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Data Sheet

Product Name: CancerSeqPlus Paraffin Tissue Curl

Catalog No.: T2235265-SC **Lot No.:** B906058

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

Pathological Diagnosis: Adenocarcinoma,Follicular

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 # B906058

symbol	type	chromosome	position	reference	mutation	quality score	allele type	Depth at this position	transcript_id	existing variation	consequence
ABL1	snp	chr9	133750321	G	A	752.93	het	47	NM_007313.2	COSM146053	synonymous_
ABL1	snp	chr9	133750330	G	A	650.202	het	44	NM_007313.2		synonymous_
APC	snp	chr5	112178839	G	T	2476.72	het	156	XM_005271975.1		missense_vari
APC	snp	chr5	112179366	C	T	1506.57	het	110	XM_005271975.1		missense_vari
ATM	snp	chr11	108117851	C	T	2287.32	het	125	NM_000051.3		synonymous_
ATM	del	chr11	108117897	ATTTTTTTTT	ATTTTTTTTT/	73.9872	het	126	NM_000051.3		intron_variant
ATM	snp	chr11	108205871	T	A	370.075	hom	17	NM_000051.3		intron_variant
AURKA	snp	chr20	54958039	A	G	736.78	het	55	NM_003600.2		splice_donor_
CCND1	snp	chr11	69471134	G	A	1814.84	het	95	NM_053056.2		downstream_
CCNE1	snp	chr19	30303987	C	T	231.493	het	43	NM_001238.2		intron_variant
CDH1	snp	chr16	68772264	C	T	2050.48	het	107	NM_004360.3		missense_vari
CDH1	ins	chr16	68857544	CAA	CAAA	995.909	het	55	NM_004360.3		intron_variant
CDKN2A	snp	chr9	21968199	C	G	18560.5	hom	606	NM_001195132	rs11515&COS	3_prime_UTR_
CDKN2A	snp	chr9	21974832	T	C	1059	het	65	NM_001195132.1		5_prime_UTR_
DDR2	ins	chr1	162740094	TTCT	TTCTCT	1238.78	het	110	XM_005245220.1		frameshift_va
DDR2	snp	chr1	162740327	T	C	7441.25	hom	236	XM_005245220	rs1780003	intron_variant
DDR2	snp	chr1	162741941	C	T	221.951	het	11	XM_005245220.1		synonymous_
DDR2	snp	chr1	162743418	G	T	926.55	hom	42	XM_005245220	rs1355287	intron_variant
DDR2	snp	chr1	162745609	C	T	619.81	het	44	XM_005245220.1		missense_vari
DDR2	snp	chr1	162746100	C	T	2012.22	hom	72	XM_005245220.1		synonymous_
ERBB2	snp	chr17	37880277	C	T	1265.32	het	84	NM_004448.2		intron_variant
ERBB2	snp	chr17	37882913	G	A	2460.57	het	119	NM_004448.2	rs112493843	splice_donor_
ERBB3	snp	chr12	56477694	AGCC	TGCC	11280.8	hom	421	NM_001982.3		splice_region_
ERBB3	complex	chr12	56477694	AGCC	TGCT	583.013	het	31	NM_001982.3		splice_region_
ERBB3	snp	chr12	56477726	T	A	1074.71	hom	62	NM_001982.3		intron_variant
ERBB3	snp	chr12	56478918	C	T	862.838	het	49	NM_001982.3		missense_vari
ESR1	snp	chr6	152420095	G	A	616.286	het	34	XM_005266856	rs2228480&C	synonymous_
FBXW7	snp	chr4	153244352	A	G	409.085	hom	15	NM_033632.3	rs34649288	intron_variant
FGFR1	snp	chr8	38271362	T	A	475.002	hom	17	NM_001174067.1		intron_variant
FGFR1	mnp	chr8	38271371	CT	AG	424.498	hom	15	NM_001174067.1		intron_variant
FGFR1	complex	chr8	38271381	TGCGT	AGGGG	503.491	hom	18	NM_001174067.1		intron_variant
FGFR1	snp	chr8	38285962	A	G	25.6385	het	80	NM_001174067.1		intron_variant
FGFR2	snp	chr10	123247559	G	A	6588.14	hom	265	NM_022970.3		synonymous_
FGFR3	del	chr4	1806012	TGGGGGGG	TGGGGGGG(	1154.82	het	248	NM_001163213.1		intron_variant
FGFR3	snp	chr4	1807894	G	A	1197.63	hom	40	NM_001163213	rs7688609	synonymous_

FOXL2	snp	chr3	138665616	C	T	270.772	het	20	NM_023067.3		5_prime_UTR
GNAQ	snp	chr9	80409521	C	T	426.835	het	23	NM_002072.3		intron_variant
GNAQ	snp	chr9	80412565	C	T	691.564	het	28	NM_002072.3		splice_accept
HRAS	snp	chr11	534298	C	T	1151.61	hom	54	NM_005343.2		missense_vari
HRAS	snp	chr11	534340	C	T	2065.65	het	87	NM_005343.2		5_prime_UTR
IDH2	snp	chr15	90631832	G	A	3526.55	het	270	NM_002168.2		missense_vari
KDR	snp	chr4	55953813	C	T	414.648	het	26	NM_002253.2		missense_vari
KIT	snp	chr4	55592089	G	A	225.569	het	14	XM_005265740.1		synonymous_
KIT	snp	chr4	55594269	G	A	656.17	het	37	XM_005265740.1		missense_vari
KIT	snp	chr4	55599367	C	T	3645.31	het	180	XM_005265740.1		intron_variant
KRAS	snp	chr12	25378732	C	T	1697.06	het	86	NM_033360.2		intron_variant
MAP2K1	snp	chr15	66727597	G	C	2699.99	het	142	NM_002755.3	rs16949924	intron_variant
MET	snp	chr7	116403291	C	T	316.299	het	16	XM_005250353.1		missense_vari
MET	snp	chr7	116423495	C	T	358.101	het	27	XM_005250353.1		missense_vari
MLH1	complex	chr3	37067097	ATA	TTT	495.57	hom	21	NM_000249.3		intron_variant
MPL	complex	chr1	43815047	GCAGGAGA	TCTCCTGC	539.715	het	121	NM_005373.2		intron_variant
MPL	complex	chr1	43815062	TGGA	GGGC	326.448	het	137	NM_005373.2		intron_variant
MYC	snp	chr8	128746547	G	A	821.519	hom	35	NM_002467.4		upstream_ger
MYCN	snp	chr2	16080157	C	G	708.858	hom	23	NM_005378.4	rs11886063	upstream_ger
MYCN	snp	chr2	16089615	T	C	209.729	het	18	NM_005378.4	rs4669018	downstream_
NOTCH1	snp	chr9	139390625	G	A	2904.71	het	217	NM_017617.3		synonymous_
NOTCH1	snp	chr9	139397809	G	T	686.017	het	29	NM_017617.3		intron_variant
NOTCH1	snp	chr9	139397893	T	A	319.683	hom	15	NM_017617.3		intron_variant
NOTCH1	snp	chr9	139399250	G	A	762.175	hom	39	NM_017617.3	COSM33752	synonymous_
NPM1	del	chr5	170837513	CTTTTTTTTT	CTTTTTTTTT	259.247	het	42	NM_002520.6		splice_region_
NRAS	snp	chr1	115252190	C	T	1573.47	het	85	NM_002524.4		splice_region_
NRAS	snp	chr1	115256663	G	A	246.115	hom	11	NM_002524.4		intron_variant
PDGFRA	snp	chr4	55141055	A	G	1619.95	hom	57	NM_006206.4	rs1873778&C	synonymous_
PDGFRA	snp	chr4	55161254	C	T	1353.29	hom	44	NM_006206.4	rs3733540	intron_variant
PDGFRA	snp	chr4	55161517	A	G	555.011	hom	18	NM_006206.4	rs7680422	3_prime_UTR
PIK3CA	complex	chr3	178916653	CACTT	AAGTG	541.028	het	28	NM_006218.2		missense_vari
PIK3R1	snp	chr5	67590439	C	T	709.892	het	31	NM_181523.2		stop_gained
PIK3R1	snp	chr5	67592095	G	A	580.084	het	25	NM_181523.2		synonymous_
PTEN	snp	chr10	89692864	C	T	781.197	hom	38	NM_000314.4	COSM134951	synonymous_
RB1	snp	chr13	48919358	T	G	1256.6	hom	46	NM_000321.2	rs198617	intron_variant
RB1	snp	chr13	49033784	A	T	508.276	hom	25	NM_000321.2		intron_variant
RET	mnp	chr10	43610190	GG	CT	327.476	het	16	NM_020975.4		splice_region_
RET	mnp	chr10	43610199	GGG	CCC	283.607	hom	12	NM_020975.4		intron_variant
SMAD4	snp	chr18	48604773	C	T	1268.15	het	62	NM_005359.5	COSM115075	missense_vari
SMO	snp	chr7	128845277	G	C	3275.71	hom	105	NM_005631.4	rs2075777	intron_variant
SMO	snp	chr7	128846328	G	C	481.995	hom	16	NM_005631.4	rs2228617	synonymous_

STK11	snp	chr19	1207152	C	T	934.273	het	58	XM_005259617.1		synonymous_
STK11	snp	chr19	1207238	G	T	5310.45	hom	183	XM_005259617	rs3764640	intron_variant
STK11	snp	chr19	1220524	G	A	415.784	het	178	XM_005259617.1		intron_variant
STK11	snp	chr19	1220826	C	T	692.848	het	49	XM_005259617.1		intron_variant
STK11	snp	chr19	1222012	G	C	11015.7	het	792	XM_005259617	rs2075607	splice_region_
STK11	snp	chr19	1226648	G	A	470.166	hom	20	XM_005259617.1		synonymous_
TERT	snp	chr5	1295349	A	G	15443.8	hom	506	NM_198253.2	rs2853669&C	upstream_gen
TP53	snp	chr17	7573983	C	T	229.074	het	15	NM_000546.5	TP53_g.16935	synonymous_
TP53	snp	chr17	7579472	G	C	1544.44	hom	52	NM_000546.5	rs1042522&T	missense_vari
TP53	mnp	chr17	7590809	AAG	CTT	100.856	het	268	NM_000546.5		5_prime_UTR_
VHL	snp	chr3	10183688	G	A	491.106	het	32	NM_000551.3		missense_vari