Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 22:52:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238621.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_SRR6238621 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238621.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 22:52:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238621.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,187,950
Mapped reads	2,630,083 / 82.5%
Unmapped reads	557,867 / 17.5%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,378 / 0.73%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	1,178,489 / 36.97%
Duplication rate	22.66%
Clipped reads	1,764,562 / 55.35%

2.2. ACGT Content

Number/percentage of A's	39,914,792 / 25.01%
Number/percentage of C's	26,967,945 / 16.89%
Number/percentage of T's	55,190,988 / 34.58%
Number/percentage of G's	37,547,543 / 23.52%
Number/percentage of N's	3,518 / 0%
GC Percentage	40.42%

2.3. Coverage

Mean	0.0516

Standard Deviation	1.107

2.4. Mapping Quality

Mean Mapping Quality	42.71

2.5. Mismatches and indels

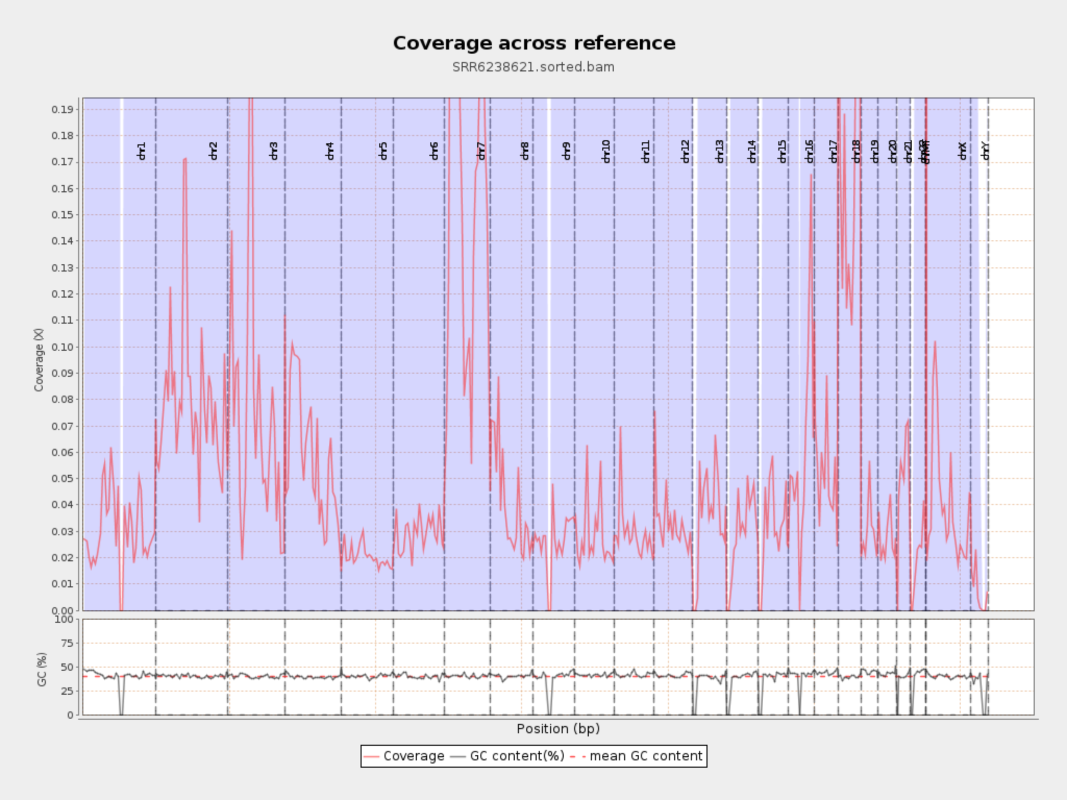
General error rate	0.63%
Mismatches	995,287
Insertions	10,502
Mapped reads with at least one insertion	0.4%
Deletions	52,479
Mapped reads with at least one deletion	1.97%
Homopolymer indels	41.38%

2.6. Chromosome stats

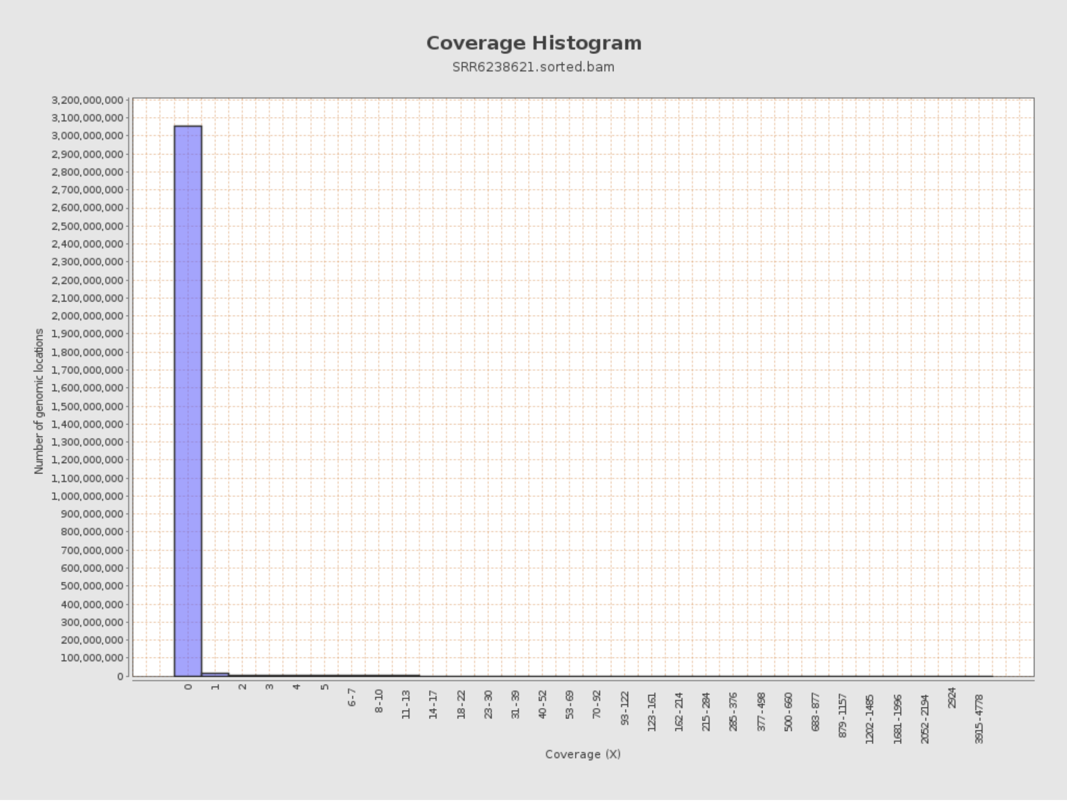
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7569279	0.0304	0.6811
chr2	243199373	19542854	0.0804	2.2766
chr3	198022430	15370486	0.0776	0.8667
chr4	191154276	11109641	0.0581	0.7393
chr5	180915260	3712654	0.0205	0.4349
chr6	171115067	5047113	0.0295	0.9386
chr7	159138663	29079678	0.1827	1.6772

chr8	146364022	5883217	0.0402	1.2485
chr9	141213431	3698220	0.0262	0.5376
chr10	135534747	3774433	0.0278	0.5628
chr11	135006516	4010233	0.0297	0.547
chr12	133851895	4472530	0.0334	0.5594
chr13	115169878	3992481	0.0347	0.7998
chr14	107349540	3234220	0.0301	0.5624
chr15	102531392	3147624	0.0307	0.6865
chr16	90354753	5311238	0.0588	0.7708
chr17	81195210	4205413	0.0518	0.691
chr18	78077248	12904298	0.1653	3.0738
chr19	59128983	1811896	0.0306	0.6554
chr20	63025520	1712095	0.0272	0.5188
chr21	48129895	2380412	0.0495	0.663
chr22	51304566	998213	0.0195	0.4311
chrMT	16571	45072	2.7199	5.0201
chrX	155270560	6275402	0.0404	0.6322
chrY	59373566	425000	0.0072	0.417

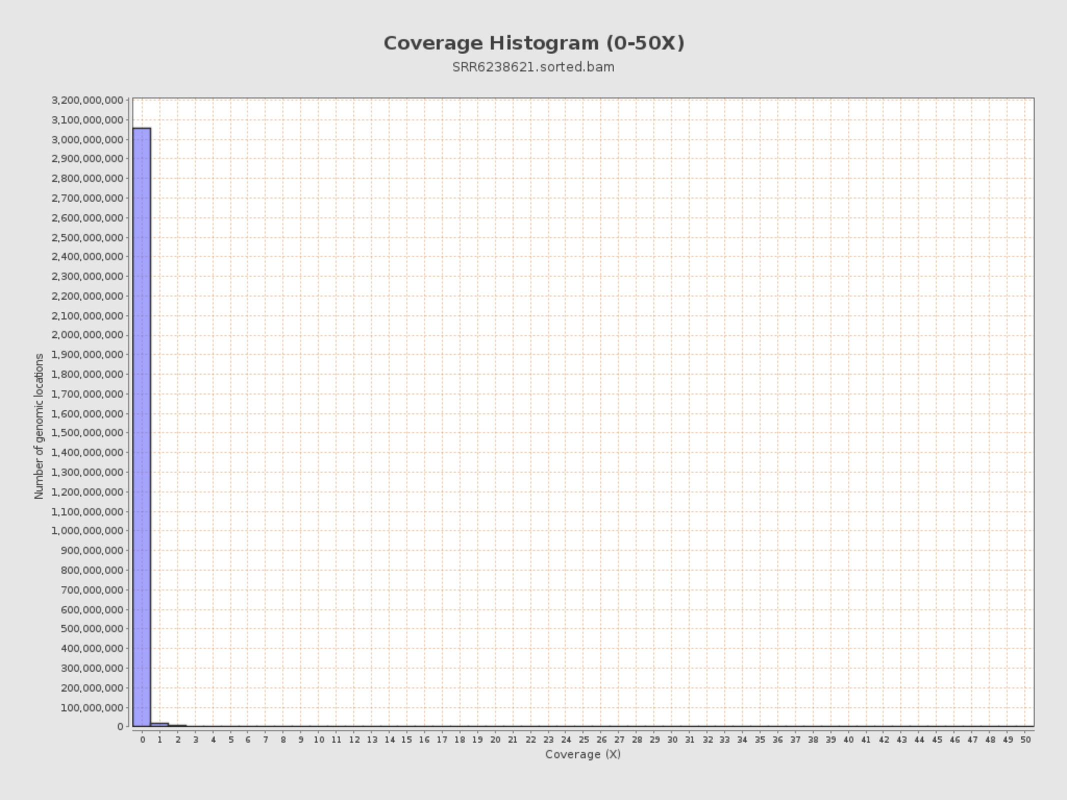
3. Results : Coverage across reference



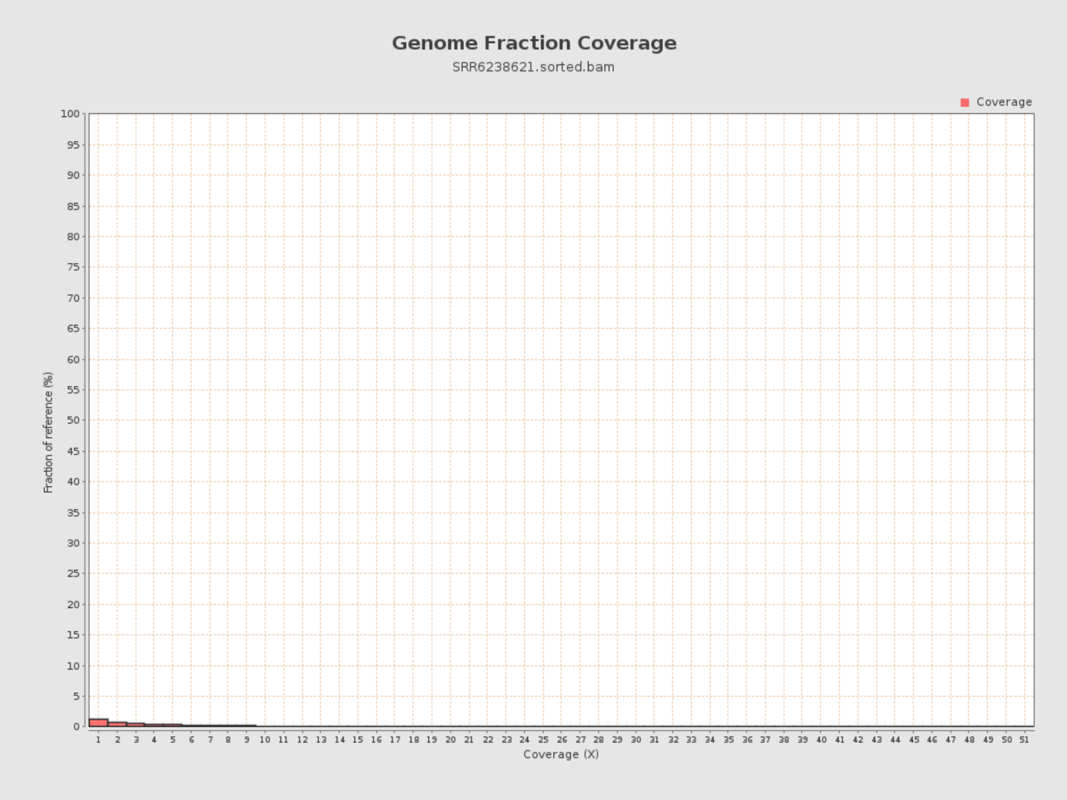
4. Results : Coverage Histogram



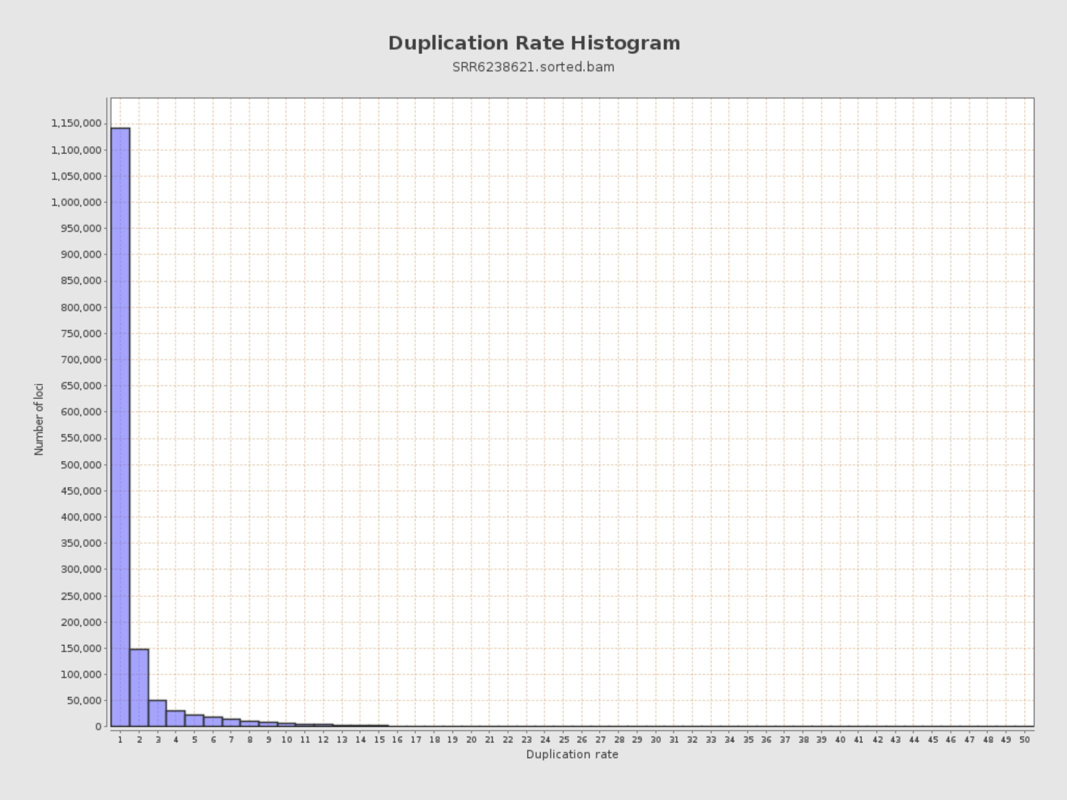
5. Results : Coverage Histogram (0-50X)



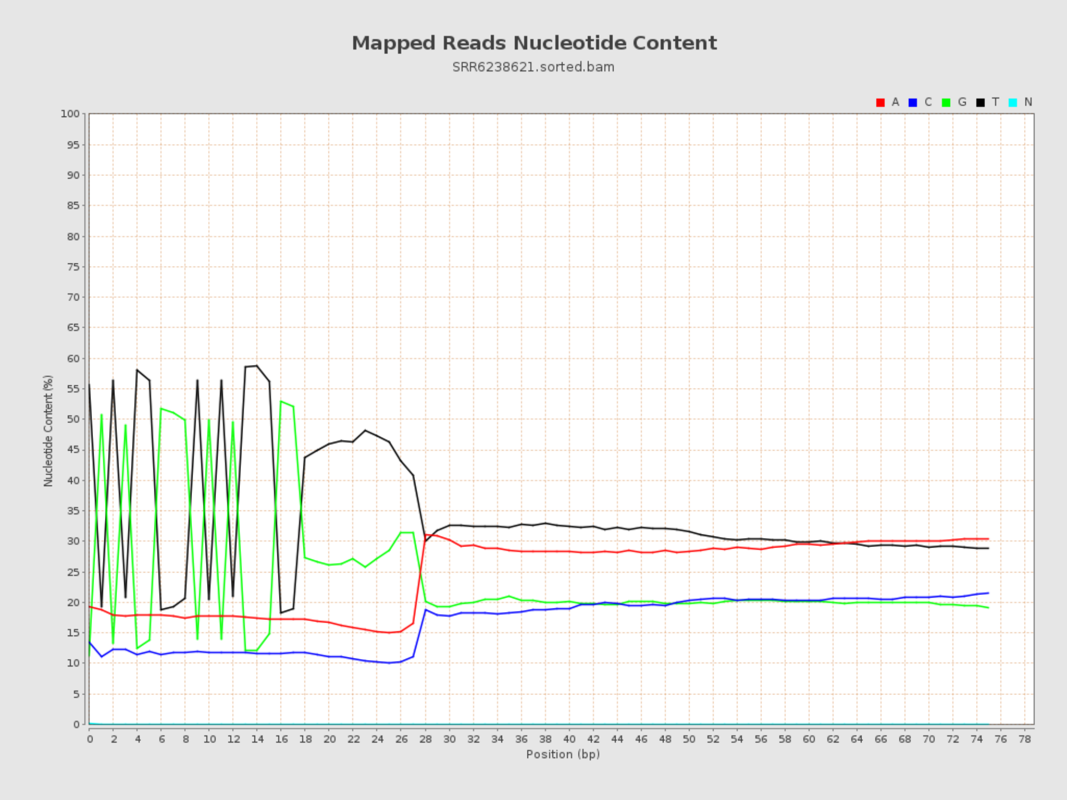
6. Results : Genome Fraction Coverage



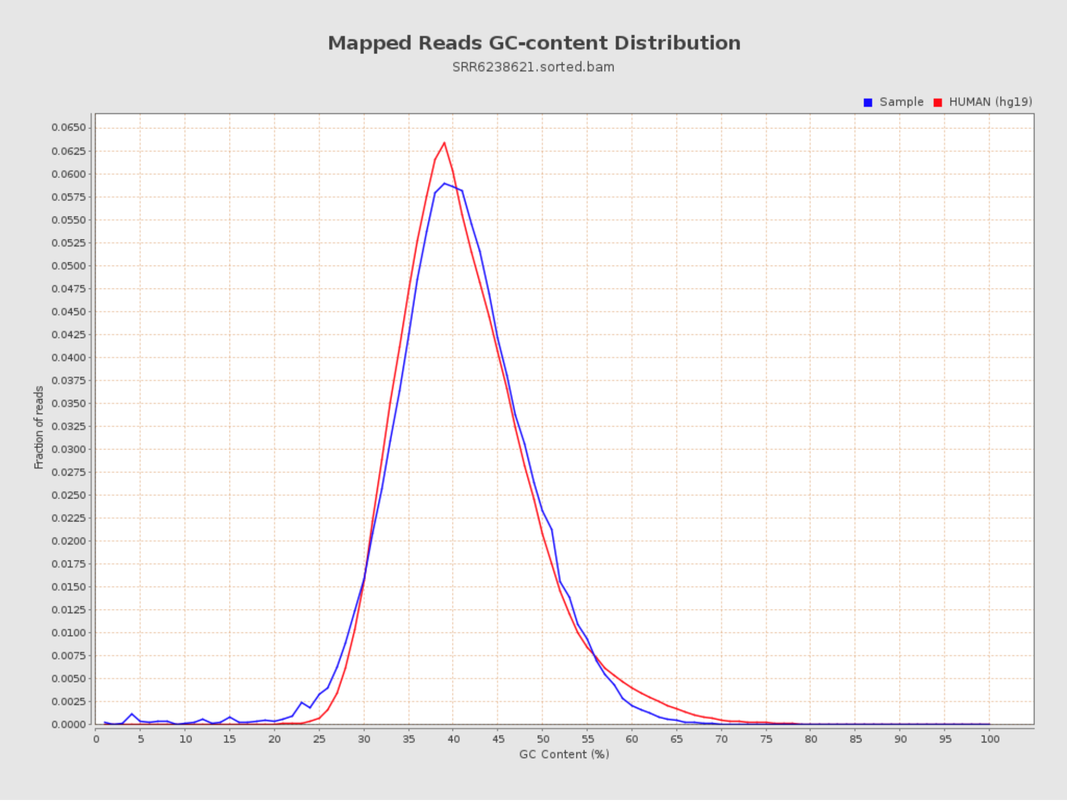
7. Results : Duplication Rate Histogram



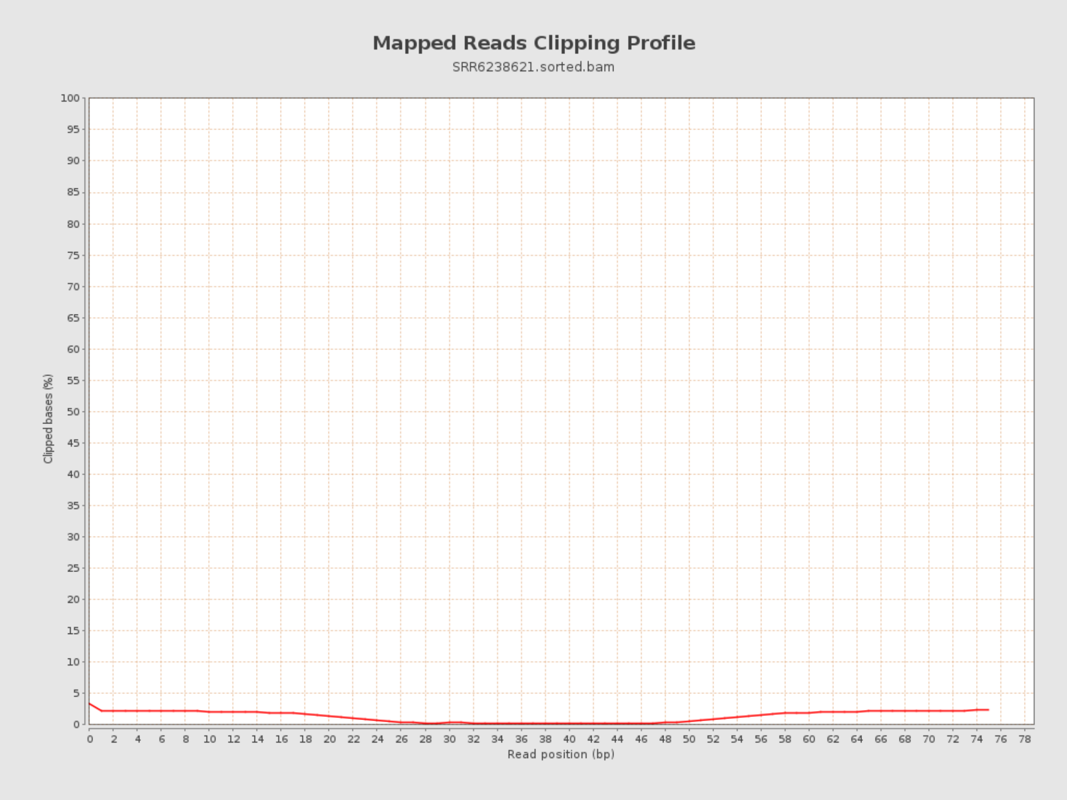
8. Results : Mapped Reads Nucleotide Content



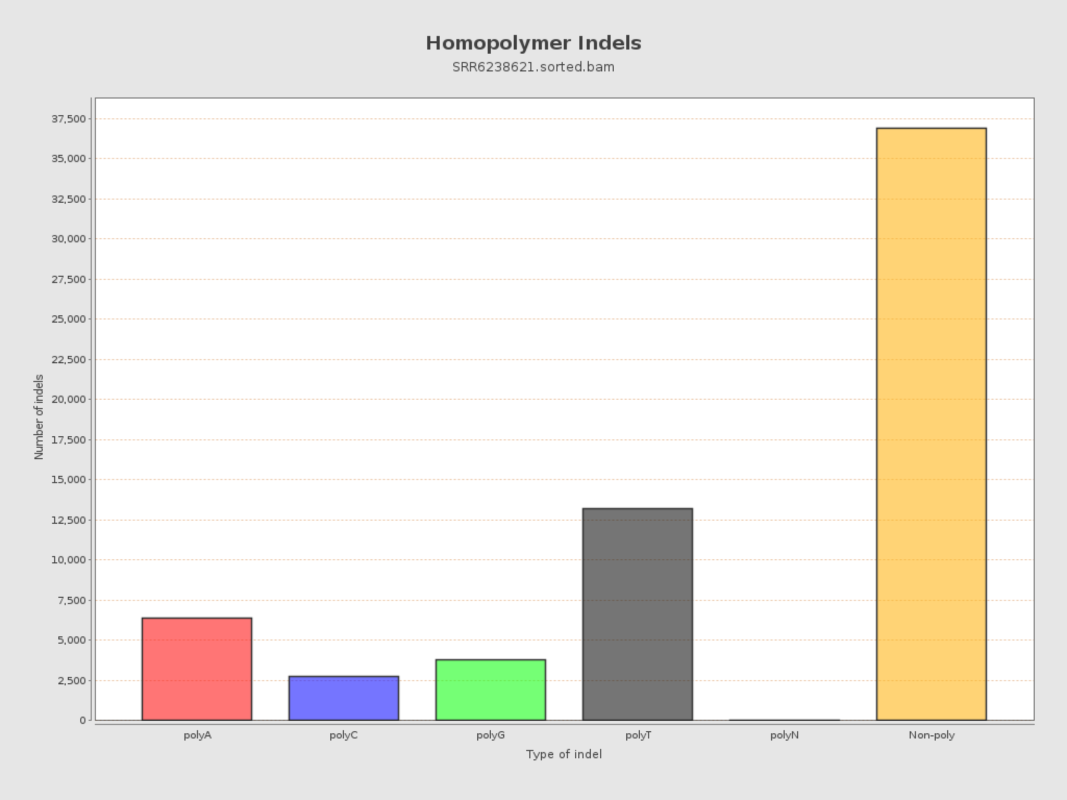
9. Results : Mapped Reads GC-content Distribution



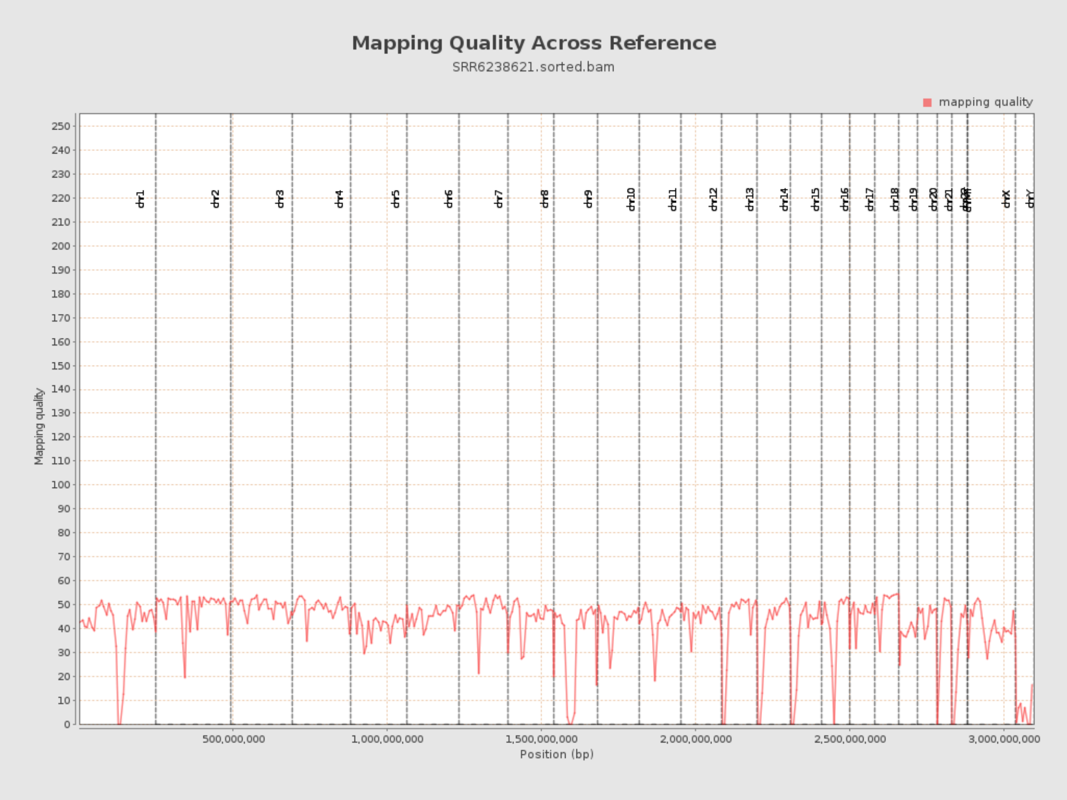
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram