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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.: B906141**

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: 68 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:** _____

B906141

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
SMO	0.32	0.01	4.82E-03	SMO	0.55	0.01	1.64E-02

symbol	type	chromosome	position	reference	mutation	quality	allele type	Depth	variant frequency	transcript_id	consequence	existing variation
ALK	snp	chr2	29445458	G	T	2050.66	hom	65	1	NM_004304	synonymous_v	rs3795850
APC	snp	chr5	112177171	G	A	866.945	hom	33	1	XM_005271	synonymous_v	rs465899
CDH1	snp	chr16	68771372	C	T	9336.55	hom	313	0.9808307	NM_004360	splice_region_v	rs3743674
CDH1	ins	chr16	68771418	CG	CGCCCCAGC	305.474	het	13	0.9230769	NM_004360	intron_variant&feature_elo	
CDH1	snp	chr16	68857441	T	C	391.285	het	32	0.59375	NM_004360	synonymous_v	rs1801552
CDK4	snp	chr12	58143125	T	C	241.032	het	18	0.6666667	NM_000075	intron_variant	
CDKN2A	snp	chr9	21968199	C	G	4933.78	het	243	0.6748971	NM_001195	3_prime_UTR_	rs11515&CO
CDKN2A	snp	chr9	21971277	G	A	615.607	het	31	0.9354839	NM_001195	intron_variant	
DDR2	snp	chr1	162740327	T	C	5912.61	hom	195	0.9948718	XM_005245	intron_variant	rs1780003
DDR2	snp	chr1	162741794	C	T	898.175	het	54	0.5925926	XM_005245	intron_variant	rs3738807
DDR2	snp	chr1	162743418	G	T	793.835	hom	27	1	XM_005245	intron_variant	rs1355287
EGFR	snp	chr7	55242609	A	G	630.951	hom	27	1	NM_005228	intron_variant	rs2017000
ERBB2	del	chr17	37882959	TCC	TC	374.056	het	193	0.1761658	NM_004448	intron_variant&feature_trur	
ERBB2	ins	chr17	37882965	AGA	AGGA	482.863	het	142	0.2323944	NM_004448	intron_variant&feature_elo	
ERBB2	snp	chr17	37882973	G	C	95.5665	het	90	0.1555556	NM_004448	intron_variant	
FGFR1	snp	chr8	38271334	G	A	264.253	het	288	0.1319444	NM_001174	intron_variant	
FGFR3	del	chr4	1806012	TGGGGGGG	TGGGGGGG	188.777	het	297	0.1245791	NM_001163	intron_variant&feature_trur	
FGFR3	snp	chr4	1807894	G	A	2262.5	hom	74	1	NM_001163	synonymous_v	rs7688609
FLT3	snp	chr13	28610183	A	G	2235.94	hom	75	1	NM_004119	splice_region_v	rs2491231
HRAS	snp	chr11	534242	A	G	2472.99	hom	79	1	NM_005343	synonymous_v	rs12628&CM
HRAS	snp	chr11	534367	C	T	293.423	het	34	0.3529412	NM_005343	5_prime_UTR_variant	
HRAS	del	chr11	534403	GCCCAGGCC	GC	975.49	hom	36	1	NM_005343	intron_variant&feature_trur	
IDH1	del	chr2	209116299	GAAAAAAA	GAAAAAAA	331.896	het	82	0.2073171	XM_005246	intron_variant&feature_trur	
KDR	snp	chr4	55980239	C	T	326.263	hom	14	0.9285714	NM_002253	intron_variant	rs7692791
MYCN	snp	chr2	16080157	C	G	1134.35	hom	36	1	NM_005378	upstream_gene	rs11886063
MYCN	snp	chr2	16089615	T	C	1522.65	het	68	0.8382353	NM_005378	downstream_g	rs4669018
NOTCH1	snp	chr9	139391636	G	A	6123.11	hom	216	0.9907407	NM_017617	synonymous_v	rs2229974
NOTCH1	snp	chr9	139397707	G	A	3415.39	hom	114	1	NM_017617	synonymous_v	rs10521&CO

NPM1	del	chr5	170837513	CTTTTTTTTT	CTTTTTTTTT	327.562	het	29	0.4827586	NM_002520	splice_region_variant&intro	
PDGFRA	snp	chr4	55141055	A	G	3906.43	hom	129	0.9844961	NM_006206	synonymous_v	rs1873778&
PDGFRA	snp	chr4	55161254	C	T	563.989	hom	19	1	NM_006206	intron_variant	rs3733540
PDGFRA	snp	chr4	55161391	T	C	366.655	hom	12	1	NM_006206	synonymous_v	rs7685117
PDGFRA	snp	chr4	55161517	A	G	836.719	hom	27	1	NM_006206	3_prime_UTR_	rs7680422
PTEN	del	chr10	89720633	CTTTTTTTTT	CTTTTTTTTT	255.608	het	38	0.3421053	NM_000314	splice_acceptor_variant&int	
RB1	snp	chr13	48919358	T	G	901.176	hom	32	1	NM_000321	intron_variant	rs198617
RB1	snp	chr13	49027122	C	T	1798.95	het	86	0.7093023	NM_000321	splice_region_v	rs180742027
RB1	snp	chr13	49033747	G	A	237.291	hom	10	1	NM_000321	intron_variant	rs198580
RB1	ins	chr13	49034022	ATT	ATTT	336.602	hom	19	0.9473684	NM_000321	intron_variant&feature_elo	
RB1	snp	chr13	49034046	T	C	232.741	hom	10	1	NM_000321	intron_variant	
RET	snp	chr10	43613843	G	T	1585.01	hom	51	1	NM_020975	synonymous_v	rs1800861&
STK11	snp	chr19	1222012	G	C	14424.7	het	946	0.5031712	XM_005259	splice_region_v	rs2075607
STK11	snp	chr19	1222268	A	G	276.763	hom	12	1	XM_005259	intron_variant	rs60977562
TERT	snp	chr5	1295349	A	G	20779.2	hom	670	0.9791045	NM_198253	upstream_gene	rs2853669&
TP53	snp	chr17	7577407	A	C	388.109	het	17	0.8823529	NM_000546	intron_variant	rs12951053
TP53	snp	chr17	7577427	G	A	372.558	het	16	0.875	NM_000546	intron_variant	rs12947788
TP53	complex	chr17	7579668	CTCCAG	CAACCCTT	258.98	het	48	0.2916667	NM_000546	intron_variant&feature_elo	
TP53	complex	chr17	7579678	CCAG	TTAC	140.49	het	52	0.25	NM_000546	intron_variant	