Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 04:00:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085139.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_SRR3085139 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085139.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 04:00:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085139.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,458,780
Mapped reads	2,241,392 / 91.16%
Unmapped reads	217,388 / 8.84%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,581 / 0.92%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	81,921 / 3.33%
Duplication rate	2.74%
Clipped reads	916,364 / 37.27%

2.2. ACGT Content

Number/percentage of A's	43,206,672 / 28.39%
Number/percentage of C's	28,211,940 / 18.54%
Number/percentage of T's	47,842,883 / 31.44%
Number/percentage of G's	32,900,693 / 21.62%
Number/percentage of N's	28,458 / 0.02%
GC Percentage	40.16%

2.3. Coverage

Mean	0.0492

Standard Deviation	0.424

2.4. Mapping Quality

Mean Mapping Quality	46.76

2.5. Mismatches and indels

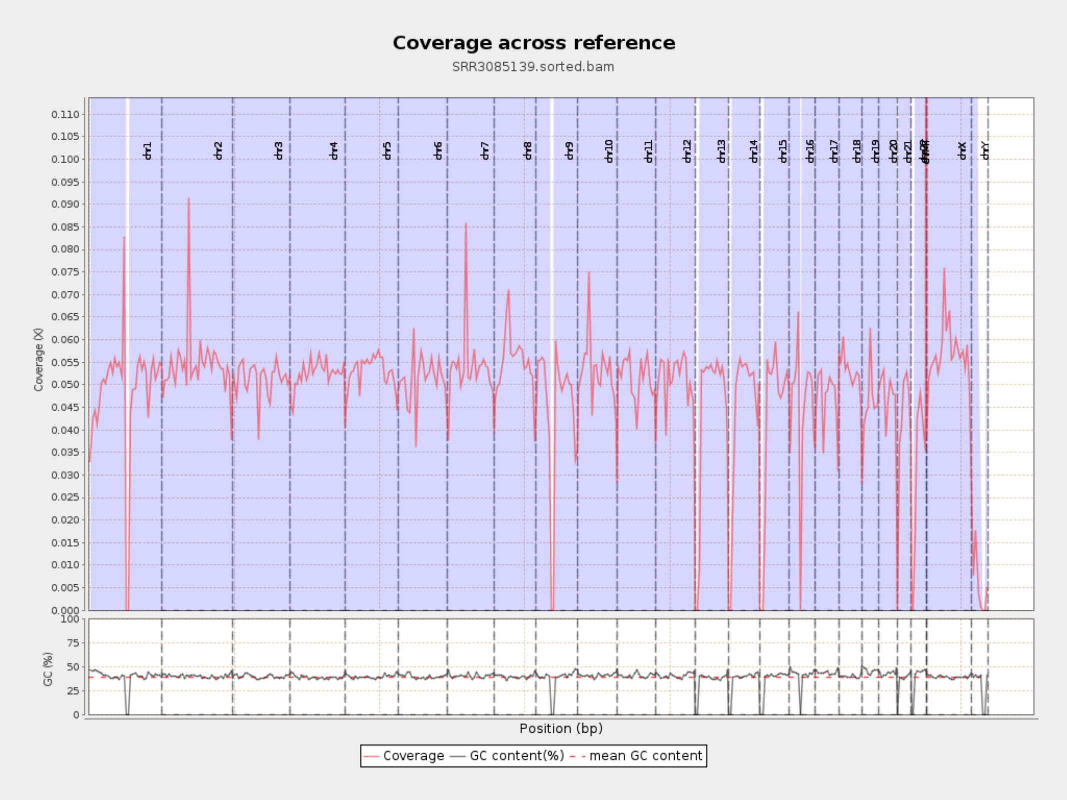
General error rate	0.9%
Mismatches	1,349,805
Insertions	12,018
Mapped reads with at least one insertion	0.53%
Deletions	35,855
Mapped reads with at least one deletion	1.58%
Homopolymer indels	47.1%

2.6. Chromosome stats

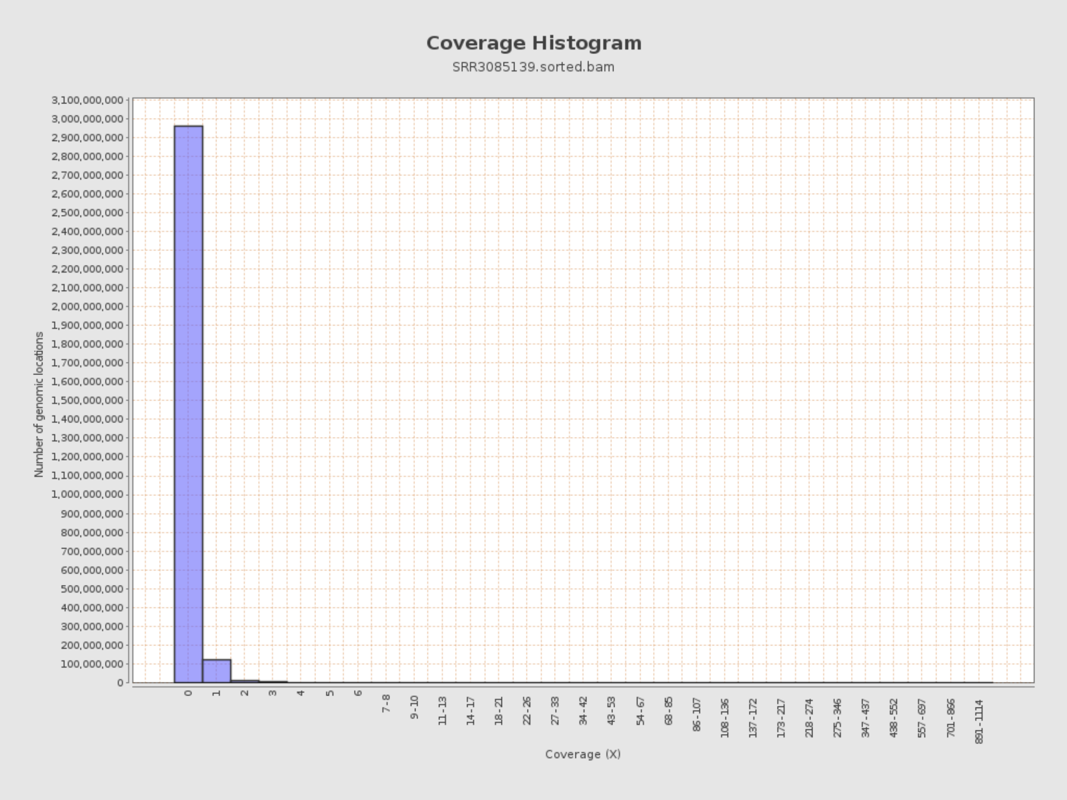
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12032508	0.0483	0.7806
chr2	243199373	13286570	0.0546	0.479
chr3	198022430	10165940	0.0513	0.2491
chr4	191154276	10031909	0.0525	0.2617
chr5	180915260	9593198	0.053	0.2546
chr6	171115067	8764400	0.0512	0.2891
chr7	159138663	8662028	0.0544	0.5542

chr8	146364022	8041137	0.0549	0.7171
chr9	141213431	6311142	0.0447	0.3693
chr10	135534747	7230771	0.0533	0.3826
chr11	135006516	6909155	0.0512	0.3582
chr12	133851895	6864634	0.0513	0.2523
chr13	115169878	5016730	0.0436	0.2299
chr14	107349540	4615787	0.043	0.2415
chr15	102531392	4333965	0.0423	0.2334
chr16	90354753	4088712	0.0453	0.2585
chr17	81195210	3785204	0.0466	0.2631
chr18	78077248	4152189	0.0532	0.692
chr19	59128983	2739065	0.0463	0.5591
chr20	63025520	2982562	0.0473	0.244
chr21	48129895	1962550	0.0408	0.2367
chr22	51304566	1523321	0.0297	0.1866
chrMT	16571	9361	0.5649	0.805
chrX	155270560	8782917	0.0566	0.2949
chrY	59373566	363095	0.0061	0.1318

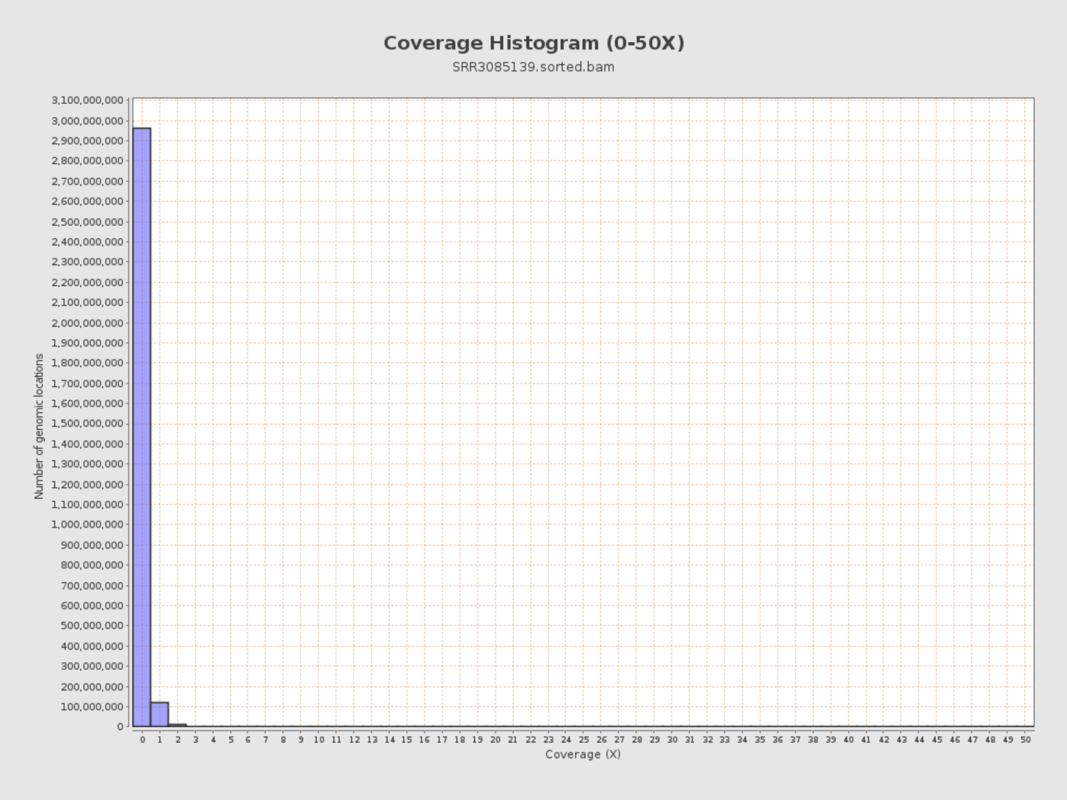
3. Results : Coverage across reference



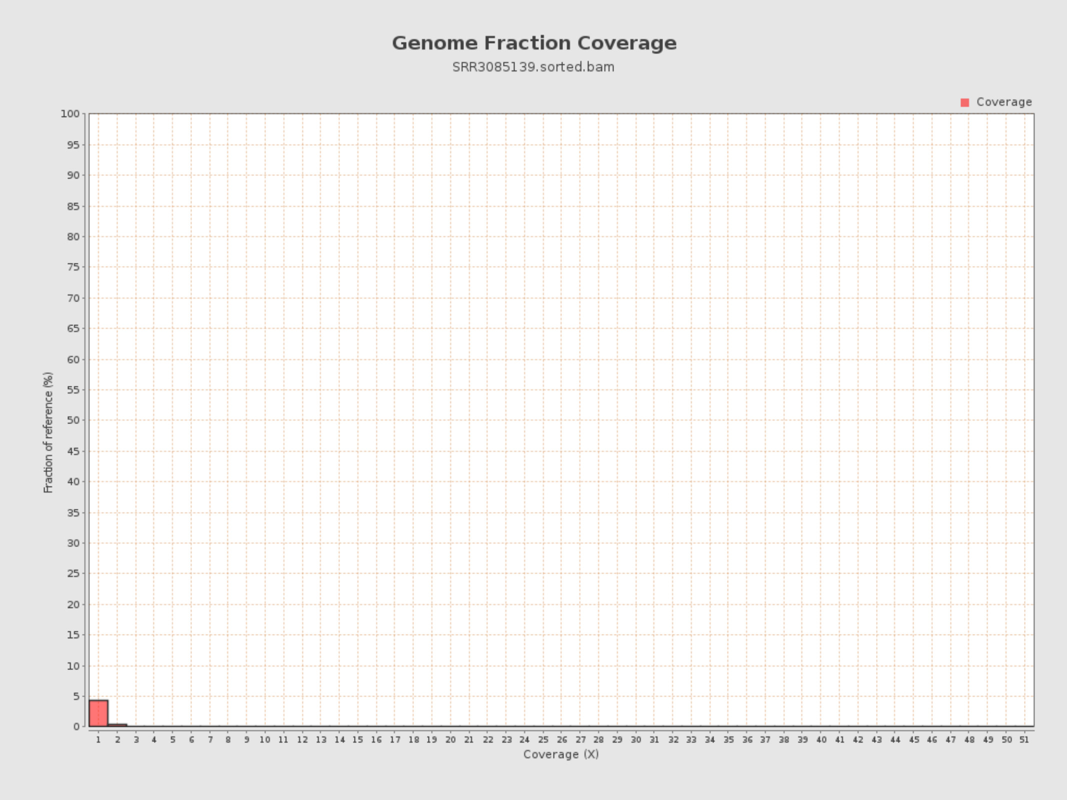
4. Results : Coverage Histogram



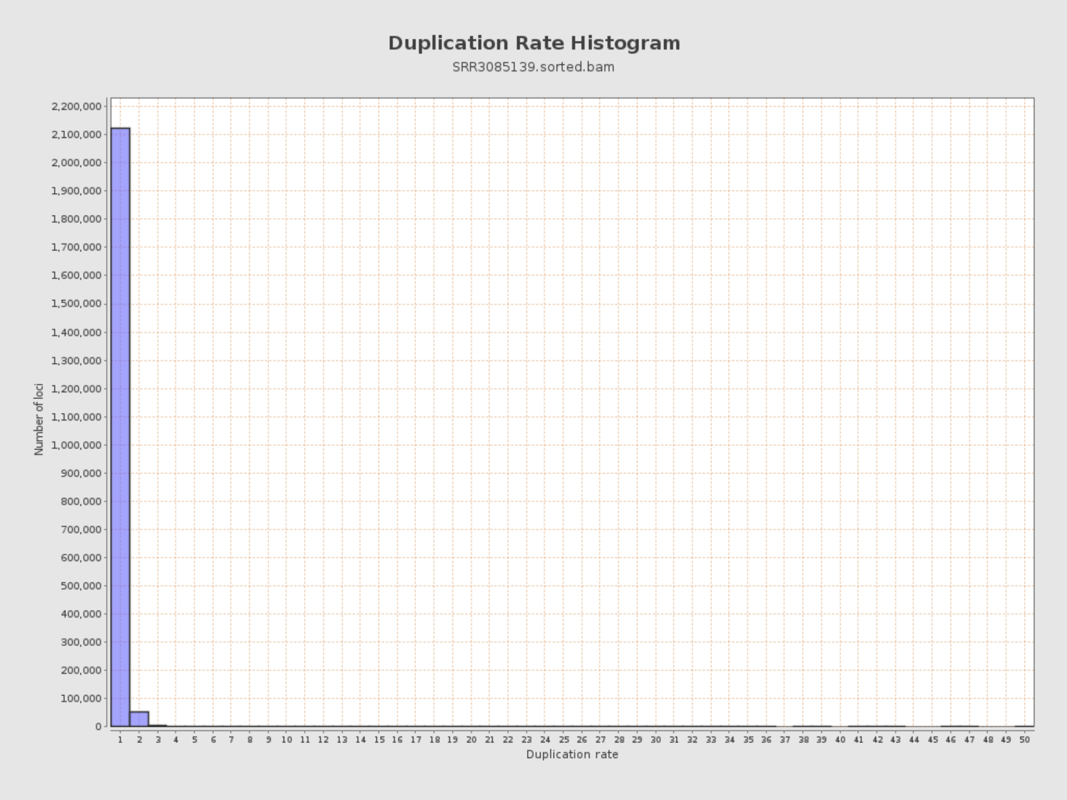
5. Results : Coverage Histogram (0-50X)



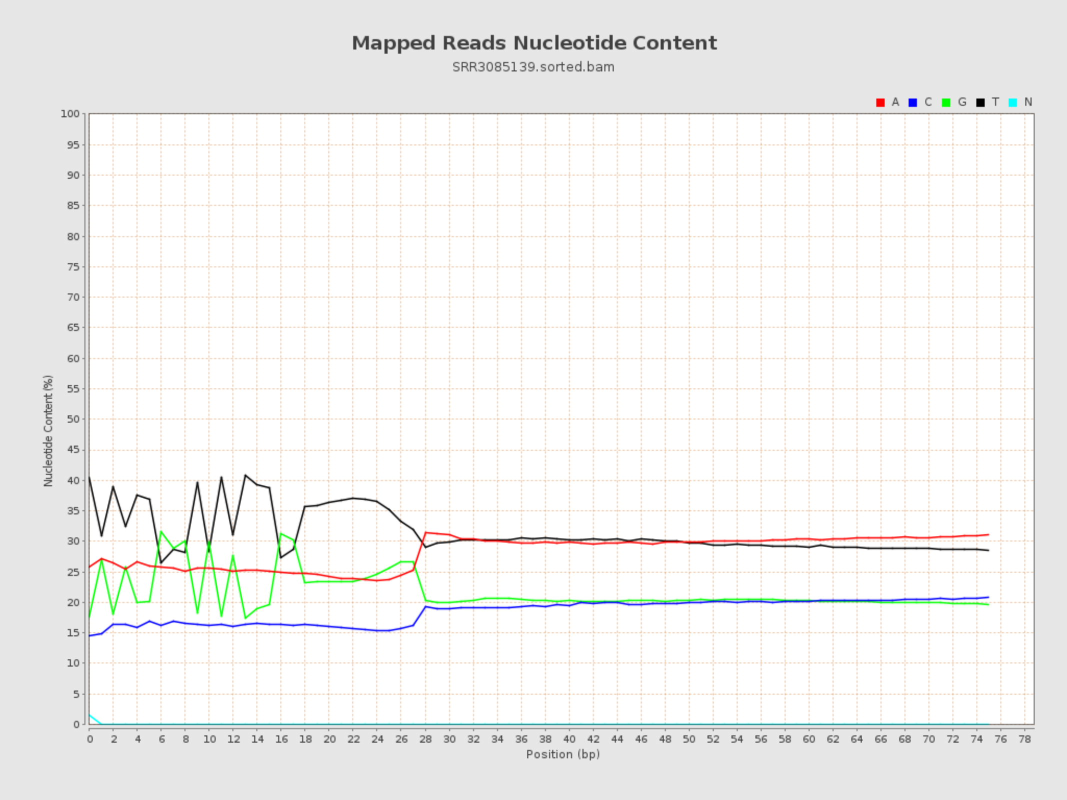
6. Results : Genome Fraction Coverage



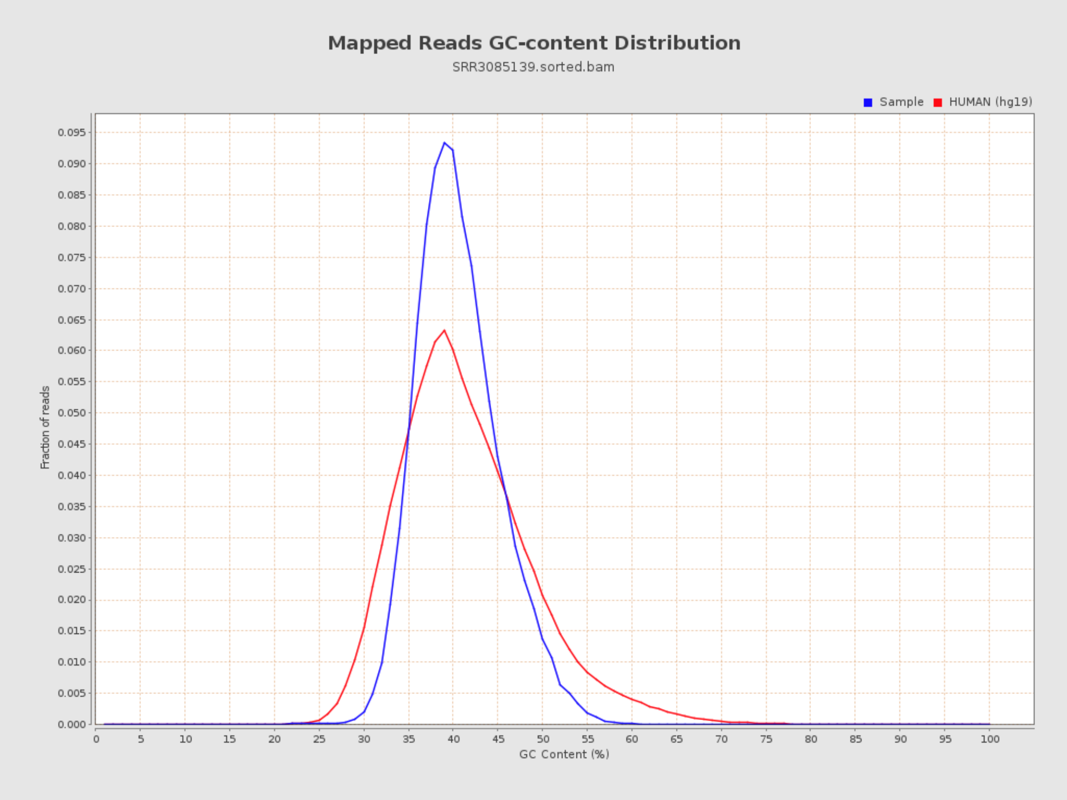
7. Results : Duplication Rate Histogram



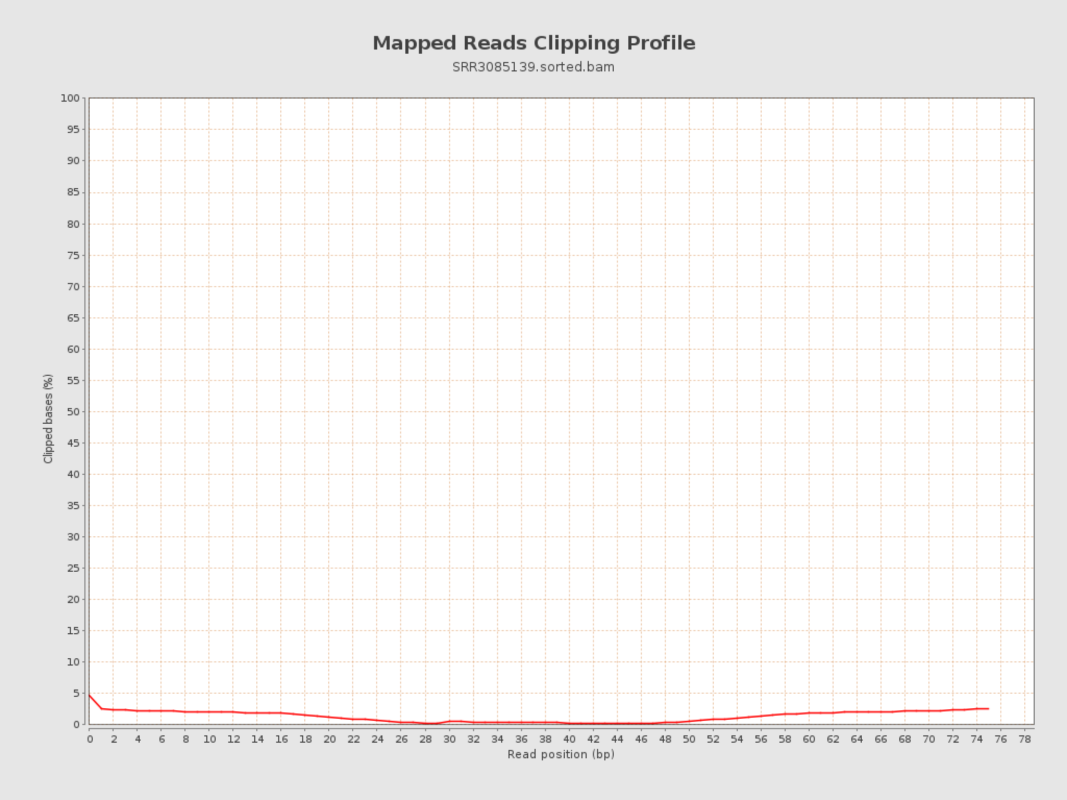
8. Results : Mapped Reads Nucleotide Content



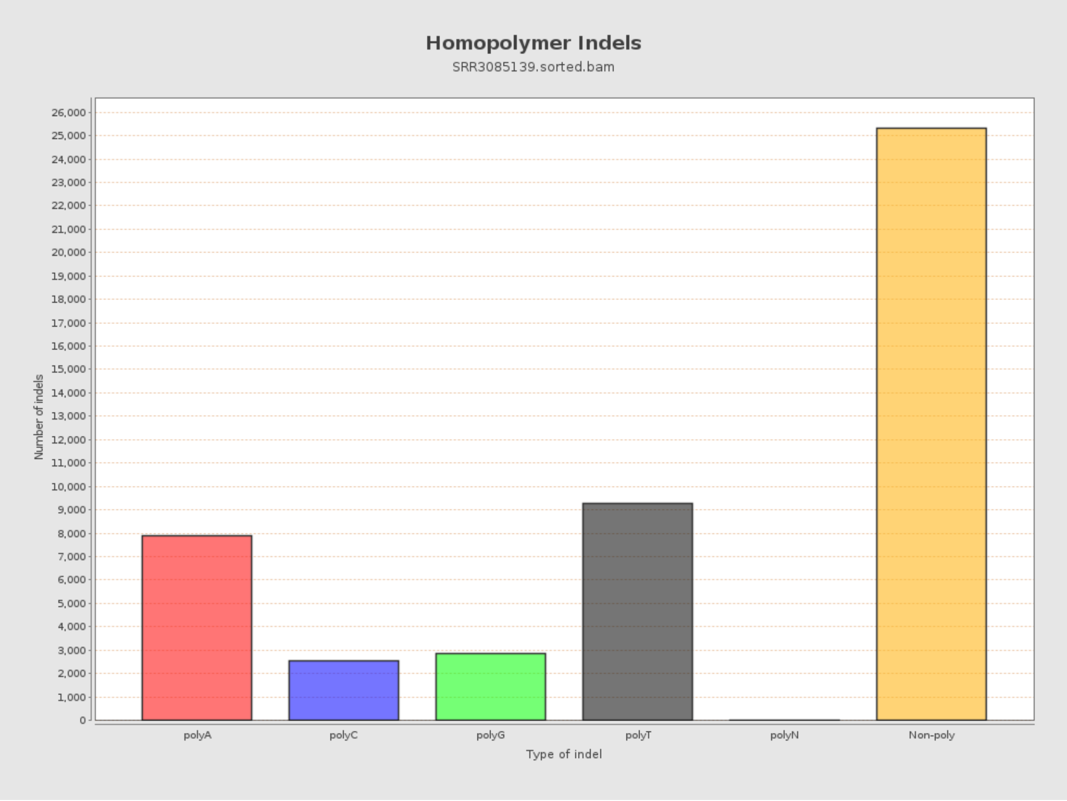
9. Results : Mapped Reads GC-content Distribution



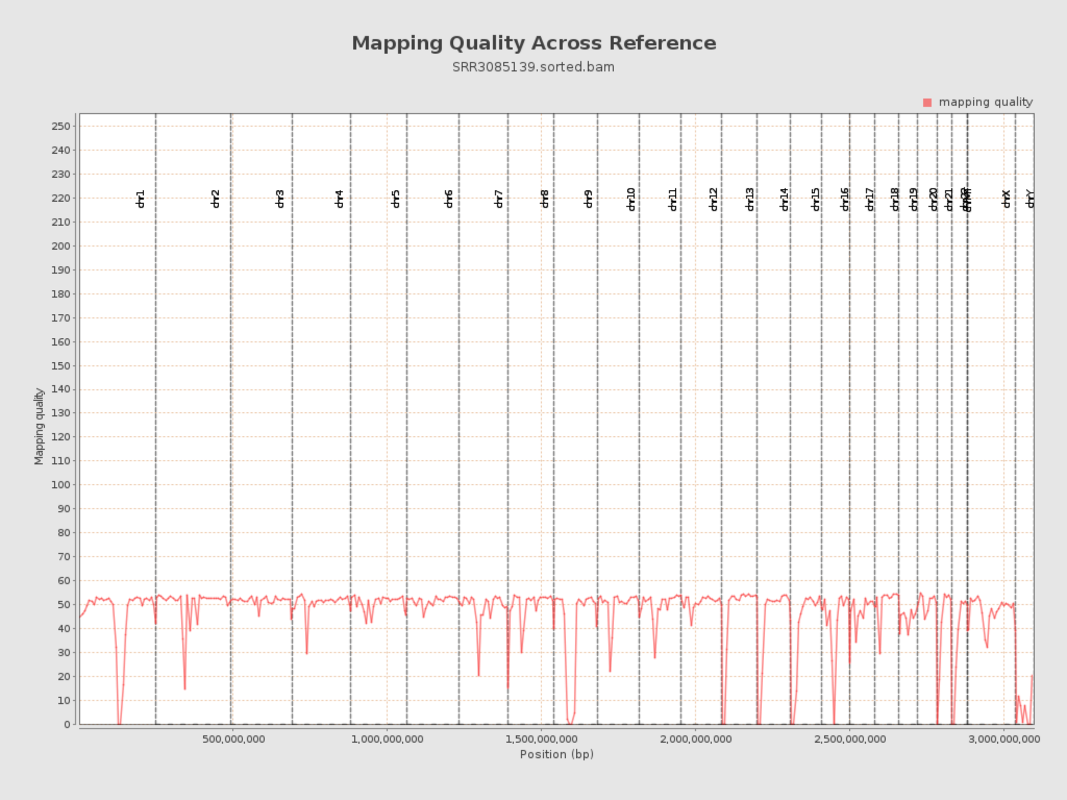
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram