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Data Sheet

Product Name: CancerSeqPlus Paraffin Tissue Curl

Catalog No.: T2235086-SC **Lot No.: B906119**

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: invasive (infiltrating) ductal 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:** _____

B906119

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
ABL1	snp	chr9	1.34E+08	C	T	341.429	het	32	0.44	NM_00731	splice_region_variant&	
ALK	snp	chr2	29445458	G	T	2253.97	hom	73	1.00	NM_00430	synonymou	rs3795850
APC	snp	chr5	1.12E+08	G	A	284.029	hom	12	1.00	XM_00527	synonymou	rs42427
APC	snp	chr5	1.12E+08	G	A	1413.53	hom	55	0.95	XM_00527	missense_variant	
AURKA	complex	chr20	54963147	CCC	ACAGATTA	227.456	het	18	0.67	NM_00360	intron_variant&feature	
CCND1	snp	chr11	69450915	G	A	495.45	het	25	0.84	NM_05305	upstream_gene_varian	
CCND1	snp	chr11	69461731	C	T	567.341	hom	20	1.00	NM_05305	intron_vari	rs647451
CDH1	snp	chr16	68771372	C	T	13645.2	hom	434	1.00	NM_00436	splice_regi	rs3743674
CDH1	snp	chr16	68842326	G	A	3771.31	het	249	0.53	NM_00436	splice_acceptor_varian	
CDH1	snp	chr16	68844207	G	A	326.615	het	23	0.57	NM_00436	synonymous_variant	
CDH1	snp	chr16	68845642	C	T	726.001	het	69	0.51	NM_00436	synonymous_variant	
CDKN2A	snp	chr9	21968159	G	A	419.427	hom	15	1.00	NM_00119	3_prime_U	rs3088440
CDKN2A	snp	chr9	21968199	C	G	14404.9	hom	460	0.99	NM_00119	3_prime_U	rs11515&C
DDR2	snp	chr1	1.63E+08	T	C	8705.91	hom	276	1.00	XM_00524	intron_vari	rs1780003
DDR2	snp	chr1	1.63E+08	G	T	655.062	hom	25	1.00	XM_00524	intron_vari	rs1355287
EGFR	snp	chr7	55242349	C	T	237.399	het	18	0.67	NM_00522	intron_variant	
ERBB3	snp	chr12	56477694	A	T	5336.85	het	280	0.69	NM_00198	splice_regi	rs2271194
FBXW7	snp	chr4	1.53E+08	G	A	610.267	hom	22	1.00	NM_03363	missense_variant	
FBXW7	snp	chr4	1.53E+08	G	A	2282.52	hom	89	0.94	NM_03363	synonymous_variant	
FBXW7	del	chr4	1.53E+08	CAAAAAAA	CAAAAAAA	210.418	het	28	0.39	NM_03363	splice_region_variant&	
FGFR2	snp	chr10	1.23E+08	C	T	1176.44	het	69	0.64	NM_02297	synonymous_variant	
FGFR3	del	chr4	1806012	TGGGGGG	TGGGGGG	1529.64	het	581	0.16	NM_00116	intron_variant&feature	
FGFR3	snp	chr4	1806056	GCCG	GCCA	6453.81	het	607	0.39	NM_00116	splice_acceptor_varian	
FGFR3	snp	chr4	1807894	G	A	2367.02	hom	78	1.00	NM_00116	synonymou	rs7688609
FLT3	snp	chr13	28610183	A	G	2219.85	hom	72	1.00	NM_00411	splice_regi	rs2491231
FOXL2	snp	chr3	1.39E+08	G	A	233.858	het	13	0.85	NM_02306	missense_variant	
FOXL2	complex	chr3	1.39E+08	TCGTAGAA	CCGTTCTA	299.49	hom	13	0.92	NM_02306	stop_gained	

GNA11	mnp	chr19	3118881	GG	AA	2222.73	het	636	0.19	NM_00206	intron_variant	
GNAS	snp	chr20	57480478	G	A	917.65	het	52	0.67	NM_08042	missense_variant	
HRAS	snp	chr11	533993	G	A	257.737	het	14	0.93	NM_00534	intron_variant	
HRAS	snp	chr11	534242	A	G	12342.2	hom	397	1.00	NM_00534	synonymou	rs12628&C
HRAS	del	chr11	534403	GCCCAGGC	GC	897.34	hom	32	1.00	NM_00534	intron_variant&feature	
IDH1	del	chr2	2.09E+08	GAAAAAAA	GAAAAAAA	570.618	het	136	0.21	XM_00524	intron_variant&feature	
JAK2	del	chr9	5073681	CTTTTTTTT	CTTTTTTTT	821.409	het	76	0.41	NM_00497	splice_region_variant&	
KDR	snp	chr4	55953884	C	T	849.722	het	72	0.54	NM_00225	synonymou	COSM1056
KDR	snp	chr4	55961159	T	C	1743.9	het	83	0.81	NM_00225	intron_vari	rs2219471
KDR	snp	chr4	55972859	T	C	286.189	het	14	0.86	NM_00225	missense_variant	
KRAS	snp	chr12	25398255	G	A	483.324	het	21	0.90	NM_03336	stop_gaine	rs1219132
MAP2K1	snp	chr15	66727485	C	T	768.524	hom	27	1.00	NM_00275	synonymous_variant	
MET	snp	chr7	1.16E+08	C	T	368.623	het	21	0.90	XM_00525	synonymous_variant	
MYC	snp	chr8	1.29E+08	C	T	1373.94	hom	52	0.96	NM_00246	intron_variant	
MYCN	snp	chr2	16089591	C	T	289.852	het	26	0.50	NM_00537	downstream_gene_va	
MYCN	snp	chr2	16089615	T	C	1766.8	hom	61	1.00	NM_00537	downstrea	rs4669018
NOTCH1	snp	chr9	1.39E+08	G	A	1530.47	hom	69	0.97	NM_01761	synonymou	rs2229974
NOTCH1	snp	chr9	1.39E+08	G	A	5005.94	hom	178	0.99	NM_01761	synonymou	rs10521&C
NPM1	del	chr5	1.71E+08	CTTTTTTTT	CTTTTTTTT	433.678	het	68	0.26	NM_00252	splice_region_variant&	
PDGFRA	snp	chr4	55141055	A	G	1216.95	hom	41	1.00	NM_00620	synonymou	rs1873788
PDGFRA	snp	chr4	55161254	C	T	2066.45	hom	65	1.00	NM_00620	intron_vari	rs3733540
PDGFRA	snp	chr4	55161391	T	C	387.35	hom	15	1.00	NM_00620	synonymou	rs7685117
PDGFRA	snp	chr4	55161517	A	G	2283.61	hom	74	1.00	NM_00620	3_prime_U	rs7680422
PTEN	snp	chr10	89720907	T	G	1234.95	hom	53	1.00	NM_00031	intron_vari	rs555895&
PTEN	snp	chr10	89725258	C	T	93.2742	het	100	0.14	NM_00031	3_prime_UTR_variant	
RET	snp	chr10	43610133	C	T	710.619	het	38	0.74	NM_02097	synonymous_variant	
RET	snp	chr10	43610281	G	A	728.148	het	40	0.93	NM_02097	intron_variant	
RET	snp	chr10	43613843	G	T	999.816	hom	33	0.97	NM_02097	synonymou	rs1800861
RET	snp	chr10	43617741	T	C	2216.41	hom	77	1.00	NM_02097	intron_variant	
SMAD4	snp	chr18	48581113	C	A	518.346	hom	24	1.00	NM_00535	intron_variant	
SMO	snp	chr7	1.29E+08	G	C	4715.32	het	222	0.80	NM_00563	intron_vari	rs2075777
STK11	snp	chr19	1222012	G	C	23696.8	het	1434	0.57	XM_00525	splice_regi	rs2075607
TP53	snp	chr17	7576844	A	T	124.394	het	38	0.29	NM_00054	intron_variant	
TP53	snp	chr17	7579619	G	T	4865.85	hom	160	0.99	NM_00054	intron_vari	rs1788332

TP53	del	chr17	7579643	CCCCCAGC	CC	6.50222	het	90	0.14	NM_00054	intron_variant&feature
TP53	snp	chr17	7580052	C	T	2800.34	hom	115	0.99	NM_00054	intron_vari rs8079544
VHL	snp	chr3	10183729	G	A	1333.81	het	78	0.63	NM_00055	synonymous_variant