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Data Sheet

Product Name: CancerSeqPlus Paraffin Tissue Curl

Catalog No.: T2235248-SC **Lot No.: B906152**

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: 69 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:** _____

B906152

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
ERBB2	3.59	0.56	3.31E-03	ERBB2	4.22	0.11	1.04E-03
KRAS	10.89	1.72	2.72E-04	KRAS	5.59	0.12	1.61E-04

symbol	type	chromosome	position	reference	mutation	quality	allele type	Depth	variant frequency	transcript_id	consequence	existing variation
ALK	snp	chr2	29445458	GC	TC	3959.12	het	216	0.5972222	NM_004304	synonymous_variant	
ALK	mnp	chr2	29445458	GC	TT	105.734	het	87	0.137931	NM_004304	missense_variant	
APC	snp	chr5	112177171	G	A	745.541	hom	27	1	XM_005271	synonymous_variant	
ATM	del	chr11	108117897	ATTTTTTTTT	ATTTTTTTTT	317.406	het	61	0.2295082	NM_000051	intron_variant&feature_t	
CDH1	snp	chr16	68771372	C	T	16168.6	het	767	0.6805737	NM_004360	splice_region_variant&in	
CDK4	snp	chr12	58144665	C	T	547.562	hom	19	1	NM_000075	intron_variant	
CDKN2A	complex	chr9	21968199	CGAG	GGAA	282.664	het	21	0.5238095	NM_001195	3_prime_UTR_variant	
CDKN2A	snp	chr9	21968199	CGAG	GGAG	28880.7	hom	929	0.977395	NM_001195	3_prime_UTR_variant	
CTNNB1	del	chr3	41265953	CTTTTTTTTT	CTTTTTTTTA	5.26187	het	134	0.1119403	XM_005264	intron_varia	rs74712418
DDR2	snp	chr1	162740327	T	C	14635.8	hom	479	0.9812109	XM_005245	intron_varia	rs12468173
DDR2	snp	chr1	162743418	G	T	1772.11	hom	59	1	XM_005245	intron_variant	
EGFR	snp	chr7	55221655	G	A	251.959	het	17	0.7647059	NM_005228	intron_variant	
ERBB3	snp	chr12	56477694	A	T	8830.64	hom	299	0.9632107	NM_001982	splice_region_variant&in	
EZH2	snp	chr7	148508833	A	G	1897.41	hom	61	1	XM_005249	intron_variant	
FBXW7	del,del	chr4	153268227	CAAAAAAAA	CAAAAAAAA	761.634	het	120	0.2666667	NM_033632	splice_regio	rs6442267
FGFR3	snp	chr4	1805662	C	A	378.228	hom	17	1	NM_001163	intron_variant	
FGFR3	del	chr4	1806012	TGGGGGGG	TGGGGGGG	598.097	het	303	0.1551155	NM_001163	intron_variant&feature_t	
FGFR3	snp	chr4	1807894	G	A	4773.24	hom	159	0.9874214	NM_001163	synonymous_variant	
FGFR3	complex	chr4	1808889	GCCAGGA	TCCTGGC	314.382	het	13	0.9230769	NM_001163	missense_va	rs2878298
FGFR3	snp	chr4	1808901	C	G	301.841	het	13	0.9230769	NM_001163	missense_variant	
FGFR3	snp	chr4	1808902	C	G	275.314	het	14	0.8571429	NM_001163	synonymous_variant	
FLT3	snp	chr13	28610183	A	G	4203.12	het	172	0.9069767	NM_004119	splice_region_variant&in	
GNA11	snp	chr19	3119006	CGCC	TGCC	4125.8	het	495	0.3111111	NM_002067	synonymous_variant	
IDH1	del	chr2	209113048	GAAAAAAAA	GAAAAAAAA	249.048	het	47	0.2553191	XM_005246	intron_variant&feature_t	
IDH1	del	chr2	209116299	GAAAAAAAA	GAAAAAAAA	848.861	het	165	0.230303	XM_005246	intron_variant&feature_t	
JAK2	del	chr9	5073681	CTTTTTTTTT	CTTTTTTTTT	491.932	het	87	0.2413793	NM_004972	splice_regio	rs7685117
KDR	snp	chr4	55961159	T	C	1775.79	het	109	0.5412844	NM_002253	intron_variant	

KDR	ins	chr4	55962545	TGG	TGGG	1.22647	het	84	0.1309524	NM_002253	intron_variant&feature_e	
MAP2K1	snp	chr15	66727597	G	C	11765.9	het	571	0.6619965	NM_002755	intron_variant	
MET	snp	chr7	116436022	G	A	820.738	hom	27	1	XM_005250	synonymous_variant	
MET	snp	chr7	116436097	G	A	1953.41	hom	64	1	XM_005250	synonymous_variant	
MYC	snp	chr8	128748815	G	A	316.287	hom	16	0.9375	NM_002467	5_prime_UTR_variant	
MYCN	snp	chr2	16080157	C	G	1675.19	hom	53	1	NM_005378	upstream_g	rs2229974
MYCN	snp	chr2	16085972	G	T	358.753	het	40	0.475	NM_005378	missense_va	rs10521&CO
MYCN	snp	chr2	16089615	T	C	4886.72	hom	167	1	NM_005378	downstream_gene_varia	
NOTCH1	snp	chr9	139391636	G	A	3498.65	hom	136	0.9926471	NM_017617	synonymous_variant	
NOTCH1	snp	chr9	139397707	G	A	3859.39	hom	126	1	NM_017617	synonymous_variant	
NOTCH1	snp	chr9	139397870	C	T	1792.55	het	203	0.3300493	NM_017617	intron_variant	
NPM1	del,del	chr5	170837513	CTTTTTTTTT	CTTTTTTTTT	1045.48	2-Jan	108	0.287037	NM_002520	splice_region_variant&in	
PDGFRA	snp	chr4	55141055	A	G	11674.3	hom	377	1	NM_006206	synonymous	rs2271194
PDGFRA	snp	chr4	55152040	C	T	7208.67	het	381	0.656168	NM_006206	synonymous	rs2069502
PDGFRA	snp	chr4	55161391	T	C	714.377	hom	24	1	NM_006206	synonymous	rs2069502
PDGFRA	snp	chr4	55161517	A	G	2875.84	hom	95	0.9789474	NM_006206	3_prime_UT	rs2069502
PIK3CA	del	chr3	178927848	ATTTTTTTTT	ATTTTTTTTT	719.324	het	61	0.442623	NM_006218	intron_variant&feature_t	
PTEN	del	chr10	89720633	CTTTTTTTTT	CTTTTTTTTT	316.559	het	69	0.2608696	NM_000314	splice_acceptor_variant&	
PTEN	snp	chr10	89720907	T	G	469.071	het	37	0.5405405	NM_000314	intron_varia	rs11390827
PTEN	del	chr10	89725293	CTTTTTTTTT	CTTTTTTTTT	38.0551	het	113	0.1150442	NM_000314	3_prime_UT	rs11390827
RB1	snp	chr13	48919358	T	G	2708.95	hom	90	1	NM_000321	intron_variant	
RB1	snp	chr13	49033747	G	A	297.737	hom	11	1	NM_000321	intron_variant	
RB1	ins	chr13	49034022	ATT	ATTT	582.322	het	38	0.7105263	NM_000321	intron_varia	rs3743674
RB1	snp	chr13	49034105	C	T	257.035	hom	10	1	NM_000321	intron_variant	
RHOA	snp	chr3	49406080	T	C	280.396	hom	12	1	NM_001664	intron_variant	
SMAD4	complex	chr18	48604775	CTC	TTT	268.164	het	59	0.2372881	NM_005359	missense_variant	
STK11	snp	chr19	1207238	G	T	10323	het	448	0.7991071	XM_005259	intron_variant	
STK11	snp	chr19	1219451	C	G	209.276	het	43	0.3255814	XM_005259	intron_variant	
STK11	snp	chr19	1220321	T	C	10518.7	het	489	0.7198364	XM_005259	intron_variant	
TP53	snp	chr17	7577407	A	C	1592.19	het	76	0.7368421	NM_000546	intron_variant	
TP53	snp	chr17	7577427	G	A	1371.63	het	62	0.7903226	NM_000546	intron_varia	rs62097315
TP53	snp	chr17	7579472	G	C	3166.99	het	209	0.507177	NM_000546	missense_va	rs9748646
TP53	snp	chr17	7579638	C	T	391.316	het	67	0.2985075	NM_000546	intron_variant	
TP53	del	chr17	7579643	CCCCCAGCC	CC	619.702	het	185	0.2108108	NM_000546	intron_variant&feature_t	
TP53	del	chr17	7579651	CCTCCAGGT	CC	806.837	het	53	0.8301887	NM_000546	intron_variant&feature_t	
TP53	complex	chr17	7579668	CTCCAG	CAACCCTT	358.923	het	227	0.1718062	NM_000546	intron_varia	rs3764640
TP53	complex	chr17	7579678	CCAG	TTAC	209.9	het	250	0.164	NM_000546	intron_varia	rs369515604