Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 12:04:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234046.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_SRR6234046 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234046.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 12:04:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234046.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,227,657
Mapped reads	2,020,686 / 90.71%
Unmapped reads	206,971 / 9.29%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,956 / 0.63%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	130,911 / 5.88%
Duplication rate	5.03%
Clipped reads	844,320 / 37.9%

2.2. ACGT Content

Number/percentage of A's	37,345,639 / 27.31%
Number/percentage of C's	26,216,453 / 19.17%
Number/percentage of T's	42,113,998 / 30.8%
Number/percentage of G's	31,048,118 / 22.71%
Number/percentage of N's	11,277 / 0.01%
GC Percentage	41.88%

2.3. Coverage

Mean	0.0442

Standard Deviation	0.4977

2.4. Mapping Quality

Mean Mapping Quality	43.37

2.5. Mismatches and indels

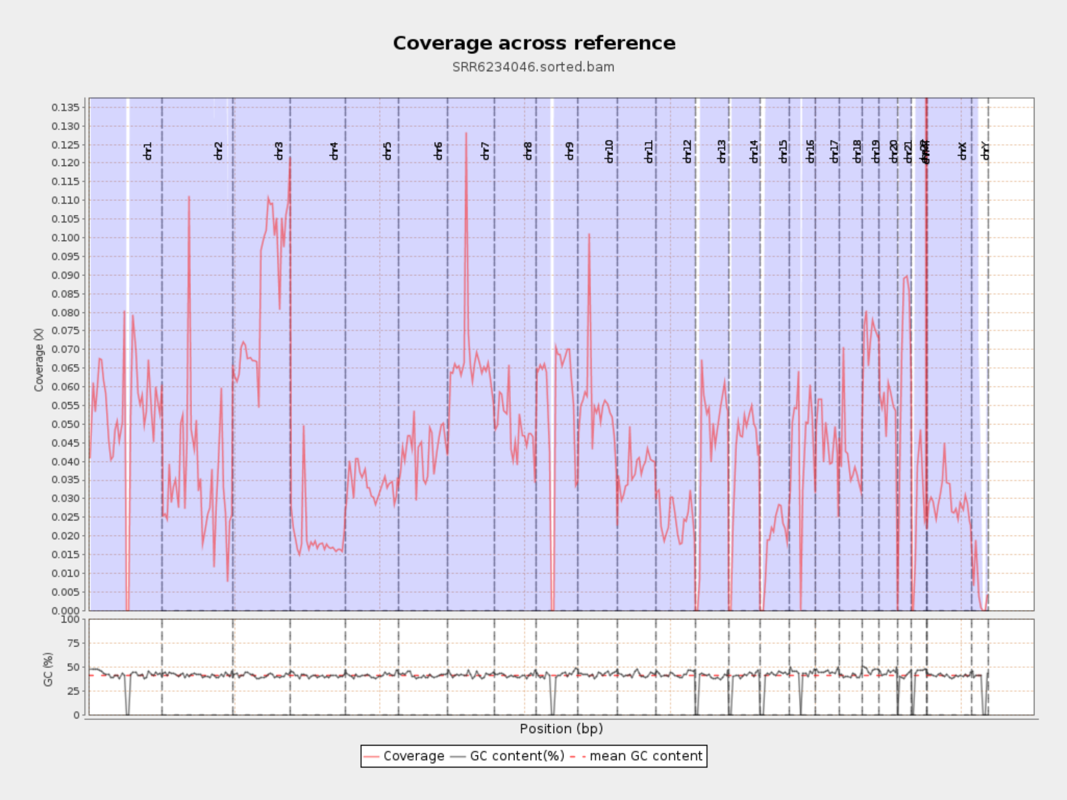
General error rate	0.85%
Mismatches	1,144,473
Insertions	12,510
Mapped reads with at least one insertion	0.61%
Deletions	38,355
Mapped reads with at least one deletion	1.88%
Homopolymer indels	44.47%

2.6. Chromosome stats

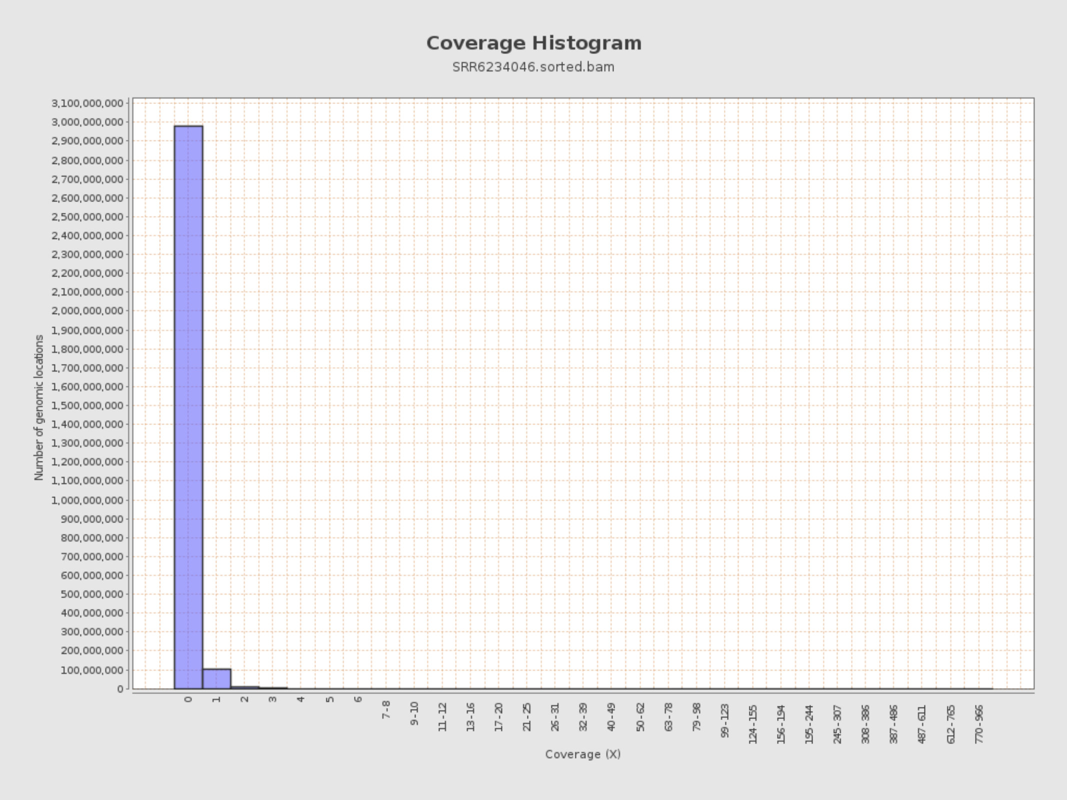
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13130457	0.0527	0.8183
chr2	243199373	8570629	0.0352	0.6809
chr3	198022430	16843620	0.0851	0.3316
chr4	191154276	3661678	0.0192	0.1954
chr5	180915260	6105170	0.0337	0.2129
chr6	171115067	7308507	0.0427	0.2937
chr7	159138663	10762560	0.0676	0.9786

chr8	146364022	7107539	0.0486	0.4525
chr9	141213431	7837682	0.0555	0.4926
chr10	135534747	7494741	0.0553	0.5274
chr11	135006516	5080420	0.0376	0.3269
chr12	133851895	3305017	0.0247	0.1916
chr13	115169878	5146631	0.0447	0.2497
chr14	107349540	4396453	0.041	0.2947
chr15	102531392	1899670	0.0185	0.1674
chr16	90354753	4089963	0.0453	0.3449
chr17	81195210	3714720	0.0458	0.2683
chr18	78077248	3213064	0.0412	1.0324
chr19	59128983	4343514	0.0735	0.5612
chr20	63025520	3419402	0.0543	0.2834
chr21	48129895	3176454	0.066	0.3247
chr22	51304566	1287607	0.0251	0.1758
chrMT	16571	28085	1.6948	1.8057
chrX	155270560	4550642	0.0293	0.249
chrY	59373566	326989	0.0055	0.1484

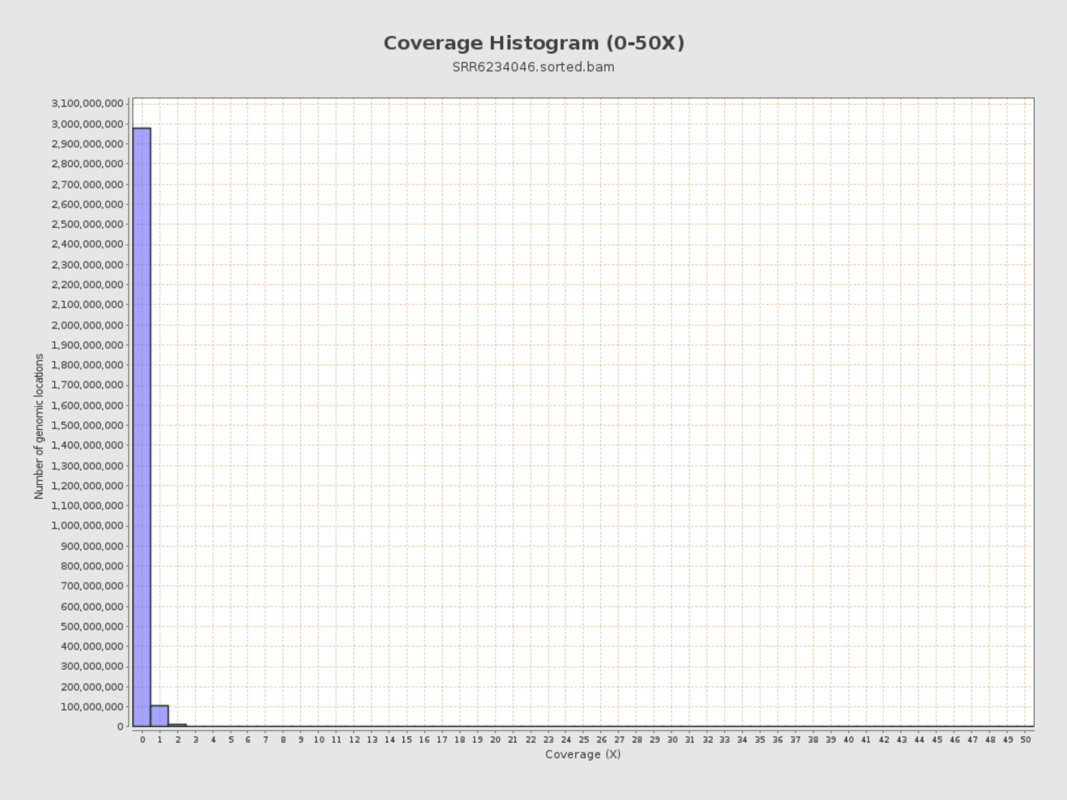
3. Results : Coverage across reference



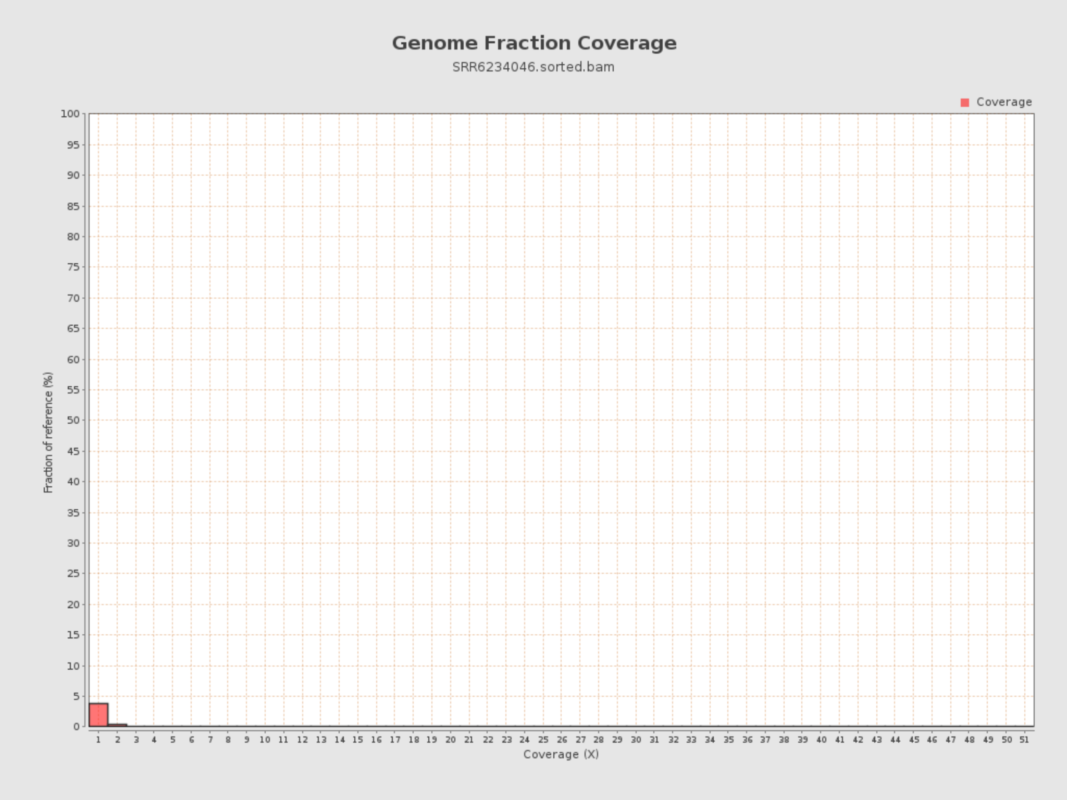
4. Results : Coverage Histogram



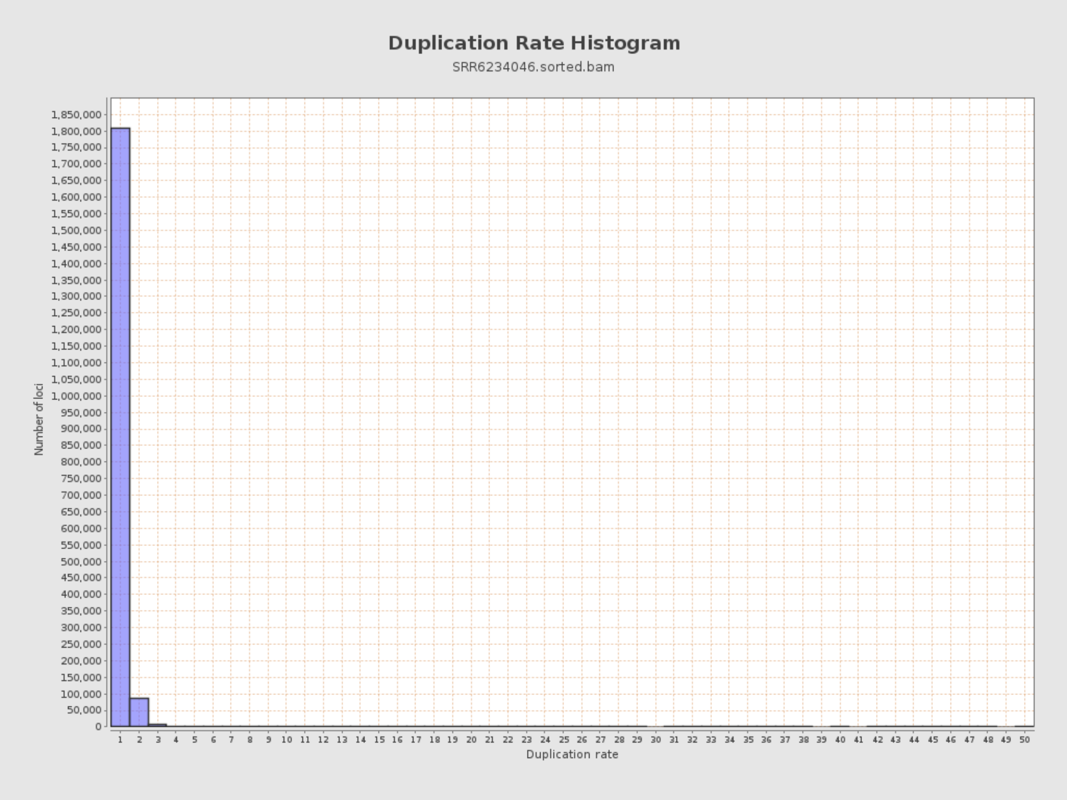
5. Results : Coverage Histogram (0-50X)



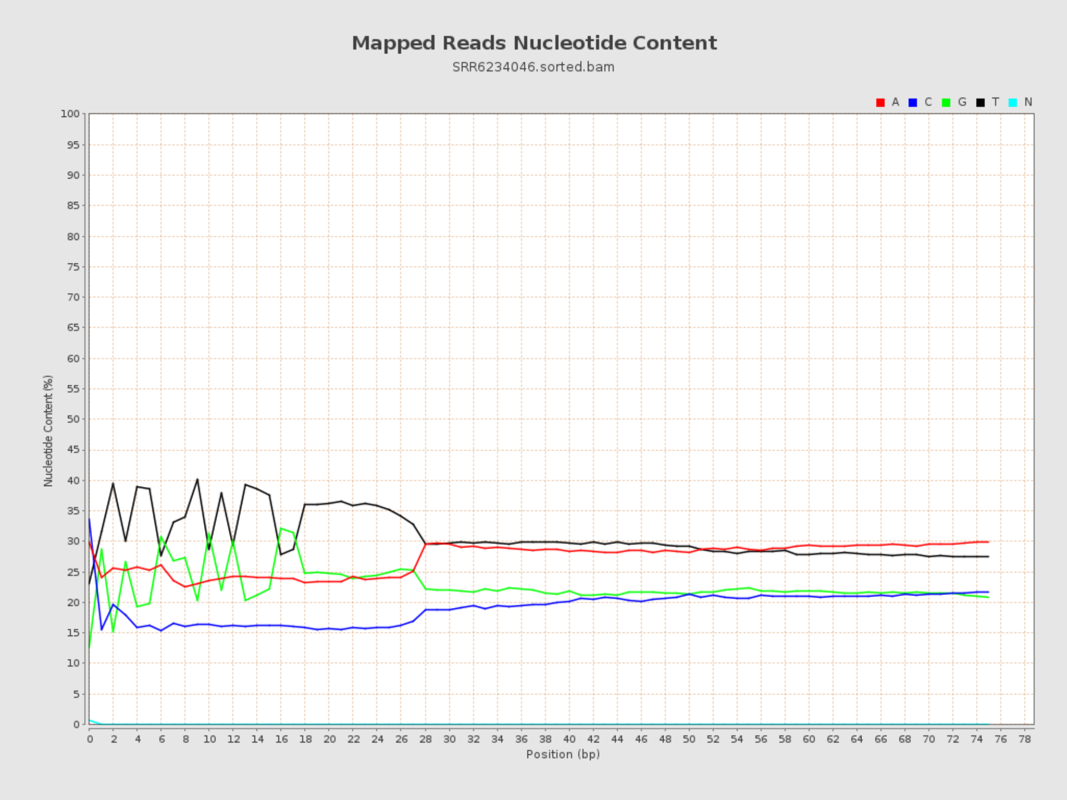
6. Results : Genome Fraction Coverage



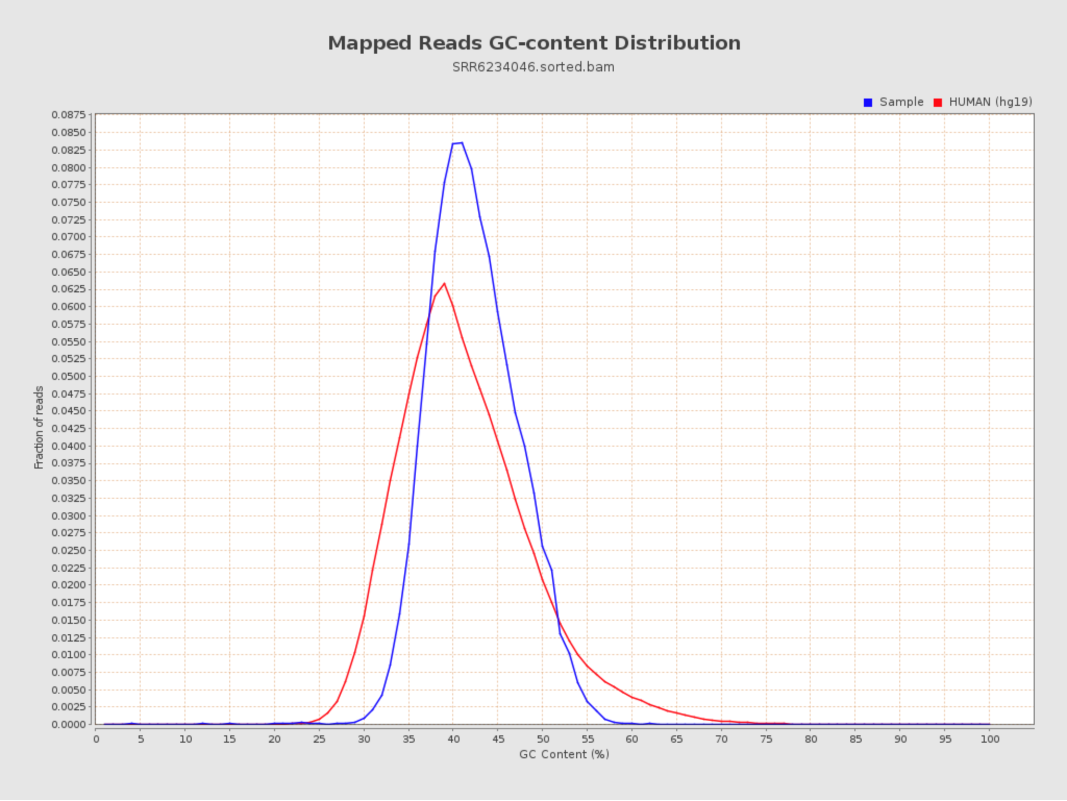
7. Results : Duplication Rate Histogram



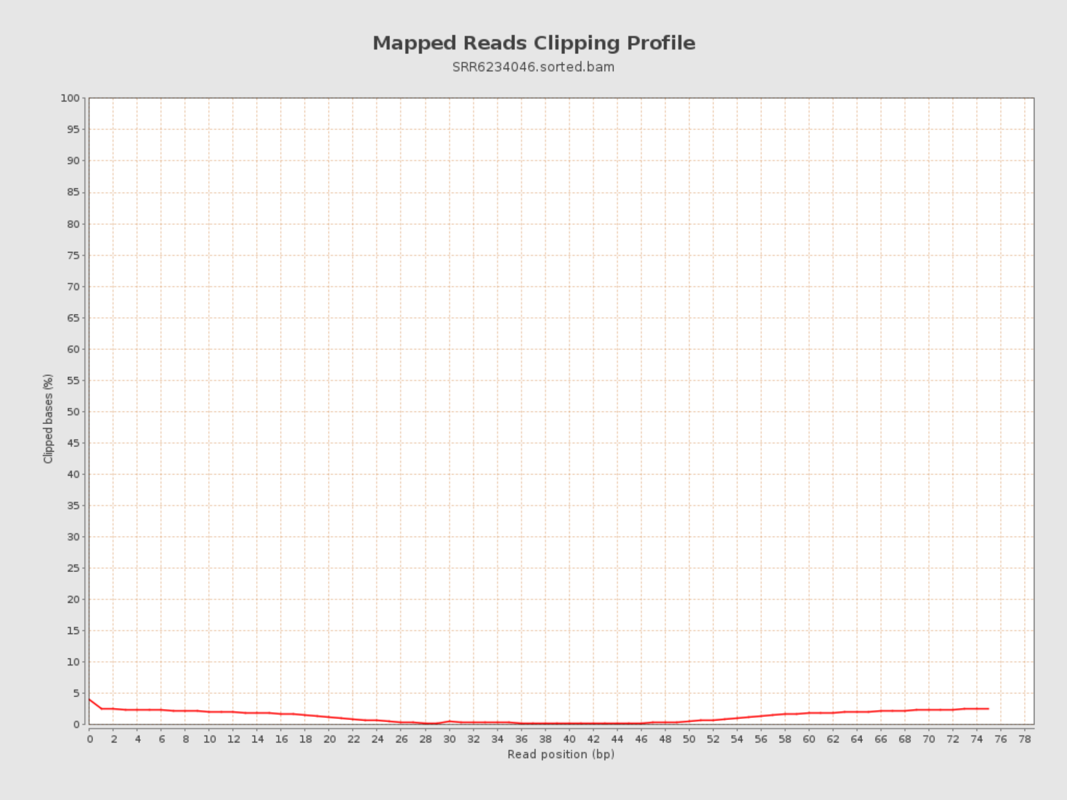
8. Results : Mapped Reads Nucleotide Content



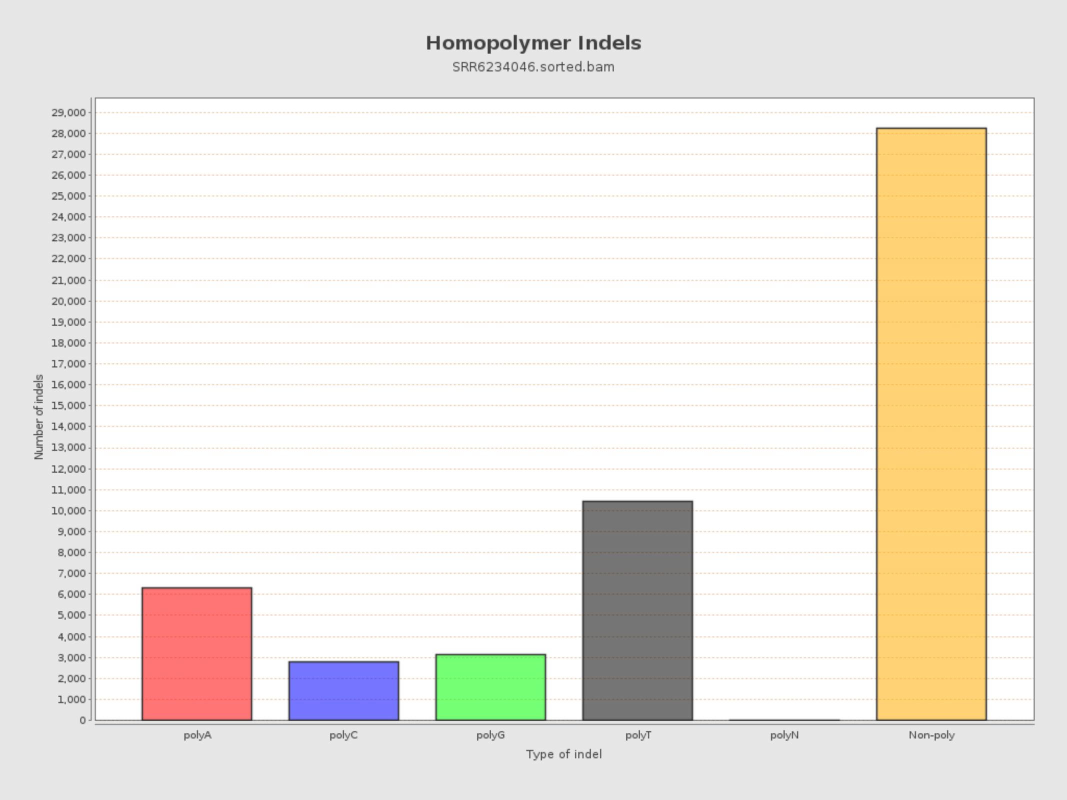
9. Results : Mapped Reads GC-content Distribution



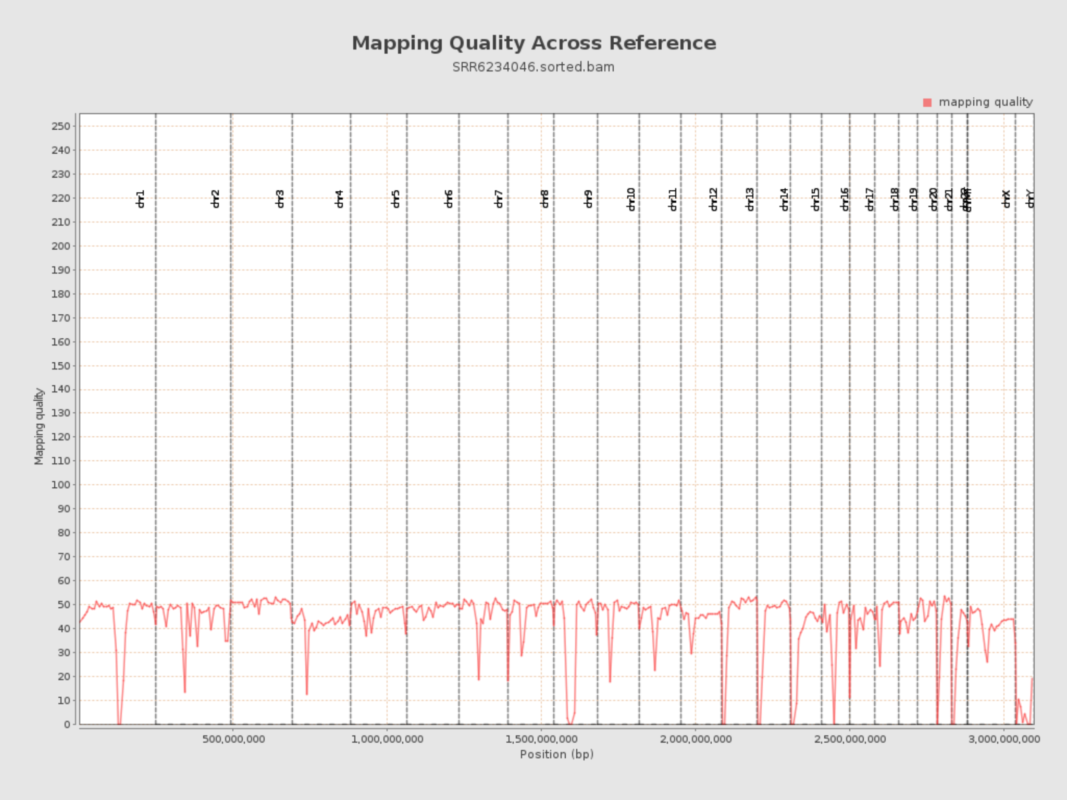
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram