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Diagnostik & molekulare Diagnostik



Laborgeräte & Service

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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.: T2235248-SC

Lot No.: B906138

Species: Human

Tissue Type: Tumor

Tissue Name: Stomach

Donor Information:

Male: 58 year(s) old

Pathological Diagnosis: Adenosquamous carcinoma

Tumor Size:

Location: stomach

Components:

1. 5 curls per package

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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
CCNE1	5.33	0.38	1.64E-03	CCNE1	3.72	0.05	8.78E-04
ERBB3	2.28	0.21	1.39E-02	ERBB3	3.54	0.07	3.03E-04

symbol	type	chromosome	position	reference	mutation	quality	allele type	Depth	variant frequency	transcript_id	existing variation	consequence
ALK	snp	chr2	29445458	G	T	3079.6	hom	98	1.00	NM_004304	rs3795850	synonymous_v
APC	snp	chr5	112177171	G	A	467.21	hom	18	1.00	XM_005271	rs465899	synonymous_v
ATM	del	chr11	108117897	ATTTTTTTTT	ATTTTTTTTT	180.24	het	63	0.17	NM_000051.3		intron_variant8
CCND1	snp	chr11	69465120	G	A	413.446	het	24	0.75	NM_053056.2		intron_variant
CDH1	snp	chr16	68771372	C	T	6199.84	hom	199	1.00	NM_004360	rs3743674	splice_region_v
CDKN2A	snp	chr9	21968199	C	G	27078	hom	866	1.00	NM_001195	rs11515&CC	3_prime_UTR_v
CTNNB1	del	chr3	41265953	CTTTTTTTTT	CTTTTTTTTA	140.395	het	96	0.15	XM_005264887.1		intron_variant8
DDR2	snp	chr1	162740327	TGTC	CGTC	6605.39	hom	231	0.94	XM_005245220.1		intron_variant
DDR2	complex	chr1	162740327	TGTC	CGTT	320.881	hom	13	0.92	XM_005245220.1		intron_variant
DDR2	snp	chr1	162743418	G	T	1349.86	hom	52	0.98	XM_005245	rs1355287	intron_variant
EGFR	ins	chr7	55242248	CG	CTG	248.842	hom	11	1.00	NM_005228.3		intron_variant8
EGFR	ins	chr7	55242254	CG	CTG	260.66	hom	11	1.00	NM_005228.3		intron_variant8
EGFR	complex	chr7	55242257	CACAG	GACG	268.588	hom	12	1.00	NM_005228.3		intron_variant8
EZH2	snp	chr7	148508833	A	G	555.831	het	29	0.69	XM_005249	rs2072407	intron_variant
FBXW7	del	chr4	153247486	CTTTTTTTTT	CTTTTTTTTT	300.805	het	50	0.26	NM_033632.3		intron_variant8
FBXW7	snp	chr4	153252061	A	G	1363.44	het	64	0.75	NM_033632	rs10033601	intron_variant
FBXW7	snp	chr4	153267968	A	G	423.054	hom	15	1.00	NM_033632	rs2714803	intron_variant
FBXW7	del,del	chr4	153268227	CAAAAAAAAA	CAAAAAAAAA	1314.02	het	140	0.35	NM_033632.3		splice_region_v
FBXW7	snp	chr4	153271120	A	G	330.318	het	24	0.54	NM_033632.3		intron_variant
FGFR3	del	chr4	1806012	TGGGGGGG	TGGGGGGG	580.701	het	185	0.18	NM_001163213.1		intron_variant8
FGFR3	snp	chr4	1807894	G	A	4040.82	hom	136	1.00	NM_001163	rs7688609	synonymous_v
FLT3	snp	chr13	28610183	A	G	3553.29	hom	119	1.00	NM_004119	rs2491231	splice_region_v
FOXL2	complex	chr3	138664790	TGTACGGCC	CGTAGTGAA	386.353	het	184	0.20	NM_023067.3		frameshift_vari
FOXL2	complex	chr3	138664804	GAGGCGGC	AATGGCCTG	474.463	het	180	0.20	NM_023067.3		frameshift_vari
IDH1	snp	chr2	209116134	C	T	5753.86	het	349	0.52	XM_005246	rs111233394	intron_variant
IDH1	del	chr2	209116299	GAAAAAAAA	GAAAAAAAA	514.822	het	100	0.24	XM_005246521.1		intron_variant8
JAK2	del	chr9	5073681	CTTTTTTTTT	CTTTTTTTTT	296.969	het	37	0.32	NM_004972.3		splice_region_v

JAK3	del	chr19	17947924	TGGGGGGC	TGGGGGGC	807.518	het	323	0.19	XM_005259896.1	splice_region_v	
KDR	snp	chr4	55961159	T	C	1567.03	hom	55	1.00	NM_002253	rs2219471	intron_variant
KDR	ins	chr4	55962545	TGG	TGGG	105.859	het	59	0.19	NM_002253.2		intron_variant8
KDR	snp	chr4	55972974	T	A	406.935	hom	14	1.00	NM_002253	rs1870377&	missense_varia
KDR	snp	chr4	55980456	C	T	2792.1	het	158	0.58	NM_002253	rs2305949	intron_variant
MYCN	snp	chr2	16080157	C	G	474.886	hom	16	1.00	NM_005378	rs11886063	upstream_gene
MYCN	snp	chr2	16089615	T	C	1516.46	hom	55	0.96	NM_005378	rs4669018	downstream_gu
NOTCH1	mnp	chr9	139391461	TG	CA	454.084	het	178	0.17	NM_017617.3		missense_varia
NOTCH1	mnp	chr9	139391467	GG	CC	504.146	het	181	0.18	NM_017617.3		missense_varia
NOTCH1	mnp	chr9	139391473	TG	CA	540.898	het	177	0.18	NM_017617.3		missense_varia
NOTCH1	snp	chr9	139391636	G	A	1748.92	hom	72	1.00	NM_017617	rs2229974	synonymous_va
NOTCH1	snp	chr9	139397707	G	A	2290.04	hom	79	1.00	NM_017617	rs10521&CC	synonymous_va
NPM1	del	chr5	170837513	CTTTTTTTT	CTTTTTTTT	290.64	het	45	0.29	NM_002520.6		splice_region_v
PDGFRA	snp	chr4	55141055	A	G	3829.93	hom	129	1.00	NM_006206	rs1873778&	synonymous_va
PDGFRA	snp	chr4	55152040	C	T	5097.76	het	227	0.87	NM_006206	rs2228230&	synonymous_va
PDGFRA	snp	chr4	55161254	C	T	945.942	het	60	0.55	NM_006206	rs3733540	intron_variant
PDGFRA	snp	chr4	55161391	T	C	302.979	hom	11	1.00	NM_006206	rs7685117	synonymous_va
PDGFRA	snp	chr4	55161517	A	G	1702.42	hom	57	0.98	NM_006206	rs7680422	3_prime_UTR_v
PIK3CA	del	chr3	178916904	CTTTTTA	CTTTTTA	326.985	het	39	0.36	NM_006218.2		frameshift_vari
PIK3R1	snp	chr5	67593337	G	A	496.249	het	41	0.46	NM_181523.2		missense_varia
PTEN	del	chr10	89720633	CTTTTTTTT	CTTTTTTTT	136.555	het	49	0.20	NM_000314.4		splice_acceptor
PTEN	snp	chr10	89720907	T	G	589.496	hom	21	1.00	NM_000314	rs555895&C	intron_variant
PTEN	del	chr10	89725293	CTTTTTTTT	CTTTTTTTT	189.993	het	64	0.19	NM_000314.4		3_prime_UTR_v
RB1	snp	chr13	48919358	T	G	988.937	hom	33	1.00	NM_000321	rs198617	intron_variant
RB1	ins	chr13	49034022	ATT	ATTT	271.289	het	20	0.65	NM_000321.2		intron_variant8
RET	snp	chr10	43610189	G	T	262.569	hom	10	1.00	NM_020975.4		splice_region_v
RET	mnp	chr10	43610190	GG	CT	262.569	hom	10	1.00	NM_020975.4		splice_region_v
RET	mnp	chr10	43610199	GGG	CCC	278.039	hom	10	1.00	NM_020975.4		intron_variant
RET	snp	chr10	43613843	G	T	1069.84	hom	36	0.97	NM_020975	rs1800861&	synonymous_va
SMO	snp	chr7	128845277	G	C	2689.81	het	127	0.74	NM_005631	rs2075777	intron_variant
STK11	snp	chr19	1207238	G	T	5024.53	hom	163	1.00	XM_005259	rs3764640	intron_variant
STK11	snp	chr19	1218523	G	T	3260.4	het	225	0.50	XM_005259	rs2075604	intron_variant
STK11	complex	chr19	1218605	TGGCACAC	GGGAAGAG	244.376	het	20	0.60	XM_005259	617.1	intron_variant
STK11	snp	chr19	1220321	T	C	2889.16	hom	92	1.00	XM_005259	rs2075606	intron_variant
TP53	snp	chr17	7577407	A	C	775.091	het	52	0.52	NM_000546	rs12951053	intron_variant
TP53	snp	chr17	7579472	G	C	1062.95	het	54	0.69	NM_000546	rs1042522&	missense_varia
TP53	del	chr17	7579643	CCCCCAGCC	CC	436.329	het	75	0.29	NM_000546.5		intron_variant8
TP53	snp	chr17	7579801	G	C	459.523	het	27	0.78	NM_000546	rs1642785	intron_variant
TP53	del	chr17	7579863	TCC	TC	18295.8	het	1481	0.40	NM_000546.5		frameshift_vari