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Data Sheet

Product Name: CancerSeqPlus Paraffin Tissue Curl

Catalog No.: T2235086-SC **Lot No.: B906120**

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: 32 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:** _____

B906120

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 frquency	transcript_id	consequence	existing variation
ABL1	snp	chr9	1.34E+08	G	A	1594.02	het	113	0.51	NM_00731	intron_variant	
ALK	snp	chr2	29443579	G	A	3955.56	het	205	0.71	NM_00430	missense_variant	
ALK	snp	chr2	29445458	G	T	3233.86	hom	102	1.00	NM_00430	synonymou	rs3795850
ALK	complex	chr2	29445472	CCC	TCT	94.1681	het	112	0.15	NM_00430	splice_acceptor_varian	
APC	snp	chr5	1.12E+08	G	A	487.389	hom	19	0.95	XM_00527	missense_v	COSM1909
APC	complex	chr5	1.12E+08	CCTCC	GATGT	477.72	hom	17	1.00	XM_00527	missense_variant	
APC	snp	chr5	1.12E+08	A	G	383.671	het	29	0.76	XM_00527	missense_variant	
CDH1	mnp	chr16	68771372	CC	TG	2317.19	hom	86	0.94	NM_00436	splice_region_variant&	
CDH1	mnp,snp	chr16	68771372	CC	TG,TC	13449.9	het	479	0.82	NM_00436	splice_region_variant&	
CDH1	snp	chr16	68857346	G	A	1720.17	het	89	0.74	NM_00436	missense_variant	
CDK4	snp	chr12	58144812	C	T	273.494	het	19	0.58	NM_00007	missense_v	COSM1924
CDKN2A	snp	chr9	21968199	C	G	9702.95	hom	322	1.00	NM_00119	3_prime_U	rs11515&C
CTNNB1	del	chr3	41265953	CTTTTTTTT	CTTTTTTTT	107.874	het	66	0.15	XM_00526	intron_variant&feature	
CTNNB1	snp	chr3	41266049	C	T	1627.88	hom	59	0.98	XM_00526	missense_variant	
DDR2	snp	chr1	1.63E+08	T	C	9468.73	hom	307	1.00	XM_00524	intron_vari	rs1780003
DDR2	snp	chr1	1.63E+08	G	T	839.967	hom	34	0.97	XM_00524	intron_vari	rs1355287
DDR2	snp	chr1	1.63E+08	G	A	708.441	hom	28	0.93	XM_00524	synonymous_variant	
DDR2	snp	chr1	1.63E+08	C	T	970.6	het	69	0.51	XM_00524	stop_gained	
ERBB2	snp	chr17	37881206	C	A	971.978	hom	50	0.98	NM_00444	intron_variant	
ERBB3	snp	chr12	56477694	A	T	2984.21	het	182	0.54	NM_00198	splice_regi	rs2271194
ERBB4	snp	chr2	2.13E+08	A	T	1859.75	het	84	0.76	NM_00523	intron_vari	rs3512391
FBXW7	snp	chr4	1.53E+08	G	A	378.39	het	23	0.65	NM_03363	missense_variant	
FBXW7	snp	chr4	1.53E+08	A	G	744.793	het	31	0.94	NM_03363	intron_vari	rs1003360
FBXW7	del,del	chr4	1.53E+08	CAAAAAAA	CAAAAAAA	853.003	het	91	0.30	NM_03363	splice_region_variant&	
FGFR1	mnp	chr8	38271371	CT	AG	940.482	hom	35	0.97	NM_00117	intron_variant	
FGFR1	complex	chr8	38271381	TGCGT	AGGGG	988.506	hom	36	1.00	NM_00117	intron_variant	
FGFR2	snp	chr10	1.23E+08	G	A	529.923	het	30	0.70	NM_02297	synonymous_variant	

FGFR2	snp	chr10	1.23E+08	G	A	325.834	het	20	0.65	NM_02297	intron_variant	
FGFR3	snp	chr4	1803704	T	C	507.113	hom	18	1.00	NM_00116	synonymou	rs2234909
FGFR3	snp	chr4	1805568	C	T	2617.16	hom	92	1.00	NM_00116	intron_vari	rs3135885
FGFR3	del	chr4	1806012	TGGGGGG	TGGGGGG	2674.72	het	771	0.19	NM_00116	intron_variant&feature	
FGFR3	snp	chr4	1807894	G	A	2624.03	hom	85	1.00	NM_00116	synonymou	rs7688609
FLT3	snp	chr13	28602438	G	A	1365.62	hom	53	0.96	NM_00411	intron_variant	
FLT3	snp	chr13	28610183	A	G	2055.63	hom	66	1.00	NM_00411	splice_regi	rs2491231
FOXL2	complex	chr3	1.39E+08	CGCAGCT	AGCTGCG	251.569	hom	11	1.00	NM_02306	synonymous_variant	
FOXL2	complex	chr3	1.39E+08	GCGGCGC	TCGGGGC	756.776	hom	27	1.00	NM_02306	missense_variant	
FOXL2	mnp	chr3	1.39E+08	CTCT	AGAG	1509.18	hom	58	1.00	NM_02306	missense_variant	
FOXL2	mnp	chr3	1.39E+08	TCGC	GAAG	712.577	hom	32	1.00	NM_02306	missense_variant	
FOXL2	snp	chr3	1.39E+08	T	G	267.119	hom	10	1.00	NM_02306	missense_variant	
FOXL2	snp	chr3	1.39E+08	G	A	267.119	hom	10	1.00	NM_02306	missense_v	CM035546
GNA11	snp	chr19	3119001	C	T	819.983	het	41	0.80	NM_00206	missense_variant	
HRAS	snp	chr11	534354	C	T	1173.22	het	62	0.71	NM_00534	5_prime_UTR_variant	
IDH1	snp	chr2	2.09E+08	C	T	1084.04	hom	42	0.95	XM_00524	missense_variant	
IDH1	del	chr2	2.09E+08	GAAAAAAA	GAAAAAAA	1111.52	het	137	0.31	XM_00524	intron_variant&feature	
JAK3	snp	chr19	17948023	C	T	482.851	hom	19	0.95	XM_00525	splice_acceptor_varian	
KDR	snp	chr4	55972919	A	G	229.749	het	18	0.56	NM_00225	missense_v	rs1439016
KDR	snp	chr4	55972974	T	A	619.868	het	27	0.89	NM_00225	missense_v	rs1870377
KDR	snp	chr4	55980456	C	T	1944.12	het	78	0.92	NM_00225	intron_vari	rs2305949
MET	snp	chr7	1.16E+08	C	T	1288.13	het	53	0.92	XM_00525	synonymou	rs3577572
MYC	snp	chr8	1.29E+08	G	A	2575.41	hom	94	0.98	NM_00246	upstream_gene_varian	
MYC	snp	chr8	1.29E+08	C	T	303.768	hom	13	1.00	NM_00246	5_prime_UTR_variant	
MYC	snp	chr8	1.29E+08	C	T	354.137	hom	15	1.00	NM_00246	5_prime_UTR_variant	
MYC	snp	chr8	1.29E+08	C	T	811.09	hom	29	1.00	NM_00246	5_prime_UTR_variant	
MYC	snp	chr8	1.29E+08	G	T	419.654	het	30	0.70	NM_00246	intron_variant	
MYCN	snp	chr2	16080157	C	G	994.112	hom	33	1.00	NM_00537	upstream_	rs1188606
MYCN	snp	chr2	16089615	T	C	1998.62	hom	71	0.99	NM_00537	downstrea	rs4669018
NOTCH1	snp	chr9	1.39E+08	G	A	1374.16	het	109	0.56	NM_01761	synonymous_variant	
NPM1	del	chr5	1.71E+08	CTTTTTTTT	CTTTTTTTT	256.037	het	34	0.32	NM_00252	splice_region_variant&	
PDGFRA	snp	chr4	55141055	A	G	2061.16	hom	76	1.00	NM_00620	synonymou	rs1873778
PDGFRA	snp	chr4	55161254	C	T	1181.57	hom	38	1.00	NM_00620	intron_vari	rs3733540
PDGFRA	snp	chr4	55161517	A	G	1690.86	hom	54	1.00	NM_00620	3_prime_U	rs7680422

PTEN	del	chr10	89720633	CTTTTTTTT	CTTTTTTTT	160.218	het	57	0.18	NM_00031	splice_acceptor_varian	
RB1	snp	chr13	48919334	A	T	312.256	hom	16	1.00	NM_00032	missense_variant&spli	
RB1	snp	chr13	48919358	T	G	1155.14	hom	41	1.00	NM_00032	intron_vari	rs198617
RB1	complex,co	chr13	48953653	CTCAAAAA	TTCAAAAA	632.012	het	58	0.21	NM_00032	intron_variant&feature	
RB1	complex,sr	chr13	48953653	CTCAAAAA	TTCAAAAA	1410.45	het	97	0.40	NM_00032	intron_variant&feature	
RB1	snp	chr13	48955568	G	A	736.342	het	50	0.80	NM_00032	missense_v	COSM1322
RET	snp	chr10	43613843	G	T	1222.87	het	54	0.81	NM_02097	synonymou	rs1800861
RET	snp	chr10	43617357	G	A	339.268	het	103	0.19	NM_02097	intron_variant	
RET	snp	chr10	43617358	A	G	11.838	het	100	0.12	NM_02097	intron_variant	
RHOA	snp	chr3	49405826	G	A	37.574	het	117	0.12	NM_00166	intron_variant	
SMAD4	snp	chr18	48581252	C	T	1715.75	hom	66	0.95	NM_00535	missense_variant	
SMARCB1	snp	chr22	24176354	C	T	415.107	het	33	0.48	XM_00526	missense_v	COSM2949
SMO	snp	chr7	1.29E+08	C	T	273.494	het	19	0.58	NM_00563	synonymous_variant	
STK11	snp	chr19	1207080	G	A	1204.36	hom	52	1.00	XM_00525	synonymou	COSM1563
STK11	snp	chr19	1207238	G	T	4109.75	hom	133	0.99	XM_00525	intron_vari	rs3764640
STK11	snp	chr19	1220321	T	C	3080.19	het	164	0.68	XM_00525	intron_vari	rs2075606
STK11	snp	chr19	1222012	G	C	21737.4	het	1123	0.66	XM_00525	splice_regi	rs2075607
TERT	snp	chr5	1295282	G	A	2213.96	hom	93	0.97	NM_19825	upstream_gene_varian	
TP53	snp	chr17	7573019	C	T	4657.11	het	254	0.65	NM_00054	intron_variant	
TP53	snp	chr17	7573046	C	T	4641.37	het	296	0.55	NM_00054	intron_variant	
TP53	snp	chr17	7579303	G	A	1051.77	het	69	0.55	NM_00054	intron_vari	rs6773642
TP53	snp	chr17	7579653	T	C	321.017	het	24	0.54	NM_00054	intron_variant	
TP53	mnp	chr17	7579658	GT	CC	394.252	het	22	0.68	NM_00054	intron_variant	