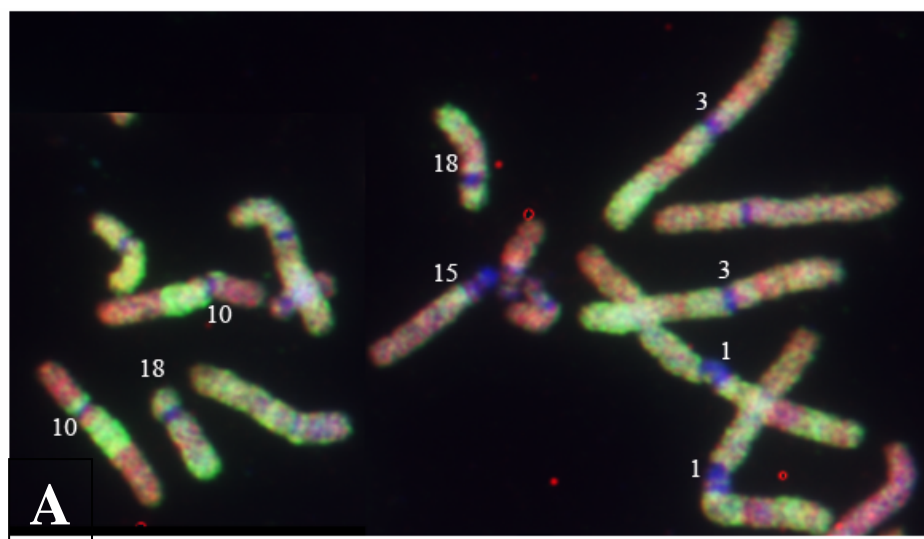


Cell line	Number of structural rearrangements																						
	chromosome																						
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	x
KH39	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0
UOK125	0	0	1	0	0	0	0	0	0	0	2	0	0	1	0	0	0	0	0	0	0	0	1
TK164	2	0	1	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
A 498	2	1	2	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	1	0	0	0	1
U2020	0	1	3	2	2	0	0	2	1	0	2	1	0	0	0	0	0	0	0	0	0	0	3
Caki2	1	1	2	0	0	3	0	1	2	0	2	2	0	0	0	1	1	1	1	1	0	0	0
UOK147	2	0	5	3	2	0	0	2	1	3	0	1	0	0	1	0	1	2	1	0	0	0	2
totally	8	3	12	6	4	4	0	6	4	4	7	4	0	1	1	1	2	3	3	2	0	0	7

Supplementary material 2. Metaphase CGH analysis of carcinoma cell lines.

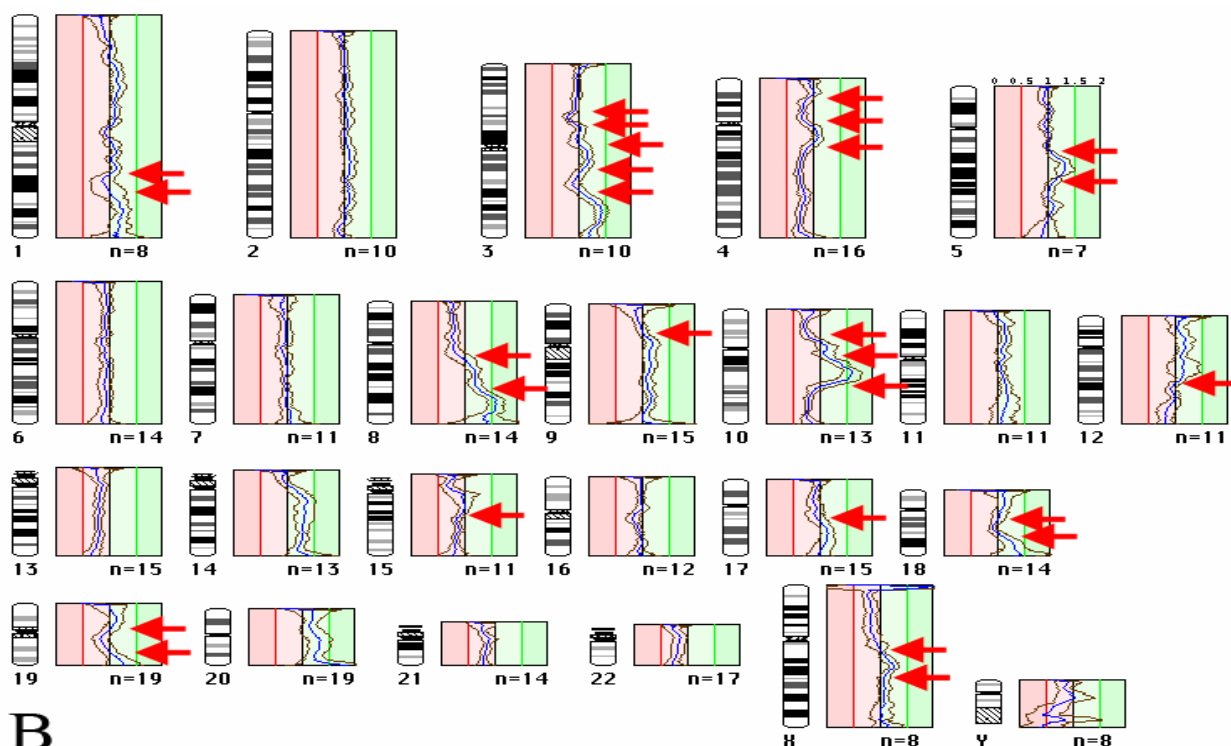
Above: Number of structural rearrangements per chromosome detected by CGH in the analysed cell lines. Three “high complexity karyotype cell lines” are highlighted (grey). Chr3 was involved in structural changes more frequently than the others (highlighted, yellow).

Below: CGH analysis of UOK147 cell line. CGH was performed as described (Alimov A et al. *Oncogene* 2000, **19**:1392-1399). Computer analysis was performed using PowerGene 710 Karyotyping, FISH and CGH system (PSI Scientific Systems) and Genus (Applied Imaging Corporation, Santa Clara, CA) software.



A. CGH identifies breaks on metaphase chromosomes 1, 3, 10, 15 and 18.

B. CGH identifies breaks on profiles (red arrows).



B