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Data Sheet

Product Name: CancerSeqPlus Paraffin Tissue Curl

Catalog No.: T2235265-SC **Lot No.: B906073**

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: _____ year(s) old
Female: 55 year(s) old

Pathological Diagnosis: Carcinoma, Papillary & folliculus

Tumor Size: N/A

Location: Thyroid

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

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

lot# B906073

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
AKT1	snp	chr14	105241403	CCG	CCA	216.98	het	71	NM_001014431.1		splice_region_variant&
AKT1	complex	chr14	105241403	CCG	TCA	109.991	het	57	NM_001014431.1		splice_region_variant&
AKT1	snp	chr14	105241495	C	T	1064.86	het	52	NM_001014431.1		missense_variant
APC	snp	chr5	112174658	C	T	319.857	hom	12	XM_005271975	CM011276&	stop_gained
APC	snp	chr5	112175679	G	A	456.755	het	21	XM_005271975.1		missense_variant
APC	snp	chr5	112178914	C	T	469.061	het	21	XM_005271975.1		synonymous_variant
APC	snp	chr5	112179377	G	A	935.718	hom	37	XM_005271975	rs3687248	missense_variant
AURKA	snp	chr20	54963197	G	A	326.493	het	18	NM_003600.2		intron_variant
CCND1	snp	chr11	69460753	G	A	517.447	het	31	NM_053056.2		intron_variant
CCNE1	complex	chr19	30308395	CACC	TACT	718.095	hom	26	NM_001238.2		missense_variant
CDH1	snp	chr16	68845772	C	T	286.984	het	12	NM_004360.3		intron_variant
CDH1	snp	chr16	68846058	G	A	2368.43	het	127	NM_004360.3		synonymous_variant
CDK4	snp	chr12	58142978	G	A	1087.87	het	45	NM_000075.3		missense_variant
CDK4	snp	chr12	58144849	C	T	255.394	het	13	NM_000075.3		missense_variant
CDKN2A	snp	chr9	21968199	C	G	1242.93	hom	43	NM_001195132	rs11515&CO	3_prime_UTR_variant
CSTF1	snp	chr20	54963197	G	A	326.493	het	18	NM_001033521.1		upstream_gene_varia
CTNNB1	snp	chr3	41266085	C	T	1283.29	hom	46	XM_005264887	COSM5750	stop_gained
CTNNB1	snp	chr3	41266101	C	T	2502.2	het	139	XM_005264887	COSM5673&	missense_variant
DDR2	snp	chr1	162740327	T	C	2580.26	hom	84	XM_005245220	rs1780003	intron_variant
DDR2	snp	chr1	162743418	G	T	421.86	hom	17	XM_005245220	rs1355287	intron_variant
DDR2	snp	chr1	162749873	T	C	378.468	het	26	XM_005245220.1		intron_variant
EGFR	snp	chr7	55221739	G	A	649.422	het	34	NM_005228.3	COSM13305	synonymous_variant
EGFR	snp	chr7	55221797	C	T	278.618	het	16	NM_005228.3		missense_variant
ERBB2	snp	chr17	37880974	C	T	1550.4	het	94	NM_004448.2		splice_region_variant&
ERBB2	snp	chr17	37881323	G	A	408.274	hom	15	NM_004448.2		missense_variant
ERBB2	snp	chr17	37882859	G	A	4076.89	het	176	NM_004448.2		missense_variant
ERBB4	snp	chr2	212652787	G	A	1488.74	hom	59	NM_005235.2		synonymous_variant
ERBB4	snp	chr2	212812308	C	T	988.276	hom	35	NM_005235.2	rs201678258	missense_variant
FBXW7	snp	chr4	153245620	G	A	874.082	hom	32	NM_033632.3		intron_variant
FBXW7	snp	chr4	153247332	T	A	640.813	hom	25	NM_033632.3		synonymous_variant
FBXW7	snp	chr4	153258961	G	A	1849.91	hom	66	NM_033632.3		missense_variant
FBXW7	snp	chr4	153259105	G	A	549.457	hom	20	NM_033632.3		intron_variant

FBXW7	snp	chr4	153273588	A	C	292.214	het	16	NM_033632.3		intron_variant
FBXW7	snp	chr4	153273589	T	A	292.214	het	16	NM_033632.3		intron_variant
FGFR1	snp	chr8	38271545	C	T	547.283	het	34	NM_001174067.1		splice_region_variant&
FGFR2	snp	chr10	123247511	G	A	5039.41	hom	178	NM_022970.3		synonymous_variant
FGFR2	mnp	chr10	123279674	GG	AT	322.929	hom	12	NM_022970.3		missense_variant
FGFR3	snp	chr4	1808467	C	T	840.152	het	48	NM_001163213.1		intron_variant
FLT3	snp	chr13	28592587	G	A	944.46	het	40	NM_004119.2		intron_variant
FLT3	snp	chr13	28592594	G	A	921.628	het	39	NM_004119.2		intron_variant
FLT3	snp	chr13	28610183	A	G	1555.44	hom	50	NM_004119.2	rs2491231	splice_region_variant&
GNA11	snp	chr19	3118897	G	A	3189.55	hom	113	NM_002067.2		intron_variant
GNAS	snp	chr20	57484213	C	T	379.735	het	22	NM_080425.2		splice_region_variant&
GNAS	snp	chr20	57484289	C	T	565.464	het	29	NM_080425.2		intron_variant
HNF1A	snp	chr12	121432181	C	T	303.655	het	17	XM_005253931.1		missense_variant
HRAS	snp	chr11	533944	C	T	483.767	hom	19	NM_005343.2		missense_variant&spli
IDH1	del	chr2	209116299	GAAAAAAA	GAAAAAAA	634.756	het	143	XM_005246521.1		intron_variant&featur
KRAS	snp	chr12	25362725	G	A	318.077	hom	11	NM_033360.2		3_prime_UTR_variant
MET	snp	chr7	116339144	G	A	1245.68	het	55	XM_005250353	COSM37024	synonymous_variant
MET	snp	chr7	116339175	G	A	1154.11	het	56	XM_005250353	COSM14474	missense_variant
MYC	snp	chr8	128749638	C	T	350.398	het	18	NM_002467.4		intron_variant
NOTCH1	snp	chr9	139390550	G	A	3583.42	hom	133	NM_017617.3	rs37012424	synonymous_variant
NOTCH1	complex	chr9	139391508	GACG	AACA	608.809	het	138	NM_017617.3		missense_variant
NOTCH1	snp	chr9	139391906	G	A	678.136	het	28	NM_017617.3		synonymous_variant
NOTCH1	snp	chr9	139399532	C	T	3899.83	het	245	NM_017617.3		synonymous_variant
NOTCH1	snp	chr9	139400045	C	T	1293.96	het	91	NM_017617.3		missense_variant
NOTCH1	snp	chr9	139400050	C	T	1314.41	het	90	NM_017617.3		missense_variant
PDGFRA	complex	chr4	55161254	CAG	TAA	466.354	hom	18	NM_006206.4		intron_variant
PDGFRA	snp	chr4	55161295	G	A	496.644	hom	19	NM_006206.4	rs141904599	synonymous_variant
PTEN	snp	chr10	89711812	G	A	1072.91	het	47	NM_000314.4	rs372870950	intron_variant
RET	snp	chr10	43615547	G	A	243.42	het	16	NM_020975.4		missense_variant
SMO	snp	chr7	128845277	G	C	984.797	hom	35	NM_005631.4	rs2075777	intron_variant
SMO	snp	chr7	128850231	G	A	494.426	hom	18	NM_005631.4		synonymous_variant
STK11	snp	chr19	1206929	C	G	1013.35	het	42	XM_005259617	COSM29463	missense_variant
STK11	snp	chr19	1207238	G	T	1019.55	hom	38	XM_005259617	rs3764640	intron_variant
STK11	snp	chr19	1218434	G	A	560.504	het	26	XM_005259617.1		synonymous_variant
STK11	snp	chr19	1218523	G	T	3013.34	hom	107	XM_005259617	rs2075604	intron_variant
STK11	snp	chr19	1220321	T	C	4440.94	hom	147	XM_005259617	rs2075606	intron_variant
STK11	snp	chr19	1220357	G	A	3455.16	hom	122	XM_005259617.1		intron_variant
STK11	snp	chr19	1220372	G	A	3187.95	hom	116	XM_005259617.1		splice_region_variant&
STK11	snp	chr19	1220414	C	A	739.984	hom	38	XM_005259617.1		missense_variant
STK11	snp	chr19	1221227	G	A	2326.71	hom	90	XM_005259617.1		synonymous_variant
STK11	snp	chr19	1223037	G	A	1117.04	hom	52	XM_005259617.1		missense_variant

TP53	snp	chr17	7576787	G	A	1068.64	het	55	NM_000546.5		intron_variant
TP53	snp	chr17	7578280	G	A	814.307	hom	37	NM_000546.5	TP53_g.126	missense_variant
TP53	snp	chr17	7579683	C	T	768.614	het	45	NM_000546.5		intron_variant
TP53	snp	chr17	7579987	G	A	275.854	hom	12	NM_000546.5		intron_variant
VHL	snp	chr3	10188185	C	T	197.411	het	22	NM_000551.3		intron_variant