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Data Sheet

Product Name: CancerSeqPlus Paraffin Tissue Curl

Catalog No.: T2235265-SC **Lot No.: B906063**

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: _____ year(s) old
Female: 23 year(s) old

Pathological Diagnosis: Adenocarcinoma, papillary

Tumor Size: 3 cm

Location: Thyroid

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

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

lot# B906063

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

CNV against	Copy Number	STDev of Copy Number	P-value	CNV against adrenal	Copy Number	STDev of Copy	P-value
ERBB4	3.34	0.98	2.57E-03	ERBB4	1.37	0.08	0.19
FBXW7	3.63	0.89	1.04E-03	FBXW7	1.69	0.10	0.03
KRAS	3.47	1.22	7.81E-04	KRAS	1.35	0.10	0.20
PTEN	4.26	0.91	7.76E-04	PTEN	1.95	0.13	0.02
RB1	4.39	0.59	7.76E-04	RB1	1.72	0.11	0.03

symbol	type	chromosome	position	reference	mutation	quality	allele type	Depth at this position	transcript_id	existing variation	consequence
ABL1	snp	chr9	133738377	C	T	2026.22	het	131	NM_007313.2		synonymous_variant
AKT1	snp	chr14	105246377	C	T	2249.91	hom	102	NM_001014431.1		intron_variant
APC	snp	chr5	112175770	G	A	2473.92	hom	89	XM_00527197	rs41115&COSN	synonymous_variant
APC	snp	chr5	112177171	G	A	1527.82	hom	57	XM_00527197	rs465899	synonymous_variant
ATM	del	chr11	108117897	ATTTTTTTTTT	ATTTTTTTTTA	544.966	het	237	NM_000051.3		intron_variant&featu
ATM	snp	chr11	108225483	C	T	490.732	hom	21	NM_000051.3	rs664982	intron_variant
CCND1	del	chr11	69450976	GAAAAAAAA	GAAAAAAAA	228.99	het	29	NM_053056.2		upstream_gene_vari
CCNE1	snp	chr19	30303617	C	T	2008.41	het	134	NM_001238.2	rs139551337	synonymous_variant
CDH1	snp	chr16	68771372	CC	TC	22296.6	het	1102	NM_004360.3		splice_region_varian
CDH1	snp	chr16	68835658	T	A	27.4024	het	85	NM_004360.3		synonymous_variant
CDH1	snp	chr16	68845801	A	G	466.933	hom	23	NM_004360.3		intron_variant
CDH1	snp	chr16	68849703	T	A	272.119	het	31	NM_004360.3		intron_variant
CDK4	snp	chr12	58143123	G	A	940.075	hom	41	NM_000075.3		intron_variant
CDK4	snp	chr12	58144665	C	T	770.552	hom	31	NM_000075.3	rs2069502	intron_variant
CDK4	complex	chr12	58144764	TTGACTGTTC	ATGGCACTTA	944.728	hom	37	NM_000075.3		missense_variant
CDK4	complex	chr12	58144778	ACTT	CGTG	852.532	hom	35	NM_000075.3		missense_variant
CDK4	complex	chr12	58144786	CC	GT	933.83	hom	35	NM_000075.3		missense_variant
CDKN2A	snp	chr9	21968159	G	A	1064.01	hom	38	NM_00119513	rs3088440&CO	3_prime_UTR_varian
CDKN2A	complex	chr9	21968199	CGAGG	GGAGA,GAA	1200.26	het	50	NM_001195132.1		3_prime_UTR_varian
CDKN2A	snp	chr9	21968199	CGAGG	GGAGG	84041.3	hom	2737	NM_001195132.1		3_prime_UTR_varian
CDKN2A	snp	chr9	21971097	C	T	723.477	het	49	NM_001195132.1		synonymous_variant
CDKN2A	snp	chr9	21971127	A	T	1458.68	het	112	NM_00119513	COSM12548	synonymous_variant
CSF1R	complex	chr5	149452950	TTGC	GTGG	904.639	het	103	NM_005211.3		missense_variant
CSF1R	complex	chr5	149452960	GGGT	ACCC	847.721	het	103	NM_005211.3		missense_variant
CSF1R	snp	chr5	149452970	C	G	1040.81	het	107	NM_005211.3		missense_variant

DDR2	snp	chr1	162740327	T	C	27092.2	hom	871	XM_00524522	rs1780003	intron_variant
DDR2	snp	chr1	162743418	G	T	4828.57	hom	164	XM_00524522	rs1355287	intron_variant
ERBB3	snp	chr12	56477694	A	T	8709.84	het	544	NM_001982.3	rs2271194	splice_region_varian
ERBB3	snp	chr12	56477726	T	A	269.275	hom	13	NM_001982.3		intron_variant
ERBB4	del	chr2	212530218	GAAAAAAAA	GAAAAAAAA	35.254	het	108	NM_005235.2		intron_variant&featu
ERBB4	del,del	chr2	212578379	TAAAAAAAA	TAAAAAAAA	1402.51	het	156	NM_005235.2		splice_region_varian
ESR1	complex	chr6	152420095	GG	AA	395.227	het	18	XM_005266856.1		missense_variant
ESR1	snp	chr6	152420095	GG	AG	13292.3	hom	442	XM_005266856.1		synonymous_variant
EZH2	snp	chr7	148508833	A	G	2291.05	hom	72	XM_00524996	rs2072407	intron_variant
FBXW7	del	chr4	153247486	CTTTTTTTTT	CTTTTTTTTT	712.197	het	120	NM_033632.3		intron_variant&featu
FBXW7	snp	chr4	153259145	T	A	482.589	hom	21	NM_033632.3		intron_variant
FBXW7	del,del	chr4	153268227	CAAAAAAAA	CAAAAAAAA	6384.46	het	695	NM_033632.3		splice_region_varian
FBXW7	snp	chr4	153271110	A	C	8882.99	het	400	NM_033632.3	rs34708673	intron_variant
FGFR3	del	chr4	1806012	TGGGGGGGG	TGGGGGGGG	3795.54	het	1471	NM_001163213.1		intron_variant&featu
FGFR3	snp	chr4	1807894	G	A	16138.6	hom	582	NM_00116321	rs7688609	synonymous_variant
FGFR3	snp	chr4	1808009	C	T	235.549	het	292	NM_001163213.1		missense_variant
FLT3	snp	chr13	28610183	A	G	9560.51	hom	314	NM_004119.2	rs2491231	splice_region_varian
FOXL2	complex	chr3	138665047	GCGGCGCCT	TCGGGGCCG	603.03	hom	22	NM_023067.3		missense_variant
HRAS	del	chr11	534403	GCCCAGGCC	GC	428.866	het	317	NM_005343.2		intron_variant&featu
IDH1	del	chr2	209113048	GAAAAAAAA	GAAAAAAAA	216.239	het	90	XM_005246521.1		intron_variant&featu
IDH1	del	chr2	209116299	GAAAAAAAA	GAAAAAAAA	6125.15	het	946	XM_005246521.1		intron_variant&featu
JAK2	del	chr9	5073681	CTTTTTTTTT	CTTTTTTTTC	461.851	het	81	NM_004972.3		splice_region_varian
KDR	snp	chr4	55960965	G	A	110.831	het	85	NM_002253.2		splice_region_varian
KDR	snp	chr4	55961159	T	C	6774.54	hom	232	NM_002253.2	rs2219471	intron_variant
KDR	snp	chr4	55972974	T	A	2516.49	hom	85	NM_002253.2	rs1870377&CM	missense_variant
MAP2K1	snp	chr15	66727444	C	T	450.94	het	35	NM_002755.3		missense_variant
MAP2K1	snp	chr15	66727597	G	C	16071.5	het	879	NM_002755.3	rs16949924	intron_variant
MET	snp	chr7	116417571	A	G	556.628	hom	29	XM_005250353.1		intron_variant
MET	snp	chr7	116436022	G	A	6771.86	hom	236	XM_00525035	rs2023748&CO	synonymous_variant
MET	snp	chr7	116436097	G	A	4676.4	hom	168	XM_00525035	rs41737&COSM	synonymous_variant
MLH1	snp	chr3	37067075	C	A	771.148	hom	28	NM_000249.3		intron_variant
MLH1	complex	chr3	37067096	TATAT	TAGTGGAGA	342.653	hom	22	NM_000249.3		intron_variant&featu
MYC	snp	chr8	128749545	G	A	388.363	het	27	NM_002467.4		intron_variant
MYCN	snp	chr2	16080073	C	T	257.19	het	23	NM_005378.4		upstream_gene_vari
MYCN	snp	chr2	16080157	C	G	2335.66	hom	74	NM_005378.4	rs11886063	upstream_gene_vari
MYCN	snp	chr2	16089442	T	A	354.137	hom	15	NM_005378.4	rs12619709	downstream_gene_v
MYCN	snp	chr2	16089615	T	C	12163	hom	419	NM_005378.4	rs4669018	downstream_gene_v
NOTCH1	snp	chr9	139391420	C	T	778.368	het	47	NM_017617.3		synonymous_variant
NOTCH1	snp	chr9	139391636	G	A	5622.01	hom	242	NM_017617.3	rs2229974	synonymous_variant
NOTCH1	snp	chr9	139397707	G	A	6361	hom	204	NM_017617.3	rs10521&COSM	synonymous_variant
NOTCH1	snp	chr9	139399229	C	T	1618.69	het	146	NM_017617.3		stop_gained

NOTCH1	snp	chr9	139399277	G	A	865.819	het	55	NM_017617.3	COSM308620	synonymous_variant
NPM1	del,del	chr5	170837513	CTTTTTTTTT	CTTTTTTTTT	4912.5	het	416	NM_002520.6		splice_region_varian
NPM1	del,del	chr5	170837513	CTTTTTTTTT	CTTTTTTTTT	4912.5	het	416	NM_002520.6		splice_region_varian
PDGFRA	snp	chr4	55141052	CCCA	CCCG	28305.1	hom	952	NM_006206.4		synonymous_variant
PDGFRA	complex	chr4	55141052	CCCA	TCCG	646.948	het	35	NM_006206.4		synonymous_variant
PDGFRA	snp	chr4	55161254	C	T	7606.23	hom	245	NM_006206.4	rs3733540	intron_variant
PDGFRA	snp	chr4	55161391	T	C	1865.48	het	75	NM_006206.4	rs7685117	synonymous_variant
PDGFRA	snp	chr4	55161517	A	G	7021.48	hom	229	NM_006206.4	rs7680422	3_prime_UTR_varian
PIK3CA	snp	chr3	178927345	T	C	3800.61	het	229	NM_006218.2	rs3729682	intron_variant
PIK3CA	del	chr3	178927848	ATTTTTTTTT	ATTTTTTTTT	2196.72	het	231	NM_006218.2		intron_variant&featu
PIK3CA	snp	chr3	178936064	A	T	646.094	het	65	NM_006218.2		missense_variant
PTEN	del	chr10	89692731	GTTTTTTTTC	GTTTTTTTC	48.4813	het	305	NM_000314.4		intron_variant&featu
PTEN	del	chr10	89720633	CTTTTTTTTT	CTTTTTTTTT	2853.35	het	544	NM_000314.4		splice_acceptor_vari
PTEN	snp	chr10	89720907	T	G	2080.28	het	116	NM_000314.4	rs555895&COS	intron_variant
PTEN	del	chr10	89725293	CTTTTTTTTT	CTTTTTTTTT	1054.96	het	246	NM_000314.4		3_prime_UTR_varian
RB1	snp	chr13	48919358	T	G	11216	hom	379	NM_000321.2	rs198617	intron_variant
RB1	del	chr13	48953654	TCAAAAAAA	TCAAAAAAA	1372.25	het	231	NM_000321.2		intron_variant&featu
RB1	snp	chr13	49033747	G	A	428.844	hom	16	NM_000321.2	rs198580	intron_variant
RB1	ins	chr13	49034022	ATT	ATTT	294.328	hom	13	NM_000321.2		intron_variant&featu
RB1	ins	chr13	49034087	TT	TTCT	265.906	het	14	NM_000321.2		intron_variant&featu
RB1	snp	chr13	49034105	C	T	289.039	hom	14	NM_000321.2	rs9562824	intron_variant
RB1	complex	chr13	49034119	TTTTTG	CTTTCC	306.491	hom	13	NM_000321.2		intron_variant
RET	snp	chr10	43610199	G	A	623.861	hom	28	NM_020975.4		intron_variant
RET	complex	chr10	43610208	AAGATC	GATCTT	558.291	het	28	NM_020975.4		intron_variant
RET	complex	chr10	43615494	CATGGC	GAGGGT	441.282	het	23	NM_020975.4		intron_variant
RET	snp	chr10	43617564	T	A	471.588	hom	22	NM_020975.4		intron_variant
SMO	snp	chr7	128845277	G	C	10793.5	hom	347	NM_005631.4	rs2075777	intron_variant
SMO	snp	chr7	128846328	G	C	6400.95	hom	204	NM_005631.4	rs2228617	synonymous_variant
STK11	snp	chr19	1207238	GC	TC	12619.5	het	706	XM_005259617.1		intron_variant
STK11	snp	chr19	1222011	CG	CC	76330.9	hom	2892	XM_005259617.1		splice_region_varian
STK11	complex	chr19	1222011	CG	TC	5988.88	hom	222	XM_005259617.1		splice_region_varian
TERT	snp	chr5	1295349	A	G	30862.5	het	1839	NM_198253.2	rs2853669&CR	upstream_gene_vari
TP53	snp	chr17	7573080	C	A	905.893	het	50	NM_000546.5		intron_variant
TP53	snp	chr17	7579472	G	C	13323.6	hom	443	NM_000546.5	rs1042522&TP	missense_variant
TP53	snp	chr17	7579563	C	T	236.107	het	11	NM_000546.5	TP53_g.11355(	missense_variant
TP53	del	chr17	7579643	CCCCCAGCCC	CC	1125.75	het	248	NM_000546.5		intron_variant&featu
TP53	snp,snp	chr17	7579801	G	C,T	1091.97	het	43	NM_000546.5	rs1642785	intron_variant
TP53	snp,snp	chr17	7579801	G	C,T	1091.97	het	43	NM_000546.5	rs1642785	intron_variant
VHL	del	chr3	10183903	AGG	AG	656.103	het	316	NM_000551.3		intron_variant&featu