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Data Sheet

Product Name: CancerSeqPlus Paraffin Tissue Curl

Catalog No.: T2235265-SC **Lot No.: B906075**

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: 22 year(s) old

Pathological Diagnosis: Carcinoma, Papillary

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# B906075

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.

CNV against colon	Copy Number	STDev of Copy Number	P-value	CNV against adrenal	Copy Number	STDev of Copy Number	P-value
DDR2	3.09	0.2	4.99E-03	DDR2	2.17	0.03	6.59E-02

symbol	type	chromosome	position	reference	mutation	quality	allele type	Depth at this position	transcript_id	existing variation	consequence
AKT1	snp	chr14	105246537	G	A	4513.08	het	268	NM_001014431.1		synonymous_varia
ALK	snp	chr2	29432728	T	A	397.996	het	47	NM_004304.4		missense_variant
ALK	snp	chr2	29445458	G	T	3379.72	hom	120	NM_004304.4	rs3795850	synonymous_varia
ATM	snp	chr11	108119856	G	A	630.789	het	43	NM_000051.3		intron_variant
ATM	snp	chr11	108172385	C	T	943.493	het	50	NM_000051.3	CM990211&	stop_gained
CCND1	snp	chr11	69460791	G	A	244.672	het	14	NM_053056.2		intron_variant
CCND1	snp	chr11	69463878	G	A	636.677	het	33	NM_053056.2		intron_variant
CCND1	snp	chr11	69465059	G	A	375.922	het	25	NM_053056.2		intron_variant
CDH1	snp	chr16	68771342	C	T	525.083	het	36	NM_004360.3		synonymous_varia
CDH1	snp	chr16	68835669	G	A	706.407	het	47	NM_004360.3		missense_variant
CDH1	snp	chr16	68853165	G	A	421.571	het	96	NM_004360.3		intron_variant
CDH1	snp	chr16	68857289	T	C	3176.36	het	194	NM_004360.3	rs2276330	intron_variant
CDH1	snp	chr16	68857321	G	A	1681.83	het	127	NM_004360.3		synonymous_varia
CDKN2A	snp	chr9	21968199	C	G	25263.8	hom	801	NM_001195132	rs11515&CO	3_prime_UTR_varia
CSF1R	snp	chr5	149452882	G	A	1773.97	het	75	NM_005211.3		missense_variant
DDR2	snp	chr1	162740327	T	C	9164.02	hom	291	XM_005245220	rs1780003	intron_variant
DDR2	snp	chr1	162743286	G	A	1215.11	het	85	XM_005245220.1		missense_variant
DDR2	snp	chr1	162743418	G	T	891.626	hom	38	XM_005245220	rs1355287	intron_variant
DDR2	snp	chr1	162745689	C	A	461.268	hom	25	XM_005245220.1		intron_variant
DDR2	snp	chr1	162746044	AC	AT	1404.74	het	237	XM_005245220.1		missense_variant
DDR2	snp	chr1	162749833	C	T	884.405	hom	38	XM_005245220.1		intron_variant
ERBB3	snp	chr12	56477694	A	T	3255.45	hom	108	NM_001982.3	rs2271194	splice_region_varia
ESR1	snp	chr6	152420095	G	A	1757.06	het	121	XM_005266856	rs2228480&	synonymous_varia
FGFR1	snp	chr8	38271443	G	A	256.789	het	12	NM_001174067.1		missense_variant
FGFR1	snp	chr8	38282138	G	A	689.039	hom	29	NM_001174067.1		synonymous_varia
FGFR1	snp	chr8	38285937	C	T	2570.53	het	132	NM_001174067	rs17182296	synonymous_varia
FGFR3	snp	chr4	1803630	G	A	3668.51	het	168	NM_001163213.1		missense_variant

FGFR3	snp	chr4	1803636	G	A	3702.09	het	166	NM_001163213.1		missense_variant
FGFR3	del	chr4	1806012	TGGGGGGGG	TGGGGGGGG	887.462	het	272	NM_001163213.1		intron_variant&fea
FGFR3	snp	chr4	1807894	G	A	615.927	hom	23	NM_001163213	rs7688609	synonymous_varia
FGFR3	snp	chr4	1807947	C	T	509.519	het	31	NM_001163213.1		intron_variant
FGFR3	snp	chr4	1808854	C	T	141.104	het	84	NM_001163213.1		synonymous_varia
FGFR3	complex	chr4	1808889	GCCAGGA	TCCTGGC	2227.12	hom	82	NM_001163213.1		missense_variant
FGFR3	complex	chr4	1808900	CCC	CGGGG	1900.51	hom	74	NM_001163213.1		frameshift_variant
FLT3	snp	chr13	28592594	G	A	2422.73	het	166	NM_004119.2		intron_variant
FLT3	snp	chr13	28610183	A	G	2020.64	het	88	NM_004119.2	rs2491231	splice_region_varia
GNAS	snp	chr20	57484425	C	T	250.092	het	22	NM_080425.2		synonymous_varia
H3F3A	snp	chr1	226252143	C	T	4678.69	het	223	NM_002107.4		missense_variant
HRAS	complex	chr11	534242	ATG	GTA	44.5977	het	84	NM_005343.2		missense_variant
HRAS	del	chr11	534403	GCCCAGGCC	GC	238.844	het	48	NM_005343.2		intron_variant&fea
IDH1	del	chr2	209116299	GAAAAAAAA	GAAAAAAAA	1313.06	het	90	XM_005246521.1		intron_variant&fea
JAK3	snp	chr19	17945727	G	A	13322.4	hom	475	XM_005259896	rs20072681	synonymous_varia
JAK3	snp	chr19	17954246	G	A	5493.61	hom	230	XM_005259896	rs19965695	synonymous_varia
JAK3	snp	chr19	17954263	G	A	5044.48	het	243	XM_005259896.1		missense_variant
KDR	snp	chr4	55955119	G	A	1382.02	hom	49	NM_002253.2		synonymous_varia
KDR	snp	chr4	55961159	T	C	214.322	het	11	NM_002253.2	rs2219471	intron_variant
KIT	snp	chr4	55593464	A	C	705.413	het	35	XM_005265740	rs3822214&	missense_variant
MAP2K1	snp	chr15	66727448	C	T	1097.83	hom	53	NM_002755.3		missense_variant
MPL	complex	chr1	43814989	GG	AA	1168.43	het	129	NM_005373.2		missense_variant
MPL	snp	chr1	43815067	C	T	13.9844	het	176	NM_005373.2		intron_variant
MYC	snp	chr8	128753017	G	A	283.101	het	25	NM_002467.4		missense_variant
MYCN	snp	chr2	16089615	T	C	291.78	het	17	NM_005378.4	rs4669018	downstream_gene
NOTCH1	snp	chr9	139397662	G	A	318.436	het	21	NM_017617.3		synonymous_varia
NOTCH1	snp	chr9	139400222	C	T	936.67	hom	37	NM_017617.3		missense_variant
NPM1	del,del	chr5	170837513	CTTTTTTTTT	CTTTTTTTTT	327.563	het	36	NM_002520.6		splice_region_varia
NRAS	snp	chr1	115251234	G	A	287.886	het	19	NM_002524.4		synonymous_varia
NRAS	snp	chr1	115252323	G	A	630.951	hom	27	NM_002524.4	COSM89423	missense_variant
PDGFRA	complex,sr	chr4	55141055	AGATG	GGATA,GGAT	2562.05	het	107	NM_006206.4		missense_variant
PDGFRA	snp	chr4	55161254	C	T	526.567	hom	18	NM_006206.4	rs3733540	intron_variant
PDGFRA	snp	chr4	55161517	A	G	1316.72	hom	51	NM_006206.4	rs7680422	3_prime_UTR_varia
PTEN	snp	chr10	89692926	C	T	510.552	hom	29	NM_000314.4	COSM5068	missense_variant
PTEN	del	chr10	89720633	CTTTTTTTTT	CTTTTTTTTT	358.354	het	69	NM_000314.4		splice_acceptor_va
RB1	snp	chr13	48919141	A	G	1850.62	het	104	NM_000321.2		intron_variant
RB1	snp	chr13	48919358	T	G	274.507	hom	10	NM_000321.2	rs198617	intron_variant
RB1	snp	chr13	48941702	G	A	394.674	hom	15	NM_000321.2	CD016053	missense_variant
RB1	snp	chr13	49037902	G	A	1491.4	het	64	NM_000321.2		synonymous_varia
RB1	snp	chr13	49037956	T	A	544.195	hom	27	NM_000321.2	CD941781	synonymous_varia
RET	complex	chr10	43610199	GGG	CCC	237.467	het	11	NM_020975.4		intron_variant

SMO	snp	chr7	128845277	G	C	3479.1	hom	119	NM_005631.4	rs2075777	intron_variant
STK11	snp	chr19	1219356	G	A	361.918	het	20	XM_005259617.1		missense_variant
STK11	snp	chr19	1220333	G	A	1129.98	het	84	XM_005259617.1		intron_variant
STK11	snp	chr19	1222012	G	C	11818.4	het	618	XM_005259617	rs2075607	splice_region_varia
STK11	snp	chr19	1223222	C	A	197.933	hom	11	XM_005259617.1		intron_variant
TERT	complex	chr5	1295221	GCCCG	ACCCA	333.425	het	97	NM_198253.2		upstream_gene_va
TP53	snp	chr17	7579472	G	C	3944.69	hom	128	NM_000546.5	rs1042522&	missense_variant
TP53	snp	chr17	7579659	T	C	636.731	het	32	NM_000546.5	rs139100308	intron_variant
VHL	complex	chr3	10183685	GAG	AAA	502.886	het	271	NM_000551.3		missense_variant
VHL	snp	chr3	10183735	G	A	482.979	hom	18	NM_000551.3	COSM18378	synonymous_varia
VHL	snp	chr3	10183876	G	C	1053.48	hom	40	NM_000551.3	rs61758376	splice_region_varia
VHL	snp	chr3	10191632	C	T	292.944	het	15	NM_000551.3	COSM18382	stop_gained