Deep Sequencing for Unbiased Genome-wide Profiling of Gene Fusions and CRISPR Targets

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Numerous diseases are rooted in the genetic abnormalities at the DNA level. Detection of disease genes and correction of genetic defects for therapy have become relatively easy with technology advances in next-generation sequencing and CRISPR genome editing. However, unbiased and highly sensitive technologies for genomic profiling are still needed for thorough assessments of treatment options, risks and benefits before clinical applications. One of the challenges in genomic profiling is the lack of prior knowledge of where in the genome to look for, especially when targets are presented at a low level, such as less than one out of 1000 cells. We have previously developed a deep sequencing method termed AMP for sensitive detection of gene fusions without prior knowledge of fusion partners even using highly degraded samples and, when combined with a DNA tag insertion, allows for genome-wide unbiased identification of CRISPR targets.