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Data Sheet

Product Name: CancerSeqPlus Paraffin Tissue Curl

Catalog No.: T2235248-SC **Lot No.: B906154**

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: _____ year(s) old
Female: 35 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:** _____

BB906154

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	consequence	existing variation
ALK	snp	chr2	29432675	G	A	909.693	hom	36	0.94	NM_004304	synonymous_variant	
ALK	snp	chr2	29432727	T	A	184.893	het	21	0.52	NM_004304	missense_variant	
ALK	snp	chr2	29445458	G	T	942.208	hom	33	1.00	NM_004304	synonymous	rs3795850
APC	snp	chr5	112173713	G	A	805.178	het	58	0.52	XM_005271	missense_variant	
CCND1	snp	chr11	69460845	C	A	237.024	hom	11	1.00	NM_053056	intron_variant	
CDH1	snp	chr16	68771372	C	T	1765.63	hom	61	1.00	NM_004360	splice_regio	rs3743674
CDH1	snp	chr16	68847342	C	T	233.524	het	12	0.83	NM_004360	stop_gained	
CDH1	snp	chr16	68849541	G	A	848.452	het	54	0.57	NM_004360	missense_variant	
CDKN2A	snp	chr9	21968199	C	G	5039.84	hom	161	0.99	NM_001195	3_prime_UT	rs11515&CO
DDR2	snp	chr1	162740327	T	C	2247.09	hom	76	0.97	XM_005245	intron_varia	rs1780003
DDR2	snp	chr1	162743418	G	T	329.677	hom	13	1.00	XM_005245	intron_varia	rs1355287
ESR1	snp	chr6	152419936	G	A	330.881	het	23	0.57	XM_005266	synonymous_variant	
FGFR3	snp	chr4	1803593	G	A	558.57	het	27	0.85	NM_001163	synonymous	rs138334098
FGFR3	snp	chr4	1803704	T	C	3321.14	hom	116	1.00	NM_001163	synonymous	rs2234909&(
FGFR3	snp	chr4	1807894	G	A	1289.3	hom	57	0.98	NM_001163	synonymous	rs7688609
HRAS	snp	chr11	534343	C	T	406.446	het	21	0.81	NM_005343	5_prime_UTR_variant	
IDH2	snp	chr15	90631878	G	A	6256.16	het	313	0.73	NM_002168	missense_variant	
KIT	snp	chr4	55599372	C	T	887.933	het	47	0.72	XM_005265	intron_variant	
MAP2K1	snp	chr15	66727597	G	C	1702.83	het	79	0.72	NM_002755	intron_varia	rs16949924
MYCN	snp	chr2	16080157	C	G	459.697	hom	16	1.00	NM_005378	upstream_g	rs11886063
MYCN	snp	chr2	16089664	C	T	564.623	het	28	0.79	NM_005378	downstream_gene_varia	
NOTCH1	snp	chr9	139391458	C	T	235.289	het	14	0.71	NM_017617	missense_va	rs201613894
NOTCH1	snp	chr9	139391461	T	C	235.289	het	14	0.71	NM_017617	missense_variant	
NOTCH1	mnp	chr9	139391467	GG	CC	236.199	het	14	0.71	NM_017617	missense_variant	
NOTCH1	mnp	chr9	139391473	TG	CA	92.1784	het	68	0.15	NM_017617	missense_variant	
NOTCH1	snp	chr9	139399403	C	T	260.66	hom	11	1.00	NM_017617	missense_variant	
PDGFRA	snp	chr4	55141033	G	A	771.607	het	51	0.55	NM_006206	missense_variant	
PDGFRA	snp	chr4	55141055	A	G	681.037	hom	22	1.00	NM_006206	synonymous	rs1873778&(
PDGFRA	snp	chr4	55161517	A	G	836.425	hom	28	1.00	NM_006206	3_prime_UT	rs7680422
RB1	snp	chr13	48941609	C	T	442.123	het	25	0.68	NM_000321	intron_variant	
STK11	snp	chr19	1207238	G	T	316.764	het	13	0.92	XM_005259	intron_varia	rs3764640
STK11	snp	chr19	1218523	G	T	1250.83	hom	44	1.00	XM_005259	intron_varia	rs2075604
STK11	mnp	chr19	1218532	CC	TT	933.653	het	51	0.69	XM_005259	intron_variant	

STK11	snp	chr19	1220321	T	C	4937.71	hom	158	0.99	XM_005259	intron_varia	rs2075606
STK11	snp	chr19	1221301	C	T	424.379	het	23	0.74	XM_005259	missense_variant	
STK11	snp	chr19	1221323	C	T	417.448	het	23	0.74	XM_005259	synonymous_variant	
TERT	snp	chr5	1295349	A	G	8389.2	het	374	0.86	NM_198253	upstream_g	rs2853669&(
TP53	snp	chr17	7579472	G	C	372.089	hom	13	1.00	NM_000546	missense_va	rs1042522&'