BioChain®
www.biochain.com
Tel: 1-888-762-2568 Fax: 1-510-783-5386 Email: info@biochain.com

Data Sheet

Product Name: CancerSeqPlus Paraffin Tissue Curl

Catalog No.: T2235152-SC **Lot No.: B911205**

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: 42 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# **B911205**

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	4.13	0.62	4.16E-04	CCNE1	3.07	0.16	6.10E-03
EGFR	4.83	0.99	4.16E-04	EGFR	7.19	0.34	6.14E-04

symbol	type	chromosome	position	reference	mutation	quality	allele type	Depth at this position	transcript_ id	existing variation	consequence
AKT1	snp	chr14	105246686	G	A	260.7	hom	11	NM_001014	rs2494738	intron_variant
ALK	snp	chr2	29445458	G	T	9567.4	hom	301	NM_00430	rs3795850	synonymous_variant
APC	snp	chr5	112175770	G	A	1133.9	hom	40	XM_00527	rs41115&C	synonymous_variant
APC	snp	chr5	112176325	G	A	521.9	hom	18	XM_00527	rs42427	synonymous_variant
APC	snp	chr5	112176559	T	G	342.4	hom	13	XM_00527	rs866006	synonymous_variant
APC	snp	chr5	112177171	G	A	6397.7	hom	241	XM_00527	rs465899	synonymous_variant
ATM	snp	chr11	108236128	G	A	1148.0	het	81	NM_00005	COSM1297	missense_variant
CCNE1	complex	chr19	30303555	CCG	ACC	11.2	het	219	NM_001238.2		intron_variant
CCNE1	del	chr19	30314458	GAAAAAAAA	GAAAAAAA	183.4	het	20	NM_001238.2		intron_variant&feature_
CDH1	snp	chr16	68771372	C	T	54775.9	hom	1738	NM_00436	rs3743674	splice_region_variant&i
CDH1	ins	chr16	68771418	CG	CGCCCCAG	457.5	het	38	NM_004360.3		intron_variant&feature_
CDH1	complex	chr16	68771429	TGC	CGT	279.1	het	41	NM_004360.3		intron_variant
CDH1	complex	chr16	68842378	CCTG	TCTGAG	253.7	het	14	NM_004360.3		frameshift_variant&feat
CDH1	complex	chr16	68842384	CTCAGAAGA	CAGGAGAG	303.5	het	17	NM_004360.3		frameshift_variant&feat
CDH1	snp	chr16	68844306	G	A	317.0	het	28	NM_004360.3		intron_variant
CDH1	snp	chr16	68857441	T	C	1163.8	hom	39	NM_00436	rs1801552	synonymous_variant
CDH1	ins	chr16	68857544	CAA	CAAA	1781.3	het	89	NM_004360.3		intron_variant&feature_
CDH1	snp	chr16	68862165	C	T	4096.0	het	186	NM_00436	COSM2077	synonymous_variant
CDKN2A	snp	chr9	21968199	C	G	38612.3	hom	1220	NM_00119	rs11515&C	3_prime_UTR_variant
CDKN2A	snp	chr9	21971004	A	T	454.6	hom	18	NM_001195132.1		synonymous_variant
CDKN2A	snp	chr9	21971008	A	T	437.7	hom	17	NM_00119	COSM1350	missense_variant
CDKN2A	complex	chr9	21971009	GGTCCACGG	GGACCTGG	234.6	hom	10	NM_001195132.1		inframe_insertion
CDKN2A	complex	chr9	21971272	GTAGAGCCC	CTACACAA	827.0	hom	44	NM_001195132.1		intron_variant&feature_
CSF1R	snp	chr5	149433815	C	A	410.7	het	34	NM_005211.3		intron_variant
DDR2	snp	chr1	162740327	TGTC	CGTC	45607.2	hom	1487	XM_005245220.1		intron_variant
DDR2	complex	chr1	162740327	TGTC	CGTT	687.3	het	37	XM_005245220.1		intron_variant

DDR2	snp	chr1	162740369	C	A	296.5	hom	13	XM_005245220.1	intron_variant
DDR2	snp	chr1	162743418	G	T	3645.5	hom	147	XM_005245	rs1355287 intron_variant
EGFR	snp	chr7	55233164	C	A	328.7	het	25	NM_00522	rs17290176 intron_variant
EGFR	snp	chr7	55242249	G	T	262.8	het	218	NM_005228.3	intron_variant
EGFR	complex	chr7	55242253	GCGTCACAG	GGCTGTGA	241.8	het	212	NM_005228.3	intron_variant&feature_
EGFR	snp	chr7	55242500	A	T	284063.0	het	13983	NM_00522	COSM1335 missense_variant
EGFR	snp	chr7	55259515	T	G	43765.7	het	2036	NM_00522	rs12143456 missense_variant
ERBB4	del	chr2	212530218	GAAAAAAAA	GAAAAAAA	156.2	het	94	NM_005235.2	intron_variant&feature_
ERBB4	del	chr2	212578379	TAAAAAAAA	TAAAAAAA	227.9	het	30	NM_005235.2	splice_region_variant&i
EZH2	snp	chr7	148508833	A	G	1427.8	het	91	XM_005249	rs2072407 intron_variant
FBXW7	snp	chr4	153252061	A	G	2881.4	hom	92	NM_033632	rs10033601 intron_variant
FBXW7	snp	chr4	153253719	C	T	1351.9	het	85	NM_033632.3	intron_variant
FBXW7	del	chr4	153268227	CAAAAAAAA	CAAAAAAA	1318.62	het	125	NM_033632.3	splice_region_variant&i
FGFR1	complex	chr8	38271422	ACGGGCAGC	CCATCACAG	453.6	het	21	NM_001174067.1	splice_region_variant&i
FGFR1	snp	chr8	38271440	T	A	442.2	het	24	NM_001174067.1	missense_variant
FGFR1	mnp	chr8	38271467	AGGT	CCAC	333.3	het	18	NM_001174067.1	missense_variant
FGFR1	complex	chr8	38271475	CAC	AAG	478.0	het	21	NM_001174067.1	missense_variant
FGFR1	complex	chr8	38271484	CTT	GTG	406.1	het	20	NM_001174067.1	missense_variant
FGFR1	snp	chr8	38273533	C	T	277.1	hom	10	NM_001174067.1	missense_variant
FGFR3	snp	chr4	1803586	T	G	351.8	het	18	NM_001163213.1	missense_variant
FGFR3	complex	chr4	1803591	GCGGGG	CCCCGC	359.4	het	17	NM_001163213.1	missense_variant
FGFR3	snp	chr4	1803601	C	A	425.5	hom	17	NM_00116	COSM1428 missense_variant
FGFR3	del	chr4	1806012	TGGGGGGGC	TGGGGGGG	2303.5	het	1470	NM_001163213.1	intron_variant&feature_
FGFR3	snp	chr4	1807894	G	A	10719.2	hom	356	NM_00116	rs7688609 synonymous_variant
FGFR3	snp	chr4	1808517	G	A	263.6	het	16	NM_001163213.1	intron_variant
FOXL2	complex	chr3	138664450	GAA	GC	285.3	hom	10	NM_023067.3	frameshift_variant&feat
FOXL2	complex	chr3	138664456	AG	ATT	314.0	hom	11	NM_023067.3	frameshift_variant&feat
GNAQ	snp	chr9	80409345	A	G	617.6	het	28	NM_00207	rs1328529 intron_variant
H3F3A	complex	chr1	226252138	GTGCG	CTTCAC	363.9	hom	13	NM_002107.4	frameshift_variant&feat
H3F3A	complex	chr1	226252148	TACTG	CAGTA	388.8	hom	14	NM_002107.4	missense_variant
H3F3A	snp	chr1	226252239	T	A	137.5	het	11	NM_002107.4	intron_variant
IDH1	del	chr2	209113048	GAAAAAAAA	GAAAAAAA	365.1	het	70	XM_005246521.1	intron_variant&feature_
IDH1	del	chr2	209116299	GAAAAAAAA	GAAAAAAA	1737.7	het	232	XM_005246521.1	intron_variant&feature_
JAK2	del	chr9	5073681	CTTTTTTTTT	CTTTTTTTT	577.9	het	84	NM_004972.3	splice_region_variant&i
KDR	snp	chr4	55980456	C	T	5642.8	het	305	NM_00225	rs2305949 intron_variant
MAP2K1	snp	chr15	66727597	G	C	10667.2	het	548	NM_002755.3	intron_variant
MET	snp	chr7	116436022	G	A	3455.4	hom	115	XM_00525	rs2023748& synonymous_variant
MET	snp	chr7	116436097	G	A	2109.4	hom	75	XM_00525	rs41737&C synonymous_variant
MLH1	snp	chr3	37067240	T	A	3287.7	het	211	NM_00024	rs63750447 missense_variant
MPL	snp	chr1	43815141	G	A	1299.2	het	90	NM_005373.2	intron_variant
MYC	snp	chr8	128748815	G	A	366.7	hom	18	NM_002467.4	5_prime_UTR_variant

MYCN	snp	chr2	16080157	C	G	15334.7	hom	484	NM_00537	rs11886063	upstream_gene_variant
MYCN	snp	chr2	16089615	T	C	8747.8	hom	301	NM_00537	rs4669018	downstream_gene_vari
NOTCH1	snp	chr9	139391636	G	A	6846.3	hom	252	NM_01761	rs2229974	synonymous_variant
NOTCH1	snp	chr9	139397707	G	A	17235.2	hom	573	NM_01761	rs10521&C	synonymous_variant
NOTCH1	complex	chr9	139399177	CACCAGGGA	TCCCTGGTG	300.7	het	14	NM_017617.3		missense_variant
NOTCH1	mnp	chr9	139399195	CCT	GTG	318.8	het	17	NM_017617.3		missense_variant
NOTCH1	complex	chr9	139399394	CTCCGGCGG	ATGCCGCC	1012.8	het	464	NM_017617.3		missense_variant
NOTCH1	snp	chr9	139399587	T	A	249.8	het	22	NM_017617.3		intron_variant
NOTCH1	snp	chr9	139399596	G	C	337.7	hom	15	NM_017617.3		intron_variant
NOTCH1	ins	chr9	139399601	TC	TGAGC	251.0	het	12	NM_01761	rs37379564	intron_variant&feature_
NOTCH1	complex	chr9	139399976	CGTCCTCCTG	AGTGCCAG	263.2	het	13	NM_017617.3		missense_variant
NOTCH1	mnp	chr9	139400164	TT	AC	251.8	het	110	NM_017617.3		missense_variant
NPM1	del	chr5	170837513	CTTTTTTTTT	CTTTTTTTT	2333.09	het	274	NM_002520.6		splice_region_variant&i
PDGFRA	snp	chr4	55141055	A	G	21901.0	hom	722	NM_00620	rs18737788	synonymous_variant
PDGFRA	snp	chr4	55161254	C	T	3819.5	het	238	NM_00620	rs3733540	intron_variant
PDGFRA	snp	chr4	55161391	T	C	1396.4	het	53	NM_00620	rs7685117	synonymous_variant
PDGFRA	snp	chr4	55161517	A	G	7159.8	hom	234	NM_00620	rs7680422	3_prime_UTR_variant
PIK3CA	del	chr3	178927848	ATTTTTTTTT	ATTTTTTTT	1008.5	het	88	NM_006218.2		intron_variant&feature_
PIK3CA	snp	chr3	178935965	G	A	314.1	het	22	NM_006218.2		intron_variant
PIK3R1	snp	chr5	67588148	G	A	3367.8	het	199	NM_18152	rs37300898	missense_variant
PIK3R1	snp	chr5	67589770	T	A	268.2	het	22	NM_181523.2		intron_variant
PTEN	del	chr10	89692731	GTTTTTTTTT	GTTTTTTTT	28.6	het	100	NM_000314.4		intron_variant&feature_
PTEN	del	chr10	89720633	CTTTTTTTTT	CTTTTTTTT	617.0	het	121	NM_000314.4		splice_acceptor_variant
PTEN	snp	chr10	89720907	T	G	1063.6	het	61	NM_00031	rs555895&C	intron_variant
PTEN	del	chr10	89725293	CTTTTTTTTT	CTTTTTTTT	528.4	het	118	NM_000314.4		3_prime_UTR_variant&t
RB1	snp	chr13	48919358	T	G	1896.8	hom	66	NM_00032	rs198617	intron_variant
RB1	del	chr13	48953655	CAAAAAAAA	CAAAAAAA	514.0	het	139	NM_000321.2		intron_variant&feature_
RB1	ins	chr13	49034022	ATT	ATTT	769.3	hom	32	NM_000321.2		intron_variant&feature_
RET	mnp	chr10	43610189	GGG	TCT	265.2	hom	11	NM_020975.4		splice_region_variant&i
RET	mnp	chr10	43610199	GGG	CCC	309.2	het	14	NM_020975.4		intron_variant
RET	snp	chr10	43613843	G	T	8707.1	hom	275	NM_02097	rs1800861&	synonymous_variant
RET	snp	chr10	43617564	T	A	379.3	het	25	NM_020975.4		intron_variant
SMO	snp	chr7	128845277	G	C	23810.3	hom	763	NM_00563	rs2075777	intron_variant
SMO	snp	chr7	128845316	G	A	841.1	hom	40	NM_005631.4		intron_variant
SMO	snp	chr7	128846328	G	C	10179.0	hom	327	NM_00563	rs2228617	synonymous_variant
SMO	snp	chr7	128846457	G	A	247.1	het	31	NM_005631.4		intron_variant
SMO	snp	chr7	128846469	A	G	494.2	hom	18	NM_00563	rs2735842	intron_variant
STK11	snp	chr19	1207238	G	T	19423.5	het	1012	XM_00525	rs3764640	intron_variant
STK11	snp	chr19	1218523	G	T	32230.2	het	1614	XM_00525	rs2075604	intron_variant
STK11	ins	chr19	1219443	GCGGGGGC	GCGGGGG	741.5	het	47	XM_005259617.1		intron_variant&feature_
STK11	snp	chr19	1219451	C	G	162.4	het	76	XM_00525	rs36951560	intron_variant

STK11	snp	chr19	1220321	T	C	23619.3	het	1219	XM_005259	rs2075606	intron_variant
STK11	complex	chr19	1222016	CCTGG	ACTGCCCCC	241.4	het	20	XM_005259617.1		intron_variant&feature_
TERT	snp	chr5	1295396	C	A	147.0	het	16	NM_198253.2		upstream_gene_variant
TP53	snp	chr17	7573080	C	A	438.5	het	33	NM_000546.5		intron_variant
TP53	complex	chr17	7579317	AAGTCA	ACC	1311.1	hom	47	NM_000546.5		feature_truncation
TP53	del	chr17	7579317	AAGTCACAG	AC	1137.1	het	323	NM_000546.5		inframe_deletion
TP53	snp	chr17	7579327	C	A	1476.2	hom	54	NM_000546	TP53_g.115	missense_variant
TP53	snp	chr17	7579472	G	C	18992.7	hom	602	NM_000546	rs1042522&	missense_variant
TP53	del	chr17	7579643	CCCCCAGCC	CC	160.4	het	229	NM_000546.5		intron_variant&feature_
TP53	snp	chr17	7579801	G	C	1945.3	hom	71	NM_000546	rs1642785	intron_variant