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Data Sheet

Product Name: CancerSeqPlus Paraffin Tissue Curl

Catalog No.: T2235086-SC **Lot No.: B906128**

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: 67 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:** _____

B906128

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.

ERBB2	12.32	1.55	1.98E-03	ERBB2	14.11	0.34	6.15E-04
NOTCH1	3.60	0.51	9.45E-03	NOTCH1	5.65	0.22	6.15E-04
STK11	3.44	0.37	9.45E-03	STK11	4.38	0.15	3.18E-03

symbol	type	chromosome	position	reference	mutation	quality	allele type	depth	variant frequency	transcript_id	consequence	existing variation
ABL1	ins	chr9	1.34E+08	GTTTTTTTC	GTTTTTTTT	639.716	het	47	0.89	NM_00731	intron_variant&feature	
AKT1	mnp	chr14	1.05E+08	CG	TA	232.416	het	293	0.13	NM_00101	intron_variant	
AKT1	snp	chr14	1.05E+08	CG	TG	9472.33	het	613	0.52	NM_00101	intron_variant	
ALK	snp	chr2	29445347	A	G	369.91	hom	18	1.00	NM_00430	intron_variant	
ALK	snp	chr2	29445458	G	T	2322.94	hom	80	1.00	NM_00430	synonymou	rs3795850
APC	complex	chr5	1.12E+08	GCAG	ACAA	6902.33	het	1075	0.26	XM_00527	missense_variant	
APC	snp	chr5	1.12E+08	G	A	2491.87	hom	88	1.00	XM_00527	synonymous_variant	
APC	snp	chr5	1.12E+08	G	A	2159.63	hom	82	0.99	XM_00527	synonymou	rs465899
ATM	snp	chr11	1.08E+08	C	T	675.021	het	37	0.70	NM_00005	synonymous_variant	
ATM	snp	chr11	1.08E+08	C	T	1115.02	hom	43	0.95	NM_00005	missense_variant	
CCND1	snp	chr11	69461870	G	A	8016.23	het	421	0.67	NM_05305	intron_variant	
CCND1	snp	chr11	69471125	G	A	8541.29	hom	306	1.00	NM_05305	downstream_gene_var	
CDH1	snp	chr16	68771372	C	T	29160	hom	938	0.99	NM_00436	splice_regi	rs3743674
CDH1	snp	chr16	68772296	G	A	2598.63	het	149	0.64	NM_00436	missense_variant	
CDH1	snp	chr16	68835723	C	T	2899.6	het	204	0.51	NM_00436	missense_variant	
CDH1	snp	chr16	68844219	G	A	1527.86	het	84	0.93	NM_00436	synonymous_variant	
CDH1	snp	chr16	68853280	C	A	189.417	het	15	0.73	NM_00436	missense_variant	
CDH1	snp	chr16	68863646	C	T	1933.24	het	115	0.62	NM_00436	synonymous_variant	
CDK4	complex	chr12	58142970	GCAG	ACAA	269.336	het	181	0.15	NM_00007	synonymous_variant	
CDK4	snp	chr12	58145480	C	T	2541.98	het	127	0.74	NM_00007	synonymous_variant	
CDKN2A	complex	chr9	21968197	CCC	TCG	5277.86	hom	193	0.99	NM_00119	3_prime_UTR_variant	
CDKN2A	complex,sr	chr9	21968197	CCC	TCG,CCG	8523.94	het	310	0.62	NM_00119	3_prime_UTR_variant	
CSF1R	snp	chr5	1.49E+08	C	T	1212.03	het	64	0.72	NM_00521	missense_variant	
DDR2	snp	chr1	1.63E+08	T	C	23198.5	hom	769	0.98	XM_00524	intron_vari	rs1780003

DDR2	snp	chr1	1.63E+08	G	A	1318.38	hom	50	0.96	XM_00524	intron_vari	rs3678066
DDR2	snp	chr1	1.63E+08	G	T	494.351	hom	21	1.00	XM_00524	intron_vari	rs1355287
ERBB2	complex	chr17	37881258	CCCAGGCC	TCCAGATG	285.771	hom	11	1.00	NM_00444	intron_variant&feature	
ERBB3	snp	chr12	56477694	AGCCC	TGCCC	21597.3	hom	783	0.93	NM_00198	splice_region_variant&	
ERBB3	complex	chr12	56477694	AGCCC	TGCCT	1056.47	het	53	0.81	NM_00198	splice_region_variant&	
ERBB4	snp	chr2	2.13E+08	C	T	12133.1	het	592	0.78	NM_00523	synonymous_variant	
ERBB4	snp	chr2	2.13E+08	C	T	2950.57	hom	116	0.94	NM_00523	splice_region_variant&	
ERBB4	snp	chr2	2.13E+08	G	A	945.188	hom	36	0.97	NM_00523	synonymous_variant	
EZH2	snp	chr7	1.49E+08	A	G	280.425	het	12	0.92	XM_00524	intron_vari	rs2072407
FBXW7	del	chr4	1.53E+08	CTTTTTTTT	CTTTTTTTT	1091.83	het	192	0.22	NM_03363	intron_variant&feature	
FBXW7	snp	chr4	1.53E+08	G	A	440.666	hom	16	1.00	NM_03363	missense_v	COSM1427
FBXW7	snp	chr4	1.53E+08	G	A	1467.01	het	91	0.59	NM_03363	synonymous_variant	
FBXW7	snp	chr4	1.53E+08	A	G	269.818	het	17	0.65	NM_03363	intron_vari	rs1003360
FGFR1	snp	chr8	38271429	G	A	1052.51	het	54	0.76	NM_00117	splice_region_variant&	
FGFR1	snp	chr8	38273481	G	A	4965.97	hom	185	0.99	NM_00117	synonymous_variant	
FGFR1	snp	chr8	38282021	G	A	308.344	het	24	0.63	NM_00117	splice_region_variant&	
FGFR1	snp	chr8	38282096	C	T	380.623	hom	19	1.00	NM_00117	stop_gained	
FGFR3	del	chr4	1806012	TGGGGGG	TGGGGGG	348.932	het	231	0.15	NM_00116	intron_variant&feature	
FGFR3	snp	chr4	1808312	G	A	3948.08	het	202	0.72	NM_00116	synonymous_variant	
FGFR3	snp	chr4	1808953	C	T	835.967	het	46	0.70	NM_00116	synonymou	rs3694240
FLT3	snp	chr13	28610183	A	G	2690.7	hom	93	1.00	NM_00411	splice_regi	rs2491231
FOXL2	complex	chr3	1.39E+08	CCCGCC	GGCGGG	902.291	hom	35	1.00	NM_02306	missense_variant	
FOXL2	complex	chr3	1.39E+08	CCTCC	TGGCG	989.891	hom	42	0.95	NM_02306	missense_variant	
GNAQ	snp	chr9	80409539	C	T	324.745	hom	12	1.00	NM_00207	intron_variant	
GNAS	snp	chr20	57484393	A	G	2937.61	het	174	0.60	NM_08042	intron_vari	rs3679091
HRAS	del	chr11	533737	GGCTC	GC	412.239	het	18	0.89	NM_00534	intron_variant&feature	
HRAS	ins	chr11	533745	GG	GAAG	410.588	het	19	0.89	NM_00534	intron_variant&feature	
HRAS	mnp	chr11	533749	AG	CA	462.845	hom	18	0.94	NM_00534	intron_variant	
HRAS	snp	chr11	533971	C	T	2476.41	het	204	0.54	NM_00534	intron_variant	
HRAS	snp	chr11	534250	G	A	6478.89	het	327	0.72	NM_00534	stop_gained	
HRAS	del	chr11	534403	GCCCAGGC	GC	2378.25	het	137	0.59	NM_00534	intron_variant&feature	
HRAS	complex	chr11	534405	CCAGGCC	TCAGC	1161.57	hom	42	1.00	NM_00534	intron_variant&feature	
IDH1	del	chr2	2.09E+08	GAAAAAAA	GAAAAAAA	407.365	het	33	0.48	XM_00524	intron_variant&feature	
JAK2	snp	chr9	5069052	T	C	319.609	het	15	0.87	NM_00497	synonymous_variant	

JAK3	snp	chr19	17947919	G	A	11135.1	het	756	0.51	XM_00525	intron_variant	
JAK3	mnp	chr19	17954206	CC	TT	787.025	het	224	0.19	XM_00525	missense_variant	
JAK3	snp	chr19	17954235	G	A	3347.07	het	177	0.74	XM_00525	missense_variant	
KDR	snp	chr4	55955100	G	A	1520.94	het	76	0.75	NM_00225	stop_gaine	rs3764327(
KDR	snp	chr4	55979488	G	A	2691.03	hom	101	0.96	NM_00225	missense_variant	
KIT	snp	chr4	55592089	G	A	283.894	het	14	0.86	XM_00526	synonymous_variant	
KIT	snp	chr4	55592178	C	T	2609.52	het	120	0.86	XM_00526	missense_variant	
KIT	snp	chr4	55593727	C	T	196.186	het	208	0.13	XM_00526	intron_variant	
KRAS	snp	chr12	25380341	G	A	615.367	het	39	0.59	NM_03336	synonymous_variant	
MAP2K1	snp	chr15	66727595	CAG	CAC	9224.44	hom	306	0.95	NM_00275	intron_variant	
MAP2K1	complex	chr15	66727595	CAG	TAC	457.885	hom	16	1.00	NM_00275	intron_variant	
MET	snp	chr7	1.16E+08	G	A	1128.58	het	69	0.59	XM_00525	synonymou	COSM1084
MET	snp	chr7	1.16E+08	G	A	351.302	het	17	0.88	XM_00525	missense_variant	
MET	snp	chr7	1.16E+08	G	A	412.791	hom	17	0.94	XM_00525	synonymou	rs41737&C
MET	snp	chr7	1.16E+08	C	T	1060.17	het	72	0.54	XM_00525	synonymou	rs3707679
MYC	snp	chr8	1.29E+08	C	T	621.261	het	44	0.52	NM_00246	stop_gained	
MYCN	snp	chr2	16080157	C	G	652.645	hom	21	1.00	NM_00537	upstream_	rs1188606
MYCN	del	chr2	16086080	AGGTGGTC	AGGTC	1360.26	het	160	0.34	NM_00537	inframe_deletion	
MYCN	snp	chr2	16089615	T	C	7367.13	hom	263	1.00	NM_00537	downstrea	rs4669018
NOTCH1	snp	chr9	1.39E+08	G	A	1055.97	het	633	0.15	NM_01761	synonymous_variant	
NOTCH1	snp	chr9	1.39E+08	G	A	3974.36	hom	139	1.00	NM_01761	synonymou	rs10521&C
NOTCH1	snp	chr9	1.39E+08	G	A	3493.32	hom	126	1.00	NM_01761	missense_variant	
NOTCH1	complex	chr9	1.39E+08	CACCAGGG	TCCCTGGT(	1144.24	hom	43	1.00	NM_01761	missense_variant	
NOTCH1	mnp	chr9	1.39E+08	CCT	GTG	1096.28	hom	40	1.00	NM_01761	missense_variant	
NOTCH1	complex	chr9	1.39E+08	CGTCCTCC	AGTGCCAG	1326.68	hom	49	0.98	NM_01761	missense_variant	
NOTCH1	snp	chr9	1.39E+08	C	T	6079.82	het	395	0.54	NM_01761	missense_variant	
NPM1	del	chr5	1.71E+08	CTTTTTTTT	CTTTTTTTT	927.029	het	85	0.46	NM_00252	splice_region_variant&	
NRAS	snp	chr1	1.15E+08	C	T	722.771	het	37	0.78	NM_00252	splice_region_variant&	
PDGFRA	snp	chr4	55141055	A	G	15316.9	hom	550	1.00	NM_00620	synonymou	rs1873778
PDGFRA	snp	chr4	55144053	C	T	273.489	hom	10	1.00	NM_00620	intron_variant	
PDGFRA	snp	chr4	55161254	C	T	10323.1	hom	324	1.00	NM_00620	intron_vari	rs3733540
PDGFRA	snp	chr4	55161517	A	G	3190.94	hom	102	1.00	NM_00620	3_prime_U	rs7680422
PIK3CA	snp	chr3	1.79E+08	G	T	132.331	het	12	0.83	NM_00621	missense_variant&spli	
PIK3CA	del	chr3	1.79E+08	CTT	CT	1655.12	het	170	0.36	NM_00621	frameshift_variant&fea	

PIK3CA	ins	chr3	1.79E+08	ATTTTTTTT	ATTTTTTTT	314.63	het	52	0.29	NM_00621	intron_variant&feature	
PIK3CA	complex	chr3	1.79E+08	TTAC	ATAAGC	239.322	het	15	0.67	NM_00621	frameshift_variant&fea	
PIK3R1	snp	chr5	67588186	C	T	2109.51	hom	80	0.95	NM_18152	missense_variant	
PIK3R1	snp	chr5	67589213	G	A	1553.52	het	63	0.92	NM_18152	missense_variant	
PIK3R1	snp	chr5	67592018	G	C	387.388	het	28	0.54	NM_18152	missense_variant	
PTEN	mnp	chr10	89711911	TA	AG	146.062	het	79	0.16	NM_00031	missense_variant	
PTEN	del	chr10	89720633	CTTTTTTTT	CTTTTTTTT	272.766	het	66	0.27	NM_00031	splice_acceptor_varian	
RET	mnp	chr10	43610189	GGG	TCT	1327.38	hom	55	0.91	NM_02097	splice_region_variant&	
RET	mnp	chr10	43610199	GGG	CCC	1475.37	hom	56	0.96	NM_02097	intron_variant	
RET	snp	chr10	43610256	G	A	498.53	het	31	0.81	NM_02097	intron_variant	
RET	mnp	chr10	43614957	GG	AA	801.719	het	162	0.23	NM_02097	intron_variant	
RET	snp	chr10	43617452	C	T	2821.63	het	163	0.63	NM_02097	missense_v	KinMutBase
RHOA	snp	chr3	49405946	T	A	1113.27	hom	52	1.00	NM_00166	missense_variant	
ROS1	snp	chr6	1.18E+08	C	A	1262.99	het	58	0.86	NM_00294	intron_variant	
SMAD4	snp	chr18	48575657	C	T	3354.95	het	158	0.83	NM_00535	splice_region_variant&	
SMAD4	snp	chr18	48604700	G	A	1716.26	hom	60	1.00	NM_00535	missense_v	CM056701
SMAD4	snp	chr18	48604729	C	A	320.105	hom	18	1.00	NM_00535	missense_variant	
SMARCB1	snp	chr22	24145490	A	G	2149.99	het	99	0.86	XM_00526	missense_variant	
STK11	mnp	chr19	1207007	CC	TT	2036.48	het	258	0.30	XM_00525	missense_variant	
STK11	snp	chr19	1207238	G	T	15289	hom	497	0.99	XM_00525	intron_vari	rs3764640
STK11	ins	chr19	1219443	GCGGGGG	GCGGGGG	4550.13	hom	173	0.96	XM_00525	intron_variant&feature	
STK11	snp	chr19	1219451	C	G	364.692	het	259	0.17	XM_00525	intron_vari	rs3695156(
STK11	snp	chr19	1220321	T	C	13658.1	het	618	0.76	XM_00525	intron_vari	rs2075606
STK11	snp	chr19	1223159	T	C	1217.03	het	50	0.92	XM_00525	missense_variant	
STK11	complex	chr19	1223164	GGTGCCCG	CGGGCACC	1232.94	hom	47	0.94	XM_00525	missense_variant&spli	
TERT	complex	chr5	1295322	GGGTCCC	ATTTTAT	2487.59	hom	94	0.96	NM_19825	upstream_gene_varian	
TP53	snp	chr17	7576844	A	T	260.938	het	28	0.68	NM_00054	intron_variant	
TP53	snp	chr17	7578265	A	G	222.706	het	18	0.56	NM_00054	missense_v	TP53_g.126
TP53	snp	chr17	7578477	G	A	1902.15	het	107	0.67	NM_00054	synonymou	TP53_g.124
TP53	snp	chr17	7579310	A	C	5512.81	het	367	0.53	NM_00054	splice_don	TP53_g.116
TP53	snp	chr17	7579472	G	C	2053.86	hom	66	1.00	NM_00054	missense_v	rs1042522
TP53	snp	chr17	7579636	C	T	505.966	het	35	0.54	NM_00054	intron_vari	rs1384540
TP53	snp	chr17	7579801	G	C	288.337	hom	13	1.00	NM_00054	intron_vari	rs1642785
TP53	snp	chr17	7590760	G	A	2314.22	het	98	0.92	NM_00054	5_prime_UTR_variant	

VHL	snp	chr3	10183529	G	A	8512.99	het	474	0.63	NM_00055	5_prime_UTR_variant
VHL	snp	chr3	10183540	G	A	8160.49	het	410	0.72	NM_00055	synonymous_variant
VHL	snp	chr3	10183549	G	A	8107.74	het	400	0.74	NM_00055	synonymous_variant
VHL	snp	chr3	10183576	G	A	1236.29	het	82	0.55	NM_00055	synonymous_variant