Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 03:05:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085132.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_SRR3085132 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085132.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 03:05:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085132.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,502,412
Mapped reads	1,327,105 / 88.33%
Unmapped reads	175,307 / 11.67%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,363 / 0.69%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	42,727 / 2.84%
Duplication rate	2.46%
Clipped reads	607,440 / 40.43%

2.2. ACGT Content

Number/percentage of A's	24,779,249 / 28.04%
Number/percentage of C's	16,409,341 / 18.57%
Number/percentage of T's	27,562,717 / 31.19%
Number/percentage of G's	19,604,079 / 22.18%
Number/percentage of N's	17,818 / 0.02%
GC Percentage	40.75%

2.3. Coverage

Mean	0.0286

Standard Deviation	0.2712

2.4. Mapping Quality

Mean Mapping Quality	45.67

2.5. Mismatches and indels

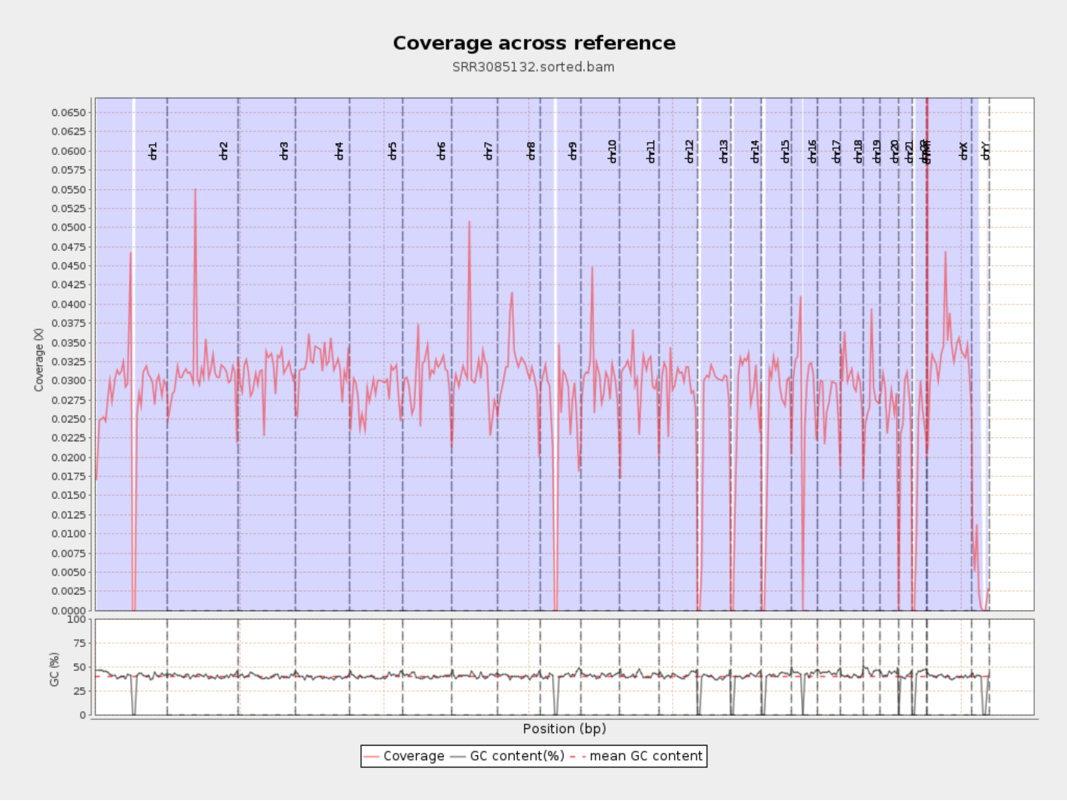
General error rate	0.9%
Mismatches	780,718
Insertions	7,052
Mapped reads with at least one insertion	0.53%
Deletions	20,756
Mapped reads with at least one deletion	1.55%
Homopolymer indels	46.58%

2.6. Chromosome stats

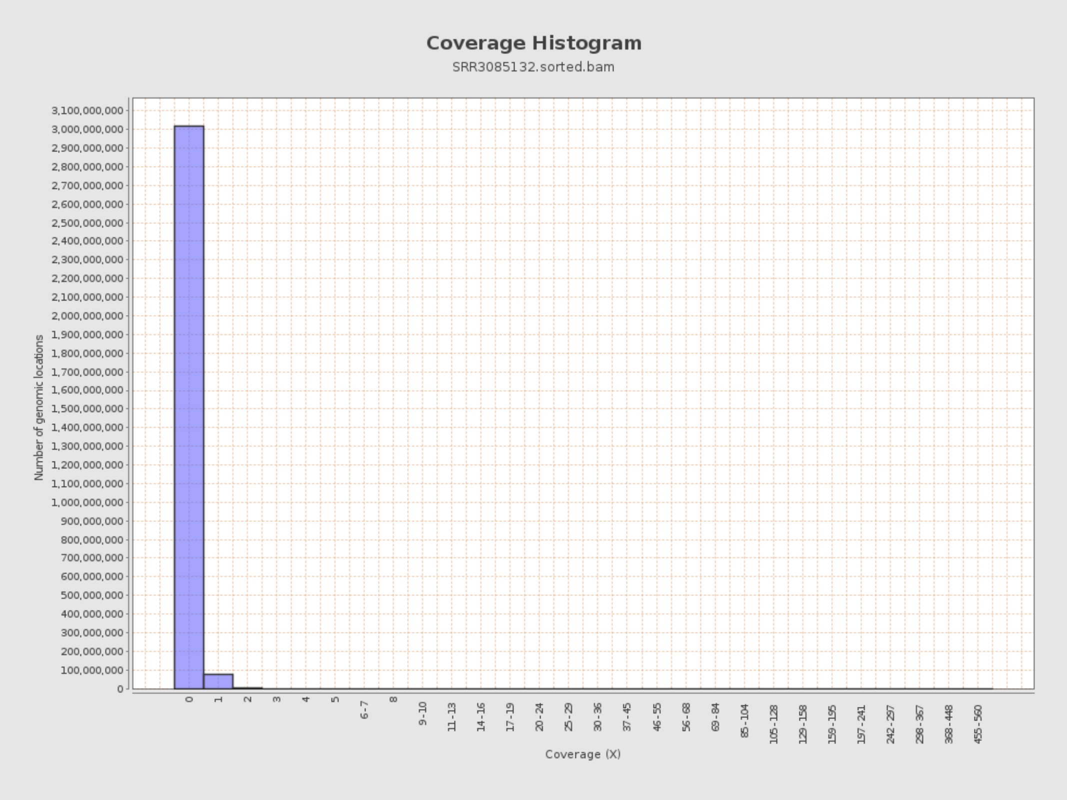
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6811225	0.0273	0.4306
chr2	243199373	7605764	0.0313	0.3454
chr3	198022430	6141466	0.031	0.1884
chr4	191154276	6126676	0.0321	0.1967
chr5	180915260	5155553	0.0285	0.1811
chr6	171115067	5243286	0.0306	0.2093
chr7	159138663	4885758	0.0307	0.3691

chr8	146364022	4611094	0.0315	0.3933
chr9	141213431	3525070	0.025	0.2531
chr10	135534747	4113817	0.0304	0.2507
chr11	135006516	4129566	0.0306	0.2453
chr12	133851895	3958190	0.0296	0.1871
chr13	115169878	2901048	0.0252	0.1692
chr14	107349540	2708341	0.0252	0.175
chr15	102531392	2513164	0.0245	0.1699
chr16	90354753	2499996	0.0277	0.1929
chr17	81195210	2203418	0.0271	0.1891
chr18	78077248	2392542	0.0306	0.4267
chr19	59128983	1651107	0.0279	0.356
chr20	63025520	1693528	0.0269	0.1795
chr21	48129895	1158110	0.0241	0.1736
chr22	51304566	919424	0.0179	0.1424
chrMT	16571	15617	0.9424	1.0912
chrX	155270560	5221469	0.0336	0.2152
chrY	59373566	221515	0.0037	0.093

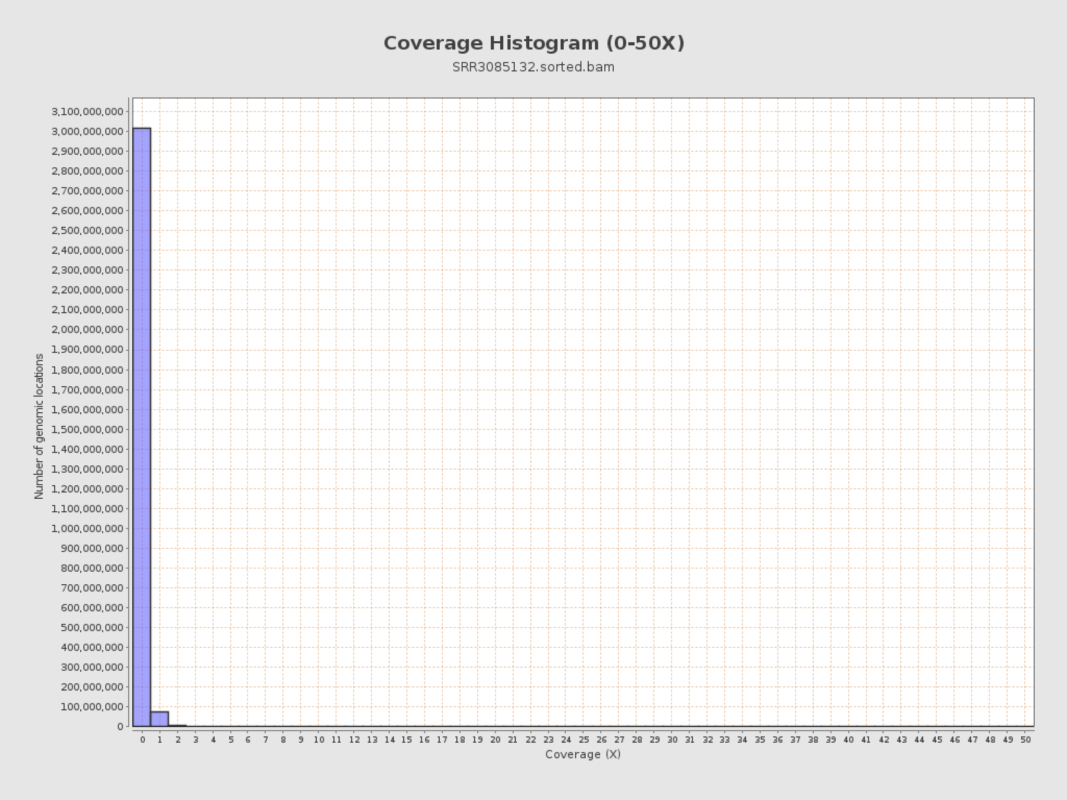
3. Results : Coverage across reference



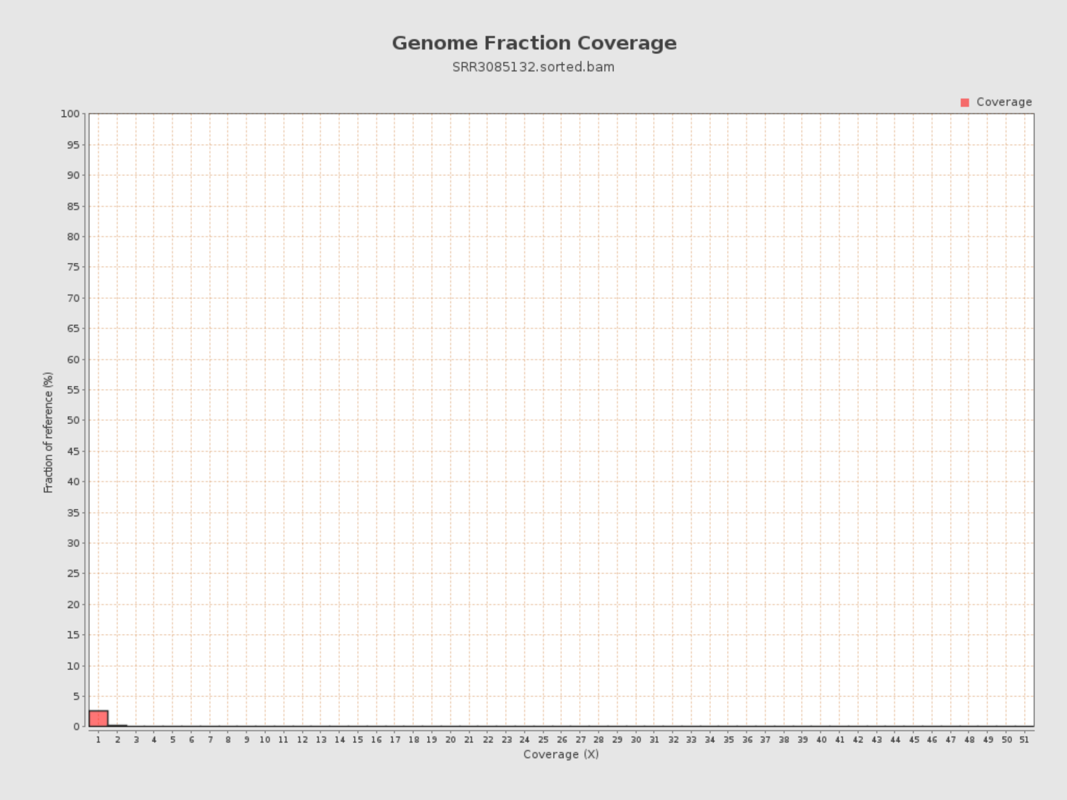
4. Results : Coverage Histogram



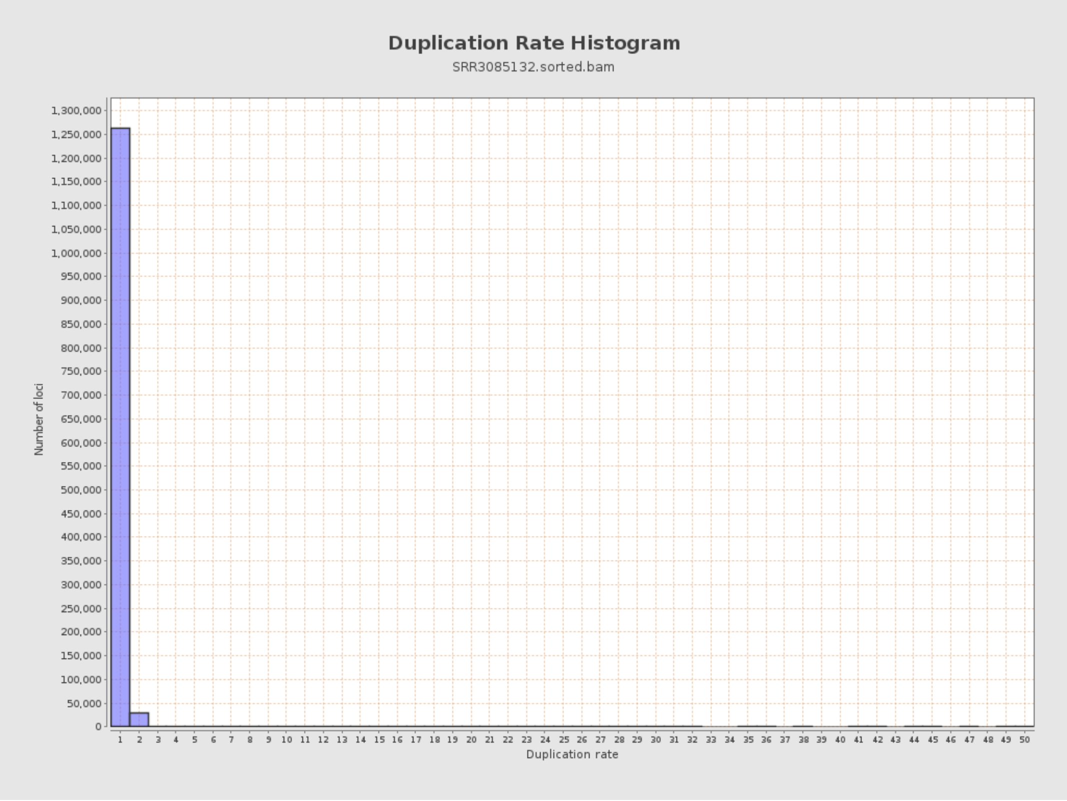
5. Results : Coverage Histogram (0-50X)



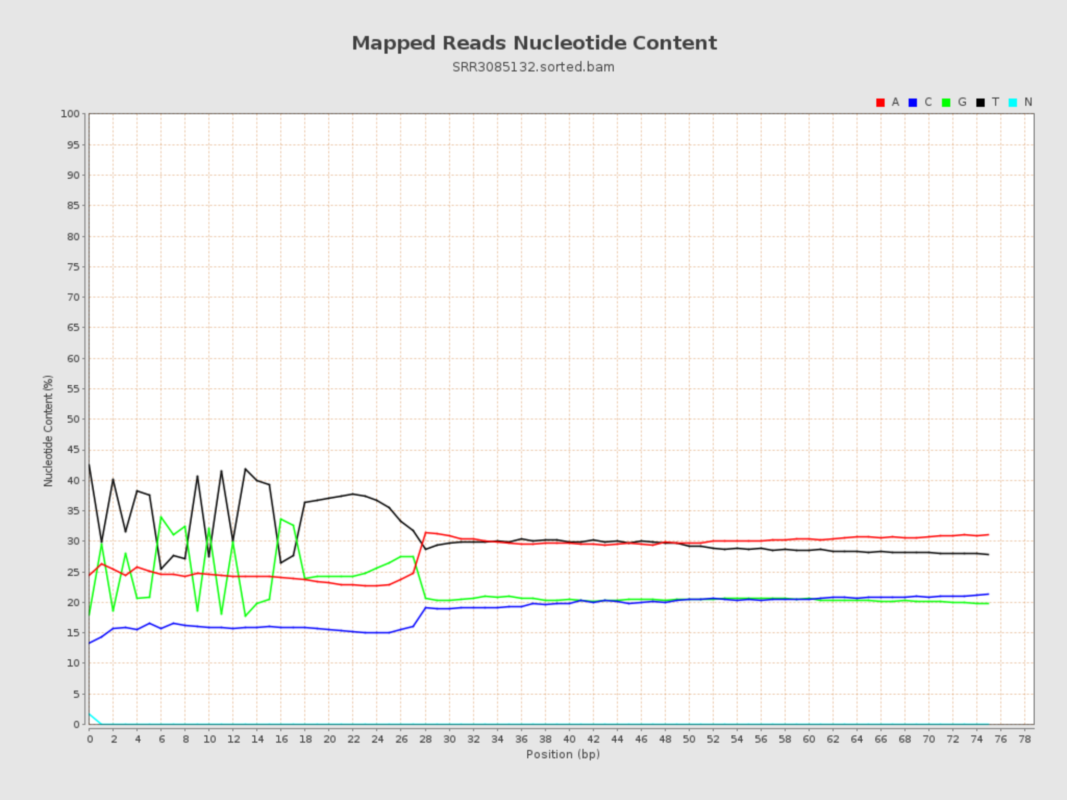
6. Results : Genome Fraction Coverage



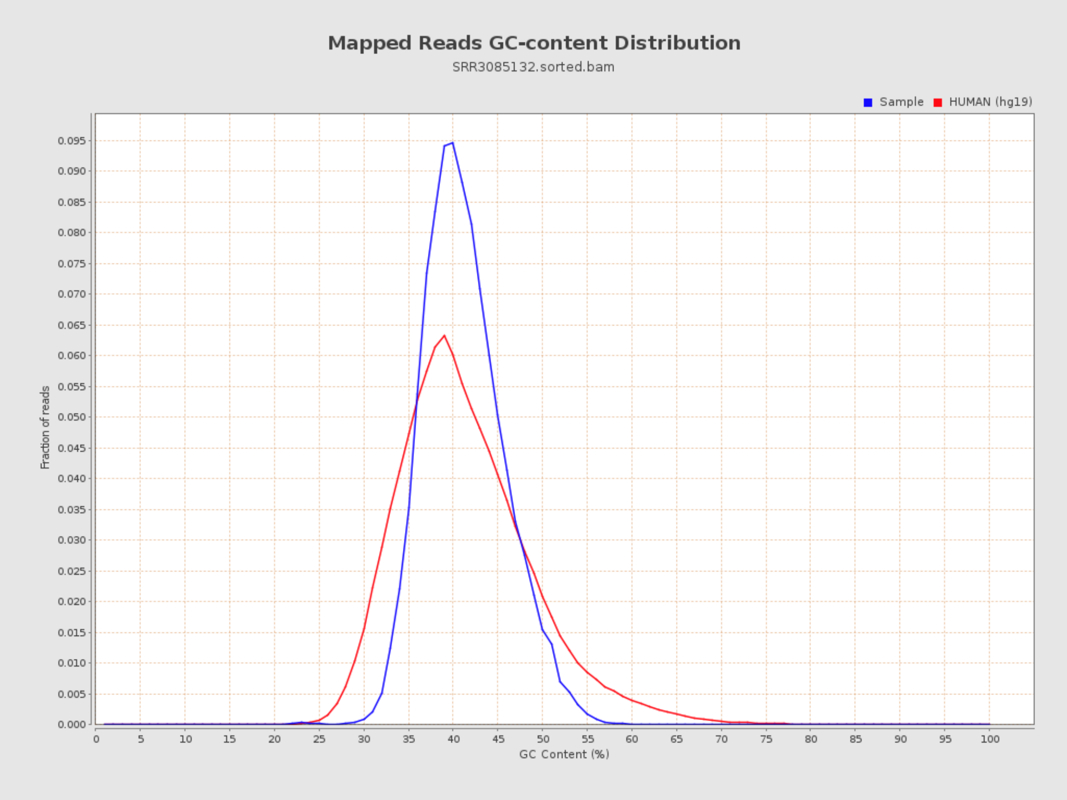
7. Results : Duplication Rate Histogram



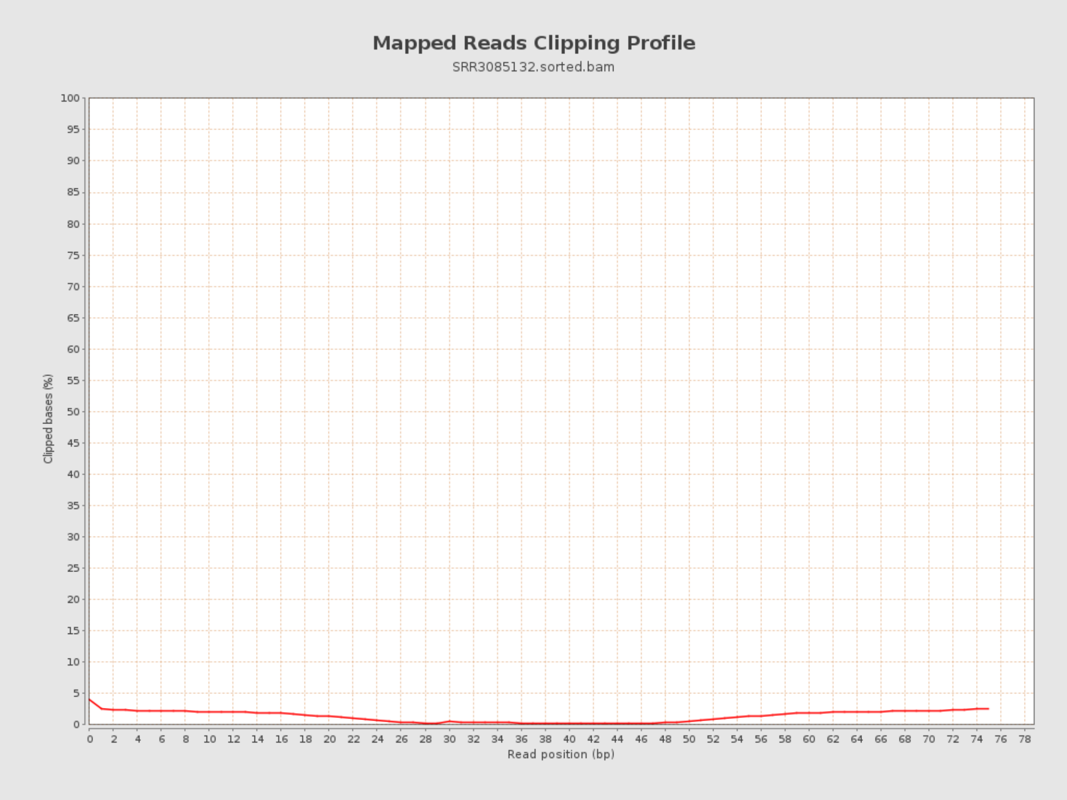
8. Results : Mapped Reads Nucleotide Content



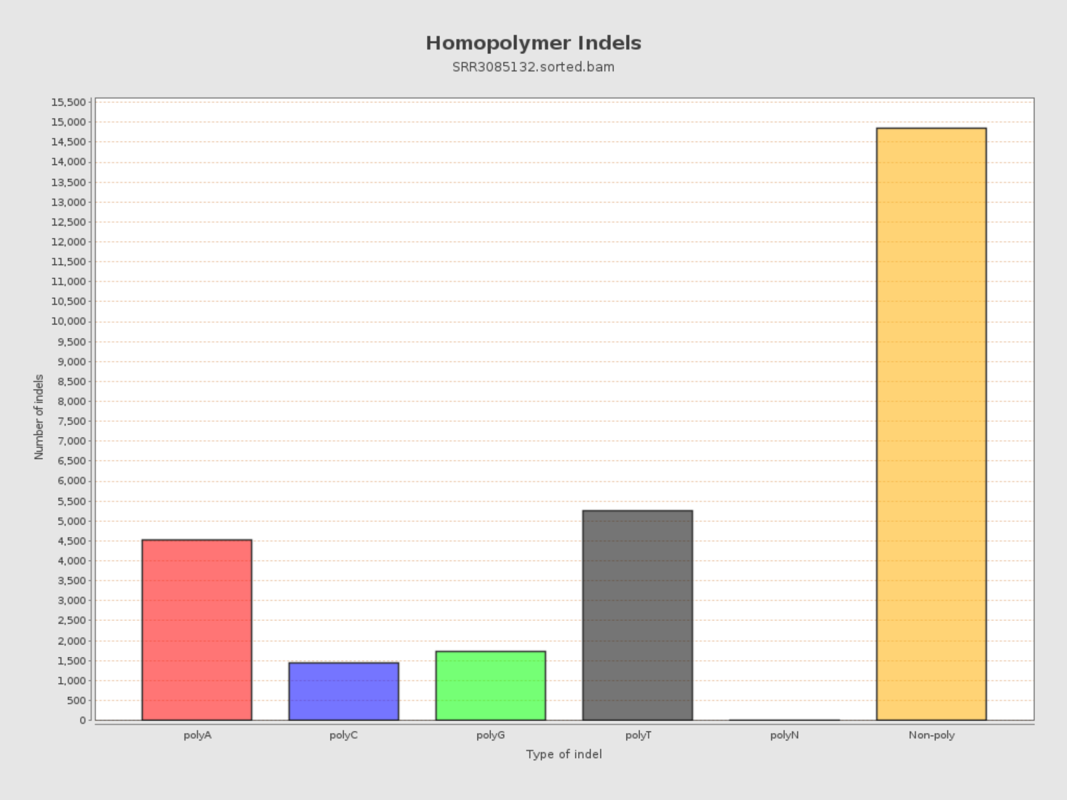
9. Results : Mapped Reads GC-content Distribution



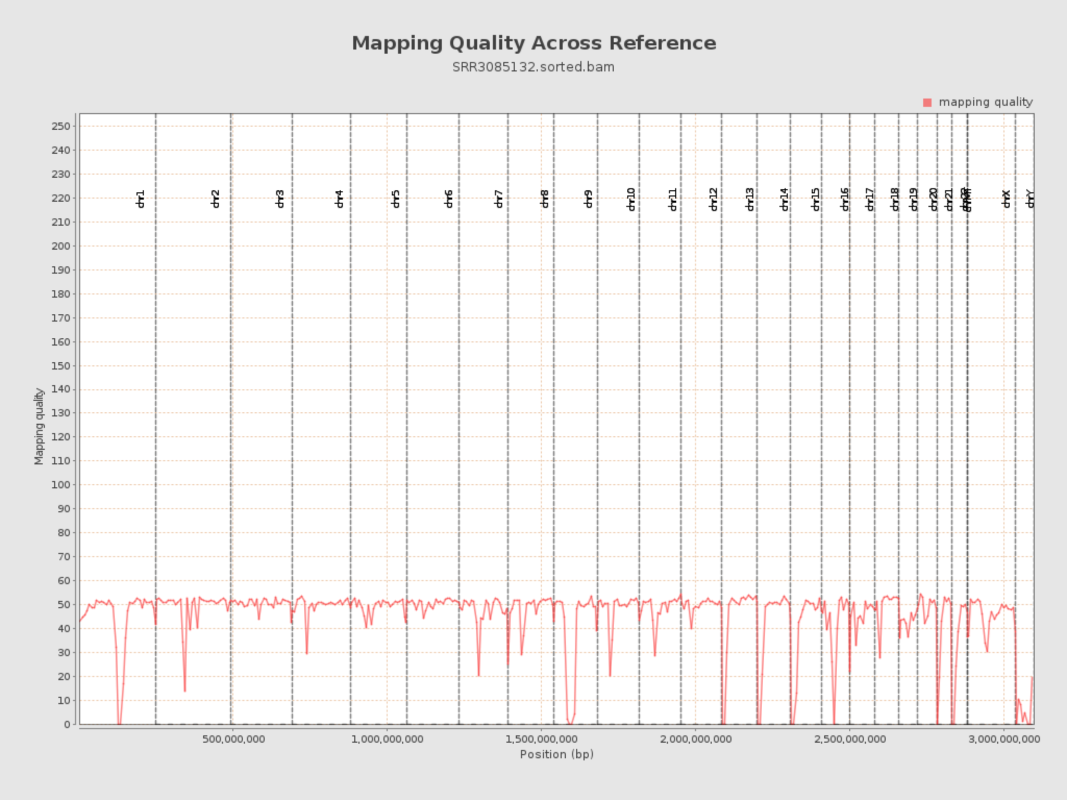
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram