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The Ion Torrent PGM sequencer delivers large volumes of whole genome data without the issue of addressing repetitive DNA which commonly occurs in the human genome. With the base calling output from Torrent Mapping Alignment Program (TMAP), insertions, deletions, and substitutions can be easily identified. Data are generated in an average unit time of 100 minutes per sample. An average of 50% of the total reads can be uniquely assigned to the reference genome (chosen from public databases). The rest of the reads can be aligned to the genome, but cannot be mapped to the human reference genome, which will be caused by the repeats in the human genome. The detection of novel variants is possible when the read depth is greater than or equal to four fold which the coverage of NGS platform. Three generations of next-generation sequencing are common in the market, including Sanger dideoxy sequencing technology (Sanger, 1984), capillary array sequencing technology (Ion Torrent, 2012), and semiconductor sequencing technology (ABI, Roche, and Illumina, 2012). Each system has its own characteristics, including DNA/RNA sequencing, the process of sequencing by polymerase chain reaction (PCR) products for diagnostics or genetic research, whole genome sequencing, and other sequencing concepts. For instance, HiSeq 2000 carries out sequencing through pyrosequencing, while PGM is based on sequencing-by-synthesis technology. The sequencing machine mainly determines the throughput, and how fast can it finish one sample! Next-generation sequencing systems present superior sequencing quality and throughput. The NGS technology is mainly used in medical research, mapping, and identifying the candidate genes associated with complex genetic disease. The current multiple GBS application focuses on the following objectives: (1) aiming to improve the identification rate of correct sibs by targeting large-scale relatedness families; (2) aiming to develop a high-resolution SNP genotyping panel for marker-assisted selection; and (3) attempting to develop a high-throughput panel of GBS SNPs for the genetics analysis of complex traits in domestic animals. Whole-genome sequencing (WGS) is another great application of NGS technology. To date, it has been widely used in the whole-genome resequencing of three model organisms: mouse, human, and rat [ 19 ]. The small genome size of humans and other nonmodel organisms makes the assembly of a high-quality genome sequence a simpler task than it is for other species [ 20 ]. Routine variant detection for human sequencing projects is usually manually verified for its accuracy. Automated variant detection is especially important for the genetics of complex disease, which relies on the detection of rare variants.

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