Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 19:00:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080697.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_SRR3080697 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080697.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 19:00:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080697.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,961,010
Mapped reads	1,613,366 / 82.27%
Unmapped reads	347,644 / 17.73%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,592 / 0.85%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	105,938 / 5.4%
Duplication rate	5.61%
Clipped reads	655,137 / 33.41%

2.2. ACGT Content

Number/percentage of A's	31,674,571 / 28.94%
Number/percentage of C's	19,955,829 / 18.24%
Number/percentage of T's	34,775,885 / 31.78%
Number/percentage of G's	23,025,211 / 21.04%
Number/percentage of N's	1,586 / 0%
GC Percentage	39.28%

2.3. Coverage

Mean	0.0354

Standard Deviation	0.3107

2.4. Mapping Quality

Mean Mapping Quality	47.21

2.5. Mismatches and indels

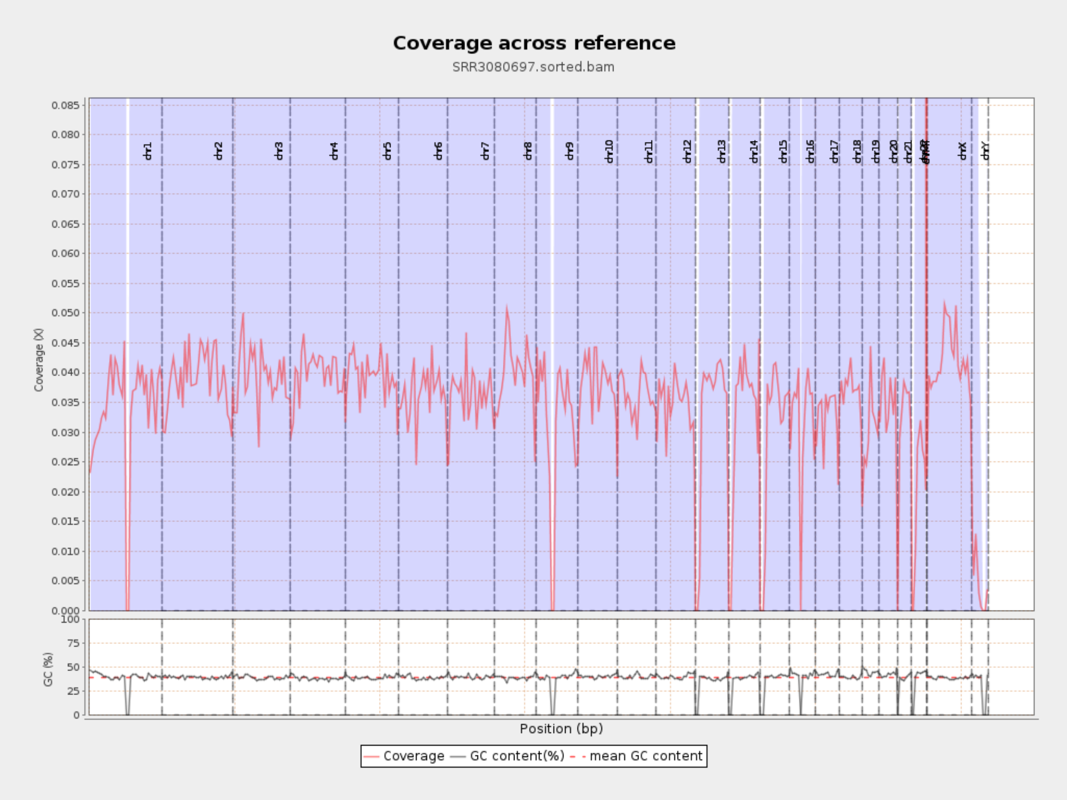
General error rate	0.81%
Mismatches	872,415
Insertions	8,542
Mapped reads with at least one insertion	0.52%
Deletions	23,031
Mapped reads with at least one deletion	1.41%
Homopolymer indels	47.93%

2.6. Chromosome stats

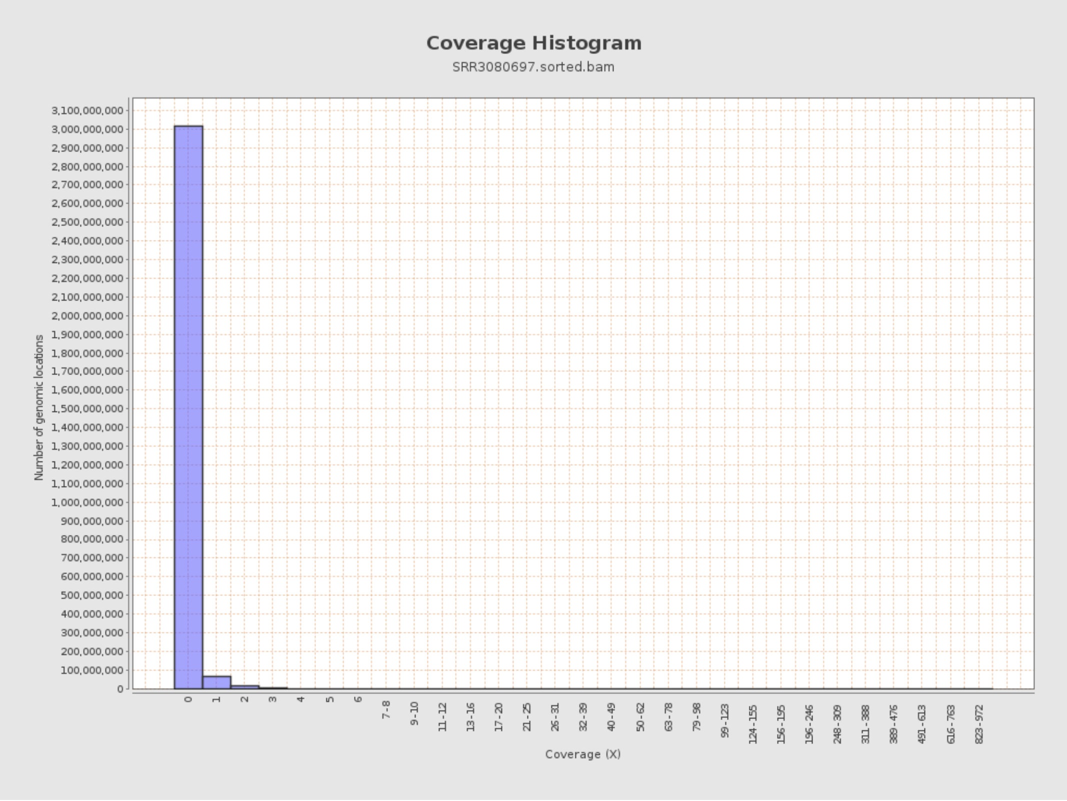
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8418465	0.0338	0.4194
chr2	243199373	9481080	0.039	0.3249
chr3	198022430	7798702	0.0394	0.2514
chr4	191154276	7606714	0.0398	0.2589
chr5	180915260	7188180	0.0397	0.2529
chr6	171115067	6229248	0.0364	0.2513
chr7	159138663	5815832	0.0365	0.3314

chr8	146364022	5832596	0.0398	0.6496
chr9	141213431	4423864	0.0313	0.2481
chr10	135534747	5241219	0.0387	0.2843
chr11	135006516	4878750	0.0361	0.2667
chr12	133851895	4659960	0.0348	0.2376
chr13	115169878	3701383	0.0321	0.2296
chr14	107349540	3378921	0.0315	0.2303
chr15	102531392	3003968	0.0293	0.2167
chr16	90354753	2856856	0.0316	0.2282
chr17	81195210	2629967	0.0324	0.2398
chr18	78077248	2914523	0.0373	0.3595
chr19	59128983	1811563	0.0306	0.3435
chr20	63025520	2222246	0.0353	0.2416
chr21	48129895	1494661	0.0311	0.231
chr22	51304566	978929	0.0191	0.1697
chrMT	16571	185214	11.177	6.6166
chrX	155270560	6464987	0.0416	0.2697
chrY	59373566	255646	0.0043	0.1081

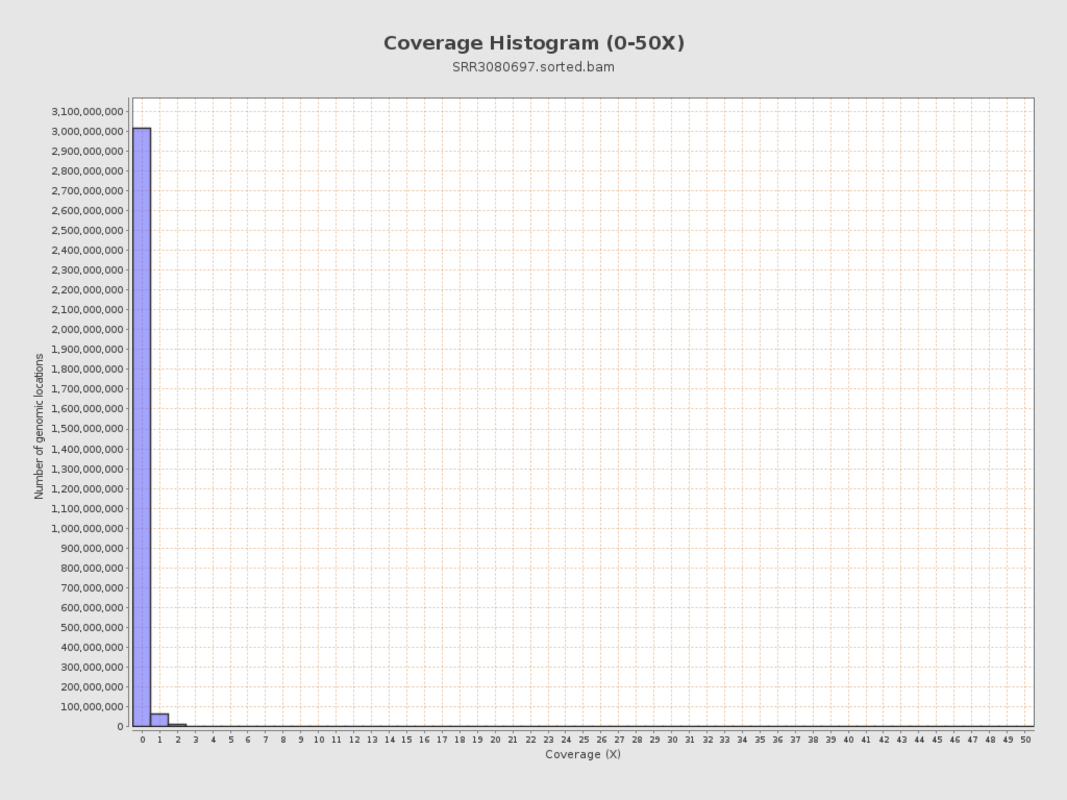
3. Results : Coverage across reference



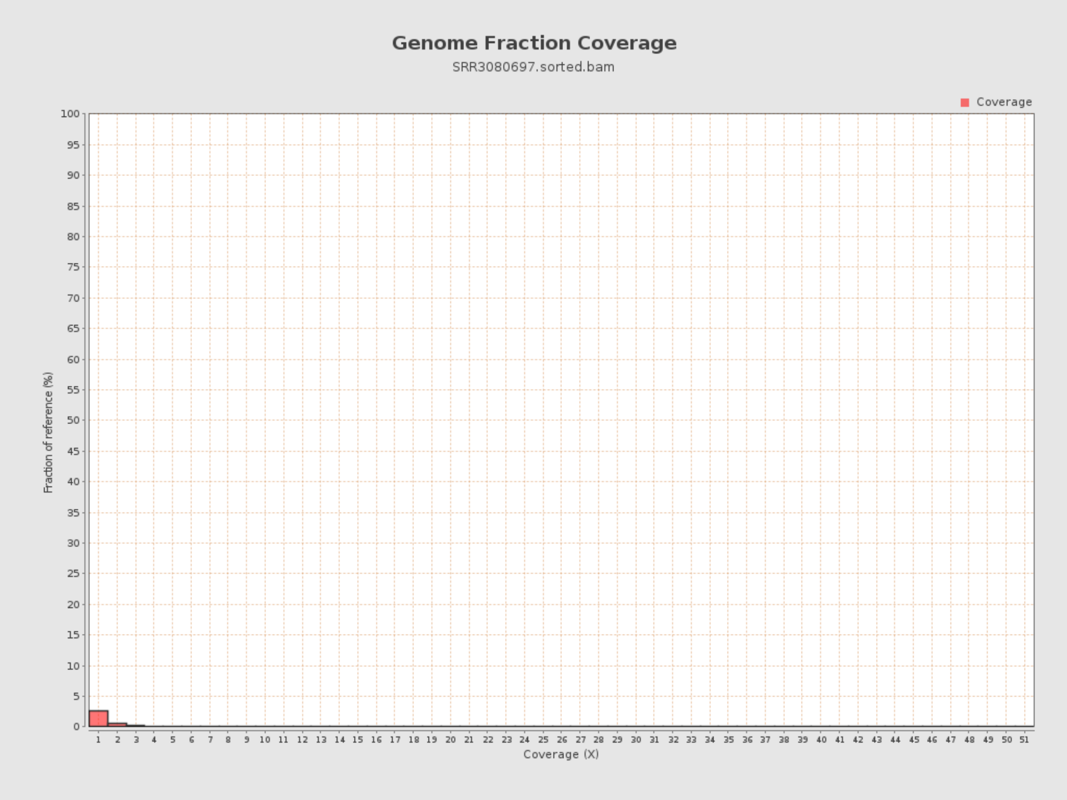
4. Results : Coverage Histogram



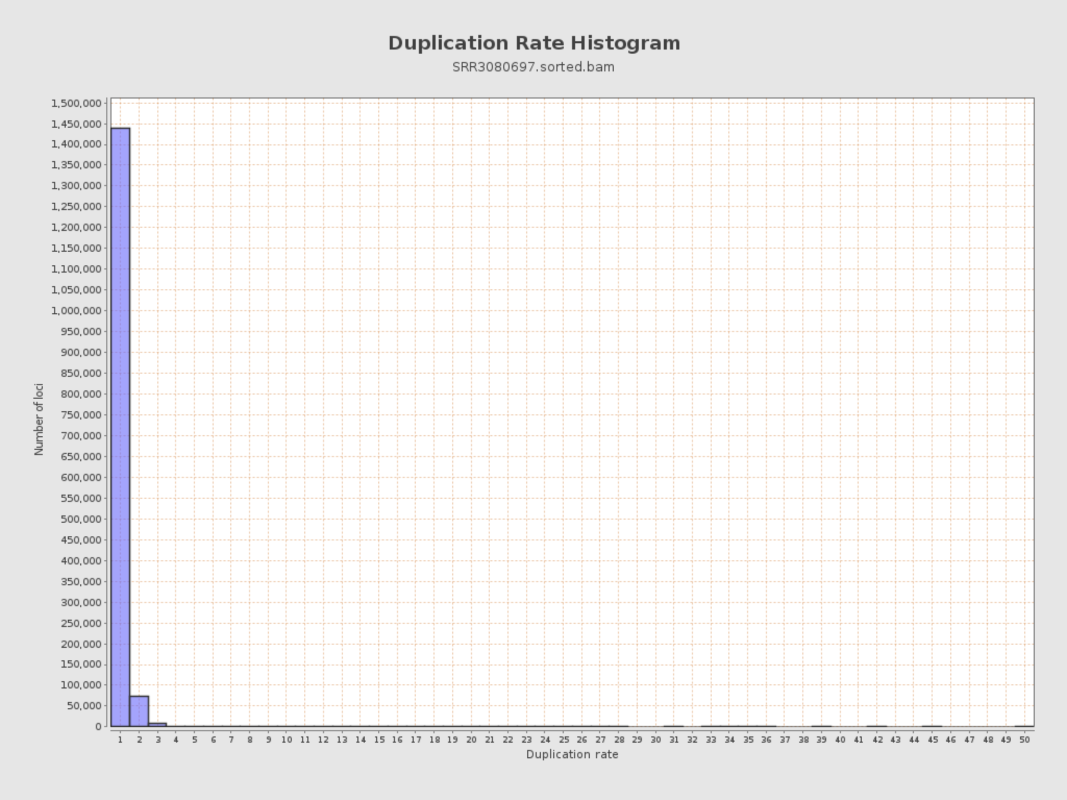
5. Results : Coverage Histogram (0-50X)



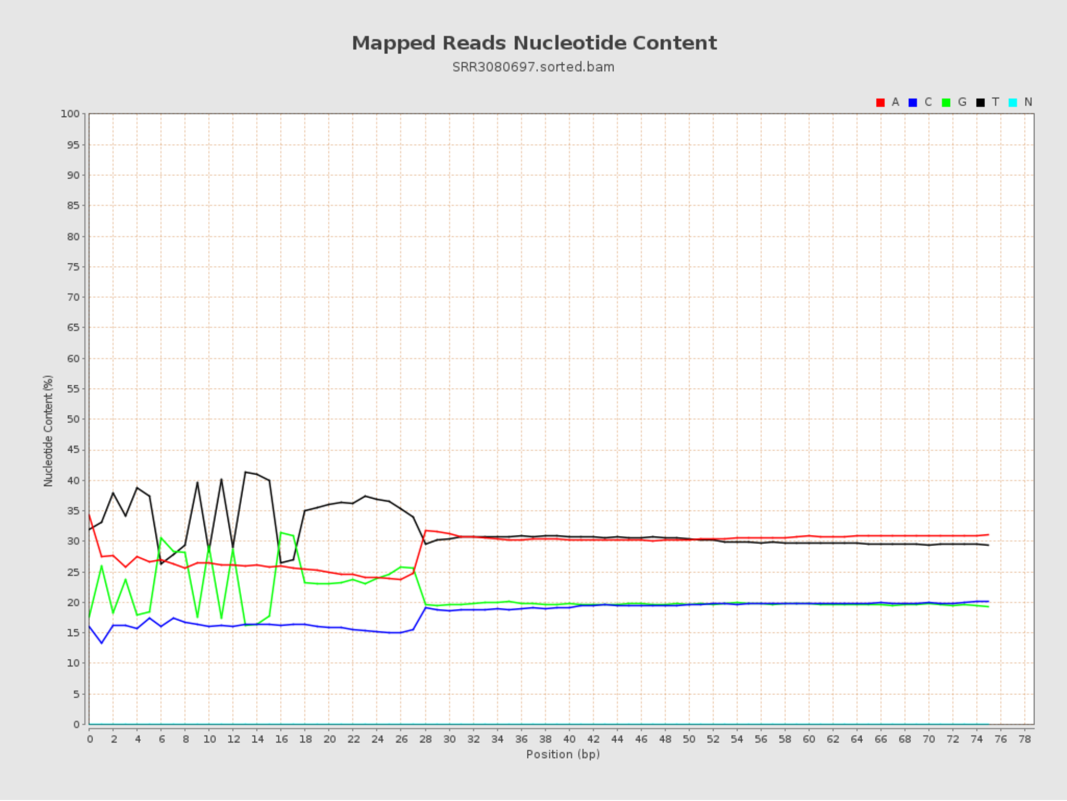
6. Results : Genome Fraction Coverage



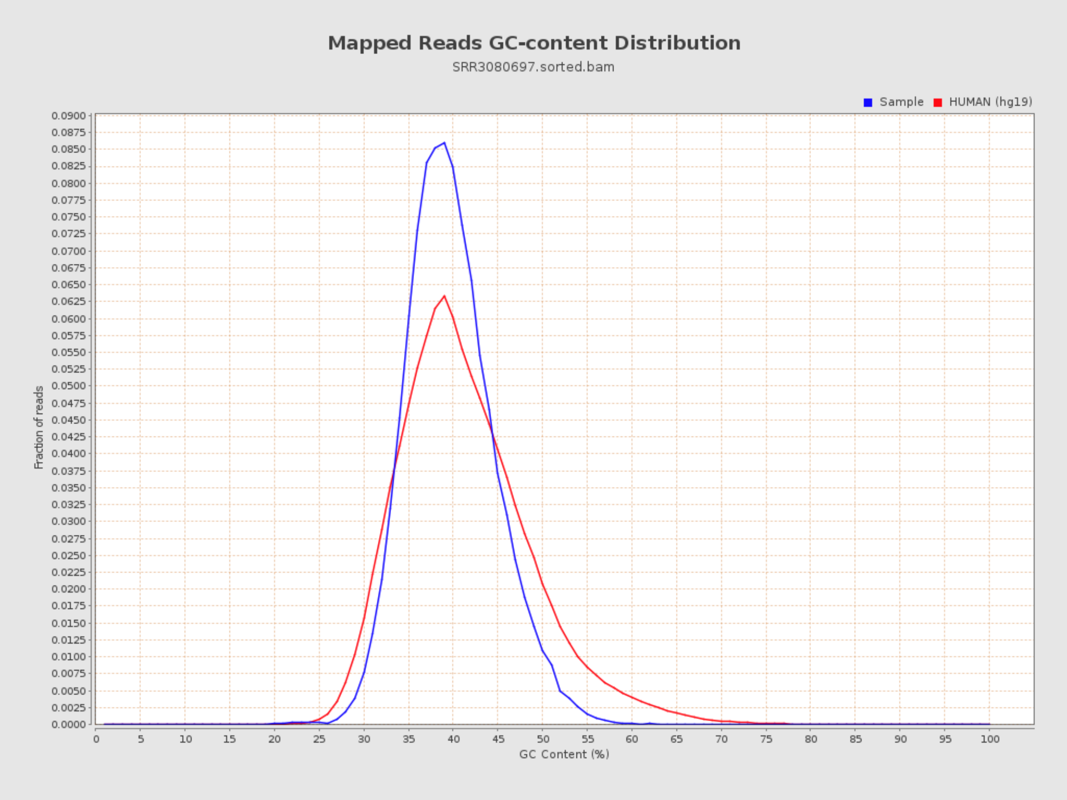
7. Results : Duplication Rate Histogram



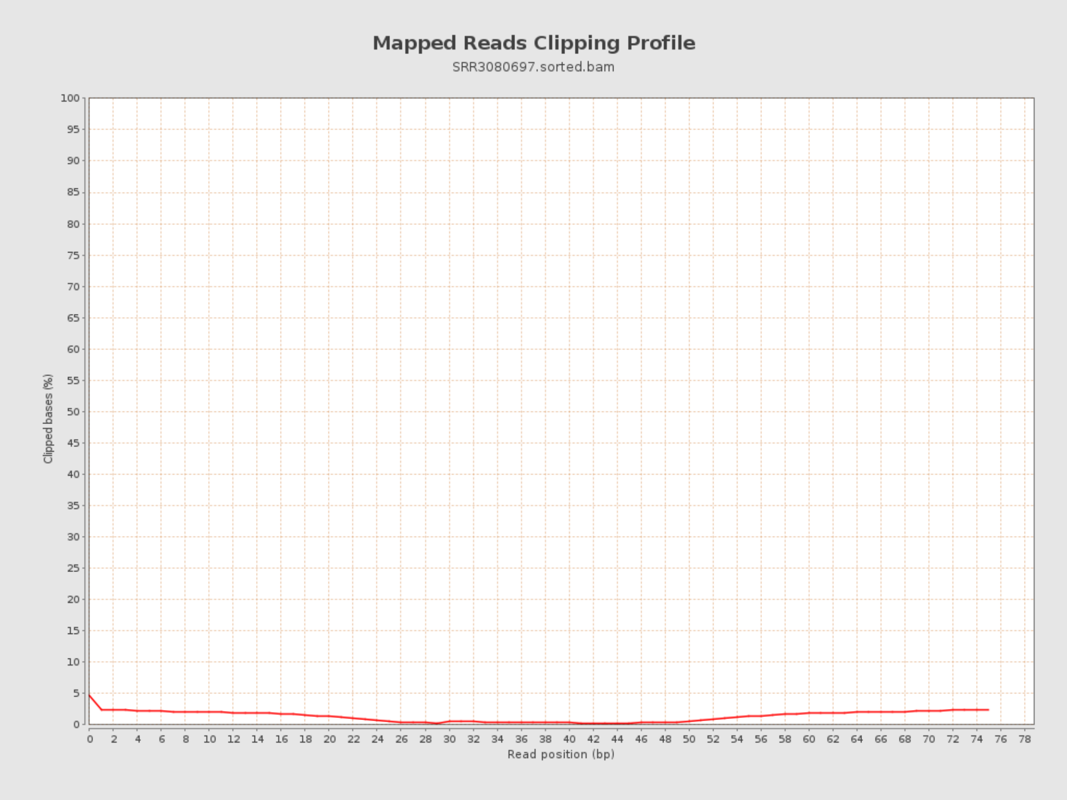
8. Results : Mapped Reads Nucleotide Content



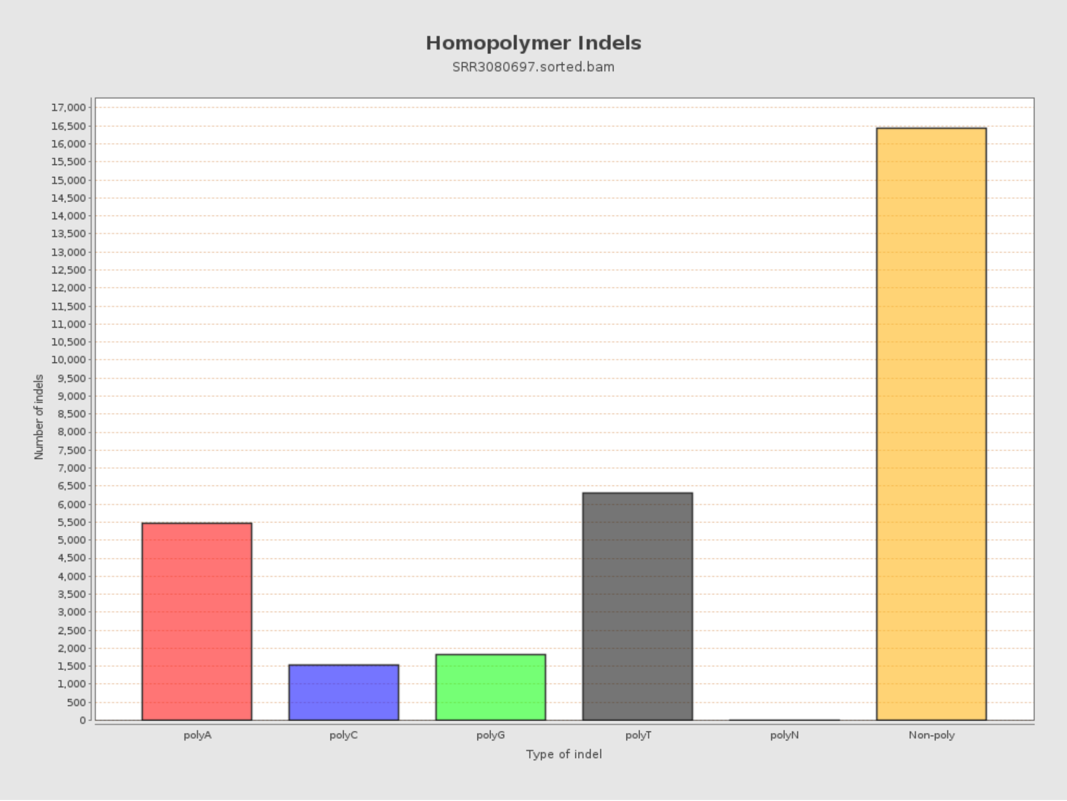
9. Results : Mapped Reads GC-content Distribution



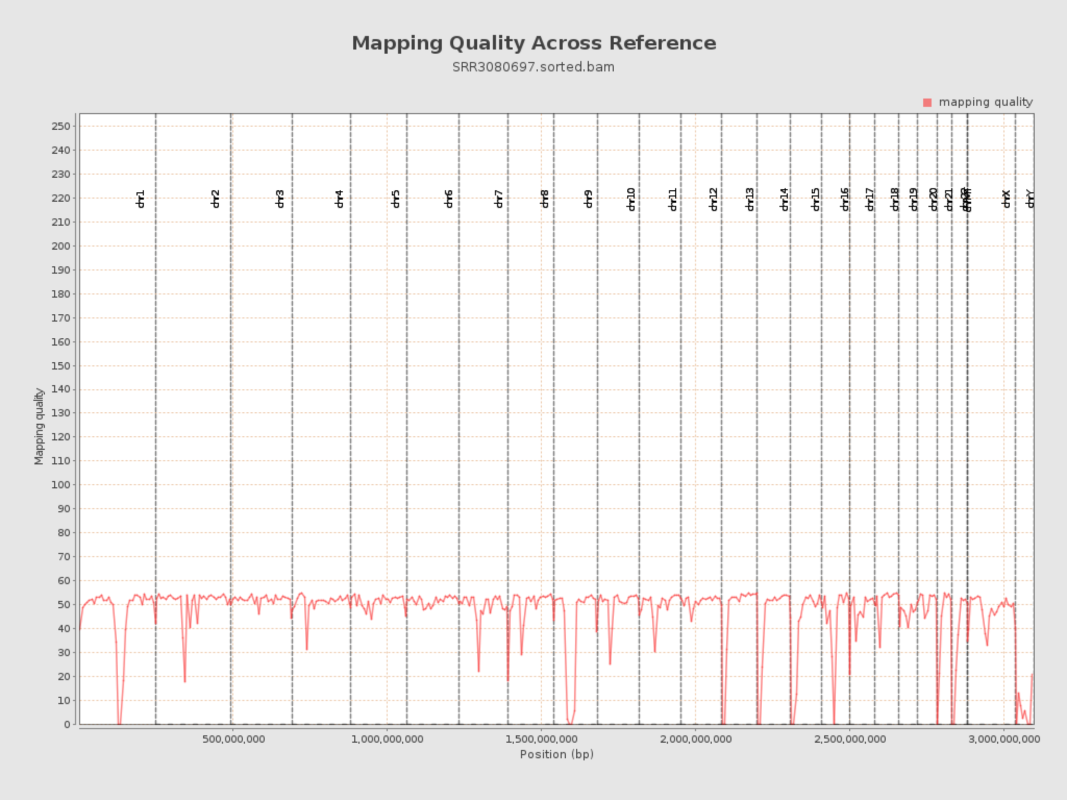
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram