



**Supplemental Fig S8.** Quantifying structural variations with ddPCR in the aneuploid K562 cell line. **(A)** DNA concentration measured with ddPCR at the six different loci targeted in our experiment. All assays were run on the same DNA and with the same 40 ng DNA input and should therefore yield the same DNA concentrations. The observed differences in DNA concentration are thus due to copy number variations. Bars show mean + Poisson sampling errors. **(B)** We hypothesized that placing the HEX reference probe physically close to the FAM probe would increase the probability that both the target and reference had the same copy numbers. To validate this approach, we compared the concentrations measured by the Chr17 HEX probe and the Chr17 AB FAM probe on mock K562 DNA with the same DNA input. The difference in measured DNA concentration was within expected sampling variability, thus validating our method. Bars show mean + total error (Poisson + sampling error).