BioChain®
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Data Sheet

Product Name: CancerSeq AMS Paraffin Tissue Curl

Catalog No.: T2235152-AC **Lot No.: C202146**

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: 56 year(s) old

Pathological Diagnosis: Adenocarcinoma

Tumor Size: 7 x 6 x 5 cm

Location: left upper 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
JAK1	chr1	65310489	T	C	Heterozygous	49.3	28981	SNP	Novel	3954	---
NRAS	chr1	115258774	T	C	Heterozygous	2.2	90	SNP	Novel	2178	---
ALK	chr2	29416366	G	C	Heterozygous	38.2	20495	SNP	Novel	3982	---
ALK	chr2	29416572	T	C	Homozygous	100	83574	SNP	Novel	3993	---
ALK	chr2	29443573	G	A	Heterozygous	1.1	15	SNP	Novel	3626	---
ALK	chr2	29445458	G	T	Heterozygous	38.1	20441	SNP	Novel	3987	---
PIK3CA	chr3	178916716	G	A	Heterozygous	1.1	15	SNP	Novel	3994	---
FGFR3	chr4	1807894	G	A	Homozygous	99.7	83342	SNP	Novel	3999	---
PDGFRA	chr4	55097835	G	C	Heterozygous	26.7	12155	SNP	Novel	3927	---
PDGFRA	chr4	55133726	T	G	Heterozygous	17.9	6945	SNP	Novel	3994	---
PDGFRA	chr4	55141055	A	G	Homozygous	99.7	83141	SNP	Novel	3998	---
PDGFRA	chr4	55152040	C	T	Heterozygous	19.8	8073	SNP	Novel	3995	---
KIT	chr4	55529200	-	A	Heterozygous	19.9	4369	INS	Novel	2380	---
KIT	chr4	55566266	G	A	Heterozygous	77.4	20496	SNP	Novel	1498	---
EGFR	chr7	55228053	A	-	Homozygous	100	78945	DEL	Novel	3985	---
EGFR	chr7	55242470	TAAGAGAA	-	Heterozygous	13.3	4260	DEL	Novel	3815	---
EGFR	chr7	55242470	TAAGAGAA	-	Heterozygous	52.3	50	DEL	Hotspot	6967	COSM12370
EGFR	chr7	55249063	G	A	Heterozygous	89	68664	SNP	Novel	3998	---
SMO	chr7	128849162	C	T	Heterozygous	1.2	21	SNP	Novel	3999	---
BRAF	chr7	140476936	G	A	Heterozygous	78.6	56895	SNP	Novel	3993	---
BRAF	chr7	140501253	A	G	Heterozygous	3.8	520	SNP	Novel	4000	---
KRAS	chr12	25386063	C	A	Homozygous	99.3	77518	SNP	Novel	3823	---
ERBB3	chr12	56477694	A	T	Homozygous	100	83623	SNP	Novel	3988	---
CDK4	chr12	58144665	C	T	Heterozygous	60.6	39228	SNP	Novel	3997	---