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Data Sheet

Product Name: CancerSeqPlus Paraffin Tissue Curl

Catalog No.: T2235248-SC **Lot No.: B906143**

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: 48 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:** _____

B906143

For CNV mutations, we utilize stringent criteria to confirm copy number variations -- using normal tissues as controls. We may have samples

CNV against colon	Copy Number	STDev of Copy Number	P-value	CNV against adrenal	Copy Number	STDev of Copy Number	P-value
ERBB2	4.28	1.53	1.90E-03	ERBB2	4.89	0.32	1.10E-03

symbol	type	chromosome	position	reference	mutation	quality	allele type	Depth	variant frequency	transcript_id	existing variation	consequence
AKT1	snp	chr14	105246325	T	A	991.33	hom	43	1.00	NM_001014	rs2494737	intron_variant
AKT1	snp	chr14	105246686	G	A	1128.17	het	71	0.73	NM_001014	rs2494738	intron_variant
ALK	snp	chr2	29445458	G	T	10558.10	het	519	0.67	NM_004304	rs3795850	synonymous_va
APC	snp	chr5	112175770	G	A	2113.07	hom	80	0.99	XM_005271	rs41115&CO	synonymous_va
APC	snp	chr5	112176325	G	A	1012.30	hom	35	1.00	XM_005271	rs42427	synonymous_va
APC	snp	chr5	112176559	T	G	545.07	hom	21	1.00	XM_005271	rs866006	synonymous_va
APC	snp	chr5	112177171	G	A	8280.64	hom	295	1.00	XM_005271	rs465899	synonymous_va
ATM	del	chr11	108117897	ATTTTTTTTT	ATTTTTTTTT	649.66	het	216	0.17	NM_000051.3		intron_variant&
ATM	snp	chr11	108170271	G	A	208.87	het	12	0.83	NM_000051	rs1150203	intron_variant
ATM	snp	chr11	108225483	C	T	464.69	het	34	0.53	NM_000051	rs664982	intron_variant
AURKA	complex	chr20	54963147	CCC	CAATTTA	355.38	het	57	0.32	NM_003600.2		intron_variant&
BRAF	snp	chr7	140481572	T	A	181.27	het	14	0.79	XM_005250045.1		intron_variant
CCND1	del	chr11	69450976	GAAAAAAAA	GAAAAAAAA	214.91	het	67	0.21	NM_053056.2		upstream_gene
CCNE1	snp	chr19	30314666	C	T	3896.04	het	250	0.52	NM_001238	rs7257694	synonymous_va
CDH1	snp	chr16	68771372	C	T	52359.70	het	2326	0.77	NM_004360	rs3743674	splice_region_v
CDH1	ins	chr16	68771418	CG	CGCCCCAGC	1493.62	het	128	0.45	NM_004360.3		intron_variant&
CDH1	complex	chr16	68771429	TGC	CGT	113.49	het	159	0.15	NM_004360.3		intron_variant
CDH1	snp	chr16	68845801	A	G	322.11	het	34	0.53	NM_004360.3		intron_variant
CDH1	snp	chr16	68857441	T	C	2947.77	het	165	0.59	NM_004360	rs1801552	synonymous_va
CDK4	snp	chr12	58144665	C	T	865.05	het	46	0.80	NM_000075	rs2069502	intron_variant
CDKN2A	snp	chr9	21968199	CG	GG	54365.40	het	2299	0.84	NM_001195132.1		3_prime_UTR_v
CSF1R	mnp	chr5	149433596	TG	GA	322.09	het	14	0.93	NM_005211.3		3_prime_UTR_v
CSF1R	snp	chr5	149433857	C	G	374.73	hom	14	1.00	NM_005211	rs41533349	intron_variant
CSF1R	snp	chr5	149452793	C	T	353.69	hom	14	1.00	NM_005211	rs10044553	intron_variant
DDR2	snp	chr1	162740327	T	C	37882.90	hom	1237	1.00	XM_005245	rs1780003	intron_variant
DDR2	complex	chr1	162740327	TGTC	CGTT	304.91	hom	15	0.73	XM_005245220.1		intron_variant
DDR2	snp	chr1	162743418	G	T	5008.16	hom	168	1.00	XM_005245	rs1355287	intron_variant
DDR2	snp	chr1	162748588	C	A	280.14	hom	11	0.91	XM_005245	rs907074	intron_variant
DDR2	snp	chr1	162749761	T	C	817.91	hom	34	1.00	XM_005245	rs1510315	intron_variant

EGFR	snp	chr7	55241727	GGTG	AGTG	6462.41	het	827	0.28	NM_005228.3		synonymous_va
EGFR	snp	chr7	55242609	A	G	2401.05	het	167	0.53	NM_005228	rs2017000	intron_variant
ERBB2	mnp	chr17	37871393	TG	CA	12.88	het	137	0.13	NM_004448.2		intron_variant
ERBB2	complex	chr17	37881258	CCCAGGCC	TCCAGATGA	449.15	het	20	0.90	NM_004448.2		intron_variant&
ERBB3	snp	chr12	56477694	A	T	12624.10	het	794	0.52	NM_001982	rs2271194	splice_region_v
ERBB4	del,del	chr2	212578379	TAAAAAAAA	TAAAAAAAA	1093.81	het	94	#VALUE!	NM_005235.2		splice_region_v
ERBB4	snp	chr2	212578519	A	T	3249.10	het	568	0.23	NM_005235	rs35123918	intron_variant
ERBB4	snp	chr2	212587321	G	A	277.13	het	19	0.58	NM_005235	rs13002712	intron_variant
EZH2	snp	chr7	148508833	A	G	2337.31	het	133	0.58	XM_005249	rs2072407	intron_variant
FBXW7	del	chr4	153247486	CTTTTTTTTT	CTTTTTTTTT	354.38	het	66	0.23	NM_033632.3		intron_variant&
FBXW7	snp	chr4	153267968	A	G	1194.81	hom	45	1.00	NM_033632	rs2714803	intron_variant
FBXW7	del,del	chr4	153268227	CAAAAAAAA	CAAAAAAAA	4355.13	het	472	248.13	NM_033632.3		splice_region_v
FGFR1	mnp	chr8	38271371	CT	AG	316.37	het	13	0.92	NM_001174067.1		intron_variant
FGFR1	complex	chr8	38271381	TGC	AGG	305.17	het	14	0.86	NM_001174067.1		intron_variant
FGFR3	del	chr4	1806012	TGGGGGGG	TGGGGGGG	13452.00	het	2948	0.21	NM_001163213.1		intron_variant&
FGFR3	complex	chr4	1807891	GACG	AACA	343.32	het	29	0.59	NM_001163213.1		synonymous_va
FGFR3	snp	chr4	1807891	GACG	GACA	29324.50	hom	1004	0.97	NM_001163213.1		synonymous_va
FGFR3	complex	chr4	1808889	GCCAGGA	TCCTGGC	1071.69	hom	42	0.95	NM_001163213.1		missense_varia
FGFR3	complex,mn	chr4	1808900	CCC	CGGGG,CGG	882.10	het	43	#VALUE!	NM_001163213.1		missense_varia
FGFR3	complex	chr4	1808903	AGC	GGA	656.72	hom	25	0.96	NM_001163213.1		missense_varia
FLT3	snp	chr13	28592546	T	C	619.22	het	33	0.76	NM_004119	rs17086226	intron_variant
FOXL2	complex	chr3	138665047	GCGGCGCCT	TCGGGGCCG	592.90	het	33	0.70	NM_023067.3		missense_varia
GNA11	snp	chr19	3119184	T	G	615.18	hom	22	1.00	NM_002067	rs308046	intron_variant
GNAQ	snp	chr9	80409345	A	G	581.47	hom	22	1.00	NM_002072	rs1328529	intron_variant
HRAS	del	chr11	534403	GCCCAGGCC	GC	1861.78	hom	71	0.99	NM_005343.2		intron_variant&
IDH1	del	chr2	209113048	GAAAAAAAA	GAAAAAAAA	464.25	het	69	0.28	XM_005246521.1		intron_variant&
IDH1	del	chr2	209116299	GAAAAAAAA	GAAAAAAAA	2552.16	het	409	0.24	XM_005246521.1		intron_variant&
JAK2	del	chr9	5073681	CTTTTTTTTT	CTTTTTTTTT	2242.57	het	264	0.30	NM_004972.3		splice_region_v
KDR	ins	chr4	55962545	TGG	TGGG	929.23	het	281	0.19	NM_002253.2		intron_variant&
KDR	snp	chr4	55980239	C	T	315.04	het	13	0.92	NM_002253	rs7692791	intron_variant
MAP2K1	snp	chr15	66727597	G	C	13864.60	het	826	0.54	NM_002755	rs16949924	intron_variant
MET	snp	chr7	116436022	G	A	7979.95	het	331	0.87	XM_005250	rs2023748&	synonymous_va
MET	snp	chr7	116436097	G	A	6045.97	het	256	0.86	XM_005250	rs41737&CC	synonymous_va
MYC	snp	chr8	128747471	C	T	232.90	het	16	0.75	NM_002467	rs4645943	upstream_gene
MYCN	snp	chr2	16080157	C	G	4097.79	hom	129	1.00	NM_005378	rs11886063	upstream_gene
MYCN	snp	chr2	16089442	T	A	431.83	hom	16	1.00	NM_005378	rs12619709	downstream_ge
MYCN	snp	chr2	16089615	T	C	15453.20	hom	518	1.00	NM_005378	rs4669018	downstream_ge
NOTCH1	snp	chr9	139390397	C	T	1706.24	hom	68	1.00	NM_017617	rs3124591	3_prime_UTR_v
NOTCH1	snp	chr9	139391636	G	A	17982.20	hom	653	1.00	NM_017617	rs2229974	synonymous_va
NOTCH1	complex,cor	chr9	139397707	GTCGG	ATCAG,ATCG	1007.14	het	43	#VALUE!	NM_017617.3		synonymous_va
NOTCH1	snp	chr9	139397707	GTCGG	ATCGG	30527.60	hom	1027	0.96	NM_017617.3		synonymous_va

NPM1	del	chr5	170837513	CTTTTTTTTT	CTTTTTTTTT	2167.64	het	269	0.31	NM_002520.6		splice_region_v
NPM1	del	chr5	170837733	CTG	CG	705.00	het	43	0.65	NM_002520.6		3_prime_UTR_v
PDGFRA	snp	chr4	55141055	A	G	32561.00	hom	1053	1.00	NM_006206	rs1873778&	synonymous_va
PDGFRA	snp	chr4	55161254	C	T	5835.08	het	296	0.68	NM_006206	rs3733540	intron_variant
PDGFRA	snp	chr4	55161391	T	C	3904.30	hom	124	1.00	NM_006206	rs7685117	synonymous_va
PDGFRA	snp	chr4	55161517	A	G	6221.13	hom	206	1.00	NM_006206	rs7680422	3_prime_UTR_v
PIK3CA	del	chr3	178927848	ATTTTTTTTT	ATTTTTTTTT	2105.89	het	210	0.36	NM_006218.2		intron_variant&
PTEN	snp	chr10	89693076	T	A	230.01	hom	10	1.00	NM_000314.4		intron_variant
PTEN	del	chr10	89720633	CTTTTTTTTT	CTTTTTTTTT	1781.71	het	346	0.26	NM_000314.4		splice_acceptor
PTEN	snp	chr10	89720907	T	G	2548.45	het	169	0.53	NM_000314	rs555895&C	intron_variant
PTEN	del	chr10	89725293	CTTTTTTTTT	CTTTTTTTTT	185.52	het	111	0.14	NM_000314.4		3_prime_UTR_v
RB1	snp	chr13	48919358	T	G	10055.50	hom	329	1.00	NM_000321	rs198617	intron_variant
RB1	del	chr13	48953655	CAAAAAAAA	CAAAAAAAA	1431.69	het	240	0.22	NM_000321.2		intron_variant&
RB1	snp	chr13	48955676	T	A	503.72	hom	19	1.00	NM_000321	rs2804086	intron_variant
RB1	snp	chr13	49033747	G	A	1118.38	hom	42	1.00	NM_000321	rs198580	intron_variant
RB1	ins	chr13	49034022	ATT	ATTT	1940.08	het	108	0.81	NM_000321.2		intron_variant&
RB1	snp	chr13	49034046	T	C	2.53	het	82	0.13	NM_000321.2		intron_variant
RB1	snp	chr13	49034105	C	T	352.38	het	20	0.80	NM_000321	rs9562824	intron_variant
RB1	snp	chr13	49034154	A	G	280.10	hom	10	1.00	NM_000321	rs198581	intron_variant
RET	mnp	chr10	43610189	GGG	TCT	320.47	hom	13	0.92	NM_020975.4		splice_region_v
RET	mnp	chr10	43610199	GGG	CCC	608.48	hom	23	0.96	NM_020975.4		intron_variant
RET	snp	chr10	43610281	G	A	257.69	het	18	0.72	NM_020975.4		intron_variant
RET	complex	chr10	43615494	CATGGC	GAGGGT	273.58	het	18	0.67	NM_020975.4		intron_variant
RHOA	snp	chr3	49406080	T	C	265.71	het	17	0.82	NM_001664	rs2878298	intron_variant
SMO	snp	chr7	128845316	G	A	225.18	het	21	0.52	NM_005631.4		intron_variant
SMO	snp	chr7	128846328	G	C	10361.60	het	604	0.56	NM_005631	rs2228617	synonymous_va
SMO	snp	chr7	128846469	A	G	588.19	het	33	0.73	NM_005631	rs2735842	intron_variant
SMO	ins	chr7	128846557	CAGT	CAGAGT	244.11	het	15	0.67	NM_005631.4		intron_variant&
STK11	snp	chr19	1218523	G	T	32809.80	het	1940	0.54	XM_005259	rs2075604	intron_variant
STK11	snp	chr19	1219274	G	A	1449.61	hom	54	1.00	XM_005259	rs34928889	intron_variant
STK11	ins	chr19	1219443	GCGGGGGC	GCGGGGGC	1170.84	het	99	0.42	XM_005259617.1		intron_variant&
STK11	snp	chr19	1219444	C	G	120.52	het	171	0.15	XM_005259617.1		intron_variant
STK11	snp	chr19	1219451	C	G	620.04	het	223	0.24	XM_005259	rs36951560	intron_variant
STK11	snp	chr19	1219553	G	T	327.14	hom	14	1.00	XM_005259	rs11084889	intron_variant
STK11	snp	chr19	1220321	TGTG	CGTG	26077.70	het	1170	0.75	XM_005259617.1		intron_variant
STK11	complex	chr19	1226625	GTCGGCC	CACTGC	278.53	het	12	0.92	XM_005259617.1		frameshift_varia
STK11	mnp	chr19	1226635	AA	TT	313.95	hom	11	1.00	XM_005259617.1		missense_varian
TERT	snp	chr5	1295347	GGA	GGG	51138.30	het	3182	0.51	NM_198253.2		upstream_gene
TP53	snp	chr17	7578115	T	C	653.01	het	34	0.85	NM_000546	rs1625895	intron_variant
TP53	snp	chr17	7579472	G	C	14339.40	het	891	0.54	NM_000546	rs1042522&	missense_varian
TP53	del	chr17	7579643	CCCCCAGCC	CC	1960.87	het	670	0.21	NM_000546.5		intron_variant&

TP53	complex	chr17	7579668	CTCCAG	CAACCCTT	1590.32	het	736	0.18	NM_000546.5		intron_variant&
TP53	complex	chr17	7579678	CCAG	TTAC	1659.08	het	671	0.21	NM_000546.5		intron_variant
TP53	snp	chr17	7579801	G	C	4750.03	het	248	0.68	NM_000546	rs1642785	intron_variant
VHL	snp	chr3	10188428	T	G	816.73	hom	29	1.00	NM_000551	rs1678607	intron_variant