Supplementary Table I. Cell lines

Breast	*Source*	*Reference*[a]
VP229, VP267, VP185, VP303	M. McCallum, Glasgow, UK	[1]
MDA-MB-157[c], MDA-MB-175, MDA-MB-435s[c], MDA-MB-361[c], MCF-7[c], DU4475[c], Hs578T[c], MDA-MB-468, MDA-MB-231[c], MDA-MB-436, BT549[c], ZR-75-1	M. Stratton, Sutton, UK	
MDA-MB-134, SK-BR-7, SK-BR-3[c]	M. O'Hare, UK	[2]
OCUB-F, OCUB-M	Riken cell bank	[3]
SUM159[c], SUM149[c], SUM102, SUM1315[c], SUM52, SUM185[c], SUM190, SUM225[c], SUM44, SUM229	S. Ethier, Michigan, USA	[4-6]
CAL51[c]	B. Dutrillaux, France	[7]
MT-3	M. Bibby, Bradford, UK	[8]
KPL1	Kurebayashi, Japan	[9]
Ovarian		
OC314, OC315, OC316	A. Alama, Genova, Italy	[10]
OVI-P, OAW41M, 59M, A2780, CH1, Hx62, LK1, LK2, OAW42/83, PA-1[c], PxN94	M. Stratton, Sutton, UK	
UCI-101, UCI-107	Carpenter, UC, USA	[11,12]
EC, KEN-3, MN-1, SHIN-3	Kiyozuka, Kansai, Japan	[13-15]
KK	Kikuchi, Japan	[16]
OVISE, OVKATE, OVMANA, OVSAHO, OVSAYO, OVTOKO	Gorai, Yokohama, Japan	[17,18]
Other		
MT-1, MaTu[b]	M. Bibby, Bradford, UK	[8,19]
HCT116[c], LoVo[c], DLD-1[c], CACO-2[c], COLO205	ATCC	

[a]References are given to lines not in the ATCC catalogue

[b]Subsequent to carrying out our analysis, we realised that these cell lines are HeLa derivatives (McLeod et al., 1999), however this fact does not substantially alter our conclusions.

[c]Screened for BUB1 mutation – no mutation found [20-22]

Supplementary Table II. Mutations in target genes

Cell line	*BAX*[a]	*BRCA1*	*hMSH3*	*hMSH6*	*IGFIIR*	*TGFβRII*	*NSEP*	*NGFR*	*BRCA2*
Ovarian									
A2780									
OC314						0, -1			-T, +A
OVI-P	0, +1	0, -1	0, -2	-1					
UCI-101									
UCI-107									
Breast									
CAL51					0, -1	-1			
MT-3	-1		-1	0, -1	0, -1	-1		0, +1	-A
OCUB-F									
OCUB-M									
Total[b]	2/8	1/8	3/8	2/8	2/8	3/8	0/8	1/8	2/8

[a]blank, normal; -1, -2, one and two bp deletions; 0, normal; +1, +2, one and two bp insertions; -T, homozygous 1 bp deletion at $(T)_{10}$ in intron 2; +A, heterozygous 1 bp insertion at $(A)_7$ in exon 11; -A, heterozygous 1 bp deletion at $(A)_8$ in exon 23.

[b]Total excludes OC314, OC315 and OCUB-F.

Supplementary Table III. Centromeric FISH data

		Chromosome modal number							
Cell line	*MSI Status*	3	7	8	9	12	15	17	18
Lymphocytes	-	2	2	2	2	2	2	2	2
A2780	+	2	2	2	2	2	2	2	2
CAL51	+	2	2	2	nd	2	2	2	nd
UCI-101	+	2	2	2	2	nd	nd	2	2
UCI-107	+	2	2	2	2	nd	nd	2	2
SUM159	-	2	2	2	2	2	2	2	2
LK-1	-	2	2	2	2	3	2	2	2
MT-3	+	2	3	2	nd	2	2	2	nd
MDA-MB-157	-	3	3	4	2	nd	nd	2	3
MDA-MB-468	-	4	nd	2	3	nd	nd	2	4
OC314[a]	+	3	4	3	3	3	2	4	2
MaTu	-	3	4	4	3	4	3	3	2
KPL1	-	4	4	3	3	4	3	4	3
OCUB-F	+	4	4	2	4	nd	nd	4	4
OCUB-M	+	4	4	4	5	nd	nd	4	3
OVI-P	+	4	5	4	3	4	4	4	4
MT-1	-	6	3	6	4	5	3	4	4

[a]The same chromosome modal numbers and similar variability were found in OC315 and OC316

SUPPLEMENTARY Table IV. Summary of molecular cytogenetic findings

MSS cell lines				MSI cell lines			
	Break index	*Modal number*	*CGH - arms with alterations*		*Break index*	*Modal number*	*CGH - arms with alterations*
MaTu	25	69	14	CAL51	0	46	3
MCF-7	99	65	25	MT-3	2	46	5
MDA-MB-134	9	44/66	22	OCUB-F	64	77	17
MDA-MB-157	43	62/116	25	OVI-P	18	92	n.d.
MDA-MB-175	10	48	27				
MDA-MB-435	38	57	21				
MDA-MB-361	57	51	12				
MT-1	71	103	27				
SK-BR-3	77	79	26				
SK-BR-7	8	43	8				
SUM159	8	47	5				
VP229	92	62	22				
VP267	98	59	24				
ZR-75-1	26	72	15				
Average	47.2		19.5		21		8.3

SUPPLEMENTARY TABLE V Details of parental cell lines

Cell line	*MT-1(MSS)*	*MT-3(MSI)*	*SUM159(MSS)*	*Normal lymphocytes*
Modal number	103	46	47	46
SKY break index	71	2	8	n.d.
Centromeric FISH				
Chromosome 3 mode (% variation)	6 (20)	2 (5)	2 (9.1)	2 (3.6)
Chromosome 8 mode (% variation)	6 (24)	2 (5.1)	2 (24)	2 (5.4)
Chromosome 15 mode (% variation)	3 (18)	2 (10)	2 (11)	2 (4.4)
Chromosome 17 mode (% variation)	4 (13)	2 (7.6)	2 (26)	2 (4.2)
6-colour FISH [a, b]				
Chromosome 4	3N	2N	2N	2N
Chromosome 5	2N, der(5)t(5;3), der(17)t(5;17), del(5), 2x der(5)t(5;10), der(5)t(5;15)	2N	2N, del(5)	2N
Chromosome 7	2N, i(7q), del(7), der(2)t(X;2;7), der(7)t(7;15)	3N	2N, der(17)t(7;17)	2N
Chromosome 8	4N, der(8)t(9;8;17),.der(8)t(6;8;17), der(22)t(8;22)	2N	2N, der(13)t(8;13), der(?)t(8;13;14)	2N
Chromosome 15	3N, der(2)t(2;11;15), 2x der(?)t(?;15;?)	2N	2N	2N
Chromosome 18	3N, del(18), der(2)t(2;18)	2N	2N	2N

[a] N, normal chromosome

[b] Translocation partners based on SKY data (Davidson et al 2000). One novel aberration, an insertion of chromosome 15 material in MT-1, was not identified in the SKY analysis due to the low resolution in detecting this type of alteration and thus the translocation partner(s) are unknown.

[c] For SUM159 the most commonly observed karyotype is given (60% of metaphases), however there were additional variant karyotypes within the parental cell line observed in more than two metaphases. These were always alternative translocations involving chromosomes 7 and 8.

Supplemental methods:

1. Chromosome number was taken into account for the clonal centromeric FISH data in the following manner. Firstly, the total number of chromosomes analysed was calculated by multiplying the number of nuclei by the modal number of signals for each chromosome (e.g. for MT-1, chromosome eight was analysed 6618 times). Secondly, the number of chromosomes that were gained/lost was calculated for each chromosome by the number of signals above/below the mode multiplied by the number of nuclei with that signal number (e.g. for MT-1 chromosome eight, there were 338 chromosome losses and 51 chromosome gains). Finally, for each cell line the values for the four chromosomes were then summed and used for chi-squared comparisons with the other cell lines.

2. Unstable alterations included chromosome breaks, chromatid breaks, acentric fragments, double minutes and dicentric chromosomes. These alterations were considered unstable as they a) would have occurred in the last division (breaks), b) would be unlikely to remain in the same form from one mitosis to the next (dicentrics), or c) would swiftly vary in number by cell division (acentrics, double minutes). Stable aberrations included new translocations, deletions, duplications and isochromosomes. If an aberration was observed in two different metaphases within the same clone, it was counted twice, however this only occurred once, in SUM159.

3. In order to compensate for the different amounts of chromosome material present in each cell line for the clonal analysis of structural aberrations, a consensus of the chromosomes was taken from the parental cell line data for centromeric FISH, comparative genomic hybridisation and SKY. For example, of the chromosomes included in the 6-colour analysis, MT-3 had two copies of chromosomes 4, 5, 8, 15 and 18, and three copies of 7, giving a total of 13 chromosomes. SUM159, with extra chromosome 5 and 8 materials, also had approximately 13 chromosomes per metaphase, while the best estimate for MT-1 including all translocations was 26 chromosomes. All statistical comparisons were done using the proportion of aberrations per total number of chromosomes analysed, i.e. for SUM159, 13 chromosomes were analysed in ten clones with a total of 303 metaphases for a grand total of 3939 chromosomes analysed. This meant that in MT-1, proportions of chromosome aberrations were lower than the raw numbers suggested; MT-1 was analysed at 7748 chromosomes.

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