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Data Sheet

Product Name: CancerSeqPlus Paraffin Tissue Curl

Catalog No.: T2235152-SC **Lot No.: C101110**

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: 69 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:** _____

C101110

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
ABL1	snp	chr9	1.34E+08	G	A	31.8357	het	87	0.13	NM_00731	synonymous_variant	
AKT1	snp	chr14	1.05E+08	TTG	TTA	2400.13	het	686	0.19	NM_00101	splice_region_variant&	
ALK	snp	chr2	29432624	C	T	1133.33	het	250	0.22	NM_00430	intron_variant	
ALK	snp	chr2	29432635	A	G	762.83	het	194	0.20	NM_00430	intron_variant	
ALK	snp	chr2	29445458	G	T	820.321	het	64	0.47	NM_00430	synonymou	rs3795850
ALK	snp	chr2	29445506	T	A	202.236	hom	11	0.91	NM_00430	intron_variant	
APC	snp	chr5	1.12E+08	A	C	241.375	het	19	0.53	XM_00527	missense_variant	
APC	snp	chr5	1.12E+08	G	A	891.244	het	517	0.15	XM_00527	missense_variant	
ATM	snp	chr11	1.08E+08	C	T	1771.66	het	81	0.86	NM_00005	missense_variant	
ATM	snp	chr11	1.08E+08	C	T	84.4777	het	65	0.15	NM_00005	intron_variant	
CCND1	snp	chr11	69465027	G	A	3426.14	het	430	0.30	NM_05305	intron_variant	
CDH1	snp	chr16	68771372	C	T	4549.63	hom	156	1.00	NM_00436	splice_regi	rs3743674
CDH1	snp	chr16	68842351	G	A	1359.8	het	87	0.57	NM_00436	missense_variant	
CDH1	snp	chr16	68863659	C	T	6063.68	het	323	0.68	NM_00436	missense_v	CD073586
CDH1	snp	chr16	68867298	A	T	5664.83	hom	274	1.00	NM_00436	missense_variant	
CDKN2A	complex	chr9	21968199	CGAGG	GGAGA	5582.13	hom	196	0.99	NM_00119	3_prime_UTR_variant	
CDKN2A	complex,sr	chr9	21968199	CGAGG	GGAGA,GG	15836.7	het	528	0.63	NM_00119	3_prime_UTR_variant	
CDKN2A	snp	chr9	21971221	C	T	5204.93	het	225	0.89	NM_00119	intron_vari	COSM1376
CDKN2A	snp	chr9	21974856	C	T	39606	hom	1338	1.00	NM_00119	5_prime_UTR_variant	
DDR2	snp	chr1	1.63E+08	T	C	29894	hom	950	1.00	XM_00524	intron_vari	rs1780003
EGFR	snp	chr7	55211147	C	T	61.8148	het	91	0.13	NM_00522	synonymous_variant	
EGFR	snp	chr7	55241649	C	A	4438.27	het	290	0.57	NM_00522	synonymou	COSM1451
ERBB2	snp	chr17	37882879	G	A	3481.9	het	214	0.57	NM_00444	missense_variant	
ERBB3	snp	chr12	56477694	A	T	3686.81	hom	128	1.00	NM_00198	splice_regi	rs2271194
ERBB4	snp	chr2	2.13E+08	C	T	548.715	het	305	0.15	NM_00523	synonymous_variant	
EZH2	snp	chr7	1.49E+08	A	G	1919.49	hom	64	1.00	XM_00524	intron_vari	rs2072407
FBXW7	del	chr4	1.53E+08	CAAAAAAA	CAAAAAAA	648.951	het	116	0.26	NM_03363	splice_region_variant&	

FGFR1	snp	chr8	38271351	G	A	1156.52	het	173	0.27	NM_00117	intron_variant	
FGFR1	snp	chr8	38271376	G	A	2410.18	het	157	0.54	NM_00117	intron_variant	
FGFR1	snp	chr8	38279311	G	A	365.217	het	100	0.20	NM_00117	splice_region_variant&	
FGFR1	snp	chr8	38279340	G	A	1721.79	het	86	0.76	NM_00117	synonymous_variant	
FGFR1	snp	chr8	38282162	C	T	1341.2	het	54	0.93	NM_00117	synonymous_variant	
FGFR2	snp	chr10	1.23E+08	G	A	187.86	het	860	0.11	NM_02297	intron_vari	rs7416062
FGFR2	snp	chr10	1.23E+08	C	T	8088.13	hom	295	0.99	NM_02297	missense_variant	
FGFR3	snp	chr4	1808964	C	T	1023	het	43	0.91	NM_00116	missense_v	rs1504520
FOXL2	snp	chr3	1.39E+08	G	A	2530.45	het	223	0.41	NM_02306	missense_variant	
GNA11	snp	chr19	3118958	G	A	287.718	het	57	0.25	NM_00206	synonymous_variant	
HNF1A	snp	chr12	1.21E+08	C	T	894.793	het	39	0.90	XM_00525	splice_region_variant&	
HRAS	snp	chr11	533736	G	A	2860.58	het	295	0.35	NM_00534	intron_variant	
HRAS	snp	chr11	533969	C	T	410.332	het	272	0.14	NM_00534	intron_variant	
HRAS	snp	chr11	534242	A	G	4325.16	hom	137	1.00	NM_00534	synonymou	rs12628&C
HRAS	snp	chr11	534259	G	A	1733.96	het	95	0.68	NM_00534	stop_gaine	rs1219177
HRAS	snp	chr11	534394	C	T	3380.37	hom	126	0.96	NM_00534	intron_variant	
HRAS	del	chr11	534403	GCCCAGGC	GC	3193.08	hom	113	1.00	NM_00534	intron_variant&feature	
IDH1	del	chr2	2.09E+08	GAAAAAAA	GAAAAAAA	165.257	het	61	0.18	XM_00524	intron_variant&feature	
IDH2	snp	chr15	90631911	A	T	12679.2	hom	597	0.99	NM_00216	missense_variant	
JAK3	snp	chr19	17945640	T	C	1252.04	het	190	0.27	XM_00525	intron_vari	rs2005216
KIT	snp	chr4	55594163	G	A	385.741	het	20	0.80	XM_00526	intron_variant	
KRAS	snp	chr12	25380308	G	A	1212.7	het	526	0.16	NM_03336	synonymous_variant	
MAP2K1	snp	chr15	66727574	A	G	221.736	het	289	0.13	NM_00275	missense_variant&spli	
MAP2K1	snp	chr15	66727597	G	C	4734.59	het	320	0.50	NM_00275	intron_vari	rs1694992
MET	snp	chr7	1.16E+08	T	C	5709.2	het	698	0.31	XM_00525	missense_variant	
MET	snp	chr7	1.16E+08	C	T	204.626	het	804	0.11	XM_00525	missense_variant	
MET	snp	chr7	1.16E+08	C	T	8234.6	het	722	0.40	XM_00525	missense_variant	
MYC	snp	chr8	1.29E+08	C	G	1355.33	het	54	0.93	NM_00246	intron_variant	
MYCN	snp	chr2	16080157	C	G	343.343	hom	12	1.00	NM_00537	upstream_	rs1188606
NOTCH1	complex	chr9	1.39E+08	GGCT	TGA	1942.77	hom	68	1.00	NM_01761	frameshift_variant&fea	
NOTCH1	snp	chr9	1.39E+08	G	A	959.37	het	742	0.14	NM_01761	missense_variant	
NOTCH1	snp	chr9	1.39E+08	C	T	3486.62	het	1363	0.17	NM_01761	missense_variant	
NOTCH1	complex	chr9	1.39E+08	AATTTGGC	CCTGTGCC	361.963	hom	15	1.00	NM_01761	stop_gained	
NPM1	del	chr5	1.71E+08	CTTTTTTTT	CTTTTTTTT	220.785	het	41	0.29	NM_00252	splice_region_variant&	

PDGFRA	snp	chr4	55141055	A	G	10385.5	hom	362	0.99	NM_00620	synonymou	rs1873778
PDGFRA	snp	chr4	55161517	A	G	1747.58	hom	55	1.00	NM_00620	3_prime_U	rs7680422
PIK3CA	snp	chr3	1.79E+08	G	A	24346.4	hom	899	0.99	NM_00621	missense_variant	
PIK3R1	snp	chr5	67586480	G	A	2624.77	het	699	0.19	NM_18152	intron_variant	
PTEN	snp	chr10	89690864	G	A	1784	hom	62	1.00	NM_00031	intron_variant	
PTEN	del	chr10	89720633	CTTTTTTTT	CTTTTTTT	150.494	het	113	0.12	NM_00031	splice_acceptor_varian	
PTPN11	snp	chr12	1.13E+08	C	T	907.272	het	55	0.60	NM_00283	stop_gained&splice_re	
RET	snp	chr10	43610063	C	T	2296.42	hom	99	1.00	NM_02097	missense_variant	
RET	snp	chr10	43615582	G	A	560.024	hom	20	1.00	NM_02097	synonymous_variant	
RET	snp	chr10	43617501	C	T	210.234	het	640	0.12	NM_02097	intron_variant	
ROS1	complex	chr6	1.18E+08	AAAG	GAAAAG	365.274	het	269	0.19	NM_00294	splice_region_variant&	
ROS1	snp	chr6	1.18E+08	C	T	752.987	het	362	0.15	NM_00294	intron_variant	
SMAD4	snp	chr18	48573660	C	T	874.027	het	39	0.90	NM_00535	missense_variant	
SMAD4	snp	chr18	48603020	C	T	195.483	het	59	0.20	NM_00535	missense_v	COSM1389
SMARCB1	complex	chr22	24143192	TTA	TCCAGG	256.199	hom	10	1.00	XM_00526	inframe_insertion	
SMARCB1	complex	chr22	24143200	CGTGC	CCACTGT	269.175	hom	10	1.00	XM_00526	frameshift_variant&fea	
SMO	snp	chr7	1.29E+08	C	T	444.557	het	27	0.63	NM_00563	missense_variant	
STK11	snp	chr19	1206878	G	A	1603.09	het	296	0.28	XM_00525	5_prime_UTR_variant	
STK11	snp	chr19	1207229	C	T	1937.35	het	456	0.21	XM_00525	intron_variant	
STK11	snp	chr19	1207238	G	T	8257.63	het	400	0.74	XM_00525	intron_vari	rs3764640
STK11	snp	chr19	1218523	G	T	2260.02	het	102	0.88	XM_00525	intron_vari	rs2075604
STK11	snp	chr19	1220321	T	C	2408.81	het	235	0.37	XM_00525	intron_vari	rs2075606
STK11	snp	chr19	1223008	G	A	1687.24	hom	60	0.98	XM_00525	synonymou	rs3763290
TERT	snp	chr5	1295349	A	G	30908	hom	1001	1.00	NM_19825	upstream_	rs2853669
TERT	snp	chr5	1295371	G	A	3693.76	het	1529	0.16	NM_19825	upstream_gene_varian	
TP53	snp	chr17	7572919	G	A	837.988	het	520	0.15	NM_00054	3_prime_UTR_variant	
TP53	snp	chr17	7577595	C	T	1603.22	het	1468	0.12	NM_00054	missense_v	TP53_g.133
TP53	snp	chr17	7578493	C	T	7025.41	hom	247	1.00	NM_00054	stop_gaine	TP53_g.124
TP53	snp	chr17	7579472	G	C	2695.68	hom	94	1.00	NM_00054	missense_v	rs1042522
TP53	snp	chr17	7579903	G	A	4988.19	het	958	0.23	NM_00054	missense_variant	
TP53	snp	chr17	7590873	C	T	7561.31	het	1090	0.27	NM_00054	upstream_gene_varian	
VHL	snp	chr3	10188237	G	A	6034.26	het	443	0.48	NM_00055	missense_v	COSM1232
VHL	snp	chr3	10188294	C	T	2470.65	hom	91	0.97	NM_00055	missense_v	CD031548
VHL	snp	chr3	10188338	T	C	247.01	het	108	0.17	NM_00055	intron_variant	

VHL	snp	chr3	10191690	G	A	920.725	hom	36	0.94	NM_00055	3_prime_UTR_variant