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Data Sheet

Product Name: CancerSeqPlus Paraffin Tissue Curl

Catalog No.: T2235152-SC **Lot No.:** C101105

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: 40 year(s) old

Pathological Diagnosis: Adenocarcinoma

Tumor Size: diameter 4.5 cm

Location: Lung, Left Upper Lobe

Components:

1. 5 curls per package
2. Certificate of Analysis

FOR IN VITRO RESEARCH USE ONLY

APPROVED BY: _____

C101105

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	C101105	EGFR	7.25	0.05	1.84E-03

symbol	type	chromosome	position	reference	mutation	quality	allele type	Depth	variant frequency	transcript_id	consequence	existing variation
ABL1	snp	chr9	133738149	G	A	360.378	het	18	0.83	NM_00731	splice_acceptor_varian	
ALK	snp	chr2	29445449	C	G	1268.52	het	70	0.69	NM_00430	synonymous_variant	
ALK	snp	chr2	29445458	G	T	3400.74	hom	108	1.00	NM_00430	synonymou	rs3795850
ATM	snp	chr11	108204615	G	A	1011.04	hom	35	1.00	NM_00005	missense_variant&spli	
ATM	snp	chr11	108206716	C	T	426.38	het	21	0.81	NM_00005	intron_variant	
AURKA	snp	chr20	54956503	G	A	800.062	hom	28	1.00	NM_00360	stop_gained	
CDH1	snp	chr16	68771372	C	T	1280.53	hom	48	0.96	NM_00436	splice_regi	rs3743674
CDH1	snp	chr16	68844127	G	A	1344.45	hom	47	1.00	NM_00436	missense_v	CM070661
CDH1	snp	chr16	68857270	G	A	1067.8	het	61	0.64	NM_00436	intron_variant	
CDKN2A	snp	chr9	21968199	C	G	16208.1	hom	509	1.00	NM_00119	3_prime_U	rs11515&C
CDKN2A	snp	chr9	21968266	G	A	5461.86	hom	205	0.97	NM_00119	intron_variant	
DDR2	snp	chr1	162740269	C	T	1824.11	het	115	0.58	XM_00524	missense_variant	
DDR2	snp	chr1	162740327	T	C	9008.46	hom	286	1.00	XM_00524	intron_vari	rs1780003
DDR2	snp	chr1	162741984	C	A	341.554	het	20	0.70	XM_00524	missense_variant	
DDR2	snp	chr1	162743389	C	T	1242.75	het	78	0.59	XM_00524	splice_region_variant&	
DDR2	snp	chr1	162743418	G	T	931.473	hom	39	1.00	XM_00524	intron_vari	rs1355287
DDR2	snp	chr1	162745689	C	A	644.471	hom	36	1.00	XM_00524	intron_variant	
EGFR	snp	chr7	55221655	G	A	1271.61	hom	57	1.00	NM_00522	intron_vari	rs4947986
EGFR	complex	chr7	55241664	GAGGATC	CAAGATCC	334.039	het	189	0.17	NM_00522	frameshift_variant&fea	
EGFR	snp	chr7	55259515	T	G	320.731	hom	11	1.00	NM_00522	missense_v	rs12143456
ERBB4	snp	chr2	212578519	A	T	9.05654	het	199	0.11	NM_00523	intron_vari	rs35123918
ESR1	snp	chr6	152420034	C	T	346.621	het	14	0.93	XM_00526	missense_variant	

FBXW7	snp	chr4	153252061	A	G	360.289	hom	13	1.00	NM_03363	intron_vari	rs10033601
FGFR3	snp	chr4	1805574	C	T	248.655	het	20	0.50	NM_00116	intron_variant	
FGFR3	snp	chr4	1805590	T	C	277.065	het	21	0.52	NM_00116	intron_variant	
FGFR3	snp	chr4	1806215	C	T	325.697	het	21	0.62	NM_00116	missense_variant	
FGFR3	snp	chr4	1808372	C	A	169.891	het	18	0.56	NM_00116	synonymous_variant	
FLT3	snp	chr13	28610183	A	G	1348.11	het	67	0.79	NM_00411	splice_regi	rs2491231
FOXL2	snp	chr3	138664520	G	C	763.527	het	42	0.69	NM_02306	missense_v	rs20184017
FOXL2	snp	chr3	138664540	C	A	259.996	het	27	0.48	NM_02306	missense_v	rs37247951
GNA11	snp	chr19	3118882	G	A	828.596	hom	33	0.94	NM_00206	intron_variant	
GNAS	snp	chr20	57480470	G	A	804.185	het	39	0.82	NM_08042	synonymous_variant	
IDH1	del	chr2	209116299	GAAAAAAAA	GAAAAAAA	1109.83	het	132	0.33	XM_00524	intron_variant&feature	
KDR	complex	chr4	55961184	CAACC	AAACT	455.166	hom	16	1.00	NM_00225	intron_variant	
KRAS	snp	chr12	25362754	G	T	198.389	het	20	0.60	NM_03336	3_prime_UTR_variant	
MAP2K1	snp	chr15	66727597	G	C	4451.32	het	224	0.65	NM_00275	intron_vari	rs16949924
MYC	snp	chr8	128749611	C	T	426.681	hom	15	1.00	NM_00246	intron_variant	
MYCN	snp	chr2	16080157	C	G	645.407	hom	21	1.00	NM_00537	upstream_	rs11886063
NOTCH1	snp	chr9	139391500	G	A	497.507	het	278	0.15	NM_01761	missense_variant	
NOTCH1	snp	chr9	139397707	G	A	2409.73	hom	84	1.00	NM_01761	synonymou	rs10521&C
PDGFRA	snp	chr4	55141055	A	G	580.522	hom	21	1.00	NM_00620	synonymou	rs18737788
PDGFRA	snp	chr4	55152040	C	T	3386.51	hom	120	0.98	NM_00620	synonymou	rs22282308
PDGFRA	snp	chr4	55161254	C	T	386.659	het	36	0.50	NM_00620	intron_vari	rs3733540
PDGFRA	snp	chr4	55161391	T	C	434.034	hom	19	1.00	NM_00620	synonymou	rs7685117
PDGFRA	snp	chr4	55161517	A	G	459.697	hom	16	1.00	NM_00620	3_prime_U	rs7680422
PIK3CA	snp	chr3	178927446	C	T	855.548	het	52	0.85	NM_00621	synonymous_variant	
ROS1	snp	chr6	117638387	C	T	3814.92	het	225	0.63	NM_00294	synonymous_variant	
SMARCB1	snp	chr22	24176287	G	A	245.106	het	17	0.59	XM_00526	intron_vari	rs50306138
SMO	snp	chr7	128845277	G	C	313.953	hom	11	1.00	NM_00563	intron_vari	rs2075777
SMO	snp	chr7	128846328	G	C	860.699	hom	30	1.00	NM_00563	synonymou	rs2228617
SMO	snp	chr7	128850423	C	T	3594.16	het	191	0.70	NM_00563	intron_variant	
STK11	snp	chr19	1206978	G	A	1952.8	het	101	0.74	XM_00525	missense_variant	
STK11	snp	chr19	1207238	G	T	523.164	het	70	0.30	XM_00525	intron_vari	rs3764640
STK11	snp	chr19	1219451	C	G	152.261	het	33	0.33	XM_00525	intron_vari	rs36951560
STK11	snp	chr19	1220321	T	C	1472.61	het	70	0.80	XM_00525	intron_vari	rs2075606
STK11	snp	chr19	1221945	C	T	4884.13	het	292	0.59	XM_00525	splice_region_variant&	

TP53	snp	chr17	7579472	G	C	1056.44	hom	43	0.95	NM_00054	missense_v	rs1042522