Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 11:52:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084401.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_SRR3084401 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084401.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 11:52:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084401.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,895,048
Mapped reads	2,650,022 / 91.54%
Unmapped reads	245,026 / 8.46%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,907 / 0.69%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	99,107 / 3.42%
Duplication rate	3.1%
Clipped reads	1,166,866 / 40.31%

2.2. ACGT Content

Number/percentage of A's	50,926,852 / 28.6%
Number/percentage of C's	33,701,607 / 18.92%
Number/percentage of T's	55,338,920 / 31.07%
Number/percentage of G's	37,896,583 / 21.28%
Number/percentage of N's	223,588 / 0.13%
GC Percentage	40.2%

2.3. Coverage

Mean	0.0575

Standard Deviation	0.384

2.4. Mapping Quality

Mean Mapping Quality	46.18

2.5. Mismatches and indels

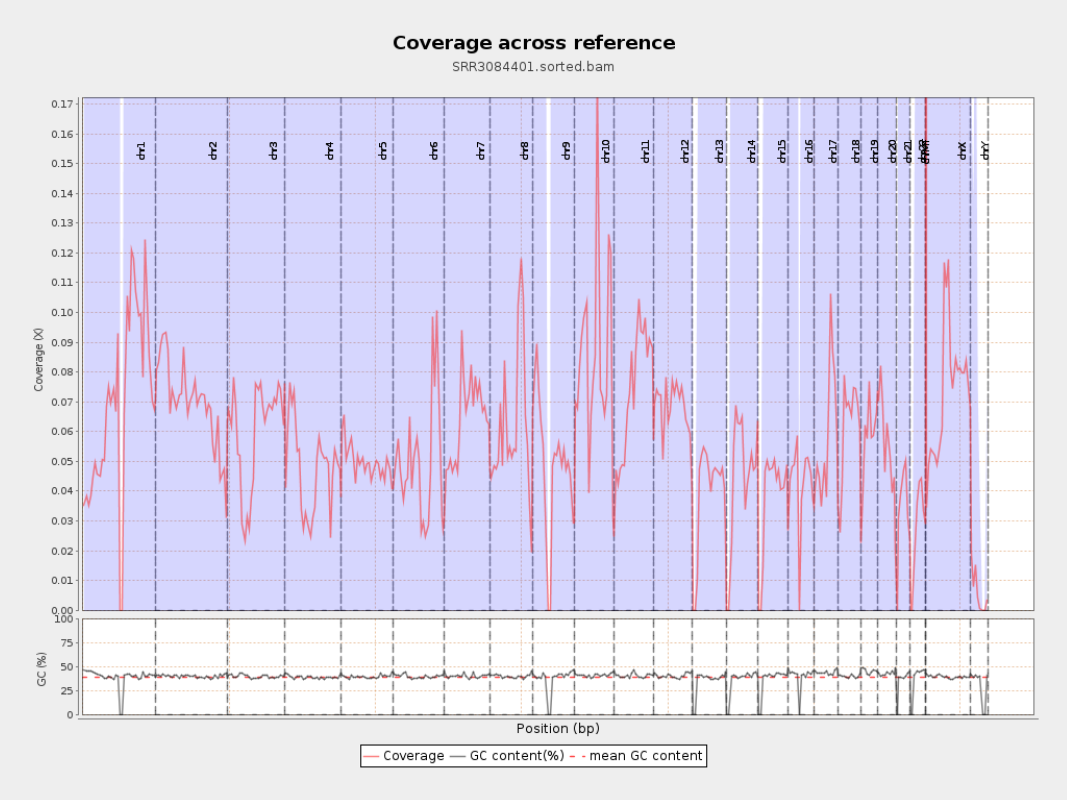
General error rate	1.01%
Mismatches	1,767,730
Insertions	12,821
Mapped reads with at least one insertion	0.48%
Deletions	36,014
Mapped reads with at least one deletion	1.35%
Homopolymer indels	46.68%

2.6. Chromosome stats

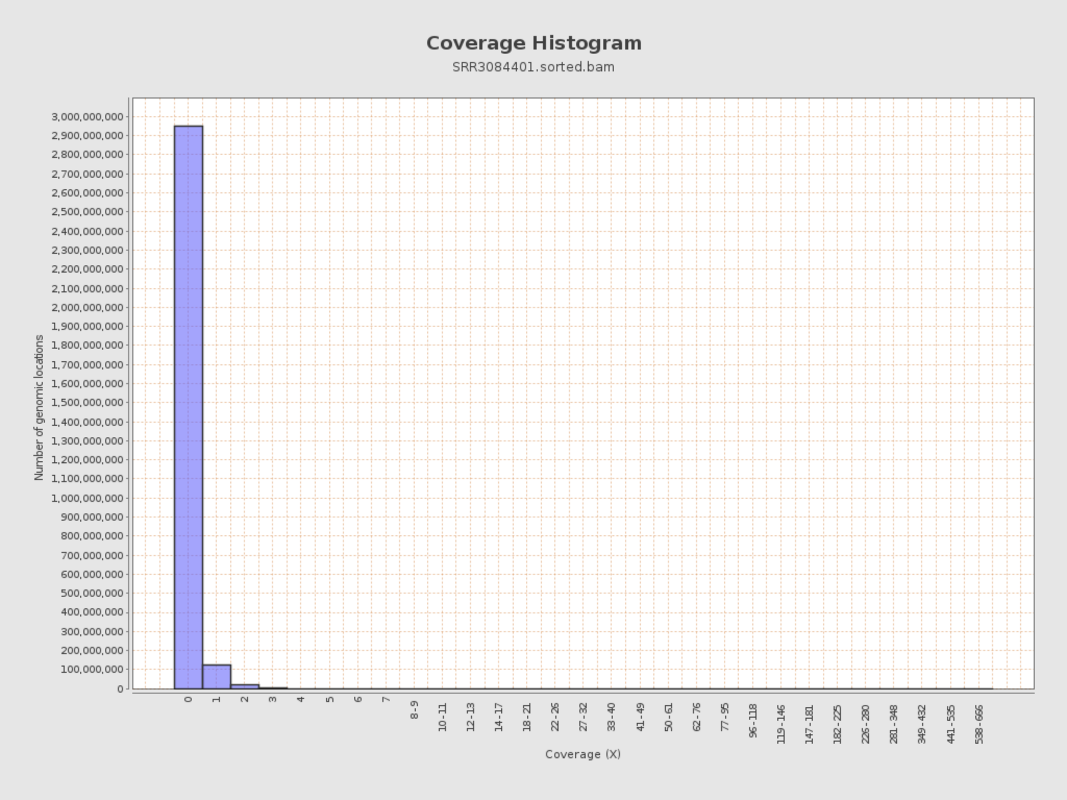
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17307184	0.0694	0.6487
chr2	243199373	17015732	0.07	0.4279
chr3	198022430	11843386	0.0598	0.2902
chr4	191154276	9023550	0.0472	0.2607
chr5	180915260	8989194	0.0497	0.2594
chr6	171115067	8699187	0.0508	0.2957
chr7	159138663	10180545	0.064	0.5252

chr8	146364022	8973118	0.0613	0.3935
chr9	141213431	6907252	0.0489	0.3286
chr10	135534747	11633554	0.0858	0.5473
chr11	135006516	9933184	0.0736	0.3809
chr12	133851895	9176358	0.0686	0.3058
chr13	115169878	4534682	0.0394	0.2305
chr14	107349540	4769951	0.0444	0.2548
chr15	102531392	3831537	0.0374	0.2301
chr16	90354753	3755475	0.0416	0.2567
chr17	81195210	4859834	0.0599	0.3078
chr18	78077248	4832467	0.0619	0.5162
chr19	59128983	3470050	0.0587	0.4775
chr20	63025520	3522899	0.0559	0.2772
chr21	48129895	1650660	0.0343	0.2263
chr22	51304566	1390414	0.0271	0.1879
chrMT	16571	42916	2.5898	2.0829
chrX	155270560	11457888	0.0738	0.3466
chrY	59373566	348465	0.0059	0.1115

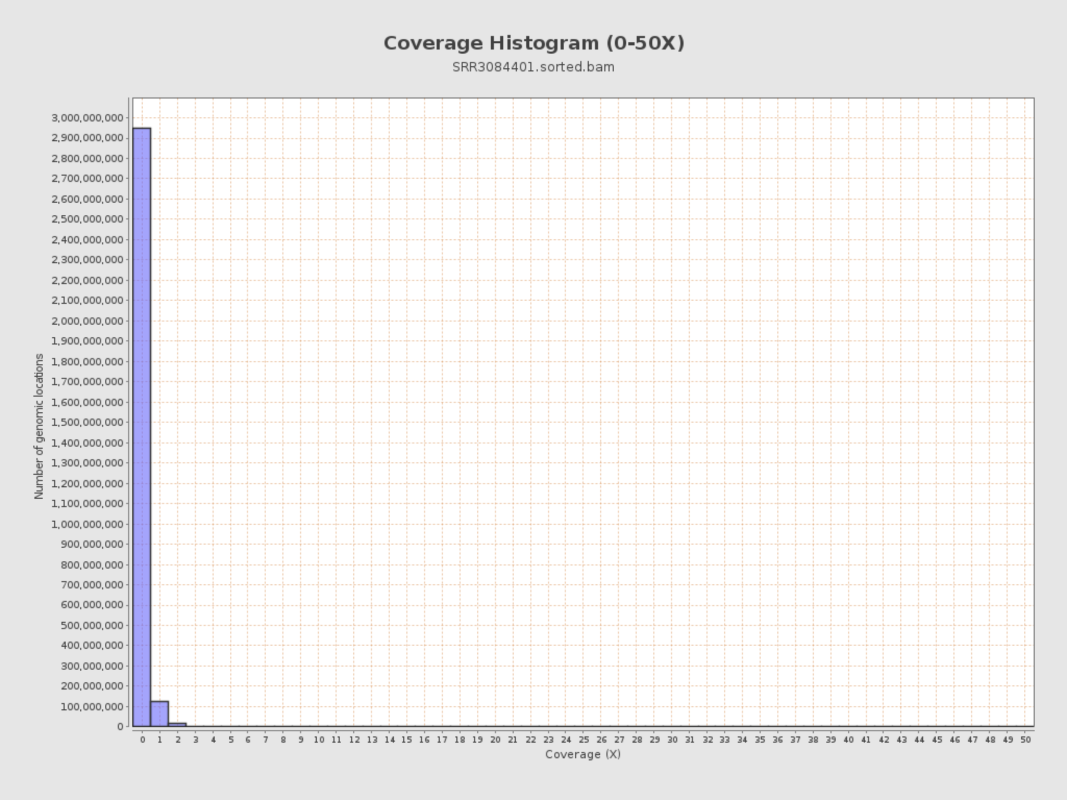
3. Results : Coverage across reference



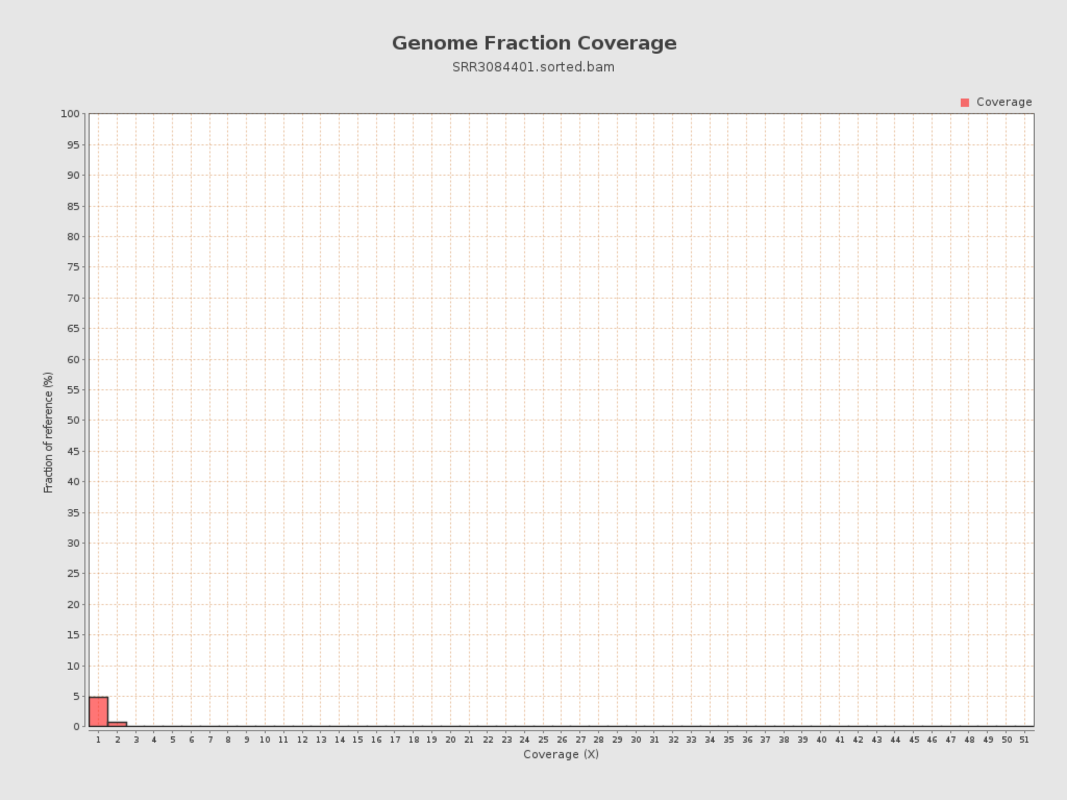
4. Results : Coverage Histogram



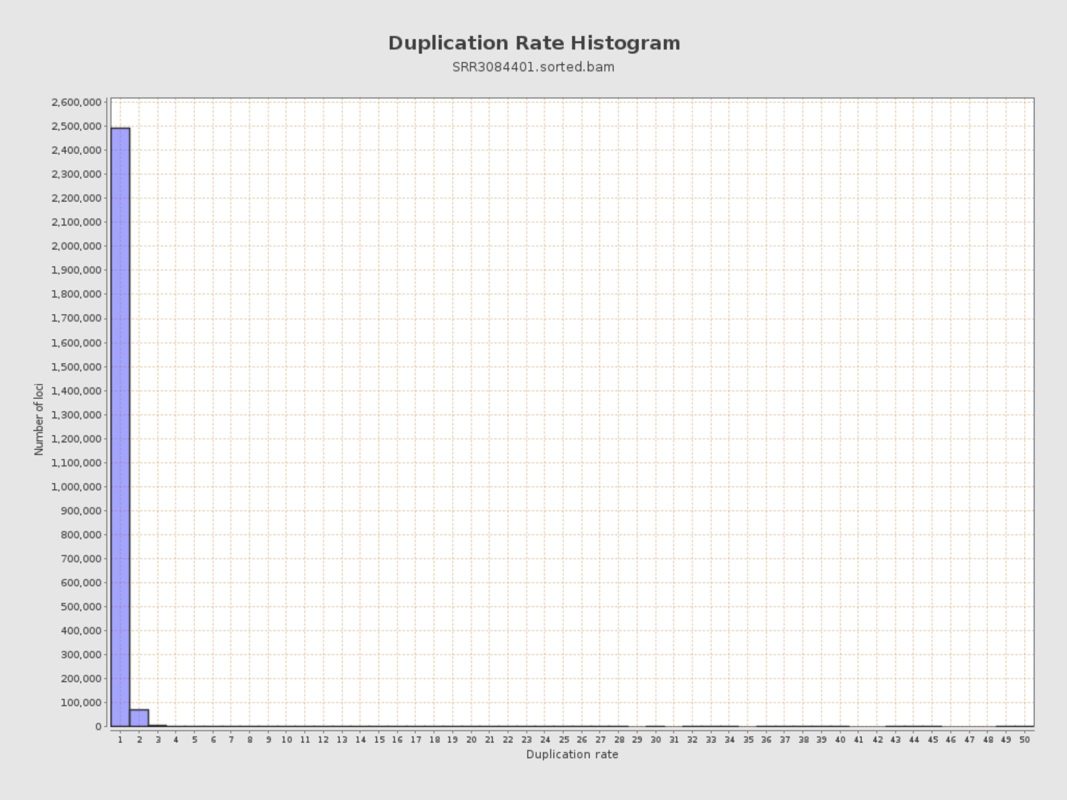
5. Results : Coverage Histogram (0-50X)



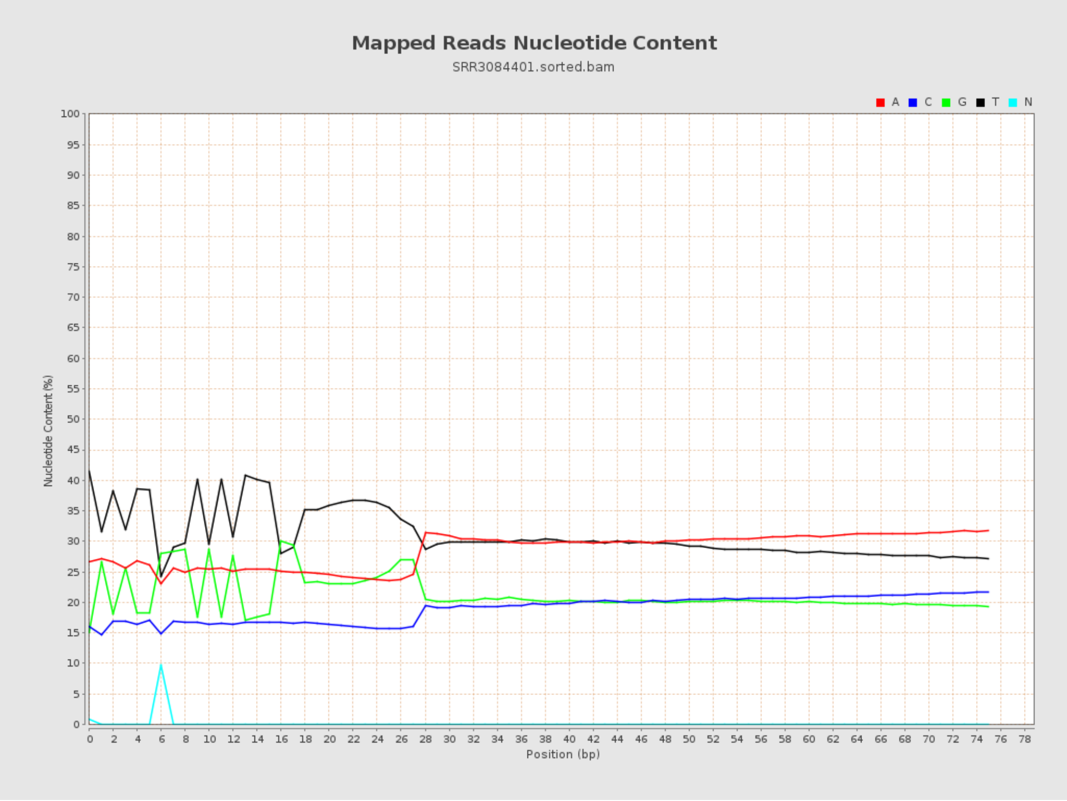
6. Results : Genome Fraction Coverage



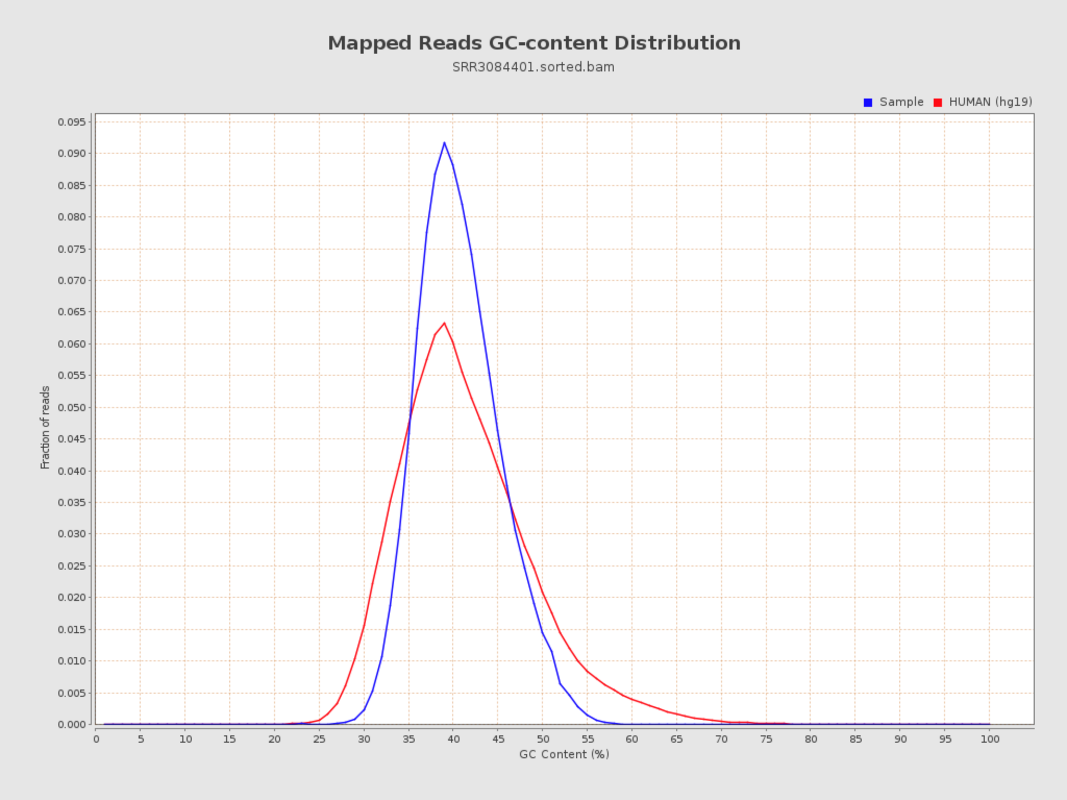
7. Results : Duplication Rate Histogram



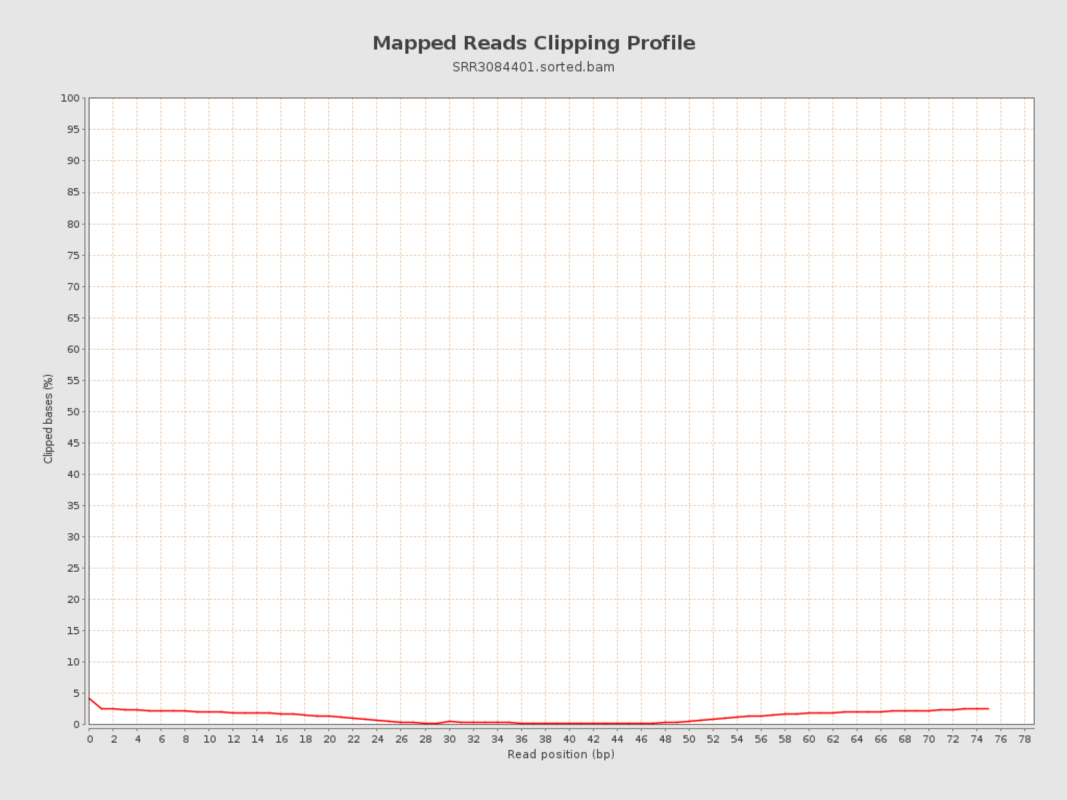
8. Results : Mapped Reads Nucleotide Content



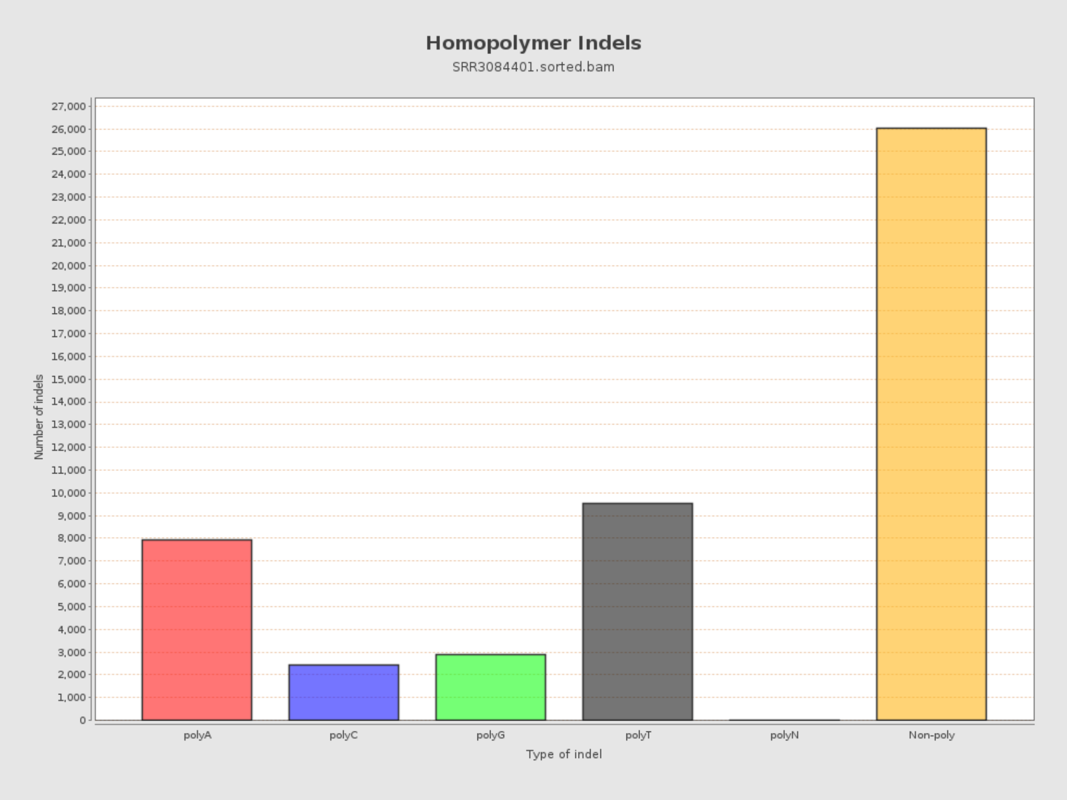
9. Results : Mapped Reads GC-content Distribution



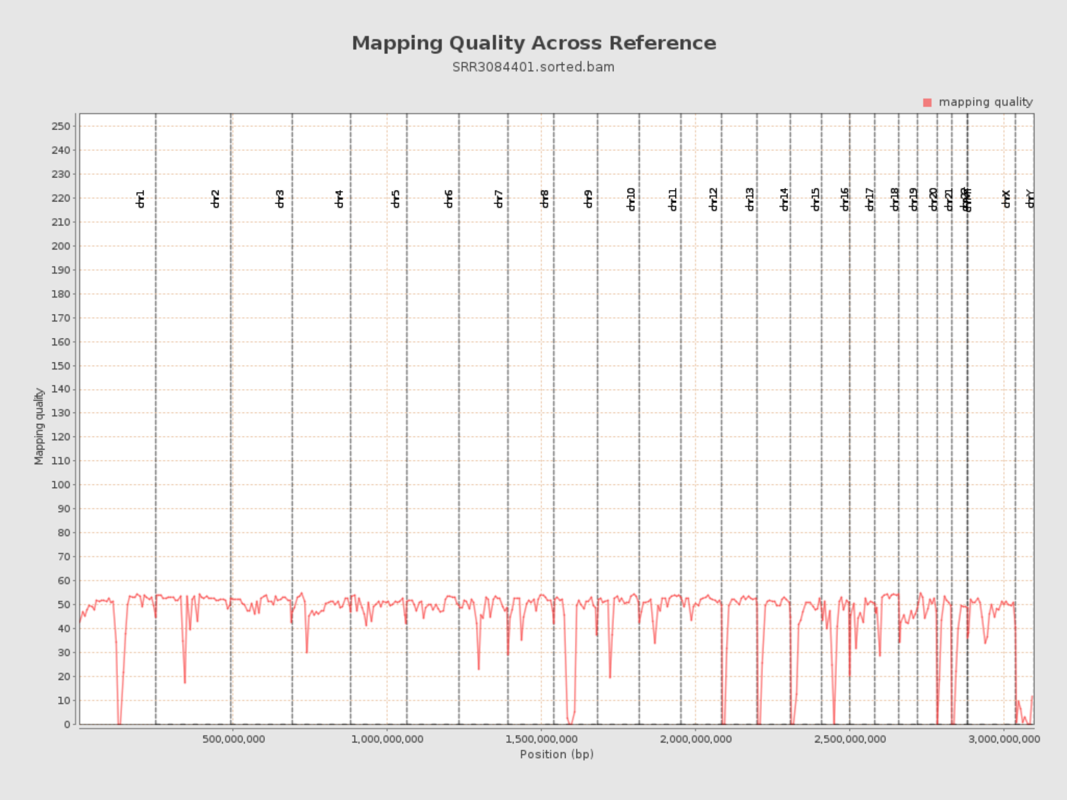
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram