Supporting Information

Highly sensitive mutation detection based on digital amplification coupled with hydrogel bead-array

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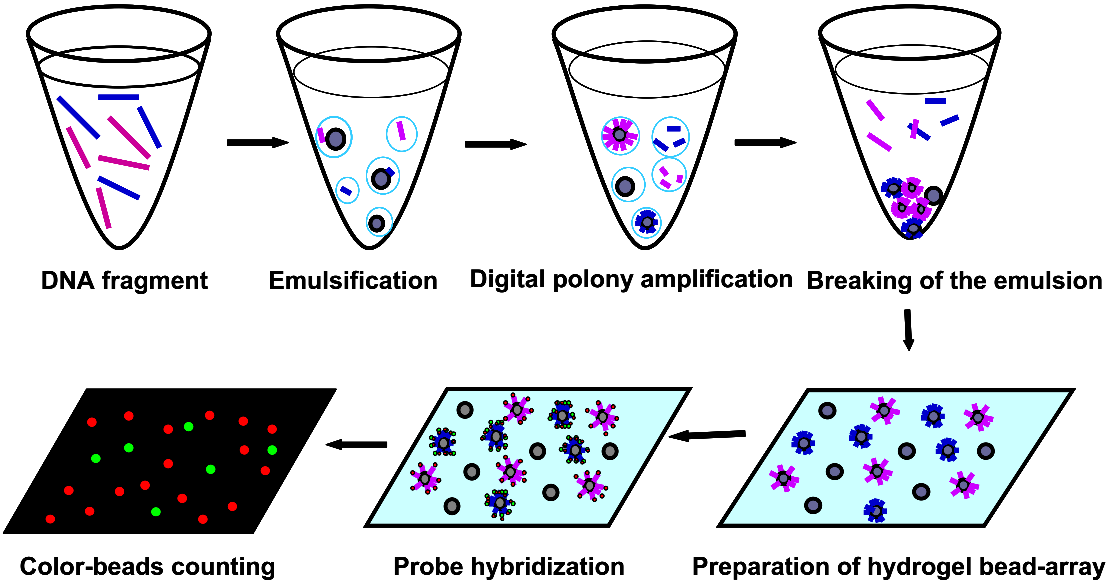
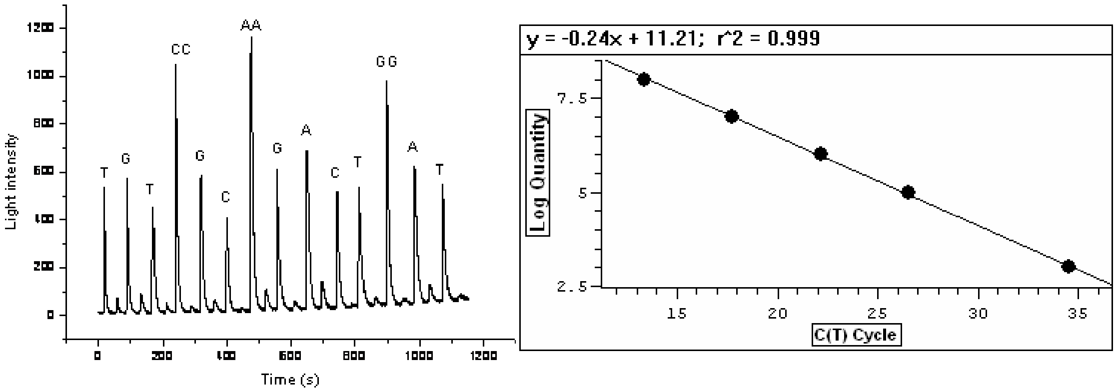
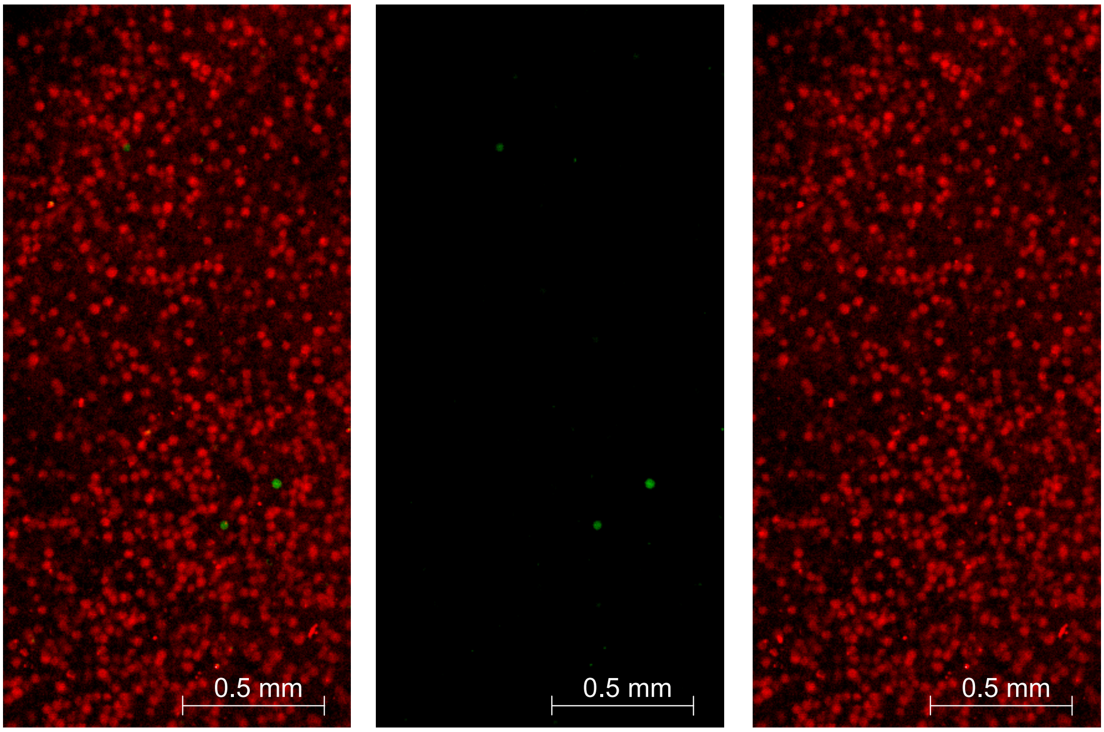


Supplemental **Fig. S1.** Schematic illustration for DABA. The procedure of DABA is as follows: emulsification, single molecule amplification, breaking of the emulsion, preparation of hydrogel bead-array, probe hybridization and color-beads counting. Based on the concepts of data analysis from Digital-PCR and the sample processing of emulsion-PCR, single molecule amplification (single DNA copy per bead) with an improved emulsion quality is performed to produce the samples for preparing the hydrogel-chip which can trap the beads with single DNA sequences. The chip was further treated with electrophoresis to remove the free and mismatched probes before allele-specific probe hybridization and chip-scan.



(A) **(B)**

Supplemental **Fig. S2.** (A) The pyrosequencing result of the amplicons on the surface of the beads. The tested sequences are TGTCCGCAAGACTGGAT. (B) The standard curve of real-time PCR for detecting the average copies of amplicons on the surface of each bead.



(A) **(B)** **(C)**

Supplemental **Fig. S3.** The images by scanning the gel-chip immobilized with beads from emulsion-PCR using the DNA sample from the tumor tissue of CRC patient as the template for detecting mutants at codon 1406 of APC gene. (A) Cy3+Cy5, (B) Cy3, (C) Cy5. Only a part of the scanning area was shown for the illustration. Every red bead originates from one wild-type molecule and every green bead is from one mutant molecule. The number of beads scored is about 2.4×10^3.