Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 03:25:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085135.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_SRR3085135 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085135.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 03:25:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085135.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,399,790
Mapped reads	1,262,718 / 90.21%
Unmapped reads	137,072 / 9.79%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,174 / 1.23%
Read min/max/mean length	30 / 76 / 76.43
Duplicated reads (estimated)	40,891 / 2.92%
Duplication rate	2.08%
Clipped reads	600,705 / 42.91%

2.2. ACGT Content

Number/percentage of A's	23,827,521 / 28.31%
Number/percentage of C's	16,070,808 / 19.09%
Number/percentage of T's	25,227,530 / 29.97%
Number/percentage of G's	19,033,614 / 22.61%
Number/percentage of N's	15,932 / 0.02%
GC Percentage	41.7%

2.3. Coverage

Mean	0.0272

Standard Deviation	0.3334

2.4. Mapping Quality

Mean Mapping Quality	43.73

2.5. Mismatches and indels

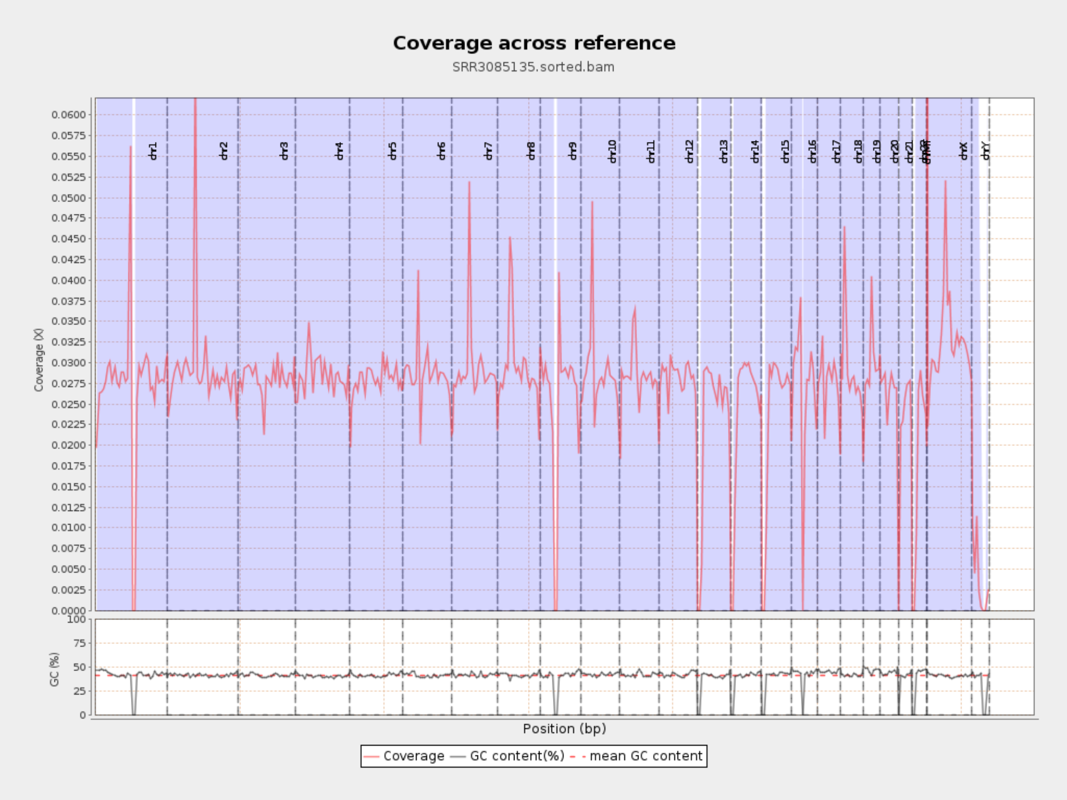
General error rate	0.89%
Mismatches	735,616
Insertions	7,516
Mapped reads with at least one insertion	0.59%
Deletions	18,052
Mapped reads with at least one deletion	1.41%
Homopolymer indels	43.77%

2.6. Chromosome stats

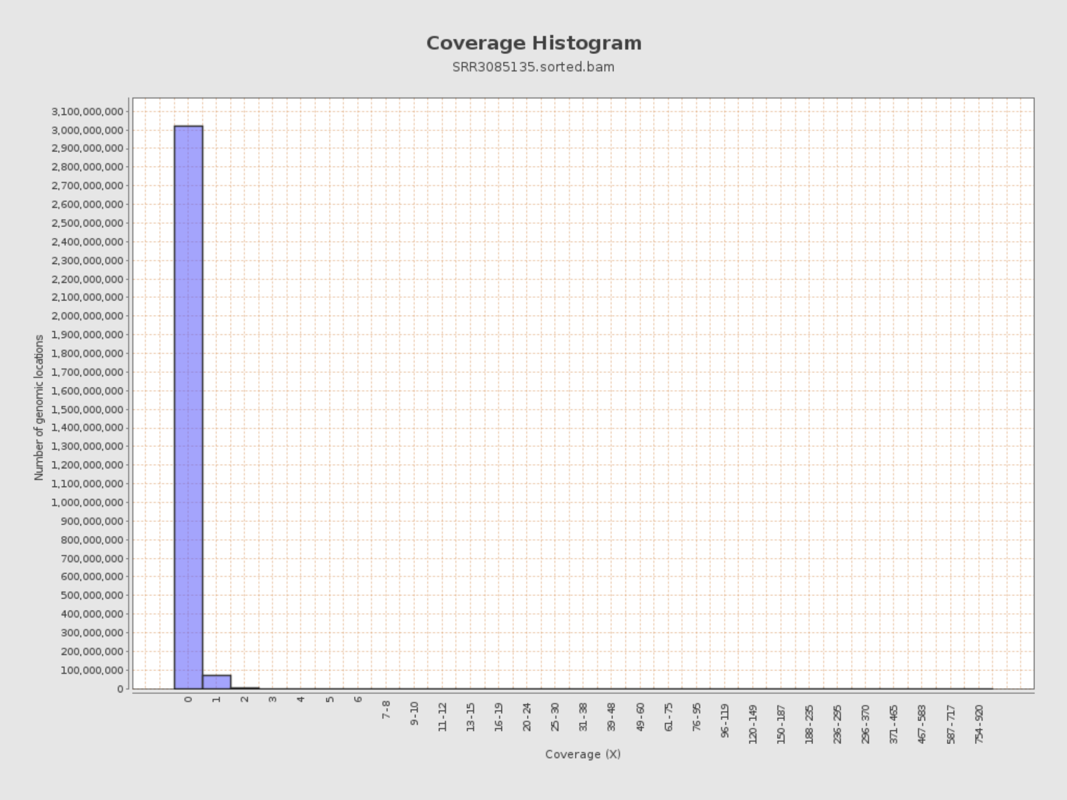
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6750842	0.0271	0.6084
chr2	243199373	7159452	0.0294	0.381
chr3	198022430	5560325	0.0281	0.1758
chr4	191154276	5446061	0.0285	0.1854
chr5	180915260	5081780	0.0281	0.1781
chr6	171115067	4893409	0.0286	0.2332
chr7	159138663	4680154	0.0294	0.337

chr8	146364022	4337528	0.0296	0.5819
chr9	141213431	3570976	0.0253	0.3082
chr10	135534747	3913703	0.0289	0.2885
chr11	135006516	3865317	0.0286	0.356
chr12	133851895	3775631	0.0282	0.1825
chr13	115169878	2598169	0.0226	0.1579
chr14	107349540	2532934	0.0236	0.1992
chr15	102531392	2371556	0.0231	0.1678
chr16	90354753	2362875	0.0262	0.2049
chr17	81195210	2243231	0.0276	0.2141
chr18	78077248	2284761	0.0293	0.6552
chr19	59128983	1762090	0.0298	0.4135
chr20	63025520	1664195	0.0264	0.179
chr21	48129895	1086015	0.0226	0.1768
chr22	51304566	929323	0.0181	0.1403
chrMT	16571	22401	1.3518	1.4169
chrX	155270560	5092810	0.0328	0.2367
chrY	59373566	219175	0.0037	0.0911

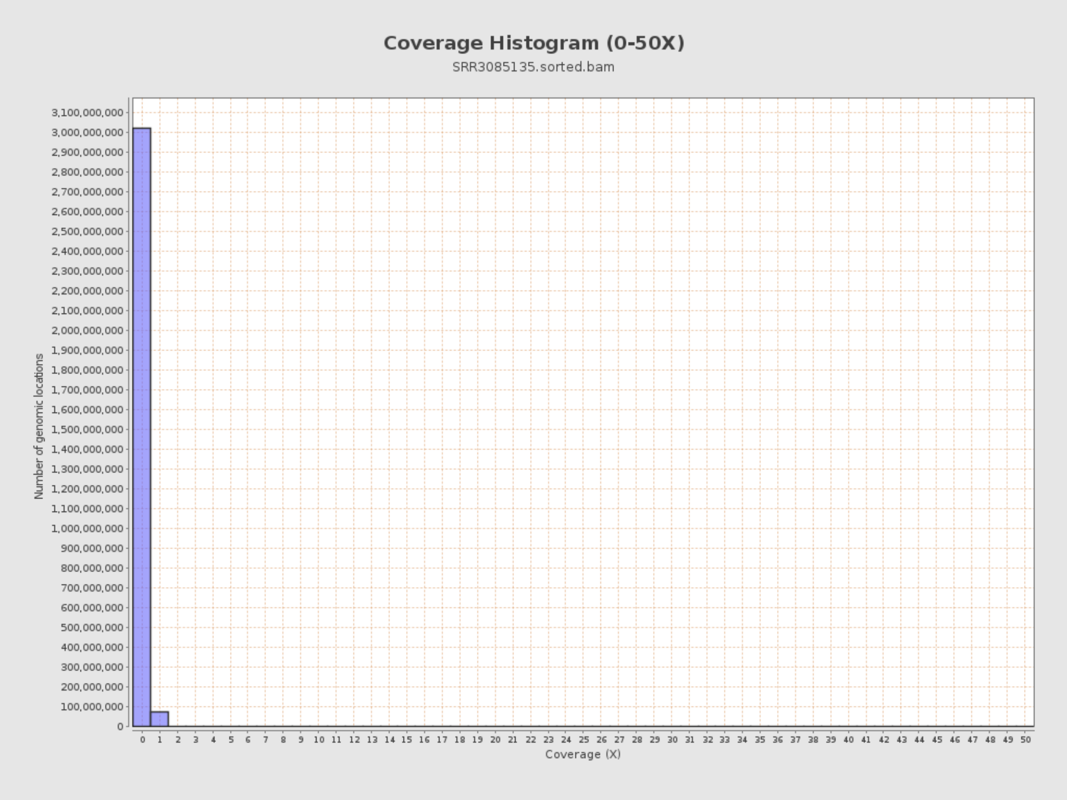
3. Results : Coverage across reference



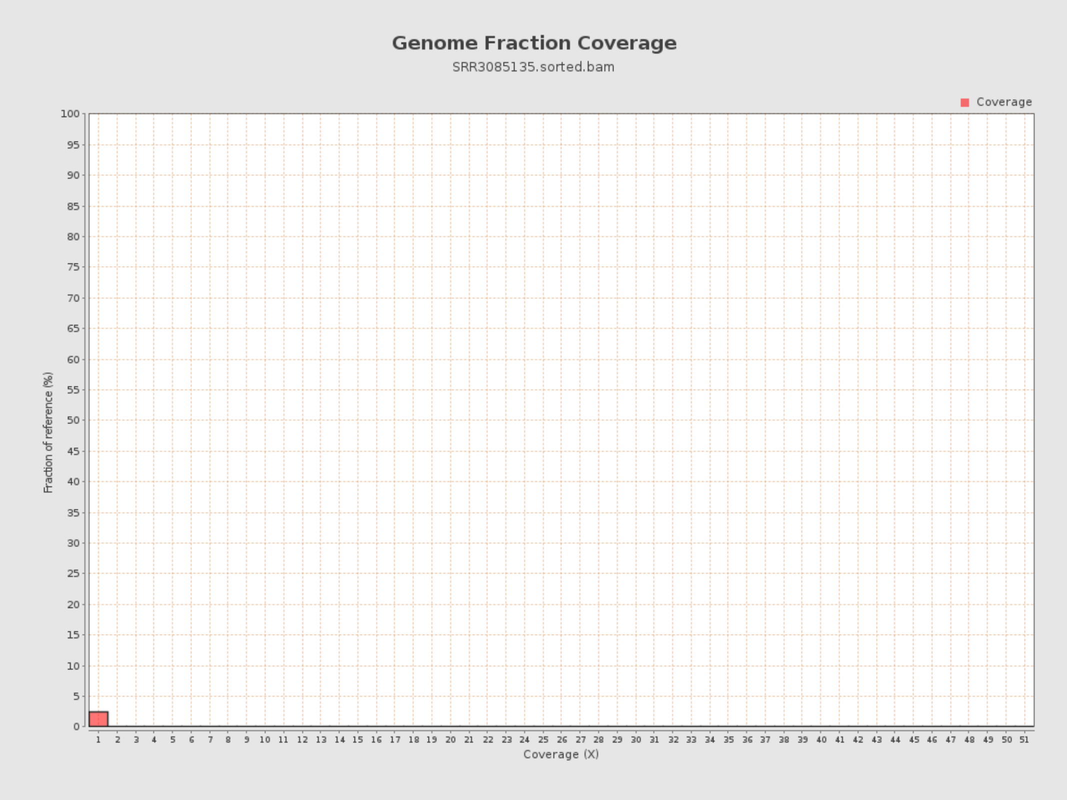
4. Results : Coverage Histogram



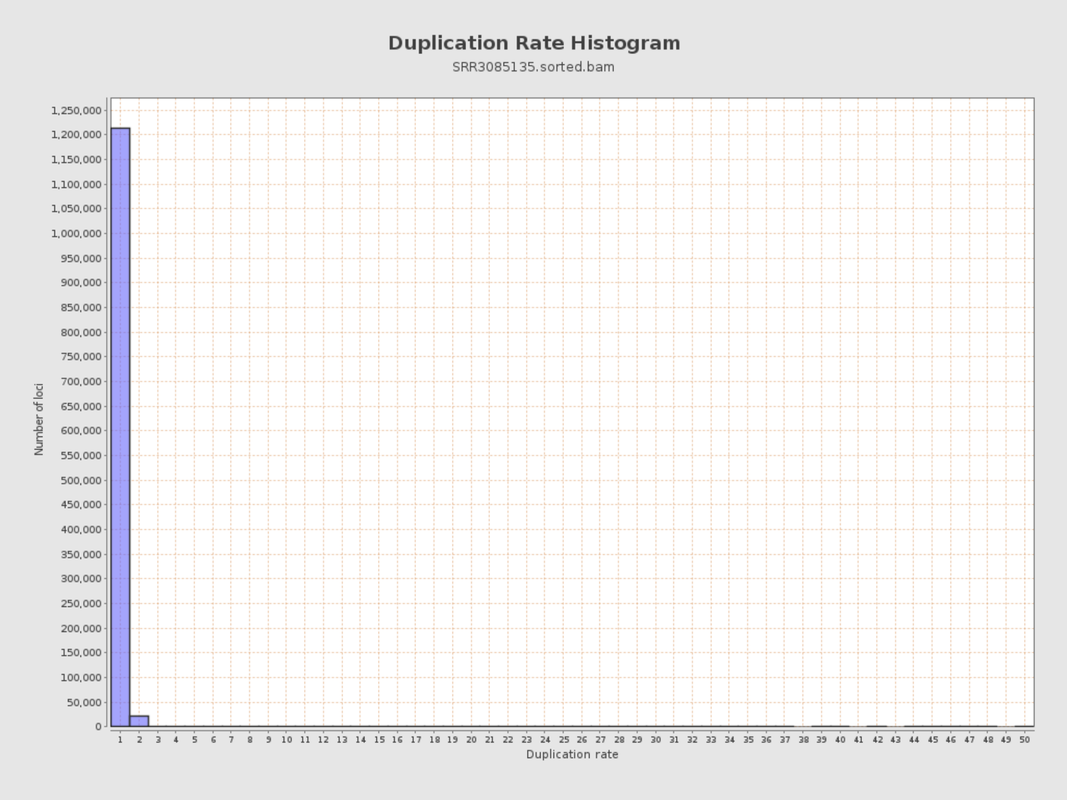
5. Results : Coverage Histogram (0-50X)



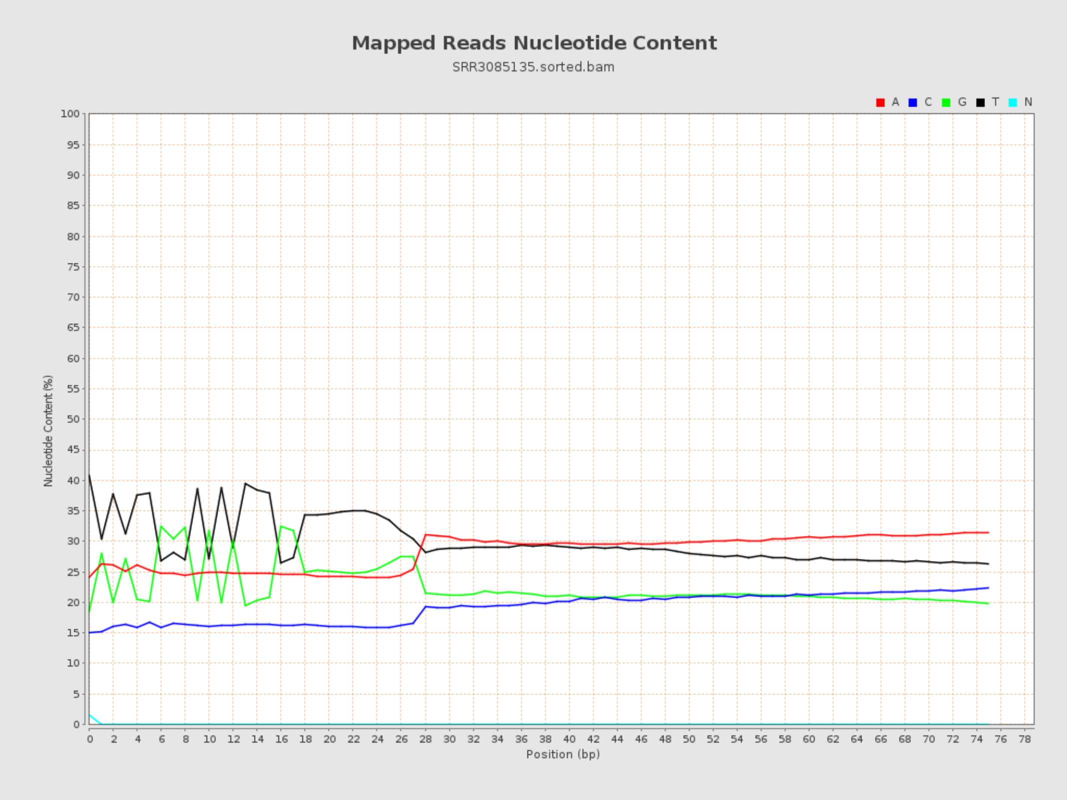
6. Results : Genome Fraction Coverage



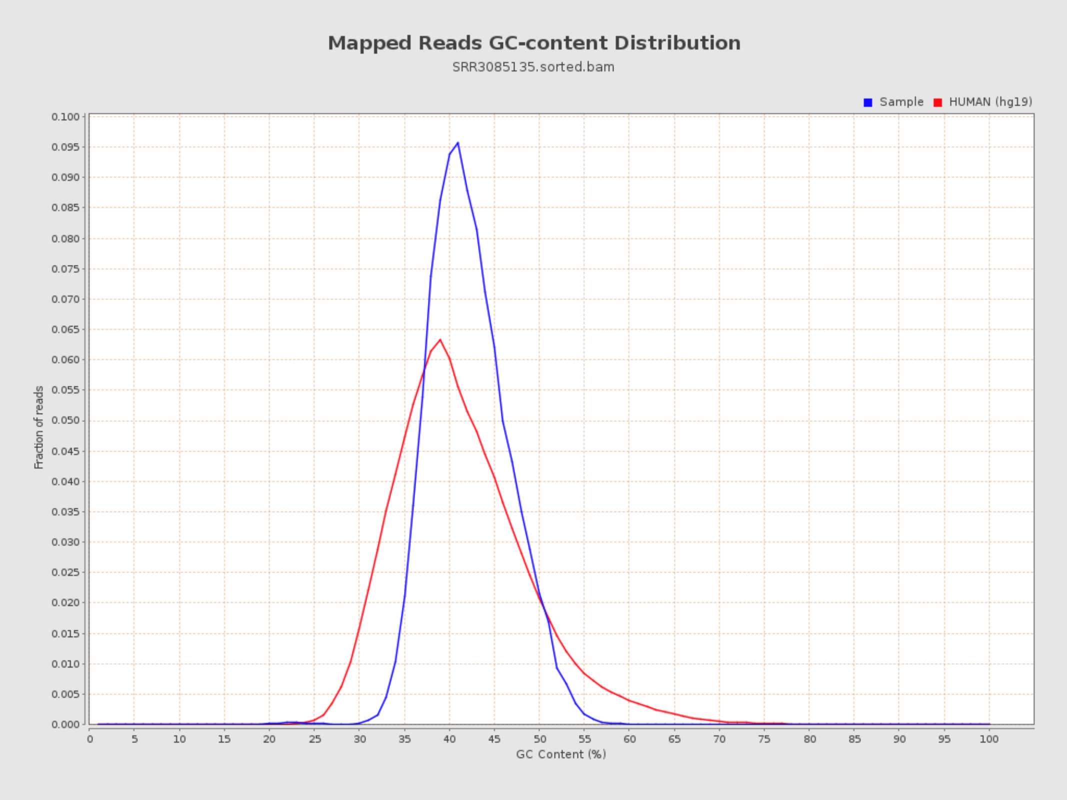
7. Results : Duplication Rate Histogram



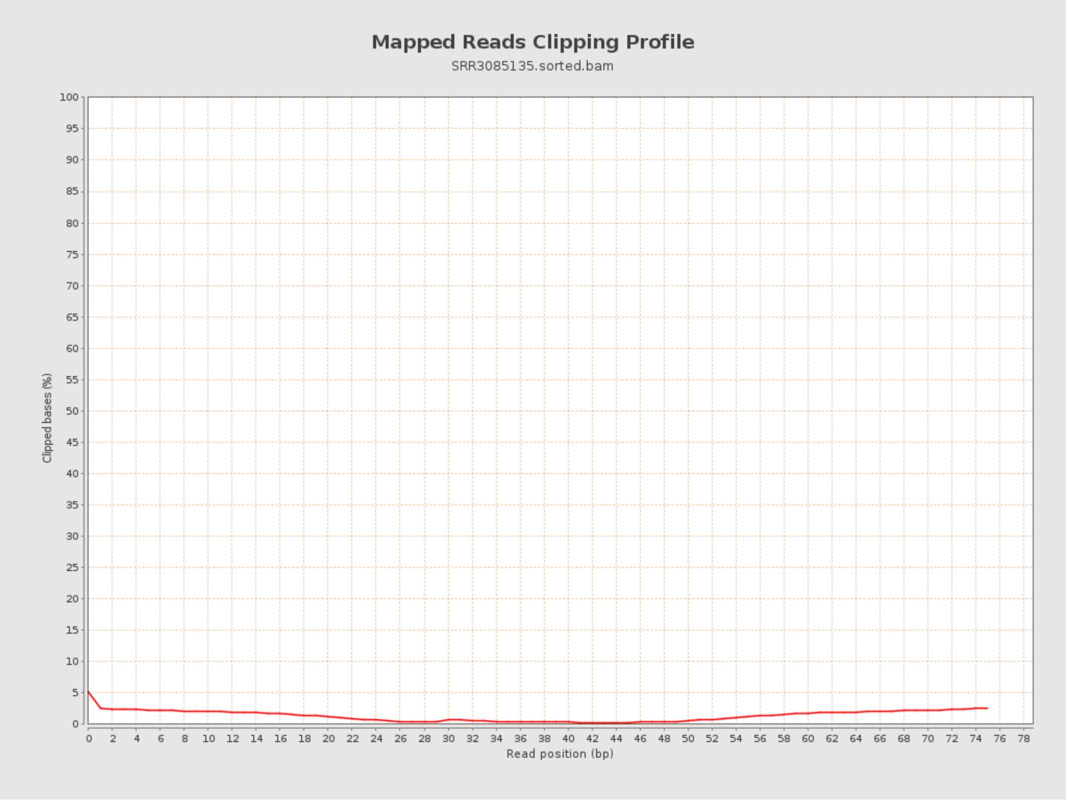
8. Results : Mapped Reads Nucleotide Content



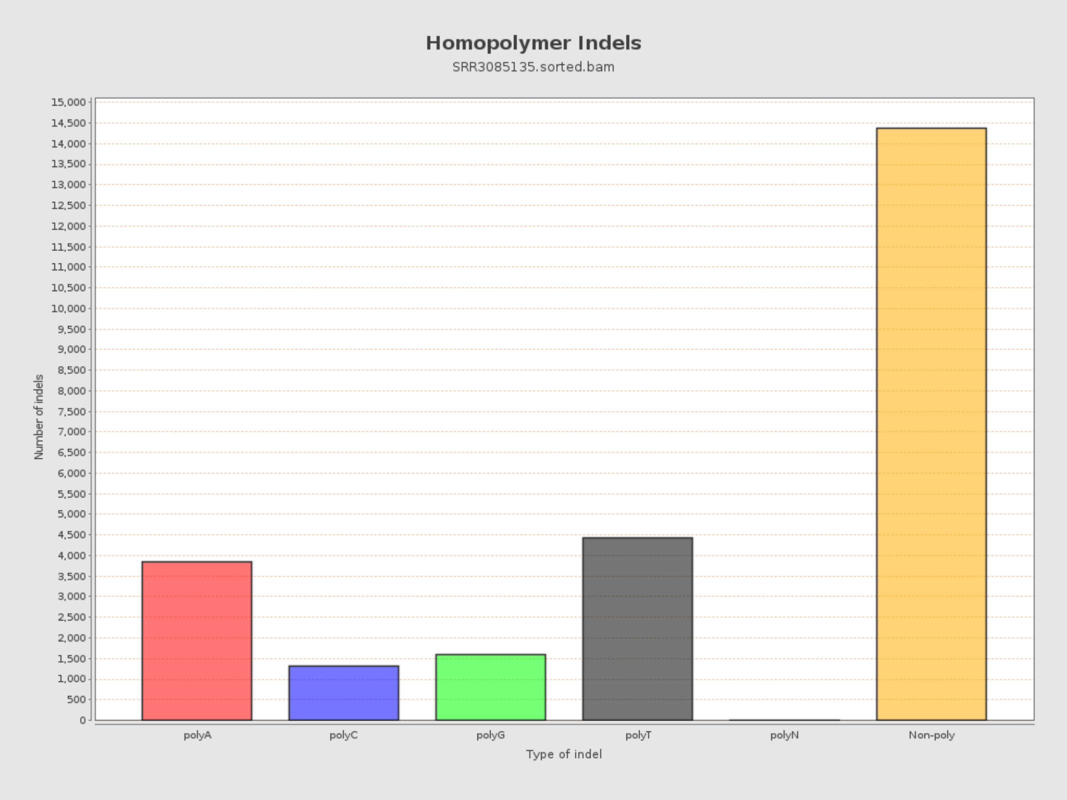
9. Results : Mapped Reads GC-content Distribution



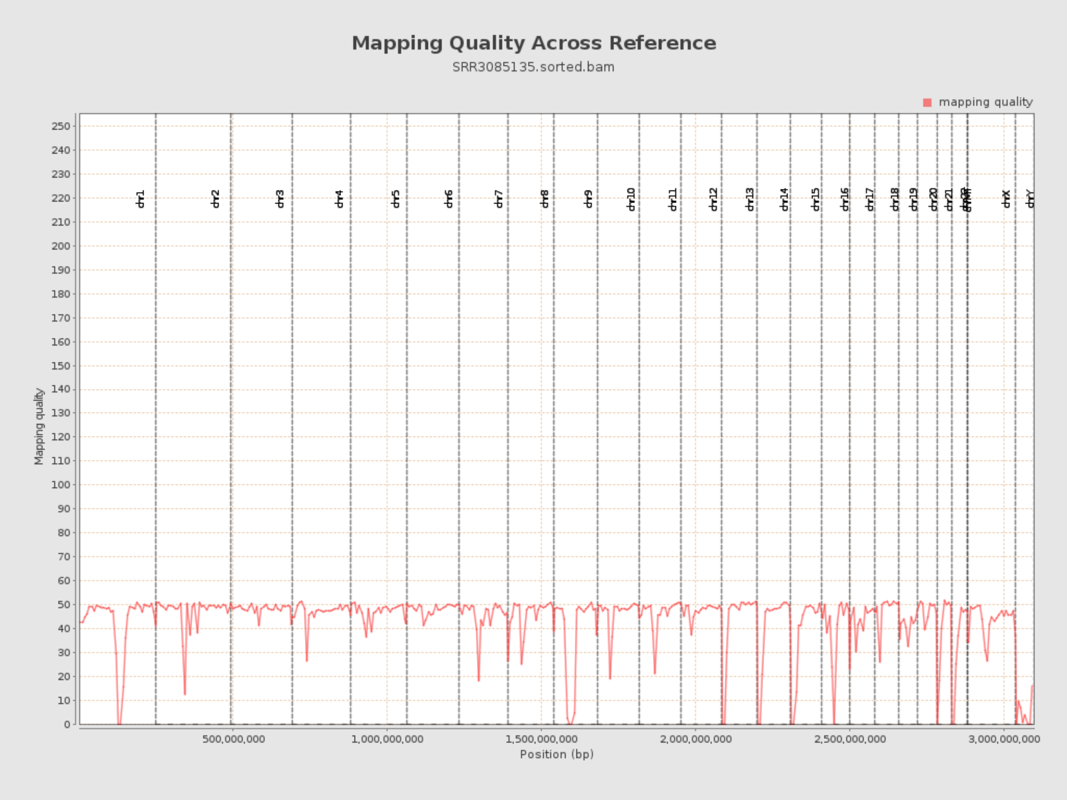
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram