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Data Sheet

Product Name: CancerSeqPlus Paraffin Tissue Curl

Catalog No.: T2235086-SC **Lot No.: B906133**

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: 43 year(s) old

Pathological Diagnosis: invasive (infiltrating) ductal carcinoma

Tumor Size: 9x6x2 (cm)

Location: breast, left

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

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

B906133

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.

PTEN	3.25	0.22	8.20E-03	PTEN	1.89	0.04	2.15E-01
MYC	3.82	0.18	3.84E-03	MYC	4.50	0.06	4.93E-03
SMO	0.29	0.03	8.20E-03	SMO	0.55	0.02	6.63E-02

symbol	type	chromosome	position	reference	mutation	quality	allele type	depth	variant frequency	transcript_id	consequence	existing variation
ALK	snp	chr2	29443665	C	T	506.291	het	42	0.57	NM_00430	synonymous_variant	
ALK	snp	chr2	29445189	G	A	560.284	het	51	0.51	NM_00430	intron_variant	
ALK	snp	chr2	29445458	G	T	2340.23	hom	76	1.00	NM_00430	synonymou	rs3795850
ATM	snp	chr11	1.08E+08	G	A	310.317	hom	11	1.00	NM_00005	missense_variant	
ATM	snp	chr11	1.08E+08	G	A	537.583	het	37	0.54	NM_00005	missense_variant	
CCND1	snp	chr11	69471093	G	A	445.313	het	30	0.60	NM_05305	downstream_gene_va	
CDH1	snp	chr16	68771372	C	T	9247.99	het	404	0.76	NM_00436	splice_regi	rs3743674
CDH1	complex	chr16	68835593	GGTCG	AATCA	843.104	het	101	0.33	NM_00436	missense_variant	
CDH1	snp	chr16	68853165	G	A	216.401	het	85	0.18	NM_00436	intron_variant	
CDH1	ins	chr16	68857544	CAA	CAAA	1545.21	hom	61	0.93	NM_00436	intron_variant&feature	
CDK4	complex	chr12	58142991	CCATC	TCATT	211.511	het	62	0.24	NM_00007	missense_variant	
CDK4	snp	chr12	58143022	G	A	1066.69	het	74	0.53	NM_00007	synonymous_variant	
CDK4	snp	chr12	58143060	C	T	778.893	het	33	0.91	NM_00007	missense_variant	
CDK4	snp	chr12	58144724	C	T	627.821	het	41	0.73	NM_00007	synonymous_variant	
CDK4	snp	chr12	58144814	G	A	1680.71	het	101	0.62	NM_00007	synonymous_variant	
CDKN2A	snp	chr9	21965764	C	T	2.9621	het	131	0.11	NM_00119	downstream_gene_va	
CDKN2A	complex	chr9	21968199	CGAGG	GGAGA	1326.63	hom	56	0.86	NM_00119	3_prime_UTR_variant	
CDKN2A	snp	chr9	21968199	CGAGG	GGAGG	18588.3	hom	656	0.91	NM_00119	3_prime_UTR_variant	
CSF1R	snp	chr5	1.49E+08	C	T	561.872	het	43	0.51	NM_00521	synonymous_variant	
CTNNB1	snp	chr3	41265971	G	A	603.95	het	42	0.55	XM_00526	intron_variant	
CTNNB1	snp	chr3	41266075	C	T	1366.43	het	81	0.58	XM_00526	synonymous_variant	
DDR2	snp	chr1	1.63E+08	GT	GC	11760.5	hom	402	0.94	XM_00524	intron_variant	
DDR2	mnp	chr1	1.63E+08	GT	TC	479.244	hom	24	0.75	XM_00524	intron_variant	
DDR2	snp	chr1	1.63E+08	G	T	483.868	hom	17	1.00	XM_00524	intron_vari	rs1355287

EGFR	snp	chr7	55232985	T	C	329.761	het	16	0.88	NM_00522	missense_variant	
EGFR	snp	chr7	55232995	G	A	368.529	het	17	0.88	NM_00522	missense_variant	
EGFR	snp	chr7	55233062	C	T	535.825	het	35	0.57	NM_00522	synonymous_variant	
ERBB2	snp	chr17	37881038	C	T	875.51	het	64	0.61	NM_00444	synonymous_variant	
ERBB3	snp	chr12	56477694	A	T	7553.54	hom	247	1.00	NM_00198	splice_regi	rs2271194
ERBB4	snp	chr2	2.13E+08	G	A	517.72	hom	22	1.00	NM_00523	intron_vari	rs13002712
ESR1	snp	chr6	1.52E+08	G	A	702.335	het	46	0.74	XM_00526	missense_variant	
EZH2	snp	chr7	1.49E+08	G	A	511.324	het	24	0.88	XM_00524	synonymous_variant	
EZH2	snp	chr7	1.49E+08	A	G	366.097	hom	12	1.00	XM_00524	intron_vari	rs2072407
FBXW7	snp	chr4	1.53E+08	A	G	286.083	het	19	0.58	NM_03363	intron_vari	rs10033601
FGFR1	snp	chr8	38271451	G	A	2880.31	het	215	0.48	NM_00117	synonymou	rs36977626
FGFR1	snp	chr8	38273424	C	T	443.722	het	36	0.58	NM_00117	synonymous_variant	
FGFR2	snp	chr10	1.23E+08	T	C	983.089	hom	36	1.00	NM_02297	missense_variant	
FGFR2	complex	chr10	1.23E+08	CT	CCAGC	888.273	hom	33	1.00	NM_02297	inframe_insertion	
FGFR2	complex	chr10	1.23E+08	CGGCT	TGACC	900.895	hom	35	1.00	NM_02297	missense_variant	
FGFR2	snp	chr10	1.23E+08	G	A	596.574	het	39	0.62	NM_02297	missense_variant	
FGFR3	mnp	chr4	1805996	AT	TC	1392.03	het	65	0.85	NM_00116	intron_variant	
FGFR3	mnp	chr4	1806004	GA	AT	1305.29	het	64	0.80	NM_00116	intron_variant	
FGFR3	mnp	chr4	1806011	GT	TG	1380.67	hom	53	0.94	NM_00116	intron_variant	
FGFR3	del	chr4	1806012	TGGGGGG	TGGGGGG	774.676	het	409	0.13	NM_00116	intron_variant&feature	
FGFR3	snp	chr4	1807894	G	A	1397.13	hom	48	1.00	NM_00116	synonymou	rs7688609
FGFR3	complex	chr4	1808889	GCCAGGA	TCCTGGC	2667.37	hom	93	1.00	NM_00116	missense_variant	
FGFR3	mnp	chr4	1808901	CCA	GGG	2432.57	hom	93	0.98	NM_00116	missense_variant	
FLT3	snp	chr13	28610183	A	G	2600.26	hom	88	0.98	NM_00411	splice_regi	rs2491231
FOXL2	snp	chr3	1.39E+08	G	A	640.233	het	72	0.46	NM_02306	synonymous_variant	
FOXL2	snp	chr3	1.39E+08	C	A	257.185	het	19	0.84	NM_02306	missense_v	rs37247951
FOXL2	snp	chr3	1.39E+08	G	A	284.029	hom	12	1.00	NM_02306	synonymous_variant	
IDH1	del	chr2	2.09E+08	GAAAAAAA	GAAAAAAA	295.39	het	74	0.22	XM_00524	intron_variant&feature	
JAK3	snp	chr19	17954225	G	A	1748.79	het	98	0.66	XM_00525	synonymous_variant	
KDR	complex	chr4	55955110	CCC	TCT	747.175	hom	27	1.00	NM_00225	missense_variant	
KDR	snp	chr4	55955192	T	A	290.853	hom	14	1.00	NM_00225	intron_variant	
KDR	snp	chr4	55961159	T	C	1000.47	hom	39	0.95	NM_00225	intron_vari	rs2219471
KDR	ins	chr4	55962545	TGG	TGGG	757.479	het	65	0.54	NM_00225	intron_variant&feature	
KDR	snp	chr4	55972974	T	A	829.318	hom	28	1.00	NM_00225	missense_v	rs18703778

KIT	snp	chr4	55561677	G	A	576.144	het	36	0.61	XM_00526	splice_acceptor_varian	
KIT	snp	chr4	55592067	C	T	779.138	het	52	0.73	XM_00526	missense_variant	
KIT	snp	chr4	55592099	C	T	831.586	het	52	0.77	XM_00526	stop_gained	
KRAS	snp	chr12	25362777	A	G	458.573	het	29	0.59	NM_03336	3_prime_U	rs1137282
KRAS	snp	chr12	25398260	G	A	755.069	het	52	0.54	NM_03336	missense_v	COSM9381
MAP2K1	snp	chr15	66727597	G	C	6713.06	het	413	0.52	NM_00275	intron_vari	rs1694992
MET	snp	chr7	1.16E+08	G	A	575.982	het	41	0.54	XM_00525	synonymous_variant	
MET	snp	chr7	1.16E+08	G	A	500.756	hom	19	1.00	XM_00525	synonymou	rs2023748
MET	snp	chr7	1.16E+08	G	A	1162.26	hom	38	1.00	XM_00525	synonymou	rs41737&C
MYC	complex	chr8	1.29E+08	CCC	TCT	53.8172	het	84	0.15	NM_00246	upstream_gene_varian	
MYC	snp	chr8	1.29E+08	G	A	191.658	het	13	0.85	NM_00246	missense_variant	
MYCN	snp	chr2	16080157	C	G	395.752	hom	13	1.00	NM_00537	upstream_	rs11886063
MYCN	complex	chr2	16089613	CAT	TAC	414.795	hom	16	1.00	NM_00537	downstream_gene_var	
MYCN	complex,sr	chr2	16089613	CAT	TAC,CAC	2535.57	het	96	0.83	NM_00537	downstream_gene_var	
NOTCH1	snp	chr9	1.39E+08	G	A	627.336	hom	27	1.00	NM_01761	missense_variant	
NOTCH1	mnp	chr9	1.39E+08	CC	TT	1217.81	hom	53	1.00	NM_01761	missense_variant	
NOTCH1	complex	chr9	1.39E+08	AGTGGTCC	GGTGCTGC	1310.9	hom	52	0.92	NM_01761	missense_variant	
NOTCH1	snp	chr9	1.39E+08	G	A	4649.62	hom	159	0.99	NM_01761	synonymou	rs10521&C
NOTCH1	snp	chr9	1.39E+08	C	T	893.354	het	65	0.63	NM_01761	missense_variant	
NOTCH1	snp	chr9	1.39E+08	G	A	257.108	het	15	0.87	NM_01761	missense_variant	
NOTCH1	snp	chr9	1.39E+08	G	A	307.398	hom	13	1.00	NM_01761	synonymou	rs3705231
NOTCH1	snp	chr9	1.39E+08	C	G	3183.59	het	142	0.89	NM_01761	synonymous_variant	
NPM1	del	chr5	1.71E+08	CTTTTTTTT	CTTTTTTTT	338.253	het	44	0.34	NM_00252	splice_region_variant&	
PDGFRA	snp	chr4	55141055	A	G	6303.35	hom	219	1.00	NM_00620	synonymou	rs1873778
PDGFRA	snp	chr4	55144565	G	A	1542.82	het	72	0.85	NM_00620	missense_variant	
PDGFRA	snp	chr4	55161254	C	T	1742.72	hom	57	0.98	NM_00620	intron_vari	rs3733540
PDGFRA	snp	chr4	55161391	T	C	482.726	hom	17	1.00	NM_00620	synonymou	rs7685117
PDGFRA	snp	chr4	55161517	A	G	1999.35	hom	64	1.00	NM_00620	3_prime_U	rs7680422
PIK3CA	snp	chr3	1.79E+08	C	T	8660.12	het	532	0.61	NM_00621	missense_variant	
PIK3R1	snp	chr5	67586426	G	A	447.613	hom	19	1.00	NM_18152	intron_variant	
PTEN	snp	chr10	89624389	G	A	373.881	hom	16	1.00	NM_00031	intron_variant	
PTEN	snp	chr10	89685335	G	A	364.216	het	29	0.52	NM_00031	intron_variant	
PTEN	snp	chr10	89717809	C	T	266.347	het	15	0.73	NM_00031	intron_variant	
PTEN	del	chr10	89720633	CTTTTTTTT	CTTTTTTTT	378	het	115	0.17	NM_00031	splice_acceptor_varian	

PTEN	del	chr10	89725293	CTTTTTTTT	CTTTTTTTT	259.799	het	59	0.22	NM_00031	3_prime_UTR_variant&	
PTPN11	snp	chr12	1.13E+08	G	A	565.095	het	31	0.71	NM_00283	missense_variant	
RB1	snp	chr13	48919358	T	G	711.3	hom	25	1.00	NM_00032	intron_vari	rs198617
RB1	snp	chr13	49027222	C	A	362.864	hom	19	0.95	NM_00032	missense_variant	
RB1	snp	chr13	49033950	G	A	2020.78	het	98	0.82	NM_00032	missense_v	CD064622
RET	mnp	chr10	43610189	GGG	TCT	420.205	hom	17	0.94	NM_02097	splice_region_variant&	
RET	mnp	chr10	43610190	GG	CT	854.301	het	250	0.19	NM_02097	splice_region_variant&	
RET	mnp	chr10	43610199	GGG	CCC	570.609	het	330	0.15	NM_02097	intron_variant	
SMO	snp	chr7	1.29E+08	G	C	2145.68	hom	73	0.99	NM_00563	intron_vari	rs2075777
SMO	snp	chr7	1.29E+08	G	C	942.722	hom	31	1.00	NM_00563	synonymou	rs2228617
SRC	snp	chr20	36031551	C	T	351.842	het	29	0.55	NM_00541	intron_variant	
STK11	snp	chr19	1207238	G	T	5176.76	hom	169	1.00	XM_00525	intron_vari	rs3764640
STK11	snp	chr19	1218521	CCG	CCT	4675.72	het	249	0.71	XM_00525	intron_variant	
STK11	complex	chr19	1218521	CCG	TCT	119.999	het	73	0.16	XM_00525	intron_variant	
STK11	snp	chr19	1220321	T	C	4602.67	het	174	0.93	XM_00525	intron_vari	rs2075606
STK11	snp	chr19	1221340	G	A	530.204	het	39	0.54	XM_00525	splice_don	COSM1523
STK11	snp	chr19	1226623	C	T	322.984	het	23	0.57	XM_00525	missense_variant	
TERT	snp	chr5	1295255	GTC	GTT	9111.74	het	765	0.41	NM_19825	upstream_gene_varian	
TERT	snp	chr5	1295349	A	G	42548.3	het	2069	0.66	NM_19825	upstream_	rs2853669&
TP53	snp	chr17	7577490	G	T	925.675	het	87	0.55	NM_00054	intron_variant	
TP53	snp	chr17	7578278	G	A	270.287	het	22	0.50	NM_00054	missense_v	TP53_g.126
TP53	snp	chr17	7579472	G	C	962.219	hom	32	1.00	NM_00054	missense_v	rs1042522&
TP53	del	chr17	7579643	CCCCCAGC	CC	185.259	het	31	0.39	NM_00054	intron_variant&feature	