Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 18:35:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238504.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_SRR6238504 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238504.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 18:35:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238504.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,584,737
Mapped reads	3,224,669 / 89.96%
Unmapped reads	360,068 / 10.04%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,856 / 0.61%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	654,173 / 18.25%
Duplication rate	16.07%
Clipped reads	2,032,297 / 56.69%

2.2. ACGT Content

Number/percentage of A's	49,383,788 / 24.86%
Number/percentage of C's	35,467,582 / 17.86%
Number/percentage of T's	65,966,556 / 33.21%
Number/percentage of G's	47,804,946 / 24.07%
Number/percentage of N's	13,489 / 0.01%
GC Percentage	41.92%

2.3. Coverage

Mean	0.0642

Standard Deviation	0.796

2.4. Mapping Quality

Mean Mapping Quality	42.64

2.5. Mismatches and indels

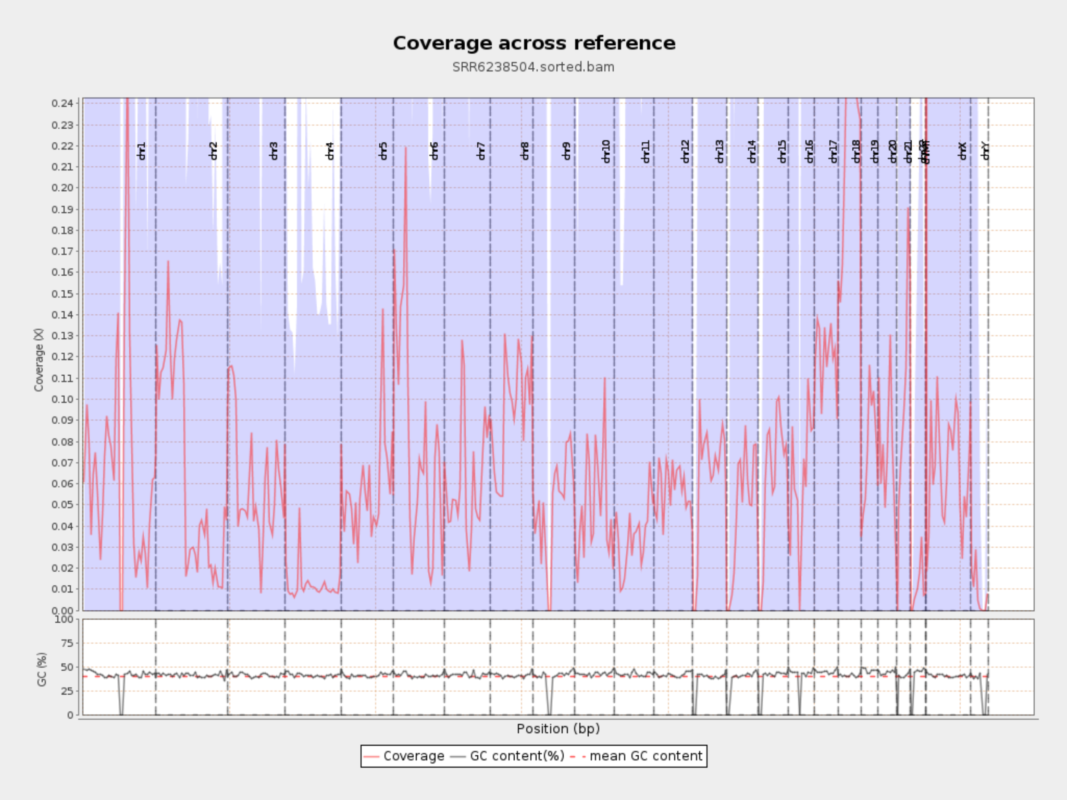
General error rate	0.62%
Mismatches	1,198,663
Insertions	13,324
Mapped reads with at least one insertion	0.41%
Deletions	64,999
Mapped reads with at least one deletion	1.99%
Homopolymer indels	42.49%

2.6. Chromosome stats

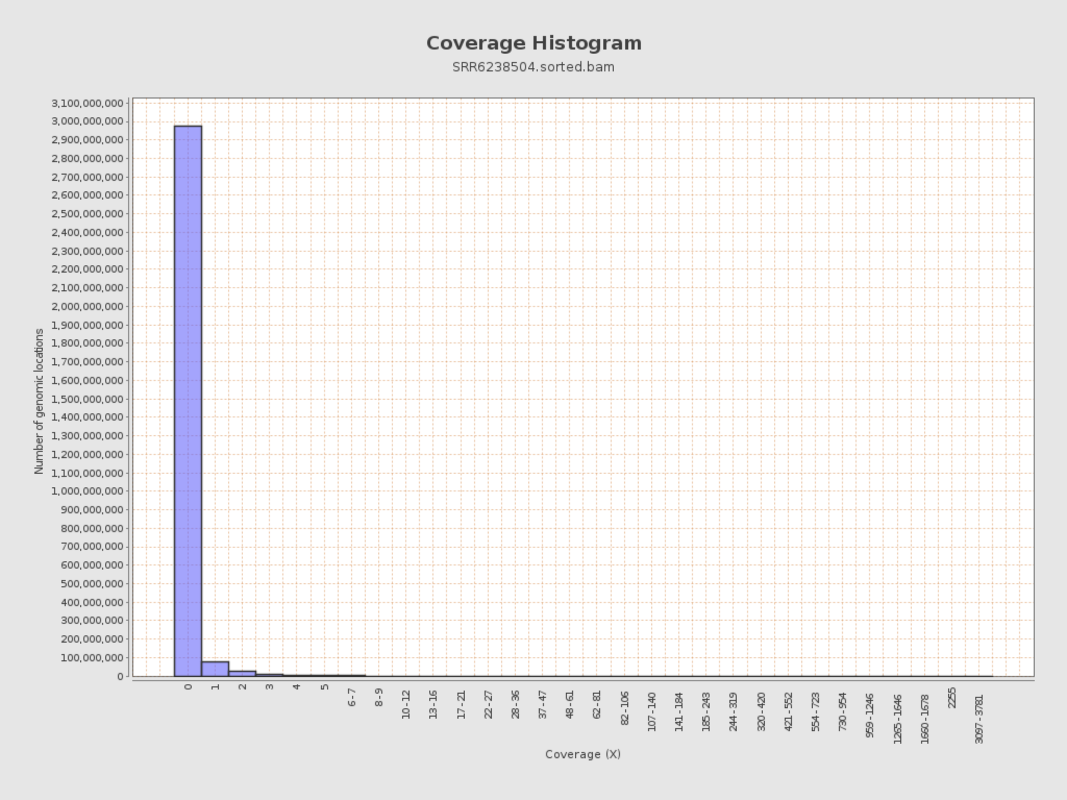
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16665621	0.0669	1.2817
chr2	243199373	15961345	0.0656	1.7371
chr3	198022430	12068655	0.0609	0.3847
chr4	191154276	2320961	0.0121	0.2012
chr5	180915260	10605486	0.0586	0.3799
chr6	171115067	13580750	0.0794	0.6435
chr7	159138663	9936633	0.0624	0.8941

chr8	146364022	13731321	0.0938	0.677
chr9	141213431	7030490	0.0498	0.46
chr10	135534747	6725340	0.0496	0.4913
chr11	135006516	4678480	0.0347	0.3415
chr12	133851895	7714744	0.0576	0.3739
chr13	115169878	7359935	0.0639	0.5141
chr14	107349540	5168364	0.0481	0.3642
chr15	102531392	6366522	0.0621	0.4796
chr16	90354753	5448053	0.0603	0.4459
chr17	81195210	9915057	0.1221	0.5665
chr18	78077248	17819521	0.2282	1.473
chr19	59128983	4612293	0.078	0.8677
chr20	63025520	4719003	0.0749	0.4502
chr21	48129895	4793435	0.0996	0.5132
chr22	51304566	602035	0.0117	0.1557
chrMT	16571	35036	2.1143	2.2721
chrX	155270560	10372659	0.0668	0.434
chrY	59373566	515913	0.0087	0.3377

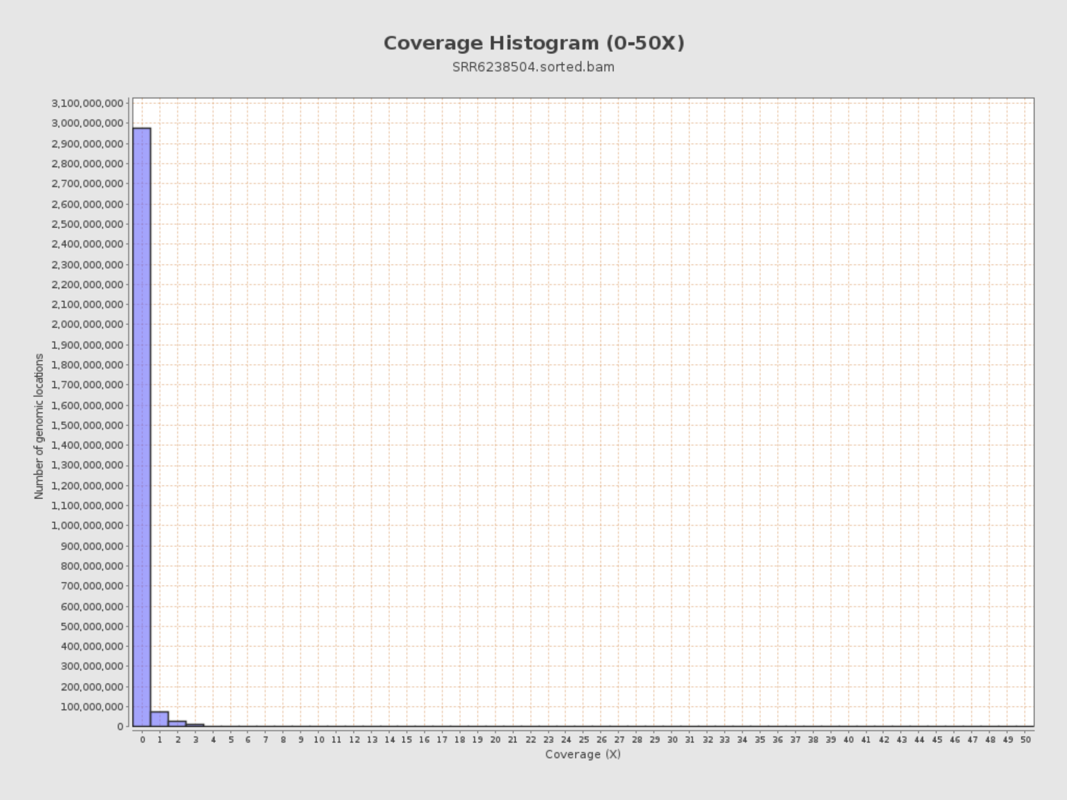
3. Results : Coverage across reference



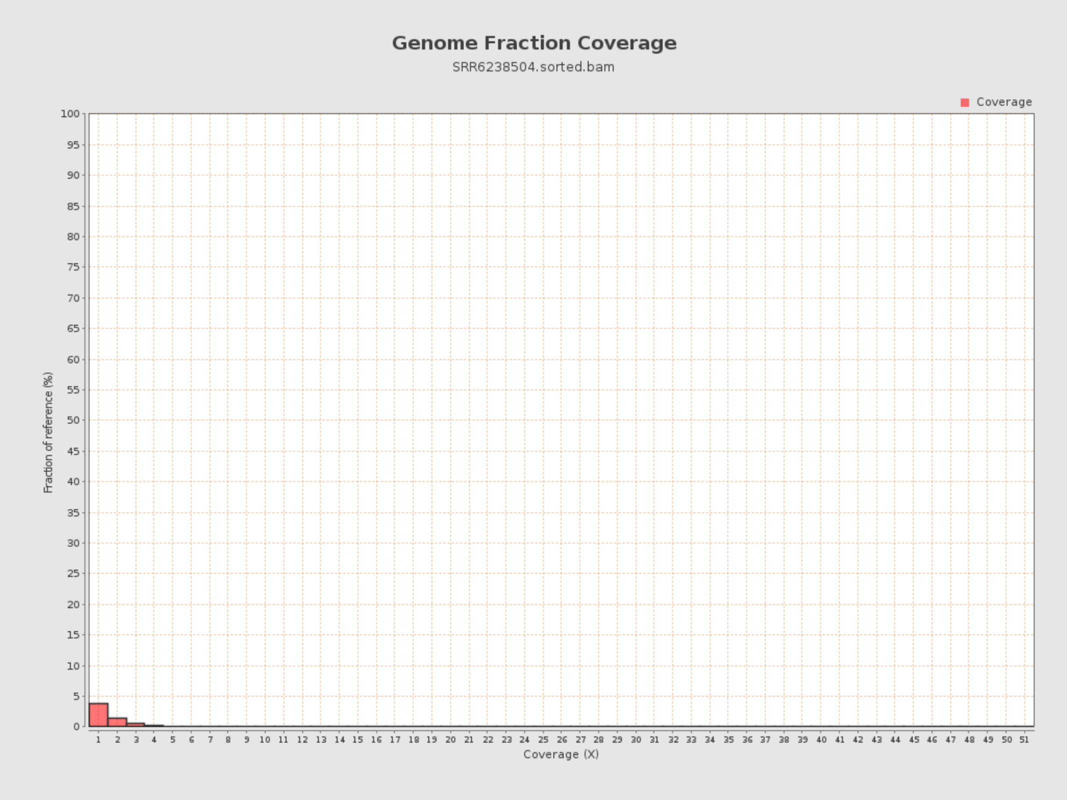
4. Results : Coverage Histogram



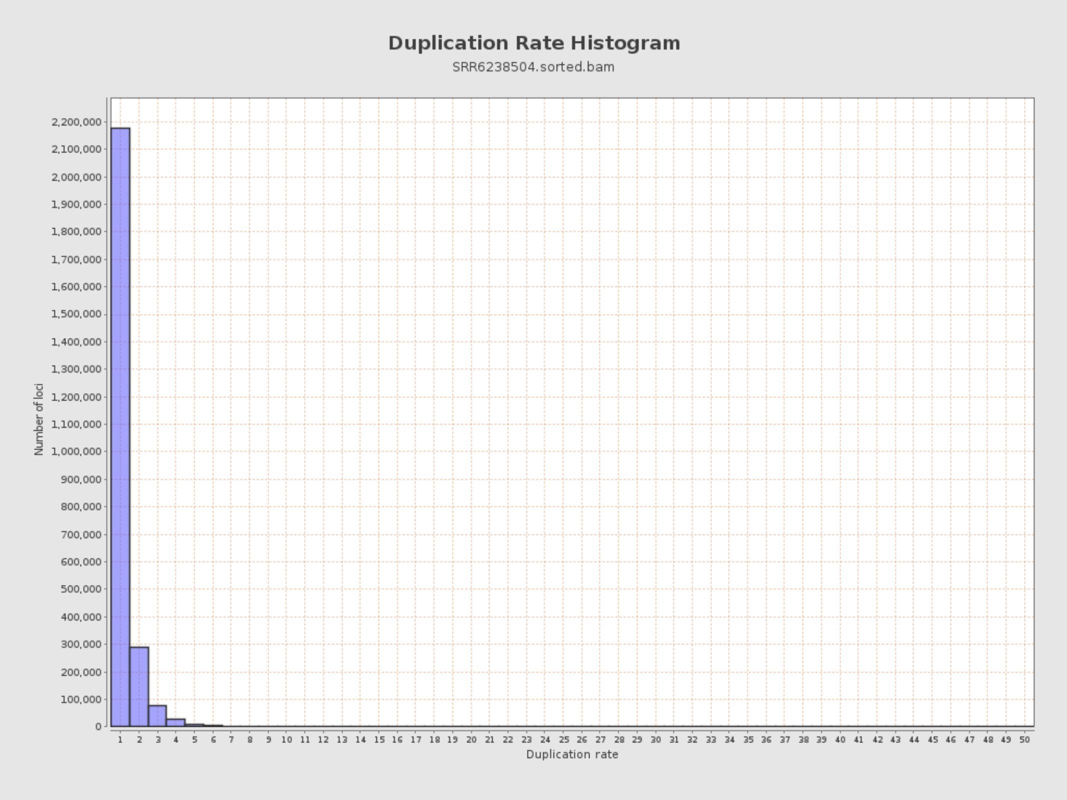
5. Results : Coverage Histogram (0-50X)



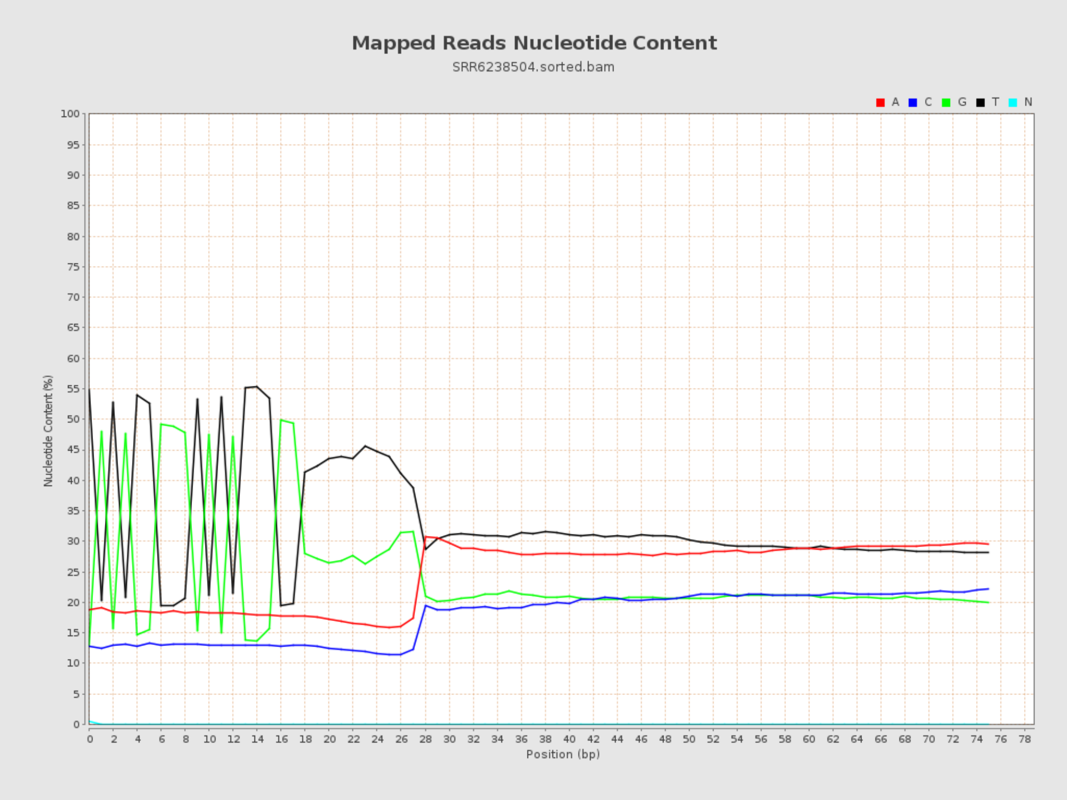
6. Results : Genome Fraction Coverage



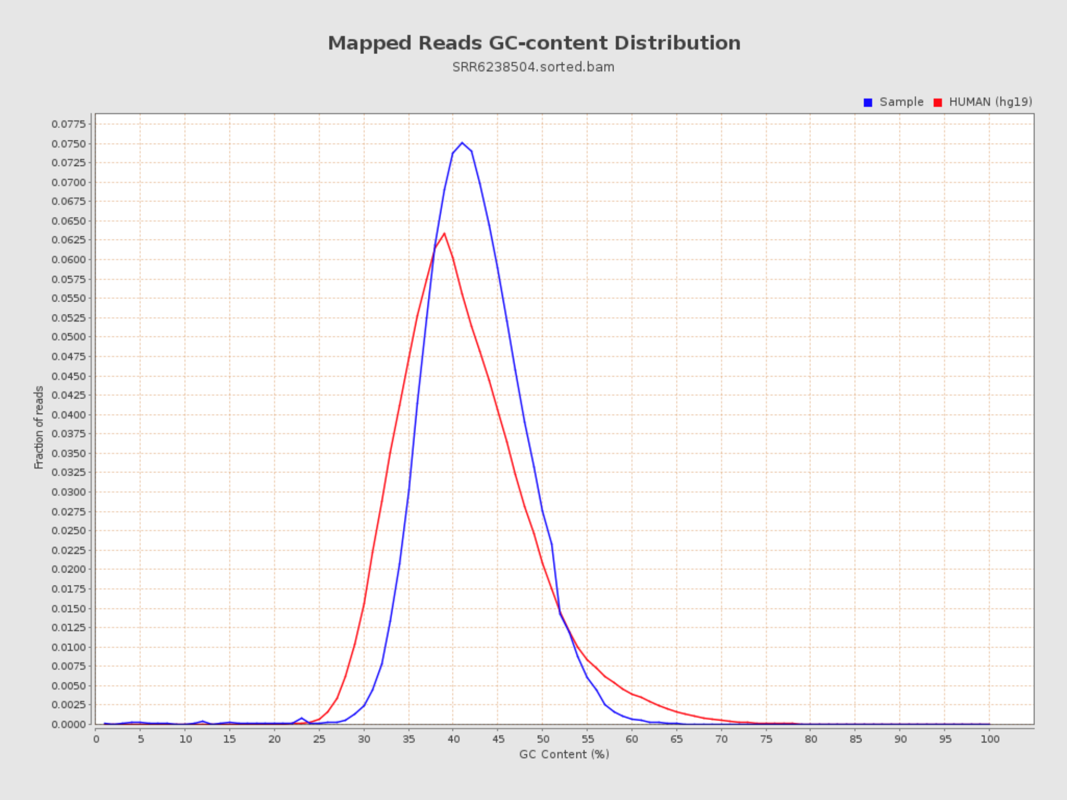
7. Results : Duplication Rate Histogram



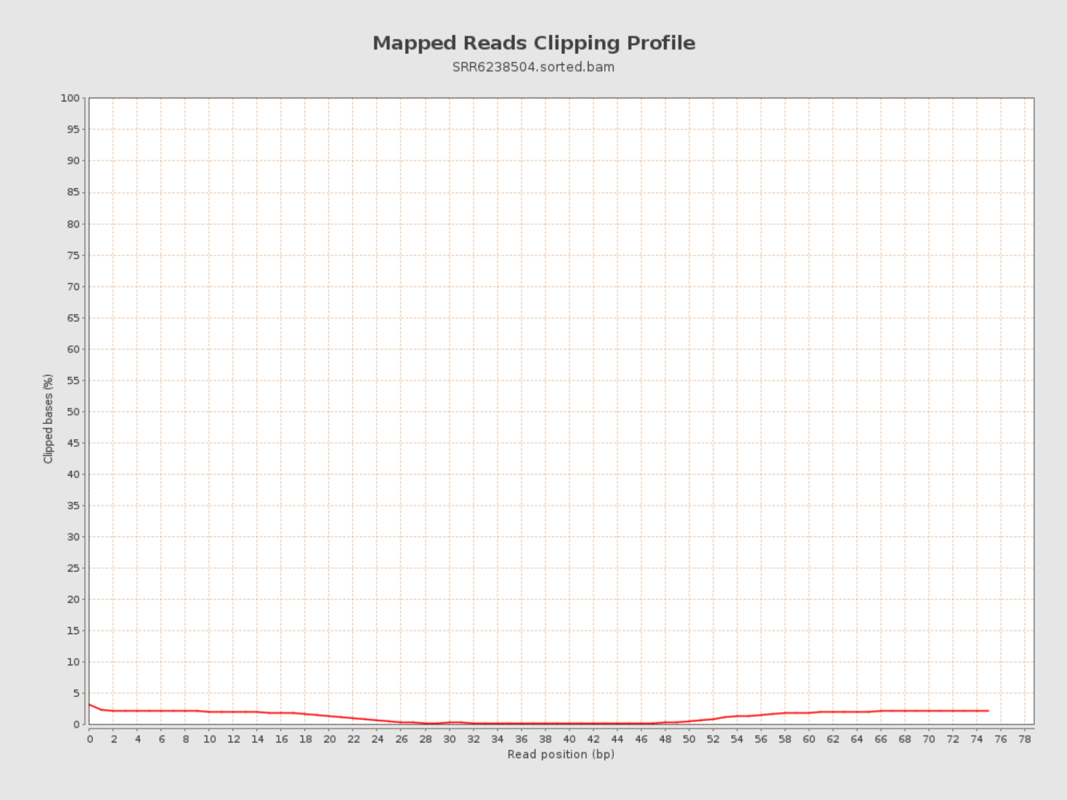
8. Results : Mapped Reads Nucleotide Content



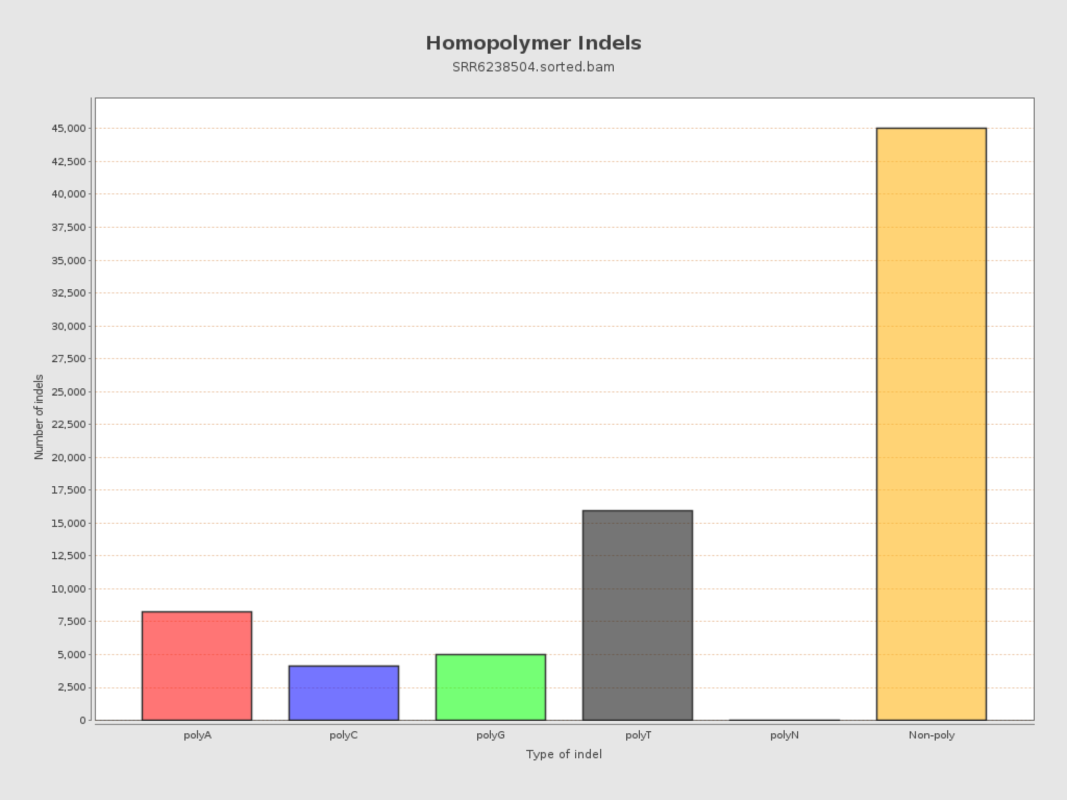
9. Results : Mapped Reads GC-content Distribution



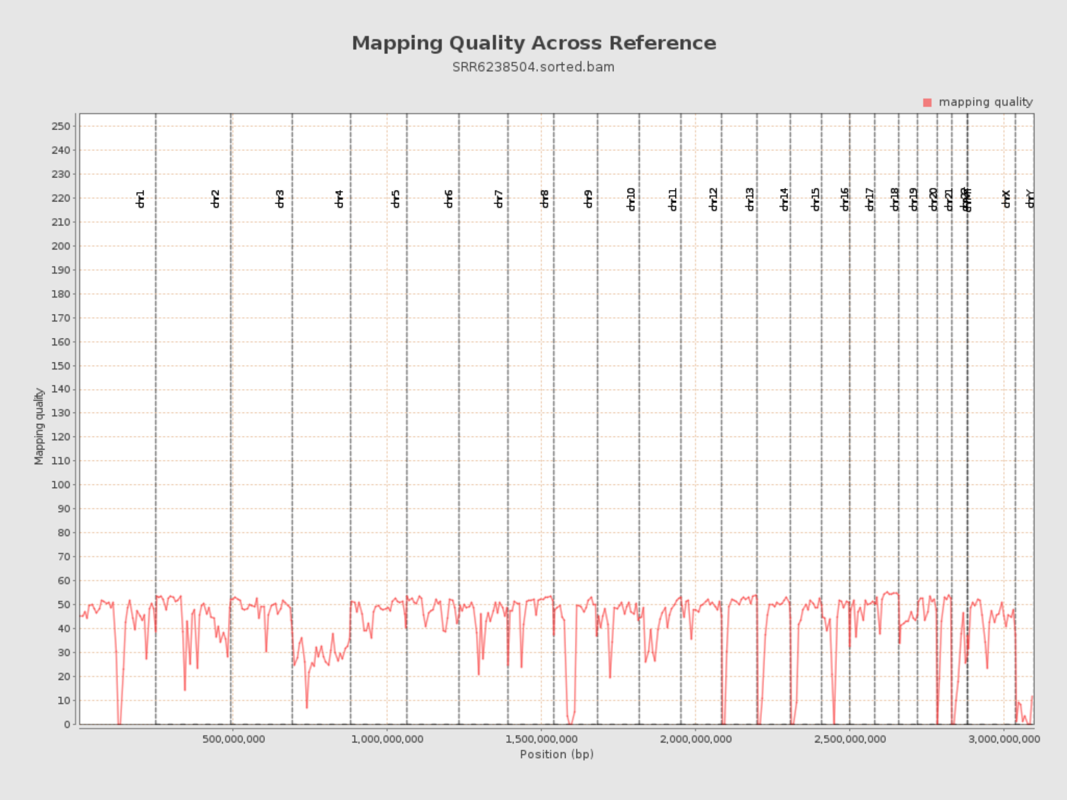
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram