Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 07:36:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080640.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_SRR3080640 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080640.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 07:36:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080640.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,104,241
Mapped reads	4,309,406 / 84.43%
Unmapped reads	794,835 / 15.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,371 / 0.5%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	204,564 / 4.01%
Duplication rate	3.77%
Clipped reads	2,101,169 / 41.17%

2.2. ACGT Content

Number/percentage of A's	78,239,250 / 27.37%
Number/percentage of C's	50,757,110 / 17.76%
Number/percentage of T's	92,797,883 / 32.46%
Number/percentage of G's	63,839,637 / 22.33%
Number/percentage of N's	234,207 / 0.08%
GC Percentage	40.09%

2.3. Coverage

Mean	0.0924

Standard Deviation	0.6383

2.4. Mapping Quality

Mean Mapping Quality	46.4

2.5. Mismatches and indels

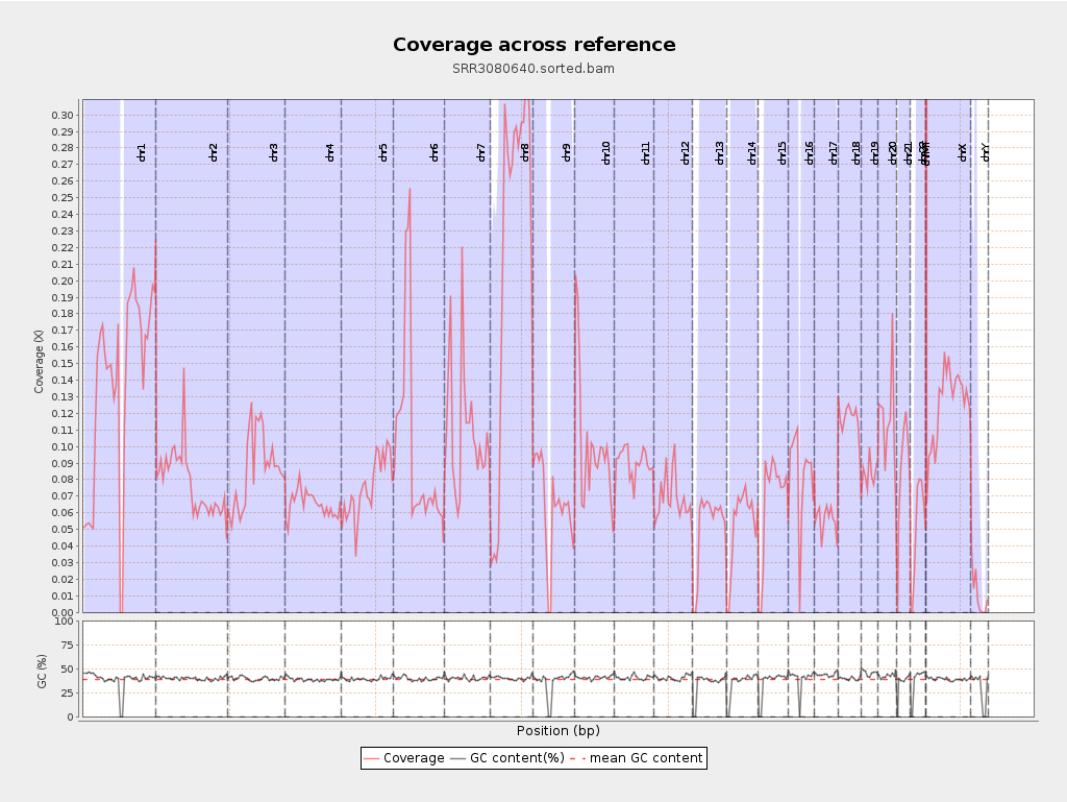
General error rate	0.9%
Mismatches	2,543,584
Insertions	24,010
Mapped reads with at least one insertion	0.55%
Deletions	69,226
Mapped reads with at least one deletion	1.59%
Homopolymer indels	47.85%

2.6. Chromosome stats

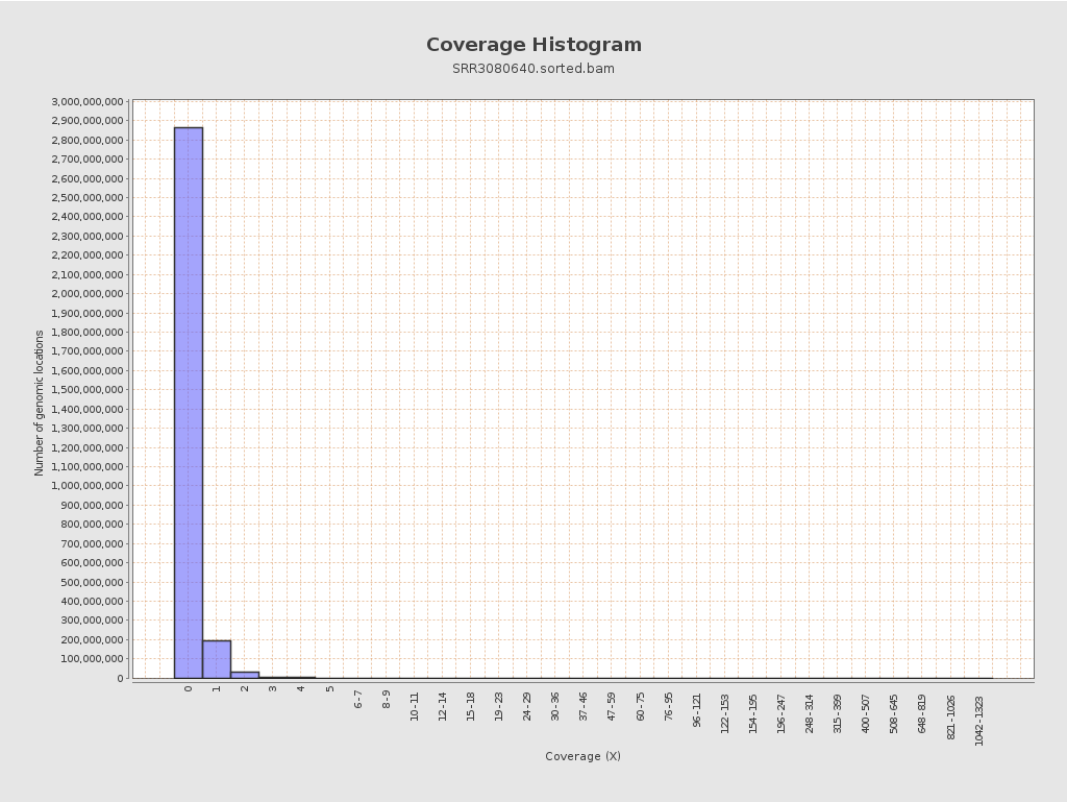
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	34275982	0.1375	0.8626
chr2	243199373	18907778	0.0777	0.7001
chr3	198022430	17137179	0.0865	0.3431
chr4	191154276	12496615	0.0654	0.3147
chr5	180915260	13549221	0.0749	0.3177
chr6	171115067	17009491	0.0994	0.6231
chr7	159138663	17488275	0.1099	1.6226

chr8	146364022	32151568	0.2197	0.8596
chr9	141213431	9032188	0.064	0.5084
chr10	135534747	13776513	0.1016	0.5208
chr11	135006516	12142869	0.0899	0.4385
chr12	133851895	9212099	0.0688	0.3136
chr13	115169878	5963372	0.0518	0.262
chr14	107349540	5705575	0.0531	0.312
chr15	102531392	6873450	0.067	0.3041
chr16	90354753	7292912	0.0807	0.3655
chr17	81195210	4588751	0.0565	0.3038
chr18	78077248	9139343	0.1171	0.8483
chr19	59128983	4969471	0.084	0.5848
chr20	63025520	7370713	0.1169	0.418
chr21	48129895	4066981	0.0845	0.3671
chr22	51304566	2627238	0.0512	0.2599
chrMT	16571	146219	8.8238	11.7267
chrX	155270560	19433673	0.1252	0.4764
chrY	59373566	623345	0.0105	0.1829

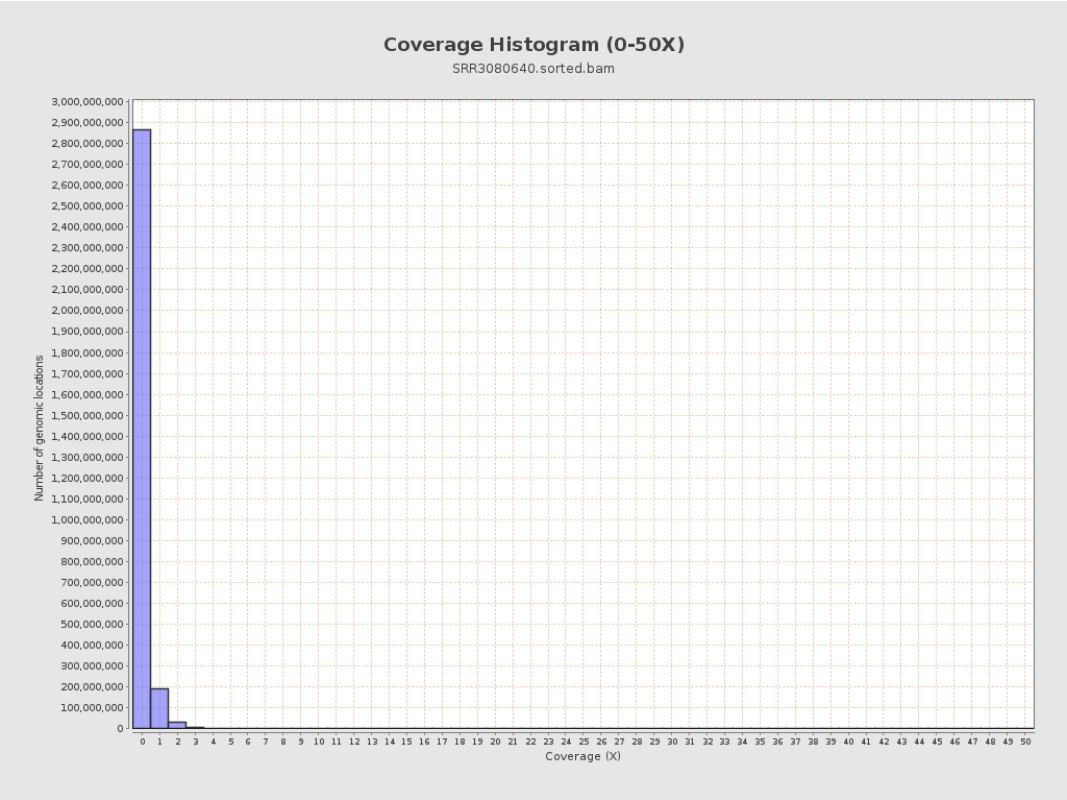
3. Results : Coverage across reference



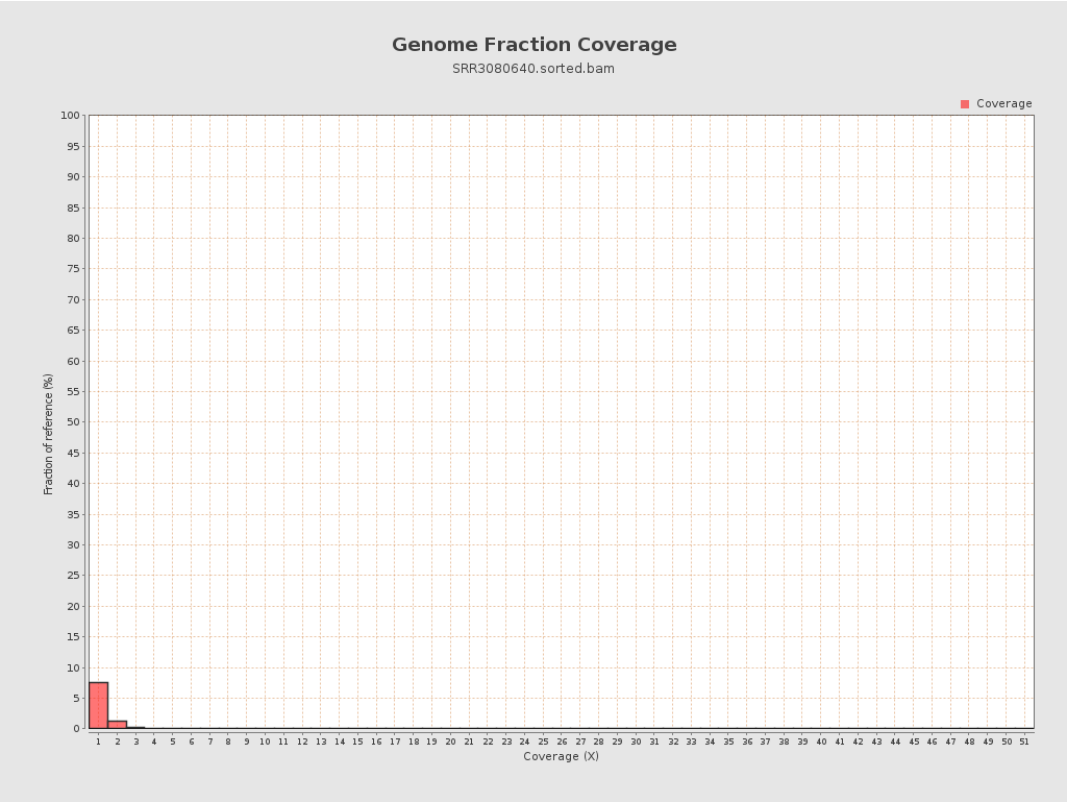
4. Results : Coverage Histogram



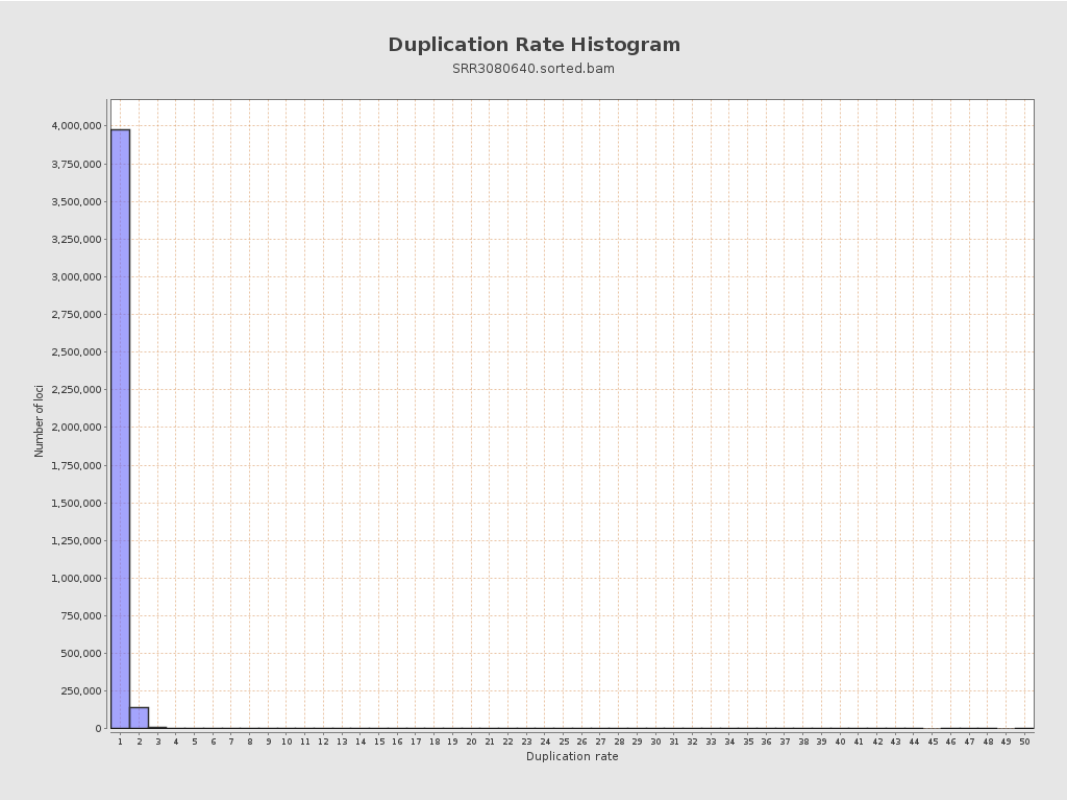
5. Results : Coverage Histogram (0-50X)



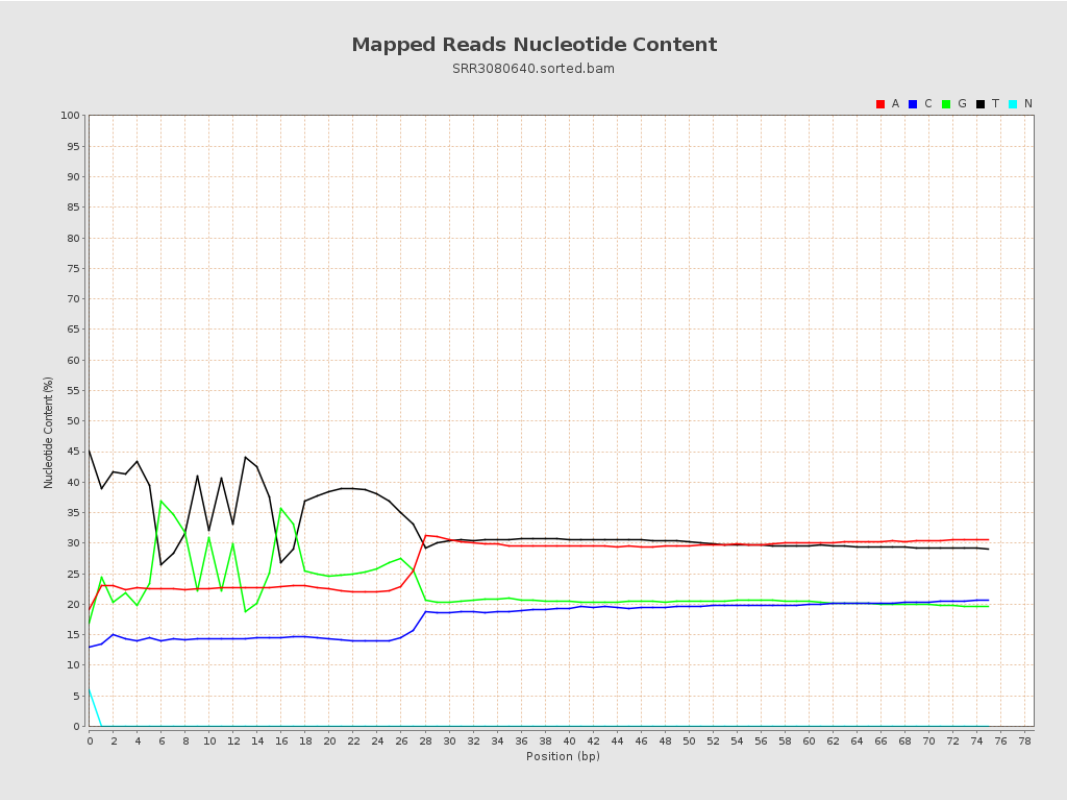
6. Results : Genome Fraction Coverage



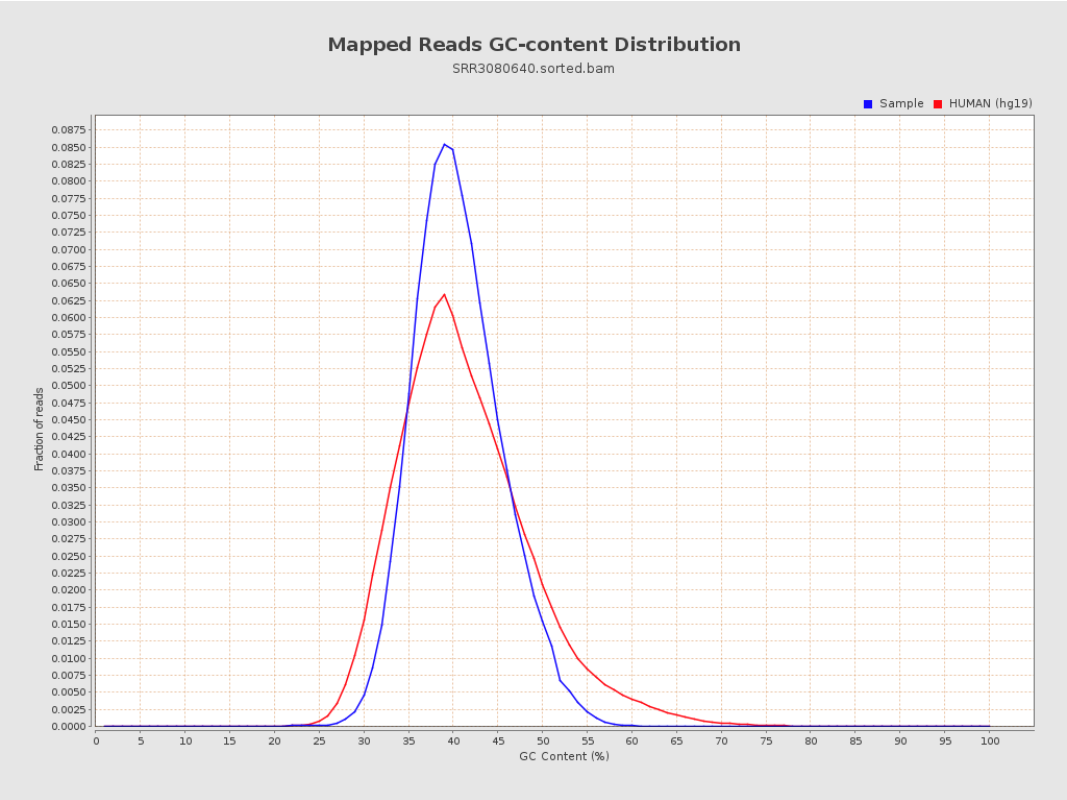
7. Results : Duplication Rate Histogram



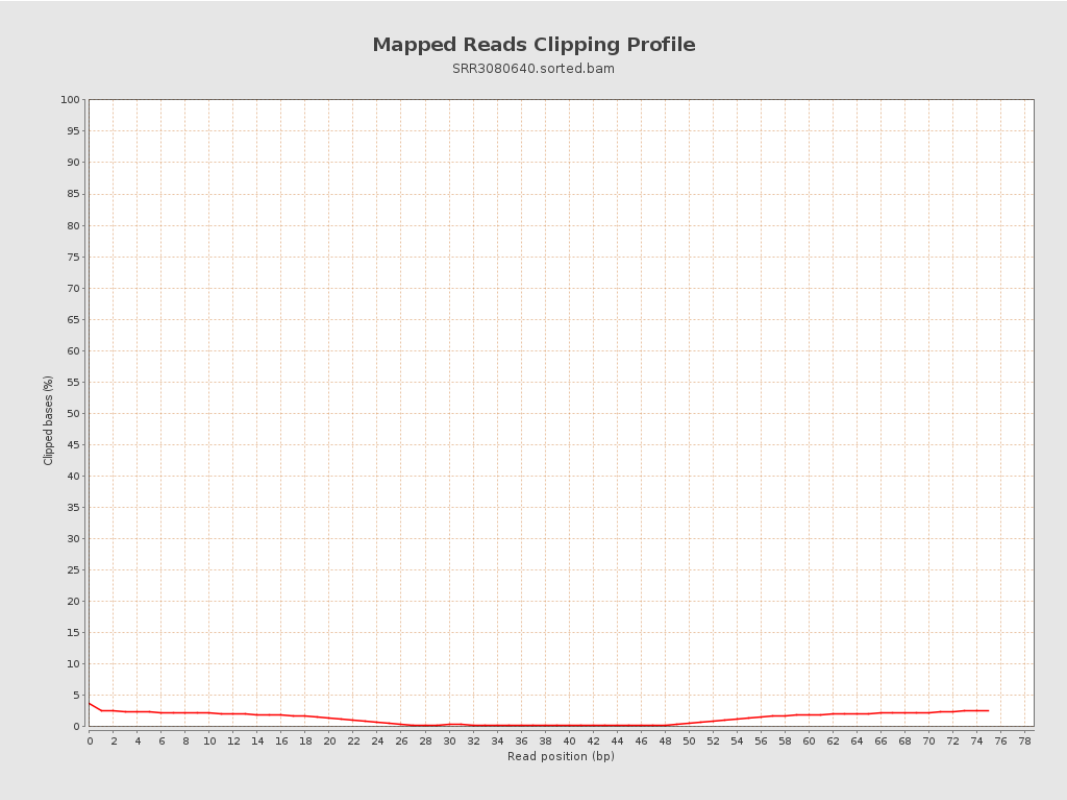
8. Results : Mapped Reads Nucleotide Content



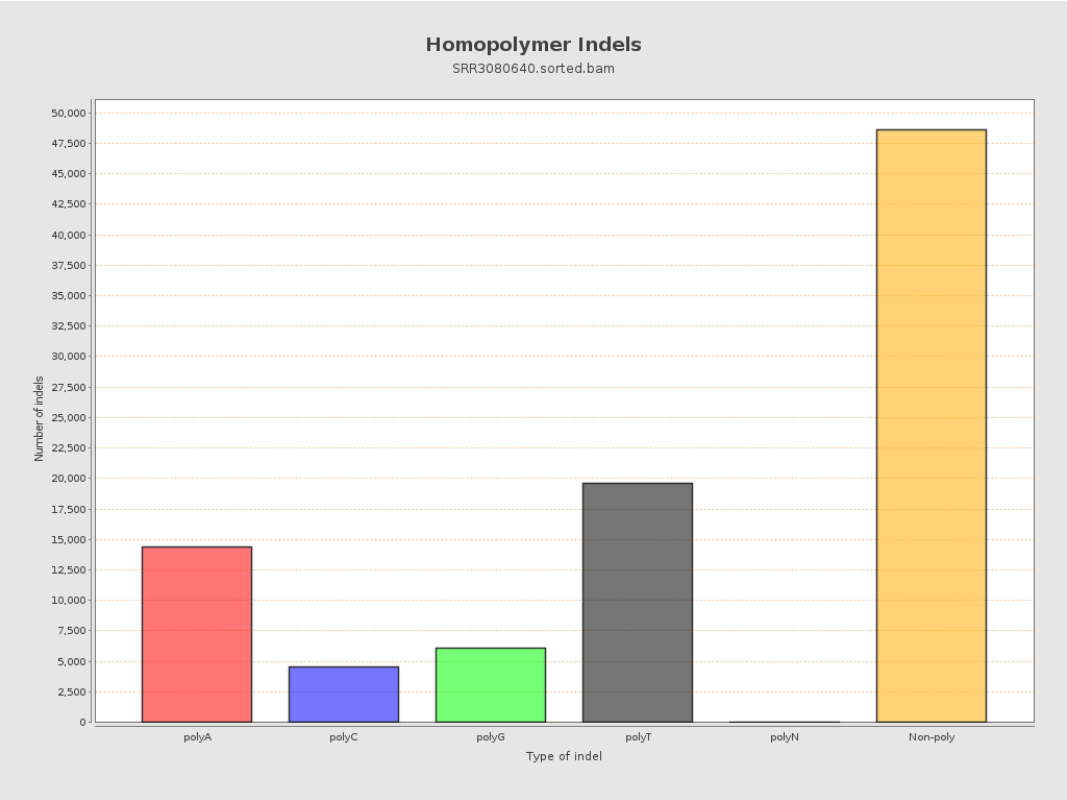
9. Results : Mapped Reads GC-content Distribution



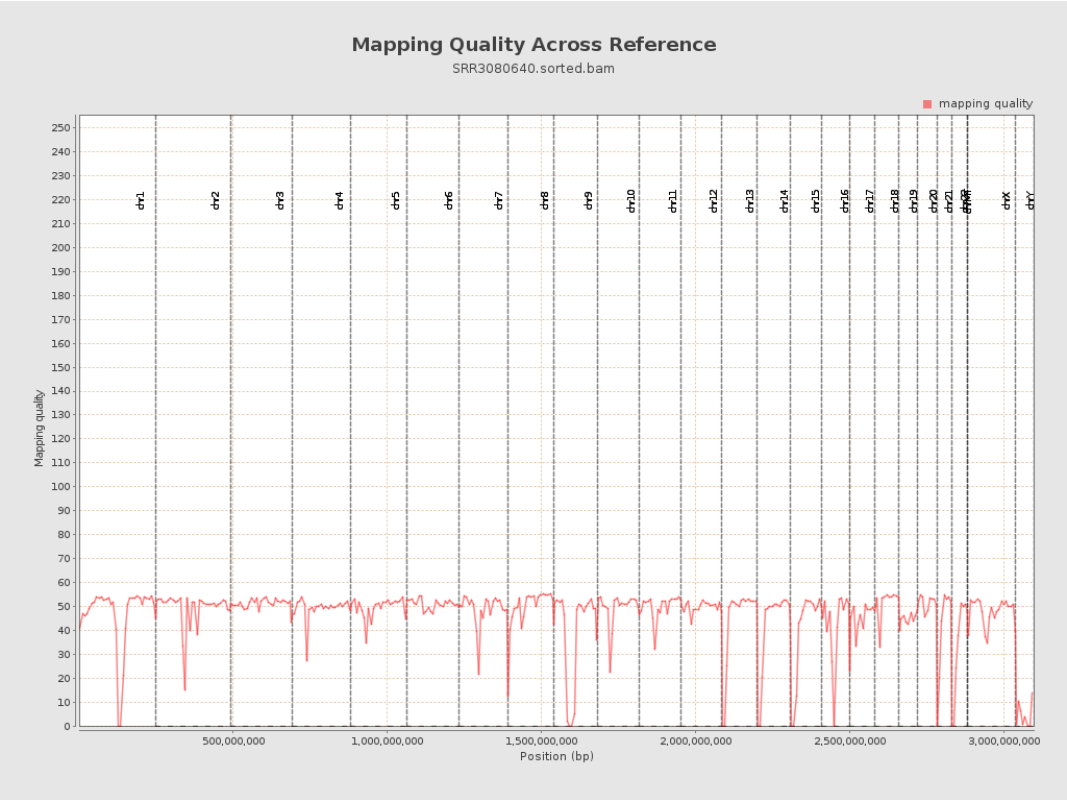
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram