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Data Sheet

Product Name: CancerSeqPlus Paraffin Tissue Curl

Catalog No.: T2235265-SC **Lot No.: B906072**

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: 26 year(s) old

Pathological Diagnosis: Carcinoma, follicular

Tumor Size: 3x2 cm

Location: Thyroid left

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

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

lot# B906072

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	isting variati	consequence
ABL2	mnp	chr1	179108864	CGGG	GTTT	357.251	hom	16	NM_007314.3		intron_variant
AKT1	snp	chr14	105246686	G	A	1209.6	het	90	NM_001014	rs2494738	intron_variant
ALK	snp	chr2	29445602	G	C	206.513	het	18	NM_004304	rs76623673	intron_variant
APC	snp	chr5	112175770	G	A	2225.78	hom	88	XM_005271	rs41115&CO	synonymous_vari
APC	snp	chr5	112176325	G	A	968.941	hom	39	XM_005271	rs42427	synonymous_vari
APC	snp	chr5	112176559	T	G	1030.12	hom	43	XM_005271	rs866006	synonymous_vari
APC	snp	chr5	112177171	G	A	9662.94	hom	352	XM_005271	rs465899	synonymous_vari
ATM	del	chr11	108117897	ATTTTTTTTT	ATTTTTTTTT	296.634	het	116	NM_000051.3		intron_variant&fe
CCND1	snp	chr11	69465283	G	A	357.156	het	20	NM_053056.2		intron_variant
CCNE1	snp	chr19	30313344	T	C	238.992	het	14	NM_001238	rs3218068	intron_variant
CCNE1	snp	chr19	30314666	C	T	5139.43	het	313	NM_001238	rs7257694	synonymous_vari
CDH1	complex,mn	chr16	68771372	CCGG	TCGA,TAGG	621.276	het	53	NM_004360.3		splice_region_var
CDH1	snp	chr16	68771372	C	T	163527	hom	5183	NM_004360	rs3743674	splice_region_var
CDH1	ins	chr16	68771418	CG	CGCCCCAGC	2767.93	het	161	NM_004360.3		intron_variant&fe
CDH1	complex	chr16	68771429	TGC	CGT	60.9583	het	222	NM_004360.3		intron_variant
CDH1	snp	chr16	68845660	C	T	21067.6	het	1234	NM_004360	rs370197479	synonymous_vari
CDH1	snp	chr16	68845801	A	G	540.193	het	40	NM_004360.3		intron_variant
CDH1	snp	chr16	68857441	T	C	2382.25	het	150	NM_004360	rs1801552	synonymous_vari
CDK4	snp	chr12	58144665	C	T	521.264	het	32	NM_000075	rs2069502	intron_variant
CDK4	snp	chr12	58144902	C	A	173.312	het	20	NM_000075.3		intron_variant
CDKN2A	snp	chr9	21968199	C	G	218806	hom	7039	NM_001195	rs11515&CO	3_prime_UTR_var
CDKN2A	complex	chr9	21968199	CGAG	GGAA	594.238	het	67	NM_001195132.1		3_prime_UTR_var
CSF1R	mnp	chr5	149433596	TG	GA	313.532	hom	14	NM_005211.3		3_prime_UTR_var
DDR2	snp	chr1	162740327	T	C	99171.7	hom	3192	XM_005245	rs1780003	intron_variant
DDR2	complex	chr1	162740327	TGTC	CGTT	267.808	het	27	XM_005245220.1		intron_variant
DDR2	snp	chr1	162740369	C	A	480.081	hom	21	XM_005245220.1		intron_variant
DDR2	snp	chr1	162743418	G	T	5677.23	hom	198	XM_005245	rs1355287	intron_variant
EGFR	snp	chr7	55221655	G	A	2818.41	het	145	NM_005228	rs4947986	intron_variant
ERBB4	del	chr2	212578379	TAAAAAAAA	TAAAAAAAA	588.053	het	77	NM_005235.2		splice_region_var
ERBB4	snp	chr2	212589986	T	C	192.934	het	13	NM_005235	rs35778743	intron_variant
EZH2	snp	chr7	148508833	A	G	5993.04	hom	191	XM_005249	rs2072407	intron_variant

FBXW7	del	chr4	153247486	CTTTTTTTTT	CTTTTTTTTT	1099.6	het	246	NM_033632.3		intron_variant&fe
FBXW7	snp	chr4	153247524	C	A	288.826	het	25	NM_033632.3		intron_variant
FBXW7	snp	chr4	153259145	T	A	186.453	het	16	NM_033632.3		intron_variant
FGFR1	snp	chr8	38271575	T	A	1441.14	het	107	NM_001174067.1		intron_variant
FGFR2	snp	chr10	123274889	C	A	234.683	het	17	NM_022970.3		intron_variant
FGFR3	snp	chr4	1805662	C	A	206.007	het	15	NM_001163213.1		intron_variant
FGFR3	del	chr4	1806012	TGGGGGGG	TGGGGGGG	26531.3	het	8438	NM_001163213.1		intron_variant&fe
FGFR3	snp	chr4	1807894	G	A	57099.4	hom	1952	NM_001163	rs7688609	synonymous_vari
FGFR3	complex	chr4	1807894	GAC	AAT	244.298	het	23	NM_001163213.1		missense_variant
FGFR3	snp	chr4	1808517	G	A	320.057	het	29	NM_001163213.1		intron_variant
FLT3	snp	chr13	28592546	T	C	493.383	hom	20	NM_004119	rs17086226	intron_variant
GNA11	snp	chr19	3119085	G	A	3473.72	het	243	NM_002067.2		intron_variant
GNAQ	snp	chr9	80409345	A	G	261.923	het	18	NM_002072	rs1328529	intron_variant
HNF1A	snp	chr12	121431545	C	A	298.958	het	25	XM_005253931.1		intron_variant
HRAS	snp	chr11	534464	C	A	375.488	het	28	NM_005343.2		intron_variant
IDH1	del	chr2	209113048	GAAAAAAA	GAAAAAAA	24.0887	het	78	XM_005246521.1		intron_variant&fe
IDH1	del	chr2	209116299	GAAAAAAA	GAAAAAAA	4019.28	het	774	XM_005246521.1		intron_variant&fe
JAK2	del	chr9	5073681	CTTTTTTTT	CTTTTTTTT	3141.3	het	379	NM_004972.3		splice_region_var
KIT	del	chr4	55599496	CTTC	CC	202.938	het	21	XM_005265740.1		intron_variant&fe
KIT	ins	chr4	55599500	AG	ATG	202.938	het	21	XM_005265740.1		intron_variant&fe
KIT	del	chr4	55599511	CAT	CT	202.938	het	21	XM_005265740.1		intron_variant&fe
KIT	ins	chr4	55599514	GG	GAAG	202.938	het	21	XM_005265740.1		intron_variant&fe
KIT	complex	chr4	55599519	GCTGAACA	ACTTAATT	205.162	het	19	XM_005265740.1		intron_variant
MET	snp	chr7	116423654	T	A	222.297	het	14	XM_005250353.1		intron_variant
MYC	snp	chr8	128750918	G	A	632.199	hom	32	NM_002467.4		missense_variant
MYCN	snp	chr2	16080157	C	G	8176.4	hom	261	NM_005378	rs11886063	upstream_gene_v
MYCN	snp	chr2	16089442	T	A	461.306	hom	17	NM_005378	rs12619709	downstream_gen
MYCN	snp	chr2	16089615	T	C	20323.1	hom	700	NM_005378	rs4669018	downstream_gen
NOTCH1	snp	chr9	139391636	G	A	45320.3	hom	1712	NM_017617	rs2229974	synonymous_vari
NOTCH1	snp	chr9	139397707	G	A	69638.7	hom	2321	NM_017617	rs10521&CC	synonymous_vari
NOTCH1	snp	chr9	139397893	T	A	433.753	het	31	NM_017617.3		intron_variant
NOTCH1	snp	chr9	139399587	T	A	196.245	hom	13	NM_017617.3		intron_variant
NPM1	del,del	chr5	170837513	CTTTTTTTT	CTTTTTTTT	4363.65	het	423	NM_002520.6		splice_region_var
NRAS	complex	chr1	115252074	AAAAA	GACGT	99.0689	het	54	NM_002524.4		intron_variant
PDGFRA	snp	chr4	55141054	CA	CG	56090.8	hom	1925	NM_006206.4		synonymous_vari
PDGFRA	mnp	chr4	55141054	CA	TG	1169.8	het	50	NM_006206.4		missense_variant
PDGFRA	snp	chr4	55161254	C	T	11517.9	hom	376	NM_006206	rs3733540	intron_variant
PDGFRA	snp	chr4	55161391	T	C	2013.3	hom	67	NM_006206	rs7685117	synonymous_vari
PDGFRA	snp	chr4	55161517	A	G	10839.3	hom	352	NM_006206	rs7680422	3_prime_UTR_var
PIK3CA	del	chr3	178927848	ATTTTTTTTT	ATTTTTTTTT	603.928	het	222	NM_006218.2		intron_variant&fe
PIK3R1	snp	chr5	67589770	T	A	174.099	het	18	NM_181523.2		intron_variant

PTEN	del	chr10	89720633	CTTTTTTTTT	CTTTTTTTTT	1557.13	het	434	NM_000314.4		splice_acceptor_v
PTEN	snp	chr10	89720907	T	G	3460.55	hom	125	NM_000314	rs555895&C	intron_variant
PTEN	del	chr10	89725293	CTTTTTTTTT	CTTTTTTTTT	750.909	het	354	NM_000314.4		3_prime_UTR_var
RB1	snp	chr13	48919358	T	G	4104.96	hom	140	NM_000321	rs198617	intron_variant
RB1	snp	chr13	48942816	T	A	268.175	hom	14	NM_000321.2		intron_variant
RB1	ins	chr13	48953655	CAAAAAAAA	CAAAAAAAA	970.606	het	178	NM_000321.2		intron_variant&fe
RB1	snp	chr13	48955676	T	A	237.291	hom	10	NM_000321	rs2804086	intron_variant
RB1	snp	chr13	49033747	G	A	656.007	hom	29	NM_000321	rs198580	intron_variant
RB1	ins	chr13	49034022	ATT	ATTT	2364.19	hom	94	NM_000321.2		intron_variant&fe
RET	snp	chr10	43610281	G	A	1653.21	hom	87	NM_020975.4		intron_variant
RET	snp	chr10	43615219	G	A	624.503	hom	28	NM_020975.4		intron_variant
RET	complex	chr10	43615494	CATGGC	GAGGGT	331.084	het	25	NM_020975.4		intron_variant
ROS1	snp	chr6	117638491	G	A	397.812	het	27	NM_002944.2		intron_variant
SMAD4	snp	chr18	48592049	T	A	258.48	het	17	NM_005359.5		intron_variant
SMARCB1	snp	chr22	24145675	G	C	355.974	hom	13	XM_005261	rs5751738	intron_variant
SMO	snp	chr7	128845277	G	C	42332.5	het	2736	NM_005631	rs2075777	intron_variant
SMO	snp	chr7	128845316	G	A	511.457	het	27	NM_005631.4		intron_variant
SMO	snp	chr7	128846469	A	G	416.803	het	33	NM_005631	rs2735842	intron_variant
STK11	snp	chr19	1219553	G	T	281.488	hom	11	XM_005259	rs11084889	intron_variant
STK11	complex	chr19	1220492	GGGCGTGG(	CGGCCACG(	67.3481	het	60	XM_005259617.1		missense_variant
STK11	snp	chr19	1222012	G	C	378032	hom	12274	XM_005259	rs2075607	splice_region_var
STK11	complex	chr19	1222012	GGCC	CGCT	252.146	het	48	XM_005259617.1		splice_region_var
STK11	snp	chr19	1223222	C	A	578.558	het	49	XM_005259617.1		intron_variant
TERT	complex	chr5	1295102	CATCGC	AGGAGG	157.835	het	14	NM_198253.2		coding_sequence_
TERT	snp	chr5	1295348	GA	GG	144931	het	9707	NM_198253.2		upstream_gene_v
TERT	snp	chr5	1295478	A	C	1144.95	het	59	NM_198253.2		upstream_gene_v
TP53	snp	chr17	7578115	T	C	442.136	hom	17	NM_000546	rs1625895	intron_variant
TP53	snp	chr17	7579472	G	C	73532.7	hom	2425	NM_000546	rs1042522&	missense_variant
TP53	complex	chr17	7579668	CTCCAG	CAACCCTT	5543.25	het	1448	NM_000546.5		intron_variant&fe
TP53	complex	chr17	7579678	CCAG	TTAC	4617.86	het	1619	NM_000546.5		intron_variant
TP53	snp	chr17	7579801	G	C	7932.42	hom	287	NM_000546	rs1642785	intron_variant
VHL	snp	chr3	10183876	G	C	22340.8	het	1321	NM_000551	rs61758376	splice_region_var
VHL	snp	chr3	10188428	T	G	1473.69	hom	54	NM_000551	rs1678607	intron_variant