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Data Sheet

Product Name: CancerSeqPlus Paraffin Tissue Curl

Catalog No.: T2235265-SC **Lot No.: B906070**

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: Thyroid

Donor Information:

Male: 35 year(s) old
Female: _____ year(s) old

Pathological Diagnosis: Adenocarcinoma, papillary

Tumor Size: 4.5x3x1.5 cm

Location: Thyroid right

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

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

lot# B906070

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 at this position	transcript_id	existing variation	consequence
APC	snp	chr5	112179098	G	A	377.506	hom	16	XM_005271975.1		missense_variar
ATM	snp	chr11	108117778	G	A	2337.7	het	116	NM_000051.3		missense_variar
ATM	snp	chr11	108236066	G	A	365.335	het	19	NM_000051.3		missense_variar
CCND1	snp	chr11	69450943	G	A	458.277	het	38	NM_053056.2		upstream_gene_
CCND1	snp	chr11	69463931	C	T	2433.26	hom	101	NM_053056.2		intron_variant
CCNE1	snp	chr19	30314648	C	T	254.39	het	15	NM_001238.2		synonymous_va
CDH1	snp	chr16	68771372	C	T	6519.12	het	286	NM_004360.3	rs3743674	splice_region_v
CDH1	complex	chr16	68835724	CAC	TAT	641.593	het	81	NM_004360.3		missense_variar
CDH1	snp	chr16	68845684	G	A	1152.45	het	63	NM_004360.3		synonymous_va
CDH1	snp	chr16	68847356	C	T	945.587	het	65	NM_004360.3		synonymous_va
CDH1	snp	chr16	68853195	G	A	1113.12	het	72	NM_004360.3		stop_gained
CDK4	snp	chr12	58144505	G	A	581.718	het	33	NM_000075.3		missense_variar
CDK4	snp	chr12	58145388	C	T	246.711	het	18	NM_000075.3		missense_variar
CDK4	ins	chr12	58145410	AGT	AGGT	166.602	het	19	NM_000075.3		frameshift_varia
CDKN2A	snp	chr9	21968197	CCC	CCG	14892.3	hom	516	NM_001195132.1		3_prime_UTR_v
CDKN2A	complex	chr9	21968197	CCC	TCG	712.367	hom	33	NM_001195132.1		3_prime_UTR_v
CTNNB1	snp	chr3	41265988	C	T	514.79	het	47	XM_005264887.1		intron_variant
DDR2	snp	chr1	162740327	T	C	8405.62	hom	290	XM_00524522(	rs1780003	intron_variant
DDR2	snp	chr1	162743418	G	T	672.098	hom	29	XM_00524522(	rs1355287	intron_variant
DDR2	snp	chr1	162746131	C	T	1214.74	het	79	XM_00524522(	rs121964863	missense_variar
ERBB3	snp	chr12	56477694	A	T	3535.56	hom	113	NM_001982.3	rs2271194	splice_region_v
ERBB3	snp	chr12	56478821	G	A	343.937	het	20	NM_001982.3		missense_variar
ERBB4	snp	chr2	212289026	C	T	699.972	het	38	NM_005235.2		missense_variar
ERBB4	snp	chr2	212587254	G	A	1078.74	het	62	NM_005235.2		synonymous_va
ERBB4	snp	chr2	212653010	G	A	280.429	het	14	NM_005235.2		intron_variant
ESR1	snp	chr6	152420095	G	A	1420.49	het	68	XM_00526685(	rs2228480&(	synonymous_va
EZH2	snp	chr7	148508833	A	G	655.571	hom	21	XM_005249962	rs2072407	intron_variant
FBXW7	snp	chr4	153249362	T	G	767.909	het	50	NM_033632.3		missense_variar
FBXW7	snp	chr4	153249392	G	A	2036.22	het	92	NM_033632.3		synonymous_va
FBXW7	del,del	chr4	153268227	CAAAAAAAA	CAAAAAAAA	420.566	het	73	NM_033632.3		splice_region_v
FBXW7	snp	chr4	153268240	A	G	135.113	het	184	NM_033632.3		intron_variant

FBXW7	del	chr4	153268249	AGA	AA	143.493	het	165	NM_033632.3		intron_variant&
FBXW7	snp	chr4	153268254	G	A	560.949	het	143	NM_033632.3		intron_variant
FGFR1	snp	chr8	38279389	G	A	546.173	het	44	NM_001174067.1		missense_variar
FGFR1	snp	chr8	38279473	C	T	1013.96	het	63	NM_001174067.1		intron_variant
FGFR3	del	chr4	1806012	TGGGGGGG	TGGGGGGG	71.9477	het	150	NM_001163213.1		intron_variant&
FGFR3	snp	chr4	1807894	G	A	459.878	hom	16	NM_00116321	rs7688609	synonymous_va
FLT3	snp	chr13	28592658	G	A	1778.84	het	85	NM_004119.2		synonymous_va
FLT3	snp	chr13	28592679	C	T	357.636	het	23	NM_004119.2		synonymous_va
FOXL2	snp	chr3	138665619	G	A	559.869	het	47	NM_023067.3		5_prime_UTR_v
IDH1	snp	chr2	209116218	G	A	1392.65	het	63	XM_005246521.1		stop_gained
IDH1	del	chr2	209116299	GAAAAAAA	GAAAAAAA	42.9498	het	84	XM_005246521.1		intron_variant&
JAK3	snp	chr19	17948032	G	A	1090.35	het	73	XM_005259896.1		intron_variant
JAK3	snp	chr19	17954272	C	T	473.515	het	37	XM_005259896.1		missense_variar
JAK3	snp	chr19	17954279	A	T	426.703	het	38	XM_005259896.1		missense_variar
KDR	snp	chr4	55953864	C	T	270.532	het	17	NM_002253.2		missense_variar
KRAS	snp	chr12	25378499	G	A	362.241	het	21	NM_033360.2		intron_variant
MAP2K1	snp	chr15	66727597	G	C	4270.34	het	269	NM_002755.3	rs16949924	intron_variant
MYC	snp	chr8	128746573	G	A	816.901	hom	36	NM_002467.4		upstream_gene
MYC	snp	chr8	128752998	C	T	403.475	het	26	NM_002467.4		missense_variar
MYC	snp	chr8	128753086	C	T	223.542	het	119	NM_002467.4		missense_variar
MYCN	snp	chr2	16080157	C	G	293.981	hom	10	NM_005378.4	rs11886063	upstream_gene
MYCN	snp	chr2	16089442	T	A	284.029	hom	12	NM_005378.4	rs12619709	downstream_ge
MYCN	snp	chr2	16089615	T	C	1625.49	hom	60	NM_005378.4	rs4669018	downstream_ge
NOTCH1	snp	chr9	139397707	G	A	2034.89	hom	74	NM_017617.3	rs10521&CO	synonymous_va
NOTCH1	complex	chr9	139399177	CACCAGGGA	TCCCTGGTG	274.862	hom	11	NM_017617.3		missense_variar
NOTCH1	snp	chr9	139399785	G	A	1075.69	het	76	NM_017617.3		synonymous_va
NOTCH1	complex	chr9	139400212	GTGAAG	CTTCAC	567.899	hom	34	NM_017617.3		stop_gained
NOTCH1	complex	chr9	139400224	AGGCA	CGAAT	714.935	het	94	NM_017617.3		missense_variar
NPM1	del	chr5	170837513	CTTTTTTTT	CTTTTTTTT	623.514	het	91	NM_002520.6		splice_region_v
NRAS	snp	chr1	115258804	G	A	559.145	het	42	NM_002524.4		splice_region_v
PDGFRA	snp	chr4	55141055	A	G	1853.1	het	94	NM_006206.4	rs1873778&C	synonymous_va
PDGFRA	snp	chr4	55152131	G	A	611.144	het	49	NM_006206.4		splice_donor_va
PDGFRA	snp	chr4	55161254	C	T	1624.9	hom	54	NM_006206.4	rs3733540	intron_variant
PDGFRA	snp	chr4	55161358	G	A	1064.97	hom	39	NM_006206.4		synonymous_va
PDGFRA	snp	chr4	55161391	T	C	542.098	hom	23	NM_006206.4	rs7685117	synonymous_va
PDGFRA	snp	chr4	55161397	C	T	594.772	hom	24	NM_006206.4	rs148629782	synonymous_va
PDGFRA	snp	chr4	55161517	A	G	667.662	hom	22	NM_006206.4	rs7680422	3_prime_UTR_v
PIK3CA	snp	chr3	178916941	G	A	1235.17	het	65	NM_006218.2	COSM6145	missense_variar
PIK3CA	snp	chr3	178921476	G	A	1976.97	het	102	NM_006218.2		missense_variar
PTEN	snp	chr10	89720907	T	G	572.756	hom	21	NM_000314.4	rs555895&C	intron_variant
PTEN	del	chr10	89725293	CTTTTTTTT	CTTTTTTTT	174.702	het	63	NM_000314.4		3_prime_UTR_v

RB1	snp	chr13	48919358	T	G	907.264	hom	34	NM_000321.2	rs198617	intron_variant
RET	complex	chr10	43615038	GAG	AAA	824.215	hom	32	NM_020975.4		missense_variar
ROS1	snp	chr6	117638275	G	A	291.411	het	15	NM_002944.2		intron_variant
SMAD4	snp	chr18	48573601	C	T	427.596	het	23	NM_005359.5		missense_variar
SMAD4	snp	chr18	48573618	C	T	544.828	het	37	NM_005359.5		missense_variar
SMAD4	snp	chr18	48581301	C	T	2162.56	het	130	NM_005359.5		missense_variar
SMAD4	snp	chr18	48581335	C	T	2163.99	het	148	NM_005359.5		synonymous_va
SMAD4	snp	chr18	48591839	G	A	354.295	het	20	NM_005359.5	COSM13890	synonymous_va
SMO	snp	chr7	128845277	G	C	3650.33	hom	127	NM_005631.4	rs2075777	intron_variant
SMO	snp	chr7	128845316	G	A	474.302	hom	22	NM_005631.4		intron_variant
SMO	snp	chr7	128846328	G	C	1670.86	hom	55	NM_005631.4	rs2228617	synonymous_va
SMO	snp	chr7	128851550	G	A	324.559	het	19	NM_005631.4		missense_variar
STK11	snp	chr19	1207238	G	T	2599.37	hom	95	XM_005259617	rs3764640	intron_variant
STK11	snp	chr19	1218523	G	T	5684.99	het	302	XM_005259617	rs2075604	intron_variant
STK11	snp	chr19	1222012	G	C	10169.3	het	499	XM_005259617	rs2075607	splice_region_v
STK11	snp	chr19	1223054	C	T	662.352	het	37	XM_005259617.1		missense_variar
TP53	snp	chr17	7573009	C	T	3274.69	het	250	NM_000546.5	TP53_g.1790	splice_acceptor_
TP53	snp	chr17	7574034	C	T	337.876	het	18	NM_000546.5	TP53_g.1688	splice_acceptor_
TP53	snp	chr17	7577490	G	T	501.576	het	35	NM_000546.5		intron_variant
TP53	snp	chr17	7577510	C	T	2568.37	het	184	NM_000546.5	TP53_g.1340	synonymous_va
TP53	snp	chr17	7578461	C	T	272.611	het	23	NM_000546.5	rs121912654	missense_variar
TP53	snp	chr17	7579472	G	C	3436.82	hom	118	NM_000546.5	rs1042522&T	missense_variar
VHL	snp	chr3	10183751	G	A	293.167	het	27	NM_000551.3	COSM14172	missense_variar