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Data Sheet

Product Name: CancerSeqPlus Paraffin Tissue Curl

Catalog No.: T2235086-SC **Lot No.: B906123**

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: 56 year(s) old

Pathological Diagnosis: medullary 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:** _____

B906123

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.

NOTCH1	2.81	0.22	3.88E-02	NOTCH1	3.92	0.07	1.53E-03
FGFR3	2.37	0.12	5.94E-02	FGFR3	3.78	0.04	1.82E-03
MYC	4.40	0.19	7.69E-03	MYC	5.04	0.05	2.97E-03
STK11	3.05	0.16	1.46E-02	STK11	3.42	0.04	1.82E-03

symbol	type	chromosome	position	reference	mutation	quality	allele type	depth	variant frequency	transcript_id	consequence	existing variation
ALK	snp	chr2	29445458	G	T	1566.24	hom	50	1.00	NM_00430	synonymou	rs3795850
APC	snp	chr5	1.12E+08	G	A	254.305	hom	10	1.00	XM_00527	synonymou	rs465899
CCND1	del	chr11	69471096	GGGTCT	GT	444.202	hom	17	1.00	NM_05305	downstream_gene_va	
CCND1	complex	chr11	69471107	CACC	GACCCAC	470.891	hom	18	1.00	NM_05305	downstream_gene_va	
CCND1	complex	chr11	69471114	CCCCT	TCACG	401.895	hom	16	0.94	NM_05305	downstream_gene_va	
CDH1	complex	chr16	68772285	ACC	TCTC	399.481	hom	15	1.00	NM_00436	frameshift_variant&fea	
CDH1	complex	chr16	68772289	GGAGAGA	CCAGGT	346.898	hom	13	1.00	NM_00436	frameshift_variant&fea	
CDH1	snp	chr16	68842417	C	A	363.433	het	33	0.64	NM_00436	missense_variant	
CDKN2A	snp	chr9	21968198	CC	CG	9324.15	hom	303	0.99	NM_00119	3_prime_UTR_variant	
CDKN2A	snp	chr9	21974758	A	G	213.833	het	28	0.39	NM_00119	synonymou	COSM1351
CDKN2A	snp	chr9	21974759	C	G	197.458	het	35	0.31	NM_00119	missense_v	CM980322
CDKN2A	snp	chr9	21974760	C	G	202.827	het	33	0.33	NM_00119	missense_v	CM056560
CTNNB1	snp	chr3	41266116	G	A	662.687	het	33	0.85	XM_00526	missense_v	COSM1423
DDR2	snp	chr1	1.63E+08	T	C	3442.95	hom	113	0.99	XM_00524	intron_vari	rs1780003
DDR2	snp	chr1	1.63E+08	C	T	684.74	het	26	0.92	XM_00524	intron_vari	rs3738807
DDR2	snp	chr1	1.63E+08	G	T	350.51	hom	15	1.00	XM_00524	intron_vari	rs1355287
ERBB2	complex	chr17	37882932	CATC	TATT	616.878	het	171	0.23	NM_00444	intron_variant	
ERBB3	snp	chr12	56477694	A	T	2257.56	het	119	0.63	NM_00198	splice_regi	rs2271194
ERBB4	snp	chr2	2.13E+08	C	T	1946.17	het	108	0.68	NM_00523	missense_variant	
FBXW7	del,del	chr4	1.53E+08	CAAAAAAA	CAAAAAAA	477.852	het	73	0.22	NM_03363	splice_region_variant&	
FBXW7	snp	chr4	1.53E+08	G	A	332.538	het	18	0.83	NM_03363	intron_variant	
FGFR1	mnp	chr8	38271371	CT	AG	114.56	het	184	0.13	NM_00117	intron_variant	
FGFR1	complex	chr8	38271381	TGC	AGG	335.169	het	125	0.18	NM_00117	intron_variant	

FGFR1	snp	chr8	38271396	G	A	1765.78	het	86	0.80	NM_00117	intron_variant	
FGFR1	snp	chr8	38273533	C	T	877.987	het	68	0.49	NM_00117	missense_variant	
FGFR3	del	chr4	1806012	TGGGGGG	TGGGGGG	1481.03	het	437	0.19	NM_00116	intron_variant&feature	
FLT3	snp	chr13	28610183	A	G	2999.77	hom	98	1.00	NM_00411	splice_regi	rs2491231
FOXL2	snp	chr3	1.39E+08	G	C	3610.47	het	209	0.64	NM_02306	missense_v	rs2018401
FOXL2	snp	chr3	1.39E+08	G	A	651.406	hom	23	1.00	NM_02306	missense_v	COSM1419
GNAQ	snp	chr9	80412479	C	T	293.953	hom	11	1.00	NM_00207	missense_variant	
GNAQ	snp	chr9	80412536	C	T	539.293	het	36	0.58	NM_00207	missense_variant	
HRAS	snp	chr11	534242	A	G	2099.51	het	134	0.52	NM_00534	synonymou	rs12628&C
HRAS	del	chr11	534403	GCCCAGGC	GC	567.018	het	191	0.18	NM_00534	intron_variant&feature	
IDH2	snp	chr15	90631944	C	T	3765.6	het	260	0.52	NM_00216	missense_variant	
MET	snp	chr7	1.16E+08	G	A	422.879	het	23	0.78	XM_00525	synonymous_variant	
MPL	complex	chr1	43814941	CTC	TTT	1194.61	het	951	0.14	NM_00537	missense_variant	
MPL	complex	chr1	43815047	GCAGGAGA	TCTCCTGC	1007.9	het	298	0.22	NM_00537	intron_variant	
MYC	snp	chr8	1.29E+08	C	T	1212.73	het	87	0.64	NM_00246	5_prime_UTR_variant	
MYCN	snp	chr2	16080157	C	G	1341.2	hom	44	1.00	NM_00537	upstream_	rs1188606
NOTCH1	snp	chr9	1.39E+08	C	T	437.655	hom	19	1.00	NM_01761	3_prime_U	rs3124591
NOTCH1	snp	chr9	1.39E+08	G	A	2804.39	hom	121	0.99	NM_01761	synonymou	rs2229974
NOTCH1	snp	chr9	1.39E+08	G	A	6343.42	hom	219	1.00	NM_01761	synonymou	rs10521&C
NOTCH1	snp	chr9	1.39E+08	G	T	184.511	hom	10	1.00	NM_01761	missense_variant	
NPM1	del	chr5	1.71E+08	CTTTTTTTT	CTTTTTTTT	462.824	het	52	0.35	NM_00252	splice_region_variant&	
PDGFRA	snp	chr4	55141055	A	G	2236.7	hom	78	0.97	NM_00620	synonymou	rs1873788
PDGFRA	snp	chr4	55161254	C	T	740.077	hom	24	1.00	NM_00620	intron_vari	rs3733540
PDGFRA	snp	chr4	55161517	A	G	828.095	hom	27	1.00	NM_00620	3_prime_U	rs7680422
PIK3CA	snp	chr3	1.79E+08	G	A	6911.5	het	486	0.51	NM_00621	missense_v	COSM1420
PIK3R1	snp	chr5	67588148	G	A	644.998	het	29	0.86	NM_18152	missense_v	rs3730898
PIK3R1	snp	chr5	67589259	A	G	250.239	het	20	0.50	NM_18152	missense_variant	
RB1	snp	chr13	48923083	G	A	769.077	het	50	0.58	NM_00032	intron_variant	
RB1	ins	chr13	49034022	ATT	ATTT	307.398	hom	13	1.00	NM_00032	intron_variant&feature	
RET	snp	chr10	43613843	G	T	622.639	het	43	0.51	NM_02097	synonymou	rs1800861
RET	snp	chr10	43615656	C	T	415.362	het	22	0.77	NM_02097	splice_region_variant&	
STK11	snp	chr19	1207238	G	T	2901.08	het	190	0.49	XM_00525	intron_vari	rs3764640
STK11	snp	chr19	1222012	G	C	57989.2	hom	1899	1.00	XM_00525	splice_regi	rs2075607
STK11	complex	chr19	1222012	GGCC	CGCT	317.941	het	38	0.34	XM_00525	splice_region_variant&	

STK11	snp	chr19	1223222	C	A	240.66	hom	11	1.00	XM_00525	intron_variant	
TP53	snp	chr17	7577142	C	T	307.489	het	24	0.50	NM_00054	missense_v	TP53_g.137
TP53	snp	chr17	7578359	C	T	180.993	het	51	0.24	NM_00054	intron_vari	TP53_g.125
TP53	del	chr17	7579643	CCCCCAGC	CC	221.818	het	42	0.36	NM_00054	intron_variant&feature	
VHL	snp	chr3	10188428	T	G	327.167	hom	15	0.93	NM_00055	intron_vari	rs1678607