Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 23:34:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085043.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_SRR3085043 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085043.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 23:34:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085043.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,957,243
Mapped reads	2,635,906 / 89.13%
Unmapped reads	321,337 / 10.87%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,872 / 0.6%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	97,373 / 3.29%
Duplication rate	2.72%
Clipped reads	1,282,157 / 43.36%

2.2. ACGT Content

Number/percentage of A's	48,900,766 / 28.08%
Number/percentage of C's	33,684,583 / 19.34%
Number/percentage of T's	52,933,702 / 30.4%
Number/percentage of G's	38,598,121 / 22.17%
Number/percentage of N's	18,466 / 0.01%
GC Percentage	41.51%

2.3. Coverage

Mean	0.0563

Standard Deviation	0.4685

2.4. Mapping Quality

Mean Mapping Quality	44.03

2.5. Mismatches and indels

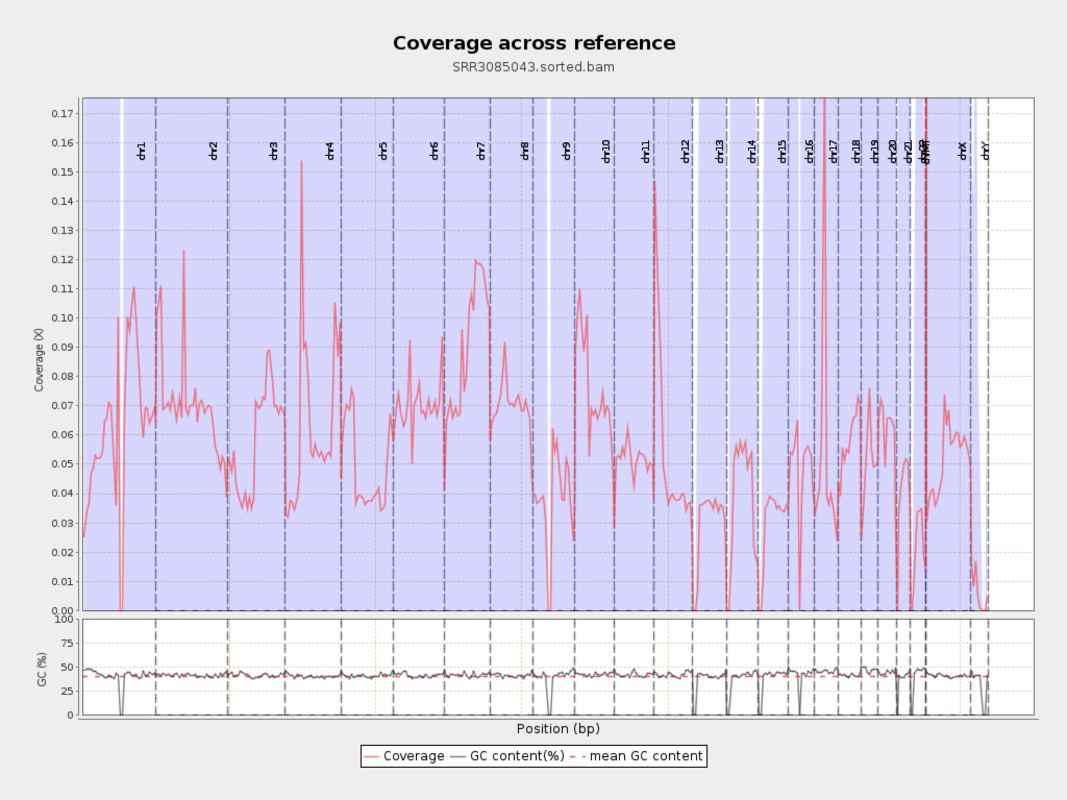
General error rate	0.93%
Mismatches	1,591,116
Insertions	12,584
Mapped reads with at least one insertion	0.47%
Deletions	34,087
Mapped reads with at least one deletion	1.28%
Homopolymer indels	45.79%

2.6. Chromosome stats

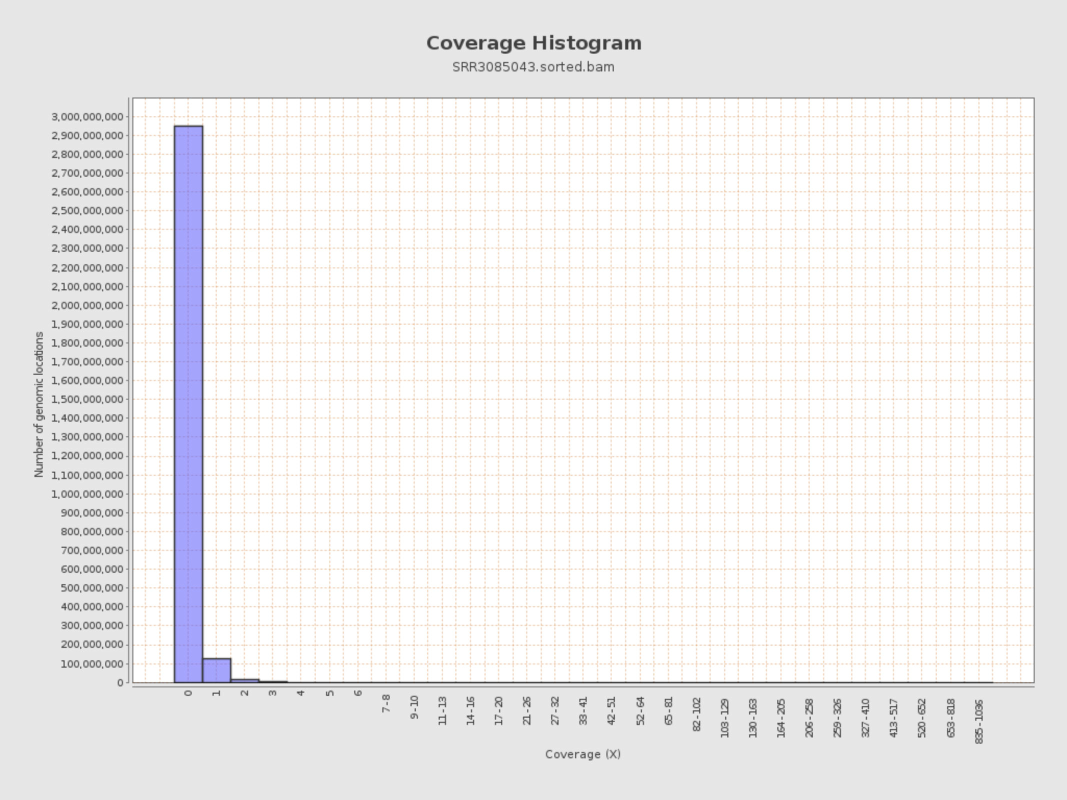
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15502162	0.0622	0.8392
chr2	243199373	17269027	0.071	0.6018
chr3	198022430	11506522	0.0581	0.2776
chr4	191154276	12086621	0.0632	0.2963
chr5	180915260	8821083	0.0488	0.2556
chr6	171115067	12072709	0.0706	0.4312
chr7	159138663	14365750	0.0903	0.5555

chr8	146364022	10273202	0.0702	0.7162
chr9	141213431	5368702	0.038	0.4401
chr10	135534747	10363775	0.0765	0.4926
chr11	135006516	6975186	0.0517	0.4357
chr12	133851895	7418841	0.0554	0.2797
chr13	115169878	3431369	0.0298	0.1946
chr14	107349540	4239722	0.0395	0.2618
chr15	102531392	2977507	0.029	0.2101
chr16	90354753	4246133	0.047	0.2792
chr17	81195210	4263000	0.0525	0.319
chr18	78077248	4559937	0.0584	0.7471
chr19	59128983	3049210	0.0516	0.5453
chr20	63025520	3943149	0.0626	0.2896
chr21	48129895	1924732	0.04	0.2481
chr22	51304566	1069637	0.0208	0.1605
chrMT	16571	40122	2.4212	2.3018
chrX	155270560	8070703	0.052	0.3178
chrY	59373566	354853	0.006	0.1124

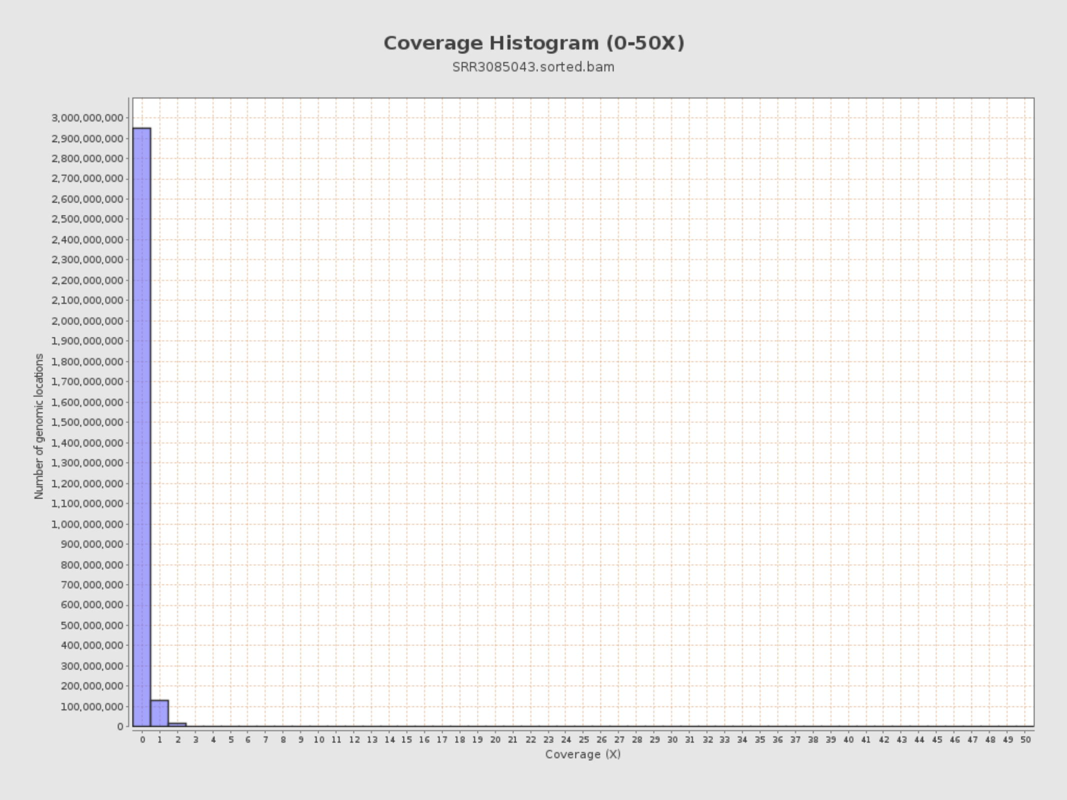
3. Results : Coverage across reference



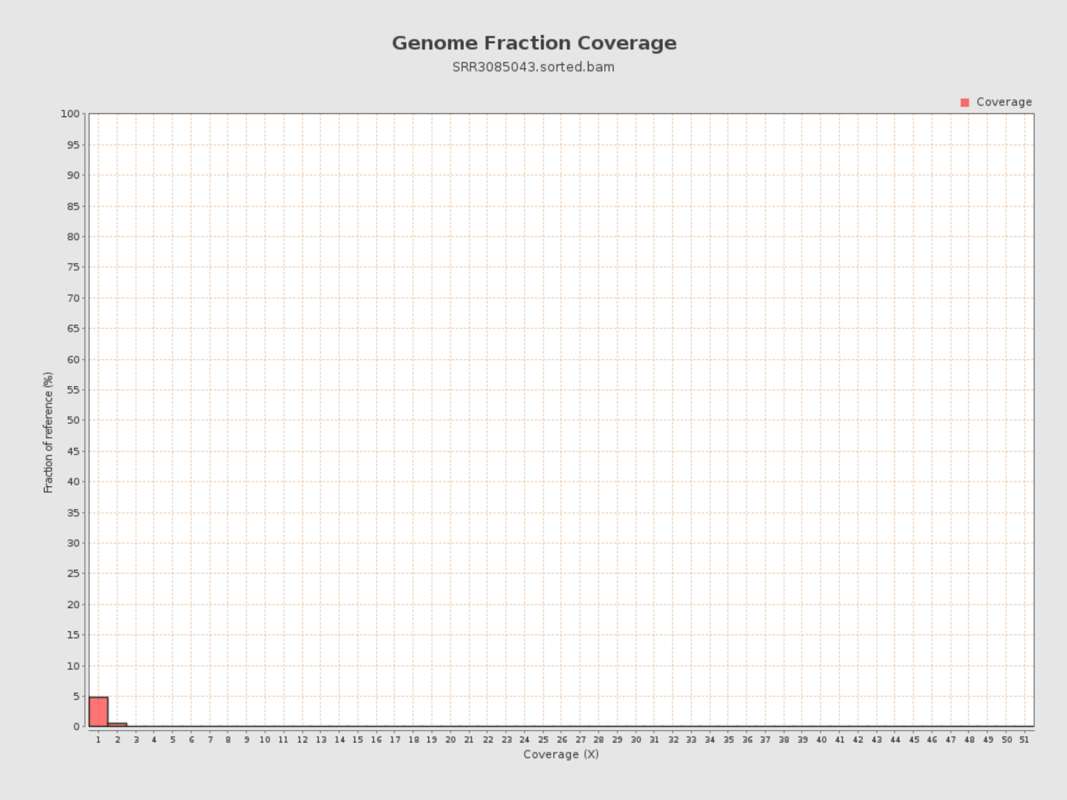
4. Results : Coverage Histogram



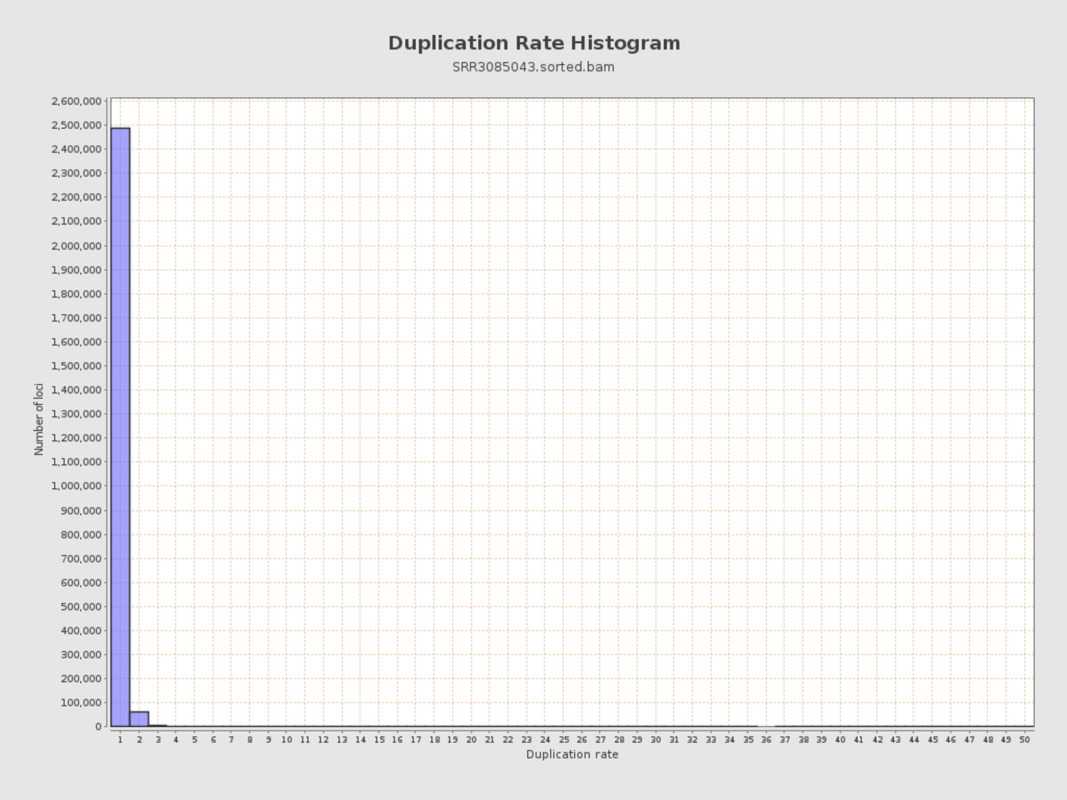
5. Results : Coverage Histogram (0-50X)



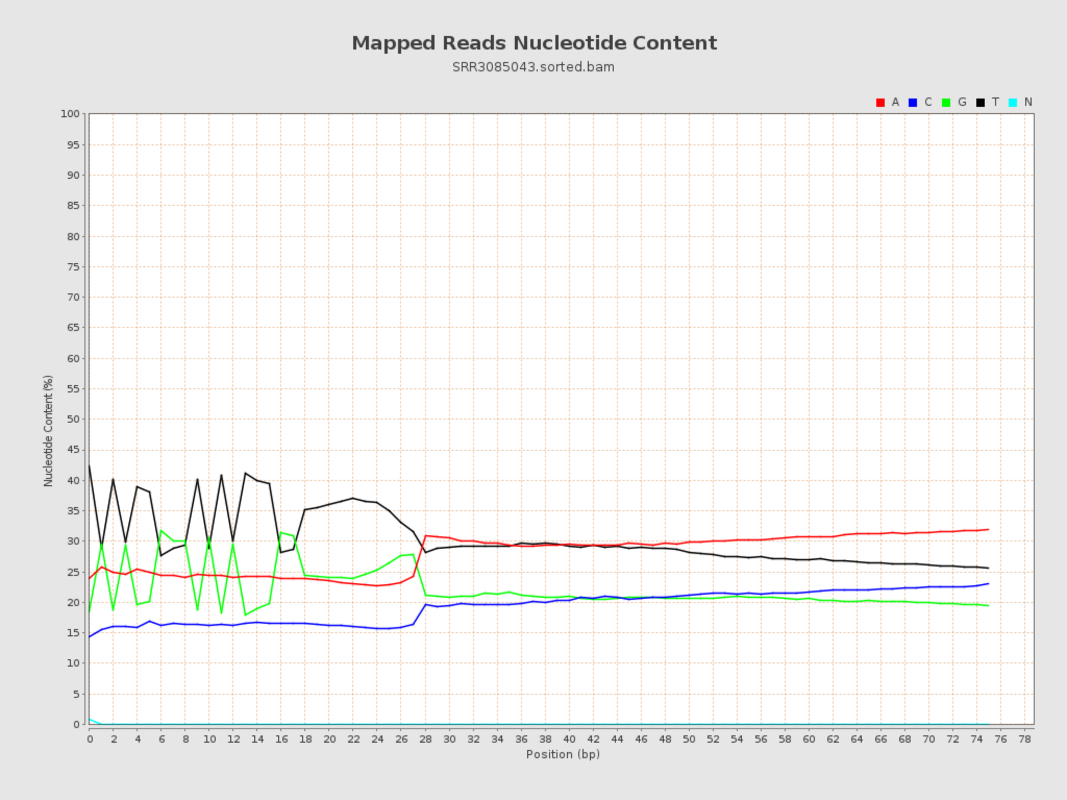
6. Results : Genome Fraction Coverage



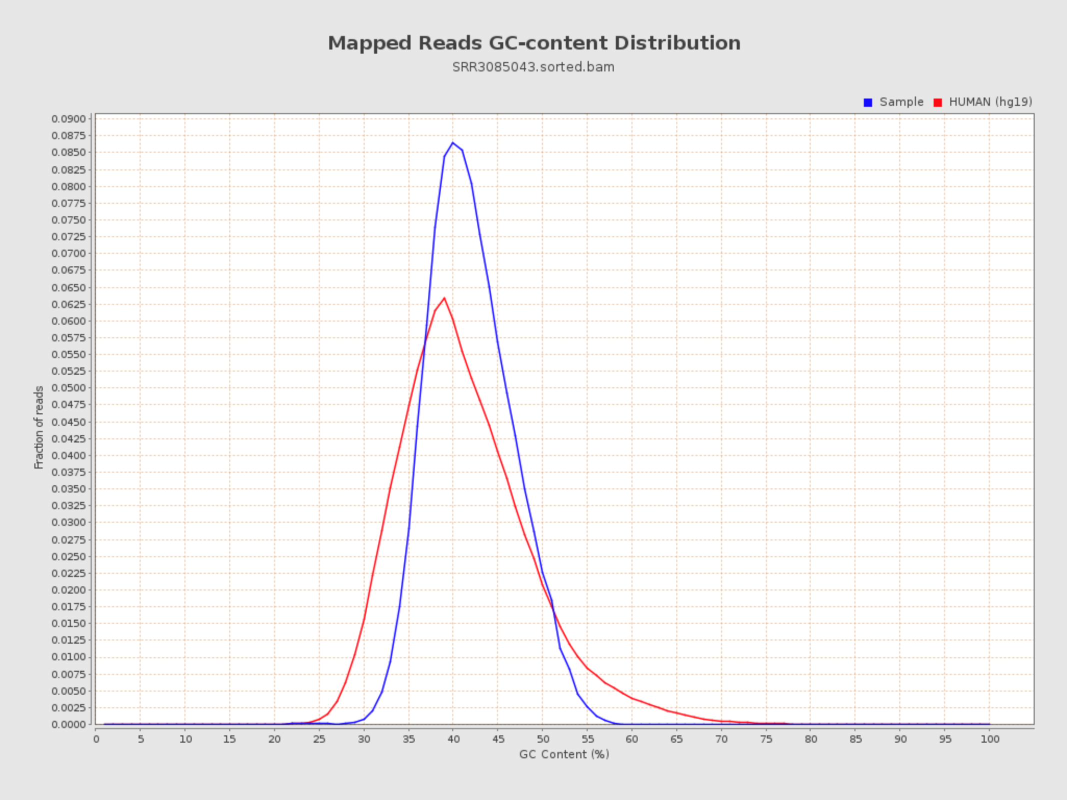
7. Results : Duplication Rate Histogram



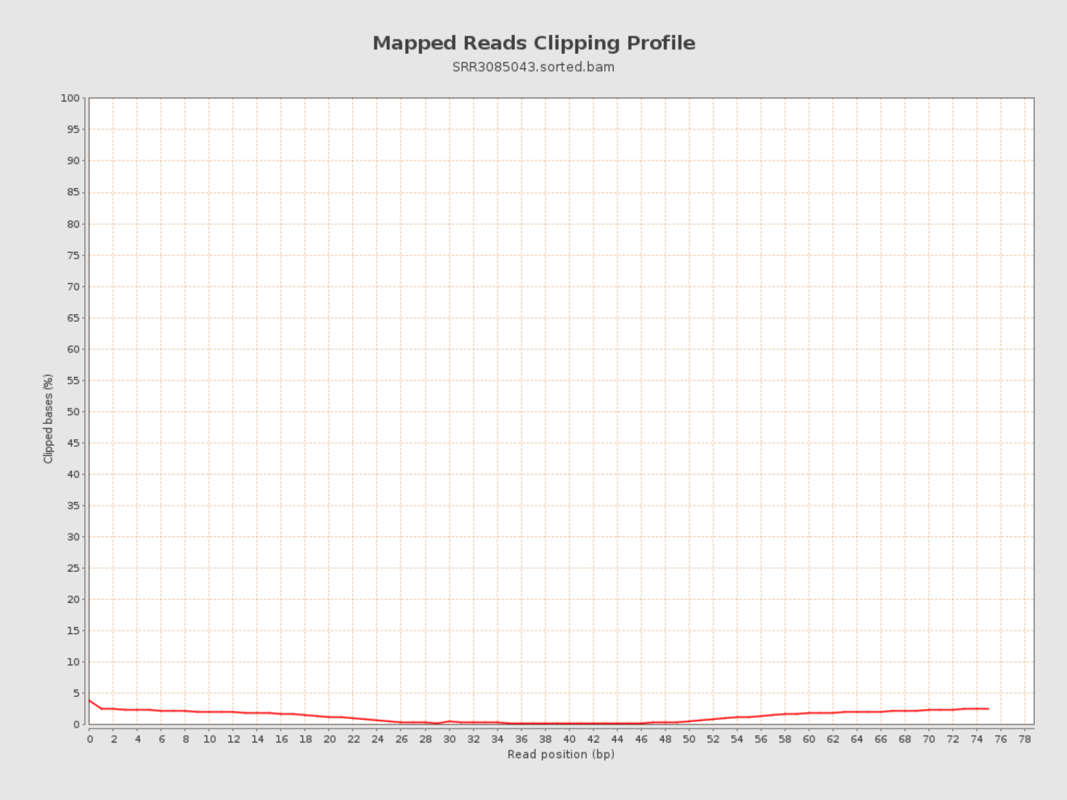
8. Results : Mapped Reads Nucleotide Content



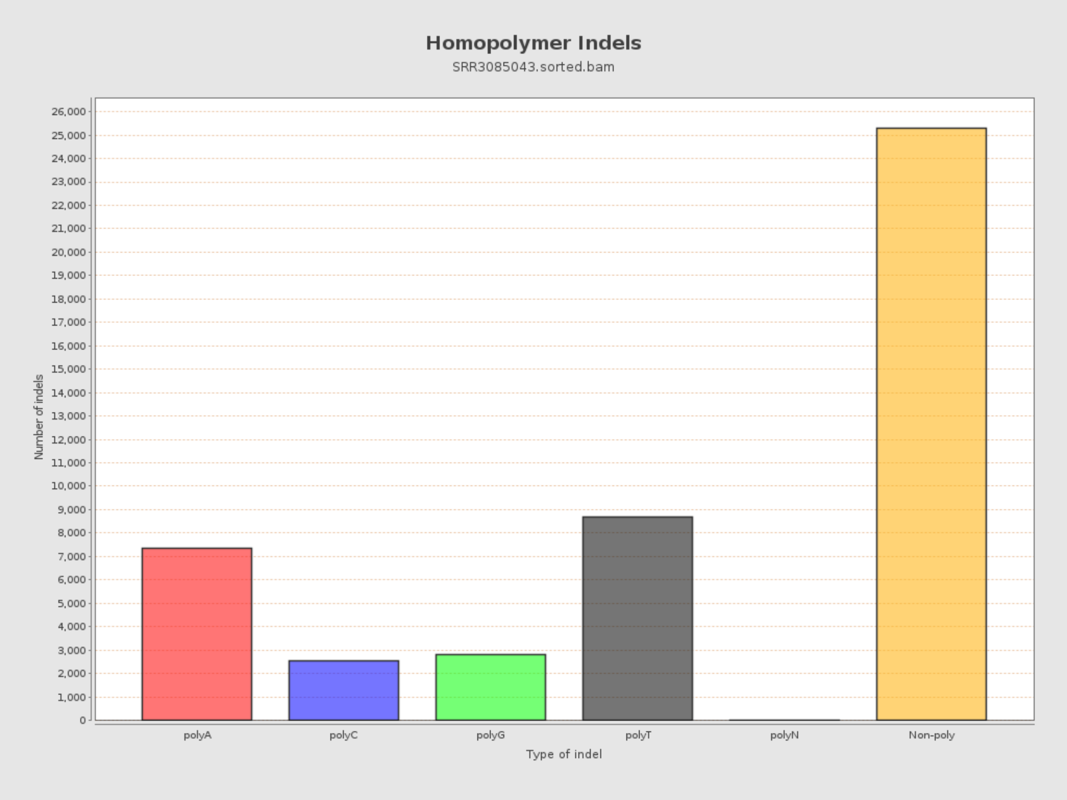
9. Results : Mapped Reads GC-content Distribution



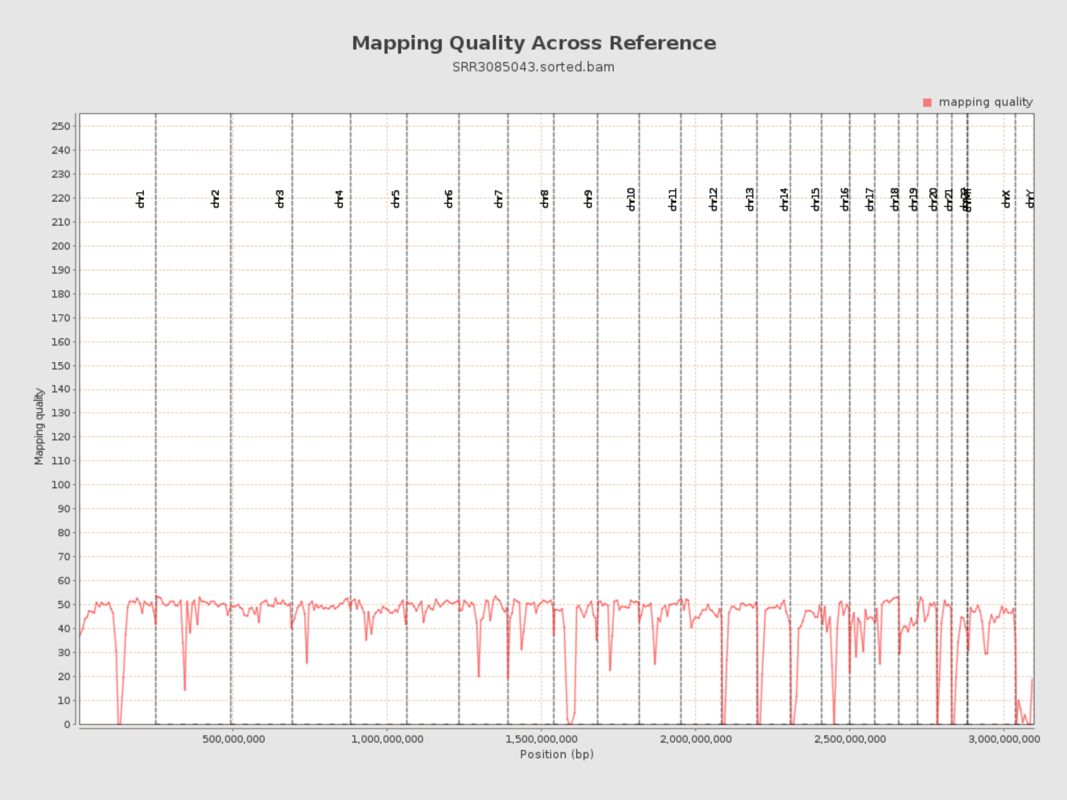
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram