Supporting Information

Cancer cells preferentially lose small chromosomes

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Supplementary Table 1

Comparison of chromosome properties and individual gain and loss rates in a total of 19,003 human solid tumors

Chromosome	**Chromosome size (bp)**	**Genes on chromosome (#)**	**Lost in tumors (# cases)**	**Rate lost in solid aneuploid tumors (%)**	**Rate lost in all solid tumors (%)**	**Gained in tumors (# cases)**	**Rate gained in solid aneuploid tumors (%)**	**Rate gained in all solid tumors (%)**	**Median rate in solid aneuploid tumors (%)**	**Median rate in all solid tumors (%)**
1	249,250,621	3141	1004	7.78	5.28	386	2.99	2.03	**-2.39**	**-1.63**
2	243,199,373	1346	853	6.61	4.49	901	6.98	4.74	**0.19**	**0.13**
3	198,022,430	1463	1152	8.93	6.06	827	6.41	4.35	**-1.26**	**-0.86**
4	191,154,276	796	1460	11.31	7.68	355	2.75	1.87	**-4.28**	**-2.91**
5	180,915,260	923	1038	8.04	5.46	1015	7.87	5.34	**-0.09**	**-0.06**
6	171,115,067	1557	1263	9.79	6.65	520	4.03	2.74	**-2.88**	**-1.95**
7	159,138,663	1150	636	4.93	3.35	2719	21.07	14.31	**8.07**	**5.48**
8	146,364,022	793	1364	10.57	7.18	1439	11.15	7.57	**0.29**	**0.20**
9	141,213,431	1149	1618	12.54	8.51	636	4.93	3.35	**-3.81**	**-2.58**
10	135,534,747	927	1829	14.17	9.62	474	3.67	2.49	**-5.25**	**-3.57**
11	135,006,516	1524	1230	9.53	6.47	569	4.41	2.99	**-2.56**	**-1.74**
12	133,851,895	1342	884	6.85	4.65	1623	12.58	8.54	**2.86**	**1.94**
13	115,169,878	633	1964	15.22	10.34	650	5.04	3.42	**-5.09**	**-3.46**
14	107,349,540	1050	1997	15.48	10.51	389	3.01	2.05	**-6.23**	**-4.23**
15	102,531,392	695	1715	13.29	9.02	454	3.52	2.39	**-4.89**	**-3.32**
16	90,354,753	880	1407	10.90	7.40	698	5.41	3.67	**-2.75**	**-1.87**
17	81,195,210	1266	1572	12.18	8.27	730	5.66	3.84	**-3.26**	**-2.22**
18	78,077,248	337	1738	13.47	9.15	836	6.48	4.40	**-3.50**	**-2.37**
19	59,128,983	1461	1300	10.07	6.84	684	5.30	3.60	**-2.39**	**-1.62**
20	63,025,520	727	953	7.39	5.01	1475	11.43	7.76	**2.02**	**1.37**
21	48,129,895	225	1496	11.59	7.87	929	7.20	4.89	**-2.20**	**-1.49**
22	51,304,566	545	2600	20.15	13.68	527	4.08	2.77	**-8.03**	**-5.45**
X	155,270,560	1098	2473	19.16	13.01	999	7.74	5.26	**-5.71**	**-3.88**
Y	59,373,566	78	2475	19.18	13.02	433	3.36	2.28	**-7.91**	**-5.37**
Overall/any	**3,095,677,412**	**25,106**	**9851**	**76.34**	**51.84**	**7562**	**58.60**	**39.79**		

Supplementary Table 2

Comparison of whole-chromosome aneuploidy rates in different human tumor types

Tumor type	**Total (# cases)**	**Chromosome loss/gain (# cases)**	**Chromosome loss/gain (%)**
All solid tumors	**19003**	**12904**	**67.91**
All carcinomas	**6005**	**4168**	**69.41**
Adenocarcinoma	3793	2679	70.63
Basal cell carcinoma	102	74	72.55
Melanoma	359	273	76.04
Squamous cell carcinoma	696	502	72.13
Transitional cell carcinoma	204	143	70.10
All lymphomas	**4317**	**2958**	**68.52**
B-cell lymphoma	1788	1242	69.46
Follicular lymphoma	1426	1011	70.90
Mantle cell lymphoma	585	323	55.21
T-cell lymphoma	168	127	75.60
All sarcomas	**2254**	**1408**	**62.47**
Ewing sarcoma	433	259	59.82
Fibrosarcoma	64	40	62.50
Leiomyosarcoma	120	78	65.00
Rhabdomyosarcoma	188	117	62.23
Synovial sarcoma	203	151	74.38
Astrocytoma	621	540	86.96
Glioblastoma	106	97	91.51
Glioma	97	84	86.60

Supplementary Table 3

Comparison of whole-chromosome aneuploidy rates in human solid tumors for different organs/tumor sites

Tumor site	Unit	Total	No whole-chromosome loss or gain	Whole-chromosome loss or gain	Whole-chromosome loss	Whole-chromosome gain	Whole-chromosome loss and gain
Bladder	#	196	60	136	122	68	54
	%	100.0	30.6	**69.4**	62.2	34.7	27.6
Brain	#	1842	305	1537	1434	567	433
	%	100.0	16.6	**83.4**	77.9	30.8	23.5
Breast	#	1120	428	692	541	407	208
	%	100.0	38.2	**61.8**	48.3	36.3	18.6
Cervix	#	84	52	32	30	26	24
	%	100.0	61.9	**38.1**	35.7	31.0	28.6
Colon	#	550	137	413	282	343	198
	%	100.0	24.9	**75.1**	51.3	62.4	36.0
Esophagus	#	59	16	43	35	24	16
	%	100.0	27.1	**72.9**	59.3	40.7	27.1
Kidney	#	1862	364	1498	1149	983	614
	%	100.0	19.5	**80.5**	61.7	52.8	33.0
Liver	#	168	43	125	59	104	37
	%	100.0	25.6	**74.4**	35.1	61.9	22.0
Lung	#	689	293	396	355	228	181
	%	100.0	42.5	**57.5**	51.5	33.1	26.3
Ovary	#	655	265	390	271	265	140
	%	100.0	40.5	**59.5**	41.4	40.5	21.4
Pancreas	#	152	42	110	102	65	51
	%	100.0	27.6	**72.4**	67.1	42.8	33.6
Prostate	#	230	87	143	115	55	19
	%	100.0	37.8	**62.2**	50.0	23.9	8.3
Salivary gland	#	489	311	178	132	83	27
	%	100.0	63.6	**36.4**	27.0	17.0	5.5
Skeleton	#	1068	388	680	490	415	214
	%	100.0	36.3	**63.7**	45.9	38.9	20.0
Skin	#	330	118	212	168	139	86
	%	100.0	35.8	**64.2**	50.9	42.1	26.1
Spleen	#	239	115	124	82	78	35
	%	100.0	48.1	**51.9**	34.3	32.6	14.6
Stomach	#	223	60	163	138	108	82
	%	100.0	26.9	**73.1**	61.9	48.4	36.8
Testis	#	358	77	281	268	243	229
	%	100.0	21.5	**78.5**	74.9	67.9	64.0
Uterus	#	779	467	312	238	138	62
	%	100.0	59.9	**40.1**	30.6	17.7	8.0
Vagina	#	72	19	53	39	37	18
	%	100.0	26.4	**73.6**	54.2	51.4	25.0

The shaded boxes indicate the bias towards chromosome loss or gain. Overall whole-chromosome aneuploidy fractions are highlighted in bold.

Supplementary Table 4

Comparison of gain and loss rates of individual chromosomes in 570 human ovarian cystadenocarcinomas

Chromosome	**Lost in tumors (# cases)**	**Rate lost in tumors (%)**	**Gained in tumors (# cases)**	**Rate gained in tumors (%)**	**Median rate in tumors (%)**
1	1	0.18	18	3.16	**1.49**
2	2	0.35	29	5.09	**2.37**
3	1	0.18	25	4.39	**2.11**
4	127	22.28	0	0.00	**-11.14**
5	13	2.28	7	1.23	**-0.53**
6	31	5.44	15	2.63	**-1.40**
7	9	1.58	40	7.02	**2.72**
8	6	1.05	15	2.63	**0.79**
9	92	16.14	5	0.88	**-7.63**
10	8	1.40	15	2.63	**0.61**
11	19	3.33	5	0.88	**-1.23**
12	6	1.05	39	6.84	**2.89**
13	160	28.07	22	3.86	**-12.11**
14	81	14.21	8	1.40	**-6.40**
15	115	20.18	4	0.70	**-9.74**
16	91	15.96	6	1.05	**-7.46**
17	97	17.02	0	0.00	**-8.51**
18	45	7.89	5	0.88	**-3.51**
19	29	5.09	0	0.00	**-2.54**
20	0	0.00	100	17.54	**8.77**
21	46	8.07	0	0.00	**-4.04**
22	246	43.16	4	0.70	**-21.23**
Overall/any chromosome	**441**	**77.37**	**170**	**29.82**	

For this analysis we used TCGA aCGH data from which information from the X and Y chromosomes was not available.

Supplementary Table 5

Comparison of gain and loss rates of individual chromosomes in 520 colorectal adenocarcinomas

Chromosome	Lost in tumors (# cases)	Rate lost in tumors (%)	Gained in tumors (# cases)	Rate gained in tumors (%)	Median rate in tumors (%)
1	7	1.35	2	0.38	**-0.48**
2	7	1.35	22	4.23	**1.44**
3	12	2.31	9	1.73	**-0.29**
4	70	13.46	1	0.19	**-6.63**
5	15	2.88	4	0.77	**-1.06**
6	12	2.31	24	4.62	**1.15**
7	1	0.19	165	31.73	**15.77**
8	5	0.96	51	9.81	**4.42**
9	26	5.00	30	5.77	**0.38**
10	24	4.62	1	0.19	**-2.21**
11	18	3.46	9	1.73	**-0.87**
12	8	1.54	47	9.04	**3.75**
13	4	0.77	263	50.58	**24.90**
14	127	24.42	6	1.15	**-11.63**
15	114	21.92	2	0.38	**-10.77**
16	6	1.15	39	7.50	**3.17**
17	24	4.62	1	0.19	**-2.21**
18	195	37.50	1	0.19	**-18.65**
19	4	0.77	14	2.69	**0.96**
20	0	0.00	160	30.77	**15.38**
21	23	4.42	0	0.00	**-2.21**
22	106	20.38	3	0.58	**-9.90**
Overall/any chromosome	**318**	**61.15**	**389**	**74.81**	

For this analysis we used TCGA aCGH data from which information from the X and Y chromosomes was not available.

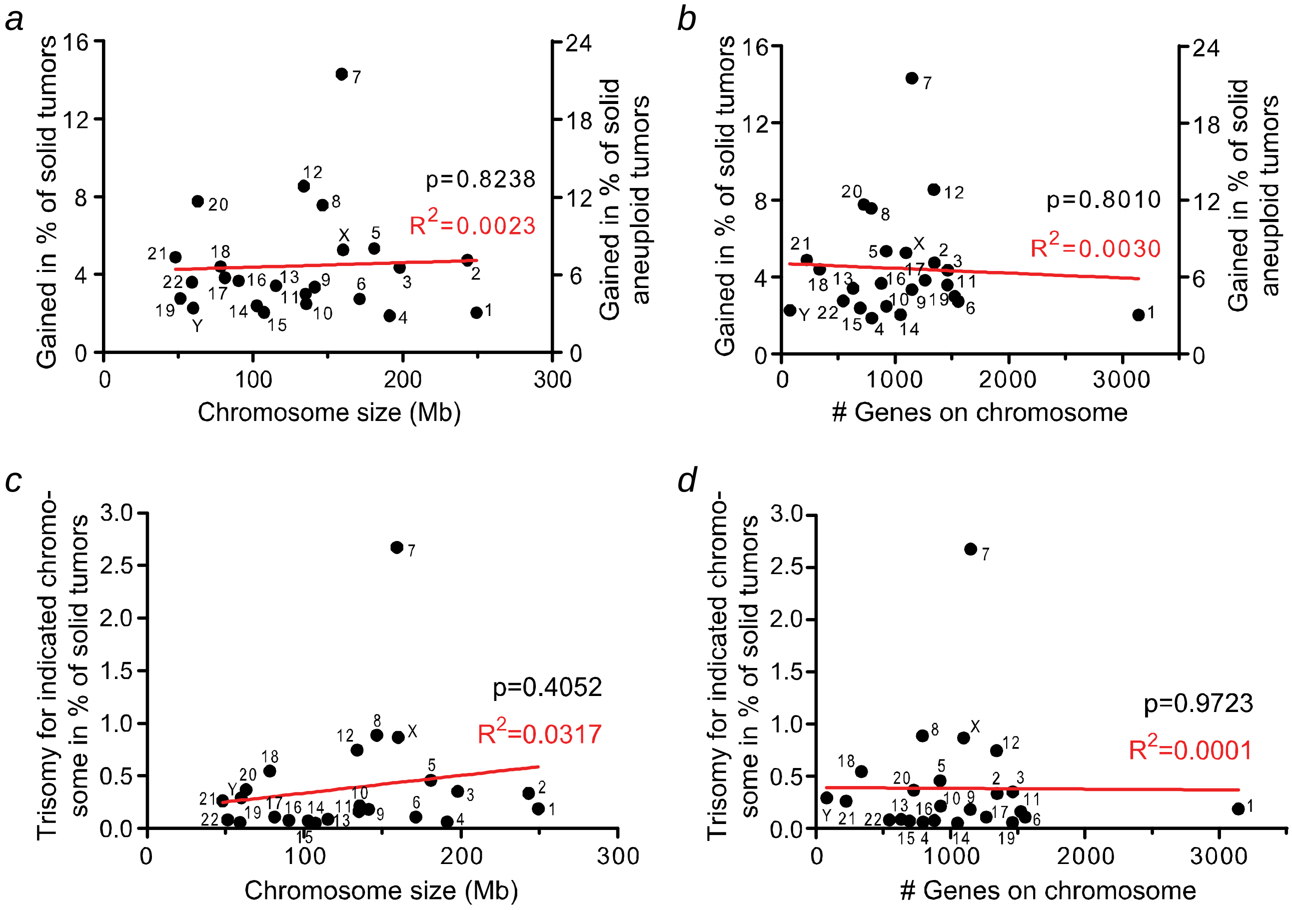
Supplementary Table 6

Comparison of gain and loss rates of individual chromosomes in 23,165 human non-solid tumors

Chromosome	**Lost in tumors (# cases)**	**Rate lost in tumors (%)**	**Gained in tumors (# cases)**	**Rate gained in tumors (%)**	**Median rate in tumors (%)**
1	532	2.30	190	0.82	**-0.74**
2	454	1.96	229	0.99	**-0.49**
3	594	2.56	559	2.41	**-0.08**
4	484	2.09	940	4.06	**0.98**
5	675	2.91	789	3.41	**0.25**
6	380	1.64	1138	4.91	**1.64**
7	1817	7.84	566	2.44	**-2.70**
8	702	3.03	2210	9.54	**3.25**
9	804	3.47	809	3.49	**0.01**
10	501	2.16	893	3.85	**0.85**
11	541	2.34	703	3.03	**0.35**
12	777	3.35	907	3.92	**0.28**
13	1295	5.59	387	1.67	**-1.96**
14	736	3.18	950	4.10	**0.46**
15	729	3.15	707	3.05	**-0.05**
16	917	3.96	205	0.88	**-1.54**
17	1071	4.62	737	3.18	**-0.72**
18	690	2.98	1121	4.84	**0.93**
19	531	2.29	937	4.04	**0.88**
20	965	4.17	367	1.58	**-1.29**
21	694	3.00	2703	11.67	**4.34**
22	749	3.23	608	2.62	**-0.30**
X	1731	7.47	1390	6.00	**-0.74**
Y	1289	5.56	377	1.63	**-1.97**
Overall/any chromosome	**8461**	**36.52**	**7834**	**33.82**	

Supplementary Figure 1

In human solid tumors, a correlation between the incidence and size or gene number of the chromosome exists neither in general nor in trisomic tumors



(a) Scatter plot of chromosome size in megabases (Mb) in relationship to the rate at which the chromosome is gained in human solid tumors.

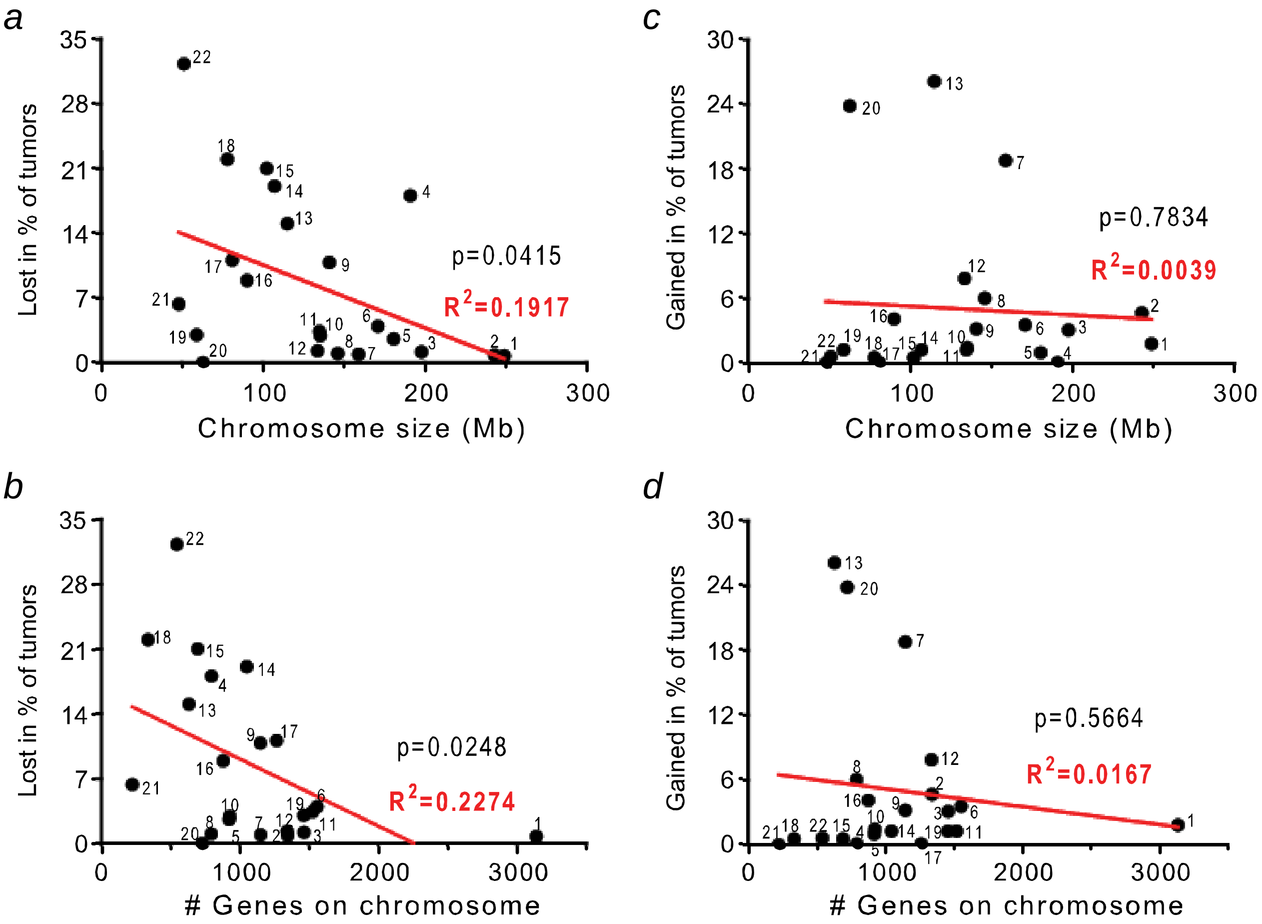
(b) Scatter plot of the number of genes on the chromosome in relationship to the rate at which the chromosome is gained in human solid tumors.

(c) Scatter plot comparing the rate at which the extra chromosome in trisomic tumors is gained to the size of the extra chromosome. Only “2n+1” tumors are included in this analysis. The indicated rates represent the fraction of all 19,003 solid tumors.

(d) Analysis as in (a) but compared to the number of genes on the extra chromosome.

Supplementary Figure 2

Ovarian serous cystadenocarcinomas and colorectal adenocarcinomas preferentially lose, but not gain, small chromosomes



(a) Scatter plot of chromosome size in megabases (Mb) in relationship to the rate at which the chromosome is lost.

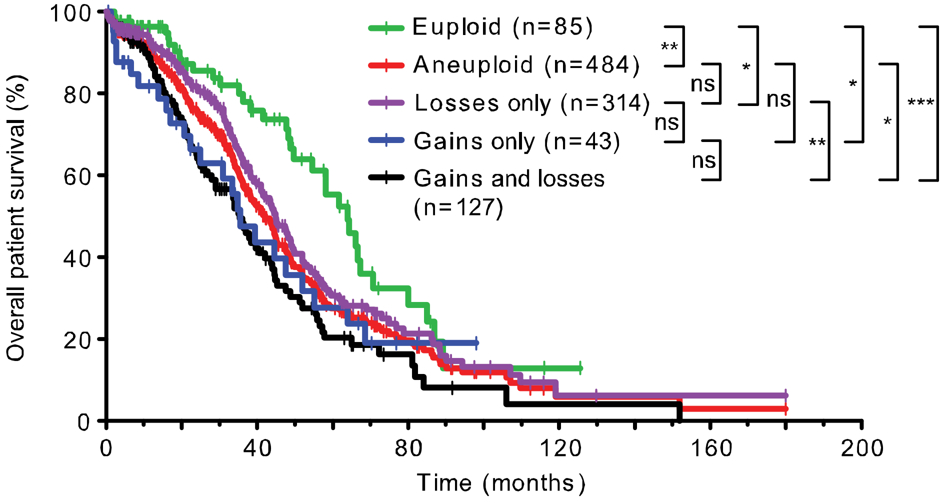
(b) Scatter plot as in (a), but for the rate at which each chromosome is gained.

(c) Scatter plot of the number of genes on the chromosome in relationship to the rate at which the chromosome is lost.

(d) Scatter plot as in (c), but for the rate at which each chromosome is gained.

Supplementary Figure 3

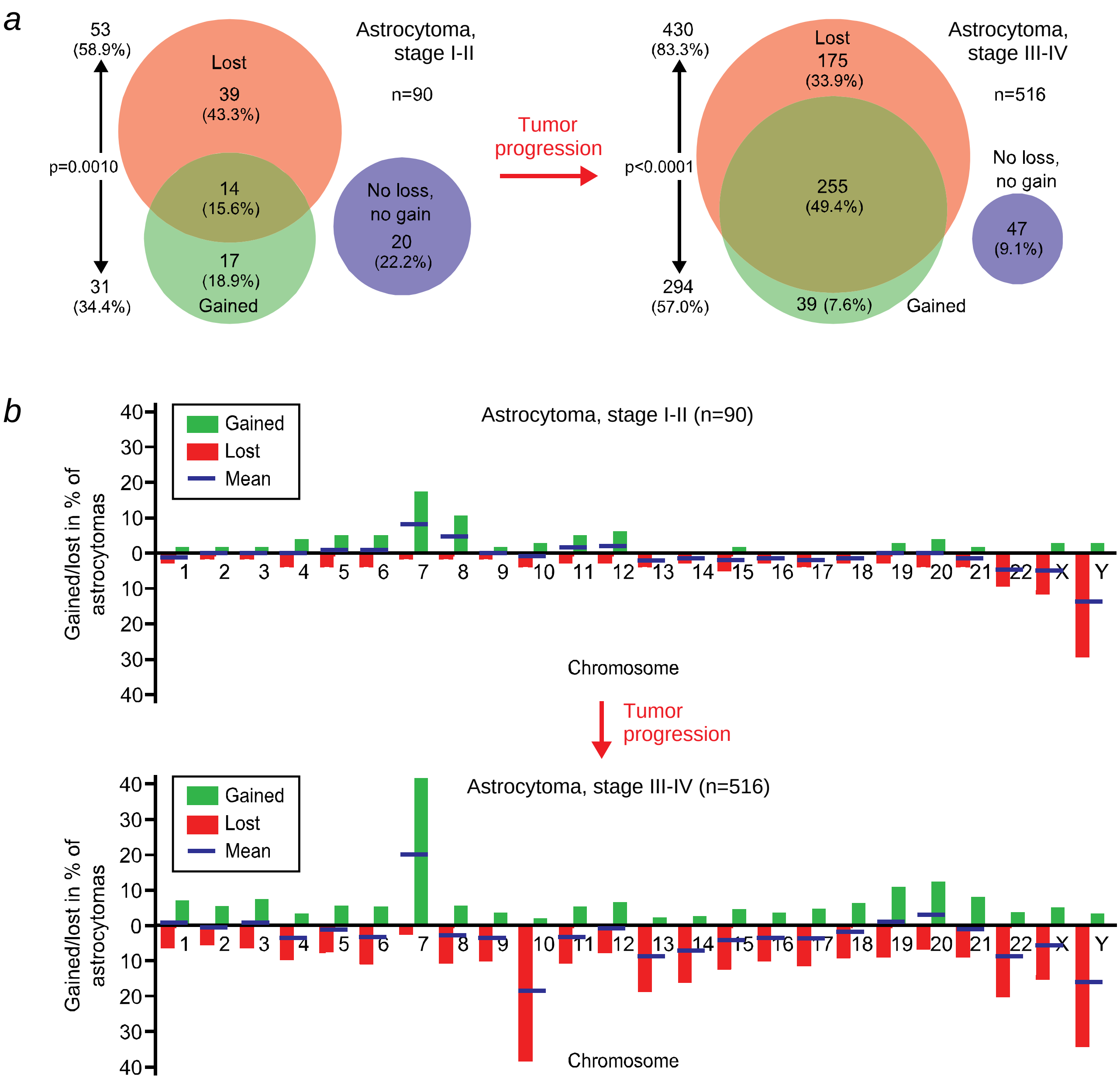
Whole-chromosome aneuploidy state of a tumor correlates with the survival of ovarian serous cystadenocarcinoma patients



The overall patient survival of subgroups of 569 ovarian serous cystadenocarcinoma patients is plotted. All p values were calculated using the log-rank (Mantel-Cox) test. See also main text. Censored patients are indicated by vertical bars on the curves. The terms “euploid” and “aneuploid” exclusively refer to numerical chromosome abnormalities in this Figure.

Supplementary Figure 4

A comparison between early- and late-stage whole-chromosome aneuploidies in human astrocytoma provides insights into tumor evolution.



(a) Area-proportional Venn diagrams as in Figure 1a, comparing whole-chromosome gain, loss and aneuploidy rates from early- and late-stage astrocytomas (n=90 and n=516, respectively).
(b) Rates at which early- and late-stage astrocytomas have gained or lost individual whole-chromosomes.