Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 21:14:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004022.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_SRR6004022 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004022.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 21:14:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004022.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,956,597
Mapped reads	2,651,105 / 89.67%
Unmapped reads	305,492 / 10.33%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,646 / 0.66%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	107,533 / 3.64%
Duplication rate	3.15%
Clipped reads	1,399,169 / 47.32%

2.2. ACGT Content

Number/percentage of A's	45,736,486 / 26.57%
Number/percentage of C's	32,451,882 / 18.85%
Number/percentage of T's	53,078,830 / 30.84%
Number/percentage of G's	40,822,482 / 23.72%
Number/percentage of N's	32,919 / 0.02%
GC Percentage	42.57%

2.3. Coverage

Mean	0.0556

Standard Deviation	0.453

2.4. Mapping Quality

Mean Mapping Quality	43.11

2.5. Mismatches and indels

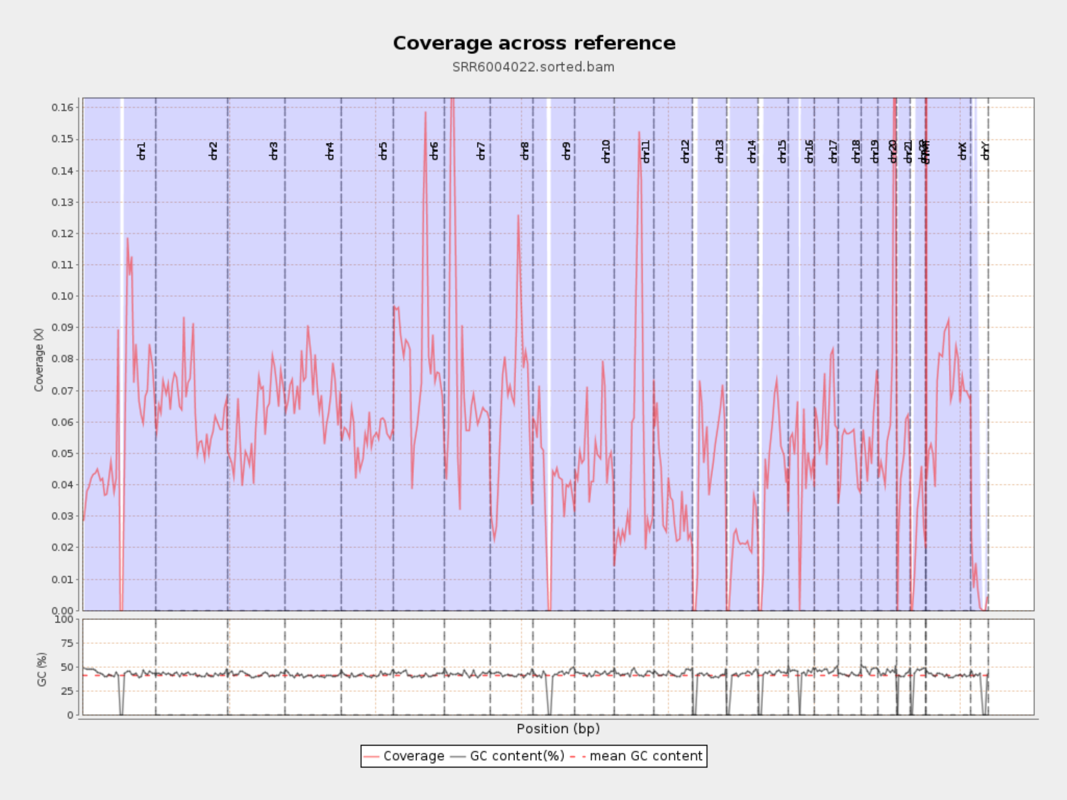
General error rate	0.86%
Mismatches	1,456,494
Insertions	13,054
Mapped reads with at least one insertion	0.49%
Deletions	51,252
Mapped reads with at least one deletion	1.91%
Homopolymer indels	45.74%

2.6. Chromosome stats

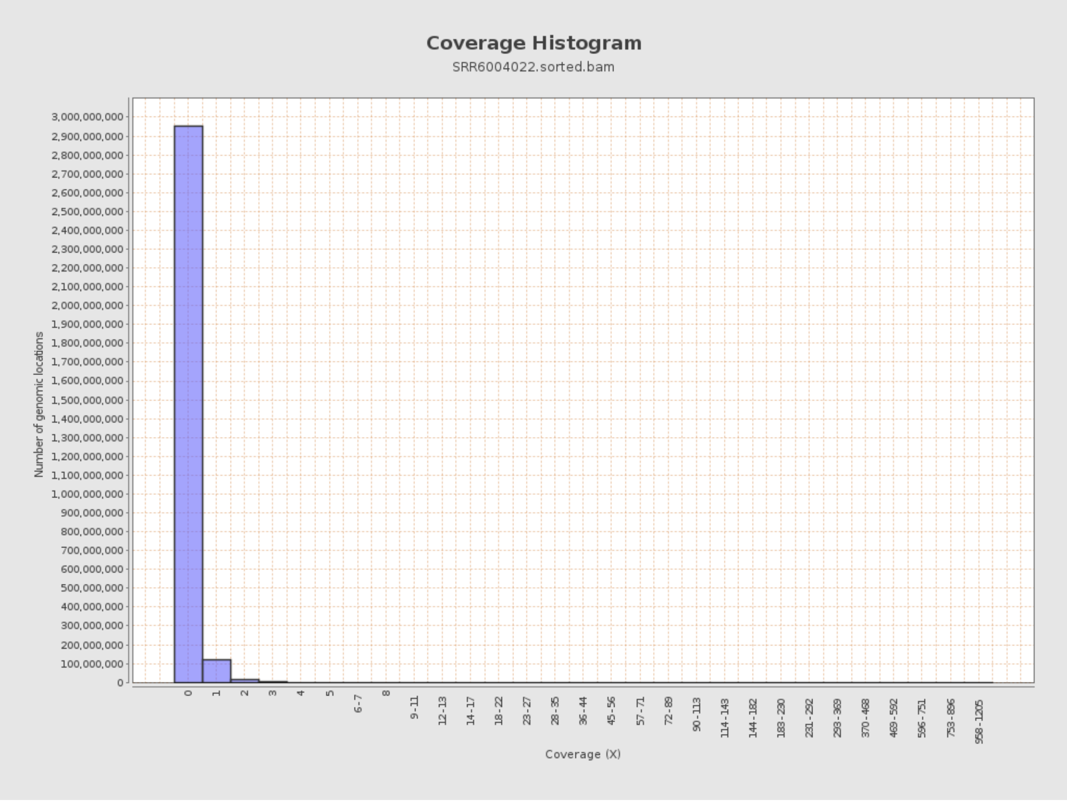
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13973462	0.0561	0.8787
chr2	243199373	15728274	0.0647	0.6135
chr3	198022430	11842117	0.0598	0.2839
chr4	191154276	13427122	0.0702	0.3089
chr5	180915260	10057752	0.0556	0.2712
chr6	171115067	14100410	0.0824	0.4197
chr7	159138663	11575544	0.0727	0.6861

chr8	146364022	9643733	0.0659	0.4569
chr9	141213431	5662119	0.0401	0.3258
chr10	135534747	6823526	0.0503	0.4064
chr11	135006516	6669119	0.0494	0.3026
chr12	133851895	4695396	0.0351	0.2235
chr13	115169878	5425650	0.0471	0.2503
chr14	107349540	2213538	0.0206	0.2183
chr15	102531392	4449752	0.0434	0.2608
chr16	90354753	4084394	0.0452	0.2684
chr17	81195210	5147609	0.0634	0.3101
chr18	78077248	3926345	0.0503	0.5288
chr19	59128983	3311488	0.056	0.647
chr20	63025520	4832846	0.0767	0.3432
chr21	48129895	2074537	0.0431	0.2514
chr22	51304566	1227324	0.0239	0.1786
chrMT	16571	75321	4.5454	4.0979
chrX	155270560	10857621	0.0699	0.3361
chrY	59373566	381045	0.0064	0.1038

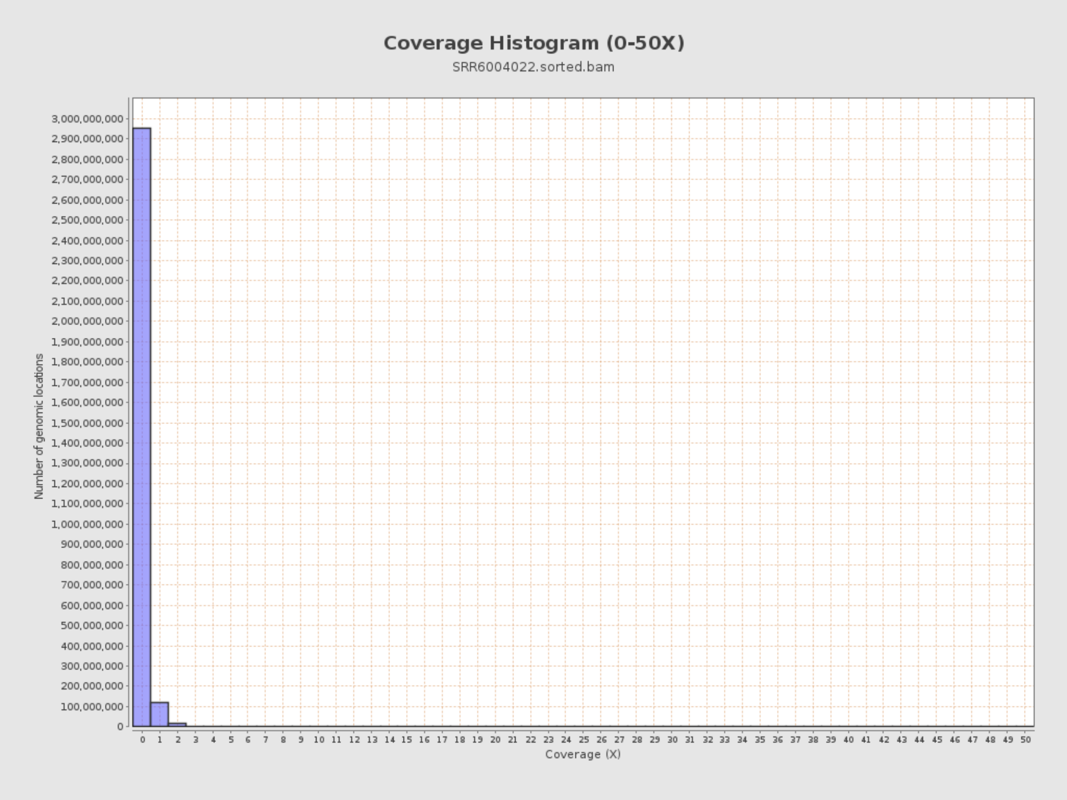
3. Results : Coverage across reference



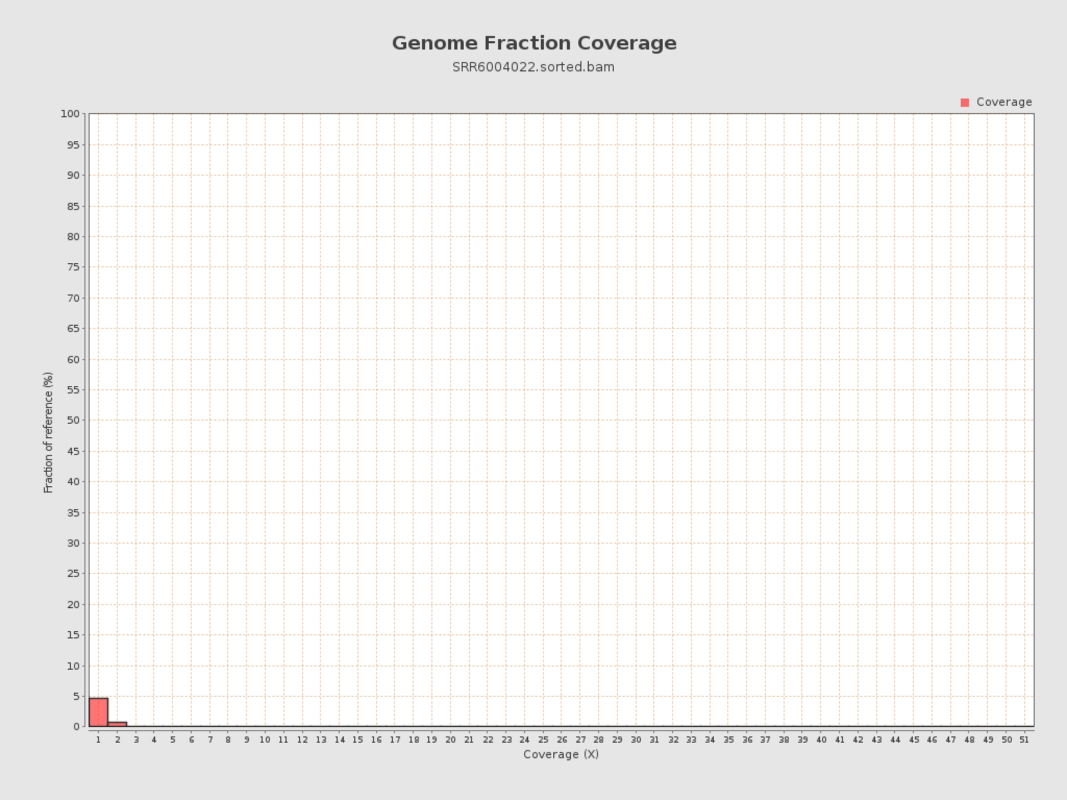
4. Results : Coverage Histogram



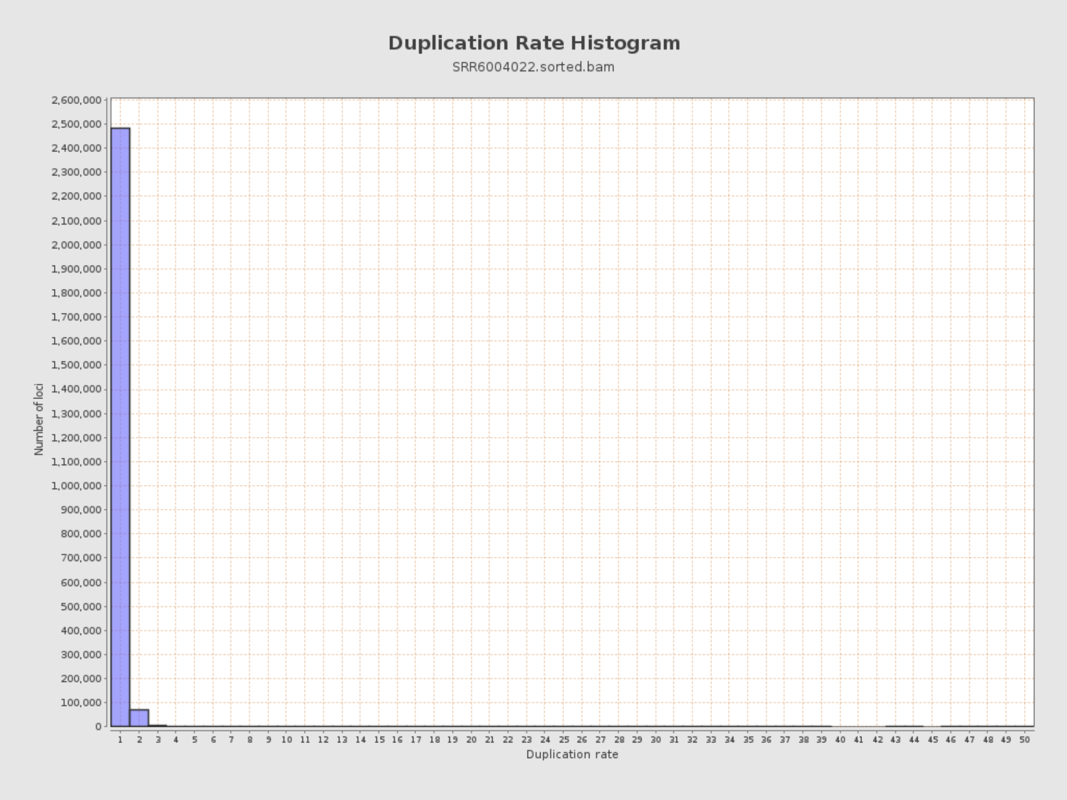
5. Results : Coverage Histogram (0-50X)



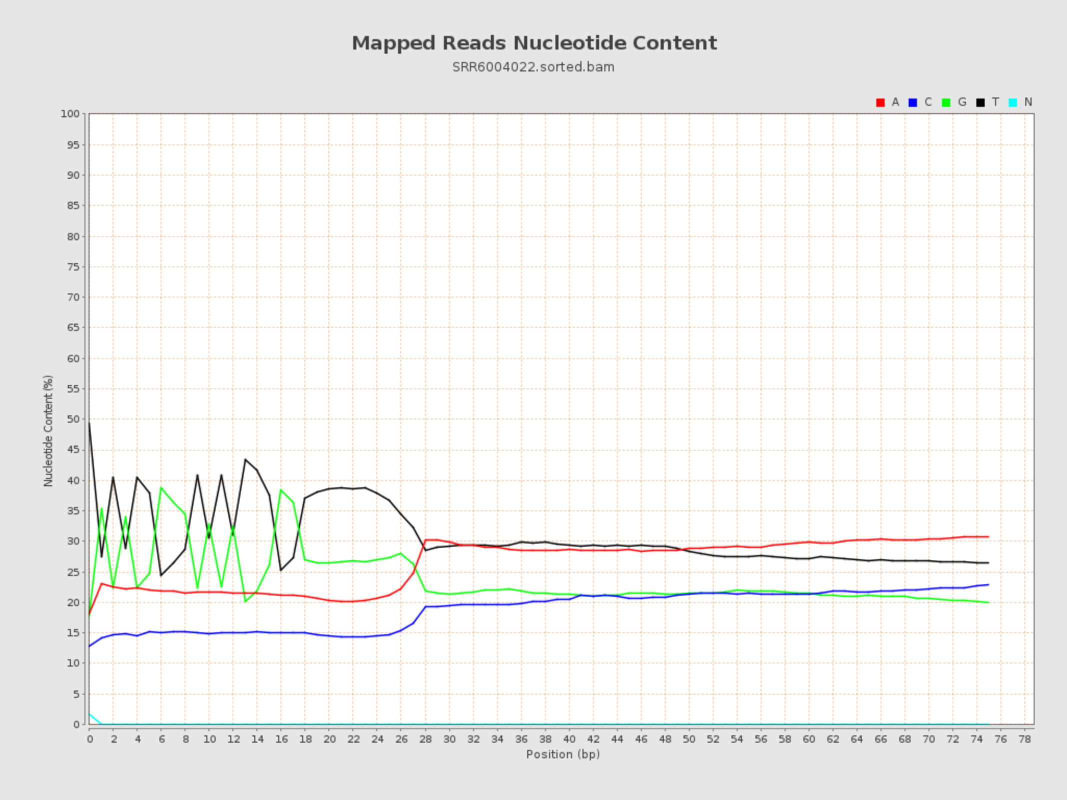
6. Results : Genome Fraction Coverage



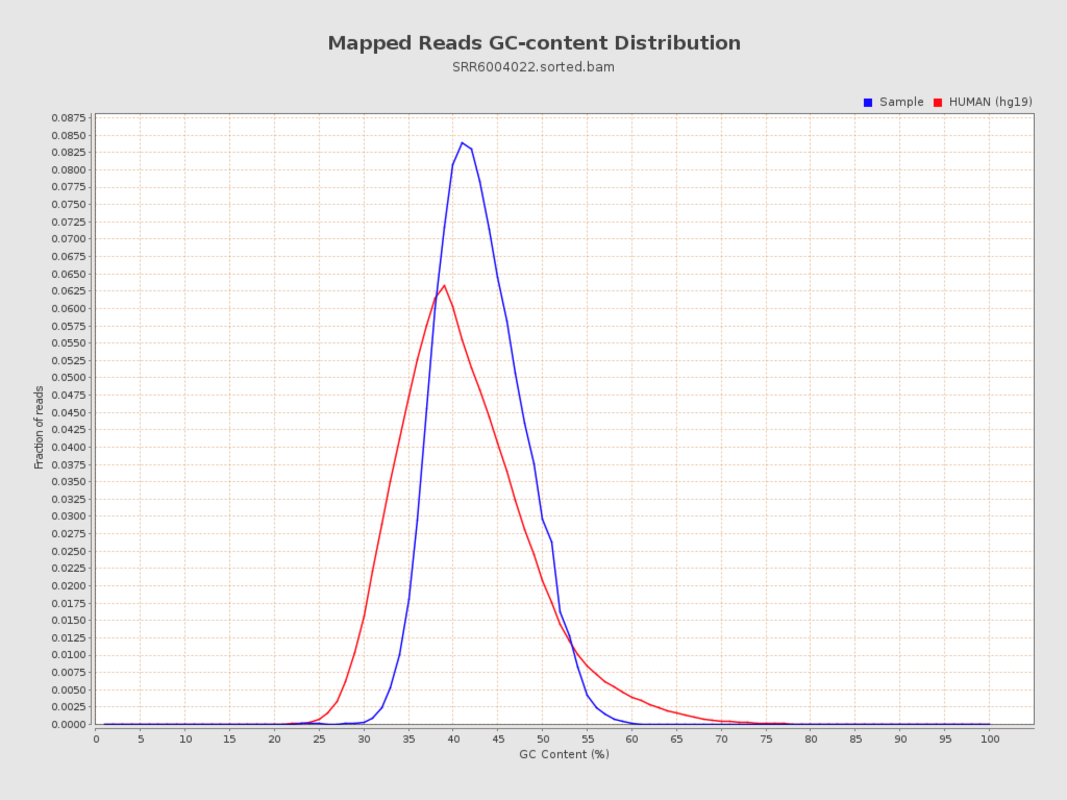
7. Results : Duplication Rate Histogram



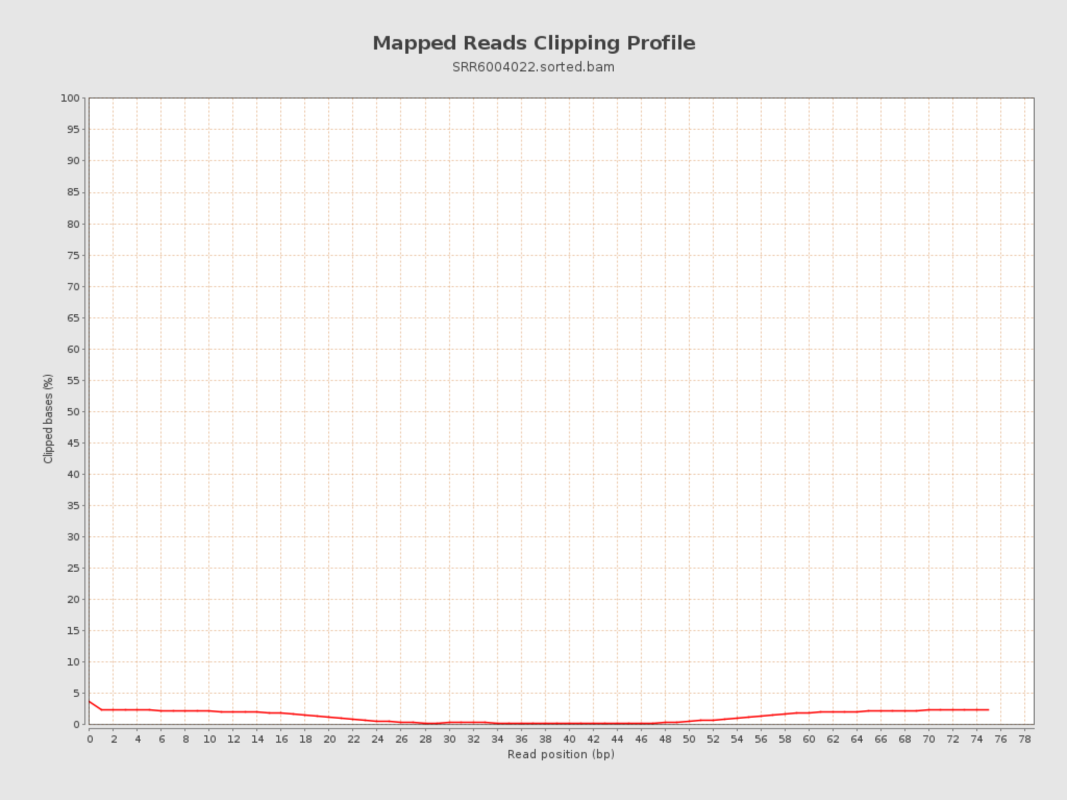
8. Results : Mapped Reads Nucleotide Content



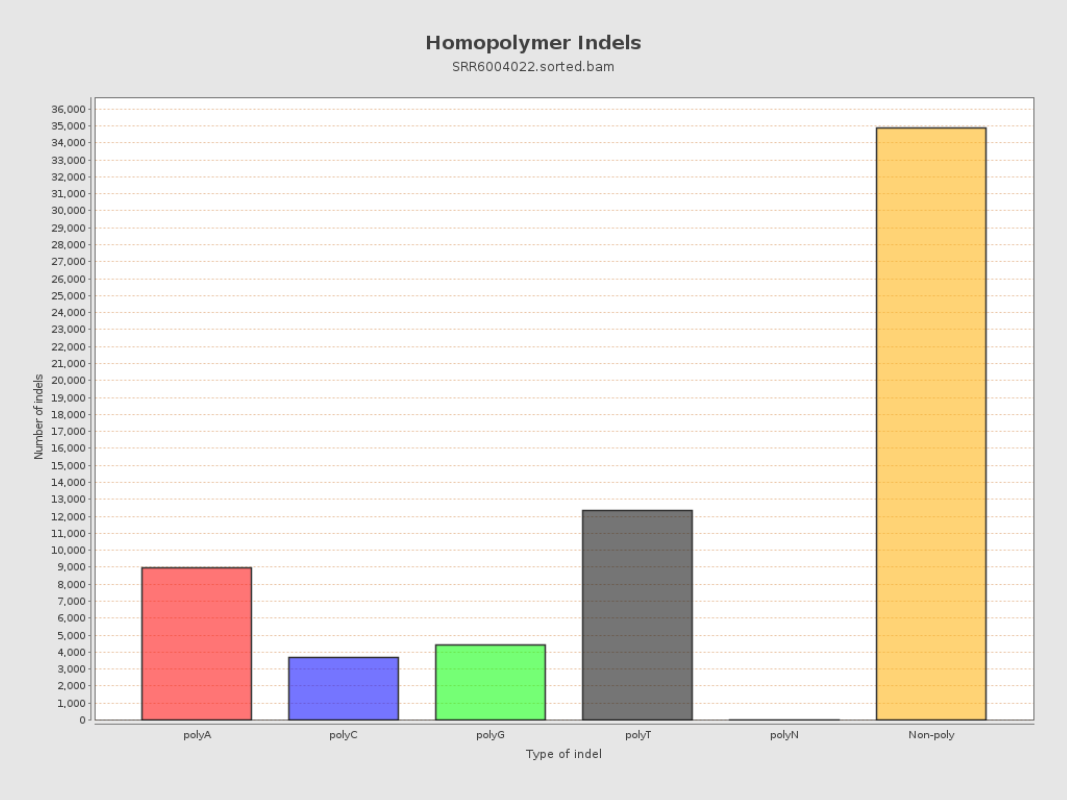
9. Results : Mapped Reads GC-content Distribution



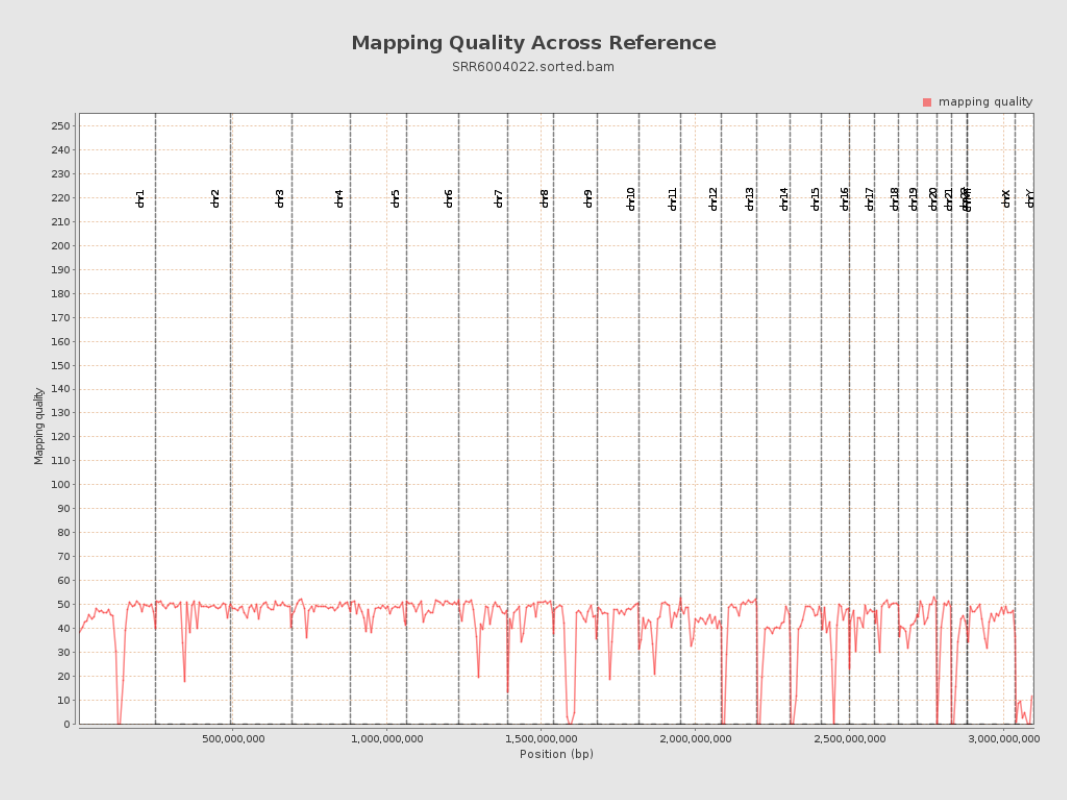
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram