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Data Sheet

Product Name: CancerSeqPlus Paraffin Tissue Curl

Catalog No.: T2235248-SC **Lot No.:** B906146

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: Stomach

Donor Information:

Male: 65 year(s) old
Female: _____ year(s) old

Pathological Diagnosis: Adenocarcinoma

Tumor Size:

Location: stomach

Components:

1. 5 curls per package
2. Certificate of Analysis

FOR IN VITRO RESEARCH USE ONLY APPROVED BY: _____

B906146

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	variant frequency	transcript_id	existing variation	consequence
ALK	snp	chr2	29445458	G	T	6227.4	het	262	0.81	NM_004304	rs3795850	synonymous
APC	snp	chr5	112175770	G	A	1775.99	hom	78	0.99	XM_005271	rs41115&CO	synonymous
APC	snp	chr5	112176559	T	G	260.66	hom	11	1.00	XM_005271	rs866006	synonymous
APC	snp	chr5	112177171	G	A	2836.25	hom	102	0.99	XM_005271	rs465899	synonymous
ATM	del	chr11	108117897	ATTTTTTTTT	ATTTTTTTTT	240.417	het	112	0.15	NM_000051.3		intron_varia
CCNE1	snp	chr19	30303714	T	G	242.478	hom	11	1.00	NM_001238.2		intron_varia
CDH1	snp	chr16	68771372	C	T	37929.7	hom	1220	1.00	NM_004360	rs3743674	splice_regio
CDH1	ins	chr16	68771418	CG	CGCCCCAGC	511.722	hom	21	0.95	NM_004360.3		intron_varia
CDKN2A	complex	chr9	21968199	CGAG	GGAA	1418.62	hom	63	0.81	NM_001195132.1		3_prime_UT
CDKN2A	snp	chr9	21968199	CGAG	GGAG	32639.9	hom	1105	0.94	NM_001195132.1		3_prime_UT
DDR2	snp	chr1	162740327	T	C	20896.2	hom	674	1.00	XM_005245	rs1780003	intron_varia
DDR2	snp	chr1	162743418	G	T	2600.39	hom	96	1.00	XM_005245	rs1355287	intron_varia
EGFR	snp	chr7	55221655	G	A	1969.91	hom	65	1.00	NM_005228	rs4947986	intron_varia
EGFR	complex	chr7	55242242	GGGCTGCG	ATATTGCTG	245.315	het	21	0.76	NM_005228.3		intron_varia
EGFR	ins	chr7	55242254	CG	CTG	372.879	het	23	0.83	NM_005228.3		intron_varia
EGFR	complex	chr7	55242257	CACAG	GACG	411.245	het	27	0.85	NM_005228.3		intron_varia
ERBB2	snp	chr17	37871480	G	A	1055.15	het	88	0.53	NM_004448.2		intron_varia
ERBB2	snp	chr17	37881206	C	A	458.953	het	35	0.80	NM_004448.2		intron_varia
ERBB2	del	chr17	37882959	TCC	TC	2203.49	het	347	0.31	NM_004448.2		intron_varia
ERBB2	ins	chr17	37882965	AGA	AGGA	2307.02	het	213	0.49	NM_004448.2		intron_varia
ERBB2	mnp	chr17	37882973	GG	CT	452.745	het	106	0.25	NM_004448.2		intron_varia
ERBB4	snp	chr2	212587321	G	A	237.291	hom	10	1.00	NM_005235	rs13002712	intron_varia
EZH2	snp	chr7	148508833	A	G	1619.31	hom	52	1.00	XM_005249	rs2072407	intron_varia
FBXW7	del	chr4	153247486	CTTTTTTTTT	CTTTTTTTTT	228.129	het	78	0.15	NM_033632.3		intron_varia
FBXW7	snp	chr4	153252061	A	G	2455.35	het	138	0.58	NM_033632	rs10033601	intron_varia
FBXW7	del,del	chr4	153268227	CAAAAAAAA	CAAAAAAAA	2414.51	het	356	0.27	NM_033632.3		splice_regio
FBXW7	snp	chr4	153271110	A	C	1633.14	het	104	0.52	NM_033632	rs34708673	intron_varia
FGFR1	ins	chr8	38271433	TA	TGACCTCCA	521.183	het	31	0.77	NM_001174067.1		splice_dono
FGFR1	complex	chr8	38271437	TGGTTG	AGGTAA	824.185	hom	35	0.89	NM_001174067.1		missense_va
FGFR1	snp	chr8	38282245	G	A	281.269	het	25	0.60	NM_001174067.1		intron_varia
FGFR1	snp	chr8	38286000	G	A	992.685	het	82	0.55	NM_001174067.1		intron_varia
FGFR1	snp	chr8	38286051	G	A	241.989	het	20	0.60	NM_001174067.1		intron_varia
FGFR3	del	chr4	1806012	TGGGGGGG	TGGGGGGG	4732.32	het	1178	0.20	NM_001163213.1		intron_varia

FGFR3	snp	chr4	1807894	G	A	5876.22	hom	205	1.00	NM_001163	rs7688609	synonymous
FLT3	snp	chr13	28609991	T	C	509.579	hom	22	1.00	NM_004119	rs2491229	intron_varia
FLT3	snp	chr13	28609997	T	C	492.393	hom	22	1.00	NM_004119	rs2491230	intron_varia
FLT3	snp	chr13	28610183	A	G	9511.43	hom	317	1.00	NM_004119	rs2491231	splice_regio
FOXL2	complex	chr3	138664905	CATC	TATGCCTCC	215.011	het	79	0.20	NM_023067.3		frameshift_v
FOXL2	complex	chr3	138664911	GCAG	CCAGATG	250.273	het	79	0.22	NM_023067.3		inframe_inse
FOXL2	snp	chr3	138664916	A	C	293.723	het	78	0.24	NM_023067.3		missense_va
FOXL2	snp	chr3	138665368	G	A	77.4942	het	142	0.13	NM_023067	CM035546	missense_va
HNF1A	snp	chr12	121432236	C	A	276.339	hom	14	1.00	XM_005253931.1		intron_varia
IDH1	del	chr2	209113048	GAAAAAAAA	GAAAAAAAA	469.558	het	49	0.37	XM_005246521.1		intron_varia
IDH1	del	chr2	209116299	GAAAAAAAA	GAAAAAAAA	1439.6	het	289	0.22	XM_005246521.1		intron_varia
JAK2	del	chr9	5073681	CTTTTTTTTT	CTTTTTTTTT	1743.94	het	190	0.32	NM_004972.3		splice_regio
JAK3	complex	chr19	17945762	GCGCCTCCC	CCGGGAGG	140.315	het	102	0.17	XM_005259896.1		missense_va
KDR	snp	chr4	55961159	T	C	3316.03	het	177	0.62	NM_002253	rs2219471	intron_varia
KDR	ins	chr4	55962545	TGG	TGGG	89.9065	het	219	0.14	NM_002253.2		intron_varia
KDR	snp	chr4	55979558	C	T	1605	het	101	0.52	NM_002253	rs2305948&	missense_va
KDR	snp	chr4	55980456	C	T	12469.8	het	708	0.56	NM_002253	rs2305949	intron_varia
KRAS	snp	chr12	25380487	G	A	256.748	het	13	0.85	NM_033360.2		intron_varia
MET	snp	chr7	116436022	G	A	4918.23	hom	158	1.00	XM_005250	rs2023748&	synonymous
MET	snp	chr7	116436097	G	A	4076.52	hom	135	0.99	XM_005250	rs41737&CC	synonymous
MYCN	snp	chr2	16080157	C	G	1316.08	hom	42	1.00	NM_005378	rs11886063	upstream_ge
NOTCH1	snp	chr9	139391636	G	A	10736	hom	415	1.00	NM_017617	rs2229974	synonymous
NOTCH1	complex	chr9	139393716	GCAACAGGC	AAGACACCT	281.091	hom	14	0.93	NM_017617.3		splice_regio
NOTCH1	snp	chr9	139397707	G	A	9120.86	hom	295	1.00	NM_017617	rs10521&CC	synonymous
NOTCH1	complex	chr9	139400272	TTGA	CTGC	439.76	hom	16	1.00	NM_017617.3		missense_va
NOTCH1	mnp	chr9	139400282	GCAG	CTGC	380.614	hom	14	1.00	NM_017617.3		missense_va
NOTCH1	snp	chr9	139400292	G	T	337.858	het	14	0.93	NM_017617	rs200099319	stop_gained
NPM1	del,del	chr5	170837513	CTTTTTTTTT	CTTTTTTTTT	1828.21	het	189	0.33	NM_002520.6		splice_regio
PDGFRA	complex	chr4	55141051	GCCCA	ACCCG	514.123	het	27	0.74	NM_006206.4		missense_va
PDGFRA	snp	chr4	55141051	GCCCA	GCCCG	19219.4	hom	650	0.96	NM_006206.4		synonymous
PDGFRA	snp	chr4	55161254	C	T	4472.07	hom	144	0.99	NM_006206	rs3733540	intron_varia
PDGFRA	snp	chr4	55161391	T	C	972.052	hom	34	1.00	NM_006206	rs7685117	synonymous
PDGFRA	snp	chr4	55161517	A	G	3142.16	hom	99	1.00	NM_006206	rs7680422	3_prime_UT
PIK3CA	del	chr3	178927848	ATTTTTTTTT	ATTTTTTTTT	1619.39	het	259	0.25	NM_006218.2		intron_varia
PTEN	del	chr10	89720633	CTTTTTTTTT	CTTTTTTTTT	446.089	het	103	0.23	NM_000314.4		splice_accep
PTEN	del	chr10	89725293	CTTTTTTTTT	CTTTTTTTTT	318.11	het	53	0.26	NM_000314.4		3_prime_UT
RB1	snp	chr13	48919358	T	G	4283.46	hom	145	0.98	NM_000321	rs198617	intron_varia
RB1	ins	chr13	48953655	CAAAAAAAA	CAAAAAAAA	768.182	het	165	0.19	NM_000321.2		intron_varia
RB1	snp	chr13	48953841	C	T	284.517	hom	10	1.00	NM_000321.2		intron_varia
RB1	ins	chr13	49034022	ATT	ATTT	639.22	het	57	0.46	NM_000321.2		intron_varia
RB1	snp	chr13	49034025	C	T	614.839	het	56	0.50	NM_000321.2		intron_varia

SMO	snp	chr7	128845088	A	G	702.654	het	51	0.51	NM_005631	rs56334250	synonymous
SMO	snp	chr7	128845277	G	C	13525.3	hom	465	0.95	NM_005631	rs2075777	intron_varia
SMO	snp	chr7	128846328	G	C	7022.8	hom	221	1.00	NM_005631	rs2228617	synonymous
SMO	snp	chr7	128846469	A	G	303.768	hom	13	1.00	NM_005631	rs2735842	intron_varia
SMO	snp	chr7	128846475	G	A	307.398	hom	13	1.00	NM_005631.4		intron_varia
SRC	snp	chr20	36031638	G	A	1368.66	het	91	0.58	NM_005417	rs11789943	synonymous
STK11	snp	chr19	1207044	G	A	1.39349	het	150	0.13	XM_005259617.1		synonymous
STK11	snp	chr19	1207238	G	T	1093.02	het	328	0.18	XM_005259	rs3764640	intron_varia
STK11	ins	chr19	1219443	GCGGGGGC	GCGGGGGC	241.638	het	34	0.32	XM_005259617.1		intron_varia
STK11	snp	chr19	1220257	C	T	686.787	hom	24	1.00	XM_005259617.1		intron_varia
STK11	complex	chr19	1220321	TGTG	CGTA	91.4094	het	184	0.13	XM_005259617.1		intron_varia
STK11	snp	chr19	1220321	TGTG	CGTG	3731.63	het	306	0.40	XM_005259617.1		intron_varia
STK11	snp	chr19	1220426	G	A	241.032	het	18	0.67	XM_005259617.1		synonymous
STK11	mnp	chr19	1220814	CC	TT	47.2768	het	95	0.13	XM_005259617.1		intron_varia
STK11	snp	chr19	1223110	GGACGAGG	GGATGAGG	405.024	het	503	0.11	XM_005259617.1		synonymous
STK11	snp	chr19	1226697	G	A	429.905	het	200	0.16	XM_005259617.1		intron_varia
TERT	snp	chr5	1295349	A	G	32829	het	1774	0.58	NM_198253	rs2853669&	upstream_ge
TP53	snp	chr17	7577407	A	C	5001.6	hom	176	1.00	NM_000546	rs12951053	intron_varia
TP53	snp	chr17	7577427	G	A	5251.96	hom	180	0.98	NM_000546	rs12947788	intron_varia
TP53	del	chr17	7579643	CCCCCAGCC	CC	1033.03	het	159	0.35	NM_000546.5		intron_varia