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

Data Sheet

Product Name: CancerSeqPlus Paraffin Tissue Curl

Catalog No.: T2235265-SC **Lot No.: B906064**

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: Thyroid

Donor Information:

Male: 26 year(s) old
Female: _____ year(s) old

Pathological Diagnosis: Adenocarcinoma, papillary

Tumor Size: 6x4x4 cm

Location: Thyroid, right

Components:
1. **5 curls per package**
2. **Certificate of Analysis**

FOR IN VITRO RESEARCH USE ONLY **APPROVED BY:** _____

lot# B906064

For CNV mutations, we utilize stringent criteria to confirm copy number variations -- using normal tissues as controls. We may have samples

CNV against	Copy Number	STDev of Copy Number	P-value	CNV against adrenal	Copy Number	STDev of Copy	P-value
NOTCH1	3.14	0.14	1.37E-01	NOTCH1	5.56	0.07	7.28E-03

symbol	type	chromosome	position	reference	mutation	quality	allele type	Depth at this position	transcript_id	existing variation	consequence
AKT1	snp	chr14	105241536	G	A	3133.69	hom	139	NM_001014431.1		synonymous_varian
ALK	snp	chr2	29445458	G	T	1189.31	het	49	NM_004304.	rs3795850	synonymous_varian
APC	snp	chr5	112179987	C	T	239.456	het	14	XM_005271975.1		3_prime_UTR_varia
ATM	snp	chr11	108137981	G	A	445.02	het	31	NM_000051.3		synonymous_varian
CDH1	snp	chr16	68771372	C	T	1955.41	hom	77	NM_004360.	rs3743674	splice_region_varia
CDH1	snp	chr16	68857289	T	C	2254.83	het	116	NM_004360.	rs2276330	intron_variant
CDH1	snp	chr16	68862186	A	T	476.19	het	28	NM_004360.3		missense_variant
CDKN2A	snp	chr9	21968199	C	G	6259.7	hom	210	NM_001195	rs11515&CO	3_prime_UTR_varia
CDKN2A	complex	chr9	21974856	CCCCC	TCCCT	1345.91	het	81	NM_001195132.1		5_prime_UTR_varia
DDR2	snp	chr1	162740327	T	C	5019.72	hom	162	XM_0052452	rs1780003	intron_variant
DDR2	snp	chr1	162743340	C	T	1819.91	hom	69	XM_005245220.1		synonymous_varian
DDR2	snp	chr1	162743418	G	T	985.011	hom	43	XM_0052452	rs1355287	intron_variant
ERBB2	snp	chr17	37881331	C	T	534.387	het	33	NM_004448.	rs373165016	synonymous_varian
ERBB4	snp	chr2	212578519	A	T	1072.52	het	75	NM_005235.	rs35123918	intron_variant
FBXW7	snp	chr4	153258936	G	A	402.3	het	21	NM_033632.3		intron_variant
FBXW7	snp	chr4	153268197	G	A	1247.28	het	69	NM_033632.3		missense_variant
FBXW7	snp	chr4	153268240	A	G	208.808	het	13	NM_033632.3		intron_variant
FGFR1	snp	chr8	38272103	G	A	732.407	het	47	NM_001174067.1		synonymous_varian
FGFR3	snp	chr4	1805662	C	A	322.603	hom	14	NM_001163213.1		intron_variant
FOXL2	snp	chr3	138664989	G	A	966.27	het	56	NM_023067.	CD025235	synonymous_varian
FOXL2	snp	chr3	138665367	C	A	949.734	hom	44	NM_023067.3		synonymous_varian
GNAS	snp	chr20	57480447	G	A	386.453	het	25	NM_080425.2		missense_variant
GNAS	snp	chr20	57484289	C	T	317.27	het	17	NM_080425.2		intron_variant
HRAS	snp	chr11	534197	C	T	918.364	hom	35	NM_005343.	rs41258054	intron_variant

IDH1	del	chr2	209116299	GAAAAAAA	GAAAAAAA	179.377	het	65	XM_005246521.1	intron_variant&feat
MYC	complex	chr8	128746417	GGCGG	AGCGA	1149.66	het	56	NM_002467.4	upstream_gene_var
MYC	snp	chr8	128750868	C	T	989.961	het	62	NM_002467.4	synonymous_varian
MYCN	snp	chr2	16089615	T	C	449.621	hom	18	NM_005378. rs4669018	downstream_gene_
NOTCH1	snp	chr9	139391954	C	T	1879.58	het	142	NM_017617.3	synonymous_varian
NOTCH1	snp	chr9	139392005	C	T	1737.46	het	99	NM_017617.3	synonymous_varian
NOTCH1	snp	chr9	139397707	G	A	1279.07	hom	45	NM_017617. rs10521&CO	synonymous_varian
NOTCH1	snp	chr9	139399974	C	T	697.27	het	52	NM_017617.3	synonymous_varian
NPM1	del,del	chr5	170837513	CTTTTTTTTT	CTTTTTTTTT	847.638	het	54	NM_002520.6	splice_region_varia
PDGFRA	snp	chr4	55141055	A	G	1116.99	hom	38	NM_006206. rs1873778&C	synonymous_varian
PDGFRA	snp	chr4	55152081	G	A	430.314	het	25	NM_006206. COSM37840	missense_variant
PDGFRA	snp	chr4	55161254	C	T	444.71	hom	15	NM_006206. rs3733540	intron_variant
PIK3R1	snp	chr5	67591998	G	A	342.238	het	31	NM_181523.2	splice_acceptor_var
SMAD4	snp	chr18	48604815	C	T	975.44	het	55	NM_005359.5	missense_variant
SMARCB1	snp	chr22	24134007	G	A	631.071	hom	22	XM_0052617 CM085717&C	missense_variant
SMARCB1	snp	chr22	24145479	C	T	192.187	het	41	XM_005261718.1	splice_region_varia
SMO	complex	chr7	128845274	CCCG	TCCC	517.051	hom	19	NM_005631.4	intron_variant
SMO	snp	chr7	128846369	G	A	358.473	hom	13	NM_005631.4	missense_variant
SMO	snp	chr7	128851646	G	A	373.881	hom	16	NM_005631.4	intron_variant
SRC	snp	chr20	36031501	C	T	510.736	hom	18	NM_005417. rs2273677	intron_variant
STK11	snp	chr19	1207238	G	T	2077.35	hom	72	XM_0052596 rs3764640	intron_variant
STK11	snp	chr19	1218523	G	T	4682.6	het	226	XM_0052596 rs2075604	intron_variant
STK11	snp	chr19	1219352	G	A	926.99	hom	32	XM_005259617.1	missense_variant
STK11	snp	chr19	1220600	G	A	830.255	het	42	XM_0052596 rs370976710	synonymous_varian
STK11	snp	chr19	1223120	C	T	648.469	het	37	XM_005259617.1	missense_variant
STK11	snp	chr19	1226477	G	A	1351.08	het	63	XM_005259617.1	synonymous_varian
TP53	mnp	chr17	7577201	GG	AA	4894.4	het	578	NM_000546.5	intron_variant
TP53	snp	chr17	7578545	C	T	1328.81	het	82	NM_000546. TP53_g.1237	missense_variant
TP53	snp	chr17	7579472	G	C	2793.66	hom	94	NM_000546. rs1042522&T	missense_variant
VHL	snp	chr3	10183830	C	T	1245.53	het	66	NM_000551.3	missense_variant
VHL	snp	chr3	10183858	C	T	1296.94	het	68	NM_000551. COSM18120	synonymous_varian