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Data Sheet

Product Name: CancerSeqPlus Paraffin Tissue Curl

Catalog No.: T2235086-SC **Lot No.: B906125**

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: 60 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:** _____

B906125

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.

CCND1	2.22	0.24	1.59E-01	CCND1	3.45	0.06	1.98E-03

symbol	type	chromosome	position	reference	mutation	quality	allele type	depth	variant frequency	transcript_id	consequence	existing variation
ABL1	snp	chr9	1.34E+08	A	T	380.039	hom	17	1.00	NM_00731	stop_gained	
ALK	snp	chr2	29432621	GGCCC	GGCCA	2776.83	het	286	0.33	NM_00430	intron_variant	
ALK	snp	chr2	29432776	T	C	862.951	het	104	0.31	NM_00430	intron_vari	rs3738867
ATM	snp	chr11	1.08E+08	G	T	571.866	hom	20	1.00	NM_00005	stop_gained	
BRAF	snp	chr7	1.4E+08	C	T	290.831	het	18	0.67	XM_00525	missense_v	rs3725699
CCNE1	mnp	chr19	30312624	TTC	GAA	241.86	het	18	0.56	NM_00123	splice_region_variant&	
CCNE1	snp	chr19	30313273	C	T	562.739	hom	20	1.00	NM_00123	intron_variant	
CDH1	snp	chr16	68771372	C	T	10641.2	het	527	0.73	NM_00436	splice_regi	rs3743674
CDH1	snp	chr16	68867230	C	A	481.216	het	35	0.54	NM_00436	missense_variant	
CDH1	snp	chr16	68867262	G	A	581.772	het	44	0.50	NM_00436	missense_variant	
CDK4	snp	chr12	58143031	G	A	1741.75	het	106	0.59	NM_00007	synonymous_variant	
CDKN2A	snp	chr9	21968199	C	G	22854.7	hom	781	0.93	NM_00119	3_prime_U	rs11515&C
CDKN2A	snp	chr9	21974742	G	A	996.895	het	59	0.68	NM_00119	missense_variant	
DDR2	mnp	chr1	1.63E+08	TG	CA	350.858	hom	14	0.93	XM_00524	intron_variant	
DDR2	snp	chr1	1.63E+08	TG	CG	15286.8	hom	502	0.97	XM_00524	intron_variant	
DDR2	snp	chr1	1.63E+08	G	T	1646.5	hom	63	1.00	XM_00524	intron_vari	rs1355287
ERBB3	snp	chr12	56477694	AGC	TGC	5049.71	hom	175	0.94	NM_00198	splice_region_variant&	
ERBB3	complex	chr12	56477694	AGC	TGT	291.226	hom	11	1.00	NM_00198	splice_region_variant&	
EZH2	snp	chr7	1.49E+08	A	G	528.825	hom	17	1.00	XM_00524	intron_vari	rs2072407
FBXW7	snp	chr4	1.53E+08	A	G	1119.53	hom	43	0.95	NM_03363	synonymous_variant	
FBXW7	snp	chr4	1.53E+08	A	G	911.59	het	57	0.54	NM_03363	intron_vari	rs1003360
FBXW7	del	chr4	1.53E+08	CAAAAAAA	CAAAAAAA	236.786	het	37	0.30	NM_03363	splice_region_variant&	
FBXW7	snp	chr4	1.53E+08	G	A	1115.36	het	56	0.82	NM_03363	intron_variant	
FGFR3	snp	chr4	1805662	C	A	300.137	hom	13	1.00	NM_00116	intron_variant	
FGFR3	del	chr4	1806012	TGGGGGG	TGGGGGG	797.752	het	305	0.17	NM_00116	intron_variant&feature	
FGFR3	snp	chr4	1806019	G	A	808.217	het	481	0.15	NM_00116	intron_variant	

FGFR3	snp	chr4	1807894	G	A	2153.41	hom	81	1.00	NM_00116	synonymou	rs7688609
FLT3	snp	chr13	28592734	G	A	865.691	het	57	0.72	NM_00411	splice_region_variant&	
FLT3	snp	chr13	28610183	A	G	4594.1	hom	147	1.00	NM_00411	splice_regi	rs2491231
FOXL2	mnp	chr3	1.39E+08	CC	TT	1699.89	het	372	0.22	NM_02306	missense_variant	
GNA11	snp	chr19	3119087	C	T	345.787	hom	16	1.00	NM_00206	intron_variant	
GNA11	complex	chr19	3119116	TCCCCTCA(	ACCCAGGT	389.658	hom	21	0.81	NM_00206	intron_variant&feature	
HNF1A	snp	chr12	1.21E+08	C	A	294.131	hom	16	1.00	XM_00525	intron_variant	
HRAS	complex	chr11	534338	TGCGGCC	GCAGGCC(	37.6326	het	166	0.13	NM_00534	5_prime_UTR_variant&	
HRAS	complex	chr11	534346	GGG	TGA	68.0951	het	168	0.14	NM_00534	5_prime_UTR_variant	
IDH1	del	chr2	2.09E+08	GAAAAAAA	GAAAAAAA	212.334	het	40	0.25	XM_00524	intron_variant&feature	
KDR	snp	chr4	55961159	T	C	2231.13	hom	79	1.00	NM_00225	intron_vari	rs2219471
KDR	snp	chr4	55972974	T	A	853.149	hom	29	1.00	NM_00225	missense_v	rs1870377&
KDR	snp	chr4	55979543	G	A	232.415	het	12	0.83	NM_00225	stop_gained	
KRAS	snp	chr12	25362777	A	G	1486.24	het	65	0.88	NM_03336	3_prime_U	rs1137282
MET	snp	chr7	1.16E+08	A	G	1048.43	het	77	0.51	XM_00525	synonymous_variant	
MYCN	snp	chr2	16080157	C	G	576.75	hom	19	1.00	NM_00537	upstream_	rs1188606:
MYCN	snp	chr2	16089615	T	C	2352.75	hom	80	1.00	NM_00537	downstrea	rs4669018
NOTCH1	snp	chr9	1.39E+08	G	A	345.977	hom	15	1.00	NM_01761	synonymou	rs2229974
NOTCH1	snp	chr9	1.39E+08	G	A	3999.51	hom	140	0.99	NM_01761	synonymou	rs10521&C
NOTCH1	snp	chr9	1.39E+08	C	T	1117.08	het	155	0.29	NM_01761	intron_variant	
NPM1	del,del	chr5	1.71E+08	CTTTTTTTT	CTTTTTTTT	544.558	het	54	0.35	NM_00252	splice_region_variant&	
PDGFRA	snp	chr4	55141055	A	G	5130.53	hom	172	1.00	NM_00620	synonymou	rs1873778&
PDGFRA	complex	chr4	55161254	CAGG	TAGA	330.559	hom	13	1.00	NM_00620	intron_variant	
PDGFRA	snp	chr4	55161254	CAGG	TAGG	3327.33	hom	121	0.88	NM_00620	intron_variant	
PDGFRA	snp	chr4	55161517	A	G	2518.92	hom	80	1.00	NM_00620	3_prime_U	rs7680422
PIK3CA	snp	chr3	1.79E+08	C	T	1092.21	het	74	0.54	NM_00621	synonymou	rs1051400
PTEN	snp	chr10	89717750	C	T	967.451	hom	34	1.00	NM_00031	missense_variant	
PTEN	del	chr10	89725293	CTTTTTTTT	CTTTTTTTT	161.712	het	55	0.18	NM_00031	3_prime_UTR_variant&	
PTPN11	snp	chr12	1.13E+08	G	T	306.915	het	25	0.64	NM_00283	missense_variant	
RET	mnp	chr10	43610189	GGG	TCT	680.637	hom	27	0.93	NM_02097	splice_region_variant&	
RET	mnp	chr10	43610199	GGG	CCC	551.922	het	600	0.13	NM_02097	intron_variant	
RET	snp	chr10	43610219	C	T	640.969	het	59	0.41	NM_02097	intron_variant	
RHOA	snp	chr3	49405934	G	A	230.659	het	18	0.56	NM_00166	synonymous_variant	
SMAD4	del	chr18	48575101	TGG	TG	271.414	het	19	0.58	NM_00535	frameshift_variant&fea	

SMAD4	snp	chr18	48581261	C	T	471.764	het	28	0.64	NM_00535	missense_v	rs1407432
SMAD4	snp	chr18	48591839	G	A	789.87	het	35	0.89	NM_00535	synonymou	COSM1389
SMARCB1	del	chr22	24133989	ACC	AC	241.306	het	82	0.20	XM_00526	frameshift_variant&fea	
SMARCB1	del	chr22	24176276	GCC	GC	51.6242	het	108	0.13	XM_00526	intron_variant&feature	
SMO	snp	chr7	1.29E+08	GGGG	CGGG	2084.15	het	107	0.72	NM_00563	intron_variant	
SMO	complex	chr7	1.29E+08	GGGG	CGGT	331.745	het	30	0.47	NM_00563	intron_variant	
SRC	snp	chr20	36031501	C	T	5748.38	hom	186	0.99	NM_00541	intron_vari	rs2273677
SRC	snp	chr20	36031602	G	A	494.044	het	37	0.62	NM_00541	synonymous_variant	
SRC	snp	chr20	36031740	C	T	403.516	het	18	0.89	NM_00541	synonymous_variant	
STK11	snp	chr19	1207238	G	T	3977.75	hom	135	0.97	XM_00525	intron_vari	rs3764640
STK11	snp	chr19	1218523	G	T	4628.58	het	321	0.49	XM_00525	intron_vari	rs2075604
STK11	snp	chr19	1219429	G	T	265.105	het	19	0.74	XM_00525	intron_variant	
STK11	snp	chr19	1220321	T	C	4213.46	het	225	0.62	XM_00525	intron_vari	rs2075606
STK11	snp	chr19	1220524	G	A	288.206	het	358	0.13	XM_00525	intron_variant	
STK11	snp	chr19	1222085	G	A	587.828	hom	25	1.00	XM_00525	intron_variant	
STK11	mnp	chr19	1226469	GG	AA	90.3957	het	807	0.11	XM_00525	missense_variant	
TERT	mnp	chr5	1295243	GA	TC	380.648	het	295	0.16	NM_19825	upstream_gene_variar	
TERT	snp	chr5	1295271	G	C	766.102	hom	31	0.94	NM_19825	upstream_gene_variar	
TERT	mnp	chr5	1295277	GCGGAGG/	CTCCTCCG(	687.362	het	31	0.94	NM_19825	upstream_gene_variar	
TERT	snp	chr5	1295349	A	G	20526.2	het	1070	0.61	NM_19825	upstream_	rs2853669
TP53	complex	chr17	7579472	GGGG	CGGA	426.334	het	21	0.86	NM_00054	missense_variant	
TP53	complex,sr	chr17	7579472	GGGG	CGGA,CGG	3860.32	het	153	0.86	NM_00054	missense_variant	