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## **Solid-phase Enzyme Catalysis of DNA end Repair Avoids Heat Treatment and Reduces GC-bias in Next-Generation Sequencing of Human Genomic DNA**

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Next-generation sequencing (NGS) has caused a revolution in both research and diagnosis. NGS analysis relies on preparation of a representative, non-biased library evenly distributed across the entire genome under investigation. This critical task has become increasingly challenging since biases found in the current methods of the NGS library preparation produce uneven coverage and compromise the quality of NGS analysis. In this report we have identified a systematic sequence bias during construction of amplification-free human DNA libraries for the Illumina sequencing platform. Our study indicates that inefficient processing of AT-rich DNA in the major steps that comprise library construction results in under-representation of the extremely high AT-content fraction in human genomic libraries. We have demonstrated a new strategy by employing DNA modifying enzymes conjugated to magnetic beads in construction of amplification-free human DNA libraries. We show that this method significantly lowers the sequence coverage bias of the libraries on Illumina sequencing platform.

### **Biography:**

Dr. Aihua Zhang graduated from Hunan medical college, Hunan, China in 1984 and did her postdoctoral training at MGH, Harvard U.S.A. She has been working as a research scientist at New England Biolabs, Inc. since 1995. Her current research interest is validating immobilized enzymes for NGS library prep.