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Data Sheet

Product Name: CancerSeqPlus Paraffin Tissue Curl

Catalog No.: T2235265-SC **Lot No.: B906066**

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: Thyroid

Donor Information:

Male: 24 year(s) old
Female: _____ year(s) old

Pathological Diagnosis: Adenocarcinoma, papillary

Tumor Size: 4x3x3 cm

Location: Thyroid, right

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

FOR IN VITRO RESEARCH USE ONLY **APPROVED BY:** _____

lot# B906066

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
NOTCH1	2.70	0.17	3.64E-02	NOTCH1	4.42	0.08	3.10E-03

symbol	type	chromosome	position	reference	mutation	quality	allele type	Depth at this position	transcript_id	existing variation	consequence
ALK	snp	chr2	29445458	G	T	1142.54	hom	37	NM_004304.4	rs3795850	synonymous_vari
CCNE1	snp	chr19	30314680	C	T	607.351	hom	23	NM_001238.2	rs141578348&C	missense_variant
CDH1	snp	chr16	68771372	C	T	5419.09	hom	170	NM_004360.3	rs3743674	splice_region_var
CDH1	complex	chr16	68842664	CCCTGTT	AACAGGG	297.018	hom	12	NM_004360.3		missense_variant
CDH1	complex	chr16	68853339	CTC	TTT	980.26	het	75	NM_004360.3		intron_variant
CDK4	snp	chr12	58144496	G	A	574.429	het	28	NM_000075.3		missense_variant
CDK4	snp	chr12	58145461	C	T	327.401	het	18	NM_000075.3		missense_variant
CDKN2A	snp	chr9	21965654	C	T	1068.93	het	59	NM_001195132.1		downstream_gen
CDKN2A	snp	chr9	21968199	C	G	6652.3	hom	214	NM_001195132	rs11515&COSM	3_prime_UTR_va
CDKN2A	complex	chr9	21971100	GGCAGC	TGCAC	430.822	het	39	NM_001195132.1		frameshift_variar
CDKN2A	complex	chr9	21971107	TCGT	ACGCT	397.337	het	39	NM_001195132.1		frameshift_variar
CDKN2A	snp	chr9	21971113	A	C	455.446	het	39	NM_001195132.1		missense_variant
DDR2	snp	chr1	162740327	T	C	5727.08	hom	182	XM_005245220	rs1780003	intron_variant
DDR2	snp	chr1	162743418	G	T	397.844	hom	14	XM_005245220	rs1355287	intron_variant
DDR2	snp	chr1	162749873	T	C	240.408	het	40	XM_005245220.1		intron_variant
ERBB2	snp	chr17	37882937	C	T	724.697	het	76	NM_004448.2		intron_variant
ERBB3	snp	chr12	56477694	A	T	1480.97	het	81	NM_001982.3	rs2271194	splice_region_var
ERBB3	complex	chr12	56482360	GG	AA	442.705	hom	17	NM_001982.3		missense_variant
EZH2	snp	chr7	148508833	A	G	879.407	hom	28	XM_005249962	rs2072407	intron_variant
FBXW7	snp	chr4	153252061	A	G	230.119	het	14	NM_033632.3	rs10033601	intron_variant
FGFR1	complex	chr8	38271390	GCAG	ACAA	312.618	het	35	NM_001174067.1		intron_variant
FGFR1	complex	chr8	38282184	CCTGC	TCTGT	507.363	het	106	NM_001174067.1		missense_variant
FGFR1	snp	chr8	38285988	T	A	340.4	hom	19	NM_001174067.1		intron_variant
FGFR3	snp	chr4	1803719	C	T	972.928	hom	35	NM_001163213.1		synonymous_vari
FGFR3	complex	chr4	1805614	CTC	TTT	411.651	het	91	NM_001163213.1		intron_variant
FGFR3	snp	chr4	1806091	C	T	576.997	hom	27	NM_001163213.1		synonymous_vari
FGFR3	snp	chr4	1808357	G	A	656.974	het	49	NM_001163213.1		synonymous_vari
FGFR3	snp	chr4	1808924	G	A	322.251	het	16	NM_001163213.1		missense_variant

FGFR3	snp	chr4	1808995	C	T	244.561	het	15	NM_001163213.1		3_prime_UTR_va
FLT3	snp	chr13	28610183	A	G	305.771	hom	11	NM_004119.2	rs2491231	splice_region_var
FOXL2	snp	chr3	138664655	C	T	2035.29	hom	83	NM_023067.3		missense_variant
FOXL2	snp	chr3	138664804	G	A	2077.34	hom	79	NM_023067.3		missense_variant
KDR	snp	chr4	55961159	T	C	1207.64	het	53	NM_002253.2	rs2219471	intron_variant
KDR	snp	chr4	55980456	C	T	1351.67	het	55	NM_002253.2	rs2305949	intron_variant
KRAS	snp	chr12	25362777	A	G	370.678	hom	13	NM_033360.2	rs1137282	3_prime_UTR_va
KRAS	snp	chr12	25380370	G	A	225.996	het	17	NM_033360.2		intron_variant
MAP2K1	snp	chr15	66727595	CAG	CAC	8116.59	hom	271	NM_002755.3		intron_variant
MAP2K1	complex	chr15	66727595	CAG	TAC	301.679	hom	10	NM_002755.3		intron_variant
MET	snp	chr7	116423529	G	A	459.434	het	29	XM_005250353.1		splice_region_var
MET	snp	chr7	116435953	G	A	627.136	het	34	XM_005250353.1		missense_variant
MET	snp	chr7	116435965	G	A	536.5	het	23	XM_005250353.1		stop_gained
MET	snp	chr7	116436022	G	A	644.718	hom	23	XM_005250353	rs2023748&COS	synonymous_vari
MPL	snp	chr1	43814947	G	A	2440.36	hom	92	NM_005373.2		synonymous_vari
MYC	snp	chr8	128749560	C	T	279.211	het	14	NM_002467.4		intron_variant
MYCN	snp	chr2	16089615	T	C	864.069	hom	33	NM_005378.4	rs4669018	downstream_gen
NOTCH1	snp	chr9	139397707	G	A	2481.06	hom	88	NM_017617.3	rs10521&COSM	synonymous_vari
NOTCH1	snp	chr9	139399412	C	T	284.029	hom	12	NM_017617.3		synonymous_vari
NOTCH1	snp	chr9	139400299	C	T	2719.13	het	182	NM_017617.3	rs150343794	missense_variant
NPM1	del,del	chr5	170837513	CTTTTTTTTTT	CTTTTTTTTT	614.505	het	73	NM_002520.6		splice_region_var
PDGFRA	snp	chr4	55141055	A	G	731.913	hom	26	NM_006206.4	rs1873778&COS	synonymous_vari
PDGFRA	snp	chr4	55161254	C	T	1680.99	hom	53	NM_006206.4	rs3733540	intron_variant
PDGFRA	snp	chr4	55161517	A	G	1351.47	hom	43	NM_006206.4	rs7680422	3_prime_UTR_va
PIK3CA	snp	chr3	178921451	T	A	1625.34	het	127	NM_006218.2		synonymous_vari
RB1	snp	chr13	48923110	T	C	817.414	het	57	NM_000321.2		synonymous_vari
RB1	complex	chr13	48953868	TGGGCA	CGGGTG	268.498	hom	11	NM_000321.2		intron_variant
RET	snp	chr10	43610114	C	T	299.067	het	22	NM_020975.4		missense_variant
ROS1	snp	chr6	117638460	G	A	783.73	het	171	NM_002944.2		intron_variant
SMAD4	snp	chr18	48573411	G	A	551.235	het	32	NM_005359.5		5_prime_UTR_va
SMARCB1	snp	chr22	24145602	C	T	919.543	het	40	XM_005261718.1		synonymous_vari
SMO	snp	chr7	128845277	G	C	1977.13	hom	63	NM_005631.4	rs2075777	intron_variant
SMO	snp	chr7	128846328	G	C	260.749	hom	10	NM_005631.4	rs2228617	synonymous_vari
SMO	snp	chr7	128850336	C	T	2112.03	hom	84	NM_005631.4		synonymous_vari
SMO	snp	chr7	128850359	C	T	2288.14	het	157	NM_005631.4		missense_variant
STK11	ins	chr19	1219443	GCGGGGGCC	GCGGGGGCC	335.524	het	20	XM_005259617.1		intron_variant&fe
STK11	snp	chr19	1220321	T	C	3250.37	het	145	XM_005259617	rs2075606	intron_variant
STK11	snp	chr19	1221853	C	T	1000.24	hom	36	XM_005259617.1		intron_variant
STK11	snp	chr19	1221907	C	T	953.671	het	75	XM_005259617.1		intron_variant
STK11	snp	chr19	1223107	C	T	317.965	het	26	XM_005259617.1		synonymous_vari
STK11	snp	chr19	1226672	G	A	540.174	het	35	XM_005259617.1		intron_variant

TERT	complex	chr5	1295216	GGAG	AGAA	1371.22	het	410	NM_198253.2		upstream_gene_
TERT	snp	chr5	1295246	CCGGGA	TCGGGA	2361.7	het	449	NM_198253.2		upstream_gene_
TERT	complex	chr5	1295349	AAGC	GAGT	285.21	het	28	NM_198253.2		upstream_gene_
TERT	snp	chr5	1295349	A	G	54182.7	hom	1706	NM_198253.2	rs2853669&CR0	upstream_gene_
TP53	snp	chr17	7572984	C	T	3831.61	het	249	NM_000546.5		synonymous_vari
TP53	snp	chr17	7573870	G	A	16.405	het	152	NM_000546.5		intron_variant
TP53	snp	chr17	7577407	A	C	1062.8	het	51	NM_000546.5	rs12951053	intron_variant
TP53	snp	chr17	7577427	G	A	745.279	het	37	NM_000546.5	rs12947788	intron_variant
TP53	snp	chr17	7577509	C	T	1581.32	het	78	NM_000546.5	rs121912652&T	missense_variant
TP53	complex	chr17	7577612	GGAG	AGAA	944.655	het	583	NM_000546.5		splice_region_var
TP53	del	chr17	7579444	TGT	TT	498.637	het	63	NM_000546.5		frameshift_variar
TP53	snp	chr17	7579470	CGG	CGC	946.407	het	87	NM_000546.5		missense_variant
TP53	complex	chr17	7579470	CGG	TGC	380.338	het	35	NM_000546.5		missense_variant