Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 12:53:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234059.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_SRR6234059 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234059.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 12:53:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234059.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,822,496
Mapped reads	5,055,965 / 86.84%
Unmapped reads	766,531 / 13.16%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	34,990 / 0.6%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	361,697 / 6.21%
Duplication rate	5.51%
Clipped reads	2,516,734 / 43.22%

2.2. ACGT Content

Number/percentage of A's	92,332,972 / 28.04%
Number/percentage of C's	59,233,558 / 17.99%
Number/percentage of T's	105,744,335 / 32.12%
Number/percentage of G's	71,911,866 / 21.84%
Number/percentage of N's	17,589 / 0.01%
GC Percentage	39.83%

2.3. Coverage

Mean	0.1064

Standard Deviation	0.9544

2.4. Mapping Quality

Mean Mapping Quality	45.94

2.5. Mismatches and indels

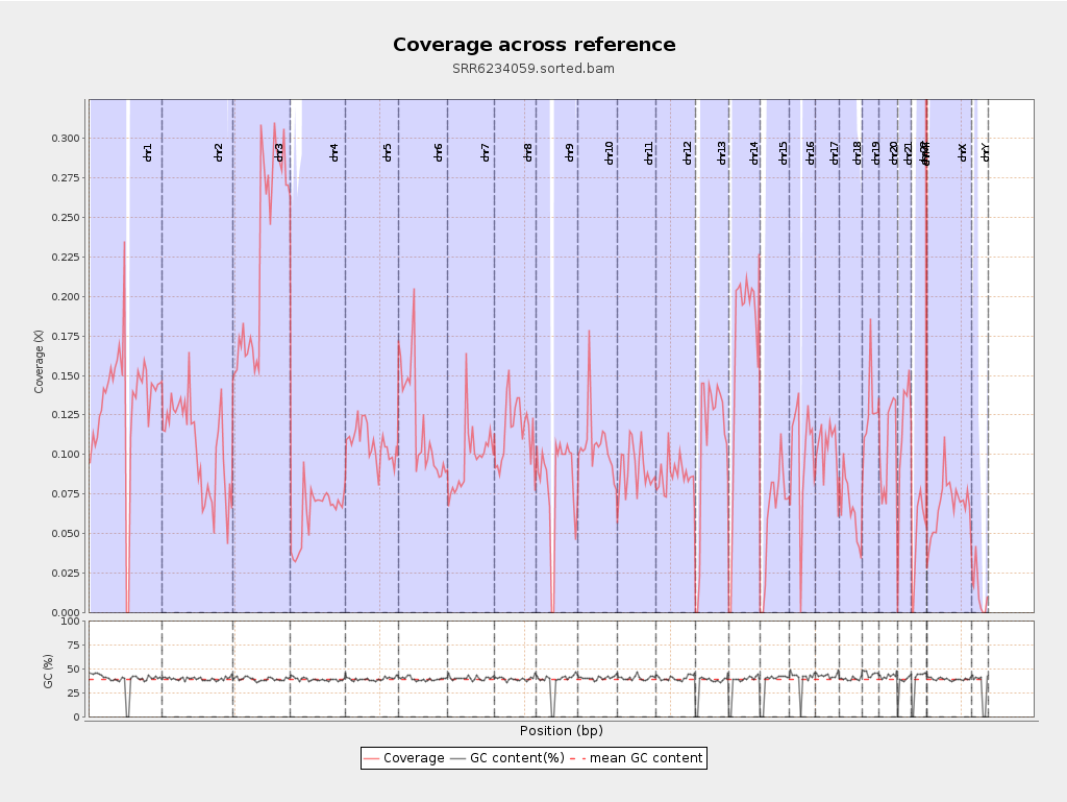
General error rate	0.77%
Mismatches	2,480,354
Insertions	23,390
Mapped reads with at least one insertion	0.46%
Deletions	111,340
Mapped reads with at least one deletion	2.18%
Homopolymer indels	44.64%

2.6. Chromosome stats

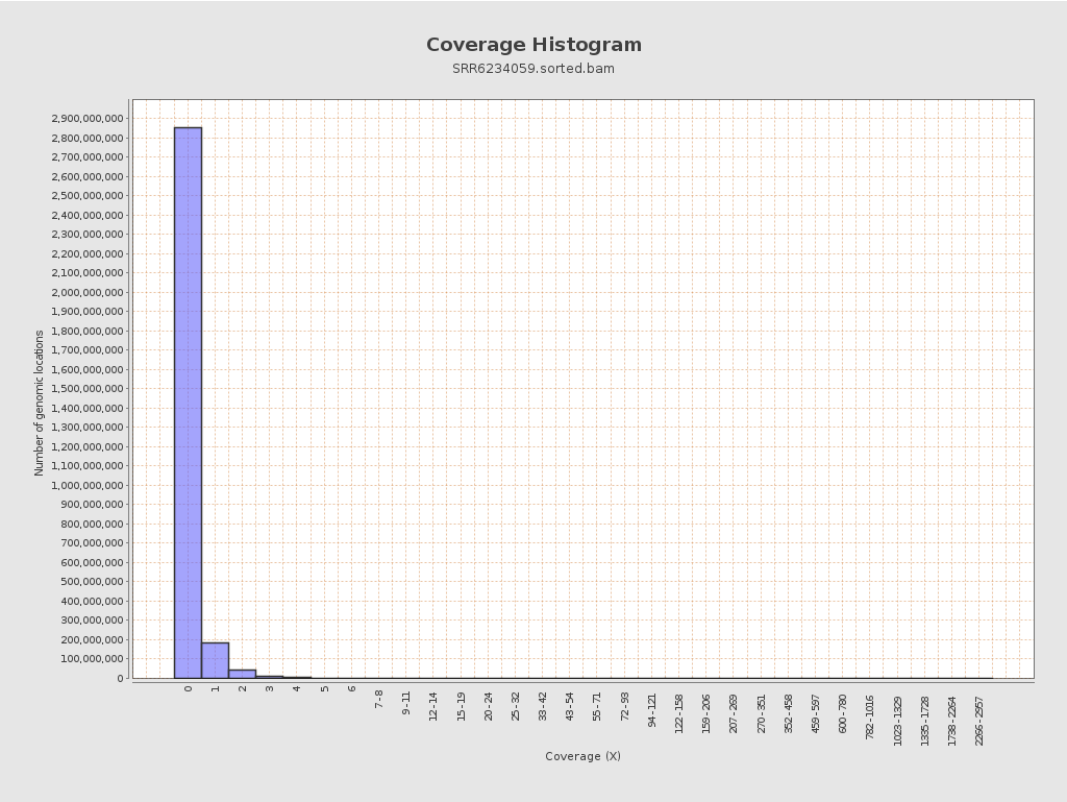
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	33181780	0.1331	2.316
chr2	243199373	25388965	0.1044	0.863
chr3	198022430	44456006	0.2245	0.6127
chr4	191154276	12031337	0.0629	0.3678
chr5	180915260	19360354	0.107	0.4261
chr6	171115067	20354178	0.119	0.6316
chr7	159138663	15575534	0.0979	0.9371

chr8	146364022	16743507	0.1144	1.4439
chr9	141213431	11510146	0.0815	0.5955
chr10	135534747	14319709	0.1057	0.88
chr11	135006516	12185528	0.0903	0.6596
chr12	133851895	11670464	0.0872	0.405
chr13	115169878	12508175	0.1086	0.4178
chr14	107349540	17553954	0.1635	0.5514
chr15	102531392	6478787	0.0632	0.324
chr16	90354753	9209543	0.1019	0.4896
chr17	81195210	8405523	0.1035	0.4874
chr18	78077248	5156100	0.066	1.3588
chr19	59128983	7569626	0.128	1.3415
chr20	63025520	6535584	0.1037	0.4506
chr21	48129895	5469201	0.1136	0.4628
chr22	51304566	2466442	0.0481	0.2675
chrMT	16571	122901	7.4166	5.1039
chrX	155270560	10477143	0.0675	0.4278
chrY	59373566	703573	0.0118	0.2365

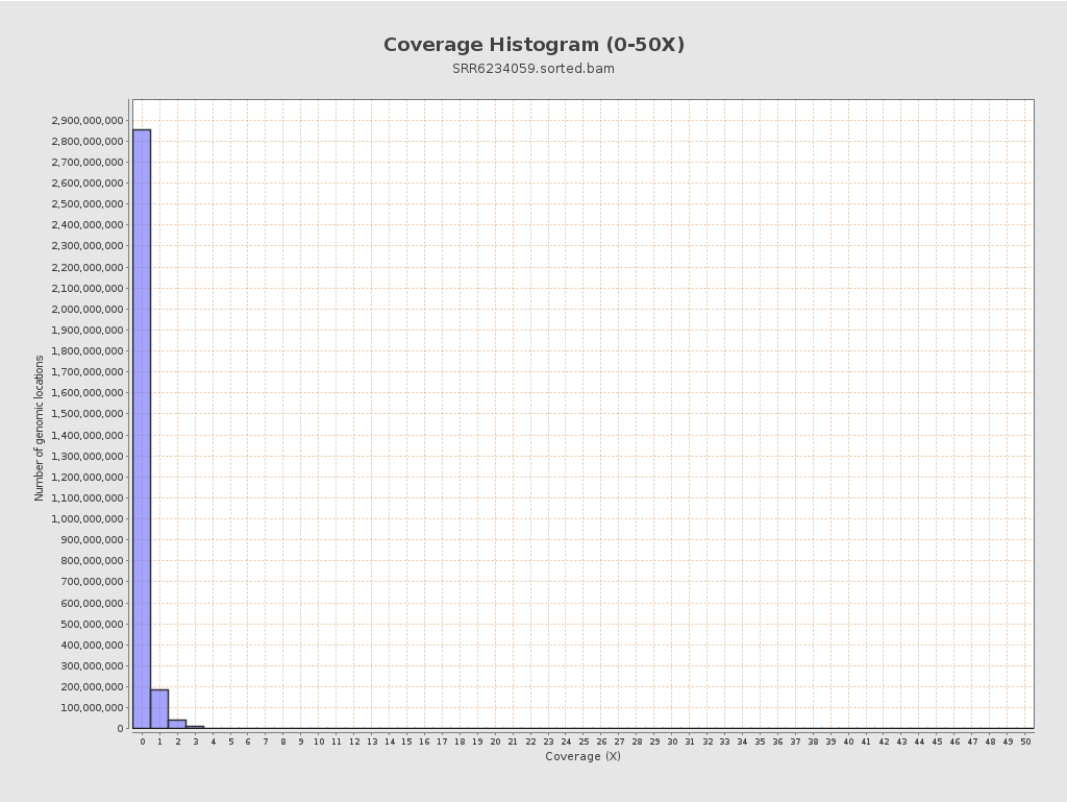
3. Results : Coverage across reference



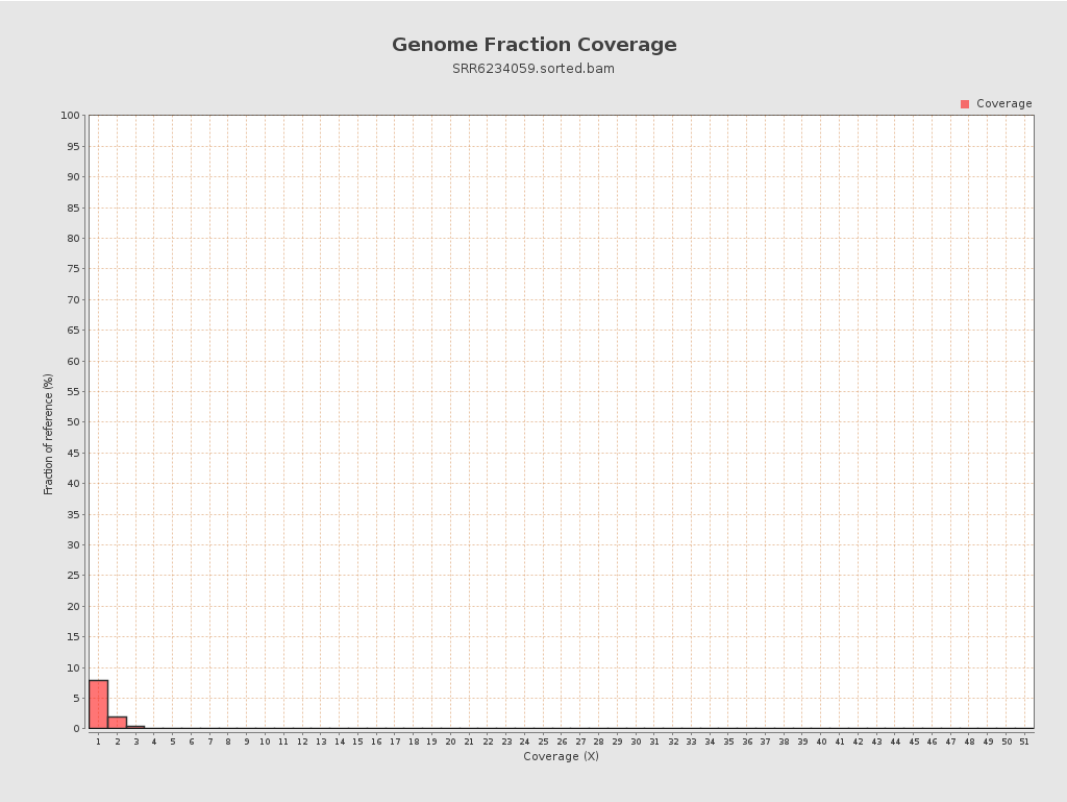
4. Results : Coverage Histogram



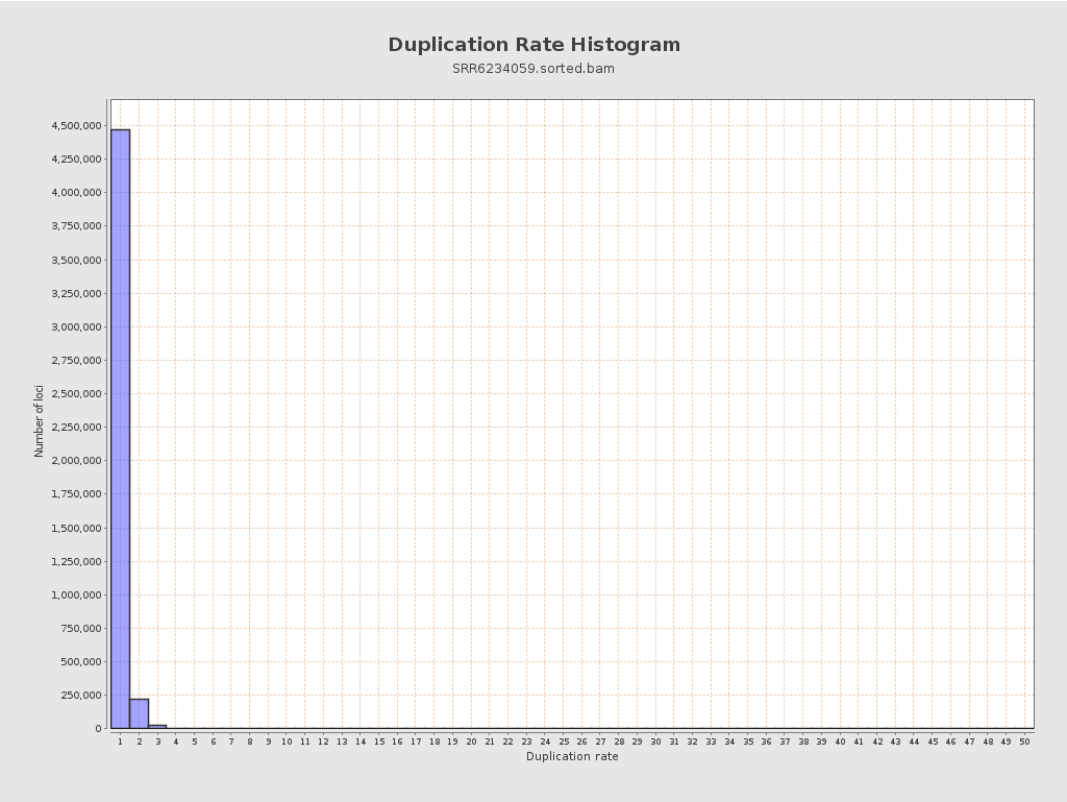
5. Results : Coverage Histogram (0-50X)



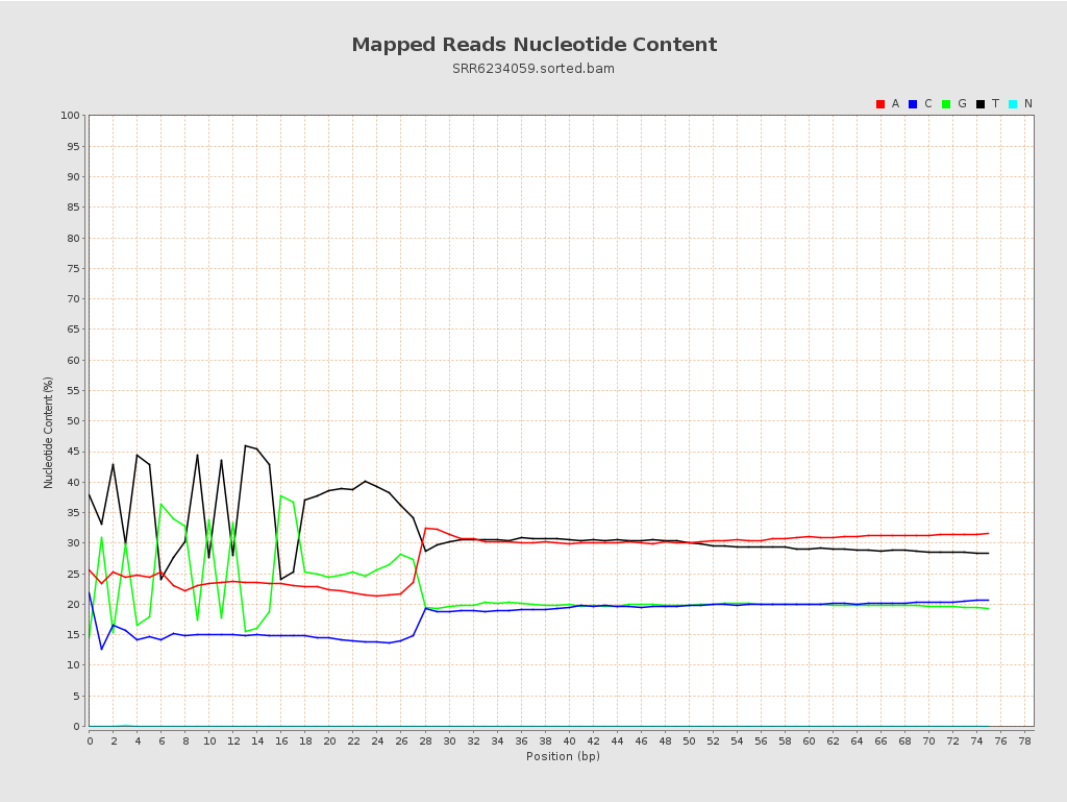
6. Results : Genome Fraction Coverage



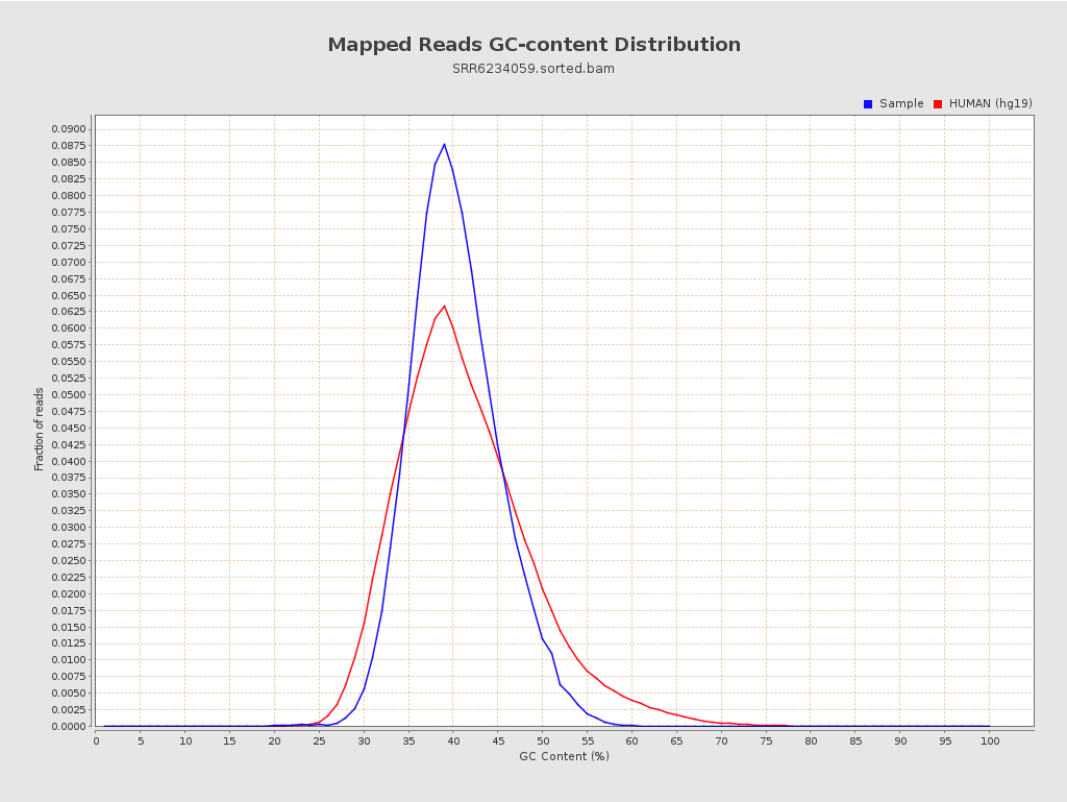
7. Results : Duplication Rate Histogram



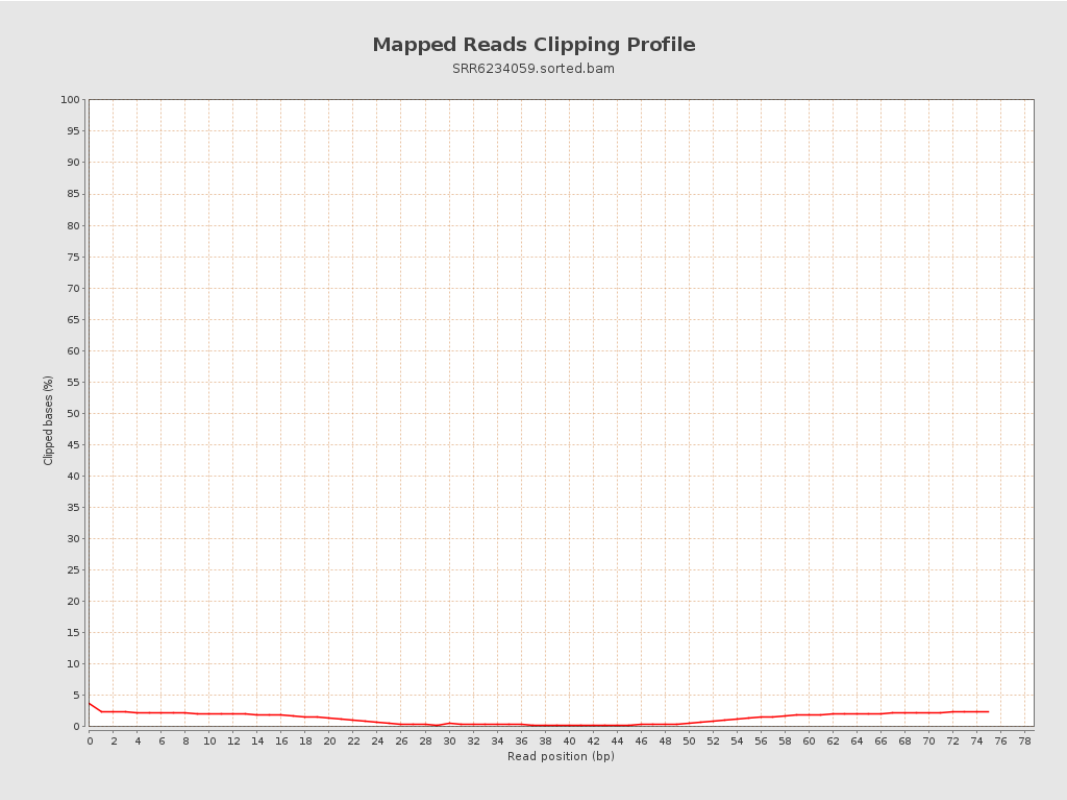
8. Results : Mapped Reads Nucleotide Content



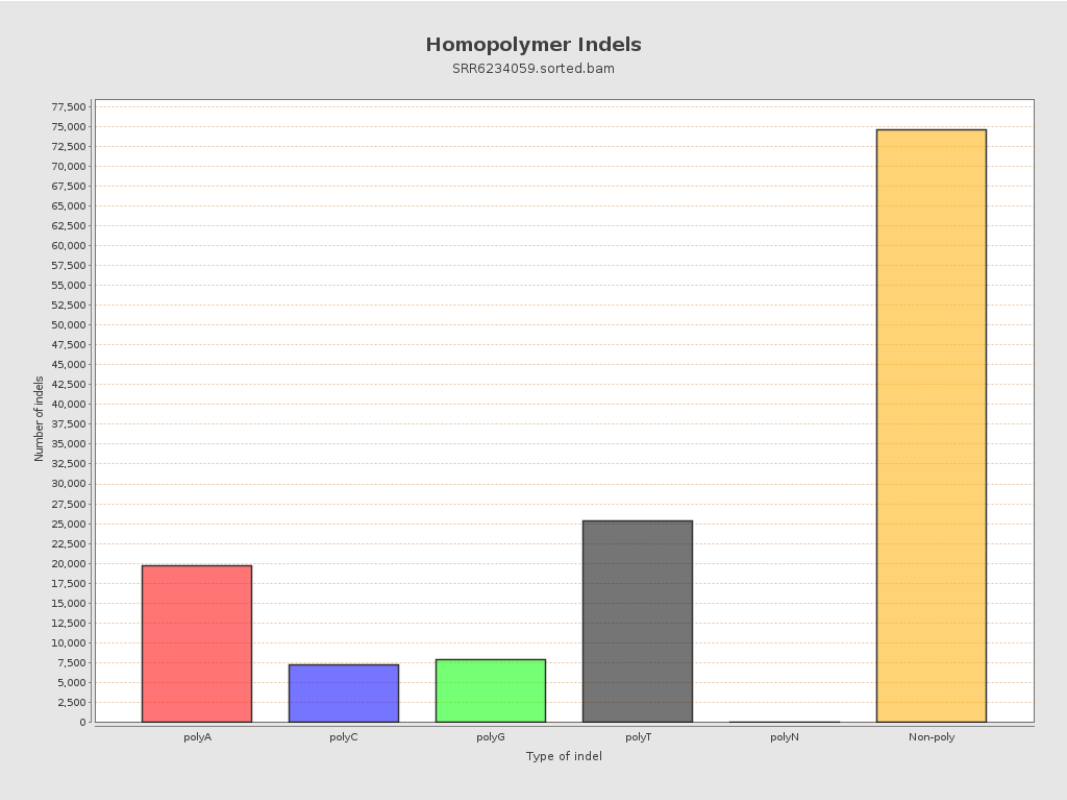
9. Results : Mapped Reads GC-content Distribution



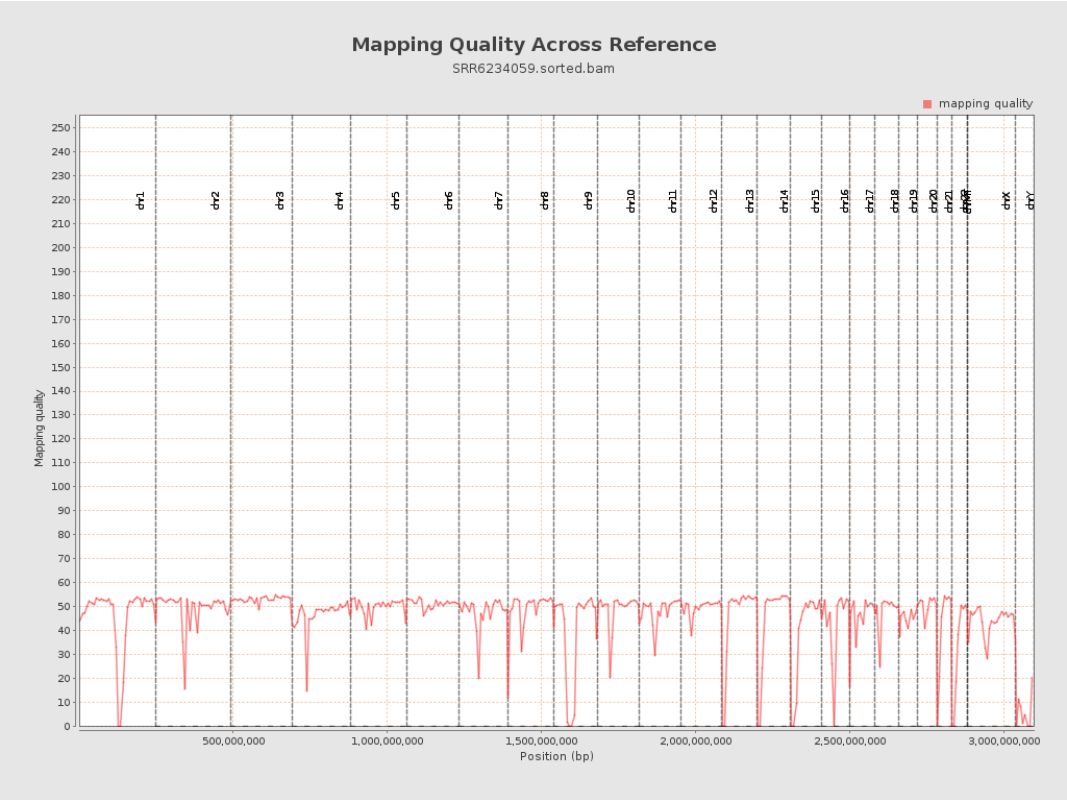
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram