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Data Sheet

Product Name: CancerSeqPlus Paraffin Tissue Curl

Catalog No.: T2235265-SC **Lot No.: B906062**

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: Adenocarcinoma, papillary

Tumor Size: 3 cm

Location: Thyroid

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

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

lot# B906062

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	3.54	0.22	2.08E-02	NOTCH1	6.02	0.11	3.40E-03

symbol	type	chromosome	position	reference	mutation	quality	allele type	Depth at this position	transcript_id	existing variation	consequence
ABL1	snp	chr9	133738459	G	A	4474.93	het	214	NM_007313.2		intron_variant
AKT1	snp	chr14	105246473	G	A	2081.84	het	84	NM_001014431	rs11555436	stop_gained
ALK	snp	chr2	29445458	G	T	1493.1	hom	54	NM_004304.4	rs3795850	synonymous_va
APC	snp	chr5	112175669	G	A	2050.88	het	128	XM_005271975.1		missense_variar
APC	snp	chr5	112175744	G	A	931.144	hom	40	XM_005271975	COSM235674&(	missense_variar
BRAF	complex	chr7	140453050	GTG	ATA	1697.32	het	140	XM_005250045.1		intron_variant
BRAF	snp	chr7	140453179	C	T	290.503	het	15	XM_005250045	rs121913340&C	missense_variar
CCND1	snp	chr11	69465016	C	T	316.424	het	242	NM_053056.2		intron_variant
CCNE1	snp	chr19	30314666	C	T	1512.47	hom	55	NM_001238.2	rs7257694	synonymous_va
CDH1	snp	chr16	68771303	G	A	15863.4	het	776	NM_004360.3		5_prime_UTR_v
CDH1	snp	chr16	68842366	C	T	3349.35	het	177	NM_004360.3	COSM1609555	missense_variar
CDH1	snp	chr16	68844129	G	A	2614.35	het	169	NM_004360.3		synonymous_va
CDH1	snp	chr16	68844200	C	T	285.319	hom	10	NM_004360.3		missense_variar
CDH1	snp	chr16	68845650	C	T	815.043	hom	44	NM_004360.3		missense_variar
CDH1	snp	chr16	68845673	C	T	2801.1	hom	99	NM_004360.3		stop_gained
CDH1	snp	chr16	68846115	G	A	5057.78	het	285	NM_004360.3		synonymous_va
CDH1	snp	chr16	68856153	C	T	718.111	het	83	NM_004360.3		intron_variant
CDH1	snp	chr16	68863549	C	T	656.489	het	41	NM_004360.3		splice_region_va
CDH1	snp	chr16	68863602	G	A	1518.03	hom	62	NM_004360.3		missense_variar
CDK4	snp	chr12	58145119	C	T	2081.95	het	107	NM_000075.3		missense_variar
CDKN2A	complex	chr9	21968199	CG	GA	799.158	hom	28	NM_001195132.1		3_prime_UTR_v
CDKN2A	snp	chr9	21968199	CG	GG	19478.5	hom	659	NM_001195132.1		3_prime_UTR_v
CDKN2A	snp	chr9	21968272	G	A	4863.6	het	203	NM_001195132.1		intron_variant
DDR2	snp	chr1	162740327	T	C	18032	hom	586	XM_005245220	rs1780003	intron_variant
DDR2	snp	chr1	162743418	G	T	400.875	hom	17	XM_005245220	rs1355287	intron_variant
DDR2	snp	chr1	162745596	C	T	2333.98	het	136	XM_005245220.1		missense_variar

DDR2	snp	chr1	162746126	C	T	611.508	het	45	XM_005245220.1		missense_variar
EGFR	snp	chr7	55249150	C	T	575.668	hom	21	NM_005228.3	COSM250049	synonymous_va
EGFR	snp	chr7	55249160	C	T	581.776	hom	21	NM_005228.3		stop_gained
EGFR	snp	chr7	55259482	C	T	725.934	het	41	NM_005228.3	COSM453249&(	missense_variar
ERBB2	snp	chr17	37881008	C	T	978.965	het	44	NM_004448.2		synonymous_va
ERBB2	snp	chr17	37881320	G	A	569.767	het	31	NM_004448.2		missense_variar
ERBB2	complex	chr17	37881468	GG	AA	834.396	het	212	NM_004448.2		intron_variant
ERBB3	snp	chr12	56477694	A	T	3074.75	hom	104	NM_001982.3	rs2271194	splice_region_va
ERBB4	snp	chr2	212589892	C	T	545.011	het	24	NM_005235.2		missense_variar
ESR1	snp	chr6	152420155	T	A	459.217	hom	20	XM_005266856.1		3_prime_UTR_v
EZH2	snp	chr7	148508833	A	G	298.211	hom	10	XM_005249962	rs2072407	intron_variant
FBXW7	snp	chr4	153249376	G	A	565.501	het	27	NM_033632.3		missense_variar
FBXW7	snp	chr4	153249410	G	A	511.273	het	28	NM_033632.3	COSM732372&(	synonymous_va
FGFR3	del	chr4	1806012	TGGGGGGGG	TGGGGGGGG	743.875	het	296	NM_001163213.1		intron_variant&
FGFR3	snp	chr4	1807894	G	A	2122.02	hom	92	NM_001163213	rs7688609	synonymous_va
FGFR3	snp	chr4	1808979	C	T	1681.31	het	103	NM_001163213.1		missense_variar
FLT3	snp	chr13	28610076	G	A	273.494	het	19	NM_004119.2	COSM1606974	missense_variar
FLT3	snp	chr13	28610183	A	G	1292.82	hom	42	NM_004119.2	rs2491231	splice_region_va
FOXL2	snp	chr3	138664500	C	T	598.498	het	31	NM_023067.3		missense_variar
FOXL2	snp	chr3	138665410	G	A	1944.85	hom	86	NM_023067.3		missense_variar
GNA11	snp	chr19	3118937	G	A	4610.99	het	272	NM_002067.2	rs376322895	synonymous_va
HNF1A	snp	chr12	121431442	C	T	1942.29	hom	74	XM_005253931.1		stop_gained
HNF1A	snp	chr12	121431488	C	T	1855.54	het	73	XM_005253931.1		missense_variar
HRAS	complex	chr11	533732	GCGTG	ACGTA	258.021	het	337	NM_005343.2		intron_variant
HRAS	complex	chr11	534197	CGGCG	TGGCA	290.952	het	269	NM_005343.2		intron_variant
HRAS	snp	chr11	534197	CGGCG	TGGCG	4322.57	het	451	NM_005343.2		intron_variant
IDH2	complex	chr15	90631846	GGT	AGC	3711.56	het	435	NM_002168.2		missense_variar
JAK3	snp	chr19	17954278	C	T	631.071	hom	22	XM_005259896.1		missense_variar
KDR	snp	chr4	55962506	C	T	447.627	het	33	NM_002253.2		missense_variar
KDR	snp	chr4	55972822	G	A	561.911	hom	20	NM_002253.2		intron_variant
MAP2K1	snp	chr15	66729095	G	A	372.089	hom	13	NM_002755.3		synonymous_va
MET	snp	chr7	116340326	C	T	353.087	het	23	XM_005250353.1		synonymous_va
MYC	snp	chr8	128746406	C	T	896.515	het	267	NM_002467.4		upstream_gene_
MYC	snp	chr8	128750889	C	T	972.867	het	64	NM_002467.4		synonymous_va
MYC	snp	chr8	128753046	G	A	1287.3	het	90	NM_002467.4		missense_variar
MYCN	snp	chr2	16089615	T	C	368.278	hom	15	NM_005378.4	rs4669018	downstream_ge
NOTCH1	snp	chr9	139391636	G	A	2785.16	hom	119	NM_017617.3	rs2229974	synonymous_va
NOTCH1	snp	chr9	139397707	G	A	875.02	hom	31	NM_017617.3	rs10521&COSM	synonymous_va
NOTCH1	snp	chr9	139399972	C	T	1064.8	het	73	NM_017617.3		missense_variar
NPM1	del,del	chr5	170837513	CTTTTTTTTTT	CTTTTTTTTTT	369.904	het	42	NM_002520.6		splice_region_va
NPM1	del,del	chr5	170837513	CTTTTTTTTTT	CTTTTTTTTTT	369.904	het	42	NM_002520.6		splice_region_va

PDGFRA	complex	chr4	55141034	GG	AA	577.494	het	33	NM_006206.4		missense_variar
PDGFRA	snp	chr4	55161254	C	T	3005.7	hom	95	NM_006206.4	rs3733540	intron_variant
PDGFRA	snp	chr4	55161517	A	G	2107.5	hom	67	NM_006206.4	rs7680422	3_prime_UTR_v
PIK3CA	snp	chr3	178952127	C	T	1143.15	het	60	NM_006218.2		missense_variar
PIK3R1	snp	chr5	67588148	G	A	970.065	hom	34	NM_181523.2	rs3730089&CM	missense_variar
RB1	snp	chr13	48953841	C	T	268.029	hom	10	NM_000321.2		intron_variant
RB1	snp	chr13	48955569	C	T	806.387	hom	28	NM_000321.2		missense_variar
RB1	snp	chr13	49033930	G	A	1036.96	het	58	NM_000321.2		synonymous_va
RET	del	chr10	43609128	GTG	GG	1698.78	het	97	NM_020975.4		splice_region_va
RET	snp	chr10	43610181	C	T	1833.56	hom	64	NM_020975.4		synonymous_va
RET	snp	chr10	43614971	G	A	449.971	het	31	NM_020975.4	rs376151644	splice_region_va
RET	snp	chr10	43615585	G	T	190.395	het	21	NM_020975.4		missense_variar
SMAD4	snp	chr18	48575669	C	T	403.345	het	18	NM_005359.5		synonymous_va
SMARCB1	snp	chr22	24134069	C	T	495.858	het	25	XM_005261718.1		intron_variant
SMO	snp	chr7	128845238	C	T	2463.83	hom	86	NM_005631.4		synonymous_va
STK11	snp	chr19	1206924	G	A	2234.2	het	144	XM_005259617.1		synonymous_va
STK11	snp	chr19	1226520	G	A	865.577	hom	32	XM_005259617.1		missense_variar
TERT	snp	chr5	1295349	A	G	53851.3	hom	1748	NM_198253.2	rs2853669&CR0	upstream_gene_
TP53	snp	chr17	7572976	G	A	826.933	hom	30	NM_000546.5		missense_variar
TP53	snp	chr17	7577407	A	C	1085.15	het	57	NM_000546.5	rs12951053	intron_variant
TP53	snp	chr17	7577427	G	A	591.943	het	24	NM_000546.5	rs12947788	intron_variant
TP53	complex	chr17	7577534	CC	TT	448.259	het	23	NM_000546.5	TP53_g.13383_	missense_variar
VHL	snp	chr3	10183836	C	T	1843.48	hom	65	NM_000551.3	CD031546	missense_variar
VHL	snp	chr3	10183882	G	A	1631.92	het	90	NM_000551.3		intron_variant