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Data Sheet

Product Name: CancerSeqPlus Paraffin Tissue Curl

Catalog No.: T2235086-SC **Lot No.: B906132**

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: 40 year(s) old

Pathological Diagnosis: carcinoma

Tumor Size: n/a

Location: breast, left

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

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

B906132

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
ALK	snp	chr2	29445458	G	T	926.839	het	54	0.61	NM_00430	synonymou	rs3795850
APC	snp	chr5	1.12E+08	G	A	237.301	het	127	0.16	XM_00527	missense_variant	
APC	snp	chr5	1.12E+08	G	A	341.474	hom	13	1.00	XM_00527	synonymou	rs465899
APC	snp	chr5	1.12E+08	C	T	375.34	het	22	0.68	XM_00527	missense_variant	
AURKA	complex	chr20	54963246	CGGTC	TGGTT	172.889	het	54	0.20	NM_00360	missense_variant	
CDH1	complex	chr16	68771372	CCG	TCA	553.785	het	117	0.23	NM_00436	splice_region_variant&	
CDH1	snp	chr16	68771372	CCG	TCG	3297.76	het	231	0.49	NM_00436	splice_region_variant&	
CDH1	snp	chr16	68771409	C	T	173.616	het	113	0.17	NM_00436	intron_variant	
CDH1	ins	chr16	68771418	CG	CGCCCCAG	403.624	het	43	0.47	NM_00436	intron_variant&feature	
CDKN2A	snp	chr9	21968199	C	G	7769.75	hom	258	1.00	NM_00119	3_prime_U	rs11515&C
DDR2	snp	chr1	1.63E+08	T	C	4699.62	hom	156	0.99	XM_00524	intron_vari	rs1780003
DDR2	snp	chr1	1.63E+08	G	T	890.378	hom	34	0.94	XM_00524	intron_vari	rs1355287
EGFR	snp	chr7	55232973	G	A	371.611	het	22	0.68	NM_00522	missense_variant&spli	
EGFR	snp	chr7	55242609	A	G	260.66	hom	11	1.00	NM_00522	intron_vari	rs2017000
ERBB3	snp	chr12	56477694	A	T	1690.02	het	94	0.60	NM_00198	splice_regi	rs2271194
FBXW7	snp	chr4	1.53E+08	G	A	629.921	het	30	0.87	NM_03363	synonymous_variant	
FBXW7	snp	chr4	1.53E+08	T	C	807.05	het	47	0.64	NM_03363	synonymous_variant	
FBXW7	snp	chr4	1.53E+08	G	A	837.141	het	41	0.80	NM_03363	synonymous_variant	
FBXW7	del,del	chr4	1.53E+08	CAAAAAAA	CAAAAAAA	474.005	het	83	0.20	NM_03363	splice_region_variant&	
FGFR3	del	chr4	1806012	TGGGGGG	TGGGGGG	2026.89	het	183	0.45	NM_00116	intron_variant&feature	
FGFR3	snp	chr4	1806016	G	A	191.13	het	361	0.12	NM_00116	intron_vari	rs3735913
FGFR3	snp	chr4	1806022	G	A	600.401	het	296	0.16	NM_00116	intron_variant	
FGFR3	snp	chr4	1806124	G	A	347.898	het	29	0.59	NM_00116	synonymous_variant	
FGFR3	snp	chr4	1807892	ACG	ACA	2146.16	hom	71	1.00	NM_00116	synonymous_variant	
FLT3	snp	chr13	28610183	A	G	1799.57	hom	60	1.00	NM_00411	splice_regi	rs2491231
FOXL2	complex	chr3	1.39E+08	ACT	ATGCC	358.96	het	41	0.41	NM_02306	frameshift_variant&fea	
FOXL2	complex	chr3	1.39E+08	GGGCGCG	GCAGACG	287.255	het	37	0.43	NM_02306	frameshift_variant&fea	
GNAS	complex	chr20	57484264	GCG	ACA	313.666	het	47	0.30	NM_08042	missense_variant	

IDH1	del	chr2	2.09E+08	GAAAAAAA	GAAAAAAA	460.011	het	75	0.27	XM_00524	intron_variant&feature	
KDR	snp	chr4	55961159	T	C	458.674	hom	16	1.00	NM_00225	intron_vari	rs2219471
KDR	ins	chr4	55962545	TGG	TGGG	359.216	het	33	0.45	NM_00225	intron_variant&feature	
KDR	snp	chr4	55972974	T	A	488.674	hom	19	0.95	NM_00225	missense_v	rs1870377
MAP2K1	snp	chr15	66727597	G	C	2091.52	het	104	0.66	NM_00275	intron_vari	rs1694992
MYCN	snp	chr2	16080157	C	G	1205.97	hom	39	1.00	NM_00537	upstream_	rs1188606
NOTCH1	snp	chr9	1.39E+08	C	T	360.917	het	23	0.83	NM_01761	missense_variant	
NOTCH1	snp	chr9	1.39E+08	G	A	891.626	hom	38	1.00	NM_01761	synonymou	rs2229974
NOTCH1	snp	chr9	1.39E+08	G	A	523.163	hom	18	1.00	NM_01761	synonymou	rs10521&C
NOTCH1	snp	chr9	1.39E+08	C	T	576.999	het	30	0.90	NM_01761	missense_variant	
PDGFRA	snp	chr4	55141055	A	G	3044.92	hom	101	1.00	NM_00620	synonymou	rs1873778
PDGFRA	snp	chr4	55161254	C	T	613.014	hom	21	1.00	NM_00620	intron_vari	rs3733540
PDGFRA	snp	chr4	55161517	A	G	496.211	hom	17	1.00	NM_00620	3_prime_U	rs7680422
PIK3CA	snp	chr3	1.79E+08	T	C	501.639	het	27	0.67	NM_00621	intron_vari	rs3729682
RB1	snp	chr13	48919358	T	G	431.479	hom	15	1.00	NM_00032	intron_vari	rs198617
RET	snp	chr10	43610119	G	A	237.399	het	18	0.67	NM_02097	missense_v	rs1799398
RET	snp	chr10	43613843	G	T	524.295	hom	17	1.00	NM_02097	synonymou	rs1800861
SMO	snp	chr7	1.29E+08	G	C	882.575	het	56	0.54	NM_00563	intron_vari	rs2075777
SMO	snp	chr7	1.29E+08	G	C	1067.52	het	55	0.69	NM_00563	synonymou	rs2228617
STK11	snp	chr19	1207238	G	T	491.861	het	61	0.31	XM_00525	intron_vari	rs3764640
STK11	snp	chr19	1220321	T	C	2053.92	het	128	0.53	XM_00525	intron_vari	rs2075606
STK11	snp	chr19	1220415	C	A	238.057	het	17	0.76	XM_00525	missense_v	rs1219133
STK11	ins	chr19	1222016	CC	CCAC	639.949	het	27	0.89	XM_00525	intron_vari	rs1865187
STK11	ins	chr19	1222019	GG	GCCCCCAG	623.281	hom	25	0.92	XM_00525	intron_variant&feature	
STK11	snp	chr19	1222025	A	C	645.29	het	26	0.92	XM_00525	intron_variant	
TERT	snp	chr5	1295349	A	G	12354.2	hom	390	1.00	NM_19825	upstream_	rs2853669
TP53	snp	chr17	7579472	G	C	708.9	het	44	0.61	NM_00054	missense_v	rs1042522
TP53	snp	chr17	7579619	G	T	1532.89	het	86	0.62	NM_00054	intron_vari	rs1788332