

# Data Sheet

Product Name: CancerSeqPlus Paraffin Tissue Curl

Catalog No.: T2235152-SC

Lot No.: B911206

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: 63 year(s) old

Female: \_\_\_\_\_ year(s) old

Pathological Diagnosis: adenocarcinoma

Tumor Size: 5 cm

Location: Lung, Right Lower Lobe

Components:

1. 5 curls per package
2. Certificate of Analysis

FOR IN VITRO RESEARCH USE ONLY

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



Lot# B911206

For CNV mutations, we utilize stringent criteria to confirm copy number variations -- using normal tissues as controls. We may have samples containing additional CNVs not listed here. Please inquire.

symbol	type	chromosome	position	reference	mutation	quality score	allele type	Depth at this position*	transcript_id	existing variation
AKT1	snp	chr14	105246686	G	A	401.478	hom	14	NM_001014431.1	rs2494738
ALK	snp	chr2	29445458	G	T	5156.33	hom	164	NM_004304.4	rs3795850
APC	snp	chr5	112177171	G	A	1032.45	het	65	XM_005271975.1	rs465899
CCND1	snp	chr11	69465287	G	A	247.752	het	14	NM_053056.2	
CCND1	snp	chr11	69471193	C	A	942.612	hom	38	NM_053056.2	rs72938078
CDH1	complex	chr16	68835779	CGC	TGT	3404.92	het	297	NM_004360.3	
CDH1	snp	chr16	68857441	T	C	382.083	hom	16	NM_004360.3	rs1801552
CDK4	complex	chr12	58144509	GCA	CCC	283.499	hom	10	NM_000075.3	
CDKN2A	snp	chr9	21968199	C	G	20103.8	hom	635	NM_001195132.1	rs11515&COSM14251
DDR2	snp	chr1	162740327	T	C	13969.1	hom	441	XM_005245220.1	rs1780003
DDR2	snp	chr1	162743418	G	T	801.538	hom	33	XM_005245220.1	rs1355287
EGFR	snp	chr7	55221655	G	A	1117.35	hom	47	NM_005228.3	rs4947986
EGFR	snp	chr7	55242609	A	G	615.793	hom	31	NM_005228.3	rs2017000
ERBB2	snp	chr17	37880971	G	A	29.0972	het	230	NM_004448.2	
ERBB2	del	chr17	37882753	AGG	AG	282.168	hom	14	NM_004448.2	
ERBB2	complex	chr17	37882759	GAGG	GGT	221.821	hom	10	NM_004448.2	
ERBB2	complex	chr17	37882768	AGCACA	TGCTAGTCC	318.067	hom	14	NM_004448.2	
ERBB3	snp	chr12	56477694	A	T	5049.92	hom	164	NM_001982.3	rs2271194
ESR1	snp	chr6	152420095	G	A	5919.48	het	361	XM_005266856.1	rs2228480&CM056948
EZH2	snp	chr7	148508833	A	G	1174.32	het	68	XM_005249962.1	rs2072407
FBXW7	del	chr4	153247486	CTTTTTTTTT	CTTTTTTTTT	229.488	het	35	NM_033632.3	
FBXW7	snp	chr4	153267968	A	G	761.493	hom	27	NM_033632.3	rs2714803
FGFR2	snp	chr10	123247764	A	G	195.431	hom	10	NM_022970.3	
FGFR2	snp	chr10	123274705	T	C	1182.58	het	102	NM_022970.3	
FGFR3	mnp	chr4	1805996	AT	TC	228.185	het	24	NM_001163213.1	
FGFR3	mnp	chr4	1806004	GA	AT	247.879	het	22	NM_001163213.1	
FGFR3	del	chr4	1806012	TGGGGGGG	TGGGGGGG	1367.89	het	483	NM_001163213.1	
FGFR3	snp	chr4	1807894	G	A	6725.74	hom	228	NM_001163213.1	rs7688609
FLT3	snp	chr13	28610183	A	G	4493.65	hom	147	NM_004119.2	rs2491231
FOXL2	complex	chr3	138664548	ACTGGTGGC	CCGCGCCA	143.843	het	44	NM_023067.3	
HNF1A	snp	chr12	121432068	G	A	373.906	hom	18	XM_005253931.1	rs137853238&CM9714

IDH1	del	chr2	209116299	GAAAAAAAA	GAAAAAAAA	800.399	het	134	XM_005246521.1	
IDH2	complex	chr15	90631973	TTGAA	ATTAT	232.873	het	11	NM_002168.2	
JAK2	del	chr9	5073681	CTTTTTTTTT	CTTTTTTTTT	447.257	het	46	NM_004972.3	
JAK2	snp	chr9	5073691	T	C	165.142	het	61	NM_004972.3	
JAK3	complex	chr19	17948104	TTAGGGGA	AAAGGTGA	1584.55	het	104	XM_005259896.1	
JAK3	mnp	chr19	17948114	ACC	CTG	1613.27	het	102	XM_005259896.1	
JAK3	complex	chr19	17948122	ACAGGTCAC	AGGTGTTCC	1519.47	het	101	XM_005259896.1	
MET	snp	chr7	116436022	G	A	735.443	het	52	XM_005250353.1	rs2023748&COSM1503
MYCN	snp	chr2	16080157	C	G	6028.9	hom	192	NM_005378.4	rs11886063
NOTCH1	snp	chr9	139391636	G	A	7907.23	hom	291	NM_017617.3	rs2229974
NOTCH1	snp	chr9	139397707	G	A	11173.3	hom	373	NM_017617.3	rs10521&COSM337478
NOTCH1	snp	chr9	139397893	T	A	206.419	het	12	NM_017617.3	
NPM1	del	chr5	170837513	CTTTTTTTTT	CTTTTTTTTT	791.607	het	78	NM_002520.6	
PDGFRA	snp	chr4	55141055	A	G	8330.84	hom	291	NM_006206.4	rs1873778&COSM2224
PDGFRA	snp	chr4	55161391	T	C	661.647	hom	23	NM_006206.4	rs7685117
PDGFRA	snp	chr4	55161517	A	G	2889.61	hom	93	NM_006206.4	rs7680422
PTEN	del	chr10	89720633	CTTTTTTTTT	CTTTTTTTTT	218.757	het	46	NM_000314.4	
PTEN	snp	chr10	89720907	T	G	857.086	hom	30	NM_000314.4	rs555895&COSM5914
RB1	snp	chr13	48919358	T	G	890.076	hom	31	NM_000321.2	rs198617
RB1	del	chr13	48953655	CAAAAAAAAA	CAAAAAAAAA	360.013	het	52	NM_000321.2	
RB1	ins	chr13	49034022	ATT	ATTT	700.042	hom	31	NM_000321.2	
RB1	snp	chr13	49039131	C	T	421.639	het	27	NM_000321.2	
RET	mnp	chr10	43610189	GGG	TCT	272.815	hom	10	NM_020975.4	
RET	mnp	chr10	43610199	GGG	CCC	332.443	hom	12	NM_020975.4	
RET	snp	chr10	43613843	G	T	5548.33	hom	179	NM_020975.4	rs1800861&CM014825
SMO	snp	chr7	128845316	G	A	394.03	hom	19	NM_005631.4	
STK11	snp	chr19	1219444	C	G	900.616	het	66	XM_005259617.1	
STK11	snp	chr19	1221161	C	T	490.751	hom	23	XM_005259617.1	rs9282860
TERT	snp	chr5	1295349	A	G	55785	hom	1762	NM_198253.2	rs2853669&CR067846
TP53	snp	chr17	7572774	C	T	424.244	hom	18	NM_000546.5	
TP53	snp	chr17	7576995	C	A	400.927	het	32	NM_000546.5	TP53_g.13923G>A&CO
TP53	snp	chr17	7577407	A	C	765.198	het	55	NM_000546.5	rs12951053
TP53	snp	chr17	7577427	G	A	699.947	het	50	NM_000546.5	rs12947788
TP53	del	chr17	7579643	CCCCCAGCC	CC	170.589	het	134	NM_000546.5	
TP53	complex	chr17	7579668	CTCCAG	CAACCTT	292.932	het	125	NM_000546.5	
TP53	complex	chr17	7579678	CCAG	TTAC	67.8779	het	178	NM_000546.5	