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Data Sheet

Product Name: CancerSeqPlus Paraffin Tissue Curl

Catalog No.: T2235152-SC **Lot No.: C101111**

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: 49 year(s) old

Pathological Diagnosis: Adenocarcinoma

Tumor Size: 6x5x3 cm

Location: Lung, Left Lower Lobe

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

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

C101111

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	359.122	het	22	0.64	NM_00731	splice_region_variant&	
AKT1	snp	chr14	1.05E+08	G	A	427.823	het	27	0.63	NM_00101	synonymous_variant	
AKT1	snp	chr14	1.05E+08	G	A	265.456	het	28	0.39	NM_00101	synonymous_variant	
ALK	snp	chr2	29445458	G	T	3657.32	hom	116	1.00	NM_00430	synonymou	rs3795850
APC	snp	chr5	1.12E+08	G	A	585.394	het	122	0.23	XM_00527	missense_variant	
BRAF	snp	chr7	1.4E+08	G	A	595.038	hom	22	1.00	XM_00525	stop_gaine	COSM5319
BRAF	snp	chr7	1.4E+08	C	T	655.128	het	26	0.92	XM_00525	intron_variant	
CDH1	snp	chr16	68771372	C	T	4314.82	het	237	0.65	NM_00436	splice_regi	rs3743674
CDH1	snp	chr16	68847416	C	T	658.343	het	159	0.21	NM_00436	intron_variant	
CDH1	snp	chr16	68857589	C	T	893.718	het	78	0.42	NM_00436	intron_variant	
CDH1	snp	chr16	68862099	G	A	268.029	hom	10	1.00	NM_00436	synonymous_variant	
CDK4	snp	chr12	58142959	C	T	5289.75	hom	183	1.00	NM_00007	splice_region_variant&	
CDK4	snp	chr12	58145016	G	A	4918.46	het	299	0.58	NM_00007	missense_variant	
CDK4	snp	chr12	58145102	G	A	4651.03	hom	164	1.00	NM_00007	missense_variant	
CDKN2A	snp	chr9	21968199	C	G	13551.5	hom	432	0.99	NM_00119	3_prime_U	rs11515&C
CDKN2A	snp	chr9	21974934	C	T	2390.3	het	251	0.43	NM_00119	5_prime_UTR_variant	
DDR2	snp	chr1	1.63E+08	T	C	14444.2	hom	458	1.00	XM_00524	intron_vari	rs1780003
DDR2	snp	chr1	1.63E+08	C	T	1747.5	hom	57	1.00	XM_00524	intron_vari	rs3738807
DDR2	snp	chr1	1.63E+08	C	T	791.352	het	39	0.79	XM_00524	synonymous_variant	
DDR2	snp	chr1	1.63E+08	C	T	4409.69	het	318	0.49	XM_00524	synonymous_variant	
EGFR	snp	chr7	55221782	C	T	214.588	het	111	0.16	NM_00522	stop_gained	
EGFR	snp	chr7	55242426	C	T	2723.9	het	290	0.34	NM_00522	synonymous_variant	
EGFR	snp	chr7	55242495	C	T	5221.21	het	362	0.51	NM_00522	synonymou	COSM1842
EGFR	snp	chr7	55259550	C	T	572.985	het	25	0.92	NM_00522	missense_v	COSM5329
ERBB2	snp	chr17	37871521	C	T	4195.19	hom	164	0.95	NM_00444	intron_variant	
ERBB2	snp	chr17	37871610	C	T	608.929	het	527	0.13	NM_00444	missense_variant&spli	
ERBB2	snp	chr17	37881178	C	T	7780.16	het	745	0.38	NM_00444	intron_variant	

ERBB2	mnp	chr17	37881474	AGG	GTC	3.46887	het	93	0.12	NM_00444	intron_variant	
ERBB3	snp	chr12	56477694	A	T	4354.08	hom	139	1.00	NM_00198	splice_regi	rs2271194
ERBB3	snp	chr12	56479005	C	T	998.733	het	76	0.47	NM_00198	intron_variant	
ERBB4	snp	chr2	2.13E+08	G	A	1472.92	het	132	0.40	NM_00523	intron_variant	
ERBB4	snp	chr2	2.13E+08	T	C	302.871	het	26	0.46	NM_00523	missense_variant	
ERBB4	snp	chr2	2.13E+08	C	T	261.703	het	144	0.15	NM_00523	synonymous_variant	
FGFR1	snp	chr8	38271342	G	A	860.757	het	393	0.16	NM_00117	intron_variant	
FGFR1	snp	chr8	38271351	G	A	1283.13	het	302	0.21	NM_00117	intron_variant	
FGFR1	snp	chr8	38271362	T	A	1278.3	hom	44	1.00	NM_00117	intron_variant	
FGFR1	mnp	chr8	38271371	CT	AG	1208.89	hom	42	1.00	NM_00117	intron_variant	
FGFR1	complex	chr8	38271381	TGC	AGG	1232.67	hom	43	1.00	NM_00117	intron_variant	
FGFR1	snp	chr8	38271460	G	A	1289.78	hom	65	0.97	NM_00117	synonymous_variant	
FGFR2	snp	chr10	1.23E+08	C	T	639.854	het	77	0.32	NM_02297	missense_variant	
FGFR2	mnp	chr10	1.23E+08	GC	TG	738.791	het	110	0.28	NM_02297	splice_region_variant&	
FGFR2	snp	chr10	1.23E+08	C	T	281.679	hom	10	1.00	NM_02297	missense_variant	
FGFR3	snp	chr4	1803565	G	A	883.578	het	125	0.29	NM_00116	missense_variant	
FGFR3	snp	chr4	1805594	C	T	1010.24	hom	37	0.97	NM_00116	intron_variant	
FGFR3	del	chr4	1806012	TGGGGGG	TGGGGGG	573.208	het	245	0.17	NM_00116	intron_variant&feature	
FGFR3	snp	chr4	1808854	C	T	534.826	het	63	0.33	NM_00116	synonymous_variant	
FLT3	snp	chr13	28610080	C	T	2816.8	hom	102	0.99	NM_00411	synonymous_variant	
FLT3	snp	chr13	28610183	A	G	3069.66	het	146	0.79	NM_00411	splice_regi	rs2491231
FOXL2	snp	chr3	1.39E+08	G	A	548.391	het	196	0.17	NM_02306	synonymous_variant	
FOXL2	snp	chr3	1.39E+08	C	T	545.418	het	213	0.17	NM_02306	synonymous_variant	
FOXL2	snp	chr3	1.39E+08	C	T	331.738	het	31	0.42	NM_02306	5_prime_UTR_variant	
GNAS	snp	chr20	57480490	G	A	2042.47	het	94	0.84	NM_08042	missense_variant	
HNF1A	snp	chr12	1.21E+08	A	G	679.565	het	188	0.20	XM_00525	splice_region_variant&	
HRAS	snp	chr11	533692	G	A	1131.43	het	800	0.16	NM_00534	intron_variant	
HRAS	snp	chr11	534197	C	T	517.272	het	59	0.36	NM_00534	intron_vari	rs4125805
HRAS	snp	chr11	534223	G	A	374.936	het	56	0.29	NM_00534	missense_variant	
HRAS	snp	chr11	534242	A	G	747.984	het	42	0.67	NM_00534	synonymou	rs12628&C
IDH1	snp	chr2	2.09E+08	G	A	1260.28	het	153	0.32	XM_00524	synonymous_variant	
KDR	snp	chr4	55980456	C	T	804.901	hom	32	0.94	NM_00225	intron_vari	rs2305949
MAP2K1	snp	chr15	66727597	G	C	2747.67	het	151	0.58	NM_00275	intron_vari	rs1694992
MDM2	snp	chr12	69230476	G	A	19.4007	het	138	0.12	NM_00239	missense_variant	

MET	snp	chr7	1.16E+08	G	A	323.359	hom	12	1.00	XM_00525	missense_v	rs3735179
MYC	snp	chr8	1.29E+08	C	T	2445.75	het	244	0.37	NM_00246	upstream_gene_variar	
MYC	snp	chr8	1.29E+08	G	A	68.187	het	192	0.13	NM_00246	5_prime_UTR_variant	
MYC	snp	chr8	1.29E+08	C	T	1383.81	het	197	0.28	NM_00246	missense_v	rs1410952
MYCN	snp	chr2	16089615	T	C	920.315	hom	34	1.00	NM_00537	downstrea	rs4669018
NOTCH1	snp	chr9	1.39E+08	C	T	4714.34	hom	168	1.00	NM_01761	missense_variant	
NOTCH1	snp	chr9	1.39E+08	G	A	366.57	het	268	0.14	NM_01761	synonymous_variant	
NOTCH1	snp	chr9	1.39E+08	G	A	240.408	het	40	0.28	NM_01761	synonymous_variant	
NOTCH1	snp	chr9	1.39E+08	G	A	179.453	het	190	0.13	NM_01761	synonymous_variant	
NOTCH1	snp	chr9	1.39E+08	C	T	1285.04	het	107	0.48	NM_01761	intron_vari	rs3754361
NPM1	del,del	chr5	1.71E+08	CTTTTTTTT	CTTTTTTTT	828.971	het	79	0.39	NM_00252	splice_region_variant&	
PDGFRA	snp	chr4	55161254	C	T	656.475	hom	23	1.00	NM_00620	intron_vari	rs3733540
PDGFRA	snp	chr4	55161517	A	G	810.704	hom	27	1.00	NM_00620	3_prime_U	rs7680422
PIK3CA	snp	chr3	1.79E+08	A	T	1378.73	het	224	0.27	NM_00621	missense_variant	
PTEN	snp	chr10	89717860	C	T	390.978	het	34	0.44	NM_00031	intron_variant	
RB1	snp	chr13	48919321	C	T	424.244	hom	18	1.00	NM_00032	synonymou	COSM1367
RB1	snp	chr13	48919358	T	G	1022.99	hom	37	1.00	NM_00032	intron_vari	rs198617
RB1	snp	chr13	49027171	G	A	837.656	het	38	0.89	NM_00032	missense_v	CM951107
RB1	snp	chr13	49037781	G	A	211.506	het	30	0.33	NM_00032	intron_variant	
RET	snp	chr10	43609947	G	A	481.582	het	23	0.87	NM_02097	synonymous_variant	
RET	snp	chr10	43610229	C	T	514.797	het	57	0.35	NM_02097	intron_variant	
RET	snp	chr10	43613834	G	A	313.953	hom	11	1.00	NM_02097	synonymou	rs1406587
SMAD4	snp	chr18	48584795	C	T	688.787	hom	24	1.00	NM_00535	synonymous_variant	
SMAD4	snp	chr18	48603062	C	T	632.064	het	92	0.28	NM_00535	stop_gained	
SMO	mnp	chr7	1.29E+08	GA	CG	339.709	hom	12	1.00	NM_00563	missense_variant	
SMO	mnp,snp	chr7	1.29E+08	GA	CG,CA	2140.95	het	84	0.86	NM_00563	missense_variant	
SMO	snp	chr7	1.29E+08	C	T	44.7864	het	301	0.11	NM_00563	intron_variant	
SMO	snp	chr7	1.29E+08	C	T	1848.7	het	322	0.25	NM_00563	intron_variant	
STK11	snp	chr19	1206905	G	A	71.3316	het	105	0.13	XM_00525	5_prime_UTR_variant	
STK11	snp	chr19	1218442	G	A	3097.9	het	173	0.65	XM_00525	missense_v	rs3756225
STK11	snp	chr19	1220336	G	A	1085.92	het	142	0.30	XM_00525	intron_variant	
STK11	snp	chr19	1221956	G	A	316.243	het	372	0.13	XM_00525	missense_variant	
STK11	snp	chr19	1222012	G	C	8316.06	hom	292	0.99	XM_00525	splice_regi	rs2075607
STK11	snp	chr19	1223083	C	T	420.612	hom	16	1.00	XM_00525	synonymous_variant	

STK11	snp	chr19	1223168	C	T	1665.71	het	473	0.19	XM_00525	missense_variant	
TERT	snp	chr5	1295178	G	A	280.423	het	334	0.13	NM_19825	upstream_gene_variar	
TERT	snp	chr5	1295229	G	A	511.022	het	131	0.24	NM_19825	upstream_gene_variar	
TERT	snp	chr5	1295349	A	G	26051.2	het	1115	0.80	NM_19825	upstream_	rs2853669
TP53	snp	chr17	7573046	C	T	104.512	het	63	0.16	NM_00054	intron_variant	
TP53	snp	chr17	7576794	G	A	512.438	het	65	0.32	NM_00054	intron_variant	
TP53	snp	chr17	7578495	C	T	1439.11	hom	53	1.00	NM_00054	synonymou	TP53_g.124
TP53	snp	chr17	7579309	G	A	4015.58	het	778	0.23	NM_00054	splice_regi	TP53_g.116
TP53	snp	chr17	7579472	G	C	5164.31	het	209	0.89	NM_00054	missense_v	rs1042522
TP53	snp	chr17	7579678	C	T	1516.3	het	147	0.37	NM_00054	intron_variant	
TP53	snp	chr17	7579683	C	T	1468.9	het	146	0.37	NM_00054	intron_variant	
VHL	snp	chr3	10183663	C	G	343.343	hom	12	1.00	NM_00055	synonymous_variant	