Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 15:57:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238312.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_SRR6238312 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238312.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 15:57:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238312.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,319,545
Mapped reads	2,981,047 / 89.8%
Unmapped reads	338,498 / 10.2%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	32,883 / 0.99%
Read min/max/mean length	30 / 76 / 76.35
Duplicated reads (estimated)	164,414 / 4.95%
Duplication rate	4.33%
Clipped reads	1,555,332 / 46.85%

2.2. ACGT Content

Number/percentage of A's	53,627,418 / 27.57%
Number/percentage of C's	36,492,719 / 18.76%
Number/percentage of T's	60,547,240 / 31.12%
Number/percentage of G's	43,825,869 / 22.53%
Number/percentage of N's	49,431 / 0.03%
GC Percentage	41.29%

2.3. Coverage

Mean	0.0629

Standard Deviation	0.515

2.4. Mapping Quality

Mean Mapping Quality	45.63

2.5. Mismatches and indels

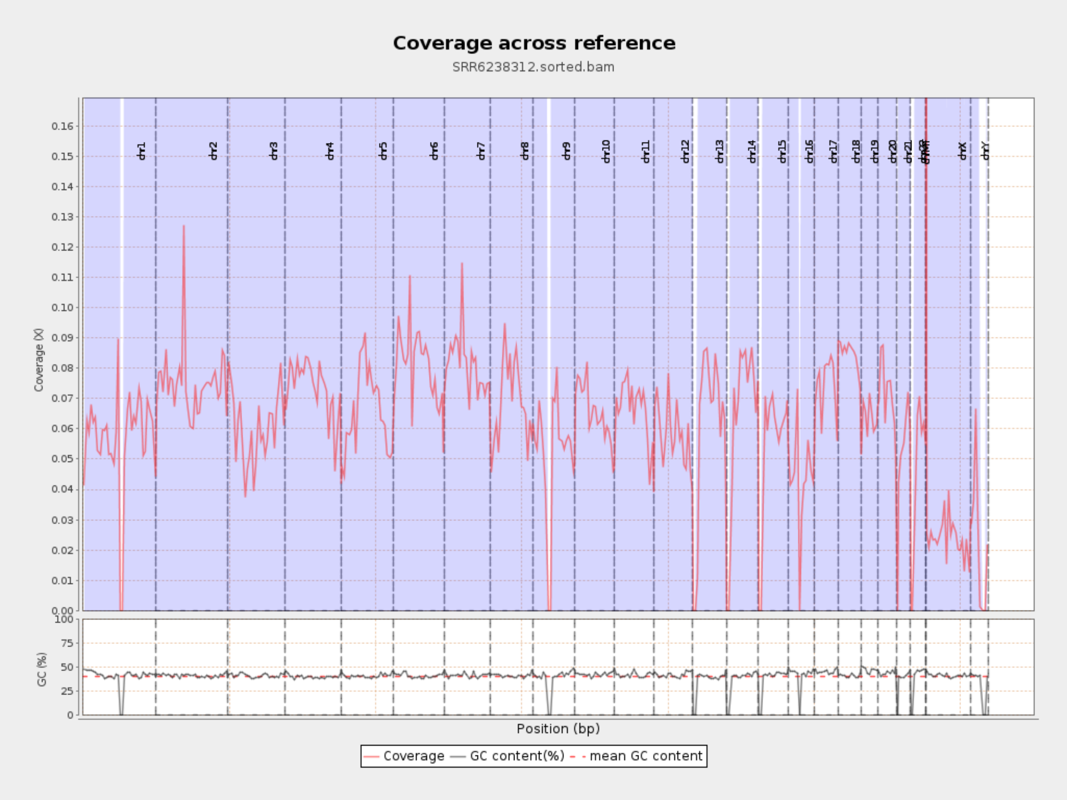
General error rate	0.85%
Mismatches	1,623,904
Insertions	14,848
Mapped reads with at least one insertion	0.49%
Deletions	52,934
Mapped reads with at least one deletion	1.76%
Homopolymer indels	45.95%

2.6. Chromosome stats

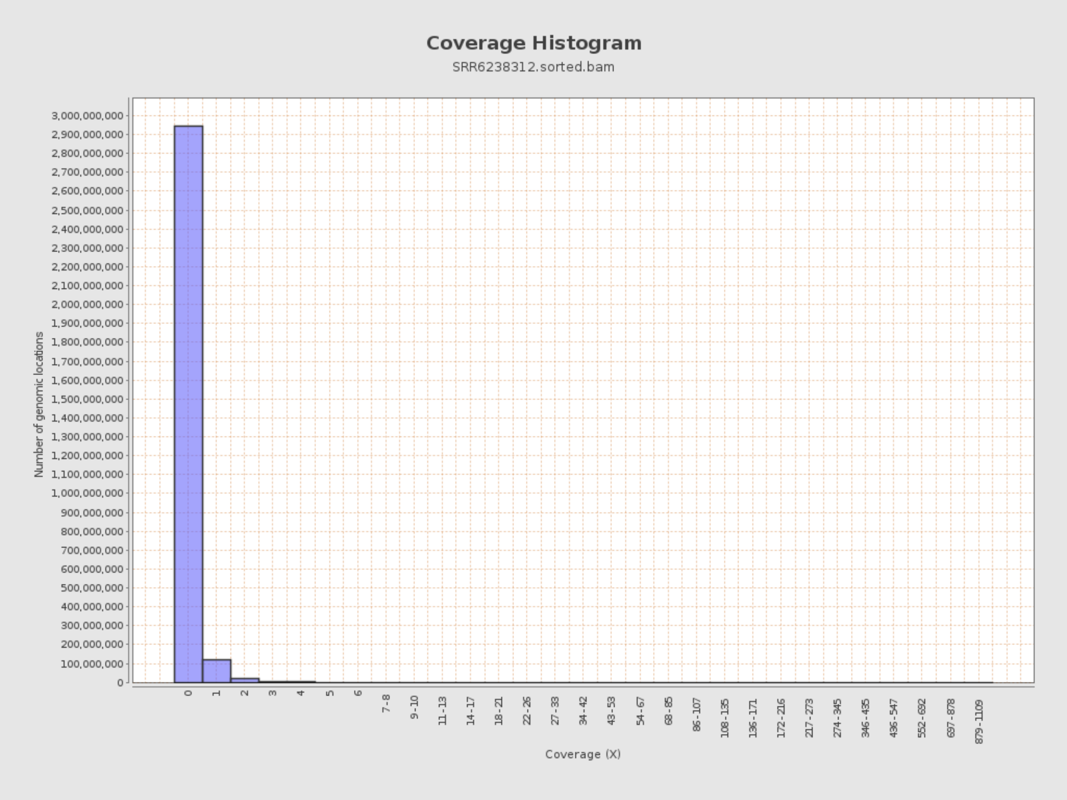
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14100248	0.0566	0.9648
chr2	243199373	18300757	0.0753	0.6597
chr3	198022430	11951766	0.0604	0.3003
chr4	191154276	14099788	0.0738	0.3394
chr5	180915260	11904956	0.0658	0.3182
chr6	171115067	13891392	0.0812	0.4612
chr7	159138663	12989013	0.0816	0.6869

chr8	146364022	10086560	0.0689	0.6595
chr9	141213431	7347352	0.052	0.4539
chr10	135534747	8930755	0.0659	0.4209
chr11	135006516	8972737	0.0665	0.4724
chr12	133851895	7863231	0.0587	0.3053
chr13	115169878	6984201	0.0606	0.3024
chr14	107349540	6919957	0.0645	0.345
chr15	102531392	5424376	0.0529	0.2926
chr16	90354753	3887844	0.043	0.2771
chr17	81195210	6109346	0.0752	0.3865
chr18	78077248	6630016	0.0849	0.7768
chr19	59128983	3779830	0.0639	0.67
chr20	63025520	4567073	0.0725	0.3434
chr21	48129895	2501998	0.052	0.3098
chr22	51304566	2283246	0.0445	0.2811
chrMT	16571	17172	1.0363	1.272
chrX	155270560	3724322	0.024	0.2469
chrY	59373566	1362040	0.0229	0.2217

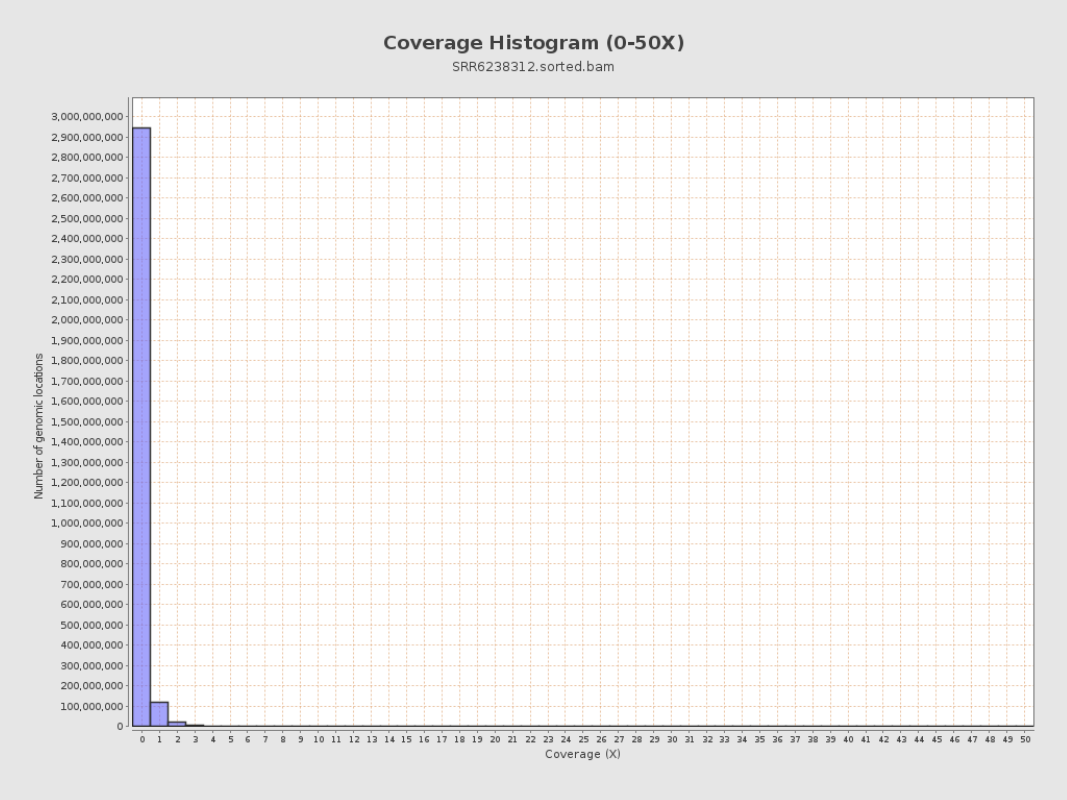
3. Results : Coverage across reference



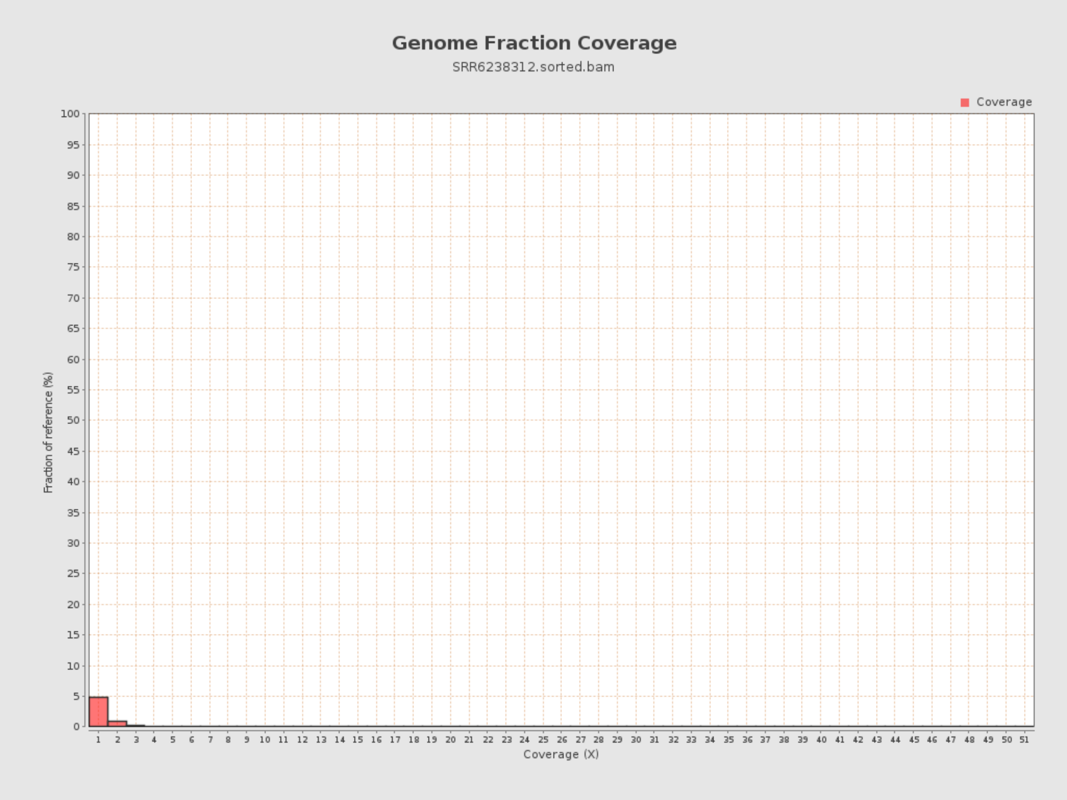
4. Results : Coverage Histogram



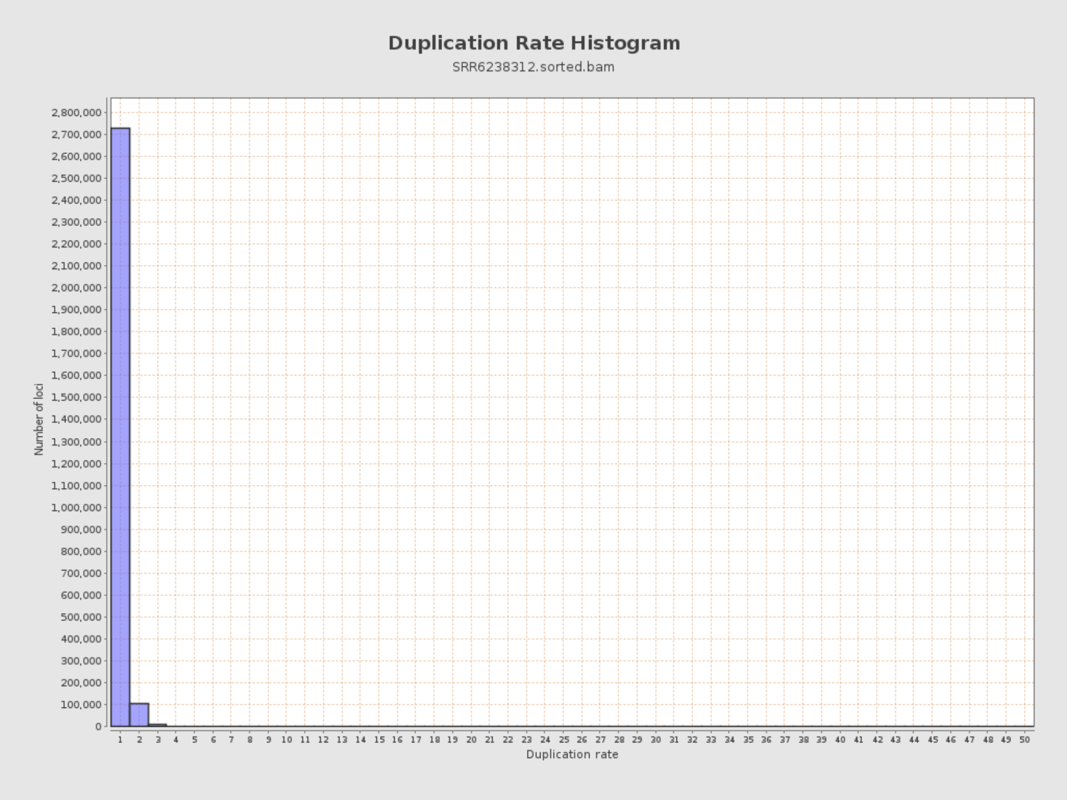
5. Results : Coverage Histogram (0-50X)



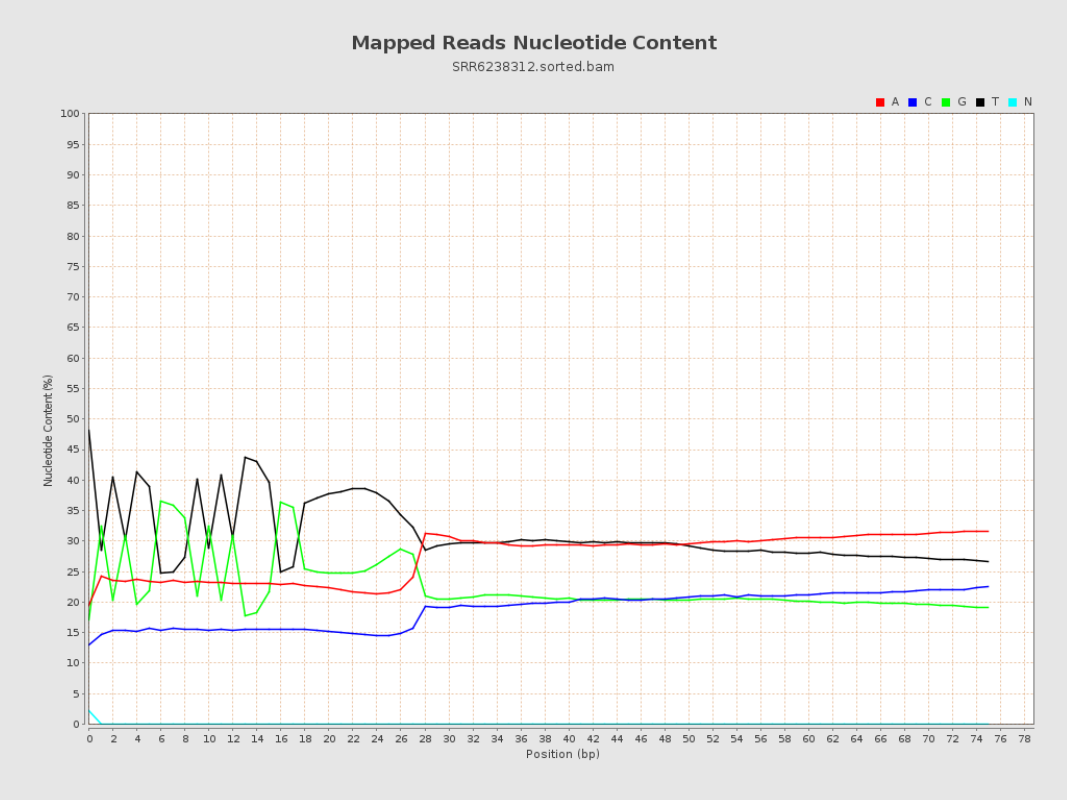
6. Results : Genome Fraction Coverage



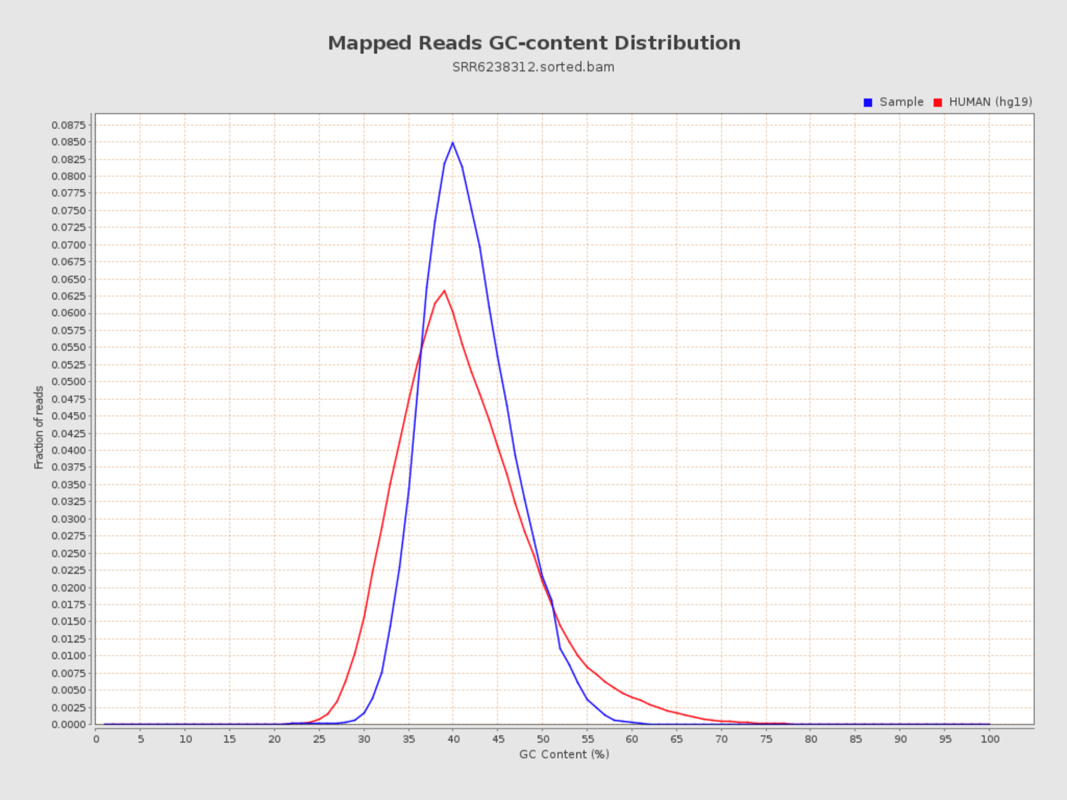
7. Results : Duplication Rate Histogram



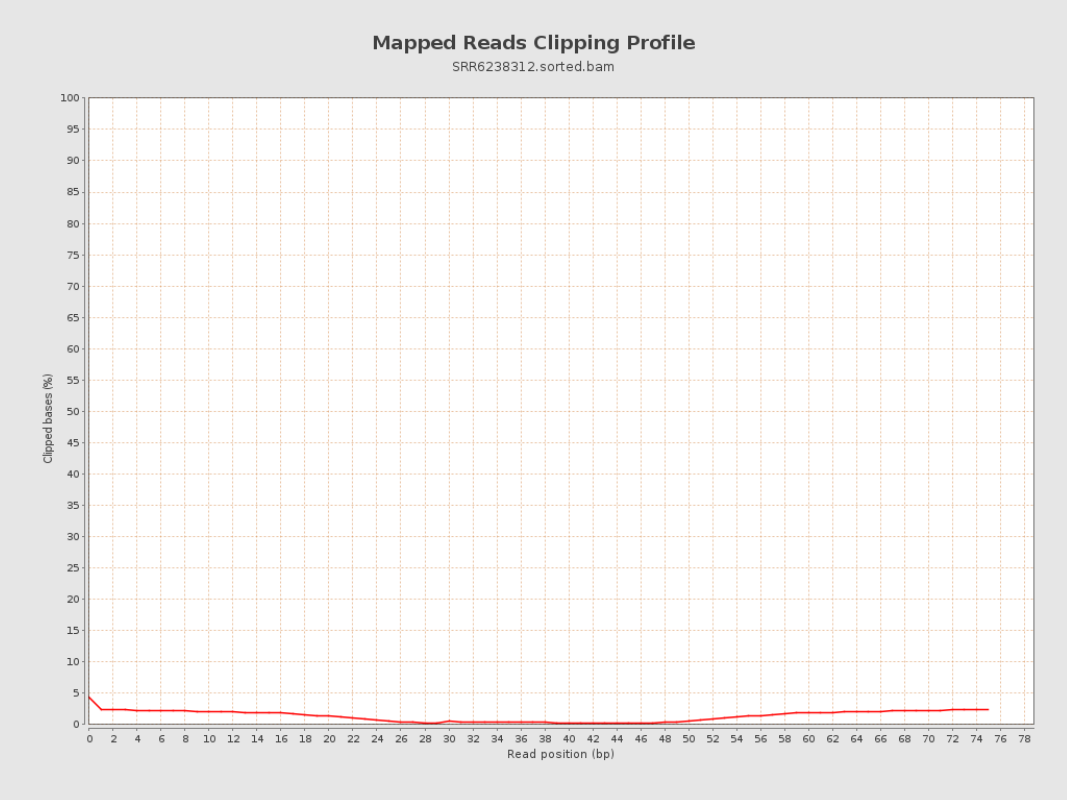
8. Results : Mapped Reads Nucleotide Content



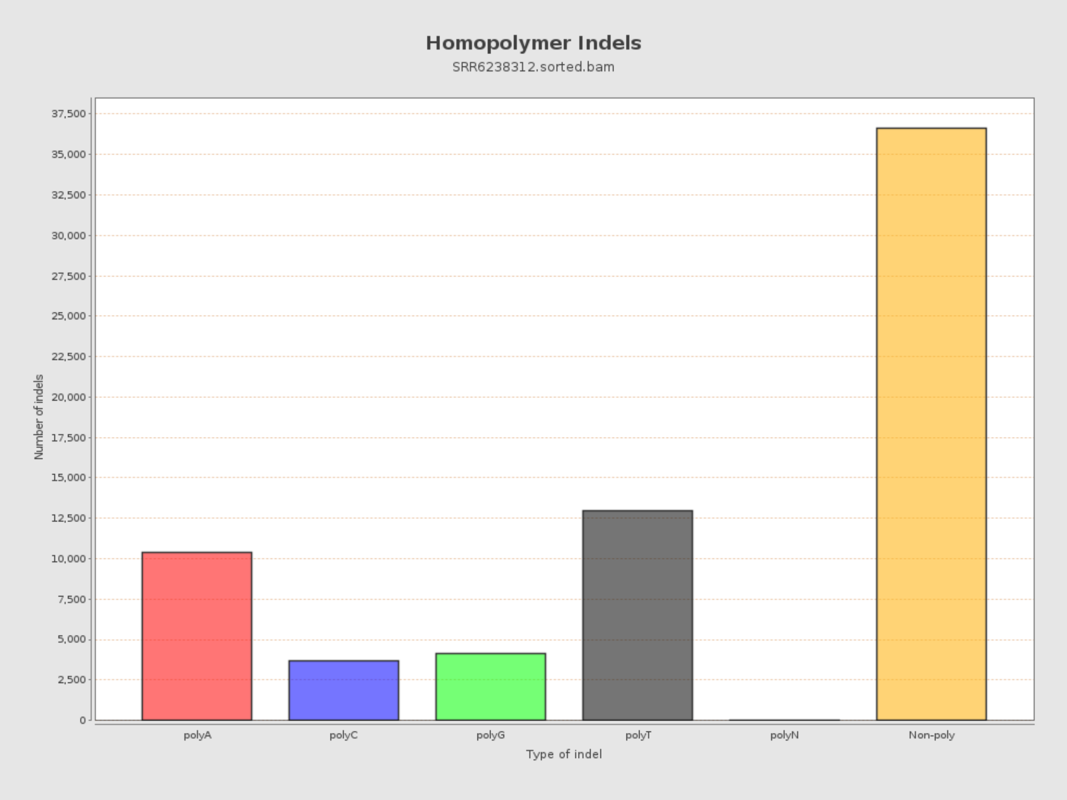
9. Results : Mapped Reads GC-content Distribution



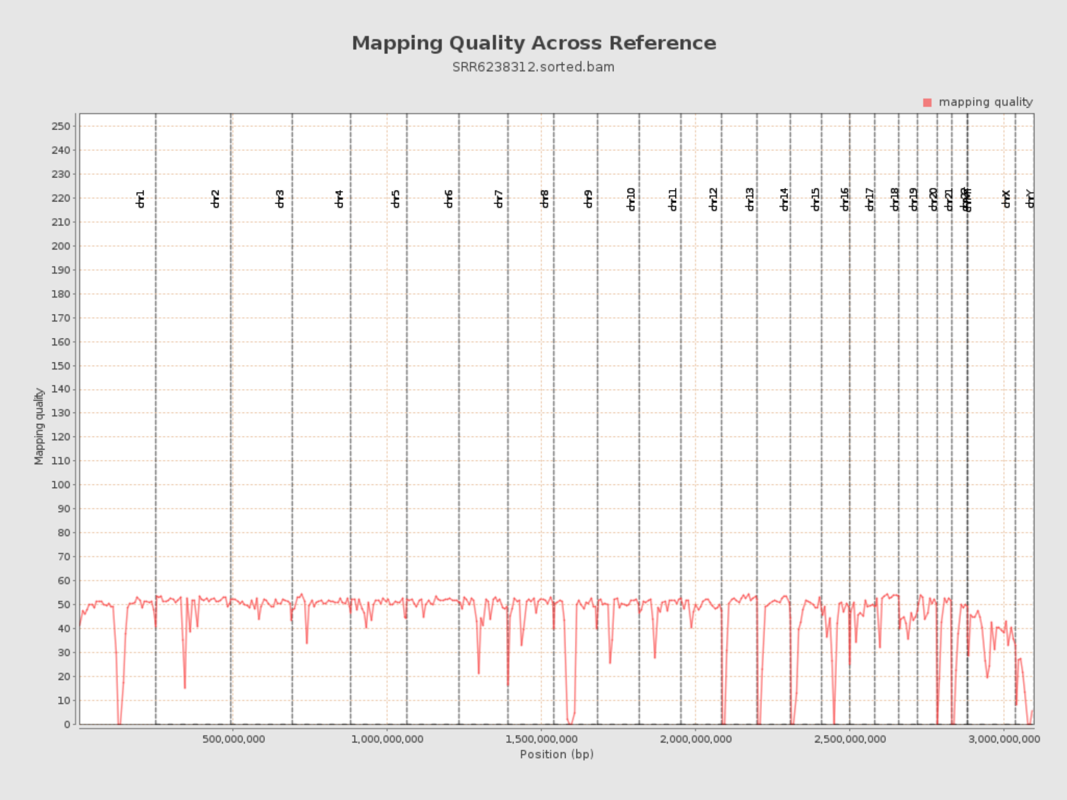
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram