Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 04:03:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085141.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_SRR3085141 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085141.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 04:03:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085141.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,435,677
Mapped reads	2,220,857 / 91.18%
Unmapped reads	214,820 / 8.82%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,347 / 0.92%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	83,697 / 3.44%
Duplication rate	2.95%
Clipped reads	880,642 / 36.16%

2.2. ACGT Content

Number/percentage of A's	43,242,509 / 28.57%
Number/percentage of C's	27,979,351 / 18.48%
Number/percentage of T's	47,757,562 / 31.55%
Number/percentage of G's	32,371,369 / 21.38%
Number/percentage of N's	28,374 / 0.02%
GC Percentage	39.87%

2.3. Coverage

Mean	0.0489

Standard Deviation	0.3959

2.4. Mapping Quality

Mean Mapping Quality	47.2

2.5. Mismatches and indels

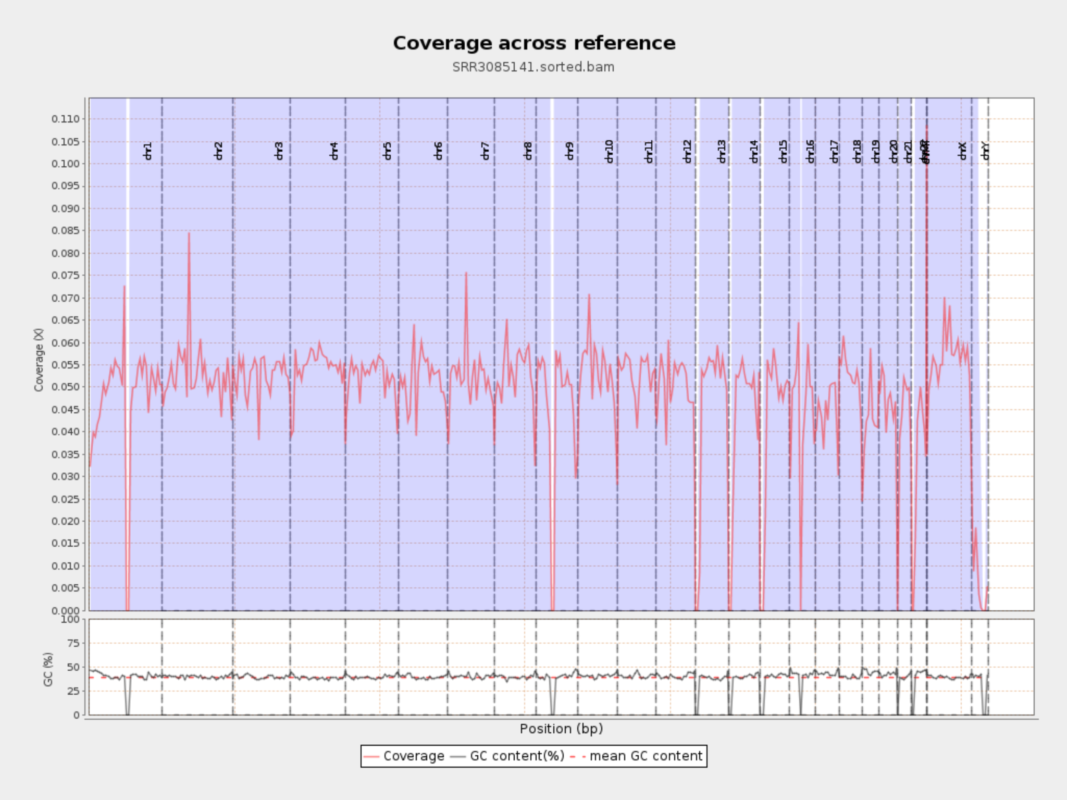
General error rate	0.88%
Mismatches	1,315,869
Insertions	11,845
Mapped reads with at least one insertion	0.53%
Deletions	33,380
Mapped reads with at least one deletion	1.49%
Homopolymer indels	47.85%

2.6. Chromosome stats

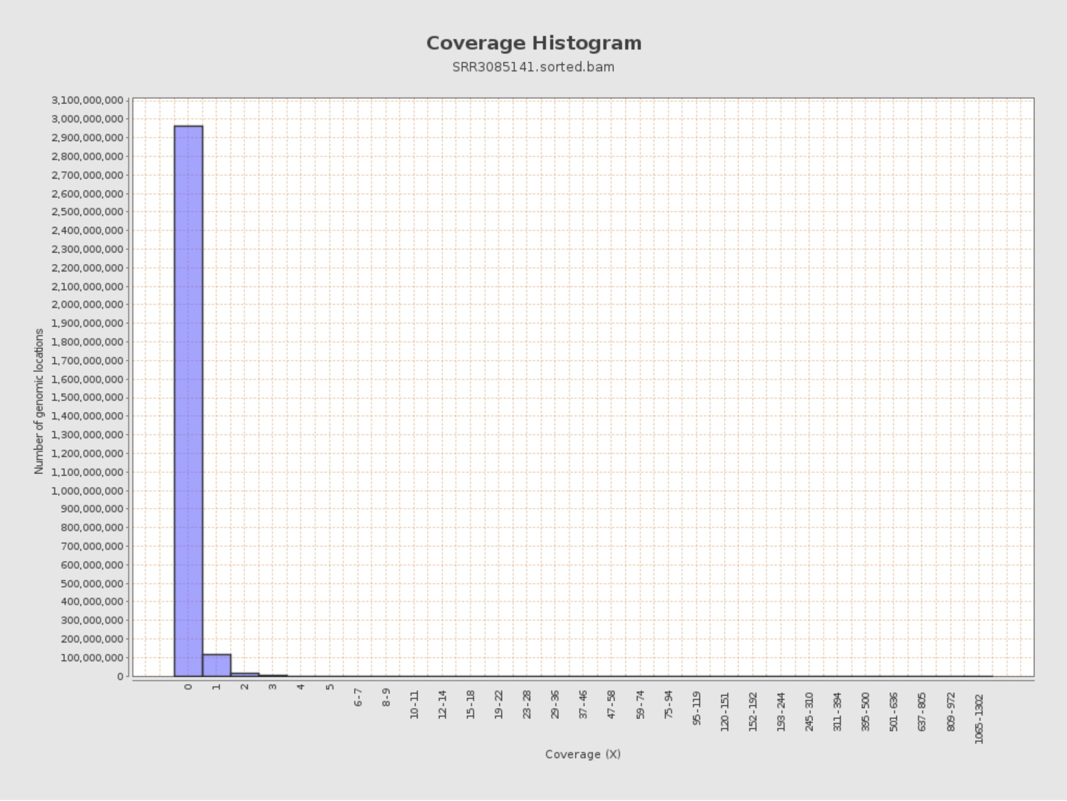
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11788223	0.0473	0.6171
chr2	243199373	12932281	0.0532	0.4438
chr3	198022430	10428811	0.0527	0.2538
chr4	191154276	10402592	0.0544	0.268
chr5	180915260	9476178	0.0524	0.2555
chr6	171115067	8849752	0.0517	0.2865
chr7	159138663	8385890	0.0527	0.4611

chr8	146364022	7715556	0.0527	0.8076
chr9	141213431	6352544	0.045	0.3553
chr10	135534747	7295000	0.0538	0.3531
chr11	135006516	7118222	0.0527	0.3452
chr12	133851895	6754818	0.0505	0.2528
chr13	115169878	5169741	0.0449	0.2358
chr14	107349540	4529374	0.0422	0.2421
chr15	102531392	4347851	0.0424	0.2338
chr16	90354753	4040549	0.0447	0.2582
chr17	81195210	3569373	0.044	0.2584
chr18	78077248	4162563	0.0533	0.6594
chr19	59128983	2551065	0.0431	0.4986
chr20	63025520	2931336	0.0465	0.2452
chr21	48129895	1977296	0.0411	0.2388
chr22	51304566	1562577	0.0305	0.1918
chrMT	16571	1800	0.1086	0.345
chrX	155270560	8717367	0.0561	0.2904
chrY	59373566	372872	0.0063	0.1401

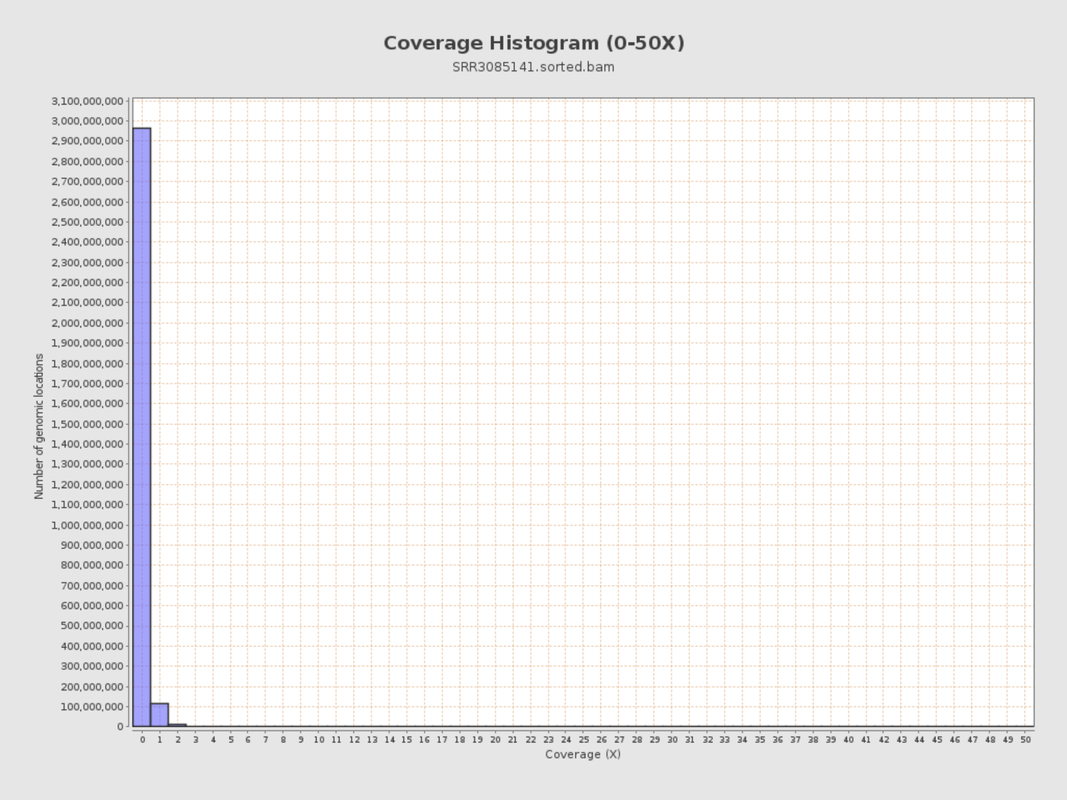
3. Results : Coverage across reference



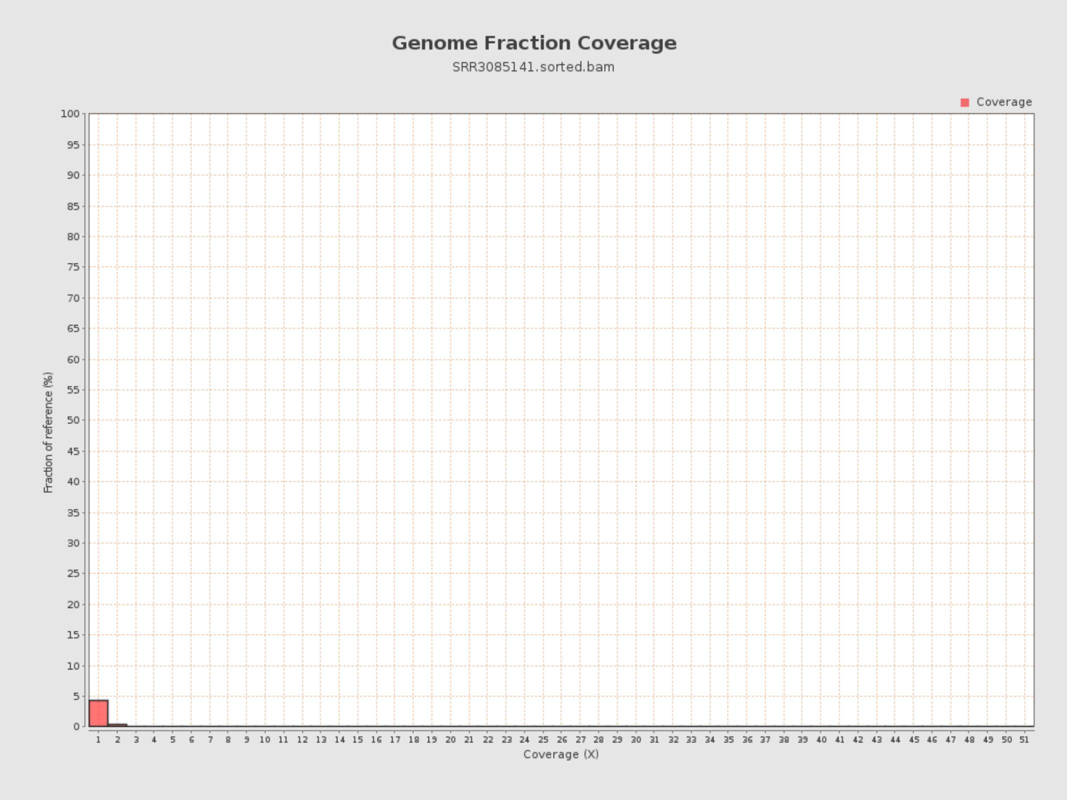
4. Results : Coverage Histogram



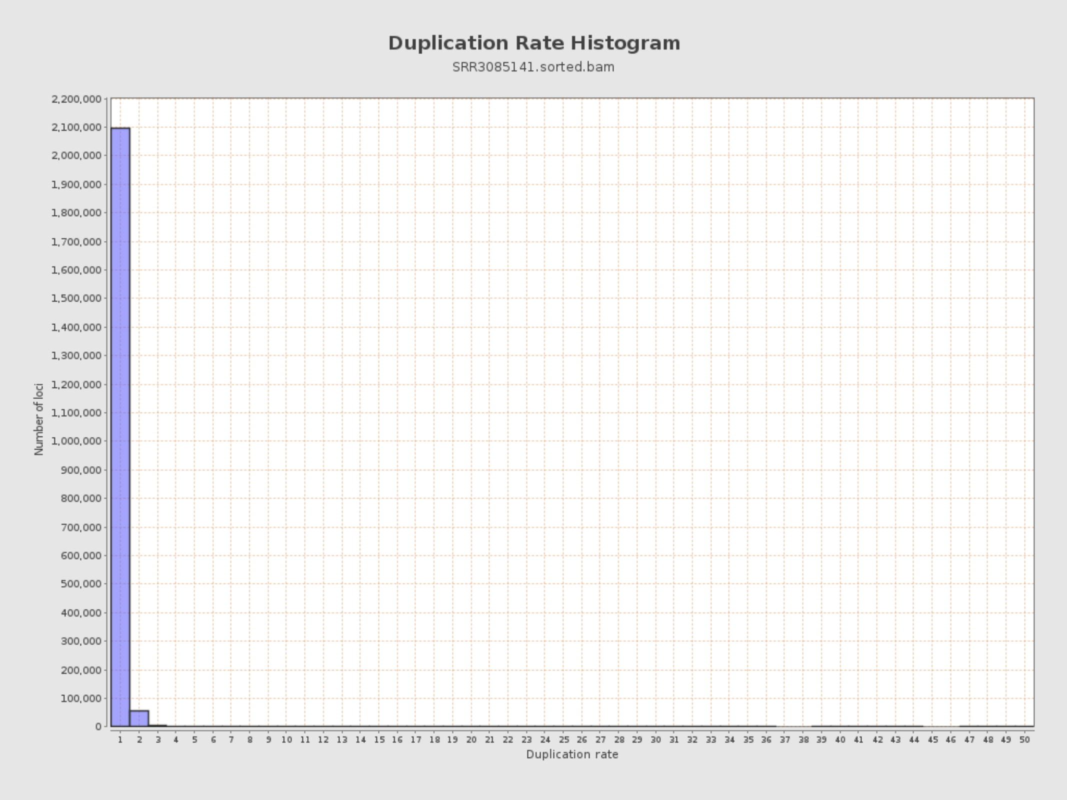
5. Results : Coverage Histogram (0-50X)



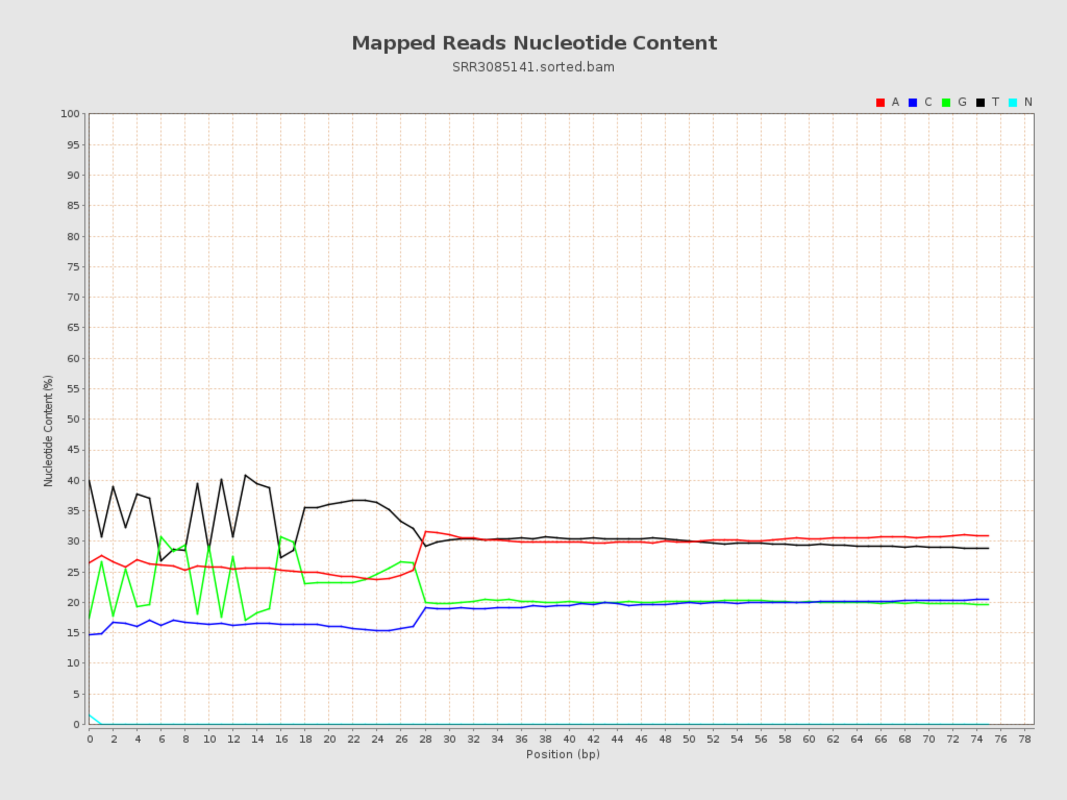
6. Results : Genome Fraction Coverage



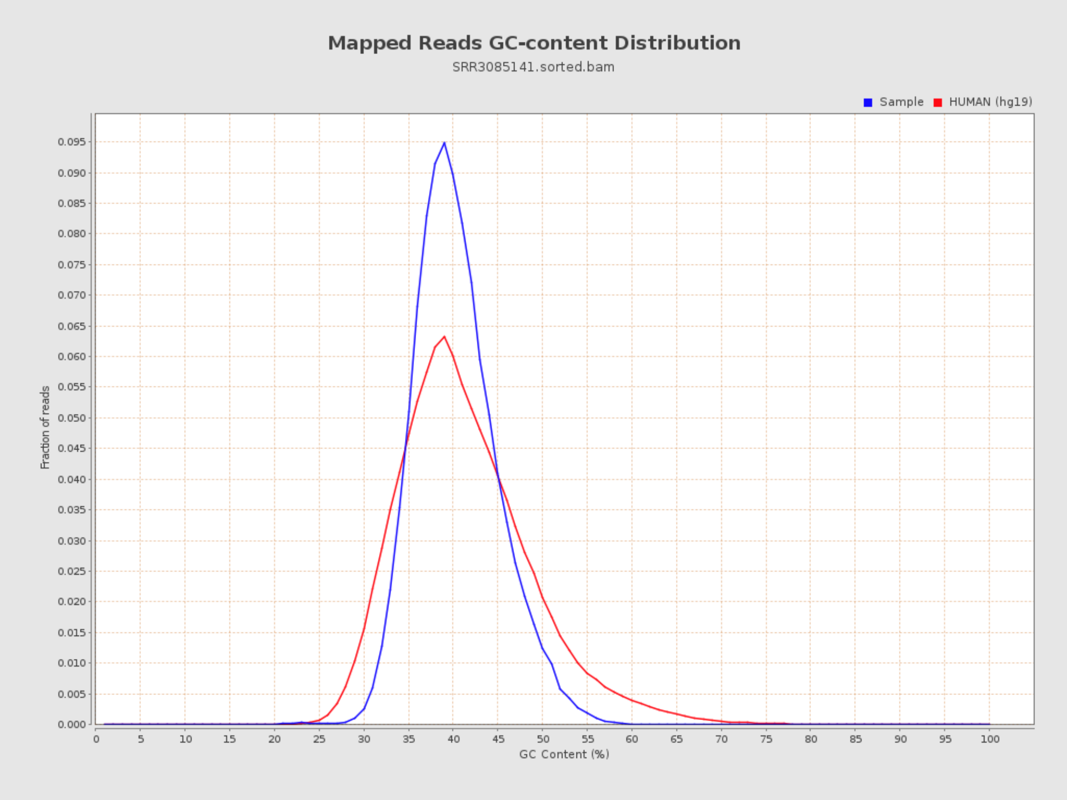
7. Results : Duplication Rate Histogram



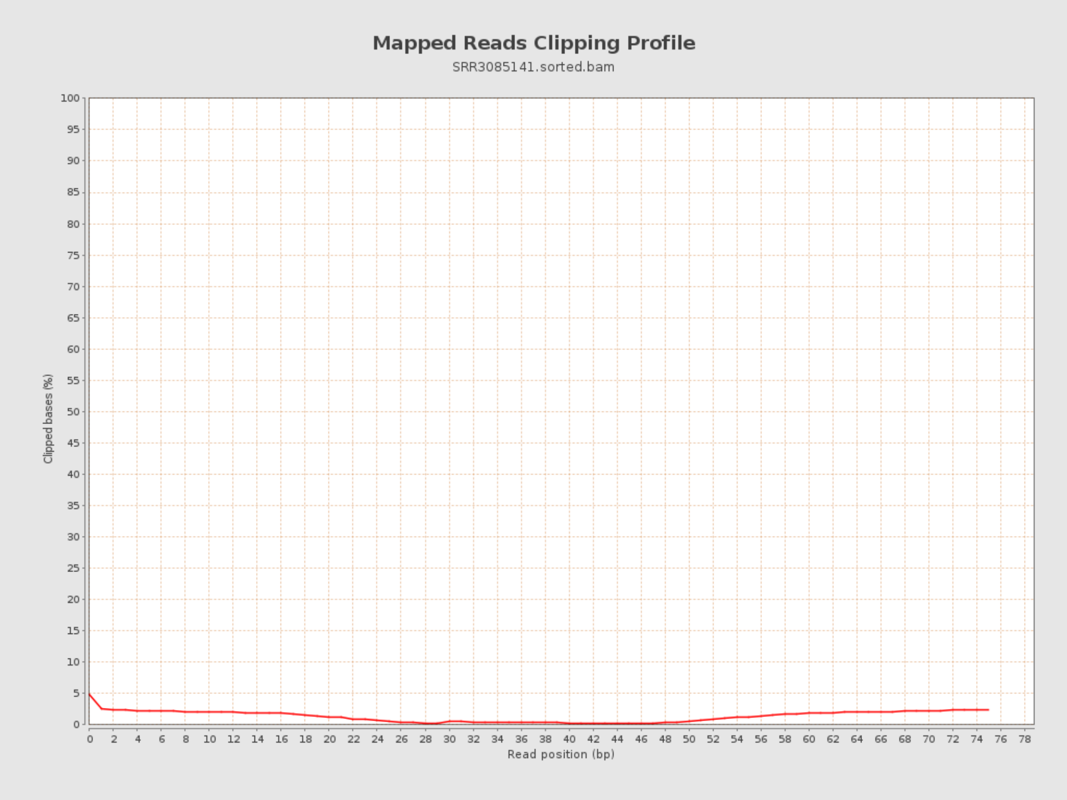
8. Results : Mapped Reads Nucleotide Content



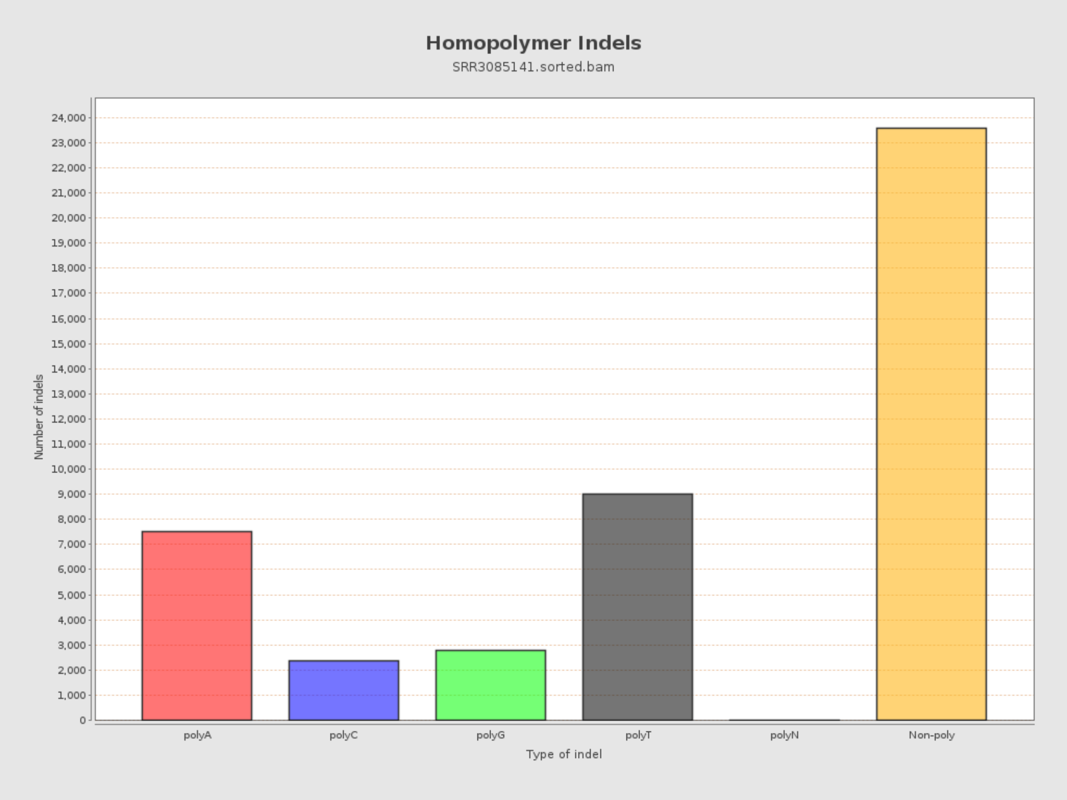
9. Results : Mapped Reads GC-content Distribution



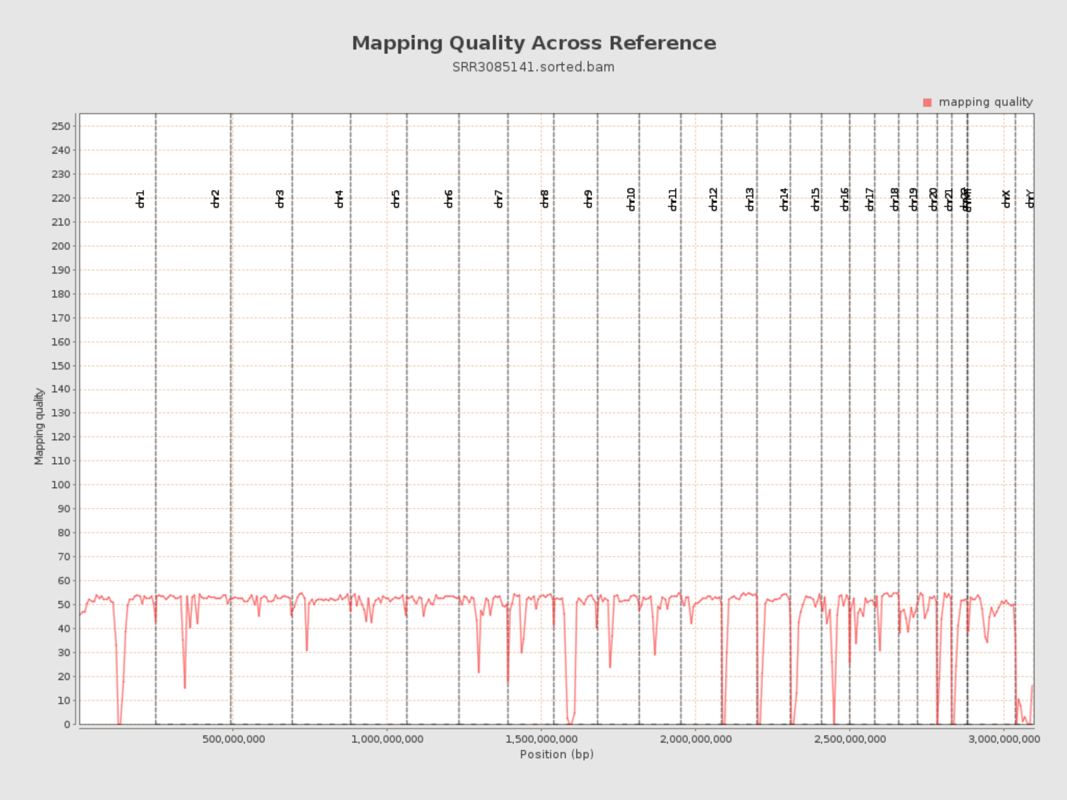
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram