G	T	Heterozygous	49.7	5754	SNP	Novel	1150	---
ERBB3	chr12	56477694	A	T	Heterozygous	45.6	17484	SNP	Novel	3984	---
CDK4	chr12	58144665	C	T	Heterozygous	41.5	10926	SNP	Novel	2903	---
IDH2	chr15	90631914	C	T	Heterozygous	3.5	19	SNP	Novel	1235	---