BioChain®
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Data Sheet

Product Name: CancerSeq AMS Paraffin Tissue Curl

Catalog No.: T2235152-AC **Lot No.: C201085**

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: _____ year(s) old
Female: 51 year(s) old

Pathological Diagnosis: Adenocarcinoma

Tumor Size: diameter 4.7 cm

Location: right lower 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)

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Gene ID	Chrom	Position	Ref	Variant	Allele Call	Frequency	Quality	Type	Allele Source	Coverage	Allele Name
MTOR	chr1	11190895	G	A	Heterozygous	3	10	SNP	Novel	1151	---
ALK	chr2	29416366	G	C	Heterozygous	38.4	4337	SNP	Novel	1295	---
ALK	chr2	29416572	T	C	Homozygous	100	29553	SNP	Novel	1860	---
ALK	chr2	29445458	G	T	Heterozygous	45.4	11684	SNP	Novel	2682	---
PIK3CA	chr3	178922274	C	A	Heterozygous	42.4	1729	SNP	Novel	439	---
FGFR3	chr4	1797741	T	C	Heterozygous	44.1	16674	SNP	Novel	3998	---
FGFR3	chr4	1807894	G	A	Homozygous	100	60251	SNP	Novel	3775	---
PDGFRA	chr4	55141055	A	G	Homozygous	100	14358	SNP	Novel	907	---
KIT	chr4	55529200	-	A	Heterozygous	37.3	1127	INS	Novel	389	---
KIT	chr4	55566266	G	A	Homozygous	100	3709	SNP	Novel	237	---
JAK2	chr9	5073802	G	A	Heterozygous	3.5	16	SNP	Novel	846	---
RET	chr10	43609953	C	T	Heterozygous	3.1	13	SNP	Novel	1242	---
RET	chr10	43613843	G	T	Heterozygous	44.9	12350	SNP	Novel	2879	---
KRAS	chr12	25386063	C	A	Homozygous	99.1	5259	SNP	Novel	338	---
KRAS	chr12	25387191	G	A	Heterozygous	3.8	18	SNP	Novel	599	---
ERBB3	chr12	56477694	A	T	Homozygous	100	22122	SNP	Novel	1381	---
CDK4	chr12	58144665	C	T	Homozygous	100	15287	SNP	Novel	962	---
MAP2K1	chr15	66729188	G	A	Heterozygous	3.5	27	SNP	Novel	1960	---