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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.: T2235086-SC **Lot No.: B906126**

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: breast

Donor Information:

Male: _____ year(s) old
Female: 54 year(s) old

Pathological Diagnosis: invasive (infiltrating) ductal carcinoma

Tumor Size: n/a

Location: breast, left

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

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

B906126

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.

DDR2	3.81	1.56	5.95E-04	DDR2	2.47	0.32	5.73E-02
NOTCH1	3.38	1.39	4.35E-03	NOTCH1	4.11	0.51	4.14E-03
AURKA	0.33	0.09	8.04E-03	AURKA	0.37	0.03	2.47E-02
ERBB4	3.17	0.69	2.82E-03	ERBB4	1.34	0.06	3.94E-01
MYC	4.05	0.95	7.34E-04	MYC	3.86	0.26	4.64E-03
SMO	0.23	0.08	3.90E-03	SMO	0.36	0.05	2.40E-02
ERBB3	3.04	1.15	4.16E-03	ERBB3	3.77	0.39	4.14E-03
VHL	3.59	1.44	5.80E-03	VHL	2.35	0.36	2.46E-01

symbol	type	chromosome	position	reference	mutation	quality	allele type	depth	variant frequency	transcript_id	consequence	existing variation
ALK	complex	chr2	29445268	GCAGC	ACAGA	2777.88	het	1350	0.17	NM_00430	missense_variant&spli	
APC	snp	chr5	1.12E+08	G	T	339.443	hom	16	1.00	XM_00527	missense_v	rs3743800
APC	snp	chr5	1.12E+08	GAAAA	AAAAA	2296.38	het	268	0.32	XM_00527	synonymous_variant	
ATM	snp	chr11	1.08E+08	C	T	1292.63	het	74	0.65	NM_00005	missense_variant	
ATM	snp	chr11	1.08E+08	A	G	310.317	hom	11	1.00	NM_00005	intron_variant	
ATM	snp	chr11	1.08E+08	T	C	305.771	hom	11	1.00	NM_00005	intron_variant	
ATM	snp	chr11	1.08E+08	A	G	310.317	hom	11	1.00	NM_00005	intron_variant	
ATM	snp	chr11	1.08E+08	A	G	1817.7	het	92	0.79	NM_00005	missense_variant&spli	
ATM	snp	chr11	1.08E+08	C	T	3653.95	hom	129	1.00	NM_00005	intron_variant	
ATM	snp	chr11	1.08E+08	G	A	802.773	hom	28	1.00	NM_00005	missense_variant	
CCND1	del	chr11	69463852	ACC	AC	357.174	het	560	0.12	NM_05305	intron_variant&feature	
CCND1	del	chr11	69471096	GGGTCT	GT	806.44	hom	34	0.91	NM_05305	downstream_gene_var	
CCND1	complex	chr11	69471107	CACC	GAC	516.135	het	28	0.82	NM_05305	downstream_gene_var	
CCND1	complex	chr11	69471117	CTGGCT	ATCACG	651.629	het	30	0.90	NM_05305	downstream_gene_var	
CCND1	snp	chr11	69471135	G	A	9213.97	het	407	0.90	NM_05305	downstream_gene_var	
CCNE1	snp	chr19	30308089	C	G	500.756	hom	19	1.00	NM_00123	missense_variant	
CDH1	snp	chr16	68771372	C	T	31027.4	het	1414	0.74	NM_00436	splice_regi	rs3743674
CDK4	snp	chr12	58144902	C	A	872.562	hom	41	0.98	NM_00007	intron_variant	
CDK4	snp	chr12	58145371	C	T	286.521	hom	13	1.00	NM_00007	missense_variant	

CDKN2A	snp	chr9	21968199	C	G	73676	hom	2334	1.00	NM_00119	3_prime_U	rs11515&C
CDKN2A	mnp	chr9	21971219	AAC	TGG	236.287	het	17	0.59	NM_00119	intron_variant	
CDKN2A	snp	chr9	21974713	G	A	4313.76	het	222	0.73	NM_00119	synonymous_variant	
CSF1R	snp	chr5	1.49E+08	G	A	285.319	hom	10	1.00	NM_00521	missense_variant	
CTNNB1	del	chr3	41265953	CTTTTTTTT	CTTTTTTTT	1321.8	het	542	0.16	XM_00526	intron_variant&feature	
DDR2	snp	chr1	1.63E+08	GGT	GGC	121746	hom	3846	0.99	XM_00524	intron_variant	
DDR2	snp	chr1	1.63E+08	T	C	278.019	hom	10	1.00	XM_00524	intron_vari	rs1780003
DDR2	complex	chr1	1.63E+08	TGTC	CGTT	11435.4	hom	421	0.91	XM_00524	intron_variant	
DDR2	snp	chr1	1.63E+08	C	T	1324.23	hom	47	1.00	XM_00524	synonymou	rs5587505(
DDR2	snp	chr1	1.63E+08	G	A	1091.13	het	57	0.75	XM_00524	missense_variant	
DDR2	snp	chr1	1.63E+08	G	T	649.803	hom	28	1.00	XM_00524	intron_vari	rs1355287
DDR2	snp	chr1	1.63E+08	G	A	6696.28	het	461	0.52	XM_00524	synonymous_variant	
DDR2	snp	chr1	1.63E+08	G	A	6326.36	het	309	0.76	XM_00524	missense_v	COSM1335
EGFR	snp	chr7	55241701	GTG	ATG	14302.1	het	709	0.75	NM_00522	missense_variant	
ERBB2	snp	chr17	37880248	C	T	11708.6	hom	429	0.97	NM_00444	synonymou	rs1397451(
ERBB3	snp	chr12	56477726	T	A	1170.42	hom	62	0.98	NM_00198	intron_variant	
ERBB4	del	chr2	2.13E+08	GAAAAAAA	GAAAAAAA	256.032	het	70	0.21	NM_00523	intron_variant&feature	
ERBB4	snp	chr2	2.13E+08	A	T	14307.3	het	765	0.59	NM_00523	intron_vari	rs3512391(
FBXW7	del	chr4	1.53E+08	CTTTTTTTT	CTTTTTTTT	697.167	het	122	0.22	NM_03363	intron_variant&feature	
FBXW7	snp	chr4	1.53E+08	C	A	251.365	het	19	0.79	NM_03363	intron_variant	
FBXW7	snp	chr4	1.53E+08	G	A	1045.28	hom	38	1.00	NM_03363	intron_variant	
FBXW7	snp	chr4	1.53E+08	G	C	7310.01	hom	290	1.00	NM_03363	missense_variant	
FBXW7	del,del	chr4	1.53E+08	AAAAAGA	AAA,AAAA	1670.74	het	190	0.25	NM_03363	intron_variant&feature	
FBXW7	snp	chr4	1.53E+08	G	A	1190.92	het	54	0.87	NM_03363	intron_vari	rs7474657(
FBXW7	snp	chr4	1.53E+08	T	C	4169.18	het	281	0.55	NM_03363	intron_variant	
FBXW7	snp	chr4	1.53E+08	A	C	2987.11	hom	94	1.00	NM_03363	intron_vari	rs3470867(
FGFR1	ins	chr8	38271325	GT	GGTT	491.864	het	32	0.59	NM_00117	splice_region_variant&	
FGFR1	complex	chr8	38271328	ATGGGCGA	GAGGTCAA	183.831	het	20	0.55	NM_00117	splice_region_variant&	
FGFR1	mnp	chr8	38271371	CT	AG	332.443	hom	12	1.00	NM_00117	intron_variant	
FGFR1	complex	chr8	38271381	TGC	AGG	348.974	het	684	0.12	NM_00117	intron_variant	
FGFR1	snp	chr8	38272162	G	A	254.779	het	13	0.85	NM_00117	intron_variant	
FGFR2	snp	chr10	1.23E+08	C	A	759.174	het	99	0.42	NM_02297	splice_acceptor_varian	
FGFR3	snp	chr4	1803577	G	A	45192.4	het	2577	0.62	NM_00116	missense_variant	
FGFR3	snp	chr4	1805580	C	T	1206.5	hom	43	1.00	NM_00116	intron_variant	

FGFR3	snp	chr4	1805591	C	T	1123.14	hom	43	0.95	NM_00116	intron_variant	
FGFR3	snp	chr4	1805614	C	T	1377.79	het	92	0.53	NM_00116	intron_variant	
FGFR3	del	chr4	1806012	TGGGGGG	TGGGGGG	4592.01	het	1188	0.20	NM_00116	intron_variant&feature	
FGFR3	snp	chr4	1807894	G	A	911.395	hom	40	0.98	NM_00116	synonymou	rs7688609
FGFR3	snp	chr4	1808403	C	T	1238.56	het	98	0.55	NM_00116	missense_variant	
FGFR3	complex	chr4	1808485	GGCAG	AGCAA	664.604	het	1017	0.12	NM_00116	intron_variant	
FLT3	snp	chr13	28608239	G	A	549.204	het	39	0.54	NM_00411	missense_variant	
FLT3	snp	chr13	28610183	A	G	11342.9	hom	359	1.00	NM_00411	splice_regi	rs2491231
GNA11	snp	chr19	3119045	C	T	36433.3	het	1888	0.68	NM_00206	synonymous_variant	
GNAQ	snp	chr9	80412487	G	A	559.679	het	40	0.55	NM_00207	missense_variant	
H3F3A	snp	chr1	2.26E+08	G	A	5311.51	hom	191	0.98	NM_00210	5_prime_UTR_variant	
HNF1A	snp	chr12	1.21E+08	G	A	1146.71	het	48	0.92	XM_00525	synonymous_variant	
IDH1	del	chr2	2.09E+08	GAAAAAAA	GAAAAAAA	1063.72	het	109	0.35	XM_00524	intron_variant&feature	
IDH1	del	chr2	2.09E+08	GAAAAAAA	GAAAAAAA	4110.01	het	344	0.41	XM_00524	intron_variant&feature	
JAK2	snp	chr9	5111838	G	A	529.254	hom	20	1.00	NM_00497	intron_variant	
JAK2	snp	chr9	5111851	A	G	576.314	hom	20	1.00	NM_00497	intron_variant	
JAK2	snp	chr9	5111879	C	T	576.314	hom	20	1.00	NM_00497	intron_variant	
JAK2	snp	chr9	5112028	T	C	471.797	hom	18	1.00	NM_00497	intron_variant	
JAK2	snp	chr9	5112040	A	G	509.83	hom	18	1.00	NM_00497	intron_variant	
JAK2	snp	chr9	5112071	G	C	517.98	hom	18	1.00	NM_00497	intron_variant	
JAK3	complex	chr19	17945706	CAC	TAT	1579.39	het	81	0.85	XM_00525	missense_variant	
KDR	snp	chr4	55961109	C	T	5580.06	hom	201	0.99	NM_00225	missense_v	rs3747523
KDR	snp	chr4	55972926	C	A	274.35	hom	15	1.00	NM_00225	synonymous_variant	
MAP2K1	snp	chr15	66727597	G	C	33554.6	het	2105	0.50	NM_00275	intron_vari	rs1694992
MDM2	snp	chr12	69207346	C	T	2624.84	hom	95	0.99	NM_00239	missense_variant	
MDM2	snp	chr12	69207414	C	T	2633.3	het	177	0.53	NM_00239	splice_region_variant&	
MET	snp	chr7	1.16E+08	G	A	835.552	het	37	0.89	XM_00525	intron_variant	
MET	snp	chr7	1.16E+08	CACCC	CACCT	2889.68	het	173	0.60	XM_00525	missense_variant	
MET	complex	chr7	1.16E+08	CACCC	TACCT	414.998	het	68	0.26	XM_00525	missense_variant	
MLH1	snp	chr3	37067337	G	A	1586.02	het	89	0.67	NM_00024	synonymous_variant	
MYC	snp	chr8	1.29E+08	C	T	8124.35	het	336	0.93	NM_00246	upstream_gene_variar	
MYC	snp	chr8	1.29E+08	G	A	6440.4	het	464	0.49	NM_00246	intron_variant	
MYCN	snp	chr2	16080157	C	G	308.541	hom	10	1.00	NM_00537	upstream_	rs1188606
MYCN	snp	chr2	16089615	T	C	4151.44	hom	146	1.00	NM_00537	downstrea	rs4669018

MYCN	snp	chr2	16091963	T	G	386.964	hom	14	1.00	NM_00537	downstrea	rs5978570
MYCN	mnp	chr2	16091988	CT	TG	393.134	hom	15	1.00	NM_00537	downstream_gene_va	
NOTCH1	mnp	chr9	1.39E+08	GG	AA	218.833	het	32	0.31	NM_01761	missense_variant	
NOTCH1	snp	chr9	1.39E+08	G	A	15599.4	hom	541	1.00	NM_01761	synonymou	rs10521&C
NOTCH1	complex	chr9	1.39E+08	CACCAGGG	TCCCTGGT/	666.673	het	1053	0.13	NM_01761	missense_variant	
NOTCH1	complex	chr9	1.39E+08	CACCAGGG	TCCCTGAT(	4764.92	het	355	0.50	NM_01761	missense_variant	
NOTCH1	mnp	chr9	1.39E+08	CC	GT	5384.2	het	369	0.53	NM_01761	missense_variant	
NOTCH1	ins	chr9	1.39E+08	GG	GACG	3524.78	hom	132	1.00	NM_01761	frameshift_variant&fea	
NOTCH1	complex	chr9	1.39E+08	AGCA	TGCT	4341.65	hom	163	0.98	NM_01761	missense_variant	
NOTCH1	del	chr9	1.39E+08	CGTC	CC	4317.57	hom	158	0.99	NM_01761	frameshift_variant&fea	
NOTCH1	snp	chr9	1.39E+08	C	T	1234.48	het	99	0.56	NM_01761	synonymous_variant	
NOTCH1	snp	chr9	1.39E+08	C	T	2358.03	het	96	0.93	NM_01761	missense_variant	
NOTCH1	snp	chr9	1.39E+08	G	A	14890.1	hom	522	1.00	NM_01761	synonymou	rs2000993
NPM1	del,del	chr5	1.71E+08	CTTTTTTTT	CTTTTTTTT	2477.4	het	235	0.31	NM_00252	splice_region_variant&	
PDGFRA	mnp	chr4	55141055	AGATG	GAATG	4936.1	hom	206	0.85	NM_00620	missense_variant	
PDGFRA	mnp,snp	chr4	55141055	AGATG	GAATG,GG	27817.7	het	1074	0.80	NM_00620	missense_variant	
PDGFRA	complex	chr4	55141134	GTG	ATA	2225.52	het	762	0.17	NM_00620	missense_variant	
PDGFRA	snp	chr4	55144551	G	A	307.489	het	23	0.52	NM_00620	synonymous_variant	
PDGFRA	snp	chr4	55161254	C	T	4783.61	hom	150	1.00	NM_00620	intron_vari	rs3733540
PDGFRA	snp	chr4	55161391	T	C	345.633	hom	13	1.00	NM_00620	synonymou	rs7685117
PDGFRA	snp	chr4	55161517	A	G	8205.93	hom	258	1.00	NM_00620	3_prime_U	rs7680422
PIK3CA	del	chr3	1.79E+08	ATTTTTTTT	ATTTTTTTT	682.818	het	124	0.24	NM_00621	intron_variant&feature	
PIK3R1	complex	chr5	67588148	GTC	ATA	387.266	hom	16	0.88	NM_18152	missense_variant	
PIK3R1	snp	chr5	67588148	GTC	ATC	6076.23	hom	216	0.92	NM_18152	missense_variant	
PIK3R1	snp	chr5	67590478	C	T	2116.21	het	114	0.68	NM_18152	missense_v	COSM1069
PTEN	snp	chr10	89624364	G	A	665.923	hom	37	0.95	NM_00031	intron_variant	
PTEN	snp	chr10	89690816	C	T	2034.63	het	113	0.66	NM_00031	missense_v	COSM3370
PTEN	del	chr10	89692731	GTTTTTTTT	GTTTTTTTT	406.674	het	54	0.31	NM_00031	intron_variant&feature	
PTEN	snp	chr10	89692751	G	A	1251.02	het	53	0.92	NM_00031	intron_variant	
PTPN11	snp	chr12	1.13E+08	C	T	4039.16	het	229	0.62	NM_00283	missense_variant	
RB1	snp	chr13	48942784	C	T	3512.97	het	168	0.79	NM_00032	intron_variant	
RB1	snp	chr13	49033785	A	T	209.509	het	12	0.92	NM_00032	intron_variant	
RB1	snp	chr13	49037813	G	A	1911.23	het	128	0.53	NM_00032	intron_variant	
RB1	snp	chr13	49037838	G	A	470.456	het	26	0.73	NM_00032	intron_variant	

RET	mnp	chr10	43610189	GGG	TCT	1089.34	hom	39	1.00	NM_02097	splice_region_variant&	
RET	mnp	chr10	43610199	GGG	CCC	1636.67	hom	62	0.97	NM_02097	intron_variant	
RET	complex	chr10	43610208	AAGATC	GATCTT	622.067	het	90	0.29	NM_02097	intron_variant	
RET	snp	chr10	43610240	G	A	644.785	het	88	0.30	NM_02097	intron_variant	
RET	snp	chr10	43610247	G	A	225.521	het	91	0.18	NM_02097	intron_variant	
RET	complex	chr10	43615494	CATGGC	GAGGGT	418.521	hom	15	1.00	NM_02097	intron_variant	
RET	snp	chr10	43615590	T	C	1618.62	het	115	0.50	NM_02097	missense_variant	
RET	complex	chr10	43615673	GCGGGGC	CCTGGGA	925.184	hom	32	1.00	NM_02097	intron_variant	
RET	snp	chr10	43615684	A	T	919.765	hom	32	1.00	NM_02097	intron_variant	
RET	snp	chr10	43615689	T	G	926.99	hom	32	1.00	NM_02097	intron_variant	
RET	complex	chr10	43621817	GTGA	CTTT	684.913	hom	26	1.00	NM_02097	intron_variant	
ROS1	snp	chr6	1.18E+08	G	T	313.211	hom	18	0.94	NM_00294	missense_variant	
SMAD4	snp	chr18	48581026	G	A	1043.51	het	58	0.69	NM_00535	intron_variant	
SMAD4	snp	chr18	48593459	G	A	5507.57	het	1175	0.21	NM_00535	missense_variant	
SMAD4	snp	chr18	48604609	C	T	3339.87	het	203	0.58	NM_00535	intron_variant	
SMAD4	snp	chr18	48604827	C	T	9046.62	het	469	0.68	NM_00535	missense_variant	
SMO	snp	chr7	1.29E+08	G	C	449.872	hom	15	1.00	NM_00563	intron_vari	rs2075777
SMO	snp	chr7	1.29E+08	G	C	4457.28	hom	146	1.00	NM_00563	synonymou	rs2228617
STK11	snp	chr19	1206905	G	A	15297.2	het	1054	0.51	XM_00525	5_prime_UTR_variant	
STK11	snp	chr19	1206933	G	A	14910.7	het	915	0.57	XM_00525	synonymous_variant	
STK11	complex,sr	chr19	1207234	CCGGG	CTGGT,CCC	28166.2	het	1119	0.77	XM_00525	intron_variant	
STK11	complex,cc	chr19	1207234	CCGGG	CTGGT,TCC	5676.04	het	259	0.57	XM_00525	intron_variant	
STK11	snp	chr19	1220371	G	A	5959.9	het	322	0.66	XM_00525	splice_acce	CS982373&
STK11	snp	chr19	1222012	GGCCCC	CGCCCC	189201	hom	6446	0.95	XM_00525	splice_region_variant&	
STK11	complex	chr19	1222012	GGCCCC	CGCCTT	301.27	hom	12	0.92	XM_00525	splice_region_variant&	
STK11	complex,cc	chr19	1222012	GGCCCC	CGCCTT,CG	5647.59	het	296	0.50	XM_00525	splice_region_variant&	
STK11	snp	chr19	1222112	G	A	14891.4	hom	641	1.00	XM_00525	intron_variant	
STK11	snp	chr19	1222117	G	A	14556.2	hom	639	0.99	XM_00525	intron_variant	
STK11	snp	chr19	1226600	C	T	1753.77	hom	62	1.00	XM_00525	synonymous_variant	
TERT	snp	chr5	1295346	GGGA	GGGG	289384	het	16144	0.57	NM_19825	upstream_gene_variar	
TERT	snp	chr5	1295349	A	G	441.117	het	20	0.90	NM_19825	upstream_	rs2853669&
TP53	snp	chr17	7576967	G	A	4656.45	het	4540	0.13	NM_00054	intron_variant	
TP53	snp	chr17	7577538	C	T	1567.38	het	98	0.57	NM_00054	missense_v	rs1154065
TP53	snp	chr17	7578466	G	A	3117.05	het	161	0.75	NM_00054	missense_v	TP53_g.124

TP53	snp	chr17	7578475	G	A	3297.67	het	165	0.75	NM_00054	missense_v	TP53_g.124
TP53	complex	chr17	7579658	GTCC	CCCT	3344.42	het	318	0.40	NM_00054	intron_variant	
VHL	snp	chr3	10183861	C	T	6665.1	het	403	0.58	NM_00055	synonymou	CX9840398
VHL	mnp	chr3	10188244	GG	AA	256.337	het	1181	0.11	NM_00055	missense_v	COSM3035
VHL	snp	chr3	10188428	T	G	3425.86	hom	156	0.99	NM_00055	intron_vari	rs1678607