Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 19:28:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080699.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_SRR3080699 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080699.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 19:28:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080699.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,203,422
Mapped reads	1,914,986 / 86.91%
Unmapped reads	288,436 / 13.09%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,668 / 0.85%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	129,427 / 5.87%
Duplication rate	5.62%
Clipped reads	791,676 / 35.93%

2.2. ACGT Content

Number/percentage of A's	37,334,672 / 28.81%
Number/percentage of C's	23,554,568 / 18.18%
Number/percentage of T's	41,392,987 / 31.94%
Number/percentage of G's	27,308,429 / 21.07%
Number/percentage of N's	1,793 / 0%
GC Percentage	39.25%

2.3. Coverage

Mean	0.0419

Standard Deviation	0.3846

2.4. Mapping Quality

Mean Mapping Quality	47.04

2.5. Mismatches and indels

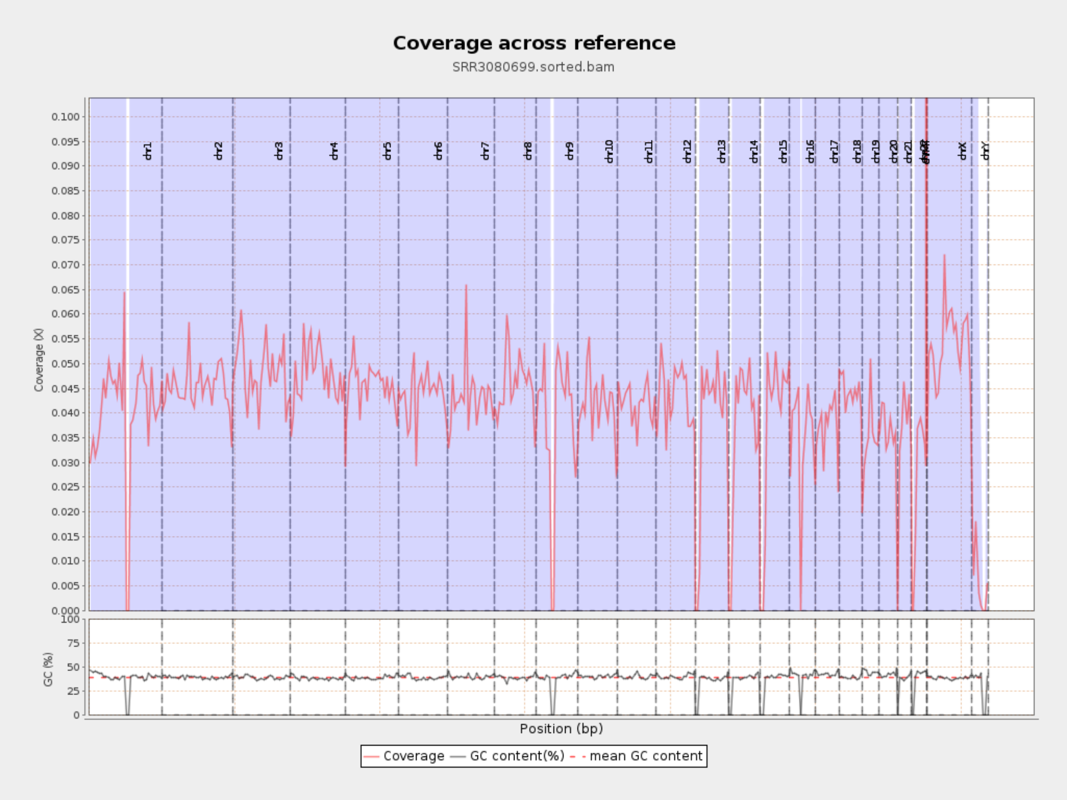
General error rate	0.84%
Mismatches	1,066,039
Insertions	10,133
Mapped reads with at least one insertion	0.52%
Deletions	27,397
Mapped reads with at least one deletion	1.42%
Homopolymer indels	47.73%

2.6. Chromosome stats

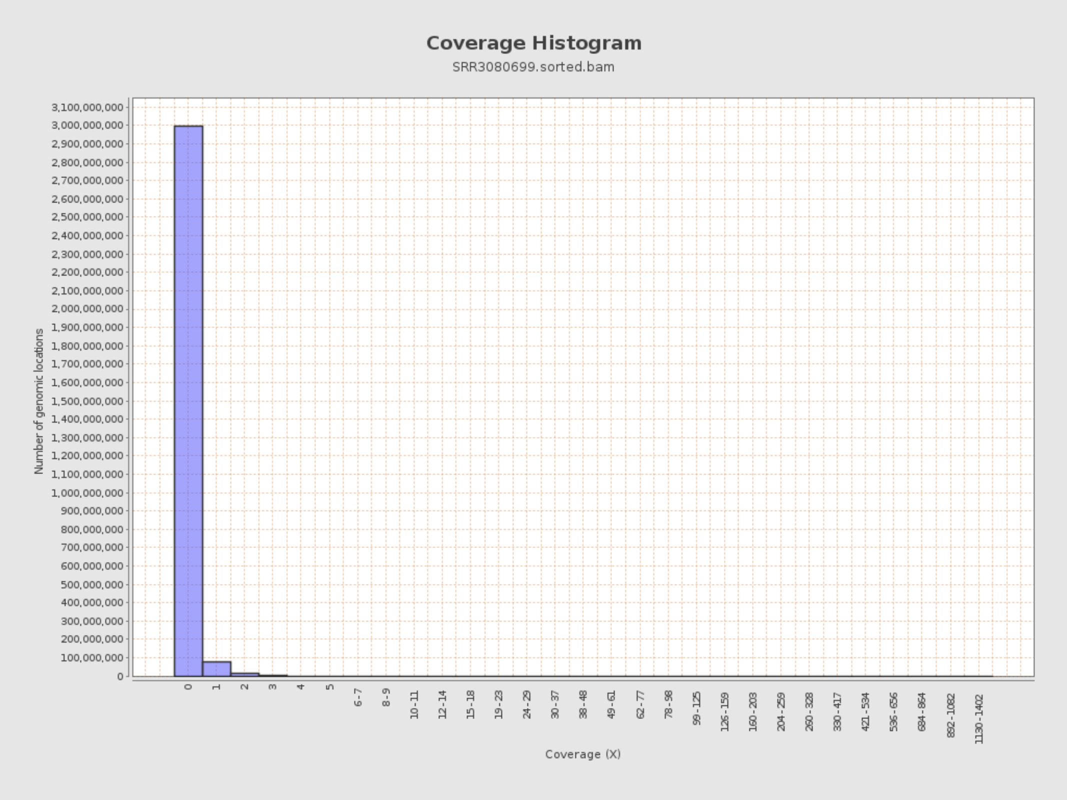
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10043432	0.0403	0.5812
chr2	243199373	11028585	0.0453	0.3864
chr3	198022430	9595510	0.0485	0.2786
chr4	191154276	9112572	0.0477	0.2877
chr5	180915260	8295634	0.0459	0.2705
chr6	171115067	7507878	0.0439	0.284
chr7	159138663	6901333	0.0434	0.4455

chr8	146364022	6685685	0.0457	0.8736
chr9	141213431	5456438	0.0386	0.313
chr10	135534747	5721551	0.0422	0.316
chr11	135006516	5650889	0.0419	0.3138
chr12	133851895	5829043	0.0435	0.2663
chr13	115169878	4308336	0.0374	0.2477
chr14	107349540	3891662	0.0363	0.2488
chr15	102531392	3836955	0.0374	0.2436
chr16	90354753	3166330	0.035	0.2469
chr17	81195210	3011916	0.0371	0.2534
chr18	78077248	3473973	0.0445	0.5018
chr19	59128983	2084269	0.0352	0.4127
chr20	63025520	2276815	0.0361	0.2438
chr21	48129895	1688966	0.0351	0.2491
chr22	51304566	1299138	0.0253	0.1962
chrMT	16571	76504	4.6167	3.2073
chrX	155270560	8350020	0.0538	0.3084
chrY	59373566	347248	0.0058	0.1529

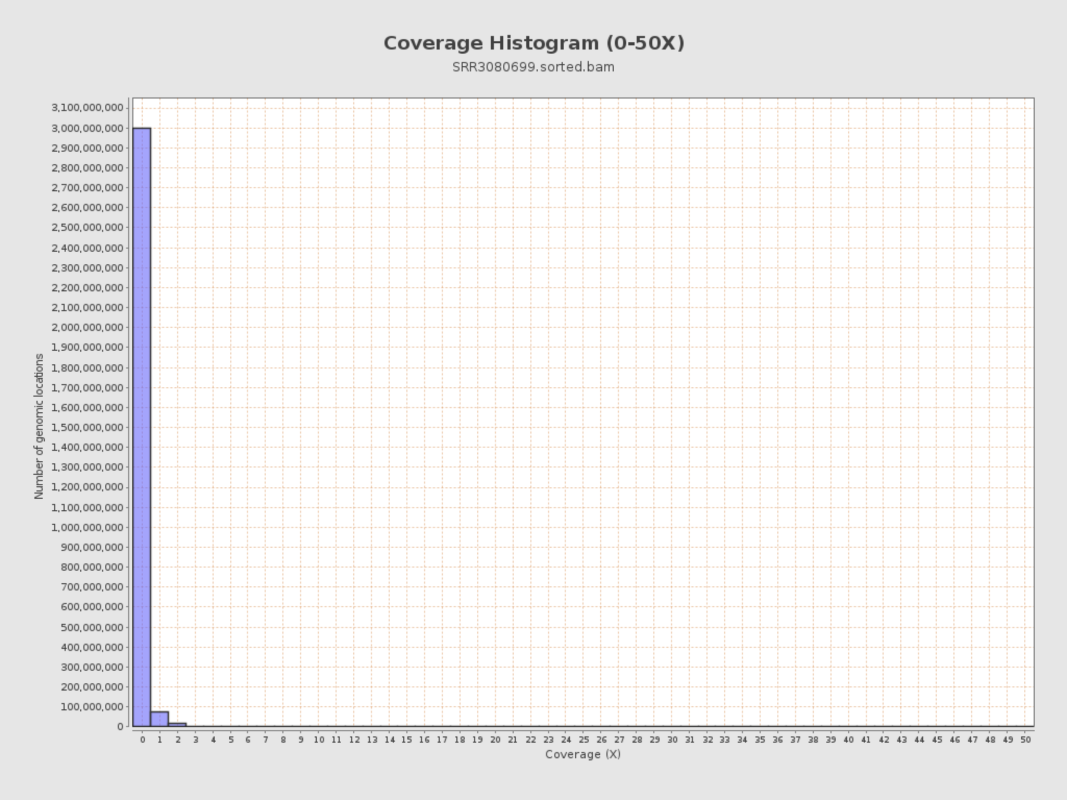
3. Results : Coverage across reference



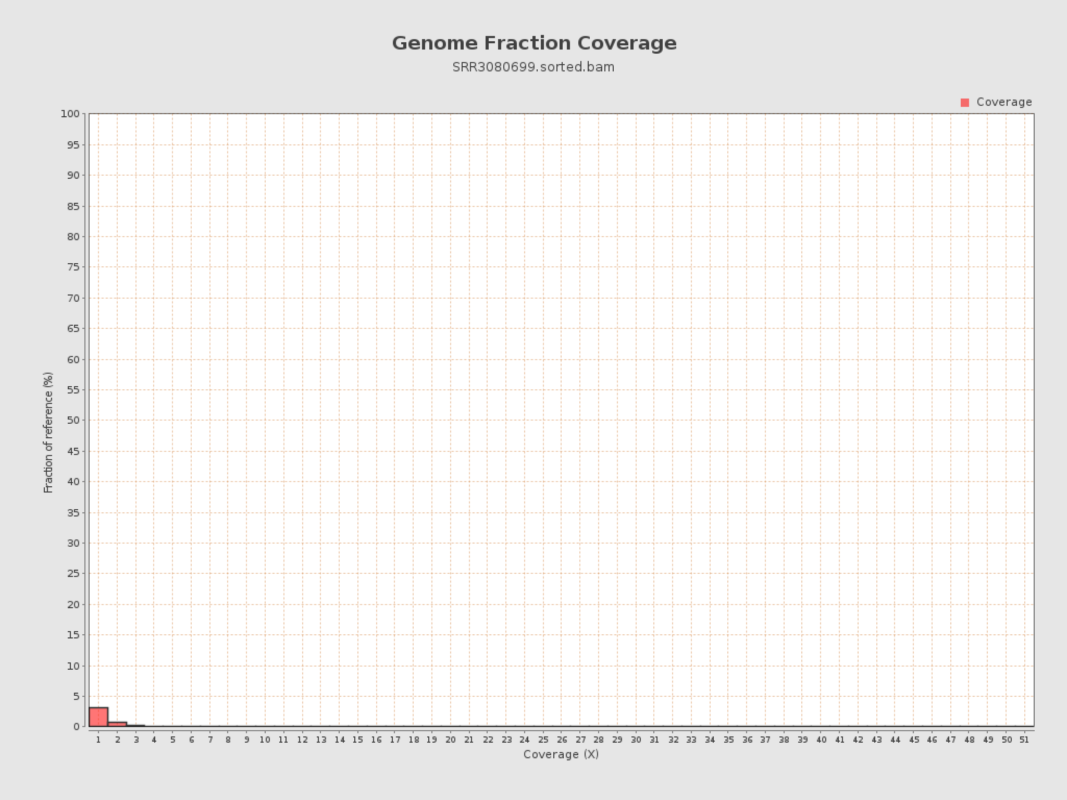
4. Results : Coverage Histogram



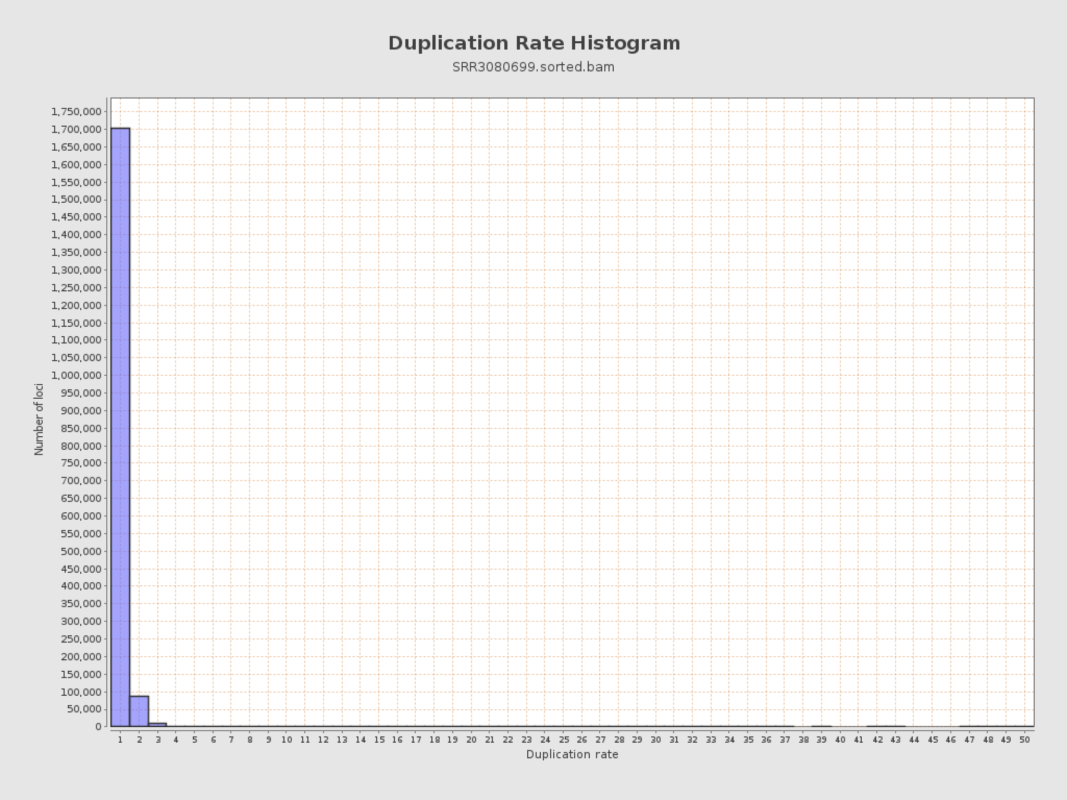
5. Results : Coverage Histogram (0-50X)



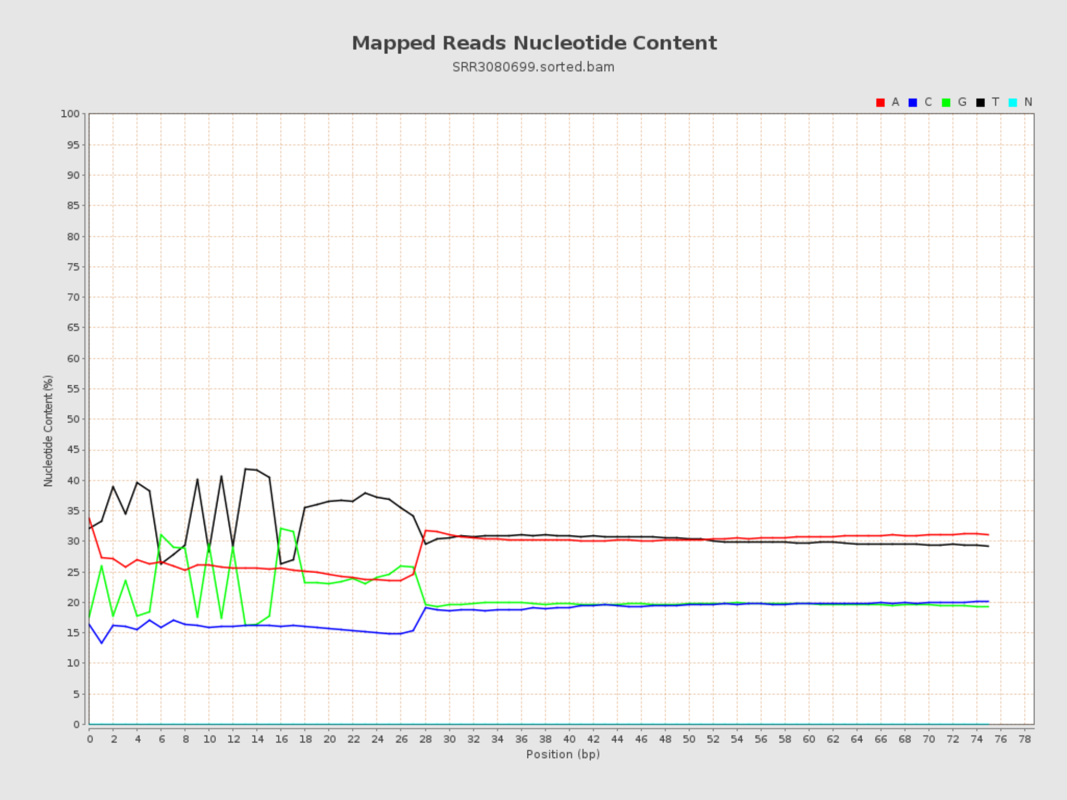
6. Results : Genome Fraction Coverage



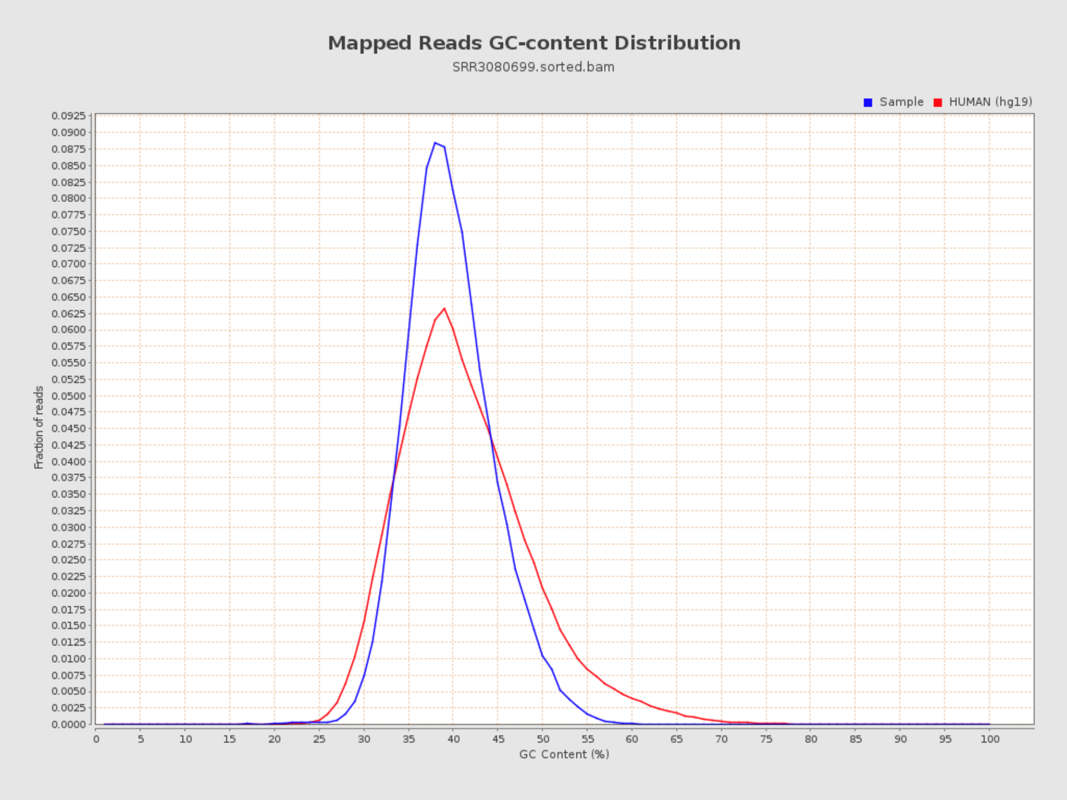
7. Results : Duplication Rate Histogram



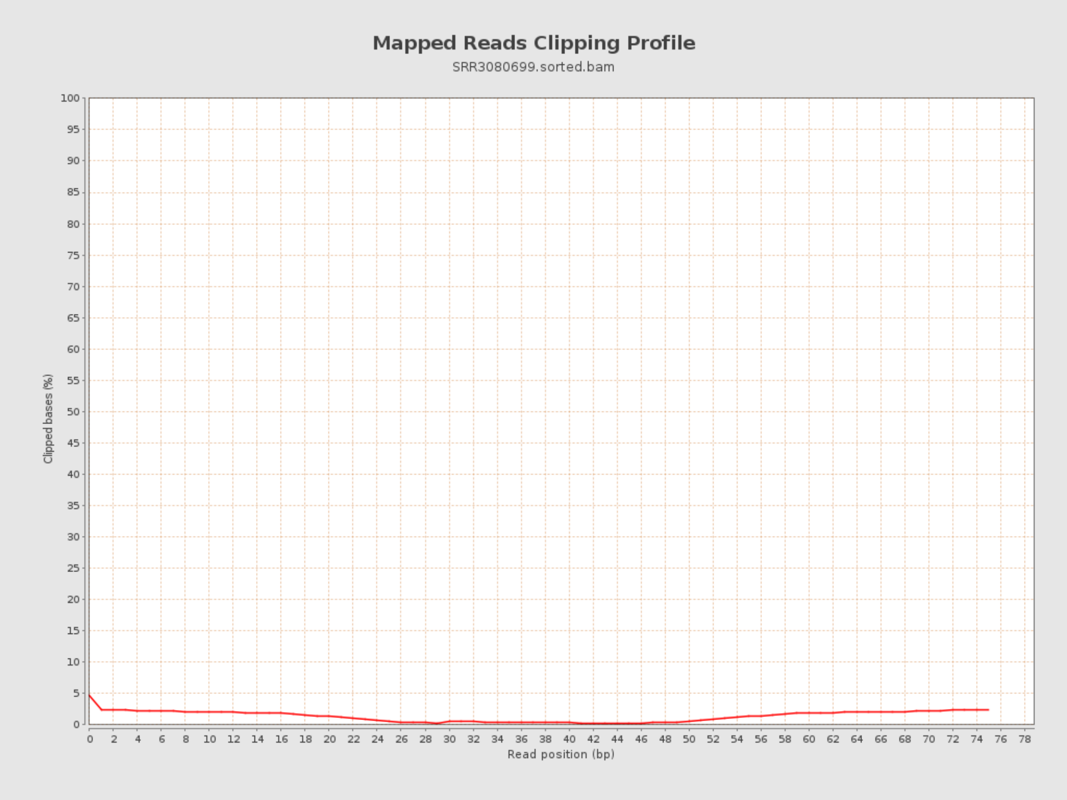
8. Results : Mapped Reads Nucleotide Content



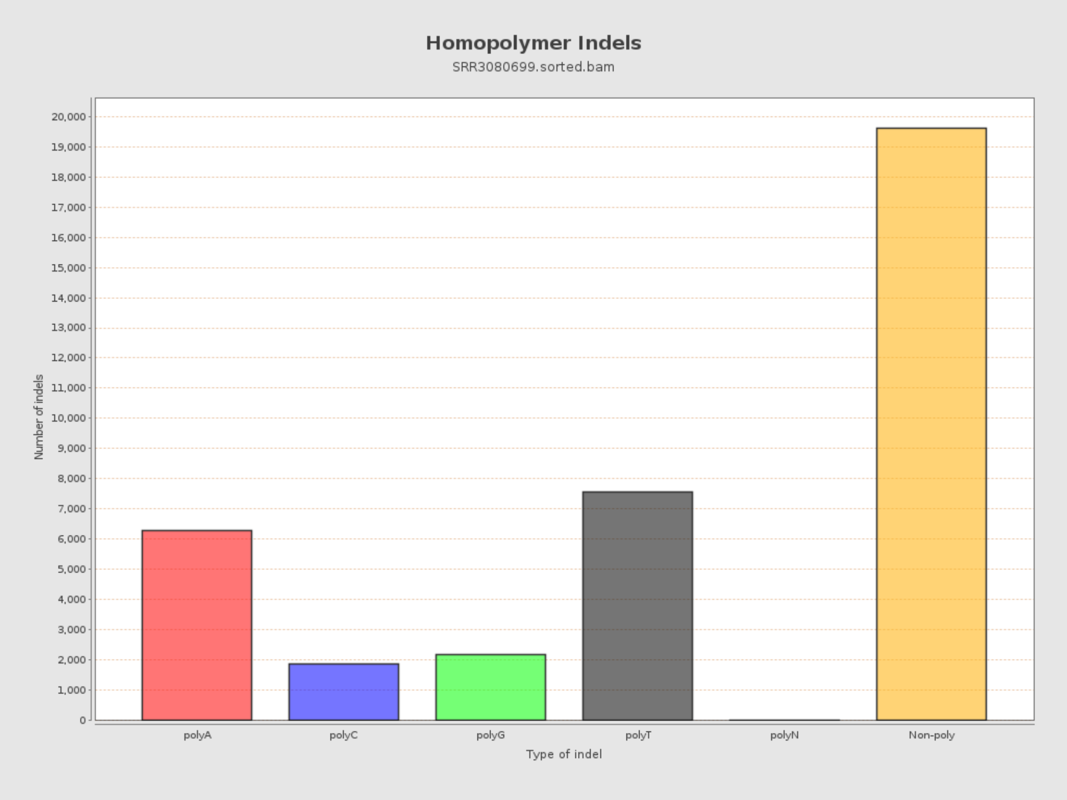
9. Results : Mapped Reads GC-content Distribution



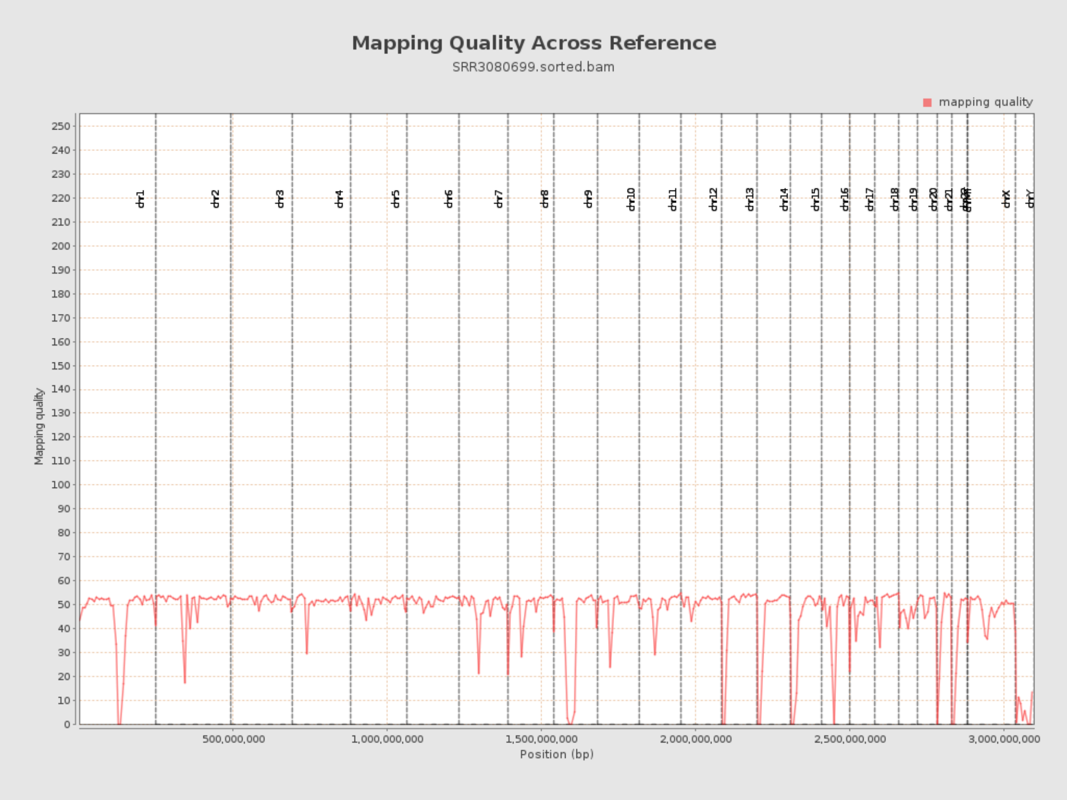
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram