BioChain®
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Data Sheet

Product Name: CancerSeq AMS Paraffin Tissue Curl

Catalog No.: T2235152-AC **Lot No.: C201040**

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

Pathological Diagnosis: Squamous cell carcinoma

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)

C201040

Gene ID	Chrom	Position	Ref	Variant	Allele Call	Frequency	Quality	Type	Allele Source	Coverage	Allele Name
MTOR	chr1	11190835	C	T	Heterozygous	4.2	23	SNP	Novel	595	---
ALK	chr2	29416366	G	C	Heterozygous	61.9	6349	SNP	Novel	901	---
ALK	chr2	29416572	T	C	Homozygous	100	14589	SNP	Novel	917	---
ALK	chr2	29416615	G	A	Heterozygous	3.8	23	SNP	Novel	938	---
ALK	chr2	29445458	G	T	Heterozygous	70.5	18764	SNP	Novel	2159	---
PIK3CA	chr3	178922274	C	A	Heterozygous	76.1	39358	SNP	Novel	3994	---
FGFR3	chr4	1807894	G	A	Homozygous	100	38352	SNP	Novel	2402	---
FGFR3	chr4	1809289	G	A	Heterozygous	5	33	SNP	Novel	497	---
PDGFRA	chr4	55097767	C	T	Heterozygous	3.5	17	SNP	Novel	960	---
PDGFRA	chr4	55097835	G	C	Heterozygous	70.5	8398	SNP	Novel	969	---
PDGFRA	chr4	55126213	C	G	Heterozygous	45.9	17309	SNP	Novel	3932	---
PDGFRA	chr4	55133726	T	G	Heterozygous	44.6	11123	SNP	Novel	2635	---
PDGFRA	chr4	55141055	A	G	Homozygous	98.5	19628	SNP	Novel	1274	---
PDGFRA	chr4	55152040	C	T	Heterozygous	44.5	7792	SNP	Novel	1853	---
KIT	chr4	55566266	G	A	Homozygous	100	9623	SNP	Novel	614	---
KIT	chr4	55598903	A	T	Heterozygous	46.3	8751	SNP	Novel	1970	---
ESR1	chr6	152419958	C	T	Heterozygous	3.1	11	SNP	Novel	922	---
EGFR	chr7	55249063	G	A	Heterozygous	48.3	3268	SNP	Novel	681	---
MET	chr7	116412010	G	A	Heterozygous	3.2	14	SNP	Novel	1172	---
RET	chr10	43613843	G	T	Homozygous	100	61946	SNP	Novel	3896	---
KRAS	chr12	25386063	C	A	Homozygous	98.5	12405	SNP	Novel	811	---
ERBB3	chr12	56477599	G	A	Heterozygous	3.3	16	SNP	Novel	1468	---
ERBB3	chr12	56477694	A	T	Homozygous	98.7	22299	SNP	Novel	1435	---
CDK4	chr12	58144665	C	T	Heterozygous	96.9	24739	SNP	Novel	1660	---
AKT1	chr14	105246475	G	A	Heterozygous	3.4	11	SNP	Novel	441	---
AKT1	chr14	105246546	G	A	Heterozygous	3.3	11	SNP	Novel	644	---
GNA11	chr19	3115022	C	T	Heterozygous	4.6	26	SNP	Novel	476	---
AR	chrX	66941793	C	T	Heterozygous	5	29	SNP	Novel	399	---
AR	chrX	66945204	C	A	Heterozygous	3.8	15	SNP	Novel	395	---