BioChain®
www.biochain.com
Tel: 1-888-762-2568 Fax: 1-510-783-5386 Email: info@biochain.com

Data Sheet

Product Name: CancerSeq AMS Paraffin Tissue Curl

Catalog No.: T2235152-AC **Lot No.: C201033**

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: 49 year(s) old

Pathological Diagnosis: Central Adenocarcinoma

Tumor Size: N/A

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
ALK	chr2	29432657	G	A	Heterozygous	4.4	11	SNP	Novel	114	---
FGFR3	chr4	1797694	C	T	Heterozygous	8.2	119	SNP	Novel	146	---
FGFR3	chr4	1797706	C	T	Heterozygous	7.3	32	SNP	Novel	151	---
FGFR3	chr4	1797736	G	A	Heterozygous	4	11	SNP	Novel	150	---
FGFR3	chr4	1801135	G	A	Heterozygous	95.5	263	SNP	Novel	22	---
FGFR3	chr4	1801225	G	A	Heterozygous	95.2	247	SNP	Novel	21	---
FGFR3	chr4	1803555	C	T	Heterozygous	4.8	15	SNP	Novel	126	---
FGFR3	chr4	1803606	A	G	Heterozygous	5.8	20	SNP	Novel	137	---
FGFR3	chr4	1803633	G	A	Heterozygous	11.7	67	SNP	Novel	137	---
FGFR3	chr4	1807894	G	A	Homozygous	100	786	SNP	Novel	49	---
FGFR3	chr4	1808320	C	T	Heterozygous	6.3	30	SNP	Novel	206	---
FGFR3	chr4	1808322	C	T	Heterozygous	7.8	46	SNP	Novel	206	---
KIT	chr4	55589790	C	T	Heterozygous	94.4	481	SNP	Novel	36	---
ROS1	chr6	117641111	C	A	Heterozygous	22.2	82	SNP	Novel	54	---
EGFR	chr7	55259537	A	G	Heterozygous	7.3	17	SNP	Novel	55	---
BRAF	chr7	140500246	G	A	Heterozygous	22.5	60	SNP	Novel	40	---
RET	chr10	43613843	G	T	Homozygous	100	835	SNP	Novel	58	---
CDK4	chr12	58145941	G	A	Heterozygous	12	42	SNP	Novel	75	---
CDK4	chr12	58146023	C	T	Heterozygous	17.6	72	SNP	Novel	74	---
ERBB2	chr17	37879665	G	A	Heterozygous	18.6	172	SNP	Novel	167	---
ERBB2	chr17	37879814	C	T	Heterozygous	21.8	180	SNP	Novel	133	---
ERBB2	chr17	37879816	G	A	Heterozygous	14.3	91	SNP	Novel	133	---
ERBB2	chr17	37879850	G	A	Heterozygous	10.5	54	SNP	Novel	133	---
ERBB2	chr17	37879891	G	A	Heterozygous	18.4	141	SNP	Novel	136	---
GNA11	chr19	3118885	C	T	Heterozygous	40.5	131	SNP	Novel	37	---
GNA11	chr19	3118973	C	T	Heterozygous	37.8	118	SNP	Novel	37	---
AR	chrX	66943564	C	T	Heterozygous	14.2	62	SNP	Novel	120	---