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Data Sheet

Product Name: CancerSeqPlus Paraffin Tissue Curl

Catalog No.: T2235086-SC **Lot No.: B906118**

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: 49 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:** _____

B906118

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
CDH1	snp	chr16	68771372	C	T	5121.49	hom	171	0.98	NM_00436	splice_regi	rs3743674
CDH1	snp	chr16	68844219	G	A	649.941	het	46	0.67	NM_00436	synonymous_variant	
CDK4	snp	chr12	58145088	C	T	965.663	het	72	0.49	NM_00007	missense_variant	
CDKN2A	snp	chr9	21968199	C	G	5966.44	hom	197	0.99	NM_00119	3_prime_U	rs11515&C
CDKN2A	complex	chr9	21971093	CCTC	TCTCACCC(	451.084	het	26	0.88	NM_00119	frameshift_variant&fea	
CDKN2A	complex	chr9	21971100	GGCAGC	TGCAC	421.739	het	26	0.88	NM_00119	frameshift_variant&fea	
CDKN2A	complex	chr9	21971107	TCGT	ACGCT	453.862	het	29	0.90	NM_00119	frameshift_variant&fea	
CDKN2A	snp	chr9	21971113	A	C	574.804	het	31	0.90	NM_00119	missense_variant	
CDKN2A	snp	chr9	21971162	G	A	1584.25	het	75	0.81	NM_00119	missense_v	COSM1362
CTNNB1	del	chr3	41265953	CTTTTTTTT	CTTTTTTTT	385.579	het	56	0.30	XM_00526	intron_variant&feature	
DDR2	snp	chr1	1.63E+08	T	C	1624.46	hom	61	0.97	XM_00524	intron_vari	rs1780003
DDR2	snp	chr1	1.63E+08	C	T	681.345	hom	24	1.00	XM_00524	intron_vari	rs3738807
DDR2	snp	chr1	1.63E+08	G	T	401.588	hom	16	1.00	XM_00524	intron_vari	rs1355287
DDR2	snp	chr1	1.63E+08	C	T	3783.55	het	206	0.67	XM_00524	synonymous_variant	
ERBB3	snp	chr12	56477612	G	A	574.138	het	24	0.92	NM_00198	missense_variant	
ERBB4	snp	chr2	2.13E+08	C	T	957.628	het	65	0.54	NM_00523	missense_v	COSM1669
ESR1	snp	chr6	1.52E+08	G	A	302.517	het	23	0.52	XM_00526	synonymou	rs2228480
EZH2	snp	chr7	1.49E+08	A	G	563.476	hom	18	1.00	XM_00524	intron_vari	rs2072407
FBXW7	snp	chr4	1.53E+08	G	A	541.459	het	30	0.70	NM_03363	missense_variant	
FBXW7	snp	chr4	1.53E+08	C	T	249.769	het	18	0.56	NM_03363	stop_gained	
FBXW7	del	chr4	1.53E+08	CAAAAAAA	CAAAAAAA	303.925	het	53	0.34	NM_03363	splice_region_variant&	
FGFR3	snp	chr4	1805561	C	T	487.891	het	28	0.68	NM_00116	intron_variant	
FGFR3	del	chr4	1806012	TGGGGGG(	TGGGGGG(	463.8	het	159	0.18	NM_00116	intron_variant&feature	
FGFR3	snp	chr4	1807894	G	A	334.19	hom	15	1.00	NM_00116	synonymou	rs7688609
FGFR3	mnp	chr4	1808964	CCAGCA	TGCTGG	730.596	het	137	0.28	NM_00116	missense_variant	
FLT3	snp	chr13	28608321	C	T	225.403	het	12	0.83	NM_00411	missense_variant	
FLT3	snp	chr13	28610183	A	G	605.099	hom	20	1.00	NM_00411	splice_regi	rs2491231
FOXL2	snp	chr3	1.39E+08	G	A	288.411	het	22	0.64	NM_02306	missense_variant	

GNAS	mnp	chr20	57484617	GG	AA	461.779	het	102	0.23	NM_08042	stop_gained	
IDH2	snp	chr15	90631943	C	T	1123.87	het	78	0.55	NM_00216	missense_variant	
JAK3	snp	chr19	17954265	C	T	198.571	het	20	0.50	XM_00525	missense_variant	
KDR	snp	chr4	55955110	C	T	553.066	het	35	0.60	NM_00225	synonymous_variant	
KDR	snp	chr4	55961092	C	T	263.942	het	26	0.50	NM_00225	missense_variant	
KDR	snp	chr4	55961159	T	C	363.213	het	30	0.50	NM_00225	intron_vari	rs2219471
KDR	snp	chr4	55962460	G	A	559.592	het	38	0.55	NM_00225	synonymous_variant	
MET	snp	chr7	1.16E+08	G	A	354.842	hom	13	1.00	XM_00525	missense_variant	
MET	snp	chr7	1.16E+08	G	A	522.659	hom	18	1.00	XM_00525	synonymou	rs41737&C
MYC	snp	chr8	1.29E+08	G	A	612.328	het	26	0.92	NM_00246	upstream_gene_variar	
MYCN	snp	chr2	16089615	T	C	1536.94	hom	52	1.00	NM_00537	downstrea	rs4669018
NOTCH1	snp	chr9	1.39E+08	G	A	1175.19	hom	42	1.00	NM_01761	synonymou	rs2229974
NOTCH1	snp	chr9	1.39E+08	G	A	1704	hom	60	0.97	NM_01761	synonymou	rs10521&C
NOTCH1	complex	chr9	1.39E+08	CACCAGGG	TCCCTGGT	133.041	het	145	0.14	NM_01761	missense_variant	
PDGFRA	snp	chr4	55141055	A	G	1388.91	hom	45	1.00	NM_00620	synonymou	rs1873778
PDGFRA	snp	chr4	55161254	C	T	669.093	hom	22	1.00	NM_00620	intron_vari	rs3733540
PDGFRA	snp	chr4	55161517	A	G	583.112	hom	19	1.00	NM_00620	3_prime_U	rs7680422
PTEN	snp	chr10	89624218	C	G	768.666	hom	26	1.00	NM_00031	5_prime_U	rs1120259
PTEN	snp	chr10	89711895	G	A	241.836	het	16	0.63	NM_00031	synonymou	COSM5179
PTEN	snp	chr10	89725333	C	T	199.986	het	23	0.43	NM_00031	3_prime_UTR_variant	
RB1	snp	chr13	48919358	T	G	1126.49	hom	38	1.00	NM_00032	intron_vari	rs198617
RET	snp	chr10	43609952	G	A	530.772	het	47	0.45	NM_02097	missense_variant	
RET	snp	chr10	43617447	C	T	1307.27	het	70	0.71	NM_02097	synonymous_variant	
SMAD4	snp	chr18	48603094	G	A	468.407	het	38	0.47	NM_00535	synonymous_variant	
SMO	snp	chr7	1.29E+08	G	C	2535.39	hom	87	0.99	NM_00563	intron_vari	rs2075777
STK11	snp	chr19	1207238	G	T	997.81	hom	34	1.00	XM_00525	intron_vari	rs3764640
STK11	snp	chr19	1218523	G	T	1597.25	het	94	0.63	XM_00525	intron_vari	rs2075604
STK11	snp	chr19	1220321	T	C	800.874	het	40	0.70	XM_00525	intron_vari	rs2075606
STK11	snp	chr19	1222012	G	C	6884.74	het	330	0.74	XM_00525	splice_regi	rs2075607
STK11	snp	chr19	1226496	G	A	3930.84	hom	153	0.96	XM_00525	missense_variant	
TERT	complex	chr5	1295346	GGGA	AGGG	1827.17	hom	76	0.87	NM_19825	upstream_gene_variar	
TERT	complex,sr	chr5	1295346	GGGA	AGGG,GGG	10512.6	het	374	0.80	NM_19825	upstream_gene_variar	
TP53	snp	chr17	7573905	G	A	1186.34	het	79	0.53	NM_00054	intron_variant	
TP53	snp	chr17	7579460	G	T	764.675	het	47	0.62	NM_00054	missense_v	TP53_g.114

TP53	snp	chr17	7579472	G	C	1385.37	hom	47	0.98	NM_00054	missense_v	rs1042522
TP53	del	chr17	7579643	CCCCCAGC	CC	189.198	het	47	0.30	NM_00054	intron_variant&feature	
TP53	snp	chr17	7579801	G	C	415.464	hom	16	1.00	NM_00054	intron_vari	rs1642785
VHL	snp	chr3	10188428	T	G	248.842	hom	11	1.00	NM_00055	intron_vari	rs1678607