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Data Sheet

Product Name: CancerSeqPlus Paraffin Tissue Curl

Catalog No.: T2235248-SC **Lot No.: B906147**

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: 60 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:** _____

B906147

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.

CNV against colon	Copy Number	STDev of Copy Number	P-value	CNV against adrenal	Copy Number	STDev of Copy Number	P-value
ERBB4	3.12	0.18	6.70E-03	ERBB4	1.58	0.01	1.34E-01
SMO	0.28	0.02	4.35E-03	SMO	0.46	0.01	2.42E-02

symbol	type	chromosome	position	reference	mutation	quality	allele type	Depth	variant frequency	transcript_id	existing variation	consequence
APC	snp	chr5	112176559	T	G	324.75	hom	12	1.00	XM_005271	rs866006	synonymous
APC	snp	chr5	112177171	G	A	990.08	hom	36	1.00	XM_005271	rs465899	synonymous
APC	snp	chr5	112179909	C	A	401.48	hom	14	1.00	XM_005271	rs1804197&	3_prime_UT
ATM	del	chr11	108117897	ATTTTTTTTT	ATTTTTTTTT	52.30	het	81	0.12	NM_000051.3		intron_varia
AURKA	complex	chr20	54963147	CCC	ACAGATTAT	257.06	hom	13	0.85	NM_003600.2		intron_varia
BRAF	snp	chr7	140481448	C	T	753.02	het	46	0.61	XM_005250045.1		missense_va
CCND1	complex	chr11	69471108	ACCC	CCCT	211.85	het	58	0.21	NM_053056.2		downstream
CCND1	snp	chr11	69471138	T	G	293.19	het	17	0.71	NM_053056.2		downstream
CDKN2A	snp	chr9	21968199	C	G	14292.10	hom	466	1.00	NM_001195	rs11515&CO	3_prime_UT
CSF1R	snp	chr5	149433815	C	A	272.91	hom	13	1.00	NM_005211.3		intron_varia
DDR2	snp	chr1	162740327	T	C	11630.30	hom	370	1.00	XM_005245	rs1780003	intron_varia
DDR2	snp	chr1	162743418	G	T	1019.57	hom	40	1.00	XM_005245	rs1355287	intron_varia
EGFR	complex	chr7	55241751	ACAGGCCTC	CCAGCCCAG	39.94	het	101	0.14	NM_005228.3		intron_varia
ERBB3	snp	chr12	56477694	A	T	4740.95	hom	156	1.00	NM_001982	rs2271194	splice_regio
EZH2	snp	chr7	148508833	A	G	296.82	het	17	0.71	XM_005249	rs2072407	intron_varia
FBXW7	del	chr4	153247486	CTTTTTTTTT	CTTTTTTTTT	359.94	het	47	0.32	NM_033632.3		intron_varia
FGFR1	snp	chr8	38271991	T	C	253.52	het	21	0.62	NM_001174067.1		intron_varia
FGFR3	snp	chr4	1803704	T	C	1109.56	hom	37	1.00	NM_001163	rs2234909&	synonymous
FGFR3	snp	chr4	1805568	C	T	3713.94	hom	135	0.96	NM_001163	rs3135885	intron_varia
FGFR3	del	chr4	1806012	TGGGGGGG	TGGGGGGG	3464.05	het	327	0.40	NM_001163213.1		intron_varia
FGFR3	snp	chr4	1807894	G	A	724.91	hom	27	0.96	NM_001163	rs7688609	synonymous
FOXL2	snp	chr3	138664822	A	G	3893.64	het	179	0.83	NM_023067.3		missense_va
IDH1	del	chr2	209116299	GAAAAAAA	GAAAAAAA	1343.13	het	176	0.29	XM_005246521.1		intron_varia
JAK2	snp	chr9	5111851	A	G	277.13	hom	10	1.00	NM_004972.3		intron_varia
KDR	snp	chr4	55972974	T	A	275.55	hom	10	1.00	NM_002253	rs1870377&	missense_va
MAP2K1	snp	chr15	66727597	G	C	4752.48	het	203	0.80	NM_002755	rs16949924	intron_varia
MET	snp	chr7	116436022	G	A	1644.46	het	74	0.84	XM_005250	rs2023748&	synonymous

MET	snp	chr7	116436097	G	A	677.49	het	49	0.61	XM_005250	rs41737&CO	synonymous
MLH1	snp	chr3	37067240	T	A	2234.24	het	108	0.69	NM_000249	rs63750447&	missense_va
MYC	snp	chr8	128746674	G	A	557.23	hom	24	1.00	NM_002467.4		upstream_ge
MYC	snp	chr8	128746711	G	A	309.47	het	23	0.65	NM_002467.4		upstream_ge
MYCN	snp	chr2	16080157	C	G	459.70	hom	16	1.00	NM_005378	rs11886063	upstream_ge
MYCN	snp	chr2	16089615	T	C	1407.40	het	89	0.55	NM_005378	rs4669018	downstream
NOTCH1	snp	chr9	139391636	G	A	981.49	hom	42	1.00	NM_017617	rs2229974	synonymous
NOTCH1	snp	chr9	139397707	G	A	10490.20	hom	341	1.00	NM_017617	rs10521&CO	synonymous
NOTCH1	complex	chr9	139399177	CACCAGGGA	TCCCTGGTG	381.77	het	180	0.16	NM_017617.3		missense_va
NPM1	del	chr5	170837513	CTTTTTTTTT	CTTTTTTTTT	494.71	het	58	0.36	NM_002520.6		splice_regior
PDGFRA	snp	chr4	55141055	A	G	4229.25	hom	140	1.00	NM_006206	rs1873778&	synonymous
PDGFRA	snp	chr4	55144038	G	A	244.56	het	15	0.67	NM_006206.4		intron_varia
PDGFRA	snp	chr4	55161254	C	T	1197.33	het	68	0.60	NM_006206	rs3733540	intron_varia
PDGFRA	snp	chr4	55161517	A	G	932.08	hom	31	1.00	NM_006206	rs7680422	3_prime_UT
PIK3R1	snp	chr5	67588148	G	A	1063.75	het	47	0.85	NM_181523	rs3730089&	missense_va
PTEN	snp	chr10	89624182	C	T	96.89	het	123	0.13	NM_000314.4		5_prime_UT
PTEN	del	chr10	89720633	CTTTTTTTTT	CTTTTTTTTT	385.68	het	103	0.22	NM_000314.4		splice_accep
PTEN	snp	chr10	89720907	T	G	416.84	hom	15	1.00	NM_000314	rs555895&C	intron_varia
RB1	snp	chr13	48919358	T	G	3657.65	hom	123	1.00	NM_000321	rs198617	intron_varia
RB1	del	chr13	48953655	CAAAAAAAA	CAAAAAAAA	600.69	het	103	0.22	NM_000321.2		intron_varia
RB1	ins	chr13	49034022	ATT	ATTT	750.84	hom	30	1.00	NM_000321.2		intron_varia
RET	snp	chr10	43613843	G	T	2957.58	hom	105	0.95	NM_020975	rs1800861&	synonymous
SMAD4	del	chr18	48584729	TGG	TG	290.99	het	38	0.32	NM_005359.5		frameshift_v
SMAD4	snp	chr18	48593417	G	A	1878.31	het	122	0.55	NM_005359	rs37776735(	missense_va
SMO	snp	chr7	128845277	G	C	1817.47	het	75	0.87	NM_005631	rs2075777	intron_varia
SMO	snp	chr7	128846328	G	C	356.76	het	20	0.65	NM_005631	rs2228617	synonymous
STK11	snp	chr19	1222012	G	C	13676.00	het	820	0.55	XM_005259	rs2075607	splice_regior
TP53	snp	chr17	7579472	G	C	2480.99	hom	86	0.98	NM_000546	rs1042522&	missense_va
TP53	del	chr17	7579643	CCCCCAGCC	CC	344.75	het	51	0.37	NM_000546.5		intron_varia
VHL	snp	chr3	10188090	C	G	260.66	hom	11	1.00	NM_000551.3		intron_varia
VHL	complex	chr3	10188095	TGA	AGCAA	220.00	hom	10	1.00	NM_000551.3		intron_varia
VHL	complex	chr3	10188101	GCCTGC	TCCTAT	236.38	hom	10	1.00	NM_000551.3		intron_varia
VHL	snp	chr3	10188114	T	C	257.02	hom	11	1.00	NM_000551.3		intron_varia