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.: B906061**

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: 18 year(s) old
Female: _____ year(s) old

Pathological Diagnosis: Adenocarcinoma, papillary

Tumor Size: 4x4.5 cm

Location: Thyroid right lobe

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

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

lot# B906061

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 at this position	transcript_id	existing variation	consequence
AKT1	snp	chr14	105241542	G	A	363.268	het	32	NM_00101443	rs145780379&C	splice_region_var
ALK	snp	chr2	29445458	G	T	11525.6	hom	362	NM_004304.4	rs3795850	synonymous_vari
APC	snp	chr5	112177171	G	A	463.532	het	53	XM_005271975	rs465899	synonymous_vari
APC	snp	chr5	112178970	G	A	530.42	het	37	XM_005271975.1		missense_variant
ATM	del	chr11	108117897	ATTTTTTTTTT	ATTTTTTTTTA	70.8173	het	104	NM_000051.3		intron_variant&fe
ATM	snp	chr11	108119916	T	A	276.763	hom	12	NM_000051.3		intron_variant
BRAF	snp	chr7	140481572	T	A	580.916	hom	30	XM_005250045.1		intron_variant
C3P1	del	chr19	10152080	ATG	AG	313.953	hom	11	NR_027300.2		non_coding_exor
C3P1	snp	chr19	10152088	A	C	292.135	hom	11	NR_027300.2		non_coding_exor
CCNE1	complex	chr19	30303623	GGAG	AGAA	873.827	het	279	NM_001238.2		synonymous_vari
CCNE1	snp	chr19	30312636	A	G	4218.35	het	193	NM_001238.2	rs149261350	missense_variant
CDH1	snp	chr16	68771372	C	T	36720.2	hom	1153	NM_004360.3	rs3743674	splice_region_var
CDH1	snp	chr16	68772100	C	T	488.59	hom	17	NM_004360.3		intron_variant
CDH1	complex	chr16	68842645	GCCAA	ACCAACA	495.157	hom	20	NM_004360.3		frameshift_variar
CDH1	complex	chr16	68842652	AGCTGACAC/	GGGTGTGTC/	579.661	hom	22	NM_004360.3		missense_variant
CDH1	snp	chr16	68857441	T	C	921.026	hom	34	NM_004360.3	rs1801552	synonymous_vari
CDK4	snp	chr12	58145156	C	T	153.989	het	117	NM_000075.3	rs2270777	intron_variant
CDKN2A	snp	chr9	21968199	CGAG	GGAG	83969.4	hom	2756	NM_001195132.1		3_prime_UTR_va
CDKN2A	complex,m	chr9	21968199	CGAG	GGAT,GAAG	2584.39	het	102	NM_001195132.1		3_prime_UTR_va
DDR2	snp	chr1	162740327	T	C	27288.8	hom	872	XM_00524522(	rs1780003	intron_variant
DDR2	complex	chr1	162741908	AGG	GGC	297.554	het	53	XM_005245220.1		missense_variant
DDR2	complex	chr1	162741916	ACACATACTC	CTGAGTATGT	227.044	het	54	XM_005245220.1		missense_variant
DDR2	complex	chr1	162741933	GCC	CCT	79.0329	het	107	XM_005245220.1		missense_variant
DDR2	snp	chr1	162743418	G	T	1953.06	hom	78	XM_00524522(	rs1355287	intron_variant
DDR2	mnp	chr1	162745953	CC	TT	408.231	het	375	XM_005245220.1		stop_gained
EGFR	snp	chr7	55249063	G	A	5441.56	het	286	NM_005228.3	rs1050171&CM	synonymous_vari
ERBB2	snp	chr17	37881206	C	A	434.196	het	27	NM_004448.2		intron_variant
ERBB3	snp	chr12	56477694	AGCC	TGCC	23712.1	hom	773	NM_001982.3		splice_region_var
ERBB3	complex	chr12	56477694	AGCC	TGCT	321.572	hom	13	NM_001982.3		splice_region_var
EZH2	snp	chr7	148508833	A	G	1909.36	hom	63	XM_005249962	rs2072407	intron_variant
FBXW7	snp	chr4	153244215	G	A	654.321	hom	28	NM_033632.3		synonymous_vari

FBXW7	del	chr4	153247486	CTTTTTTTTTT	CTTTTTTTTTT	372.776	het	64	NM_033632.3		intron_variant&fe
FBXW7	snp	chr4	153252061	A	G	3524.27	het	185	NM_033632.3	rs10033601	intron_variant
FBXW7	mnp	chr4	153268068	TT	GC	214.728	het	109	NM_033632.3		intron_variant
FBXW7	del,del	chr4	153268227	CAAAAAAAA	CAAAAAAAA	2758.29	het	409	NM_033632.3		splice_region_var
FBXW7	snp	chr4	153268239	A	G	980.203	het	770	NM_033632.3		intron_variant
FBXW7	snp	chr4	153271110	A	C	2324.93	het	149	NM_033632.3	rs34708673	intron_variant
FGFR1	snp	chr8	38285988	T	A	1021.96	het	59	NM_001174067.1		intron_variant
FGFR3	snp	chr4	1805478	C	T	3362.06	het	178	NM_00116321	rs2305185	intron_variant
FGFR3	del	chr4	1806012	TGGGGGGGG	TGGGGGGGG	4501.19	het	1512	NM_001163213.1		intron_variant&fe
FGFR3	snp	chr4	1807894	G	A	16474.7	hom	544	NM_00116321	rs7688609	synonymous_vari
FLT3	snp	chr13	28610183	A	G	8395.97	hom	277	NM_004119.2	rs2491231	splice_region_var
IDH1	del	chr2	209116299	GAAAAAAAA	GAAAAAAAA	3361.23	het	438	XM_005246521.1		intron_variant&fe
JAK2	del	chr9	5073681	CTTTTTTTTT	CTTTTTTTTC	1121.01	het	110	NM_004972.3		splice_region_var
KDR	mnp	chr4	55962554	CC	TT	563.315	hom	28	NM_002253.2		intron_variant
KIT	snp	chr4	55593762	G	A	320.412	hom	16	XM_005265740.1		intron_variant
KIT	snp	chr4	55597450	C	T	237.51	het	17	XM_005265740.1		intron_variant
MET	snp	chr7	116340198	G	A	502.453	het	45	XM_005250353.1		missense_variant
MYC	snp	chr8	128752902	C	T	940.725	het	57	NM_002467.4		stop_gained
MYCN	snp	chr2	16080157	C	G	4115.87	hom	132	NM_005378.4	rs11886063	upstream_gene_v
MYCN	snp	chr2	16089615	T	C	9434.78	hom	323	NM_005378.4	rs4669018	downstream_gen
NOTCH1	snp	chr9	139391636	G	A	5094.46	hom	218	NM_017617.3	rs2229974	synonymous_vari
NOTCH1	snp	chr9	139397707	G	A	13594.5	hom	462	NM_017617.3	rs10521&COSM	synonymous_vari
NOTCH1	snp	chr9	139397893	T	A	323.51	hom	14	NM_017617.3		intron_variant
NPM1	del	chr5	170837513	CTTTTTTTTT	CTTTTTTTTT	2084.16	het	269	NM_002520.6		splice_region_var
PDGFRA	snp	chr4	55141055	A	G	17940.9	hom	587	NM_006206.4	rs1873778&CO	synonymous_vari
PDGFRA	snp	chr4	55144715	T	A	486.208	hom	21	NM_006206.4		intron_variant
PDGFRA	snp	chr4	55161254	C	T	7454.92	hom	237	NM_006206.4	rs3733540	intron_variant
PDGFRA	snp	chr4	55161391	T	C	521.925	hom	18	NM_006206.4	rs7685117	synonymous_vari
PDGFRA	snp	chr4	55161517	A	G	5628.5	hom	179	NM_006206.4	rs7680422	3_prime_UTR_va
PIK3CA	del	chr3	178927848	ATTTTTTTTT	ATTTTTTTTT	290.71	het	60	NM_006218.2		intron_variant&fe
PIK3CA	snp	chr3	178947890	T	A	305.846	het	23	NM_006218.2		missense_variant
PIK3R1	snp	chr5	67589770	T	A	222.068	het	17	NM_181523.2		intron_variant
PLCD3	snp	chr17	43198634	T	C	331.807	hom	13	NM_133373.3		missense_variant
PTEN	del	chr10	89692731	GTTTTTTTTC	GTTTTTTTC	199.485	het	96	NM_000314.4		intron_variant&fe
PTEN	snp	chr10	89693076	T	A	511.246	hom	23	NM_000314.4		intron_variant
PTEN	ins	chr10	89711927	TAAAGAATCA	TAAAGAATCA	401.733	het	70	NM_000314.4		frameshift_variar
PTEN	del	chr10	89720633	CTTTTTTTTT	CTTTTTTTTT	1277.93	het	214	NM_000314.4		splice_acceptor_v
PTEN	snp	chr10	89725256	C	T	330.026	het	207	NM_000314.4		3_prime_UTR_va
PTEN	del	chr10	89725293	CTTTTTTTTT	CTTTTTTTTT	614.643	het	249	NM_000314.4		3_prime_UTR_va
PTPN11	complex	chr12	112888121	GAAG	AAAA	382.761	het	134	NM_002834.3		splice_acceptor_v
RB1	snp	chr13	48919358	T	G	3208.02	hom	109	NM_000321.2	rs198617	intron_variant

RB1	snp	chr13	48953543	G	A	506.05	het	36	NM_000321.2		intron_variant
RB1	ins	chr13	48953655	CAAAAAAAA	CAAAAAAAA	218.254	het	65	NM_000321.2		intron_variant&fe
RET	snp	chr10	43610189	G	T	294.862	hom	11	NM_020975.4		splice_region_var
RET	mnp	chr10	43610190	GG	CT	299.299	het	13	NM_020975.4		splice_region_var
RET	mnp	chr10	43610199	GGG	CCC	325.889	hom	14	NM_020975.4		intron_variant
RET	snp	chr10	43610281	G	A	566.788	hom	27	NM_020975.4		intron_variant
RET	complex	chr10	43615494	CATGGC	GAGGGT	383.161	hom	15	NM_020975.4		intron_variant
RET	snp	chr10	43615633	C	G	2308.92	het	143	NM_020975.4	rs1800863&CM	synonymous_vari
RET	snp	chr10	43617518	A	T	39694.4	het	2355	NM_020975.4	rs3026772	intron_variant
RET	snp	chr10	43617564	T	A	246.793	het	18	NM_020975.4		intron_variant
SMAD4	snp	chr18	48592049	T	A	300.137	hom	13	NM_005359.5		intron_variant
SMO	snp	chr7	128845277	GGGG	CGGG	22804.2	hom	757	NM_005631.4		intron_variant
SMO	complex,co	chr7	128845277	GGGG	CGTG,CGGA	519.855	het	23	NM_005631.4		intron_variant
SMO	snp	chr7	128845316	G	A	229.101	hom	10	NM_005631.4		intron_variant
SMO	snp	chr7	128846328	G	C	6791.94	hom	220	NM_005631.4	rs2228617	synonymous_vari
SMO	complex	chr7	128850391	TGGGCA	AGGGGC	419.46	hom	17	NM_005631.4		splice_donor_var
SMO	snp	chr7	128850401	A	T	401.529	hom	16	NM_005631.4		intron_variant
SMO	complex	chr7	128850406	GCCCCT	TGCCCA	472.285	hom	17	NM_005631.4		intron_variant
SMO	complex	chr7	128850427	TCAC	AGAGC	329.248	het	31	NM_005631.4		intron_variant&fe
SRC	snp	chr20	36031501	C	T	12171	het	683	NM_005417.4	rs2273677	intron_variant
STK11	snp	chr19	1207238	G	T	14634.4	het	1088	XM_005259617	rs3764640	intron_variant
STK11	ins	chr19	1219443	GCGGGGGCC	GCGGGGGCC	416.01	het	52	XM_005259617.1		intron_variant&fe
STK11	snp	chr19	1219451	C	G	90.0063	het	84	XM_005259617	rs369515604	intron_variant
TP53	snp	chr17	7573918	G	C	447.916	hom	16	NM_000546.5		intron_variant
TP53	mnp	chr17	7573925	ACCTG	CAGGT	433.416	hom	16	NM_000546.5		splice_donor_var
TP53	snp	chr17	7579472	G	C	15127.7	hom	492	NM_000546.5	rs1042522&TP5	missense_variant
TP53	del	chr17	7579643	CCCCCAGCCC	CC	1006.99	het	295	NM_000546.5		intron_variant&fe
TP53	complex	chr17	7579668	CTCCAG	CAACCCTT	1004.11	het	324	NM_000546.5		intron_variant&fe
TP53	complex	chr17	7579678	CCAG	TTAC	609.231	het	402	NM_000546.5		intron_variant
TP53	snp	chr17	7579801	G	C	3486.65	hom	121	NM_000546.5	rs1642785	intron_variant
TP53	snp	chr17	7590628	C	T	339.443	hom	16	NM_000546.5		intron_variant
VHL	mnp	chr3	10183657	GTC	AGA	372.45	hom	14	NM_000551.3		missense_variant
VHL	mnp	chr3	10183664	CC	GG	367.831	hom	15	NM_000551.3		missense_variant
VHL	mnp	chr3	10183672	ACT	GTC	326.401	hom	13	NM_000551.3		missense_variant