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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.: T2235265-SC **Lot No.: B906057**

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: 35 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 # B906057

symbol	type	chromosome	position	reference	mutation	quality score	allele type	Depth at this position	transcript_id	existing variation	consequence
ALK	snp	chr2	29445458	G	T	2702.47	hom	87	NM_004304.4	rs3795850	synonymous_variant
APC	snp	chr5	112174714	C	T	439.518	het	29	XM_005271975.1		synonymous_variant
APC	snp	chr5	112177171	G	A	423.28	het	30	XM_005271975.	rs465899	synonymous_variant
ATM	snp	chr11	108180928	A	G	321.884	het	21	NM_000051.3		missense_variant
CCND1	snp	chr11	69465102	G	A	875.601	hom	37	NM_053056.2		intron_variant
CCNE1	complex	chr19	30303985	CCC	TCT	311.993	het	41	NM_001238.2		intron_variant
CDH1	snp	chr16	68857473	C	T	202.211	het	20	NM_004360.3		missense_variant
CDH1	snp	chr16	68862081	G	A	1101.42	het	65	NM_004360.3		synonymous_variant
CDH1	snp	chr16	68867402	G	A	3249.08	het	168	NM_004360.3	rs67389265	stop_retained_variant
CDKN2A	snp	chr9	21968199	C	G	28317.8	hom	895	NM_001195132	rs11515&COS	3_prime_UTR_variant
CDKN2A	snp	chr9	21971194	C	T	2042	het	127	NM_001195132	COSM13602	missense_variant
CDKN2A	complex	chr9	21971207	CCTGC	TCTGT	1988.61	het	181	NM_001195132.1		splice_acceptor_variant&c
DDR2	snp	chr1	162740327	T	C	4168.49	hom	136	XM_005245220.	rs1780003	intron_variant
DDR2	snp	chr1	162743418	G	T	693.833	hom	30	XM_005245220.	rs1355287	intron_variant
EGFR	snp	chr7	55242582	G	A	260.66	hom	11	NM_005228.3	rs17337135	intron_variant
ERBB2	del	chr17	37882959	TCC	TC	542.198	het	94	NM_004448.2		intron_variant&feature_tr
ERBB2	ins	chr17	37882965	AGA	AGGA	307.285	hom	27	NM_004448.2		intron_variant&feature_el
ERBB2	complex	chr17	37882972	GGGAAGG	GCTCTTAC	441.616	hom	26	NM_004448.2		intron_variant&feature_el
ERBB3	snp	chr12	56477694	A	T	5471.71	het	272	NM_001982.3	rs2271194	splice_region_variant&intr
ERBB4	snp	chr2	212578519	A	T	1519.32	het	210	NM_005235.2	rs35123918	intron_variant
EZH2	snp	chr7	148508833	A	G	670.169	hom	22	XM_005249962.	rs2072407	intron_variant
FBXW7	snp	chr4	153250968	G	A	1783.78	het	82	NM_033632.3		intron_variant
FBXW7	snp	chr4	153251907	G	A	262.663	het	24	NM_033632.3	COSM22964&	stop_gained
FBXW7	snp	chr4	153252037	C	T	267.56	het	21	NM_033632.3		intron_variant
FBXW7	del,del	chr4	153268227	CAAAAAA	CAAAAAA	686.364	het	99	NM_033632.3		splice_region_variant&intr
FBXW7	snp	chr4	153273817	C	T	407.21	het	31	NM_033632.3		intron_variant
FGFR3	del	chr4	1806012	TGGGGGG	TGGGGGG	659.847	het	333	NM_001163213.1		intron_variant&feature_tr
FGFR3	snp	chr4	1807894	G	A	782.769	hom	28	NM_001163213	rs7688609	synonymous_variant
FLT3	snp	chr13	28610183	A	G	3090.31	hom	101	NM_004119.2	rs2491231	splice_region_variant&intr
FOXL2	snp	chr3	138665213	C	T	394.523	het	32	NM_023067.3	CM082718	missense_variant
H3F3A	snp	chr1	226252044	C	T	424.244	hom	18	NM_002107.4		5_prime_UTR_variant
HRAS	snp	chr11	534332	G	A	3249.77	het	197	NM_005343.2	rs41294870	5_prime_UTR_variant
IDH1	del	chr2	209116299	GAAAAAA	GAAAAAA	831.07	het	113	XM_005246521.1		intron_variant&feature_tr
JAK3	snp	chr19	17945673	C	T	2603.01	het	140	XM_005259896.1		synonymous_variant
KIT	snp	chr4	55595589	G	A	320.93	het	19	XM_005265740.1		synonymous_variant
MET	complex	chr7	116339303	CATTCTAC	GATGCTC	292.805	hom	14	XM_005250353.1		frameshift_variant&featur

MET	ins	chr7	116339313	GA	GTA	324.378	het	16	XM_005250353.1		frameshift_variant&featur
MET	complex	chr7	116339316	CATC	AATG	291	het	16	XM_005250353.1		missense_variant
MET	snp	chr7	116339367	G	A	432.633	hom	18	XM_005250353.	rs372320153	missense_variant
MET	snp	chr7	116339510	C	T	935.711	hom	36	XM_005250353.1		synonymous_variant
MYCN	snp	chr2	16080157	C	G	637.264	hom	21	NM_005378.4	rs11886063	upstream_gene_variant
NOTCH1	snp	chr9	139390723	A	G	476.867	het	32	NM_017617.3		missense_variant
NOTCH1	snp	chr9	139391429	C	G	693.355	hom	37	NM_017617.3		missense_variant
NOTCH1	complex	chr9	139391497	TGAGGG	CAAGGAC	293.761	het	15	NM_017617.3		frameshift_variant&featur
NOTCH1	snp	chr9	139391636	G	A	684.815	hom	32	NM_017617.3	rs2229974	synonymous_variant
NOTCH1	complex	chr9	139400109	ACGG	GCGA	324.307	het	183	NM_017617.3		synonymous_variant
NPM1	del,del	chr5	170837513	CTTTTTTT	CTTTTTTT	508.126	het	43	NM_002520.6		splice_region_variant&intı
PDGFRA	snp	chr4	55141055	A	G	1647.74	hom	56	NM_006206.4	rs1873778&C(	synonymous_variant
PDGFRA	snp	chr4	55161254	C	T	1868.1	hom	62	NM_006206.4	rs3733540	intron_variant
PDGFRA	snp	chr4	55161391	T	C	625.006	hom	23	NM_006206.4	rs7685117	synonymous_variant
PDGFRA	snp	chr4	55161517	A	G	1325.17	hom	44	NM_006206.4	rs7680422	3_prime_UTR_variant
PIK3R1	snp	chr5	67586621	G	A	540.635	het	46	NM_181523.2		intron_variant
PTEN	del	chr10	89720633	CTTTTTTT	CTTTTTTT	313.77	het	88	NM_000314.4		splice_acceptor_variant&i
PTEN	snp	chr10	89720957	A	T	131.253	het	39	NM_000314.4		intron_variant
PTEN	del	chr10	89725293	CTTTTTTT	CTTTTTTT	132.843	het	49	NM_000314.4		3_prime_UTR_variant&fea
RB1	snp	chr13	48919358	T	G	638.437	hom	22	NM_000321.2	rs198617	intron_variant
RB1	snp	chr13	48941657	G	A	479.663	het	37	NM_000321.2	CM030501&C(	missense_variant
RB1	complex	chr13	48942709	GTG	ATA	367.438	het	28	NM_000321.2		missense_variant
RET	snp	chr10	43609957	G	A	299.314	het	24	NM_020975.4	CD034000	missense_variant
RET	mnp	chr10	43610189	GGG	TCT	532.268	hom	22	NM_020975.4		splice_region_variant&intı
RET	mnp	chr10	43610199	GGG	CCC	572.97	hom	23	NM_020975.4		intron_variant
STK11	snp	chr19	1221285	G	A	330.049	het	21	XM_005259617.1		missense_variant
STK11	snp	chr19	1222012	G	C	17500.9	hom	599	XM_005259617.	rs2075607	splice_region_variant&intı
TERT	snp	chr5	1295349	A	G	13659.2	het	871	NM_198253.2	rs2853669&CF	upstream_gene_variant
TP53	snp	chr17	7577082	C	T	732.948	het	48	NM_000546.5	TP53_g.13836	missense_variant
TP53	snp	chr17	7579472	G	C	1563.76	het	72	NM_000546.5	rs1042522&TF	missense_variant
TP53	snp	chr17	7579619	G	T	1453.56	het	85	NM_000546.5	rs17883323	intron_variant