Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 02:03:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238670.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_SRR6238670 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238670.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 02:03:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238670.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,828,913
Mapped reads	3,551,179 / 92.75%
Unmapped reads	277,734 / 7.25%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	26,495 / 0.69%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	359,902 / 9.4%
Duplication rate	8.57%
Clipped reads	2,144,674 / 56.01%

2.2. ACGT Content

Number/percentage of A's	55,796,000 / 25.12%
Number/percentage of C's	39,892,301 / 17.96%
Number/percentage of T's	73,115,695 / 32.91%
Number/percentage of G's	53,341,134 / 24.01%
Number/percentage of N's	11,726 / 0.01%
GC Percentage	41.97%

2.3. Coverage

Mean	0.0718

Standard Deviation	0.6538

2.4. Mapping Quality

Mean Mapping Quality	43.98

2.5. Mismatches and indels

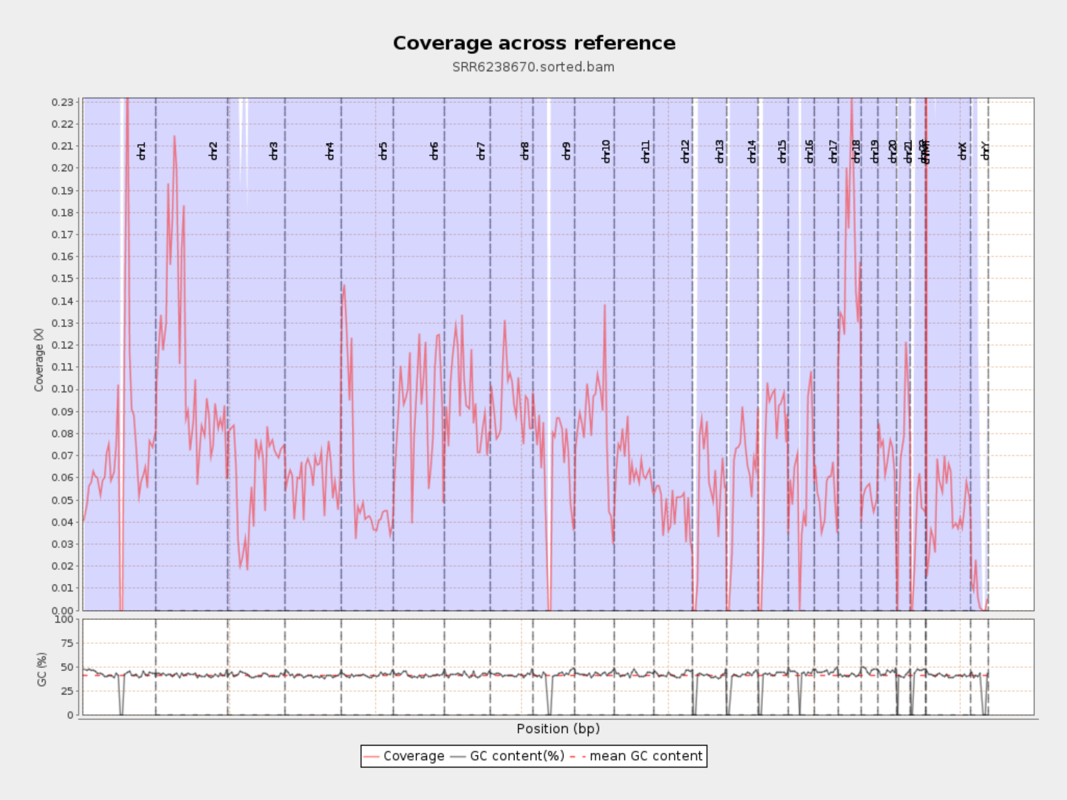
General error rate	0.57%
Mismatches	1,234,594
Insertions	14,533
Mapped reads with at least one insertion	0.41%
Deletions	59,768
Mapped reads with at least one deletion	1.67%
Homopolymer indels	43.06%

2.6. Chromosome stats

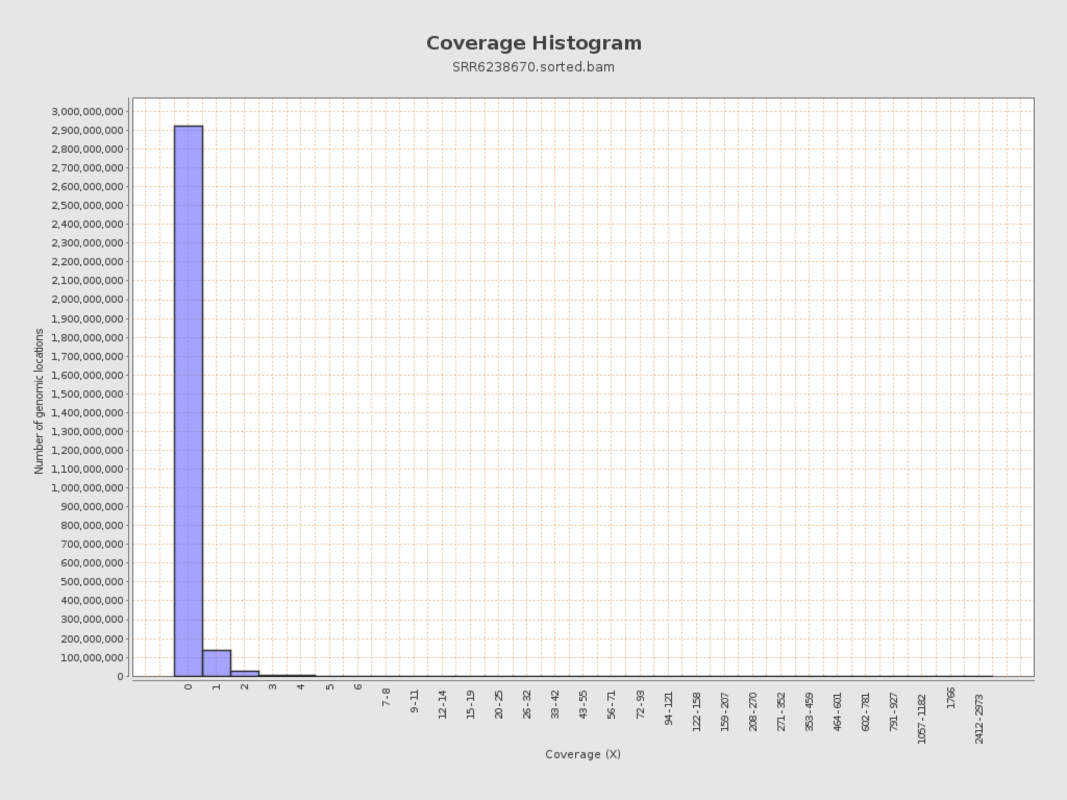
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17663385	0.0709	0.7473
chr2	243199373	27225749	0.1119	1.4698
chr3	198022430	11951589	0.0604	0.3096
chr4	191154276	11535211	0.0603	0.3137
chr5	180915260	10984849	0.0607	0.3151
chr6	171115067	15938296	0.0931	0.5903
chr7	159138663	15045264	0.0945	0.8815

chr8	146364022	13790309	0.0942	0.7008
chr9	141213431	9190882	0.0651	0.5853
chr10	135534747	11491537	0.0848	0.4556
chr11	135006516	8856626	0.0656	0.4367
chr12	133851895	6166921	0.0461	0.2943
chr13	115169878	6102151	0.053	0.3636
chr14	107349540	6238643	0.0581	0.3581
chr15	102531392	7541472	0.0736	0.3827
chr16	90354753	5134061	0.0568	0.3628
chr17	81195210	4304409	0.053	0.3106
chr18	78077248	12507347	0.1602	1.1997
chr19	59128983	3079603	0.0521	0.5529
chr20	63025520	4412223	0.07	0.3617
chr21	48129895	3596514	0.0747	0.3681
chr22	51304566	1844105	0.0359	0.2286
chrMT	16571	40504	2.4443	2.309
chrX	155270560	7208609	0.0464	0.3371
chrY	59373566	410320	0.0069	0.1976

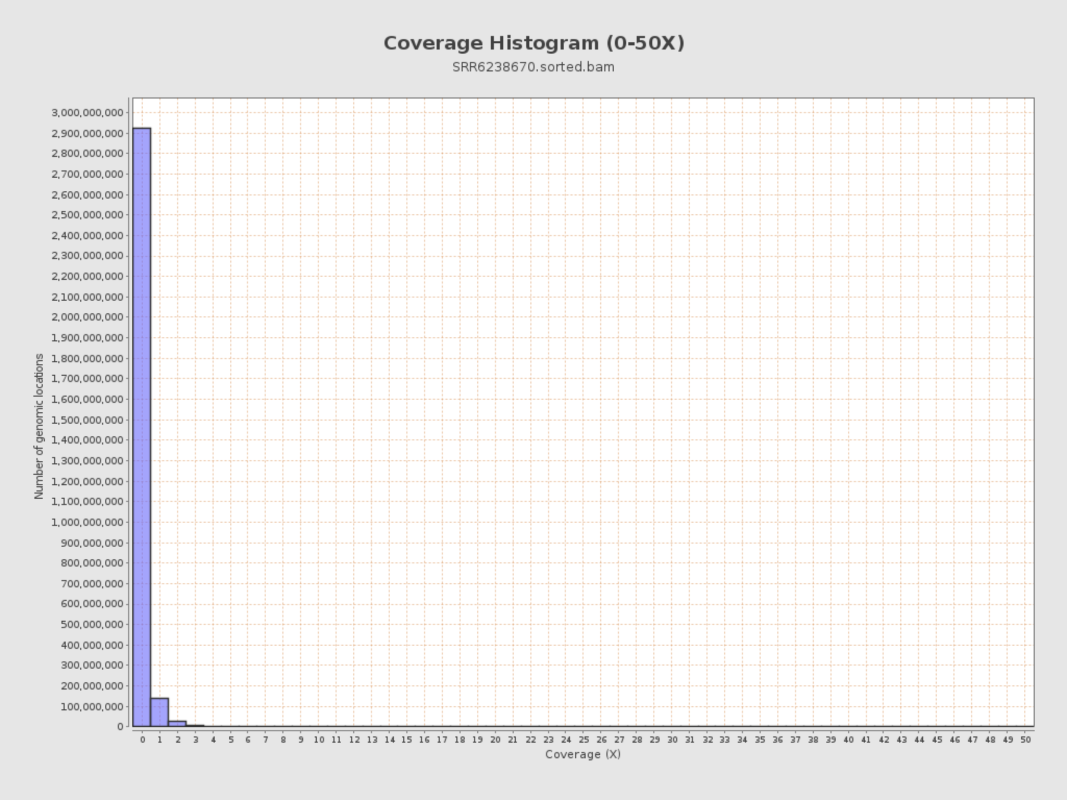
3. Results : Coverage across reference



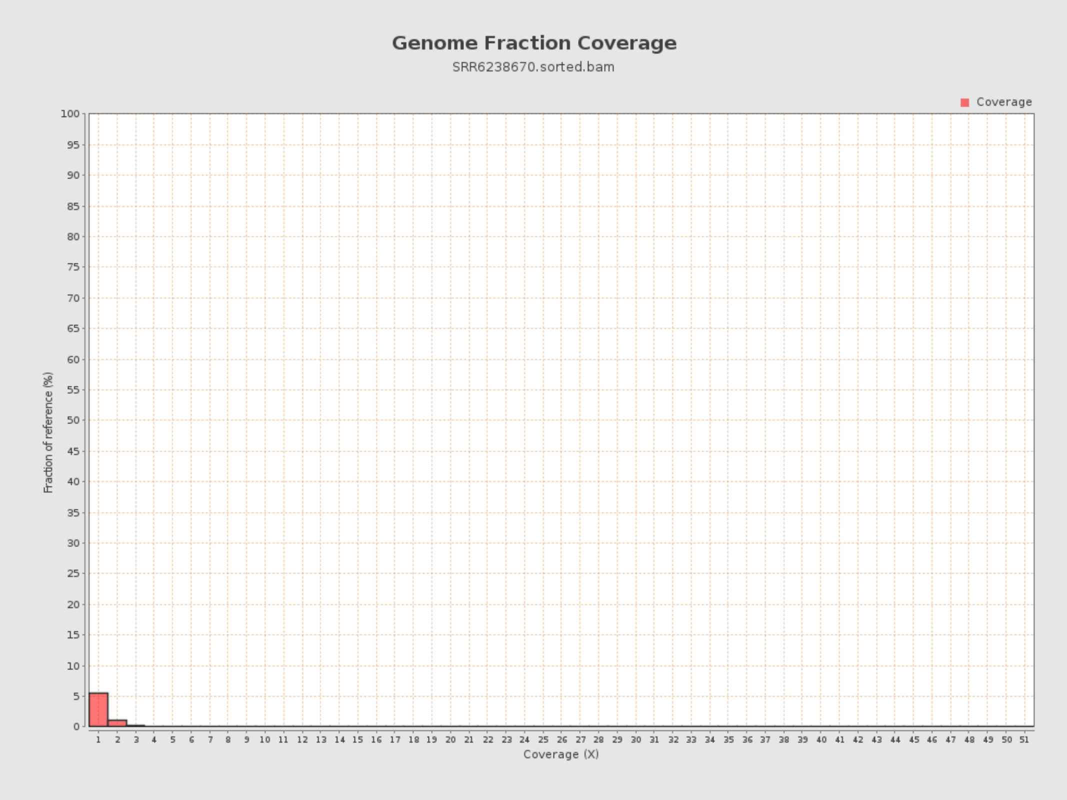
4. Results : Coverage Histogram



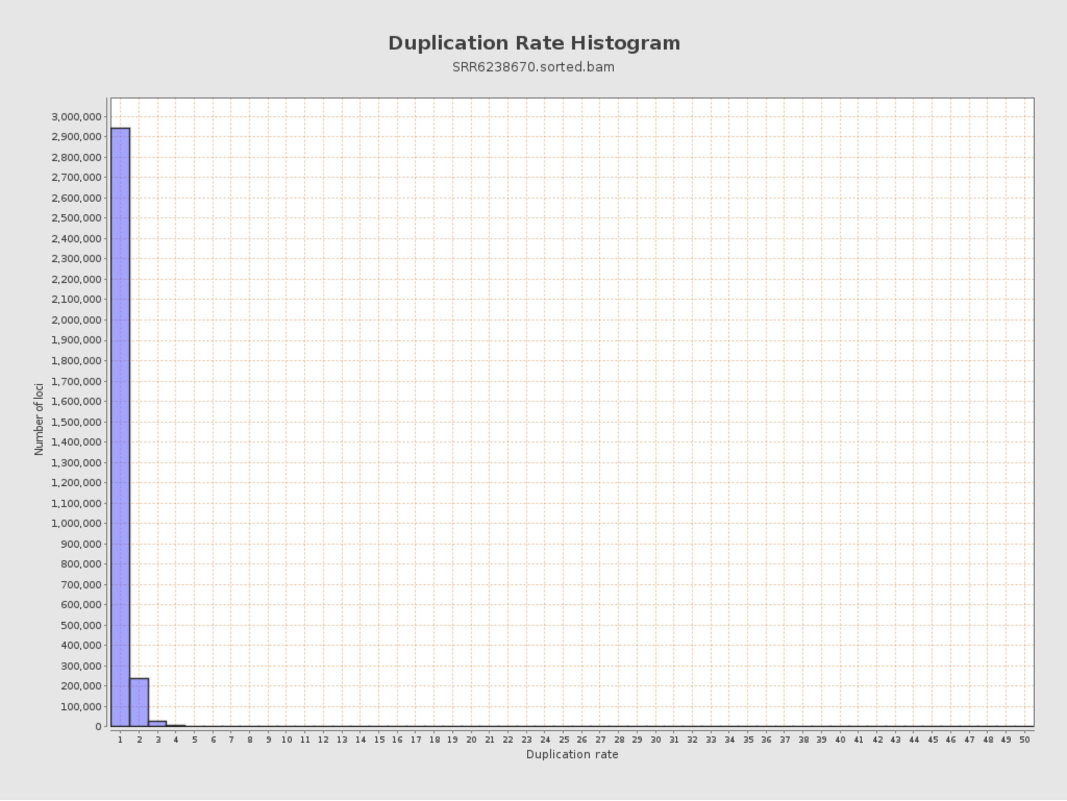
5. Results : Coverage Histogram (0-50X)



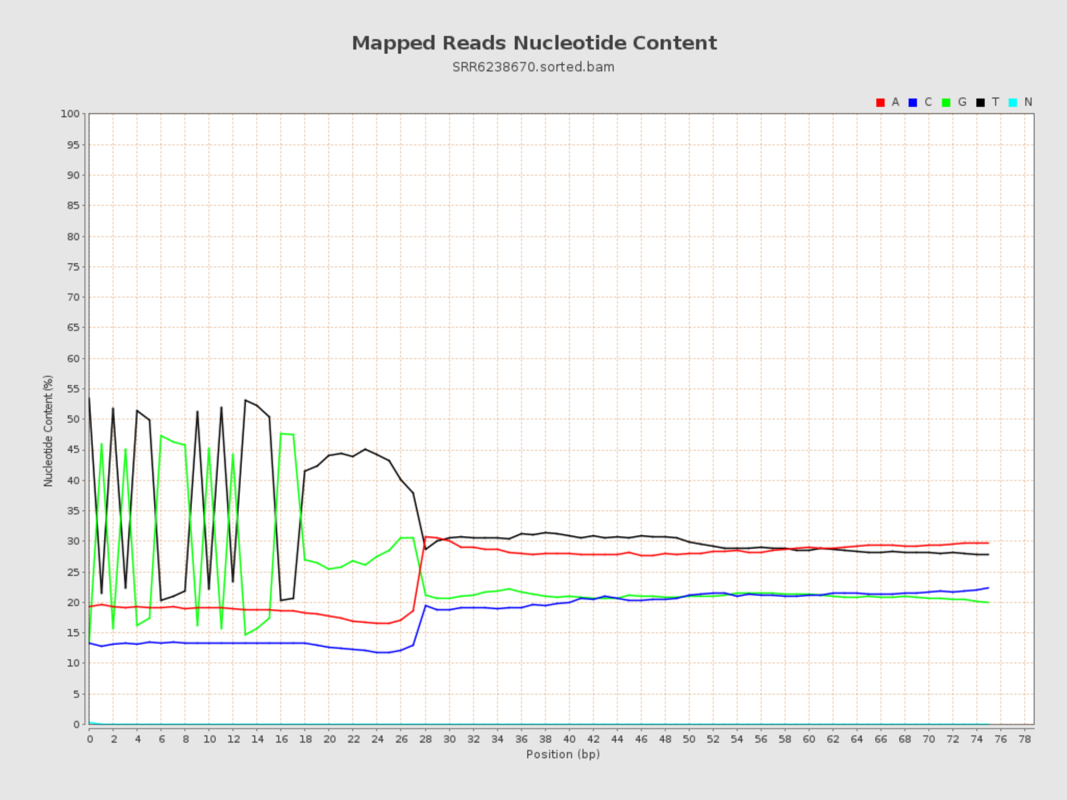
6. Results : Genome Fraction Coverage



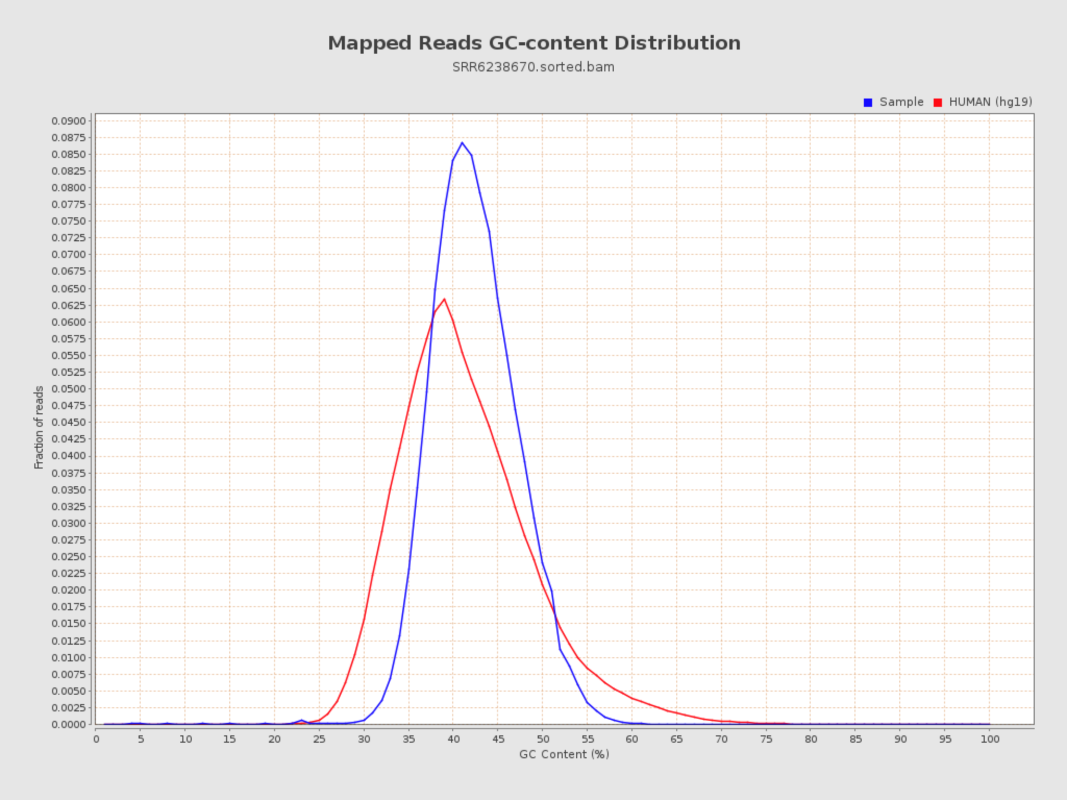
7. Results : Duplication Rate Histogram



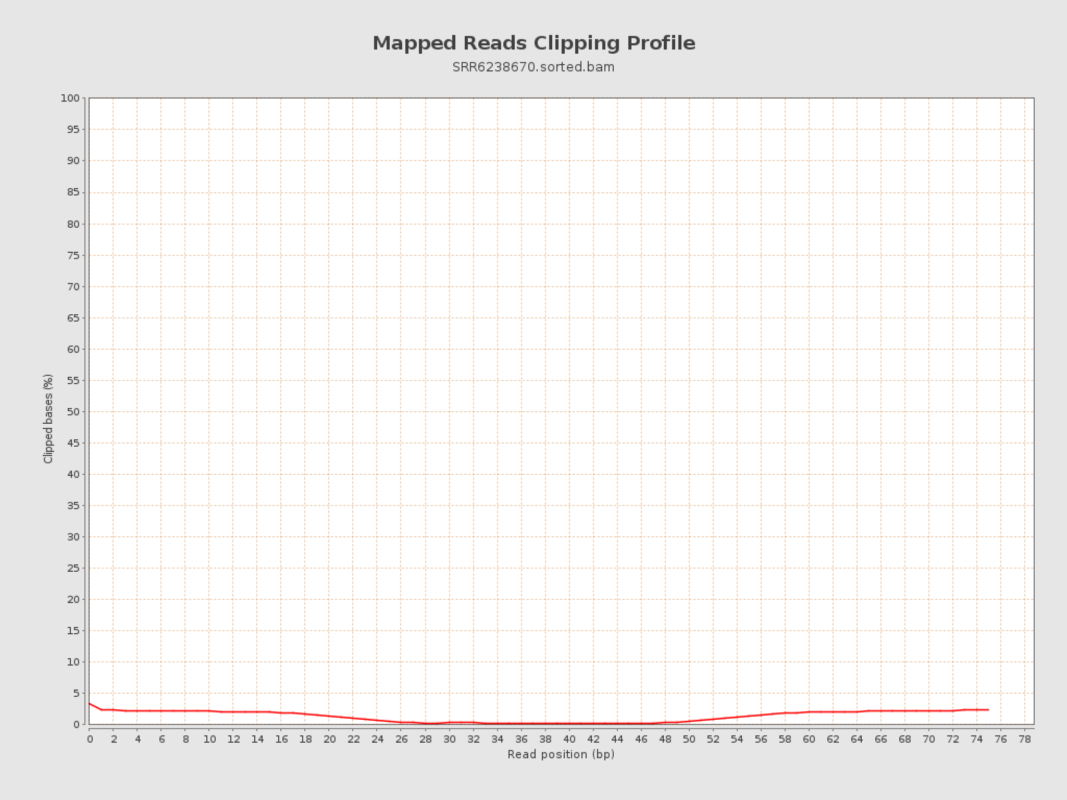
8. Results : Mapped Reads Nucleotide Content



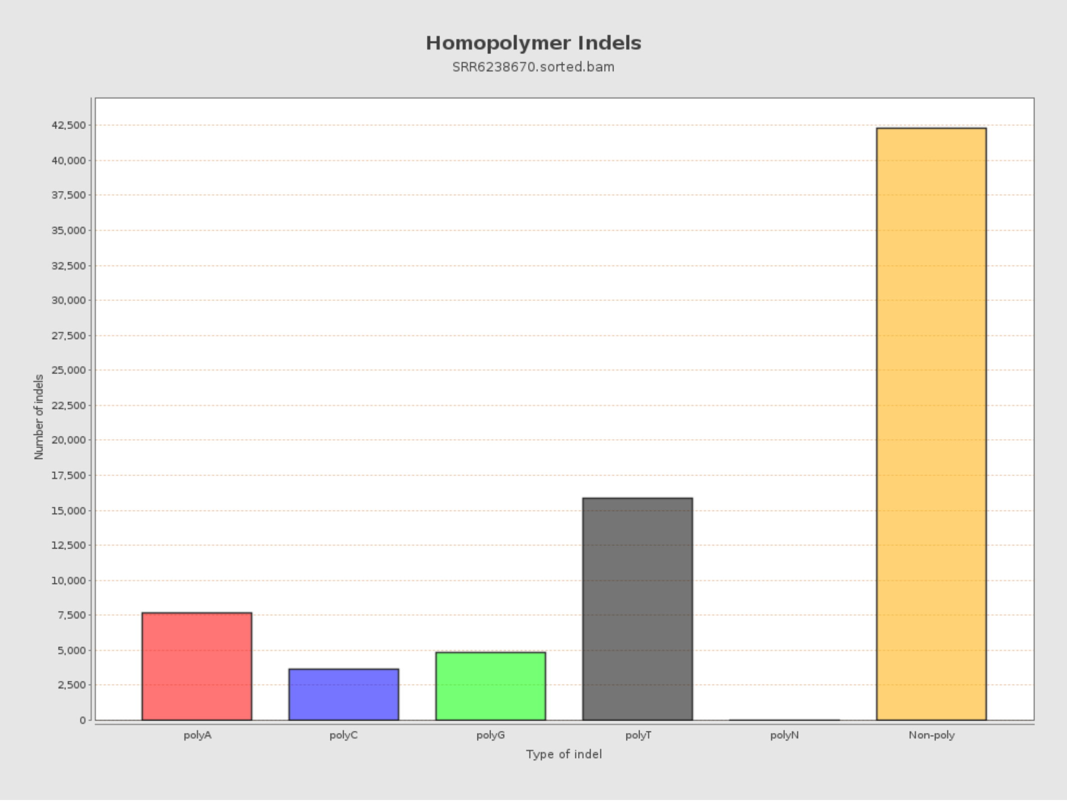
9. Results : Mapped Reads GC-content Distribution



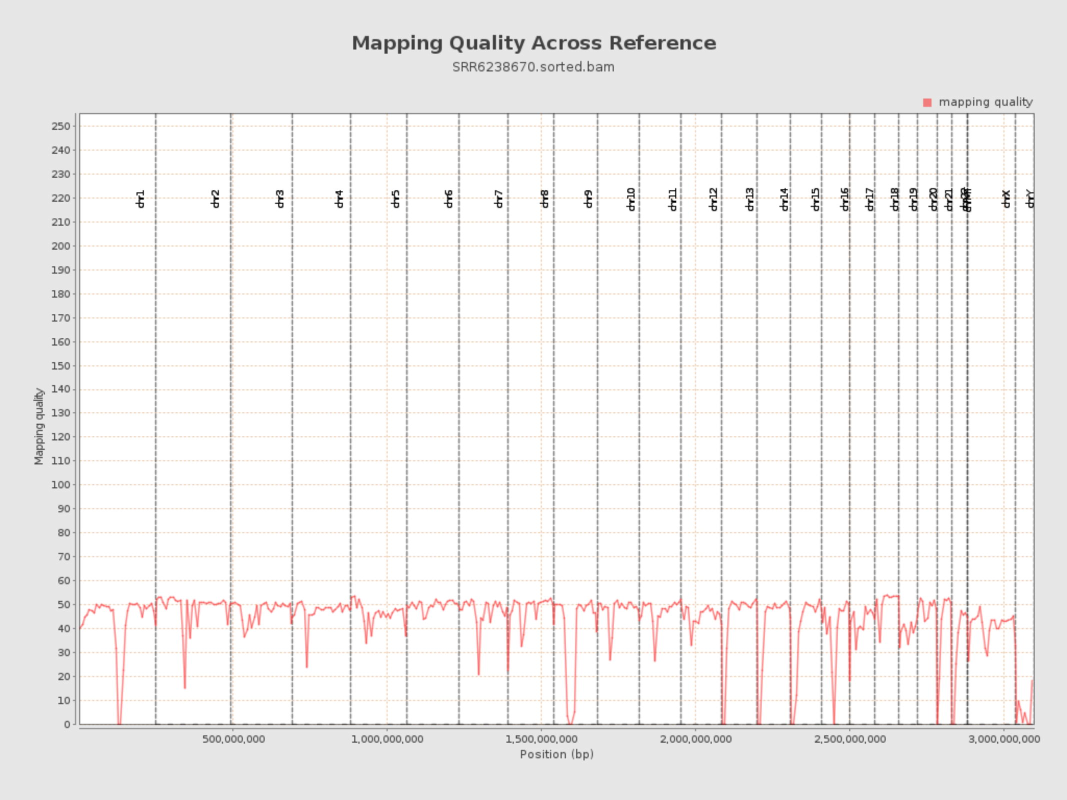
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram