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Data Sheet

Product Name: CancerSeqPlus Paraffin Tissue Curl

Catalog No.: T2235265-SC **Lot No.: B906059**

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

Pathological Diagnosis: Sarcomatoid carcinoma

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# B906059

symbol	type	chromosome	position	reference	mutation	quality score	allele type	Depth at this position	transcript_id	existing variation	consequence
AKT1	snp	chr14	105246325	T	A	216.361	hom	10	NM_00101443	rs2494737	intron_variant
APC	snp	chr5	112175770	G	A	787.625	hom	30	XM_005271975	rs41115&CO	synonymous_va
APC	snp	chr5	112176559	T	G	330.767	hom	14	XM_005271975	rs866006	synonymous_va
APC	snp	chr5	112177171	G	A	364.297	hom	14	XM_005271975	rs465899	synonymous_va
APC	snp	chr5	112178116	G	A	300.17	het	15	XM_005271975.1		synonymous_va
APC	snp	chr5	112179909	C	A	1432.52	het	80	XM_005271975	rs1804197&	3_prime_UTR_v
ATM	del	chr11	108117897	ATTTTTTTTT	ATTTTTTTTT	202.026	het	197	NM_000051.3		intron_variant&
CDH1	snp	chr16	68771372	C	T	93988.2	hom	3005	NM_004360.3	rs3743674	splice_region_v
CDH1	ins	chr16	68771418	CG	CGCCCCAGC	2251.45	het	166	NM_004360.3		intron_variant&
CDH1	complex	chr16	68771429	TGC	CGT	1529.46	het	205	NM_004360.3		intron_variant
CDH1	complex	chr16	68771437	TTCCTC	AGCCC	316.732	het	87	NM_004360.3		intron_variant&
CDH1	complex	chr16	68771444	CCC	GCG	389.516	het	88	NM_004360.3		intron_variant
CDH1	snp	chr16	68772386	C	A	916.625	het	95	NM_004360.3		intron_variant
CDH1	snp	chr16	68857441	T	C	1651.53	hom	56	NM_004360.3	rs1801552	synonymous_va
CDK4	complex	chr12	58145395	TCTTGAGG	CCCACAGTG	420.145	het	84	NM_000075.3		frameshift_varia
CDKN2A	complex	chr9	21968199	CGAGG	GGAGA	1540.92	het	81	NM_001195132.1		3_prime_UTR_v
CDKN2A	snp	chr9	21968199	CGAGG	GGAGG	93179.2	hom	3092	NM_001195132.1		3_prime_UTR_v
DDR2	snp	chr1	162740327	TGTC	CGTC	32838.3	hom	1085	XM_005245220.1		intron_variant
DDR2	complex	chr1	162740327	TGTC	CGTT	318.41	het	20	XM_005245220.1		intron_variant
DDR2	snp	chr1	162743418	G	T	4988.8	hom	182	XM_005245220	rs1355287	intron_variant
EGFR	snp	chr7	55221655	G	A	781.391	hom	31	NM_005228.3	rs4947986	intron_variant
EGFR	snp	chr7	55259608	C	A	608.125	hom	29	NM_005228.3	rs369725826	intron_variant
ERBB3	snp	chr12	56477694	A	T	22770.7	hom	744	NM_001982.3	rs2271194	splice_region_v
ERBB4	del,del	chr2	212578379	TAAAAAAAA	TAAAAAAAA	444.172	het	51	NM_005235.2		splice_region_v
ERBB4	snp	chr2	212578516	TAAA	TAAT	8101.47	het	598	NM_005235.2		intron_variant
ESR1	snp	chr6	152420095	G	A	15670.6	hom	502	XM_005266856	rs2228480&	synonymous_va
EZH2	snp	chr7	148508833	A	G	3230.87	hom	105	XM_005249962	rs2072407	intron_variant
FBXW7	del	chr4	153247486	CTTTTTTTTT	CTTTTTTTTT	232.523	het	63	NM_033632.3		intron_variant&
FBXW7	snp	chr4	153259145	T	A	267.613	het	20	NM_033632.3		intron_variant
FBXW7	del,del	chr4	153268227	CAAAAAAAA	CAAAAAAAA	1138.99	het	169	NM_033632.3		splice_region_v
FGFR1	snp	chr8	38271362	T	A	1007.08	het	85	NM_001174067.1		intron_variant
FGFR1	mnp	chr8	38271371	CT	AG	1894.11	hom	74	NM_001174067.1		intron_variant
FGFR1	complex,cor	chr8	38271381	TGCGT	AGGG,AGGG	1502.52	het	65	NM_001174067.1		intron_variant&
FGFR1	complex	chr8	38271966	TTTCTC	CCTCTT	275.154	het	49	NM_001174067.1		intron_variant
FGFR1	mnp	chr8	38271976	GGG	CCC	277.671	het	50	NM_001174067.1		intron_variant
FGFR1	snp	chr8	38272185	C	A	175.144	het	19	NM_001174067.1		intron_variant

FGFR1	complex	chr8	38282181	AAC	CAT	568.34	het	24	NM_001174067.1		missense_varia
FGFR1	mnp	chr8	38282189	TT	AA	627.036	hom	25	NM_001174067.1		missense_varia
FGFR1	snp	chr8	38282196	A	G	658.897	hom	25	NM_001174067.1		missense_varia
FGFR2	snp	chr10	123274889	C	A	370.981	hom	17	NM_022970.3		intron_variant
FGFR3	snp	chr4	1807593	C	T	903.493	hom	39	NM_001163213.1		stop_gained
FGFR3	snp	chr4	1807894	G	A	18357.1	hom	644	NM_001163213	rs7688609	synonymous_va
FGFR3	complex	chr4	1808889	GCCAGGA	TCCTGGC	945.217	het	39	NM_001163213.1		missense_varia
FGFR3	complex	chr4	1808900	CCC	CGGGG	707.155	het	42	NM_001163213.1		frameshift_varia
FGFR3	mnp	chr4	1809031	CCACCCT	AGGGTGG	578.007	het	68	NM_001163213.1		3_prime_UTR_v
FGFR3	complex	chr4	1809044	GGT	AGG	756.259	het	47	NM_001163213.1		3_prime_UTR_v
FLT3	snp	chr13	28592546	T	C	303.953	hom	11	NM_004119.2	rs17086226	intron_variant
FLT3	snp	chr13	28609991	T	C	308.612	hom	12	NM_004119.2	rs2491229	intron_variant
FLT3	snp	chr13	28609997	T	C	512.937	hom	20	NM_004119.2	rs2491230	intron_variant
FLT3	snp	chr13	28610183	A	G	10043.9	hom	341	NM_004119.2	rs2491231	splice_region_v
FOXL2	complex	chr3	138664790	TGTACGGCC	CGTAGTGAA	3702.33	het	261	NM_023067.3		frameshift_varia
FOXL2	complex	chr3	138664804	GAGGCGGC	AATGGCCTG	4445.53	het	230	NM_023067.3		frameshift_varia
FOXL2	complex	chr3	138665047	GCGGCGCCT	TCGGGGCCG	316.089	hom	14	NM_023067.3		missense_varia
HNF1A	del	chr12	121431996	CAT	CT	327.901	hom	12	XM_005253931.1		frameshift_varia
HNF1A	complex	chr12	121432000	ACA	TCT	294.765	hom	13	XM_005253931.1		missense_varia
HRAS	snp	chr11	534492	G	A	395.314	het	21	NM_005343.2		intron_variant
IDH1	del	chr2	209113048	GAAAAAAA	GAAAAAAA	126.582	het	79	XM_005246521.1		intron_variant&
IDH1	del	chr2	209116299	GAAAAAAA	GAAAAAAA	1925.08	het	389	XM_005246521.1		intron_variant&
JAK2	del	chr9	5073681	CTTTTTTTTT	CTTTTTTTTT	1200.43	het	198	NM_004972.3		splice_region_v
JAK3	snp	chr19	17954349	G	A	254.415	het	19	XM_005259896.1		intron_variant
KDR	snp	chr4	55972974	T	A	1232.17	het	78	NM_002253.2	rs1870377&	missense_varia
MAP2K1	complex	chr15	66727559	TGGTCAT	ATGACCA	327.649	hom	13	NM_002755.3		missense_varia
MDM2	snp	chr12	69207458	T	A	218.181	hom	10	NM_002392.5		intron_variant
MET	snp	chr7	116417571	A	G	236.332	hom	18	XM_005250353.1		intron_variant
MET	snp	chr7	116436097	G	A	1694.56	het	91	XM_005250353	rs41737&CC	synonymous_va
MYCN	snp	chr2	16080157	C	G	2040.4	hom	65	NM_005378.4	rs11886063	upstream_gene
MYCN	snp	chr2	16089615	T	C	7298.58	hom	254	NM_005378.4	rs4669018	downstream_ge
NOTCH1	mnp	chr9	139390571	GG	CC	171.944	het	40	NM_017617.3		missense_varia
NOTCH1	mnp	chr9	139390579	TGGAGAC	GTCTCCA	425.818	het	33	NM_017617.3		missense_varia
NOTCH1	mnp	chr9	139390592	GG	CC	256.65	het	43	NM_017617.3		missense_varia
NOTCH1	snp	chr9	139391636	G	A	19344.6	hom	821	NM_017617.3	rs2229974	synonymous_va
NOTCH1	snp	chr9	139397707	G	A	20216.7	hom	663	NM_017617.3	rs10521&CC	synonymous_va
NOTCH1	complex	chr9	139400089	AATTTGGCG	CCTGTGCCC	380.997	het	21	NM_017617.3		stop_gained
NPM1	del,del	chr5	170837513	CTTTTTTTTT	CTTTTTTTTT	1397.14	het	155	NM_002520.6		splice_region_v
PDGFRA	snp	chr4	55141055	A	G	29122.3	hom	970	NM_006206.4	rs1873778&	synonymous_va
PDGFRA	snp	chr4	55161254	C	T	6608.21	hom	211	NM_006206.4	rs3733540	intron_variant
PDGFRA	snp	chr4	55161391	T	C	949.241	hom	32	NM_006206.4	rs7685117	synonymous_va

PDGFRA	snp	chr4	55161517	A	G	4508.83	hom	151	NM_006206.4	rs7680422	3_prime_UTR_v
PIK3CA	del	chr3	178927848	ATTTTTTTTT	ATTTTTTTTT	174.465	het	88	NM_006218.2		intron_variant&
PTEN	del	chr10	89720633	CTTTTTTTTT	CTTTTTTTTT	631.546	het	241	NM_000314.4		splice_acceptor
PTEN	del	chr10	89725293	CTTTTTTTTT	CTTTTTTTTT	86.1027	het	134	NM_000314.4		3_prime_UTR_v
RB1	snp	chr13	48919358	T	G	4068.09	hom	139	NM_000321.2	rs198617	intron_variant
RB1	ins	chr13	48953655	CAAAAAAAA	CAAAAAAAA	1737.75	het	237	NM_000321.2		intron_variant&
RB1	snp	chr13	49033747	G	A	380.039	hom	17	NM_000321.2	rs198580	intron_variant
RB1	ins	chr13	49034022	ATT	ATTT	593.302	het	32	NM_000321.2		intron_variant&
RET	complex	chr10	43610075	TCCGGAG	CACAGGATG	721.767	hom	37	NM_020975.4		frameshift_varia
RET	complex	chr10	43610083	CCCG	CCTCTGTCTC	657.101	hom	36	NM_020975.4		inframe_insertio
RET	complex	chr10	43610091	GG	GCTGGCCTC	681.978	hom	31	NM_020975.4		frameshift_varia
RET	mnp	chr10	43610189	GGG	TCT	675.211	het	105	NM_020975.4		splice_region_v
RET	mnp	chr10	43610199	GGG	CCC	852.291	het	110	NM_020975.4		intron_variant
RET	snp	chr10	43613843	G	T	4630.11	het	245	NM_020975.4	rs1800861&	synonymous_va
RET	snp	chr10	43617564	T	A	599.222	hom	35	NM_020975.4		intron_variant
SMAD4	snp	chr18	48592049	T	A	321.497	hom	15	NM_005359.5		intron_variant
SMO	snp	chr7	128845276	CG	CC	28303.9	hom	957	NM_005631.4		intron_variant
SMO	mnp	chr7	128845276	CG	TC	503.236	het	26	NM_005631.4		intron_variant
SMO	snp	chr7	128846328	G	C	9962.14	hom	328	NM_005631.4	rs2228617	synonymous_va
SND1	snp	chr7	127719709	G	C	253.395	hom	10	NM_014390.2	rs14048467	intron_variant
STK11	snp	chr19	1207238	G	T	10963	het	715	XM_005259617	rs3764640	intron_variant
STK11	snp	chr19	1218523	G	T	29776.4	het	1824	XM_005259617	rs2075604	intron_variant
STK11	ins	chr19	1219443	GCGGGGGC	GCGGGGGC	1260.89	het	196	XM_005259617.1		intron_variant&
STK11	snp	chr19	1219444	C	G	480.003	het	234	XM_005259617.1		intron_variant
STK11	snp	chr19	1219451	C	G	448.304	het	308	XM_005259617	rs369515604	intron_variant
TERT	snp	chr5	1295349	A	G	111964	het	5970	NM_198253.2	rs2853669&	upstream_gene
TP53	snp	chr17	7573989	C	T	316.376	het	17	NM_000546.5	TP53_g.169	synonymous_va
TP53	mnp	chr17	7579322	ACA	TGT	675.591	hom	28	NM_000546.5		missense_varia
TP53	complex	chr17	7579330	GGCT	GCACG	567.482	hom	26	NM_000546.5		frameshift_varia
TP53	snp	chr17	7579472	G	C	7961.39	het	448	NM_000546.5	rs1042522&	missense_varia
TP53	del	chr17	7579643	CCCCCAGCC	CC	115.97	het	300	NM_000546.5		intron_variant&
TP53	snp	chr17	7579653	T	C	216.234	het	35	NM_000546.5		intron_variant
TP53	mnp	chr17	7579658	GT	CC	175.653	het	48	NM_000546.5		intron_variant
TP53	snp	chr17	7579801	G	C	1081.53	hom	41	NM_000546.5	rs1642785	intron_variant
TP53	complex	chr17	7579911	ATGGCAGTG	GGGTCACTG	541.587	het	27	NM_000546.5		coding_sequenc
VHL	snp	chr3	10183700	G	A	274.269	het	14	NM_000551.3	COSM14304	missense_varia
VHL	mnp	chr3	10183712	CCC	TAG	231.899	het	15	NM_000551.3		stop_gained