

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 23:45:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8751232.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR8751232 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8751232.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 23:45:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8751232.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,861,118
Mapped reads	4,541,480 / 93.42%
Unmapped reads	319,638 / 6.58%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	171,943 / 3.54%
Read min/max/mean length	30 / 101 / 102.46
Duplicated reads (estimated)	141,661 / 2.91%
Duplication rate	1.62%
Clipped reads	884,557 / 18.2%

2.2. ACGT Content

Number/percentage of A's	130,211,539 / 29.16%
Number/percentage of C's	92,979,273 / 20.82%
Number/percentage of T's	130,946,763 / 29.33%
Number/percentage of G's	92,385,875 / 20.69%
Number/percentage of N's	2,553 / 0%
GC Percentage	41.51%

2.3. Coverage

Mean	0.1443

Standard Deviation	1.4158
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2.4. Mapping Quality

Mean Mapping Quality	51.17
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2.5. Mismatches and indels

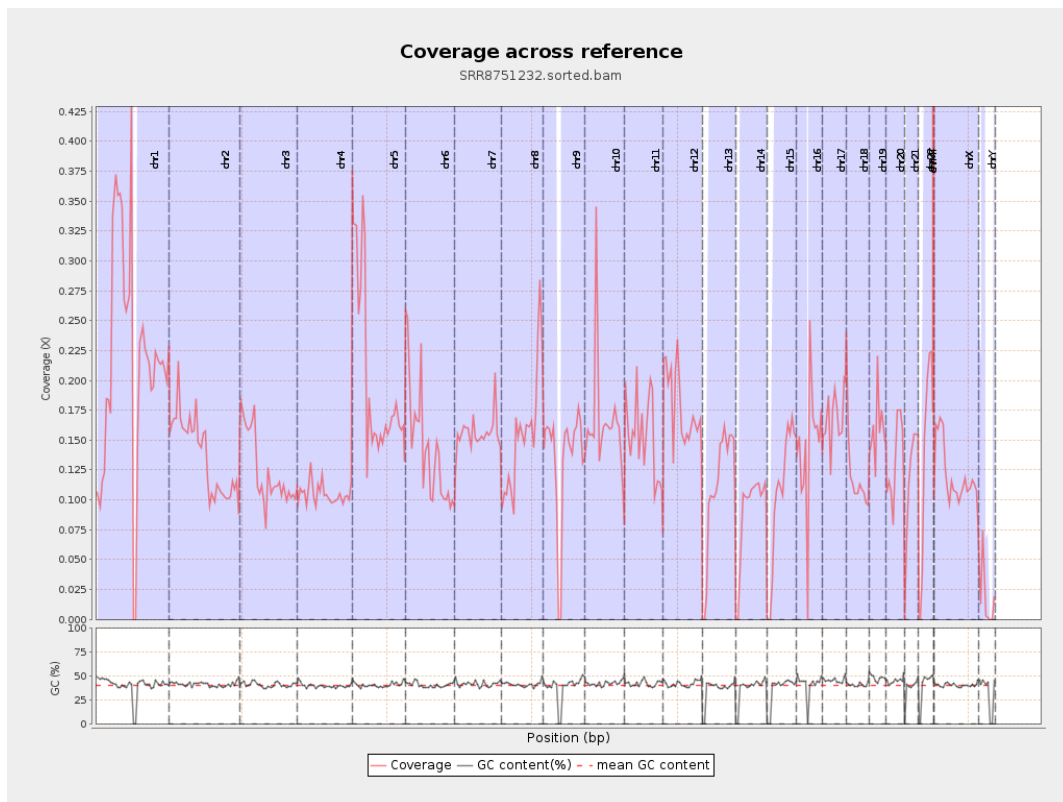
General error rate	0.44%
Mismatches	1,724,872
Insertions	180,485
Mapped reads with at least one insertion	3.86%
Deletions	63,423
Mapped reads with at least one deletion	1.37%
Homopolymer indels	51.23%

2.6. Chromosome stats

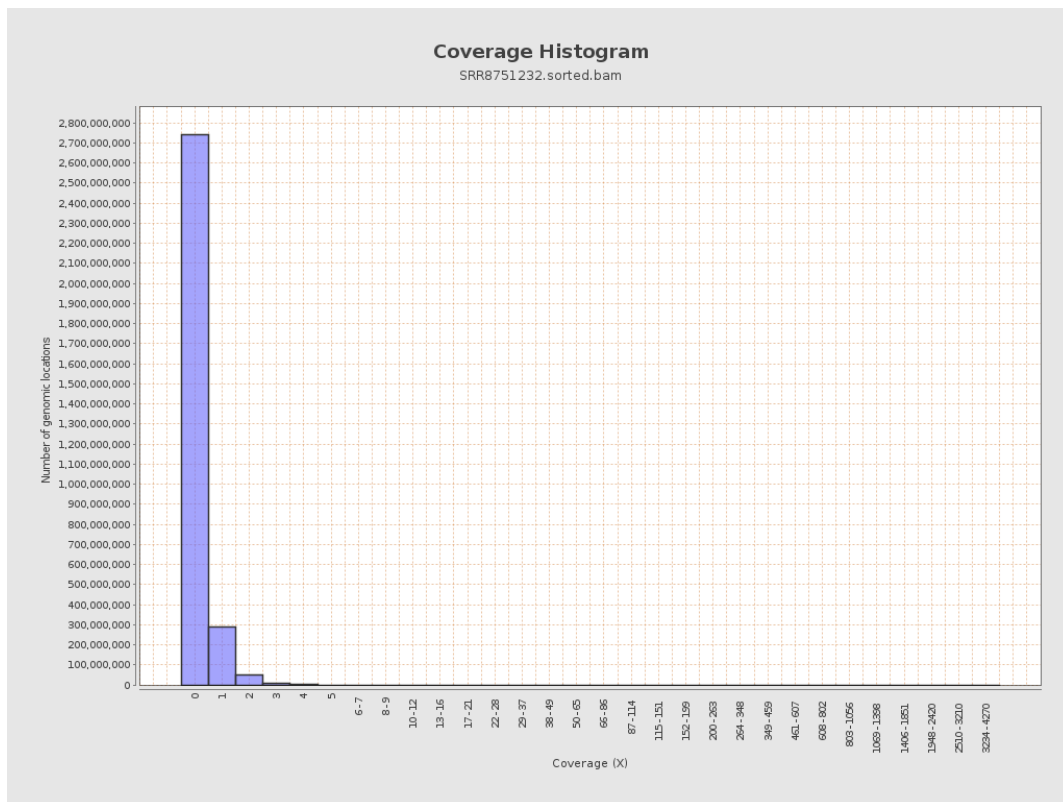
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	54032173	0.2168	4.0007
chr2	243199373	33359967	0.1372	0.5935
chr3	198022430	24562256	0.124	0.451
chr4	191154276	20082200	0.1051	0.4776
chr5	180915260	35820802	0.198	0.5189
chr6	171115067	24565298	0.1436	0.9107
chr7	159138663	24913090	0.1565	0.8093

chr8	146364022	22807244	0.1558	0.5478
chr9	141213431	18998724	0.1345	0.6505
chr10	135534747	22302512	0.1646	1.8955
chr11	135006516	20562310	0.1523	0.7005
chr12	133851895	23814287	0.1779	0.4912
chr13	115169878	12637102	0.1097	0.3817
chr14	107349540	9588884	0.0893	0.3692
chr15	102531392	10898664	0.1063	0.3744
chr16	90354753	13028131	0.1442	0.9475
chr17	81195210	13794902	0.1699	0.7153
chr18	78077248	9256235	0.1186	1.3398
chr19	59128983	9461449	0.16	2.7552
chr20	63025520	8277142	0.1313	0.4315
chr21	48129895	5619628	0.1168	0.4559
chr22	51304566	6876575	0.134	0.4323
chrMT	16571	1738545	104.9149	39.4295
chrX	155270560	18616458	0.1199	0.4676
chrY	59373566	1050396	0.0177	0.6788

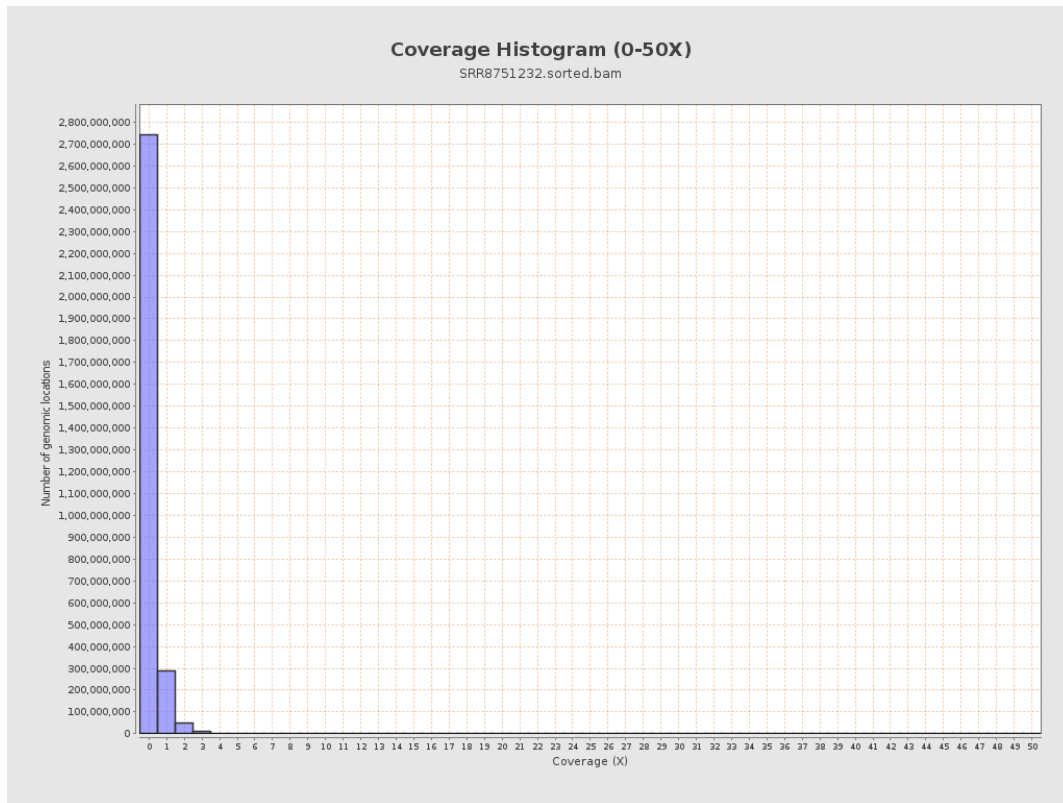
3. Results : Coverage across reference



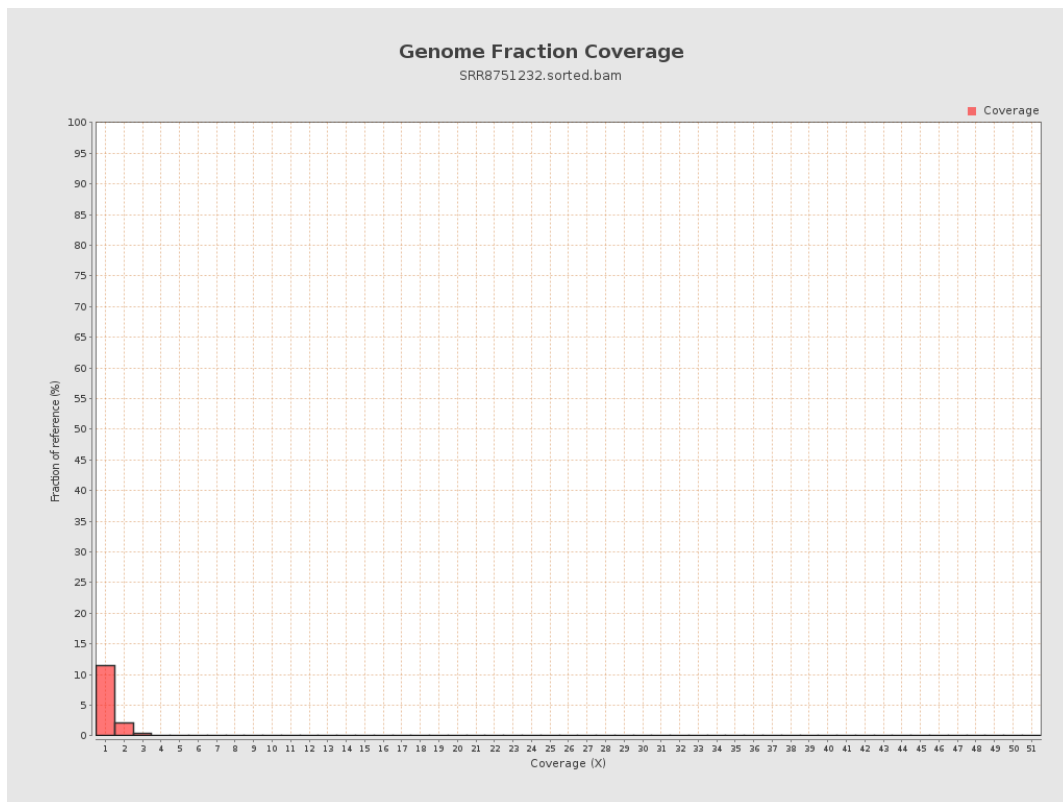
4. Results : Coverage Histogram



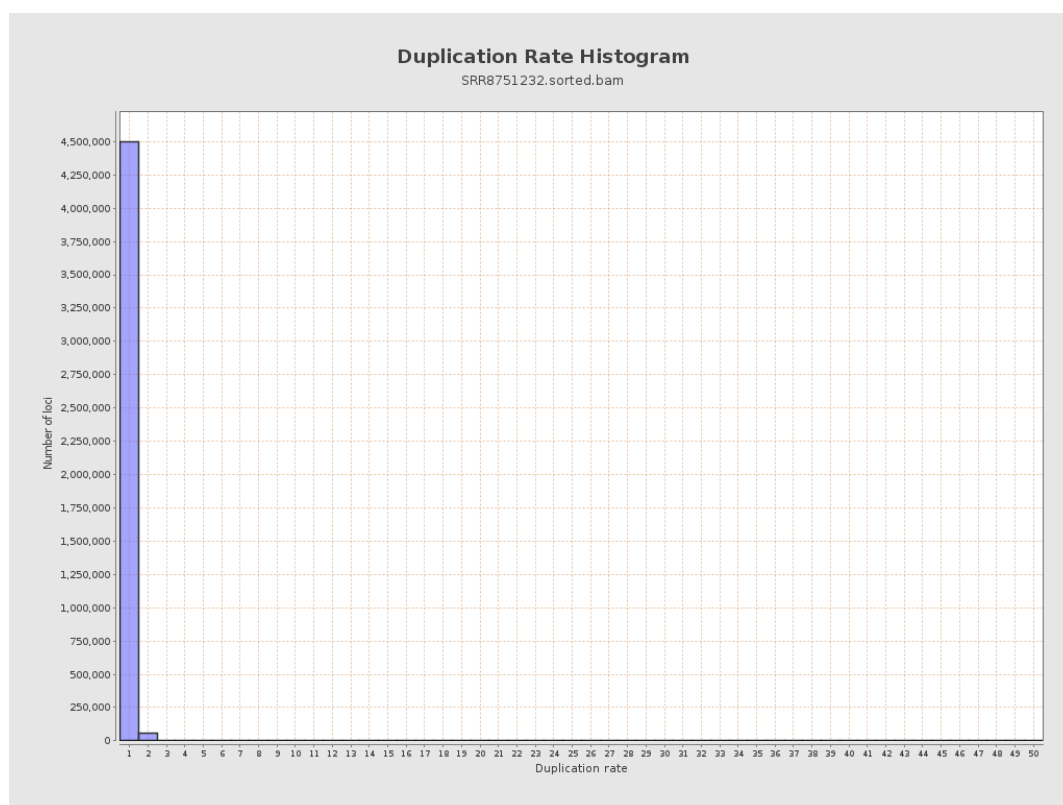
5. Results : Coverage Histogram (0-50X)



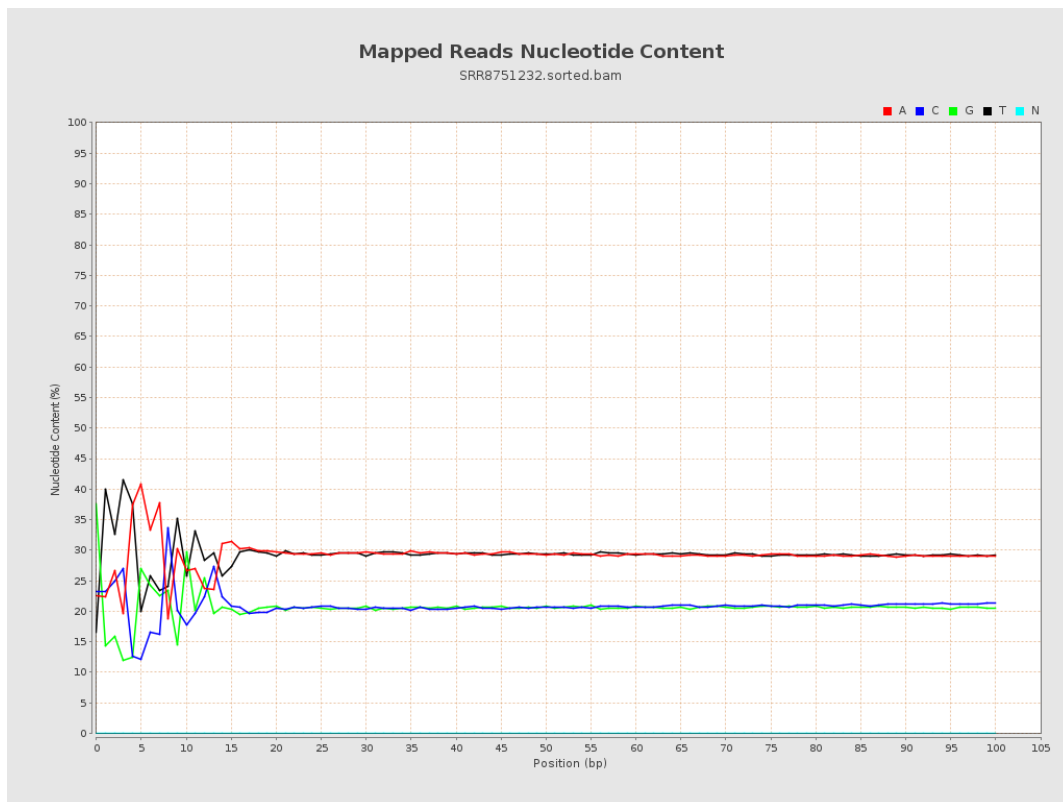
6. Results : Genome Fraction Coverage



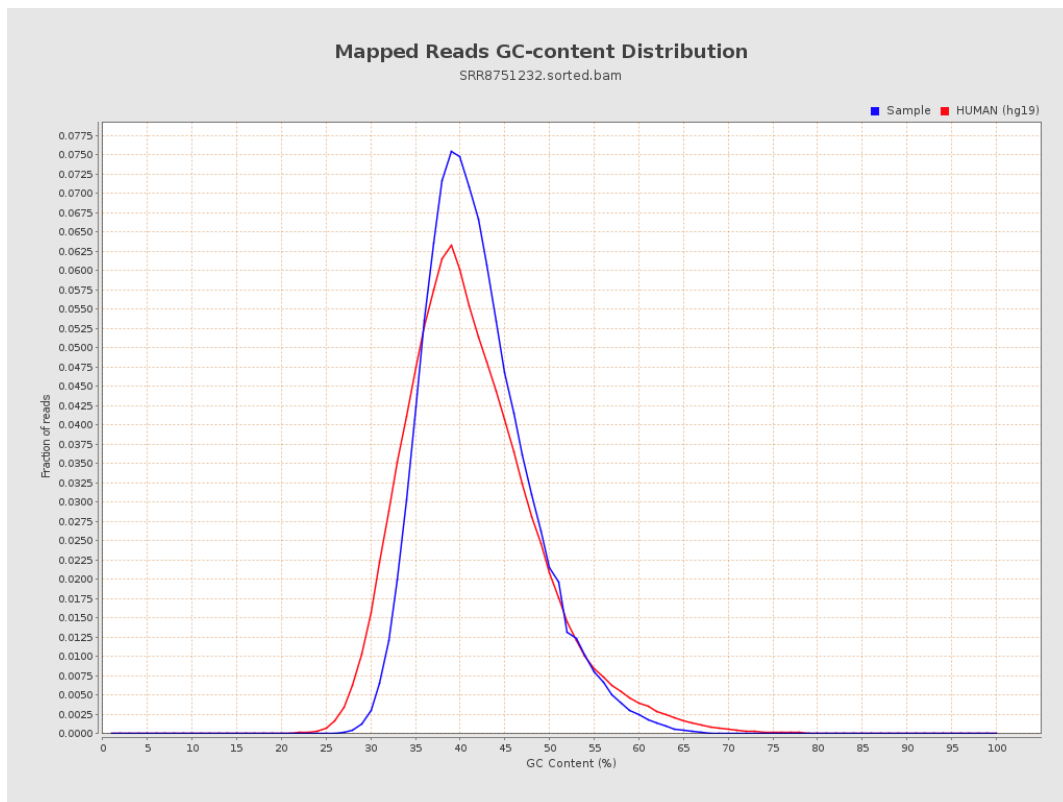
7. Results : Duplication Rate Histogram



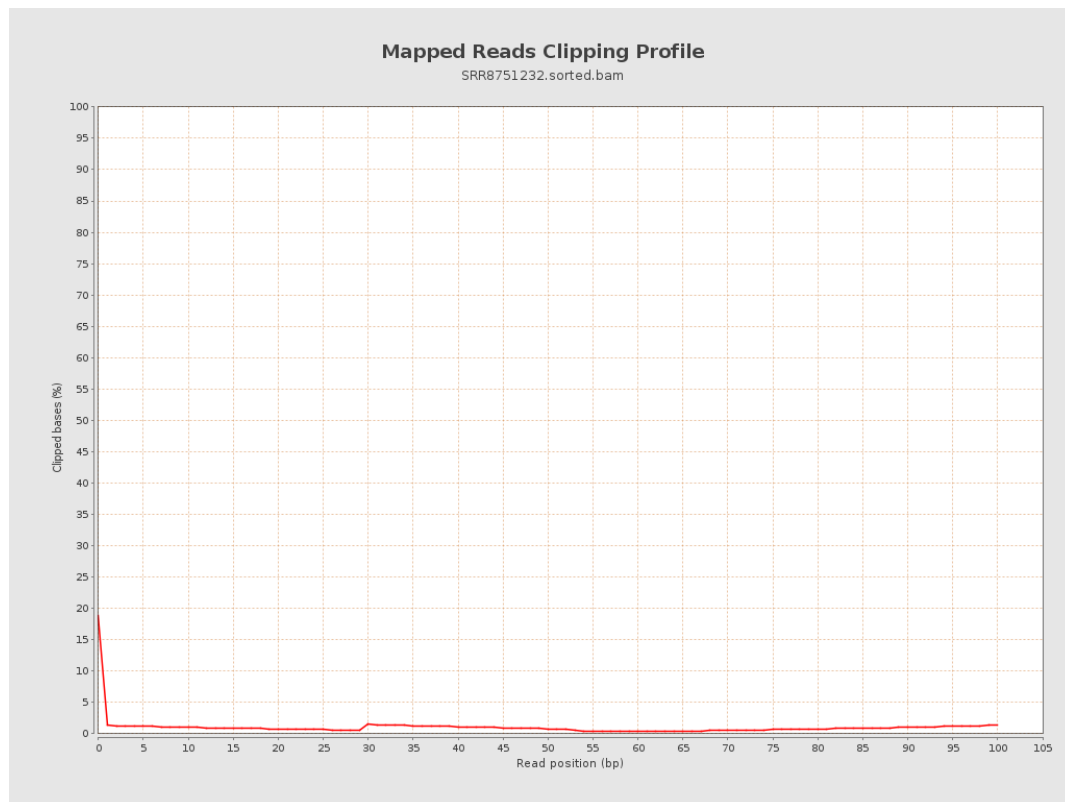
8. Results : Mapped Reads Nucleotide Content



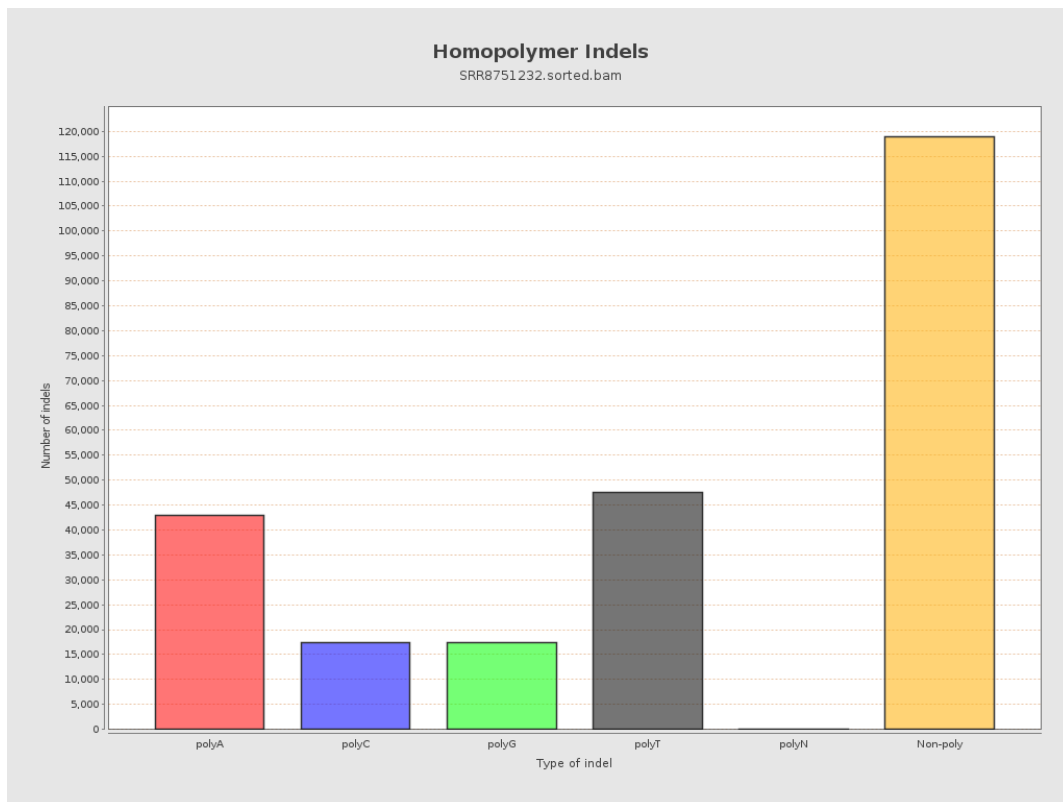
9. Results : Mapped Reads GC-content Distribution



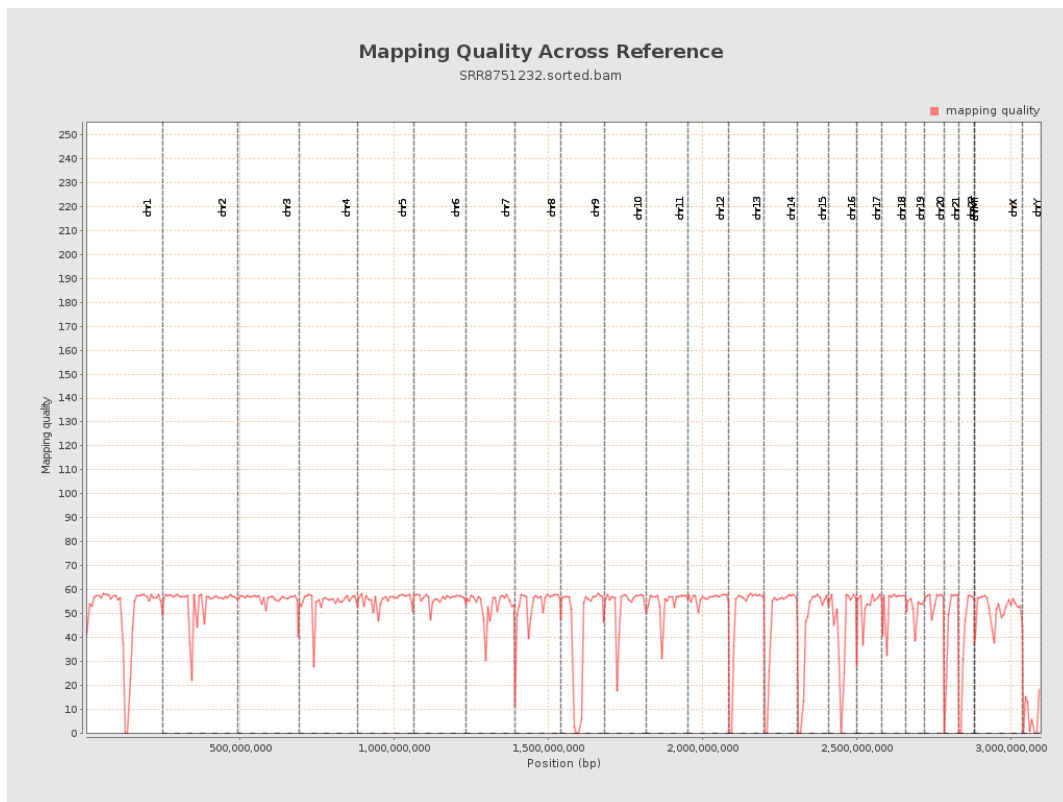
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

