

# LETTERS

## Transcriptome genetics using second generation sequencing in a Caucasian population

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Gene expression is an important phenotype that informs about genetic and environmental effects on cellular state. Many studies have previously identified genetic variants for gene expression phenotypes using custom and commercially available microarrays<sup>1–5</sup>. Second generation sequencing technologies are now providing

in one lane of an Illumina GAI analyzer and yielded  $16.9 \pm 5.9$  (mean  $\pm$  s.d.) million reads that were then mapped to the NCBI36 assembly of the human genome (Supplementary Fig. 1) using MAQ<sup>16</sup>. We subsequently filtered reads that had low mapping quality, mapped sex chromosomes or mitochondrial DNA and were not correctly