Questions to consider while doing this mapping exercise

Coverage

What was the (approximate) average coverage?
What was the maximum coverage?
What was the minimum coverage?
Was coverage across the ‘genome’ even?

Mapping

Were all of your reads mappable?
Where did the unmappable reads come from?
In a real sequencing dataset, why might there be unmappable reads?
What fraction of reads mapped unambiguously (uniquely)?
Did you identify any sequencing errors?
Did you identify any variants (SNPs)?

Speed

What was your mapping speed (how many reads per minute did you map)?
How does that compare to the speed of mapping software like bowtie or bwa?
Could you have mapped faster with more workers in your group?