Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 05:10:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240073.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_SRR6240073 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240073.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 05:10:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240073.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,301,432
Mapped reads	1,835,352 / 79.75%
Unmapped reads	466,080 / 20.25%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,207 / 0.7%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	282,403 / 12.27%
Duplication rate	11.31%
Clipped reads	936,662 / 40.7%

2.2. ACGT Content

Number/percentage of A's	34,344,611 / 28.49%
Number/percentage of C's	22,566,804 / 18.72%
Number/percentage of T's	38,181,729 / 31.67%
Number/percentage of G's	25,453,232 / 21.11%
Number/percentage of N's	11,115 / 0.01%
GC Percentage	39.83%

2.3. Coverage

Mean	0.039

Standard Deviation	0.4593

2.4. Mapping Quality

Mean Mapping Quality	46.68

2.5. Mismatches and indels

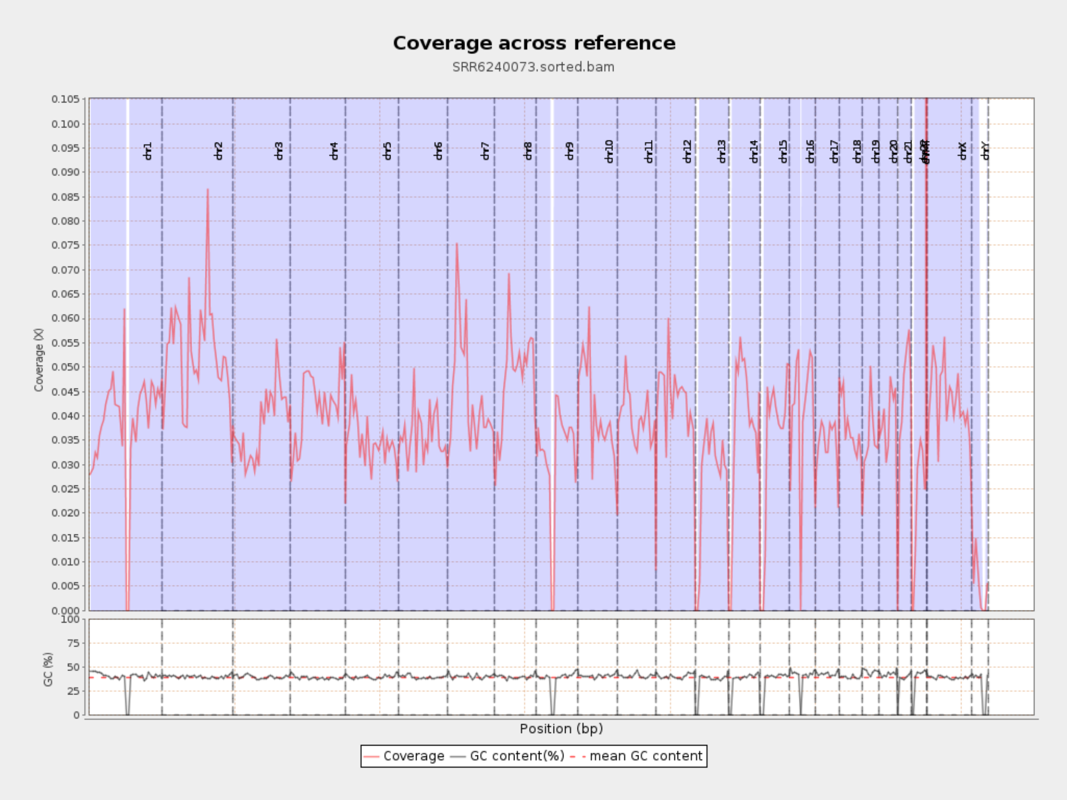
General error rate	0.86%
Mismatches	1,025,180
Insertions	8,724
Mapped reads with at least one insertion	0.47%
Deletions	34,316
Mapped reads with at least one deletion	1.85%
Homopolymer indels	48.34%

2.6. Chromosome stats

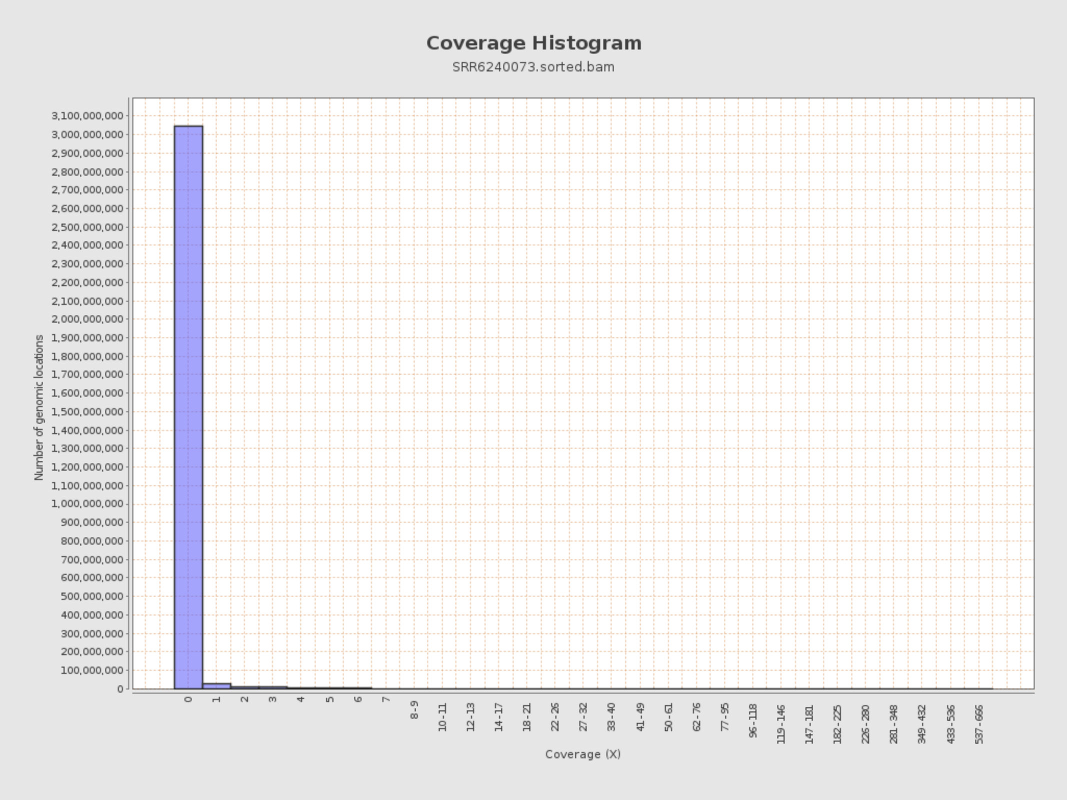
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9596237	0.0385	0.6528
chr2	243199373	12890538	0.053	0.5268
chr3	198022430	7554658	0.0382	0.3771
chr4	191154276	8061361	0.0422	0.4061
chr5	180915260	6335616	0.035	0.3688
chr6	171115067	6141522	0.0359	0.4025
chr7	159138663	7142440	0.0449	0.5815

chr8	146364022	7006360	0.0479	0.5932
chr9	141213431	4475182	0.0317	0.4141
chr10	135534747	5585604	0.0412	0.4467
chr11	135006516	5317408	0.0394	0.4675
chr12	133851895	5853245	0.0437	0.4076
chr13	115169878	3117606	0.0271	0.3211
chr14	107349540	3983825	0.0371	0.3911
chr15	102531392	3505560	0.0342	0.3731
chr16	90354753	3663026	0.0405	0.3899
chr17	81195210	2773162	0.0342	0.3642
chr18	78077248	2932591	0.0376	0.6185
chr19	59128983	2105422	0.0356	0.4689
chr20	63025520	2451171	0.0389	0.3795
chr21	48129895	2033928	0.0423	0.4084
chr22	51304566	1088248	0.0212	0.2661
chrMT	16571	20146	1.2157	2.1605
chrX	155270560	6663865	0.0429	0.4167
chrY	59373566	318720	0.0054	0.1307

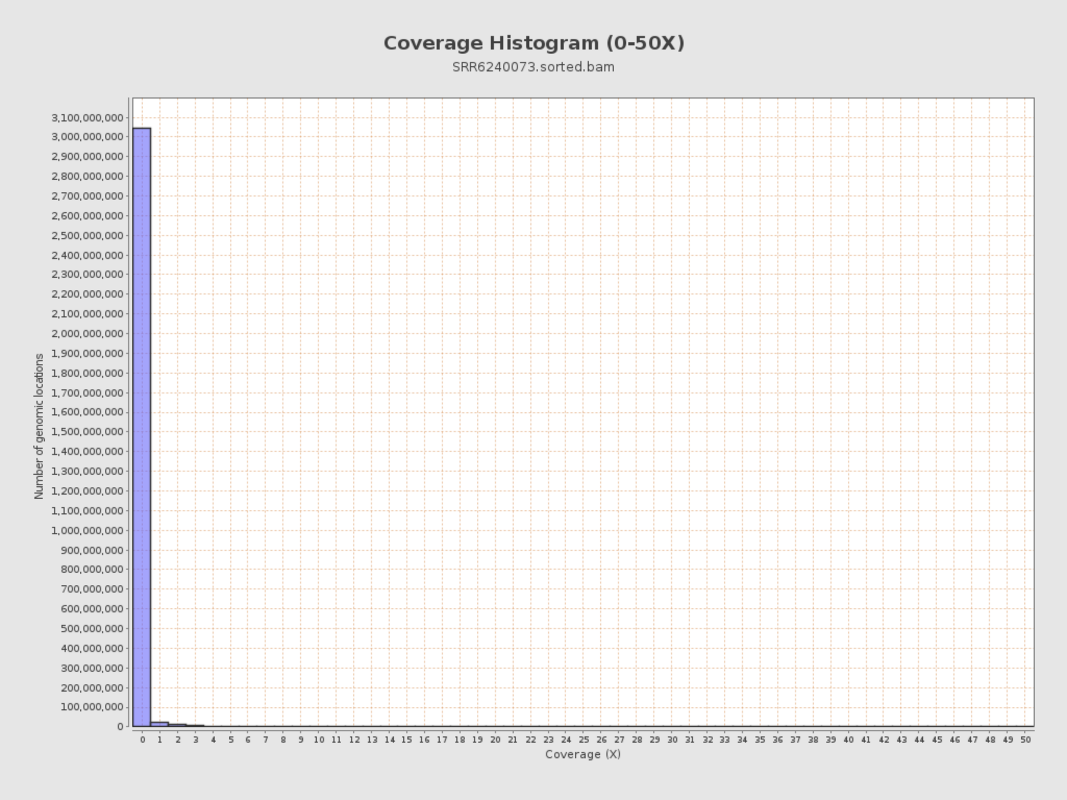
3. Results : Coverage across reference



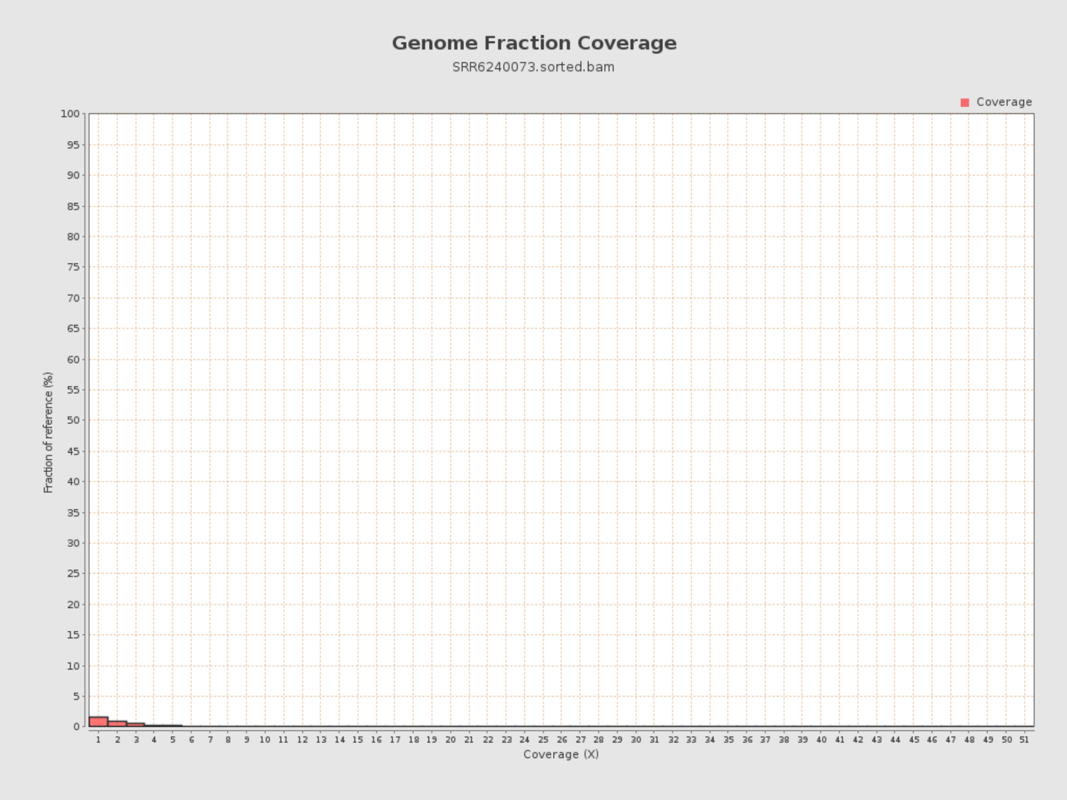
4. Results : Coverage Histogram



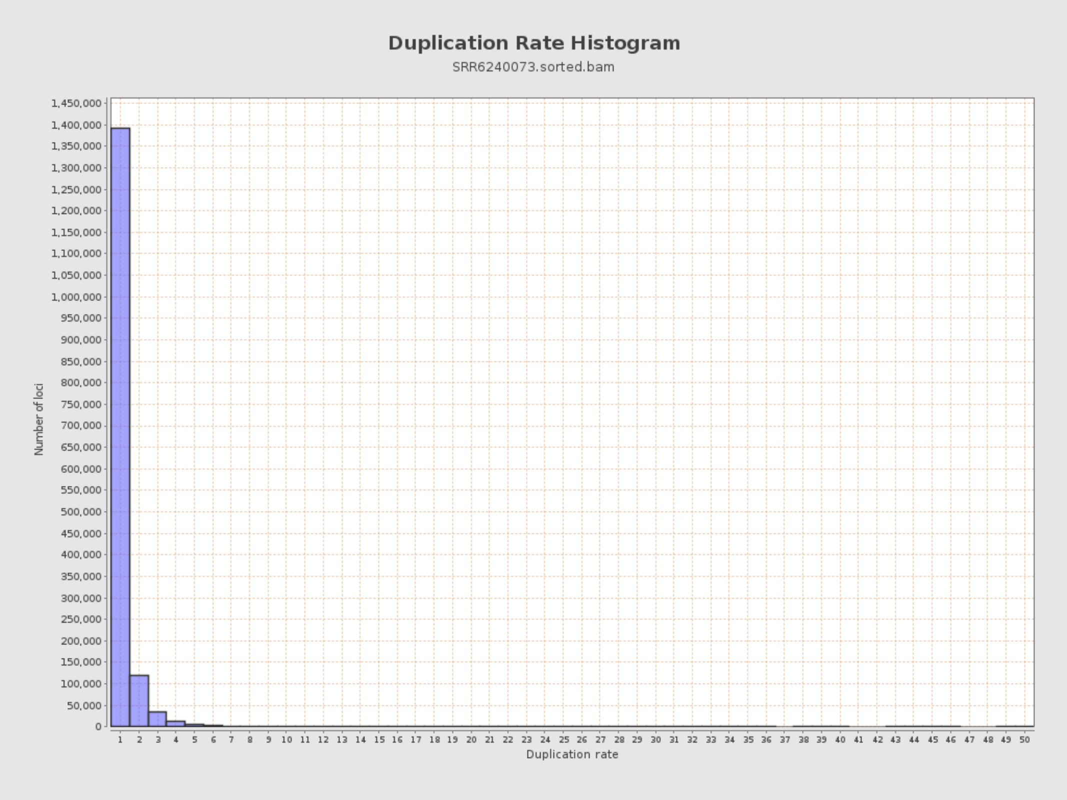
5. Results : Coverage Histogram (0-50X)



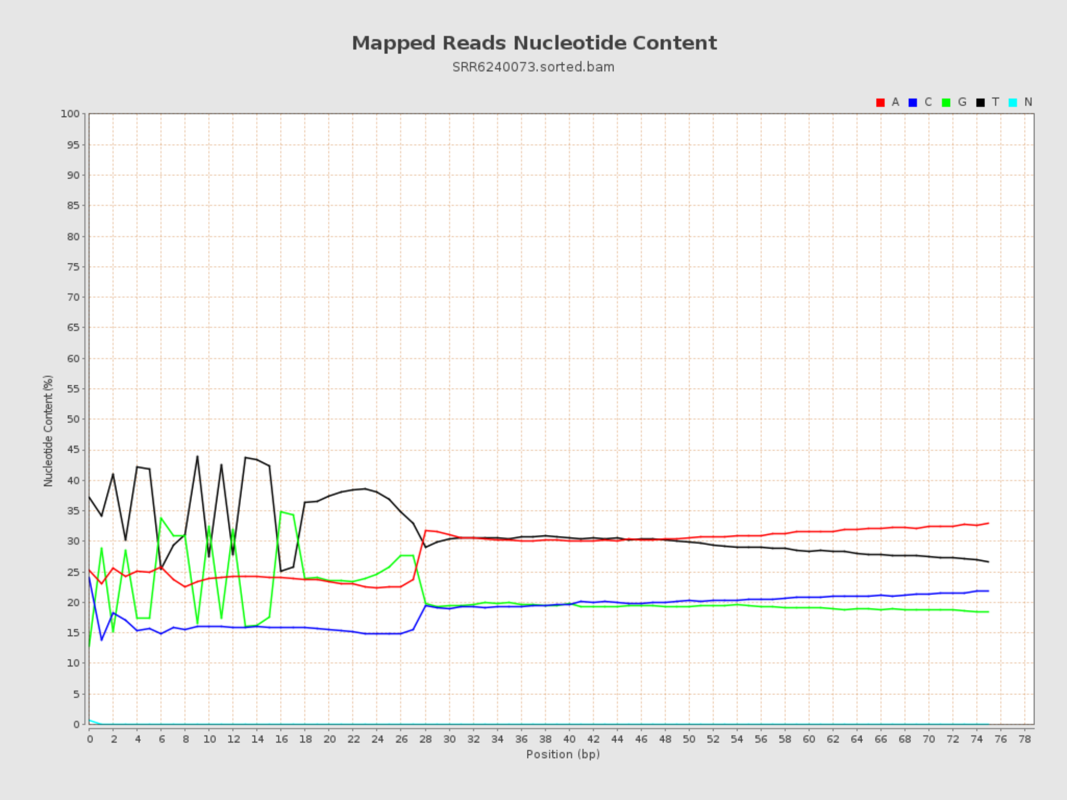
6. Results : Genome Fraction Coverage



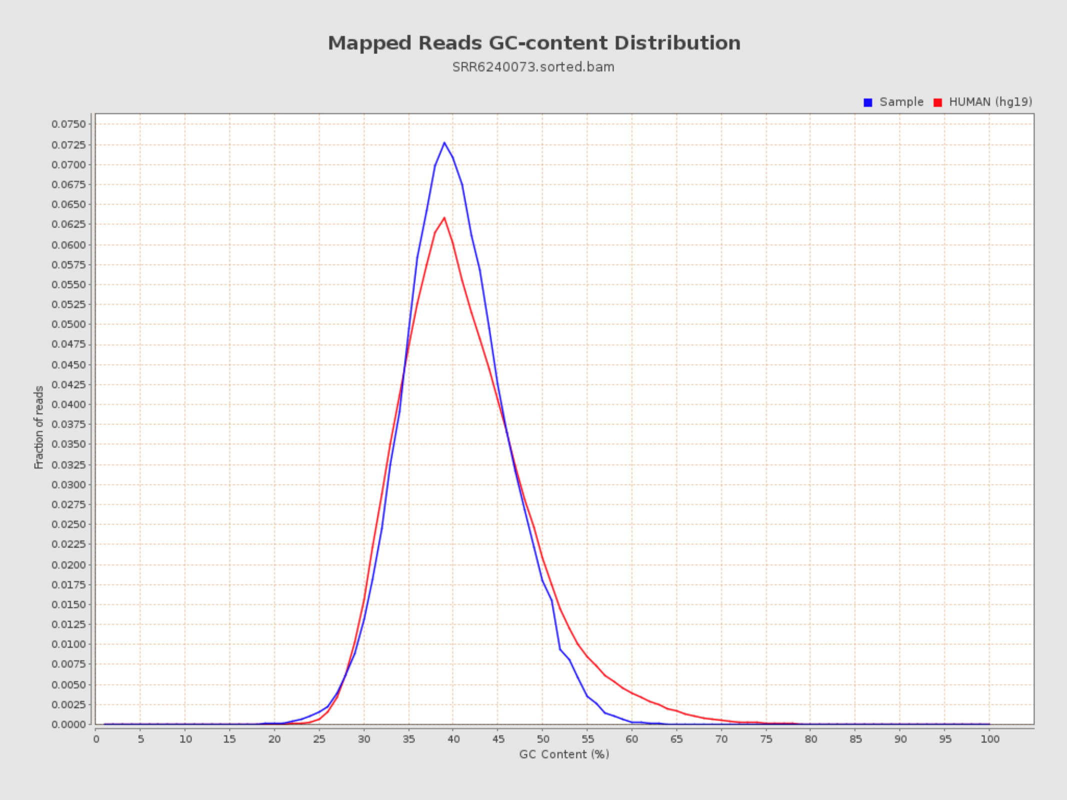
7. Results : Duplication Rate Histogram



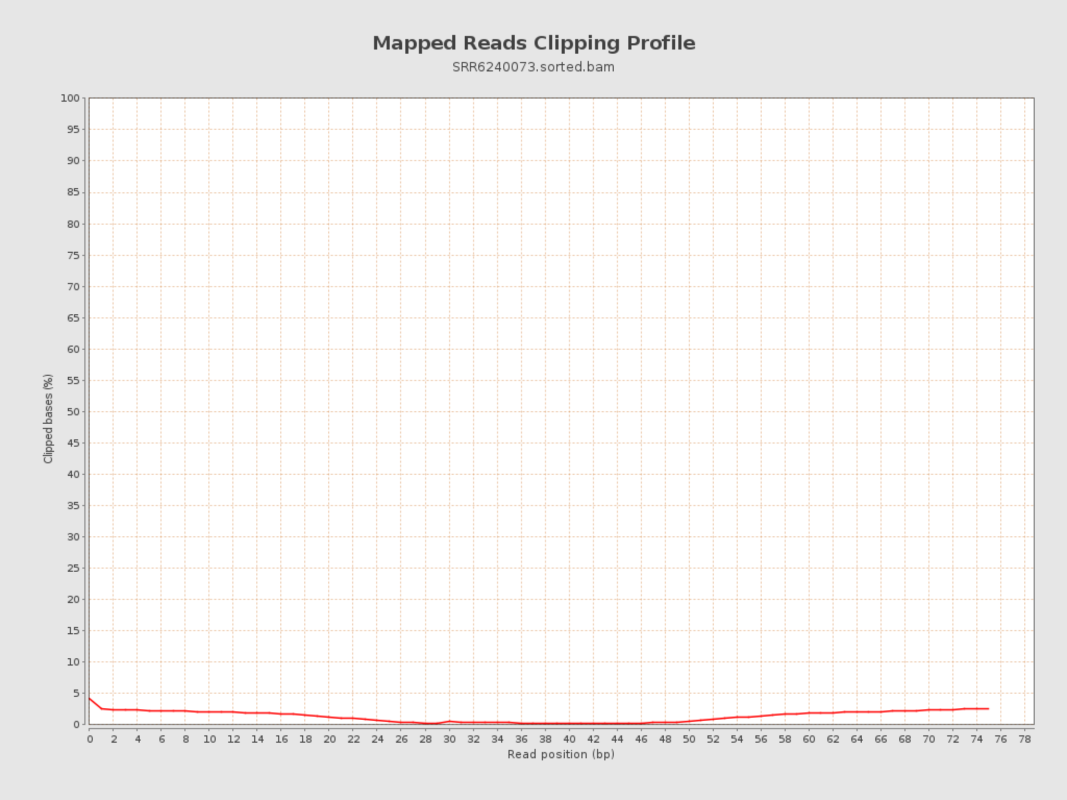
8. Results : Mapped Reads Nucleotide Content



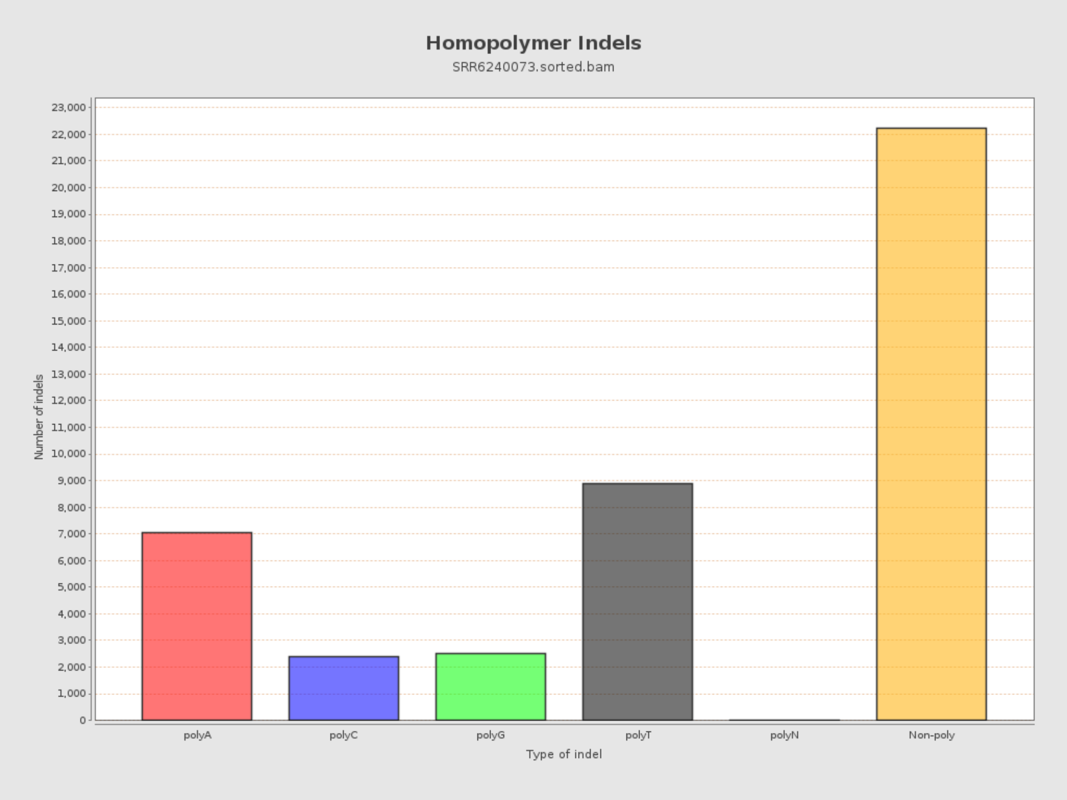
9. Results : Mapped Reads GC-content Distribution



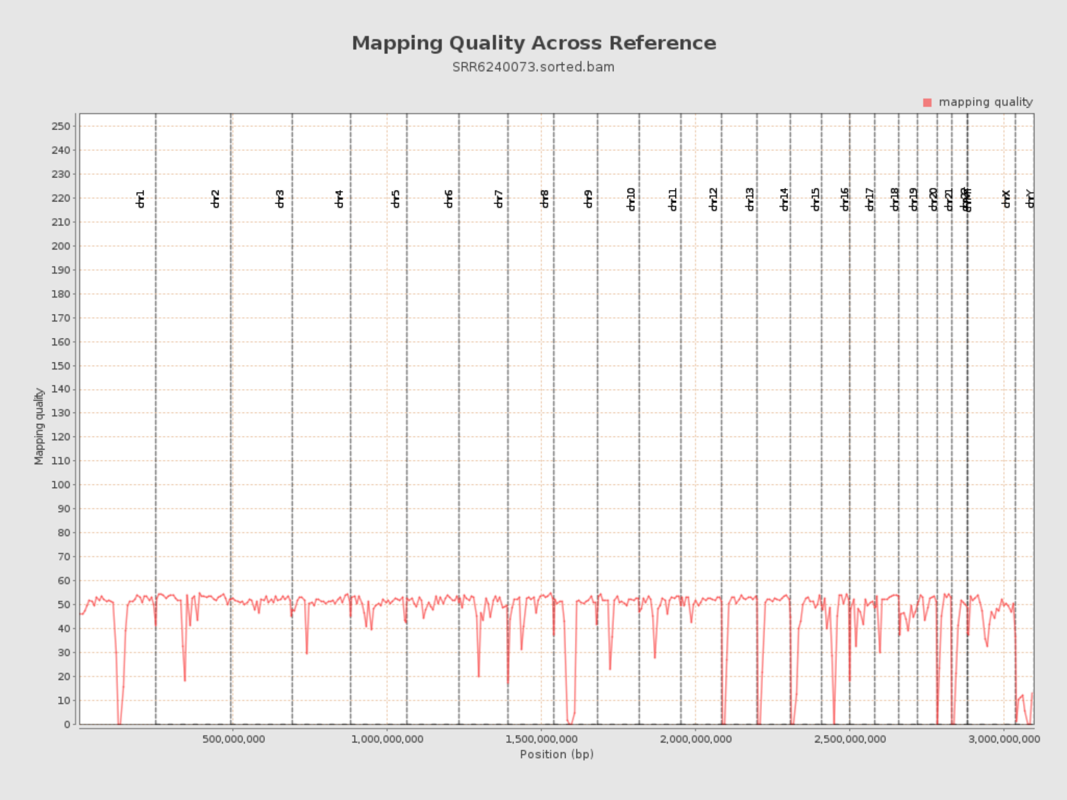
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram