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Data Sheet

Product Name: CancerSeqPlus Paraffin Tissue Curl

Catalog No.: T2235265-SC **Lot No.: B906074**

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: 25 year(s) old

Pathological Diagnosis: Carcinoma, Papillary

Tumor Size: diameter 1.5cm

Location: Thyroid, right

Components:

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

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

lot # B906074

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
NOTCH1	2.60	0.12	6.80E-02	NOTCH1	3.74	0.05	3.41E-03

symbol	type	chromosome	position	reference	mutation	quality	allele type	Depth at this position	transcript_id	existing variation	consequence
ABL1	snp	chr9	133738163	C	T	382.491	het	22	NM_007313.2		missense_variant
ABL1	snp	chr9	133750284	G	A	331.153	het	23	NM_007313.2		missense_variant
AKT1	complex	chr14	105246552	CCC	TCT	2890.13	het	282	NM_001014431.1		splice_acceptor_v
ALK	snp	chr2	29445458	G	T	654.707	hom	22	NM_004304.4	rs3795850	synonymous_varia
BRAF	snp	chr7	140453053	G	A	271.196	het	21	XM_005250045.1		intron_variant
BRAF	snp	chr7	140481323	G	A	1427.19	hom	51	XM_005250045.1		intron_variant
CCNE1	snp	chr19	30303670	C	T	639.836	het	46	NM_001238.2		missense_variant
CCNE1	snp	chr19	30312639	C	T	847.839	het	53	NM_001238.2		missense_variant
CDH1	snp	chr16	68771353	TGCTGCTGCT	TGCGGCTGC	1889.68	het	985	NM_004360.3		missense_variant
CDH1	snp	chr16	68771370	CCC	CCT	28106.9	hom	913	NM_004360.3		splice_region_vari
CDH1	snp	chr16	68845597	G	A	326.134	het	25	NM_004360.3		synonymous_varia
CDH1	snp	chr16	68847232	C	T	1064.37	het	58	NM_004360.3		missense_variant
CDK4	snp	chr12	58145497	C	T	1707.88	het	87	NM_000075.3		missense_variant
CDK4	snp	chr12	58145502	C	T	269.786	het	93	NM_000075.3		5_prime_UTR_var
CDKN2A	snp,snp	chr9	21968199	C	A,G	10072	het	354	NM_001195132	rs11515&COS	3_prime_UTR_var
CDKN2A	snp	chr9	21968258	G	A	810.184	het	54	NM_001195132.1		intron_variant
CDKN2A	snp	chr9	21970913	C	T	323.335	het	20	NM_001195132	CM034219	missense_variant
DDR2	snp	chr1	162740241	C	T	738.784	het	39	XM_005245220.1		synonymous_varia
DDR2	snp	chr1	162740327	T	C	9360.52	hom	300	XM_005245220	rs1780003	intron_variant
DDR2	snp	chr1	162743418	G	T	1660.4	hom	63	XM_005245220	rs1355287	intron_variant
DDR2	snp	chr1	162745512	G	A	1084.03	hom	42	XM_005245220.1		missense_variant
EGFR	snp	chr7	55232979	G	A	343.741	het	19	NM_005228.3		missense_variant
EGFR	snp	chr7	55233102	C	T	857.802	hom	32	NM_005228.3		missense_variant
EGFR	snp	chr7	55233122	C	T	810.513	het	43	NM_005228.3		synonymous_varia
EGFR	snp	chr7	55241667	G	A	972.363	het	60	NM_005228.3		synonymous_varia
ERBB2	snp	chr17	37871576	C	T	4650.42	het	323	NM_004448.2		stop_gained

ERBB2	complex	chr17	37881301	GGGG	AGGA	469.571	het	269	NM_004448.2		splice_acceptor_v
ERBB3	complex	chr12	56477667	CCGAC	TCGAT	1797.09	het	246	NM_001982.3		missense_variant
ERBB3	snp	chr12	56477694	A	T	8671.98	hom	282	NM_001982.3	rs2271194	splice_region_vari
ERBB3	snp	chr12	56478975	C	T	1510.54	het	89	NM_001982.3		intron_variant
ERBB3	snp	chr12	56482435	C	T	310.751	het	16	NM_001982.3		missense_variant
ESR1	snp	chr6	152419936	G	A	5718.12	het	356	XM_005266856.1		synonymous_varia
ESR1	snp	chr6	152420095	G	A	1506.94	het	97	XM_005266856	rs2228480&C	synonymous_varia
FGFR2	snp	chr10	123274661	G	A	1424.65	het	73	NM_022970.3		synonymous_varia
FGFR2	snp	chr10	123274680	G	A	1430.12	het	70	NM_022970.3	rs372348666	missense_variant
FGFR2	snp	chr10	123274710	G	A	656.911	hom	29	NM_022970.3		missense_variant
FGFR3	snp	chr4	1805600	C	T	993.42	het	49	NM_001163213.1		intron_variant
FGFR3	snp	chr4	1808979	C	T	1525.23	het	83	NM_001163213.1		missense_variant
FLT3	snp	chr13	28610183	A	G	2797.22	hom	89	NM_004119.2	rs2491231	splice_region_vari
FOXL2	snp	chr3	138665063	C	T	5153.49	het	366	NM_023067.3		missense_variant
GNAS	snp	chr20	57480506	C	T	741.625	hom	27	NM_080425.2		synonymous_varia
GNAS	snp	chr20	57480544	C	T	785.009	hom	28	NM_080425.2		intron_variant
HNF1A	snp	chr12	121431343	G	A	991.509	het	54	XM_005253931.1		missense_variant
HNF1A	snp	chr12	121431999	C	G	1741.13	het	99	XM_005253931.1		stop_gained
HRAS	complex	chr11	533768	GTACTGGTGG	GCCTGGA	899.929	hom	35	NM_005343.2		feature_truncatio
HRAS	complex	chr11	533786	AAA	CCT	905.114	hom	36	NM_005343.2		missense_variant
HRAS	snp	chr11	533970	C	T	1041.76	het	146	NM_005343.2		intron_variant
HRAS	snp	chr11	534242	A	G	1015.28	het	58	NM_005343.2	rs12628&CM	synonymous_varia
HRAS	del	chr11	534403	GCCCAGGCCC	GC	1143.44	het	146	NM_005343.2		intron_variant&fe
HRAS	complex	chr11	534409	GC	AG	453.172	het	176	NM_005343.2		intron_variant
HRAS	snp	chr11	534415	C	G	675.066	het	183	NM_005343.2	rs61877782	intron_variant
IDH1	del	chr2	209116299	GAAAAAAAA	GAAAAAAA	1198.65	hom	56	XM_005246521.1		intron_variant&fe
IDH2	snp	chr15	90631868	G	T	2590.59	hom	94	NM_002168.2		missense_variant
IDH2	snp	chr15	90631903	C	T	4720.59	het	294	NM_002168.2		synonymous_varia
IDH2	snp	chr15	90631923	C	T	11273.8	het	824	NM_002168.2		missense_variant
IDH2	snp	chr15	90631978	C	T	12430.3	het	863	NM_002168.2		splice_region_vari
KDR	snp	chr4	55946085	G	A	369.166	het	41	NM_002253.2		3_prime_UTR_var
KDR	snp	chr4	55953776	G	A	522.482	hom	19	NM_002253.2		splice_region_vari
KDR	snp	chr4	55960991	G	A	584.634	het	43	NM_002253.2		synonymous_varia
KDR	snp	chr4	55961159	T	C	317.938	hom	12	NM_002253.2	rs2219471	intron_variant
KIT	snp	chr4	55589810	C	T	502.727	het	25	XM_005265740.1		missense_variant
KIT	snp	chr4	55593688	C	T	295.731	het	19	XM_005265740.1		missense_variant
MDM2	snp	chr12	69230475	G	A	287.229	het	21	NM_002392.5	rs373451300	synonymous_varia
MET	snp	chr7	116411978	G	A	3719.04	het	212	XM_005250353.1		missense_variant
MET	snp	chr7	116411991	T	A	1073.36	het	72	XM_005250353.1		synonymous_varia
NOTCH1	complex	chr9	139391575	GT	TG	859.129	hom	33	NM_017617.3		missense_variant
NOTCH1	complex	chr9	139391583	AG	CT	1040.6	hom	39	NM_017617.3		missense_variant

NOTCH1	ins	chr9	139391589	TC	TCACCC	594.706	hom	24	NM_017617.3		frameshift_varian
NOTCH1	snp	chr9	139391593	C	T	1063.99	hom	41	NM_017617.3		missense_variant
NOTCH1	snp	chr9	139399420	C	T	3183.55	hom	141	NM_017617.3		missense_variant
NOTCH1	snp	chr9	139399976	C	A	246.189	hom	10	NM_017617.3	rs200495793	missense_variant
NOTCH1	complex	chr9	139399977	GTCCTCCTGG	GTGCCAGGA	246.189	hom	10	NM_017617.3		missense_variant
NOTCH1	snp	chr9	139400085	G	A	7599.38	het	411	NM_017617.3		synonymous_varia
NPM1	del	chr5	170837513	CTTTTTTTTTT	CTTTTTTTT	219.677	het	35	NM_002520.6		splice_region_vari
NRAS	snp	chr1	115258821	G	A	944.587	hom	41	NM_002524.4		intron_variant
PDGFRA	snp	chr4	55141055	A	G	933.859	hom	34	NM_006206.4	rs1873778&C	synonymous_varia
PDGFRA	snp	chr4	55161254	C	T	278.649	het	35	NM_006206.4	rs3733540	intron_variant
PDGFRA	snp	chr4	55161517	A	G	801.584	hom	28	NM_006206.4	rs7680422	3_prime_UTR_var
PIK3CA	snp	chr3	178916935	C	T	1484.91	het	94	NM_006218.2		missense_variant
PIK3CA	snp	chr3	178927810	G	A	413.375	het	35	NM_006218.2		intron_variant
PIK3R1	snp	chr5	67588148	G	A	1180.74	hom	45	NM_181523.2	rs3730089&C	missense_variant
PIK3R1	snp	chr5	67588196	C	T	526.419	het	37	NM_181523.2		splice_region_vari
PIK3R1	snp	chr5	67592126	G	A	643.478	hom	28	NM_181523.2		missense_variant
PTEN	snp	chr10	89717840	A	G	1189.88	het	79	NM_000314.4		intron_variant
RB1	snp	chr13	48919358	T	G	1123.55	hom	41	NM_000321.2	rs198617	intron_variant
RET	snp	chr10	43609035	G	A	679.563	het	39	NM_020975.4		synonymous_varia
RET	complex	chr10	43613959	CCAC	TCAT	700.862	het	76	NM_020975.4		intron_variant
RET	snp	chr10	43617414	G	T	705.77	hom	37	NM_020975.4		missense_variant
SMAD4	snp	chr18	48581249	C	T	257.688	hom	12	NM_005359.5		missense_variant
SMARCB1	snp	chr22	24145595	C	T	1349.57	het	95	XM_005261718.1		missense_variant
SMO	snp	chr7	128845277	G	C	4682.35	hom	172	NM_005631.4	rs2075777	intron_variant
SMO	snp	chr7	128850279	C	T	2842.57	het	169	NM_005631.4		synonymous_varia
SRC	snp	chr20	36031578	G	A	473.581	het	22	NM_005417.4		missense_variant
STK11	snp	chr19	1207238	G	T	4778.98	het	285	XM_005259617	rs3764640	intron_variant
STK11	snp	chr19	1218523	G	T	7011.69	hom	245	XM_005259617	rs2075604	intron_variant
STK11	snp	chr19	1219424	G	A	2193.42	het	102	XM_005259617	rs113069959	intron_variant
STK11	snp	chr19	1220321	T	C	9834.02	hom	314	XM_005259617	rs2075606	intron_variant
STK11	snp	chr19	1220361	G	A	2794.53	het	172	XM_005259617.1		intron_variant
STK11	snp	chr19	1220415	C	A	830.112	het	53	XM_005259617	rs121913323	missense_variant
STK11	snp	chr19	1220733	C	T	2821.63	hom	109	XM_005259617.1		intron_variant
STK11	complex	chr19	1223125	CGAC	TGAT	2125.7	het	193	XM_005259617.1		synonymous_varia
TP53	snp	chr17	7573941	G	A	410.249	het	29	NM_000546.5		synonymous_varia
TP53	snp	chr17	7577407	A	C	817.964	het	45	NM_000546.5	rs12951053	intron_variant
TP53	snp	chr17	7577427	G	A	529.476	het	26	NM_000546.5	rs12947788	intron_variant
TP53	snp	chr17	7578277	G	A	546.97	het	34	NM_000546.5	TP53_g.1264	missense_variant
TP53	snp	chr17	7579348	G	A	2038.78	het	118	NM_000546.5	TP53_g.1157	synonymous_varia