Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 18:42:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238506.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_SRR6238506 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238506.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 18:42:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238506.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,362,997
Mapped reads	2,095,163 / 88.67%
Unmapped reads	267,834 / 11.33%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,717 / 0.75%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	405,238 / 17.15%
Duplication rate	15.76%
Clipped reads	1,341,486 / 56.77%

2.2. ACGT Content

Number/percentage of A's	31,665,830 / 24.65%
Number/percentage of C's	22,692,373 / 17.66%
Number/percentage of T's	42,653,257 / 33.2%
Number/percentage of G's	31,467,230 / 24.49%
Number/percentage of N's	8,639 / 0.01%
GC Percentage	42.15%

2.3. Coverage

Mean	0.0415

Standard Deviation	0.5693

2.4. Mapping Quality

Mean Mapping Quality	39.29

2.5. Mismatches and indels

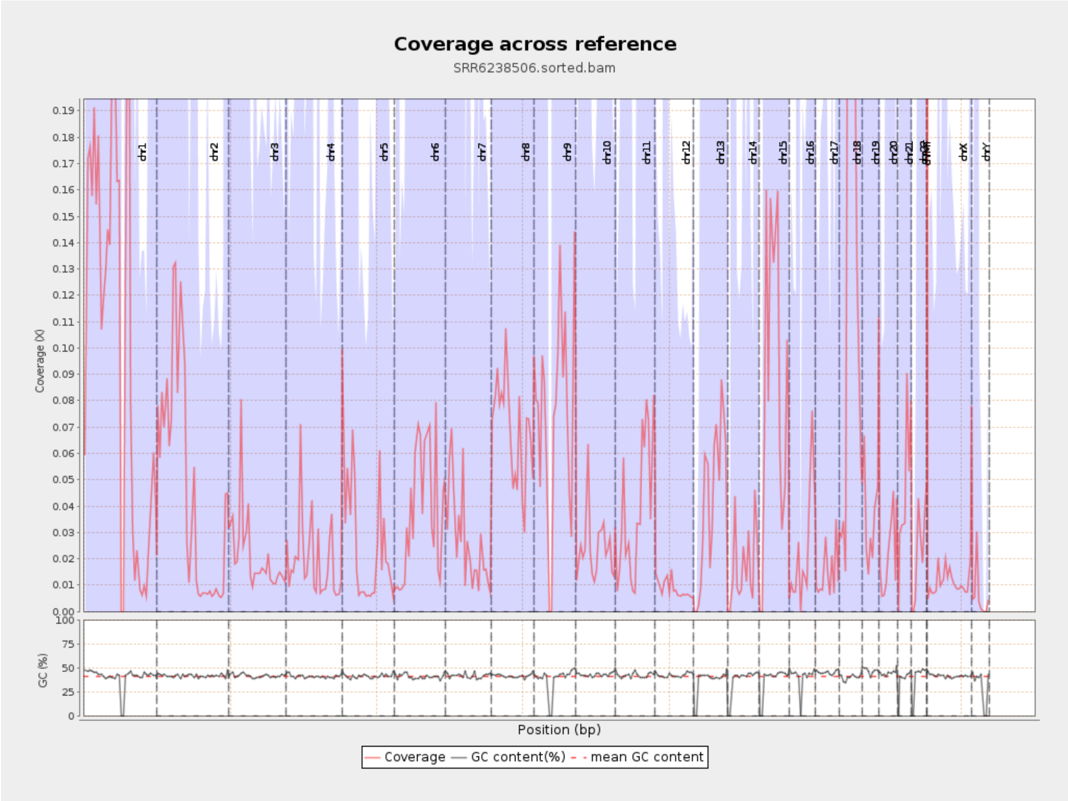
General error rate	0.62%
Mismatches	782,619
Insertions	8,444
Mapped reads with at least one insertion	0.4%
Deletions	42,283
Mapped reads with at least one deletion	1.99%
Homopolymer indels	41.05%

2.6. Chromosome stats

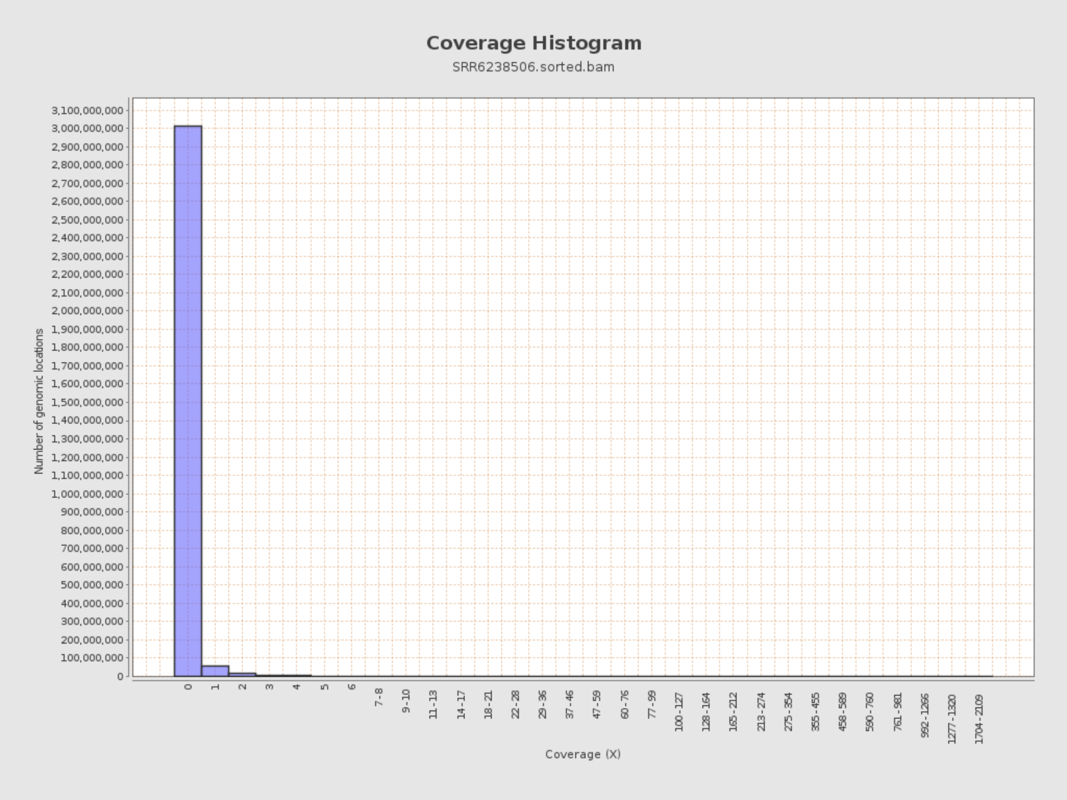
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	25067114	0.1006	1.1244
chr2	243199373	11255300	0.0463	1.0048
chr3	198022430	4226132	0.0213	0.2145
chr4	191154276	3707526	0.0194	0.2597
chr5	180915260	4606790	0.0255	0.2399
chr6	171115067	6488112	0.0379	0.4253
chr7	159138663	4325279	0.0272	0.4749

chr8	146364022	9999491	0.0683	0.4782
chr9	141213431	10506651	0.0744	0.6242
chr10	135534747	3228662	0.0238	0.3921
chr11	135006516	5203412	0.0385	0.3084
chr12	133851895	1167411	0.0087	0.2265
chr13	115169878	4817619	0.0418	0.3358
chr14	107349540	1850993	0.0172	0.3566
chr15	102531392	9046263	0.0882	0.4654
chr16	90354753	2007393	0.0222	0.342
chr17	81195210	1174553	0.0145	0.1811
chr18	78077248	10624872	0.1361	1.0796
chr19	59128983	2226698	0.0377	0.7057
chr20	63025520	1291365	0.0205	0.2399
chr21	48129895	2246358	0.0467	0.3914
chr22	51304566	1119682	0.0218	0.2163
chrMT	16571	95951	5.7903	4.5556
chrX	155270560	1906395	0.0123	0.2175
chrY	59373566	371355	0.0063	0.3471

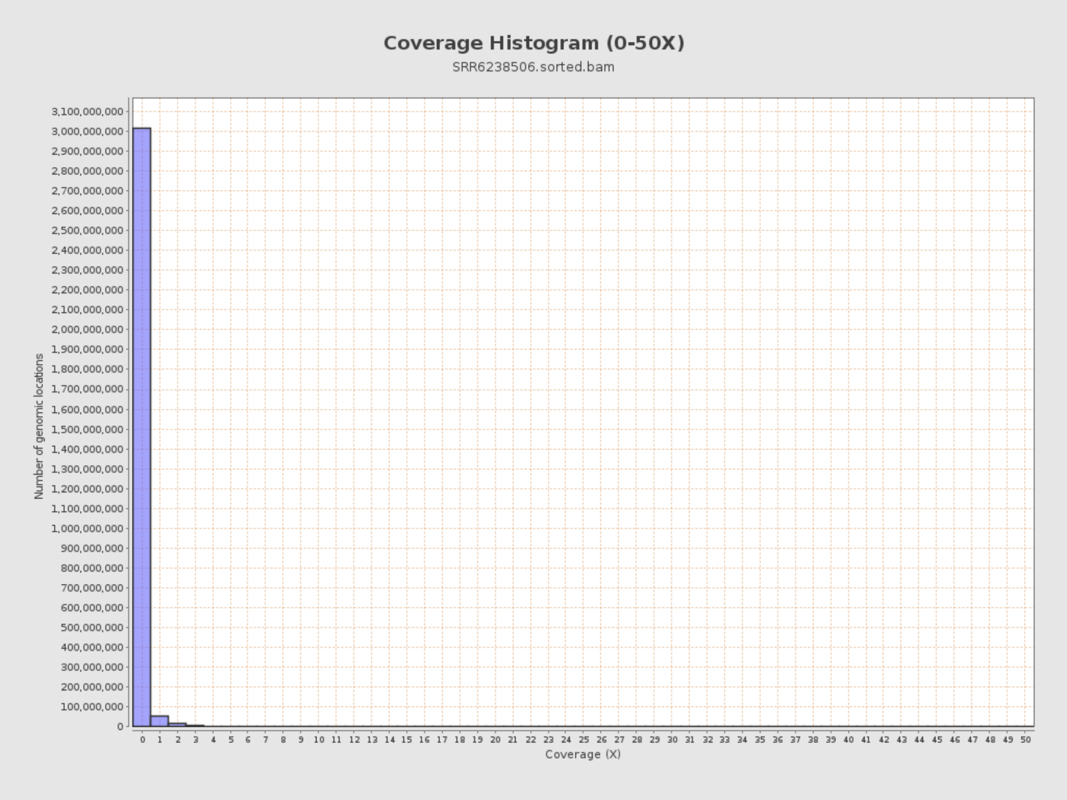
3. Results : Coverage across reference



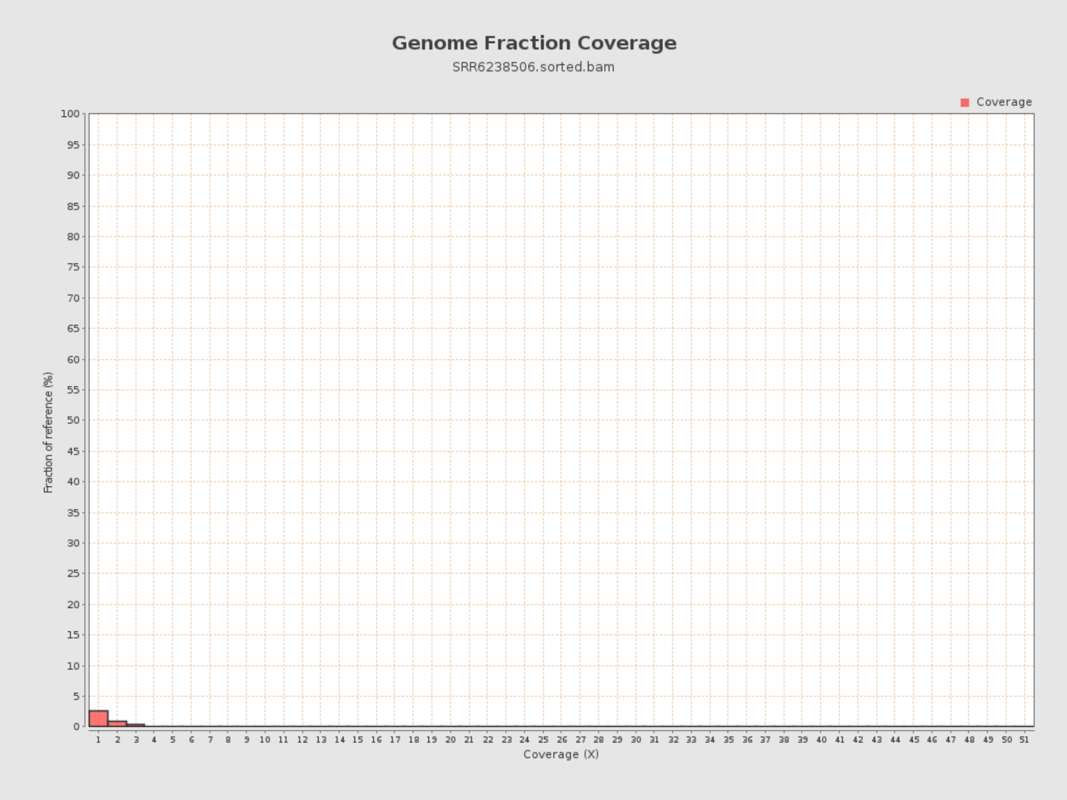
4. Results : Coverage Histogram



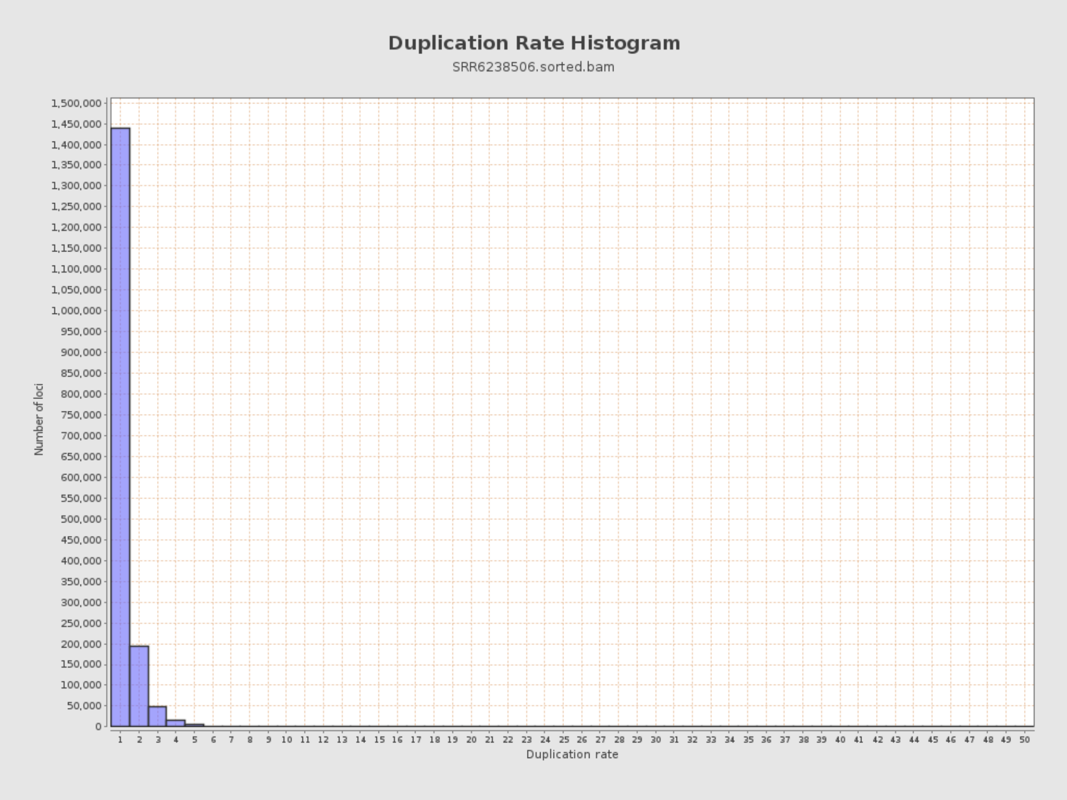
5. Results : Coverage Histogram (0-50X)



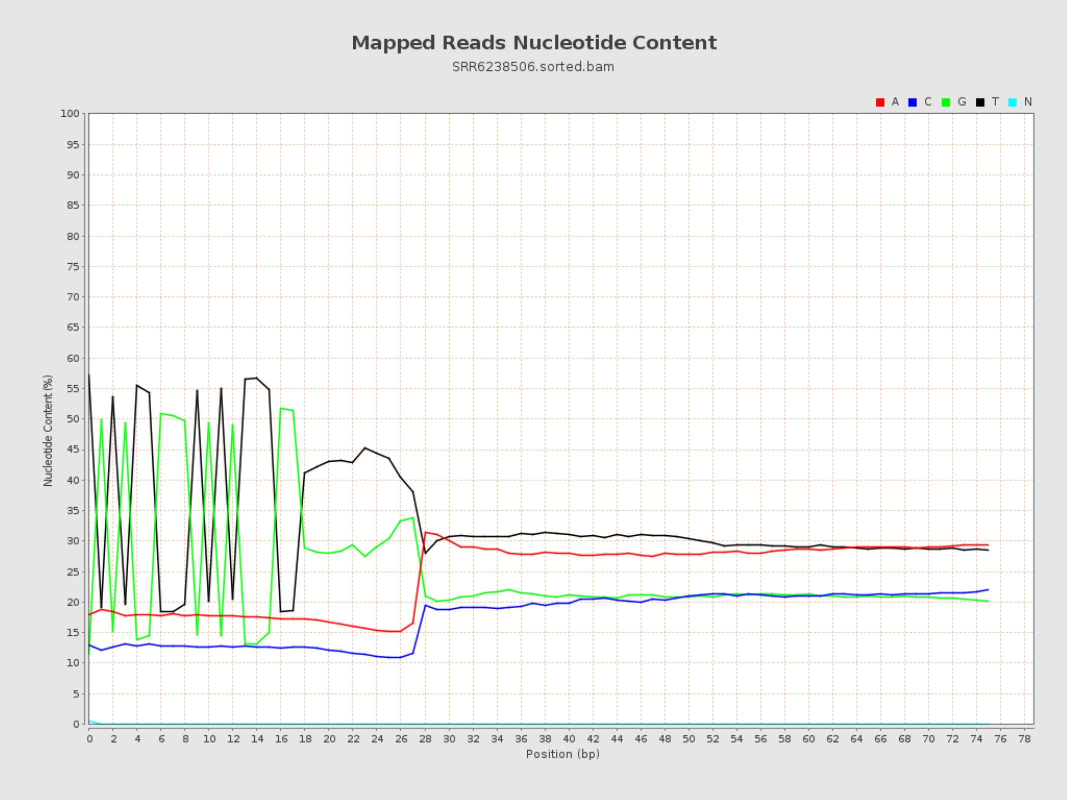
6. Results : Genome Fraction Coverage



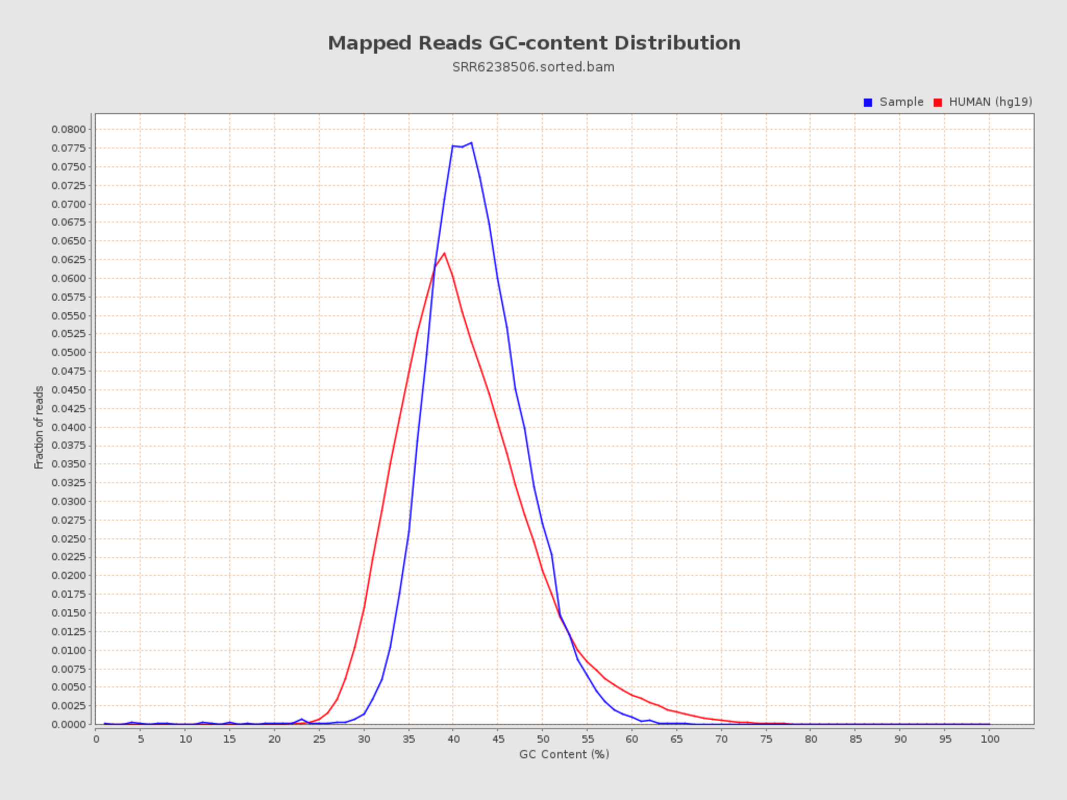
7. Results : Duplication Rate Histogram



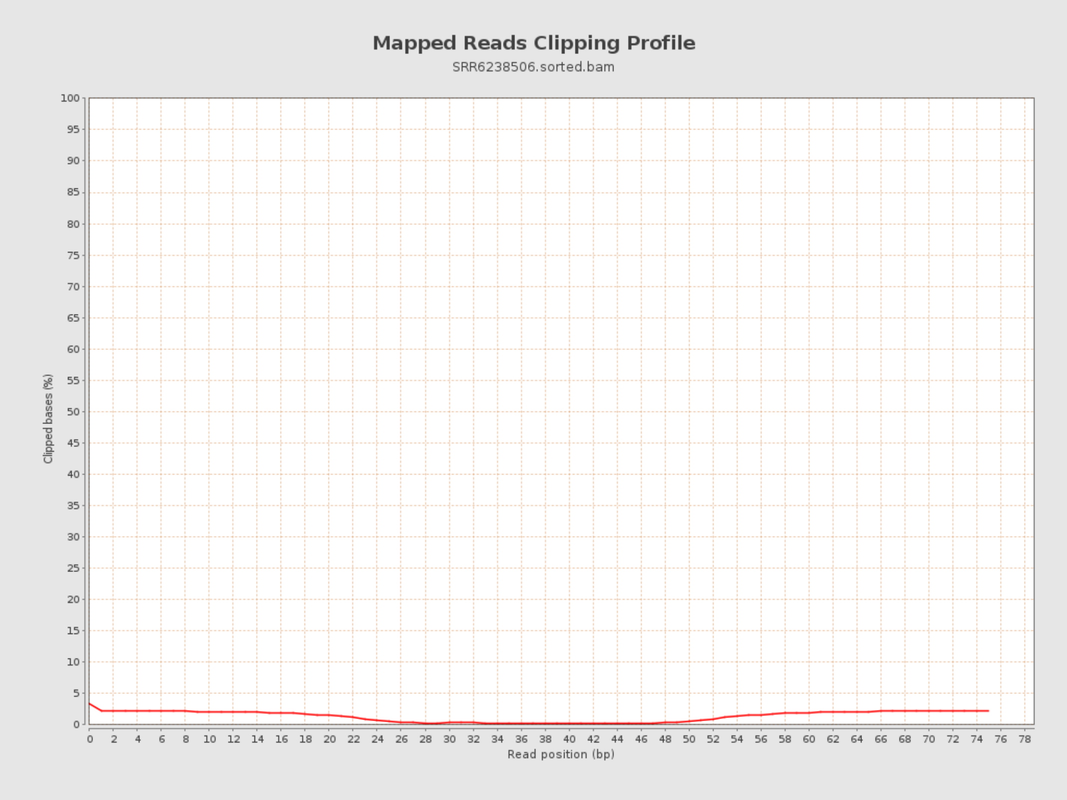
8. Results : Mapped Reads Nucleotide Content



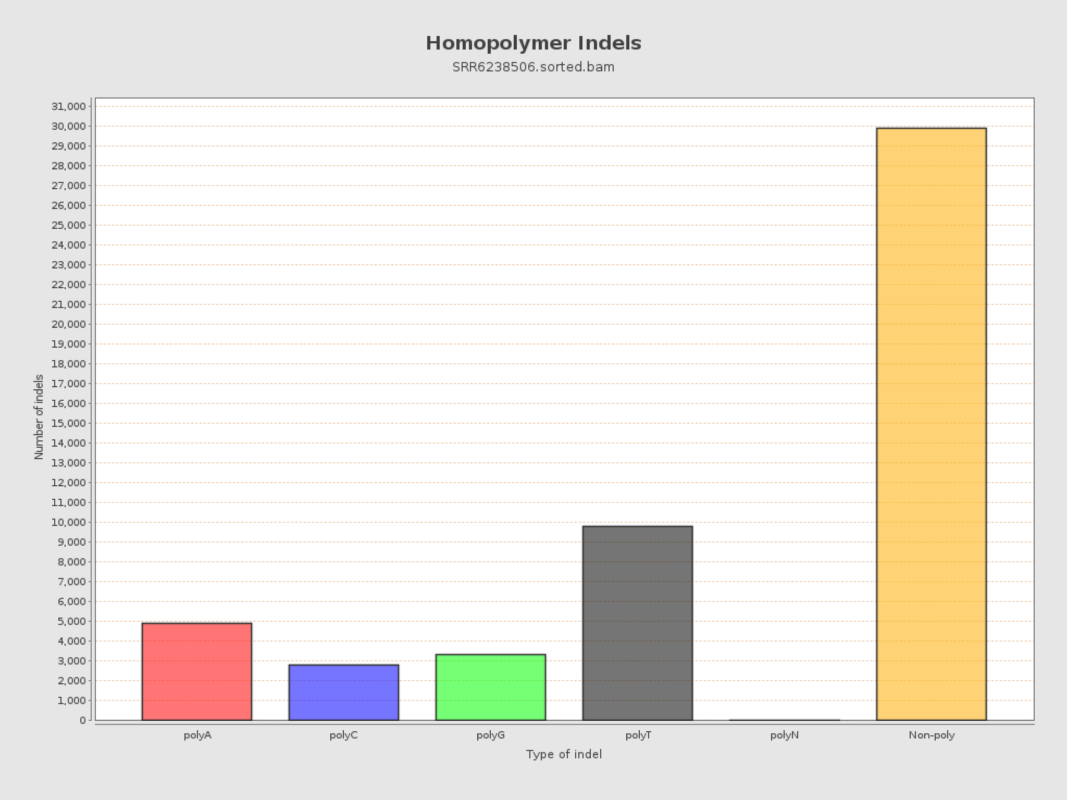
9. Results : Mapped Reads GC-content Distribution



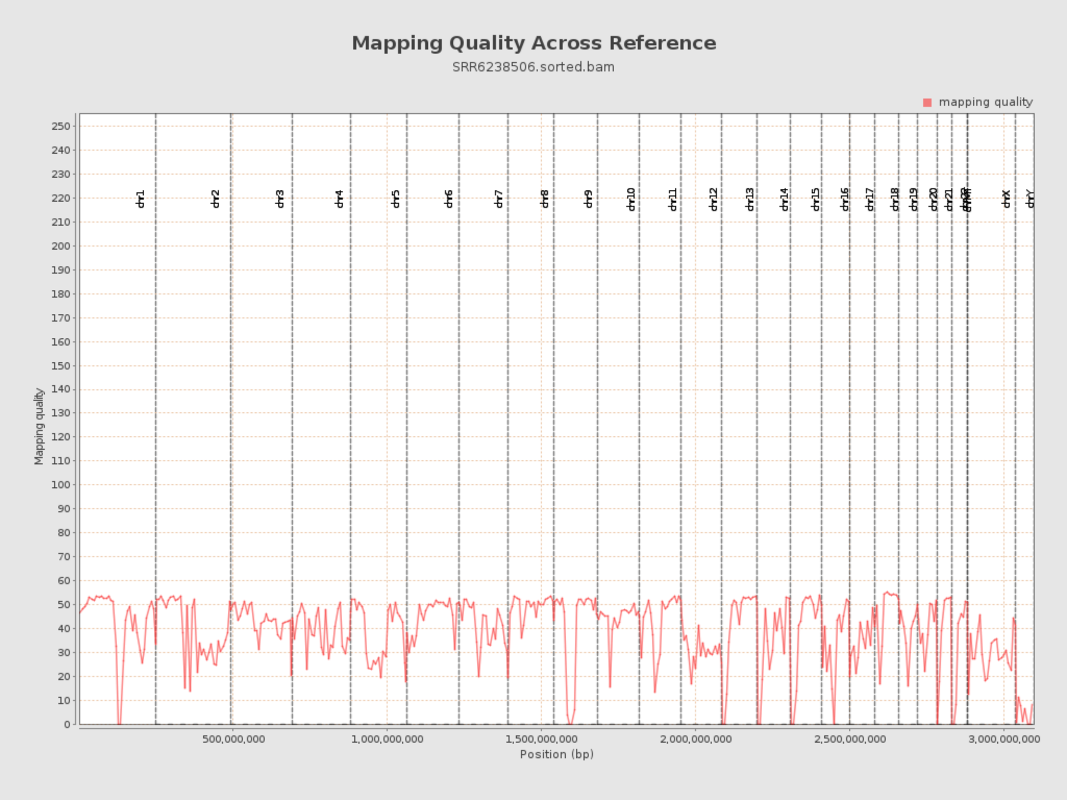
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram