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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.: C101106**

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: 48 year(s) old

Pathological Diagnosis: Adenocarcinoma

Tumor Size: diameter 5 cm

Location: Lung, Left Upper Lobe

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

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

C101106

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.

tissue type	Lot #	Strong Evidence compared with **GIAB** (NA12878)	Copy Number	STDev of Copy Number	P-value
Lung	C101106	MDM2	4.66	0.20	8.94E-04

symbol	type	chromosome	position	reference	mutation	quality	allele type	Depth	variant frequency	transcript_id	consequence	existing variation
AKT1	snp	chr14	1.05E+08	T	A	1553.09	hom	69	0.99	NM_00101	intron_vari	rs2494737
ALK	snp	chr2	29432625	C	A	10014	het	491	0.66	NM_00430	intron_vari	rs3738868
ALK	snp	chr2	29432776	T	C	5397.62	het	315	0.59	NM_00430	intron_vari	rs3738867
ALK	snp	chr2	29443746	CTGG	CTGT	8587.65	het	416	0.69	NM_00430	intron_variant	
ALK	complex	chr2	29443746	CTGG	TTGT	71.037	het	125	0.13	NM_00430	intron_variant	
ALK	snp	chr2	29445458	G	T	2334.05	het	113	0.68	NM_00430	synonymou	rs3795850
APC	snp	chr5	1.12E+08	G	A	946.264	hom	38	0.95	XM_00527	synonymou	rs465899
APC	snp	chr5	1.12E+08	G	A	409.755	hom	18	1.00	XM_00527	missense_variant	
ATM	snp	chr11	1.08E+08	C	T	474.042	hom	24	1.00	NM_00005	intron_variant	
ATM	snp	chr11	1.08E+08	C	T	420.622	hom	18	1.00	NM_00005	intron_vari	rs1819242
ATM	snp	chr11	1.08E+08	G	A	2504.67	hom	93	0.96	NM_00005	missense_variant	
ATM	snp	chr11	1.08E+08	T	A	847.952	het	54	0.85	NM_00005	missense_variant	
BRAF	snp	chr7	1.4E+08	C	T	298.208	het	17	0.76	XM_00525	missense_variant	
CCND1	snp	chr11	69462061	G	A	624.503	hom	28	1.00	NM_05305	intron_variant	
CCNE1	snp	chr19	30303617	C	T	616.322	het	31	0.84	NM_00123	synonymou	rs1395513
CDH1	snp	chr16	68771372	CC	TC	42300.3	hom	1414	0.98	NM_00436	splice_region_variant&	
CDH1	mnp	chr16	68771372	CC	TT	558.507	het	27	0.85	NM_00436	splice_region_variant&	
CDH1	snp	chr16	68857441	T	C	2580.19	het	120	0.86	NM_00436	synonymou	rs1801552
CDH1	snp	chr16	68867447	C	A	1181.44	hom	57	1.00	NM_00436	3_prime_UTR_variant	
CDK4	snp	chr12	58144665	C	T	409.586	hom	15	1.00	NM_00007	intron_vari	rs2069502
CDK4	complex	chr12	58144753	AGTCA	TGGCCTG	321.657	hom	20	1.00	NM_00007	frameshift_variant&fea	

CDK4	snp	chr12	58144838	G	A	1213.72	hom	43	1.00	NM_00007	synonymous_variant	
CDKN2A	snp	chr9	21968193	G	A	1943.14	het	116	0.59	NM_00119	3_prime_UTR_variant	
CDKN2A	snp	chr9	21968199	C	G	3337.88	hom	114	0.93	NM_00119	3_prime_U	rs11515&C
CSF1R	mnp	chr5	1.49E+08	TG	GA	373.881	hom	16	1.00	NM_00521	3_prime_UTR_variant	
CTNNB1	del	chr3	41266268	CTT	CT	1296.77	het	146	0.35	XM_00526	intron_variant&feature	
DDR2	snp	chr1	1.63E+08	T	C	18575	hom	594	1.00	XM_00524	intron_vari	rs1780003
DDR2	snp	chr1	1.63E+08	G	T	3388.9	hom	115	1.00	XM_00524	intron_vari	rs1355287
DDR2	complex	chr1	1.63E+08	ATAC	GTAT	193.237	het	13	0.77	XM_00524	intron_variant	
DDR2	mnp	chr1	1.63E+08	AT	TC	191.22	het	12	0.83	XM_00524	intron_variant	
DDR2	snp	chr1	1.63E+08	T	C	2366.41	hom	104	1.00	XM_00524	intron_vari	rs1510315
EGFR	snp	chr7	55241472	C	T	496.938	hom	24	0.96	NM_00522	intron_variant	
ERBB2	complex	chr17	37882836	GTCG	CTTA	730.749	hom	26	1.00	NM_00444	stop_gained	
ERBB2	snp	chr17	37882845	G	C	747.922	hom	26	1.00	NM_00444	missense_variant	
ERBB2	complex	chr17	37882850	CGG	AGA	706.78	hom	25	1.00	NM_00444	synonymous_variant	
ERBB2	del	chr17	37882887	ACCCCCA	ACCCCA	1886.22	het	795	0.17	NM_00444	frameshift_variant&fea	
ERBB3	snp	chr12	56477694	A	T	7974.43	hom	267	0.99	NM_00198	splice_regi	rs2271194
EZH2	snp	chr7	1.49E+08	A	G	749.295	hom	25	1.00	XM_00524	intron_vari	rs2072407
FBXW7	snp	chr4	1.53E+08	A	G	940.193	hom	31	1.00	NM_03363	intron_vari	rs10033601
FBXW7	del	chr4	1.53E+08	CAAAAAAAA	CAAAAAAA	210.119	het	41	0.29	NM_03363	splice_region_variant&	
FGFR1	complex	chr8	38279256	TGCTCCCCCC	CCCTCGCC	776.655	hom	36	0.97	NM_00117	intron_variant	
FGFR1	snp	chr8	38279345	G	T	805.58	het	74	0.51	NM_00117	missense_variant	
FGFR2	snp	chr10	1.23E+08	A	C	3191.7	het	155	0.88	NM_02297	intron_vari	rs3135802
FGFR2	snp	chr10	1.23E+08	G	T	302.209	het	54	0.48	NM_02297	intron_variant	
FGFR3	ins	chr4	1806012	TGGGGGGGG	TGGGGGG	725.113	het	338	0.16	NM_00116	intron_variant&feature	
FGFR3	snp	chr4	1806080	G	A	2090.44	het	135	0.61	NM_00116	missense_variant	
FGFR3	snp	chr4	1807894	G	A	2673.51	hom	93	1.00	NM_00116	synonymou	rs7688609
FLT3	snp	chr13	28609991	T	C	289.605	het	25	0.56	NM_00411	intron_vari	rs2491229
FLT3	snp	chr13	28609997	T	C	284.867	het	24	0.58	NM_00411	intron_vari	rs2491230
FLT3	snp	chr13	28610183	A	G	2019.94	het	112	0.63	NM_00411	splice_regi	rs2491231
GNAS	snp	chr20	57484335	G	A	971.462	het	88	0.50	NM_08042	intron_variant	
HRAS	snp	chr11	534197	C	T	1698.39	het	98	0.66	NM_00534	intron_vari	rs4125805
IDH1	del	chr2	2.09E+08	GAAAAAAAA	GAAAAAAA	1648.09	het	277	0.25	XM_00524	intron_variant&feature	
KDR	snp	chr4	55972974	T	A	879.432	het	45	0.78	NM_00225	missense_v	rs1870377
MPL	mnp	chr1	43814949	TGAC	ATCT	554.345	hom	21	0.95	NM_00537	missense_variant	

MYC	snp	chr8	1.29E+08	C	T	354.137	hom	15	1.00	NM_00246	missense_variant	
MYCN	snp	chr2	16080157	C	G	1377.28	hom	45	1.00	NM_00537	upstream_	rs1188606
MYCN	snp	chr2	16081072	C	T	373.881	hom	16	1.00	NM_00537	intron_variant	
MYCN	snp	chr2	16089615	T	C	4751.17	hom	164	1.00	NM_00537	downstrea	rs4669018
NOTCH1	snp	chr9	1.39E+08	G	A	1312.27	hom	56	1.00	NM_01761	synonymou	rs2229974
NOTCH1	snp	chr9	1.39E+08	G	A	1031.84	hom	36	1.00	NM_01761	synonymou	rs10521&C
NOTCH1	snp	chr9	1.39E+08	C	T	1340.34	het	103	0.53	NM_01761	synonymous_variant	
PDGFRA	snp	chr4	55141055	A	G	19544.7	hom	651	1.00	NM_00620	synonymou	rs1873778
PDGFRA	snp	chr4	55152040	C	T	4346.38	het	288	0.50	NM_00620	synonymou	rs2228308
PDGFRA	snp	chr4	55161391	T	C	624.394	hom	23	1.00	NM_00620	synonymou	rs7685117
PDGFRA	snp	chr4	55161517	A	G	982.063	het	44	0.84	NM_00620	3_prime_U	rs7680422
PIK3CA	del	chr3	1.79E+08	ATTTTTTTTTT	ATTTTTTTT	1059.09	het	262	0.20	NM_00621	intron_variant&feature	
PIK3R1	snp	chr5	67589182	T	C	467.467	hom	19	0.95	NM_18152	synonymou	rs1784731
PIK3R1	snp	chr5	67593456	G	A	227.334	het	45	0.29	NM_18152	3_prime_UTR_variant	
PTEN	snp	chr10	89720907	T	G	507.77	hom	22	1.00	NM_00031	intron_vari	rs555895&
PTPN11	snp	chr12	1.13E+08	A	T	220.373	het	26	0.50	NM_00283	missense_v	rs3975075
RB1	snp	chr13	48919358	T	G	514.358	hom	18	1.00	NM_00032	intron_vari	rs198617
RB1	snp	chr13	48953600	C	T	555.434	hom	26	0.96	NM_00032	intron_variant	
RB1	snp	chr13	49037948	G	T	75.9093	het	41	0.24	NM_00032	missense_variant	
RET	snp	chr10	43610281	G	A	267.46	hom	13	1.00	NM_02097	intron_variant	
RET	snp	chr10	43613843	G	T	6275.55	het	317	0.65	NM_02097	synonymou	rs1800861
RET	snp	chr10	43615060	G	A	1449.91	het	101	0.57	NM_02097	missense_variant	
SMARCB1	snp	chr22	24134013	C	T	1107.94	het	79	0.54	XM_00526	missense_variant	
SMARCB1	snp	chr22	24145670	G	A	245.206	hom	11	1.00	XM_00526	intron_variant	
SMO	snp	chr7	1.29E+08	G	C	7969.94	hom	255	1.00	NM_00563	intron_vari	rs2075777
SMO	snp	chr7	1.29E+08	G	C	2614.39	hom	87	1.00	NM_00563	synonymou	rs2228617
SRC	snp	chr20	36031501	C	T	15240.6	hom	492	1.00	NM_00541	intron_vari	rs2273677
STK11	del	chr19	1206796	CTTTTTTTTTT	CTTTTTTTT	257.483	het	53	0.28	XM_00525	5_prime_UTR_variant&	
STK11	snp	chr19	1207238	G	T	6555.59	hom	214	0.99	XM_00525	intron_vari	rs3764640
STK11	complex	chr19	1218464	GGTGG	AGTGA	535.222	het	792	0.13	XM_00525	missense_variant	
STK11	snp	chr19	1219274	G	A	720.816	hom	31	1.00	XM_00525	intron_vari	rs3492888
STK11	complex	chr19	1219435	AGGGT	GGGGG	34.0379	het	93	0.15	XM_00525	intron_variant	
STK11	snp	chr19	1219444	C	G	404.816	het	47	0.45	XM_00525	intron_variant	
STK11	snp	chr19	1219451	C	G	44.279	het	46	0.22	XM_00525	intron_vari	rs3695156

STK11	snp	chr19	1221422	G	A	233.691	het	12	0.92	XM_00525	intron_variant	
STK11	snp	chr19	1222012	G	C	26835.3	hom	865	1.00	XM_00525	splice_regi	rs2075607
STK11	snp	chr19	1226508	G	A	2198.08	het	89	0.93	XM_00525	missense_variant	
TP53	del	chr17	7579643	CCCCCAGCCC	CC	569.085	het	165	0.25	NM_00054	intron_variant&feature	
TP53	complex	chr17	7579668	CTCCAG	CAACCCTT	2446.16	het	280	0.41	NM_00054	intron_variant&feature	
TP53	complex	chr17	7579678	CCAG	TTAC	2117.03	het	284	0.40	NM_00054	intron_variant	