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Data Sheet

Product Name: CancerSeqPlus Paraffin Tissue Curl

Catalog No.: T2235248-SC **Lot No.: B906153**

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: 65 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:** _____

B906153

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
CDKN2A	4.54	0.12	9.54E-03	CDKN2A	5.18	0.06	8.68E-03
NOTCH1	4.56	0.28	1.90E-02	NOTCH1	6.73	0.11	8.68E-03

symbol	type	chromosome	position	reference	mutation	quality	allele type	Depth	variant frequency	transcript_id	consequence	existing variation
ALK	snp	chr2	29432675	G	A	718.532	hom	25	1.00	NM_004304	synonymous_variant	
ALK	snp	chr2	29432727	T	A	179.575	het	19	0.58	NM_004304	missense_variant	
ALK	snp	chr2	29445458	G	T	1575.55	het	71	0.79	NM_004304	synonymous	rs3795850
CDH1	snp	chr16	68771372	C	T	6907.34	het	460	0.52	NM_004360	splice_regio	rs3743674
CDH1	snp	chr16	68842640	C	T	866.677	het	68	0.59	NM_004360	synonymous_variant	
CDH1	snp	chr16	68842662	C	T	2097.28	het	108	0.72	NM_004360	missense_variant	
CDH1	snp	chr16	68844159	G	A	895.469	het	52	0.63	NM_004360	synonymous_variant	
CDH1	snp	chr16	68853317	C	T	649.379	het	48	0.50	NM_004360	missense_variant	
CDKN2A	snp	chr9	21968199	C	G	21043.6	hom	663	1.00	NM_001195	3_prime_UT	rs11515&CO
CDKN2A	snp	chr9	21974818	C	T	350.421	het	20	0.75	NM_001195	synonymous_variant	
DDR2	snp	chr1	162740327	T	C	4274.89	hom	139	0.99	XM_005245	intron_varia	rs1780003
DDR2	snp	chr1	162743383	C	T	685.866	hom	24	1.00	XM_005245	missense_variant	
DDR2	snp	chr1	162743418	G	T	376.599	hom	16	1.00	XM_005245	intron_varia	rs1355287
EGFR	snp	chr7	55241727	G	A	933.69	hom	31	1.00	NM_005228	synonymous	rs55959834&
EGFR	snp	chr7	55259451	G	A	630.146	het	34	0.71	NM_005228	missense_variant	
ERBB3	snp	chr12	56477694	A	T	2142.61	het	99	0.81	NM_001982	splice_regio	rs2271194
ERBB4	snp	chr2	212578484	T	C	1048.3	het	72	0.53	NM_005235	intron_variant	
FGFR2	snp	chr10	123274695	T	A	350.564	hom	18	0.94	NM_022970	missense_variant	
FGFR3	snp	chr4	1803704	T	C	1562.32	het	83	0.69	NM_001163	synonymous	rs2234909&
FGFR3	snp	chr4	1805662	C	A	303.768	hom	13	1.00	NM_001163	intron_variant	
FGFR3	del	chr4	1806012	TGGGGGGG	TGGGGGGG	350.774	het	67	0.27	NM_001163	intron_variant&feature_t	
FGFR3	snp	chr4	1807894	G	A	607.581	hom	26	1.00	NM_001163	synonymous	rs7688609
GNA11	snp	chr19	3119006	C	T	4163.77	het	238	0.62	NM_002067	synonymous_variant	
H3F3A	snp	chr1	226252173	C	T	992.521	het	62	0.58	NM_002107	missense_variant	
IDH2	snp	chr15	90631933	C	T	4615.81	het	311	0.52	NM_002168	synonymous_variant	
KIT	snp	chr4	55599372	C	T	563.351	het	29	0.76	XM_005265	intron_variant	
MYCN	snp	chr2	16080157	C	G	722.148	hom	25	1.00	NM_005378	upstream_g	rs11886063

MYCN	snp	chr2	16085972	G	T	378.06	hom	18	1.00	NM_005378	missense_variant	
MYCN	snp	chr2	16089615	T	C	799.469	hom	29	1.00	NM_005378	downstream	rs4669018
NOTCH1	snp	chr9	139391595	G	A	2832.38	het	182	0.57	NM_017617	missense_variant	
NOTCH1	snp	chr9	139391636	G	A	813.393	hom	35	1.00	NM_017617	synonymous	rs2229974
NOTCH1	snp	chr9	139397870	C	T	1864.16	het	90	0.80	NM_017617	intron_variant	
NPM1	del	chr5	170837513	CTTTTTTTTT	CTTTTTTTTT	337.809	het	62	0.24	NM_002520	splice_region_variant&in	
PDGFRA	snp	chr4	55141055	A	G	1050.81	hom	35	1.00	NM_006206	synonymous	rs1873778&
PDGFRA	snp	chr4	55152040	C	T	4208.27	hom	150	0.99	NM_006206	synonymous	rs2228230&
PDGFRA	snp	chr4	55161517	A	G	874.327	hom	28	1.00	NM_006206	3_prime_UT	rs7680422
PIK3CA	snp	chr3	178951889	G	A	1392.98	het	84	0.58	NM_006218	missense_va	COSM14209
PIK3R1	snp	chr5	67589679	A	G	1474.53	hom	51	1.00	NM_181523	intron_variant	
PTEN	snp	chr10	89624188	T	C	32.8652	het	79	0.13	NM_000314	5_prime_UTR_variant	
RET	complex	chr10	43609004	GGGG	AGGA	297.237	het	44	0.30	NM_020975	missense_variant&splice_	
RET	snp	chr10	43609004	GGGG	GGGA	1354.8	het	95	0.52	NM_020975	missense_variant&splice_	
SMAD4	snp	chr18	48581322	C	T	926.99	hom	32	1.00	NM_005359	missense_variant	
SMAD4	complex	chr18	48604775	CTC	TTT	542.829	hom	20	1.00	NM_005359	missense_variant	
SMO	snp	chr7	128846328	G	C	517.065	hom	18	1.00	NM_005631	synonymous	rs2228617
SMO	del	chr7	128850245	CCAT	CT	434.779	het	54	0.33	NM_005631	frameshift_variant&featu	
SMO	snp	chr7	128850251	C	A	474.841	het	39	0.46	NM_005631	missense_va	COSM32652
STK11	snp	chr19	1207238	G	T	9829.05	hom	319	0.99	XM_005259	intron_varia	rs3764640
STK11	snp	chr19	1220321	T	C	9234.92	het	405	0.80	XM_005259	intron_varia	rs2075606
STK11	snp	chr19	1220368	G	A	3224.18	het	193	0.60	XM_005259	splice_regio	CS055618
TERT	snp	chr5	1295236	G	A	2530.55	het	123	0.74	NM_198253	upstream_gene_variant	
TP53	snp	chr17	7577407	A	C	947.998	het	48	0.67	NM_000546	intron_varia	rs12951053
TP53	snp	chr17	7577427	G	A	762.836	het	32	0.88	NM_000546	intron_varia	rs12947788
TP53	snp	chr17	7579472	G	C	511.448	het	25	0.84	NM_000546	missense_va	rs1042522&
TP53	snp	chr17	7579600	G	T	207.756	het	19	0.58	NM_000546	intron_variant	
TP53	del	chr17	7579651	CCTCCAGGT	CC	615.876	het	52	0.60	NM_000546	intron_variant&feature_t	