Supporting Information

Valind et al. 10.1073/pnas.1311163110

Table S1. Estimation of AI in fibroblast lines (F1 and F2) by single- versus dual-color FISH

Cell-chr-probe*	AI† single color	AI† dual color	Single/dual
F1-chr2-R	5.23×10^{-3}	9.60E-04	5
F1-chr2-G	5.56×10^{-3}		6
F1-chr17-R	1.26×10^{-2}	1.60E-03	8
F1-chr17-B	2.37×10^{-2}		15
F2-chr2-R	7.71×10^{-3}	1.50E-03	5
F2-chr2-G	1.57×10^{-2}		10
F2-chr17-R	1.10×10^{-2}	1.80E-03	6
F2-chr17-B	2.04×10^{-2}		11
Mean	12.7×10^{-3}	1.47E-03	9

Further details of the analytic methods and detailed data are found in Valind et al. (1). Chr, chromosome.
*R, red (spectrum orange); G, green (spectrum green); B, blue (spectrum aqua).
†AI, aneusomy index per pair of homologous chromosomes.

1. Valind A, Jin Y, Gisselsson D (2013) Elevated tolerance to aneuploidy in cancer cells: estimating the fitness effects of chromosome number alterations by in silico modelling of somatic genome evolution. *PLoS ONE* 8(7):e70445.

Table S2. Estimation of AI in normal cells by chromosome banding

Cell type*	Number of cells analyzed	Number of aneuploid cells	Percentage aneuploid cells, %	AI†
Lymphocytes	17,545	244	1.66	7.24E-04
Amniotic fluid cells	17,262	220	1.46	6.35E-04
Fibroblasts	240	4	1.67	7.25E-04
Mean			1.60	0.69E-03

*Data for lymphocytes and amniotic fluid cells were obtained from Peterson and Mitelman (1); fibroblast data were obtained from 14 karyotypically normal skin biopsy samples.
†AI, aneusomy index per pair of homologous chromosomes.

1. Petersson H, Mitelman F (1985) Nonrandom de novo chromosome aberrations in human lymphocytes and amniotic cells. *Hereditas* 102(1):33–38.

Table S3. Bonferroni corrected *P* values for Fisher's exact test

Sample	Chromosome	Bonferroni-corrected *P* value
D1	2	1
D1	17	1
D2	2	1
D2	17	1
D3	2	1
D3	17	9.758593e-01
E1	2	1
E1	17	2.842892e-01
P1	2	1
P1	17	1
W1	2	1
W1	17	1
DT1	2	4.609277e-01
DT1	17	1
T1	2	1.218186e-03
T1	17	1.639000e-05
T2	2	1.830400e-09
T2	17	6.270000e-14
DLD1	2	8.196892e-03
DLD1	17	2.773782e-04
SW480	2	4.356000e-17
SW480	16	1.273800e-06

P values are from Fisher's exact test comparing each sample against pooled data from the two euploid controls (F1 and F2) for each chromosome in separation.

D1, D2, D3, from Down syndrome; DT1, from double trisomy 2 and 21; E1, from Edwards syndrome; P1, from Patau syndrome; W1, from complete trisomy 8/Warkany syndrome.

Table S4. Frequencies of losses and gains for each chromosome for each of the samples

Case number	Phenotype	M-1 chromosome 2, %	M+1 chromosome 2, %	Other aneusomy chromosome 2, %	M-1 chromosome 17 (16)*, %	M+1 chromosome 17 (16)*, %	Other aneusomy chromosome 17 (16)*, %
F1	Normal	0.06	0.03	0	0.14	0.03	0
F2	Normal	0.09	0.06	0	0.15	0.03	0
D1	Down syndrome	0.20	0	0	0.20	0	0
D2	Down syndrome	0.20	0.20	0	0.20	0	0
D3	Down syndrome	0.10	0.30	0	0.29	0.05	0
P1	Patau syndrome	0.10	0.10	0	0.29	0.19	0
E1	Edwards syndrome	0.20	0	0	0.50	0.20	0
W1	Fetal death	0.05	0.10	0	0.25	0.10	0
DT1	Fetal death	0.33	0	0.10	0.19	0.13	0
T1	Triploidy	0.40	0	0.26	0.86	0	0.13
T2	Triploidy	1.05	0	0.20	1.7	0	0.13
DLD1	Colorectal cancer	0.60	0.60	0	1.4	0.37	0
SW480	Colorectal cancer	3.0	0.95	0.79	2.2	0.20	0

M, modal chromosome copy number.

*In SW480 data for chromosome 16 were used in replacement for chromosome 17, as the latter was subject to complex structural rearrangements.