Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 02:12:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238672.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_SRR6238672 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238672.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 02:12:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238672.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,715,776
Mapped reads	4,063,491 / 86.17%
Unmapped reads	652,285 / 13.83%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	32,422 / 0.69%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	1,534,265 / 32.53%
Duplication rate	21.39%
Clipped reads	2,574,256 / 54.59%

2.2. ACGT Content

Number/percentage of A's	61,261,201 / 24.52%
Number/percentage of C's	45,356,909 / 18.15%
Number/percentage of T's	82,217,467 / 32.91%
Number/percentage of G's	61,013,408 / 24.42%
Number/percentage of N's	12,466 / 0%
GC Percentage	42.57%

2.3. Coverage

Mean	0.0808

Standard Deviation	1.3362

2.4. Mapping Quality

Mean Mapping Quality	43.06

2.5. Mismatches and indels

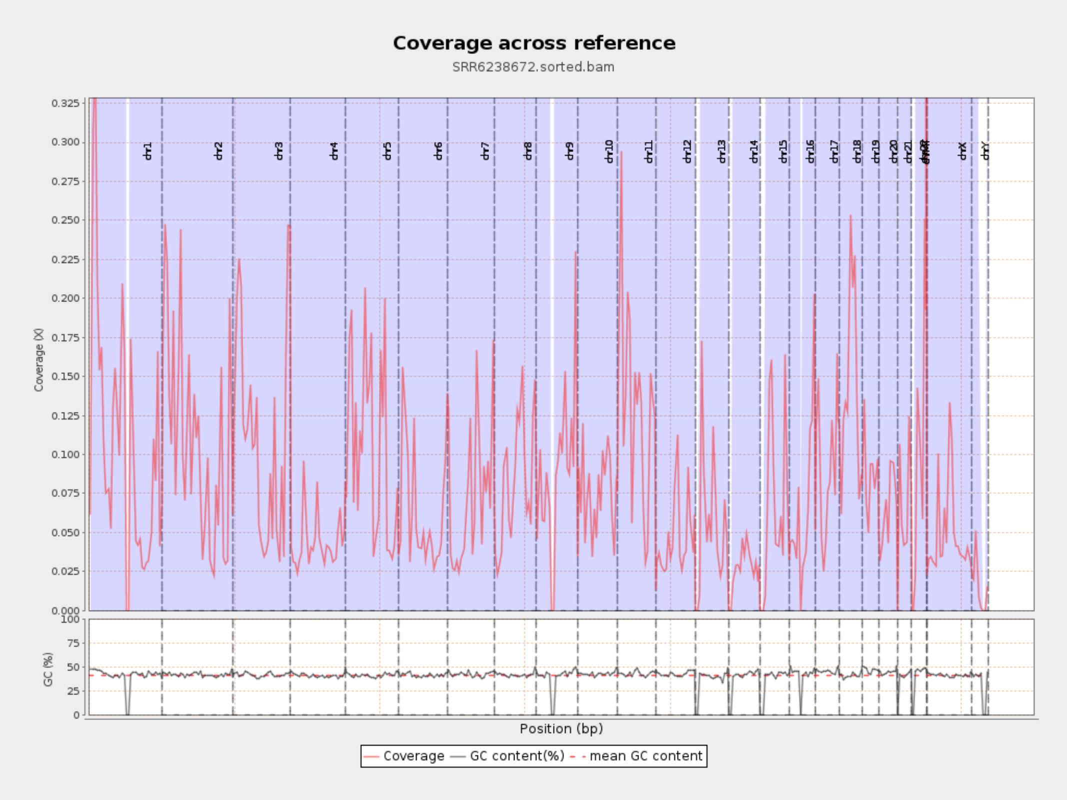
General error rate	0.62%
Mismatches	1,523,711
Insertions	17,970
Mapped reads with at least one insertion	0.44%
Deletions	68,817
Mapped reads with at least one deletion	1.68%
Homopolymer indels	40.69%

2.6. Chromosome stats

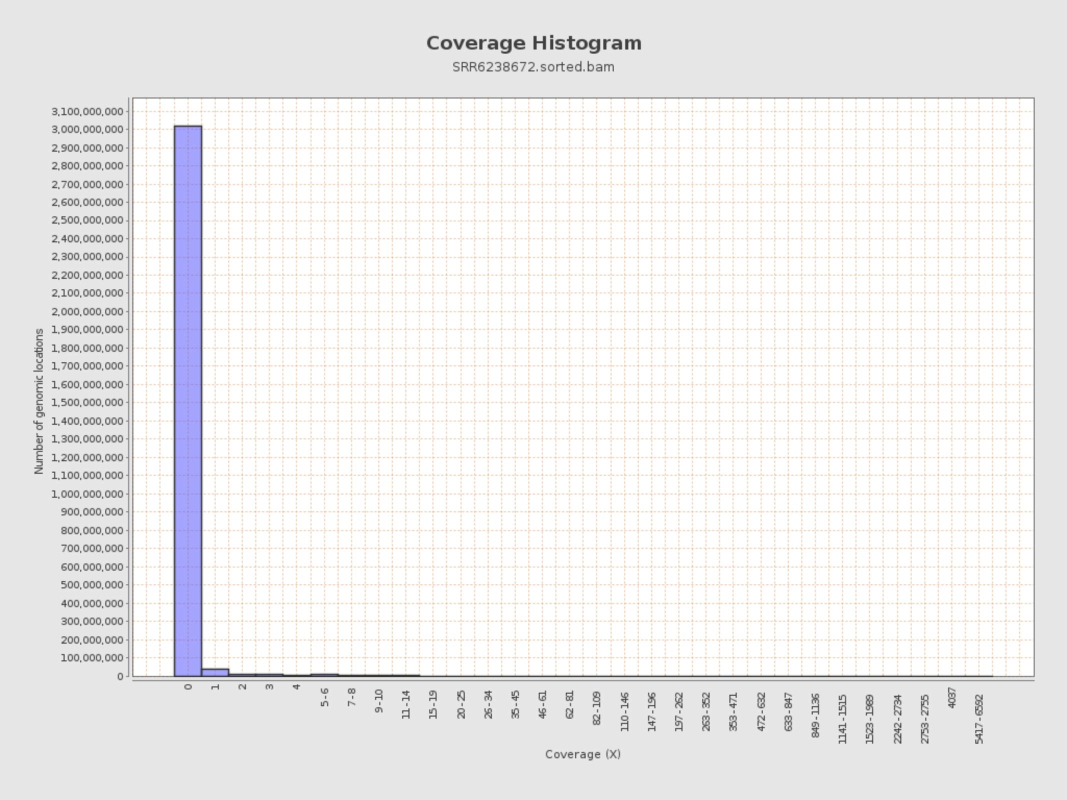
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	26898972	0.1079	1.7224
chr2	243199373	26446794	0.1087	3.0773
chr3	198022430	21477623	0.1085	0.9009
chr4	191154276	8323425	0.0435	0.5426
chr5	180915260	19049726	0.1053	0.8623
chr6	171115067	10781416	0.063	1.1582
chr7	159138663	11337374	0.0712	0.9134

chr8	146364022	11914656	0.0814	1.0045
chr9	141213431	12581074	0.0891	0.9463
chr10	135534747	10148475	0.0749	0.7882
chr11	135006516	17689968	0.131	1.1359
chr12	133851895	6244549	0.0467	0.5741
chr13	115169878	6454283	0.056	0.836
chr14	107349540	2881473	0.0268	0.4259
chr15	102531392	7008262	0.0684	0.9095
chr16	90354753	6186544	0.0685	0.9345
chr17	81195210	7429724	0.0915	0.8514
chr18	78077248	11192329	0.1433	2.7396
chr19	59128983	5109002	0.0864	1.3097
chr20	63025520	4134205	0.0656	0.7128
chr21	48129895	3270811	0.068	0.7397
chr22	51304566	4834981	0.0942	0.879
chrMT	16571	75712	4.5689	5.4244
chrX	155270560	7651558	0.0493	0.6372
chrY	59373566	856694	0.0144	0.5743

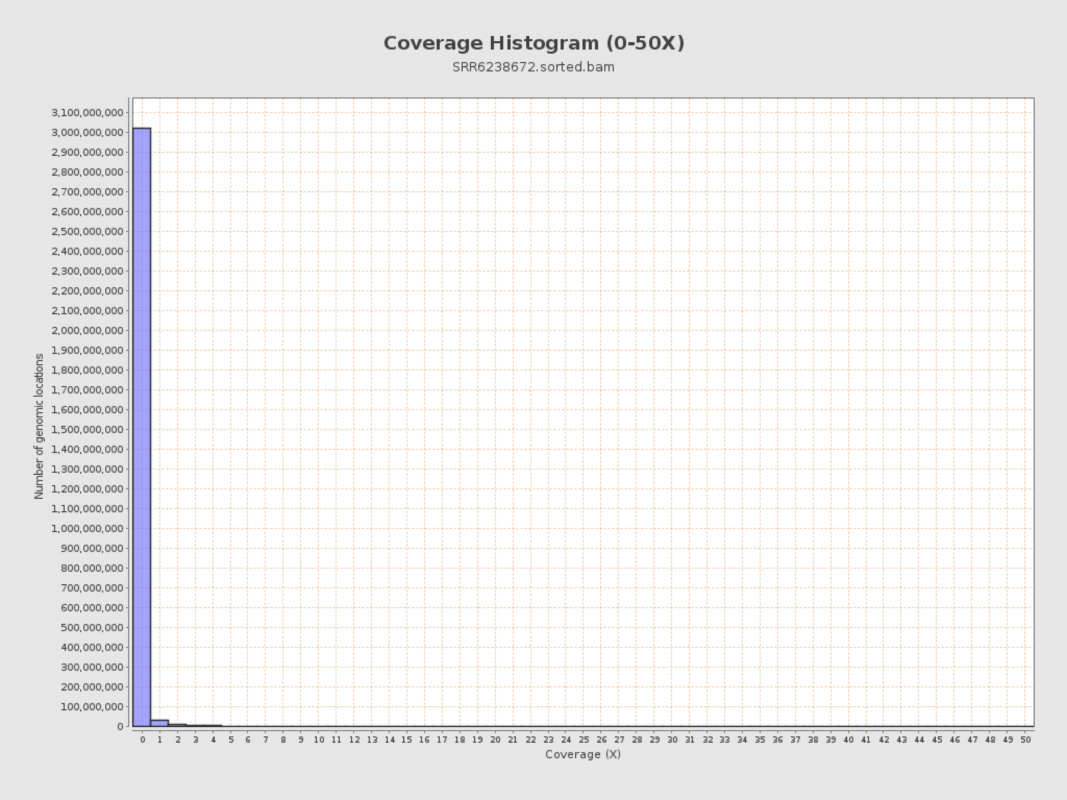
3. Results : Coverage across reference



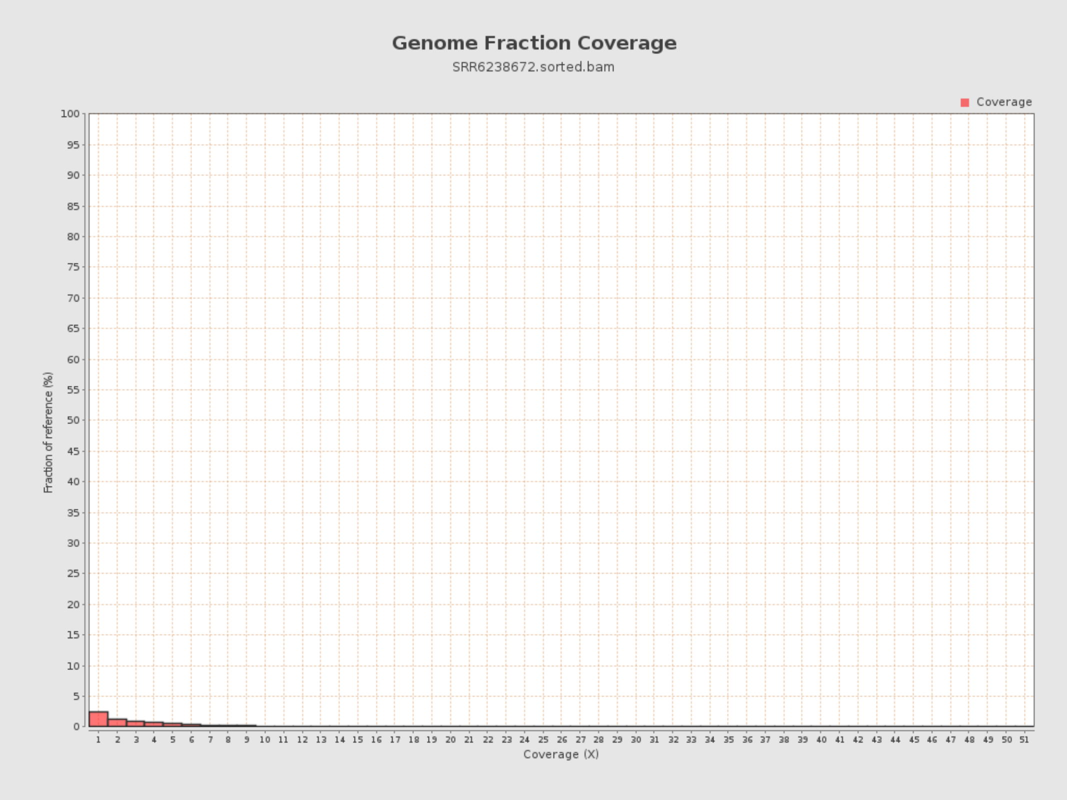
4. Results : Coverage Histogram



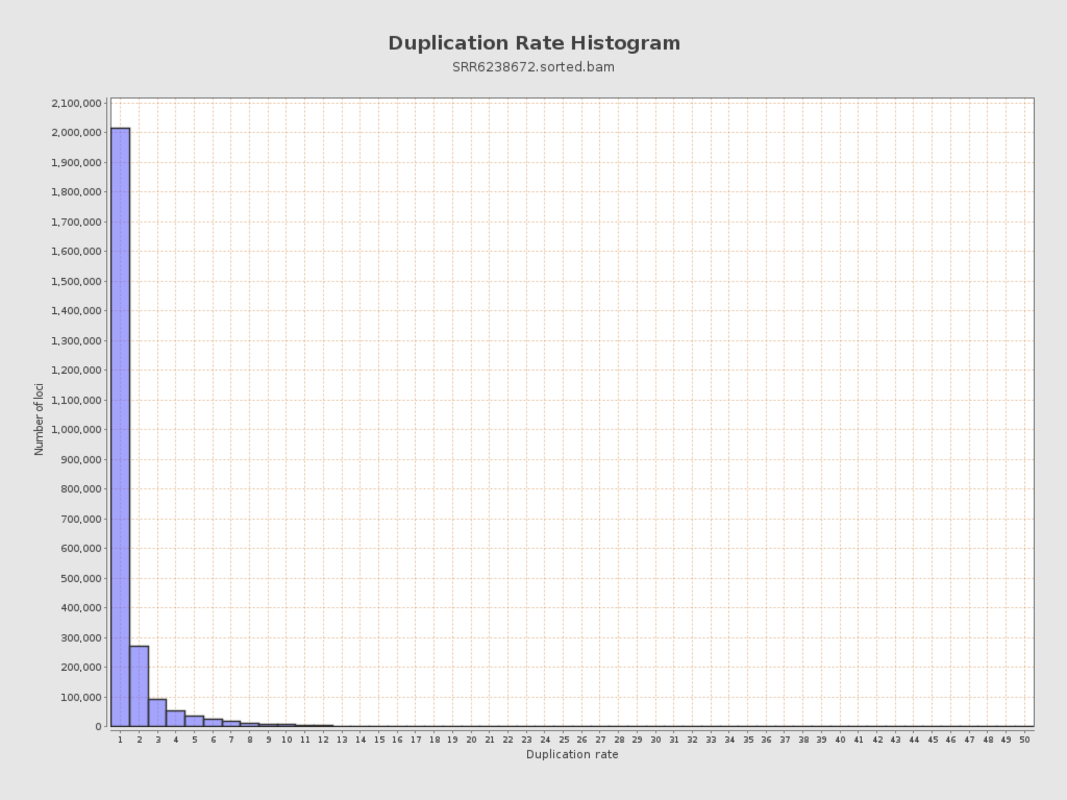
5. Results : Coverage Histogram (0-50X)



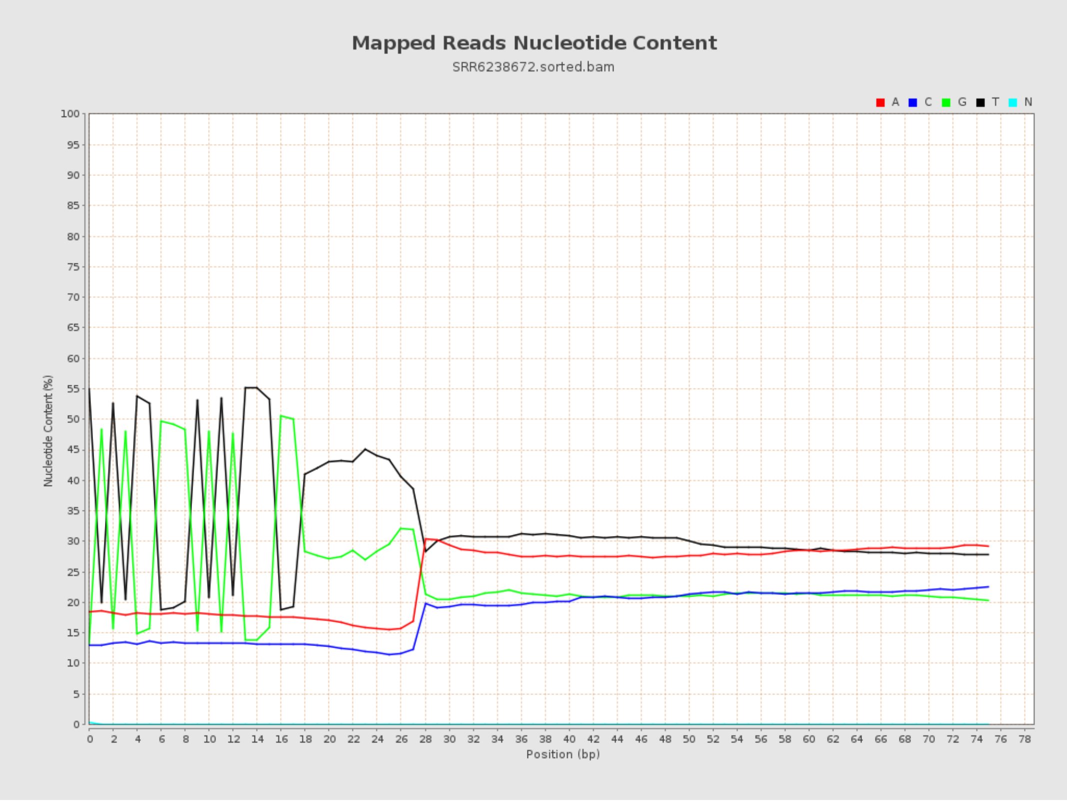
6. Results : Genome Fraction Coverage



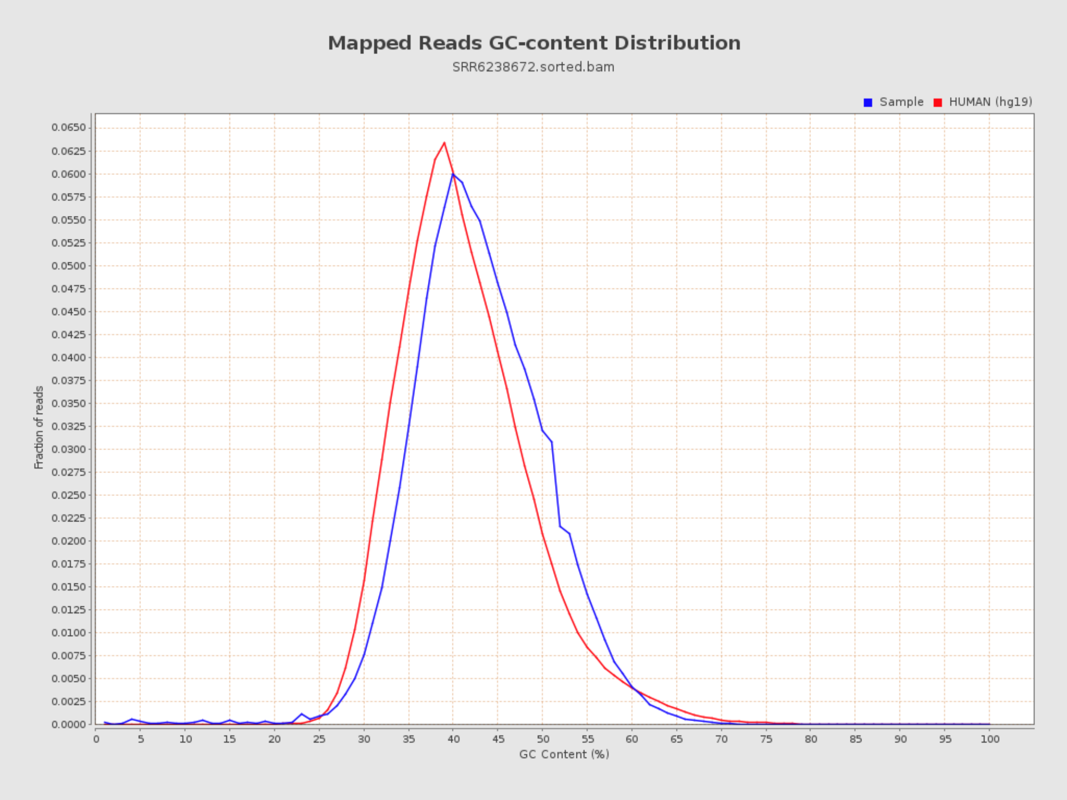
7. Results : Duplication Rate Histogram



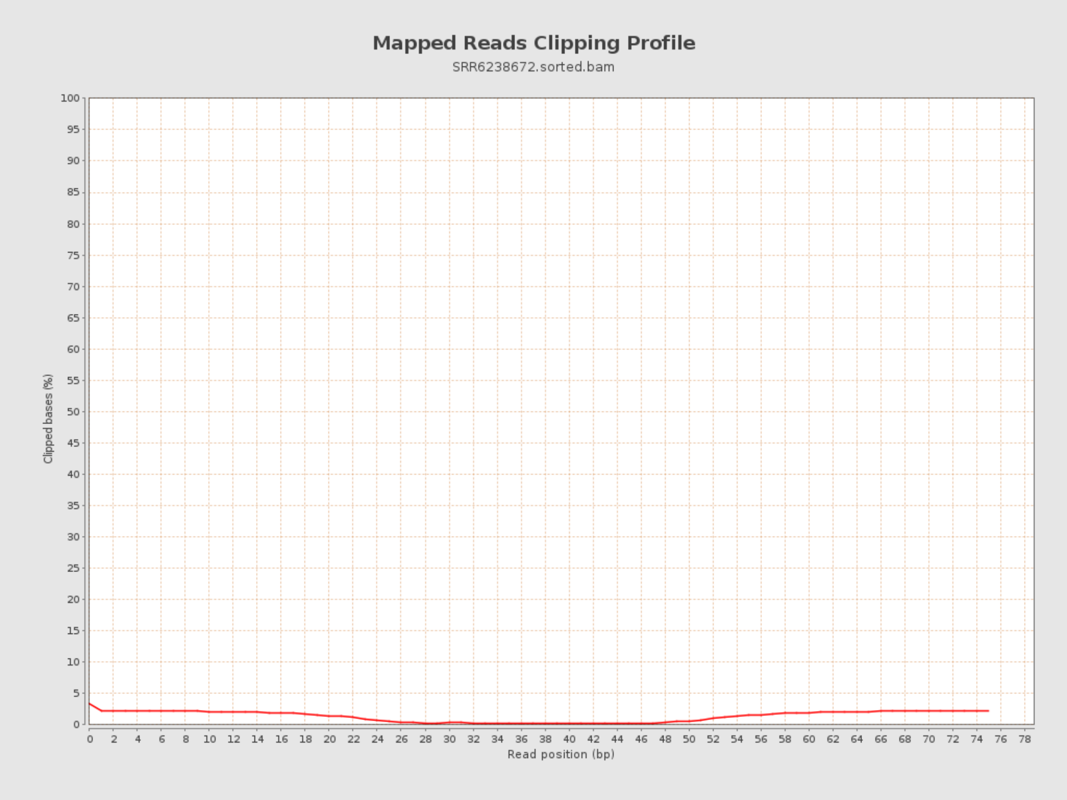
8. Results : Mapped Reads Nucleotide Content



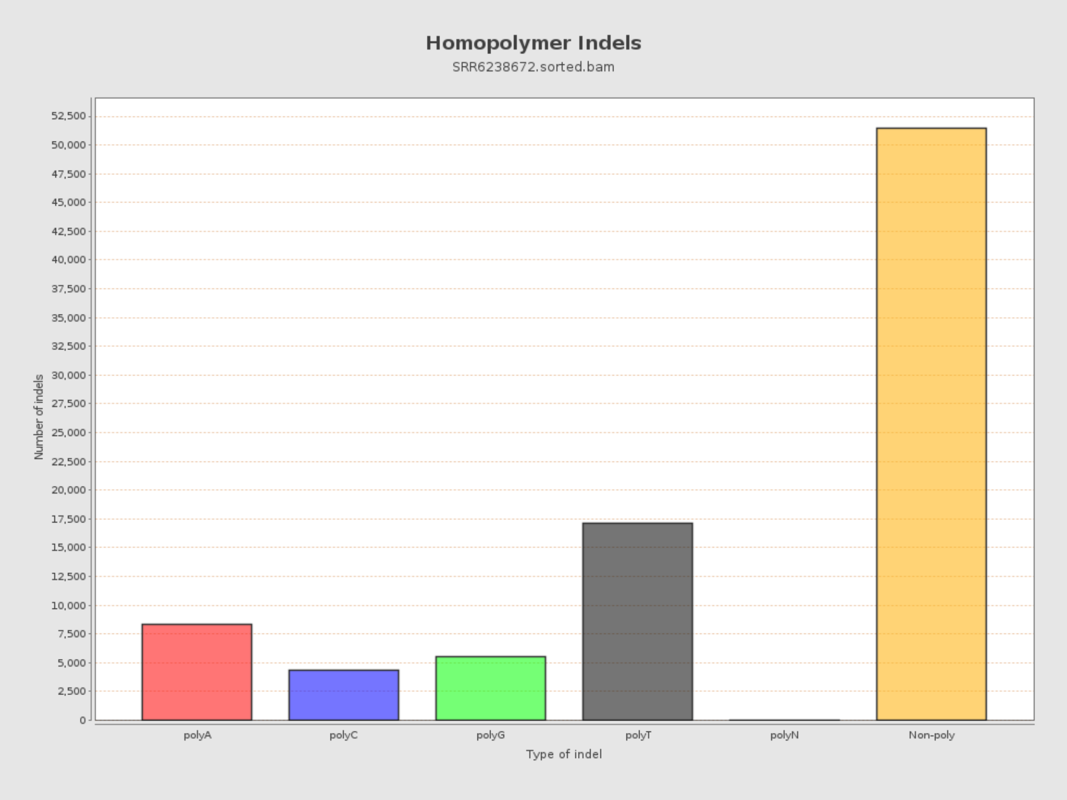
9. Results : Mapped Reads GC-content Distribution



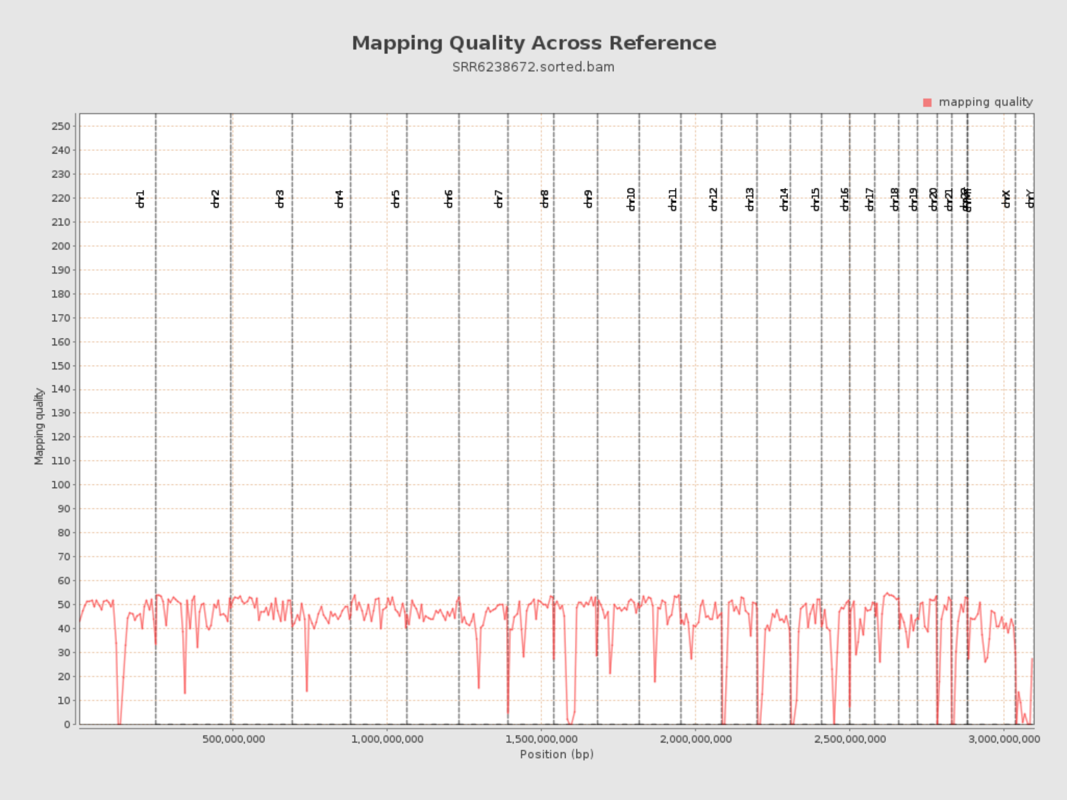
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram