Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/19 00:03:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1163162.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_SRR1163162 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1163162.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 19 00:03:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1163162.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	36,641,548
Mapped reads	36,075,286 / 98.45%
Unmapped reads	566,262 / 1.55%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	412,573 / 1.13%
Read min/max/mean length	30 / 100 / 100.46
Duplicated reads (estimated)	15,835,199 / 43.22%
Duplication rate	40.64%
Clipped reads	2,219,648 / 6.06%

2.2. ACGT Content

Number/percentage of A's	943,071,095 / 26.29%
Number/percentage of C's	850,682,350 / 23.72%
Number/percentage of T's	955,640,970 / 26.64%
Number/percentage of G's	834,572,581 / 23.27%
Number/percentage of N's	2,647,330 / 0.07%
GC Percentage	46.99%

2.3. Coverage

Mean	1.1588

Standard Deviation	11.2722

2.4. Mapping Quality

Mean Mapping Quality	49.53

2.5. Mismatches and indels

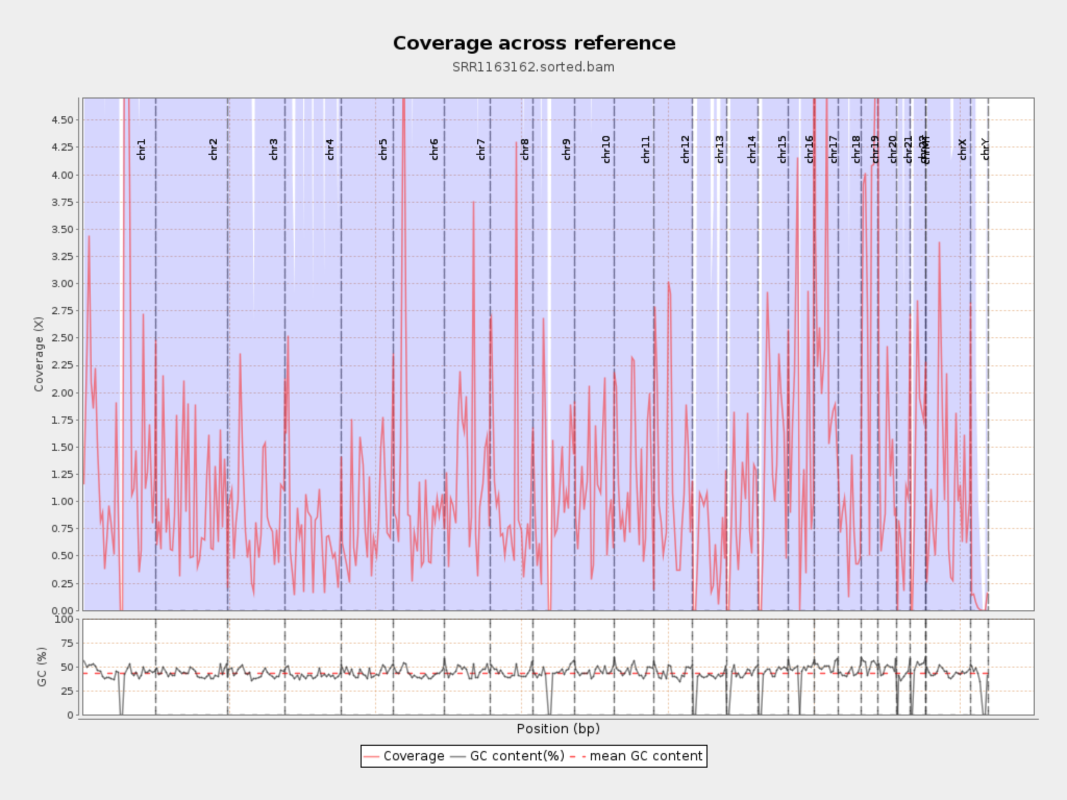
General error rate	0.78%
Mismatches	27,577,431
Insertions	268,121
Mapped reads with at least one insertion	0.73%
Deletions	314,438
Mapped reads with at least one deletion	0.86%
Homopolymer indels	46.07%

2.6. Chromosome stats

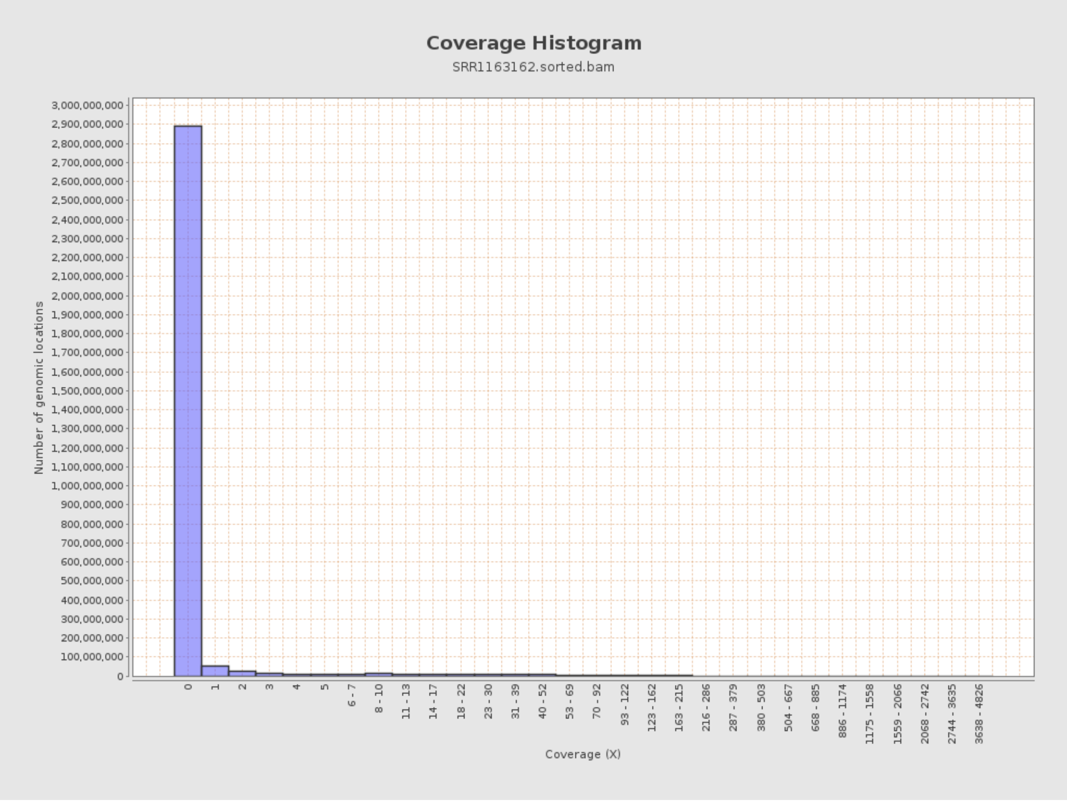
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	401640114	1.6114	14.1103
chr2	243199373	244277893	1.0044	9.6293
chr3	198022430	173212673	0.8747	7.8963
chr4	191154276	138630709	0.7252	9.5838
chr5	180915260	166101862	0.9181	11.6508
chr6	171115067	188965837	1.1043	10.4115
chr7	159138663	203906232	1.2813	13.534

chr8	146364022	153822185	1.051	13.6973
chr9	141213431	145186368	1.0281	8.9301
chr10	135534747	146478629	1.0807	9.5421
chr11	135006516	167394496	1.2399	9.7721
chr12	133851895	174619180	1.3046	10.3053
chr13	115169878	64995605	0.5643	6.5643
chr14	107349540	99270466	0.9247	8.4637
chr15	102531392	142602074	1.3908	11.1064
chr16	90354753	140712804	1.5573	12.6084
chr17	81195210	194548534	2.3961	16.052
chr18	78077248	57754568	0.7397	7.9587
chr19	59128983	209512144	3.5433	20.4411
chr20	63025520	77179979	1.2246	10.4876
chr21	48129895	43136501	0.8963	11.6186
chr22	51304566	75713903	1.4758	11.6895
chrMT	16571	19840	1.1973	1.4236
chrX	155270560	173706559	1.1187	13.1707
chrY	59373566	3861996	0.065	6.4611

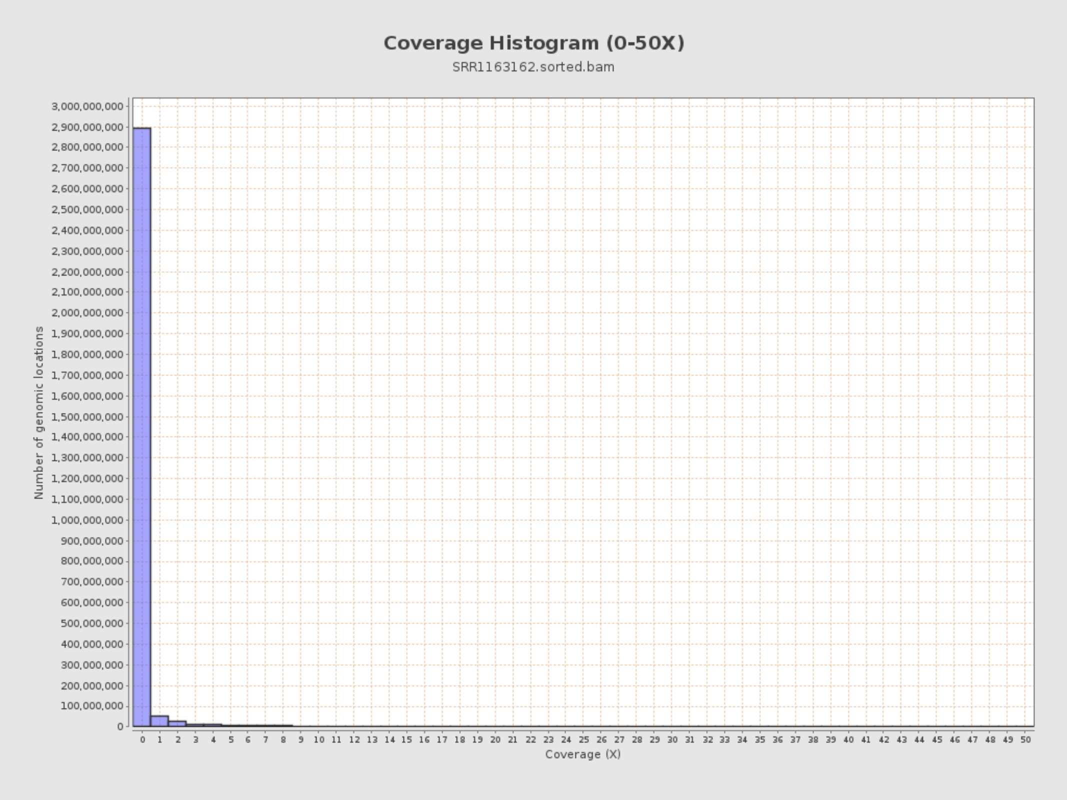
3. Results : Coverage across reference



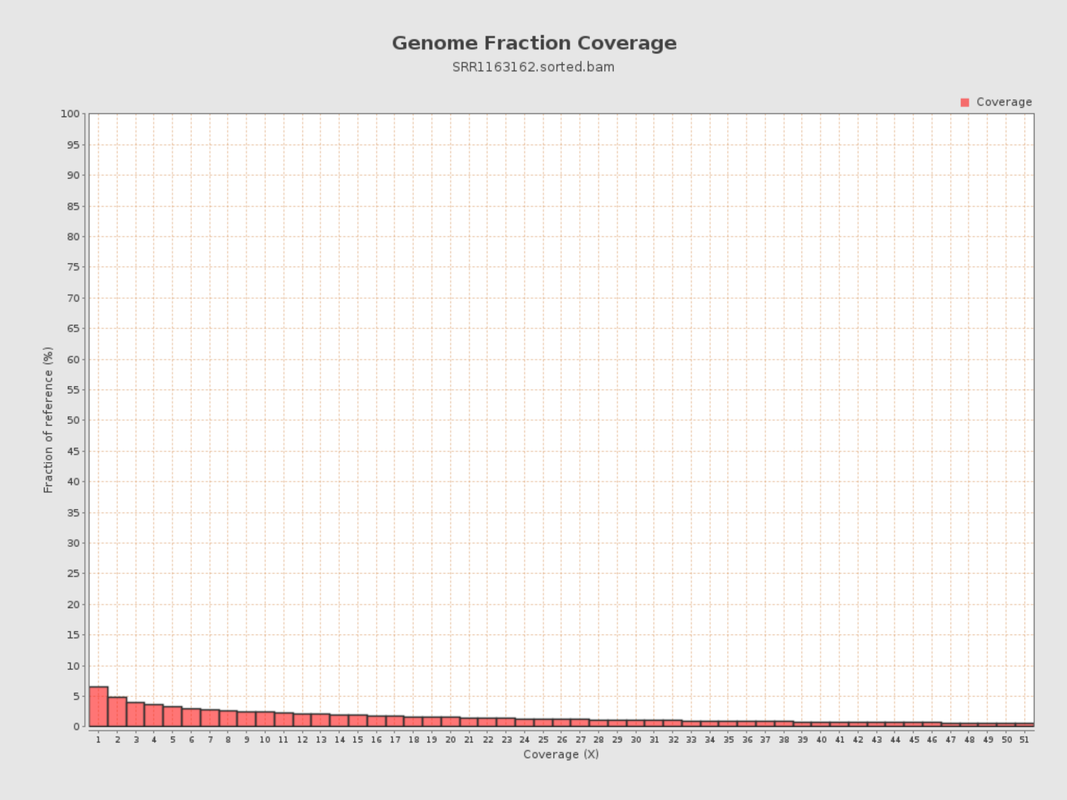
4. Results : Coverage Histogram



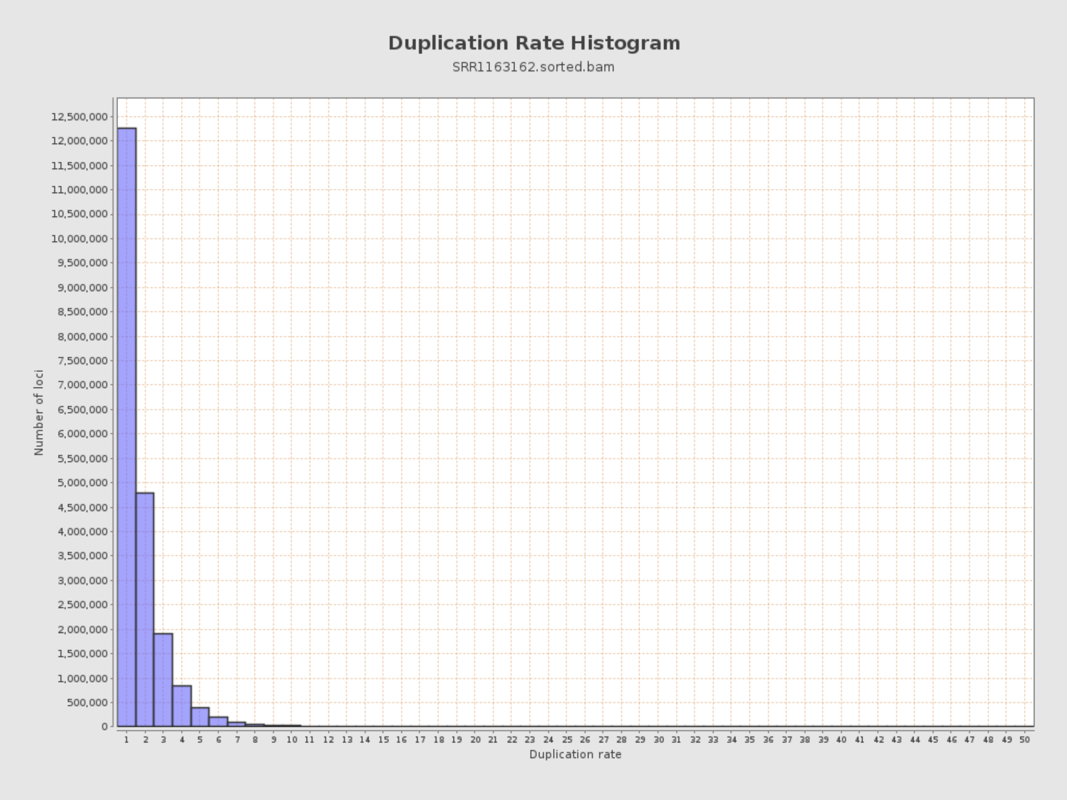
5. Results : Coverage Histogram (0-50X)



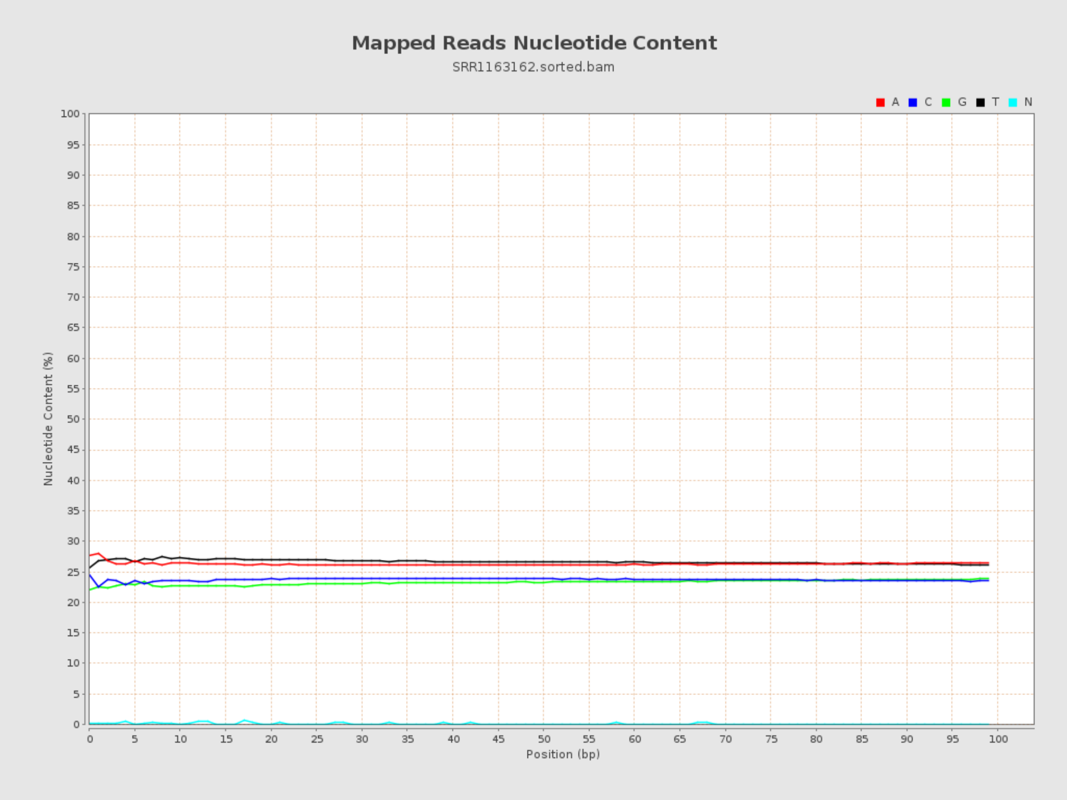
6. Results : Genome Fraction Coverage



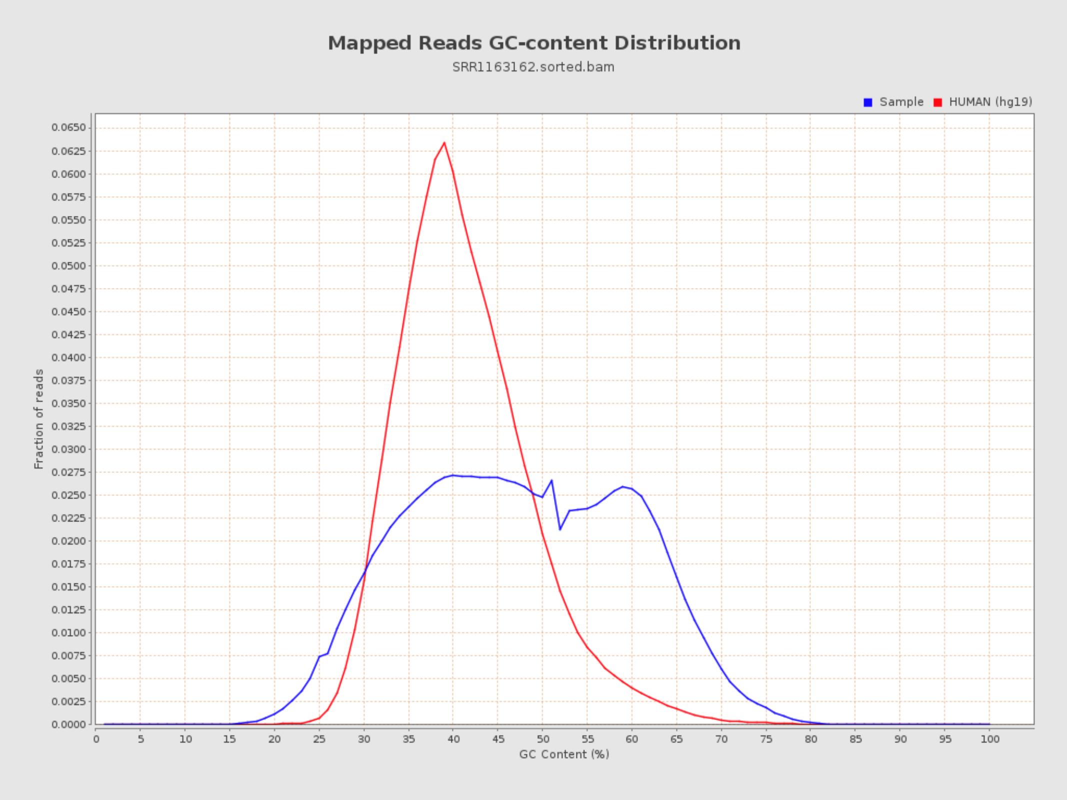
7. Results : Duplication Rate Histogram



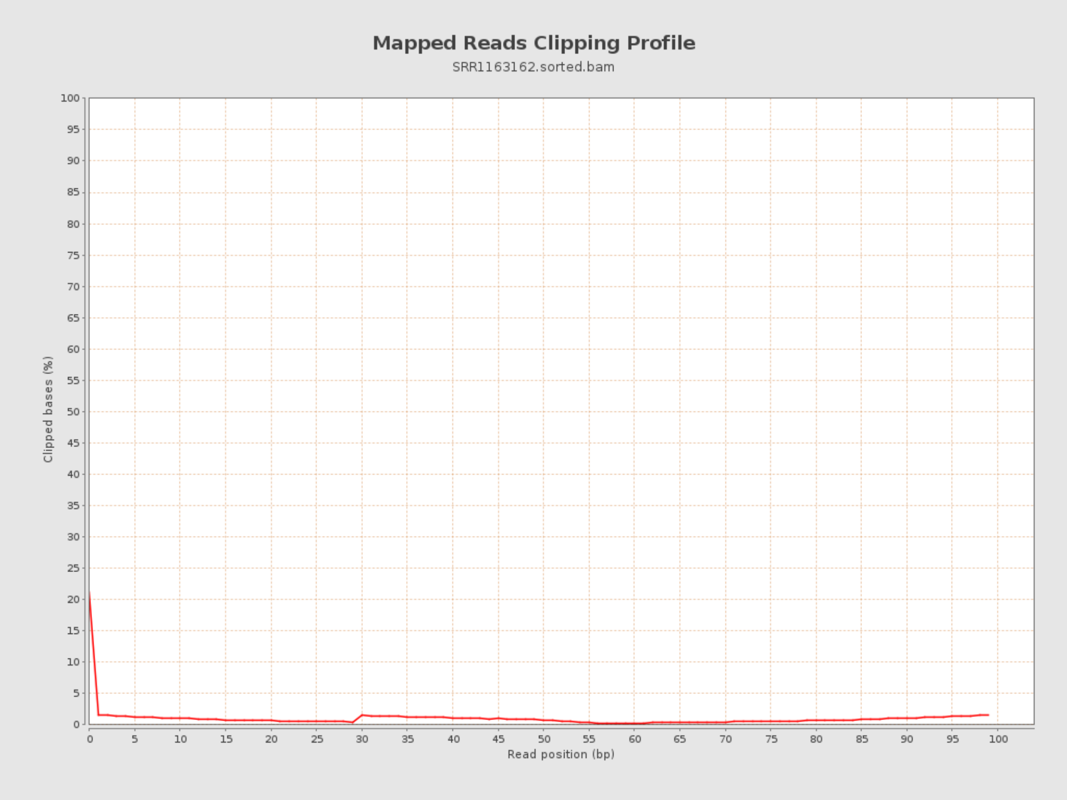
8. Results : Mapped Reads Nucleotide Content



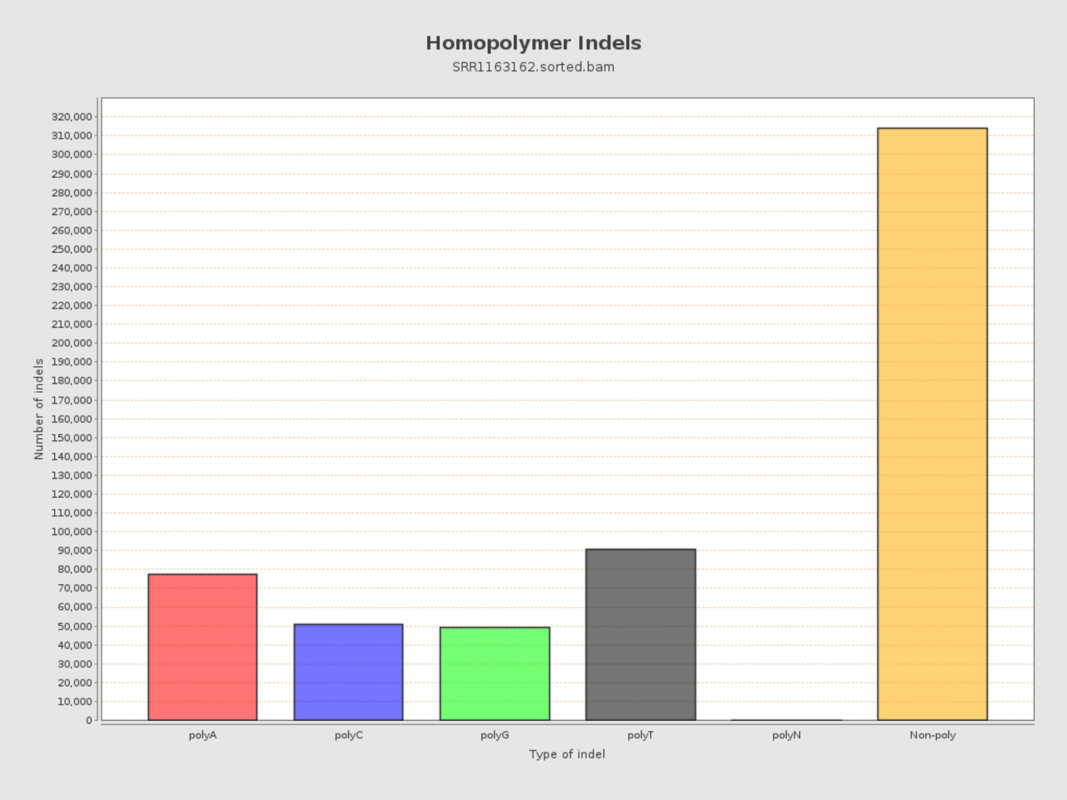
9. Results : Mapped Reads GC-content Distribution



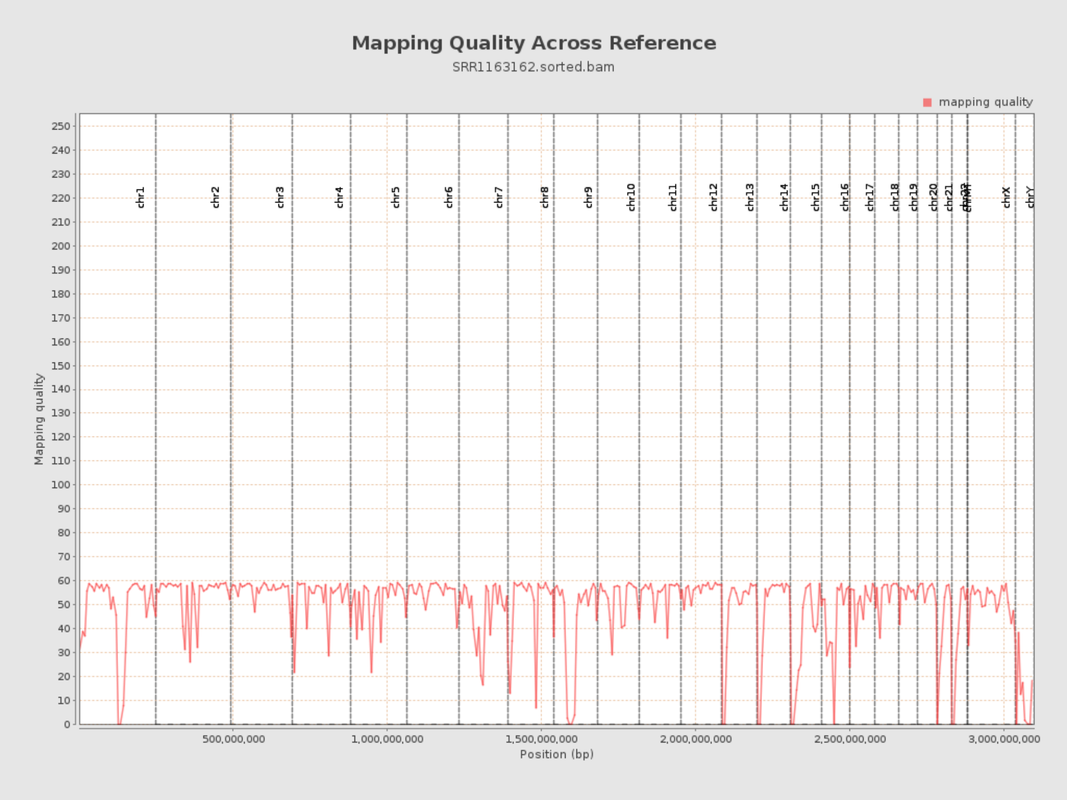
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram