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Data Sheet

Product Name: CancerSeqPlus Paraffin Tissue Curl

Catalog No.: T2235248-SC **Lot No.: B906142**

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:** _____

B906142

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
ABL1	snp	chr9	133750286	G	A	733.891	het	52	0.52	NM_007313.2		missense_varian
AKT1	snp	chr14	105246325	T	A	373.881	hom	16	1.00	NM_001014	rs2494737	intron_variant
ALK	snp	chr2	29445458	G	T	1877.48	het	113	0.56	NM_004304	rs3795850	synonymous_va
APC	snp	chr5	112175770	G	A	637.37	hom	25	1.00	XM_005271	rs41115&CO	synonymous_va
APC	snp	chr5	112177171	G	A	2246.17	hom	80	0.99	XM_005271	rs465899	synonymous_va
CCND1	snp	chr11	69471170	C	T	475.059	het	32	0.75	NM_053056.2		downstream_ge
CCND1	mnp	chr11	69471204	TGT	ACA	268.753	het	42	0.36	NM_053056.2		downstream_ge
CCND1	complex	chr11	69471210	AC	AGA	257.863	het	41	0.34	NM_053056.2		downstream_ge
CCNE1	snp	chr19	30314666	C	T	352.491	het	22	0.59	NM_001238	rs7257694	synonymous_va
CDH1	snp	chr16	68771372	C	T	8652.05	het	458	0.61	NM_004360	rs3743674	splice_region_va
CDH1	complex	chr16	68771429	TGC	CGT	726.037	hom	37	0.95	NM_004360.3		intron_variant
CDH1	complex	chr16	68771437	TTCCTC	AGCCC	665.083	hom	35	0.89	NM_004360.3		intron_variant&
CDH1	complex	chr16	68771444	CCC	GCG	668.673	hom	34	0.91	NM_004360.3		intron_variant
CDH1	snp	chr16	68849456	C	T	1565.58	het	92	0.61	NM_004360	rs11486146	synonymous_va
CDH1	complex	chr16	68853397	TCTTTTGG	CCAAAAGA	271.275	hom	13	0.92	NM_004360.3		intron_variant
CDH1	complex	chr16	68853410	AGA	GGG	240.429	hom	12	1.00	NM_004360.3		intron_variant
CDKN2A	snp	chr9	21968199	C	G	18891.1	hom	597	1.00	NM_001195	rs11515&CO	3_prime_UTR_va
CTNNB1	del	chr3	41265953	CTTTTTTTTT	CTTTTTTTA	16.6281	het	93	0.12	XM_005264887.1		intron_variant&
DDR2	snp	chr1	162740327	T	C	9684.25	hom	319	1.00	XM_005245	rs1780003	intron_variant
DDR2	snp	chr1	162743418	G	T	678.718	hom	25	1.00	XM_005245	rs1355287	intron_variant
EGFR	snp	chr7	55242609	A	G	403.239	hom	15	1.00	NM_005228	rs2017000	intron_variant
ERBB4	snp	chr2	212578519	A	T	2991.87	het	173	0.57	NM_005235	rs35123918	intron_variant
FBXW7	snp	chr4	153245534	G	A	313.619	het	21	0.76	NM_033632.3		missense_varian
FBXW7	del,del	chr4	153268227	CAAAAAAAA	CAAAAAAAA	1225.91	het	129	0.02	NM_033632.3		splice_region_va
FGFR3	del	chr4	1806012	TGGGGGGG	TGGGGGGG	4374.94	het	294	0.60	NM_001163213.1		intron_variant&
FGFR3	snp	chr4	1807894	G	A	5183.72	hom	182	0.99	NM_001163	rs7688609	synonymous_va
FGFR3	snp	chr4	1808766	G	C	434.709	het	25	0.88	NM_001163213.1		intron_variant
FGFR3	ins	chr4	1808773	CC	CCACCTC	387.456	het	26	0.77	NM_001163213.1		intron_variant&
FGFR3	complex	chr4	1808777	GGCACAGAC	TGCCCAG	416.026	het	29	0.79	NM_001163213.1		intron_variant&
FGFR3	snp	chr4	1808805	C	T	526.804	het	37	0.68	NM_001163213.1		intron_variant
FLT3	snp	chr13	28610183	A	G	3829.74	hom	125	1.00	NM_004119	rs2491231	splice_region_va
FOXL2	complex	chr3	138664450	GAA	GC	393.314	hom	14	1.00	NM_023067.3		frameshift_varia
FOXL2	complex	chr3	138664456	AG	ATT	401.478	hom	14	1.00	NM_023067.3		frameshift_varia

FOXL2	snp	chr3	138664464	G	T	397.85	hom	14	1.00	NM_023067	rs14327288	synonymous_va
IDH1	del	chr2	209116299	GAAAAAAA	GAAAAAAA	1047.01	het	118	0.33	XM_005246	521.1	intron_variant&
KDR	snp	chr4	55961159	TAC	CAC	2489.46	hom	93	0.88	NM_002253	.2	intron_variant
KDR	complex	chr4	55961159	TAC	CAG	279.901	hom	11	0.91	NM_002253	.2	intron_variant
KDR	snp	chr4	55972974	T	A	648.86	hom	22	1.00	NM_002253	rs1870377&	missense_varian
KIT	snp	chr4	55593481	A	G	1365.15	het	81	0.57	XM_005265	rs55986963	synonymous_va
MAP2K1	snp	chr15	66727597	G	C	4246.38	het	242	0.57	NM_002755	rs16949924	intron_variant
MET	snp	chr7	116436022	G	A	863.866	het	50	0.64	XM_005250	rs2023748&	synonymous_va
MET	snp	chr7	116436097	G	A	640.313	het	40	0.60	XM_005250	rs41737&CO	synonymous_va
MYCN	snp	chr2	16080157	C	G	1204.26	hom	38	1.00	NM_005378	rs11886063	upstream_gene_
MYCN	snp	chr2	16089615	T	C	2162.85	het	117	0.64	NM_005378	rs4669018	downstream_ge
NOTCH1	snp	chr9	139390581	G	C	260.423	het	16	0.75	NM_017617	.3	missense_varian
NOTCH1	snp	chr9	139390584	A	C	255.736	het	14	0.86	NM_017617	.3	missense_varian
NOTCH1	snp	chr9	139391510	CGG	TGG	10647.8	het	957	0.36	NM_017617	.3	synonymous_va
NOTCH1	snp	chr9	139391636	G	A	1581.68	hom	56	1.00	NM_017617	rs2229974	synonymous_va
NOTCH1	snp	chr9	139397707	G	A	8984.23	hom	290	1.00	NM_017617	rs10521&CO	synonymous_va
NOTCH1	ins	chr9	139399204	GG	GACG	350.528	hom	13	1.00	NM_017617	.3	frameshift_varia
NOTCH1	complex	chr9	139399209	AGCA	TGCT	447.916	hom	16	1.00	NM_017617	.3	missense_varian
NOTCH1	del	chr9	139399216	CGTC	CC	448.822	hom	16	1.00	NM_017617	.3	frameshift_varia
NOTCH1	complex	chr9	139399224	GC	GAA	433.416	hom	16	1.00	NM_017617	COSM30860	frameshift_varia
NPM1	del	chr5	170837513	CTTTTTTTT	CTTTTTTTT	282.234	het	30	0.43	NM_002520	.6	splice_region_va
PDGFRA	snp	chr4	55141055	A	G	6034.89	hom	195	1.00	NM_006206	rs1873778&	synonymous_va
PDGFRA	snp	chr4	55161391	T	C	353.69	hom	14	1.00	NM_006206	rs7685117	synonymous_va
PDGFRA	snp	chr4	55161517	A	G	1188.93	hom	43	0.98	NM_006206	rs7680422	3_prime_UTR_va
PIK3CA	snp	chr3	178938938	C	T	285.319	hom	10	1.00	NM_006218	.2	missense_varian
PIK3R1	snp	chr5	67588148	G	A	1311.38	het	79	0.57	NM_181523	rs3730089&	missense_varian
PTEN	del	chr10	89720633	CTTTTTTTT	CTTTTTTTT	218.959	het	71	0.18	NM_000314	.4	splice_acceptor_
PTEN	snp	chr10	89720907	T	G	649.537	het	60	0.50	NM_000314	rs555895&C	intron_variant
RB1	snp	chr13	48919358	T	G	1256.09	hom	42	1.00	NM_000321	rs198617	intron_variant
RB1	ins	chr13	49034022	ATT	ATTT	330.767	hom	14	1.00	NM_000321	.2	intron_variant&
RET	snp	chr10	43613843	G	T	1923.04	hom	66	0.98	NM_020975	rs1800861&	synonymous_va
RET	snp	chr10	43615633	C	G	822.256	het	37	0.86	NM_020975	rs1800863&	synonymous_va
RET	snp	chr10	43617564	T	A	301.739	hom	14	1.00	NM_020975	.4	intron_variant
SMAD4	snp	chr18	48581116	A	T	300.87	het	19	0.68	NM_005359	.5	intron_variant
SMAD4	snp	chr18	48581229	C	T	538.984	het	40	0.65	NM_005359	rs37776733	missense_varian
SMO	snp	chr7	128845277	G	C	4863.68	hom	165	1.00	NM_005631	rs2075777	intron_variant
SMO	snp	chr7	128846328	G	C	2261.52	hom	72	1.00	NM_005631	rs2228617	synonymous_va
STK11	snp	chr19	1207238	G	T	2749.22	hom	93	0.99	XM_005259	rs3764640	intron_variant
STK11	snp	chr19	1220321	T	C	7508.46	hom	237	1.00	XM_005259	rs2075606	intron_variant
STK11	complex	chr19	1220695	TCTGG	CCTGA	113.986	het	50	0.20	XM_005259617.1		stop_gained
STK11	snp	chr19	1221423	G	C	172.704	het	32	0.69	XM_005259617.1		intron_variant

STK11	snp	chr19	1226772	C	T	237.291	hom	10	1.00	XM_005259	rs2277746	intron_variant
TP53	snp	chr17	7578115	T	C	230.011	hom	10	1.00	NM_000546	rs1625895	intron_variant
TP53	snp	chr17	7579619	G	T	2769.46	het	123	0.82	NM_000546	rs17883323	intron_variant
TP53	del	chr17	7579643	CCCCCAGCC	CC	244.041	het	53	0.28	NM_000546.5		intron_variant&
TP53	snp	chr17	7580052	C	T	878.103	het	50	0.88	NM_000546	rs8079544	intron_variant