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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.: C101118**

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: diameter 7.5 cm

Location: Lung, Right Lower Lobe

Components:
1. **5 curls per package**
2. **Certificate of Analysis**

FOR IN VITRO RESEARCH USE ONLY **APPROVED BY:** _____

C101118

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	allele type	Depth	variant frequency	transcript_id	consequence	existing variation
ALK	snp	chr2	29432625	C	A	18284.1	het	1000	0.59	NM_00430	intron_vari	rs3738868
ALK	snp	chr2	29432776	T	C	15282.7	het	774	0.68	NM_00430	intron_vari	rs3738867
ALK	snp	chr2	29432807	T	A	276.763	hom	12	1.00	NM_00430	intron_variant	
ALK	snp	chr2	29443749	G	T	13411.7	het	575	0.79	NM_00430	intron_vari	rs8015297
APC	snp	chr5	1.12E+08	A	G	665.078	het	43	0.58	XM_00527	missense_variant	
APC	snp	chr5	1.12E+08	G	A	3111.59	hom	135	1.00	XM_00527	synonymou	rs41115&C
APC	snp	chr5	1.12E+08	G	A	260.66	hom	11	1.00	XM_00527	synonymou	rs42427
APC	snp	chr5	1.12E+08	T	G	467.362	hom	20	1.00	XM_00527	synonymou	rs866006
APC	snp	chr5	1.12E+08	G	A	401.697	hom	16	1.00	XM_00527	synonymou	rs465899
APC	snp	chr5	1.12E+08	G	A	477.771	het	31	0.77	XM_00527	missense_v	COSM1186
ATM	del	chr11	1.08E+08	ATTTTTTTT	ATTTTTTTT	82.1873	het	254	0.11	NM_00005	intron_variant&feature	
ATM	snp	chr11	1.08E+08	T	C	408.575	het	38	0.50	NM_00005	intron_variant	
ATM	snp	chr11	1.08E+08	C	T	1114.25	het	74	0.69	NM_00005	intron_variant	
ATM	snp	chr11	1.08E+08	C	T	1019.8	het	64	0.75	NM_00005	intron_vari	rs664982
BRAF	complex	chr7	1.4E+08	GTTA	ATTG	19.8141	het	129	0.12	XM_00525	intron_variant	
CCND1	mnp	chr11	69461913	TTACTT	AAGTAA	525.382	hom	23	0.83	NM_05305	intron_variant	
CCND1	mnp	chr11	69461925	TCA	AGG	610.71	hom	23	1.00	NM_05305	intron_variant	
CCNE1	snp	chr19	30312737	G	A	353.183	het	111	0.20	NM_00123	intron_variant	
CCNE1	snp	chr19	30312874	C	T	233.651	hom	10	1.00	NM_00123	intron_vari	rs3218066
CDH1	snp	chr16	68771372	C	T	20907.9	hom	688	1.00	NM_00436	splice_regi	rs3743674
CDH1	complex	chr16	68771414	TCCGC	CCCGT	930.782	hom	50	0.98	NM_00436	intron_variant	
CDH1	complex	chr16	68842670	TGGTG	TTC	710.985	hom	28	0.96	NM_00436	frameshift_variant&fea	
CDH1	complex	chr16	68842679	TATTATTGA	TCAATAATA	645.54	hom	29	0.90	NM_00436	stop_gained	
CDK4	snp	chr12	58144665	C	T	1819.12	hom	79	1.00	NM_00007	intron_vari	rs2069502
CDK4	snp	chr12	58145438	G	A	2927.45	het	201	0.52	NM_00007	synonymous_variant	
CDKN2A	snp	chr9	21968087	G	T	304.17	hom	15	0.93	NM_00119	3_prime_UTR_variant	
CDKN2A	snp	chr9	21968199	C	G	52770.7	hom	1691	0.99	NM_00119	3_prime_U	rs11515&C

CSF1R	mnp	chr5	1.49E+08	TG	GA	215.451	hom	10	1.00	NM_00521	3_prime_UTR_variant	
DDR2	snp	chr1	1.63E+08	T	C	36539.3	hom	1172	1.00	XM_00524	intron_vari	rs1780003
DDR2	snp	chr1	1.63E+08	G	T	6783.69	hom	231	1.00	XM_00524	intron_vari	rs1355287
EGFR	snp	chr7	55242609	A	G	2829.41	hom	122	1.00	NM_00522	intron_vari	rs2017000
ERBB2	snp	chr17	37881206	C	A	254.013	het	28	0.50	NM_00444	intron_variant	
ERBB3	snp	chr12	56477694	A	T	15411.1	het	619	0.91	NM_00198	splice_regi	rs2271194
ERBB4	del	chr2	2.13E+08	TAAAAAAA	TAAAAAAA	346.632	het	54	0.35	NM_00523	splice_region_variant&	
ERBB4	complex	chr2	2.13E+08	TTAAA	CTATC	855.564	hom	34	0.97	NM_00523	intron_variant	
ERBB4	mnp	chr2	2.13E+08	TAGC	GCTA	828.576	hom	32	0.97	NM_00523	intron_variant	
ERBB4	snp	chr2	2.13E+08	G	T	715.674	hom	30	0.97	NM_00523	intron_variant	
ERBB4	snp	chr2	2.13E+08	G	A	400.875	hom	17	1.00	NM_00523	intron_vari	rs13002712
FBXW7	snp	chr4	1.53E+08	A	G	731.78	hom	29	1.00	NM_03363	intron_vari	rs2714803
FBXW7	del	chr4	1.53E+08	CAAAAAAA	CAAAAAAA	2084.63	het	414	0.23	NM_03363	splice_region_variant&	
FGFR1	snp	chr8	38271575	T	A	259.103	hom	14	1.00	NM_00117	intron_variant	
FGFR2	snp	chr10	1.23E+08	A	G	387.925	hom	16	0.94	NM_02297	missense_variant	
FGFR2	snp	chr10	1.23E+08	T	A	360.407	hom	17	0.88	NM_02297	missense_variant	
FGFR2	snp	chr10	1.23E+08	G	C	360.407	hom	17	0.88	NM_02297	missense_variant	
FGFR3	del	chr4	1806012	TGGGGGG	TGGGGGG	7409.92	het	1781	0.21	NM_00116	intron_variant&feature	
FGFR3	snp	chr4	1807894	G	A	15702.4	hom	520	1.00	NM_00116	synonymou	rs7688609
FGFR3	snp	chr4	1807932	GTCAT	ATCAT	184.914	het	542	0.11	NM_00116	intron_variant	
FGFR3	snp	chr4	1808461	CC	CG	414.18	het	239	0.20	NM_00116	intron_variant	
FGFR3	complex	chr4	1808889	GCCAGGA	TCCTGGC	568.169	hom	20	1.00	NM_00116	missense_variant	
FGFR3	complex	chr4	1808900	CCC	CGGGG	528.349	hom	20	1.00	NM_00116	frameshift_variant&fea	
FLT3	snp	chr13	28609991	T	C	260.66	hom	11	1.00	NM_00411	intron_vari	rs2491229
FLT3	snp	chr13	28609997	T	C	260.66	hom	11	1.00	NM_00411	intron_vari	rs2491230
FLT3	snp	chr13	28610183	A	G	10464.8	het	496	0.74	NM_00411	splice_regi	rs2491231
FOXL2	snp	chr3	1.39E+08	C	A	177.408	het	12	0.83	NM_02306	missense_v	rs3724795
H3F3A	snp	chr1	2.26E+08	T	A	670.565	hom	37	1.00	NM_00210	intron_variant	
HRAS	snp	chr11	533970	C	T	776.252	het	483	0.14	NM_00534	intron_variant	
HRAS	snp	chr11	534197	C	T	3087.19	het	166	0.86	NM_00534	intron_vari	rs4125805
HRAS	del	chr11	534403	GCCCAGGC	GC	705.265	hom	27	1.00	NM_00534	intron_variant&feature	
HRAS	complex	chr11	534405	CCAGGCC	TCAGC	458.791	hom	16	1.00	NM_00534	intron_variant&feature	
IDH1	del	chr2	2.09E+08	GAAAAAAA	GAAAAAAA	13351	het	2331	0.24	XM_00524	intron_variant&feature	
JAK2	del	chr9	5073681	CTTTTTTTT	CTTTTTTTT	1440.61	het	175	0.31	NM_00497	splice_region_variant&	

KDR	snp	chr4	55979517	G	A	4448.87	het	287	0.56	NM_00225	synonymous_variant	
KDR	snp	chr4	55979558	C	T	4286.51	het	254	0.63	NM_00225	missense_v	rs2305948
KDR	snp	chr4	55979577	G	A	1206.65	het	143	0.48	NM_00225	synonymous_variant	
KDR	snp	chr4	55980239	C	T	1314.9	hom	57	1.00	NM_00225	intron_vari	rs7692791
KIT	snp	chr4	55593464	A	C	1301.71	het	65	0.71	XM_00526	missense_v	rs3822148
KIT	snp	chr4	55602701	T	C	1171.9	hom	42	1.00	XM_00526	missense_variant	
KIT	mnp	chr4	55602708	CT	AC	1138.6	hom	42	0.95	XM_00526	missense_variant	
KIT	mnp	chr4	55602720	GT	AG	1197.16	hom	42	1.00	XM_00526	missense_variant	
KIT	snp	chr4	55602728	G	A	1186.72	hom	41	1.00	XM_00526	missense_v	CM057993
KIT	snp	chr4	55602765	G	C	4893.22	het	234	0.69	XM_00526	synonymou	rs3733542
MET	snp	chr7	1.16E+08	G	A	5303.9	het	233	0.87	XM_00525	synonymou	rs41737&C
MLH1	snp	chr3	37067050	A	G	19301.4	het	1018	0.66	NM_00024	intron_vari	rs1112974
MLH1	complex	chr3	37067398	CCTGCTGA	ACTTCAGC	89.2916	het	71	0.17	NM_00024	missense_variant	
MLH1	snp	chr3	37067414	C	G	122.228	het	67	0.18	NM_00024	missense_variant	
MPL	snp	chr1	43814897	C	T	574.268	hom	25	1.00	NM_00537	intron_variant	
MYCN	snp	chr2	16080157	C	G	2441.8	hom	77	1.00	NM_00537	upstream_	rs1188606
MYCN	snp	chr2	16089615	T	C	10414.7	hom	364	1.00	NM_00537	downstrea	rs4669018
NOTCH1	snp	chr9	1.39E+08	G	A	9347.34	hom	322	1.00	NM_01761	synonymou	rs2229974
NOTCH1	snp	chr9	1.39E+08	G	A	13547.1	hom	432	1.00	NM_01761	synonymou	rs10521&C
NPM1	del	chr5	1.71E+08	CTTTTTTTT	CTTTTTTTT	925.921	het	116	0.33	NM_00252	splice_region_variant&	
PDGFRA	snp	chr4	55141055	A	G	32753.7	hom	1052	1.00	NM_00620	synonymou	rs1873778
PDGFRA	snp	chr4	55144447	T	C	264.954	hom	12	1.00	NM_00620	intron_vari	rs1907820
PDGFRA	snp	chr4	55161254	C	T	10950.2	hom	367	0.99	NM_00620	intron_vari	rs3733540
PDGFRA	snp	chr4	55161391	T	C	4753.12	hom	162	1.00	NM_00620	synonymou	rs7685117
PDGFRA	snp	chr4	55161517	A	G	4093.39	hom	137	1.00	NM_00620	3_prime_U	rs7680422
PIK3CA	del	chr3	1.79E+08	ATTTTTTTT	ATTTTTTTT	1490.44	het	419	0.18	NM_00621	intron_variant&feature	
PIK3CA	snp	chr3	1.79E+08	G	A	1736.18	het	151	0.51	NM_00621	intron_variant	
PIK3R1	snp	chr5	67587994	C	T	514.102	hom	22	1.00	NM_18152	intron_vari	rs3730087
PIK3R1	snp	chr5	67588148	G	A	14938	het	752	0.68	NM_18152	missense_v	rs3730089
PIK3R1	snp	chr5	67588273	T	G	220.449	het	27	0.52	NM_18152	intron_variant	
PIK3R1	snp	chr5	67592274	T	A	263.639	hom	14	1.00	NM_18152	intron_variant	
PTEN	snp	chr10	89717717	C	T	749.709	hom	38	0.95	NM_00031	missense_variant	
PTEN	del	chr10	89720633	CTTTTTTTT	CTTTTTTTT	684.579	het	377	0.15	NM_00031	splice_acceptor_varian	
PTEN	snp	chr10	89720907	T	G	5291.21	hom	187	1.00	NM_00031	intron_vari	rs555895&

RB1	snp	chr13	48919358	T	G	8700.01	hom	293	1.00	NM_00032	intron_vari	rs198617
RB1	ins	chr13	48953655	CAAAAAAA	CAAAAAAA	2082.8	het	403	0.23	NM_00032	intron_variant&feature	
RB1	snp	chr13	48955603	A	G	225.805	het	185	0.16	NM_00032	intron_variant	
RB1	snp	chr13	48955647	G	A	844.888	hom	36	1.00	NM_00032	intron_variant	
RB1	snp	chr13	49033747	G	A	1130	hom	44	1.00	NM_00032	intron_vari	rs198580
RB1	ins	chr13	49034022	ATT	ATTT	1922.6	hom	82	0.99	NM_00032	intron_variant&feature	
RB1	ins	chr13	49034087	TT	TTCT	507.237	het	40	0.63	NM_00032	intron_variant&feature	
RB1	complex	chr13	49034103	CTC	CTTT	527.118	hom	24	0.96	NM_00032	intron_variant&feature	
RB1	complex,sr	chr13	49034103	CTC	CTTT,CTT	1007.75	het	46	0.50	NM_00032	intron_variant&feature	
RB1	ins	chr13	49034111	CTT	CTTT	301.943	het	39	0.59	NM_00032	intron_variant&feature	
RB1	snp	chr13	49034115	C	T	322.86	het	44	0.36	NM_00032	intron_vari	rs5638805
RB1	snp	chr13	49034119	T	C	507.936	het	48	0.48	NM_00032	intron_variant	
RET	complex	chr10	43615494	CATGGC	GAGGGT	365.847	hom	14	1.00	NM_02097	intron_variant	
ROS1	complex	chr6	1.18E+08	AAA	GAAAACGA	319.174	het	15	0.80	NM_00294	splice_region_variant&	
SMAD4	mnp	chr18	48584516	GG	AA	2719.66	hom	119	1.00	NM_00535	missense_variant	
SMAD4	complex	chr18	48584757	AATTTGC	AGGTGTGT	658.741	hom	24	1.00	NM_00535	frameshift_variant&fea	
SMAD4	snp	chr18	48586132	A	G	783.484	het	70	0.50	NM_00535	intron_variant	
SMARCB1	snp	chr22	24145675	G	C	607.982	hom	28	0.96	XM_00526	intron_vari	rs5751738
SMO	complex	chr7	1.29E+08	CCCG	TCCC	4107.39	hom	147	0.98	NM_00563	intron_variant	
SMO	complex,sr	chr7	1.29E+08	CCCG	TCCC,CCCC	31054.9	het	1114	0.86	NM_00563	intron_variant	
SMO	snp	chr7	1.29E+08	G	C	25986.7	hom	825	1.00	NM_00563	synonymou	rs2228617
SMO	snp	chr7	1.29E+08	A	G	513.959	hom	23	1.00	NM_00563	intron_vari	rs2735842
STK11	snp	chr19	1207238	G	T	7502.16	het	402	0.62	XM_00525	intron_vari	rs3764640
STK11	snp	chr19	1219436	GGGT	GGGG	60.7259	het	109	0.16	XM_00525	intron_variant	
STK11	snp	chr19	1222012	G	C	43455.5	het	2252	0.63	XM_00525	splice_regi	rs2075607
STK11	snp	chr19	1222075	G	A	449.544	het	673	0.14	XM_00525	intron_vari	rs1817329
TP53	snp	chr17	7579472	G	C	13240.2	hom	423	1.00	NM_00054	missense_v	rs1042522
TP53	del	chr17	7579643	CCCCCAGC	CC	2591.6	het	393	0.33	NM_00054	intron_variant&feature	
TP53	complex	chr17	7579678	CCAG	TTAC	3.51942	het	91	0.13	NM_00054	intron_variant	
TP53	snp	chr17	7579801	G	C	1705.92	hom	58	1.00	NM_00054	intron_vari	rs1642785