BioChain®
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Data Sheet

Product Name: CancerSeq AMS Paraffin Tissue Curl

Catalog No.: T2235152-AC **Lot No.: C202141**

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: 60 year(s) old

Pathological Diagnosis: Adenocarcinoma

Tumor Size: diameter 3 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	11174378	C	T	Heterozygous	25	144	SNP	Novel	64	---
MTOR	chr1	11188013	C	A	Heterozygous	8.6	35	SNP	Novel	70	---
MTOR	chr1	11188048	G	T	Heterozygous	7	27	SNP	Novel	71	---
MTOR	chr1	11188069	C	T	Heterozygous	14.1	73	SNP	Novel	71	---
JAK1	chr1	65311202	G	A	Heterozygous	6.3	101	SNP	Novel	271	---
JAK1	chr1	65311232	T	C	Heterozygous	1.4	11	SNP	Novel	281	---
JAK1	chr1	65311250	G	A	Heterozygous	2.9	31	SNP	Novel	280	---
NRAS	chr1	115256513	G	A	Heterozygous	4.4	27	SNP	Novel	113	---
NRAS	chr1	115256514	G	A	Heterozygous	15	150	SNP	Novel	113	---
NRAS	chr1	115256524	C	T	Heterozygous	7.1	51	SNP	Novel	113	---
ALK	chr2	29416572	T	C	Homozygous	100	424	SNP	Novel	29	---
ALK	chr2	29445223	C	T	Heterozygous	16	22	SNP	Novel	25	---
ALK	chr2	29445448	C	T	Heterozygous	37.5	138	SNP	Novel	40	---
ALK	chr2	29445458	G	T	Heterozygous	50	211	SNP	Novel	40	---
IDH1	chr2	209113120	G	A	Heterozygous	6.5	10	SNP	Novel	31	---
PIK3CA	chr3	178947891	G	A	Heterozygous	4.8	42	SNP	Novel	146	---
FGFR3	chr4	1797673	G	A	Heterozygous	9.2	35	SNP	Novel	65	---
FGFR3	chr4	1797701	C	T	Heterozygous	10.8	44	SNP	Novel	65	---
FGFR3	chr4	1805788	C	T	Heterozygous	23.8	181	SNP	Novel	80	---
FGFR3	chr4	1807855	G	A	Heterozygous	6.8	15	SNP	Novel	44	---
FGFR3	chr4	1807894	G	A	Homozygous	100	662	SNP	Novel	41	---
FGFR3	chr4	1808328	C	T	Heterozygous	3.4	38	SNP	Novel	263	---
FGFR3	chr4	1808361	C	T	Heterozygous	3	32	SNP	Novel	266	---
PDGFRA	chr4	55144138	A	G	Heterozygous	2.9	20	SNP	Novel	138	---
PDGFRA	chr4	55161899	G	A	Heterozygous	9.1	10	SNP	Novel	22	---
PDGFRA	chr4	55161910	C	T	Heterozygous	13.6	15	SNP	Novel	22	---
EGFR	chr7	55221865	C	T	Heterozygous	31.6	100	SNP	Novel	38	---
EGFR	chr7	55259429	G	A	Heterozygous	44.8	116	SNP	Novel	29	---
MET	chr7	116339333	T	C	Heterozygous	11.8	21	SNP	Novel	34	---
MET	chr7	116339401	C	T	Heterozygous	20.6	46	SNP	Novel	34	---
MET	chr7	116340296	C	T	Heterozygous	18.6	55	SNP	Novel	43	---
MET	chr7	116423409	C	T	Heterozygous	12.6	103	SNP	Novel	103	---
MET	chr7	116423432	G	T	Heterozygous	4.8	27	SNP	Novel	104	---
MET	chr7	116423434	G	A	Heterozygous	2.9	14	SNP	Novel	105	---
SMO	chr7	128846383	C	A	Heterozygous	10.7	81	SNP	Novel	103	---

BRAF	chr7	140476891	G	A	Heterozygous	7.9	28	SNP	Novel	63	---
BRAF	chr7	140481445	C	T	Heterozygous	8.5	21	SNP	Novel	47	---
BRAF	chr7	140494207	T	C	Heterozygous	4.5	15	SNP	Novel	67	---
RET	chr10	43613843	G	T	Heterozygous	34.2	300	SNP	Novel	79	---
FGFR2	chr10	123274816	C	T	Heterozygous	42.9	69	SNP	Novel	21	---
FGFR2	chr10	123284147	C	G	Heterozygous	39.1	69	SNP	Novel	23	---
KRAS	chr12	25380277	G	A	Heterozygous	13.7	44	SNP	Novel	51	---
ERBB3	chr12	56481624	G	A	Heterozygous	6.5	35	SNP	Novel	93	---
ERBB3	chr12	56482570	G	A	Heterozygous	30.8	99	SNP	Novel	39	---
CDK4	chr12	58142959	C	T	Heterozygous	7.7	21	SNP	Novel	52	---
CDK4	chr12	58143295	G	A	Heterozygous	4.3	10	SNP	Novel	46	---
CDK4	chr12	58145957	C	T	Heterozygous	7.3	75	SNP	Novel	151	---
MAP2K1	chr15	66727455	G	A	Heterozygous	40	151	SNP	Novel	40	---
MAP2K1	chr15	66727495	A	G	Heterozygous	14.3	36	SNP	Novel	42	---
MAP2K1	chr15	66729222	G	A	Heterozygous	6.7	10	SNP	Novel	30	---
ERBB2	chr17	37879639	G	A	Heterozygous	11.8	82	SNP	Novel	93	---
ERBB2	chr17	37879668	G	A	Heterozygous	11.8	82	SNP	Novel	93	---
ERBB2	chr17	37879683	G	A	Heterozygous	11.8	82	SNP	Novel	93	---
ERBB2	chr17	37879830	C	T	Heterozygous	23.3	156	SNP	Novel	73	---
ERBB2	chr17	37880976	C	T	Heterozygous	19.4	96	SNP	Novel	62	---
ERBB2	chr17	37880998	-	TGT	Heterozygous	80.6	828	INS	Hotspot	62	COSM12553
ERBB2	chr17	37881004	G	A	Heterozygous	4.8	15	SNP	Novel	63	---
ERBB2	chr17	37881005	C	T	Heterozygous	25.4	145	SNP	Novel	63	---
ERBB2	chr17	37881395	G	A	Heterozygous	55	244	SNP	Novel	40	---
ERBB2	chr17	37882926	G	A	Heterozygous	19.4	96	SNP	Novel	62	---
JAK3	chr19	17945926	G	T	Heterozygous	9.5	21	SNP	Novel	42	---
JAK3	chr19	17948782	G	T	Heterozygous	23.1	97	SNP	Novel	52	---
JAK3	chr19	17948860	C	T	Heterozygous	28.8	134	SNP	Novel	52	---
JAK3	chr19	17949134	G	A	Heterozygous	4.1	15	SNP	Novel	73	---
AR	chrX	66906915	G	A	Heterozygous	7.4	10	SNP	Novel	27	---