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Data Sheet

Product Name: CancerSeqPlus Paraffin Tissue Curl

Catalog No.: T2235248-SC **Lot No.: B906157**

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: 45 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:** _____

B906157

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	29445081	C	T	390.808	het	26	0.73	NM_004304.4		intron_varia
APC	snp	chr5	112175770	G	A	341.069	het	25	0.52	XM_005271	rs41115&CO	synonymous
CDH1	snp	chr16	68771371	CC	CT	15873.3	hom	562	0.92	NM_004360.3		splice_regio
CDH1	mnp	chr16	68771371	CC	TT	825.76	het	42	0.74	NM_004360.3		splice_regio
CDH1	ins	chr16	68771418	CG	CGCCCCAGC	260.751	het	13	0.92	NM_004360.3		intron_varia
CDKN2A	mnp	chr9	21968199	CG	GA	1175.81	hom	38	1.00	NM_001195132.1		3_prime_UT
CDKN2A	snp	chr9	21968199	CG	GG	21096.5	hom	705	0.94	NM_001195132.1		3_prime_UT
CDKN2A	snp	chr9	21971277	G	A	218.181	hom	10	1.00	NM_001195132.1		intron_varia
CSF1R	mnp	chr5	149433596	TG	GA	354.337	het	21	0.81	NM_005211.3		3_prime_UT
DDR2	snp	chr1	162740327	T	C	10758.2	hom	355	1.00	XM_005245	rs1780003	intron_varia
DDR2	snp	chr1	162741794	C	T	2341.61	het	104	0.78	XM_005245	rs3738807	intron_varia
DDR2	snp	chr1	162743418	G	T	1334.53	hom	49	1.00	XM_005245	rs1355287	intron_varia
EGFR	snp	chr7	55221655	G	A	719.144	hom	27	0.96	NM_005228	rs4947986	intron_varia
EGFR	snp	chr7	55242279	C	T	1619.74	het	132	0.54	NM_005228.3		intron_varia
ERBB3	snp	chr12	56477694	A	T	7050.42	het	297	0.81	NM_001982	rs2271194	splice_regio
ESR1	snp	chr6	152420095	G	A	3227.05	het	198	0.53	XM_005266	rs2228480&	synonymous
FBXW7	snp	chr4	153244352	A	G	572.789	het	37	0.57	NM_033632	rs34649288	intron_varia
FBXW7	del,del	chr4	153268227	CAAAAAAAA	CAAAAAAAA	1076.07	het	143	0.26	NM_033632.3		splice_regio
FGFR3	snp	chr4	1803704	TG	CG	2416.53	het	265	0.31	NM_001163213.1		synonymous
FGFR3	del	chr4	1806012	TGGGGGGG	TGGGGGGG	1130.49	het	496	0.16	NM_001163213.1		intron_varia
FGFR3	snp	chr4	1807894	G	A	7180.9	hom	230	1.00	NM_001163	rs7688609	synonymous
FLT3	snp	chr13	28610183	A	G	1858.44	het	97	0.66	NM_004119	rs2491231	splice_regio
H3F3A	snp	chr1	226252239	T	A	394.827	hom	21	1.00	NM_002107.4		intron_varia
HRAS	complex	chr11	534244	GGTT	AGTC	12.8281	het	122	0.11	NM_005343.2		missense_va
HRAS	snp	chr11	534244	GGTT	AGTT	469.801	het	148	0.18	NM_005343.2		missense_va
IDH1	del	chr2	209116299	GAAAAAAAA	GAAAAAAAA	431.412	het	107	0.20	XM_005246521.1		intron_varia
JAK2	del	chr9	5073681	CTTTTTTTTT	CTTTTTTTTT	439.024	het	45	0.38	NM_004972.3		splice_regio
KDR	snp	chr4	55961159	T	C	3209.25	het	159	0.71	NM_002253	rs2219471	intron_varia
KDR	ins	chr4	55962545	TGG	TGGG	325.853	het	76	0.22	NM_002253.2		intron_varia
KDR	snp	chr4	55972974	T	A	565.798	het	36	0.56	NM_002253	rs1870377&	missense_va
MAP2K1	snp	chr15	66727597	G	C	4500.17	het	275	0.52	NM_002755	rs16949924	intron_varia
MET	snp	chr7	116436022	G	A	1743.48	hom	59	1.00	XM_005250	rs2023748&	synonymous
MET	snp	chr7	116436097	G	A	1746.1	hom	58	1.00	XM_005250	rs41737&CO	synonymous

MPL	complex	chr1	43815047	GCAGGAGA	TCTCCTGC	4.98507	het	226	0.14	NM_005373.2		intron_varia
MYCN	snp	chr2	16080157	C	G	2260.45	hom	71	1.00	NM_005378	rs11886063	upstream_ge
MYCN	snp	chr2	16089615	T	C	2708.54	hom	91	1.00	NM_005378	rs4669018	downstream
NOTCH1	mnp	chr9	139390563	ATG	CGA	182.073	het	14	0.79	NM_017617.3		missense_va
NOTCH1	snp	chr9	139391385	C	T	858.154	het	53	0.77	NM_017617.3		missense_va
NOTCH1	snp	chr9	139391636	G	A	3646.33	hom	149	1.00	NM_017617	rs2229974	synonymous
NOTCH1	snp	chr9	139397707	G	A	7258.9	hom	237	0.99	NM_017617	rs10521&CC	synonymous
NOTCH1	del	chr9	139397820	TTCCTCCTCC	TTCCTCCC	15.8833	het	225	0.12	NM_017617.3		intron_varia
NPM1	del,del	chr5	170837513	CTTTTTTTTT	CTTTTTTTTT	580.562	het	50	0.34	NM_002520.6		splice_regio
PDGFRA	snp	chr4	55141055	A	G	9132.61	hom	299	1.00	NM_006206	rs1873778&	synonymous
PDGFRA	snp	chr4	55161254	C	T	4117.3	hom	133	1.00	NM_006206	rs3733540	intron_varia
PDGFRA	snp	chr4	55161391	T	C	841.754	hom	29	1.00	NM_006206	rs7685117	synonymous
PDGFRA	snp	chr4	55161517	A	G	2163.53	hom	71	1.00	NM_006206	rs7680422	3_prime_UT
PIK3CA	ins	chr3	178927848	ATTTTTTTTT	ATTTTTTTTT	219.155	het	52	0.21	NM_006218.2		intron_varia
PTEN	del	chr10	89720633	CTTTTTTTTT	CTTTTTTTTT	260.346	het	63	0.22	NM_000314.4		splice_accep
RB1	snp	chr13	48919358	T	G	1645.74	hom	55	1.00	NM_000321	rs198617	intron_varia
RB1	snp	chr13	48942784	C	T	234.973	het	118	0.16	NM_000321.2		intron_varia
RB1	ins	chr13	48953655	CAAAAAAAA	CAAAAAAAA	255.723	het	27	0.41	NM_000321.2		intron_varia
RB1	snp	chr13	49033747	G	A	313.953	hom	11	1.00	NM_000321	rs198580	intron_varia
RB1	ins	chr13	49034022	ATT	ATTT	369.948	hom	14	1.00	NM_000321.2		intron_varia
RET	snp	chr10	43610119	G	A	1607.83	het	105	0.51	NM_020975	rs1799939&	missense_va
RET	snp	chr10	43613843	G	T	3617.01	het	171	0.70	NM_020975	rs1800861&	synonymous
SMAD4	del	chr18	48586214	ATTTTTG	ATTG	817.292	het	171	0.22	NM_005359.5		intron_varia
SMO	snp	chr7	128845277	G	C	8458.14	hom	271	1.00	NM_005631	rs2075777	intron_varia
SMO	snp	chr7	128846328	G	C	3954.5	hom	133	0.94	NM_005631	rs2228617	synonymous
STK11	snp	chr19	1218523	G	T	7959.78	het	447	0.58	XM_005259	rs2075604	intron_varia
STK11	ins	chr19	1219443	GCGGGGGC	GCGGGGGC	305.885	het	37	0.38	XM_005259617.1		intron_varia
STK11	snp	chr19	1219451	C	G	273.458	het	89	0.26	XM_005259	rs369515604	intron_varia
TERT	snp	chr5	1295349	AAGC	GAGC	20524.3	het	1170	0.59	NM_198253.2		upstream_ge
TP53	snp	chr17	7579472	G	C	5786.57	het	329	0.61	NM_000546	rs1042522&	missense_va
TP53	del	chr17	7579643	CCCCCAGCC	CC	396.776	het	119	0.23	NM_000546.5		intron_varia
TP53	complex	chr17	7579668	CTCCAG	CAACCCTT	696.394	het	154	0.26	NM_000546.5		intron_varia
TP53	complex	chr17	7579678	CCAG	TTAC	591.774	het	163	0.26	NM_000546.5		intron_varia
TP53	snp	chr17	7579801	G	C	310.587	het	20	0.60	NM_000546	rs1642785	intron_varia