Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 16:22:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238319.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_SRR6238319 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238319.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 16:22:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238319.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,736,146
Mapped reads	2,517,266 / 92%
Unmapped reads	218,880 / 8%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,292 / 0.81%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	102,060 / 3.73%
Duplication rate	2.88%
Clipped reads	1,108,818 / 40.52%

2.2. ACGT Content

Number/percentage of A's	47,220,319 / 28.13%
Number/percentage of C's	31,517,141 / 18.77%
Number/percentage of T's	52,155,321 / 31.07%
Number/percentage of G's	36,944,162 / 22.01%
Number/percentage of N's	42,963 / 0.03%
GC Percentage	40.78%

2.3. Coverage

Mean	0.0543

Standard Deviation	0.5119

2.4. Mapping Quality

Mean Mapping Quality	45.63

2.5. Mismatches and indels

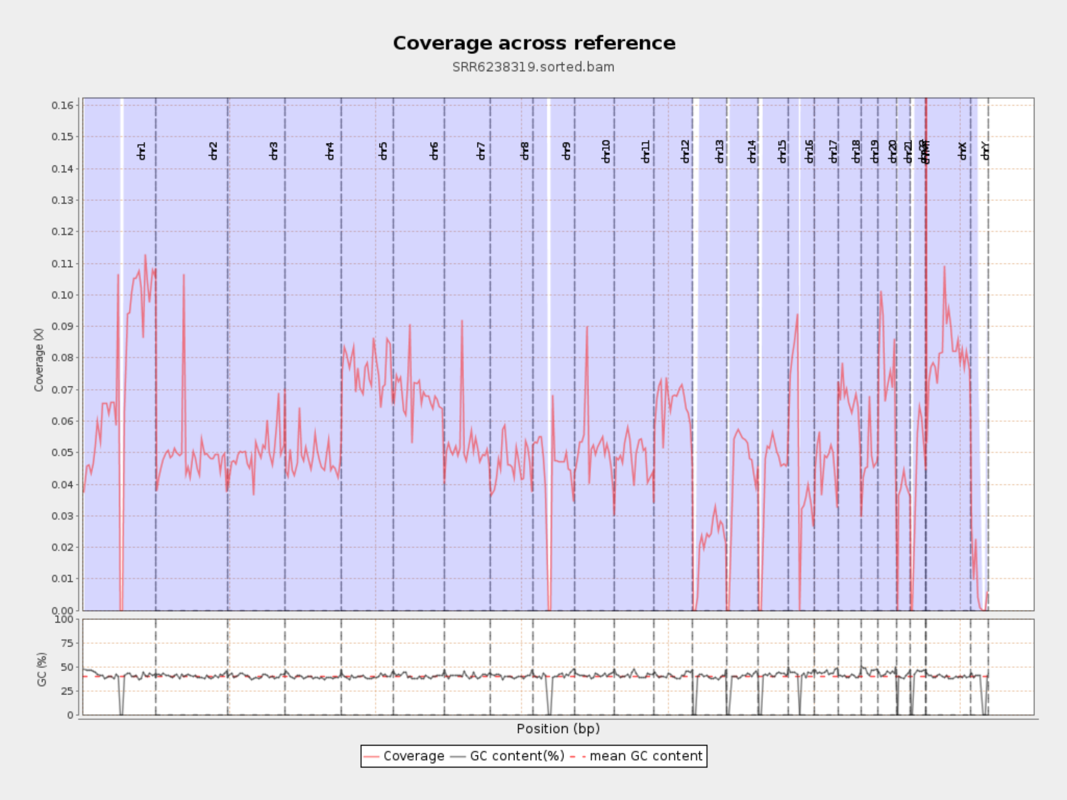
General error rate	0.83%
Mismatches	1,370,477
Insertions	12,569
Mapped reads with at least one insertion	0.5%
Deletions	47,247
Mapped reads with at least one deletion	1.86%
Homopolymer indels	46.13%

2.6. Chromosome stats

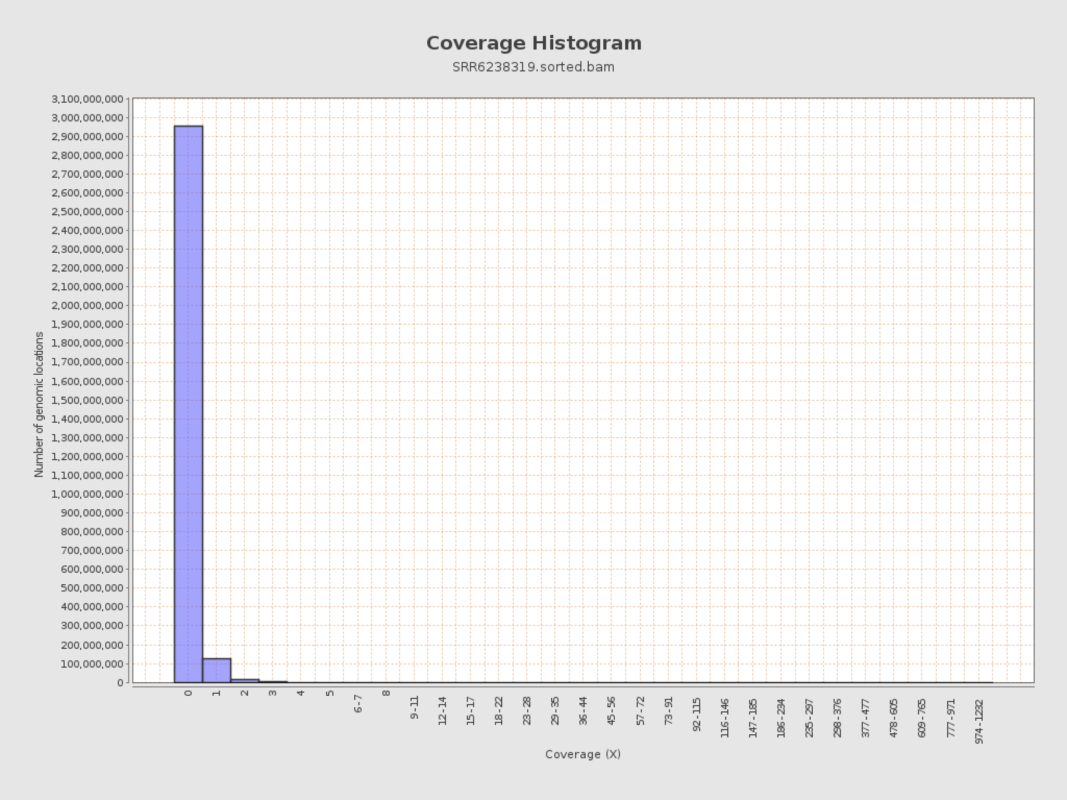
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	18200176	0.073	1.063
chr2	243199373	12008656	0.0494	0.5779
chr3	198022430	9938911	0.0502	0.2535
chr4	191154276	9179785	0.048	0.2724
chr5	180915260	13743477	0.076	0.3168
chr6	171115067	11700460	0.0684	0.3914
chr7	159138663	8342682	0.0524	0.6436

chr8	146364022	6773744	0.0463	0.6436
chr9	141213431	6148823	0.0435	0.4735
chr10	135534747	7087920	0.0523	0.4476
chr11	135006516	6534316	0.0484	0.3908
chr12	133851895	8815941	0.0659	0.301
chr13	115169878	2416018	0.021	0.1634
chr14	107349540	4655963	0.0434	0.2878
chr15	102531392	4176754	0.0407	0.2338
chr16	90354753	4432578	0.0491	0.2929
chr17	81195210	3854402	0.0475	0.2923
chr18	78077248	5239156	0.0671	0.8639
chr19	59128983	2838643	0.048	0.7207
chr20	63025520	4967251	0.0788	0.3274
chr21	48129895	1703836	0.0354	0.2514
chr22	51304566	2077056	0.0405	0.2263
chrMT	16571	9354	0.5645	0.9939
chrX	155270560	12638151	0.0814	0.3812
chrY	59373566	477352	0.008	0.1757

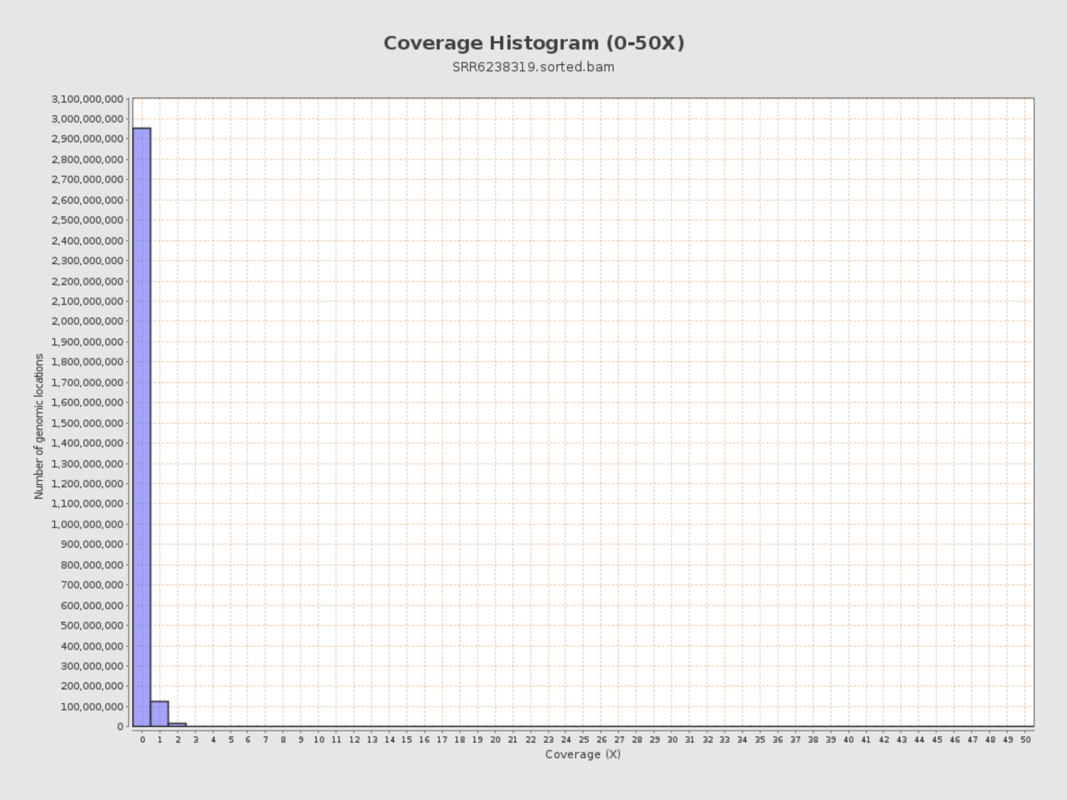
3. Results : Coverage across reference



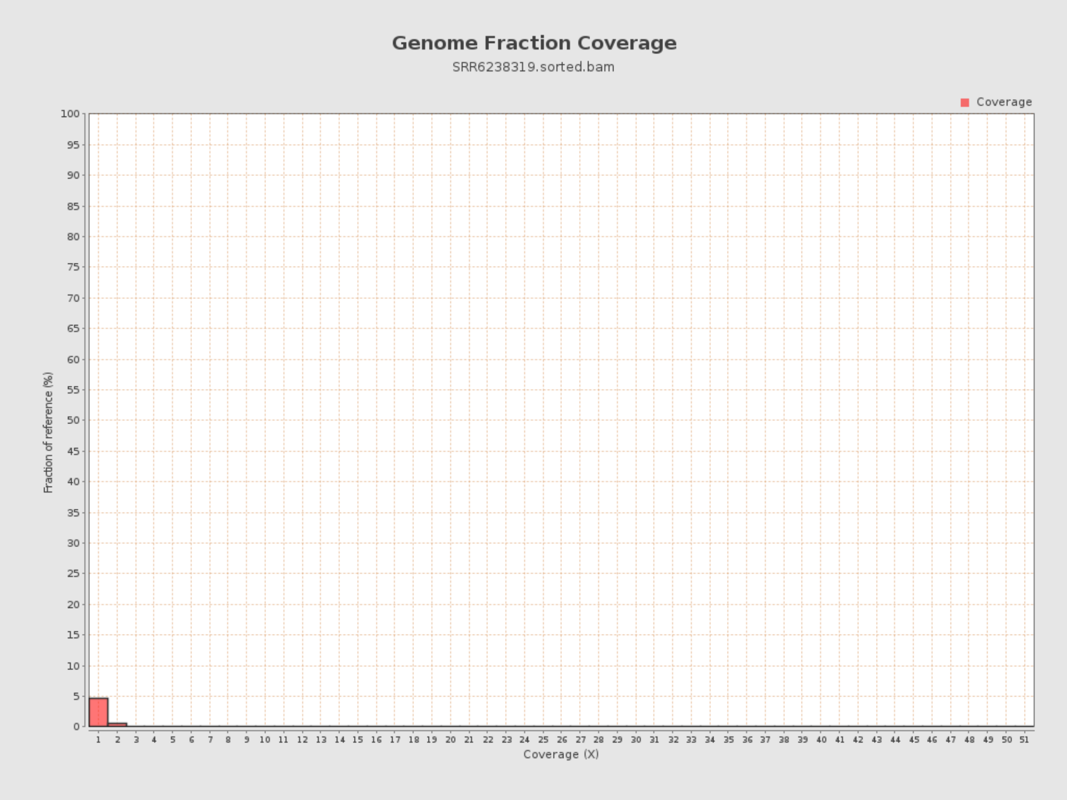
4. Results : Coverage Histogram



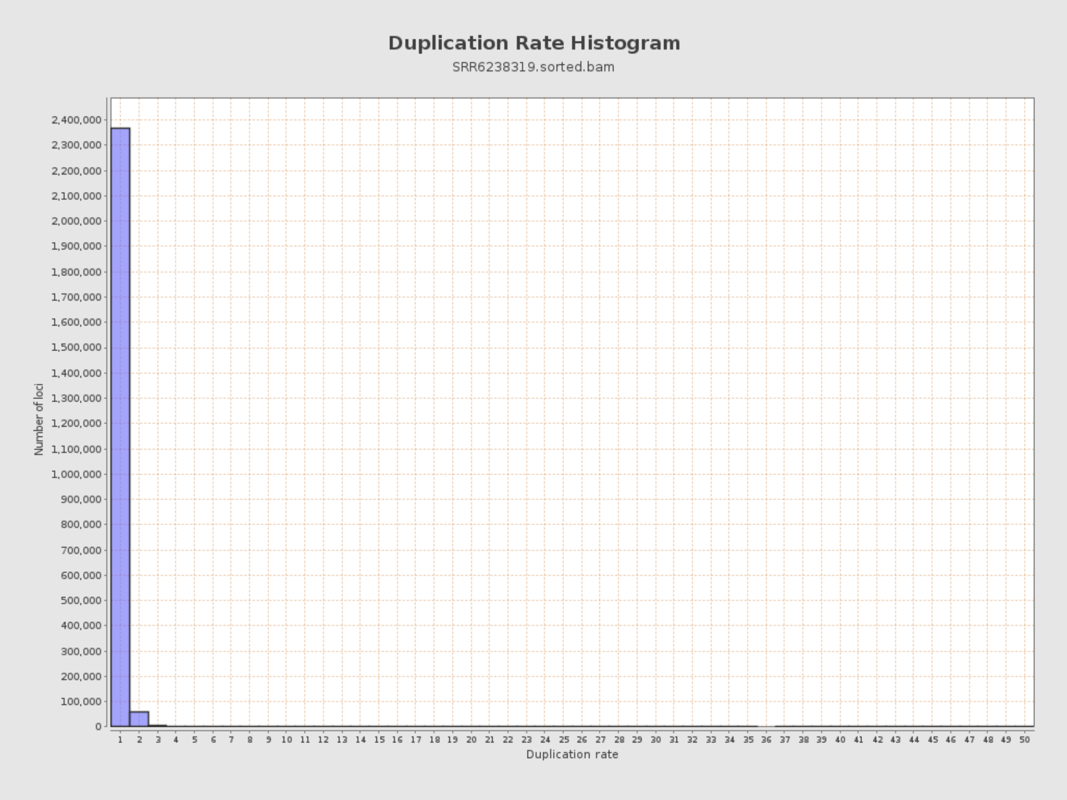
5. Results : Coverage Histogram (0-50X)



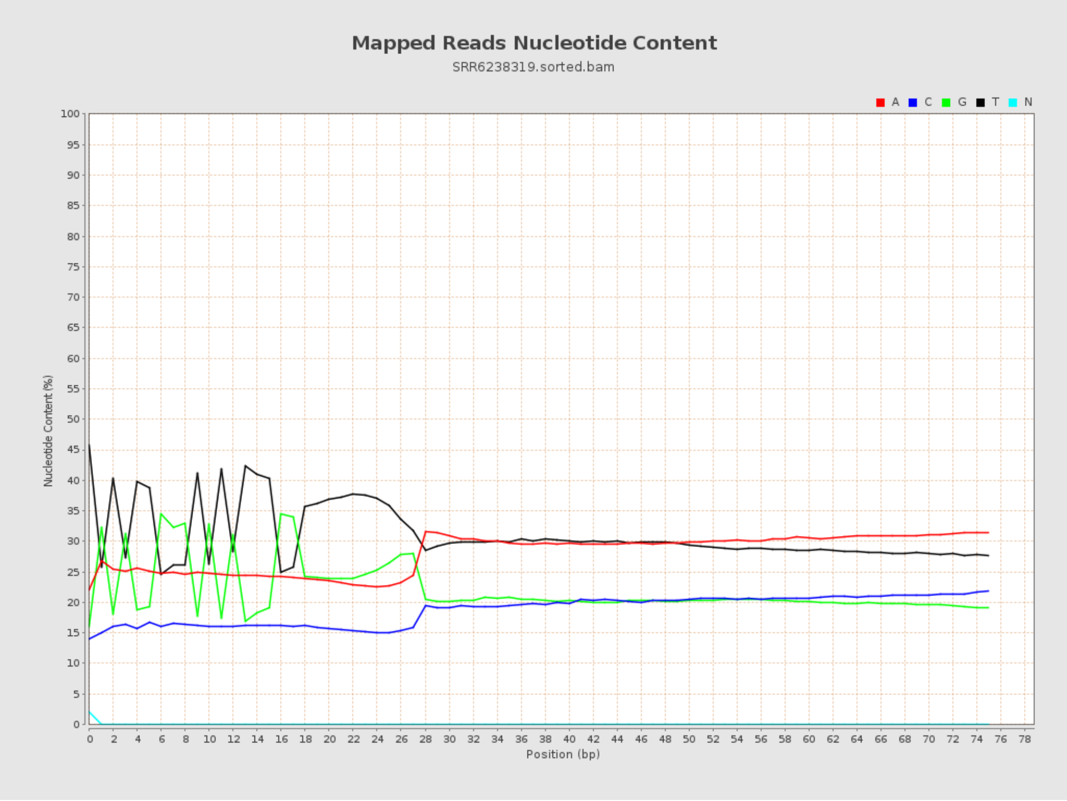
6. Results : Genome Fraction Coverage



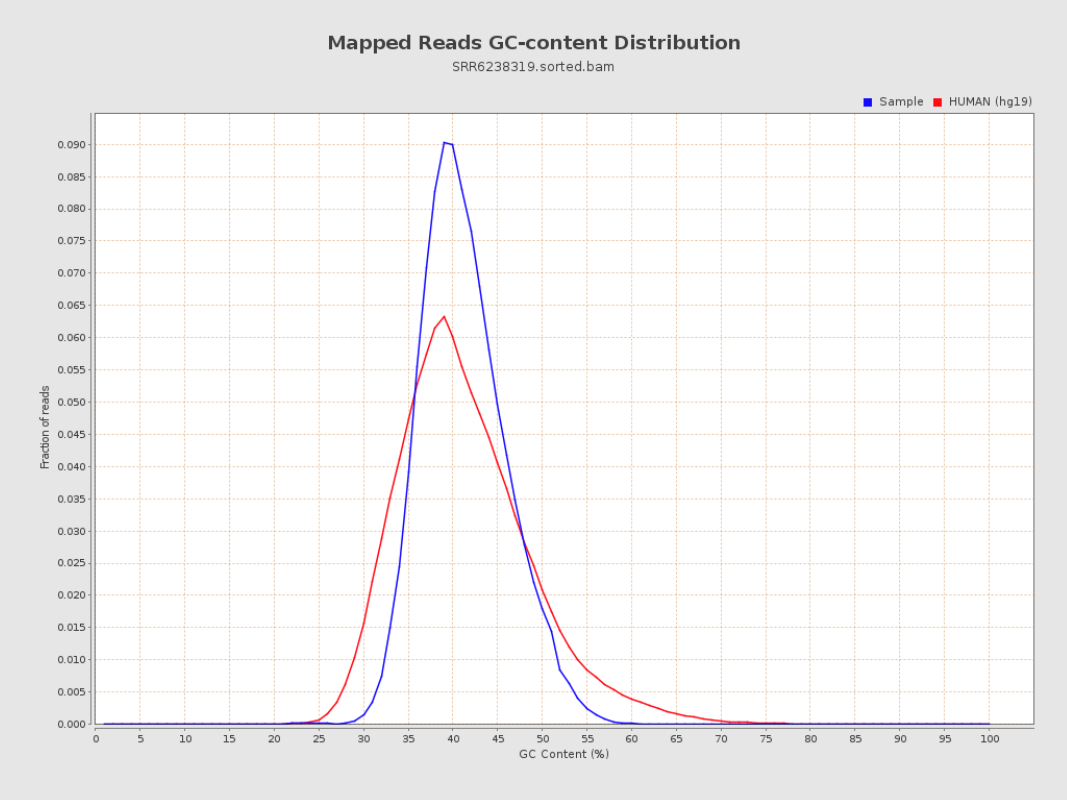
7. Results : Duplication Rate Histogram



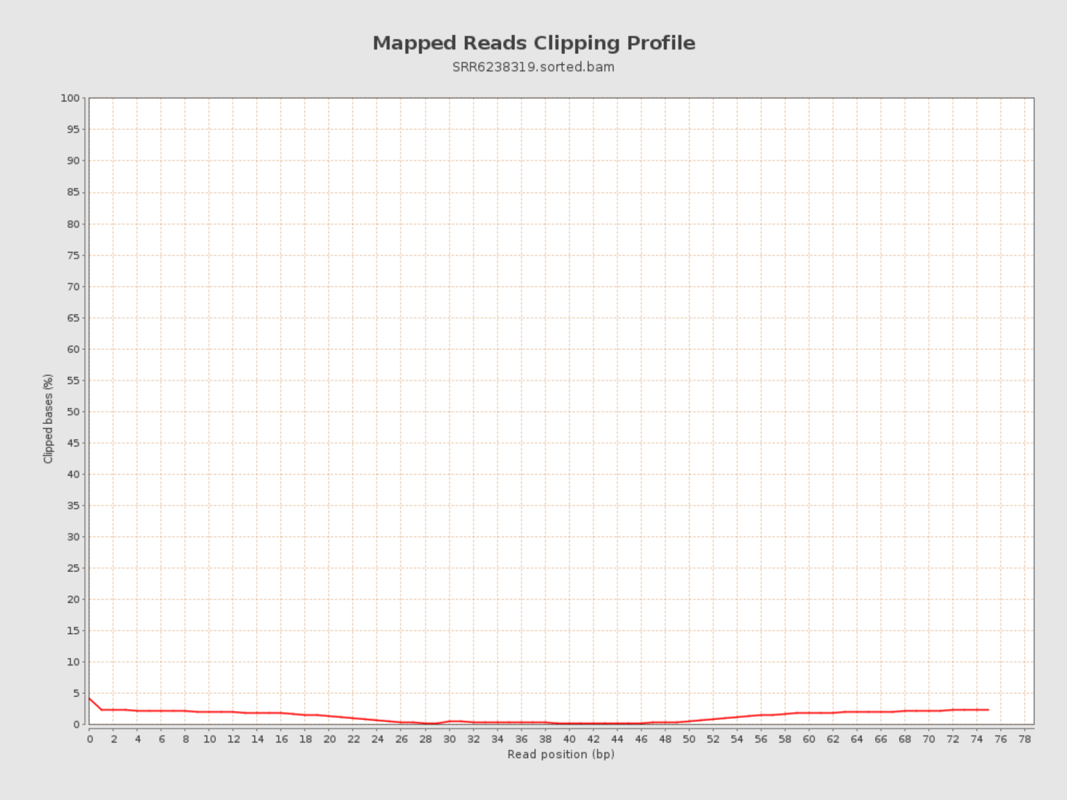
8. Results : Mapped Reads Nucleotide Content



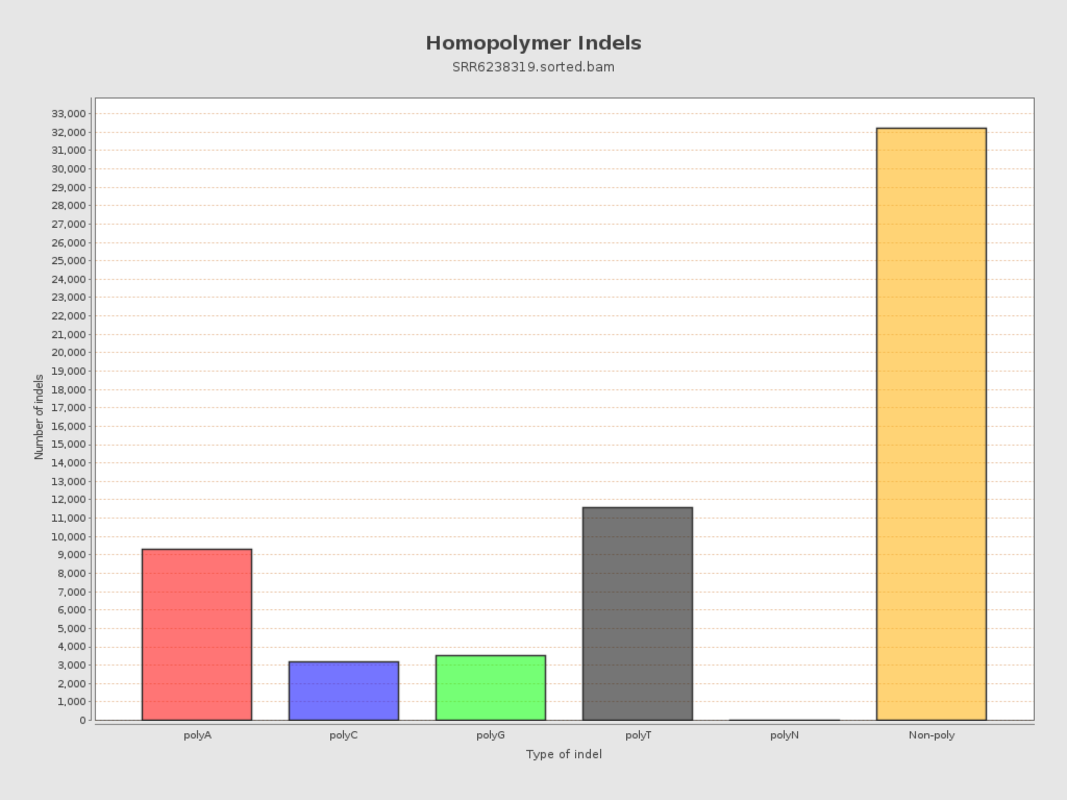
9. Results : Mapped Reads GC-content Distribution



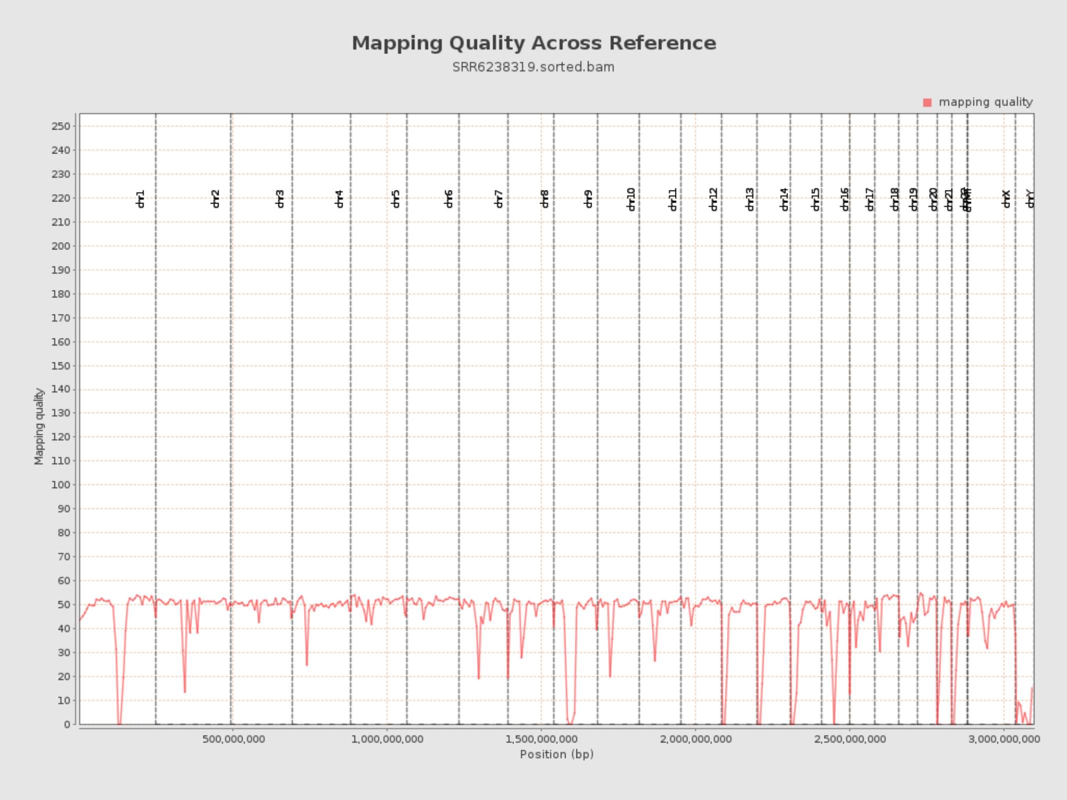
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram