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Data Sheet

Product Name: CancerSeqPlus Paraffin Tissue Curl

Catalog No.: T2235248-SC **Lot No.: B906148**

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: _____ year(s) old
Female: 32 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:** _____

B906148

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	Copy Number	STDev of	P-value	CNV	Copy	STDev of	P-value
CCNE1	4.19	0.30	1.22E-03	CCNE1	2.87	0.03	2.05E-03

symbol	type	chromosome	position	reference	mutation	quality	allele type	Depth	variant frequency	transcript_id	existing variation	consequence
ATM	del	chr11	108117897	ATTTTTTTTT	ATTTTTTTTT	169.149	het	107	0.14	NM_000051	intron_variant&feature_t	
CCNE1	snp	chr19	30301731	C	A	266.209	hom	10	1.00	NM_001238	upstream_gene_variant	
CDH1	snp	chr16	68771372	C	T	13270	het	579	0.76	NM_004360	splice_regio	rs3743674
CDH1	complex	chr16	68771429	TGC	CGT	202.428	het	15	0.73	NM_004360	intron_variant	
CDH1	mnp	chr16	68771437	TT	AG	235.911	het	16	0.75	NM_004360	intron_variant	
CDH1	snp	chr16	68857441	T	C	519.343	het	30	0.63	NM_004360	synonymous	rs1801552
CDK4	snp	chr12	58145156	C	T	223.581	het	99	0.17	NM_000075	intron_varia	rs2270777
CDKN2A	snp	chr9	21968199	C	G	30342.3	hom	965	1.00	NM_001195	3_prime_UT	rs11515&CO
DDR2	snp	chr1	162740327	T	C	15979.1	hom	514	0.99	XM_005245	intron_varia	rs1780003
DDR2	snp	chr1	162743418	G	T	2204.34	hom	80	1.00	XM_005245	intron_varia	rs1355287
EGFR	snp	chr7	55242609	A	G	417.24	het	24	0.71	NM_005228	intron_varia	rs2017000
ERBB3	snp	chr12	56477694	A	T	9676.39	het	400	0.86	NM_001982	splice_regio	rs2271194
ERBB4	snp	chr2	212578519	A	T	1920.23	het	378	0.22	NM_005235	intron_varia	rs35123918
FBXW7	del	chr4	153247486	CTTTTTTTTT	CTTTTTTTTT	276.586	het	81	0.17	NM_033632	intron_variant&feature_t	
FBXW7	snp	chr4	153267968	A	G	596.097	hom	24	1.00	NM_033632	intron_varia	rs2714803
FBXW7	del,del	chr4	153268227	CAAAAAAAA	CAAAAAAAA	1024.3	2-Jan	148	#VALUE!	NM_033632	splice_region_variant&in	
FBXW7	del,del	chr4	153268227	CAAAAAAAA	CAAAAAAAA	1024.3	2-Jan	148	#VALUE!	NM_033632	splice_region_variant&in	
FGFR1	snp	chr8	38271362	T	A	471.764	het	28	0.64	NM_001174	intron_variant	
FGFR1	mnp	chr8	38271371	CT	AG	662.513	hom	25	0.96	NM_001174	intron_variant	
FGFR1	complex	chr8	38271381	TGC	AGG	720.807	hom	26	1.00	NM_001174	intron_variant	
FGFR3	del	chr4	1806012	TGGGGGGG	TGGGGGGG	2622.06	het	789	0.18	NM_001163	intron_variant&feature_t	
FGFR3	snp	chr4	1807894	G	A	5117.14	hom	166	1.00	NM_001163	synonymous	rs7688609
FLT3	snp	chr13	28610183	A	G	3938.9	het	249	0.52	NM_004119	splice_regio	rs2491231
FOXL2	complex	chr3	138664785	GCG	ACA	218.141	het	256	0.13	NM_023067	missense_variant	
FOXL2	complex	chr3	138665047	GCGGCGCCT	TCGGGGCCG	1002.01	hom	35	1.00	NM_023067	missense_variant	
HRAS	del	chr11	534403	GCCCAGGCC	GC	458.696	hom	17	1.00	NM_005343	intron_variant&feature_t	
IDH1	del	chr2	209116299	GAAAAAAAA	GAAAAAAAA	1260.23	het	213	0.24	XM_005246	intron_variant&feature_t	
JAK2	del	chr9	5073681	CTTTTTTTTT	CTTTTTTTTT	797.228	het	95	0.32	NM_004972	splice_region_variant&in	
KIT	snp	chr4	55593464	A	C	1672.45	het	75	0.79	XM_005265	missense_va	rs3822214&

KIT	snp	chr4	55602765	G	C	2541.99	het	125	0.70	XM_005265	synonymous	rs3733542&
MAP2K1	snp	chr15	66727597	G	C	10263.5	het	576	0.57	NM_002755	intron_varia	rs16949924
MET	snp	chr7	116436022	G	A	1579.9	het	87	0.61	XM_005250	synonymous	rs2023748&
MYCN	snp	chr2	16080157	C	G	3152.86	hom	99	1.00	NM_005378	upstream_g	rs11886063
MYCN	snp	chr2	16089615	T	C	5507.77	hom	182	1.00	NM_005378	downstream	rs4669018
NOTCH1	snp	chr9	139391636	G	A	2241.77	het	116	0.82	NM_017617	synonymous	rs2229974
NOTCH1	snp	chr9	139397707	G	A	4416.99	het	216	0.70	NM_017617	synonymous	rs10521&CO
NOTCH1	snp	chr9	139399633	G	T	395.51	hom	15	1.00	NM_017617	intron_variant	
NPM1	del	chr5	170837513	CTTTTTTTTT	CTTTTTTTTT	1020.29	het	130	0.31	NM_002520	splice_region_variant&in	
PDGFRA	complex	chr4	55141051	GCCCA	ACCCG	384.454	het	28	0.57	NM_006206	missense_variant	
PDGFRA	snp	chr4	55141051	GCCCA	GCCCG	11544	hom	399	0.93	NM_006206	synonymous_variant	
PDGFRA	snp	chr4	55161254	C	T	1702.82	het	93	0.61	NM_006206	intron_varia	rs3733540
PDGFRA	snp	chr4	55161391	T	C	1163.48	hom	38	1.00	NM_006206	synonymous	rs7685117
PDGFRA	snp	chr4	55161517	A	G	4423.68	hom	141	1.00	NM_006206	3_prime_UT	rs7680422
PIK3CA	del	chr3	178927848	ATTTTTTTTT	ATTTTTTTTT	641.685	het	128	0.21	NM_006218	intron_variant&feature_t	
PTEN	del	chr10	89720633	CTTTTTTTTT	CTTTTTTTTT	411.211	het	123	0.17	NM_000314	splice_acceptor_variant&	
PTEN	snp	chr10	89720907	T	G	1153.75	het	50	0.88	NM_000314	intron_varia	rs555895&C
PTEN	del	chr10	89725293	CTTTTTTTTT	CTTTTTTTTT	321.448	het	99	0.18	NM_000314	3_prime_UTR_variant&fe	
RB1	snp	chr13	48919358	T	G	3581.94	hom	120	1.00	NM_000321	intron_varia	rs198617
RB1	snp	chr13	49033747	G	A	287.286	hom	11	1.00	NM_000321	intron_varia	rs198580
RB1	ins	chr13	49034022	ATT	ATTT	585.954	hom	25	1.00	NM_000321	intron_variant&feature_e	
RET	complex	chr10	43610208	AAGATC	GATCTT	247.789	het	19	0.53	NM_020975	intron_variant	
RET	complex	chr10	43621817	GTGA	CTTT	346.673	hom	13	1.00	NM_020975	intron_variant	
SMO	snp	chr7	128845277	G	C	9888.78	hom	329	0.99	NM_005631	intron_varia	rs2075777
SMO	snp	chr7	128846328	G	C	7502.92	hom	250	0.95	NM_005631	synonymous	rs2228617
SMO	snp	chr7	128846469	A	G	556.828	hom	21	1.00	NM_005631	intron_varia	rs2735842
STK11	snp	chr19	1222012	G	C	28810	het	1316	0.74	XM_005259	splice_regio	rs2075607
TERT	snp	chr5	1295349	A	G	17099.9	het	1047	0.51	NM_198253	upstream_g	rs2853669&
TP53	snp	chr17	7577298	G	A	563.854	hom	22	0.95	NM_000546	intron_variant	
TP53	snp	chr17	7578115	T	C	358.843	hom	14	1.00	NM_000546	intron_varia	rs1625895
TP53	snp	chr17	7579472	G	C	4327.69	het	218	0.68	NM_000546	missense_va	rs1042522&
TP53	del	chr17	7579643	CCCCCAGCC	CC	1347.21	het	179	0.38	NM_000546	intron_variant&feature_t	
TP53	complex	chr17	7579678	CCAG	TTAC	201.127	het	32	0.38	NM_000546	intron_variant	
VHL	snp	chr3	10188428	T	G	230.011	hom	10	1.00	NM_000551	intron_varia	rs1678607