Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/18 13:44:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1163152.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_SRR1163152 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1163152.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 18 13:44:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1163152.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	149,748,722
Mapped reads	148,335,243 / 99.06%
Unmapped reads	1,413,479 / 0.94%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	781,730 / 0.52%
Read min/max/mean length	30 / 100 / 100.21
Duplicated reads (estimated)	94,516,128 / 63.12%
Duplication rate	48.21%
Clipped reads	12,402,686 / 8.28%

2.2. ACGT Content

Number/percentage of A's	3,583,294,733 / 24.48%
Number/percentage of C's	3,735,880,544 / 25.53%
Number/percentage of T's	3,588,681,332 / 24.52%
Number/percentage of G's	3,727,067,199 / 25.47%
Number/percentage of N's	479,682 / 0%
GC Percentage	50.99%

2.3. Coverage

Mean	4.7282

Standard Deviation	59.177

2.4. Mapping Quality

Mean Mapping Quality	49.32

2.5. Mismatches and indels

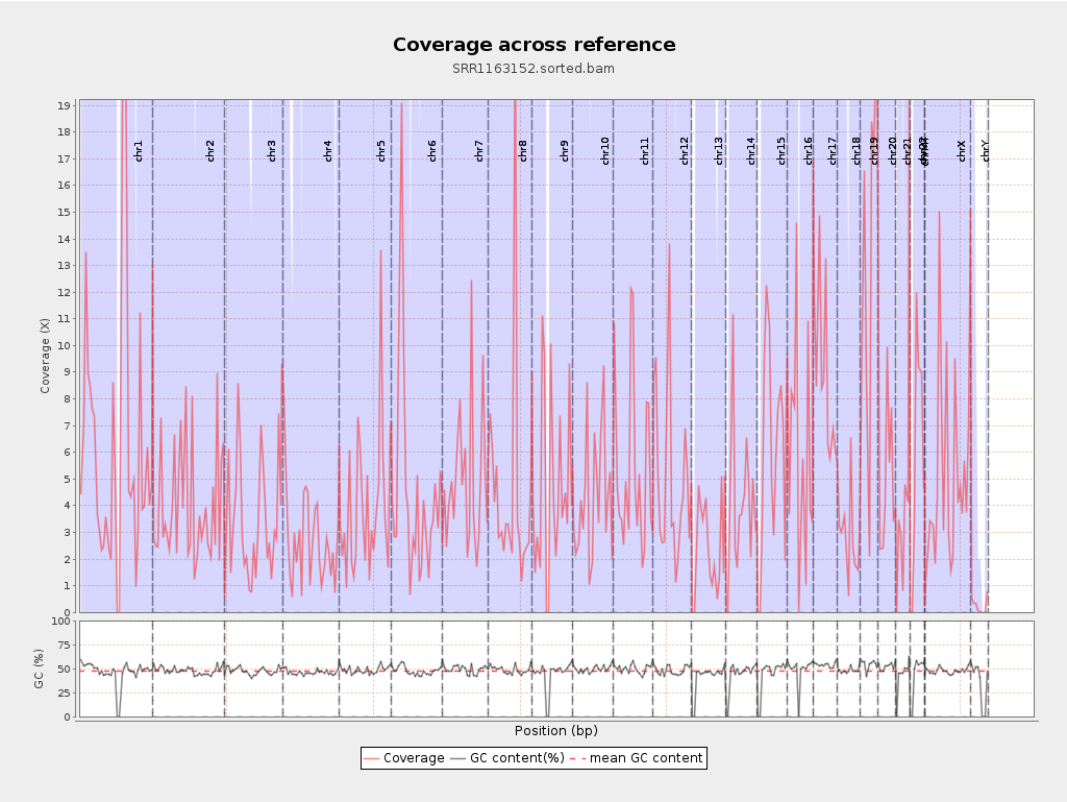
General error rate	0.32%
Mismatches	45,089,076
Insertions	1,047,951
Mapped reads with at least one insertion	0.7%
Deletions	734,109
Mapped reads with at least one deletion	0.49%
Homopolymer indels	45.53%

2.6. Chromosome stats

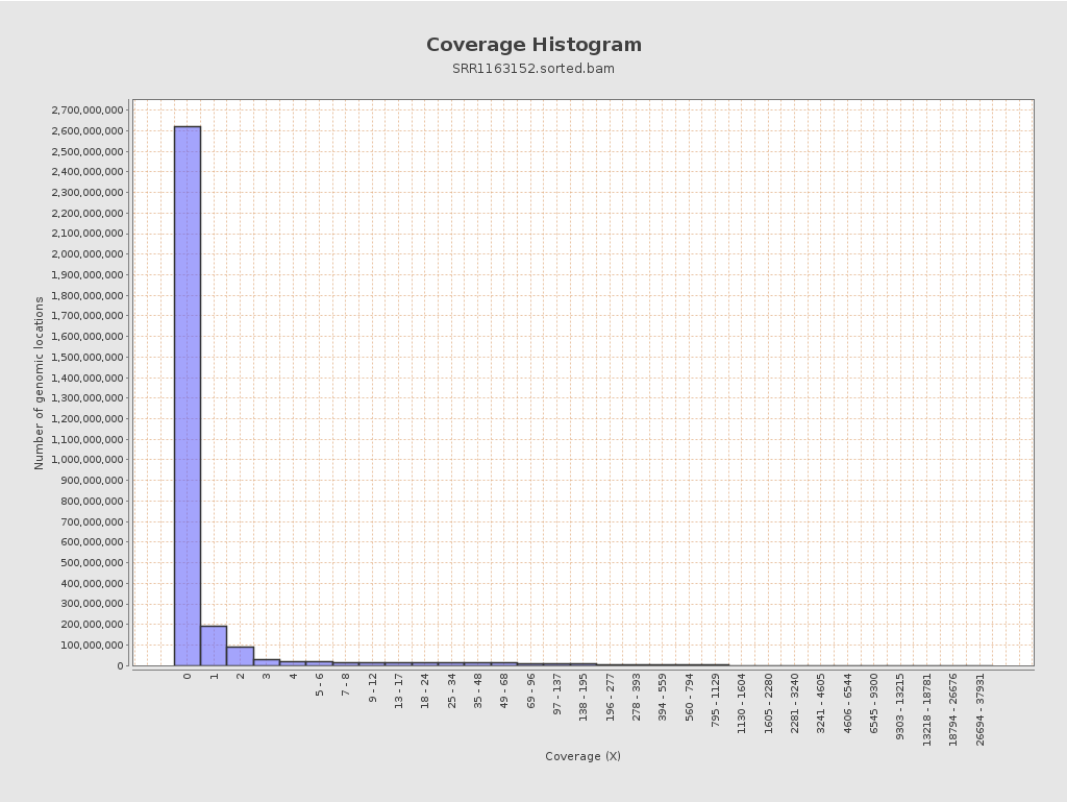
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	1603859531	6.4347	66.0298
chr2	243199373	972325427	3.9981	46.448
chr3	198022430	702186554	3.546	42.6021
chr4	191154276	523561506	2.7389	38.4638
chr5	180915260	729730998	4.0336	58.553
chr6	171115067	768175885	4.4892	53.397
chr7	159138663	782591731	4.9177	56.3408

chr8	146364022	651880971	4.4538	76.614
chr9	141213431	651936477	4.6167	58.6392
chr10	135534747	592135170	4.3689	49.9857
chr11	135006516	743657393	5.5083	56.9996
chr12	133851895	684284215	5.1122	55.2871
chr13	115169878	273784931	2.3772	33.8691
chr14	107349540	427312429	3.9806	45.6941
chr15	102531392	599765632	5.8496	58.2321
chr16	90354753	535695697	5.9288	53.2541
chr17	81195210	720166759	8.8696	76.8876
chr18	78077248	221656469	2.8389	38.1142
chr19	59128983	789574811	13.3534	95.1952
chr20	63025520	334562104	5.3084	57.6293
chr21	48129895	219886465	4.5686	166.0804
chr22	51304566	304723550	5.9395	61.0573
chrMT	16571	3620	0.2185	0.5891
chrX	155270560	789041223	5.0817	62.289
chrY	59373566	14639503	0.2466	14.4555

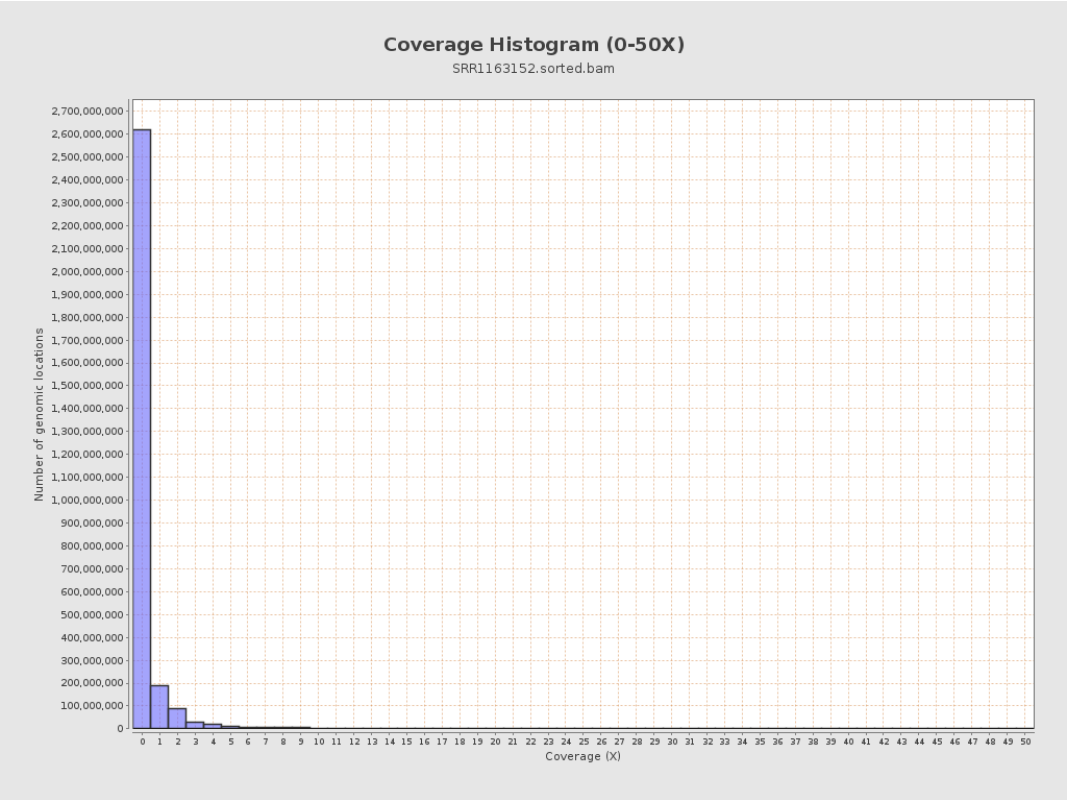
3. Results : Coverage across reference



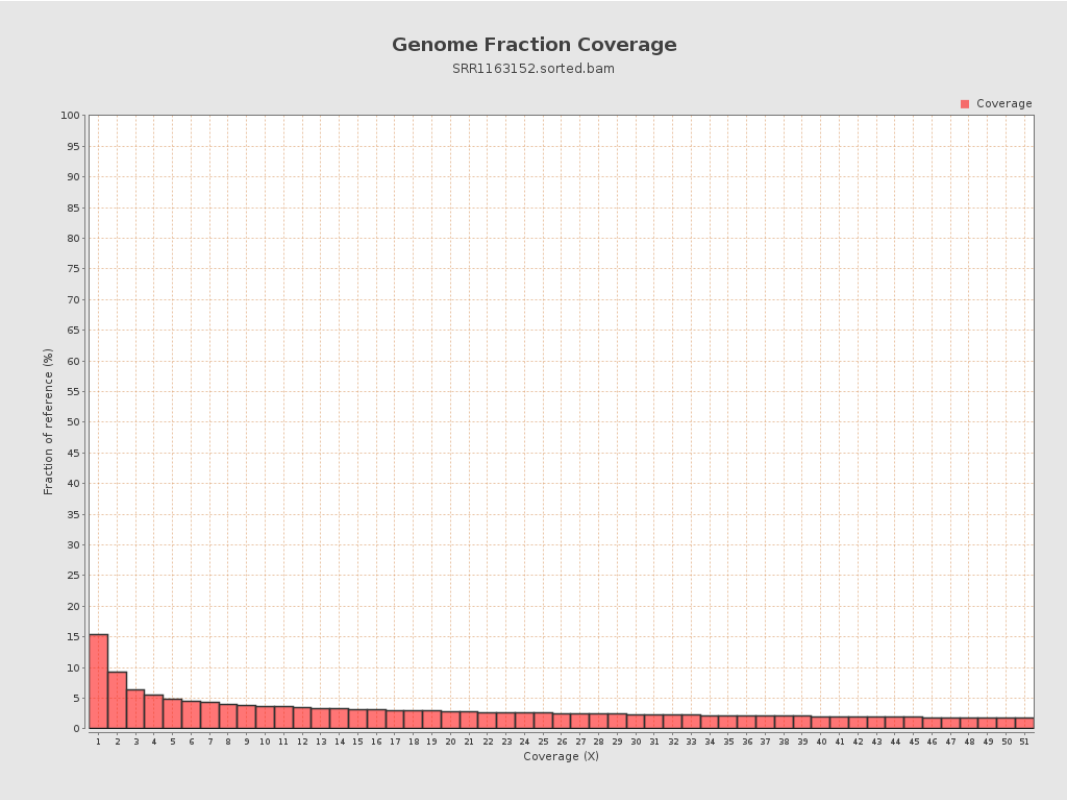
4. Results : Coverage Histogram



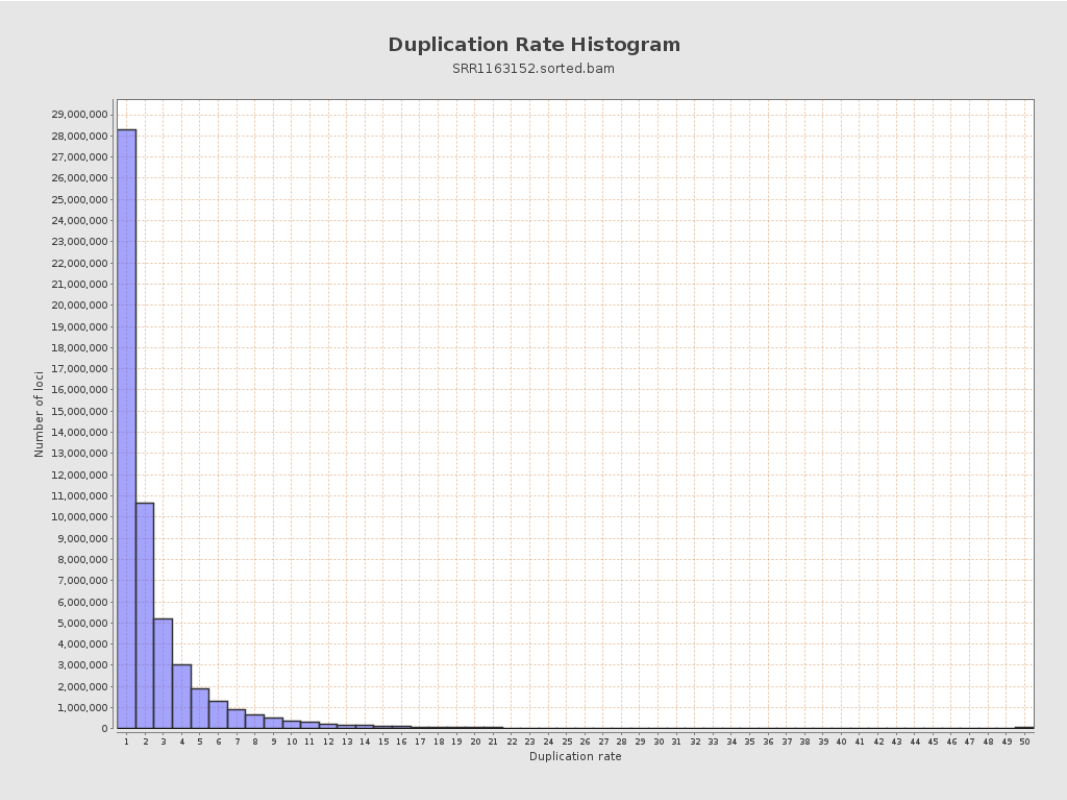
5. Results : Coverage Histogram (0-50X)



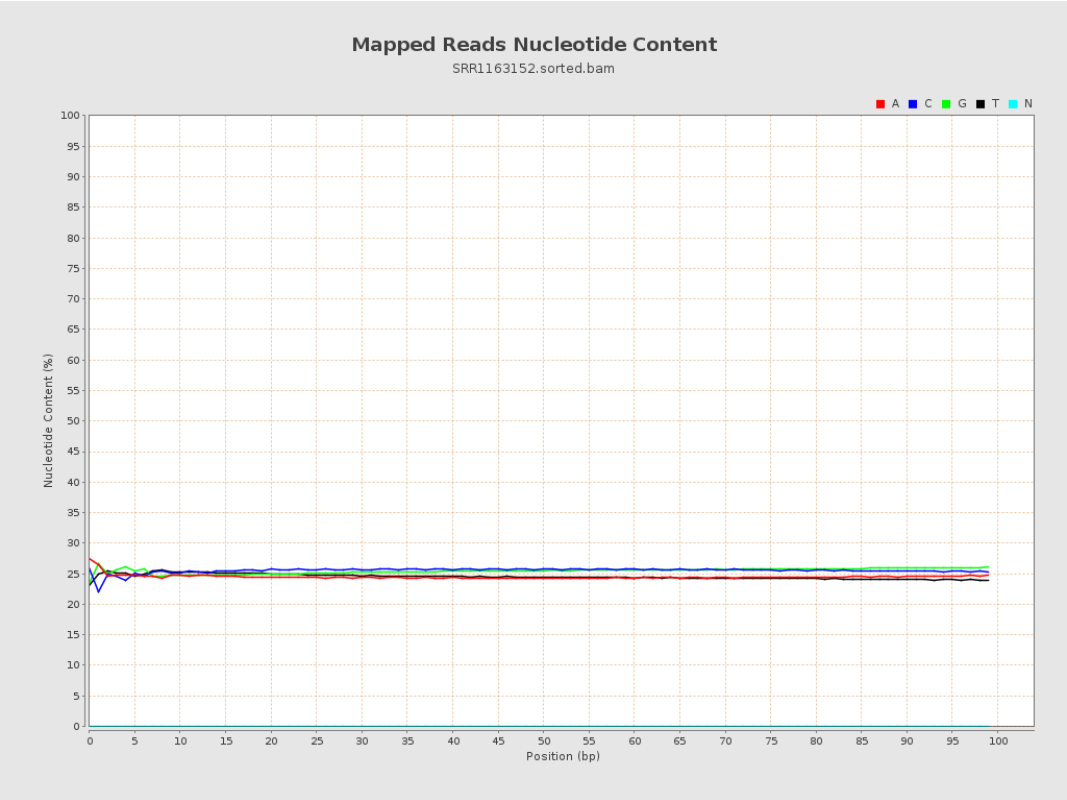
6. Results : Genome Fraction Coverage



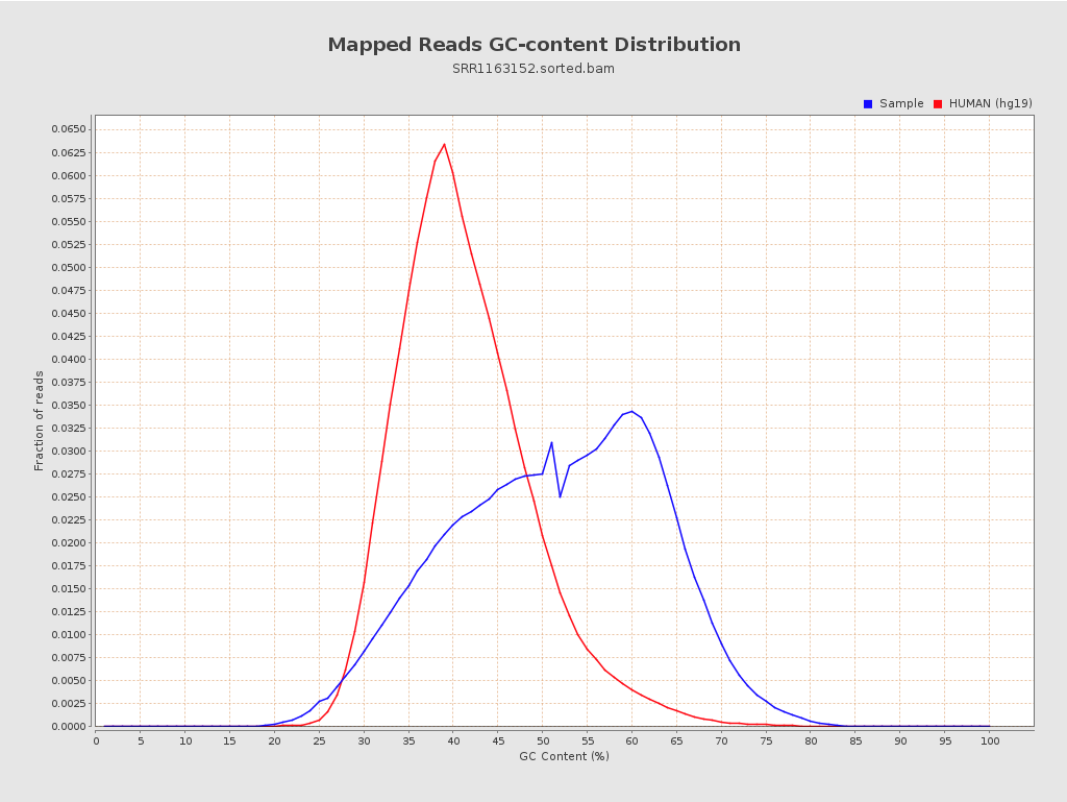
7. Results : Duplication Rate Histogram



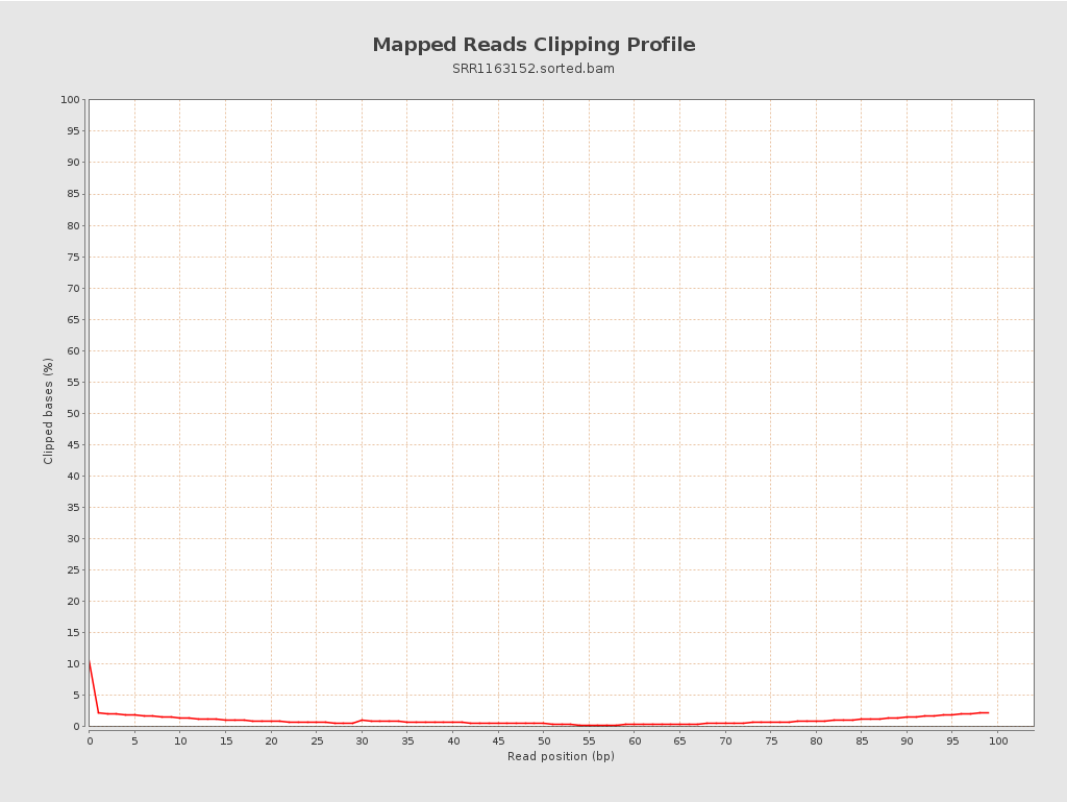
8. Results : Mapped Reads Nucleotide Content



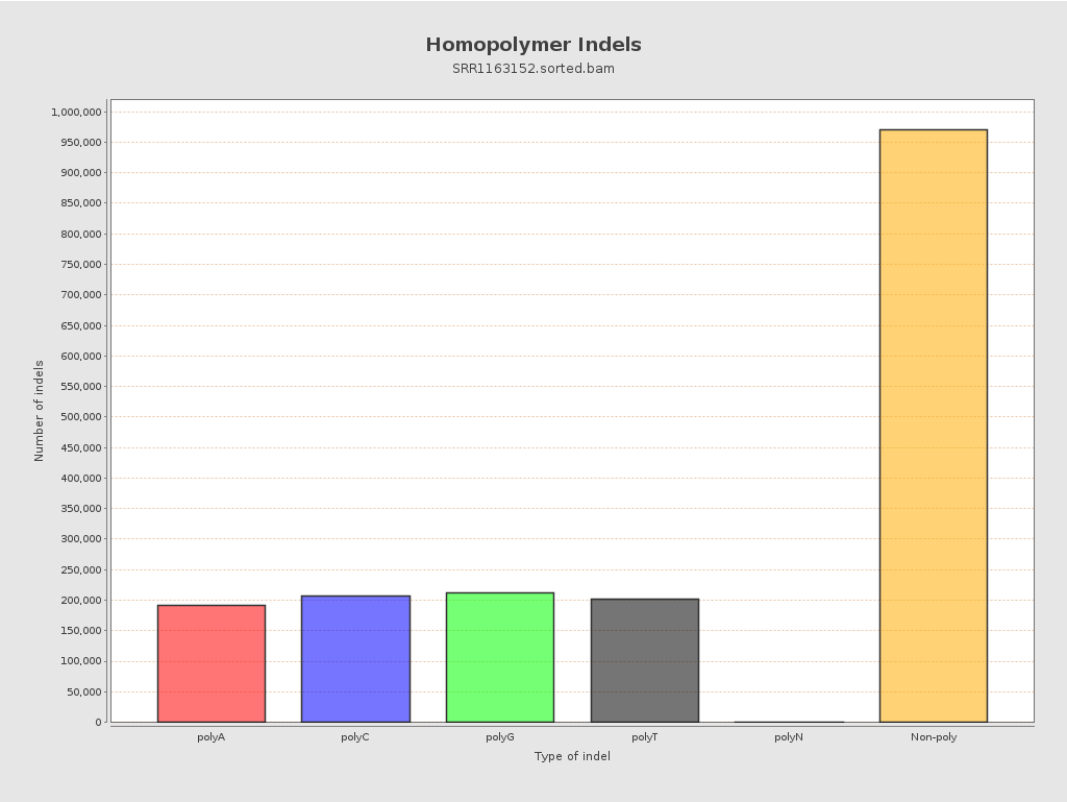
9. Results : Mapped Reads GC-content Distribution



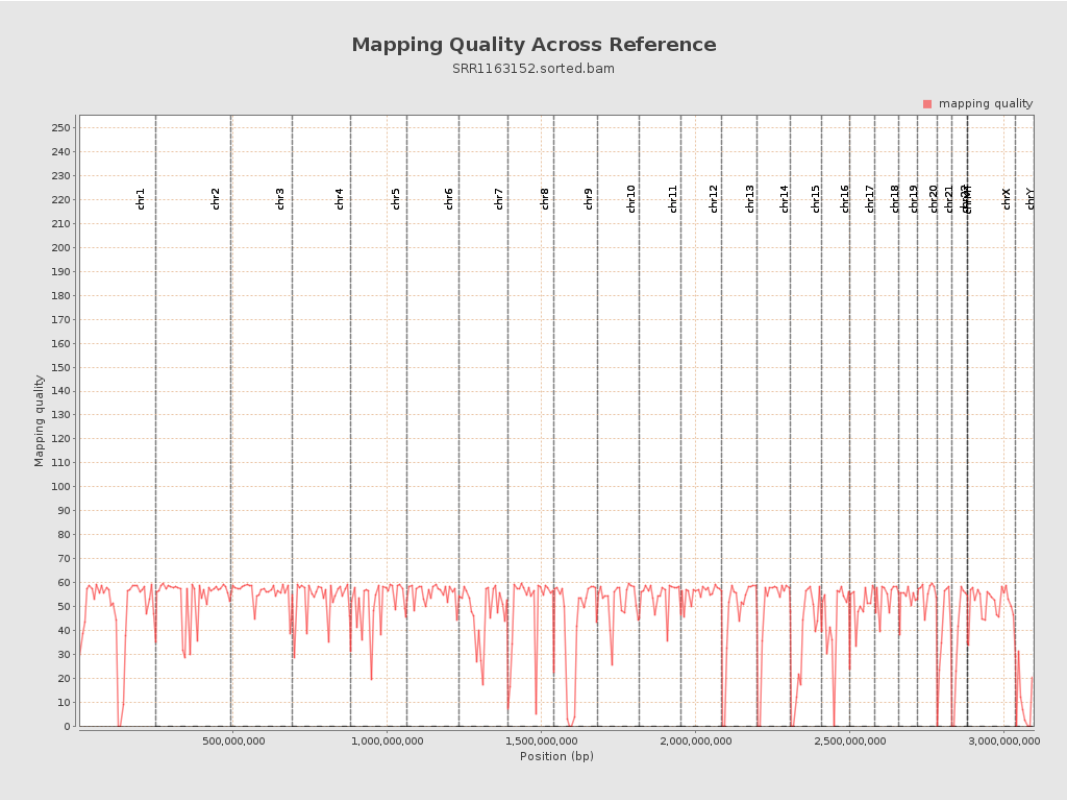
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram