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Data Sheet

Product Name: CancerSeqPlus Paraffin Tissue Curl

Catalog No.: T2235265-SC **Lot No.: B906076**

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: 41 year(s) old

Pathological Diagnosis: Carcinoma, Papillary

Tumor Size: 3X2X2

Location: Thyroid

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

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

lot# B906076

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
ABL1	snp	chr9	133738438	C	G	3221.09	het	171	NM_007313.2	rs12551730	intron_variant
ALK	snp	chr2	29445458	G	T	4413.83	hom	144	NM_004304.4	rs3795850	synonymous_variant
APC	complex	chr5	112173798	CATC	GATG	290.042	het	24	XM_005271975.1		stop_gained
APC	mnp	chr5	112173809	AG	GC	266.191	het	23	XM_005271975.1		missense_variant
APC	snp	chr5	112176559	T	G	424.244	hom	18	XM_005271975.	rs866006	synonymous_variant
ATM	snp	chr11	108119916	T	A	311.523	hom	15	NM_000051.3		intron_variant
ATM	snp	chr11	108170489	C	T	1863.93	het	75	NM_000051.3		missense_variant
CCND1	snp	chr11	69471133	G	A	903.178	het	42	NM_053056.2		downstream_gene_v
CDH1	complex	chr16	68771340	CTCTCGGC	GCCGAGAG	41.8258	het	525	NM_004360.3		missense_variant
CDH1	snp	chr16	68771353	T	G	456.26	het	582	NM_004360.3		missense_variant
CDH1	snp	chr16	68771370	CCC	CCT	10270.8	hom	359	NM_004360.3		splice_region_varian
CDH1	complex	chr16	68771370	CCC	TCT	874.681	hom	32	NM_004360.3		splice_region_varian
CDH1	snp	chr16	68844166	G	A	1575.66	het	116	NM_004360.3		missense_variant
CDH1	complex	chr16	68846101	ACAGCAACA(	GCTGTTGCTG	704.572	het	35	NM_004360.3		missense_variant
CDH1	complex	chr16	68846115	GATC	GCTTA	727.4	hom	32	NM_004360.3		frameshift_variant&t
CDKN2A	snp	chr9	21968199	C	G	28814.9	hom	911	NM_001195132.	rs11515&CO	3_prime_UTR_variar
DDR2	snp	chr1	162740327	T	C	10532.4	hom	336	XM_005245220.	rs1780003	intron_variant
DDR2	snp	chr1	162743418	G	T	2941.65	hom	129	XM_005245220.	rs1355287	intron_variant
EGFR	complex	chr7	55221791	GTGAACC	TTGC	431.52	hom	17	NM_005228.3		feature_truncation
EGFR	mnp	chr7	55221800	GA	TC	514.358	hom	18	NM_005228.3		missense_variant
EGFR	snp	chr7	55249063	G	A	525.794	het	26	NM_005228.3	rs1050171&(	synonymous_variant
ERBB2	complex	chr17	37880147	CCTCCTCT	TTTCACA	444.573	hom	30	NM_004448.2		intron_variant&featu
ERBB2	snp	chr17	37880159	G	C	1489.05	hom	57	NM_004448.2		splice_region_varian
ERBB2	complex	chr17	37880163	AGGGCATCT(	ATCAGGGAT(	1261.69	hom	48	NM_004448.2		splice_acceptor_vari
ERBB2	del	chr17	37882959	TCC	TC	1941.99	het	166	NM_004448.2		intron_variant&featu
ERBB2	ins	chr17	37882965	AGA	AGGA	1860.27	hom	86	NM_004448.2		intron_variant&featu
ERBB2	mnp	chr17	37882973	GG	CT	1972.67	hom	88	NM_004448.2		intron_variant
ERBB3	snp	chr12	56477694	A	T	3434.32	het	219	NM_001982.3	rs2271194	splice_region_varian
ESR1	snp	chr6	152420095	G	A	5578.26	het	330	XM_005266856.	rs2228480&(	synonymous_variant
EZH2	snp	chr7	148508833	A	G	300.859	het	15	XM_005249962.	rs2072407	intron_variant
FBXW7	del	chr4	153247486	CTTTTTTTTT	CTTTTTTTTT	353.275	het	59	NM_033632.3		intron_variant&featu

FGFR1	mnp	chr8	38271371	CT	AG	235.008	het	13	NM_001174067.1		intron_variant
FGFR1	complex	chr8	38271381	TGC	AGG	257.882	het	15	NM_001174067.1		intron_variant
FGFR3	del	chr4	1806012	TGGGGGGGG	TGGGGGGGG	1017.09	het	354	NM_001163213.1		intron_variant&featu
FGFR3	snp	chr4	1808372	C	A	368.892	het	52	NM_001163213.1		synonymous_variant
FGFR3	mnp	chr4	1808375	CC	TT	309.384	het	21	NM_001163213.1		missense_variant
FOXL2	mnp	chr3	138665030	CCA	AGG	1296.61	hom	51	NM_023067.3		missense_variant
FOXL2	complex	chr3	138665040	CCCGCC	GGCGGG	1377.17	hom	53	NM_023067.3		missense_variant
HRAS	del	chr11	534403	GCCCAGGCC	GC	16.2773	het	219	NM_005343.2		intron_variant&featu
IDH1	del	chr2	209116299	GAAAAAAAA	GAAAAAAAA	559.658	het	124	XM_005246521.1		intron_variant&featu
JAK2	del	chr9	5073681	CTTTTTTTTT	CTTTTTTTTC	736.54	het	69	NM_004972.3		splice_region_varian
KDR	snp	chr4	55955192	T	A	257.64	het	20	NM_002253.2		intron_variant
KDR	snp	chr4	55961159	T	C	724.228	het	42	NM_002253.2	rs2219471	intron_variant
MAP2K1	snp	chr15	66727550	C	T	452.447	hom	16	NM_002755.3		missense_variant
MAP2K1	complex	chr15	66727559	TGGTCAT	ATGACCA	452.447	hom	16	NM_002755.3		missense_variant
MAP2K1	snp	chr15	66727597	G	C	7676.47	het	415	NM_002755.3	rs16949924	intron_variant
MAP2K1	snp	chr15	66729250	C	T	3160.73	het	166	NM_002755.3	rs16949939	intron_variant
MET	snp	chr7	116436097	G	A	851.303	het	49	XM_005250353.	rs41737&CO	synonymous_variant
MYC	snp	chr8	128748687	C	T	1292.54	het	75	NM_002467.4		5_prime_UTR_variar
MYCN	snp	chr2	16080157	C	G	906.118	hom	30	NM_005378.4	rs11886063	upstream_gene_vari
MYCN	snp	chr2	16089551	C	T	256.008	het	18	NM_005378.4		downstream_gene_v
NOTCH1	snp	chr9	139391446	C	T	1354.65	het	67	NM_017617.3	rs369457922	missense_variant
NOTCH1	snp	chr9	139391539	GTGGC	GTGGT	8560.1	het	1318	NM_017617.3		synonymous_variant
NOTCH1	snp	chr9	139391636	G	A	541.089	hom	23	NM_017617.3	rs2229974	synonymous_variant
NOTCH1	snp	chr9	139397707	G	A	2806.59	hom	106	NM_017617.3	rs10521&CO	synonymous_variant
NOTCH1	complex	chr9	139399226	GGCCCAGCC	CGCCGAGGG	281.081	het	18	NM_017617.3		missense_variant
NOTCH1	mnp	chr9	139399246	GC	CT	308.111	het	25	NM_017617.3		missense_variant
NOTCH1	complex	chr9	139399976	CGTCCTCCTG	AGTGCCAGG	471.03	hom	20	NM_017617.3		missense_variant
NPM1	del,del	chr5	170837513	CTTTTTTTTT	CTTTTTTTTT	884.022	het	94	NM_002520.6		splice_region_varian
PDGFRA	snp	chr4	55141055	A	G	5534.41	hom	183	NM_006206.4	rs1873778&(	synonymous_variant
PDGFRA	snp	chr4	55161254	C	T	631.547	het	40	NM_006206.4	rs3733540	intron_variant
PDGFRA	snp	chr4	55161517	A	G	1678.99	hom	54	NM_006206.4	rs7680422	3_prime_UTR_variar
PIK3CA	snp	chr3	178927345	T	C	534.905	het	24	NM_006218.2	rs3729682	intron_variant
PTEN	snp	chr10	89685286	C	T	1287.32	het	59	NM_000314.4	rs121909236	missense_variant
PTEN	snp	chr10	89711976	G	A	407.65	het	27	NM_000314.4	COSM5853	missense_variant
PTEN	del	chr10	89720633	CTTTTTTTTT	CTTTTTTTTT	220.447	het	70	NM_000314.4		splice_acceptor_vari
PTEN	del	chr10	89725293	CTTTTTTTTT	CTTTTTTTTT	341.798	het	85	NM_000314.4		3_prime_UTR_variar
RB1	snp	chr13	48919358	T	G	1124.26	hom	39	NM_000321.2	rs198617	intron_variant
RET	mnp	chr10	43610190	GG	CT	87.8536	het	189	NM_020975.4		splice_region_varian
RET	snp	chr10	43613843	G	T	2374.9	het	122	NM_020975.4	rs1800861&(	synonymous_variant
RET	snp	chr10	43617537	C	T	394.991	het	466	NM_020975.4		intron_variant
SMARCB1	snp	chr22	24134018	G	A	577.175	het	39	XM_005261718.1		missense_variant

SMO	snp	chr7	128845178	G	A	281.226	hom	11	NM_005631.4	rs148484943	synonymous_variant
SMO	complex	chr7	128845189	AGGACAT	TGGT	256.435	hom	10	NM_005631.4		feature_truncation
SMO	snp	chr7	128845198	A	T	263.715	hom	10	NM_005631.4		missense_variant
SMO	snp	chr7	128845277	G	C	1141.8	hom	37	NM_005631.4	rs2075777	intron_variant
SMO	snp	chr7	128846328	G	C	3116.58	hom	99	NM_005631.4	rs2228617	synonymous_variant
SRC	snp	chr20	36031545	G	A	705.689	het	41	NM_005417.4		intron_variant
SRC	snp	chr20	36031669	C	T	850.468	hom	31	NM_005417.4		stop_gained
SRC	snp	chr20	36031779	C	T	399.844	het	31	NM_005417.4	rs146973968	synonymous_variant
STK11	complex	chr19	1219399	TGCCAGGCC(	GGCCTGGCA(	977.172	het	53	XM_005259617.1		splice_donor_varian
STK11	complex	chr19	1220727	CGCCCCCCC	GGGGGGGC(	318.777	hom	15	XM_005259617.1		intron_variant
STK11	complex	chr19	1220743	CACCACA	TACAGGG	305.367	hom	14	XM_005259617.1		intron_variant
STK11	snp	chr19	1222011	CG	CC	9617.82	het	992	XM_005259617.1		splice_region_varian
TERT	snp	chr5	1295349	A	G	17031.7	het	1058	NM_198253.2	rs2853669&(	upstream_gene_vari
TP53	snp	chr17	7573969	G	A	570.056	het	45	NM_000546.5		missense_variant
TP53	snp	chr17	7579472	G	C	5994.2	het	226	NM_000546.5	rs1042522&T	missense_variant
TP53	del	chr17	7579643	CCCCCAGCC(	CC	243.936	het	85	NM_000546.5		intron_variant&featu
TP53	mnp	chr17	7579658	GT	CC	193.719	het	99	NM_000546.5		intron_variant
TP53	complex	chr17	7579668	CTCCAG	CAACCCTT	470.686	het	123	NM_000546.5		intron_variant&featu
TP53	complex	chr17	7579678	CCAG	TTAC	577.317	het	118	NM_000546.5		intron_variant
TP53	complex	chr17	7590817	AACTTTTA	GACTG	491.763	hom	21	NM_000546.5		5_prime_UTR_varian
TP53	complex	chr17	7590828	CCAGTC	CTAAAAGTT	488.749	het	22	NM_000546.5		5_prime_UTR_varian
VHL	snp	chr3	10191497	C	T	852.589	het	44	NM_000551.3	rs5030819&(	stop_gained