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Data Sheet

Product Name: CancerSeqPlus Paraffin Tissue Curl

Catalog No.: T2235248-SC **Lot No.: B906139**

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: 71 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:** _____

B906139

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
CCNE1	8.13	0.22	6.12E-04	CCNE1	6.03	0.03	1.00E-03
ERBB2	3.96	0.27	5.37E-03	ERBB2	4.61	0.05	1.47E-03
FGFR2	24.13	1.80	2.73E-04	FGFR2	16.85	0.34	2.70E-04

symbol	type	chromosome	position	reference	mutation	quality	allele type	Depth	variant frequency	transcript_id	existing variation	consequence
ALK	snp	chr2	29443749	G	T	1052.71	het	70	0.5	NM_004304.4	rs80152976	intron_variant
ALK	snp	chr2	29445154	C	T	691.647	het	47	0.7021277	NM_004304.4		intron_variant
ALK	snp	chr2	29445458	G	T	1142.44	het	60	0.6333333	NM_004304.4	rs3795850	synonymous_v
APC	snp	chr5	112177171	G	A	248.009	hom	10	1	XM_00527197	rs465899	synonymous_v
ATM	del	chr11	108117897	ATTTTTTTTT	ATTTTTTTT	223.332	het	46	0.2391304	NM_000051.3		intron_variant&
CDH1	snp	chr16	68771371	CC	CT	9341.67	hom	307	0.9576547	NM_004360.3		splice_region_v
CDH1	mnp	chr16	68771371	CC	TT	341.337	hom	13	1	NM_004360.3		splice_region_v
CDKN2A	snp	chr9	21968199	C	G	20046.5	hom	634	0.9984227	NM_00119513	rs11515&CO	3_prime_UTR_
CDKN2A	del	chr9	21968257	AGA	AA	82.5033	het	228	0.1184211	NM_001195132.1		intron_variant&
CDKN2A	snp	chr9	21968258	G	A	5443.4	het	382	0.5	NM_001195132.1		intron_variant
DDR2	snp	chr1	162740327	T	C	5622.53	hom	179	0.9944134	XM_00524522	rs1780003	intron_variant
DDR2	snp	chr1	162743418	G	T	750.32	hom	28	0.9642857	XM_00524522	rs1355287	intron_variant
EGFR	snp	chr7	55221655	G	A	364.095	het	19	0.7894737	NM_005228.3	rs4947986	intron_variant
EZH2	snp	chr7	148508833	A	G	582.213	hom	19	1	XM_00524996	rs2072407	intron_variant
FBXW7	del,del	chr4	153268227	CAAAAAAAA	CAAAAAAAA	265.06	het	54	#VALUE!	NM_033632.3		splice_region_v
FGFR1	snp	chr8	38271338	G	A	345.182	het	16	0.875	NM_001174067.1		intron_variant
FGFR1	mnp	chr8	38271371	CT	AG	336.114	hom	14	0.8571429	NM_001174067.1		intron_variant
FGFR1	complex	chr8	38271381	TGC	AGG	437.041	hom	16	1	NM_001174067.1		intron_variant
FGFR1	snp	chr8	38282106	T	C	2343.69	het	153	0.5555556	NM_001174067.1		missense_varia
FGFR3	del	chr4	1806012	TGGGGGGG	TGGGGGGG	1561.45	het	493	0.1724138	NM_001163213.1		intron_variant&
FGFR3	snp	chr4	1807894	G	A	6064.46	hom	244	0.9877049	NM_00116321	rs7688609	synonymous_v
FGFR3	snp	chr4	1809021	C	A	156.177	het	12	0.8333333	NM_00116321	rs148257939	3_prime_UTR_
FLT3	snp	chr13	28610183	A	G	2775.51	hom	92	1	NM_004119.2	rs2491231	splice_region_v
FOXL2	snp	chr3	138664615	G	A	1215.88	hom	57	0.9298246	NM_023067.3		missense_varia

HRAS	snp	chr11	534483	C	G	327.139	hom	14	1	NM_005343.2		intron_variant
IDH1	del	chr2	209116299	GAAAAAAAA	GAAAAAAAA	1092.07	het	199	0.2311558	XM_005246521.1		intron_variant&
JAK2	del	chr9	5073681	CTTTTTTTTT	CTTTTTTTTT	400.14	het	38	0.3947368	NM_004972.3		splice_region_v
KDR	snp	chr4	55980456	C	T	1027.99	het	74	0.5	NM_002253.2	rs2305949	intron_variant
MAP2K1	snp	chr15	66727595	CAG	CAC	1171.14	het	185	0.2486486	NM_002755.3		intron_variant
MET	snp	chr7	116436022	G	A	1733.19	hom	60	0.9833333	XM_00525035	rs2023748&	synonymous_v
MET	snp	chr7	116436091	C	T	503.974	het	34	0.5588235	XM_005250353.1		synonymous_v
MET	snp	chr7	116436097	G	A	1142.73	hom	38	1	XM_00525035	rs41737&CO	synonymous_v
MPL	complex	chr1	43815047	GCAGGAGA	TCTCCTGC	86.0981	het	212	0.1367925	NM_005373.2		intron_variant
MYC	snp	chr8	128748655	C	T	2256.62	het	167	0.5988024	NM_002467.4		5_prime_UTR_
MYCN	snp	chr2	16080157	C	G	1764.13	hom	57	1	NM_005378.4	rs11886063	upstream_gene
MYCN	snp	chr2	16081359	G	A	237.933	hom	11	1	NM_005378.4		intron_variant
NOTCH1	snp	chr9	139391636	G	A	1981.62	hom	72	1	NM_017617.3	rs2229974	synonymous_v
NOTCH1	snp	chr9	139397707	G	A	2048.11	het	91	0.8681319	NM_017617.3	rs10521&CO	synonymous_v
NPM1	del	chr5	170837513	CTTTTTTTTT	CTTTTTTTTT	505.164	het	62	0.3225806	NM_002520.6		splice_region_v
PDGFRA	snp	chr4	55141055	A	G	5603.35	hom	179	1	NM_006206.4	rs1873778&	synonymous_v
PDGFRA	snp	chr4	55161254	C	T	1236.53	hom	42	0.9761905	NM_006206.4	rs3733540	intron_variant
PDGFRA	snp	chr4	55161517	A	G	1464.8	hom	48	1	NM_006206.4	rs7680422	3_prime_UTR_
PIK3CA	complex	chr3	178921384	CTA	ATGTCA	757.643	hom	33	0.8787879	NM_006218.2		inframe_insert
PIK3CA	ins	chr3	178921388	AG	ATGG	761.055	het	31	0.9354839	NM_006218.2		frameshift_vari
PIK3CA	snp	chr3	178921392	A	C	802.608	het	34	0.9117647	NM_006218.2		missense_varia
PIK3CA	del	chr3	178927848	ATTTTTTTTT	ATTTTTTTTT	214.489	het	41	0.2439024	NM_006218.2		intron_variant&
PIK3R1	snp	chr5	67588148	G	A	585.857	het	32	0.6875	NM_181523.2	rs3730089&	missense_varia
PTEN	del	chr10	89720633	CTTTTTTTTT	CTTTTTTTTT	374.436	het	51	0.372549	NM_000314.4		splice_acceptor
RB1	snp	chr13	48919358	T	G	1665.67	hom	57	1	NM_000321.2	rs198617	intron_variant
RB1	snp	chr13	48953647	C	T	1131.67	het	57	0.8596491	NM_000321.2		intron_variant
RB1	ins	chr13	49034022	ATT	ATTT	330.563	hom	15	1	NM_000321.2		intron_variant&
RET	del	chr10	43614958	GCCCCCT	GCCCCT	878.361	het	187	0.2566845	NM_020975.4		intron_variant&
RET	snp	chr10	43615031	C	T	2756.95	het	184	0.5271739	NM_020975.4		synonymous_v
RET	snp	chr10	43615084	G	A	798.849	het	51	0.8431373	NM_020975.4		missense_varia
SMAD4	snp	chr18	48604746	G	A	515.984	het	40	0.6	NM_005359.5		missense_varia
SMO	snp	chr7	128845277	G	C	5511.33	hom	183	0.989071	NM_005631.4	rs2075777	intron_variant
SMO	snp	chr7	128846328	G	C	2388.45	hom	76	1	NM_005631.4	rs2228617	synonymous_v
STK11	snp	chr19	1207238	G	T	4109.21	hom	142	0.971831	XM_00525961	rs3764640	intron_variant
STK11	snp	chr19	1219451	C	G	113.808	het	41	0.2682927	XM_00525961	rs369515604	intron_variant
STK11	complex	chr19	1220317	CCCCT	TCCCC	551.227	het	146	0.1986301	XM_005259617.1		intron_variant
STK11	complex	chr19	1221306	GACTGTGGC	CACAGTCGC	123.894	het	324	0.1820988	XM_005259617.1		frameshift_vari
STK11	snp	chr19	1221321	C	A	727.175	het	340	0.1852941	XM_00525961	CD035104	missense_varia
STK11	snp	chr19	1222012	G	C	19311.2	het	1029	0.6180758	XM_00525961	rs2075607	splice_region_v
TP53	snp	chr17	7577407	A	C	824.774	het	34	0.8823529	NM_000546.5	rs12951053	intron_variant
TP53	snp	chr17	7577427	G	A	547.562	het	25	0.84	NM_000546.5	rs12947788	intron_variant

TP53	del	chr17	7579643	CCCCCAGCC	CC	522.034	het	54	0.5	NM_000546.5		intron_variant&
TP53	mnp	chr17	7579658	GT	CC	201.686	het	54	0.2222222	NM_000546.5		intron_variant