Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 17:15:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238336.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_SRR6238336 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238336.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 17:15:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238336.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,425,954
Mapped reads	2,155,130 / 88.84%
Unmapped reads	270,824 / 11.16%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,910 / 0.78%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	103,310 / 4.26%
Duplication rate	3.65%
Clipped reads	1,065,622 / 43.93%

2.2. ACGT Content

Number/percentage of A's	39,636,891 / 27.84%
Number/percentage of C's	27,389,253 / 19.24%
Number/percentage of T's	43,764,400 / 30.74%
Number/percentage of G's	31,558,869 / 22.16%
Number/percentage of N's	41,721 / 0.03%
GC Percentage	41.4%

2.3. Coverage

Mean	0.046

Standard Deviation	0.4154

2.4. Mapping Quality

Mean Mapping Quality	45.82

2.5. Mismatches and indels

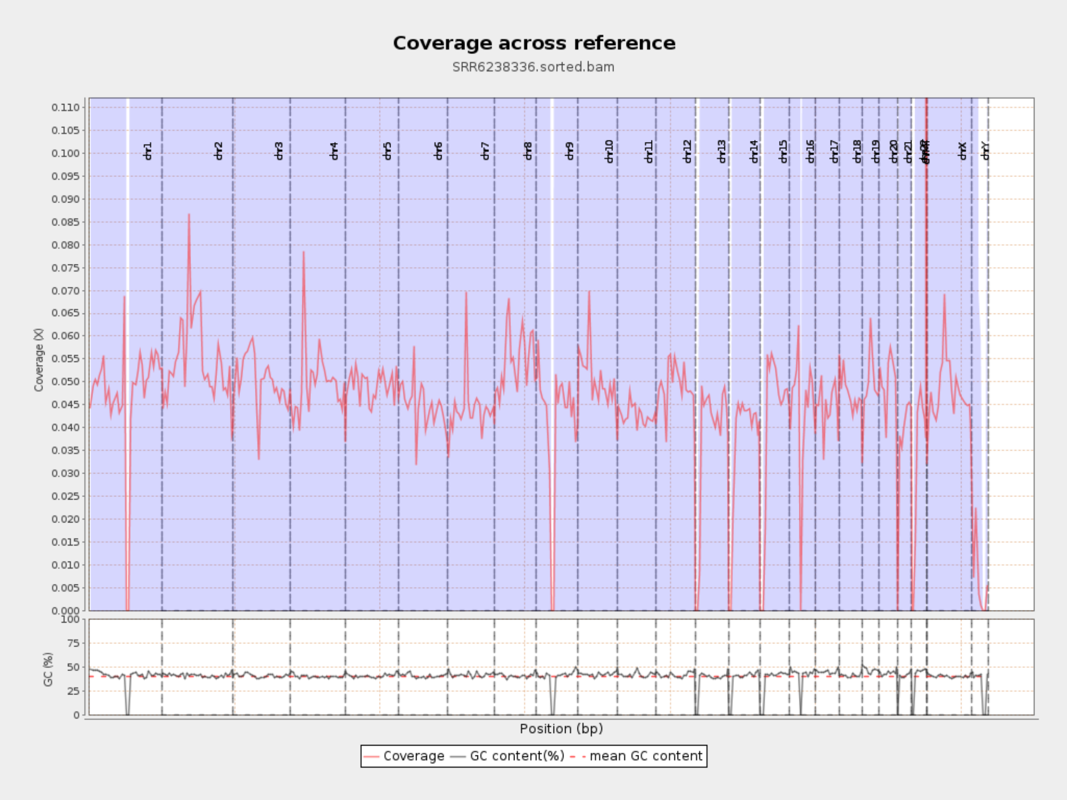
General error rate	0.87%
Mismatches	1,222,177
Insertions	11,603
Mapped reads with at least one insertion	0.53%
Deletions	40,072
Mapped reads with at least one deletion	1.84%
Homopolymer indels	46.13%

2.6. Chromosome stats

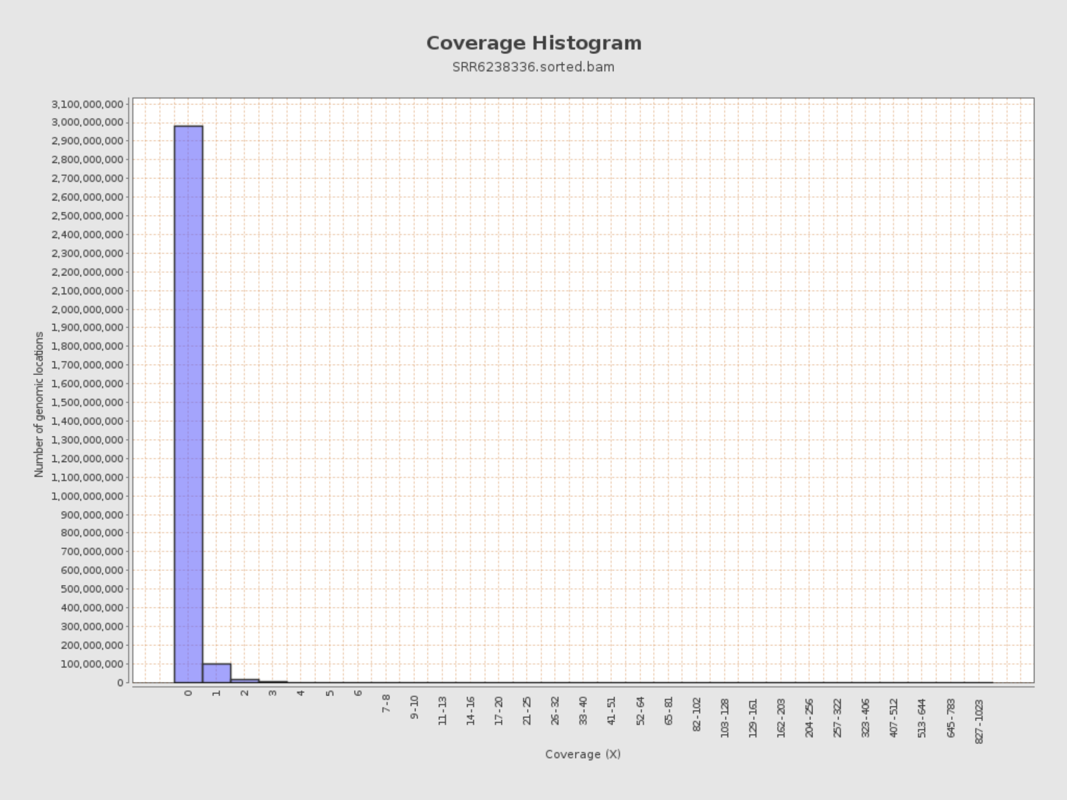
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11794483	0.0473	0.6834
chr2	243199373	13446767	0.0553	0.5212
chr3	198022430	9925521	0.0501	0.2651
chr4	191154276	9497450	0.0497	0.3157
chr5	180915260	8929512	0.0494	0.2668
chr6	171115067	7668222	0.0448	0.3098
chr7	159138663	7043233	0.0443	0.4832

chr8	146364022	8010045	0.0547	0.6744
chr9	141213431	5777382	0.0409	0.3697
chr10	135534747	6912519	0.051	0.3797
chr11	135006516	5750205	0.0426	0.4434
chr12	133851895	6566441	0.0491	0.2717
chr13	115169878	4270003	0.0371	0.229
chr14	107349540	3852663	0.0359	0.2441
chr15	102531392	4194539	0.0409	0.2538
chr16	90354753	3955108	0.0438	0.2735
chr17	81195210	3604515	0.0444	0.2913
chr18	78077248	3713447	0.0476	0.6385
chr19	59128983	2959827	0.0501	0.4776
chr20	63025520	3135023	0.0497	0.2798
chr21	48129895	1800874	0.0374	0.2633
chr22	51304566	1575405	0.0307	0.2042
chrMT	16571	243731	14.7083	12.9904
chrX	155270560	7431904	0.0479	0.2976
chrY	59373566	401126	0.0068	0.1772

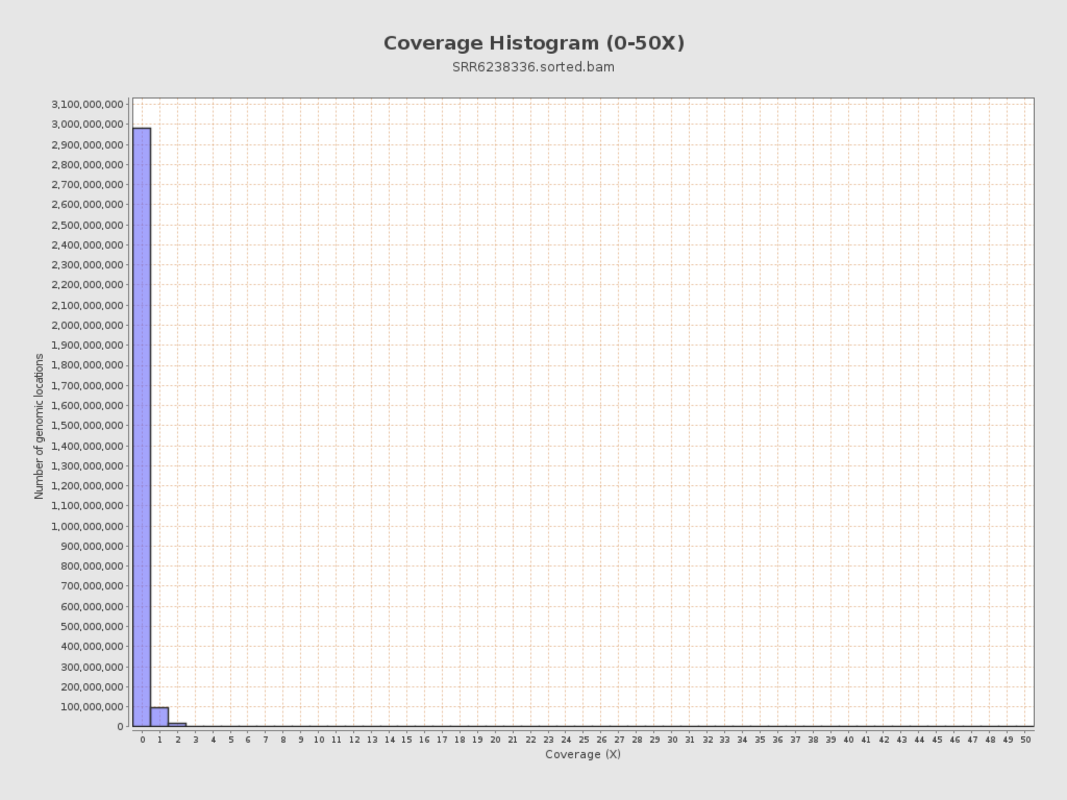
3. Results : Coverage across reference



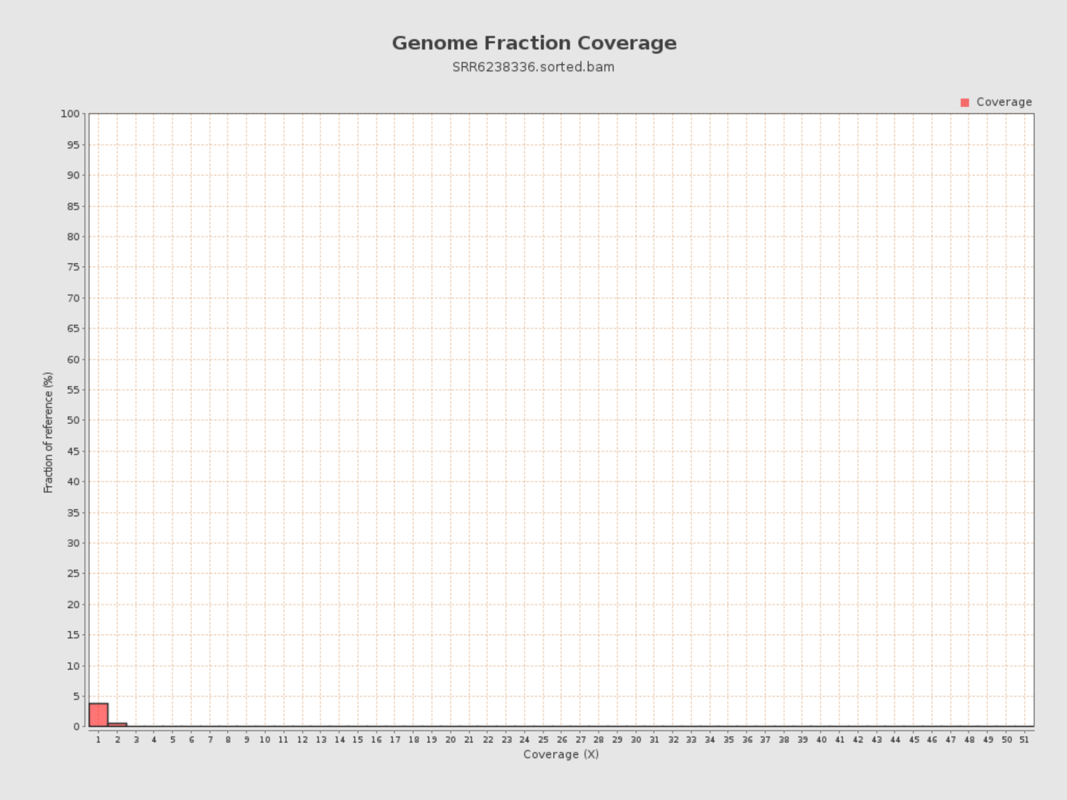
4. Results : Coverage Histogram



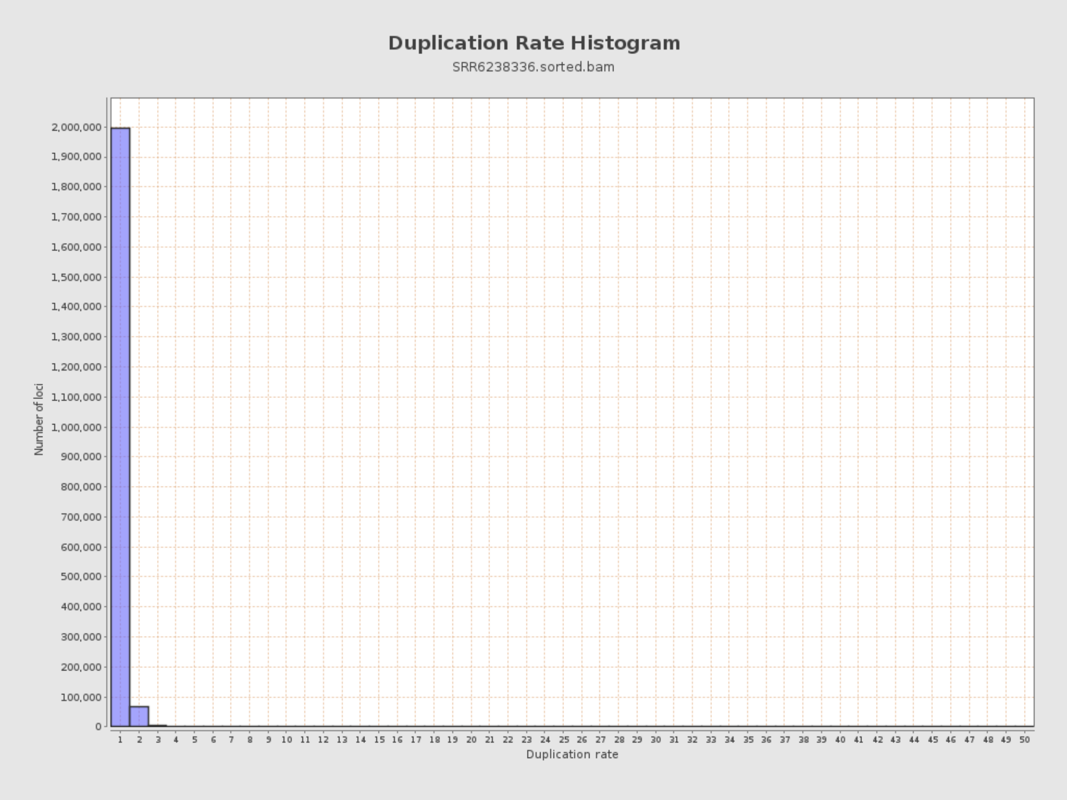
5. Results : Coverage Histogram (0-50X)



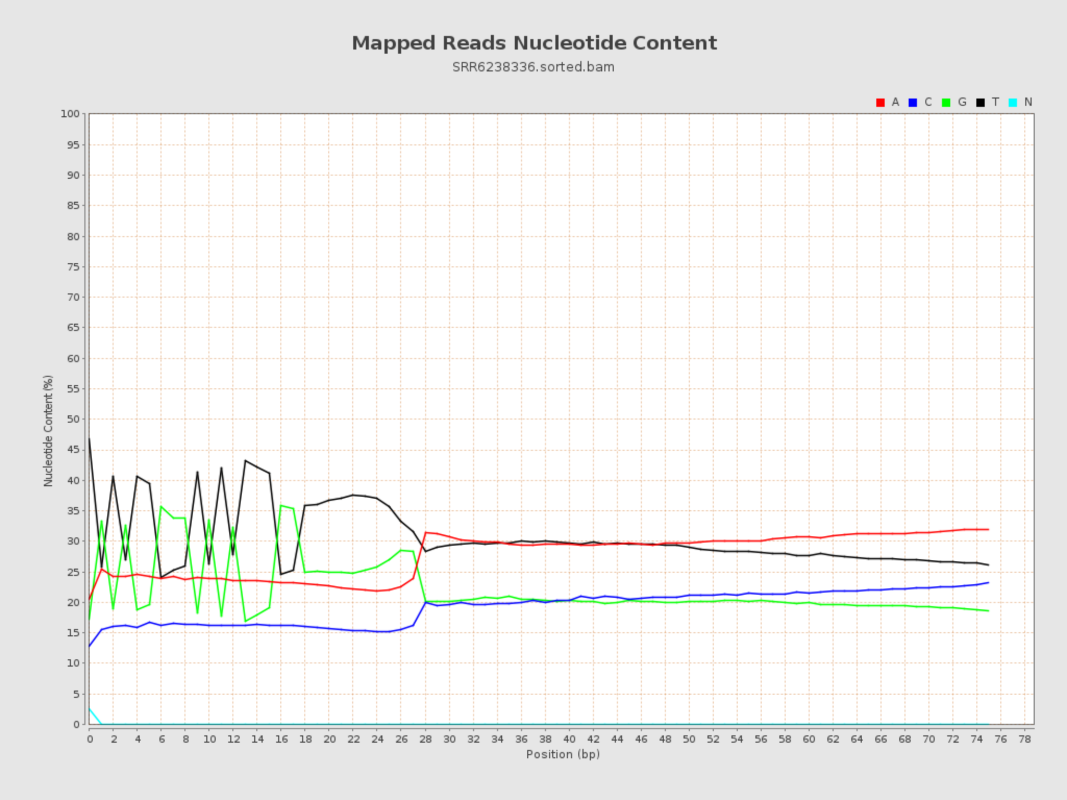
6. Results : Genome Fraction Coverage



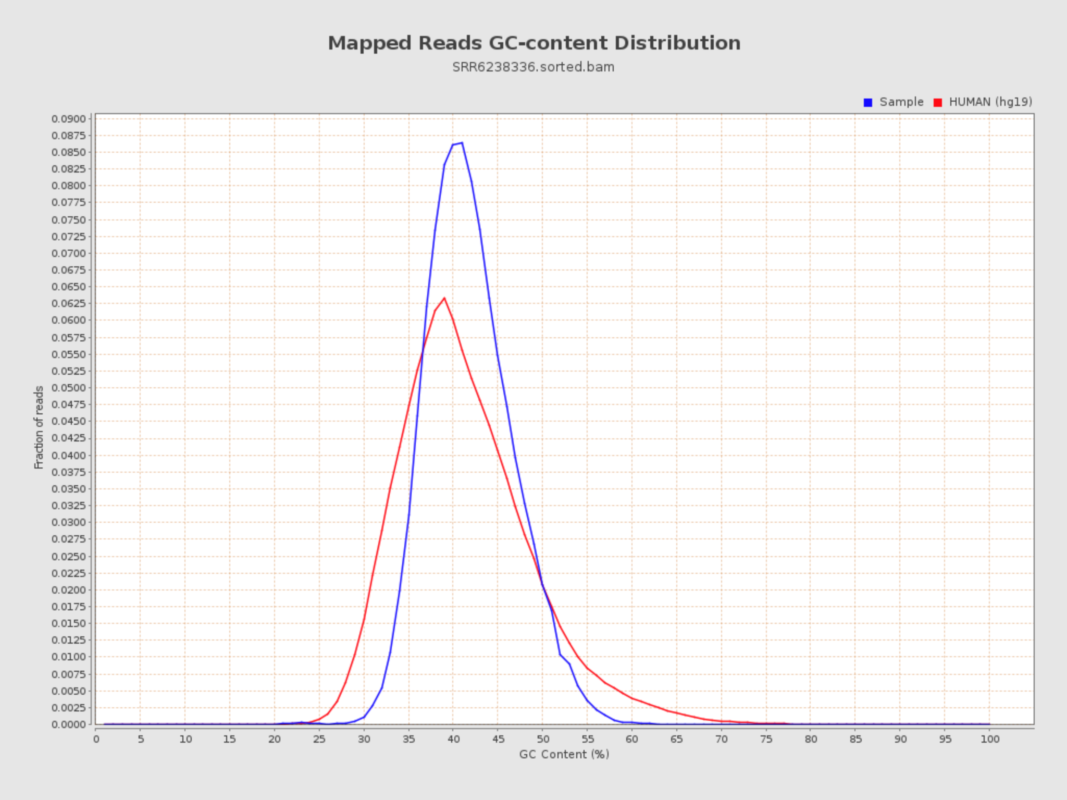
7. Results : Duplication Rate Histogram



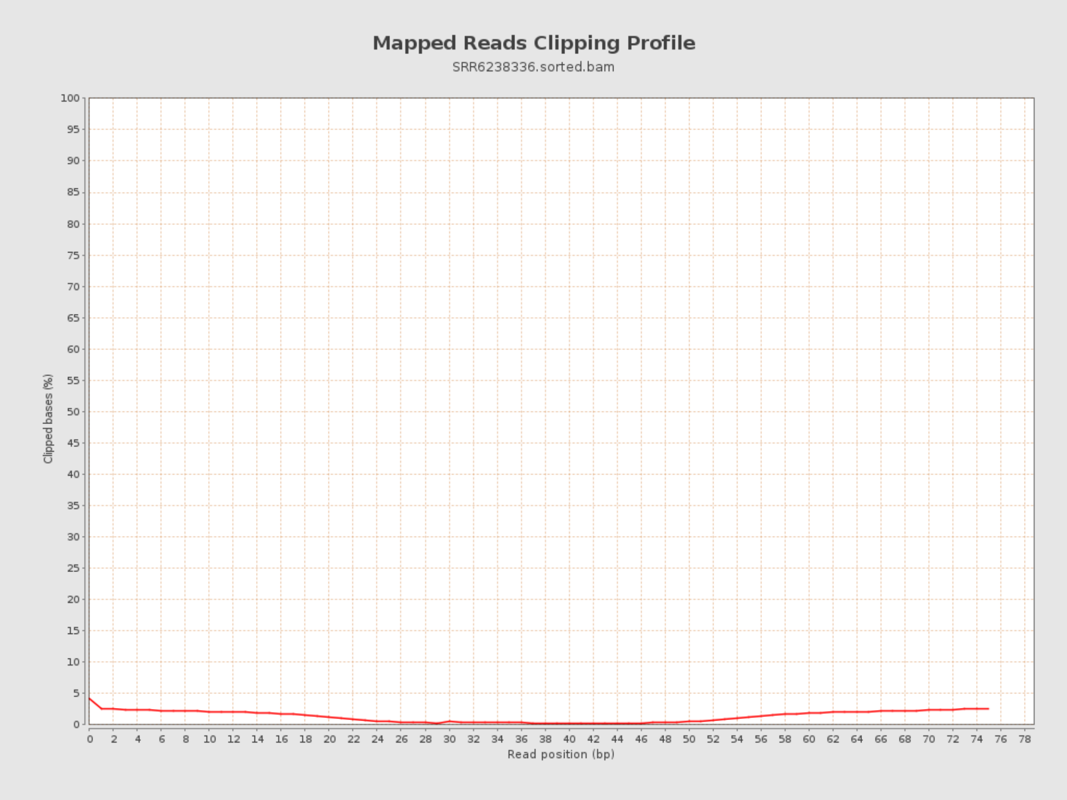
8. Results : Mapped Reads Nucleotide Content



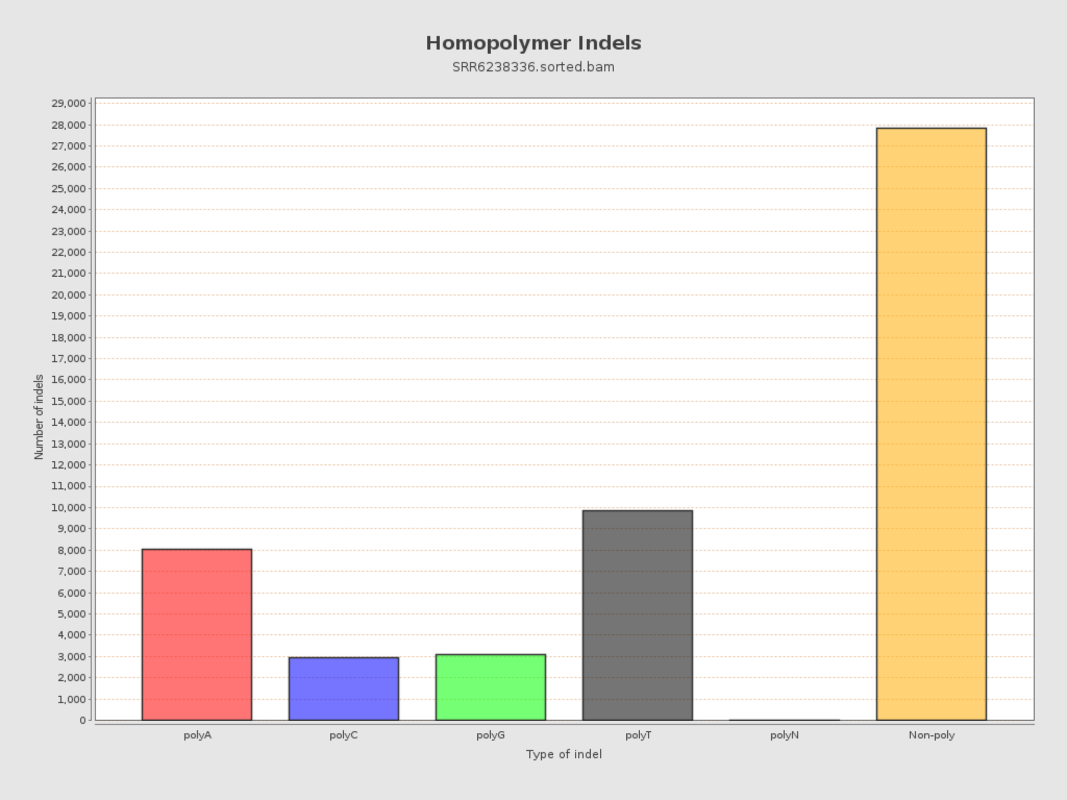
9. Results : Mapped Reads GC-content Distribution



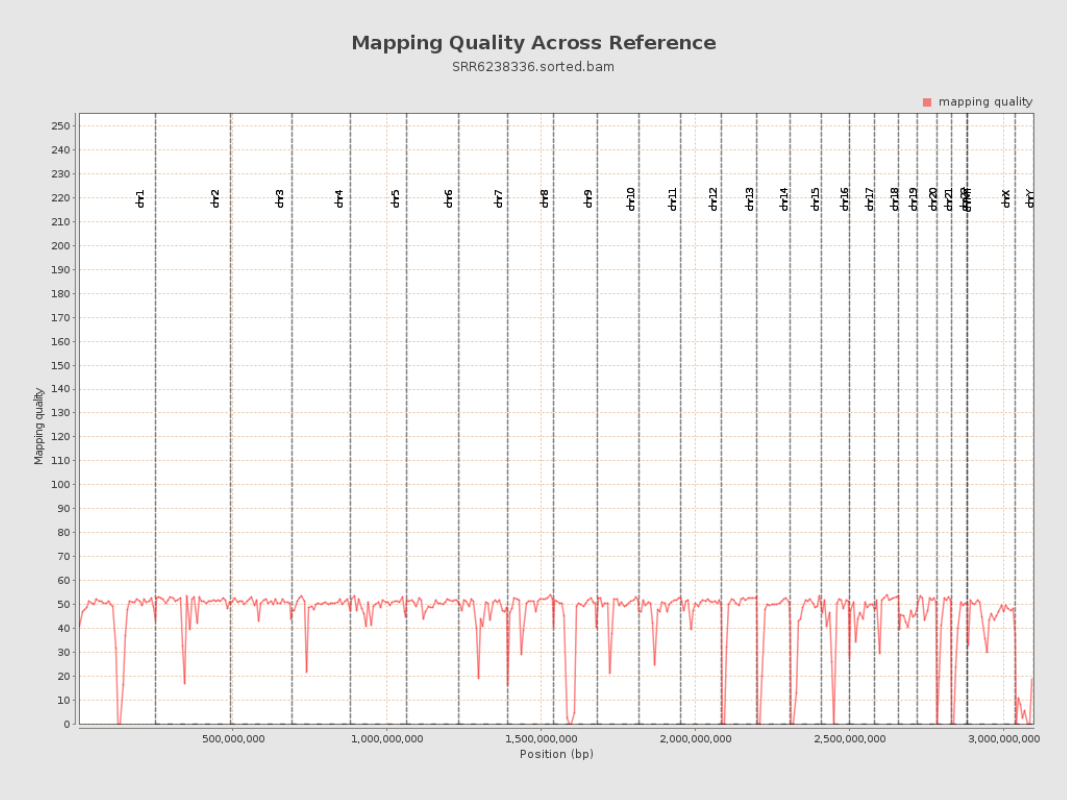
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram