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Data Sheet

Product Name: CancerSeqPlus Paraffin Tissue Curl

Catalog No.: T2235248-SC **Lot No.: B906140**

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: 54 year(s) old
Female: _____year(s) old

Pathological Diagnosis: Adenosquamous carcinoma

Tumor Size:

Location: stomach

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

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

B906140

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	3.07	0.16	4.43E-03	CCNE1	2.25	0.02	1.08E-02
FGFR2	25.42	1.91	2.71E-04	FGFR2	18.01	0.36	2.70E-04

symbol	type	chromosome	position	reference	mutation	quality	allele type	Depth	variant frequency	transcript_id	existing variation	consequence
ALK	snp	chr2	29445154	C	T	683.646	het	54	0.57	NM_004304.4		intron_variant
ALK	snp	chr2	29445458	G	T	2087.15	hom	66	1.00	NM_004304.4	rs3795850	synonymous_va
APC	snp	chr5	112177171	G	A	730.004	hom	27	1.00	XM_0052719	rs465899	synonymous_va
CCNE1	snp	chr19	30311662	C	T	1439.91	het	99	0.53	NM_001238.1	COSM99439	synonymous_va
CCNE1	snp	chr19	30314666	C	T	1325.21	het	84	0.52	NM_001238.1	rs7257694	synonymous_va
CDH1	snp	chr16	68771372	C	T	9941.64	hom	316	1.00	NM_004360.3	rs3743674	splice_region_va
CDH1	ins	chr16	68771418	CG	CGCCCCAGC	315.436	hom	12	1.00	NM_004360.3		intron_variant&
CDKN2A	snp	chr9	21968199	C	G	13954.8	het	557	0.89	NM_0011951	rs11515&CO	3_prime_UTR_v
CDKN2A	snp	chr9	21968258	G	A	6099.16	het	372	0.58	NM_001195132.1		intron_variant
CDKN2A	snp	chr9	21971277	G	A	345.977	hom	15	1.00	NM_001195132.1		intron_variant
CTNNB1	ins	chr3	41265953	CTTTTTTTTT	CTTTTTTTTT	119.744	het	72	0.15	XM_005264887.1		intron_variant&
DDR2	snp	chr1	162740327	T	C	6760.55	hom	216	1.00	XM_0052452	rs1780003	intron_variant
DDR2	snp	chr1	162743418	G	T	675.746	hom	23	1.00	XM_0052452	rs1355287	intron_variant
EGFR	snp	chr7	55242609	A	G	517.72	hom	22	1.00	NM_005228.3	rs2017000	intron_variant
ERBB2	del	chr17	37882959	TCC	TC	196.117	het	166	0.16	NM_004448.2		intron_variant&
ERBB2	ins	chr17	37882965	AGA	AGGA	349.279	het	93	0.26	NM_004448.2		intron_variant&
FGFR1	snp	chr8	38271338	G	A	469.605	het	25	0.76	NM_001174067.1		intron_variant
FGFR1	mnp	chr8	38271371	CT	AG	718.532	hom	25	1.00	NM_001174067.1		intron_variant
FGFR1	complex	chr8	38271381	TGC	AGG	733.461	hom	26	1.00	NM_001174067.1		intron_variant
FGFR3	del	chr4	1806012	TGGGGGGG	TGGGGGGG	1531.44	het	419	0.19	NM_001163213.1		intron_variant&
FGFR3	snp	chr4	1807894	G	A	6420.68	hom	249	0.98	NM_0011632	rs7688609	synonymous_va
FLT3	del	chr13	28602226	AAGAGAGA	AAGAGAGA	160.095	hom	9	0.78	NM_004119.2		intron_variant&
FLT3	snp	chr13	28610183	A	G	2725.47	hom	89	1.00	NM_004119.1	rs2491231	splice_region_va
HRAS	snp	chr11	534242	A	G	3585	hom	115	1.00	NM_005343.1	rs12628&CN	synonymous_va
HRAS	del	chr11	534403	GCCCAGGCC	GC	1296.06	hom	46	1.00	NM_005343.2		intron_variant&
HRAS	snp	chr11	534415	C	G	897.6	hom	31	1.00	NM_005343.1	rs61877782	intron_variant
IDH1	del	chr2	209116299	GAAAAAAA	GAAAAAAA	800.461	het	150	0.24	XM_005246521.1		intron_variant&

JAK2	del	chr9	5073681	CTTTTTTTTT	CTTTTTTTTT	342.308	het	39	0.33	NM_004972.3		splice_region_va
KDR	snp	chr4	55980239	C	T	377.658	hom	15	1.00	NM_002253.1	rs7692791	intron_variant
MET	snp	chr7	116436022	G	A	850.704	het	47	0.68	XM_0052503	rs2023748&	synonymous_va
MYC	snp	chr8	128748655	C	T	2050.34	het	136	0.71	NM_002467.4		5_prime_UTR_v
MYCN	snp	chr2	16080157	C	G	1763.19	hom	56	1.00	NM_005378.4	rs11886063	upstream_gene_
MYCN	snp	chr2	16089615	T	C	2105.31	het	94	0.87	NM_005378.4	rs4669018	downstream_ge
NOTCH1	snp	chr9	139391636	G	A	5879.8	hom	199	1.00	NM_017617.1	rs2229974	synonymous_va
NOTCH1	snp	chr9	139397707	G	A	2737.04	hom	92	1.00	NM_017617.1	rs10521&CC	synonymous_va
NPM1	del	chr5	170837513	CTTTTTTTTT	CTTTTTTTTT	345.404	het	35	0.43	NM_002520.6		splice_region_va
PDGFRA	snp	chr4	55141055	A	G	6388.64	hom	203	1.00	NM_006206.4	rs1873778&	synonymous_va
PDGFRA	snp	chr4	55161254	C	T	717.994	hom	24	1.00	NM_006206.4	rs3733540	intron_variant
PDGFRA	snp	chr4	55161517	A	G	1494.14	hom	48	1.00	NM_006206.4	rs7680422	3_prime_UTR_v
PIK3CA	complex	chr3	178921384	CTA	ATGTCA	843.566	hom	35	0.89	NM_006218.2		inframe_insertio
PIK3CA	ins	chr3	178921388	AG	ATGG	775.999	hom	31	0.94	NM_006218.2		frameshift_varia
PIK3CA	snp	chr3	178921392	A	C	806.356	het	38	0.87	NM_006218.2		missense_variar
PTEN	del	chr10	89720633	CTTTTTTTTT	CTTTTTTTTT	288.493	het	82	0.20	NM_000314.4		splice_acceptor_
RB1	snp	chr13	48919358	T	G	1499.66	hom	52	1.00	NM_000321.2	rs198617	intron_variant
RB1	del	chr13	48953655	CAAAAAAAA	CAAAAAAAA	225.867	het	24	0.42	NM_000321.2		intron_variant&
RET	snp	chr10	43613843	G	T	1624.07	hom	52	1.00	NM_020975.4	rs1800861&	synonymous_va
RET	del	chr10	43614958	GCCCCCT	GCCCCT	798.018	het	93	0.40	NM_020975.4		intron_variant&
RET	snp	chr10	43615031	C	T	2000.97	het	122	0.61	NM_020975.4		synonymous_va
SMO	snp	chr7	128845277	G	C	1553.85	het	92	0.55	NM_005631.4	rs2075777	intron_variant
STK11	complex	chr19	1220317	CCCCT	TCCCC	93.1008	het	193	0.12	XM_005259617.1		intron_variant
STK11	complex	chr19	1221306	GACTGTGGC	CACAGTCGC	159.656	het	292	0.19	XM_005259617.1		frameshift_varia
STK11	snp	chr19	1221321	C	A	729.074	het	316	0.19	XM_0052596	CD035104	missense_variar
TP53	snp	chr17	7577407	A	C	608.477	het	27	0.85	NM_000546.5	rs12951053	intron_variant
TP53	snp	chr17	7577427	G	A	540.578	het	24	0.83	NM_000546.5	rs12947788	intron_variant
TP53	del	chr17	7579643	CCCCCAGCC	CC	509.033	het	52	0.46	NM_000546.5		intron_variant&
TP53	complex	chr17	7579668	CTCCAG	CAACCCTT	73.3973	het	63	0.17	NM_000546.5		intron_variant&
TP53	complex	chr17	7579678	CCAG	TTAC	1.29017	het	67	0.15	NM_000546.5		intron_variant