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Data Sheet

Product Name: CancerSeqPlus Paraffin Tissue Curl

Catalog No.: T2235248-SC **Lot No.: B906149**

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:** _____

B906149

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	29445458	G	T	4097.48	hom	138	0.9710145	NM_004304	synonymous	rs3795850
APC	snp	chr5	112175770	G	A	254.485	het	16	0.75	XM_005271	synonymous	rs41115&CO
CDH1	snp	chr16	68771372	C	T	11120.7	het	508	0.7165354	NM_004360	splice_regio	rs3743674
CDKN2A	snp	chr9	21968199	C	G	29703.3	hom	939	0.9957401	NM_001195	3_prime_UT	rs11515&CO
CTNNB1	del	chr3	41265953	CTTTTTTTTT	CTTTTTTTTA	123.203	het	127	0.1338583	XM_005264	intron_variant&feature_t	
DDR2	snp	chr1	162740327	T	C	16986.9	hom	537	0.9944134	XM_005245	intron_varia	rs1780003
DDR2	snp	chr1	162743418	G	T	1220.29	hom	50	1	XM_005245	intron_varia	rs1355287
EGFR	snp	chr7	55221986	G	A	257.024	hom	11	1	NM_005228	intron_varia	rs41344849
ERBB3	snp	chr12	56477694	A	T	5806.43	het	258	0.7674419	NM_001982	splice_regio	rs2271194
ERBB4	snp	chr2	212578519	A	T	142.448	het	344	0.1133721	NM_005235	intron_varia	rs35123918
FBXW7	snp	chr4	153267968	A	G	435.766	hom	18	1	NM_033632	intron_varia	rs2714803
FBXW7	del,del	chr4	153268227	CAAAAAAAA	CAAAAAAAA	894.532	het	96	0.28125	NM_033632	splice_region_variant&in	
FGFR3	del	chr4	1806012	TGGGGGGG	TGGGGGGG	2802.68	het	717	0.1938633	NM_001163	intron_variant&feature_t	
FGFR3	snp	chr4	1807894	G	A	5606.19	hom	188	1	NM_001163	synonymous	rs7688609
FGFR3	complex	chr4	1808889	GCCAGGA	TCCTGGC	396.943	hom	14	1	NM_001163	missense_variant	
FGFR3	complex	chr4	1808900	CCC	CGGGG	325.634	hom	15	0.8666667	NM_001163	frameshift_variant&featu	
FLT3	snp	chr13	28610183	A	G	3857.68	het	191	0.7015707	NM_004119	splice_regio	rs2491231
FOXL2	complex	chr3	138665047	GCGGCGCCT	TCGGGGCCG	665.07	hom	24	1	NM_023067	missense_variant	
HRAS	snp	chr11	534197	C	T	3528.79	het	226	0.6106195	NM_005343	intron_varia	rs41258054
IDH1	del	chr2	209116299	GAAAAAAAA	GAAAAAAAA	524.914	het	154	0.1818182	XM_005246	intron_variant&feature_t	
JAK2	del	chr9	5073681	CTTTTTTTTT	CTTTTTTTTT	1028.92	het	65	0.5538462	NM_004972	splice_region_variant&in	
MAP2K1	complex	chr15	66727559	TGGTCAT	ATGACCA	339.743	hom	14	0.8571429	NM_002755	missense_variant	
MYCN	snp	chr2	16080157	C	G	2334.81	hom	76	0.9736842	NM_005378	upstream_g	rs11886063
MYCN	snp	chr2	16089615	T	C	3644.93	hom	125	0.984	NM_005378	downstream	rs4669018
NOTCH1	snp	chr9	139391685	C	T	180.747	het	12	0.8333333	NM_017617	missense_variant	
NOTCH1	snp	chr9	139397707	G	A	3012.89	het	161	0.6335404	NM_017617	synonymous	rs10521&CO
IDH1	snp	chr9	139399633	G	T	341.095	hom	13	1	NM_017617	intron_variant	
NPM1	del	chr5	170837513	CTTTTTTTTT	CTTTTTTTTT	708.245	het	86	0.3255814	NM_002520	splice_region_variant&in	
PDGFRA	complex	chr4	55141051	GCCCA	ACCCG	707.611	hom	32	0.8125	NM_006206	missense_variant	
PDGFRA	snp	chr4	55141051	GCCCA	GCCCG	6331.85	hom	236	0.8644068	NM_006206	synonymous_variant	
PDGFRA	snp	chr4	55161254	C	T	2430.65	hom	78	1	NM_006206	intron_varia	rs3733540
PDGFRA	snp	chr4	55161391	T	C	850.344	hom	30	1	NM_006206	synonymous	rs7685117
PDGFRA	snp	chr4	55161517	A	G	3147.1	hom	101	0.990099	NM_006206	3_prime_UT	rs7680422

PIK3CA	del	chr3	178927848	ATTTTTTTTT	ATTTTTTTTT	241.656	het	83	0.1807229	NM_006218	intron_variant&feature_t	
PTEN	del	chr10	89720633	CTTTTTTTTT	CTTTTTTTTT	377.151	het	86	0.2325581	NM_000314	splice_acceptor_variant&	
PTEN	snp	chr10	89720907	T	G	1098.7	het	55	0.8909091	NM_000314	intron_varia	rs555895&C
PTEN	del	chr10	89725293	CTTTTTTTTT	CTTTTTTTTT	134.928	het	89	0.1460674	NM_000314	3_prime_UTR_variant&fe	
RB1	snp	chr13	48919358	T	G	2548.41	hom	86	1	NM_000321	intron_varia	rs198617
RB1	ins	chr13	48953655	CAAAAAAAA	CAAAAAAAA	283.024	het	42	0.2857143	NM_000321	intron_variant&feature_e	
RB1	ins	chr13	49034022	ATT	ATTT	257.155	het	15	0.8666667	NM_000321	intron_variant&feature_e	
RET	snp	chr10	43610190	G	C	257.288	het	14	0.7857143	NM_020975	splice_region_variant&in	
RET	snp	chr10	43610191	G	T	292.348	het	12	0.9166667	NM_020975	splice_region_variant&in	
RET	mnp	chr10	43610198	CG	GA	631.071	hom	22	1	NM_020975	intron_variant	
RET	mnp,snp	chr10	43610198	CG	GA,CC	1034.5	het	38	0.5789474	NM_020975	intron_variant	
RET	mnp	chr10	43610200	GG	CC	414.002	het	41	0.3902439	NM_020975	intron_variant	
RET	complex	chr10	43610208	AAGATC	GATCTT	412.443	het	38	0.4210526	NM_020975	intron_variant	
RET	snp	chr10	43613843	G	T	3447.56	hom	112	0.9821429	NM_020975	synonymous	rs1800861&(
SMO	snp	chr7	128845277	G	C	6043.61	het	327	0.6330275	NM_005631	intron_varia	rs2075777
SMO	snp	chr7	128846328	G	C	3823.91	het	190	0.6736842	NM_005631	synonymous	rs2228617
STK11	snp	chr19	1222012	G	C	34254.4	het	1784	0.6261211	XM_005259	splice_regio	rs2075607
TP53	snp	chr17	7577298	G	A	363.919	hom	13	1	NM_000546	intron_variant	
TP53	snp	chr17	7579472	G	C	3036.53	het	156	0.6538462	NM_000546	missense_va	rs1042522&7
TP53	snp	chr17	7579563	C	T	1484.87	het	89	0.6067416	NM_000546	missense_va	TP53_g.1135
TP53	del	chr17	7579643	CCCCCAGCC	CC	632.914	het	152	0.2697368	NM_000546	intron_variant&feature_t	
TP53	complex	chr17	7579668	CTCCAG	CAACCCTT	505.143	het	151	0.2251656	NM_000546	intron_variant&feature_e	
TP53	complex	chr17	7579678	CCAG	TTAC	433.11	het	148	0.2364865	NM_000546	intron_variant	