



Figure S1. Block-wise normalization was conducted and the Bayes regression approach was used to identify the regions with chromosomal copy number changes. **(A)** Array images of self-hybridization of reference DNA (left) and co-hybridization of patient DNA and reference DNA (right) are shown. The \log_2 ratio of these two arrays after block-wise normalization is shown in the lower panels. The \log_2 ratio of array of lung cancer patient was more deviated from 0 than that of reference sample. **(B)** The schematic illustrations show the \log_2 ratio of all BAC probes on chromosome 3 in two patients. The values of +1, 0, or -1 were assigned to a region where gene dosage is higher, uncertain, or lower than those of the neighboring regions, respectively. **(C)** Merged data of alteration frequency, in which the gain chromosome region with 50% frequency (+1) at the position 20~32 10^6 bp and the loss chromosome region with 100% frequency (-2) at the position 32~48 10^6 bp on chromosome 3, for patient 1 and patient 2 is shown. **(D)** Data from a total of 40 lung cancer patients were merged, and the results show two alteration regions with gain at 3p13-14.1 and loss at 3p21.3-22.3.