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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.: B906155**

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: 40 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:** _____

B906155

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	3.39	0.16	2.97E-03	CDKN2A	3.92	0.06	1.32E-02
NOTCH1	2.76	0.17	4.42E-03	NOTCH1	4.16	0.07	2.46E-03

symbol	type	chromosome	position	reference	mutation	quality	allele type	Depth	variant frequency	transcript_id	consequence	existing variation
ABL1	complex	chr9	133736212	AGCTGACA	TCCTGGCGG	236.628	hom	11	0.9090909	NM_007313	intron_variant&feature_e	
ABL1	snp	chr9	133736221	T	A	321.543	hom	12	1	NM_007313	intron_variant	
ABL1	snp	chr9	133738147	C	T	1496.19	het	84	0.6666667	NM_007313	splice_region_variant&in	
ALK	snp	chr2	29445458	G	T	1324.37	het	63	0.7142857	NM_004304	synonymous	rs3795850
CCND1	snp	chr11	69461893	G	A	1257.89	het	66	0.7121212	NM_053056	intron_variant	
CCND1	snp	chr11	69465136	C	T	1021.86	hom	40	0.95	NM_053056	intron_variant	
CDH1	snp	chr16	68771372	C	T	4636.2	hom	145	1	NM_004360	splice_regio	rs3743674
CDH1	snp	chr16	68835640	G	A	773.264	het	57	0.5087719	NM_004360	synonymous_variant	
CDH1	snp	chr16	68849637	G	A	1012.56	het	68	0.5441176	NM_004360	missense_variant	
CDH1	snp	chr16	68856070	C	T	2310.11	het	96	0.9166667	NM_004360	synonymous_variant	
CDH1	snp	chr16	68857347	G	A	726.441	hom	36	0.9444444	NM_004360	missense_variant	
CDH1	snp	chr16	68857441	T	C	767.556	hom	33	1	NM_004360	synonymous	rs1801552
CDKN2A	snp	chr9	21968199	C	G	27040	hom	851	0.9964747	NM_001195	3_prime_UT	rs11515&CO
CDKN2A	snp	chr9	21974768	G	A	230.284	het	14	0.8571429	NM_001195	missense_va	COSM16481
CTNNB1	snp	chr3	41265943	A	G	362.544	het	22	0.6818182	XM_005264	intron_variant	
DDR2	snp	chr1	162740327	T	C	10190	hom	329	0.9969605	XM_005245	intron_varia	rs1780003
DDR2	mnp	chr1	162743381	TG	AT	396.513	het	29	0.5172414	XM_005245	missense_variant	
DDR2	snp	chr1	162743418	G	T	446.302	hom	19	0.9473684	XM_005245	intron_varia	rs1355287
EGFR	snp	chr7	55249016	C	T	929.702	het	61	0.5409836	NM_005228	missense_variant	
ERBB2	del	chr17	37871620	CTGT	CT	1590.76	het	168	0.3333333	NM_004448	intron_variant&feature_t	
ERBB3	snp	chr12	56477694	AGCC	TGCC	5773.47	hom	206	0.9029126	NM_001982	splice_region_variant&in	
ERBB3	complex	chr12	56477694	AGCC	TGCT	525.955	hom	20	0.95	NM_001982	splice_region_variant&in	
FBXW7	snp	chr4	153268194	G	A	3111.04	het	183	0.6502732	NM_033632	missense_variant	
FBXW7	del,del	chr4	153268227	CAAAAAAA	CAAAAAAA	716.44	2-Jan	94	0.2553191	NM_033632	splice_region_variant&in	
FBXW7	snp	chr4	153268254	G	A	4003.65	hom	151	0.9602649	NM_033632	intron_variant	
FGFR1	snp	chr8	38271575	T	A	346.693	hom	16	1	NM_001174	intron_variant	
FGFR1	del	chr8	38282180	CAA	CA	261.598	het	65	0.2153846	NM_001174	frameshift_variant&featu	

FGFR3	snp	chr4	1803636	G	A	12130.4	het	560	0.8553571	NM_001163	missense_variant	
FGFR3	snp	chr4	1806173	C	T	1678.41	hom	64	0.953125	NM_001163	synonymous_variant	
FLT3	snp	chr13	28610183	A	G	1644.71	het	77	0.7532468	NM_004119	splice_regio	rs2491231
FOXL2	snp	chr3	138664540	C	A	1406.36	hom	64	1	NM_023067	missense_va	rs372479512
FOXL2	mnp	chr3	138665192	CC	TT	716.832	het	49	0.5714286	NM_023067	missense_variant	
HRAS	del	chr11	534403	GCCCAGGCC	GC	1588.11	het	125	0.464	NM_005343	intron_variant&feature_t	
KIT	snp	chr4	55561688	A	G	1132.1	het	63	0.6666667	XM_005265	synonymous_variant	
KIT	snp	chr4	55561706	G	A	1641.04	hom	65	0.9384615	XM_005265	synonymous_variant	
MAP2K1	snp	chr15	66727597	G	C	3219.58	het	208	0.4951923	NM_002755	intron_varia	rs16949924
MYC	snp	chr8	128746465	G	T	706.015	het	53	0.490566	NM_002467	upstream_gene_variant	
MYC	snp	chr8	128748722	C	T	3719.87	het	209	0.6267943	NM_002467	5_prime_UTR_variant	
MYCN	snp	chr2	16080157	C	G	593.076	hom	19	1	NM_005378	upstream_g	rs11886063
NOTCH1	snp	chr9	139391456	C	T	1083.66	hom	43	0.9534884	NM_017617	synonymous_variant	
NOTCH1	snp	chr9	139391636	G	A	1499.22	hom	64	1	NM_017617	synonymous	rs2229974
NOTCH1	snp	chr9	139399856	T	A	934.686	het	70	0.6571429	NM_017617	stop_gained	
NOTCH1	snp	chr9	139400119	G	A	1641.91	het	118	0.5084746	NM_017617	missense_variant	
NOTCH1	snp	chr9	139400144	T	A	452.882	hom	20	1	NM_017617	missense_variant	
NPM1	del,del	chr5	170837513	CTTTTTTTTT	CTTTTTTTTT	921.561	2-Jan	52	0.3846154	NM_002520	splice_region_variant&in	
PDGFRA	snp	chr4	55161254	C	T	4025.97	hom	130	1	NM_006206	intron_varia	rs3733540
PDGFRA	snp	chr4	55161343	C	T	248.746	het	17	0.5882353	NM_006206	synonymous_variant	
PDGFRA	snp	chr4	55161517	A	G	2105.24	hom	67	1	NM_006206	3_prime_UT	rs7680422
RB1	ins	chr13	48953655	CAAAAAAAA	CAAAAAAAA	279.404	het	63	0.2222222	NM_000321	intron_variant&feature_e	
RET	snp	chr10	43609046	G	T	700.622	het	58	0.5689655	NM_020975	missense_variant	
RET	snp	chr10	43613843	G	T	3845.58	hom	123	0.9837398	NM_020975	synonymous	rs1800861&
SMO	snp	chr7	128845277	G	C	5340.38	hom	175	0.9771429	NM_005631	intron_varia	rs2075777
SMO	snp	chr7	128846328	G	C	605.3	hom	21	1	NM_005631	synonymous	rs2228617
SMO	snp	chr7	128851491	G	A	781.078	het	37	0.8378378	NM_005631	missense_variant	
STK11	snp	chr19	1207235	CGGG	CGGT	16042.5	hom	570	0.9210526	XM_005259	intron_variant	
STK11	complex	chr19	1207235	CGGG	TGGT	623.576	het	42	0.6190476	XM_005259	intron_variant	
STK11	snp	chr19	1218523	G	T	6829.43	het	339	0.7315634	XM_005259	intron_varia	rs2075604
STK11	ins	chr19	1219443	GCGGGGGC	GCGGGGGC	469.567	hom	19	1	XM_005259	intron_variant&feature_e	
STK11	snp	chr19	1220321	T	C	8585.49	hom	274	1	XM_005259	intron_varia	rs2075606
STK11	snp	chr19	1220399	G	A	1002.03	hom	40	0.95	XM_005259	synonymous_variant	
STK11	snp	chr19	1223064	G	A	1042.94	het	59	0.6610169	XM_005259	missense_variant	
TP53	snp	chr17	7573932	G	A	592.422	het	42	0.5238095	NM_000546	synonymous_variant	
TP53	snp	chr17	7577110	G	A	3393.74	het	143	0.9160839	NM_000546	synonymous	TP53_g.1380
TP53	snp	chr17	7578495	C	T	1273.54	het	61	0.8196721	NM_000546	synonymous	TP53_g.1242
TP53	complex	chr17	7579468	CACGG	TACGC	2061.71	hom	75	0.9733333	NM_000546	missense_variant	
TP53	complex,snp	chr17	7579468	CACGG	TACGC,CAC	6224.36	2-Jan	244	300	NM_000546	missense_variant	
TP53	complex,snp	chr17	7579468	CACGG	TACGC,CAC	6224.36	2-Jan	244	300	NM_000546	missense_variant	
TP53	del	chr17	7579643	CCCCCAGCC	CC	336.833	het	30	0.6	NM_000546	intron_variant&feature_t	

TP53	snp	chr17	7579706	G	A	514.12	hom	24	0.9583333	NM_000546	synonymous	rs37099229
TP53	snp	chr17	7590794	C	T	4662.86	hom	176	0.9659091	NM_000546	5_prime_UTR_variant	