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Data Sheet

Product Name: CancerSeqPlus Paraffin Tissue Curl

Catalog No.: T2235086-SC **Lot No.: B906121**

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: 44 year(s) old

Pathological Diagnosis: invasive (infiltrating) ductal carcinoma

Tumor Size: n/a

Location: breast, right

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

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

B906121

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.

ERBB4	3.13	0.18	9.20E-03	ERBB4	1.55	0.02	2.33E-01
MYC	3.54	0.22	6.66E-03	MYC	4.00	0.08	2.53E-03
CDKN2A	2.97	0.16	6.66E-03	CDKN2A	3.18	0.06	1.92E-03
EGFR	10.42	0.59	1.22E-03	EGFR	13.91	0.14	1.22E-03

symbol	type	chromosome	position	reference	mutation	quality	allele type	depth	variant frequency	transcript_id	consequence	existing variation
ALK	snp	chr2	29445347	A	G	183.01	het	13	0.85	NM_00430	intron_variant	
ALK	snp	chr2	29445458	G	T	2145.07	het	91	0.85	NM_00430	synonymou	rs3795850
APC	snp	chr5	1.12E+08	G	A	522.721	het	34	0.59	XM_00527	synonymou	CD991577&
ATM	ins	chr11	1.08E+08	TAA	TAAA	334.788	het	36	0.39	NM_00005	intron_variant&feature	
CCND1	snp	chr11	69461920	G	A	764.663	het	55	0.53	NM_05305	intron_variant	
CCND1	snp	chr11	69461939	G	A	720.9	het	52	0.52	NM_05305	intron_variant	
CCNE1	ins	chr19	30303583	CC	CCGGGC	1205.15	het	111	0.43	NM_00123	intron_variant&feature	
CDH1	snp	chr16	68771372	C	T	37490.4	hom	1188	0.99	NM_00436	splice_regi	rs3743674
CDH1	complex	chr16	68772282	GCC	ACT	316.838	het	294	0.15	NM_00436	missense_variant	
CDH1	snp	chr16	68849703	T	A	313.688	het	25	0.72	NM_00436	intron_variant	
CDH1	snp	chr16	68855925	C	T	466.93	het	33	0.55	NM_00436	missense_variant	
CDH1	complex	chr16	68862162	CAAC	TAAT	1881.14	het	172	0.41	NM_00436	synonymous_variant	
CDH1	complex	chr16	68863656	CCCC	TCCT	1053.82	het	90	0.43	NM_00436	missense_variant	
CDK4	snp	chr12	58145105	G	A	3710.76	het	211	0.64	NM_00007	missense_variant	
CDKN2A	snp	chr9	21968199	C	G	37796.8	hom	1195	1.00	NM_00119	3_prime_U	rs11515&C
DDR2	snp	chr1	1.63E+08	T	C	10663.8	hom	337	1.00	XM_00524	intron_vari	rs1780003
DDR2	snp	chr1	1.63E+08	G	T	761.06	hom	31	1.00	XM_00524	intron_vari	rs1355287
EGFR	snp	chr7	55259608	C	A	1072.04	het	63	0.89	NM_00522	intron_vari	rs36972582
ERBB3	snp	chr12	56477694	A	T	5377.52	hom	170	1.00	NM_00198	splice_regi	rs2271194
ERBB4	snp	chr2	2.13E+08	C	T	864.625	het	49	0.65	NM_00523	missense_variant	
FBXW7	del	chr4	1.53E+08	TACA	TA	794.214	het	44	0.75	NM_03363	intron_variant&feature	
FBXW7	snp	chr4	1.53E+08	A	G	2892.04	hom	98	0.97	NM_03363	intron_vari	rs10033601
FBXW7	snp	chr4	1.53E+08	G	A	1157.44	het	62	0.69	NM_03363	missense_v	COSM3059

FBXW7	del,del	chr4	1.53E+08	CAAAAAAA	CAAAAAAA	639.821	het	60	0.23	NM_03363	splice_region_variant&	
FGFR3	del	chr4	1806012	TGGGGGG	TGGGGGG	972.04	het	558	0.15	NM_00116	intron_variant&feature	
FGFR3	snp	chr4	1806196	C	T	396.71	het	31	0.55	NM_00116	synonymous_variant	
FGFR3	snp	chr4	1807894	G	A	3357.28	hom	135	0.99	NM_00116	synonymou	rs7688609
FLT3	snp	chr13	28610183	A	G	1531.9	hom	49	1.00	NM_00411	splice_regi	rs2491231
FOXL2	complex	chr3	1.39E+08	GCGGCGC	TCGGGGC	450.635	hom	16	1.00	NM_02306	missense_variant	
GNA11	snp	chr19	3119085	G	A	257.06	het	13	0.92	NM_00206	intron_variant	
IDH1	del	chr2	2.09E+08	GAAAAAAA	GAAAAAAA	827.804	het	58	0.55	XM_00524	intron_variant&feature	
JAK2	snp	chr9	5072650	C	T	494.624	het	38	0.50	NM_00497	intron_vari	rs1410729
KDR	snp	chr4	55961159	T	C	1425.02	het	68	0.82	NM_00225	intron_vari	rs2219471
KDR	snp	chr4	55972974	T	A	572.694	hom	20	1.00	NM_00225	missense_v	rs1870377
KDR	snp	chr4	55972995	C	T	470.171	het	20	0.90	NM_00225	intron_variant	
MAP2K1	snp	chr15	66727550	C	T	339.709	hom	12	1.00	NM_00275	missense_variant	
MET	snp	chr7	1.16E+08	G	A	858.258	het	38	0.89	XM_00525	synonymou	rs3738575
MYCN	snp	chr2	16080157	C	G	865.782	hom	29	0.97	NM_00537	upstream_	rs1188606
MYCN	snp	chr2	16089615	T	C	1608.25	hom	57	1.00	NM_00537	downstrea	rs4669018
NOTCH1	snp	chr9	1.39E+08	G	A	617.437	hom	22	1.00	NM_01761	synonymou	rs10521&C
NOTCH1	snp	chr9	1.39E+08	C	T	920.902	hom	33	1.00	NM_01761	missense_variant	
NOTCH1	complex	chr9	1.39E+08	AGCA	TGCT	253.094	het	84	0.19	NM_01761	missense_variant	
NOTCH1	snp	chr9	1.39E+08	G	A	36.9666	het	85	0.13	NM_01761	missense_variant	
NOTCH1	mnp	chr9	1.39E+08	GTC	CAG	256.002	het	82	0.20	NM_01761	missense_variant	
NOTCH1	snp	chr9	1.39E+08	C	T	1594.3	het	94	0.85	NM_01761	missense_v	COSM1461
NOTCH1	snp	chr9	1.39E+08	C	T	1476.71	het	90	0.87	NM_01761	synonymous_variant	
NOTCH1	snp	chr9	1.39E+08	C	T	1666.88	het	121	0.64	NM_01761	synonymou	COSM1461
NOTCH1	complex	chr9	1.39E+08	CGTCCTCC	AGTGCCAG	1626.28	hom	66	0.91	NM_01761	missense_variant	
NOTCH1	mnp	chr9	1.39E+08	GG	AA	451.409	het	888	0.12	NM_01761	missense_variant	
NPM1	del	chr5	1.71E+08	CTTTTTTTT	CTTTTTTTT	554.527	het	74	0.30	NM_00252	splice_region_variant&	
PDGFRA	snp	chr4	55141055	A	G	3701.24	hom	122	1.00	NM_00620	synonymou	rs1873778
PDGFRA	complex	chr4	55161254	CAGG	TAGA	352.493	hom	14	1.00	NM_00620	intron_variant	
PDGFRA	complex,sr	chr4	55161254	CAGG	TAGA,TAG	1634.91	het	61	0.77	NM_00620	intron_variant	
PDGFRA	snp	chr4	55161517	A	G	1182.55	hom	39	1.00	NM_00620	3_prime_U	rs7680422
PIK3CA	ins	chr3	1.79E+08	ATTTTTTTT	ATTTTTTTT	533.365	het	81	0.26	NM_00621	intron_variant&feature	
PIK3R1	snp	chr5	67588918	T	A	271.905	hom	10	1.00	NM_18152	intron_variant	
PIK3R1	complex	chr5	67588923	TTTCAGGG	CTTCTTCC	286.118	hom	12	1.00	NM_18152	splice_acceptor_varian	

PIK3R1	snp	chr5	67591201	C	T	166.97	het	118	0.14	NM_18152	intron_variant	
PIK3R1	complex	chr5	67592207	ATGAA	TTCAT	394.138	het	20	0.80	NM_18152	intron_variant	
PTEN	snp	chr10	89685257	G	A	673.416	het	33	0.79	NM_00031	intron_vari	COSM5922
PTEN	snp	chr10	89690686	C	T	191.233	het	12	0.83	NM_00031	intron_variant	
PTEN	del	chr10	89720633	CTTTTTTTT	CTTTTTTTT	432.468	het	86	0.28	NM_00031	splice_acceptor_varian	
RB1	snp	chr13	48919358	T	G	1815.53	hom	65	1.00	NM_00032	intron_vari	rs198617
RB1	snp	chr13	48942734	C	T	524.627	het	26	0.85	NM_00032	missense_v	CD951845
RB1	snp	chr13	49033816	T	C	226.479	het	14	0.71	NM_00032	splice_region_variant&	
RET	snp	chr10	43609966	G	A	561.809	het	39	0.56	NM_02097	missense_variant	
RET	mnp	chr10	43610189	GGG	TCT	809.303	hom	31	0.94	NM_02097	splice_region_variant&	
RET	mnp	chr10	43610199	GGG	CCC	906.796	hom	33	0.97	NM_02097	intron_variant	
RET	snp	chr10	43610281	G	A	392.808	hom	21	0.95	NM_02097	intron_variant	
RET	snp	chr10	43615611	G	A	220.399	het	12	0.83	NM_02097	missense_v	rs7608719
RET	snp	chr10	43615616	G	A	224.949	het	12	0.83	NM_02097	missense_variant	
SMAD4	snp	chr18	48581050	G	A	1757.3	het	82	0.84	NM_00535	intron_variant	
SMAD4	snp	chr18	48584588	C	T	1196.11	hom	44	0.98	NM_00535	missense_variant	
SMAD4	snp	chr18	48604760	C	T	869.567	het	50	0.68	NM_00535	missense_variant	
SMO	snp	chr7	1.29E+08	G	C	971.333	het	52	0.65	NM_00563	synonymou	rs2228617
SMO	mnp	chr7	1.29E+08	CC	TT	189.24	het	45	0.22	NM_00563	synonymous_variant	
STK11	snp	chr19	1207238	G	T	7438.19	het	334	0.79	XM_00525	intron_vari	rs3764640
STK11	snp	chr19	1218523	G	T	20630.7	hom	672	1.00	XM_00525	intron_vari	rs2075604
STK11	complex	chr19	1218605	TGGCAC	GGGAAG	307.624	hom	17	0.88	XM_00525	intron_variant	
STK11	ins	chr19	1219443	GCGGGGG	GCGGGGG	520.003	het	50	0.42	XM_00525	intron_variant&feature	
STK11	snp	chr19	1219454	G	A	192.975	het	134	0.16	XM_00525	intron_variant	
STK11	snp	chr19	1220321	T	C	10302	hom	335	1.00	XM_00525	intron_vari	rs2075606
STK11	mnp	chr19	1221896	GG	AA	36.5817	het	99	0.14	XM_00525	intron_variant	
TERT	snp	chr5	1295396	C	A	240.429	hom	12	1.00	NM_19825	upstream_gene_varian	
TP53	snp	chr17	7577405	GGA	GGC	545.302	het	140	0.19	NM_00054	intron_variant	
TP53	snp	chr17	7577457	G	A	1267.89	het	102	0.59	NM_00054	intron_vari	TP53_g.134
TP53	snp	chr17	7579472	G	C	2706.23	het	122	0.84	NM_00054	missense_v	rs1042522
TP53	del	chr17	7579643	CCCCCAGC	CC	116.288	het	68	0.21	NM_00054	intron_variant&feature	