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Data Sheet

Product Name: CancerSeqPlus Paraffin Tissue Curl

Catalog No.: T2235086-SC **Lot No.: B906131**

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: 53 year(s) old

Pathological Diagnosis: 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:** _____

B906131

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	variant frequency	transcript_id	consequence	existing variation
ALK	snp	chr2	29445458	G	T	2758.47	hom	96	0.95	NM_00430	synonymou	rs3795850
ATM	snp	chr11	1.08E+08	G	A	297.379	het	27	0.59	NM_00005	synonymous_variant	
CCND1	snp	chr11	69461978	G	T	704.673	hom	30	1.00	NM_05305	intron_variant	
CCND1	snp	chr11	69465081	G	A	701.997	het	51	0.55	NM_05305	intron_variant	
CCND1	del	chr11	69471179	GGTCT	GT	1183.25	het	109	0.51	NM_05305	downstream_gene_var	
CCND1	ins	chr11	69471188	AC	AGACC	1247.14	het	114	0.50	NM_05305	downstream_gene_var	
CCNE1	snp	chr19	30311577	C	T	233.651	hom	10	1.00	NM_00123	intron_variant	
CDH1	snp	chr16	68771034	C	A	286.521	hom	13	1.00	NM_00436	upstream_	rs16260&C
CDH1	snp	chr16	68771372	C	T	17176.8	hom	544	1.00	NM_00436	splice_regi	rs3743674
CDH1	snp	chr16	68847356	C	T	958.349	het	63	0.57	NM_00436	synonymous_variant	
CDKN2A	snp	chr9	21968159	G	A	769.97	het	35	0.89	NM_00119	3_prime_U	rs3088440
CDKN2A	snp	chr9	21968199	C	G	26723.5	hom	854	0.99	NM_00119	3_prime_U	rs11515&C
CDKN2A	snp	chr9	21971014	A	T	881.058	het	44	0.77	NM_00119	missense_v	CM004887
CSF1R	complex	chr5	1.49E+08	CTTGC	GGTGG	766.821	hom	29	1.00	NM_00521	missense_variant	
CSF1R	mnp	chr5	1.49E+08	GGGT	ACCC	775.855	hom	29	1.00	NM_00521	missense_variant	
CSF1R	snp	chr5	1.49E+08	C	G	836.87	hom	30	1.00	NM_00521	missense_variant	
CSF1R	snp	chr5	1.49E+08	G	A	897.6	hom	31	1.00	NM_00521	synonymous_variant	
DDR2	snp	chr1	1.63E+08	T	C	10089.6	hom	328	1.00	XM_00524	intron_vari	rs1780003
DDR2	snp	chr1	1.63E+08	G	T	1393.63	hom	52	1.00	XM_00524	intron_vari	rs1355287
EZH2	snp	chr7	1.49E+08	A	G	365.316	hom	12	1.00	XM_00524	intron_vari	rs2072407
FBXW7	snp	chr4	1.53E+08	A	G	985.561	het	65	0.54	NM_03363	intron_vari	rs1003360
FBXW7	del	chr4	1.53E+08	CAAAAAAA	CAAAAAAA	299.391	het	37	0.38	NM_03363	splice_region_variant&	
FGFR1	mnp	chr8	38271371	CT	AG	482.144	hom	19	0.95	NM_00117	intron_variant	
FGFR1	complex	chr8	38271381	TGCGT	AGGGG	391.205	hom	16	0.94	NM_00117	intron_variant	
FGFR3	del	chr4	1806012	TGGGGGG	TGGGGGG	2043.69	het	508	0.20	NM_00116	intron_variant&feature	
FGFR3	snp	chr4	1806018	G	A	2334.98	het	858	0.17	NM_00116	intron_vari	rs3718987
FGFR3	snp	chr4	1807894	G	A	1966.14	hom	67	0.99	NM_00116	synonymou	rs7688609
FOXL2	mnp	chr3	1.39E+08	GG	AA	1251.69	het	516	0.17	NM_02306	missense_variant	

FOXL2	complex	chr3	1.39E+08	GCTG	ACTA	1118.72	hom	54	0.94	NM_02306	missense_variant	
FOXL2	complex,sr	chr3	1.39E+08	GCTG	ACTA,GCTA	1571.54	het	74	0.69	NM_02306	missense_variant	
FOXL2	complex	chr3	1.39E+08	GCGGCGCC	TCGGGGCC	779.28	hom	28	1.00	NM_02306	missense_variant	
HRAS	snp	chr11	534242	A	G	2810.78	het	143	0.66	NM_00534	synonymou	rs12628&C
HRAS	del	chr11	534403	GCCCAGGC	GC	604.93	het	160	0.20	NM_00534	intron_variant&feature	
IDH1	del	chr2	2.09E+08	GAAAAAAA	GAAAAAAA	284.073	het	88	0.19	XM_00524	intron_variant&feature	
KDR	snp	chr4	55972974	T	A	375.849	het	27	0.52	NM_00225	missense_v	rs1870377&
MET	snp	chr7	1.16E+08	G	A	971.767	hom	34	1.00	XM_00525	synonymou	rs2023748&
MET	snp	chr7	1.16E+08	G	A	776.72	hom	26	1.00	XM_00525	synonymou	rs41737&C
MYC	snp	chr8	1.29E+08	C	T	1293.54	het	66	0.76	NM_00246	upstream_gene_varian	
MYCN	snp	chr2	16089615	T	C	739.299	het	40	0.73	NM_00537	downstrea	rs4669018
NOTCH1	mnp	chr9	1.39E+08	GTGG	CCAC	214.986	het	32	0.34	NM_01761	missense_variant	
NOTCH1	snp	chr9	1.39E+08	G	T	158.59	het	27	0.41	NM_01761	synonymous_variant	
NOTCH1	snp	chr9	1.39E+08	G	C	158.59	het	27	0.41	NM_01761	synonymous_variant	
NOTCH1	snp	chr9	1.39E+08	C	T	547.45	het	38	0.68	NM_01761	missense_variant	
NOTCH1	snp	chr9	1.39E+08	C	T	705.73	het	41	0.66	NM_01761	missense_variant	
NOTCH1	snp	chr9	1.39E+08	G	A	257.024	hom	11	1.00	NM_01761	synonymou	rs2229974
NOTCH1	snp	chr9	1.39E+08	G	A	1707.14	het	76	0.84	NM_01761	synonymou	rs10521&C
NOTCH1	snp	chr9	1.39E+08	C	T	1462.47	het	93	0.74	NM_01761	synonymous_variant	
PDGFRA	complex,cc	chr4	55141052	CCCA	CACG,GCCC	389.02	het	20	0.50	NM_00620	missense_variant	
PDGFRA	snp	chr4	55141052	CCCA	CCCG	5330.55	hom	202	0.90	NM_00620	synonymous_variant	
PDGFRA	snp	chr4	55161254	C	T	3021.69	hom	97	1.00	NM_00620	intron_vari	rs3733540
PDGFRA	snp	chr4	55161517	A	G	1349.47	hom	44	1.00	NM_00620	3_prime_U	rs7680422
PIK3CA	del	chr3	1.79E+08	ATTTTTTTT	ATTTTTTTT	270.546	het	55	0.24	NM_00621	intron_variant&feature	
PTEN	del	chr10	89720633	CTTTTTTTT	CTTTTTTTT	254.405	het	75	0.21	NM_00031	splice_acceptor_varian	
PTEN	complex	chr10	89720907	TTGAC	GTGAT	234.561	hom	10	1.00	NM_00031	intron_variant	
PTEN	complex,sr	chr10	89720907	TTGAC	GTGAT,GTC	619.906	het	26	0.62	NM_00031	intron_variant	
PTEN	del	chr10	89725293	CTTTTTTTT	CTTTTTTTT	217.124	het	90	0.17	NM_00031	3_prime_UTR_variant&	
RB1	snp	chr13	48919358	T	G	556.713	hom	20	1.00	NM_00032	intron_vari	rs198617
RET	snp	chr10	43610072	C	T	350.537	het	19	0.89	NM_02097	missense_variant	
RET	complex	chr10	43610208	AAGATC	GATCTT	217.486	het	227	0.13	NM_02097	intron_variant	
RET	snp	chr10	43613843	G	T	1382.55	hom	50	0.98	NM_02097	synonymou	rs1800861&
ROS1	snp	chr6	1.18E+08	G	A	221.821	hom	10	1.00	NM_00294	intron_variant	
SMO	snp	chr7	1.29E+08	G	C	4183.09	hom	134	1.00	NM_00563	intron_vari	rs2075777

SMO	snp	chr7	1.29E+08	C	T	489.1	het	33	0.64	NM_00563	synonymous_variant	
SMO	snp	chr7	1.29E+08	G	C	2789.62	hom	94	1.00	NM_00563	synonymou	rs2228617
STK11	snp	chr19	1207238	G	T	2990.52	hom	99	0.99	XM_00525	intron_vari	rs3764640
STK11	snp	chr19	1222012	GGCCC	CGCCC	14780.2	het	737	0.68	XM_00525	splice_region_variant&	
STK11	snp	chr19	1222095	G	A	603.966	hom	26	1.00	XM_00525	intron_variant	
TP53	snp	chr17	7573080	C	A	686.386	hom	32	1.00	NM_00054	intron_variant	
TP53	snp	chr17	7577407	A	C	1637.6	hom	52	1.00	NM_00054	intron_vari	rs1295105
TP53	snp	chr17	7577427	G	A	751.108	hom	24	1.00	NM_00054	intron_vari	rs1294778
TP53	del	chr17	7579643	CCCCCAGC	CC	149.326	het	61	0.23	NM_00054	intron_variant&feature	
TP53	del	chr17	7579651	CCTCCAGG	CC	203.212	het	11	0.91	NM_00054	intron_variant&feature	
TP53	snp	chr17	7579679	C	T	227.917	het	97	0.18	NM_00054	intron_variant	