Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 20:35:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8751209.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_SRR8751209 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8751209.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 20:35:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8751209.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,504,611
Mapped reads	4,062,169 / 90.18%
Unmapped reads	442,442 / 9.82%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	195,888 / 4.35%
Read min/max/mean length	30 / 101 / 102.8
Duplicated reads (estimated)	119,272 / 2.65%
Duplication rate	1.4%
Clipped reads	863,834 / 19.18%

2.2. ACGT Content

Number/percentage of A's	118,735,303 / 29.65%
Number/percentage of C's	81,479,114 / 20.35%
Number/percentage of T's	119,356,067 / 29.81%
Number/percentage of G's	80,841,776 / 20.19%
Number/percentage of N's	2,906 / 0%
GC Percentage	40.54%

2.3. Coverage

Mean	0.1294

Standard Deviation	1.4431

2.4. Mapping Quality

Mean Mapping Quality	51

2.5. Mismatches and indels

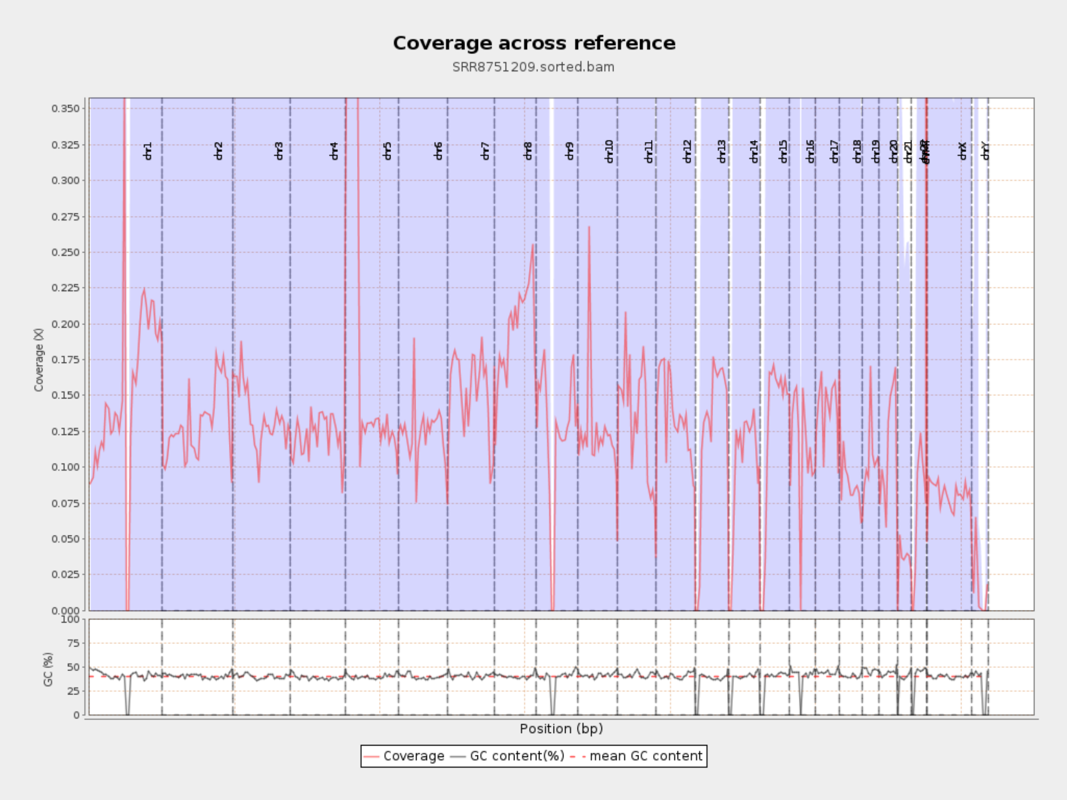
General error rate	0.44%
Mismatches	1,472,394
Insertions	223,099
Mapped reads with at least one insertion	5.3%
Deletions	58,391
Mapped reads with at least one deletion	1.41%
Homopolymer indels	52.08%

2.6. Chromosome stats

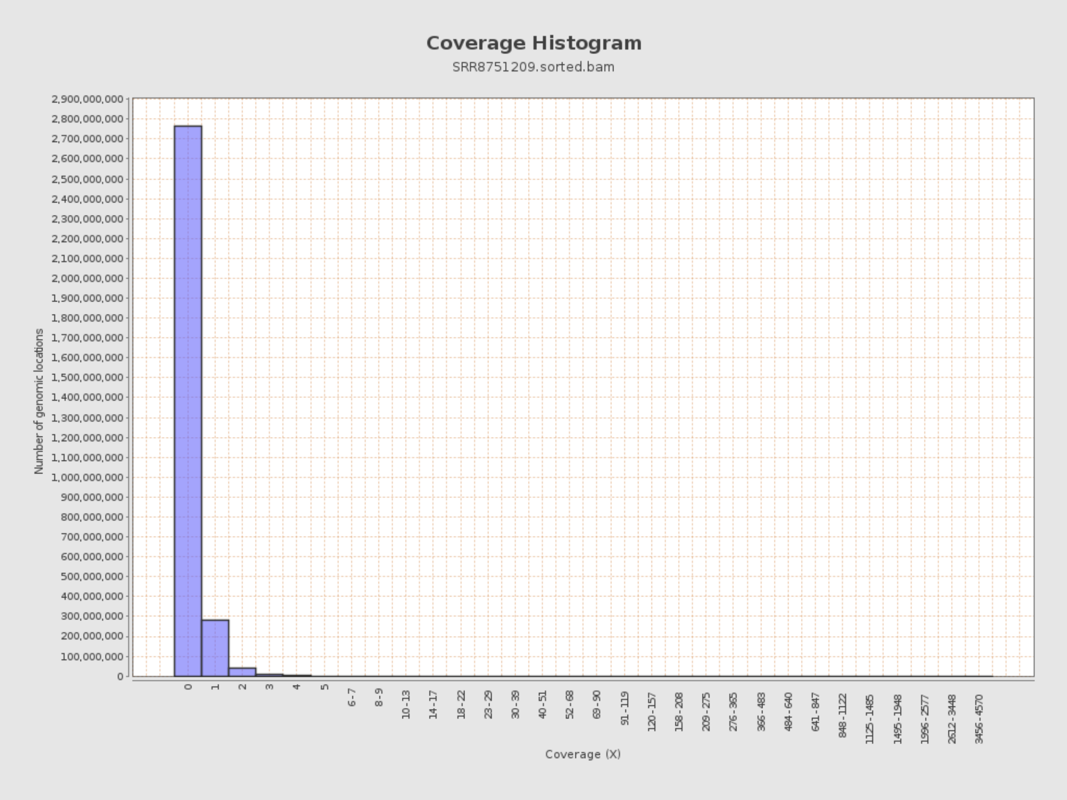
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	38029430	0.1526	4.237
chr2	243199373	31811903	0.1308	0.6084
chr3	198022430	26868407	0.1357	0.4501
chr4	191154276	23239250	0.1216	0.4152
chr5	180915260	35606680	0.1968	0.5213
chr6	171115067	21251066	0.1242	0.7837
chr7	159138663	24612454	0.1547	0.9458

chr8	146364022	28817206	0.1969	0.9589
chr9	141213431	17650691	0.125	0.8343
chr10	135534747	17016829	0.1256	1.5953
chr11	135006516	18254526	0.1352	0.6194
chr12	133851895	18329173	0.1369	0.4211
chr13	115169878	14226776	0.1235	0.3916
chr14	107349540	10733074	0.1	0.3769
chr15	102531392	12778360	0.1246	0.3952
chr16	90354753	10119752	0.112	0.6124
chr17	81195210	11385243	0.1402	0.7084
chr18	78077248	7109057	0.0911	1.5441
chr19	59128983	6320054	0.1069	2.8275
chr20	63025520	7347185	0.1166	0.3953
chr21	48129895	1711395	0.0356	0.2456
chr22	51304566	3564462	0.0695	0.299
chrMT	16571	323516	19.523	8.7008
chrX	155270560	12550567	0.0808	0.3759
chrY	59373566	885204	0.0149	0.6612

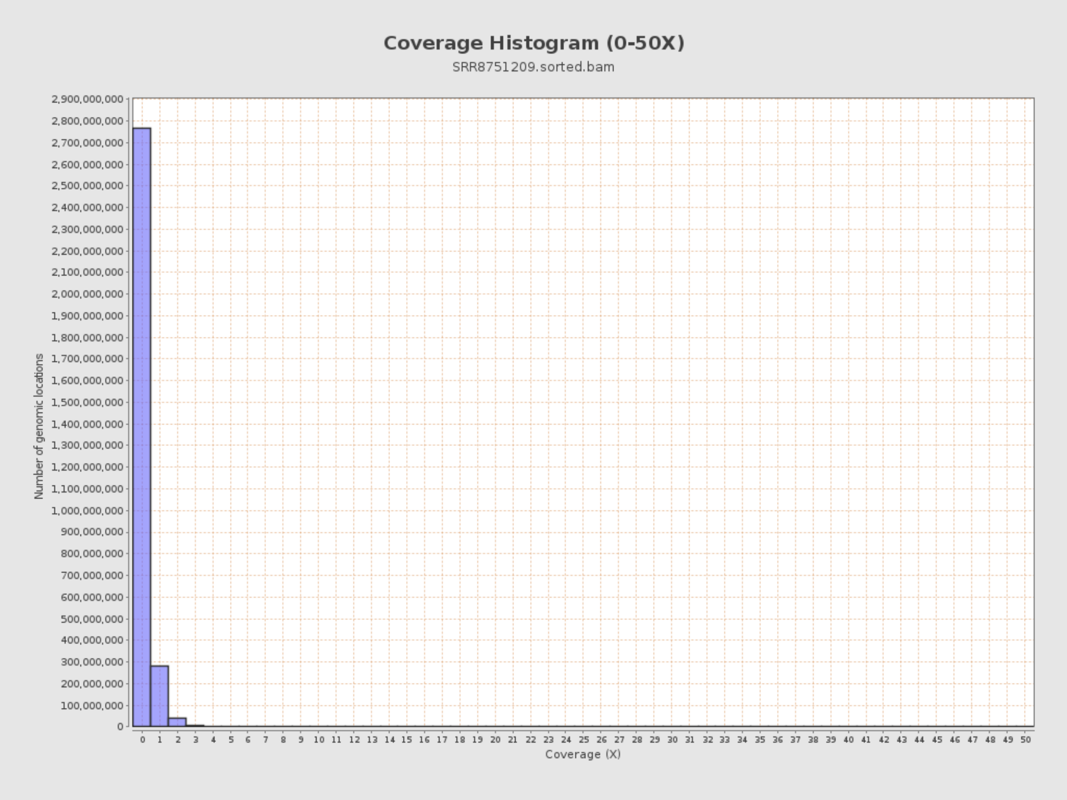
3. Results : Coverage across reference



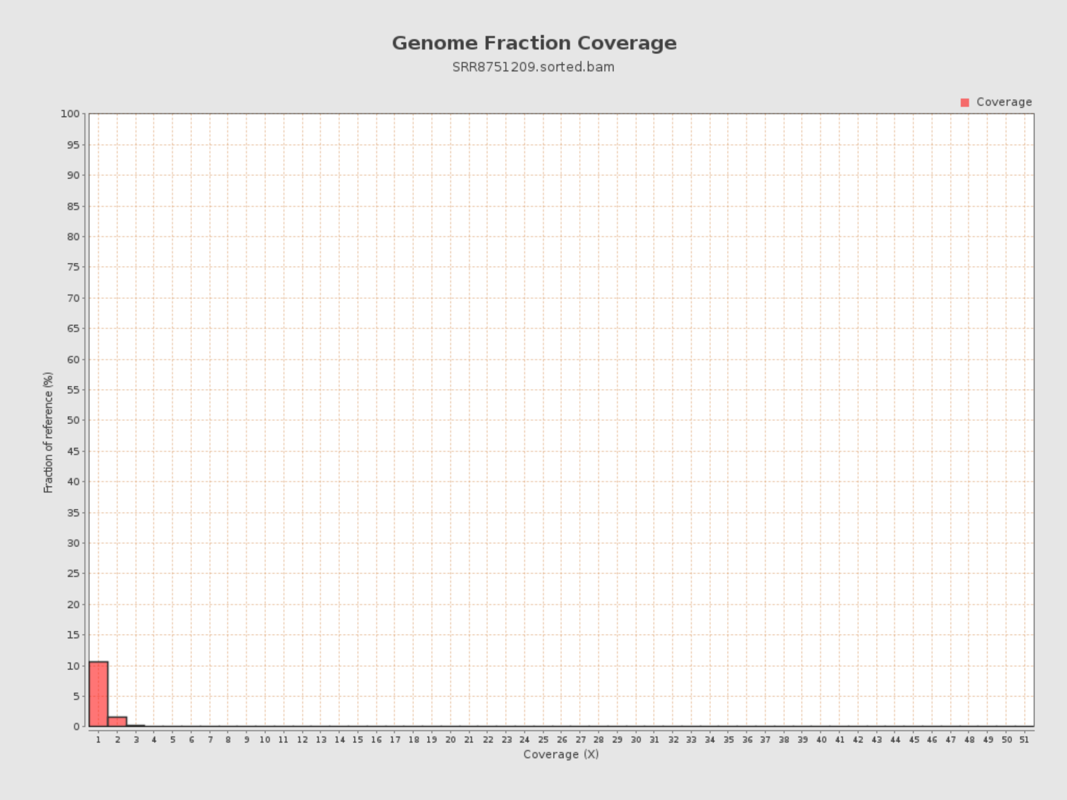
4. Results : Coverage Histogram



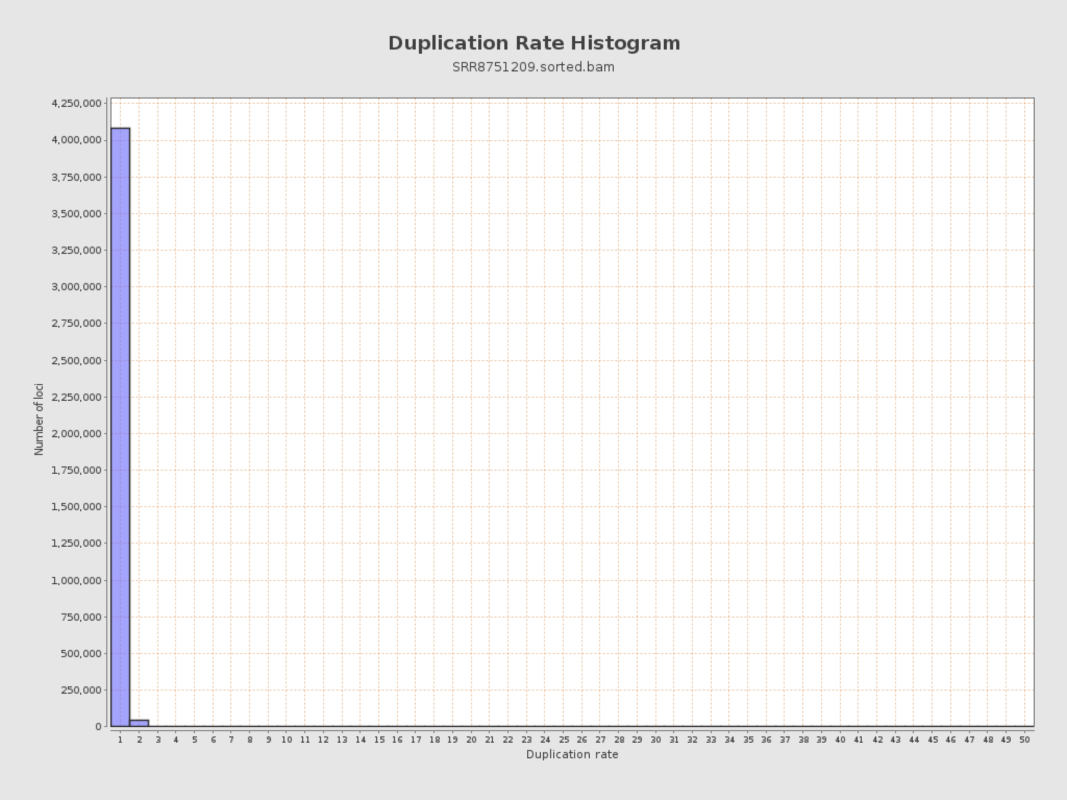
5. Results : Coverage Histogram (0-50X)



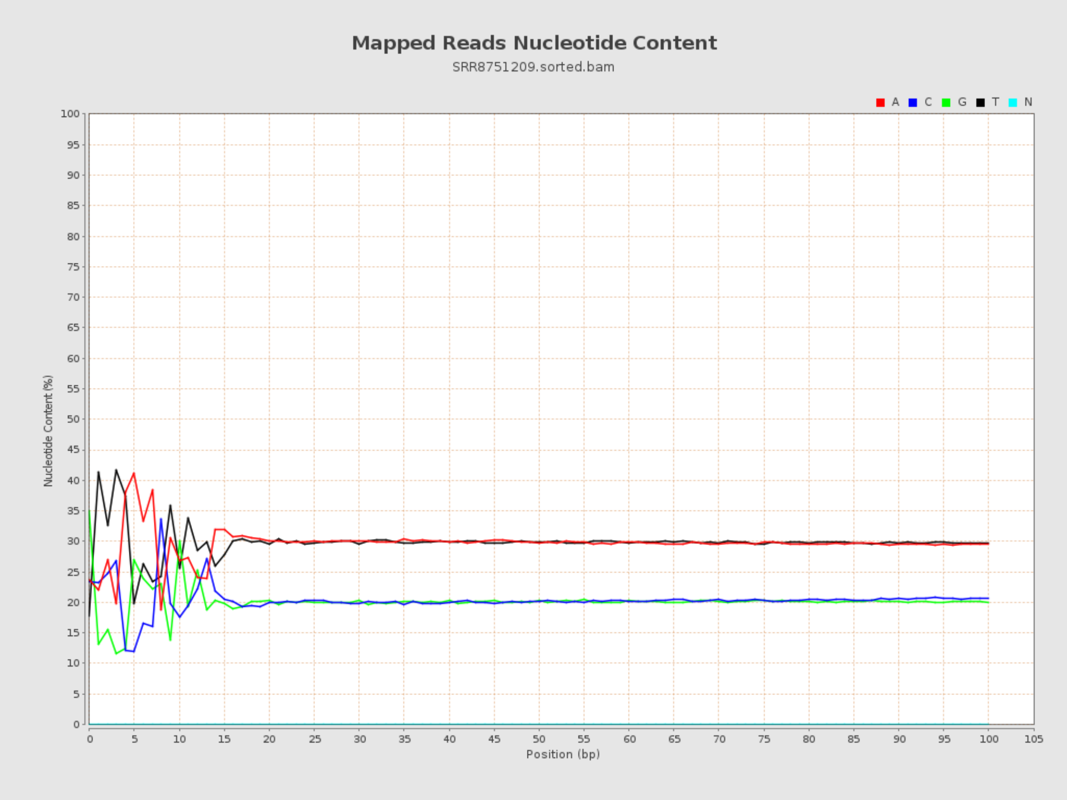
6. Results : Genome Fraction Coverage



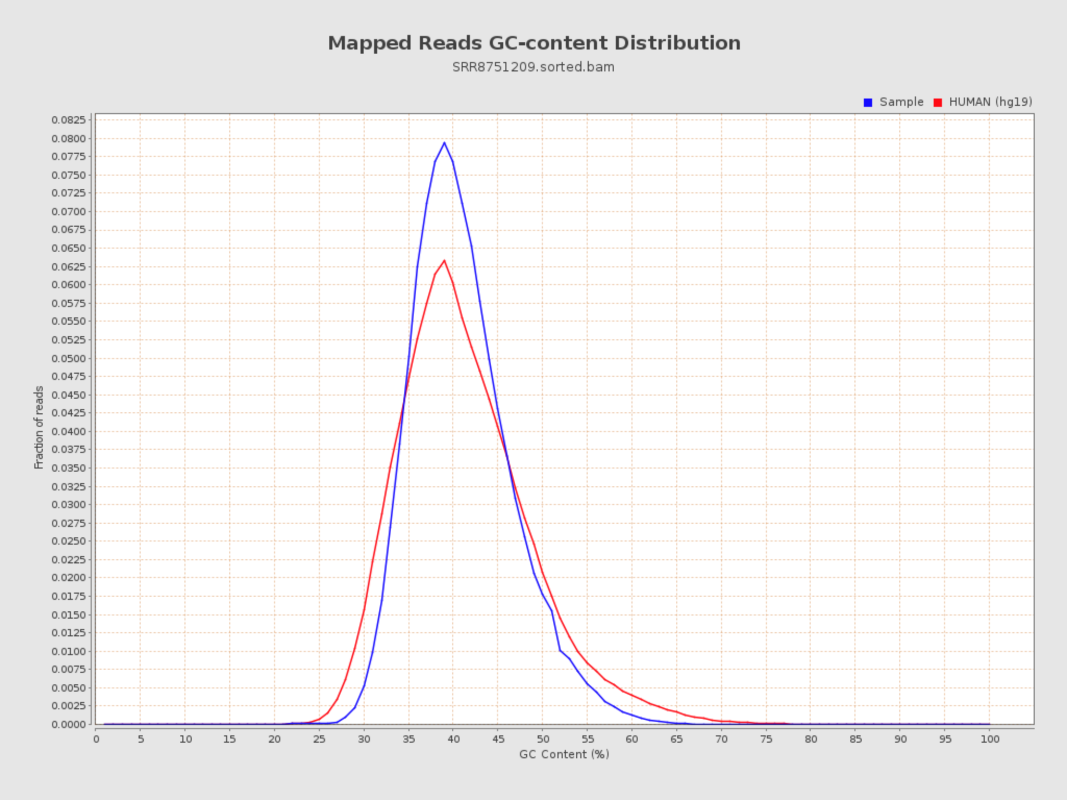
7. Results : Duplication Rate Histogram



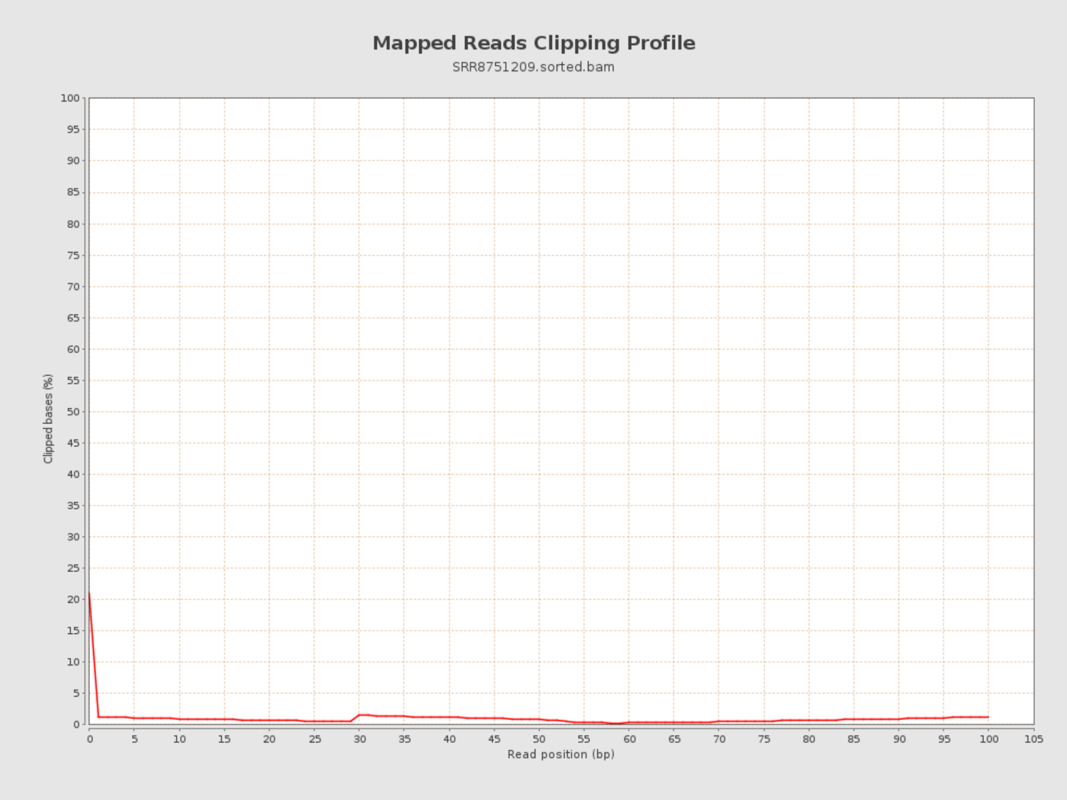
8. Results : Mapped Reads Nucleotide Content



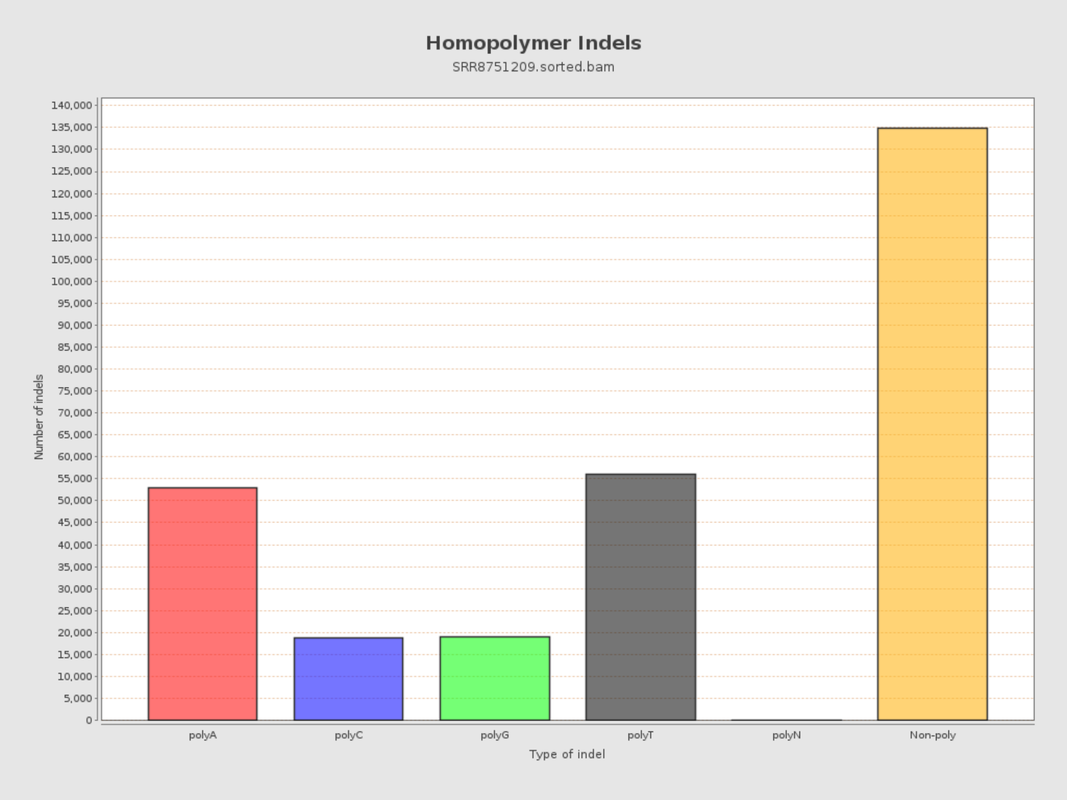
9. Results : Mapped Reads GC-content Distribution



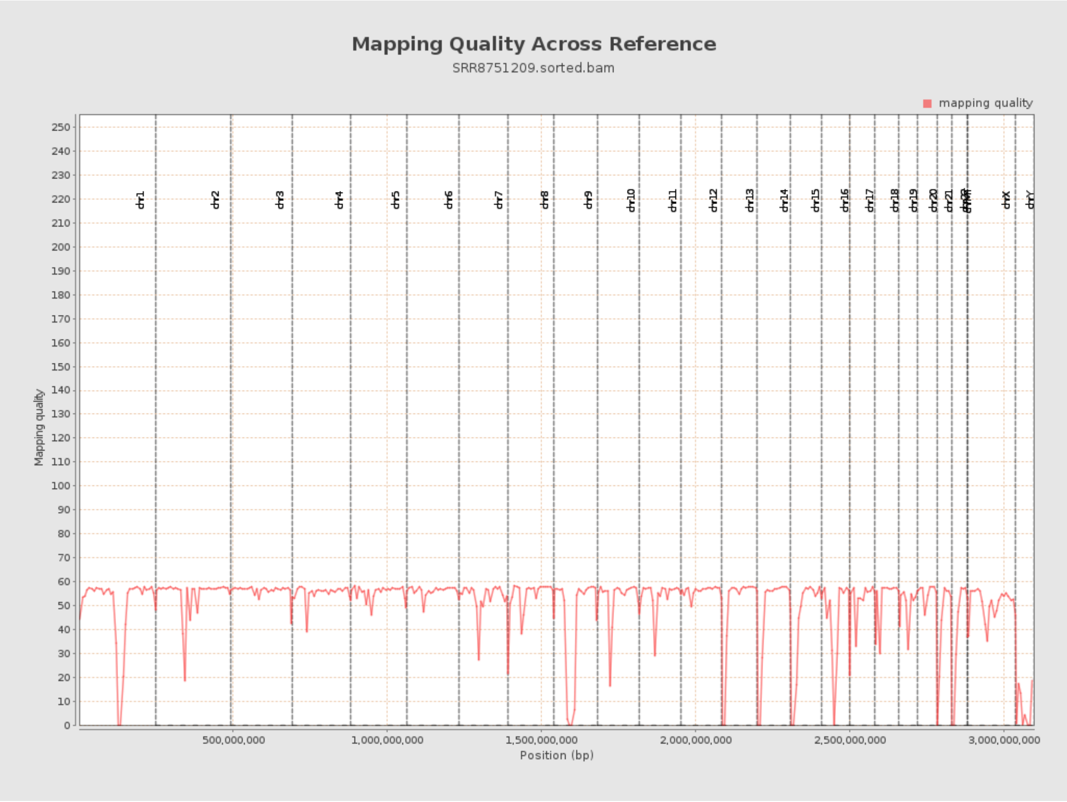
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram