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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.: C101104**

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: 57 year(s) old

Pathological Diagnosis: Adenocarcinoma

Tumor Size: diameter 4 cm

Location: Lung, Right Lower Lobe

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

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

C101104

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	C101104	DDR2	3.88	0.37	3.72E-03
		TP53	4.23	0.25	2.18E-04

symbol	type	chromosome	position	reference	mutation	quality	allele type	Depth	variant frequency	transcript_id	consequence	existing variation
ABL1	snp	chr9	133738434	C	T	2805.73	het	129	0.83	NM_00731	intron_variant	
ABL1	snp	chr9	133748254	C	T	2740.14	het	130	0.81	NM_00731	synonymous_variant	
AKT1	snp	chr14	105246479	G	A	9590.69	het	656	0.51	NM_00101	missense_variant	
ALK	snp	chr2	29432662	C	T	4218.5	het	255	0.60	NM_00430	missense_variant	
ALK	snp	chr2	29445458	G	T	4742.23	het	283	0.54	NM_00430	synonymou	rs3795850
CCND1	complex	chr11	69461845	CGGCTCCC	GGGAGCCC	2236.68	hom	77	1.00	NM_05305	intron_variant	
CDH1	snp	chr16	68771372	C	T	44529	hom	1383	1.00	NM_00436	splice_regi	rs3743674
CDH1	snp	chr16	68772322	C	T	10205.9	hom	365	0.98	NM_00436	splice_region_variant&	
CDK4	snp	chr12	58145111	C	T	3474.44	hom	121	0.98	NM_00007	missense_variant	
CDKN2A	snp	chr9	21968199	C	G	53998.8	hom	1732	1.00	NM_00119	3_prime_U	rs11515&C
CDKN2A	snp	chr9	21974894	C	T	3161.67	het	133	0.91	NM_00119	5_prime_UTR_variant	
CSF1R	snp	chr5	149453037	C	T	1554.31	het	107	0.51	NM_00521	synonymous_variant	
CTNNB1	snp	chr3	41266124	A	G	8568.12	het	527	0.57	XM_00526	missense_v	COSM5716
DDR2	mnp	chr1	162740326	GT	AC	4424.04	het	231	0.69	XM_00524	intron_variant	
DDR2	snp	chr1	162740326	GT	GC	99854.1	hom	3437	0.93	XM_00524	intron_variant	
DDR2	snp	chr1	162740327	T	C	280.011	hom	10	1.00	XM_00524	intron_vari	rs1780003
DDR2	snp	chr1	162740369	C	A	806.971	hom	36	1.00	XM_00524	intron_variant	
DDR2	snp	chr1	162741794	C	T	1858.1	het	84	0.87	XM_00524	intron_vari	rs3738807
DDR2	snp	chr1	162741963	G	A	1870.93	het	88	0.88	XM_00524	missense_v	COSM8987
DDR2	snp	chr1	162746040	C	T	11656.4	hom	506	1.00	XM_00524	synonymous_variant	
DDR2	snp	chr1	162748470	A	G	6913.11	het	473	0.51	XM_00524	missense_variant	

DDR2	snp	chr1	162749873	T	C	270.085	hom	10	1.00	XM_00524	intron_variant	
EGFR	snp	chr7	55211016	G	A	1166.78	het	76	0.55	NM_00522	missense_variant	
EGFR	snp	chr7	55221777	C	T	10290.9	het	661	0.54	NM_00522	missense_v	COSM1651
EGFR	snp	chr7	55249063	G	A	3873.22	het	161	0.92	NM_00522	synonymou	rs1050171
EGFR	snp	chr7	55259608	C	A	6541.66	hom	293	1.00	NM_00522	intron_vari	rs3697258
ERBB2	snp	chr17	37881134	C	T	18399.5	het	1196	0.54	NM_00444	synonymous_variant	
ERBB2	snp	chr17	37882633	A	T	432.946	hom	28	1.00	NM_00444	intron_variant	
ERBB2	snp	chr17	37882689	C	T	14693.6	hom	514	1.00	NM_00444	intron_variant	
ERBB2	complex	chr17	37882752	GAGGGGA	CAGGAGG	292.476	hom	12	1.00	NM_00444	intron_variant	
ERBB2	ins	chr17	37882762	GC	GTC	396.172	hom	18	1.00	NM_00444	intron_variant&feature	
ERBB2	snp	chr17	37882763	C	T	137.385	het	28	0.36	NM_00444	intron_variant	
ERBB2	complex	chr17	37882768	AGCACA	TGCTAGTC	424.076	hom	19	1.00	NM_00444	intron_variant&feature	
ERBB2	snp	chr17	37882778	G	C	291.11	het	23	0.78	NM_00444	intron_variant	
ERBB3	snp	chr12	56477694	A	T	7766.14	hom	248	0.99	NM_00198	splice_regi	rs2271194
ERBB4	snp	chr2	212289026	C	T	1088.61	hom	38	1.00	NM_00523	missense_variant&spli	
ERBB4	snp	chr2	212578519	A	T	29597.3	hom	932	1.00	NM_00523	intron_vari	rs3512391
FBXW7	del	chr4	153268227	CAAAAAAAA	CAAAAAAA	215.321	het	28	0.39	NM_03363	splice_region_variant&	
FGFR2	snp	chr10	123279745	C	T	212.247	het	138	0.16	NM_02297	intron_vari	rs2981448
FGFR3	del	chr4	1806012	TGGGGGGGG	TGGGGGG	5886.35	het	1085	0.24	NM_00116	intron_variant&feature	
FGFR3	mnp	chr4	1806215	CAC	GTG	88.199	het	68	0.15	NM_00116	missense_variant	
FLT3	snp	chr13	28610123	C	T	247.06	het	16	0.63	NM_00411	missense_variant	
FLT3	snp	chr13	28610181	CTA	CTG	4916.09	het	306	0.51	NM_00411	splice_acceptor_varian	
FOXL2	snp	chr3	138665245	CT	TT	3701.09	het	2015	0.16	NM_02306	missense_variant	
FOXL2	snp	chr3	138665607	C	T	1975.13	het	114	0.62	NM_02306	5_prime_UTR_variant	
HRAS	snp	chr11	533853	C	T	1287.9	hom	47	0.98	NM_00534	missense_variant	
HRAS	complex	chr11	534397	AGCCA	GGCTG	1580.38	hom	58	0.98	NM_00534	intron_variant	
HRAS	mnp	chr11	534406	CA	TG	1504.18	hom	58	0.95	NM_00534	intron_variant	
IDH1	del	chr2	209116299	GAAAAAAAA	GAAAAAAA	371.557	het	97	0.21	XM_00524	intron_variant&feature	
IDH2	snp	chr15	90631910	A	T	2122.79	het	197	0.65	NM_00216	missense_variant	
JAK3	snp	chr19	17945675	G	A	11445	het	771	0.51	XM_00525	synonymous_variant	
KDR	snp	chr4	55946145	G	A	284.948	het	16	0.75	NM_00225	missense_variant	
KDR	snp	chr4	55946158	G	A	283.894	het	14	0.86	NM_00225	stop_gained	
KDR	snp	chr4	55953872	C	T	1928.97	het	83	0.90	NM_00225	synonymous_variant	
KIT	snp	chr4	55597543	G	A	637.737	het	44	0.55	XM_00526	missense_variant	

KRAS	snp	chr12	25362754	G	A	4720.58	het	240	0.71	NM_03336	3_prime_UTR_variant	
MAP2K1	snp	chr15	66727483	G	T	770.238	het	60	0.83	NM_00275	missense_v	CM076269
MAP2K1	snp	chr15	66727515	C	T	3023.87	het	143	0.87	NM_00275	synonymous_variant	
MAP2K1	snp	chr15	66727597	G	C	49263.2	het	2822	0.55	NM_00275	intron_vari	rs16949924
MET	snp	chr7	116411924	G	A	12302.3	het	790	0.54	XM_00525	missense_v	rs45607832
MET	snp	chr7	116436093	C	T	940.936	het	73	0.48	XM_00525	missense_variant	
MPL	mnp	chr1	43815066	CC	AT	223.13	het	509	0.12	NM_00537	intron_variant	
MYCN	snp	chr2	16080157	C	G	2049.26	hom	66	1.00	NM_00537	upstream_	rs11886063
MYCN	snp	chr2	16089615	T	C	530.743	hom	19	1.00	NM_00537	downstrea	rs4669018
NOTCH1	snp	chr9	139391636	G	A	19642.3	hom	851	1.00	NM_01761	synonymou	rs2229974
NOTCH1	snp	chr9	139391945	G	A	1419.01	het	94	0.56	NM_01761	synonymous_variant	
NOTCH1	complex	chr9	139399177	CACCAGGGA	TCCCTGGT	2255.27	hom	85	0.98	NM_01761	missense_variant	
NOTCH1	mnp	chr9	139399195	CCT	GTG	2486.21	hom	94	0.99	NM_01761	missense_variant	
NOTCH1	snp	chr9	139399210	G	A	2346.13	het	121	0.78	NM_01761	synonymou	COSM3086
NOTCH1	snp	chr9	139400322	GCC	GCT	3857.37	het	560	0.27	NM_01761	missense_variant	
NPM1	del	chr5	170837513	CTTTTTTTTT	CTTTTTTT	2816.43	het	362	0.29	NM_00252	splice_region_variant&	
PDGFRA	snp	chr4	55141055	A	G	6349.41	hom	218	1.00	NM_00620	synonymou	rs18737788
PDGFRA	complex	chr4	55161254	CAG	TAA	759.826	hom	27	1.00	NM_00620	intron_variant	
PDGFRA	snp	chr4	55161254	CAG	TAG	9411.48	hom	324	0.92	NM_00620	intron_variant	
PDGFRA	snp	chr4	55161517	A	G	11174.9	hom	350	1.00	NM_00620	3_prime_U	rs7680422
PIK3CA	snp	chr3	178921453	C	T	1053.5	het	75	0.52	NM_00621	missense_variant	
PIK3R1	snp	chr5	67589552	G	A	230.849	het	13	0.85	NM_18152	missense_variant	
PTEN	snp	chr10	89624214	C	T	2234.19	het	143	0.87	NM_00031	5_prime_UTR_variant	
PTEN	snp	chr10	89692926	C	T	791.026	hom	28	1.00	NM_00031	missense_v	COSM5068
PTEN	del	chr10	89725293	CTTTTTTTTT	CTTTTTTT	1237.69	het	471	0.16	NM_00031	3_prime_UTR_variant&	
PTEN	snp	chr10	89725294	T	C	364.117	het	77	0.23	NM_00031	3_prime_U	rs1044487
RET	snp	chr10	43613843	G	T	5191.15	hom	163	1.00	NM_02097	synonymou	rs18008618
RET	complex	chr10	43615494	CATGGC	GAGGGT	352.344	hom	13	1.00	NM_02097	intron_variant	
ROS1	snp	chr6	117638364	A	T	261.659	hom	10	1.00	NM_00294	missense_variant	
ROS1	complex	chr6	117638391	AGAC	TGGA	5622.24	het	283	0.75	NM_00294	missense_variant	
SMAD4	snp	chr18	48603128	G	A	2686.18	hom	97	1.00	NM_00535	missense_variant	
SMARCB1	snp	chr22	24145506	G	A	1315.15	het	64	0.78	XM_00526	synonymous_variant	
SMARCB1	snp	chr22	24145670	G	A	996.741	hom	43	1.00	XM_00526	intron_variant	
SMO	snp	chr7	128846415	C	T	1558.69	het	105	0.53	NM_00563	synonymous_variant	

STK11	snp	chr19	1207178	C	T	667.201	het	30	0.90	XM_00525	missense_variant	
STK11	snp	chr19	1207238	G	T	49651.1	hom	1564	1.00	XM_00525	intron_vari	rs3764640
STK11	snp	chr19	1220321	T	C	9838.49	hom	311	0.99	XM_00525	intron_vari	rs2075606
TERT	mnp,mnp	chr5	1295349	AA	GG,GT	673.295	het	37	0.46	NM_19825	upstream_gene_varian	
TERT	snp	chr5	1295349	A	G	265611	hom	8607	1.00	NM_19825	upstream_	rs2853669
TP53	snp	chr17	7573870	G	A	570.504	het	911	0.12	NM_00054	intron_variant	
TP53	snp	chr17	7576835	G	A	11931.5	het	524	0.89	NM_00054	intron_vari	rs3734649
TP53	snp	chr17	7577054	G	A	565.464	het	29	0.79	NM_00054	missense_	TP53_g.138
TP53	snp	chr17	7577407	A	C	3157.73	hom	106	1.00	NM_00054	intron_vari	rs1295105
TP53	snp	chr17	7577427	G	A	2941.53	hom	100	1.00	NM_00054	intron_vari	rs1294778
TP53	snp	chr17	7578441	G	A	577.51	het	30	0.77	NM_00054	synonymou	TP53_g.124
TP53	del	chr17	7579643	CCCCCAGCC(	CC	71.1169	het	107	0.17	NM_00054	intron_variant&feature	