Suppl. 6: Real-time PCR quantification of mtDNA copy numbers per ng total DNA in 16 (I - XVI) segmented central adenocarcinoma sections.

A: Shown are the numbers of tumor containing segments and total segments, the minimum (min), first quantile (1st Q), median, third quantile (3rd Q) and maximum values as well as the histological growth pattern (predominant is underlined) for the respective tumor.

#	Number of segments (tumor/total)	Min	1st Q	Median	3rd Q	Max	Growth pattern
I	19/19	127,900	245,500	289,500	329,000	524,100	<u>papillary</u>
II	15/15	11,090	17,190	20,580	34,300	46,380	<u>acinar</u>, micropapillary
III	11/12	6,321	23,510	26,860	35,210	68,630	<u>acinar</u>, micropapillary, lepidic
IV	9/15	83	390	1,020	1,634	8,756	<u>acinar</u>, micropapillary
V	7/11	68,590	82,740	115,400	127,600	171,500	<u>papillary</u>, acinar, micropapillary
VI	13/13	21,740	75,150	83,780	154,500	804,600	<u>acinar</u>, solid, micropapillary
VII	28/33	28,470	44,010	60,690	75,420	105,000	<u>solid</u>, acinar
VIII	21/34	38,420	56,160	65,980	79,410	161,200	<u>lepidic</u>, acinar
IX	5/15	30,660	51,980	79,380	126,900	229,700	<u>lepidic</u>, acinar
X	33/41	15,040	57,750	66,890	102,800	328,000	<u>solid</u>
XI	26/41	29,850	189,000	265,400	302,900	963,800	<u>solid</u>, acinar
XII	36/48	84,450	165,100	204,200	252,100	597,300	<u>papillary</u>, acinar
XIII	15/16	71,000	105,500	125,800	156,100	217,200	<u>micropapillary</u>, solid, papillary, lepidic
XIV	12/13	19,020	56,970	71,250	85,760	137,000	<u>solid</u>, acinar
XV	22/25	55,460	113,500	125,900	158,200	231,100	<u>acinar</u>, papillary, lepidic
XVI	16/20	53,600	84,620	95,680	136,600	212,600	<u>acinar</u>, solid
total	288/371	83	57,700	97,200	183,500	963,800	

B: mtDNA copy numbers per nanogram total DNA in the segments of central sections of 16 ADC

Segment	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV	XVI
A1	409423	20583	36614	704	115368	n/a	138449	38440	80538	232475	n/a	n/a	73792	n/a	119029	108129
A2	349801	42867	25272	117	171533	154523	103398	57078	79375	136406	273594	146037	188759	74286	157573	88482
A3	315678	34554	24644	390	121654	804566	33959	73874	92719	102780	247667	257098	106555	71253	131934	139067
A4	234672	34055	39449	n/a	51141	94346	66247	68842	61920	45214	290827	131660	149676	52242	155026	140712
A5	n/a	19767	n/a	n/a	n/a	n/a	91120	79410	108799	58466	286052	312403	n/a	n/a	118975	107325
A6	n/a	n/a	n/a	n/a	n/a	n/a	72843	69765	n/a	92555	368332	176638	n/a	n/a	109825	n/a
A7	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	257010	303126	145251	n/a	n/a	106256	n/a
A8	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	423918	n/a	n/a	n/a	n/a	n/a
A9	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	177952	n/a	n/a	n/a	n/a	n/a
B1	393307	14231	68634	8756	68594	62103	74947	60388	81189	162278	n/a	174101	94372	19018	158475	53597
B2	524065	32125	22373	1504	74034	81730	45129	88378	126915	90179	209400	249046	217243	91621	231143	193920
B3	292966	28055	26865	113	55980	195040	93137	53034	30656	47474	167871	205936	196524	54594	116630	73052
B4	232136	14241	10494	n/a	84357	107809	32119	54020	51985	62090	229233	597328	132577	51786	177308	92067
B5	226011	43650	n/a	n/a	n/a	43513	71474	65751	133644	55731	272097	363522	n/a	79890	165177	69221
B6	n/a	n/a	n/a	n/a	n/a	n/a	104979	69797	n/a	67073	160090	271698	n/a	n/a	99420	n/a
B7	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	66889	963844	180795	n/a	n/a	n/a	n/a
B8	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	29854	n/a	n/a	n/a	n/a	n/a
B9	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	686606	n/a	n/a	n/a	n/a	n/a
C1	127884	17180	32579	5089	133513	75148	81732	63427	74272	233180	n/a	180802	71001	56104	124594	n/a
C2	214308	46383	35823	1634	91439	75688	57294	57575	229658	69423	356478	128121	162604	117226	194280	99076
C3	310712	20359	6321	2492	100240	83779	36222	65976	79384	93461	152037	168840	127693	57841	112475	72708
C4	289544	11093	34588	n/a	n/a	212301	44936	69809	106084	46073	388694	346290	105586	67895	151620	104534
C5	256374	17205	n/a	n/a	n/a	21744	68453	94684	87239	66498	258694	227986	n/a	136967	117914	143538
C6	n/a	n/a	n/a	n/a	n/a	n/a	58327	126348	n/a	58254	245365	236995	n/a	n/a	61843	n/a
C7	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	75169	289113	242090	n/a	n/a	n/a	n/a
C8	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	181717	n/a	n/a	n/a	n/a	n/a
C9	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
D1	260793	n/a	n/a	1020	n/a	n/a	52971	38417	n/a	111972	n/a	261093	125762	n/a	n/a	n/a
D2	264151	n/a	n/a	83	n/a	n/a	69492	51929	n/a	37988	418466	145722	121197	n/a	169949	90132
D3	308603	n/a	n/a	3458	n/a	n/a	28467	161227	n/a	58795	149897	291446	105494	n/a	127222	212625
D4	342381	n/a	n/a	n/a	n/a	n/a	76822	39658	n/a	32993	97644	122851	112786	n/a	82253	135813
D5	271795	n/a	n/a	n/a	n/a	n/a	51869	96761	n/a	31700	210988	369598	n/a	n/a	60685	n/a
D6	n/a	n/a	n/a	n/a	n/a	n/a	38798	74327	n/a	15043	282143	416908	n/a	n/a	n/a	n/a
D7	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	58090	246429	372195	n/a	n/a	n/a	n/a
D8	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	177967	n/a	n/a	n/a	n/a	n/a
D9	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
E1	n/a	n/a	n/a	2647	n/a	n/a	n/a	30022	n/a	189026	n/a	170452	n/a	n/a	n/a	n/a
E2	n/a	n/a	n/a	336	n/a	n/a	52976	58207	n/a	62795	270972	171751	n/a	n/a	n/a	139578
E3	n/a	n/a	n/a	2732	n/a	n/a	84773	56163	n/a	69727	166299	84454	n/a	n/a	130823	92289
E4	n/a	n/a	n/a	n/a	n/a	n/a	37625	85462	n/a	145786	304341	198203	n/a	n/a	55462	143251
E5	n/a	n/a	n/a	n/a	n/a	n/a	58033	63814	n/a	57748	367565	240376	n/a	n/a	n/a	n/a
E6	n/a	n/a	n/a	n/a	n/a	n/a	63045	n/a	n/a	328035	309704	153687	n/a	n/a	n/a	n/a
E7	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	317491	222092	169371	n/a	n/a	n/a	n/a
E8	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
E9	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
F1	n/a	n/a	n/a	n/a	n/a	n/a	n/a	39234	n/a	n/a	n/a	202405	n/a	n/a	n/a	n/a
F2	n/a	n/a	n/a	n/a	n/a	n/a	n/a	36199	n/a	292936	n/a	238531	n/a	n/a	n/a	n/a
F3	n/a	n/a	n/a	n/a	n/a	n/a	53921	49752	n/a	215742	315124	89745	n/a	n/a	n/a	n/a
F4	n/a	n/a	n/a	n/a	n/a	n/a	52267	65060	n/a	210942	281655	277083	n/a	n/a	n/a	n/a
F5	n/a	n/a	n/a	n/a	n/a	n/a	52525	53860	n/a	249772	302264	226747	n/a	n/a	n/a	n/a
F6	n/a	n/a	n/a	n/a	n/a	n/a	41225	n/a	n/a	562387	254145	104548	n/a	n/a	n/a	n/a
F7	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	330341	192144	166678	n/a	n/a	n/a	n/a
F8	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
F9	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
G1	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	105865	n/a	n/a	n/a	n/a
G2	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	147180	n/a	n/a	n/a	n/a
G3	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	207024	n/a	n/a	n/a	n/a
G4	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	138074	n/a	n/a	n/a	n/a
G5	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	109845	n/a	n/a	n/a	n/a
G6	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	65139	n/a	n/a	n/a	n/a
G7	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	109445	n/a	n/a	n/a	n/a
G8	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
G9	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a