Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 06:10:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240201.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_SRR6240201 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240201.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 06:10:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240201.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,874,051
Mapped reads	1,528,756 / 81.57%
Unmapped reads	345,295 / 18.43%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,921 / 0.58%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	159,200 / 8.49%
Duplication rate	8.56%
Clipped reads	877,027 / 46.8%

2.2. ACGT Content

Number/percentage of A's	27,020,315 / 27.76%
Number/percentage of C's	17,568,623 / 18.05%
Number/percentage of T's	31,105,217 / 31.96%
Number/percentage of G's	21,608,747 / 22.2%
Number/percentage of N's	24,026 / 0.02%
GC Percentage	40.25%

2.3. Coverage

Mean	0.0315

Standard Deviation	0.3225

2.4. Mapping Quality

Mean Mapping Quality	46.04

2.5. Mismatches and indels

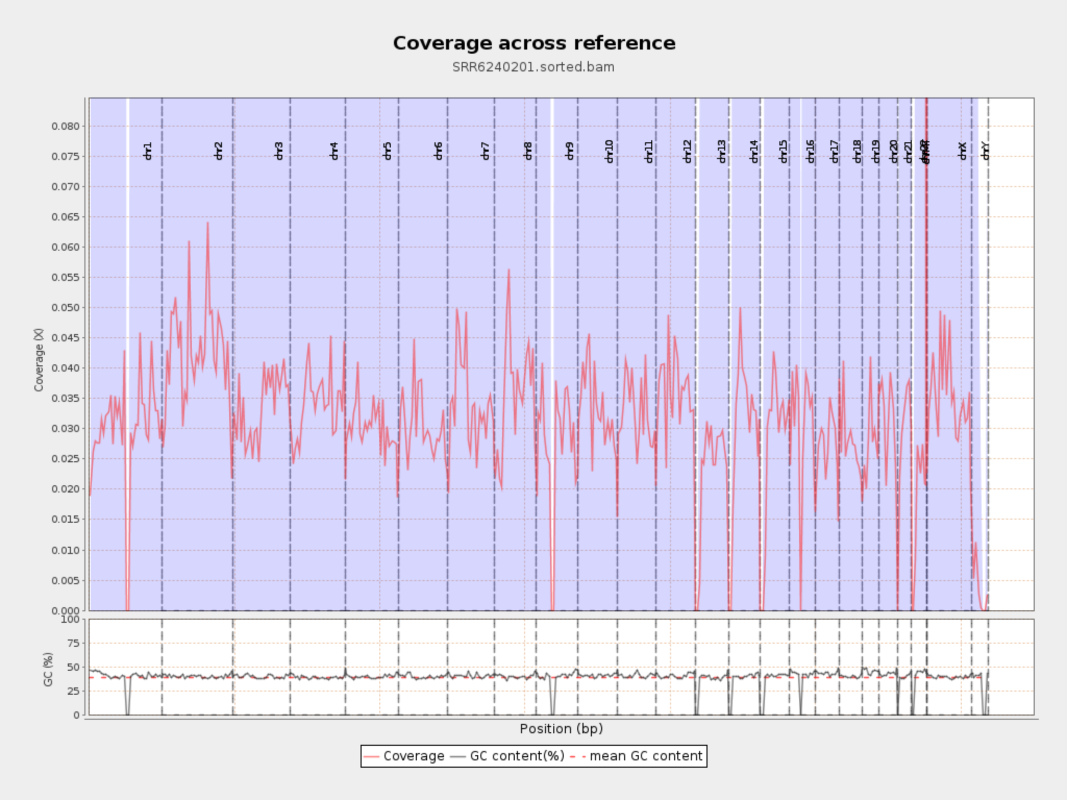
General error rate	0.88%
Mismatches	839,968
Insertions	6,888
Mapped reads with at least one insertion	0.45%
Deletions	26,231
Mapped reads with at least one deletion	1.7%
Homopolymer indels	48.31%

2.6. Chromosome stats

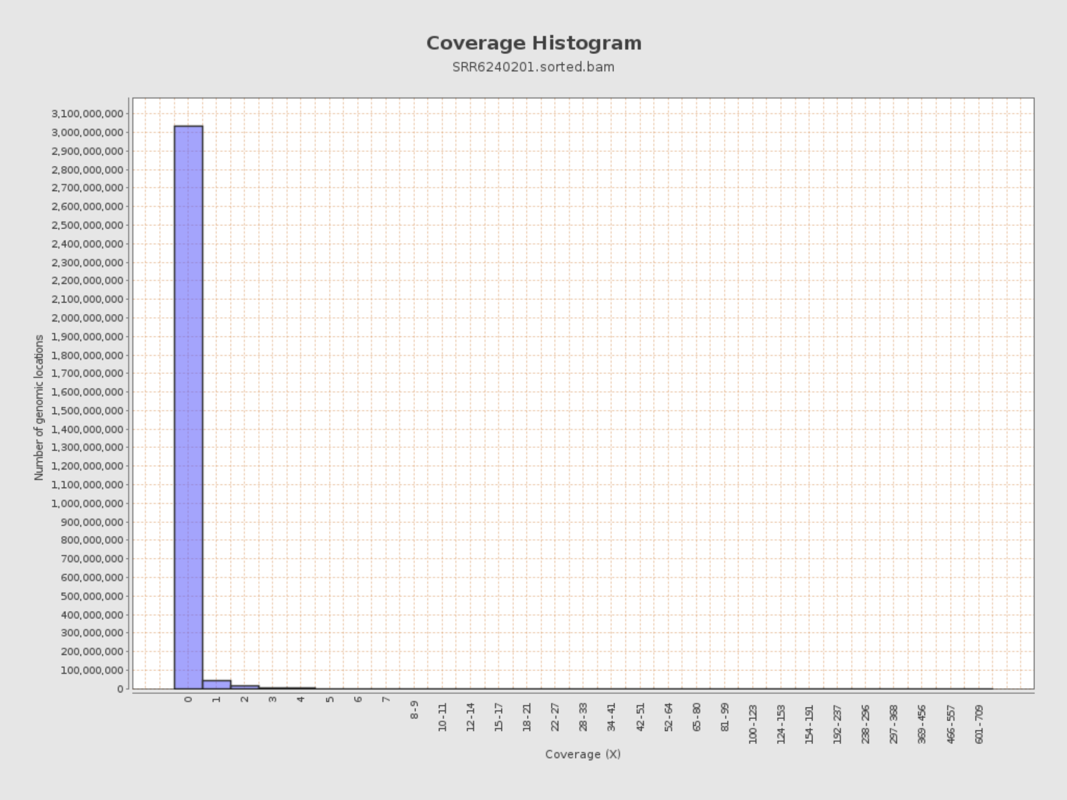
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7430049	0.0298	0.4372
chr2	243199373	10351937	0.0426	0.4
chr3	198022430	6665453	0.0337	0.2625
chr4	191154276	6544748	0.0342	0.2722
chr5	180915260	5483664	0.0303	0.25
chr6	171115067	5192700	0.0303	0.2715
chr7	159138663	5479343	0.0344	0.3777

chr8	146364022	5254385	0.0359	0.513
chr9	141213431	3886614	0.0275	0.3077
chr10	135534747	4557899	0.0336	0.2991
chr11	135006516	4383267	0.0325	0.3073
chr12	133851895	4848829	0.0362	0.2728
chr13	115169878	2570107	0.0223	0.2147
chr14	107349540	3223178	0.03	0.2566
chr15	102531392	2785901	0.0272	0.2398
chr16	90354753	2735570	0.0303	0.2514
chr17	81195210	2193695	0.027	0.2432
chr18	78077248	2198964	0.0282	0.457
chr19	59128983	1655073	0.028	0.3568
chr20	63025520	1951629	0.031	0.251
chr21	48129895	1378062	0.0286	0.2462
chr22	51304566	868054	0.0169	0.1794
chrMT	16571	21245	1.2821	1.6965
chrX	155270560	5486840	0.0353	0.2816
chrY	59373566	225194	0.0038	0.0926

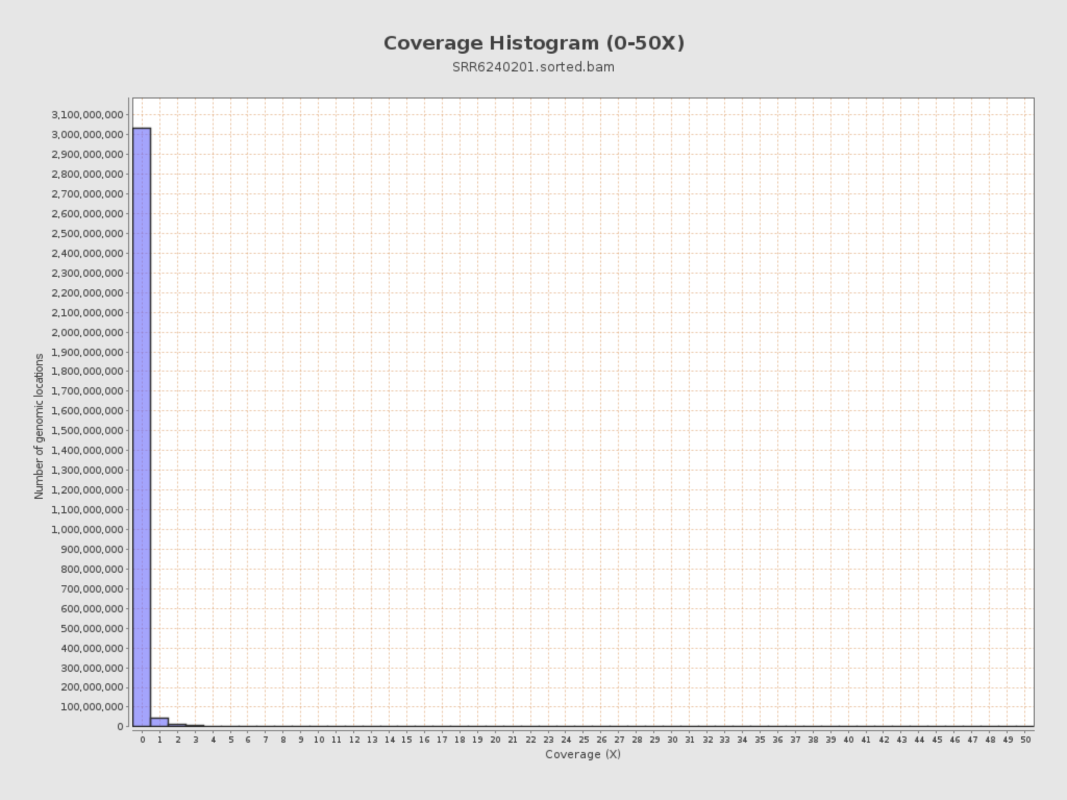
3. Results : Coverage across reference



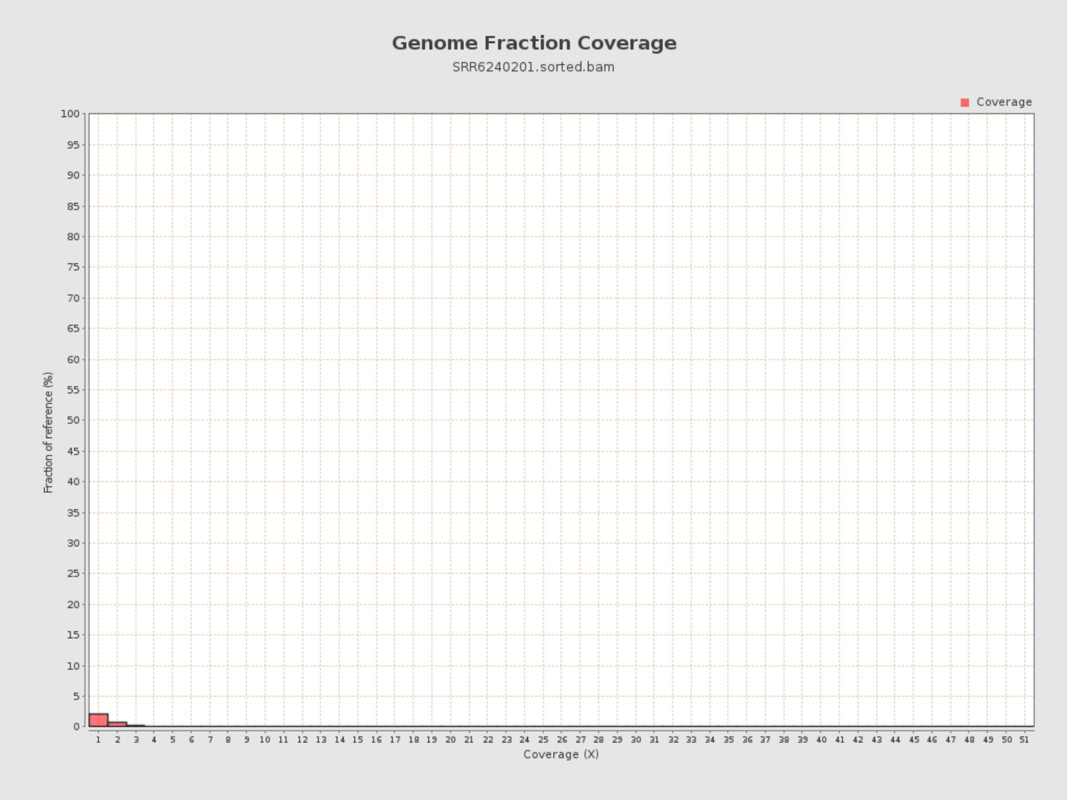
4. Results : Coverage Histogram



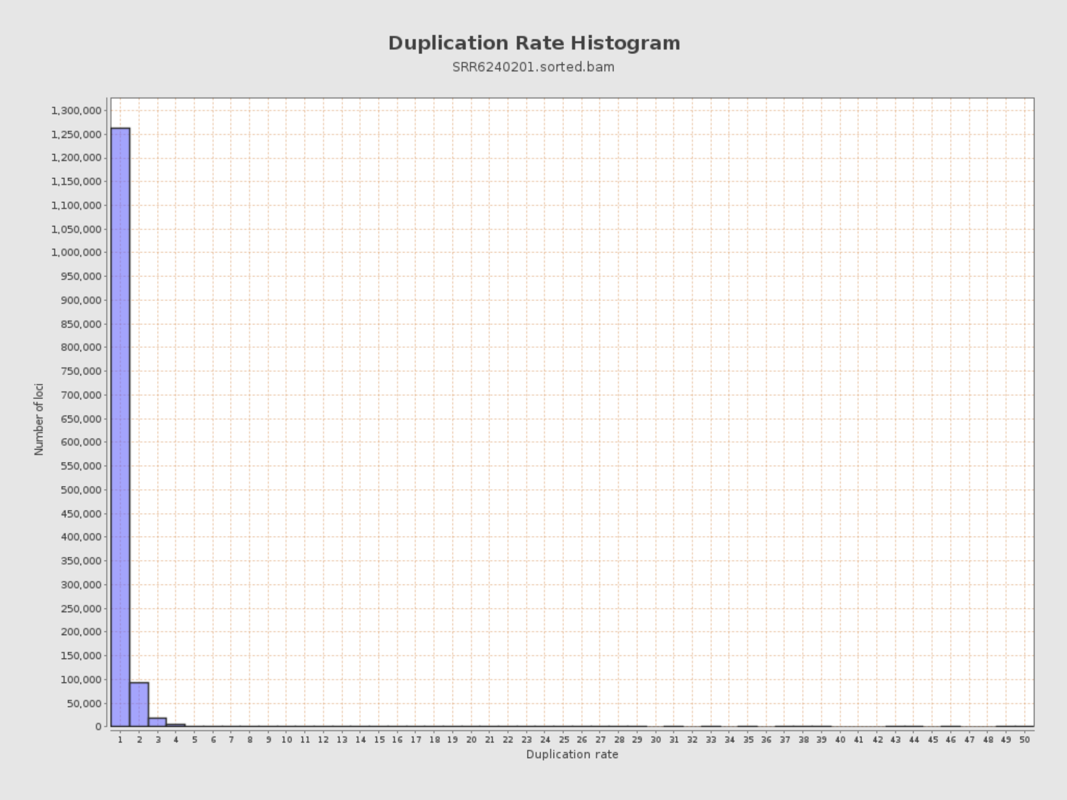
5. Results : Coverage Histogram (0-50X)



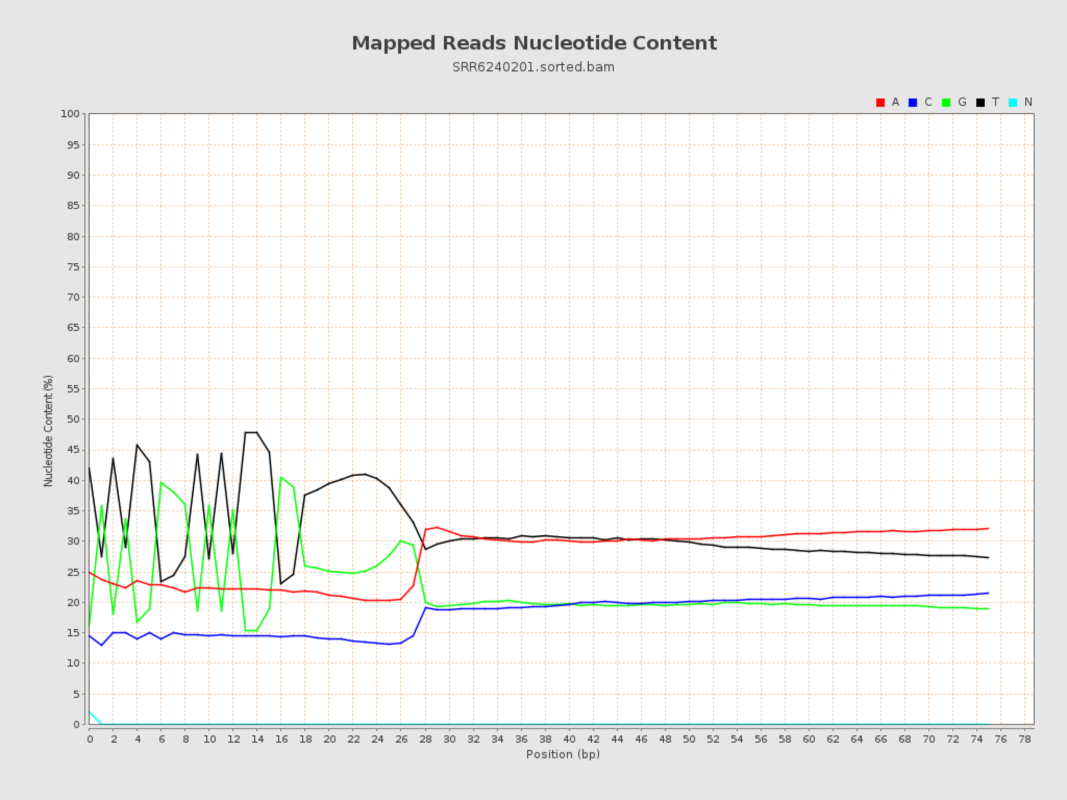
6. Results : Genome Fraction Coverage



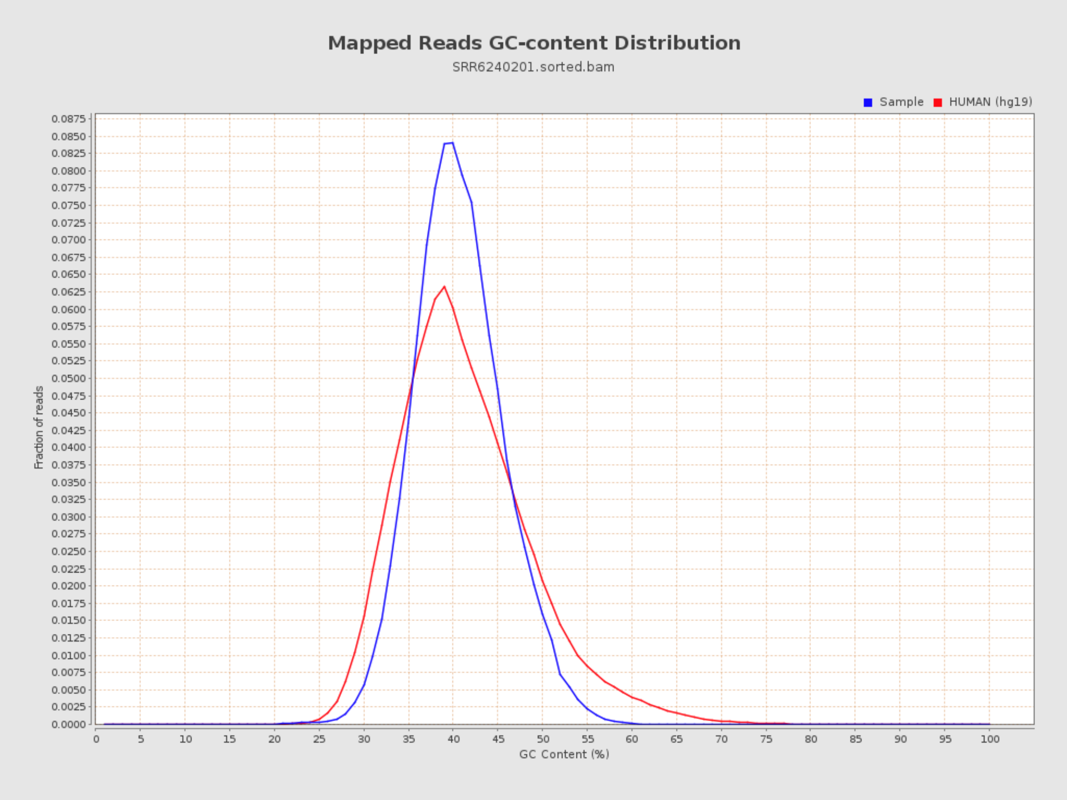
7. Results : Duplication Rate Histogram



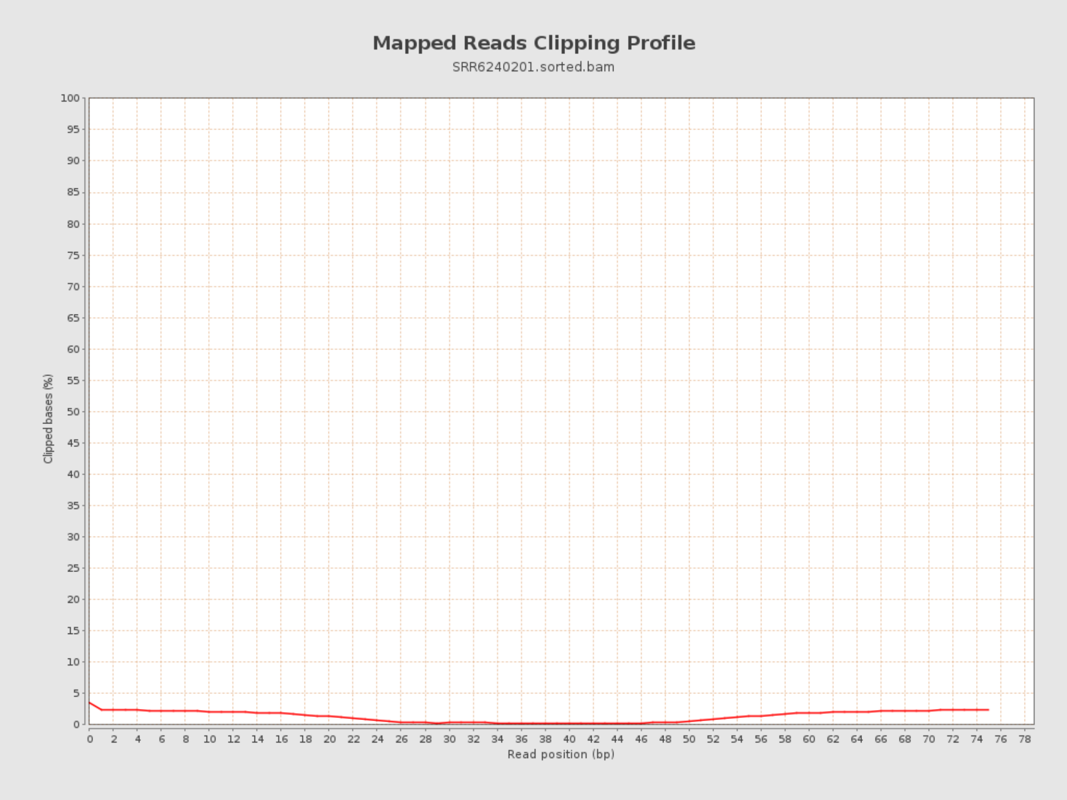
8. Results : Mapped Reads Nucleotide Content



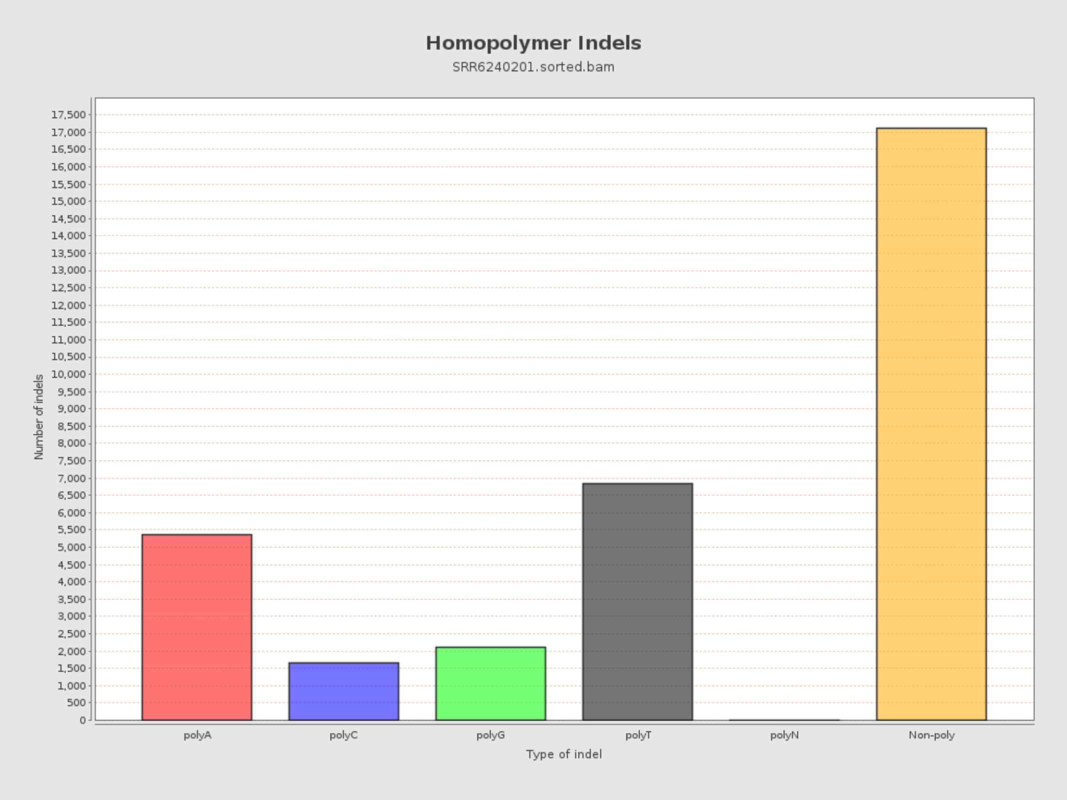
9. Results : Mapped Reads GC-content Distribution



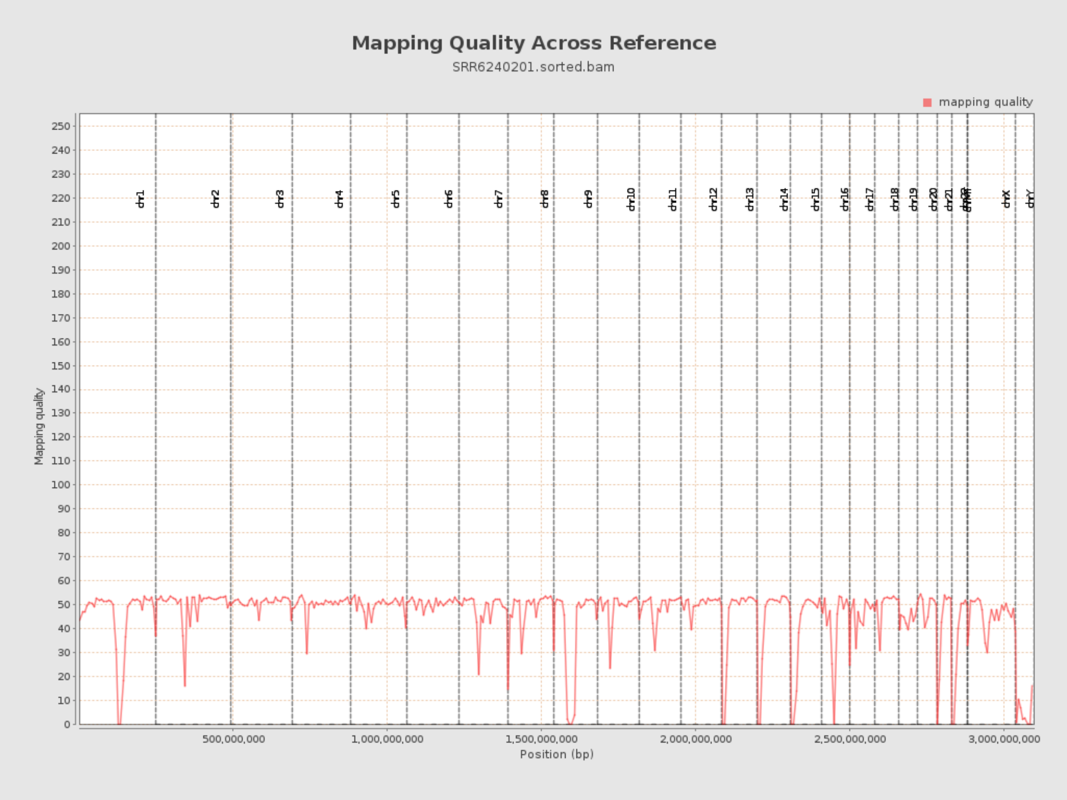
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram