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Data Sheet

Product Name: CancerSeqPlus Paraffin Tissue Curl

Catalog No.: T2235086-SC **Lot No.: B906127**

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: 55 year(s) old

Pathological Diagnosis: invasive (infiltrating) ductal carcinoma

Tumor Size: 4.5x4x4 (cm)

Location: breast, right

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

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

B906127

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.

symbol	type	chromosome	position	reference	mutation	quality	allele type	depth	variant frequency	transcript_id	consequence	existing variation
APC	snp	chr5	1.12E+08	G	A	819.443	het	52	0.62	XM_00527	synonymou	rs465899
CCNE1	snp	chr19	30314666	C	T	673.604	het	39	0.59	NM_00123	synonymou	rs7257694
CDH1	snp	chr16	68771372	C	T	11363.4	hom	359	1.00	NM_00436	splice_regi	rs3743674
CDH1	ins	chr16	68771418	CG	CGCCCCAG	305.451	het	20	0.85	NM_00436	intron_variant&feature	
CDH1	del	chr16	68835572	GTGAATT	GT	510.42	het	82	0.26	NM_00436	frameshift_variant&sp	
CDH1	snp	chr16	68857289	T	C	4420.9	het	232	0.66	NM_00436	intron_vari	rs2276330
CDH1	snp	chr16	68857441	T	C	437.493	het	24	0.71	NM_00436	synonymou	rs1801552
CDKN2A	snp	chr9	21968199	C	G	14896.6	hom	488	1.00	NM_00119	3_prime_U	rs11515&C
CTNNB1	del	chr3	41265953	CTTTTTTTT	CTTTTTTTT	44.8598	het	129	0.12	XM_00526	intron_variant&feature	
DDR2	snp	chr1	1.63E+08	T	C	8830.29	hom	292	1.00	XM_00524	intron_vari	rs1780003
DDR2	snp	chr1	1.63E+08	G	T	1458.68	hom	54	1.00	XM_00524	intron_vari	rs1355287
EGFR	snp	chr7	55249063	G	A	2231.23	hom	73	1.00	NM_00522	synonymou	rs1050171
ERBB3	snp	chr12	56477694	AGCCC	TGCCC	6443.46	hom	228	0.92	NM_00198	splice_region_variant&	
ERBB3	complex	chr12	56477694	AGCCC	TGCCT	271.535	hom	16	0.75	NM_00198	splice_region_variant&	
ERBB4	snp	chr2	2.13E+08	C	T	42.5371	het	77	0.13	NM_00523	splice_acce	COSM1530
EZH2	snp	chr7	1.49E+08	A	G	960.423	het	58	0.57	XM_00524	intron_vari	rs2072407
FBXW7	del,del	chr4	1.53E+08	CAAAAAAA	CAAAAAAA	886.993	het	85	0.33	NM_03363	splice_region_variant&	
FGFR1	snp	chr8	38271575	T	A	282.72	het	26	0.58	NM_00117	intron_variant	
FGFR2	del	chr10	1.23E+08	ACA	AA	2884.87	het	152	0.64	NM_02297	intron_variant&feature	
FGFR2	snp	chr10	1.23E+08	C	A	126.197	het	65	0.17	NM_02297	intron_vari	rs4647915
FGFR3	snp	chr4	1805662	C	A	225.461	hom	10	1.00	NM_00116	intron_variant	
FGFR3	del	chr4	1806012	TGGGGGG	TGGGGGG	2667.86	het	536	0.24	NM_00116	intron_variant&feature	
FGFR3	snp	chr4	1807894	G	A	3063.09	hom	102	1.00	NM_00116	synonymou	rs7688609
FLT3	snp	chr13	28609991	T	C	291.831	hom	11	1.00	NM_00411	intron_vari	rs2491229
FLT3	snp	chr13	28609997	T	C	320.42	hom	12	1.00	NM_00411	intron_vari	rs2491230
FLT3	snp	chr13	28610183	A	G	4118.62	hom	135	1.00	NM_00411	splice_regi	rs2491231
FOXL2	snp	chr3	1.39E+08	GA	GC	12249	het	751	0.55	NM_02306	synonymous_variant	
GNA11	snp	chr19	3119085	G	A	577.355	het	42	0.74	NM_00206	intron_variant	

HRAS	del	chr11	534403	GCCCAGGC	GC	452.26	het	172	0.17	NM_00534	intron_variant&feature	
IDH1	del	chr2	2.09E+08	GAAAAAAA	GAAAAAAA	899.776	het	196	0.22	XM_00524	intron_variant&feature	
JAK2	del	chr9	5073681	CTTTTTTTT	CTTTTTTTT	230.281	het	41	0.24	NM_00497	splice_region_variant&	
MAP2K1	snp	chr15	66727597	G	C	8226.7	hom	273	0.99	NM_00275	intron_vari	rs1694924
MET	snp	chr7	1.16E+08	G	A	213.055	het	15	0.73	XM_00525	synonymou	rs1176221
MLH1	snp	chr3	37067050	A	G	2955.54	het	203	0.51	NM_00024	intron_vari	rs1112974
MYCN	snp	chr2	16080157	C	G	906.248	hom	29	1.00	NM_00537	upstream_	rs1188606
NPM1	del	chr5	1.71E+08	CTTTTTTTT	CTTTTTTTT	215.03	het	29	0.34	NM_00252	splice_region_variant&	
PDGFRA	snp	chr4	55141055	A	G	8826.82	hom	295	1.00	NM_00620	synonymou	rs1873778
PDGFRA	snp	chr4	55161254	C	T	1509.57	hom	52	0.98	NM_00620	intron_vari	rs3733540
PDGFRA	snp	chr4	55161391	T	C	668.613	hom	22	1.00	NM_00620	synonymou	rs7685117
PDGFRA	snp	chr4	55161517	A	G	1890.29	hom	62	1.00	NM_00620	3_prime_U	rs7680422
PIK3CA	snp	chr3	1.79E+08	C	A	3272.13	hom	118	0.99	NM_00621	intron_vari	rs2699895
PIK3CA	del	chr3	1.79E+08	ATTTTTTTT	ATTTTTTTT	1148.9	het	89	0.49	NM_00621	intron_variant&feature	
PTEN	del	chr10	89720633	CTTTTTTTT	CTTTTTTTT	500.17	het	114	0.24	NM_00031	splice_acceptor_varian	
PTEN	del	chr10	89725293	CTTTTTTTT	CTTTTTTTT	327.473	het	77	0.21	NM_00031	3_prime_UTR_variant&	
RB1	snp	chr13	48919358	T	G	1742.17	hom	59	1.00	NM_00032	intron_vari	rs198617
RB1	ins	chr13	48953655	CAAAAAAA	CAAAAAAA	572.751	het	78	0.28	NM_00032	intron_variant&feature	
RB1	ins	chr13	49034022	ATT	ATTT	415.46	het	34	0.62	NM_00032	intron_variant&feature	
RET	snp	chr10	43613843	G	T	2128.8	hom	68	1.00	NM_02097	synonymou	rs1800861
ROS1	snp	chr6	1.18E+08	G	A	270.234	het	15	0.93	NM_00294	intron_variant	
SMO	snp	chr7	1.29E+08	G	C	7306.93	hom	246	1.00	NM_00563	intron_vari	rs2075777
SMO	snp	chr7	1.29E+08	G	C	2914.78	hom	94	1.00	NM_00563	synonymou	rs2228617
STK11	snp	chr19	1207238	G	T	2159.08	het	107	0.74	XM_00525	intron_vari	rs3764640
STK11	snp	chr19	1218523	G	T	6503.98	het	295	0.76	XM_00525	intron_vari	rs2075604
STK11	snp	chr19	1220321	T	C	3927.27	het	197	0.67	XM_00525	intron_vari	rs2075606
STK11	snp	chr19	1222268	A	G	225.206	hom	11	1.00	XM_00525	intron_vari	rs6097756
TP53	snp	chr17	7579472	G	C	1786.13	het	94	0.66	NM_00054	missense_v	rs1042522
TP53	del	chr17	7579643	CCCCCAGC	CC	285.631	het	57	0.32	NM_00054	intron_variant&feature	
TP53	snp	chr17	7579801	G	C	579.584	hom	25	0.96	NM_00054	intron_vari	rs1642785