The figure shows the percentage of unique reads for different sequencing techniques:

- **RNA-Seq:**
  - Single-end: Shows a higher percentage of unique reads compared to paired-end.
  - Paired-end: Lower percentage of unique reads.

- **Exome:**
  - High percentage of unique reads for both single-end and paired-end methods.

- **Genome:**
  - Very high percentage of unique reads for both single-end and paired-end methods.

- **ChIP-Seq:**
  - Single-end: Shows a lower percentage of unique reads compared to paired-end.

The x-axis represents different samples or conditions labeled as 1, 2, 3, 4, and 5. The y-axis represents the percentage of unique reads ranging from 0% to 100%. The bar chart indicates the difference in read coverage between single-end and paired-end sequencing methods for each sample type.