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Lieferung & Zahlungsart

siehe unsere Liefer- und Versandbedingungen

Zuschläge

- Mindermengenzuschlag
- Trockeneiszuschlag
- Gefahrgutzuschlag
- Expressversand

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Data Sheet

Product Name: CancerSeqPlus Paraffin Tissue Curls

Catalog No.: T2235152-SC **Lot No.: B906042**

Species: Human

Tissue Type: Tumor

Tissue Name: Lung

Donor Information:

Male: 66 year(s) old

Pathological Diagnosis: adenocarcinoma

Tumor Size: 5 cm

Location: Lung, Right Upper Lobe

Components:

1. **5 curls per package**

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Lot# **B906042**

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
CCND1	3.08	0.11	8.31E-03	CCND1	5.39	0.10	1.73E-03
NOTCH1	2.20	0.10	8.31E-03	NOTCH1	3.31	0.05	1.29E-03

symbol	type	chromosome	position	reference	mutation	quality score	allele type	Depth at this position	transcript_id	existing variation
ALK	snp	chr2	29445458	G	T	2400.56	hom	78	NM_004304.4	rs3795850
APC	snp	chr5	112177171	G	A	2711.26	hom	110	XM_005271975.1	rs465899
APC	snp	chr5	112178032	T	G	275.96	het	17	XM_005271975.1	
CCND1	del	chr11	69450976	GAAAAAAAA	GAAAAAAAA	265.413	het	84	NM_053056.2	
CCND1	complex	chr11	69464071	GTGACTG	CAGTCAC	658.763	het	93	NM_053056.2	
CCND1	ins	chr11	69464081	TG	TGGCGG	354.68	het	43	NM_053056.2	
CCND1	snp	chr11	69464085	A	G	390.056	het	65	NM_053056.2	
CCND1	complex	chr11	69464086	TGTTGCT	GGTAAGCG	331.541	hom	23	NM_053056.2	
CCND1	snp	chr11	69465142	T	A	1104.03	hom	58	NM_053056.2	
CDH1	snp	chr16	68867251	T	C	690.754	het	51	NM_004360.3	
CDKN2A	snp	chr9	21968199	C	G	8283.45	hom	263	NM_001195132.1	rs11515&COSM14251
DDR2	snp	chr1	162740327	T	C	17620.4	hom	563	XM_005245220.1	rs1780003
DDR2	snp	chr1	162743418	G	T	499.926	hom	17	XM_005245220.1	rs1355287
EGFR	del	chr7	55242465	GGAATTAAG	GA	1917.92	hom	74	NM_005228.3	COSM26513
ERBB2	del	chr17	37882959	TCC	TC	1445.41	het	213	NM_004448.2	
ERBB2	ins	chr17	37882965	AGA	AGGA	1212.71	het	94	NM_004448.2	
ERBB2	complex	chr17	37882972	GGGA	GCTCTT	1389.88	het	95	NM_004448.2	
ERBB3	snp	chr12	56477694	A	T	2290.1	het	108	NM_001982.3	rs2271194
ESR1	snp	chr6	152420095	G	A	3977.58	het	168	XM_005266856.1	rs2228480&CM056948
FBXW7	snp	chr4	153268038	G	T	188.59	het	14	NM_033632.3	
FGFR1	snp	chr8	38271575	T	A	318.599	hom	16	NM_001174067.1	
FGFR2	snp	chr10	123274889	C	A	237.024	hom	11	NM_022970.3	
FGFR3	del	chr4	1806012	TGGGGGGG	TGGGGGGG	1690.15	het	744	NM_001163213.1	
FGFR3	snp	chr4	1807894	G	A	2989.66	hom	100	NM_001163213.1	rs7688609
FOXL2	snp	chr3	138665110	G	A	5.63117	het	149	NM_023067.3	
IDH2	complex	chr15	90631835	TGCCTGCCA	GGCACGCC	593.427	het	483	NM_002168.2	

KRAS	snp	chr12	25362777	A	G	1191.72	het	59	NM_033360.2	rs1137282
MAP2K1	snp	chr15	66729188	G	A	4144.9	hom	169	NM_002755.3	rs139364105
MLH1	snp	chr3	37067379	G	T	367.357	hom	17	NM_000249.3	
MYCN	snp	chr2	16080157	C	G	2865.72	hom	95	NM_005378.4	rs11886063
MYCN	snp	chr2	16089615	T	C	864.787	hom	33	NM_005378.4	rs4669018
MYCNOS	snp	chr2	16080157	C	G	2865.72	hom	95	NR_026766.1	rs11886063
NOTCH1	snp	chr9	139399435	C	T	2200.18	het	194	NM_017617.3	
PDGFRA	snp	chr4	55141055	A	G	4667.02	hom	151	NM_006206.4	rs1873778&COSM22242&
PDGFRA	snp	chr4	55161254	C	T	1380.89	hom	44	NM_006206.4	rs3733540
PDGFRA	snp	chr4	55161391	T	C	473.188	hom	19	NM_006206.4	rs7685117
PDGFRA	snp	chr4	55161517	A	G	2289.5	hom	80	NM_006206.4	rs7680422
PIK3CA	del	chr3	178927848	ATTTTTTTTT	ATTTTTTTTT	204.666	het	78	NM_006218.2	
PIK3R1	snp	chr5	67588148	G	A	1110.4	het	77	NM_181523.2	rs3730089&CM080497
PTEN	snp	chr10	89717749	C	T	257.475	hom	13	NM_000314.4	COSM921131
PTEN	del	chr10	89725293	CTTTTTTTTT	CTTTTTTTT	212.446	het	35	NM_000314.4	
RB1	snp	chr13	48919358	T	G	556.206	hom	21	NM_000321.2	rs198617
RET	mnp	chr10	43610190	GG	CT	292.135	hom	11	NM_020975.4	
RET	mnp	chr10	43610199	GGG	CCC	343.343	hom	12	NM_020975.4	
RET	snp	chr10	43613843	G	T	2007.76	hom	75	NM_020975.4	rs1800861&CM014825
RET	complex	chr10	43614991	TCA	ACGA	357.394	het	21	NM_020975.4	
RET	complex	chr10	43614994	TCGT	TGAGGA	354.608	hom	19	NM_020975.4	
SMAD4	snp	chr18	48584746	C	T	552.2	het	29	NM_005359.5	
SMO	snp	chr7	128845277	G	C	4205.49	hom	142	NM_005631.4	rs2075777
SMO	snp	chr7	128846328	G	C	2305.42	hom	80	NM_005631.4	rs2228617
SMO	snp	chr7	128846457	G	A	267.679	hom	12	NM_005631.4	
STK11	complex	chr19	1206922	GTGGA	CTTGG	715.545	hom	27	XM_005259617.1	
STK11	complex	chr19	1206931	CA	CTTGCGGC	642.491	hom	25	XM_005259617.1	
STK11	snp	chr19	1207238	G	T	273.908	het	138	XM_005259617.1	rs3764640
STK11	snp	chr19	1219451	C	G	119.226	het	51	XM_005259617.1	rs369515604
STK11	mnp	chr19	1220637	TTCC	GGAA	583.665	het	173	XM_005259617.1	
STK11	complex	chr19	1220645	GCCC	GGG	559.356	het	175	XM_005259617.1	
STK11	snp	chr19	1221438	G	A	247.024	hom	11	XM_005259617.1	
STK11	mnp	chr19	1221911	TGCCC	TGTTC	4982.95	het	505	XM_005259617.1	
STK11	mnp	chr19	1221913	CC	TT	5014.62	het	454	XM_005259617.1	
TERT	snp	chr5	1295349	A	G	25796.3	hom	814	NM_198253.2	rs2853669&CR067846
TP53	snp	chr17	7576853	C	T	484.058	het	34	NM_000546.5	rs11575996&TP53_g.1406
TP53	snp	chr17	7577407	A	C	2342.78	hom	80	NM_000546.5	rs12951053
TP53	snp	chr17	7577427	G	A	1838.93	hom	64	NM_000546.5	rs12947788
TP53	del	chr17	7579643	CCCCCAGCC(	CC	420.604	het	93	NM_000546.5	
TP53	complex	chr17	7579668	CTCCAG	CAACCCTT	801.692	het	152	NM_000546.5	
TP53	complex	chr17	7579678	CCAG	TTAC	627.077	het	161	NM_000546.5	

TP53	snp	chr17	7579683	C	T	236.311	het	111	NM_000546.5	