Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 22:55:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085032.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_SRR3085032 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085032.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 22:55:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085032.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,544,833
Mapped reads	2,323,785 / 91.31%
Unmapped reads	221,048 / 8.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,710 / 0.62%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	75,602 / 2.97%
Duplication rate	2.56%
Clipped reads	1,002,191 / 39.38%

2.2. ACGT Content

Number/percentage of A's	43,544,804 / 27.87%
Number/percentage of C's	30,128,674 / 19.28%
Number/percentage of T's	47,870,631 / 30.64%
Number/percentage of G's	34,695,939 / 22.21%
Number/percentage of N's	3,828 / 0%
GC Percentage	41.49%

2.3. Coverage

Mean	0.0505

Standard Deviation	0.364

2.4. Mapping Quality

Mean Mapping Quality	45.28

2.5. Mismatches and indels

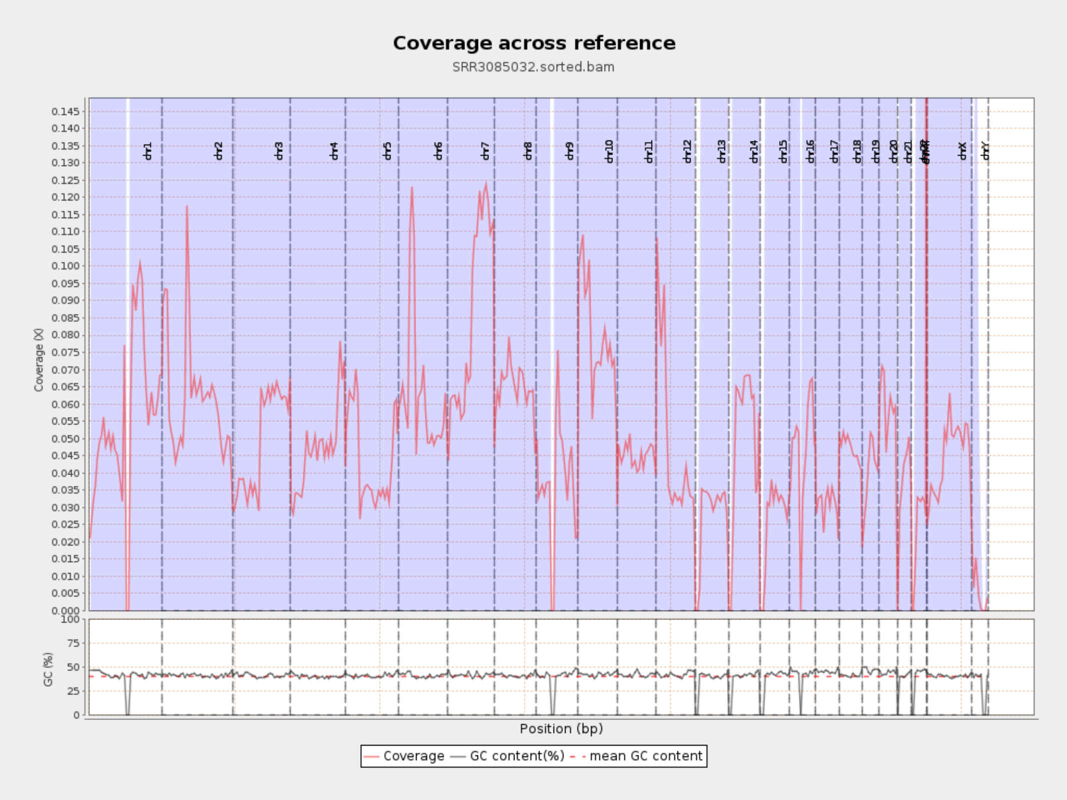
General error rate	0.83%
Mismatches	1,277,146
Insertions	10,829
Mapped reads with at least one insertion	0.46%
Deletions	31,637
Mapped reads with at least one deletion	1.35%
Homopolymer indels	46.82%

2.6. Chromosome stats

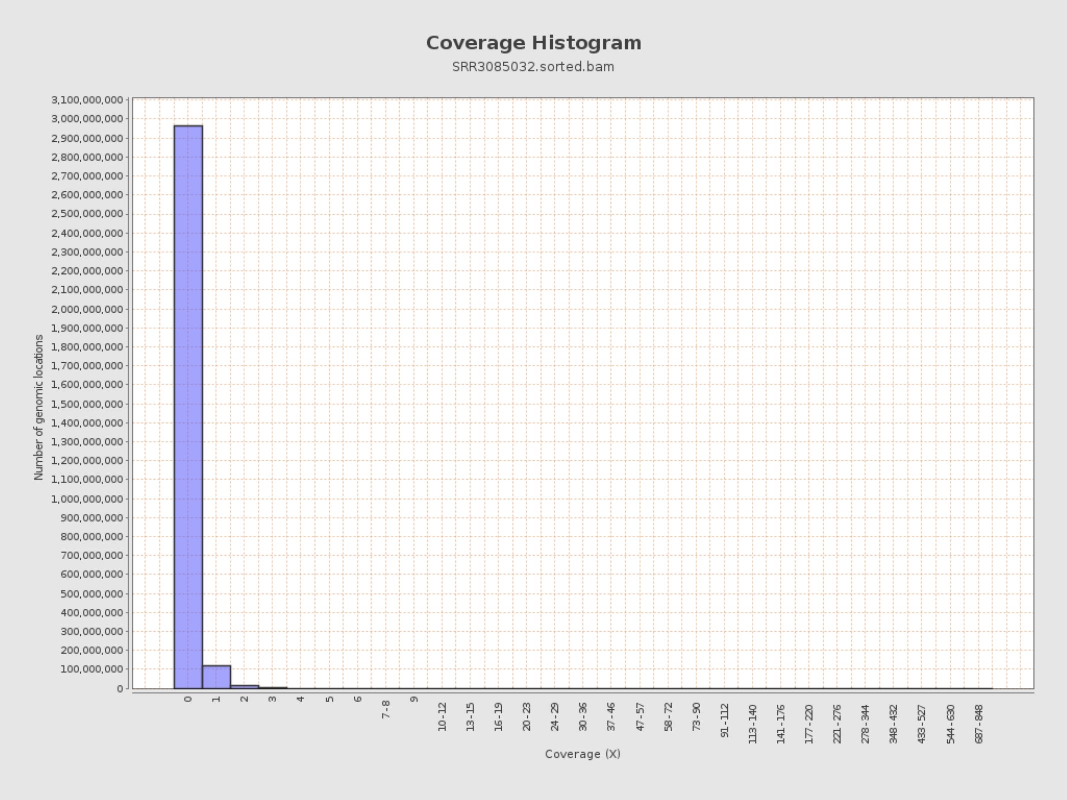
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13754398	0.0552	0.5216
chr2	243199373	15158646	0.0623	0.4944
chr3	198022430	9682315	0.0489	0.2532
chr4	191154276	9028529	0.0472	0.2503
chr5	180915260	7932763	0.0438	0.2369
chr6	171115067	10888169	0.0636	0.3586
chr7	159138663	13840719	0.087	0.4165

chr8	146364022	9500107	0.0649	0.5837
chr9	141213431	5211798	0.0369	0.327
chr10	135534747	10974591	0.081	0.4983
chr11	135006516	6057856	0.0449	0.3254
chr12	133851895	6522177	0.0487	0.2541
chr13	115169878	3121278	0.0271	0.1856
chr14	107349540	5275012	0.0491	0.2665
chr15	102531392	2667543	0.026	0.1915
chr16	90354753	4280114	0.0474	0.2597
chr17	81195210	2479680	0.0305	0.2104
chr18	78077248	3674822	0.0471	0.5262
chr19	59128983	2383571	0.0403	0.3929
chr20	63025520	3689032	0.0585	0.2791
chr21	48129895	1757722	0.0365	0.2248
chr22	51304566	1157104	0.0226	0.1671
chrMT	16571	16808	1.0143	1.3099
chrX	155270560	6939438	0.0447	0.2655
chrY	59373566	304078	0.0051	0.1018

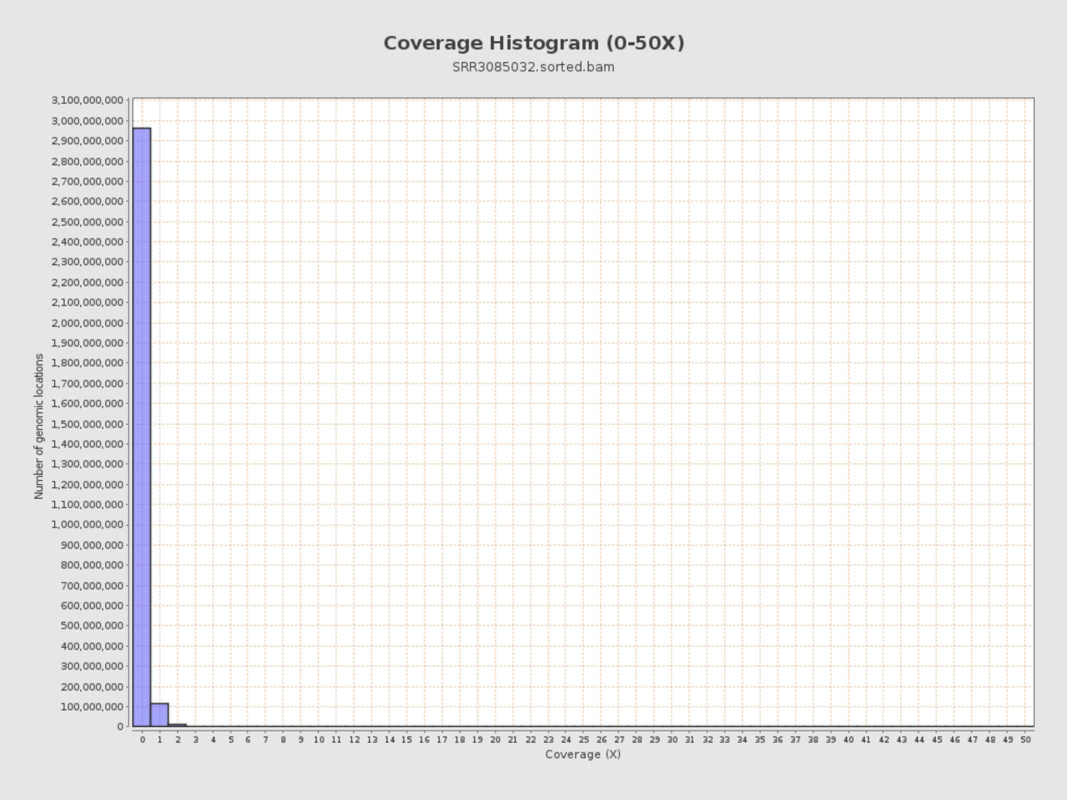
3. Results : Coverage across reference



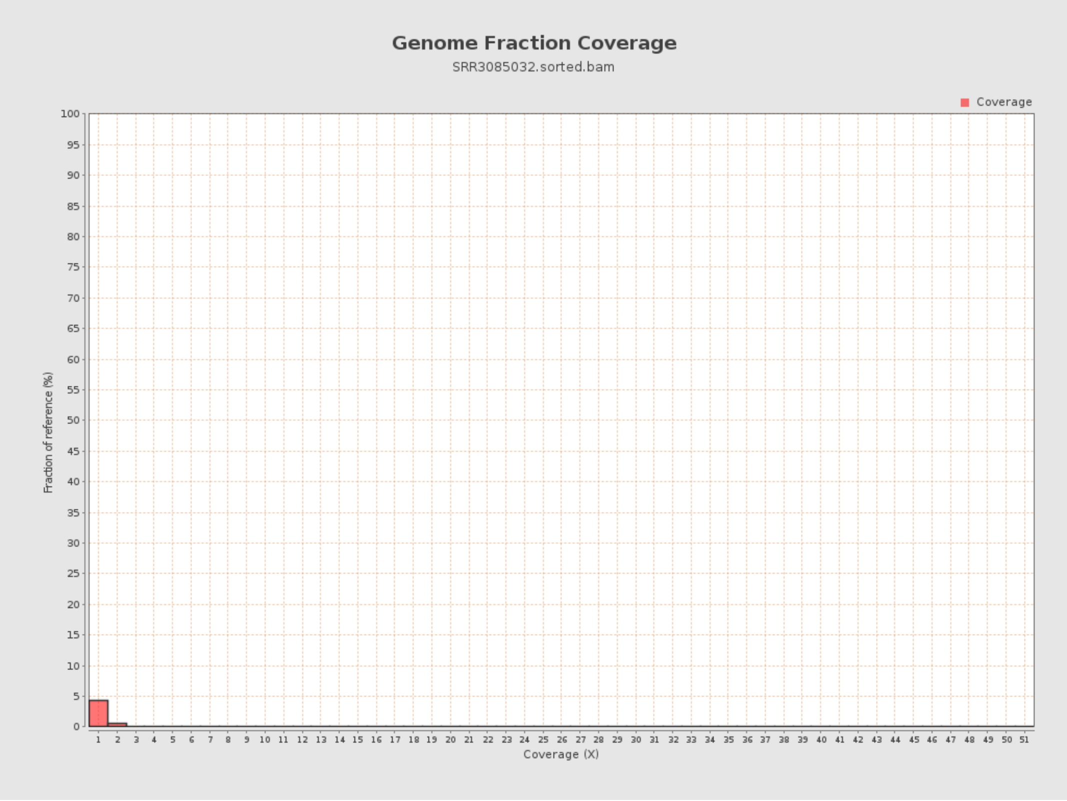
4. Results : Coverage Histogram



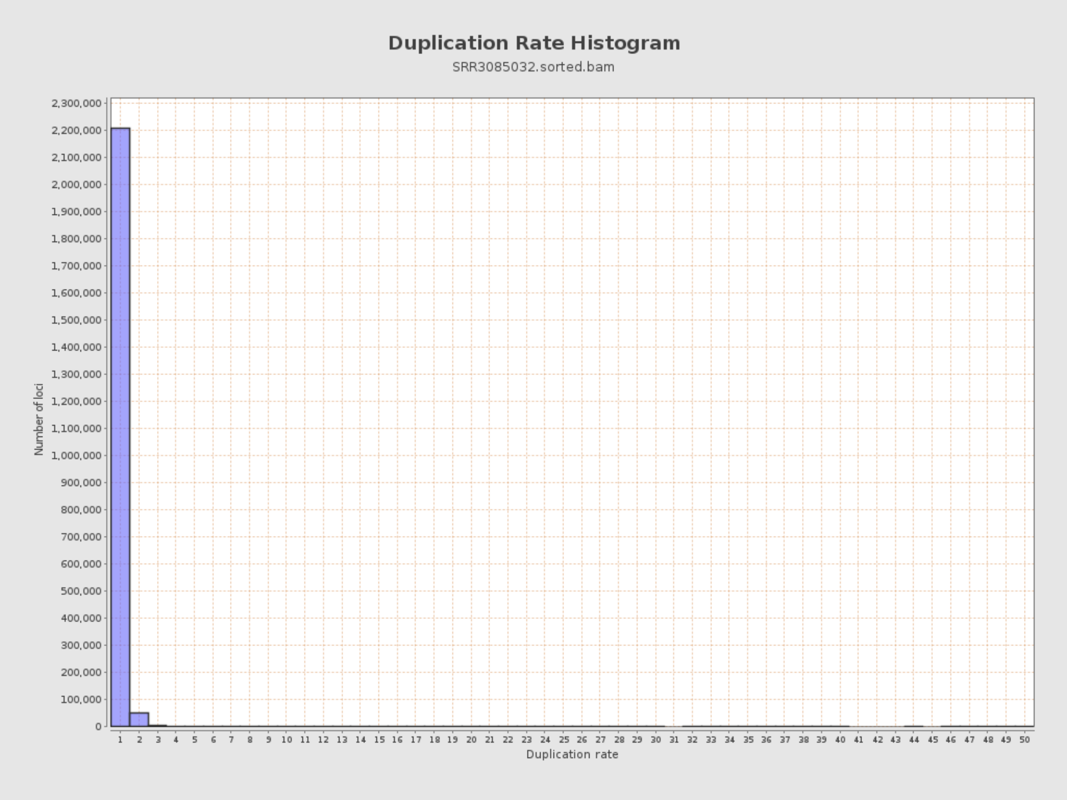
5. Results : Coverage Histogram (0-50X)



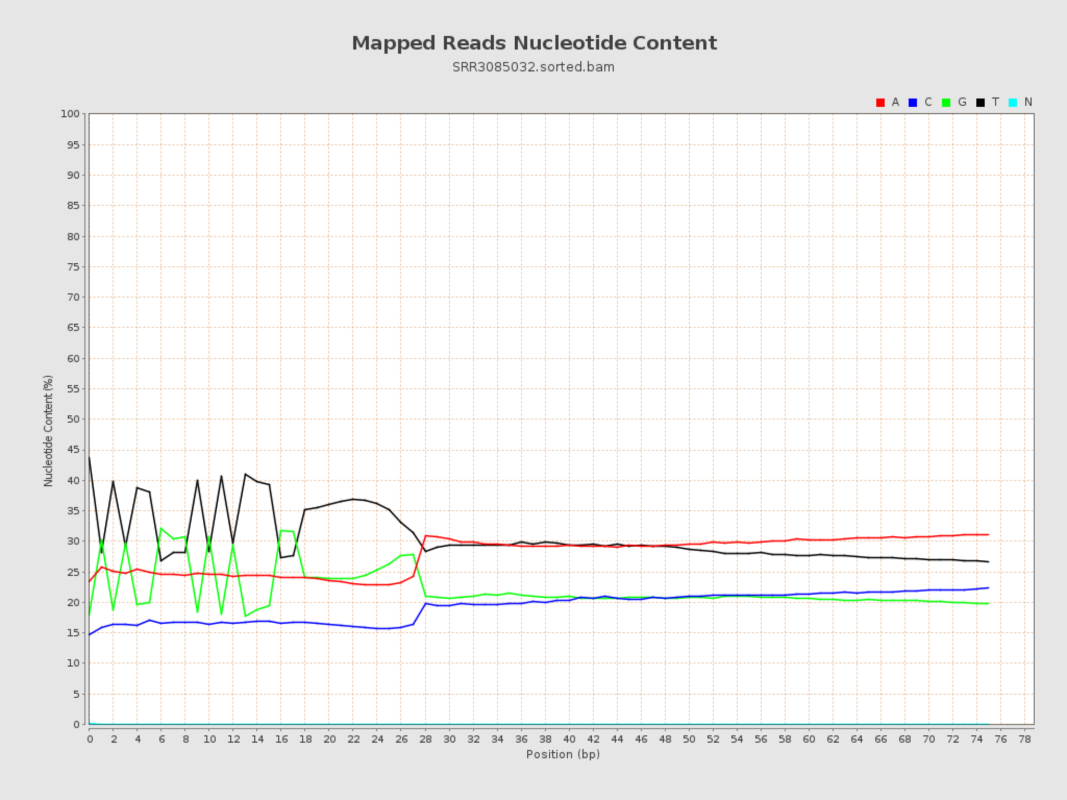
6. Results : Genome Fraction Coverage



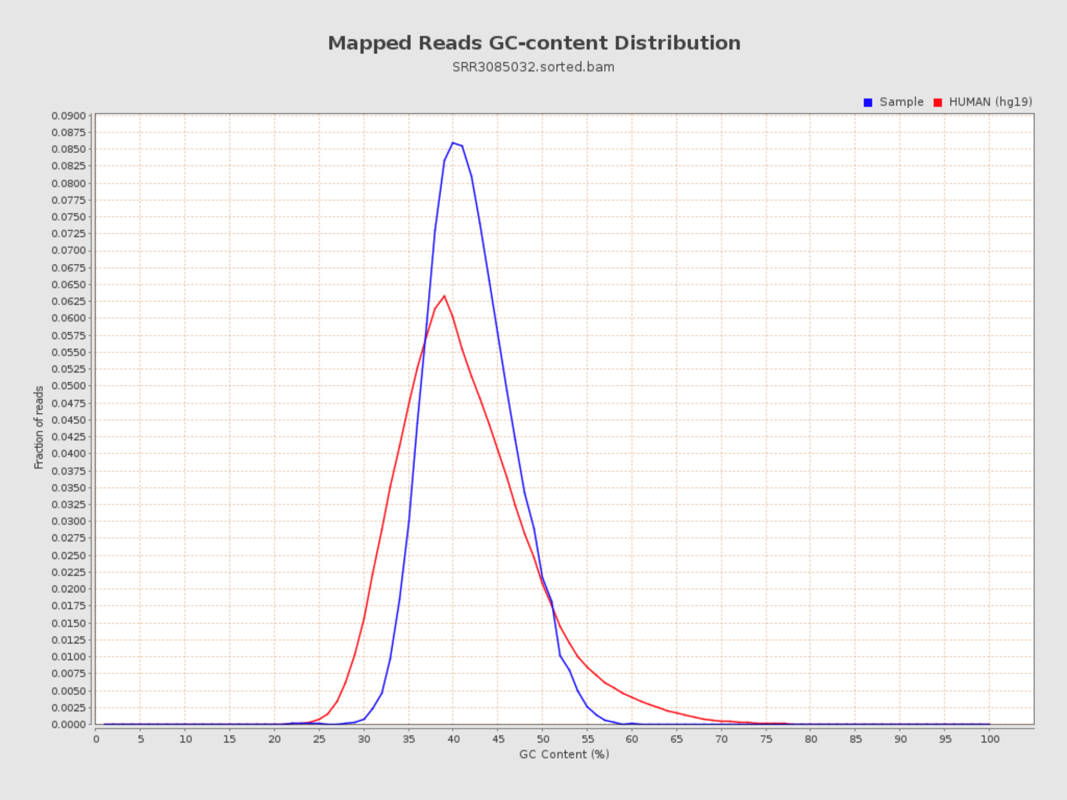
7. Results : Duplication Rate Histogram



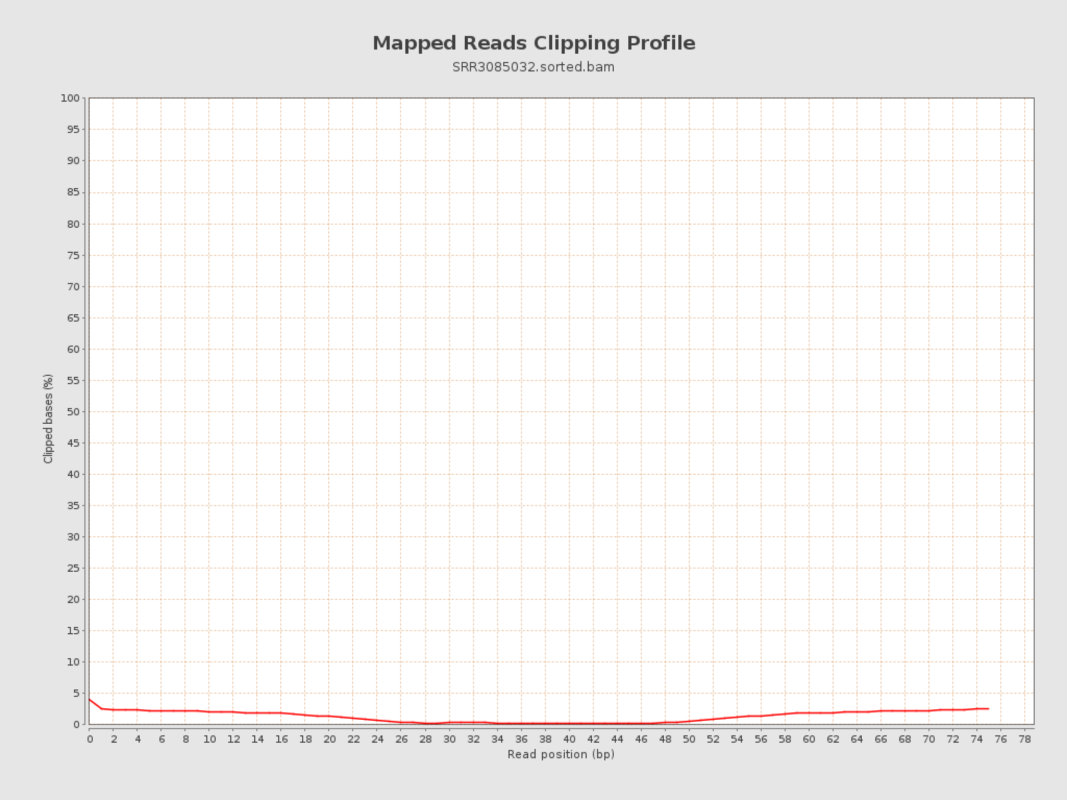
8. Results : Mapped Reads Nucleotide Content



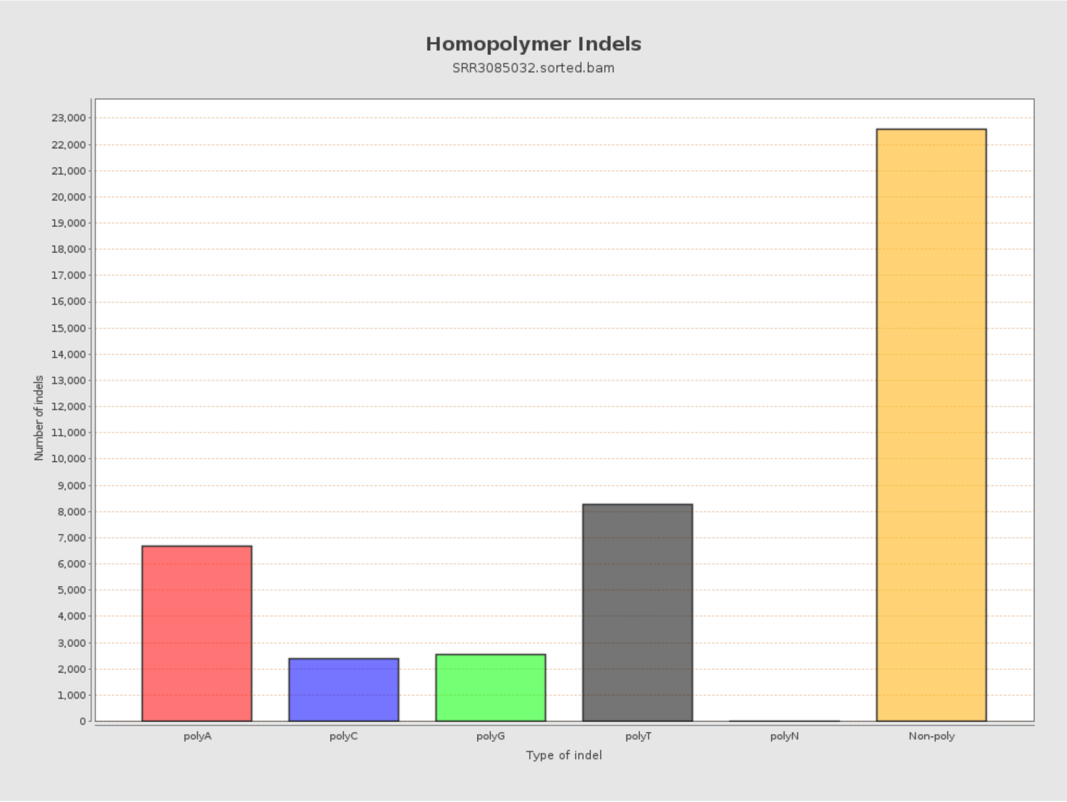
9. Results : Mapped Reads GC-content Distribution



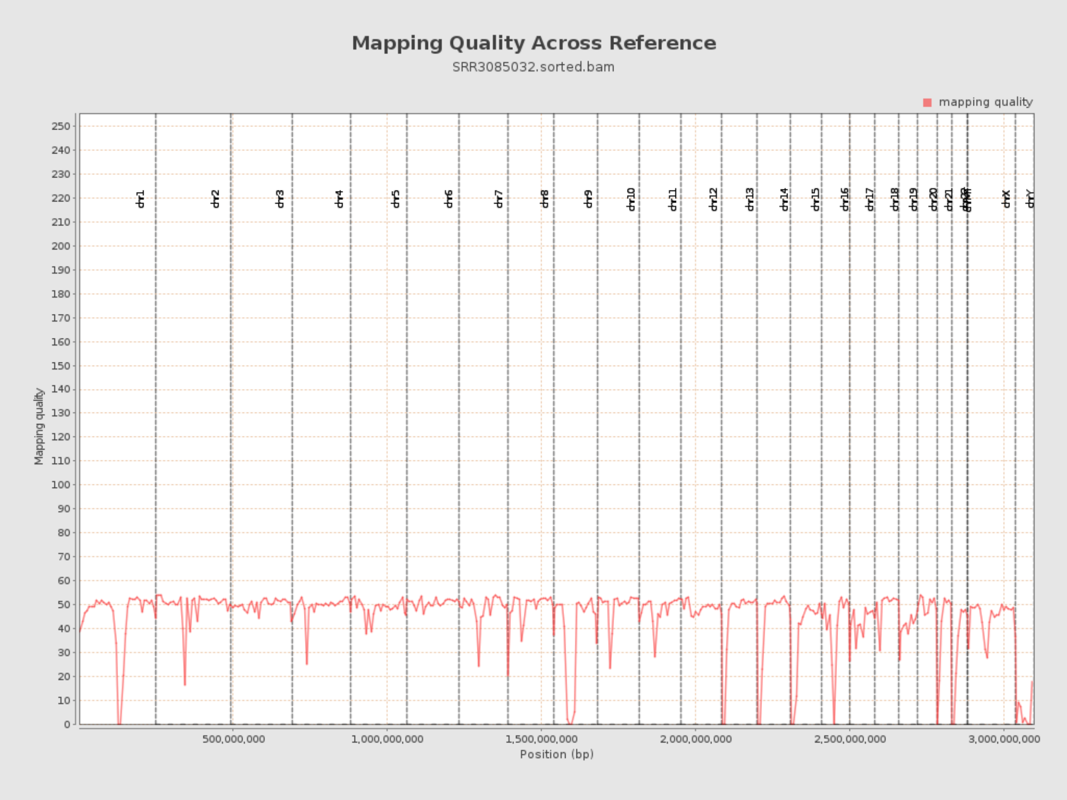
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram