Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 17:12:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238335.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_SRR6238335 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238335.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 17:12:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238335.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,207,495
Mapped reads	2,926,952 / 91.25%
Unmapped reads	280,543 / 8.75%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	27,570 / 0.86%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	123,088 / 3.84%
Duplication rate	2.95%
Clipped reads	1,334,799 / 41.61%

2.2. ACGT Content

Number/percentage of A's	54,699,381 / 28.05%
Number/percentage of C's	37,454,081 / 19.2%
Number/percentage of T's	59,592,853 / 30.56%
Number/percentage of G's	43,219,785 / 22.16%
Number/percentage of N's	62,185 / 0.03%
GC Percentage	41.37%

2.3. Coverage

Mean	0.063

Standard Deviation	0.5737

2.4. Mapping Quality

Mean Mapping Quality	44.77

2.5. Mismatches and indels

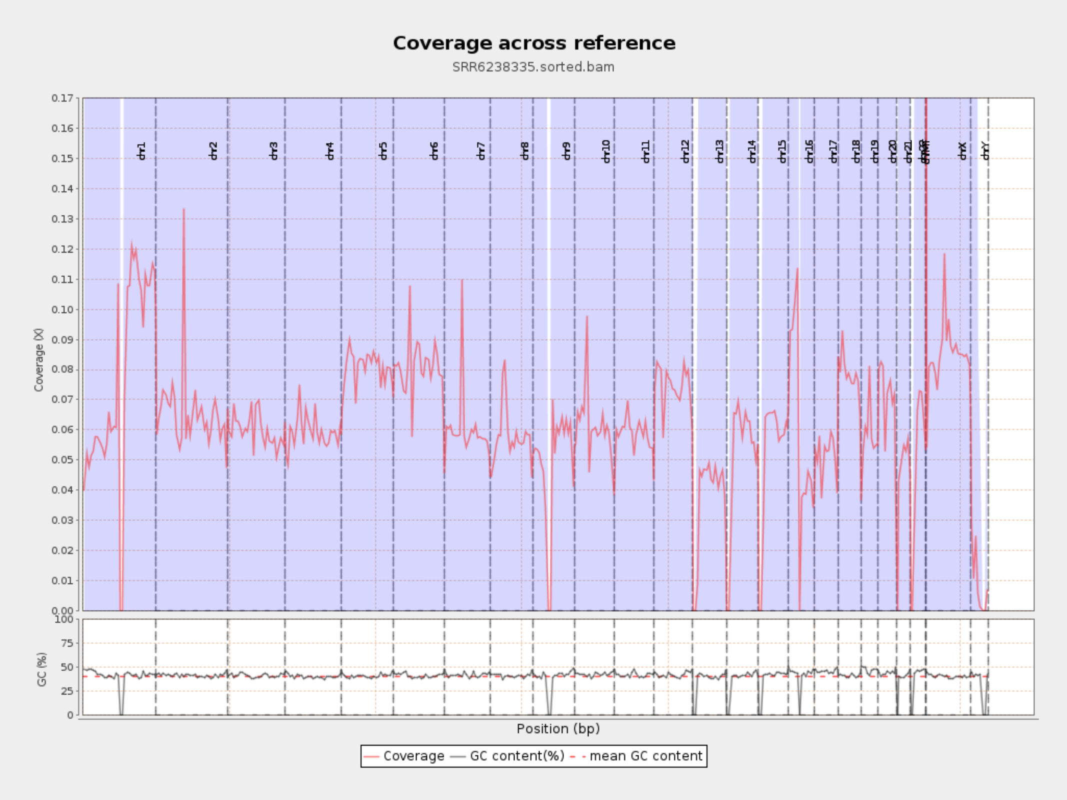
General error rate	0.85%
Mismatches	1,627,752
Insertions	14,363
Mapped reads with at least one insertion	0.49%
Deletions	53,041
Mapped reads with at least one deletion	1.79%
Homopolymer indels	45.68%

2.6. Chromosome stats

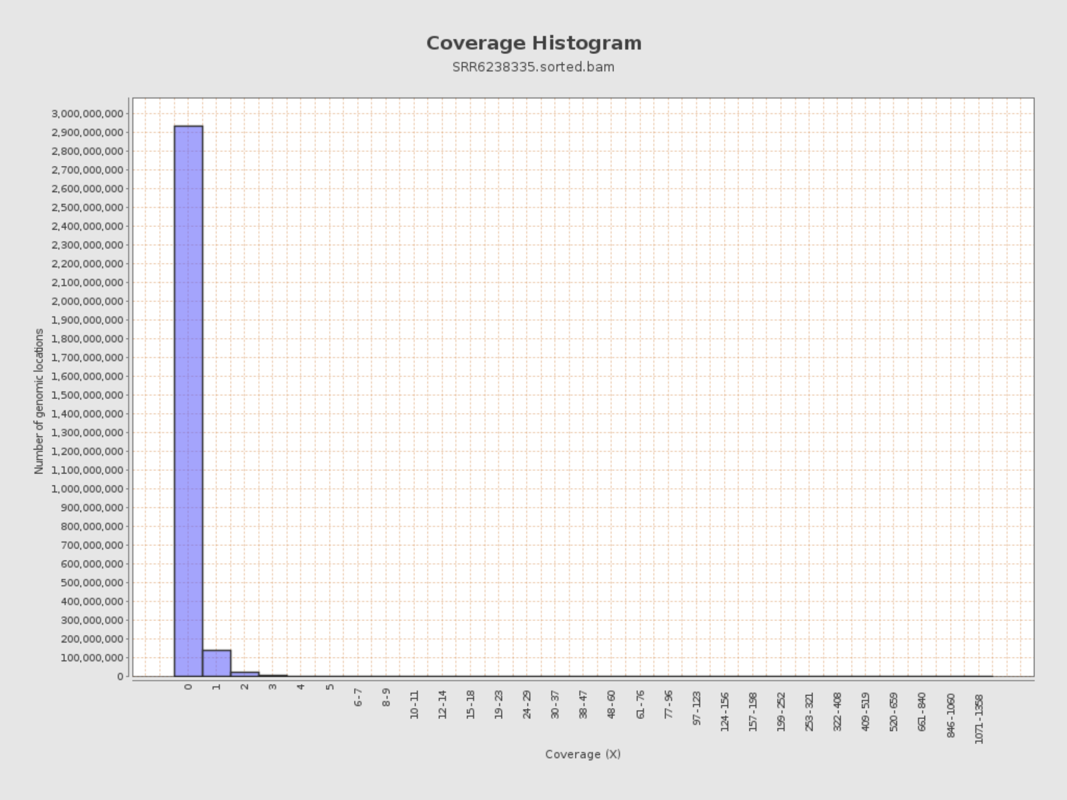
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	19053771	0.0764	1.1484
chr2	243199373	16039521	0.066	0.6736
chr3	198022430	11855770	0.0599	0.2804
chr4	191154276	11352570	0.0594	0.3014
chr5	180915260	14542884	0.0804	0.3308
chr6	171115067	13879681	0.0811	0.4553
chr7	159138663	9589082	0.0603	0.7418

chr8	146364022	8468599	0.0579	0.7842
chr9	141213431	6915585	0.049	0.514
chr10	135534747	8325228	0.0614	0.4994
chr11	135006516	7939248	0.0588	0.439
chr12	133851895	10049438	0.0751	0.3295
chr13	115169878	4282117	0.0372	0.2225
chr14	107349540	5576687	0.0519	0.3059
chr15	102531392	5222842	0.0509	0.268
chr16	90354753	5284993	0.0585	0.3319
chr17	81195210	4208923	0.0518	0.3077
chr18	78077248	6149410	0.0788	0.9952
chr19	59128983	3474622	0.0588	0.8486
chr20	63025520	4499854	0.0714	0.3175
chr21	48129895	2202719	0.0458	0.2775
chr22	51304566	2459377	0.0479	0.2518
chrMT	16571	12437	0.7505	0.9932
chrX	155270560	13207426	0.0851	0.4065
chrY	59373566	527048	0.0089	0.1874

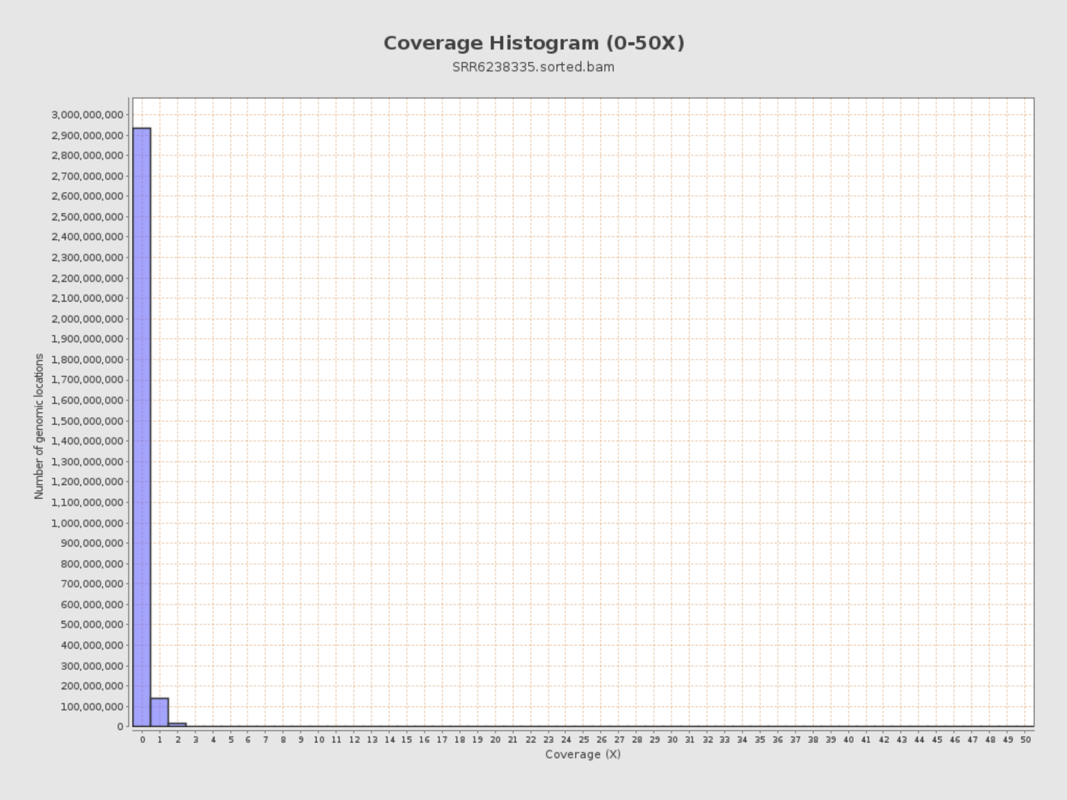
3. Results : Coverage across reference



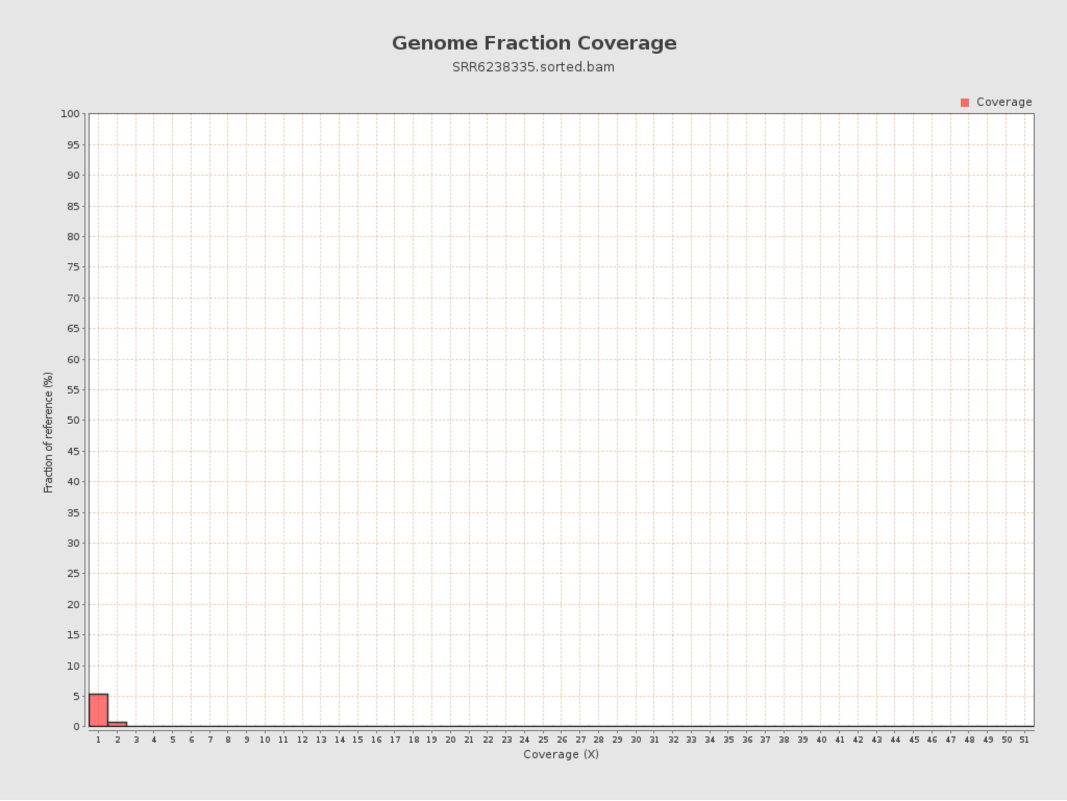
4. Results : Coverage Histogram



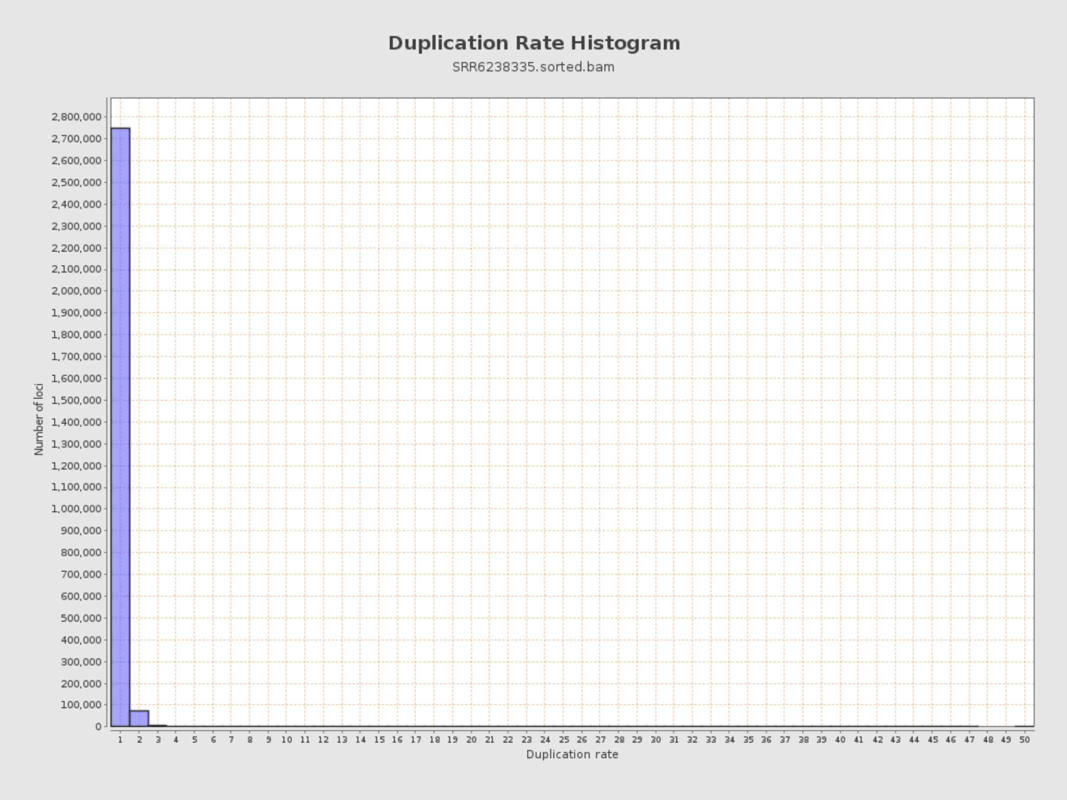
5. Results : Coverage Histogram (0-50X)



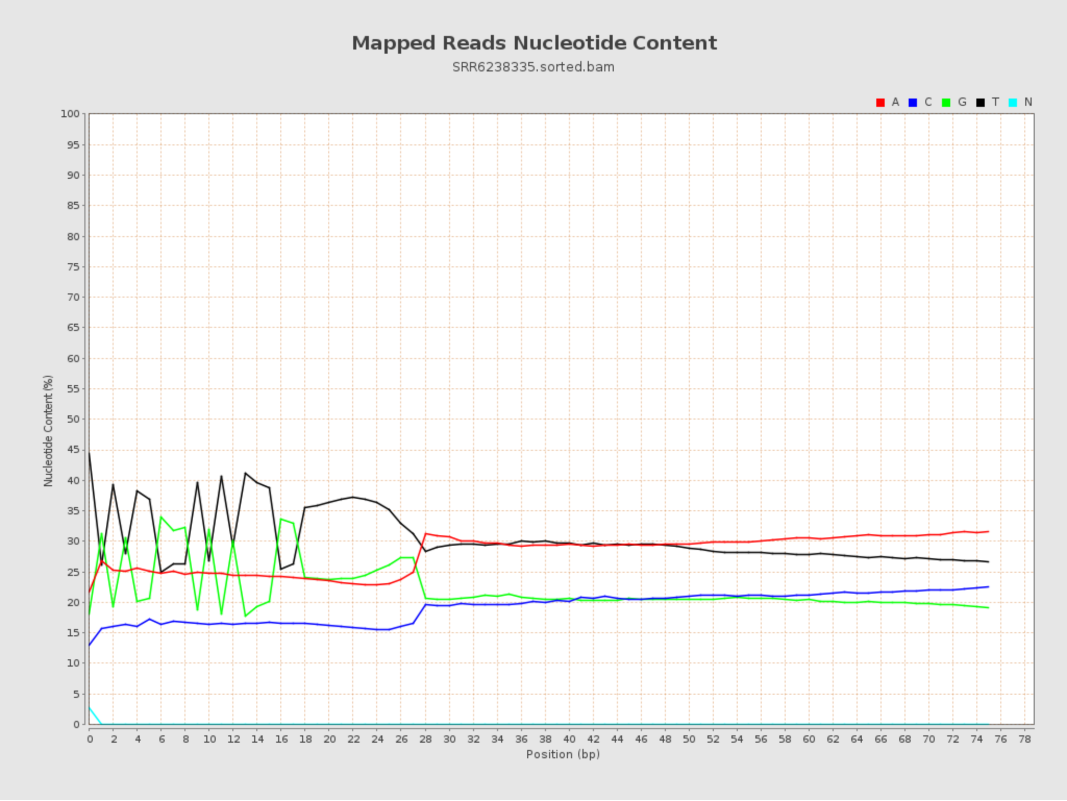
6. Results : Genome Fraction Coverage



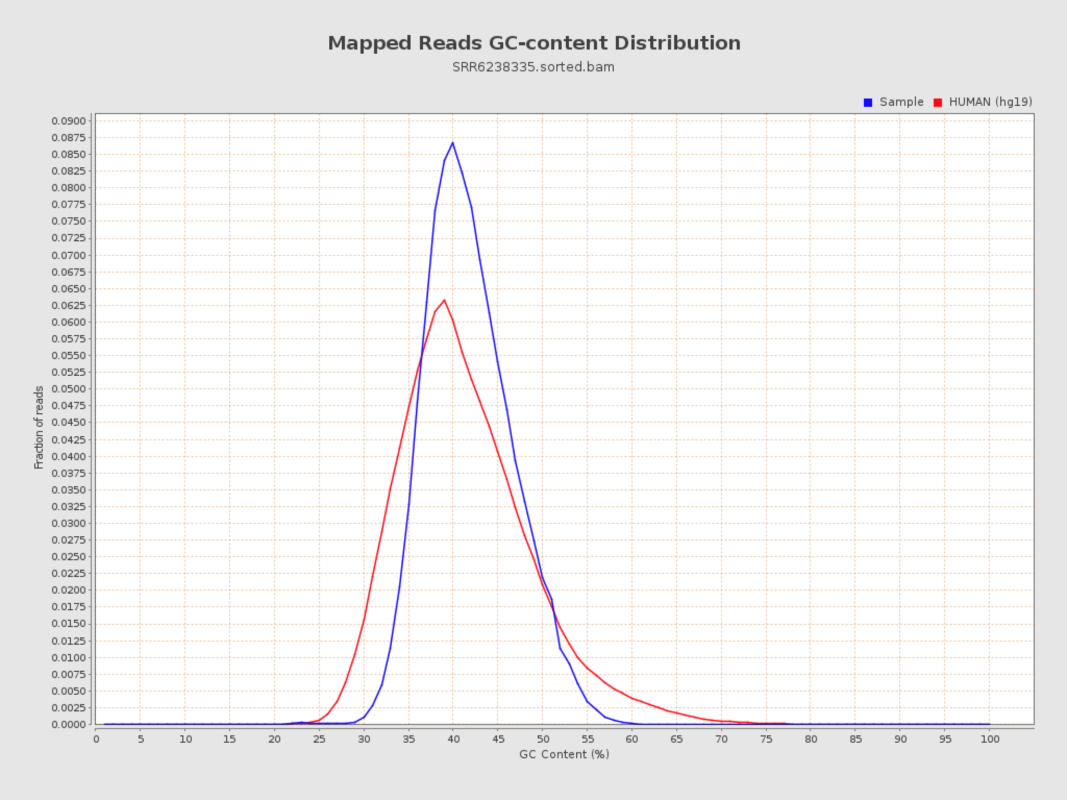
7. Results : Duplication Rate Histogram



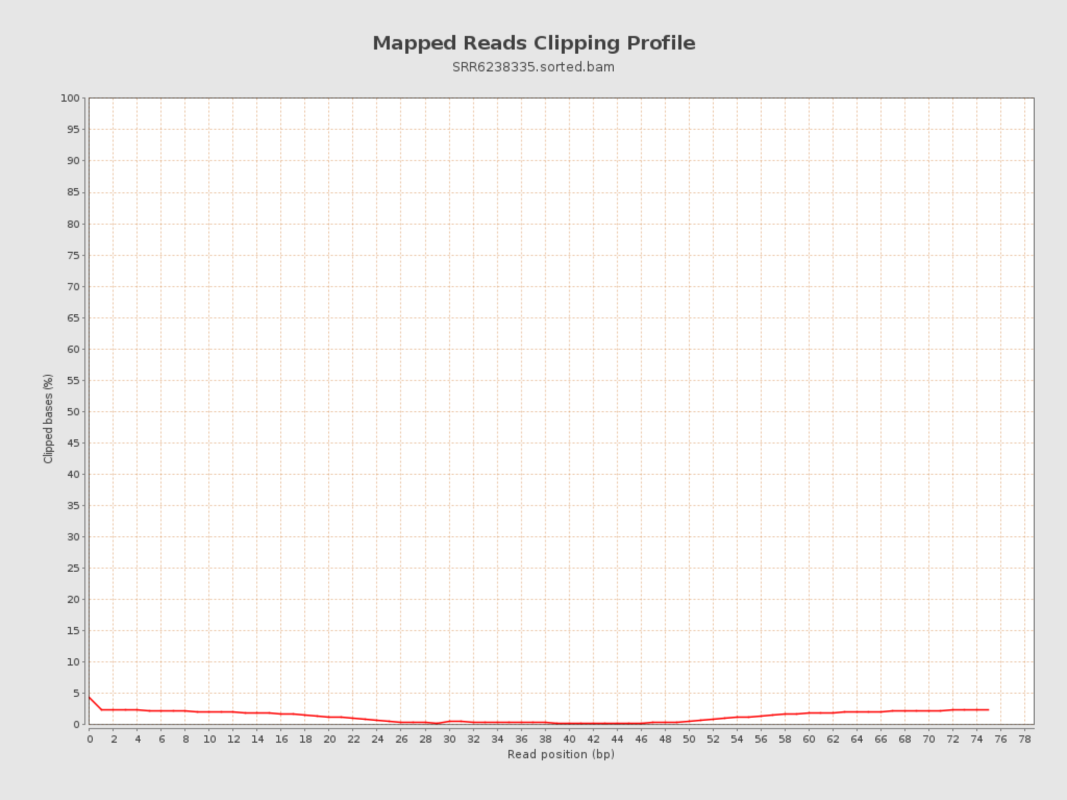
8. Results : Mapped Reads Nucleotide Content



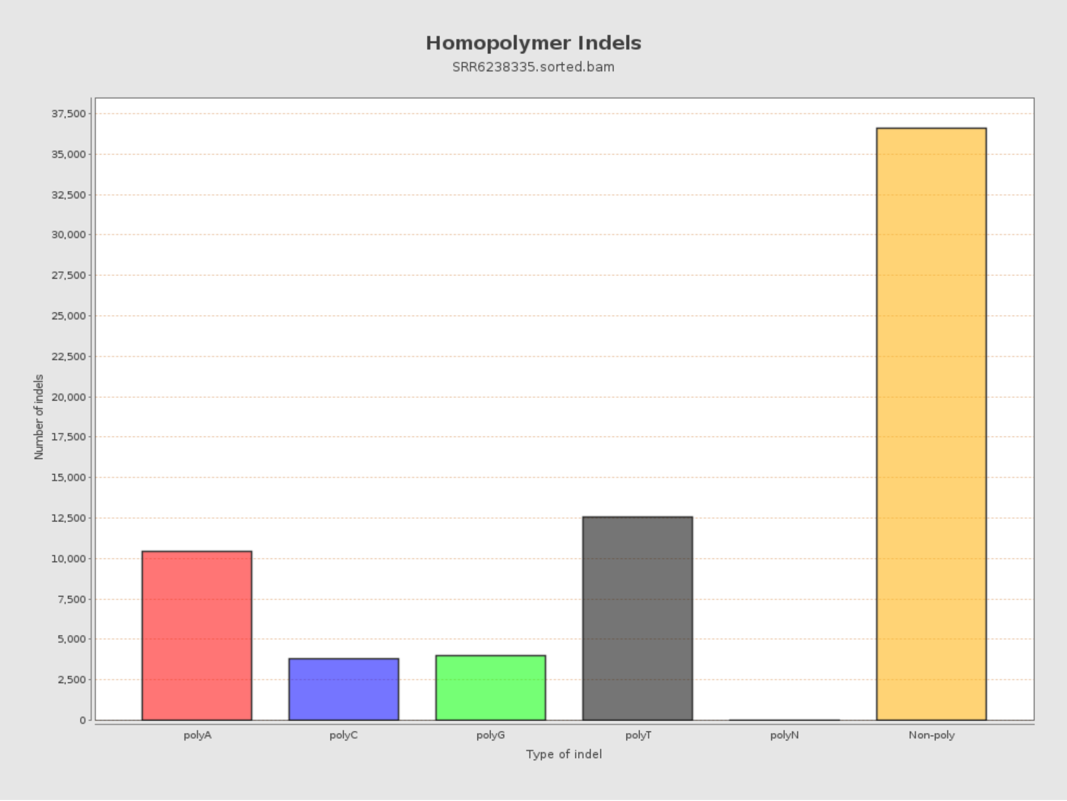
9. Results : Mapped Reads GC-content Distribution



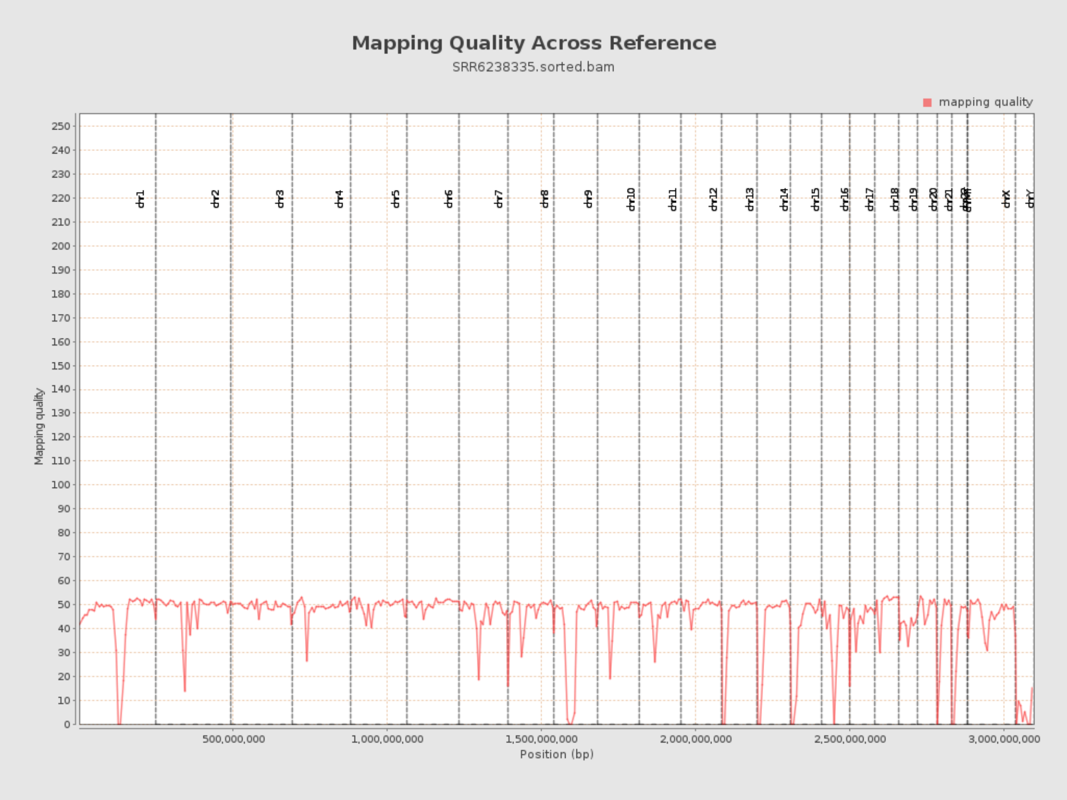
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram