Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 03:18:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085134.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_SRR3085134 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085134.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 03:17:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085134.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,084,631
Mapped reads	1,885,437 / 90.44%
Unmapped reads	199,194 / 9.56%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,195 / 1.06%
Read min/max/mean length	30 / 76 / 76.37
Duplicated reads (estimated)	88,770 / 4.26%
Duplication rate	3.9%
Clipped reads	857,358 / 41.13%

2.2. ACGT Content

Number/percentage of A's	35,928,674 / 28.41%
Number/percentage of C's	23,536,444 / 18.61%
Number/percentage of T's	39,774,712 / 31.46%
Number/percentage of G's	27,177,024 / 21.49%
Number/percentage of N's	25,995 / 0.02%
GC Percentage	40.11%

2.3. Coverage

Mean	0.0409

Standard Deviation	0.3318

2.4. Mapping Quality

Mean Mapping Quality	46.87

2.5. Mismatches and indels

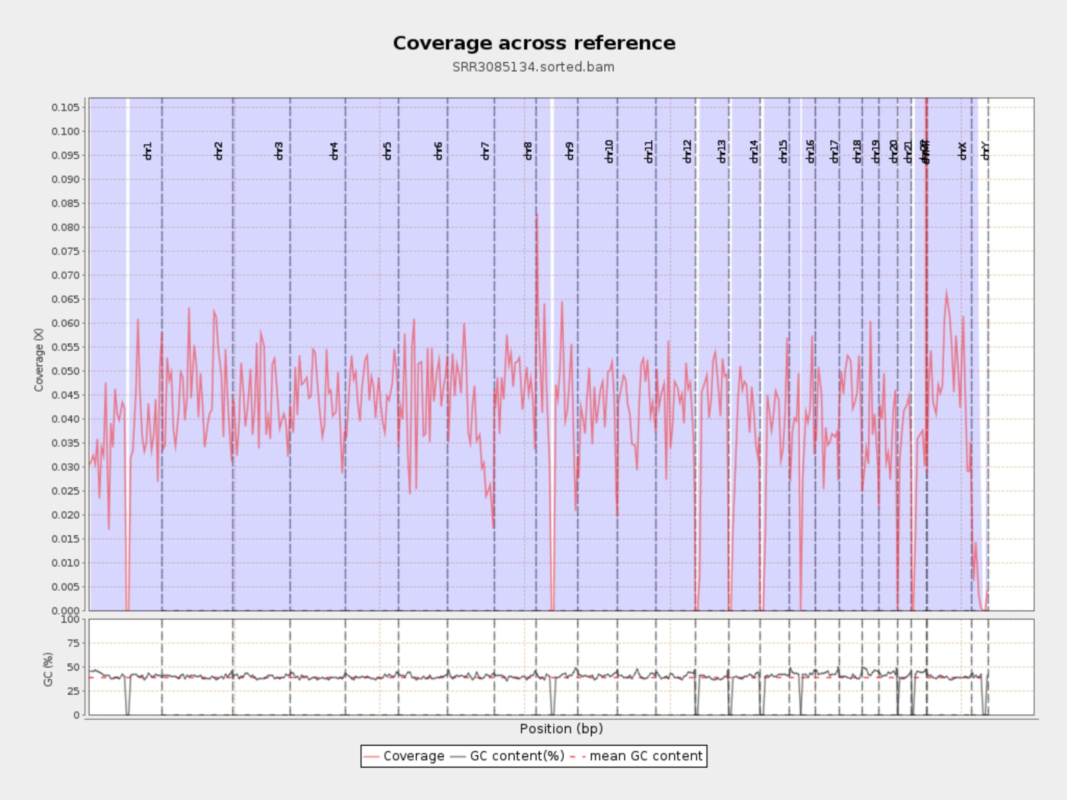
General error rate	0.91%
Mismatches	1,137,503
Insertions	9,809
Mapped reads with at least one insertion	0.52%
Deletions	29,726
Mapped reads with at least one deletion	1.56%
Homopolymer indels	47.69%

2.6. Chromosome stats

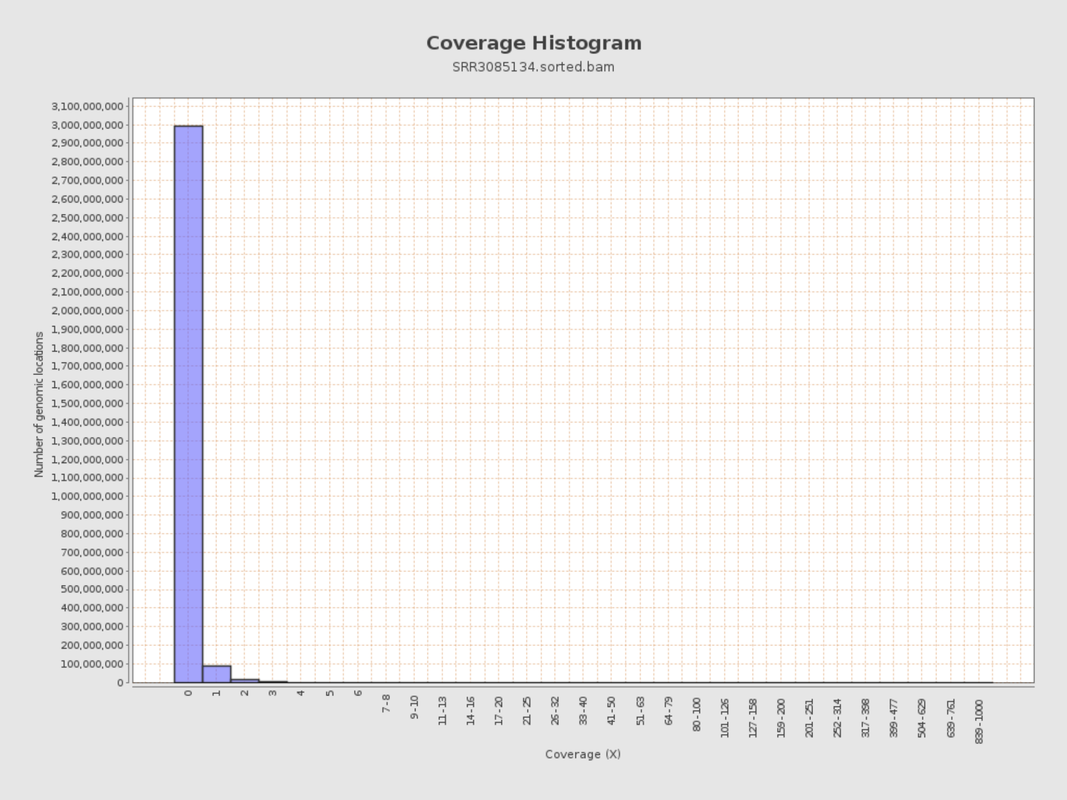
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8797545	0.0353	0.4676
chr2	243199373	11069334	0.0455	0.3811
chr3	198022430	8551412	0.0432	0.2436
chr4	191154276	8509406	0.0445	0.2573
chr5	180915260	8317379	0.046	0.2526
chr6	171115067	7654823	0.0447	0.2794
chr7	159138663	6266901	0.0394	0.3379

chr8	146364022	6922273	0.0473	0.6404
chr9	141213431	5873809	0.0416	0.3055
chr10	135534747	5772728	0.0426	0.295
chr11	135006516	5812204	0.0431	0.3171
chr12	133851895	5807266	0.0434	0.2468
chr13	115169878	4545682	0.0395	0.2358
chr14	107349540	3746443	0.0349	0.2281
chr15	102531392	3452870	0.0337	0.2204
chr16	90354753	3292362	0.0364	0.2353
chr17	81195210	3012268	0.0371	0.2421
chr18	78077248	3716463	0.0476	0.5103
chr19	59128983	2139986	0.0362	0.3692
chr20	63025520	2395501	0.038	0.2346
chr21	48129895	1694545	0.0352	0.2302
chr22	51304566	1278913	0.0249	0.1839
chrMT	16571	128274	7.7409	4.8473
chrX	155270560	7446667	0.048	0.2747
chrY	59373566	285533	0.0048	0.1022

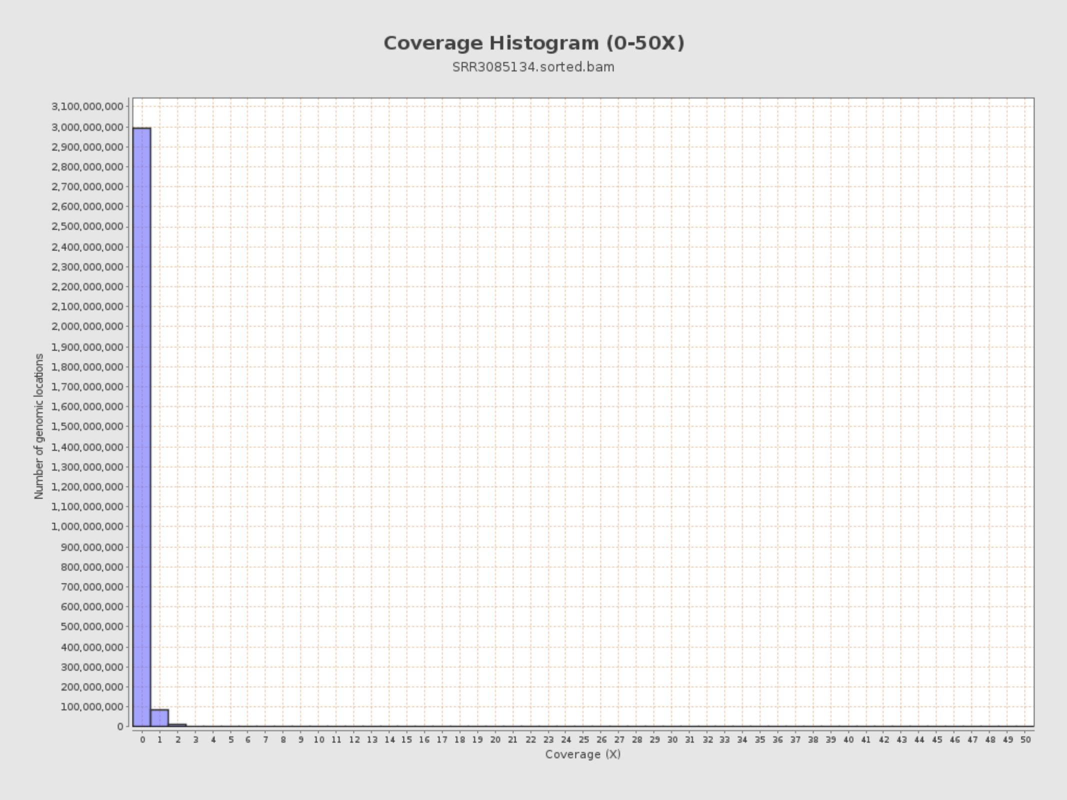
3. Results : Coverage across reference



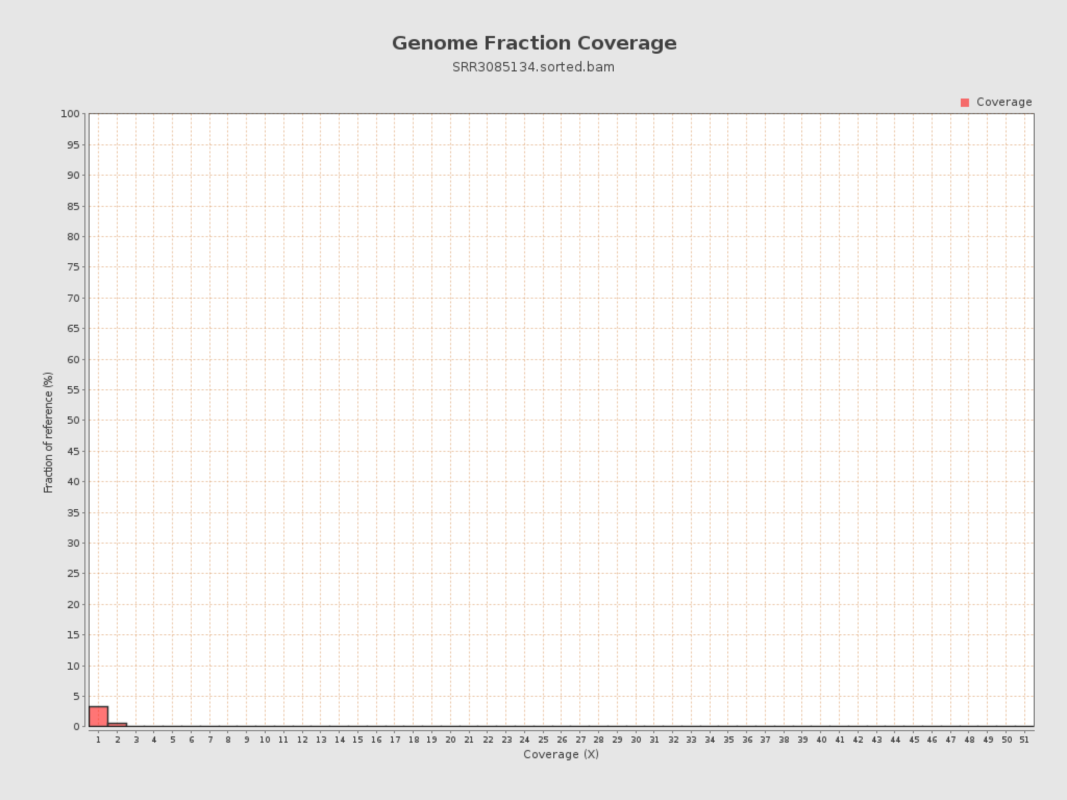
4. Results : Coverage Histogram



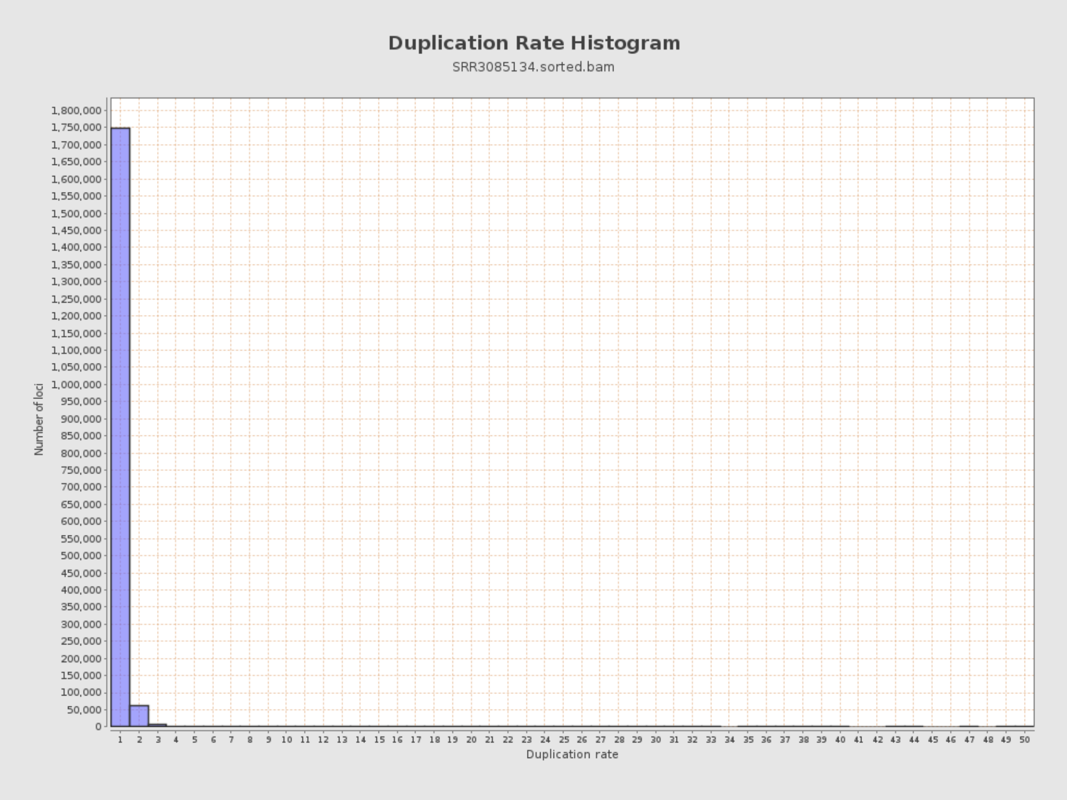
5. Results : Coverage Histogram (0-50X)



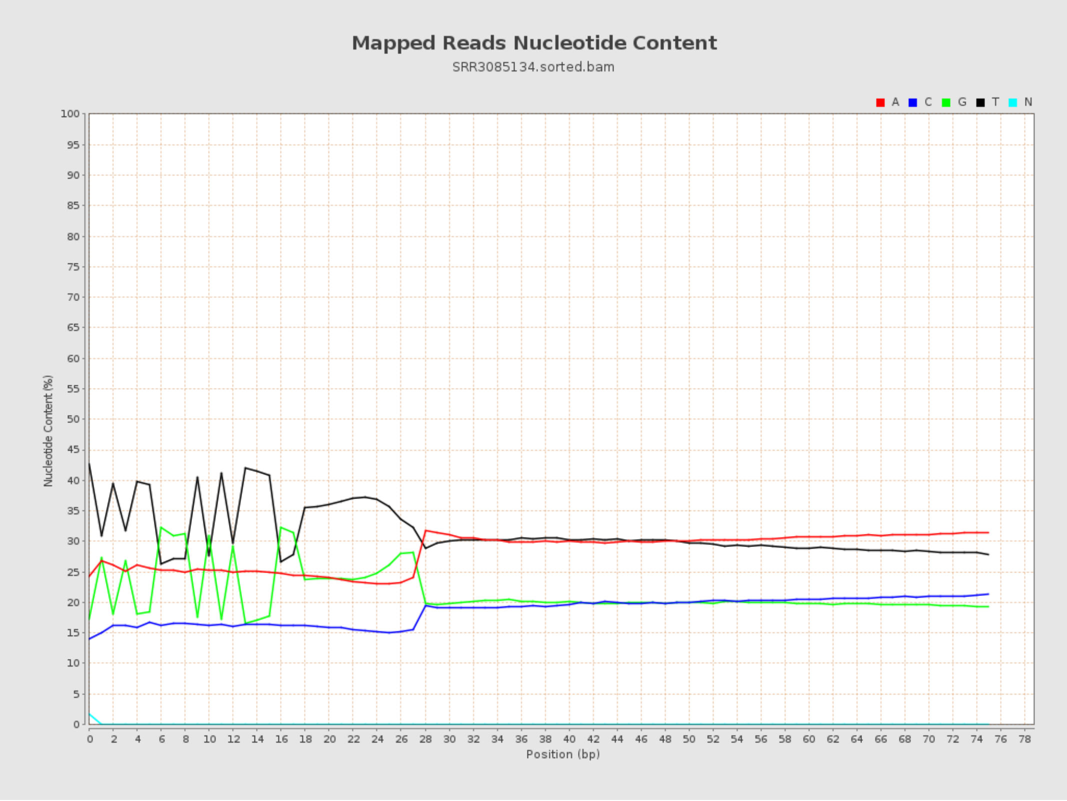
6. Results : Genome Fraction Coverage



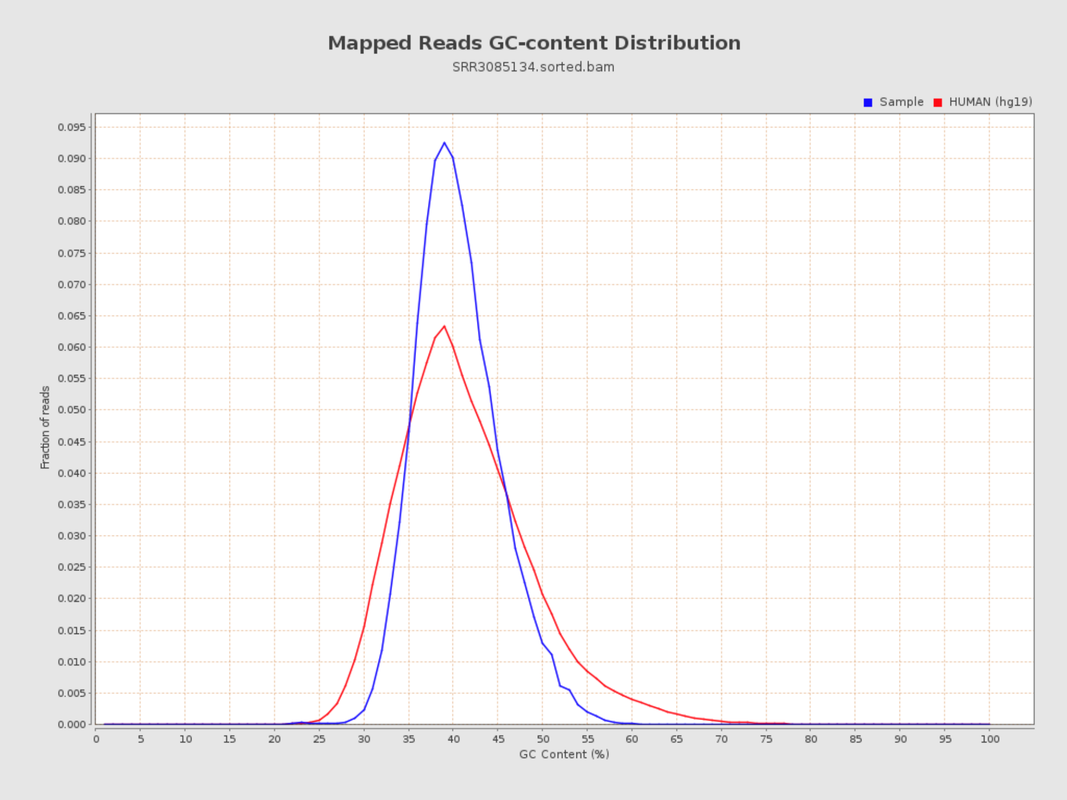
7. Results : Duplication Rate Histogram



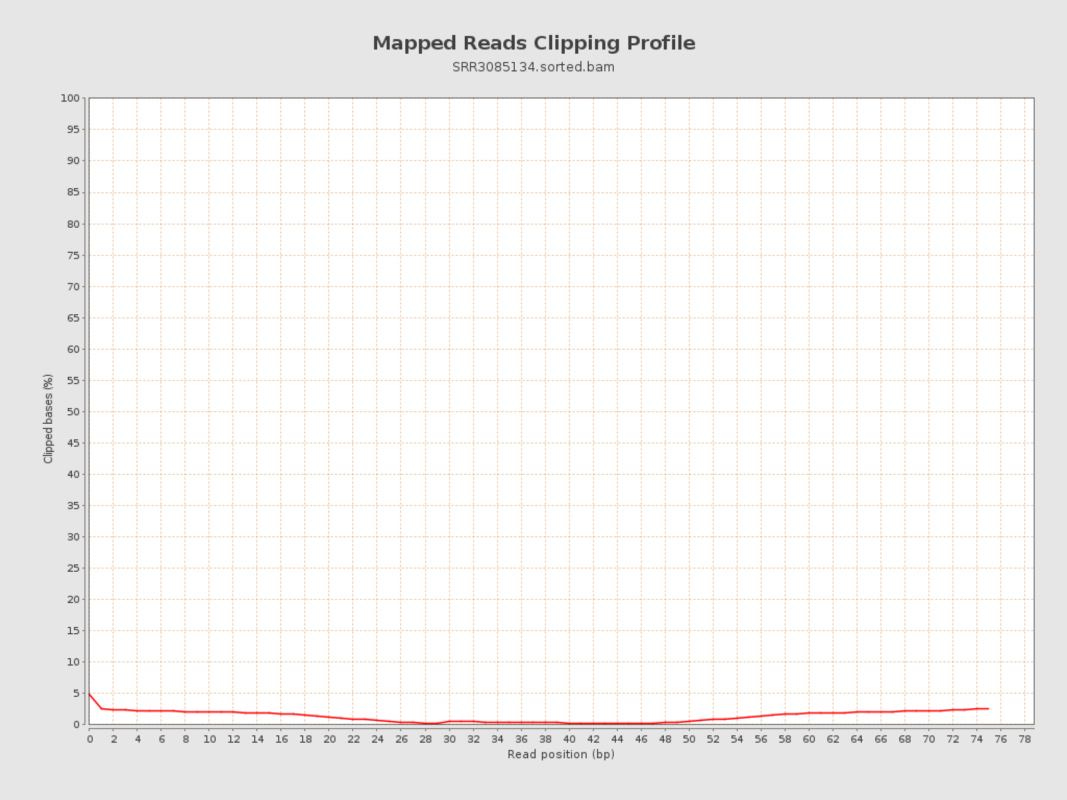
8. Results : Mapped Reads Nucleotide Content



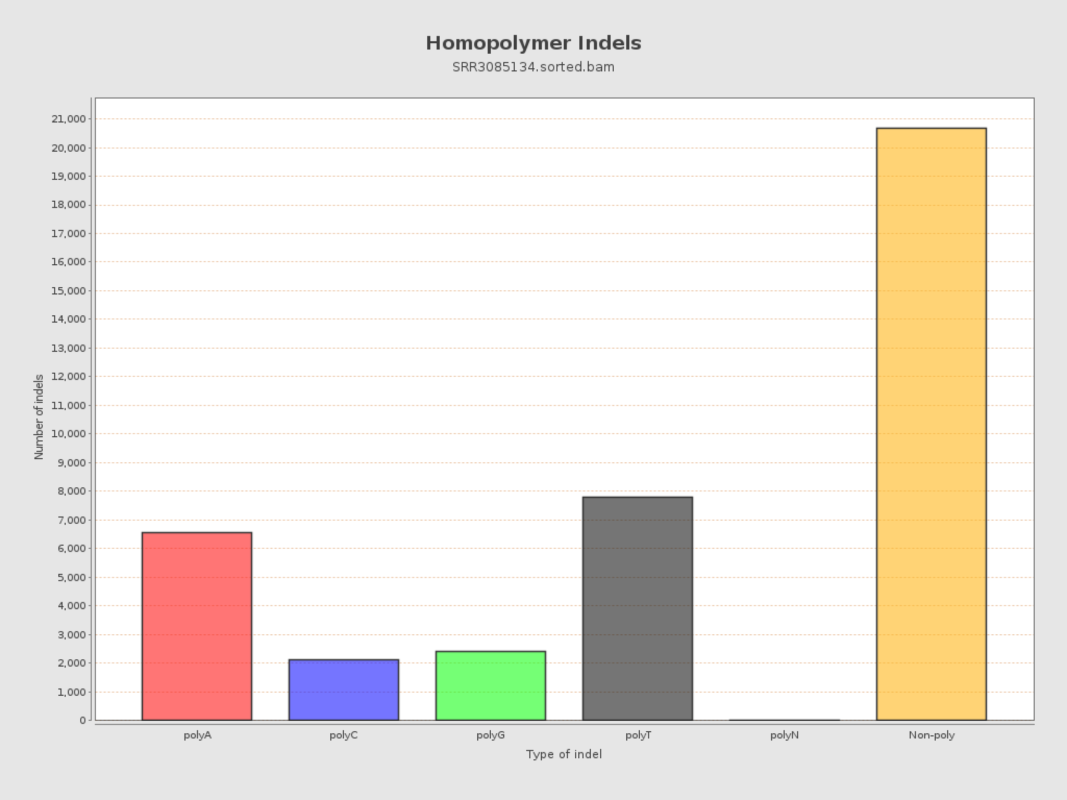
9. Results : Mapped Reads GC-content Distribution



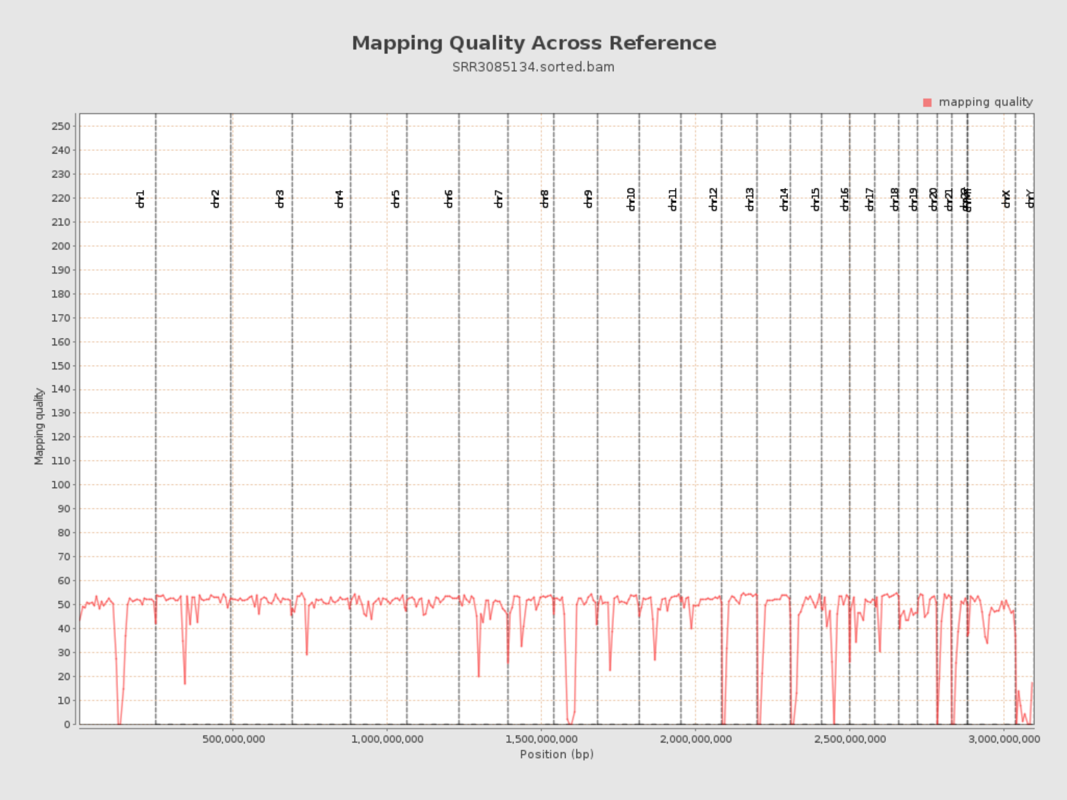
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram