

# Data Sheet

Product Name: CancerSeqPlus Paraffin Tissue Curl

Catalog No.: T2235152-SC

Lot No.: B906046

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: 56 year(s) old

Pathological Diagnosis: adenocarcinoma

Tumor Size: 7x6x5cm

Location: Lung, Left Upper Lobe

Components:

1. 5 curls per package
2. Certificate of Analysis

FOR IN VITRO RESEARCH USE ONLY

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



Lot# **B906046**

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.

CNV against colon	Copy Number	STDev of Copy Number	P-value	CNV against adrenal	Copy Number	STDev of Copy Number	P-value
CCNE1	3.46	0.30	2.55E-04	CCNE1	2.26	0.09	8.60E-03
EGFR	7.50	1.26	2.55E-04	EGFR	9.98	0.44	4.74E-04
ERBB2	6.45	0.61	2.55E-04	ERBB2	7.37	0.41	4.74E-04
GNAS	4.59	1.17	2.03E-03	GNAS	3.60	0.25	2.45E-03
KRAS	5.47	0.40	1.44E-04	KRAS	2.61	0.11	1.79E-03
RB1 (-)	0.41	0.08	1.72E-03	RB1 (-)	0.17	0.01	5.54E-04

symbol	type	chromosome	position	reference	mutation	quality score	allele type	Depth at this position	transcript_id	existing variation
ABL1	snp	chr9	133748476	G	A	783.158	hom	42	NM_007313.2	
AKT1	snp	chr14	105241644	G	A	292.421	het	21	NM_001014431.1	
AKT1	snp	chr14	105246686	G	A	899.621	hom	37	NM_001014431.1	rs2494738
ALK	snp	chr2	29432625	C	A	14483.1	het	736	NM_004304.4	rs3738868
ALK	snp	chr2	29432776	T	C	13503.5	het	672	NM_004304.4	rs3738867
ALK	snp	chr2	29443749	G	T	5914.36	het	333	NM_004304.4	rs80152976
APC	snp	chr5	112175770	G	A	1651.99	hom	71	XM_005271975.1	rs41115&COSM19714
APC	snp	chr5	112176559	T	G	545.181	hom	19	XM_005271975.1	rs866006
APC	snp	chr5	112177171	G	A	5117.4	hom	177	XM_005271975.1	rs465899
ATM	del	chr11	108117897	ATTTTTTTTT	ATTTTTTTTT	68.9061	het	80	NM_000051.3	
ATM	snp	chr11	108205805	C	G	2387.06	het	101	NM_000051.3	
ATM	snp	chr11	108225661	A	G	261.685	het	29	NM_000051.3	rs664143
CCND1	complex	chr11	69465243	ACTCCACCCG	CCTCGGGTG	759.421	het	47	NM_053056.2	
CCND1	complex	chr11	69471196	TCCC	TCG	49.4391	het	83	NM_053056.2	
CCNE1	snp	chr19	30313344	T	C	1308.75	hom	54	NM_001238.2	rs3218068
CDK4	snp	chr12	58144665	C	T	433.317	hom	16	NM_000075.3	rs2069502
CDKN2A	snp	chr9	21968199	C	G	46771.5	hom	1476	NM_001195132.1	rs11515&COSM14251
CDKN2A	mnp	chr9	21971136	GT	CA	1087.8	hom	50	NM_001195132.1	
CDKN2A	complex	chr9	21971144	AGTTGGGCTC	GGAGCCCA	1211.36	hom	51	NM_001195132.1	
CSF1R	mnp	chr5	149433596	TG	GA	504.217	het	25	NM_005211.3	

DDR2	snp	chr1	162740327	T	C	33959.3	hom	1110	XM_005245220.1	rs1780003
DDR2	snp	chr1	162741794	C	T	5868.17	het	327	XM_005245220.1	rs3738807
DDR2	snp	chr1	162741891	A	G	208.501	het	14	XM_005245220.1	
DDR2	snp	chr1	162741892	A	G	203.641	het	13	XM_005245220.1	
DDR2	snp	chr1	162743418	G	T	2541.81	hom	90	XM_005245220.1	rs1355287
DDR2	snp	chr1	162745689	C	A	174.911	het	20	XM_005245220.1	
EGFR	del	chr7	55211186	GAGGCTGGG	GA	406.916	het	22	NM_005228.3	
EGFR	snp	chr7	55221655	G	A	13454.3	het	651	NM_005228.3	rs4947986
EGFR	snp	chr7	55222171	G	A	663.387	het	38	NM_005228.3	
EGFR	mnp	chr7	55240763	AA	GC	476.706	hom	17	NM_005228.3	
EGFR	snp	chr7	55240769	C	G	465.065	hom	19	NM_005228.3	
EGFR	del	chr7	55242469	TTAAGAGAA	TC	2359.58	hom	104	NM_005228.3	
EGFR	complex	chr7	55242469	TTAAGAGAA	TCGAAAGCC	676.739	het	55	NM_005228.3	
EGFR	mnp	chr7	55242483	ATCTC	GGAAT	441.062	het	39	NM_005228.3	
EGFR	snp	chr7	55242609	A	G	5905.61	het	308	NM_005228.3	rs2017000
EGFR	snp	chr7	55242782	T	C	248.949	het	17	NM_005228.3	rs712831
EGFR	snp	chr7	55249063	G	A	52308.9	het	2217	NM_005228.3	rs1050171&CM067987&C
ERBB2	complex	chr17	37881258	CCCAGGCC	TCCAGATGA	446.92	hom	17	NM_004448.2	
ERBB3	snp	chr12	56477694	A	T	10440.4	hom	343	NM_001982.3	rs2271194
ERBB4	snp	chr2	212587321	G	A	487.095	het	31	NM_005235.2	rs13002712
EZH2	snp	chr7	148508833	A	G	7684.34	hom	243	XM_005249962.1	rs2072407
FBXW7	del	chr4	153247486	CTTTTTTTTT	CTTTTTTTTT	361.013	het	47	NM_033632.3	
FBXW7	snp	chr4	153252061	A	G	3321.34	hom	108	NM_033632.3	rs10033601
FBXW7	del,del	chr4	153268227	CAAAAAAAAA	CAAAAAAAAA	1396.48	het	133	NM_033632.3	
FGFR1	mnp	chr8	38271371	CT	AG	329.248	het	31	NM_001174067.1	
FGFR1	snp	chr8	38271383	C	G	419.542	het	35	NM_001174067.1	rs376538647
FGFR1	mnp	chr8	38271410	TCTG	CAGA	419.143	hom	17	NM_001174067.1	
FGFR1	complex	chr8	38271418	TGGCA	AGGCC	367.531	hom	15	NM_001174067.1	
FGFR1	snp	chr8	38271575	T	A	385.534	het	42	NM_001174067.1	
FGFR1	snp	chr8	38282294	C	T	490.868	het	27	NM_001174067.1	rs2280846
FGFR1	complex	chr8	38285891	TTTCTTT	ATGATGA	327.998	het	17	NM_001174067.1	
FGFR1	mnp	chr8	38285905	GA	TC	336.719	het	18	NM_001174067.1	
FGFR3	snp	chr4	1803431	T	G	1443.72	het	59	NM_001163213.1	
FGFR3	del	chr4	1806012	TGGGGGGGG	TGGGGGGGG	5302.55	het	1822	NM_001163213.1	
FGFR3	complex	chr4	1807891	GACG	AACA	827.288	hom	41	NM_001163213.1	
FGFR3	snp	chr4	1807891	GACG	GACA	18860.5	hom	668	NM_001163213.1	
FLT3	snp	chr13	28609991	T	C	377.658	hom	15	NM_004119.2	rs2491229
FLT3	snp	chr13	28609997	T	C	390.713	hom	16	NM_004119.2	rs2491230
FLT3	snp	chr13	28610183	A	G	4486.04	hom	155	NM_004119.2	rs2491231
FOXL2	complex	chr3	138665047	GCGGCGCCT	TCGGGGCCG	446.45	het	20	NM_023067.3	
GNA11	snp	chr19	3119184	T	G	407.065	hom	20	NM_002067.2	rs308046

HRAS	snp	chr11	533693	C	T	257.127	het	11	NM_005343.2	
HRAS	snp	chr11	533762	T	C	294.328	het	17	NM_005343.2	
HRAS	snp	chr11	533767	T	A	262.075	het	14	NM_005343.2	
HRAS	snp	chr11	533772	T	A	339.709	hom	12	NM_005343.2	
HRAS	snp	chr11	533777	G	A	235.854	het	13	NM_005343.2	
HRAS	mnp	chr11	533778	ATGT	ACCC	275.711	hom	12	NM_005343.2	
HRAS	snp	chr11	534596	G	A	200.718	het	17	NM_005343.2	
IDH1	del	chr2	209113048	GAAAAAAAA	GAAAAAAAA	142.995	het	81	XM_005246521.1	
IDH1	snp	chr2	209116197	T	G	251.072	het	11	XM_005246521.1	
IDH1	complex	chr2	209116203	ATTCCCAA	TTTGGGAAT	248.919	hom	10	XM_005246521.1	
IDH1	complex	chr2	209116216	TCGT	TAAAGA	248.009	hom	10	XM_005246521.1	
IDH1	del	chr2	209116299	GAAAAAAAA	GAAAAAAAA	2020.02	het	250	XM_005246521.1	
JAK2	del	chr9	5073681	CTTTTTTTTT	CTTTTTTTTT	1005.94	het	133	NM_004972.3	
JAK3	mnp	chr19	17948159	ACACA	TGTGT	667.499	het	44	XM_005259896.1	
JAK3	mnp	chr19	17948170	CCA	ATG	644.08	het	43	XM_005259896.1	
KDR	snp	chr4	55961159	T	C	1987.72	hom	67	NM_002253.2	rs2219471
KDR	ins	chr4	55962545	TGG	TGGG	1496.83	het	143	NM_002253.2	
KDR	snp	chr4	55972974	T	A	2353.95	hom	78	NM_002253.2	rs1870377&CM074306&C
KIT	snp	chr4	55599436	T	C	555.545	het	46	XM_005265740.1	rs1008658
MAP2K1	snp	chr15	66727597	G	C	11972.8	het	556	NM_002755.3	rs16949924
MAP2K1	snp	chr15	66729330	C	A	292.667	hom	14	NM_002755.3	
MLH1	snp	chr3	37067240	T	A	4383.11	het	220	NM_000249.3	rs63750447&MMR_c.115
MYCN	snp	chr2	16080157	C	G	7189.9	hom	227	NM_005378.4	rs11886063
MYCN	mnp	chr2	16081196	G G G G	C C C C	271.173	het	17	NM_005378.4	
MYCN	complex	chr2	16081206	T C C A A G G G	C T C C A G G G	283.415	het	19	NM_005378.4	
MYCN	snp	chr2	16081231	AGA	AGG	11451.9	het	606	NM_005378.4	
MYCN	snp	chr2	16081233	A	G	933.948	hom	33	NM_005378.4	rs117839276
MYCN	snp	chr2	16081359	G	A	370.256	hom	16	NM_005378.4	
MYCN	snp	chr2	16089442	T	A	350.51	hom	15	NM_005378.4	rs12619709
MYCNOS	snp	chr2	16080157	C	G	7189.9	hom	227	NR_026766.1	rs11886063
MYCNOS	mnp	chr2	16081196	G G G G	C C C C	271.173	het	17	NR_026766.1	
MYCNOS	complex	chr2	16081206	T C C A A G G G	C T C C A G G G	283.415	het	19	NR_026766.1	
MYCNOS	snp	chr2	16081231	AGA	AGG	11451.9	het	606	NR_026766.1	
MYCNOS	snp	chr2	16081233	A	G	933.948	hom	33	NR_026766.1	rs117839276
MYCNOS	snp	chr2	16081359	G	A	370.256	hom	16	NR_026766.1	
NPM1	del,del	chr5	170837513	CTTTTTTTTT	CTTTTTTTTT	643.784	het	73	NM_002520.6	
NRAS	complex	chr1	115252133	ACC	GCA	208.501	het	14	NM_002524.4	
PDGFRA	snp	chr4	55141055	A	G	17395.1	hom	568	NM_006206.4	rs1873778&COSM222428
PDGFRA	snp	chr4	55161254	C	T	2380.62	het	103	NM_006206.4	rs3733540
PDGFRA	snp	chr4	55161391	T	C	1346.08	hom	47	NM_006206.4	rs7685117
PDGFRA	snp	chr4	55161517	A	G	2328.66	hom	78	NM_006206.4	rs7680422

PIK3CA	complex	chr3	178916653	CACTT	AAGTG	267.716	het	37	NM_006218.2	
PIK3CA	mnp	chr3	178916666	CA	AC	280.002	het	37	NM_006218.2	
PIK3CA	del	chr3	178927848	ATTTTTTTTT	ATTTTTTTTT	530.086	het	119	NM_006218.2	
PIK3CA	mnp	chr3	178938881	CA	AG	423.478	het	30	NM_006218.2	
PIK3R1	snp	chr5	67591901	C	T	222.731	hom	10	NM_181523.2	
PIK3R1	snp	chr5	67591905	A	C	222.731	hom	10	NM_181523.2	
PIK3R1	snp	chr5	67591906	G	A	222.731	hom	10	NM_181523.2	
PIK3R1	del	chr5	67591910	AGTG	AGG	222.731	hom	10	NM_181523.2	
PTEN	del	chr10	89720633	CTTTTTTTTT	CTTTTTTTTT	417.971	het	80	NM_000314.4	
RB1	snp	chr13	48919358	T	G	492.729	hom	18	NM_000321.2	rs198617
RB1	ins	chr13	49034022	ATT	ATTT	307.871	het	18	NM_000321.2	
RET	complex	chr10	43615494	CATGGC	GAGGGT	319.957	het	18	NM_020975.4	
RET	snp	chr10	43615496	T	G	178.333	het	15	NM_020975.4	
SMARCB1	snp	chr22	24176287	G	A	8483.5	het	533	XM_005261718.1	rs5030613&COSM1090
SMO	snp	chr7	128846457	G	A	427.088	het	41	NM_005631.4	
SRC	snp	chr20	36031501	C	T	8435.87	het	546	NM_005417.4	rs2273677
STK11	snp	chr19	1219274	G	A	271.377	het	13	XM_005259617.1	rs34928889
STK11	snp	chr19	1221096	C	T	224.752	het	20	XM_005259617.1	
STK11	complex	chr19	1221543	TCCG	ACCTG	227.727	het	13	XM_005259617.1	
STK11	ins	chr19	1221547	AA	ACA	169.452	het	11	XM_005259617.1	
STK11	snp	chr19	1221550	T	C	233.691	het	12	XM_005259617.1	
STK11	snp	chr19	1221555	C	A	214.285	hom	13	XM_005259617.1	
STK11	complex	chr19	1221995	CGGCAGCAC	GGGCGGCTC	439.439	het	22	XM_005259617.1	
TERT	snp	chr5	1295349	A	G	87646.7	hom	2773	NM_198253.2	rs2853669&CR067846
TP53	complex	chr17	7577494	CTGACC	ATCACAC	381.644	hom	19	NM_000546.5	
TP53	mnp	chr17	7577504	GTCT	AGAC	394.476	het	20	NM_000546.5	
TP53	del	chr17	7577512	GTG	GG	507.388	het	23	NM_000546.5	
TP53	snp	chr17	7577610	T	A	35190.1	het	2017	NM_000546.5	TP53_g.13308A>T&TP53
TP53	snp	chr17	7578115	T	C	326.179	hom	13	NM_000546.5	rs1625895
TP53	snp	chr17	7578645	C	T	333.44	hom	13	NM_000546.5	rs2909430
TP53	snp	chr17	7579472	G	C	28661.9	hom	957	NM_000546.5	rs1042522&TP53_g.1144C
TP53	del	chr17	7579643	CCCCAGCCC	CC	301.959	het	340	NM_000546.5	
TP53	complex	chr17	7579668	CTCCAG	CAACCCTT	1026.2	het	430	NM_000546.5	
TP53	complex	chr17	7579678	CCAG	TTAC	1103.82	het	494	NM_000546.5	
TP53	snp	chr17	7579801	G	C	2497.03	hom	90	NM_000546.5	rs1642785