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Data Sheet

Product Name: CancerSeqPlus Paraffin Tissue Curl

Catalog No.: T2235265-SC **Lot No.: B906071**

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: 35 year(s) old

Pathological Diagnosis: Carcinoma, papillary

Tumor Size: 3x3x2.5 cm

Location: Thyroid

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

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

lot# B906071

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	mnp	chr9	133748451	CC	TT	788.128	het	172	NM_007313.2		intron_variant
ALK	snp	chr2	29445458	G	T	2147.89	hom	71	NM_004304.4	rs3795850	synonymous_variant
ALK	snp	chr2	29445505	G	A	556.124	het	31	NM_004304.4		intron_variant
CDH1	snp	chr16	68771372	C	T	11185.8	hom	362	NM_004360.3	rs3743674	splice_region_varian
CDK4	snp	chr12	58143031	G	A	1902.14	het	110	NM_000075.3		synonymous_variant
CDKN2A	snp	chr9	21968199	C	G	18185	hom	580	NM_001195132	rs11515&CO	3_prime_UTR_varian
CDKN2A	snp	chr9	21968310	C	A	366.989	het	38	NM_001195132.1		intron_variant
CDKN2A	snp	chr9	21971185	C	T	1525	het	74	NM_001195132	rs36204273	missense_variant
DDR2	snp	chr1	162740327	T	C	9707.36	hom	308	XM_005245220	rs1780003	intron_variant
DDR2	snp	chr1	162746195	A	G	306.99	hom	15	XM_005245220.1		intron_variant
ERBB3	snp	chr12	56477694	A	T	2502.8	het	132	NM_001982.3	rs2271194	splice_region_varian
ERBB4	snp	chr2	212578280	C	T	354.382	hom	16	NM_005235.2		missense_variant
FBXW7	snp	chr4	153252061	A	G	642.146	het	42	NM_033632.3	rs10033601	intron_variant
FBXW7	del	chr4	153268227	CAAAAAAAA	CAAAAAAAA	202.061	het	40	NM_033632.3		splice_region_varian
FGFR2	snp	chr10	123258090	G	A	845.43	het	44	NM_022970.3		synonymous_variant
FGFR3	snp	chr4	1803690	C	T	343.532	het	24	NM_001163213.1		missense_variant
FGFR3	snp	chr4	1806017	G	A	587.812	het	78	NM_001163213	rs200683551	intron_variant
FGFR3	snp	chr4	1806215	C	T	279.565	het	17	NM_001163213.1		missense_variant
FGFR3	snp	chr4	1807894	G	A	1579.29	hom	57	NM_001163213	rs7688609	synonymous_variant
FGFR3	mnp	chr4	1808919	GG	AA	1334.81	het	161	NM_001163213.1		missense_variant
FLT3	snp	chr13	28610183	A	G	3712.77	hom	125	NM_004119.2	rs2491231	splice_region_varian
FOXL2	ins	chr3	138664543	GG	GCG	1168.37	hom	51	NM_023067.3		frameshift_variant&f
FOXL2	complex	chr3	138664546	GCACTGGTG	CCACCAGTG	1076.71	hom	51	NM_023067.3		frameshift_variant&f
IDH1	del	chr2	209116299	GAAAAAAAA	GAAAAAAAA	536.925	het	85	XM_005246521.1		intron_variant&featu
JAK2	del	chr9	5073681	CTTTTTTTTT	CTTTTTTTTT	993.112	het	86	NM_004972.3		splice_region_varian
MET	snp	chr7	116340162	C	T	647.092	hom	28	XM_005250353	COSM10843	missense_variant
MLH1	snp	chr3	37067240	T	A	1887.04	het	95	NM_000249.3	rs63750447	missense_variant
MYC	snp	chr8	128749566	C	T	754.2	hom	31	NM_002467.4		intron_variant
MYCN	snp	chr2	16089615	T	C	732.196	hom	27	NM_005378.4	rs4669018	downstream_gene_v
NOTCH1	complex	chr9	139390558	ACTGCATG	TCTCCGA	253.415	het	16	NM_017617.3		frameshift_variant&f
NOTCH1	mnp	chr9	139390571	GG	CC	300.848	het	17	NM_017617.3		missense_variant
NOTCH1	snp	chr9	139390954	G	A	1.16911	het	208	NM_017617.3	rs37567929	missense_variant

NOTCH1	snp	chr9	139391039	C	T	341.67	het	172	NM_017617.3		synonymous_variant
NOTCH1	snp	chr9	139391636	G	A	1587.96	hom	72	NM_017617.3	rs2229974	synonymous_variant
NOTCH1	snp	chr9	139397707	G	A	2586.11	hom	88	NM_017617.3	rs10521&CO	synonymous_variant
NOTCH1	snp	chr9	139397735	G	A	1779.05	het	86	NM_017617.3		missense_variant
NOTCH1	snp	chr9	139397742	G	A	1732.82	het	85	NM_017617.3		stop_gained
NPM1	del,del	chr5	170837513	CTTTTTTTTT	CTTTTTTTTT	723.679	het	67	NM_002520.6		splice_region_varian
PDGFRA	snp	chr4	55141055	A	G	11233.8	hom	382	NM_006206.4	rs1873778&	synonymous_variant
PDGFRA	snp	chr4	55144523	C	T	497.347	het	28	NM_006206.4		splice_region_varian
PDGFRA	snp	chr4	55152040	C	T	4322.5	het	280	NM_006206.4	rs2228230&	synonymous_variant
PDGFRA	snp	chr4	55161517	A	G	1519.49	hom	49	NM_006206.4	rs7680422	3_prime_UTR_varian
PIK3CA	snp	chr3	178927345	T	C	1396.61	hom	47	NM_006218.2	rs3729682	intron_variant
PIK3CA	del	chr3	178927848	ATTTTTTTTT	ATTTTTTTTT	661.298	het	64	NM_006218.2		intron_variant&featu
PTEN	snp	chr10	89693076	T	A	420.025	hom	23	NM_000314.4		intron_variant
PTEN	del	chr10	89720633	CTTTTTTTTT	CTTTTTTTTT	596.211	het	154	NM_000314.4		splice_acceptor_vari
PTEN	snp	chr10	89720768	G	A	260.46	het	14	NM_000314.4		missense_variant
PTEN	del	chr10	89725293	CTTTTTTTTT	CTTTTTTTTT	315.956	het	52	NM_000314.4		3_prime_UTR_varian
RB1	snp	chr13	48919334	A	T	159.252	het	17	NM_000321.2		missense_variant&sp
RB1	snp	chr13	48919358	T	G	2125.81	hom	78	NM_000321.2	rs198617	intron_variant
RB1	snp	chr13	49034025	C	T	756.72	hom	33	NM_000321.2		intron_variant
RET	mnp	chr10	43610189	GGG	TCT	700.929	hom	27	NM_020975.4		splice_region_varian
RET	mnp	chr10	43610199	GGG	CCC	769.511	het	32	NM_020975.4		intron_variant
RET	snp	chr10	43610281	G	A	515.804	hom	27	NM_020975.4		intron_variant
SMO	snp	chr7	128845018	C	T	407.65	het	27	NM_005631.4	rs2703091	intron_variant
SMO	snp	chr7	128845277	G	C	3701.63	hom	119	NM_005631.4	rs2075777	intron_variant
SMO	snp	chr7	128846328	G	C	740.057	hom	25	NM_005631.4	rs2228617	synonymous_variant
SRC	snp	chr20	36031501	C	T	5729.23	het	283	NM_005417.4	rs2273677	intron_variant
STK11	snp	chr19	1207238	G	T	3335.73	het	246	XM_005259617	rs3764640	intron_variant
STK11	snp	chr19	1219419	G	A	190.463	het	19	XM_005259617.1		splice_region_varian
STK11	snp	chr19	1221459	G	A	1201.61	hom	51	XM_005259617.1		intron_variant
STK11	snp	chr19	1222012	G	C	30142.7	hom	976	XM_005259617	rs2075607	splice_region_varian
TERT	snp	chr5	1295349	A	G	9087.01	het	563	NM_198253.2	rs2853669&	upstream_gene_vari
TP53	snp	chr17	7579472	G	C	3154.45	hom	100	NM_000546.5	rs1042522&	missense_variant
TP53	del	chr17	7579643	CCCCCAGCC	CC	453.808	het	81	NM_000546.5		intron_variant&featu