

# Data Sheet

Product Name: CancerSeq AMS Paraffin Tissue Curl

Catalog No.: T2235152-AC

Lot No.: C201059

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 3.5 cm

Location: right middle lobe

Components:

1. 5 curls per package
2. Certificate of Analysis

FOR IN VITRO RESEARCH USE ONLY

APPROVED BY: \_\_\_\_\_



## 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
<b>Gene ID</b>	The Gene symbol for the gene located at this position
<b>Chrom</b>	The chromosome where the target region is located
<b>Position</b>	The genomic position of the variant in the build of the genome database
<b>Ref</b>	The reference allele of the variation
<b>Variant</b>	The alternate allele of the variation
<b>Allele Call</b>	The type of variation, either heterozygous or homozygous
<b>Frequency</b>	The percentage of reads for the sample that includes the variant
<b>Quality</b>	The quality score of the variant
<b>Type</b>	The variant type, which can be SNP, MNP, Ins, Del, and Complex
<b>Allele Source</b>	Listed as Hotspot for alleles found within the hotspots sequencing file and Novel for all other alleles
<b>Coverage</b>	The number of reads that cover the region
<b>Allele Name</b>	The allele name that is defined within the hotspots sequencing file (if Novel allele, then there is no name)

C201059

Gene ID	Chrom	Position	Ref	Variant	Allele Call	Frequency	Quality	Type	Allele Source	Coverage	Allele Name
MTOR	chr1	11188180	G	A	Heterozygous	3.2	14	SNP	Novel	1452	---
MTOR	chr1	11188244	G	A	Heterozygous	3.6	24	SNP	Novel	1506	---
ALK	chr2	29416366	G	C	Heterozygous	70.6	16462	SNP	Novel	1885	---
ALK	chr2	29416399	C	T	Heterozygous	2.9	12	SNP	Novel	1901	---
ALK	chr2	29416451	C	T	Heterozygous	3.1	13	SNP	Novel	1897	---
ALK	chr2	29416572	T	C	Homozygous	100	26575	SNP	Novel	1667	---
ALK	chr2	29436861	G	A	Heterozygous	3.3	17	SNP	Novel	1392	---
ALK	chr2	29445458	G	T	Heterozygous	65.7	26312	SNP	Novel	3378	---
ALK	chr2	29498014	C	T	Heterozygous	3.8	20	SNP	Novel	707	---
PIK3CA	chr3	178916698	G	A	Heterozygous	5.3	30	SNP	Novel	337	---
PIK3CA	chr3	178916716	G	A	Heterozygous	4.1	16	SNP	Novel	338	---
PIK3CA	chr3	178916731	G	A	Heterozygous	4.4	19	SNP	Novel	341	---
PIK3CA	chr3	178916849	G	A	Heterozygous	5.8	22	SNP	Novel	154	---
PIK3CA	chr3	178922274	C	A	Heterozygous	92.9	4053	SNP	Novel	294	---
PIK3CA	chr3	178936080	C	T	Heterozygous	4.9	26	SNP	Novel	366	---
PIK3CA	chr3	178938950	G	A	Heterozygous	3.3	13	SNP	Novel	914	---
PIK3CA	chr3	178952004	C	T	Heterozygous	3.1	11	SNP	Novel	1168	---
FGFR3	chr4	1807894	G	A	Homozygous	100	63949	SNP	Novel	3995	---
PDGFRA	chr4	55097758	C	T	Heterozygous	4.3	35	SNP	Novel	971	---
PDGFRA	chr4	55121601	C	T	Heterozygous	3.3	13	SNP	Novel	1012	---
PDGFRA	chr4	55141055	A	G	Heterozygous	96.9	10558	SNP	Novel	678	---
PDGFRA	chr4	55141054	CA	TG	Heterozygous	3.1	10558	MNP	Novel	678	---
KIT	chr4	55566266	G	A	Heterozygous	32.1	374	SNP	Novel	159	---
KIT	chr4	55573044	G	A	Heterozygous	3.8	11	SNP	Novel	239	---
KIT	chr4	55599271	C	T	Heterozygous	3.5	16	SNP	Novel	794	---
EGFR	chr7	55228053	A	-	Homozygous	100	7415	DEL	Novel	499	---
MET	chr7	116403179	C	T	Heterozygous	4.4	24	SNP	Novel	528	---
BRAF	chr7	140476660	C	T	Heterozygous	3.9	32	SNP	Novel	1325	---
RET	chr10	43613843	G	T	Heterozygous	43.2	15994	SNP	Novel	3980	---
RET	chr10	43615625	G	A	Heterozygous	4.2	35	SNP	Novel	1115	---
FGFR2	chr10	123350124	C	T	Heterozygous	4.3	14	SNP	Novel	211	---
KRAS	chr12	25386054	C	G	Heterozygous	5.1	26	SNP	Novel	335	---
KRAS	chr12	25386063	C	A	Heterozygous	42.3	1318	SNP	Novel	336	---
KRAS	chr12	25391239	G	C	Heterozygous	50.4	2165	SNP	Novel	425	---
KRAS	chr12	25398198	C	T	Heterozygous	3.5	24	SNP	Novel	1728	---

KRAS	chr12	25398297	C	T	Heterozygous	3.6	29	SNP	Novel	1765	---
KRAS	chr12	25400206	G	T	Heterozygous	53	4453	SNP	Novel	809	---
ERBB3	chr12	56477694	A	T	Heterozygous	42.2	10081	SNP	Novel	2607	---
ERBB3	chr12	56482620	C	T	Heterozygous	3	14	SNP	Novel	2297	---
CDK4	chr12	58142328	C	T	Heterozygous	3.3	18	SNP	Novel	1743	---
CDK4	chr12	58144665	C	T	Heterozygous	44.1	5610	SNP	Novel	1344	---
MAP2K1	chr15	66774085	C	T	Heterozygous	3.3	15	SNP	Novel	1469	---
IDH2	chr15	90631892	C	T	Heterozygous	4.7	37	SNP	Novel	718	---
GNA11	chr19	3115000	G	A	Heterozygous	4	37	SNP	Novel	1449	---
GNA11	chr19	3115051	C	T	Heterozygous	3.6	25	SNP	Novel	1506	---
MAP2K2	chr19	4117531	C	T	Heterozygous	3.1	11	SNP	Novel	1131	---
MAP2K2	chr19	4117558	C	T	Heterozygous	3.2	13	SNP	Novel	1150	---
MAP2K2	chr19	4117641	C	T	Heterozygous	2.7	12	SNP	Novel	1049	---
AR	chrX	66866192	G	A	Heterozygous	3.5	15	SNP	Novel	866	---
AR	chrX	66915246	G	A	Heterozygous	6.7	114	SNP	Novel	914	---
AR	chrX	66917714	C	T	Heterozygous	3.5	13	SNP	Novel	572	---
AR	chrX	66941763	C	T	Heterozygous	5.1	46	SNP	Novel	688	---
AR	chrX	66941789	G	A	Heterozygous	3.2	13	SNP	Novel	1016	---