Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 19:13:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6236073.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_SRR6236073 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6236073.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 19:13:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6236073.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,395,244
Mapped reads	2,055,636 / 85.82%
Unmapped reads	339,608 / 14.18%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,568 / 0.57%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	112,033 / 4.68%
Duplication rate	4.46%
Clipped reads	725,855 / 30.3%

2.2. ACGT Content

Number/percentage of A's	40,133,778 / 28.42%
Number/percentage of C's	26,287,046 / 18.62%
Number/percentage of T's	44,240,811 / 31.33%
Number/percentage of G's	30,455,817 / 21.57%
Number/percentage of N's	77,650 / 0.05%
GC Percentage	40.19%

2.3. Coverage

Mean	0.0456

Standard Deviation	0.4357

2.4. Mapping Quality

Mean Mapping Quality	46.57

2.5. Mismatches and indels

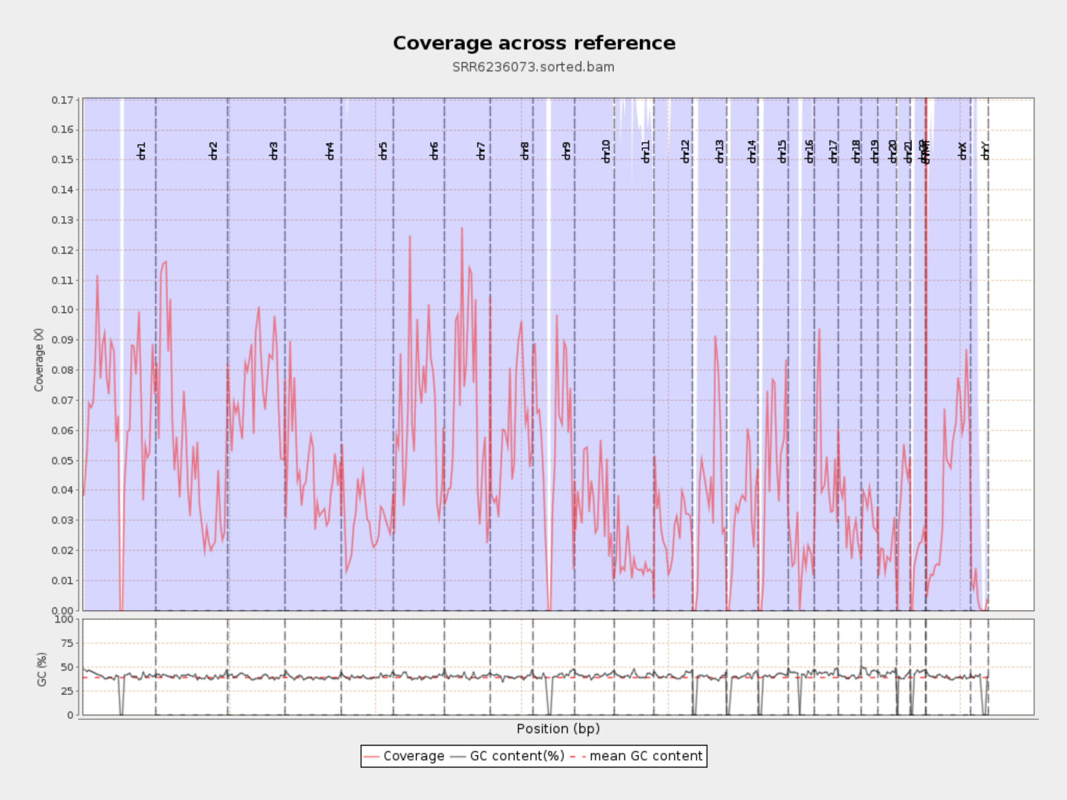
General error rate	0.81%
Mismatches	1,126,232
Insertions	9,859
Mapped reads with at least one insertion	0.48%
Deletions	44,821
Mapped reads with at least one deletion	2.15%
Homopolymer indels	47.7%

2.6. Chromosome stats

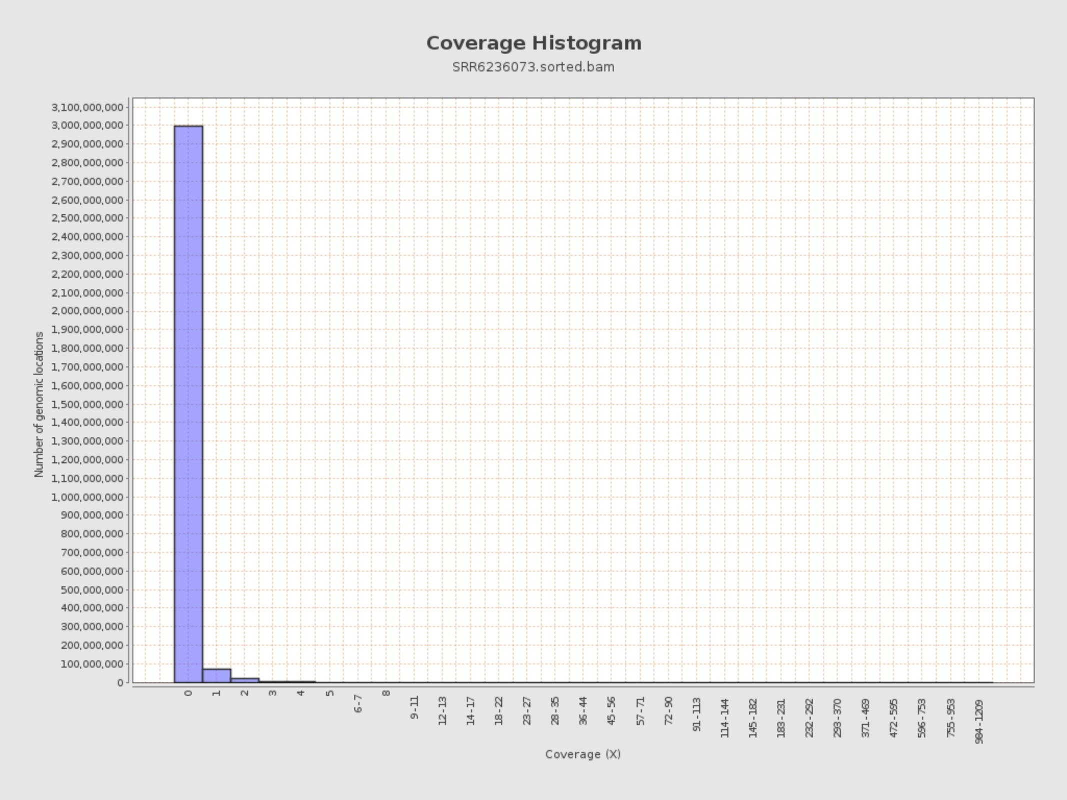
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16675200	0.0669	0.5427
chr2	243199373	12671738	0.0521	0.362
chr3	198022430	14796928	0.0747	0.3621
chr4	191154276	8655163	0.0453	0.2865
chr5	180915260	5548253	0.0307	0.2318
chr6	171115067	11379579	0.0665	0.5921
chr7	159138663	10613930	0.0667	0.9528

chr8	146364022	8576394	0.0586	0.8231
chr9	141213431	7729048	0.0547	0.3573
chr10	135534747	4847004	0.0358	0.3534
chr11	135006516	2206276	0.0163	0.1995
chr12	133851895	3869020	0.0289	0.2386
chr13	115169878	4504127	0.0391	0.263
chr14	107349540	3368937	0.0314	0.242
chr15	102531392	4768121	0.0465	0.2874
chr16	90354753	1593781	0.0176	0.1958
chr17	81195210	3948459	0.0486	0.3214
chr18	78077248	2412278	0.0309	0.4364
chr19	59128983	1989216	0.0336	0.3539
chr20	63025520	1230489	0.0195	0.1887
chr21	48129895	1896391	0.0394	0.269
chr22	51304566	872235	0.017	0.1689
chrMT	16571	71213	4.2974	3.3489
chrX	155270560	6775133	0.0436	0.2901
chrY	59373566	274713	0.0046	0.1131

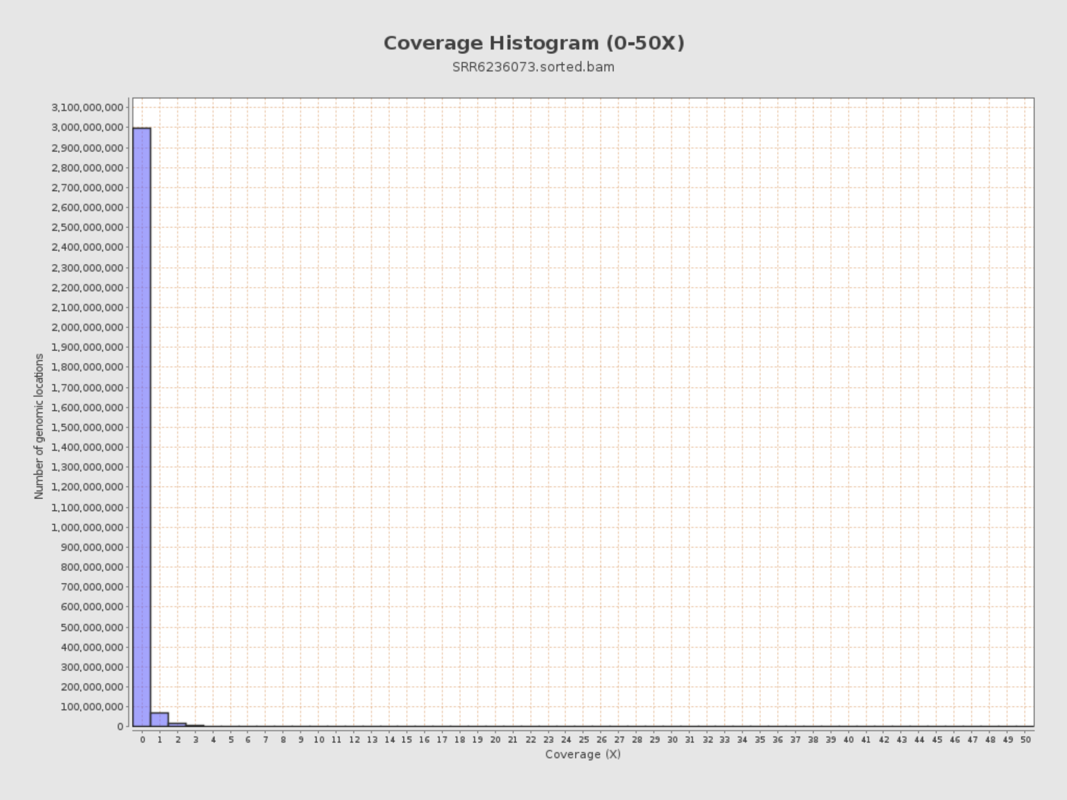
3. Results : Coverage across reference



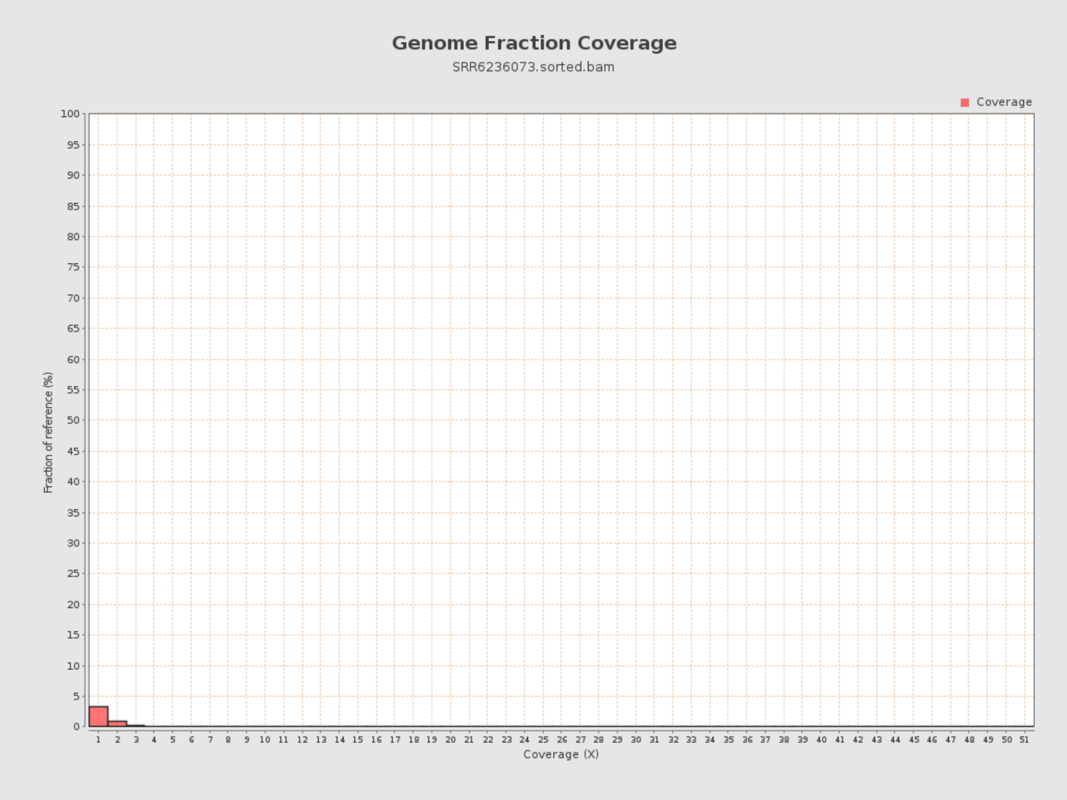
4. Results : Coverage Histogram



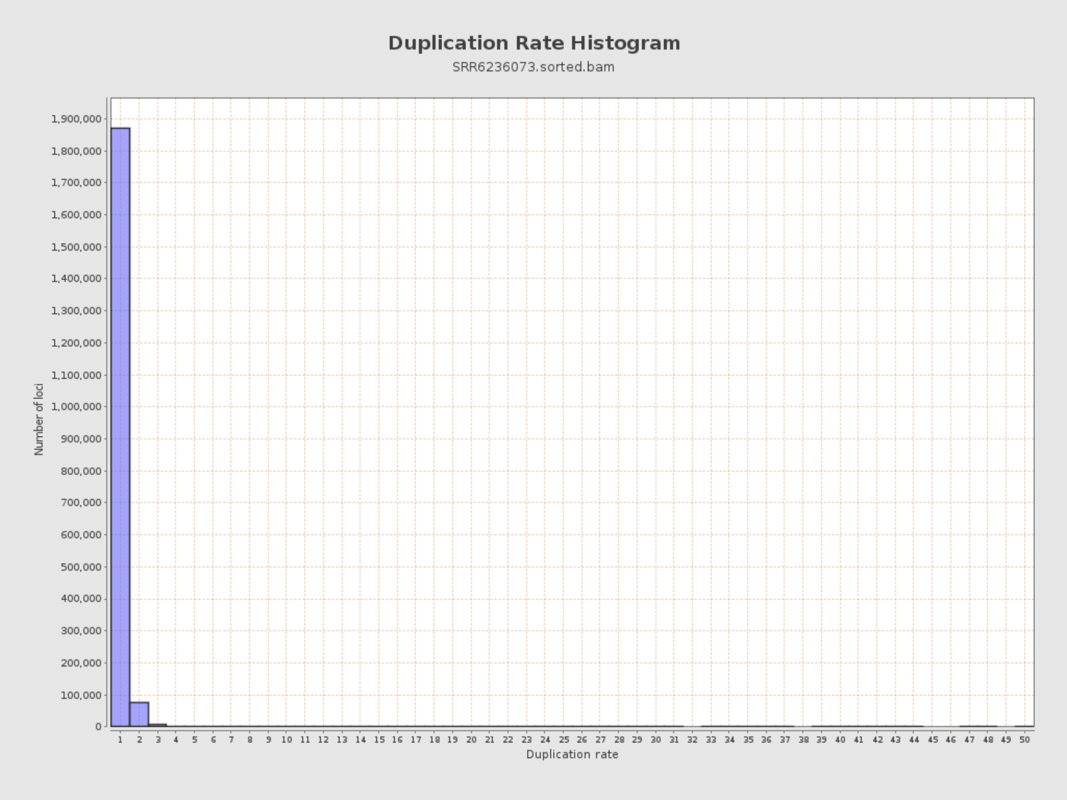
5. Results : Coverage Histogram (0-50X)



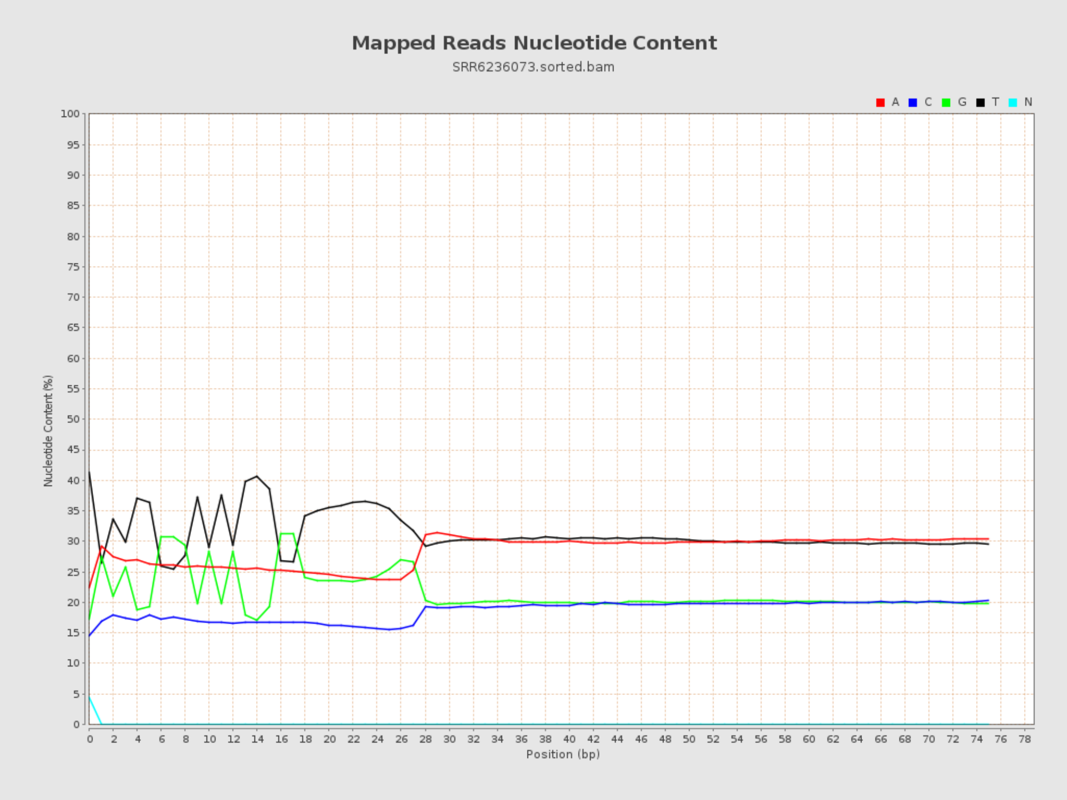
6. Results : Genome Fraction Coverage



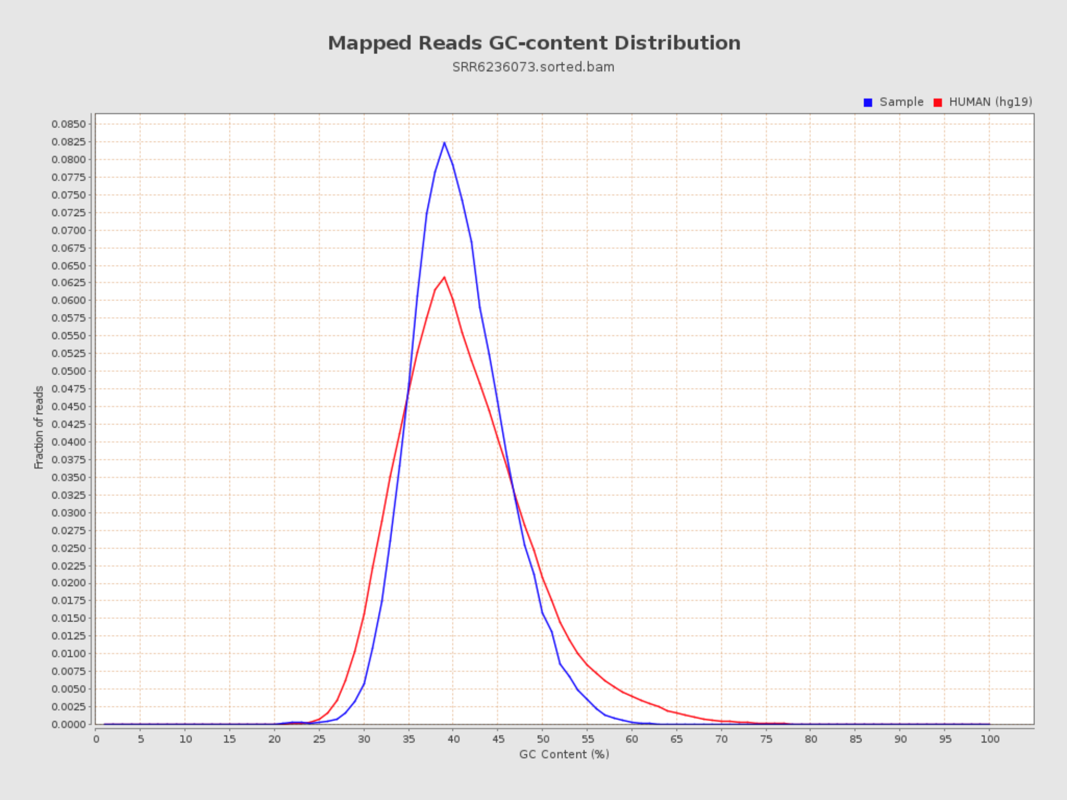
7. Results : Duplication Rate Histogram



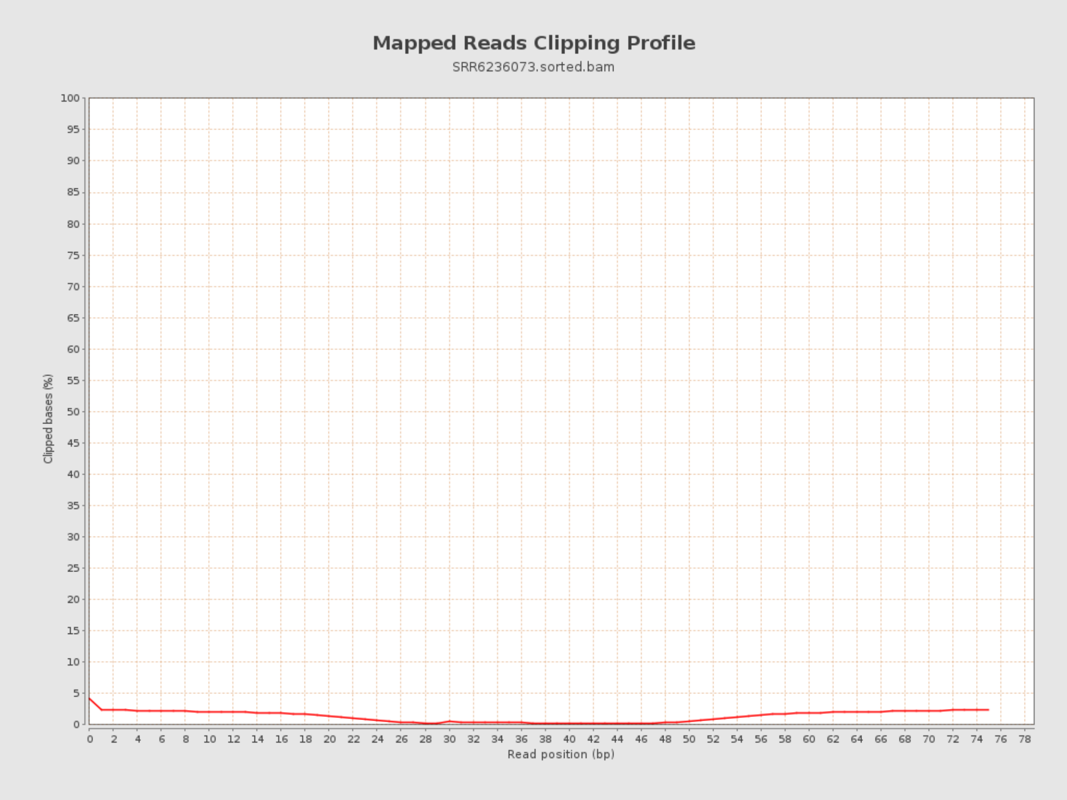
8. Results : Mapped Reads Nucleotide Content



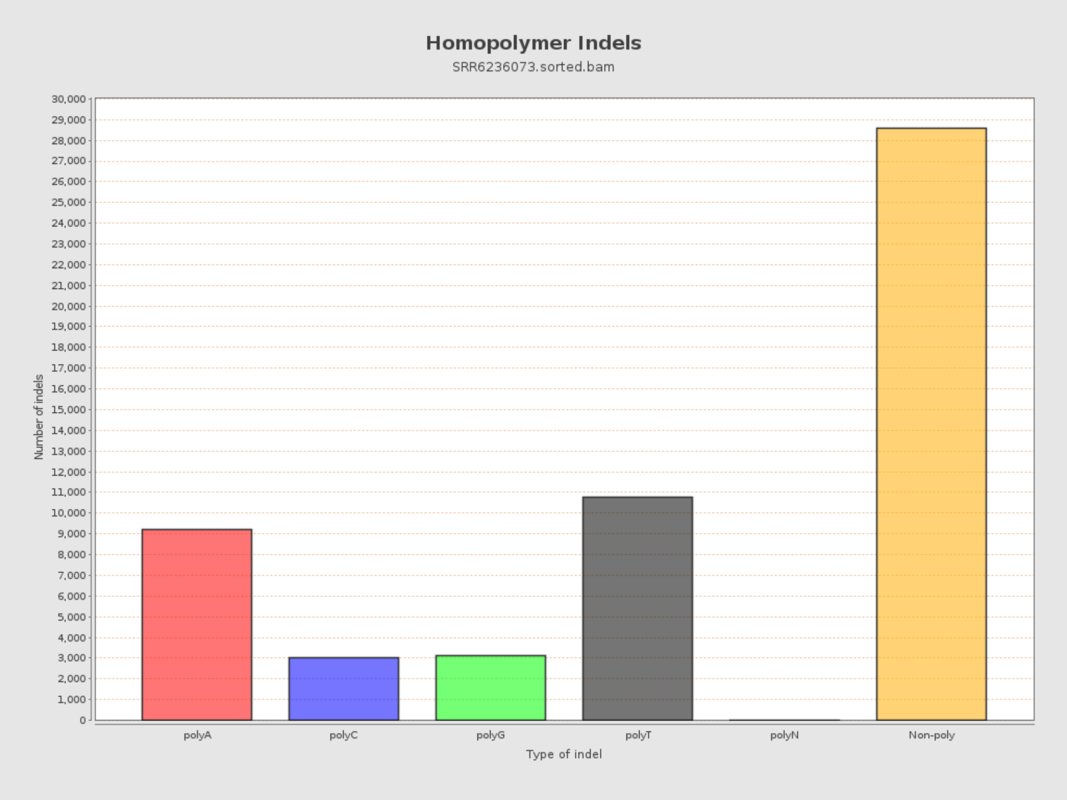
9. Results : Mapped Reads GC-content Distribution



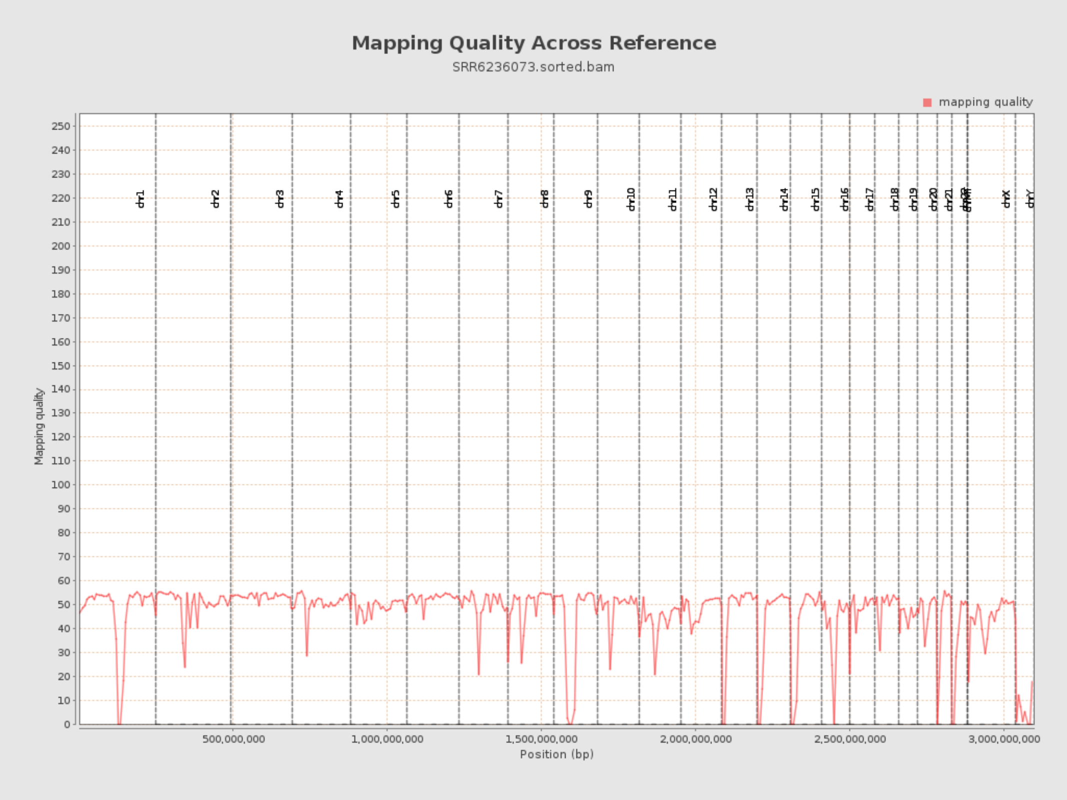
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram