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Data Sheet

Product Name: CancerSeqPlus Paraffin Tissue Curl

Catalog No.: T2235265-SC **Lot No.: B906065**

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

Pathological Diagnosis: Adenocarcinoma, papillary

Tumor Size: 4x3x3 cm

Location: Thyroid, right

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

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

Lot# B906065

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
CDKN2A	3.12	0.32	2.88E-03	CDKN2A	3.23	0.09	3.16E-03
FGFR3	2.16	0.27	6.09E-02	FGFR3	3.61	0.09	1.45E-03
NOTCH1	2.98	0.45	2.88E-03	NOTCH1	4.9	0.23	3.87E-04
STK11	2.89	0.37	2.88E-03	STK11	3.12	0.09	2.08E-03

symbol	type	chromosome	position	reference	mutation	quality	allele type	Depth at this position	transcript_id	existing variation	consequence
ABL1	snp	chr9	133748455	G	A	547.98	het	326	NM_007313.2		intron_variant
APC	snp	chr5	112175717	G	A	1115.1	het	96	XM_005271975.1		missense_variant
APC	snp	chr5	112176927	C	T	704.673	hom	30	XM_005271975.1		missense_variant
APC	snp	chr5	112176982	C	T	1329.62	het	62	XM_005271975.1		synonymous_varia
APC	snp	chr5	112176993	C	T	1545.75	het	76	XM_005271975	rs72541814	missense_variant
APC	snp	chr5	112177171	G	A	4153.82	hom	156	XM_005271975	rs465899	synonymous_varia
ATM	snp	chr11	108137926	G	A	329.689	het	14	NM_000051.3	rs199875915	missense_variant
ATM	snp	chr11	108155022	C	T	2396.17	het	149	NM_000051.3		missense_variant
CCND1	snp	chr11	69463948	G	A	2260.93	hom	92	NM_053056.2		intron_variant
CCND1	snp	chr11	69465108	G	A	2515.46	hom	88	NM_053056.2		intron_variant
CCNE1	snp	chr19	30311657	G	T	658.689	hom	32	NM_001238.2		missense_variant
CDH1	complex,sn	chr16	68771370	CCC	TCT,CCT	37069.3	het	1340	NM_004360.3		splice_region_varia
CDH1	complex	chr16	68771370	CCC	TCT,CTT	7481.05	het	292	NM_004360.3		splice_region_varia
CDH1	snp	chr16	68771372	C	T	604.107	hom	21	NM_004360.3	rs3743674	splice_region_varia
CDH1	complex	chr16	68835697	CC	TT	787.08	het	85	NM_004360.3		missense_variant
CDH1	snp	chr16	68845648	C	T	658.666	het	42	NM_004360.3	rs139110184	synonymous_varia
CDH1	snp	chr16	68853280	C	A	508.601	het	58	NM_004360.3		missense_variant
CDH1	snp	chr16	68857340	G	A	1369.37	het	68	NM_004360.3		missense_variant
CDH1	snp	chr16	68857557	C	T	969.881	het	56	NM_004360.3		intron_variant
CDKN2A	complex	chr9	21968199	CGAGG	GGAGA	638.038	het	47	NM_001195132.1		3_prime_UTR_vari
CDKN2A	snp	chr9	21968199	CGAGG	GGAGG	61809.2	hom	2006	NM_001195132.1		3_prime_UTR_vari
CSF1R	snp	chr5	149453030	C	T	621.526	het	41	NM_005211.3		missense_variant
CTNNB1	snp	chr3	41266225	C	T	362.104	hom	13	XM_005264887.1		synonymous_varia
DDR2	snp	chr1	162740327	T	C	16620.1	hom	538	XM_005245220	rs1780003	intron_variant

DDR2	snp	chr1	162741866	C	T	290.317	hom	11	XM_005245220.1		synonymous_varia
DDR2	ins	chr1	162741873	GC	GTC	305.193	hom	12	XM_005245220.1		frameshift_variant
DDR2	complex	chr1	162741877	AGGCTGAC	CCTCTGC	273.953	hom	11	XM_005245220.1		frameshift_variant
DDR2	complex	chr1	162741891	AA	GG	311.551	hom	12	XM_005245220.1		missense_variant
DDR2	snp	chr1	162741935	C	T	360.289	hom	13	XM_005245220.1		synonymous_varia
DDR2	snp	chr1	162743418	G	T	2989.05	hom	123	XM_005245220	rs1355287	intron_variant
DDR2	snp	chr1	162745533	C	A	181.063	het	15	XM_005245220.1		missense_variant
DDR2	snp	chr1	162749921	C	T	1539.82	het	79	XM_005245220.1		missense_variant
EGFR	snp	chr7	55211036	C	T	1322.4	het	107	NM_005228.3		synonymous_varia
EGFR	snp	chr7	55232921	G	A	902.996	het	47	NM_005228.3		intron_variant
EGFR	snp	chr7	55233102	C	T	262.71	het	15	NM_005228.3		missense_variant
ERBB2	snp	chr17	37871455	G	T	2870.85	het	151	NM_004448.2		intron_variant
ERBB3	snp	chr12	56477668	C	T	2283.46	het	123	NM_001982.3		synonymous_varia
ERBB3	snp	chr12	56477694	A	T	6565.02	hom	207	NM_001982.3	rs2271194	splice_region_varia
ERBB3	snp	chr12	56482356	G	A	1225.78	het	63	NM_001982.3		missense_variant
ERBB4	snp	chr2	212578519	A	T	4192.71	het	256	NM_005235.2	rs35123918	intron_variant
ERBB4	snp	chr2	212812162	G	A	4736.45	het	302	NM_005235.2		synonymous_varia
EZH2	snp	chr7	148508833	A	G	285.319	hom	10	XM_005249962	rs2072407	intron_variant
FBXW7	snp	chr4	153249392	G	A	1561.45	hom	57	NM_033632.3		synonymous_varia
FBXW7	snp	chr4	153252061	A	G	1436.96	hom	47	NM_033632.3	rs10033601	intron_variant
FBXW7	del,del	chr4	153268227	CAAAAAAAA	CAAAAAAAA	1047.28	het	128	NM_033632.3		splice_region_varia
FBXW7	snp	chr4	153273884	C	T	274.243	het	70	NM_033632.3		intron_variant
FGFR2	complex	chr10	123274694	GTCTG	ATCTA	345.66	het	55	NM_022970.3		missense_variant
FGFR3	del	chr4	1806012	TGGGGGGGG	TGGGGGGG	4961.64	het	1770	NM_001163213.1		intron_variant&fea
FGFR3	complex	chr4	1806182	CCC	TCT	1517.82	het	83	NM_001163213.1		missense_variant
FGFR3	snp	chr4	1807894	G	A	12733.7	hom	455	NM_001163213	rs7688609	synonymous_varia
FLT3	snp	chr13	28610099	C	T	872.139	het	45	NM_004119.2		stop_gained
FLT3	snp	chr13	28610183	A	G	2733.97	hom	86	NM_004119.2	rs2491231	splice_region_varia
GNA11	snp	chr19	3118979	G	A	8655.85	het	521	NM_002067.2		synonymous_varia
H3F3A	del	chr1	226252094	TAA	TA	376.278	het	211	NM_002107.4		frameshift_variant
HRAS	snp	chr11	533913	C	T	4502.71	het	316	NM_005343.2		missense_variant
JAK2	snp	chr9	5069050	G	A	423.054	hom	15	NM_004972.3		missense_variant
JAK2	snp	chr9	5078436	C	T	1097.35	het	55	NM_004972.3		missense_variant
JAK3	snp	chr19	17945631	G	A	3185.74	het	250	XM_005259896	rs57005908	intron_variant
KDR	snp	chr4	55961159	T	C	573.633	hom	21	NM_002253.2	rs2219471	intron_variant
KDR	snp	chr4	55962528	G	A	356.021	het	32	NM_002253.2		intron_variant
KDR	snp	chr4	55972974	T	A	338.37	hom	12	NM_002253.2	rs1870377&CM	missense_variant
KDR	snp	chr4	55980456	C	T	3410.84	het	171	NM_002253.2	rs2305949	intron_variant
KIT	snp	chr4	55561695	G	A	256.359	het	16	XM_005265740.1		missense_variant
KIT	snp	chr4	55599309	G	A	2334.64	het	137	XM_005265740	KinMutBase_KIT	missense_variant
KIT	snp	chr4	55599314	G	A	2256.74	het	133	XM_005265740.1		missense_variant

MAP2K1	snp	chr15	66727597	G	C	7001.18	hom	221	NM_002755.3	rs16949924	intron_variant
MDM2	snp	chr12	69222646	G	A	4887.73	het	296	NM_002392.5		missense_variant
MDM2	snp	chr12	69222655	G	A	5442.86	het	305	NM_002392.5		missense_variant
MPL	snp	chr1	43815103	G	A	5848.44	hom	251	NM_005373.2		intron_variant
MYC	snp	chr8	128748662	C	T	223.837	het	19	NM_002467.4		5_prime_UTR_vari
MYCN	snp	chr2	16080157	C	G	1232.49	hom	39	NM_005378.4	rs11886063	upstream_gene_va
MYCN	snp	chr2	16089608	G	A	1590.28	het	116	NM_005378.4		downstream_gene
MYCN	snp	chr2	16089615	T	C	4500.76	hom	158	NM_005378.4	rs4669018	downstream_gene
NOTCH1	snp	chr9	139391066	G	A	4136.12	het	194	NM_017617.3		synonymous_varia
NOTCH1	snp	chr9	139391074	G	A	284.029	hom	12	NM_017617.3		synonymous_varia
NOTCH1	snp	chr9	139391636	G	A	10476.1	hom	452	NM_017617.3	rs2229974	synonymous_varia
NOTCH1	snp	chr9	139397732	G	A	1584.59	het	104	NM_017617.3		missense_variant
NOTCH1	snp	chr9	139397870	C	T	289.265	het	379	NM_017617.3		intron_variant
NOTCH1	snp	chr9	139399824	C	T	1631.92	het	78	NM_017617.3		synonymous_varia
NOTCH1	snp	chr9	139399845	A	T	1681.85	het	75	NM_017617.3		missense_variant
NPM1	del	chr5	170837513	CTTTTTTTTTT	CTTTTTTTTT	860.398	het	90	NM_002520.6		splice_region_varia
NRAS	snp	chr1	115252296	C	T	261.659	hom	10	NM_002524.4		missense_variant
PDGFRA	snp	chr4	55141055	A	G	3237.58	hom	104	NM_006206.4	rs1873778&COS	synonymous_varia
PDGFRA	snp	chr4	55141083	C	T	1011.38	het	71	NM_006206.4		missense_variant
PDGFRA	snp	chr4	55161254	C	T	2257.79	hom	73	NM_006206.4	rs3733540	intron_variant
PDGFRA	snp	chr4	55161517	A	G	1822.86	hom	58	NM_006206.4	rs7680422	3_prime_UTR_vari
PIK3R1	snp	chr5	67588148	G	A	1915.65	het	112	NM_181523.2	rs3730089&CM	missense_variant
PIK3R1	snp	chr5	67590478	C	T	290.876	het	16	NM_181523.2	COSM1069601&	missense_variant
PIK3R1	snp	chr5	67592281	G	A	814.307	hom	36	NM_181523.2	rs895304	intron_variant
PTEN	snp	chr10	89653826	C	T	574.252	hom	23	NM_000314.4		missense_variant
PTEN	snp	chr10	89693076	T	A	584.429	hom	31	NM_000314.4		intron_variant
PTEN	snp	chr10	89711918	G	T	288.005	hom	17	NM_000314.4	COSM5249	missense_variant
PTEN	del	chr10	89720633	CTTTTTTTTT	CTTTTTTTTT	812.823	het	197	NM_000314.4		splice_acceptor_va
PTEN	snp	chr10	89720789	G	A	1040.78	hom	47	NM_000314.4	COSM5305&CO	missense_variant
PTEN	snp	chr10	89725326	C	T	123.751	het	69	NM_000314.4		3_prime_UTR_vari
PTPN11	snp	chr12	112926857	A	G	2064.12	het	120	NM_002834.3		missense_variant
RB1	snp	chr13	48919179	G	A	877.259	het	41	NM_000321.2		intron_variant
RB1	snp	chr13	48919358	T	G	1369.35	hom	47	NM_000321.2	rs198617	intron_variant
RB1	snp	chr13	48953849	G	A	1096.57	hom	40	NM_000321.2		intron_variant
RB1	snp	chr13	48953863	C	T	1203.67	hom	44	NM_000321.2		intron_variant
RB1	complex	chr13	48953868	TGGGCA	AGGGTG	1125.29	hom	43	NM_000321.2		intron_variant
RB1	snp	chr13	48953879	G	C	535.663	hom	23	NM_000321.2		intron_variant
RB1	complex	chr13	48953887	AGGCATCAA	GGAATTCAT	554.513	hom	24	NM_000321.2		intron_variant
RB1	complex	chr13	48953911	AA	CG	557.225	hom	24	NM_000321.2		intron_variant
RB1	snp	chr13	48953917	G	A	376.649	het	31	NM_000321.2		intron_variant
RB1	ins	chr13	49034022	ATT	ATTT	284.029	hom	12	NM_000321.2		intron_variant&fea

RB1	del	chr13	49039094	CTTTTTTTTTT	CTTTTTTTTTT	84.9771	het	32	NM_000321.2		intron_variant&fea
RET	snp	chr10	43613843	G	T	3227.13	het	197	NM_020975.4	rs1800861&CM	synonymous_varia
RET	snp	chr10	43615133	C	T	2822.45	hom	107	NM_020975.4		synonymous_varia
RET	complex	chr10	43615494	CATGGC	GAGGGT	289.822	hom	12	NM_020975.4		intron_variant
RHOA	snp	chr3	49405852	G	A	2414.87	het	159	NM_001664.2		intron_variant
ROS1	snp	chr6	117638341	G	T	386.266	het	36	NM_002944.2		missense_variant
SMAD4	snp	chr18	48575140	G	A	837.277	hom	32	NM_005359.5		missense_variant
SMAD4	snp	chr18	48581063	G	A	436.342	het	26	NM_005359.5		intron_variant
SMAD4	snp	chr18	48591986	G	A	1789.01	het	113	NM_005359.5		intron_variant
SMAD4	snp	chr18	48604760	C	T	2032.84	het	128	NM_005359.5		missense_variant
SMO	snp	chr7	128845277	G	C	7614.19	het	391	NM_005631.4	rs2075777	intron_variant
SMO	snp	chr7	128846328	G	C	1770.1	het	88	NM_005631.4	rs2228617	synonymous_varia
SRC	snp	chr20	36031586	G	A	505.55	het	31	NM_005417.4		missense_variant
STK11	snp	chr19	1207035	G	A	1557.57	het	243	XM_005259617.1		synonymous_varia
STK11	snp	chr19	1218523	G	T	16533.9	het	981	XM_005259617	rs2075604	intron_variant
STK11	snp	chr19	1220321	T	C	7972.97	het	442	XM_005259617	rs2075606	intron_variant
STK11	complex	chr19	1220593	TCGCGGCGG	CCGCCGCGA	944.878	hom	34	XM_005259617.1		missense_variant
STK11	snp	chr19	1220702	G	A	958.123	hom	41	XM_005259617.1		synonymous_varia
STK11	complex	chr19	1221246	GGG	AGA	1185.82	het	1651	XM_005259617.1		missense_variant
STK11	complex	chr19	1221286	GGAG	AGAA	3719.39	het	873	XM_005259617.1		missense_variant
STK11	complex	chr19	1222008	GAGCG	AAGCC	1992.93	het	2176	XM_005259617.1		splice_region_varia
STK11	snp	chr19	1222008	GAGCG	GAGCC	51264.3	het	3884	XM_005259617.1		splice_region_varia
TP53	complex	chr17	7579678	CCAG	TTAC	187.66	het	24	NM_000546.5		intron_variant
TP53	snp	chr17	7580007	G	A	5930.27	hom	262	NM_000546.5		intron_variant
VHL	snp	chr3	10183556	G	A	3759.69	het	248	NM_000551.3		missense_variant