Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 12:11:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238079.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_SRR6238079 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238079.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 12:11:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238079.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,833,864
Mapped reads	1,637,450 / 89.29%
Unmapped reads	196,414 / 10.71%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,054 / 0.55%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	63,895 / 3.48%
Duplication rate	2.26%
Clipped reads	748,840 / 40.83%

2.2. ACGT Content

Number/percentage of A's	29,649,060 / 27.34%
Number/percentage of C's	20,288,199 / 18.71%
Number/percentage of T's	32,970,555 / 30.4%
Number/percentage of G's	25,343,068 / 23.37%
Number/percentage of N's	210,007 / 0.19%
GC Percentage	42.07%

2.3. Coverage

Mean	0.0351

Standard Deviation	0.445

2.4. Mapping Quality

Mean Mapping Quality	43.49

2.5. Mismatches and indels

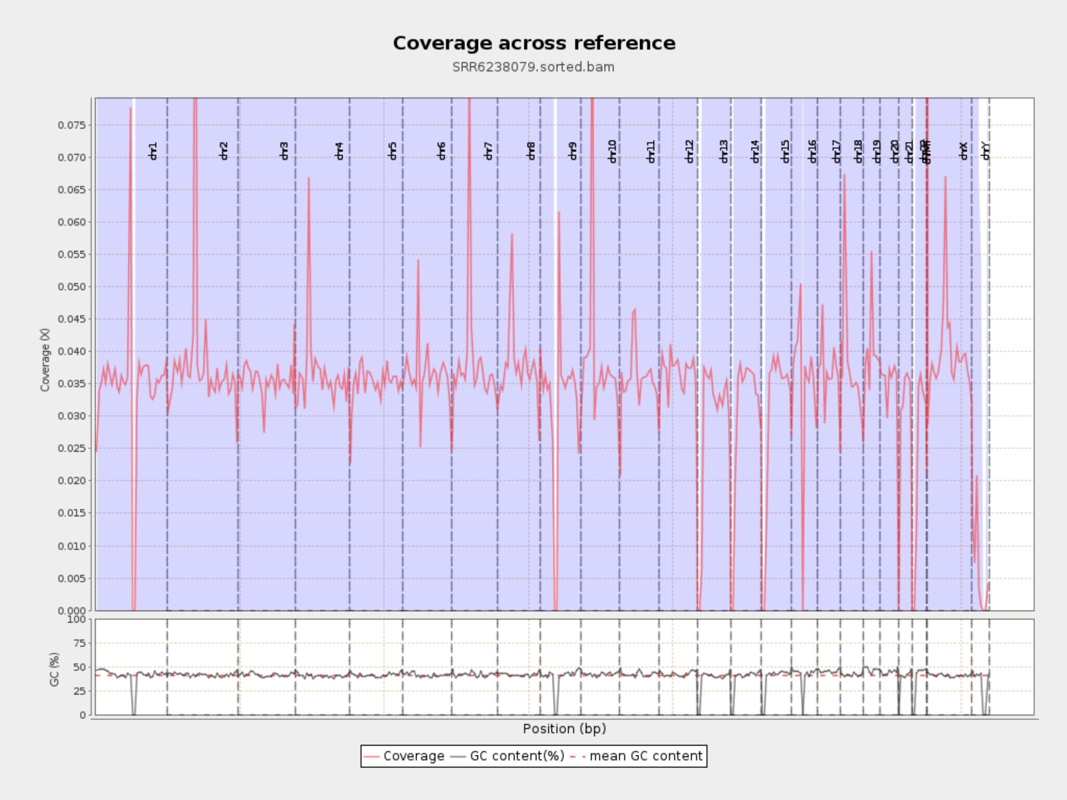
General error rate	0.96%
Mismatches	1,026,666
Insertions	10,299
Mapped reads with at least one insertion	0.62%
Deletions	29,086
Mapped reads with at least one deletion	1.76%
Homopolymer indels	46.88%

2.6. Chromosome stats

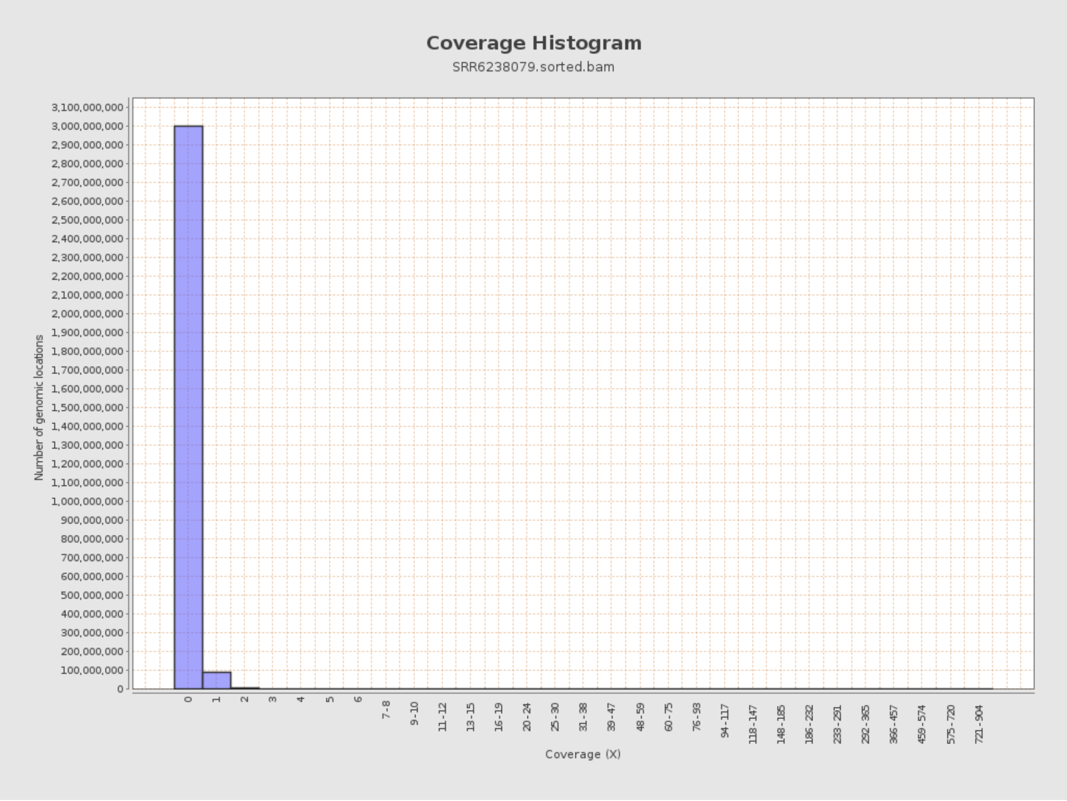
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8594797	0.0345	0.7971
chr2	243199373	9433842	0.0388	0.5954
chr3	198022430	7029732	0.0355	0.2142
chr4	191154276	7021077	0.0367	0.2494
chr5	180915260	6404622	0.0354	0.2083
chr6	171115067	6226087	0.0364	0.3029
chr7	159138663	6154384	0.0387	0.608

chr8	146364022	5569990	0.0381	0.3939
chr9	141213431	4501670	0.0319	0.4998
chr10	135534747	5339937	0.0394	0.5538
chr11	135006516	4884831	0.0362	0.3662
chr12	133851895	4917534	0.0367	0.2204
chr13	115169878	3255073	0.0283	0.1793
chr14	107349540	3198103	0.0298	0.2476
chr15	102531392	3056369	0.0298	0.1887
chr16	90354753	3114219	0.0345	0.2705
chr17	81195210	2984508	0.0368	0.2715
chr18	78077248	2991248	0.0383	0.9611
chr19	59128983	2362500	0.04	0.5719
chr20	63025520	2204292	0.035	0.2328
chr21	48129895	1447053	0.0301	0.238
chr22	51304566	1193977	0.0233	0.1633
chrMT	16571	83357	5.0303	3.7039
chrX	155270560	6185452	0.0398	0.2877
chrY	59373566	355194	0.006	0.1744

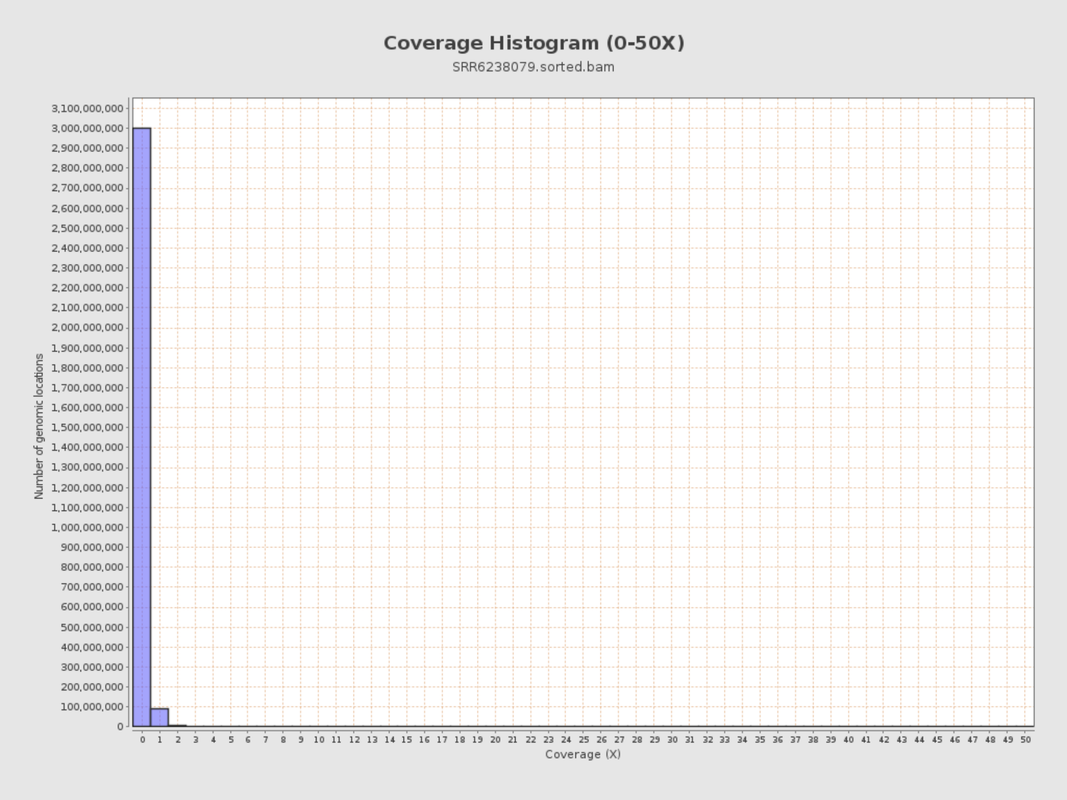
3. Results : Coverage across reference



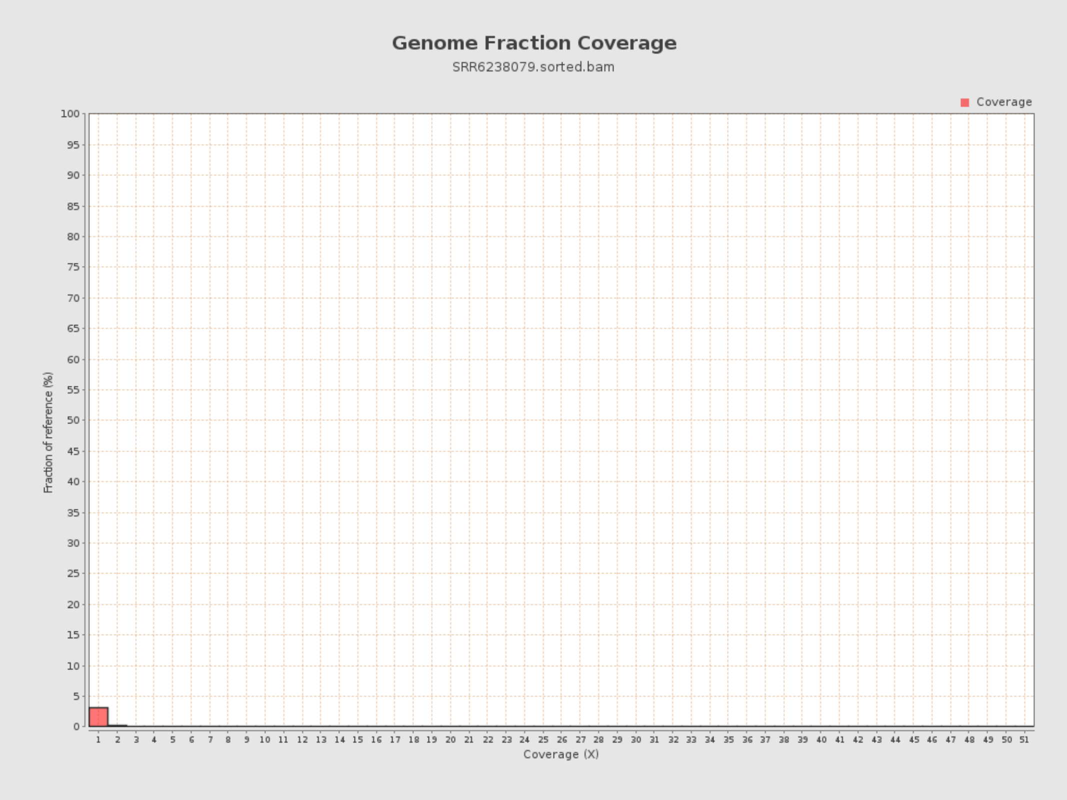
4. Results : Coverage Histogram



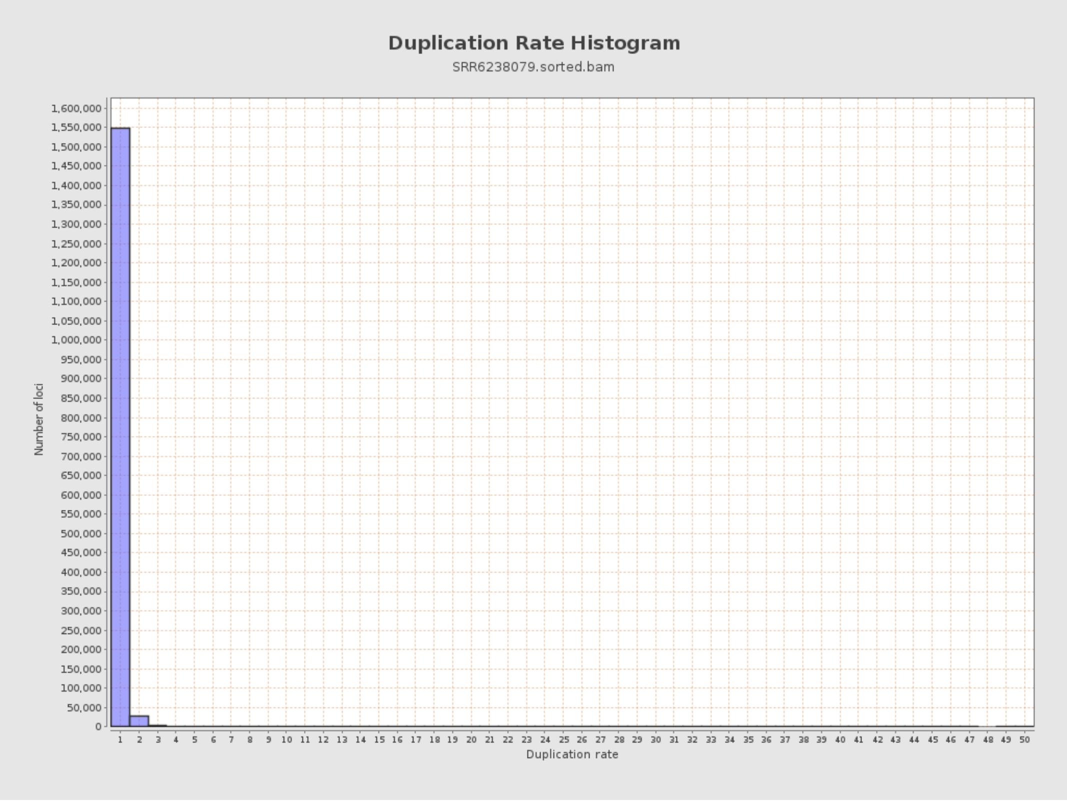
5. Results : Coverage Histogram (0-50X)



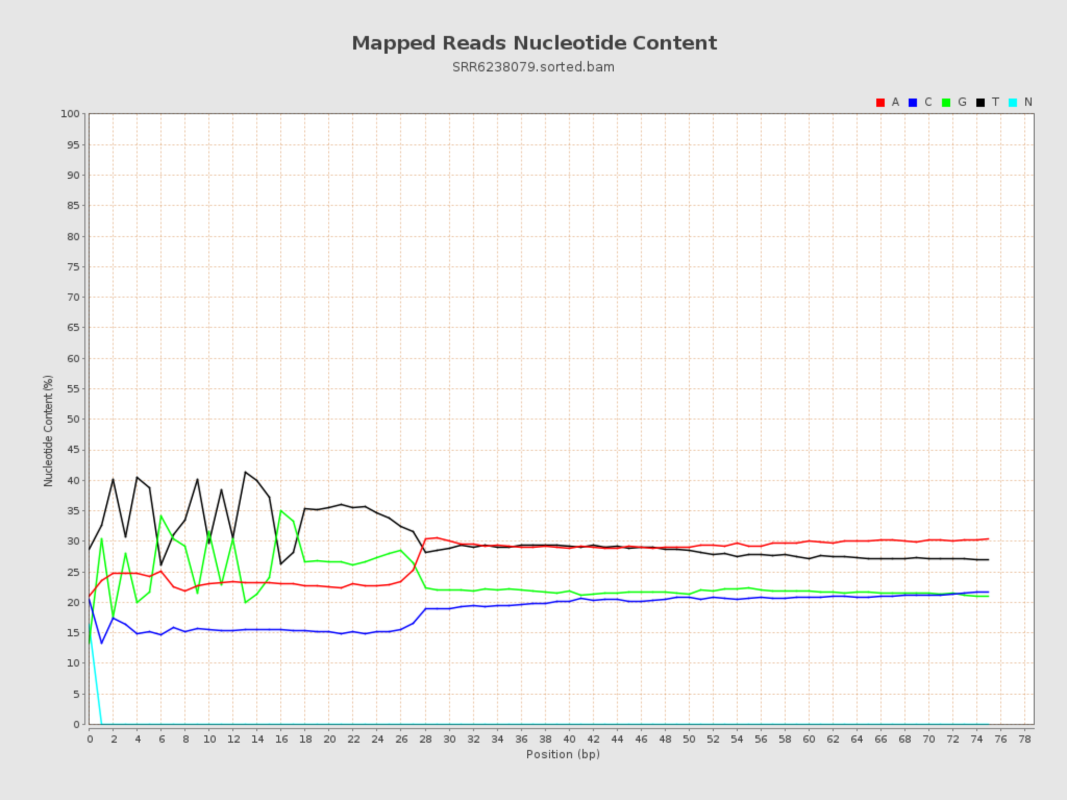
6. Results : Genome Fraction Coverage



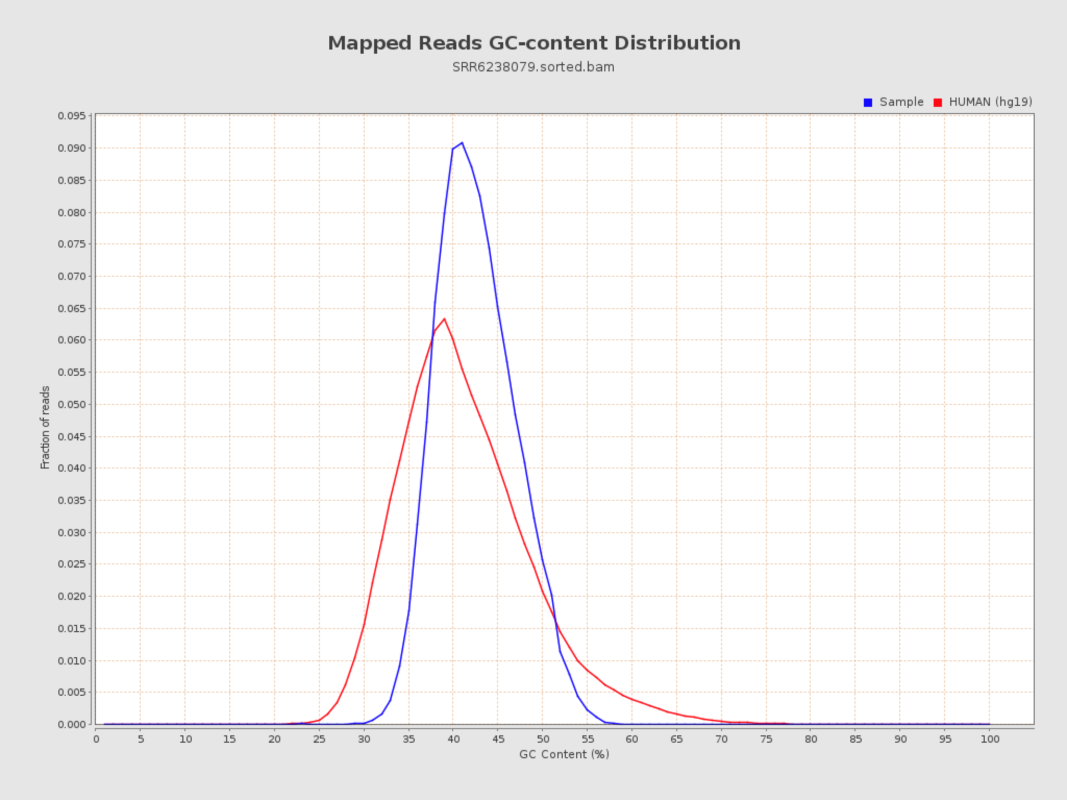
7. Results : Duplication Rate Histogram



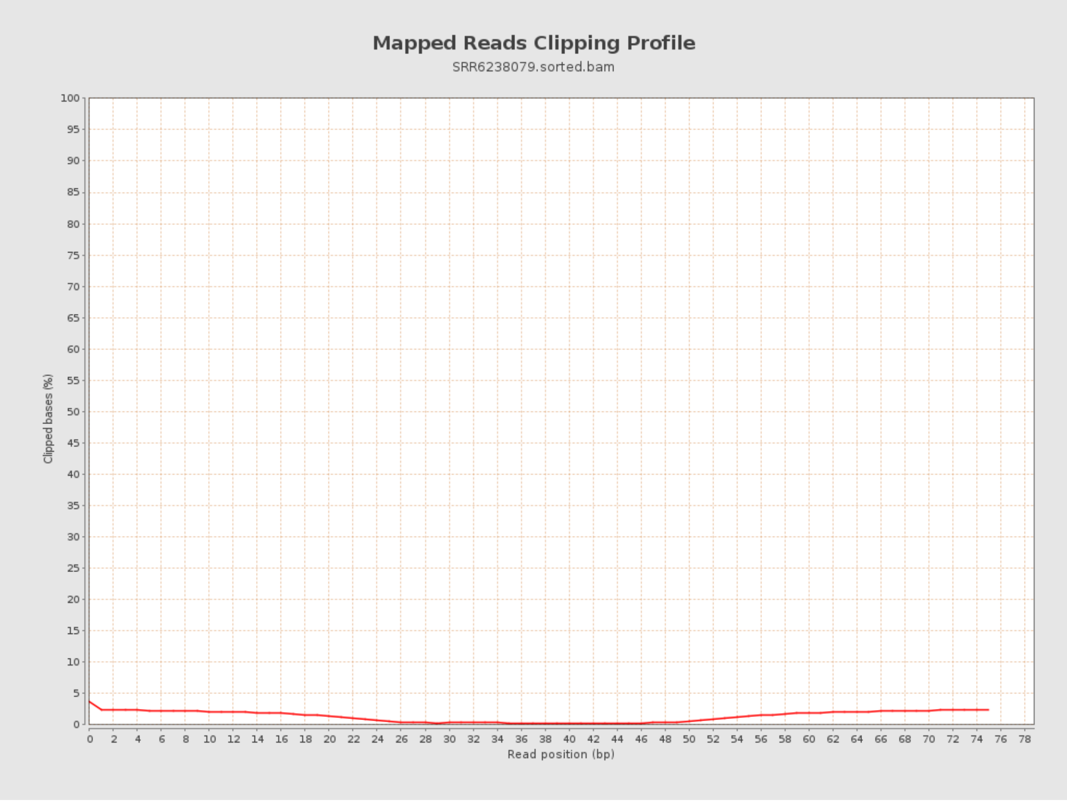
8. Results : Mapped Reads Nucleotide Content



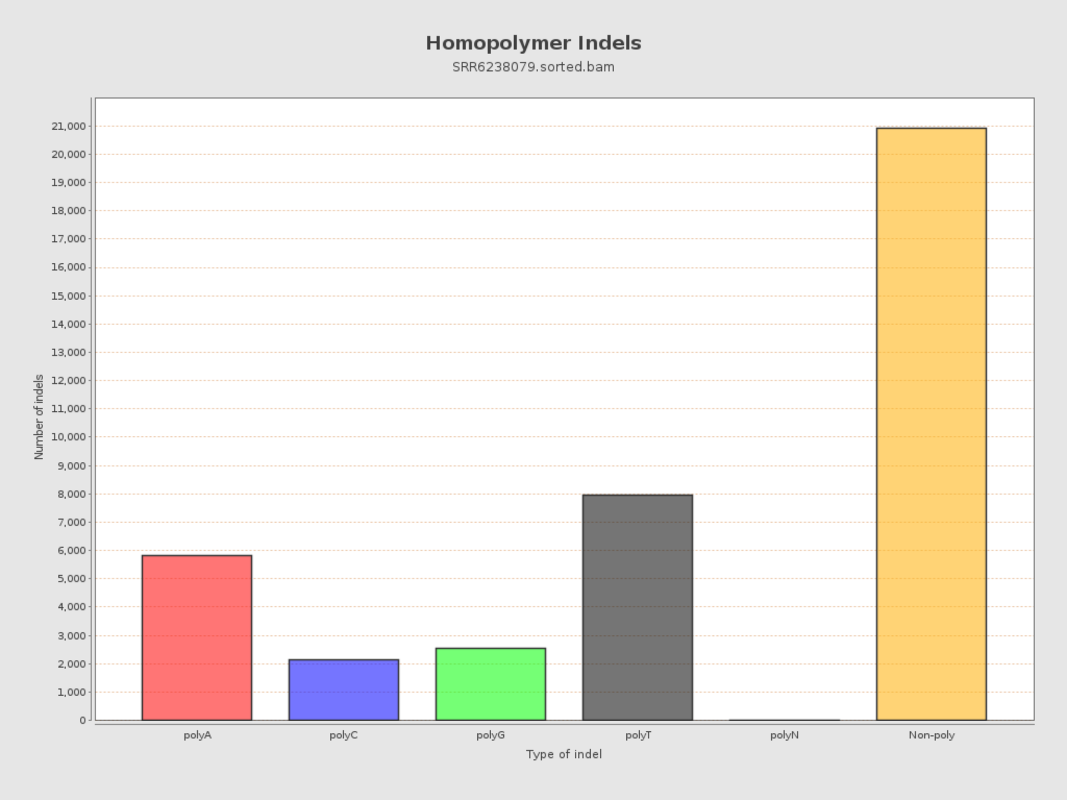
9. Results : Mapped Reads GC-content Distribution



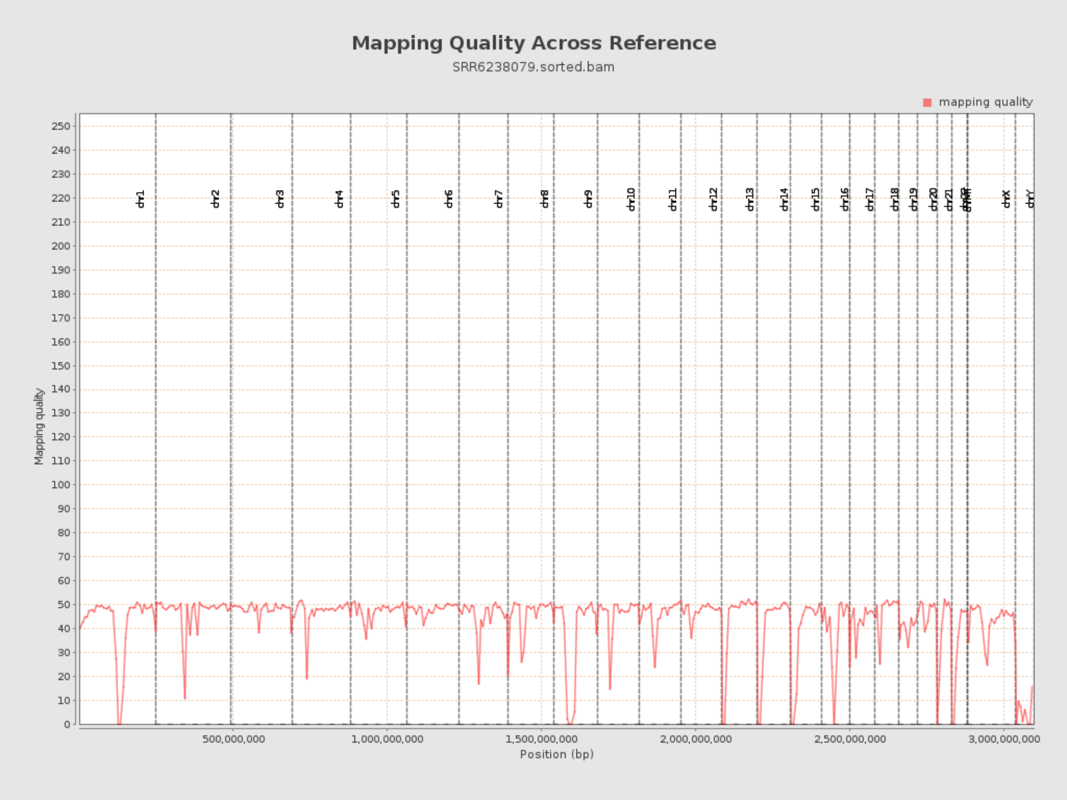
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram