Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 22:18:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085022.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_SRR3085022 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085022.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 22:18:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085022.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,427,293
Mapped reads	2,165,751 / 89.22%
Unmapped reads	261,542 / 10.78%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,786 / 0.57%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	71,378 / 2.94%
Duplication rate	2.51%
Clipped reads	1,102,649 / 45.43%

2.2. ACGT Content

Number/percentage of A's	38,733,793 / 27.26%
Number/percentage of C's	27,534,560 / 19.38%
Number/percentage of T's	43,006,039 / 30.27%
Number/percentage of G's	32,785,684 / 23.08%
Number/percentage of N's	5,387 / 0%
GC Percentage	42.46%

2.3. Coverage

Mean	0.0459

Standard Deviation	0.3633

2.4. Mapping Quality

Mean Mapping Quality	43.15

2.5. Mismatches and indels

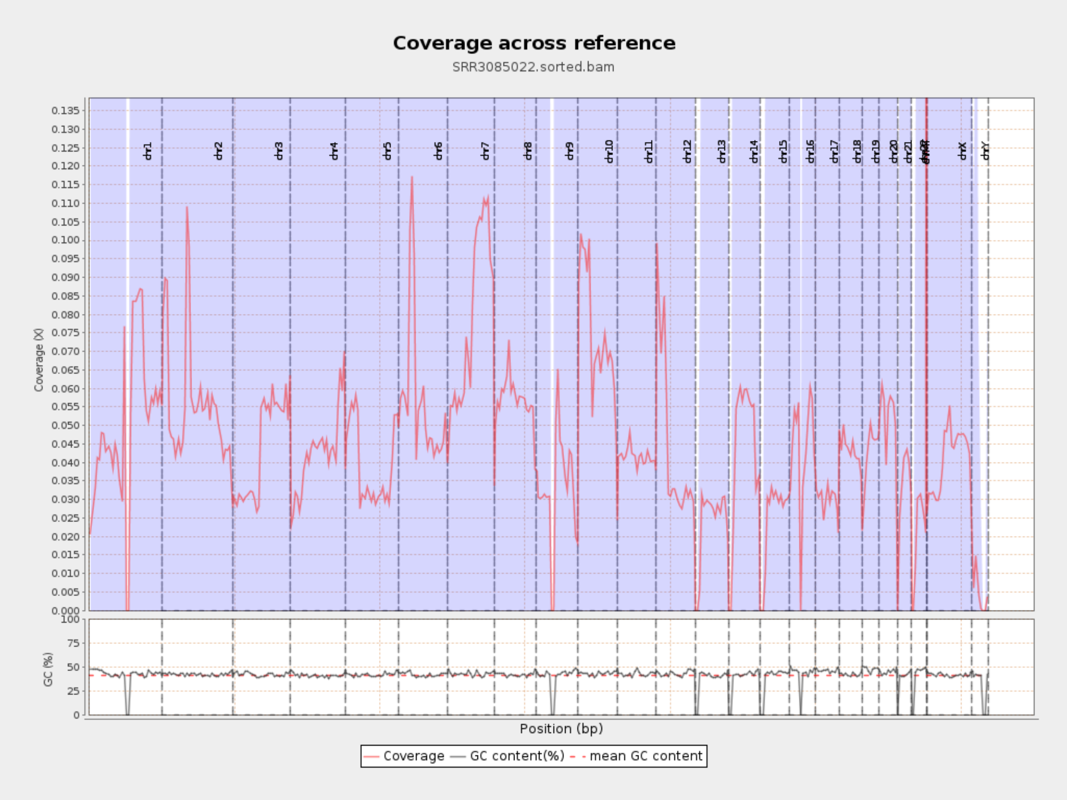
General error rate	0.89%
Mismatches	1,247,413
Insertions	10,090
Mapped reads with at least one insertion	0.46%
Deletions	28,813
Mapped reads with at least one deletion	1.32%
Homopolymer indels	45.87%

2.6. Chromosome stats

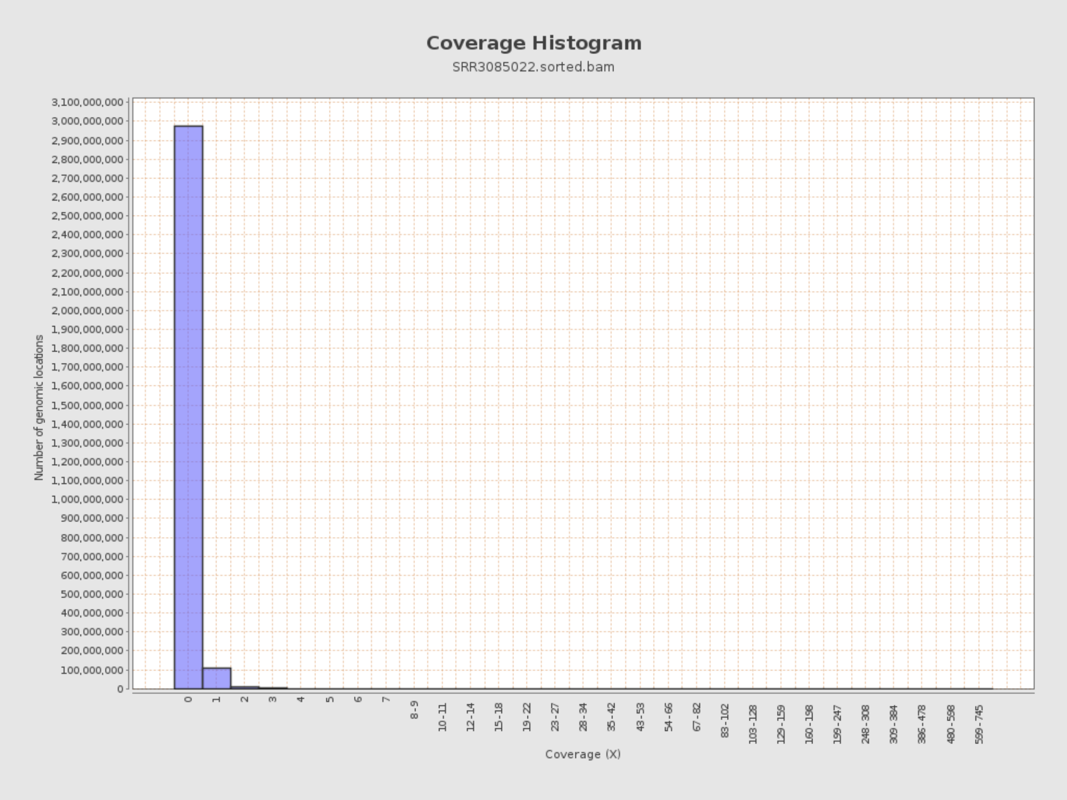
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12421183	0.0498	0.5616
chr2	243199373	13787179	0.0567	0.495
chr3	198022430	8583298	0.0433	0.2358
chr4	191154276	8170583	0.0427	0.238
chr5	180915260	7096732	0.0392	0.2224
chr6	171115067	9792973	0.0572	0.3541
chr7	159138663	12633239	0.0794	0.422

chr8	146364022	8329195	0.0569	0.5475
chr9	141213431	4665464	0.033	0.34
chr10	135534747	10278329	0.0758	0.4894
chr11	135006516	5576108	0.0413	0.3247
chr12	133851895	5938897	0.0444	0.2429
chr13	115169878	2717067	0.0236	0.1699
chr14	107349540	4706646	0.0438	0.2511
chr15	102531392	2515056	0.0245	0.1934
chr16	90354753	3992962	0.0442	0.253
chr17	81195210	2429918	0.0299	0.2145
chr18	78077248	3400636	0.0436	0.5342
chr19	59128983	2522836	0.0427	0.4084
chr20	63025520	3308432	0.0525	0.2629
chr21	48129895	1575579	0.0327	0.2174
chr22	51304566	1011809	0.0197	0.156
chrMT	16571	10049	0.6064	0.9112
chrX	155270560	6353233	0.0409	0.2569
chrY	59373566	297326	0.005	0.1015

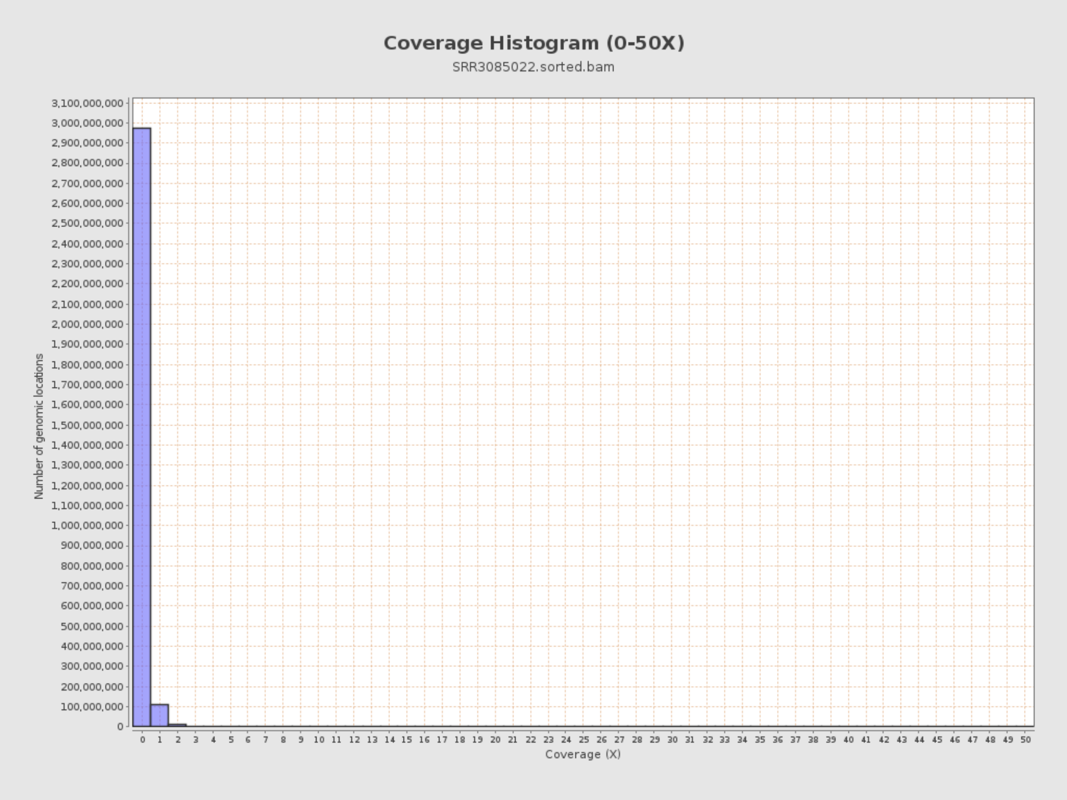
3. Results : Coverage across reference



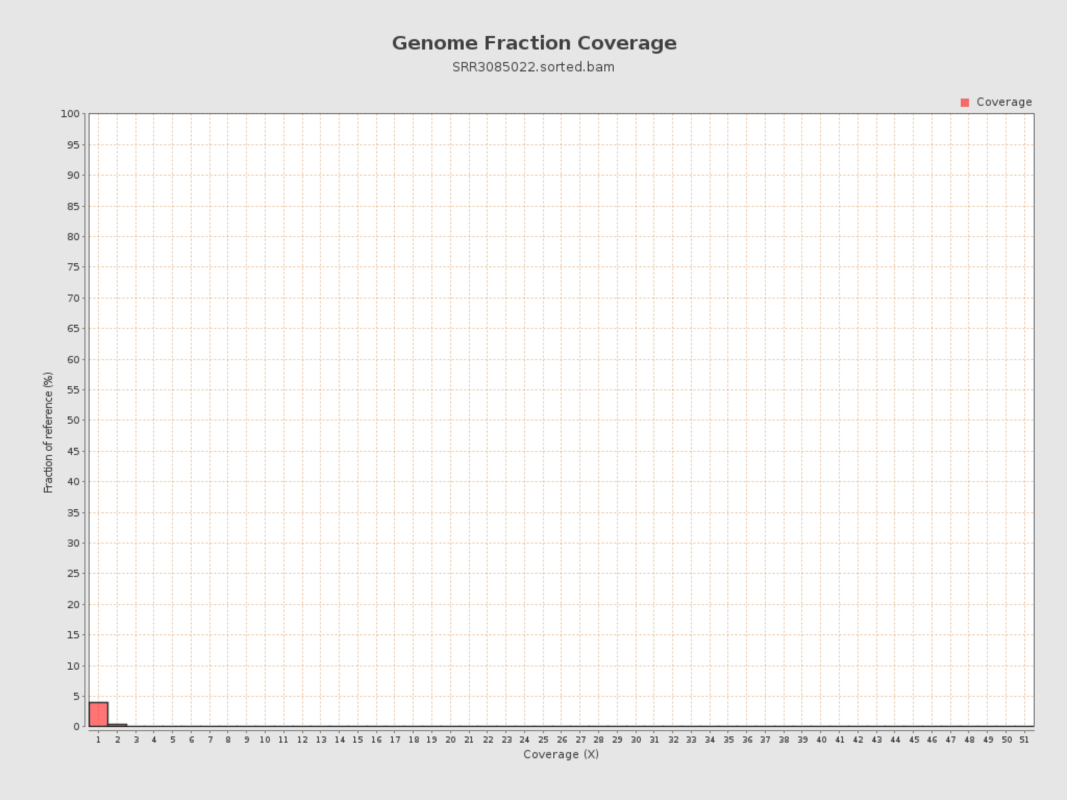
4. Results : Coverage Histogram



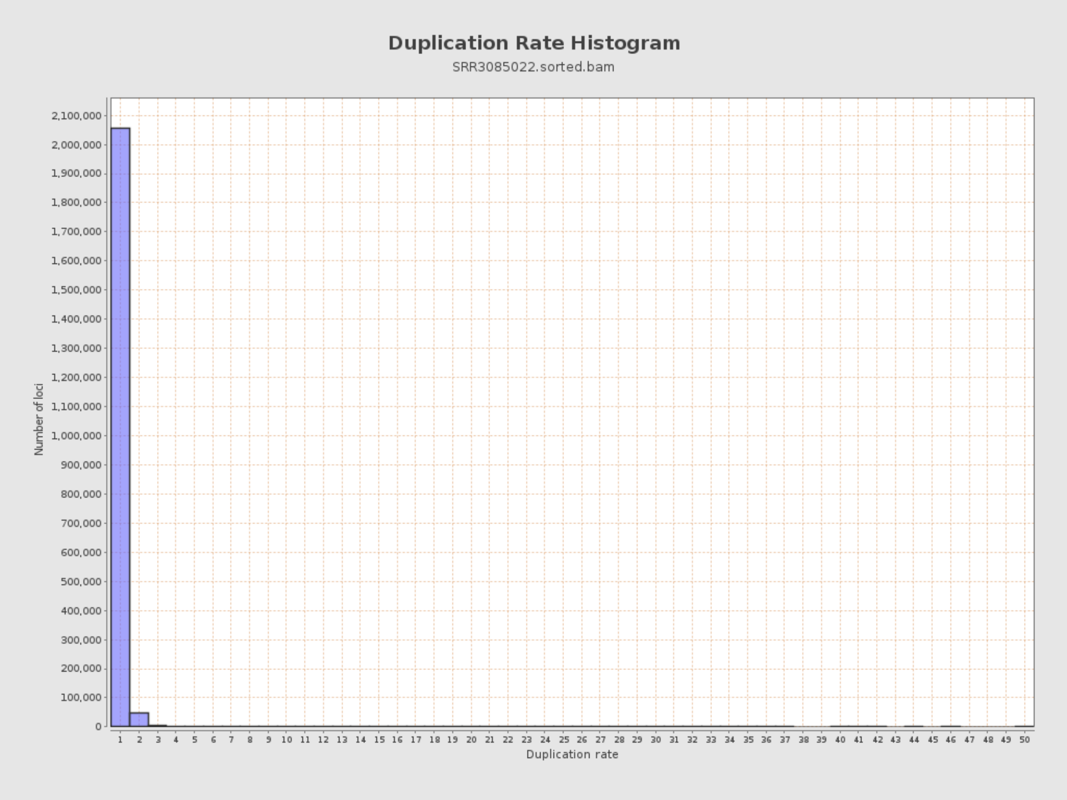
5. Results : Coverage Histogram (0-50X)



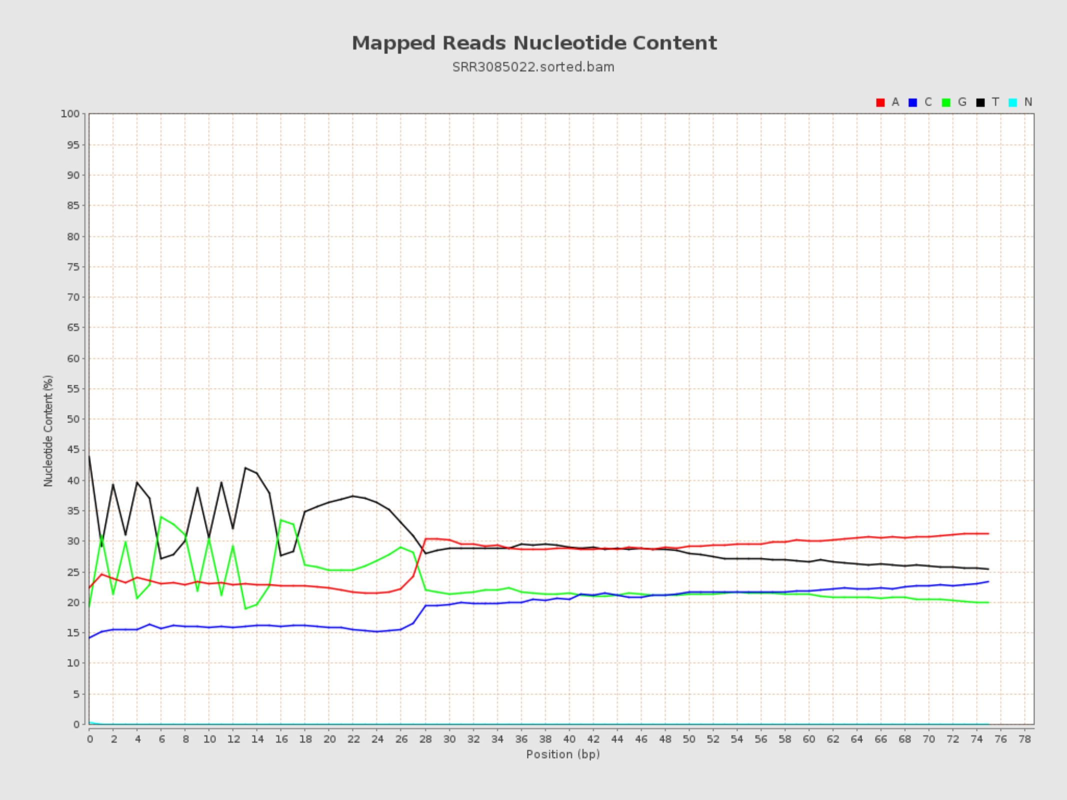
6. Results : Genome Fraction Coverage



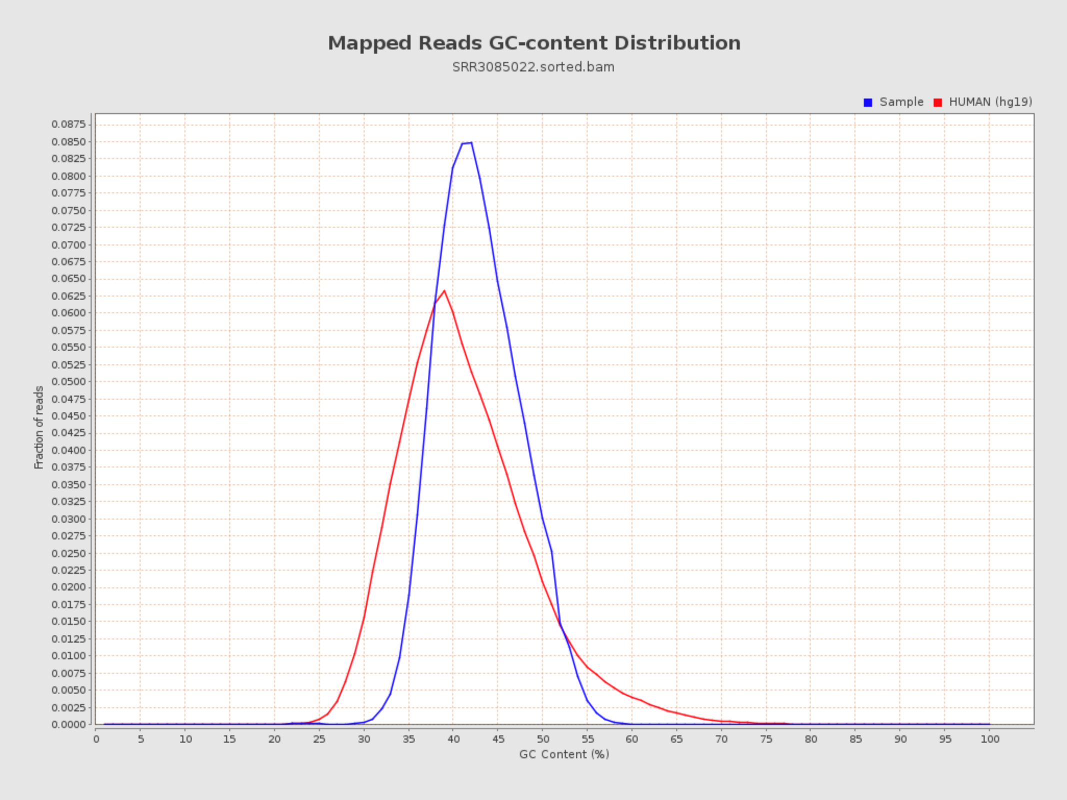
7. Results : Duplication Rate Histogram



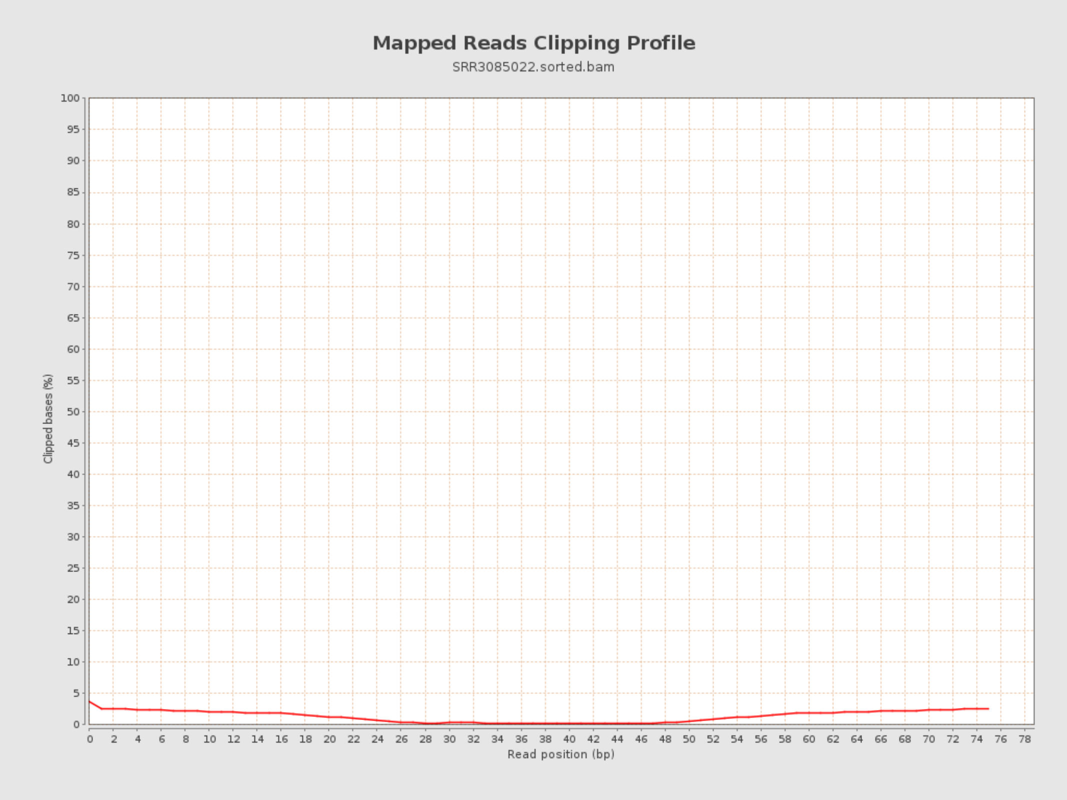
8. Results : Mapped Reads Nucleotide Content



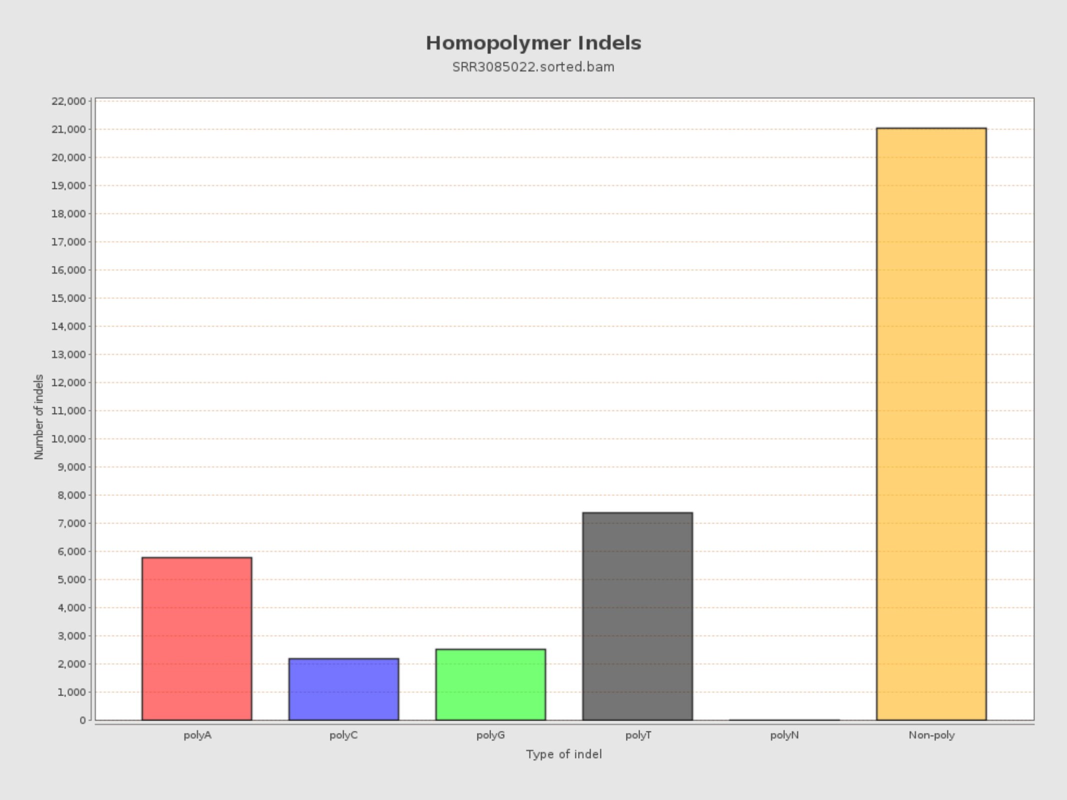
9. Results : Mapped Reads GC-content Distribution



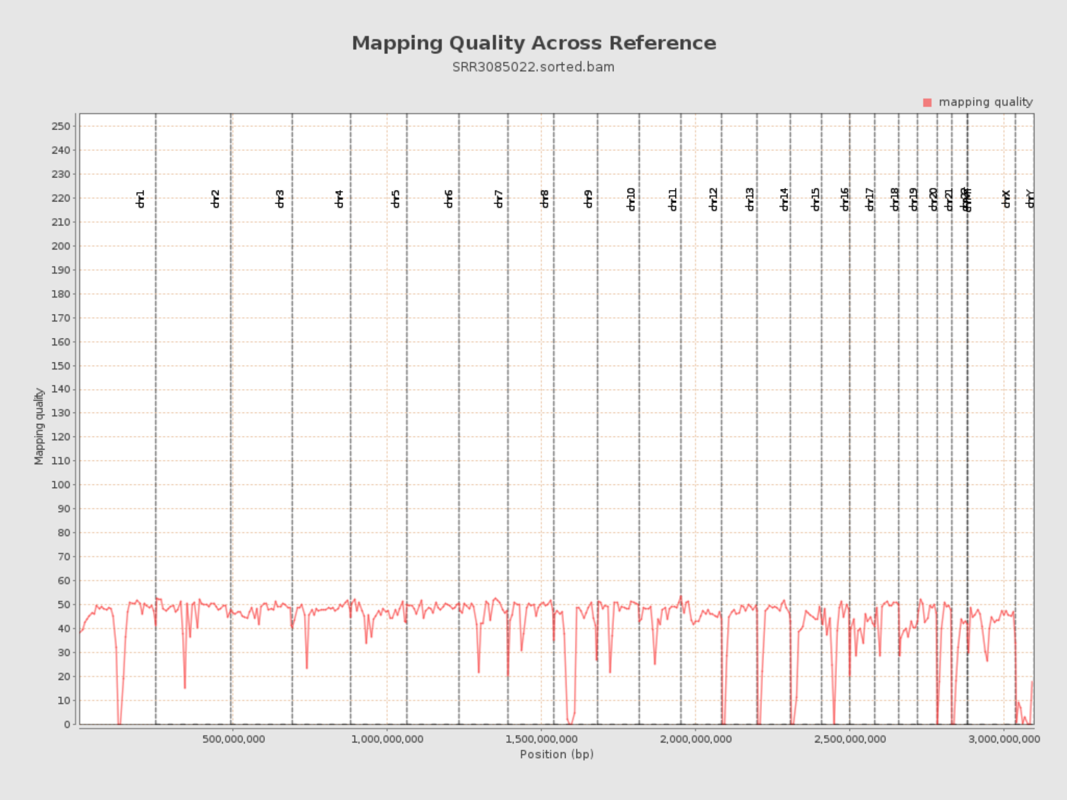
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram