Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 18:09:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230338.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_SRR6230338 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230338.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 18:09:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6230338.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,257,585
Mapped reads	2,768,033 / 84.97%
Unmapped reads	489,552 / 15.03%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,837 / 0.61%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	130,105 / 3.99%
Duplication rate	3.5%
Clipped reads	1,283,549 / 39.4%

2.2. ACGT Content

Number/percentage of A's	50,354,500 / 27.47%
Number/percentage of C's	31,949,914 / 17.43%
Number/percentage of T's	60,808,294 / 33.17%
Number/percentage of G's	39,836,286 / 21.73%
Number/percentage of N's	357,478 / 0.2%
GC Percentage	39.16%

2.3. Coverage

Mean	0.0592

Standard Deviation	0.5521

2.4. Mapping Quality

Mean Mapping Quality	47.28

2.5. Mismatches and indels

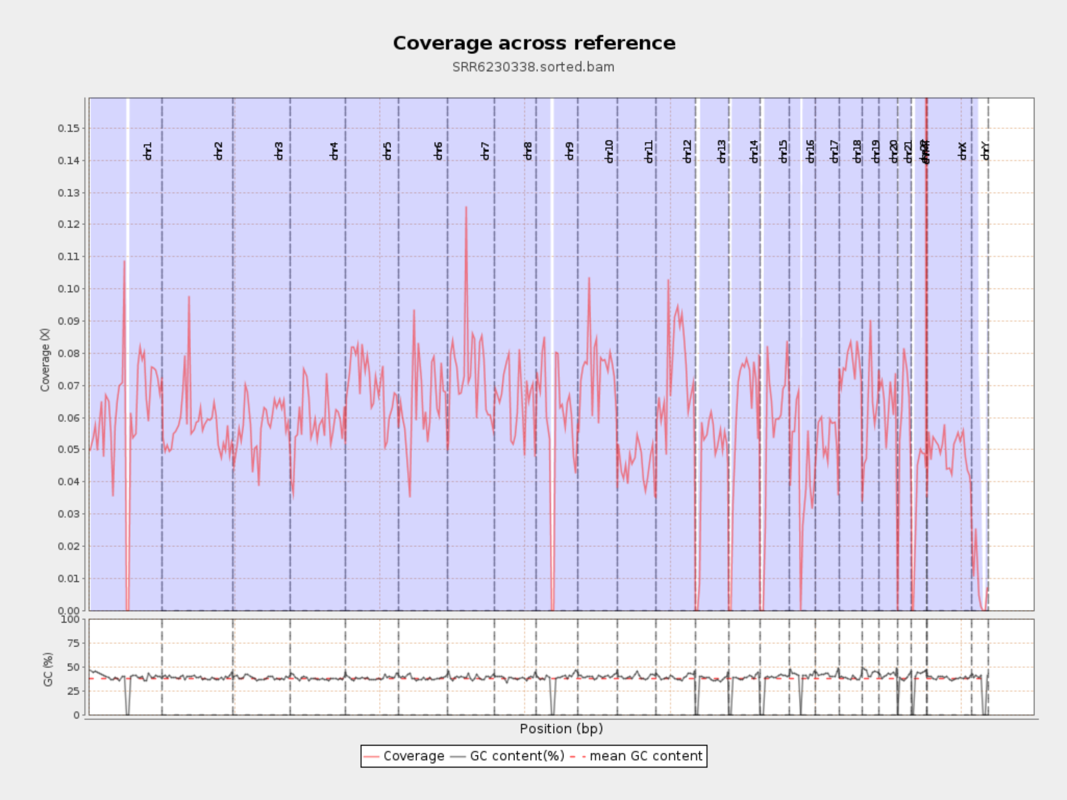
General error rate	1.02%
Mismatches	1,837,134
Insertions	16,762
Mapped reads with at least one insertion	0.6%
Deletions	47,312
Mapped reads with at least one deletion	1.69%
Homopolymer indels	48.61%

2.6. Chromosome stats

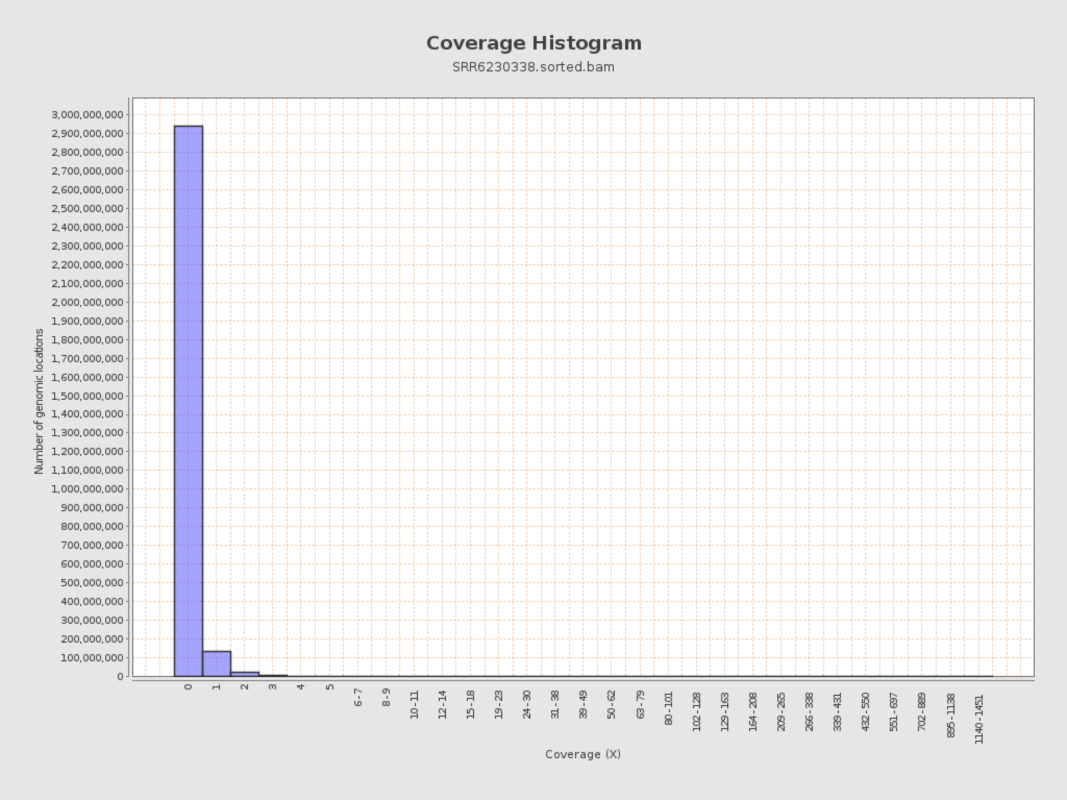
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15234265	0.0611	1.1409
chr2	243199373	14122988	0.0581	0.504
chr3	198022430	11345487	0.0573	0.2741
chr4	191154276	11160292	0.0584	0.3136
chr5	180915260	12707324	0.0702	0.309
chr6	171115067	10975584	0.0641	0.4003
chr7	159138663	11929375	0.075	0.806

chr8	146364022	9533955	0.0651	0.9174
chr9	141213431	8222674	0.0582	0.4814
chr10	135534747	10188748	0.0752	0.4724
chr11	135006516	6112961	0.0453	0.3769
chr12	133851895	9955524	0.0744	0.3212
chr13	115169878	5255184	0.0456	0.2435
chr14	107349540	6345467	0.0591	0.3094
chr15	102531392	5615638	0.0548	0.2682
chr16	90354753	3890892	0.0431	0.2791
chr17	81195210	4296832	0.0529	0.2996
chr18	78077248	5999357	0.0768	0.8851
chr19	59128983	3664620	0.062	0.6721
chr20	63025520	4026290	0.0639	0.3122
chr21	48129895	2804508	0.0583	0.318
chr22	51304566	1752173	0.0342	0.2092
chrMT	16571	117583	7.0957	4.2121
chrX	155270560	7667144	0.0494	0.2899
chrY	59373566	459279	0.0077	0.1773

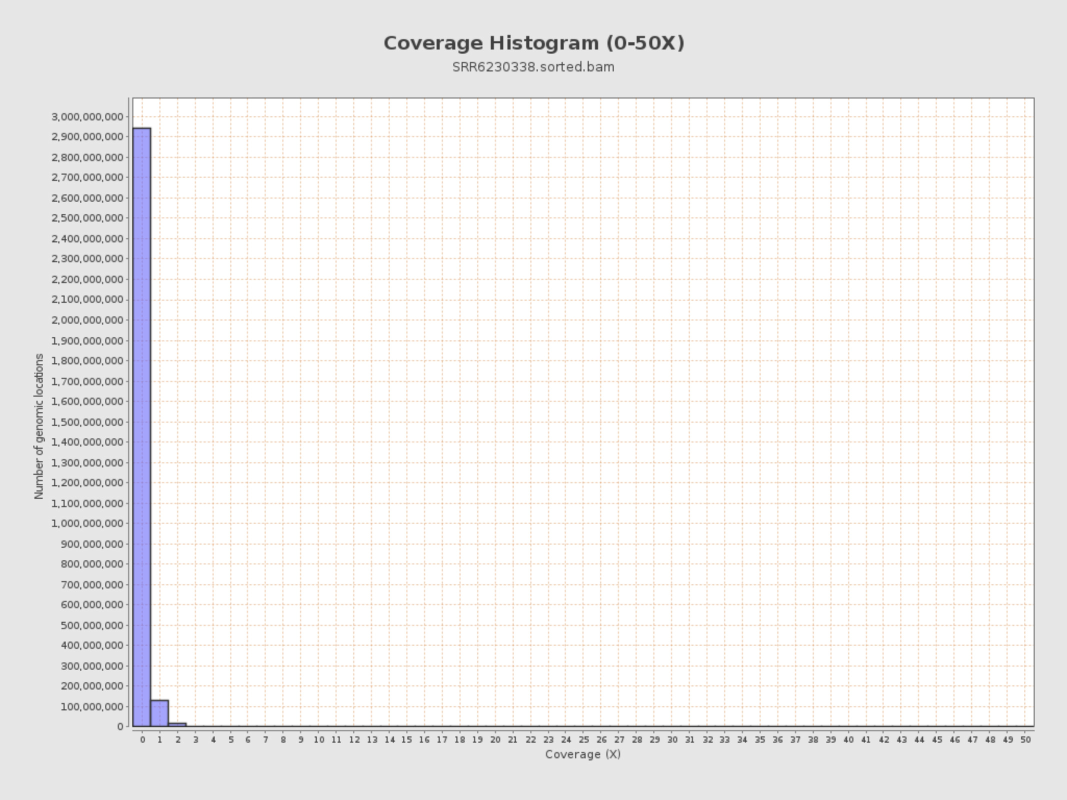
3. Results : Coverage across reference



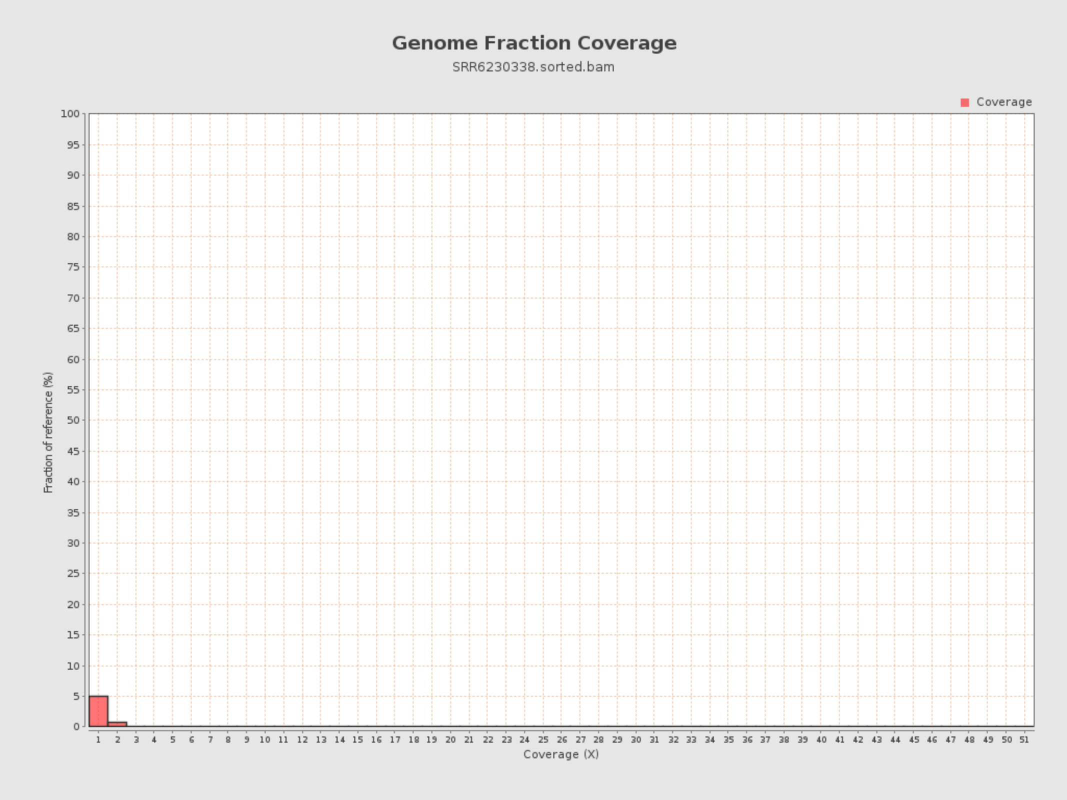
4. Results : Coverage Histogram



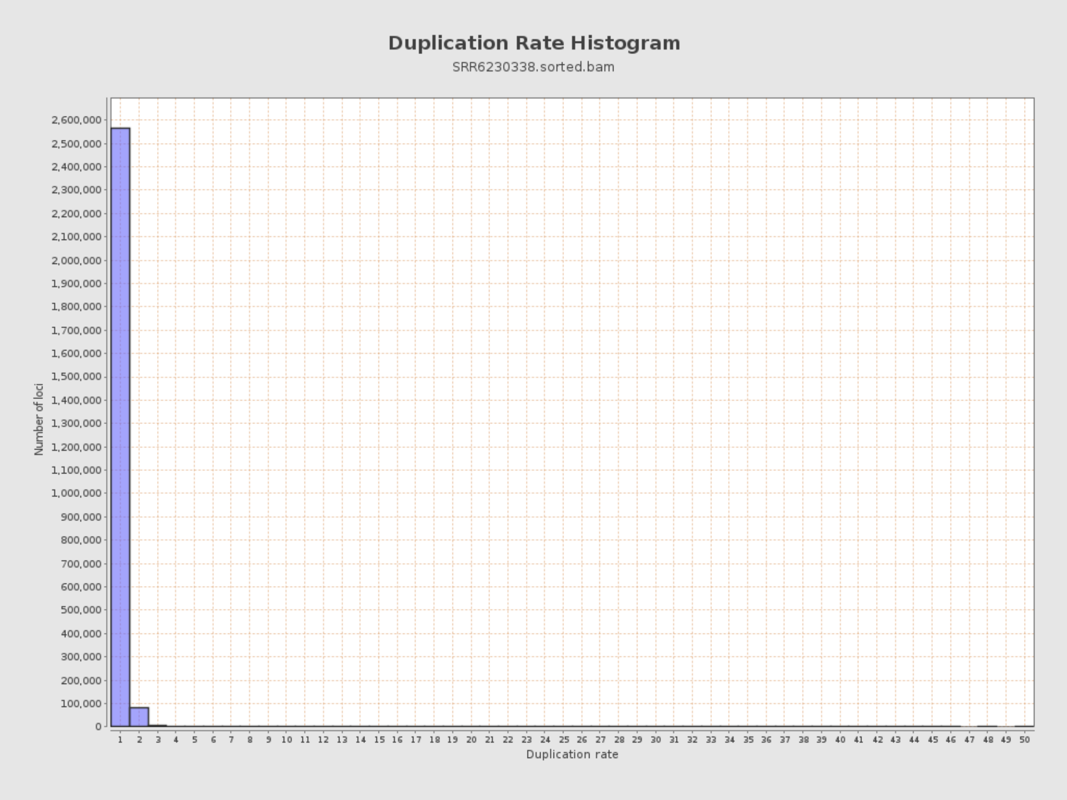
5. Results : Coverage Histogram (0-50X)



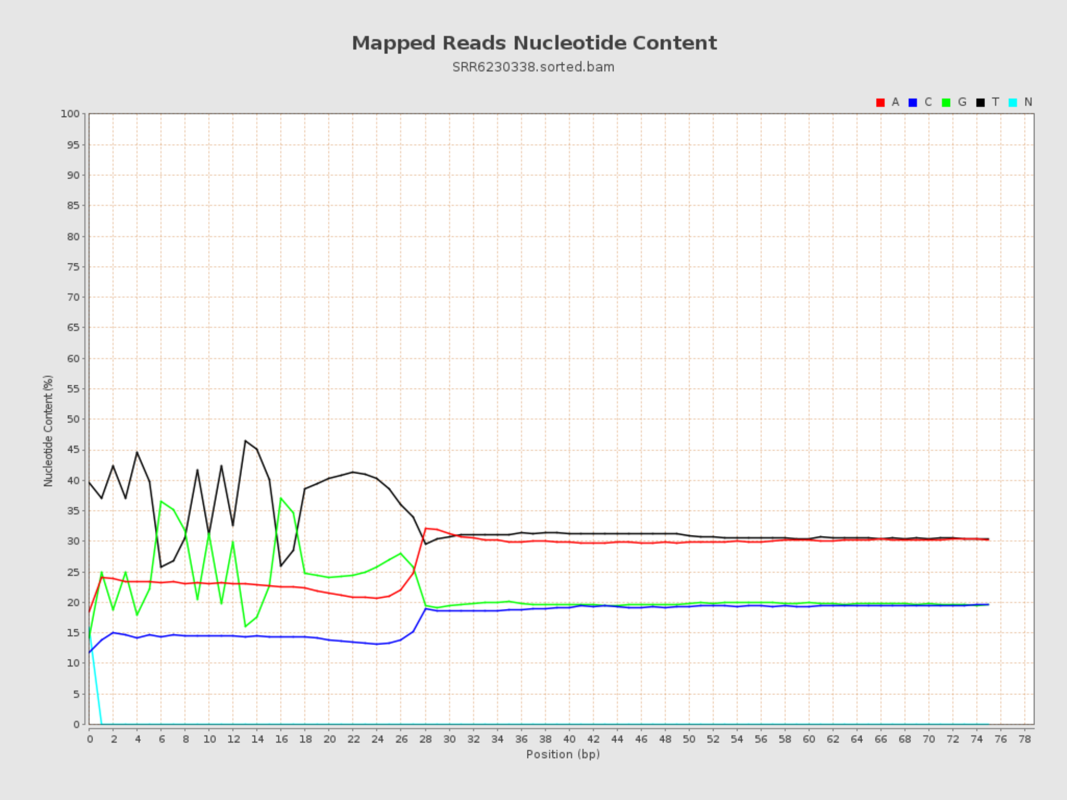
6. Results : Genome Fraction Coverage



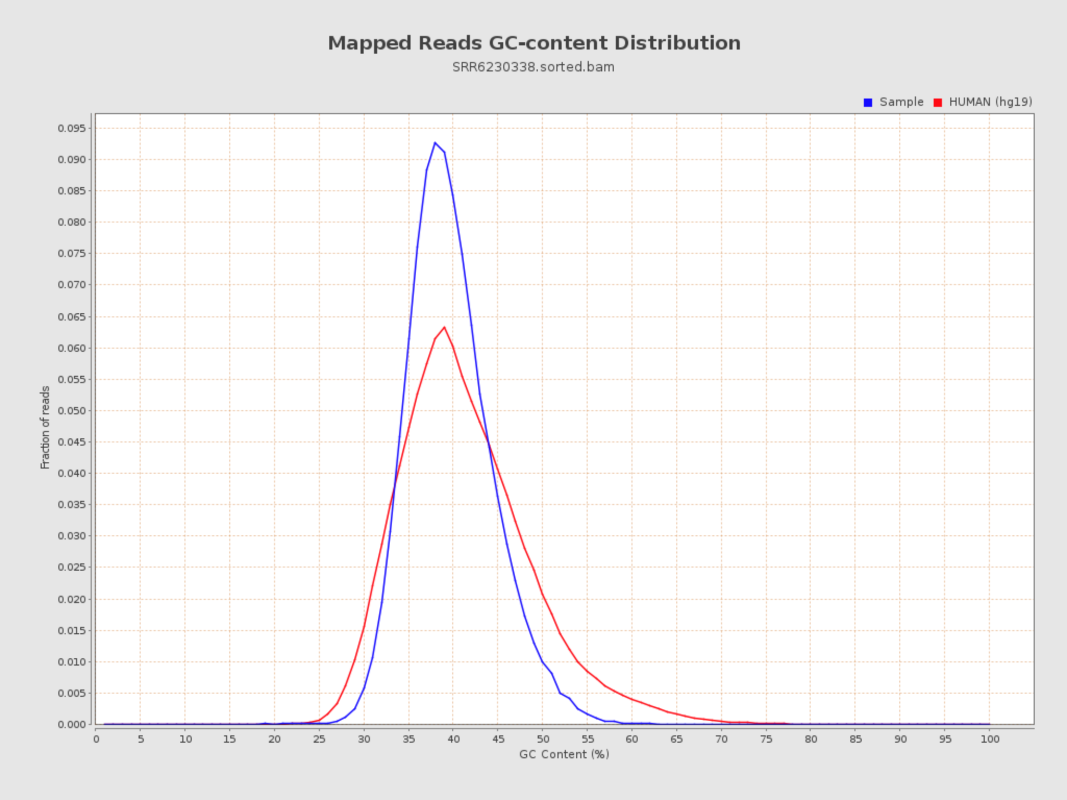
7. Results : Duplication Rate Histogram



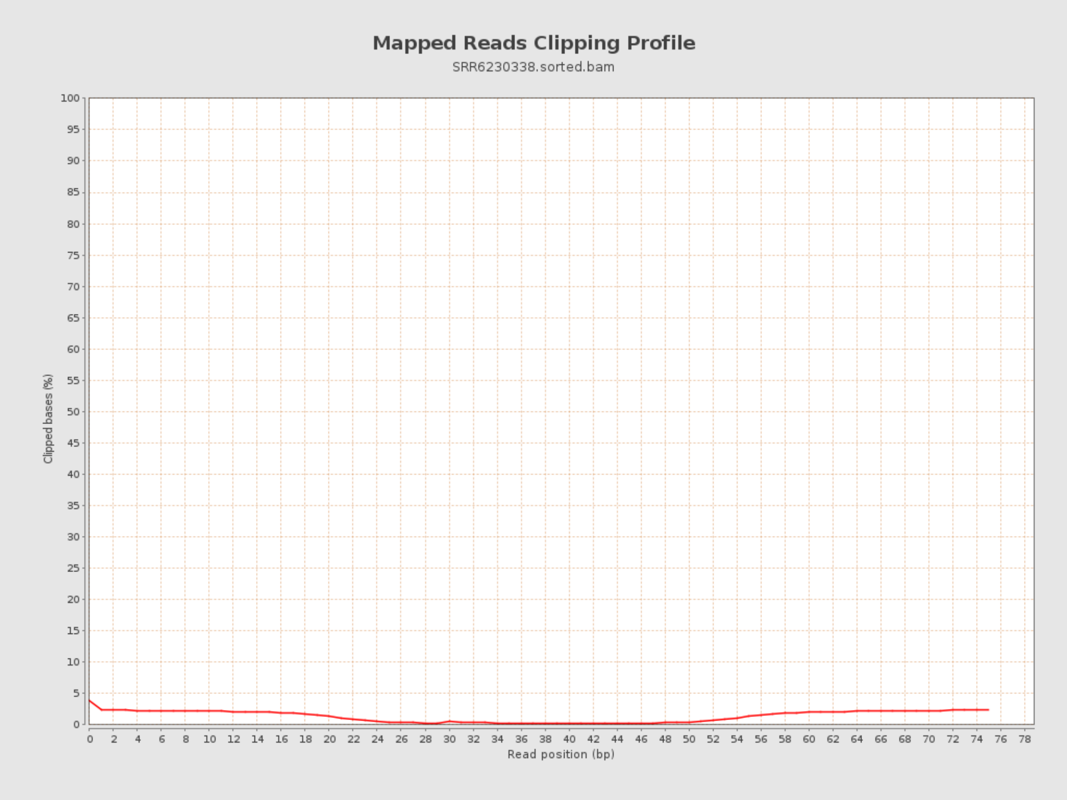
8. Results : Mapped Reads Nucleotide Content



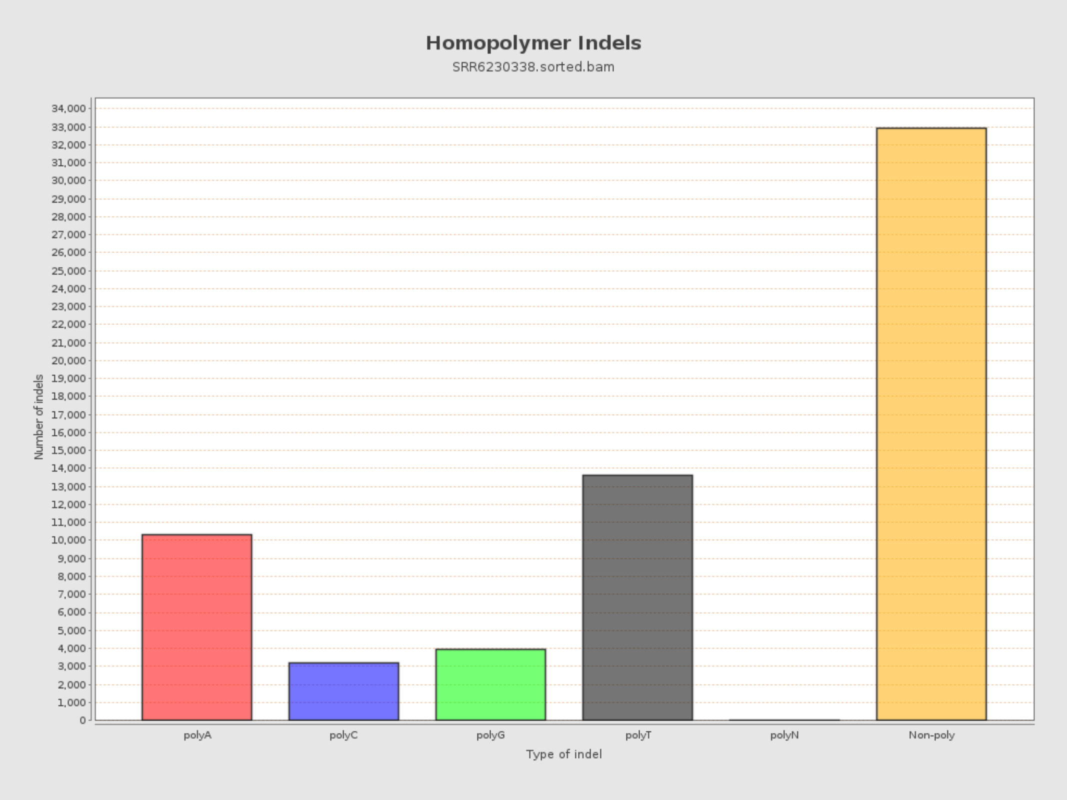
9. Results : Mapped Reads GC-content Distribution



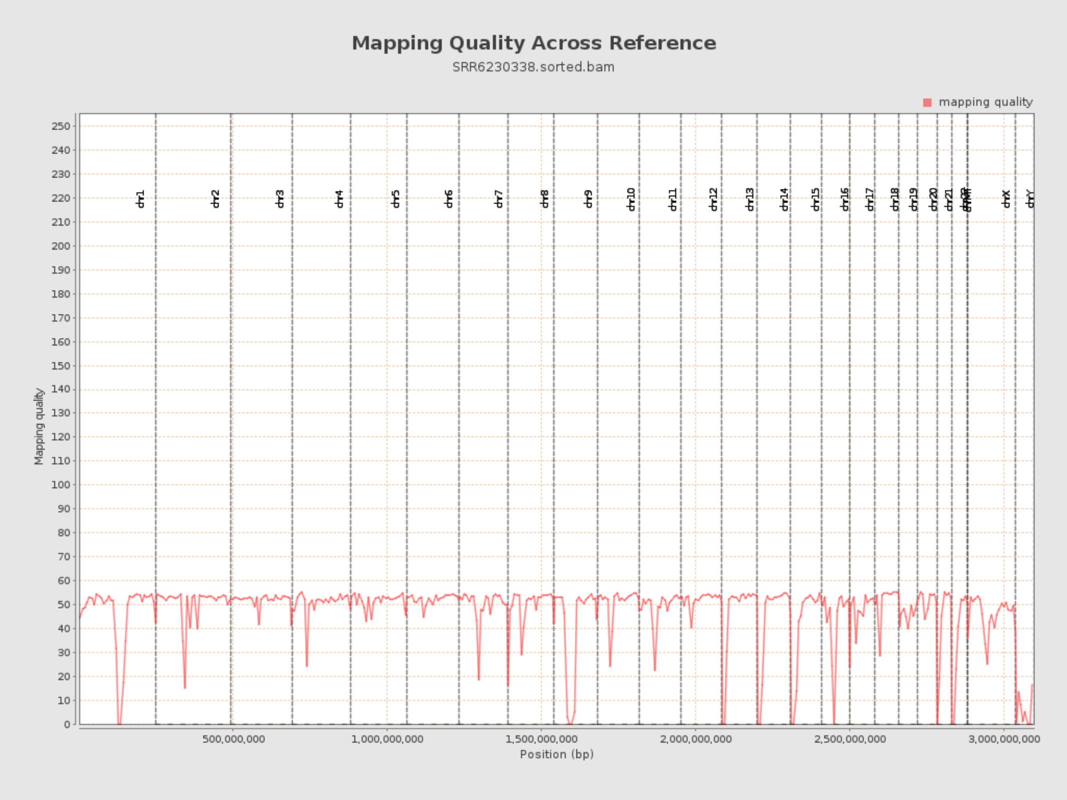
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram