Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 13:28:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238262.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_SRR6238262 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238262.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 13:28:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238262.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,752,196
Mapped reads	1,371,756 / 78.29%
Unmapped reads	380,440 / 21.71%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,337 / 0.82%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	156,939 / 8.96%
Duplication rate	8.99%
Clipped reads	815,918 / 46.57%

2.2. ACGT Content

Number/percentage of A's	24,435,621 / 28.13%
Number/percentage of C's	16,411,578 / 18.89%
Number/percentage of T's	26,948,452 / 31.02%
Number/percentage of G's	19,051,622 / 21.93%
Number/percentage of N's	19,850 / 0.02%
GC Percentage	40.82%

2.3. Coverage

Mean	0.0281

Standard Deviation	0.3229

2.4. Mapping Quality

Mean Mapping Quality	45.24

2.5. Mismatches and indels

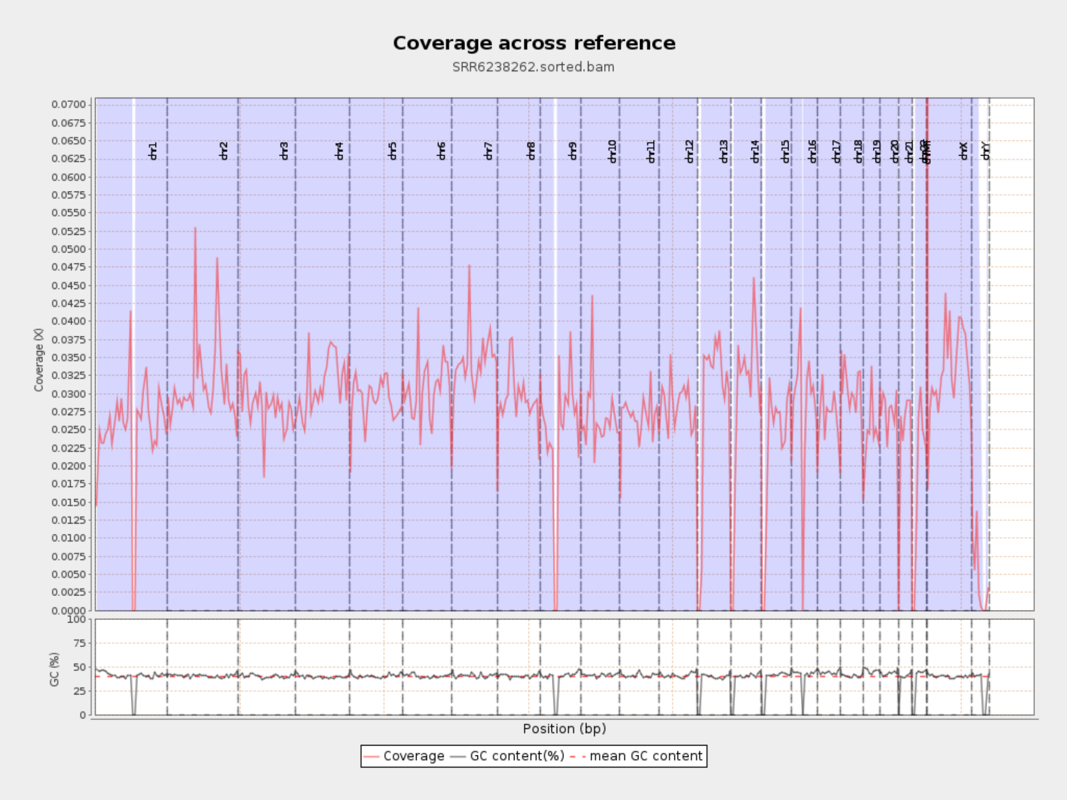
General error rate	1%
Mismatches	856,464
Insertions	7,290
Mapped reads with at least one insertion	0.53%
Deletions	32,204
Mapped reads with at least one deletion	2.32%
Homopolymer indels	46.54%

2.6. Chromosome stats

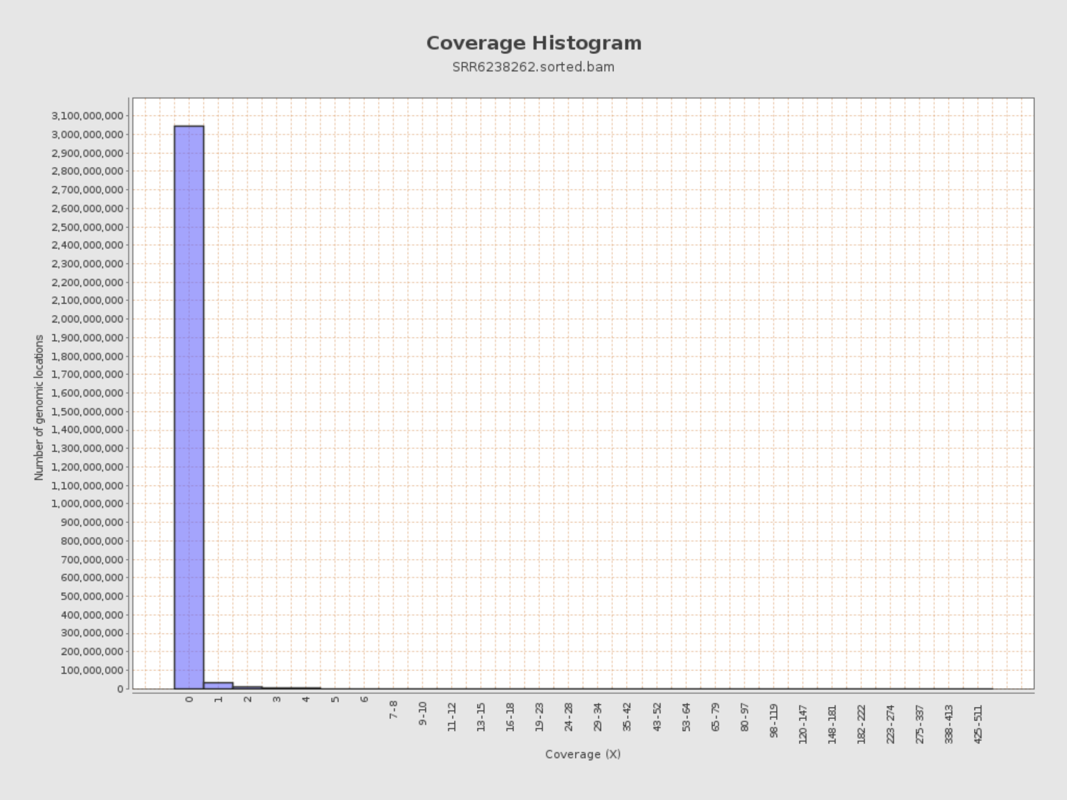
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6175005	0.0248	0.4635
chr2	243199373	7675493	0.0316	0.3836
chr3	198022430	5634010	0.0285	0.2555
chr4	191154276	5995257	0.0314	0.2778
chr5	180915260	5331587	0.0295	0.2595
chr6	171115067	5250967	0.0307	0.3076
chr7	159138663	5491815	0.0345	0.4052

chr8	146364022	4314675	0.0295	0.4018
chr9	141213431	3458864	0.0245	0.2766
chr10	135534747	3622877	0.0267	0.2878
chr11	135006516	3631024	0.0269	0.2736
chr12	133851895	3812517	0.0285	0.2566
chr13	115169878	3249046	0.0282	0.2603
chr14	107349540	3101003	0.0289	0.321
chr15	102531392	2312234	0.0226	0.3349
chr16	90354753	2517961	0.0279	0.2569
chr17	81195210	2185106	0.0269	0.2602
chr18	78077248	2384643	0.0305	0.4363
chr19	59128983	1473418	0.0249	0.3358
chr20	63025520	1715501	0.0272	0.2491
chr21	48129895	1161638	0.0241	0.2372
chr22	51304566	941825	0.0184	0.1975
chrMT	16571	17441	1.0525	1.8467
chrX	155270560	5220689	0.0336	0.2967
chrY	59373566	245540	0.0041	0.1166

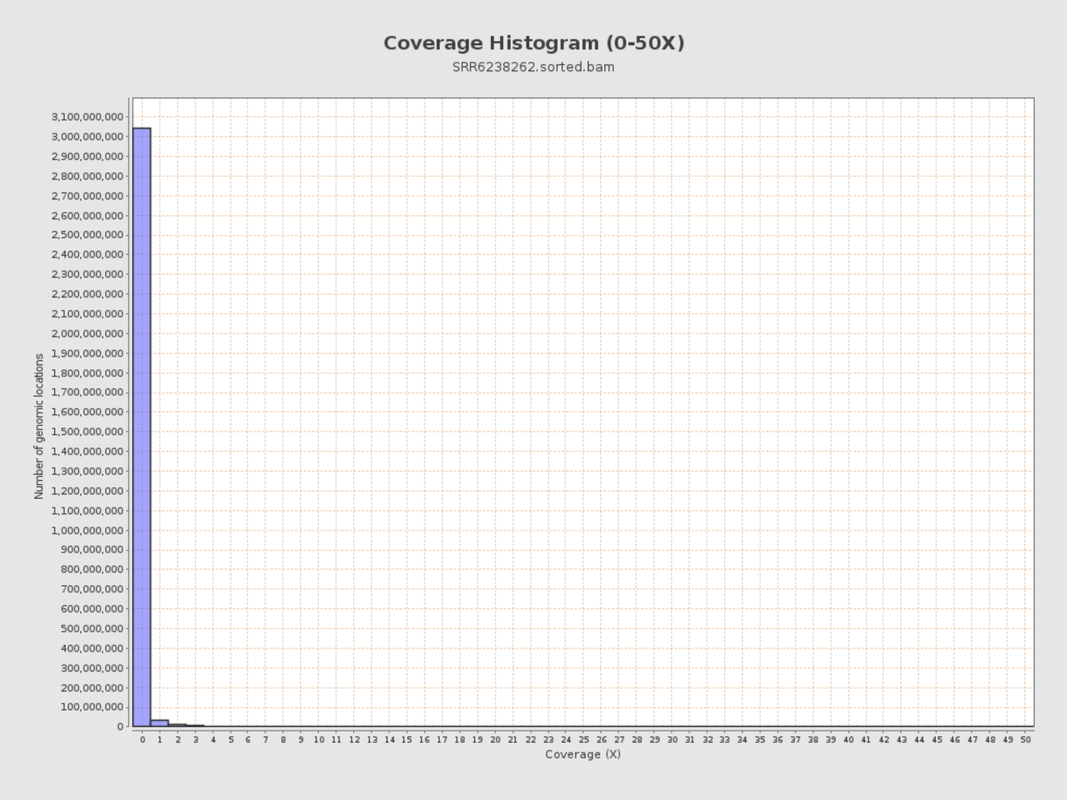
3. Results : Coverage across reference



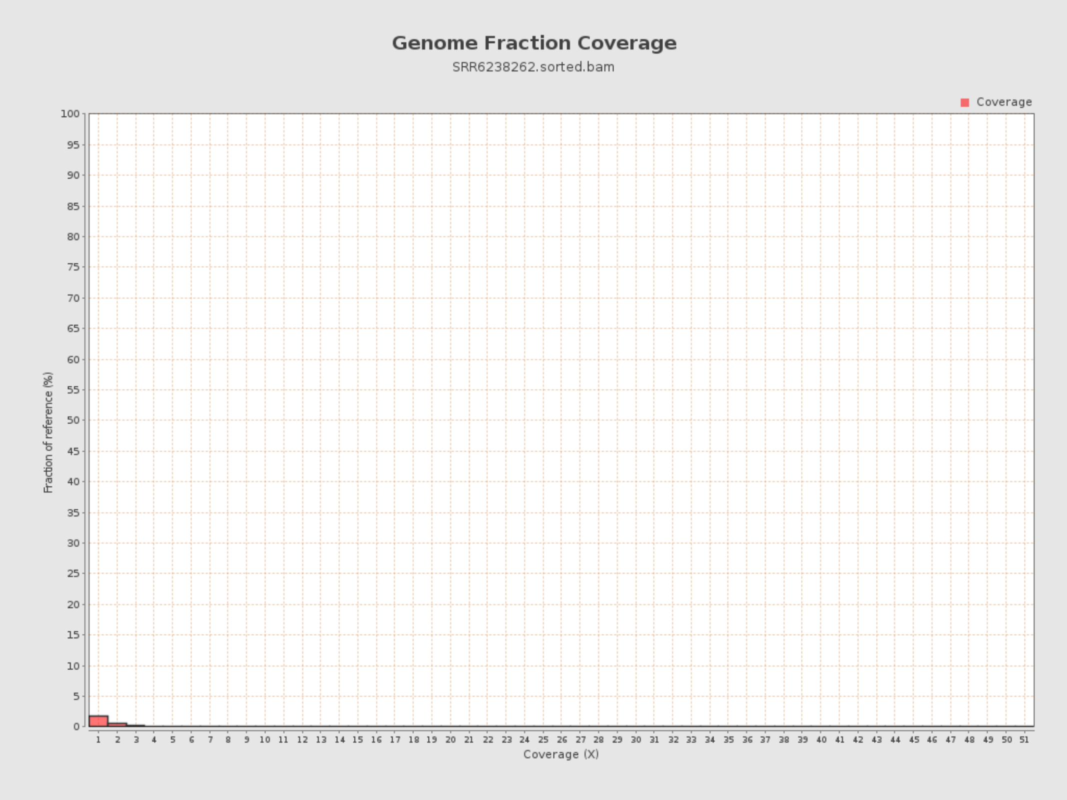
4. Results : Coverage Histogram



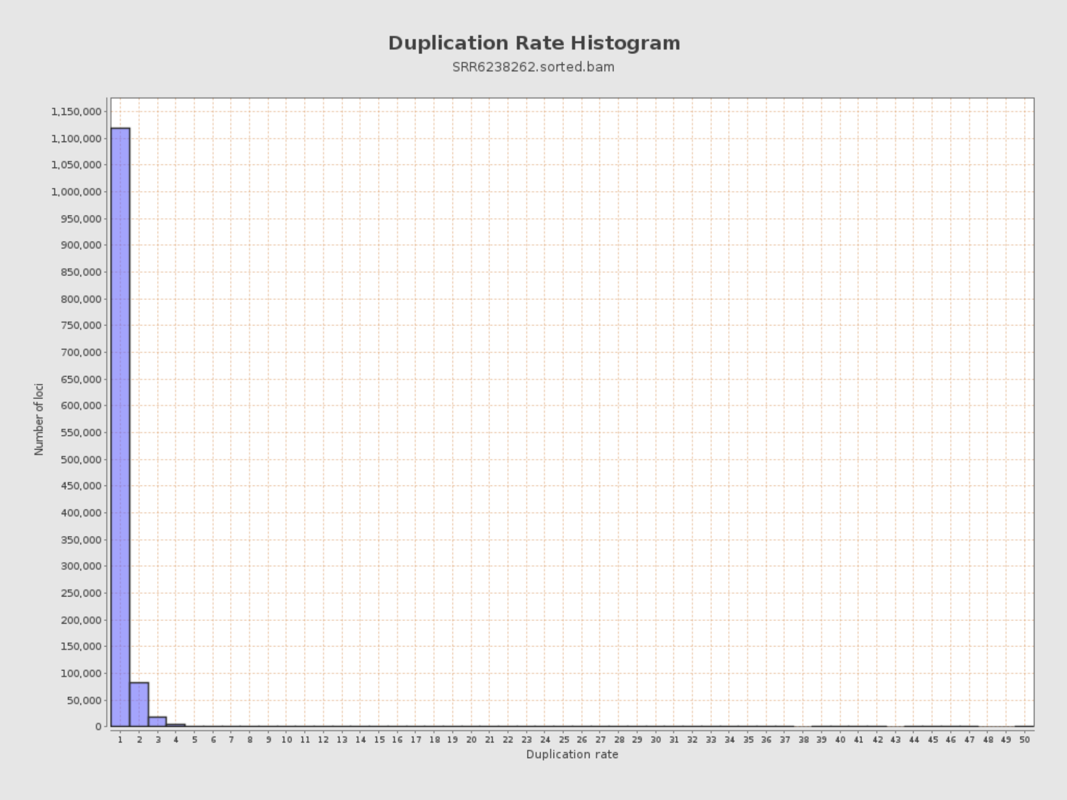
5. Results : Coverage Histogram (0-50X)



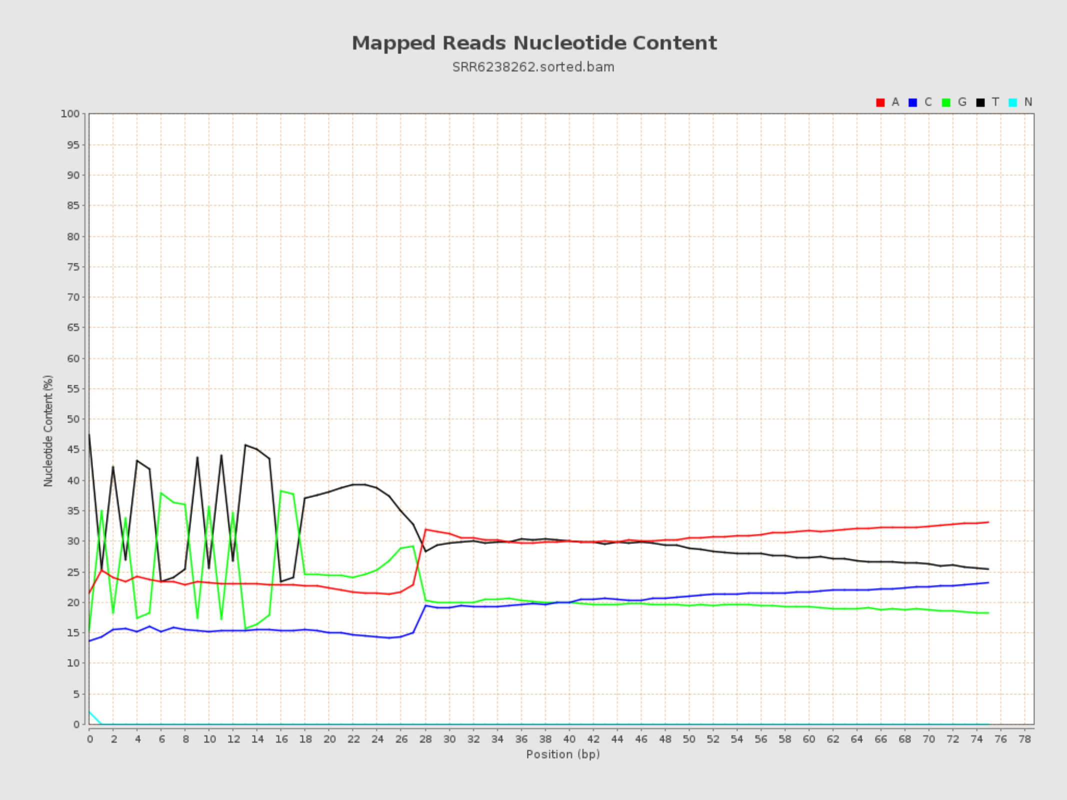
6. Results : Genome Fraction Coverage



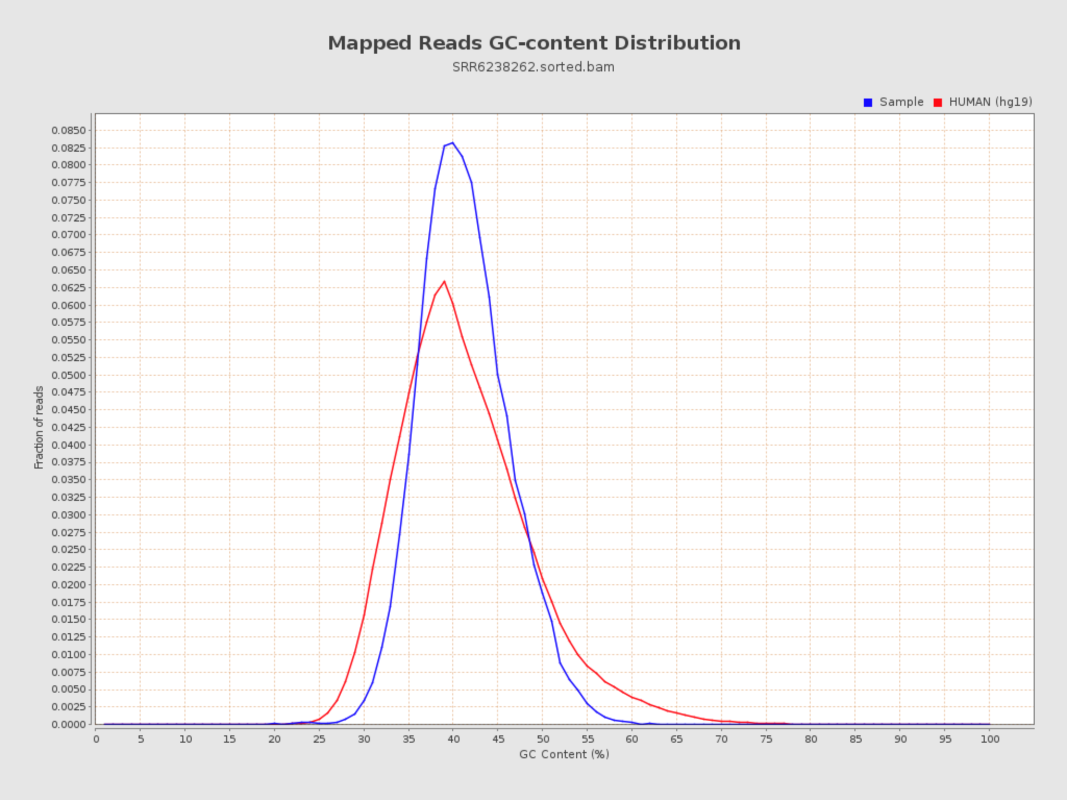
7. Results : Duplication Rate Histogram



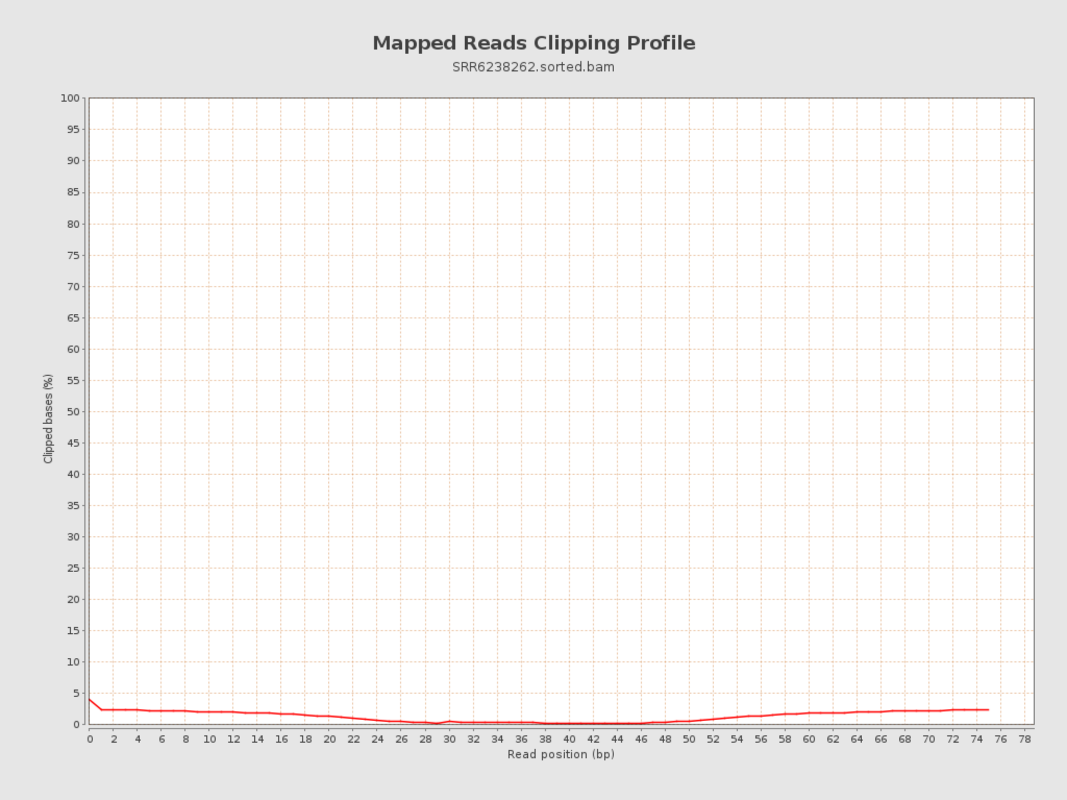
8. Results : Mapped Reads Nucleotide Content



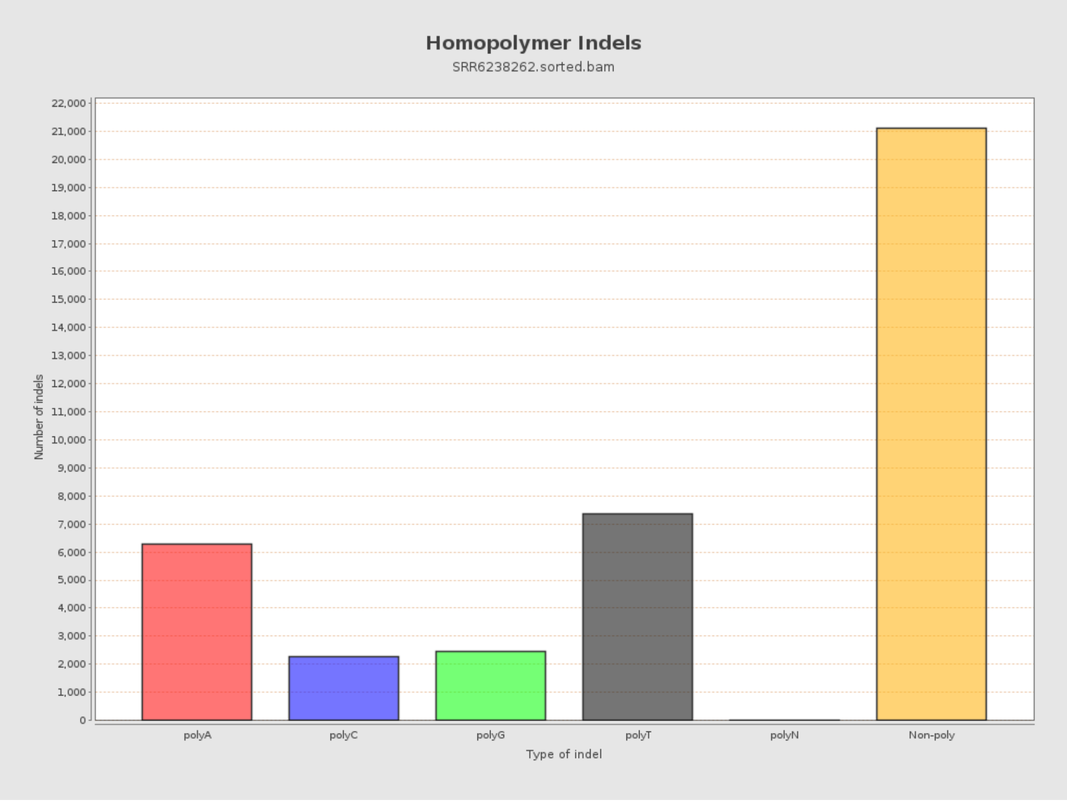
9. Results : Mapped Reads GC-content Distribution



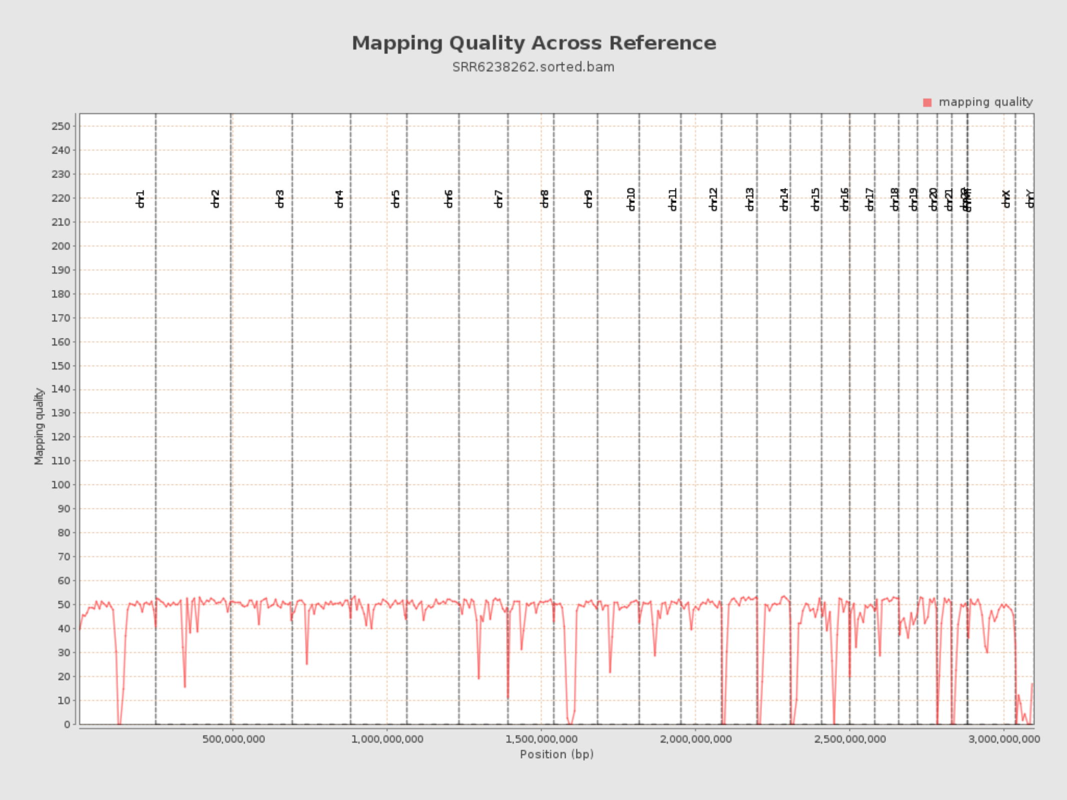
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram