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Tel: 1-888-762-2568 Fax: 1-510-783-5386 Email: info@biochain.com

Data Sheet

Product Name: CancerSeqPlus Paraffin Tissue Curl

Catalog No.: T2235248-SC **Lot No.:** B906151

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: 53 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: _____

B906151

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
AKT1	snp	chr14	105246686	G	A	232.906	het	20	0.6	NM_001014	intron_varia	rs2494738
ALK	snp	chr2	29445458	G	T	5957.9	hom	191	1	NM_004304	synonymous	rs3795850
APC	snp	chr5	112175770	G	A	330.767	hom	14	1	XM_005271	synonymous	rs41115&CO
APC	snp	chr5	112176325	G	A	351.561	hom	12	1	XM_005271	synonymous	rs42427
APC	snp	chr5	112176559	T	G	562.149	hom	21	0.952381	XM_005271	synonymous	rs866006
APC	snp	chr5	112177171	G	A	1888.95	hom	66	1	XM_005271	synonymous	rs465899
CDH1	snp	chr16	68771372	C	T	16120.8	hom	519	0.9980732	NM_004360	splice_regio	rs3743674
CDH1	ins	chr16	68771418	CG	CGCCCCAGC	171.447	het	12	0.8333333	NM_004360	intron_variant&feature_e	
CDH1	snp	chr16	68857441	T	C	1107.01	het	60	0.6333333	NM_004360	synonymous	rs1801552
CDKN2A	snp	chr9	21968199	C	G	31395.2	hom	1025	0.9863415	NM_001195	3_prime_UT	rs11515&CO
DDR2	snp	chr1	162740327	T	C	11346.7	hom	372	0.9946237	XM_005245	intron_varia	rs1780003
DDR2	snp	chr1	162743418	G	T	1494.38	hom	51	1	XM_005245	intron_varia	rs1355287
DDR2	snp	chr1	162749761	T	C	237.291	hom	10	1	XM_005245	intron_varia	rs1510315
ERBB3	snp	chr12	56477694	A	T	8842.57	hom	287	1	NM_001982	splice_regio	rs2271194
ERBB4	del	chr2	212530218	GAAAAAAAA	GAAAAAAAA	87.3532	het	96	0.125	NM_005235	intron_variant&feature_t	
ERBB4	snp	chr2	212812097	T	C	289.818	het	13	0.9230769	NM_005235	intron_varia	rs839541
ESR1	snp	chr6	152420095	G	A	6131.24	het	305	0.652459	XM_005266	synonymous	rs2228480&
EZH2	snp	chr7	148508833	A	G	1742.1	hom	56	1	XM_005249	intron_varia	rs2072407
FBXW7	del	chr4	153247486	CTTTTTTTTT	CTTTTTTTTT	255.336	het	74	0.1621622	NM_033632	intron_variant&feature_t	
FBXW7	snp	chr4	153252061	A	G	2412.3	het	149	0.5234899	NM_033632	intron_varia	rs10033601
FBXW7	del,del	chr4	153268227	CAAAAAAAA	CAAAAAAAA	1353.51	het	144	0.3125	NM_033632	splice_region_variant&in	
FGFR1	snp	chr8	38271362	T	A	343.343	hom	12	1	NM_001174	intron_variant	
FGFR1	mnp	chr8	38271371	CT	AG	343.343	hom	12	1	NM_001174	intron_variant	
FGFR1	complex	chr8	38271381	TGCGT	AGGGG	318.924	het	13	0.9230769	NM_001174	intron_variant	
FGFR3	snp	chr4	1805662	C	A	225.658	het	14	0.8571429	NM_001163	intron_variant	
FGFR3	del	chr4	1806012	TGGGGGGG	TGGGGGGG	1804.14	het	768	0.1510417	NM_001163	intron_variant&feature_t	
FGFR3	snp	chr4	1807894	G	A	9706.69	hom	320	0.996875	NM_001163	synonymous	rs7688609
FLT3	snp	chr13	28609991	T	C	278.039	hom	10	1	NM_004119	intron_varia	rs2491229
FLT3	snp	chr13	28609997	T	C	362.328	hom	13	1	NM_004119	intron_varia	rs2491230
FLT3	snp	chr13	28610183	A	G	6394.2	hom	211	1	NM_004119	splice_regio	rs2491231
FOXL2	complex	chr3	138664548	ACTGGTGGC	CCGCGCCCA	247.039	het	52	0.2692308	NM_023067	missense_variant	
IDH1	del	chr2	209116299	GAAAAAAAA	GAAAAAAAA	1628.84	het	191	0.3089005	XM_005246	intron_variant&feature_t	
JAK2	del	chr9	5073681	CTTTTTTTTT	CTTTTTTTTT	948.062	het	122	0.295082	NM_004972	splice_region_variant&in	

KDR	snp	chr4	55961159	T	C	2143.4	het	96	0.8229167	NM_002253	intron_varia	rs2219471
KDR	ins	chr4	55962545	TGG	TGGG	172.824	het	76	0.1710526	NM_002253	intron_variant&feature_e	
KDR	snp	chr4	55980239	C	T	353.69	hom	14	1	NM_002253	intron_varia	rs7692791
MYCN	snp	chr2	16080157	C	G	1865.77	hom	60	1	NM_005378	upstream_g	rs11886063
NOTCH1	snp	chr9	139391636	G	A	2564.78	hom	100	0.99	NM_017617	synonymous	rs2229974
NOTCH1	snp	chr9	139397707	G	A	10939.7	hom	356	1	NM_017617	synonymous	rs10521&CO
NOTCH1	complex	chr9	139399976	CGTCCTCCTC	AGTGCCAGG	414.894	hom	15	1	NM_017617	missense_variant	
NPM1	del	chr5	170837513	CTTTTTTTTT	CTTTTTTTTT	604.182	het	82	0.304878	NM_002520	splice_region_variant&in	
PDGFRA	snp	chr4	55141055	A	G	12221.4	hom	403	0.9950372	NM_006206	synonymous	rs1873778&
PDGFRA	snp	chr4	55161254	C	T	3057.53	hom	100	1	NM_006206	intron_varia	rs3733540
PDGFRA	snp	chr4	55161391	T	C	934.047	hom	31	1	NM_006206	synonymous	rs7685117
PDGFRA	snp	chr4	55161517	A	G	2581.73	hom	86	1	NM_006206	3_prime_UT	rs7680422
PIK3CA	del	chr3	178927848	ATTTTTTTTT	ATTTTTTTTT	353.291	het	69	0.2318841	NM_006218	intron_variant&feature_t	
PIK3CA	snp	chr3	178935957	A	G	722.744	het	40	0.625	NM_006218	intron_varia	rs3729686
PTEN	del	chr10	89720633	CTTTTTTTTT	CTTTTTTTTT	452.605	het	121	0.214876	NM_000314	splice_acceptor_variant&	
RB1	snp	chr13	48919358	T	G	1985.55	hom	65	1	NM_000321	intron_varia	rs198617
RB1	ins	chr13	48923061	GTTTTTTTTC	GTTTTTTTTT	1400.5	het	121	0.3966942	NM_000321	intron_variant&feature_e	
RB1	ins	chr13	48953655	CAAAAAAAA	CAAAAAAAA	513.788	het	64	0.3125	NM_000321	intron_variant&feature_e	
RB1	snp	chr13	49033747	G	A	723.322	hom	26	1	NM_000321	intron_varia	rs198580
RB1	snp	chr13	49034022	A	C	237.585	het	25	0.48	NM_000321	intron_variant	
RB1	ins	chr13	49034022	ATT	ATTT	421.7	het	22	0.7727273	NM_000321	intron_variant&feature_e	
RET	snp	chr10	43613843	G	T	2228.1	het	146	0.5	NM_020975	synonymous	rs1800861&
SMARCB1	snp	chr22	24145675	G	C	213.011	het	14	0.7142857	XM_005261	intron_varia	rs5751738
SMO	snp	chr7	128845277	G	C	4729.65	het	261	0.6091954	NM_005631	intron_varia	rs2075777
SMO	snp	chr7	128846328	G	C	2272.72	het	137	0.5474453	NM_005631	synonymous	rs2228617
STK11	snp	chr19	1207238	G	T	5550.35	hom	192	0.9739583	XM_005259	intron_varia	rs3764640
STK11	snp	chr19	1219444	C	G	194.776	het	31	0.3548387	XM_005259	intron_variant	
STK11	snp	chr19	1222012	G	C	19934.6	het	1109	0.5843102	XM_005259	splice_regio	rs2075607
TP53	snp	chr17	7577407	A	C	3406.22	hom	119	1	NM_000546	intron_varia	rs12951053
TP53	snp	chr17	7577427	G	A	4016.76	hom	144	0.9791667	NM_000546	intron_varia	rs12947788
TP53	snp	chr17	7578115	T	C	529.265	hom	20	1	NM_000546	intron_varia	rs1625895
TP53	del	chr17	7578262	CGG	CG	5923.33	het	428	0.4602804	NM_000546	frameshift_v	TP53_g.1265
TP53	del	chr17	7579643	CCCCCAGCC	CC	983.165	het	148	0.3175676	NM_000546	intron_variant&feature_t	
TP53	mnp	chr17	7579658	GT	CC	64.1978	het	142	0.1267606	NM_000546	intron_variant	
TP53	snp	chr17	7579668	C	T	212.913	het	34	0.2941176	NM_000546	intron_variant	
TP53	complex	chr17	7579668	CTCCAG	CAACCCTT	434.719	het	244	0.1762295	NM_000546	intron_variant&feature_e	
TP53	complex	chr17	7579678	CCAG	TTAC	494.217	het	243	0.2016461	NM_000546	intron_variant	
VHL	snp	chr3	10188428	T	G	707.284	hom	26	0.9615385	NM_000551	intron_varia	rs1678607