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Data Sheet

Product Name: CancerSeqPlus Paraffin Tissue Curl

Catalog No.: T2235152-SC **Lot No.: C101103**

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: 58 year(s) old

Pathological Diagnosis: Adenocarcinoma

Tumor Size: diameter 7 cm

Location: Lung, Right Upper Lobe

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

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

C101103

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	29443662	C	T	2549.81	het	154	0.863636	NM_00430	synonymous_variant	
ALK	snp	chr2	29443702	C	T	5386.86	het	253	0.901186	NM_00430	splice_acceptor_varian	
ALK	snp	chr2	29445458	G	T	3917.63	het	214	0.593458	NM_00430	synonymou	rs3795850
APC	snp	chr5	1.12E+08	T	C	524.467	het	44	0.545455	XM_00527	synonymous_variant	
ATM	snp	chr11	1.08E+08	C	T	1935.39	het	134	0.522388	NM_00005	splice_region_variant&	
ATM	snp	chr11	1.08E+08	A	T	167.221	hom	10	1	NM_00005	intron_variant	
ATM	snp	chr11	1.08E+08	G	A	464.304	het	27	0.666667	NM_00005	missense_variant	
ATM	snp	chr11	1.08E+08	G	A	352.847	het	26	0.538462	NM_00005	missense_variant	
CCND1	snp	chr11	69450892	G	A	1598.76	het	118	0.483051	NM_05305	upstream_gene_variar	
CCNE1	snp	chr19	30303926	G	A	969.69	het	52	0.711538	NM_00123	synonymous_variant	
CCNE1	snp	chr19	30308281	G	C	1050.54	hom	48	0.979167	NM_00123	intron_variant	
CCNE1	snp	chr19	30312728	G	A	1135.6	het	164	0.286585	NM_00123	splice_region_variant&	
CCNE1	snp	chr19	30313252	G	A	1250.03	het	70	0.671429	NM_00123	missense_variant	
CDH1	snp	chr16	68771372	C	T	23462.7	hom	745	0.997315	NM_00436	splice_regi	rs3743674
CDH1	snp	chr16	68847310	C	T	1384.65	het	92	0.695652	NM_00436	missense_variant	
CDH1	snp	chr16	68849703	T	A	811.928	hom	41	1	NM_00436	intron_variant	
CDH1	snp	chr16	68857330	G	A	1936.74	het	99	0.767677	NM_00436	synonymous_variant	
CDK4	snp	chr12	58144559	T	A	391.395	hom	17	1	NM_00007	intron_variant	
CDK4	snp	chr12	58145316	C	T	489.827	hom	21	1	NM_00007	missense_variant	
CDKN2A	snp	chr9	21968199	C	G	86947.2	hom	2756	0.998549	NM_00119	3_prime_U	rs11515&C
CDKN2A	complex	chr9	21968199	CGAGG	GGAGA	478.386	hom	24	0.75	NM_00119	3_prime_UTR_variant	
CTNNB1	snp	chr3	41266048	ACC	ACT	1621.43	het	199	0.306533	XM_00526	missense_variant	
CTNNB1	complex	chr3	41266048	ACC	GCT	613.868	het	138	0.224638	XM_00526	missense_variant	
DDR2	snp	chr1	1.63E+08	T	C	23353.6	hom	745	0.997315	XM_00524	intron_vari	rs1780003
DDR2	snp	chr1	1.63E+08	G	T	3255.52	hom	132	1	XM_00524	intron_vari	rs1355287
ERBB2	snp	chr17	37871530	C	T	5169.28	het	258	0.806202	NM_00444	intron_variant	
ERBB2	snp	chr17	37881206	C	A	1260.26	hom	67	0.985075	NM_00444	intron_variant	

ERBB3	snp	chr12	56477694	A	T	10750.4	hom	340	1	NM_00198	splice_regi	rs2271194
EZH2	snp	chr7	1.49E+08	A	G	409.276	hom	14	1	XM_00524	intron_vari	rs2072407
FBXW7	snp	chr4	1.53E+08	G	A	1054.47	het	65	0.584615	NM_03363	synonymous_variant	
FBXW7	snp	chr4	1.53E+08	C	T	284.029	hom	12	1	NM_03363	missense_variant	
FBXW7	snp	chr4	1.53E+08	C	T	663.262	hom	24	1	NM_03363	intron_variant	
FBXW7	snp	chr4	1.53E+08	A	G	641.562	hom	24	1	NM_03363	intron_vari	rs1003360
FBXW7	del	chr4	1.53E+08	CAAAAAAA	CAAAAAAA	859.921	het	156	0.262821	NM_03363	splice_region_variant&	
FGFR1	snp	chr8	38271460	G	A	3620.58	het	152	0.934211	NM_00117	synonymous_variant	
FGFR3	snp	chr4	1805662	C	A	303.768	hom	13	1	NM_00116	intron_variant	
FGFR3	del	chr4	1806012	TGGGGGG	TGGGGGG	490.909	het	534	0.117978	NM_00116	intron_variant&feature	
FGFR3	snp	chr4	1807894	G	A	4074.7	hom	141	1	NM_00116	synonymou	rs7688609
FLT3	snp	chr13	28608259	A	T	1268.97	het	137	0.49635	NM_00411	stop_gained	
FLT3	snp	chr13	28610183	A	G	12708.6	hom	410	0.997561	NM_00411	splice_regi	rs2491231
H3F3A	snp	chr1	2.26E+08	C	T	300.137	hom	13	1	NM_00210	intron_variant	
HRAS	complex	chr11	534396	CAGCCAGG	GGGCCTGG	1107.48	hom	40	1	NM_00534	intron_variant	
IDH1	snp	chr2	2.09E+08	G	A	571.092	hom	22	0.954545	XM_00524	missense_v	COSM9653
JAK2	snp	chr9	5069093	G	A	427.978	hom	16	1	NM_00497	synonymous_variant	
JAK2	del	chr9	5073681	CTTTTTTTT	CTTTTTTTT	1206.64	het	211	0.236967	NM_00497	splice_region_variant&	
KDR	snp	chr4	55961159	T	C	2985.87	hom	105	1	NM_00225	intron_vari	rs2219471
KDR	snp	chr4	55962489	G	A	3284.21	het	210	0.566667	NM_00225	missense_variant	
KDR	snp	chr4	55979510	G	A	335.993	het	16	0.875	NM_00225	synonymous_variant	
MAP2K1	snp	chr15	66727597	G	C	11112.1	het	532	0.708647	NM_00275	intron_vari	rs1694992
MET	snp	chr7	1.16E+08	G	A	974.633	het	62	0.580645	XM_00525	missense_variant	
MET	snp	chr7	1.16E+08	G	A	925.291	het	60	0.583333	XM_00525	missense_variant	
MET	snp	chr7	1.16E+08	G	A	295.299	het	23	0.782609	XM_00525	missense_variant	
MET	snp	chr7	1.16E+08	C	T	510.716	het	30	0.866667	XM_00525	synonymous_variant	
MET	snp	chr7	1.16E+08	G	A	789.452	hom	40	1	XM_00525	synonymous_variant	
MET	snp	chr7	1.16E+08	C	T	2512.94	het	129	0.744186	XM_00525	synonymous_variant	
MET	snp	chr7	1.16E+08	G	A	1396.9	het	89	0.573034	XM_00525	missense_variant	
MET	snp	chr7	1.16E+08	G	A	1673.67	het	87	0.701149	XM_00525	synonymou	rs41737&C
MYCN	snp	chr2	16080157	C	G	1785.39	hom	57	1	NM_00537	upstream_	rs1188606
MYCN	snp	chr2	16089615	T	C	2069.68	hom	76	1	NM_00537	downstrea	rs4669018
NOTCH1	snp	chr9	1.39E+08	G	A	1780.5	hom	64	0.984375	NM_01761	synonymous_variant	
NOTCH1	mnp	chr9	1.39E+08	TG	CA	1568.32	het	107	0.53271	NM_01761	missense_variant	

NOTCH1	mnp	chr9	1.39E+08	GG	CC	1627.93	het	122	0.491803	NM_01761	missense_variant	
NOTCH1	mnp	chr9	1.39E+08	TG	CA	1322.8	het	249	0.240964	NM_01761	missense_variant	
NOTCH1	snp	chr9	1.39E+08	G	A	3228.34	hom	142	1	NM_01761	synonymou	rs2229974
NOTCH1	snp	chr9	1.39E+08	G	A	1114.22	het	82	0.621951	NM_01761	synonymous_variant	
NOTCH1	complex	chr9	1.39E+08	GTCG	ATCA	3240.46	hom	126	0.992063	NM_01761	synonymous_variant	
NOTCH1	complex,sr	chr9	1.39E+08	GTCG	ATCA,ATCG	12583.2	het	455	0.723077	NM_01761	synonymous_variant	
NOTCH1	snp	chr9	1.39E+08	T	A	440.371	hom	19	1	NM_01761	intron_variant	
NPM1	del	chr5	1.71E+08	CTTTTTTTT	CTTTTTTTT	792.454	het	87	0.390805	NM_00252	splice_region_variant&	
PDGFRA	complex	chr4	55141053	CCA	TCG	3201.3	hom	121	0.975207	NM_00620	missense_variant	
PDGFRA	complex,sr	chr4	55141053	CCA	TCG,CCG	12665.2	het	485	0.750515	NM_00620	missense_variant	
PDGFRA	snp	chr4	55161254	C	T	2726.02	het	172	0.523256	NM_00620	intron_vari	rs3733540
PDGFRA	snp	chr4	55161391	T	C	1568.96	hom	55	1	NM_00620	synonymou	rs7685117
PDGFRA	snp	chr4	55161517	A	G	2998.97	hom	100	1	NM_00620	3_prime_U	rs7680422
PIK3R1	snp	chr5	67589065	C	A	214.296	hom	11	1	NM_18152	intron_variant	
PIK3R1	snp	chr5	67589770	T	A	216.692	het	30	0.5	NM_18152	intron_variant	
PIK3R1	snp	chr5	67590364	G	A	2388.76	het	121	0.727273	NM_18152	missense_variant&spli	
PIK3R1	snp	chr5	67592170	G	A	999.636	het	85	0.541176	NM_18152	splice_donor_variant	
PIK3R1	snp	chr5	67593296	T	C	6257.87	het	435	0.508046	NM_18152	missense_variant	
PTEN	snp	chr10	89624136	C	T	330.767	hom	14	1	NM_00031	5_prime_UTR_variant	
PTEN	snp	chr10	89692757	C	T	285.319	hom	10	1	NM_00031	intron_variant	
PTEN	snp	chr10	89725271	C	T	569.436	het	32	0.75	NM_00031	3_prime_UTR_variant	
RB1	snp	chr13	48919358	T	G	4977.4	hom	189	1	NM_00032	intron_vari	rs198617
RB1	ins	chr13	48953655	CAAAAAAA	CAAAAAAA	906.692	het	210	0.214286	NM_00032	intron_variant&feature	
RB1	mnp	chr13	48953924	TG	CA	58.831	het	65	0.153846	NM_00032	intron_variant	
RB1	snp	chr13	49037916	T	A	2471.57	het	161	0.590062	NM_00032	missense_variant	
RET	snp	chr10	43609167	C	T	173.15	het	328	0.121951	NM_02097	intron_variant	
RET	complex	chr10	43615494	CATGGC	GAGGGT	307.044	het	15	0.866667	NM_02097	intron_variant	
ROS1	snp	chr6	1.18E+08	C	T	3412.23	het	272	0.555147	NM_00294	splice_region_variant&	
SMAD4	snp	chr18	48593587	G	A	4648.94	het	241	0.780083	NM_00535	intron_variant	
SMARCB1	snp	chr22	24176231	C	T	236.115	hom	11	1	XM_00526	intron_variant	
SMO	snp	chr7	1.29E+08	C	T	2874.91	het	206	0.495146	NM_00563	missense_variant	
SMO	snp	chr7	1.29E+08	G	C	11348.8	hom	363	0.988981	NM_00563	intron_vari	rs2075777
SMO	snp	chr7	1.29E+08	G	C	5857.96	hom	186	1	NM_00563	synonymou	rs2228617
SMO	snp	chr7	1.29E+08	C	A	2168.39	het	136	0.595588	NM_00563	synonymous_variant	

SRC	snp	chr20	36031596	G	A	534.042	hom	29	1	NM_00541	synonymous_variant	
STK11	snp	chr19	1207235	CGGG	CGGT	10825.5	hom	396	0.901515	XM_00525	intron_variant	
STK11	complex	chr19	1207235	CGGG	TGGT	806.089	het	37	0.837838	XM_00525	intron_variant	
STK11	snp	chr19	1218523	G	T	20345.5	hom	662	0.995468	XM_00525	intron_vari	rs2075604
STK11	snp	chr19	1220321	T	C	18380.1	hom	586	1	XM_00525	intron_vari	rs2075606
STK11	snp	chr19	1220460	A	T	1278	hom	56	1	XM_00525	missense_variant	
STK11	snp	chr19	1220749	AC	AT	4101.23	het	218	0.706422	XM_00525	intron_variant	
STK11	mnp	chr19	1220749	AC	GT	150.087	het	63	0.174603	XM_00525	intron_variant	
TERT	snp	chr5	1295349	A	G	25923.2	het	1442	0.571429	NM_19825	upstream_	rs2853669
TP53	mnp	chr17	7573918	GTCA	TGAC	269.175	hom	10	1	NM_00054	splice_region_variant&	
TP53	ins	chr17	7573925	AC	AGCCC	280.095	hom	10	1	NM_00054	splice_don	TP53_g.169
TP53	snp	chr17	7573929	G	T	343.343	hom	12	1	NM_00054	splice_region_variant&	
TP53	snp	chr17	7577407	A	C	948.365	het	44	0.75	NM_00054	intron_vari	rs1295105
TP53	snp	chr17	7577427	G	A	501.054	het	30	0.633333	NM_00054	intron_vari	rs1294778
TP53	snp	chr17	7579468	CACGG	CACGC	6458.83	het	561	0.377897	NM_00054	missense_variant	
TP53	del	chr17	7579643	CCCCCAGC	CC	1174.19	het	213	0.323944	NM_00054	intron_variant&feature	
TP53	mnp	chr17	7579645	CC	TT	1110.01	het	72	0.597222	NM_00054	intron_variant	
TP53	del	chr17	7579651	CCTCCAGG	CC	338.558	het	67	0.283582	NM_00054	intron_variant&feature	
TP53	complex	chr17	7579668	CTCCAG	CAACCCTT	472.576	het	62	0.33871	NM_00054	intron_variant&feature	
TP53	complex	chr17	7579678	CCAG	TTAC	884.094	het	80	0.4875	NM_00054	intron_variant	
TP53	snp	chr17	7579997	G	A	3319.27	het	217	0.700461	NM_00054	intron_variant	
VHL	snp	chr3	10183556	G	A	5239.43	het	289	0.650519	NM_00055	missense_variant	