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Data Sheet

Product Name: CancerSeqPlus Paraffin Tissue Curl

Catalog No.: T2235086-SC **Lot No.: B906124**

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: 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:** _____

B906124

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	3.49	0.15	6.04E-04	DDR2	2.61	0.03	5.27E-03
ERBB2	20.12	1.11	6.11E-04	ERBB2	21.26	0.25	1.21E-03

symbol	type	chromosome	position	reference	mutation	quality	allele type	depth	variant frequency	transcript_id	consequence	existing variation
AKT1	snp	chr14	1.05E+08	C	T	5305.78	het	217	0.92	NM_00101	splice_region_variant&	
ALK	snp	chr2	29443638	G	A	343.822	het	22	0.77	NM_00430	synonymous_variant	
ALK	snp	chr2	29445458	G	T	931.101	het	40	0.85	NM_00430	synonymou	rs3795850
APC	snp	chr5	1.12E+08	G	A	489.939	het	30	0.63	XM_00527	missense_variant	
APC	snp	chr5	1.12E+08	T	A	568.903	hom	33	0.94	XM_00527	missense_v	rs3705811
ATM	snp	chr11	1.08E+08	C	T	362.483	het	22	0.64	NM_00005	synonymous_variant	
ATM	snp	chr11	1.08E+08	C	T	1008.38	het	56	0.66	NM_00005	intron_variant	
ATM	snp	chr11	1.08E+08	A	G	755.544	het	50	0.58	NM_00005	missense_variant	
CCND1	snp	chr11	69461850	C	T	2462.6	het	133	0.61	NM_05305	intron_vari	rs3690103
CDH1	snp	chr16	68771342	C	T	5835.87	het	269	0.83	NM_00436	synonymous_variant	
CDH1	mnp	chr16	68771371	CC	TT	5593.51	het	247	0.88	NM_00436	splice_region_variant&	
CDH1	snp	chr16	68772208	T	C	830.965	hom	29	1.00	NM_00436	synonymous_variant	
CDH1	mnp	chr16	68772213	TCT	AGA	758.923	hom	27	1.00	NM_00436	missense_variant	
CDH1	snp	chr16	68772220	G	A	839.097	hom	29	1.00	NM_00436	synonymous_variant	
CDH1	snp	chr16	68863645	C	T	240.4	het	16	0.63	NM_00436	missense_variant	
CDKN2A	snp	chr9	21965743	C	T	1031.07	het	55	0.69	NM_00119	downstream_gene_va	
CDKN2A	snp	chr9	21968199	C	G	21275.5	hom	690	0.99	NM_00119	3_prime_U	rs11515&C
CDKN2A	snp	chr9	21970926	G	A	359.824	het	20	0.70	NM_00119	synonymous_variant	
CDKN2A	snp	chr9	21974646	C	T	1516.84	het	84	0.64	NM_00119	intron_variant	
DDR2	snp	chr1	1.63E+08	T	C	11140.4	hom	356	0.99	XM_00524	intron_vari	rs1780003
DDR2	snp	chr1	1.63E+08	G	T	802.743	hom	32	1.00	XM_00524	intron_vari	rs1355287
EGFR	snp	chr7	55241724	C	T	809.717	het	37	0.89	NM_00522	synonymous_variant	
EGFR	snp	chr7	55259608	C	A	517.576	hom	23	1.00	NM_00522	intron_vari	rs3697258
ERBB2	complex	chr17	37880186	GAG	AAA	367.053	het	308	0.14	NM_00444	missense_variant	
ERBB3	snp	chr12	56477694	A	T	2237.46	hom	82	0.94	NM_00198	splice_regi	rs2271194

ERBB4	snp	chr2	2.13E+08	A	T	227.596	het	30	0.33	NM_00523	intron_vari	rs3512391
ERBB4	snp	chr2	2.13E+08	C	T	1824.19	het	128	0.51	NM_00523	missense_v	rs1436624
FBXW7	snp	chr4	1.53E+08	G	A	2293.67	het	103	0.90	NM_03363	missense_variant&spli	
FBXW7	del,del	chr4	1.53E+08	CAAAAAAA	CAAAAAAA	456.083	het	71	0.23	NM_03363	splice_region_variant&	
FGFR1	snp	chr8	38271526	C	T	1492.13	het	72	0.78	NM_00117	synonymous_variant	
FGFR3	snp	chr4	1803719	C	T	298.498	hom	11	1.00	NM_00116	synonymous_variant	
FGFR3	snp	chr4	1805987	G	A	12395	het	657	0.68	NM_00116	intron_variant	
FGFR3	snp	chr4	1806229	C	T	856.357	het	62	0.50	NM_00116	synonymous_variant	
FGFR3	snp	chr4	1807894	G	A	257.024	hom	11	1.00	NM_00116	synonymou	rs7688609
FLT3	snp	chr13	28610183	A	G	276.788	het	13	0.85	NM_00411	splice_regi	rs2491231
FOXL2	complex	chr3	1.39E+08	GCG	ACA	69.4118	het	220	0.12	NM_02306	missense_variant	
GNA11	snp	chr19	3118904	G	A	6281.77	het	403	0.54	NM_00206	intron_variant	
GNAS	snp	chr20	57484433	C	T	1678.87	het	103	0.60	NM_08042	missense_variant	
IDH1	del	chr2	2.09E+08	GAAAAAAA	GAAAAAAA	968.118	het	69	0.51	XM_00524	intron_variant&feature	
JAK2	snp	chr9	5073653	G	A	912.815	het	41	0.85	NM_00497	intron_vari	rs1891099
JAK3	snp	chr19	17948048	G	A	1000.59	het	59	0.86	XM_00525	intron_variant	
KDR	snp	chr4	55961159	T	C	907.251	het	45	0.78	NM_00225	intron_vari	rs2219471
KDR	snp	chr4	55980456	C	T	4182.88	het	162	0.93	NM_00225	intron_vari	rs2305949
KIT	snp	chr4	55593669	G	A	302.365	het	21	0.57	XM_00526	missense_v	CD057857
MYCN	snp	chr2	16080157	C	G	1091.81	hom	37	0.97	NM_00537	upstream_	rs1188606
NOTCH1	snp	chr9	1.39E+08	G	A	275.938	het	19	0.58	NM_01761	missense_variant	
NOTCH1	snp	chr9	1.39E+08	G	A	759.414	het	280	0.17	NM_01761	intron_variant	
NOTCH1	complex	chr9	1.39E+08	CACCAGGG	TCCCTGGT	812.492	het	175	0.23	NM_01761	missense_variant	
NOTCH1	snp	chr9	1.39E+08	G	A	564.484	het	37	0.57	NM_01761	intron_variant	
NPM1	del,del	chr5	1.71E+08	CTTTTTTTT	CTTTTTTTT	488.634	het	42	0.33	NM_00252	splice_region_variant&	
PDGFRA	complex	chr4	55141055	AGATG	GGATA	1210.26	hom	45	0.98	NM_00620	missense_variant	
PDGFRA	complex,sr	chr4	55141055	AGATG	GGATA,GG	7430.84	het	286	0.84	NM_00620	missense_variant	
PDGFRA	snp	chr4	55161254	C	T	2138.31	hom	68	1.00	NM_00620	intron_vari	rs3733540
PDGFRA	snp	chr4	55161517	A	G	2242.05	hom	77	1.00	NM_00620	3_prime_U	rs7680422
PIK3CA	snp	chr3	1.79E+08	C	T	307.398	hom	13	1.00	NM_00621	intron_variant	
PIK3R1	snp	chr5	67593231	C	T	512.071	het	32	0.59	NM_18152	intron_vari	rs1437715
PTEN	snp	chr10	89692970	C	T	1726.02	het	79	0.86	NM_00031	synonymou	COSM1349
PTEN	del	chr10	89720633	CTTTTTTTT	CTTTTTTTT	271.283	het	61	0.23	NM_00031	splice_acceptor_varian	
PTEN	snp	chr10	89725334	C	T	274.939	het	59	0.27	NM_00031	3_prime_UTR_variant	

RET	snp	chr10	43613843	G	T	2043.95	hom	69	0.99	NM_02097	synonymou	rs1800861
RET	snp	chr10	43615585	G	A	323.704	het	14	0.93	NM_02097	missense_variant	
RET	snp	chr10	43615628	G	A	307.768	het	13	0.92	NM_02097	missense_variant	
SMAD4	snp	chr18	48604803	C	T	1615.16	het	80	0.75	NM_00535	missense_variant	
SMARCB1	snp	chr22	24145647	C	T	950.067	het	60	0.75	XM_00526	intron_variant	
SMO	snp	chr7	1.29E+08	G	C	1327.99	hom	42	1.00	NM_00563	intron_vari	rs2075777
SMO	snp	chr7	1.29E+08	G	C	1049.53	hom	35	1.00	NM_00563	synonymou	rs2228617
STK11	snp	chr19	1207194	C	T	441.017	het	21	0.86	XM_00525	synonymous_variant	
STK11	snp	chr19	1207238	G	T	365.39	het	28	0.54	XM_00525	intron_vari	rs3764640
STK11	snp	chr19	1218441	C	T	4251.66	het	187	0.79	XM_00525	missense_variant	
STK11	snp	chr19	1218505	C	T	1948.93	het	95	0.77	XM_00525	splice_region_variant&	
STK11	snp	chr19	1218523	G	T	3312.04	het	163	0.75	XM_00525	intron_vari	rs2075604
STK11	ins	chr19	1219443	GCGGGGG	GCGGGGG	349.252	het	23	0.83	XM_00525	intron_variant&feature	
STK11	snp	chr19	1220321	T	C	4604.05	het	204	0.88	XM_00525	intron_vari	rs2075606
STK11	snp	chr19	1220588	C	T	5807.16	het	299	0.71	XM_00525	synonymous_variant	
STK11	snp	chr19	1220639	C	T	5767.58	hom	215	0.98	XM_00525	synonymou	COSM9622
STK11	snp	chr19	1220667	G	A	2520.2	hom	109	1.00	XM_00525	missense_variant	
TERT	snp	chr5	1295337	CCGCC	TCGCC	290.836	het	1121	0.11	NM_19825	upstream_gene_varian	
TP53	del	chr17	7579470	CGGGGGG	CGGGGGA	1070.8	het	60	0.65	NM_00054	frameshift_variant&fe	
TP53	snp	chr17	7579472	G	C	299.397	het	81	0.20	NM_00054	missense_v	rs1042522