Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 14:03:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234072.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_SRR6234072 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234072.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 14:03:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234072.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,848,014
Mapped reads	5,539,939 / 94.73%
Unmapped reads	308,075 / 5.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	33,588 / 0.57%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	575,655 / 9.84%
Duplication rate	8.56%
Clipped reads	2,976,273 / 50.89%

2.2. ACGT Content

Number/percentage of A's	90,560,041 / 25.43%
Number/percentage of C's	65,429,686 / 18.38%
Number/percentage of T's	114,723,836 / 32.22%
Number/percentage of G's	85,302,025 / 23.96%
Number/percentage of N's	34,127 / 0.01%
GC Percentage	42.33%

2.3. Coverage

Mean	0.1151

Standard Deviation	1.1418

2.4. Mapping Quality

Mean Mapping Quality	40.81

2.5. Mismatches and indels

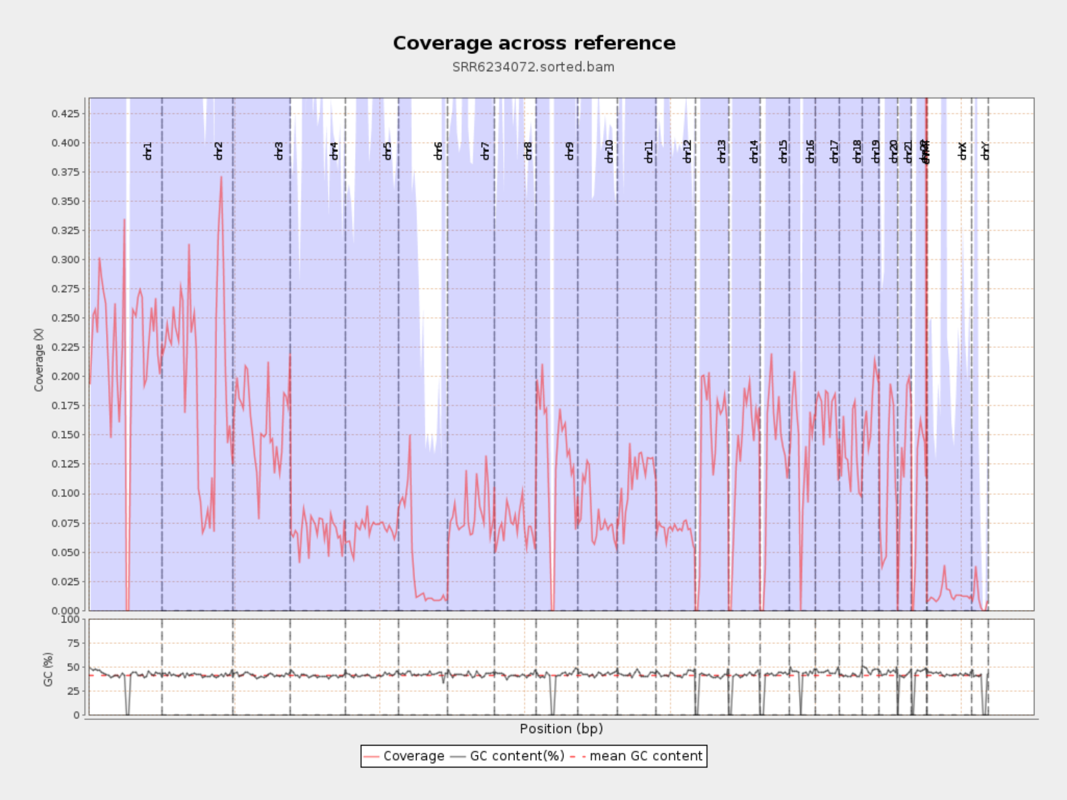
General error rate	0.54%
Mismatches	1,897,770
Insertions	23,462
Mapped reads with at least one insertion	0.42%
Deletions	78,245
Mapped reads with at least one deletion	1.4%
Homopolymer indels	44.57%

2.6. Chromosome stats

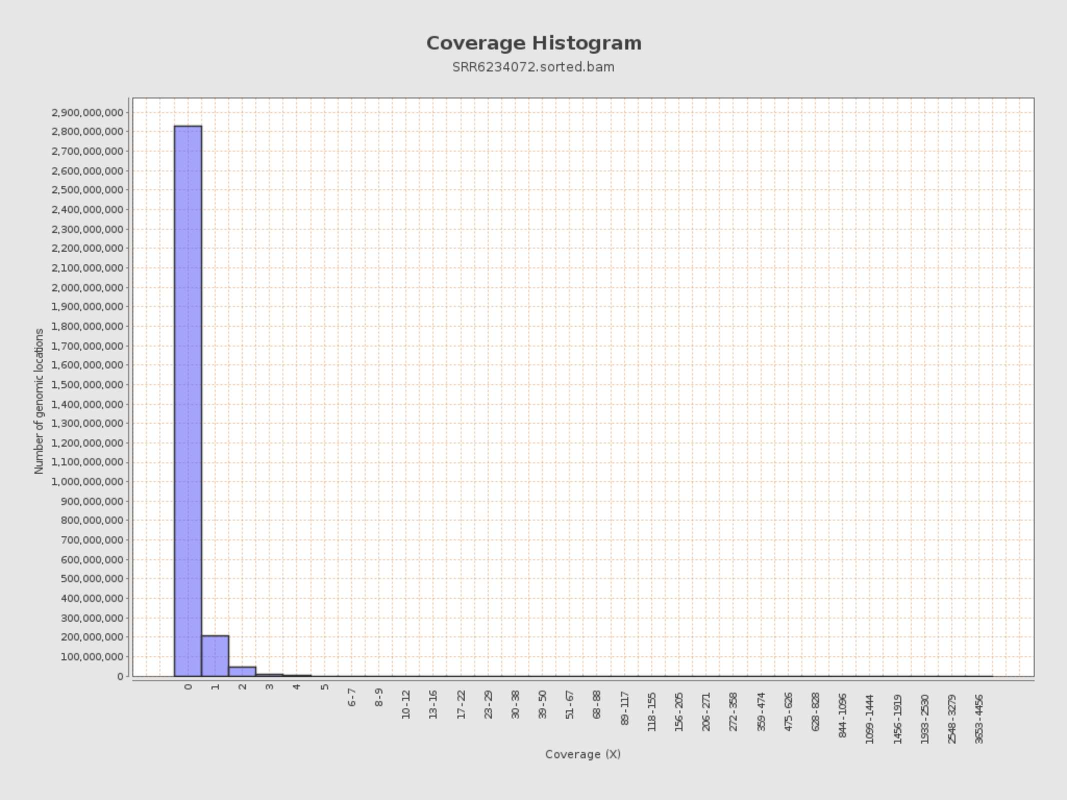
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	55202126	0.2215	2.5726
chr2	243199373	48744364	0.2004	2.1381
chr3	198022430	31433470	0.1587	0.5108
chr4	191154276	12918354	0.0676	0.3725
chr5	180915260	12460896	0.0689	0.3582
chr6	171115067	6469281	0.0378	0.5202
chr7	159138663	13276259	0.0834	0.7379

chr8	146364022	10516483	0.0719	1.0349
chr9	141213431	18248885	0.1292	0.7846
chr10	135534747	10965341	0.0809	0.6246
chr11	135006516	15176732	0.1124	0.7674
chr12	133851895	9256231	0.0692	0.3647
chr13	115169878	16399577	0.1424	0.5357
chr14	107349540	14158930	0.1319	0.5237
chr15	102531392	13172859	0.1285	0.5074
chr16	90354753	12490703	0.1382	0.5762
chr17	81195210	13630856	0.1679	0.6613
chr18	78077248	10453888	0.1339	1.8522
chr19	59128983	10149042	0.1716	1.5778
chr20	63025520	6442556	0.1022	0.474
chr21	48129895	6451203	0.134	0.4925
chr22	51304566	5155694	0.1005	0.3966
chrMT	16571	295497	17.8322	10.8605
chrX	155270560	2124065	0.0137	0.3679
chrY	59373566	593141	0.01	0.253

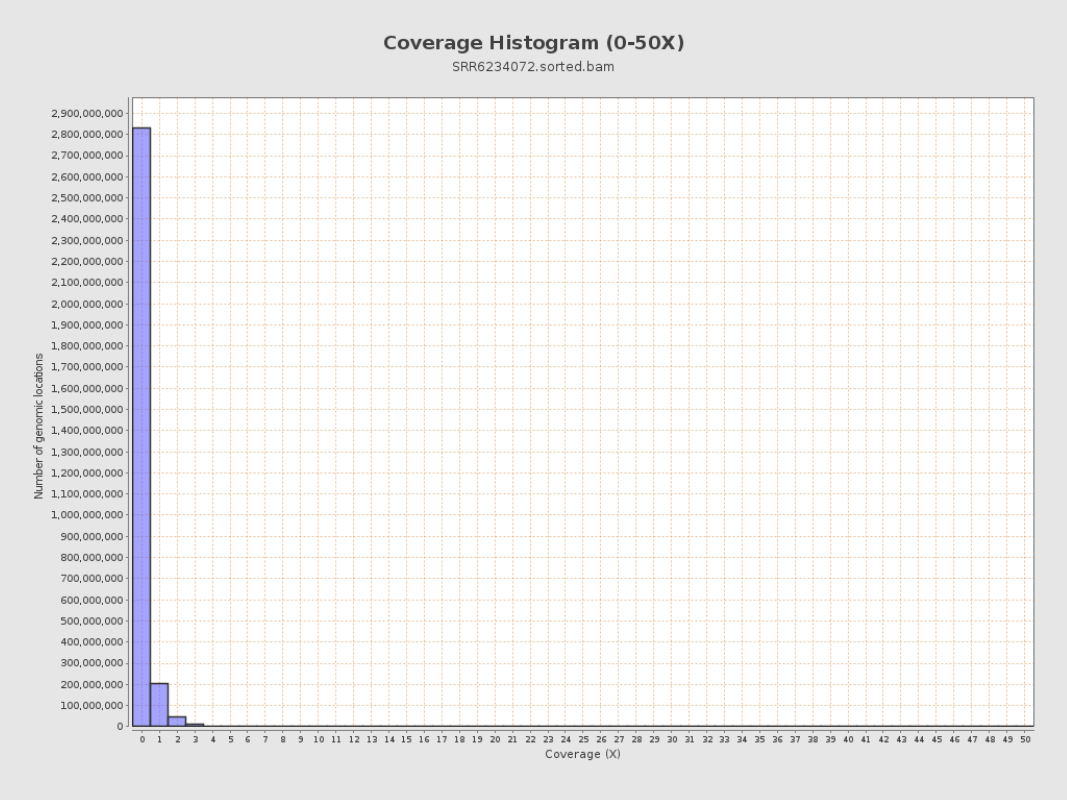
3. Results : Coverage across reference



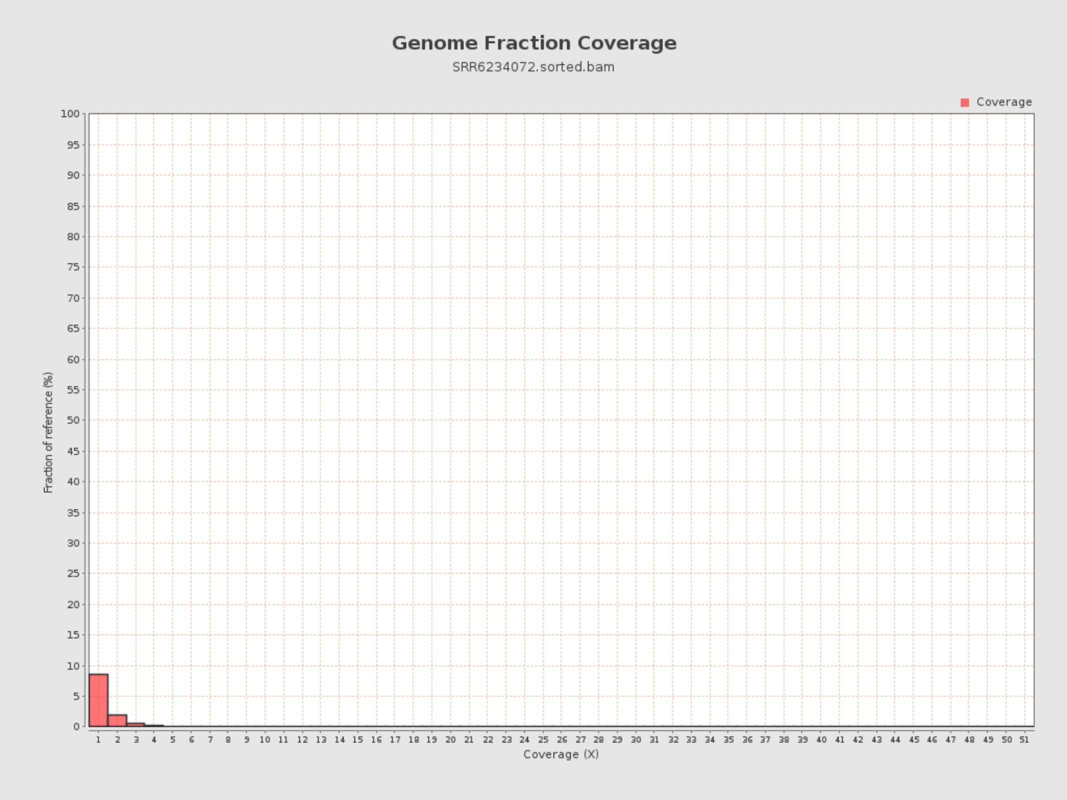
4. Results : Coverage Histogram



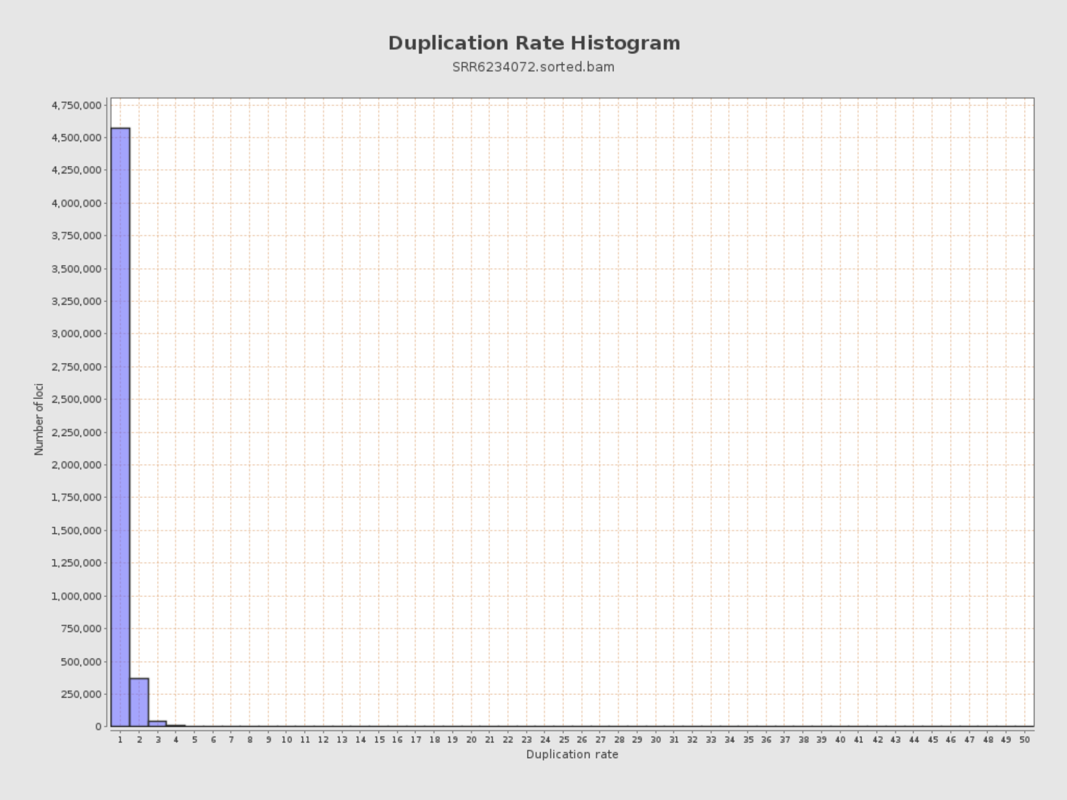
5. Results : Coverage Histogram (0-50X)



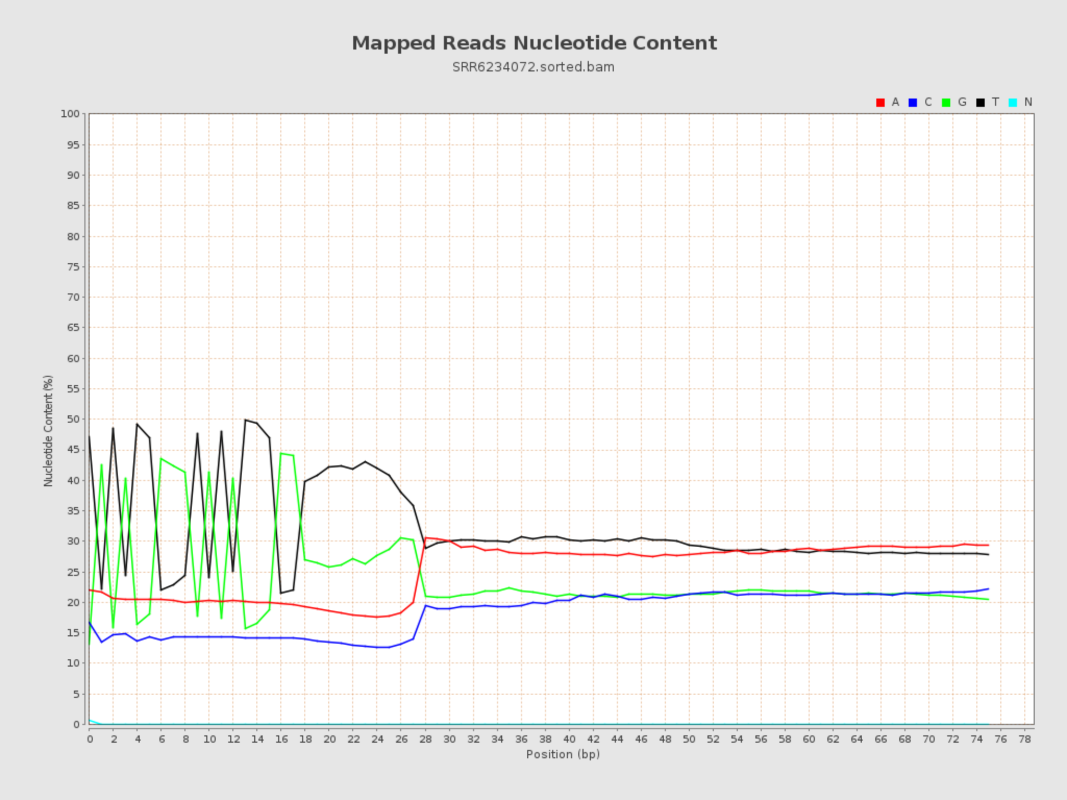
6. Results : Genome Fraction Coverage



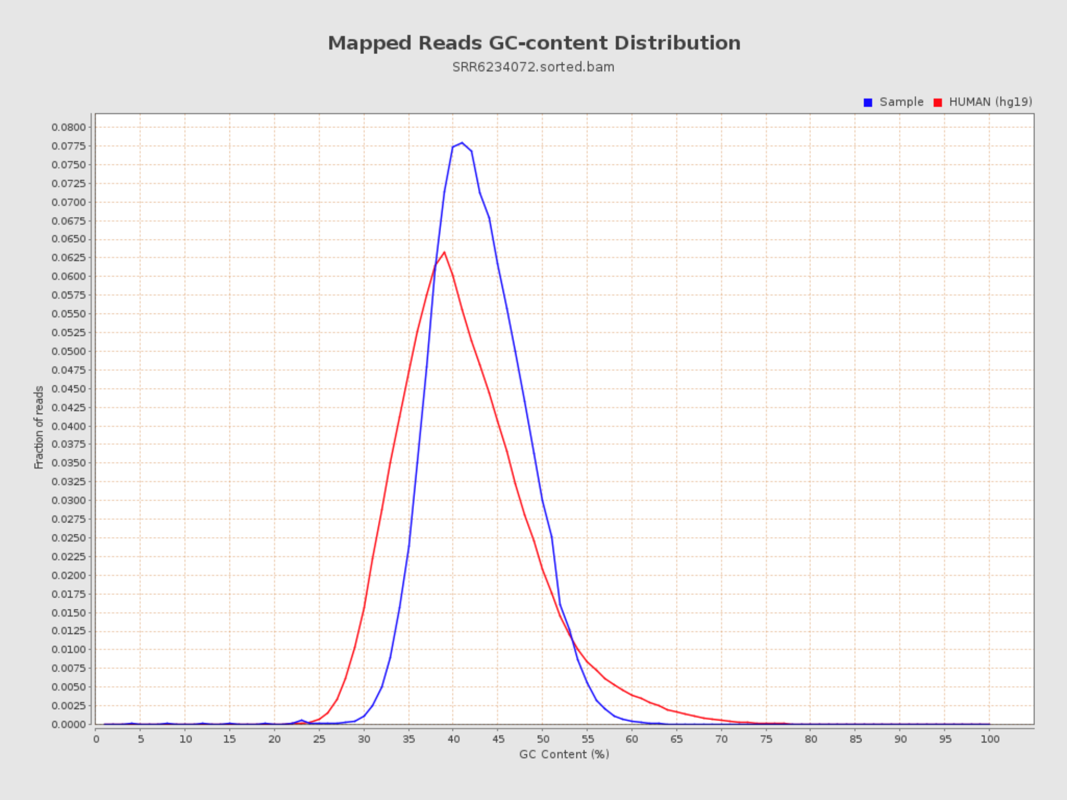
7. Results : Duplication Rate Histogram



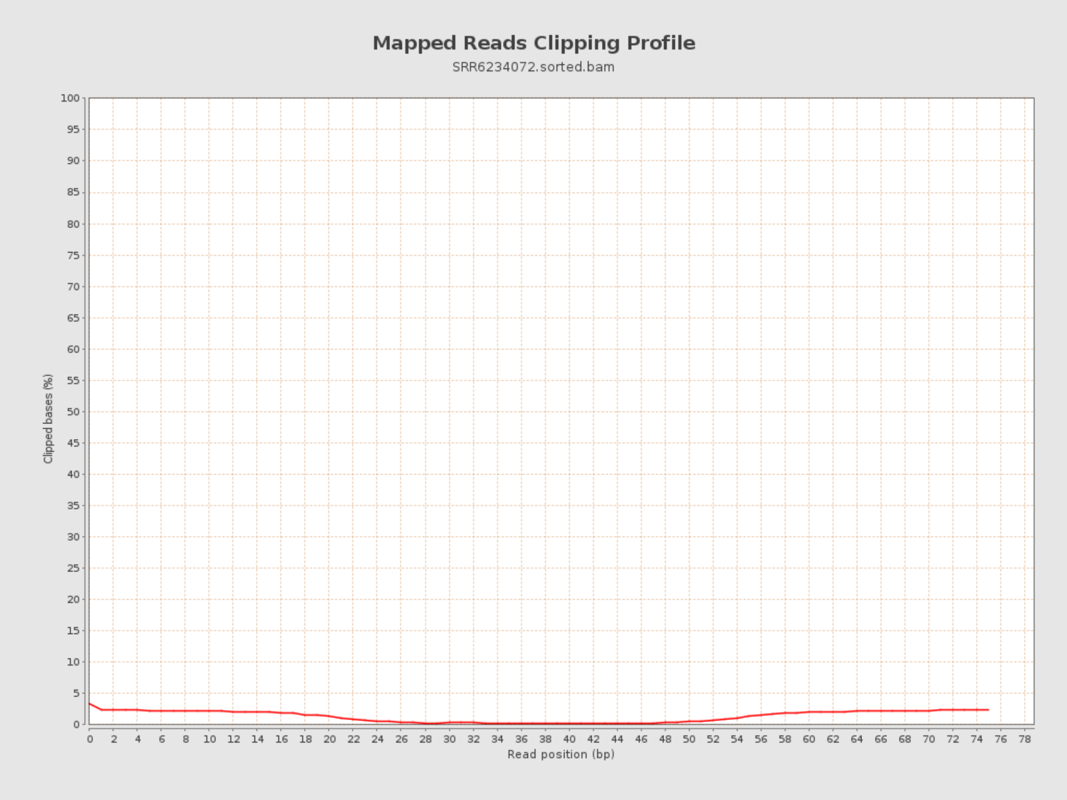
8. Results : Mapped Reads Nucleotide Content



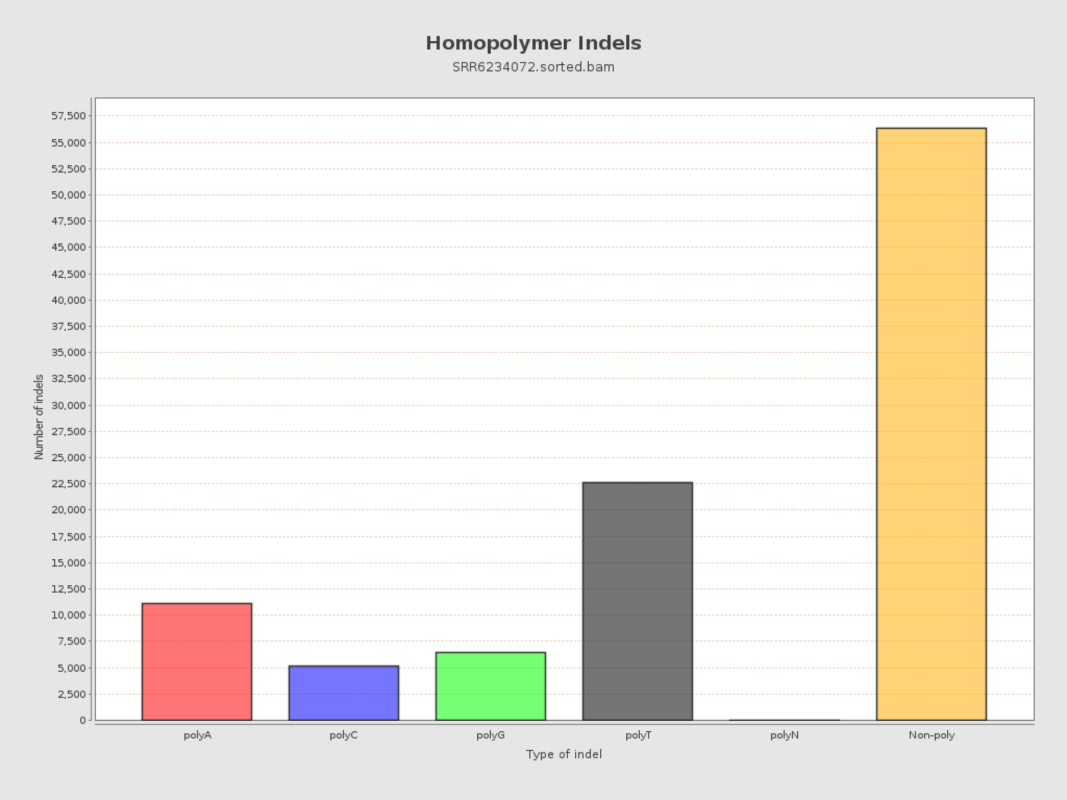
9. Results : Mapped Reads GC-content Distribution



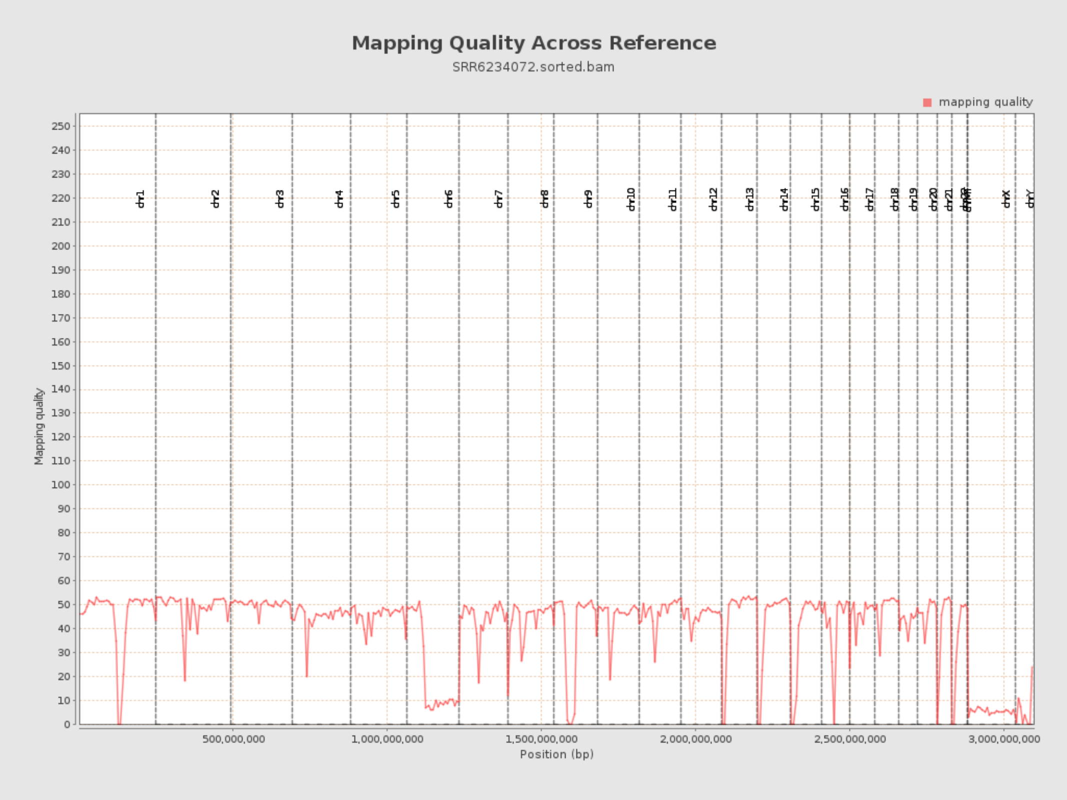
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram