

ABSTRACT

A position identification unit (110) maps a plurality of tumor sample reads to a human genome sequence, and identifies, for each target gene, a target position which is a genome position of a base, the genome position having changed with respect to the human genome sequence. A frequency calculation unit (120) calculates a variant allele frequency for each target position of each target gene. A distance calculation unit (130) calculates, for each target gene, a feature distance equivalent to a difference between a variant allele frequency corresponding to a peak density and a reference variant allele frequency in a density distribution indicating a density of the number of mapping reads with respect to the variant allele frequency. A coefficient calculation unit (140) calculates a correction coefficient using the feature distance of each target gene. A copy-number calculation unit (150) calculates the copy number of each target gene in the cancer cell using the copy number per target gene in a tumor sample and a correction coefficient.