



### Supplementary figure S3. Posttetraploid cell lines display variable aneuploidy

(A) Frequency of all normal and derivative chromosomes that were identified in HCT116 and in its posttetraploid derivatives HPT1 (B) and HPT2 (C). Bars represent median and interquartile range of 10 cells that were scored for each cell line. Constitutive derivative chromosomes that were described for HCT116 are marked in red. Note that several novel derivative chromosomes in posttetraploid cell lines arose from balanced translocations and thus did not affect the total copy number. At least 10 cells was evaluated for each cell line. (D) The frequency of chromosomal aberrations calculated as aberration ratio is increased in posttetraploid cell line in comparison to the parental HCT116, but the difference is not statistically significant. (E) Chromosome numbers of the posttetraploid cell lines determined by standard karyotyping. At least 25 cells was scored for each cell line.