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Data Sheet

Product Name: CancerSeqPlus Paraffin Tissue Curl

Catalog No.: T2235248-SC **Lot No.:** B906145

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: Stomach

Donor Information:

Male: 30 year(s) old
Female: _____ year(s) old

Pathological Diagnosis: Adenocarcinoma

Tumor Size:

Location: stomach

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

FOR IN VITRO RESEARCH USE ONLY APPROVED BY: _____

B906145

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	existing variation	consequence
AKT1	snp	chr14	105246325	T	A	986.826	hom	45	0.98	NM_001014	rs2494737	intron_variant
ALK	snp	chr2	29445458	G	T	14383.2	het	552	0.91	NM_004304	rs3795850	synonymous_v
APC	snp	chr5	112175770	G	A	2635.58	hom	100	1.00	XM_005271	rs41115&CC	synonymous_v
APC	snp	chr5	112176325	G	A	381.979	hom	13	1.00	XM_005271	rs42427	synonymous_v
APC	snp	chr5	112176559	T	G	628.011	hom	23	1.00	XM_005271	rs866006	synonymous_v
APC	snp	chr5	112177171	G	A	7225.65	hom	255	1.00	XM_005271	rs465899	synonymous_v
ATM	del	chr11	108117897	ATTTTTTTTT	ATTTTTTTTT	808.045	het	178	0.20	NM_000051.3		intron_variant
CCND1	del	chr11	69450976	GAAAAAAAA	GAAAAAAAA	241.354	het	38	0.29	NM_053056.2		upstream_gen
CDH1	snp	chr16	68771372	C	T	37811.5	het	1829	0.69	NM_004360	rs3743674	splice_region_
CDH1	ins	chr16	68771418	CG	CGCCCCAGC	503.617	het	75	0.31	NM_004360.3		intron_variant
CDH1	complex	chr16	68771429	TGC	CGT	9.59855	het	87	0.14	NM_004360.3		intron_variant
CDH1	snp	chr16	68857441	T	C	1521.24	het	104	0.51	NM_004360	rs1801552	synonymous_v
CDK4	snp	chr12	58144665	C	T	364.098	het	29	0.52	NM_000075	rs2069502	intron_variant
CDK4	snp	chr12	58145156	C	T	44.387	het	308	0.11	NM_000075	rs2270777	intron_variant
CDKN2A	complex,mn	chr9	21968199	CGAG	GGAA,GAAG	1931.16	het	93	#VALUE!	NM_001195132.1		3_prime_UTR_
CDKN2A	snp	chr9	21968199	CGAG	GGAG	67474.4	hom	2279	0.96	NM_001195132.1		3_prime_UTR_
DDR2	snp	chr1	162740327	TGTC	CGTC	35741.9	hom	1182	0.99	XM_005245220.1		intron_variant
DDR2	complex	chr1	162740327	TGTC	CGTT	328.023	hom	17	0.71	XM_005245220.1		intron_variant
DDR2	snp	chr1	162743418	G	T	3900.88	hom	136	1.00	XM_005245	rs1355287	intron_variant
DDR2	snp	chr1	162749761	T	C	580.532	hom	22	1.00	XM_005245	rs1510315	intron_variant
EGFR	snp	chr7	55221655	G	A	2026.76	het	123	0.54	NM_005228	rs4947986	intron_variant
EGFR	snp	chr7	55238874	T	A	361.538	hom	12	1.00	NM_005228	rs2227984	synonymous_v
EGFR	snp	chr7	55241727	GGTG	AGTG	5947.67	het	674	0.31	NM_005228.3		synonymous_v
EGFR	ins	chr7	55242254	CG	CTG	39.2914	het	67	0.15	NM_005228.3		intron_variant
EGFR	snp	chr7	55242609	A	G	1933.9	het	107	0.70	NM_005228	rs2017000	intron_variant
EGFR	snp	chr7	55259608	C	A	244.542	het	24	0.50	NM_005228	rs36972582	intron_variant
ERBB2	complex	chr17	37881258	CCCAGGCC	TCCAGATGA	8.79927	het	74	0.14	NM_004448.2		intron_variant
ERBB4	del	chr2	212578379	TAAAAAAAA	TAAAAAAAA	620.888	het	72	0.33	NM_005235.2		splice_region_
ERBB4	snp	chr2	212587321	G	A	359.48	het	22	0.68	NM_005235	rs13002712	intron_variant
EZH2	snp	chr7	148508833	A	G	2973.06	het	133	0.77	XM_005249	rs2072407	intron_variant
FBXW7	del	chr4	153247486	CTTTTTTTTT	CTTTTTTTTT	256.203	het	96	0.15	NM_033632.3		intron_variant
FBXW7	snp	chr4	153267968	A	G	559.13	hom	20	1.00	NM_033632	rs2714803	intron_variant
FGFR1	ins	chr8	38271433	TA	TGACCTCCA	416.416	het	26	0.69	NM_001174067.1		splice_donor_v

FGFR1	complex	chr8	38271437	TGGTTG	AGGTAA	674.631	hom	29	0.90	NM_001174067.1		missense_varia
FGFR3	del	chr4	1806012	TGGGGGGG	TGGGGGGG	7445.1	het	2299	0.18	NM_001163213.1		intron_variant
FGFR3	snp	chr4	1807894	G	A	22618.8	hom	755	1.00	NM_001163	rs7688609	synonymous_v
FGFR3	complex	chr4	1808889	GCCAGGA	TCCTGGC	571.939	het	26	0.88	NM_001163213.1		missense_varia
FGFR3	complex	chr4	1808900	CCC	CGGGG	407.767	het	27	0.63	NM_001163213.1		frameshift_var
FLT3	snp	chr13	28592546	T	C	294.101	hom	11	1.00	NM_004119	rs17086226	intron_variant
FOXL2	mnp	chr3	138665008	TA	CC	280.317	hom	11	1.00	NM_023067.3		missense_varia
GNA11	snp	chr19	3119184	T	G	294.667	hom	11	1.00	NM_002067	rs308046	intron_variant
GNAQ	snp	chr9	80409345	A	G	347.94	het	19	0.84	NM_002072	rs1328529	intron_variant
HNF1A	snp	chr12	121431272	T	A	271.595	hom	10	1.00	XM_005253	rs2071190	intron_variant
HRAS	del	chr11	534403	GCCCAGGCC	GC	553.121	het	670	0.13	NM_005343.2		intron_variant
IDH1	del	chr2	209113048	GAAAAAAAA	GAAAAAAAA	593.936	het	77	0.30	XM_005246521.1		intron_variant
IDH1	del	chr2	209116299	GAAAAAAAA	GAAAAAAAA	3237.26	het	438	0.28	XM_005246521.1		intron_variant
JAK2	del	chr9	5073681	CTTTTTTTTT	CTTTTTTTTT	2515.3	het	273	0.33	NM_004972.3		splice_region_
MET	snp	chr7	116436022	G	A	6046.11	het	254	0.85	XM_005250	rs2023748&	synonymous_v
MET	snp	chr7	116436097	G	A	5193.59	het	217	0.84	XM_005250	rs41737&CC	synonymous_v
MYCN	snp	chr2	16080157	C	G	2558.06	hom	80	1.00	NM_005378	rs11886063	upstream_gen
MYCN	snp	chr2	16089615	T	C	6619.25	het	403	0.56	NM_005378	rs4669018	downstream_g
NOTCH1	snp	chr9	139390397	C	T	1182.6	hom	45	1.00	NM_017617	rs3124591	3_prime_UTR_
NOTCH1	complex	chr9	139391341	TGCTGG	CCCACC	85.6762	het	144	0.15	NM_017617.3		missense_varia
NOTCH1	complex	chr9	139391351	AGA	TGT	148.955	het	161	0.16	NM_017617.3		missense_varia
NOTCH1	complex	chr9	139391358	ACA	TCT	100.668	het	159	0.14	NM_017617.3		missense_varia
NOTCH1	snp	chr9	139391636	G	A	16123.3	hom	606	0.99	NM_017617	rs2229974	synonymous_v
NOTCH1	complex	chr9	139393716	GCAACAGGC	AAGACACCT	197.691	hom	11	0.91	NM_017617.3		splice_region_
NOTCH1	complex	chr9	139395301	TGCAGAGGC	AGGCCCGCG	317.938	hom	12	1.00	NM_017617.3		splice_accepto
NOTCH1	snp	chr9	139395311	G	T	292.169	hom	13	0.85	NM_017617	rs11574908	intron_variant
NOTCH1	snp	chr9	139395312	A	T	350.528	hom	13	1.00	NM_017617.3		intron_variant
NOTCH1	snp	chr9	139395317	G	T	216.341	hom	10	1.00	NM_017617.3		intron_variant
NOTCH1	complex,cor	chr9	139397707	GTCGG	ATCAG,ATCC	1188.74	het	47	#VALUE!	NM_017617.3		synonymous_v
NOTCH1	snp	chr9	139397707	GTCGG	ATCGG	22690.2	hom	785	0.94	NM_017617.3		synonymous_v
NOTCH1	complex	chr9	139399177	CACCAGGGA	TCCCTGGTG	278.173	het	18	0.67	NM_017617.3		missense_varia
NOTCH1	snp	chr9	139399195	C	G	380.009	het	22	0.68	NM_017617	COSM33751	missense_varia
NOTCH1	complex	chr9	139400272	TTGA	CTGC	300.943	het	14	0.86	NM_017617.3		missense_varia
NOTCH1	snp	chr9	139400282	G	C	253.698	het	13	0.85	NM_017617.3		missense_varia
NOTCH1	snp	chr9	139400283	C	T	253.698	het	13	0.85	NM_017617.3		synonymous_v
NOTCH1	snp	chr9	139400284	A	G	305.951	het	13	0.92	NM_017617.3		missense_varia
NOTCH1	snp	chr9	139400292	G	T	253.698	het	13	0.85	NM_017617	rs200099319	stop_gained
NPM1	del	chr5	170837513	CTTTTTTTTT	CTTTTTTTTT	2124.3	het	240	0.35	NM_002520.6		splice_region_
NPM1	del	chr5	170837733	CTG	CG	265.856	het	30	0.43	NM_002520.6		3_prime_UTR_
PDGFRA	snp	chr4	55141052	CCCA	CCCG	31920.7	hom	1046	0.99	NM_006206.4		synonymous_v
PDGFRA	snp	chr4	55161254	C	T	5280.53	het	271	0.64	NM_006206	rs3733540	intron_variant

PDGFRA	snp	chr4	55161391	T	C	3355.81	hom	109	0.99	NM_006206	rs7685117	synonymous_v
PDGFRA	snp	chr4	55161517	A	G	5778.46	hom	191	0.99	NM_006206	rs7680422	3_prime_UTR_
PIK3CA	del	chr3	178927848	ATTTTTTTTT	ATTTTTTTTT	2064.32	het	266	0.28	NM_006218.2		intron_variant
PTEN	del	chr10	89720633	CTTTTTTTTT	CTTTTTTTTT	1102.15	het	238	0.22	NM_000314.4		splice_accepto
PTEN	snp	chr10	89720907	T	G	2192.73	het	137	0.55	NM_000314	rs555895&C	intron_variant
PTEN	del	chr10	89725293	CTTTTTTTTT	CTTTTTTTTT	197.38	het	119	0.15	NM_000314.4		3_prime_UTR_
RB1	snp	chr13	48919358	T	G	8577.19	hom	284	0.99	NM_000321	rs198617	intron_variant
RB1	del	chr13	48953655	CAAAAAAAA	CAAAAAAAA	1425.1	het	247	0.22	NM_000321.2		intron_variant
RB1	snp	chr13	48955676	T	A	307.398	hom	13	1.00	NM_000321	rs2804086	intron_variant
RB1	snp	chr13	49033747	G	A	836.407	hom	30	1.00	NM_000321	rs198580	intron_variant
RB1	ins	chr13	49034022	ATT	ATTT	1664.73	het	104	0.68	NM_000321.2		intron_variant
RB1	snp	chr13	49034025	C	T	520.153	het	103	0.27	NM_000321.2		intron_variant
RB1	snp	chr13	49034046	T	C	256.889	het	54	0.28	NM_000321.2		intron_variant
RB1	snp	chr13	49034050	T	C	139.894	het	51	0.22	NM_000321.2		intron_variant
RB1	snp	chr13	49034054	T	C	123.813	het	55	0.20	NM_000321.2		intron_variant
RB1	snp	chr13	49034058	T	C	131.937	het	53	0.21	NM_000321.2		intron_variant
RB1	snp	chr13	49034062	T	C	133.804	het	50	0.22	NM_000321.2		intron_variant
RB1	snp	chr13	49034066	T	C	117.335	het	48	0.21	NM_000321.2		intron_variant
RB1	ins	chr13	49034087	TT	TTCT	245.549	het	24	0.42	NM_000321.2		intron_variant
RB1	snp	chr13	49034105	C	T	372.492	het	18	0.89	NM_000321	rs9562824	intron_variant
RB1	snp	chr13	49034154	A	G	259.435	hom	10	1.00	NM_000321	rs198581	intron_variant
RET	mnp	chr10	43610190	GG	CT	364.827	hom	13	1.00	NM_020975.4		splice_region_
RET	mnp	chr10	43610199	GGG	CCC	354.532	hom	14	0.93	NM_020975.4		intron_variant
RET	snp	chr10	43610281	G	A	393.652	hom	19	0.95	NM_020975.4		intron_variant
SMO	snp	chr7	128845276	CG	CC	16704.8	het	895	0.61	NM_005631.4		intron_variant
SMO	snp	chr7	128846328	G	C	10763.3	het	519	0.68	NM_005631	rs2228617	synonymous_v
SMO	snp	chr7	128846469	A	G	405.217	het	25	0.84	NM_005631	rs2735842	intron_variant
STK11	snp	chr19	1219274	G	A	685.429	het	31	0.90	XM_005259	rs34928889	intron_variant
STK11	ins	chr19	1219443	GCGGGGGC	GCGGGGGC	575.391	het	89	0.27	XM_005259617.1		intron_variant
STK11	snp	chr19	1219444	C	G	441.431	het	138	0.22	XM_005259617.1		intron_variant
STK11	snp	chr19	1219451	C	G	409.237	het	175	0.22	XM_005259	rs36951560	intron_variant
STK11	snp	chr19	1219553	G	T	237.291	hom	10	1.00	XM_005259	rs11084889	intron_variant
STK11	snp	chr19	1220257	C	T	546.019	hom	19	1.00	XM_005259617.1		intron_variant
STK11	snp	chr19	1220321	TGTG	CGTG	13280.5	het	829	0.51	XM_005259617.1		intron_variant
STK11	snp	chr19	1226772	C	T	254.561	hom	10	1.00	XM_005259	rs2277746	intron_variant
TERT	snp	chr5	1295349	A	G	41572.8	het	2570	0.51	NM_198253	rs2853669&	upstream_gen
TP53	snp	chr17	7578115	T	C	499.438	hom	20	1.00	NM_000546	rs1625895	intron_variant
TP53	snp	chr17	7579472	G	C	13727.3	het	637	0.76	NM_000546	rs1042522&	missense_vari
TP53	del	chr17	7579643	CCCCCAGCC	CC	2562.7	het	550	0.26	NM_000546.5		intron_variant
TP53	complex	chr17	7579668	CTCCAG	CAACCCTT	1811.82	het	504	0.22	NM_000546.5		intron_variant
TP53	complex	chr17	7579678	CCAG	TTAC	1456.52	het	542	0.22	NM_000546.5		intron_variant

TP53	snp	chr17	7579801	G	C	4180.34	het	185	0.85	NM_000546	rs1642785	intron_variant
TP53	snp	chr17	7580182	G	A	180.153	het	15	0.67	NM_000546.5		intron_variant
VHL	snp	chr3	10188428	T	G	368.458	hom	13	1.00	NM_000551	rs1678607	intron_variant