Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 15:31:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8751175.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_SRR8751175 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8751175.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 15:31:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8751175.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,396,861
Mapped reads	3,692,652 / 83.98%
Unmapped reads	704,209 / 16.02%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	221,563 / 5.04%
Read min/max/mean length	30 / 101 / 103.08
Duplicated reads (estimated)	167,569 / 3.81%
Duplication rate	2.25%
Clipped reads	939,361 / 21.36%

2.2. ACGT Content

Number/percentage of A's	106,526,149 / 29.38%
Number/percentage of C's	74,515,127 / 20.55%
Number/percentage of T's	107,143,211 / 29.55%
Number/percentage of G's	74,357,664 / 20.51%
Number/percentage of N's	2,013 / 0%
GC Percentage	41.06%

2.3. Coverage

Mean	0.1172

Standard Deviation	1.5924

2.4. Mapping Quality

Mean Mapping Quality	50.94

2.5. Mismatches and indels

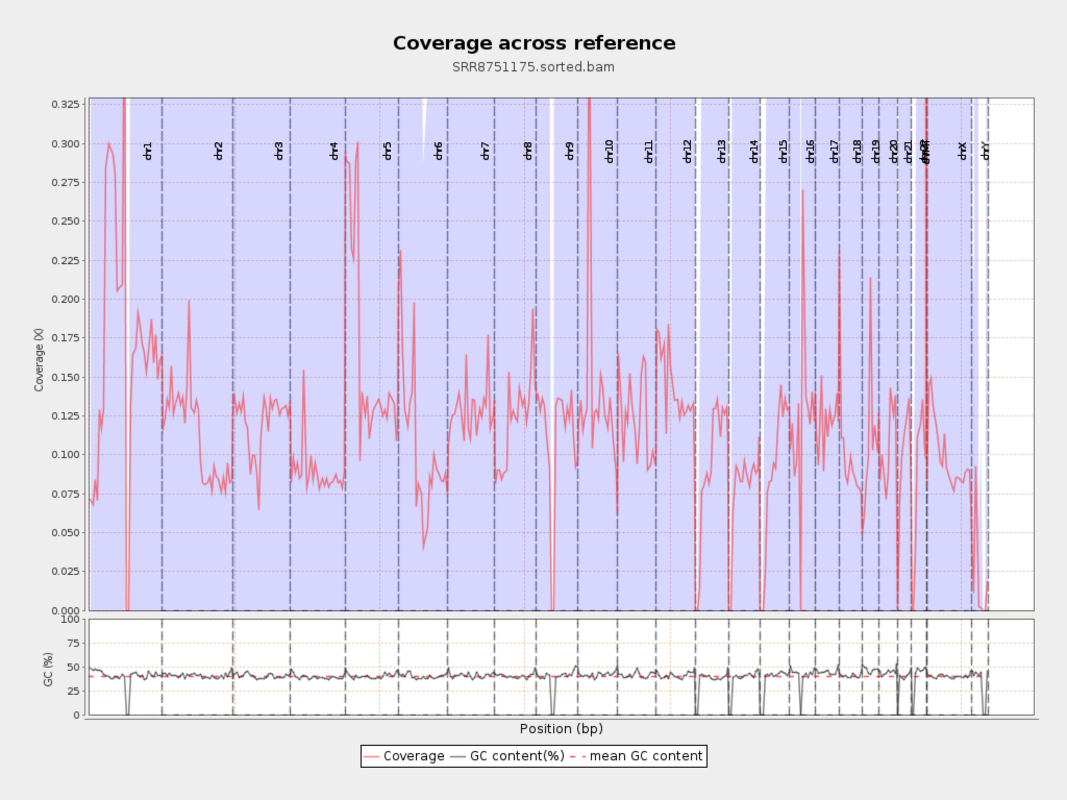
General error rate	0.55%
Mismatches	1,639,039
Insertions	257,654
Mapped reads with at least one insertion	6.69%
Deletions	57,907
Mapped reads with at least one deletion	1.53%
Homopolymer indels	52.79%

2.6. Chromosome stats

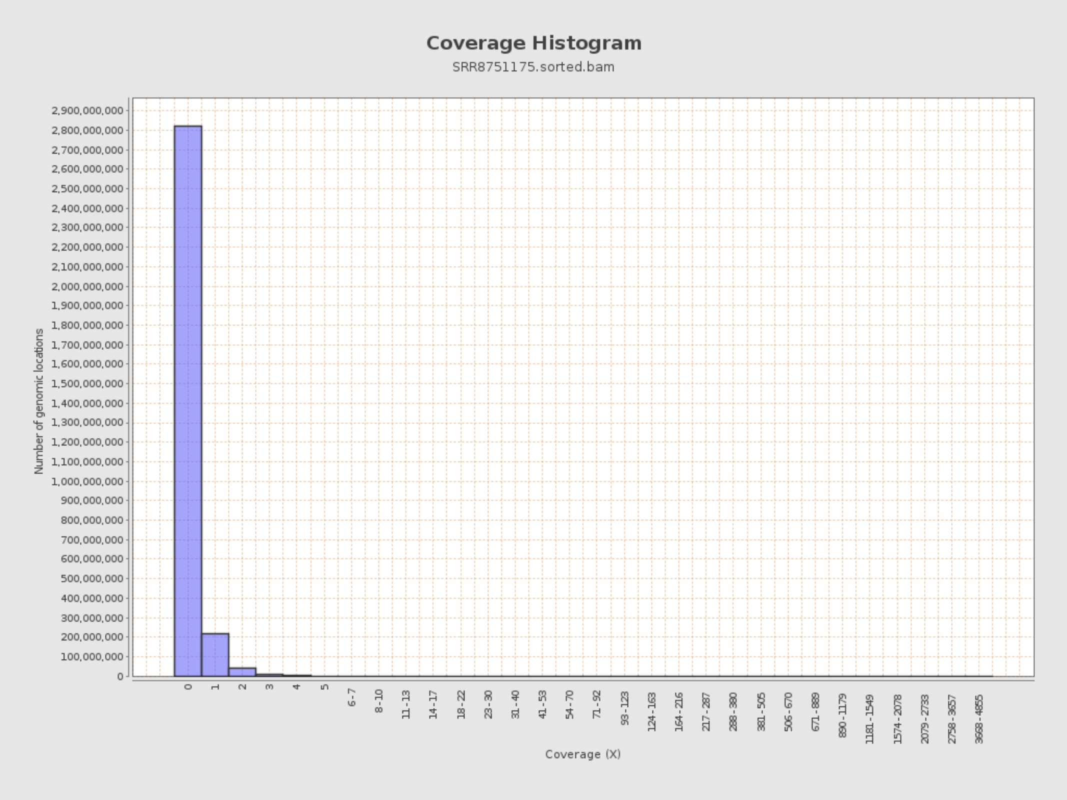
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	42786368	0.1717	4.5518
chr2	243199373	27317048	0.1123	0.6625
chr3	198022430	23954537	0.121	0.5218
chr4	191154276	16934914	0.0886	0.6169
chr5	180915260	29704877	0.1642	0.5001
chr6	171115067	18241847	0.1066	0.928
chr7	159138663	20577261	0.1293	0.9799

chr8	146364022	17950669	0.1226	0.5907
chr9	141213431	15662522	0.1109	0.7229
chr10	135534747	19051968	0.1406	2.3595
chr11	135006516	16548306	0.1226	0.7434
chr12	133851895	19259488	0.1439	0.4692
chr13	115169878	10454552	0.0908	0.3647
chr14	107349540	8143176	0.0759	0.4232
chr15	102531392	9017020	0.0879	0.3633
chr16	90354753	11047926	0.1223	1.1206
chr17	81195210	9776461	0.1204	0.7217
chr18	78077248	7565184	0.0969	1.548
chr19	59128983	6449669	0.1091	3.194
chr20	63025520	6554219	0.104	0.4313
chr21	48129895	4585579	0.0953	0.4969
chr22	51304566	4122514	0.0804	0.3525
chrMT	16571	511344	30.8578	11.6442
chrX	155270560	15318340	0.0987	0.4594
chrY	59373566	1136465	0.0191	0.8801

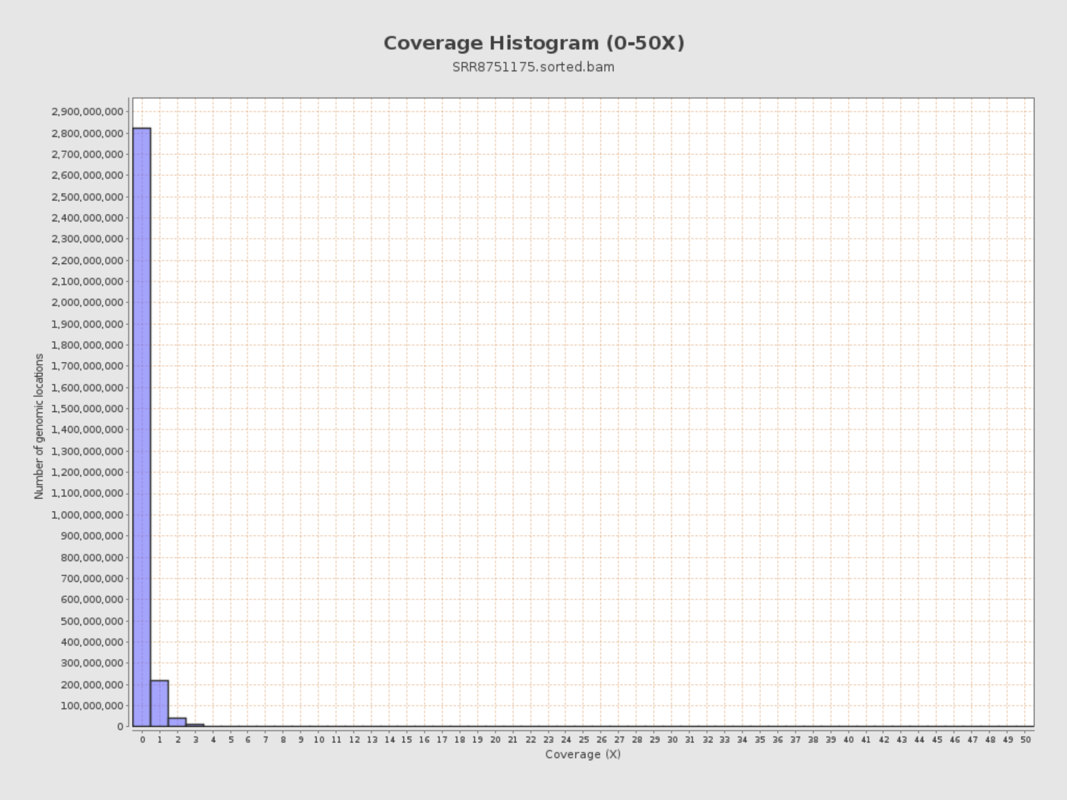
3. Results : Coverage across reference



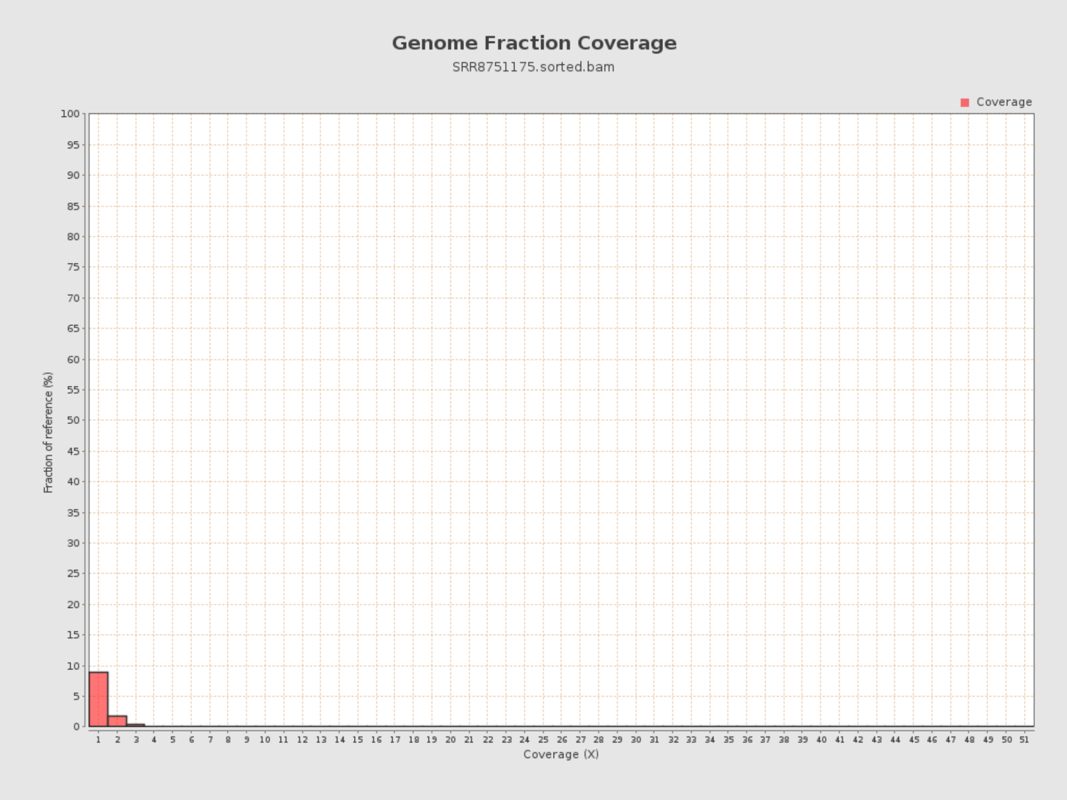
4. Results : Coverage Histogram



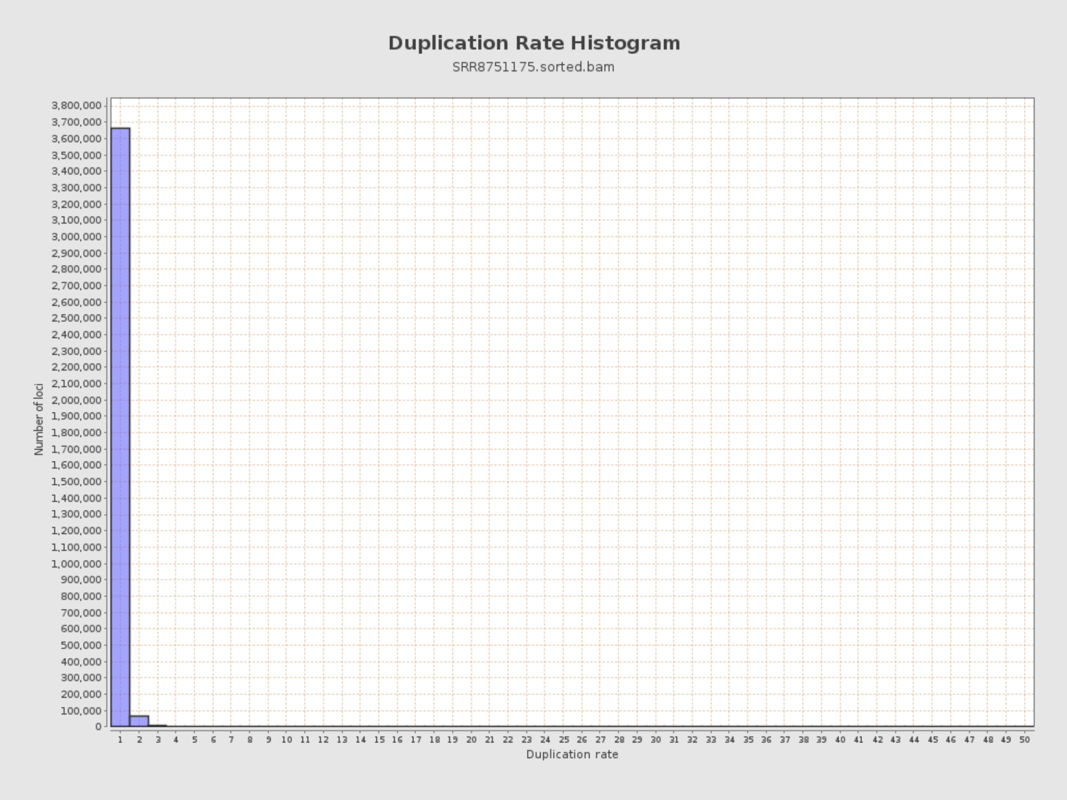
5. Results : Coverage Histogram (0-50X)



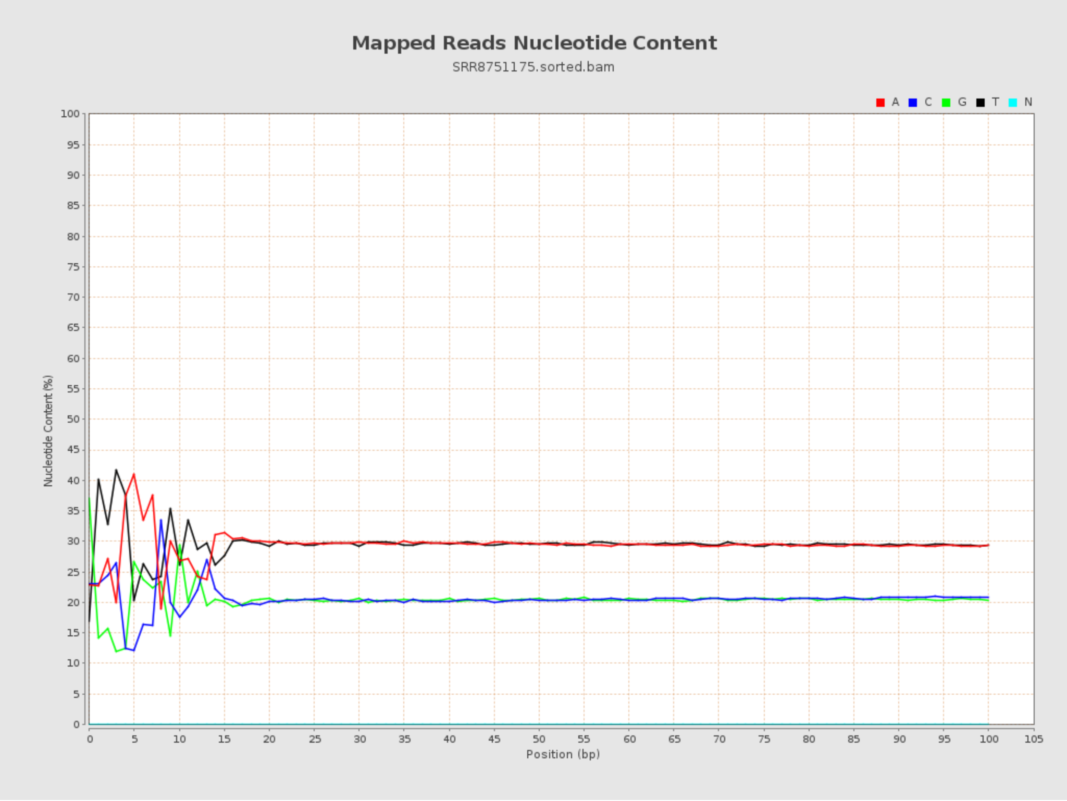
6. Results : Genome Fraction Coverage



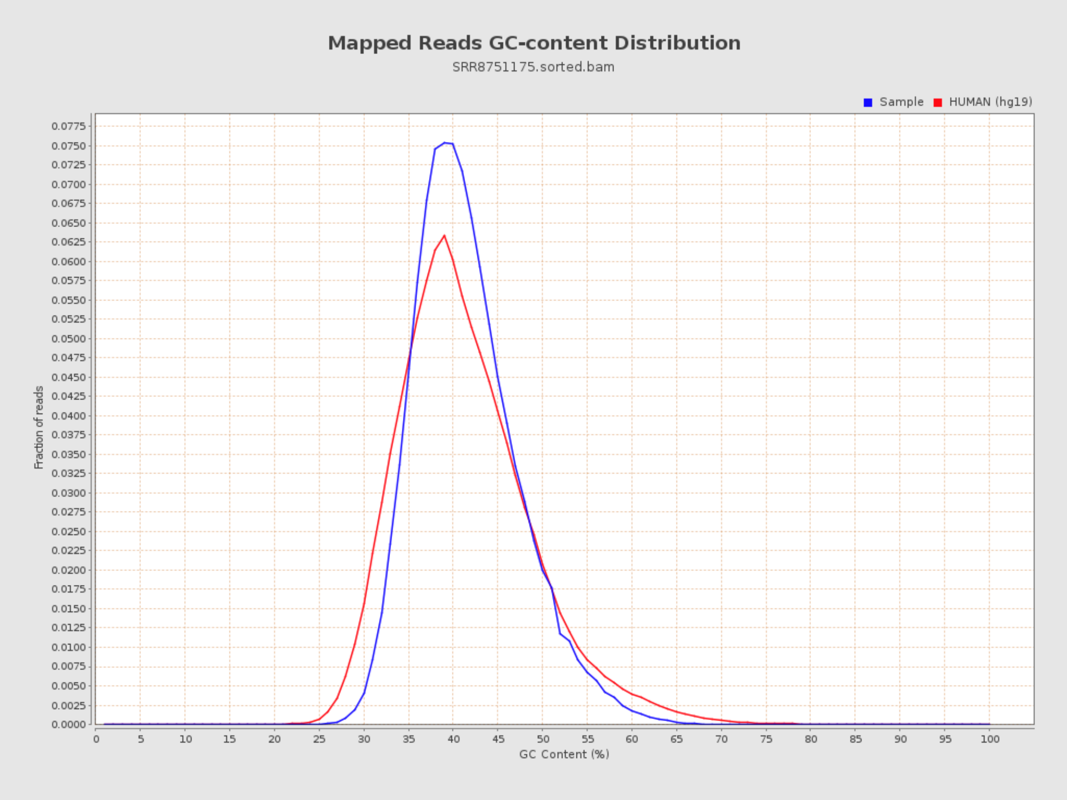
7. Results : Duplication Rate Histogram



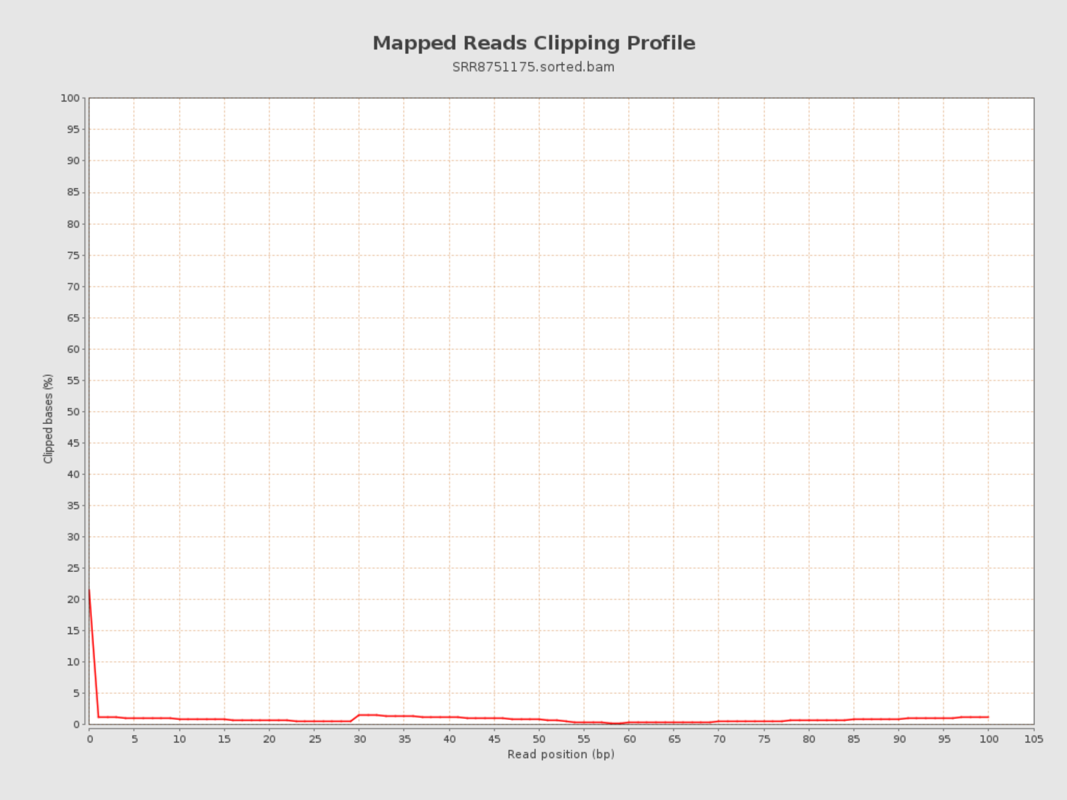
8. Results : Mapped Reads Nucleotide Content



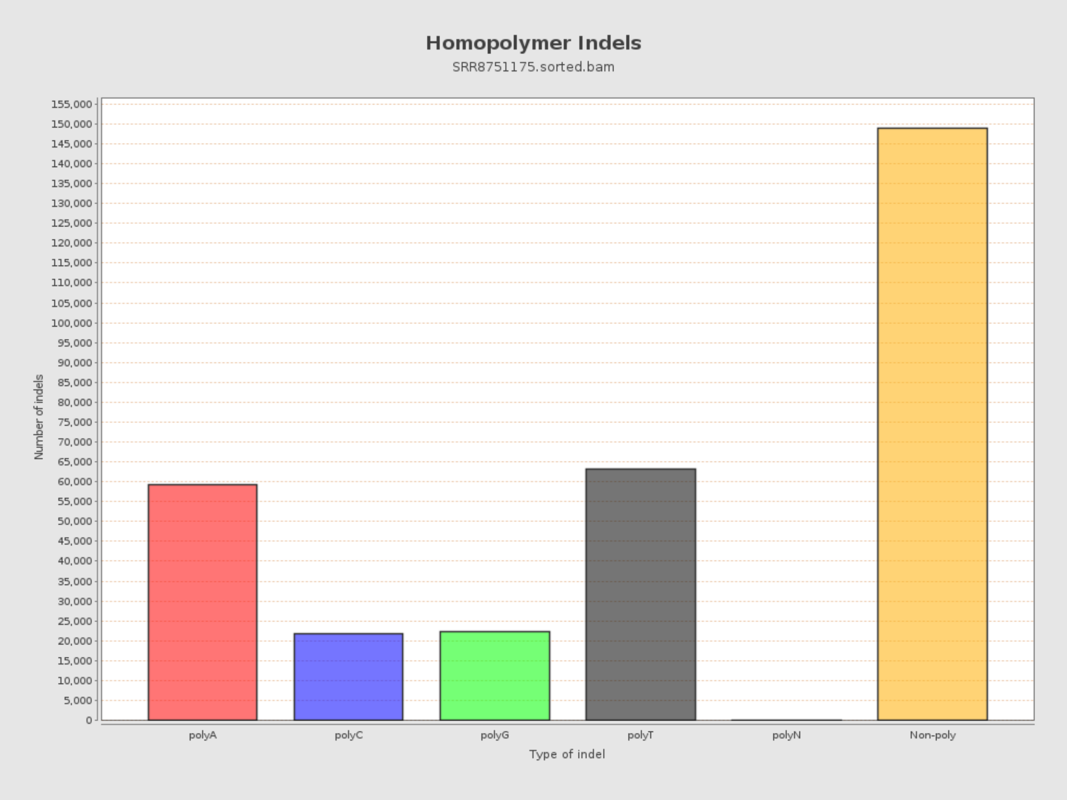
9. Results : Mapped Reads GC-content Distribution



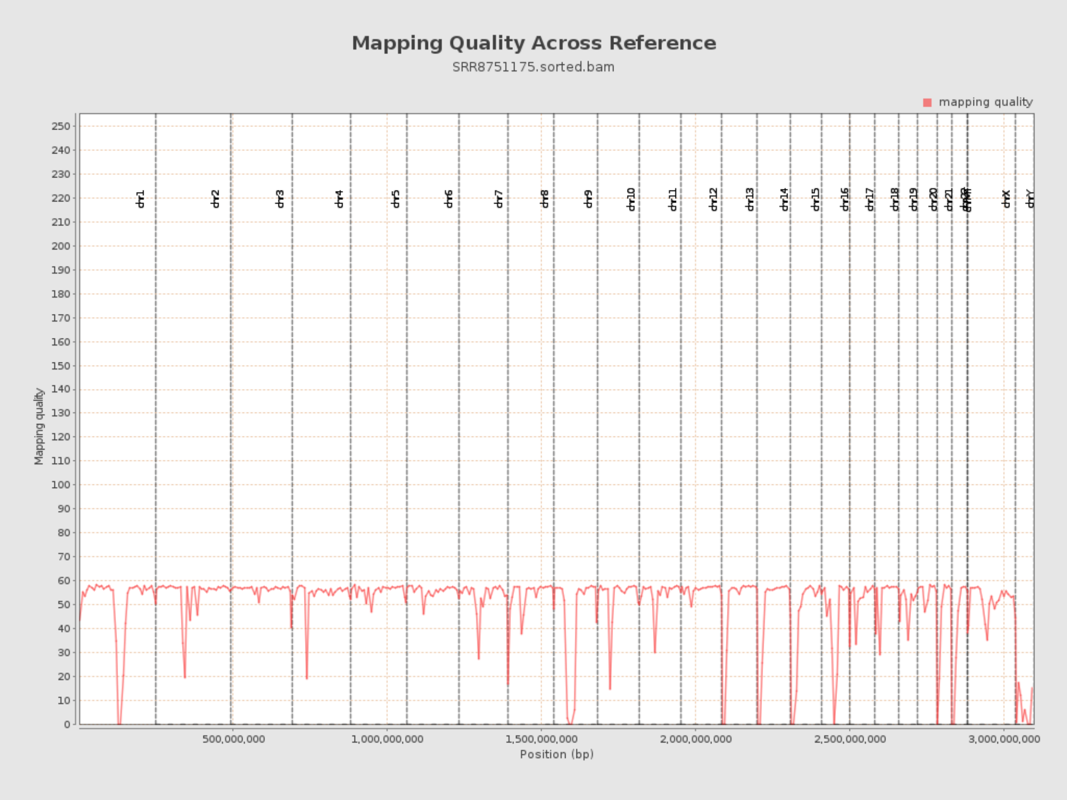
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram