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.: B906060**

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: _____ year(s) old
Female: 46 year(s) old

Pathological Diagnosis: Adenocarcinoma, papillary

Tumor Size: N/A

Location: Thyroid

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

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

lot# B906060

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
ABL1	snp	chr9	133738293	C	T	373.906	hom	18	NM_007313.2		synonymous_variant
AKT1	complex	chr14	105241302	CAG	AAGTG	256.852	het	21	NM_001014431.1		frameshift_variant&featu
AKT1	snp	chr14	105246387	C	T	985.927	het	51	NM_00101443	rs36770138(	intron_variant
ALK	snp	chr2	29445458	G	T	4164.95	hom	135	NM_004304.4	rs3795850	synonymous_variant
APC	snp	chr5	112175010	G	A	221.525	het	15	XM_005271975.1		missense_variant
APC	snp	chr5	112175770	G	A	879.892	hom	38	XM_00527197	rs41115&CO	synonymous_variant
APC	snp	chr5	112176559	T	G	569.367	hom	20	XM_00527197	rs866006	synonymous_variant
APC	snp	chr5	112177171	G	A	1211.45	hom	42	XM_00527197	rs465899	synonymous_variant
ATM	del	chr11	108117897	ATTTTTTT	ATTTTTTT	429.388	het	150	NM_000051.3		intron_variant&feature_t
ATM	snp	chr11	108170573	T	G	441.369	het	28	NM_000051.3		missense_variant
AURKA	complex	chr20	54963147	CCC	CAATTTA	329.562	het	38	NM_003600.2		intron_variant&feature_e
CCND1	del	chr11	69461849	TCC	TC	131.465	het	445	NM_053056.2		intron_variant&feature_t
CDH1	snp	chr16	68771372	C	T	15440.6	het	908	NM_004360.3	rs3743674	splice_region_variant&int
CDH1	ins	chr16	68771418	CG	CGCCCCAC	370.05	het	116	NM_004360.3		intron_variant&feature_e
CDH1	snp	chr16	68857441	T	C	680.089	het	48	NM_004360.3	rs1801552	synonymous_variant
CDKN2A	mnp	chr9	21965622	GC	CA	1278.8	het	171	NM_001195132.1		downstream_gene_varian
CDKN2A	complex	chr9	21965628	CCCGAGGC	GCCTCGGC	1296.7	het	188	NM_001195132.1		downstream_gene_varian
CDKN2A	snp	chr9	21968198	CC	CG	60636.5	hom	1970	NM_001195132.1		3_prime_UTR_variant
CDKN2A	mnp	chr9	21968198	CC	TG	733.162	hom	28	NM_001195132.1		3_prime_UTR_variant
CDKN2A	snp	chr9	21968366	G	A	535.93	het	34	NM_001195132.1		intron_variant
DDR2	snp	chr1	162740327	T	C	22033.4	hom	713	XM_00524522	rs1780003	intron_variant
DDR2	mnp	chr1	162741973	TGG	GTT	278.596	hom	13	XM_005245220.1		stop_gained
DDR2	complex	chr1	162741983	CCCCAGGA	TCCTGGGC	395.353	hom	16	XM_005245220.1		missense_variant
DDR2	snp	chr1	162743418	G	T	3020.13	hom	114	XM_00524522	rs1355287	intron_variant
ERBB2	snp	chr17	37880345	G	A	280.396	hom	12	NM_004448.2		intron_variant
ERBB2	complex	chr17	37882993	TATGCC	CATGC	398.039	het	26	NM_004448.2		intron_variant&feature_t
ERBB2	complex	chr17	37883001	GCC	CCTTC	405.128	het	26	NM_004448.2		intron_variant&feature_e
ERBB2	complex	chr17	37883005	CTCACGGA	GTGAGGG	168.596	het	27	NM_004448.2		intron_variant&feature_t
ERBB2	snp	chr17	37883022	G	A	462.936	het	28	NM_004448.2	rs371178334	intron_variant
ERBB2	snp	chr17	37883027	G	A	514.12	hom	24	NM_004448.2		intron_variant
ERBB3	snp	chr12	56477694	AGCCC	TGCCC	7169.6	hom	268	NM_001982.3		splice_region_variant&int
ERBB3	complex	chr12	56477694	AGCCC	TGCCT	605.361	hom	24	NM_001982.3		splice_region_variant&int

ERBB4	del,del	chr2	212578379	TAAAAAA	TAAAAAA	345.172	het	43	NM_005235.2		splice_region_variant&int
ERBB4	del,del	chr2	212578379	TAAAAAA	TAAAAAA	345.172	het	43	NM_005235.2		splice_region_variant&int
EZH2	snp	chr7	148508833	A	G	1136.45	hom	38	XM_00524996	rs2072407	intron_variant
FBXW7	snp	chr4	153267968	A	G	319.882	hom	14	NM_033632.3	rs2714803	intron_variant
FBXW7	del,del	chr4	153268227	CAAAAAA	CAAAAAA	803.451	2-Jan	144	NM_033632.3		splice_region_variant&int
FBXW7	del,del	chr4	153268227	CAAAAAA	CAAAAAA	803.451	2-Jan	144	NM_033632.3		splice_region_variant&int
FGFR3	mnp	chr4	1805996	AT	TC	781.246	het	43	NM_001163213.1		intron_variant
FGFR3	mnp	chr4	1806004	GA	AT	757.345	het	42	NM_001163213.1		intron_variant
FGFR3	mnp	chr4	1806011	GT	TG	615.641	het	34	NM_001163213.1		intron_variant
FGFR3	del	chr4	1806012	TGGGGGG	TGGGGGG	1314.32	het	542	NM_001163213.1		intron_variant&feature_t
FGFR3	snp	chr4	1807894	G	A	7634.96	hom	273	NM_00116321	rs7688609	synonymous_variant
FGFR3	complex	chr4	1808431	TCCACTGG	ACCCCTGA	220.648	het	110	NM_001163213.1		intron_variant&feature_e
FGFR3	complex	chr4	1808440	TCCT	ACCCAGTC	182.113	het	108	NM_001163213.1		intron_variant&feature_e
FLT3	snp	chr13	28592777	G	A	724.429	hom	31	NM_004119.2	rs377040701	intron_variant
FLT3	snp	chr13	28610183	A	G	3657.19	het	216	NM_004119.2	rs2491231	splice_region_variant&int
FLT3	snp	chr13	28610213	G	A	222.344	het	18	NM_004119.2		intron_variant
FOXL2	complex	chr3	138664543	GGCGC	CGCGCCC	226.617	het	150	NM_023067.3		frameshift_variant&featu
FOXL2	complex	chr3	138664550	TGGTGGG	CAGTGCG	350.077	het	143	NM_023067.3		frameshift_variant&featu
HNF1A	snp	chr12	121432113	G	A	494.864	hom	20	XM_005253931.1		missense_variant
HRAS	snp	chr11	534197	C	T	4625.18	hom	175	NM_005343.2	rs41258054	intron_variant
IDH1	del	chr2	209116299	GAAAAAA	GAAAAAA	1663.03	het	227	XM_005246521.1		intron_variant&feature_t
JAK2	del	chr9	5073681	CTTTTTTT	CTTTTTTT	446.616	het	47	NM_004972.3		splice_region_variant&int
JAK3	snp	chr19	17947914	G	A	1084.99	het	67	XM_005259896.1		intron_variant
JAK3	ins	chr19	17948116	CTGG	CTGTGG	630.237	het	62	XM_005259896.1		intron_variant&feature_e
JAK3	complex	chr19	17948123	CAGGTCA	GGTGTTC	688.665	het	67	XM_005259896.1		intron_variant
KDR	mnp	chr4	55962412	GG	AA	545.292	het	511	NM_002253.2		missense_variant
KRAS	snp	chr12	25380448	G	A	473.454	het	39	NM_033360.2		intron_variant
MAP2K1	complex	chr15	66727559	TGGTCAT	ATGACCA	631.153	hom	23	NM_002755.3		missense_variant
MDM2	snp	chr12	69210628	C	T	773.783	het	37	NM_002392.5		stop_gained
MPL	complex	chr1	43814885	CGGGGCT	TCAGACTT	171.037	het	12	NM_005373.2		intron_variant
MYC	mnp	chr8	128748681	CC	TT	2493.99	het	399	NM_002467.4		5_prime_UTR_variant
MYCN	complex	chr2	16080153	ACTAC	TCTAG	372.45	hom	14	NM_005378.4		upstream_gene_variant
MYCN	complex,s	chr2	16080153	ACTAC	TCTAG,AC	936.834	2-Jan	34	NM_005378.4		upstream_gene_variant
MYCN	complex,s	chr2	16080153	ACTAC	TCTAG,AC	936.834	2-Jan	34	NM_005378.4		upstream_gene_variant
MYCN	snp	chr2	16089615	T	C	4535.97	hom	167	NM_005378.4	rs4669018	downstream_gene_varian
NOTCH1	mnp	chr9	139390571	GG	CC	265.202	het	13	NM_017617.3		missense_variant
NOTCH1	snp	chr9	139390755	G	A	218.181	hom	10	NM_017617.3		missense_variant
NOTCH1	snp	chr9	139390840	G	A	241.688	het	17	NM_017617.3		synonymous_variant
NOTCH1	snp	chr9	139391636	G	A	5779.84	hom	251	NM_017617.3	rs2229974	synonymous_variant
NOTCH1	snp	chr9	139397707	G	A	6029.02	hom	201	NM_017617.3	rs10521&CO	synonymous_variant
NOTCH1	snp	chr9	139397893	T	A	350.318	hom	16	NM_017617.3		intron_variant

NPM1	del	chr5	170837513	CTTTTTTT	CTTTTTTT	1470.89	het	209	NM_002520.6		splice_region_variant&int
PDGFRA	snp	chr4	55141052	CCCA	CCCG	14131.7	hom	495	NM_006206.4		synonymous_variant
PDGFRA	complex	chr4	55141052	CCCA	TCCG	329.919	hom	16	NM_006206.4		synonymous_variant
PDGFRA	snp	chr4	55161254	C	T	3927.75	hom	133	NM_006206.4	rs3733540	intron_variant
PDGFRA	snp	chr4	55161391	T	C	1565.73	hom	53	NM_006206.4	rs7685117	synonymous_variant
PDGFRA	snp	chr4	55161517	A	G	2857.89	hom	95	NM_006206.4	rs7680422	3_prime_UTR_variant
PIK3CA	del	chr3	178927848	ATTTTTTT	ATTTTTTT	598.252	het	86	NM_006218.2		intron_variant&feature_t
PIK3CA	snp	chr3	178938891	G	A	208.044	het	35	NM_006218.2		synonymous_variant
PIK3R1	snp	chr5	67589155	C	T	225.451	het	15	NM_181523.2		synonymous_variant
PTEN	complex	chr10	89624247	GATCG	AATCA	545.666	het	134	NM_000314.4		missense_variant
PTEN	del	chr10	89720633	CTTTTTTT	CTTTTTTT	786.122	het	160	NM_000314.4		splice_acceptor_variant&i
PTEN	snp	chr10	89720907	T	G	741.373	hom	30	NM_000314.4	rs555895&C	intron_variant
PTEN	del	chr10	89725293	CTTTTTTT	CTTTTTTT	1041.3	het	200	NM_000314.4		3_prime_UTR_variant&fea
RB1	snp	chr13	48919358	T	G	5277.43	hom	181	NM_000321.2	rs198617	intron_variant
RB1	ins	chr13	48953655	CAAAAAA	CAAAAAA	447.102	het	72	NM_000321.2		intron_variant&feature_e
RB1	ins	chr13	49034022	ATT	ATTT	634.936	het	29	NM_000321.2		intron_variant&feature_e
RB1	del	chr13	49034085	CTTTTC	CTTTC	238.352	hom	12	NM_000321.2		intron_variant&feature_t
RB1	snp	chr13	49034099	C	T	230.011	hom	10	NM_000321.2		intron_variant
RET	mnp	chr10	43610198	CG	GA	974.178	hom	34	NM_020975.4		intron_variant
RET	complex	chr10	43610208	AAGATC	GATCTT	968.098	hom	39	NM_020975.4		intron_variant
RET	snp	chr10	43617324	C	T	274.058	het	19	NM_020975.4		intron_variant
SMAD4	snp	chr18	48575275	G	A	260.66	hom	11	NM_005359.5		intron_variant
SMAD4	complex	chr18	48584716	CTACC	TTACT	553.7	het	278	NM_005359.5		missense_variant
SMO	snp	chr7	128845277	G	C	8544.36	hom	284	NM_005631.4	rs2075777	intron_variant
SMO	snp	chr7	128846328	G	C	6250.6	hom	202	NM_005631.4	rs2228617	synonymous_variant
STK11	ins	chr19	1219443	GCGGGGG	GCGGGGG	440.275	het	42	XM_005259617.1		intron_variant&feature_e
STK11	snp	chr19	1219444	C	G	149.645	het	64	XM_005259617.1		intron_variant
STK11	snp	chr19	1222012	G	C	38926.6	het	2322	XM_00525961	rs2075607	splice_region_variant&int
STK11	snp	chr19	1223222	C	A	247.491	hom	13	XM_005259617.1		intron_variant
STK11	complex	chr19	1226569	CGGGCCC	CTTGCGG	405.823	hom	19	XM_005259617.1		inframe_insertion
STK11	snp	chr19	1226588	G	T	476.883	hom	19	XM_005259617.1		synonymous_variant
TP53	snp	chr17	7573080	C	A	747.484	hom	35	NM_000546.5		intron_variant
TP53	snp	chr17	7579472	G	C	14735	hom	481	NM_000546.5	rs1042522&	missense_variant
TP53	del	chr17	7579643	CCCCCAG	CC	469.723	het	144	NM_000546.5		intron_variant&feature_t
TP53	mnp	chr17	7579658	GT	CC	333.483	het	191	NM_000546.5		intron_variant
TP53	snp	chr17	7579801	G	C	1687.2	hom	62	NM_000546.5	rs1642785	intron_variant
TP53	mnp	chr17	7580062	TGGAG	CTCCA	1173.66	het	61	NM_000546.5		intron_variant
TP53	snp	chr17	7580073	A	G	1324.82	hom	57	NM_000546.5		intron_variant