Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 18:44:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081099.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_SRR3081099 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081099.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 18:44:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081099.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,612,093
Mapped reads	2,398,596 / 91.83%
Unmapped reads	213,497 / 8.17%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,599 / 0.83%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	121,433 / 4.65%
Duplication rate	3.45%
Clipped reads	1,014,255 / 38.83%

2.2. ACGT Content

Number/percentage of A's	44,814,790 / 27.69%
Number/percentage of C's	30,260,544 / 18.7%
Number/percentage of T's	50,726,395 / 31.35%
Number/percentage of G's	36,015,423 / 22.26%
Number/percentage of N's	1,757 / 0%
GC Percentage	40.96%

2.3. Coverage

Mean	0.0523

Standard Deviation	0.5931

2.4. Mapping Quality

Mean Mapping Quality	45.69

2.5. Mismatches and indels

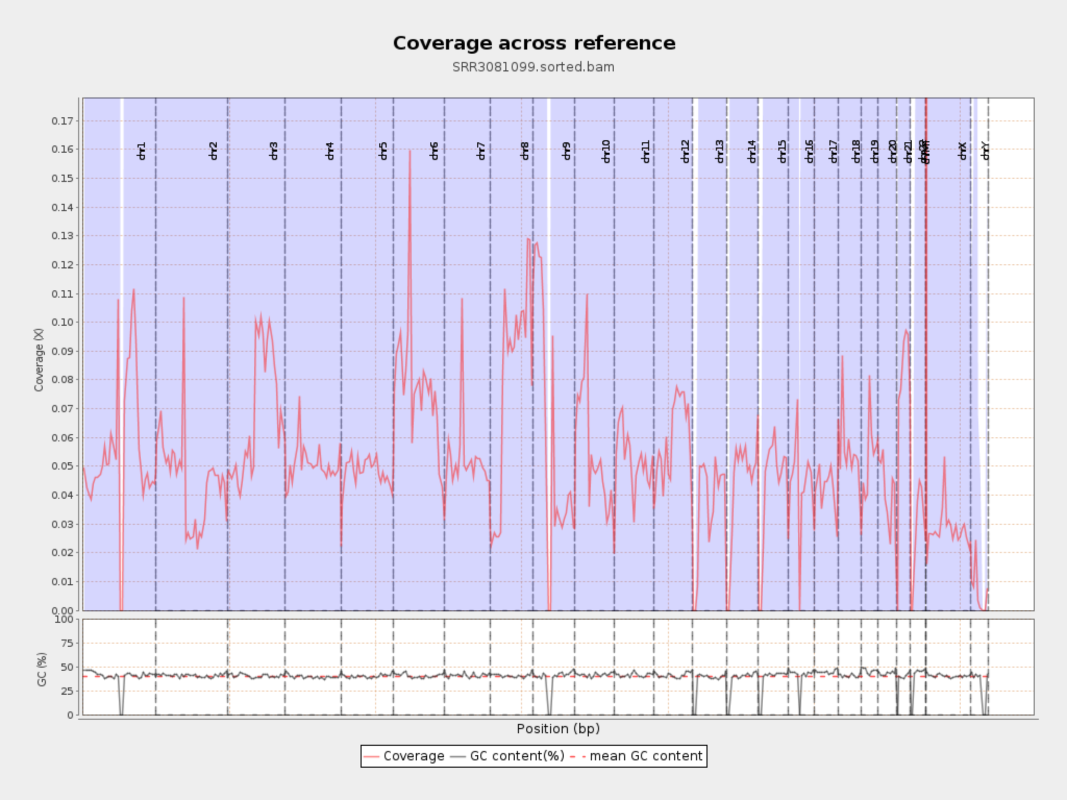
General error rate	0.93%
Mismatches	1,484,249
Insertions	12,626
Mapped reads with at least one insertion	0.52%
Deletions	35,718
Mapped reads with at least one deletion	1.47%
Homopolymer indels	46.19%

2.6. Chromosome stats

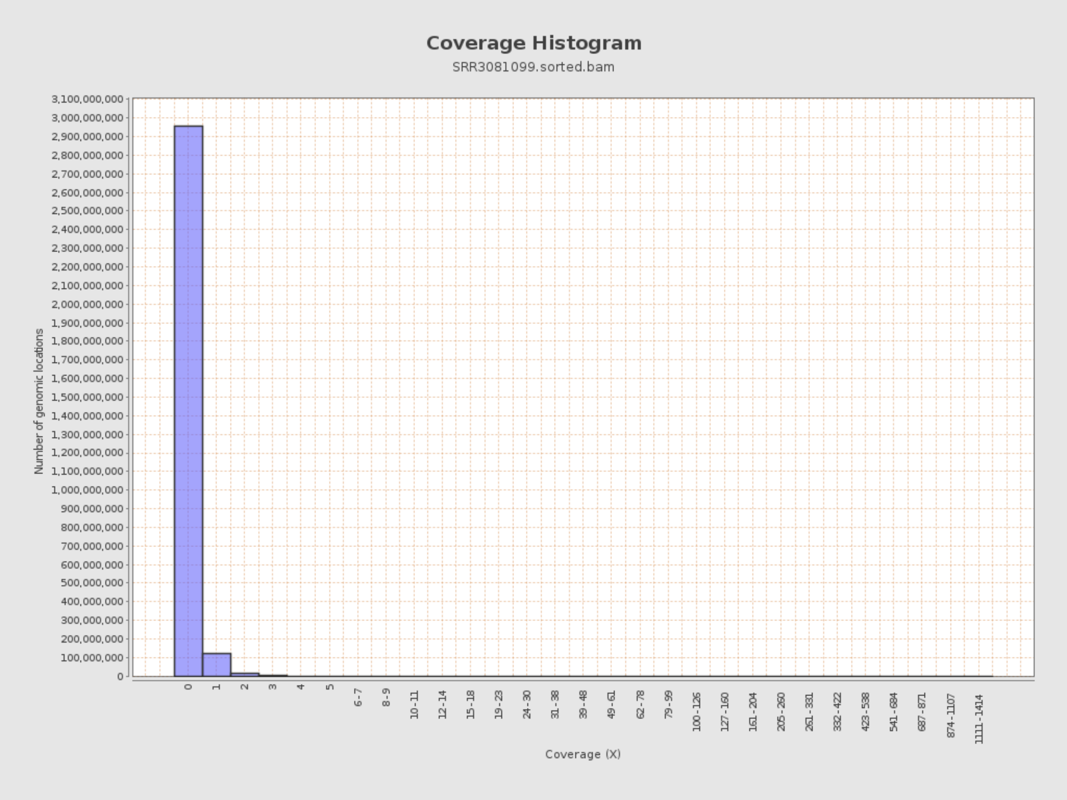
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13761115	0.0552	1.1514
chr2	243199373	11083369	0.0456	0.5917
chr3	198022430	13408511	0.0677	0.3011
chr4	191154276	9734798	0.0509	0.2715
chr5	180915260	8722438	0.0482	0.258
chr6	171115067	13488113	0.0788	0.7318
chr7	159138663	8359041	0.0525	0.6908

chr8	146364022	11700724	0.0799	0.5875
chr9	141213431	8386621	0.0594	0.6957
chr10	135534747	7517743	0.0555	0.5551
chr11	135006516	7065405	0.0523	0.446
chr12	133851895	8007064	0.0598	0.3121
chr13	115169878	4160153	0.0361	0.2114
chr14	107349540	4645823	0.0433	0.3661
chr15	102531392	4363077	0.0426	0.2328
chr16	90354753	3847565	0.0426	0.3954
chr17	81195210	3481809	0.0429	0.264
chr18	78077248	4378767	0.0561	1.3759
chr19	59128983	3121459	0.0528	0.8184
chr20	63025520	2629413	0.0417	0.2719
chr21	48129895	3734825	0.0776	0.3845
chr22	51304566	1400724	0.0273	0.1828
chrMT	16571	81454	4.9155	3.303
chrX	155270560	4400175	0.0283	0.2818
chrY	59373566	396777	0.0067	0.1713

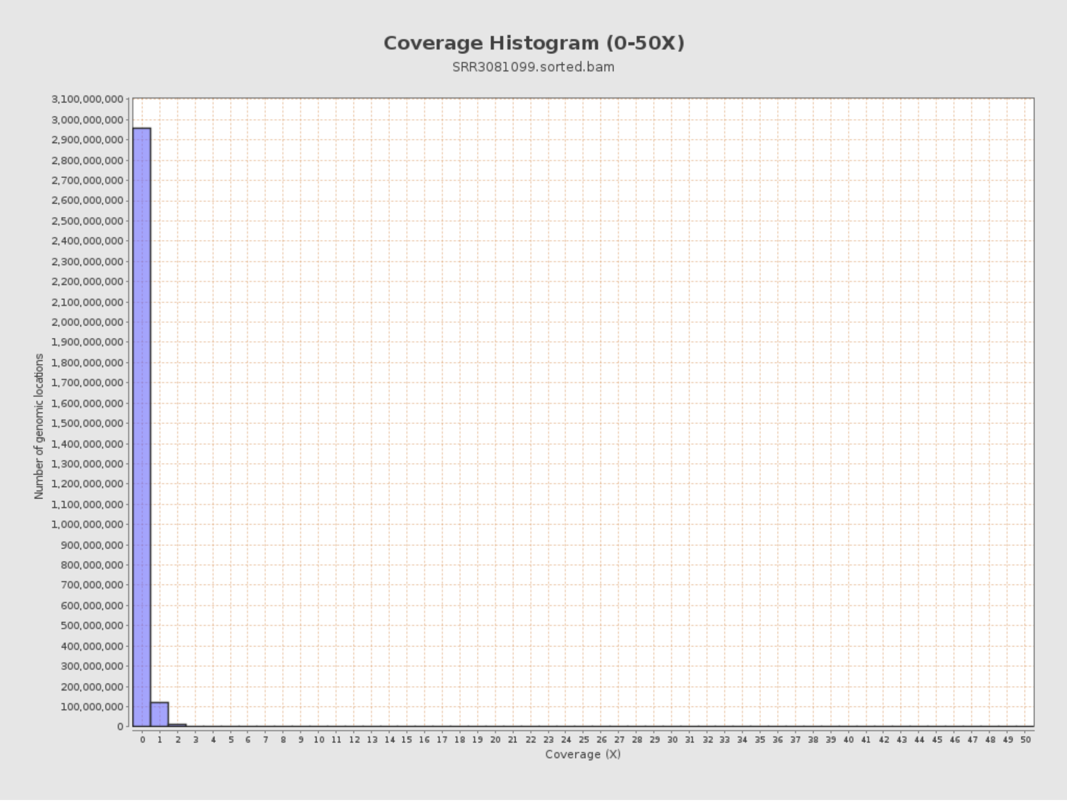
3. Results : Coverage across reference



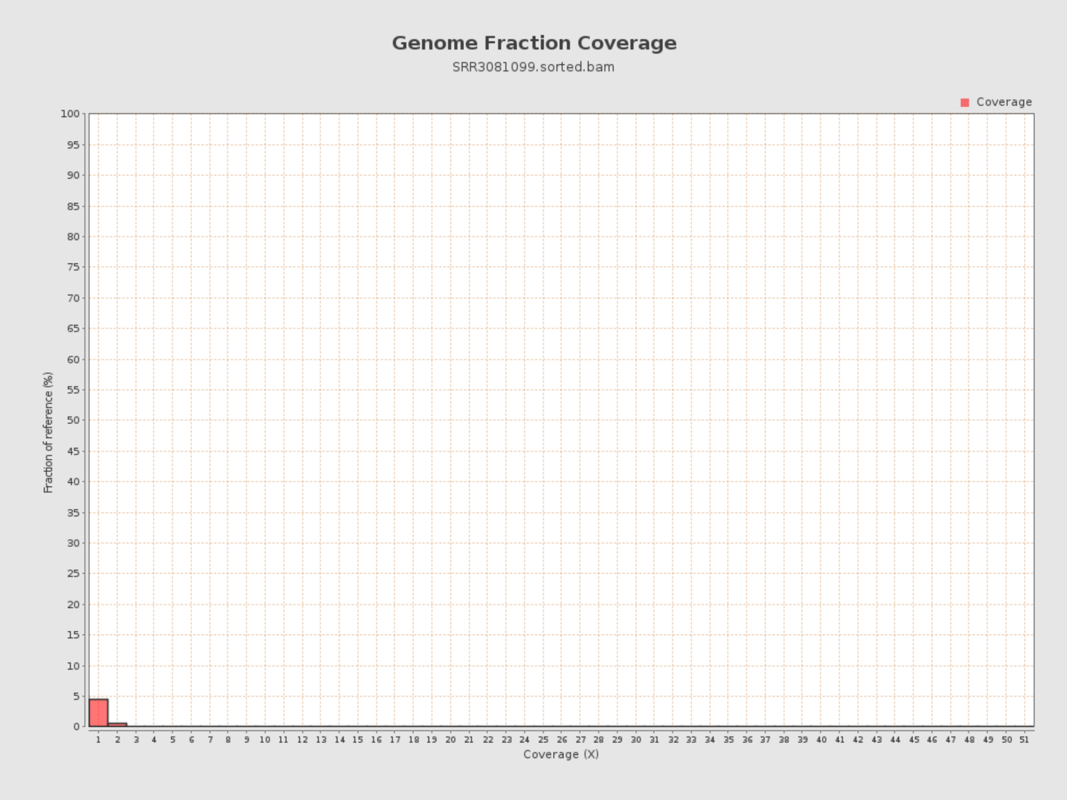
4. Results : Coverage Histogram



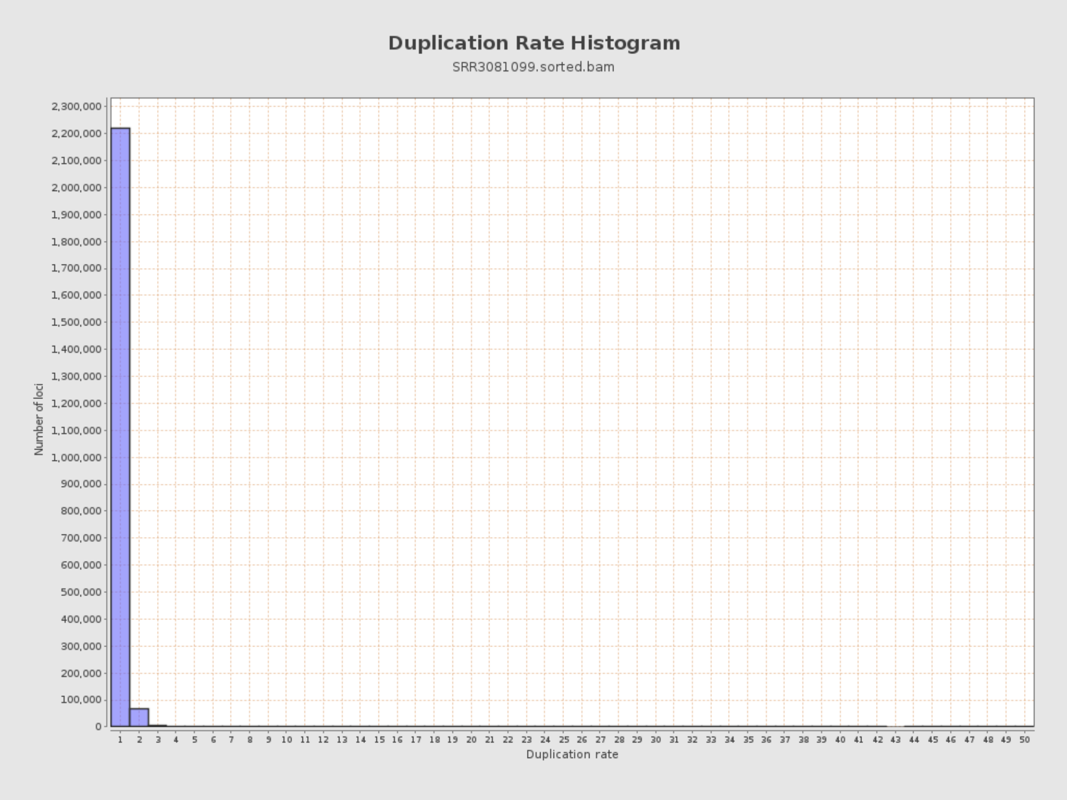
5. Results : Coverage Histogram (0-50X)



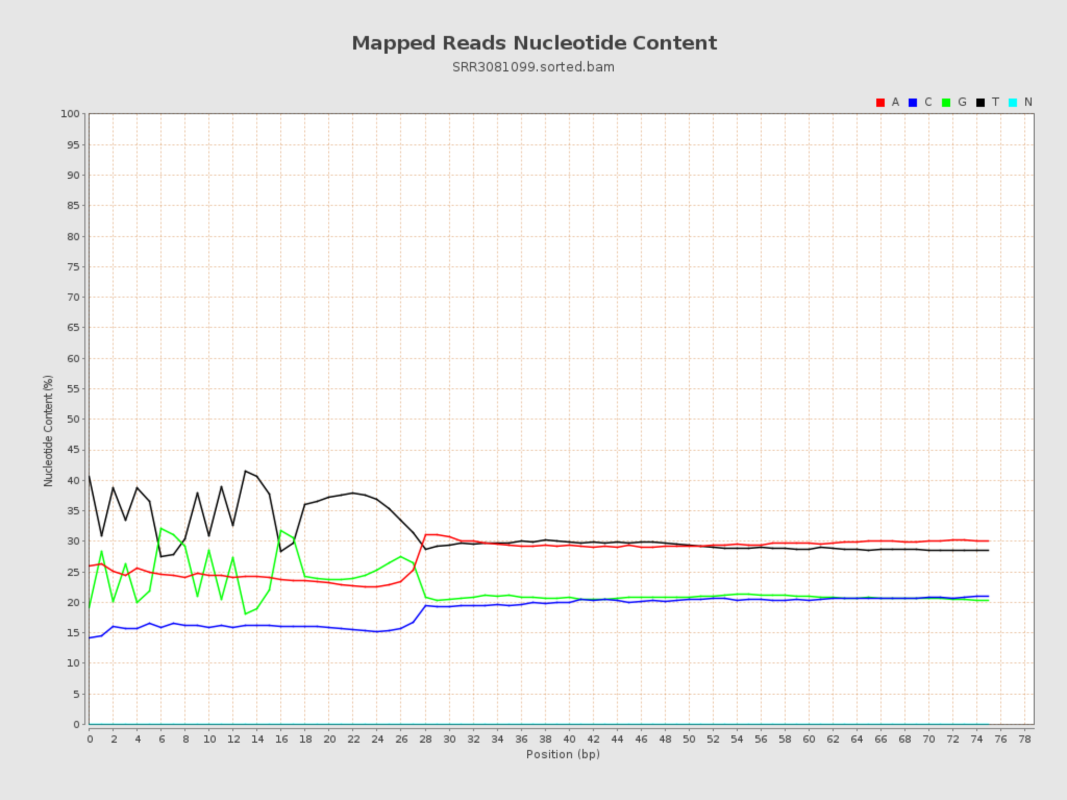
6. Results : Genome Fraction Coverage



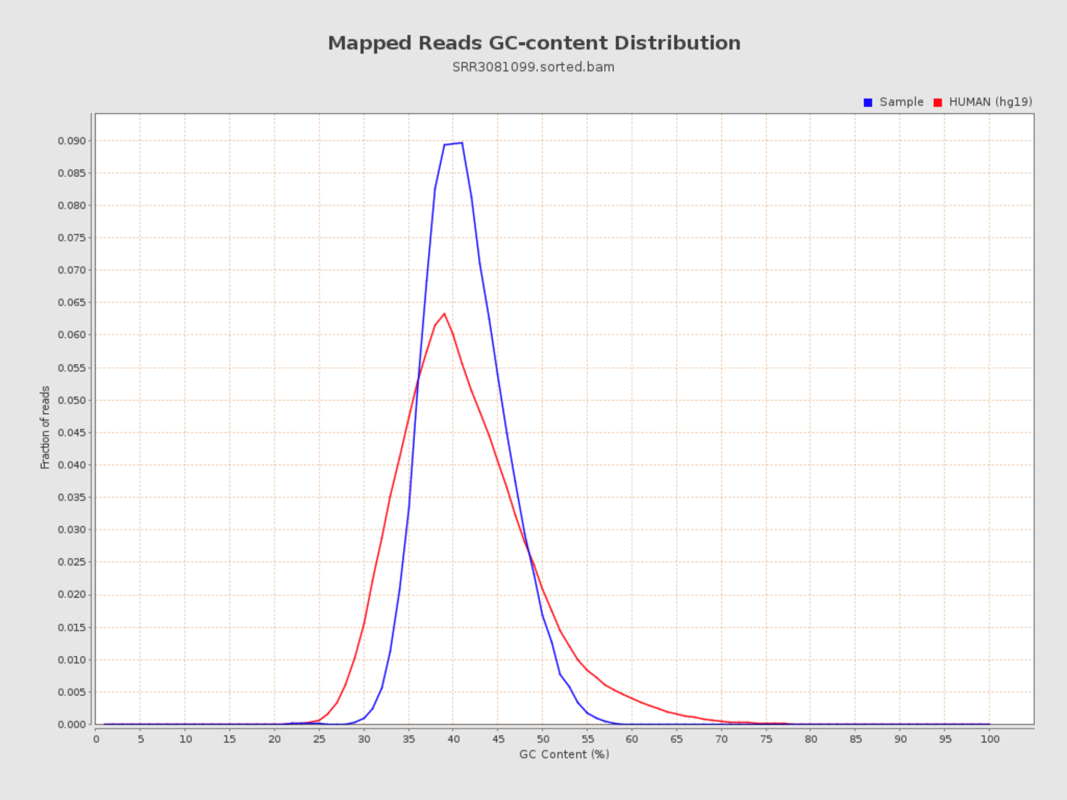
7. Results : Duplication Rate Histogram



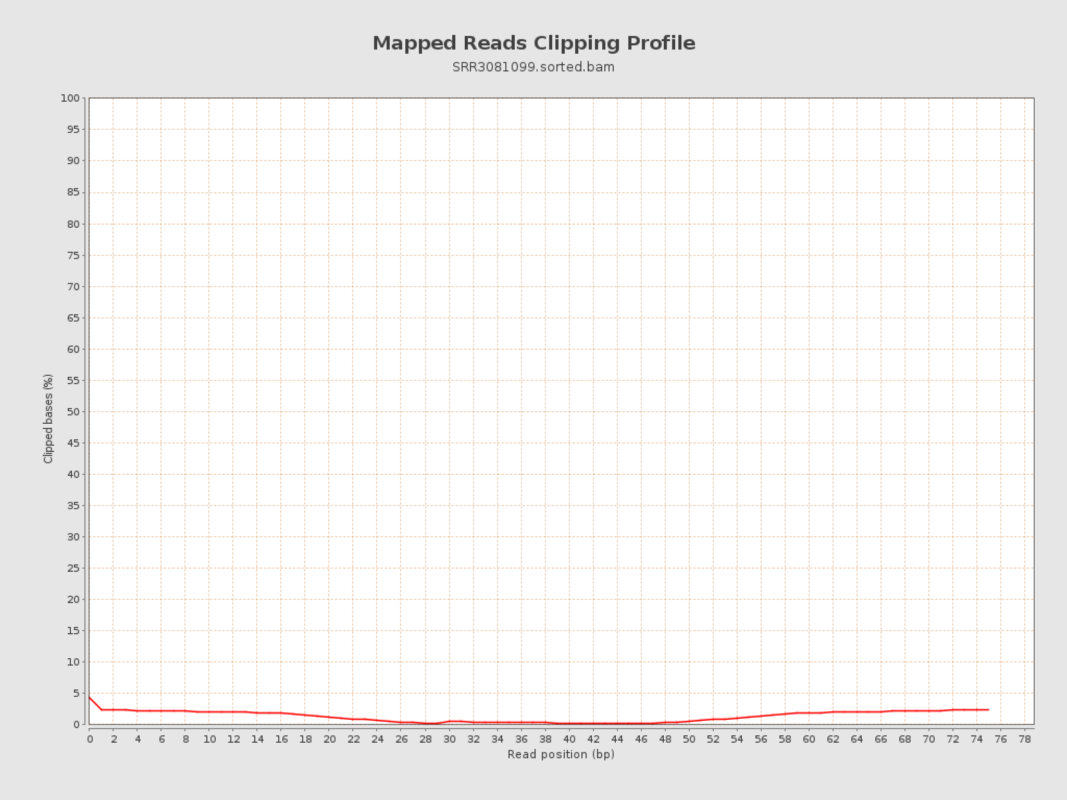
8. Results : Mapped Reads Nucleotide Content



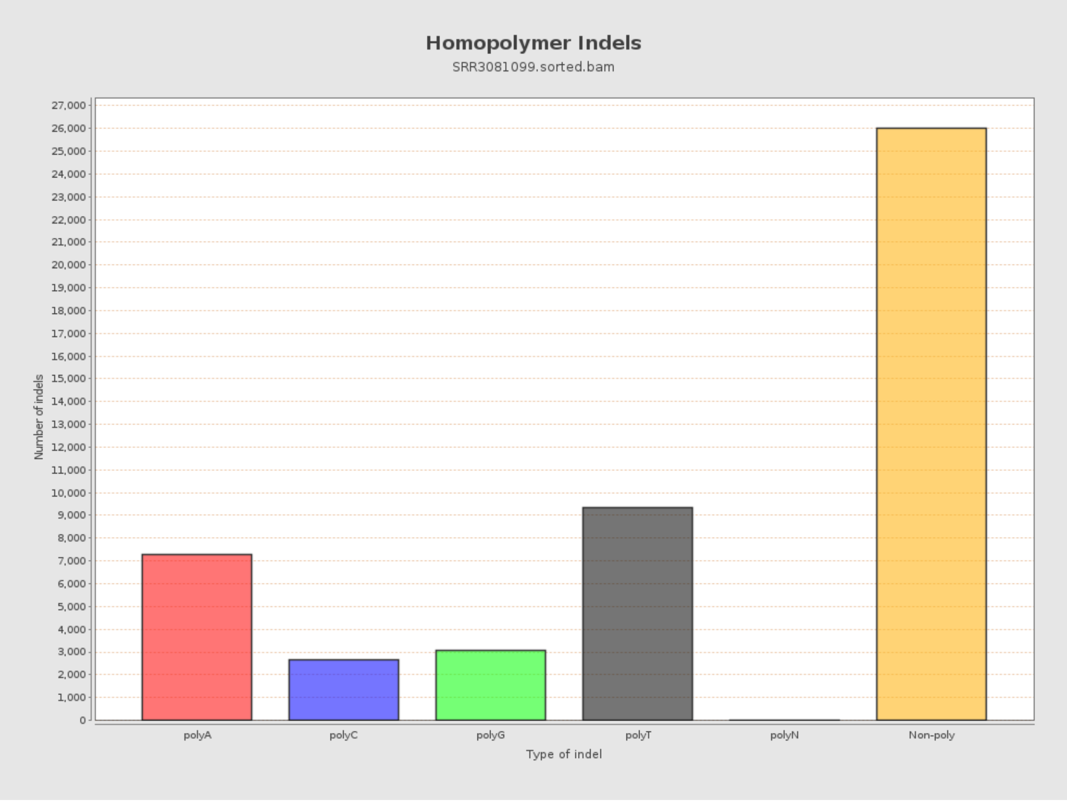
9. Results : Mapped Reads GC-content Distribution



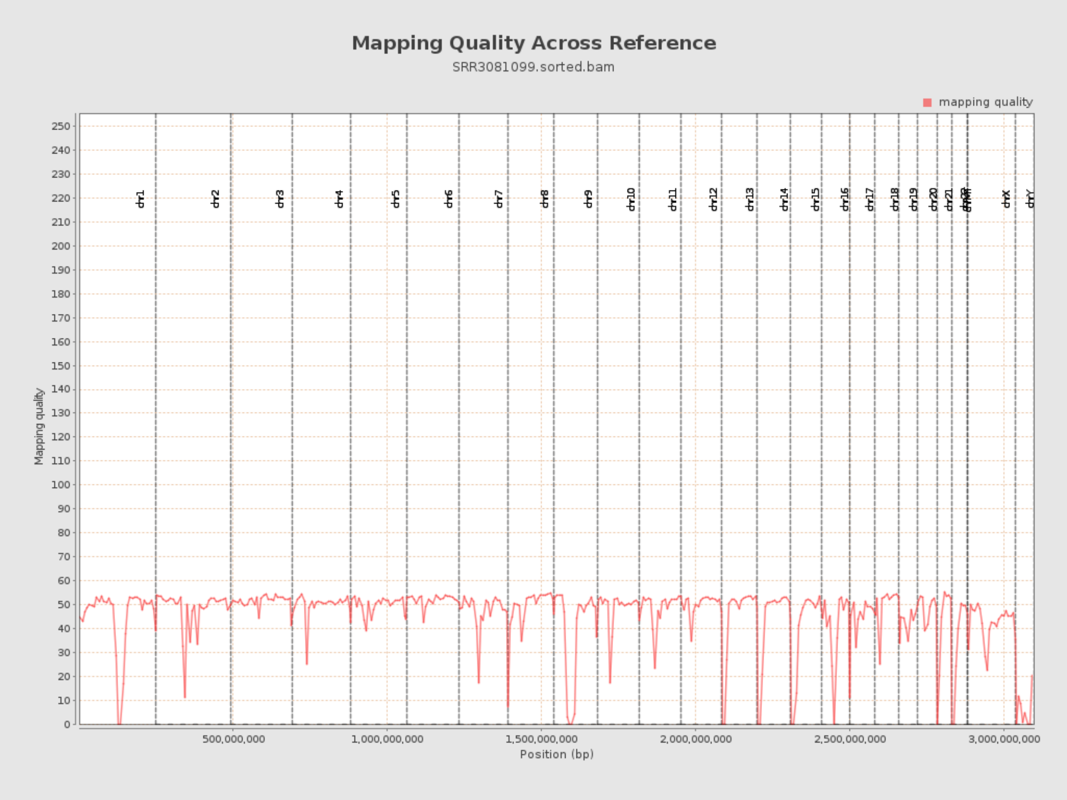
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram