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Data Sheet

Product Name: CancerSeqPlus Paraffin Tissue Curl

Catalog No.: T2235086-SC **Lot No.: B906136**

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: 59 year(s) old

Pathological Diagnosis: invasive (infiltrating) ductal carcinoma

Tumor Size: 10x10x10 (cm)

Location: breast, left

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

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

B906136

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	1158.89	hom	44	1.00	XM_00527	synonymou	rs41115&C
APC	snp	chr5	1.12E+08	G	A	766.564	hom	29	1.00	XM_00527	synonymou	rs465899
APC	snp	chr5	1.12E+08	G	A	792.7	het	42	0.76	XM_00527	missense_variant	
ATM	snp	chr11	1.08E+08	T	C	1078	hom	36	1.00	NM_00005	missense_v	rs1800568
CCNE1	snp	chr19	30304010	G	A	357.643	het	41	0.41	NM_00123	intron_variant	
CDH1	snp	chr16	68771372	C	T	19116.5	hom	609	1.00	NM_00436	splice_regi	rs3743674
CDH1	ins	chr16	68771418	CG	CGCCCCAG	626.17	hom	27	1.00	NM_00436	intron_variant&feature	
CDKN2A	complex,m	chr9	21968199	CGA	GGC,GCA	923.907	het	49	0.63	NM_00119	3_prime_UTR_variant	
CDKN2A	snp	chr9	21968199	CG	GG	32129.3	hom	1070	0.97	NM_00119	3_prime_UTR_variant	
CSF1R	complex	chr5	1.49E+08	TTGC	GTGG	282.461	het	168	0.15	NM_00521	missense_variant	
CSF1R	mnp	chr5	1.49E+08	GGGT	ACCC	110.121	het	173	0.13	NM_00521	missense_variant	
CSF1R	snp	chr5	1.49E+08	C	G	489.258	het	105	0.24	NM_00521	missense_variant	
DDR2	snp	chr1	1.63E+08	T	C	15444.2	hom	496	1.00	XM_00524	intron_vari	rs1780003
DDR2	snp	chr1	1.63E+08	G	T	1468.46	hom	52	1.00	XM_00524	intron_vari	rs1355287
EGFR	snp	chr7	55249063	G	A	710.467	hom	23	1.00	NM_00522	synonymou	rs1050171
ERBB2	complex	chr17	37881012	TATGTCTC	GAAGGCG	147.85	het	135	0.16	NM_00444	missense_variant	
ERBB3	snp	chr12	56477694	A	T	8368.45	hom	268	1.00	NM_00198	splice_regi	rs2271194
ERBB4	snp	chr2	2.13E+08	T	A	268.588	hom	12	1.00	NM_00523	intron_variant	
ESR1	snp	chr6	1.52E+08	G	A	6848.29	hom	216	1.00	XM_00526	synonymou	rs2228480
FBXW7	del,del	chr4	1.53E+08	CAAAAAAA	CAAAAAAA	313.77	het	55	0.25	NM_03363	splice_region_variant&	
FGFR3	del	chr4	1806012	TGGGGGG	TGGGGGG	1658.44	het	437	0.20	NM_00116	intron_variant&feature	
FGFR3	snp	chr4	1807894	G	A	2852.6	hom	94	0.99	NM_00116	synonymou	rs7688609
FGFR3	snp	chr4	1808517	G	A	475.351	hom	21	1.00	NM_00116	intron_variant	
FLT3	snp	chr13	28610183	A	G	59.6042	het	96	0.13	NM_00411	splice_regi	rs2491231
FOXL2	mnp	chr3	1.39E+08	GG	AA	496.671	het	64	0.38	NM_02306	missense_variant	
FOXL2	snp	chr3	1.39E+08	G	A	805.635	het	65	0.57	NM_02306	synonymous_variant	
HNF1A	snp	chr12	1.21E+08	G	C	505.163	het	27	0.89	XM_00525	synonymou	rs5634858
IDH1	del	chr2	2.09E+08	GAAAAAAA	GAAAAAAA	1699.64	het	213	0.30	XM_00524	intron_variant&feature	

JAK2	del	chr9	5073681	CTTTTTTTT	CTTTTTTTT	404.295	het	55	0.29	NM_00497	splice_region_variant&	
KDR	snp	chr4	55972974	T	A	623.643	het	40	0.58	NM_00225	missense_v	rs1870377
KDR	snp	chr4	55979558	C	T	399.926	het	23	0.74	NM_00225	missense_v	rs2305948
KDR	snp	chr4	55980456	C	T	1933.22	het	96	0.69	NM_00225	intron_vari	rs2305949
MET	snp	chr7	1.16E+08	G	A	814.304	het	40	0.75	XM_00525	synonymou	rs41737&C
MLH1	snp	chr3	37067050	A	G	3489.79	hom	122	0.99	NM_00024	intron_vari	rs1112974
MYC	snp	chr8	1.29E+08	G	A	2555.41	het	171	0.61	NM_00246	5_prime_UTR_variant	
MYC	snp	chr8	1.29E+08	G	A	568.862	hom	27	0.96	NM_00246	5_prime_UTR_variant	
MYCN	snp	chr2	16080157	C	G	658.385	hom	21	1.00	NM_00537	upstream_	rs1188606
NOTCH1	snp	chr9	1.39E+08	G	A	3257.94	hom	125	1.00	NM_01761	synonymou	rs2229974
NPM1	del	chr5	1.71E+08	CTTTTTTTT	CTTTTTTTT	701.753	het	97	0.29	NM_00252	splice_region_variant&	
NRAS	del	chr1	1.15E+08	TGG	TG	37.1748	het	70	0.14	NM_00252	frameshift_variant&fea	
PDGFRA	snp	chr4	55141055	A	G	7007.75	hom	231	1.00	NM_00620	synonymou	rs1873778
PDGFRA	snp	chr4	55161254	C	T	1849.35	hom	61	0.98	NM_00620	intron_vari	rs3733540
PDGFRA	snp	chr4	55161517	A	G	1220.19	hom	41	1.00	NM_00620	3_prime_U	rs7680422
PIK3CA	del	chr3	1.79E+08	ATTTTTTTT	ATTTTTTTT	606.234	het	50	0.46	NM_00621	intron_variant&feature	
PIK3CA	snp	chr3	1.79E+08	C	T	516.145	hom	19	1.00	NM_00621	stop_gaine	rs1219132
PIK3R1	snp	chr5	67588148	G	A	2480.93	het	136	0.60	NM_18152	missense_v	rs3730089
PIK3R1	snp	chr5	67589770	T	A	284.554	hom	16	0.94	NM_18152	intron_variant	
PTEN	snp	chr10	89692843	C	T	546.841	het	41	0.63	NM_00031	synonymous_variant	
PTEN	del	chr10	89720633	CTTTTTTTT	CTTTTTTTT	1115.97	het	256	0.23	NM_00031	splice_acceptor_varian	
PTEN	snp	chr10	89725281	C	T	48.268	het	73	0.14	NM_00031	3_prime_UTR_variant	
RB1	snp	chr13	48919358	T	G	1135.83	hom	39	1.00	NM_00032	intron_vari	rs198617
RET	snp	chr10	43613843	G	T	1917.2	hom	63	0.98	NM_02097	synonymou	rs1800861
SMO	snp	chr7	1.29E+08	G	C	3168.06	hom	106	0.98	NM_00563	intron_vari	rs2075777
SMO	snp	chr7	1.29E+08	G	C	2378.54	hom	80	0.99	NM_00563	synonymou	rs2228617
STK11	snp	chr19	1221422	G	A	246.115	hom	11	1.00	XM_00525	intron_variant	
STK11	snp	chr19	1222012	G	C	51485.8	hom	1673	1.00	XM_00525	splice_regi	rs2075607
TERT	snp	chr5	1295349	A	G	24314.6	het	1342	0.58	NM_19825	upstream_	rs2853669
TP53	snp	chr17	7578208	T	C	3159.48	het	168	0.62	NM_00054	missense_v	TP53_g.127
TP53	snp	chr17	7579472	G	C	2646.02	hom	86	1.00	NM_00054	missense_v	rs1042522
TP53	del	chr17	7579643	CCCCCAGC	CC	427.261	het	112	0.27	NM_00054	intron_variant&feature	
TP53	snp	chr17	7579801	G	C	586.307	hom	25	0.96	NM_00054	intron_vari	rs1642785