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Data Sheet

Product Name: CancerSeqPlus Paraffin Tissue Curl

Catalog No.: T2235086-SC **Lot No.: B906135**

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: 2.5x2x2 (cm)

Location: breast, left

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

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

B906135

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.

MYC	2.73	0.34	3.50E-03	MYC	3.04	0.08	2.71E-03

symbol	type	chromosome	position	reference	mutation	quality	allele type	depth	variant frequency	transcript_id	consequence	existing variation
APC	snp	chr5	1.12E+08	G	A	983.579	het	65	0.55	XM_00527	synonymou	rs465899
CCND1	snp	chr11	69471193	C	A	592.903	hom	23	1.00	NM_05305	downstrea	rs7293807
CCNE1	complex	chr19	30314666	CGGGC	TGGGT	962.631	hom	36	0.97	NM_00123	missense_variant	
CCNE1	complex,sr	chr19	30314666	CGGGC	TGGGT,TG	4466.74	het	160	0.77	NM_00123	synonymous_variant	
CDH1	snp	chr16	68771372	C	T	12215.5	hom	385	1.00	NM_00436	splice_regi	rs3743674
CDH1	snp	chr16	68772208	T	C	430.307	hom	15	1.00	NM_00436	synonymous_variant	
CDH1	mnp	chr16	68772213	TCT	AGA	444.291	hom	16	1.00	NM_00436	missense_variant	
CDH1	snp	chr16	68772220	G	A	430.307	hom	15	1.00	NM_00436	synonymous_variant	
CDH1	snp	chr16	68855975	C	T	254.196	het	24	0.50	NM_00436	missense_variant	
CDH1	snp	chr16	68857289	T	C	23432.4	hom	779	1.00	NM_00436	intron_vari	rs2276330
CDKN2A	mnp	chr9	21968199	CG	GA	852.07	het	44	0.73	NM_00119	3_prime_UTR_variant	
CDKN2A	snp	chr9	21968199	CG	GG	57479.5	hom	1884	0.98	NM_00119	3_prime_UTR_variant	
CDKN2A	snp	chr9	21974728	C	T	800.582	het	50	0.62	NM_00119	synonymou	COSM1354
DDR2	snp	chr1	1.63E+08	T	C	32435.3	hom	1024	1.00	XM_00524	intron_vari	rs1780003
DDR2	snp	chr1	1.63E+08	G	T	1909.59	hom	84	0.99	XM_00524	intron_vari	rs1355287
EGFR	snp	chr7	55232966	G	A	747.744	het	51	0.55	NM_00522	splice_region_variant&	
EGFR	snp	chr7	55233102	C	T	1451.91	het	77	0.69	NM_00522	missense_variant	
EGFR	snp	chr7	55249063	G	A	1518.3	het	79	0.72	NM_00522	synonymou	rs1050171
ERBB2	snp	chr17	37883079	G	A	837.665	hom	36	1.00	NM_00444	synonymous_variant	
ERBB3	snp	chr12	56477694	A	T	21697.9	hom	691	0.99	NM_00198	splice_regi	rs2271194
ERBB3	snp	chr12	56482444	G	A	74.3787	het	112	0.16	NM_00198	splice_region_variant&	
ERBB4	del	chr2	2.13E+08	TAAAAAAA	TAAAAAAA	233.993	het	28	0.39	NM_00523	splice_region_variant&	
FBXW7	del	chr4	1.53E+08	CTTTTTTTT	CTTTTTTTT	381.727	het	82	0.20	NM_03363	intron_variant&feature	
FBXW7	del,del	chr4	1.53E+08	CAAAAAAA	CAAAAAAA	2368.98	het	332	0.23	NM_03363	splice_region_variant&	
FGFR2	snp	chr10	1.23E+08	A	C	3649.5	het	170	0.78	NM_02297	intron_vari	rs3135802
FGFR3	snp	chr4	1803704	T	C	4739.63	hom	166	1.00	NM_00116	synonymou	rs2234909

FGFR3	snp	chr4	1805502	C	T	1193.93	het	60	0.72	NM_00116	intron_vari	rs4647928
FGFR3	del,del	chr4	1806012	TGGGGGG	TGGGGGG	12839.1	het	810	0.63	NM_00116	intron_variant&feature	
FGFR3	snp	chr4	1806151	G	A	778.163	het	50	0.60	NM_00116	synonymous_variant	
FGFR3	snp	chr4	1807894	G	A	8625.86	hom	284	1.00	NM_00116	synonymou	rs7688609
FGFR3	complex	chr4	1808889	GCCAGGA	TCCTGGC	537.399	hom	20	1.00	NM_00116	missense_variant	
FGFR3	complex	chr4	1808900	CCC	CGGGG	419.427	hom	17	0.94	NM_00116	frameshift_variant&fea	
FLT3	snp	chr13	28610183	A	G	7924.59	hom	262	1.00	NM_00411	splice_regi	rs2491231
FOXL2	complex	chr3	1.39E+08	GCGGCGCC	TCGGGGCC	1512.58	hom	59	0.95	NM_02306	missense_variant	
FOXL2	snp	chr3	1.39E+08	G	A	205.441	hom	10	1.00	NM_02306	5_prime_UTR_variant	
HNF1A	snp	chr12	1.21E+08	C	T	1254.03	het	71	0.66	XM_00525	missense_v	COSM4644
IDH1	del	chr2	2.09E+08	GAAAAAAA	GAAAAAAA	443.299	het	68	0.28	XM_00524	intron_variant&feature	
IDH1	del	chr2	2.09E+08	GAAAAAAA	GAAAAAAA	1537.77	het	252	0.24	XM_00524	intron_variant&feature	
JAK2	del	chr9	5073681	CTTTTTTTT	CTTTTTTTT	530.416	het	49	0.43	NM_00497	splice_region_variant&	
JAK3	complex	chr19	17947960	GTG	ATA	872.085	het	761	0.14	XM_00525	missense_variant	
MAP2K1	complex	chr15	66727548	GCC	CCT	388.778	hom	14	1.00	NM_00275	missense_variant	
MAP2K1	complex	chr15	66727561	GTCATG	ATCAG	270.759	hom	10	1.00	NM_00275	frameshift_variant&fea	
MET	snp	chr7	1.16E+08	G	A	702.694	het	36	0.78	XM_00525	synonymou	rs2023748
MET	snp	chr7	1.16E+08	G	A	2236.77	het	135	0.59	XM_00525	synonymou	rs41737&C
MLH1	snp	chr3	37067050	A	G	18478.5	het	993	0.66	NM_00024	intron_vari	rs1112974
MPL	complex	chr1	43814889	GCTC	ACTT	301.575	het	39	0.38	NM_00537	intron_variant	
MPL	mnp	chr1	43814899	GGGT	ACCC	290.684	het	42	0.38	NM_00537	intron_variant	
MYC	snp	chr8	1.29E+08	G	A	483.52	het	27	0.89	NM_00246	5_prime_UTR_variant	
MYCN	snp	chr2	16080157	C	G	1541.8	hom	50	1.00	NM_00537	upstream_	rs1188606
MYCN	snp	chr2	16090091	C	T	347.529	het	23	0.61	NM_00537	downstream_gene_va	
NOTCH1	snp	chr9	1.39E+08	G	A	2019.96	hom	77	1.00	NM_01761	synonymou	rs2229974
NOTCH1	snp	chr9	1.39E+08	G	A	3474.24	het	199	0.59	NM_01761	synonymou	rs10521&C
NPM1	del	chr5	1.71E+08	CTTTTTTTT	CTTTTTTTT	1681.1	het	218	0.29	NM_00252	splice_region_variant&	
PDGFRA	snp	chr4	55141055	A	G	11469.9	hom	385	0.99	NM_00620	synonymou	rs1873788
PDGFRA	snp	chr4	55161254	C	T	6789.32	hom	217	1.00	NM_00620	intron_vari	rs3733540
PDGFRA	snp	chr4	55161391	T	C	1326.34	hom	43	1.00	NM_00620	synonymou	rs7685117
PDGFRA	snp	chr4	55161517	A	G	5655.59	hom	186	0.99	NM_00620	3_prime_U	rs7680422
PIK3CA	del	chr3	1.79E+08	ATTTTTTTT	ATTTTTTTT	505.196	het	109	0.22	NM_00621	intron_variant&feature	
PIK3CA	snp	chr3	1.79E+08	C	T	192.57	het	63	0.19	NM_00621	intron_variant	
PTEN	snp	chr10	89717683	C	T	193.572	het	14	0.71	NM_00031	synonymous_variant	

PTEN	snp	chr10	89717708	C	T	199.032	het	14	0.71	NM_00031	stop_gaine	CM981673
PTEN	del	chr10	89720633	CTTTTTTTT	CTTTTTTTT	945.239	het	177	0.24	NM_00031	splice_acceptor_varian	
PTEN	snp	chr10	89720709	C	G	739.558	hom	34	0.94	NM_00031	stop_gaine	COSM1349
PTEN	snp	chr10	89720996	C	T	14157.3	het	649	0.78	NM_00031	intron_variant	
PTEN	snp	chr10	89725197	G	A	204.176	het	28	0.39	NM_00031	missense_variant	
RB1	snp	chr13	48919358	T	G	2359.44	hom	81	1.00	NM_00032	intron_vari	rs198617
RB1	ins	chr13	48953655	CAAAAAAA	CAAAAAAA	142.599	het	81	0.15	NM_00032	intron_variant&feature	
RB1	ins	chr13	49034022	ATT	ATTT	548.888	het	36	0.69	NM_00032	intron_variant&feature	
RET	snp	chr10	43610281	G	A	308.127	hom	16	0.94	NM_02097	intron_variant	
RET	snp	chr10	43613843	G	T	5624.06	het	293	0.63	NM_02097	synonymou	rs1800861
SMO	snp	chr7	1.29E+08	G	C	13880.7	hom	459	1.00	NM_00563	intron_vari	rs2075777
SMO	snp	chr7	1.29E+08	G	C	6385.61	hom	204	1.00	NM_00563	synonymou	rs2228617
STK11	snp	chr19	1207271	C	A	193.611	hom	10	1.00	XM_00525	intron_variant	
STK11	snp	chr19	1219451	C	G	100.614	het	52	0.23	XM_00525	intron_vari	rs3695156
STK11	snp	chr19	1220310	A	C	313.953	hom	11	1.00	XM_00525	intron_variant	
STK11	snp	chr19	1220316	A	T	296.68	hom	11	1.00	XM_00525	intron_variant	
STK11	complex	chr19	1220322	GTGAG	TTGCA	333.351	hom	12	1.00	XM_00525	intron_variant	
STK11	snp	chr19	1226559	G	A	1120.99	het	84	0.61	XM_00525	missense_variant	
TERT	snp	chr5	1295349	A	G	52695.7	het	2839	0.58	NM_19825	upstream_	rs2853669
TP53	snp	chr17	7579579	C	T	3873.54	het	209	0.70	NM_00054	synonymou	rs1800370
TP53	del	chr17	7579651	CCTCCAGG	CC	224.719	het	24	0.50	NM_00054	intron_variant&feature	
TP53	snp	chr17	7580117	C	G	216.115	hom	11	1.00	NM_00054	intron_vari	rs1406995
VHL	snp	chr3	10183929	C	A	385.007	hom	20	1.00	NM_00055	intron_variant	