Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 23:06:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085035.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_SRR3085035 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085035.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 23:06:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085035.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,354,159
Mapped reads	2,111,414 / 89.69%
Unmapped reads	242,745 / 10.31%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,650 / 0.54%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	80,735 / 3.43%
Duplication rate	3.19%
Clipped reads	866,045 / 36.79%

2.2. ACGT Content

Number/percentage of A's	38,972,554 / 27.35%
Number/percentage of C's	27,480,826 / 19.29%
Number/percentage of T's	43,877,221 / 30.79%
Number/percentage of G's	32,139,302 / 22.56%
Number/percentage of N's	14,903 / 0.01%
GC Percentage	41.84%

2.3. Coverage

Mean	0.046

Standard Deviation	0.3299

2.4. Mapping Quality

Mean Mapping Quality	46.09

2.5. Mismatches and indels

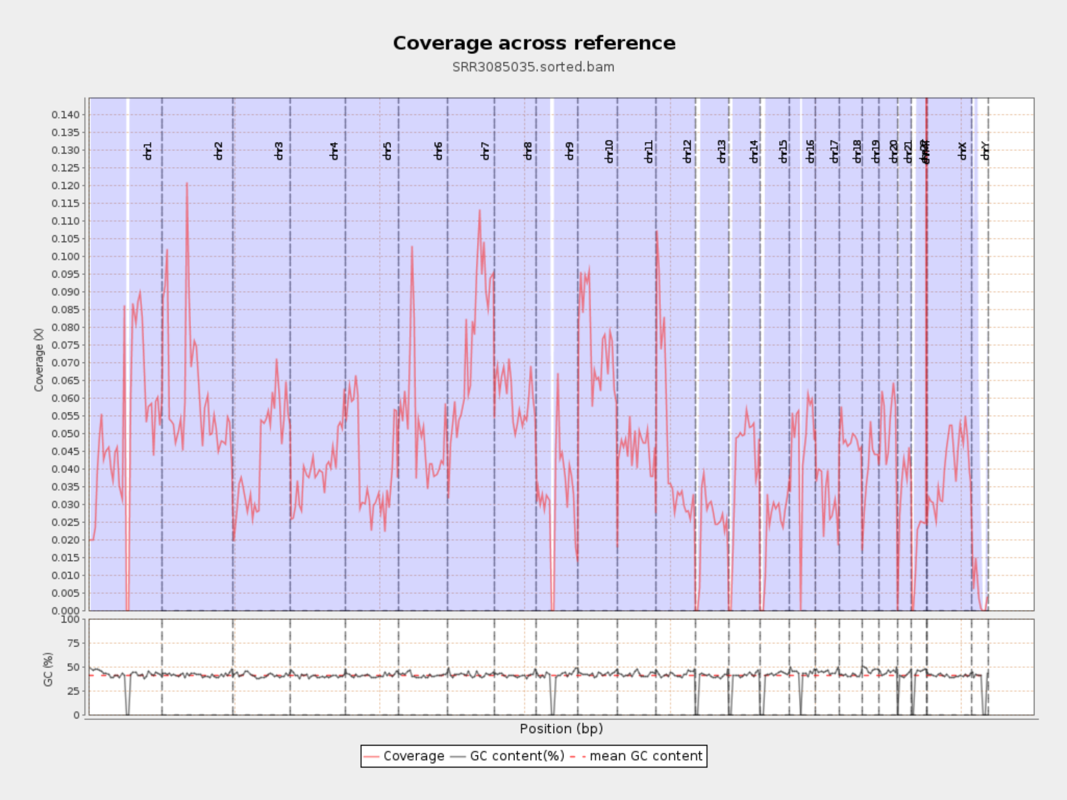
General error rate	0.9%
Mismatches	1,263,887
Insertions	9,537
Mapped reads with at least one insertion	0.45%
Deletions	29,866
Mapped reads with at least one deletion	1.4%
Homopolymer indels	48.26%

2.6. Chromosome stats

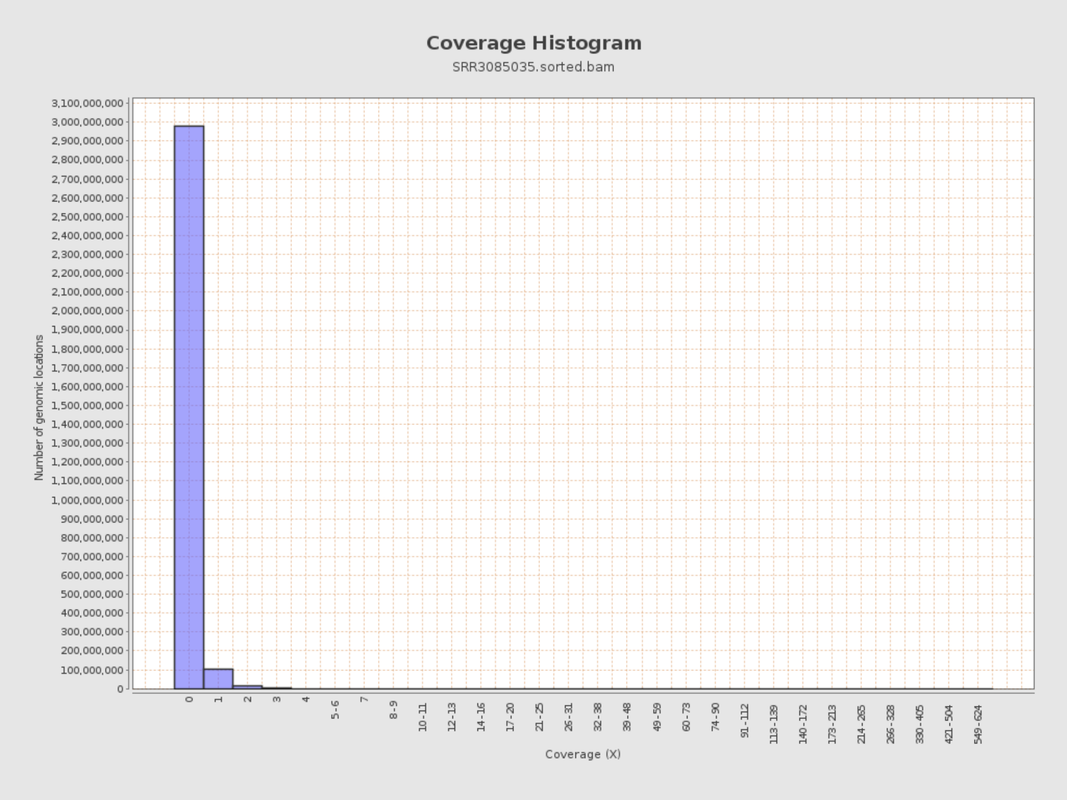
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12491228	0.0501	0.4811
chr2	243199373	14878310	0.0612	0.4089
chr3	198022430	8675099	0.0438	0.2448
chr4	191154276	7596966	0.0397	0.2398
chr5	180915260	7331526	0.0405	0.2339
chr6	171115067	8893982	0.052	0.3192
chr7	159138663	11842711	0.0744	0.4469

chr8	146364022	8823986	0.0603	0.4695
chr9	141213431	4582705	0.0325	0.269
chr10	135534747	10281168	0.0759	0.4223
chr11	135006516	6122830	0.0454	0.3481
chr12	133851895	6177741	0.0462	0.2533
chr13	115169878	2714350	0.0236	0.1771
chr14	107349540	4335110	0.0404	0.2382
chr15	102531392	2369870	0.0231	0.1804
chr16	90354753	4316906	0.0478	0.2619
chr17	81195210	2538668	0.0313	0.2392
chr18	78077248	3796264	0.0486	0.4283
chr19	59128983	2388684	0.0404	0.3542
chr20	63025520	3323038	0.0527	0.2735
chr21	48129895	1645081	0.0342	0.2248
chr22	51304566	881086	0.0172	0.15
chrMT	16571	7137	0.4307	0.7451
chrX	155270560	6225658	0.0401	0.2482
chrY	59373566	297086	0.005	0.1121

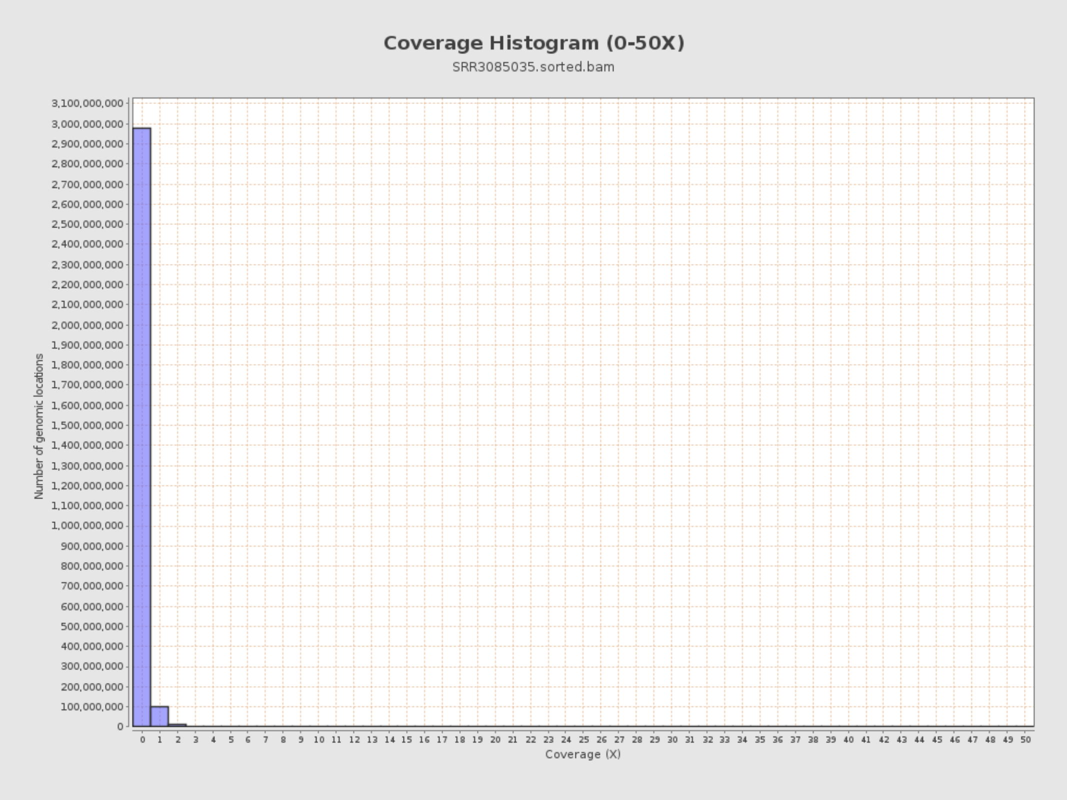
3. Results : Coverage across reference



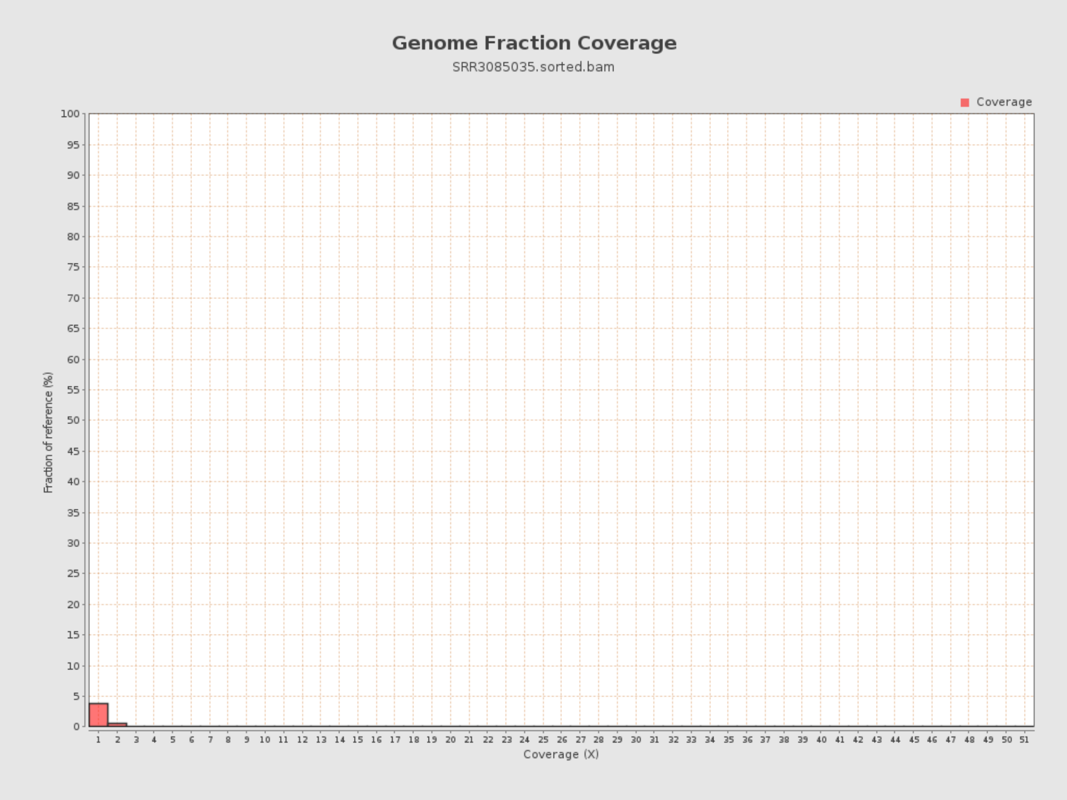
4. Results : Coverage Histogram



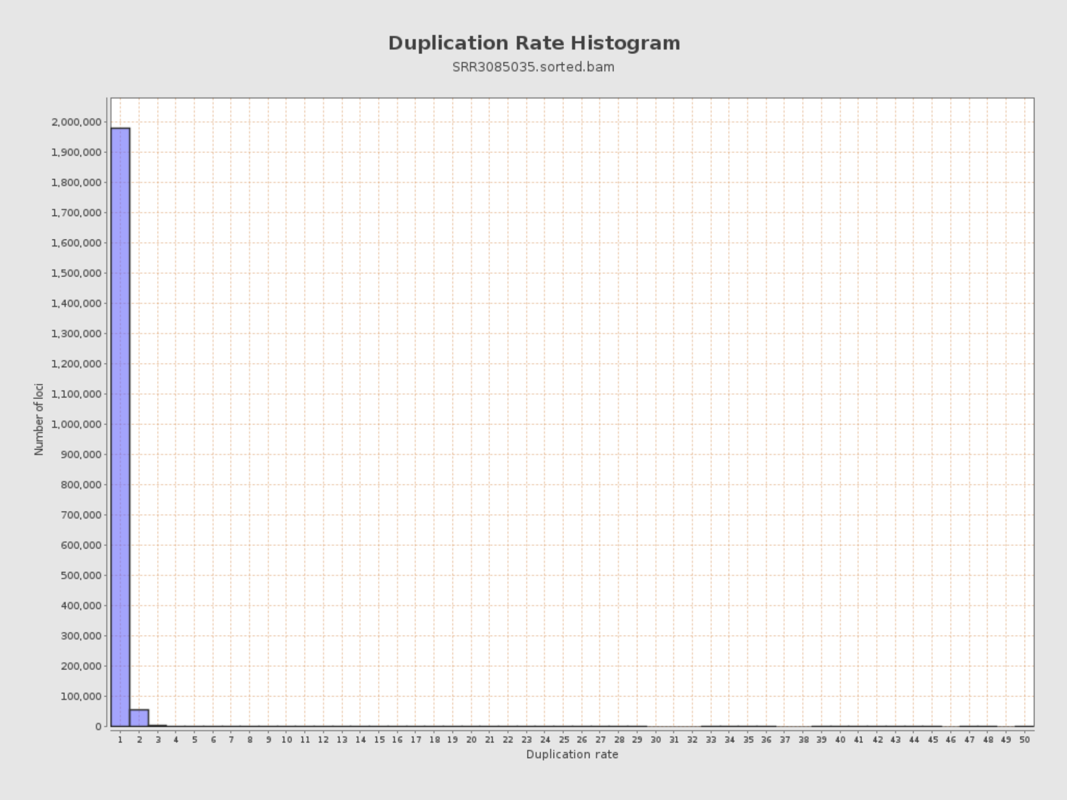
5. Results : Coverage Histogram (0-50X)



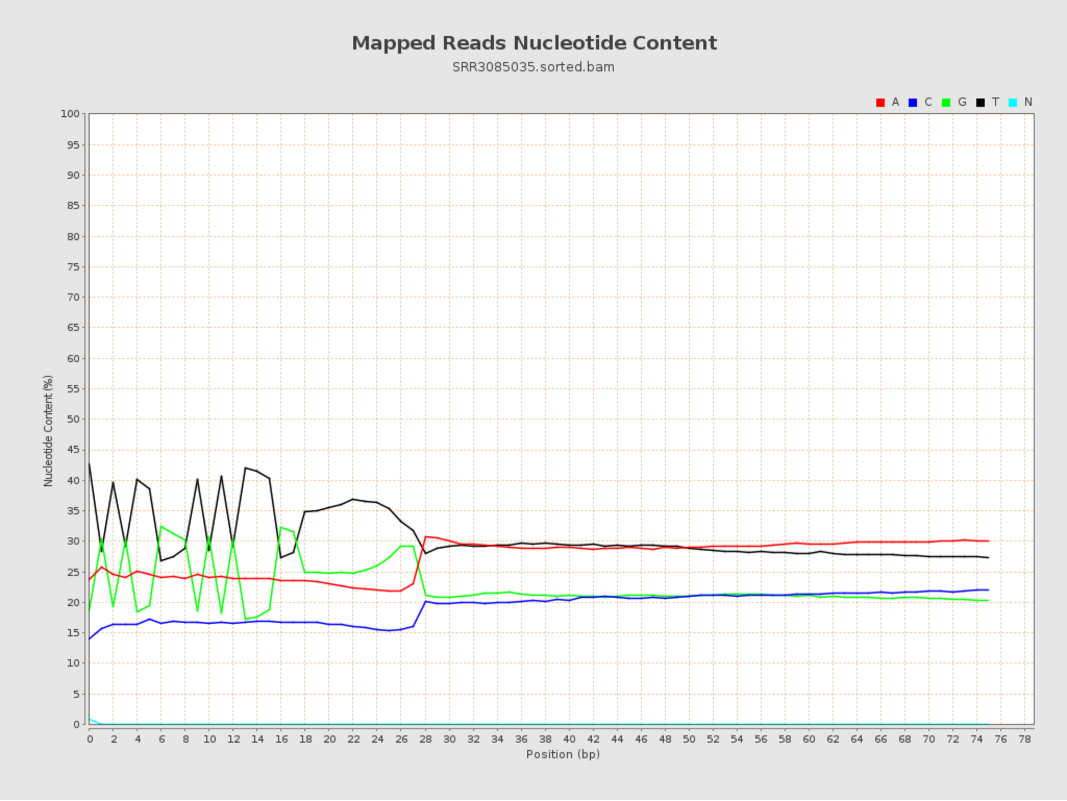
6. Results : Genome Fraction Coverage



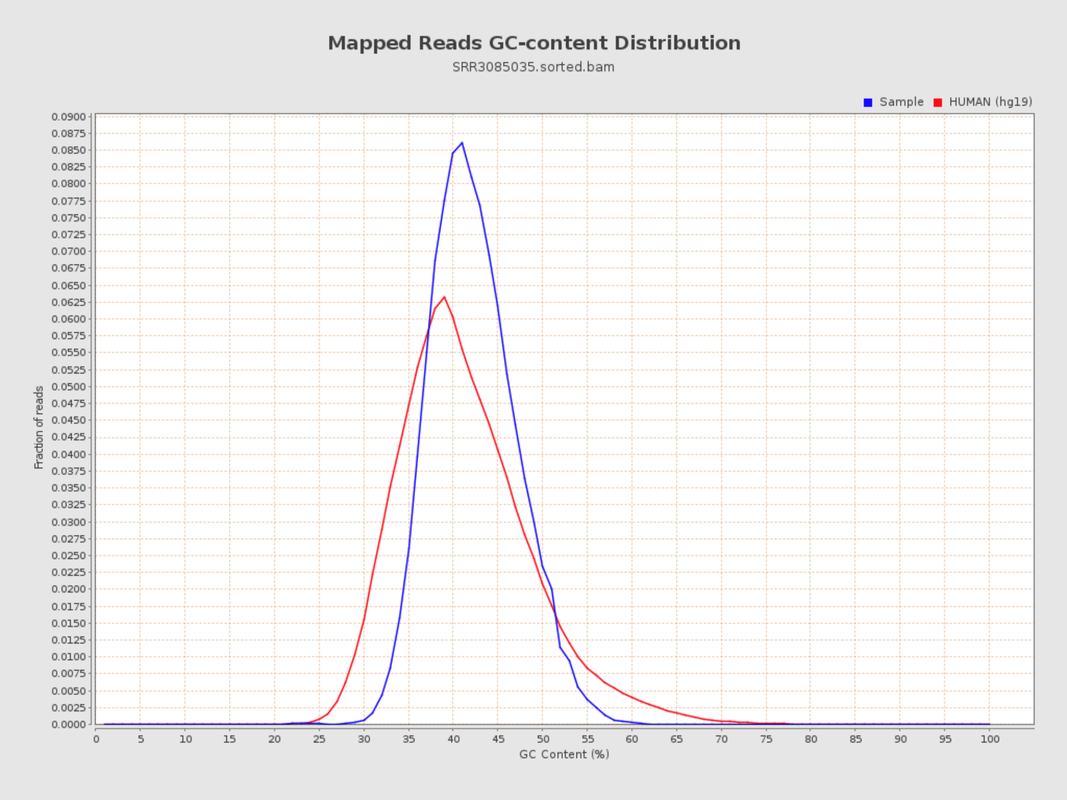
7. Results : Duplication Rate Histogram



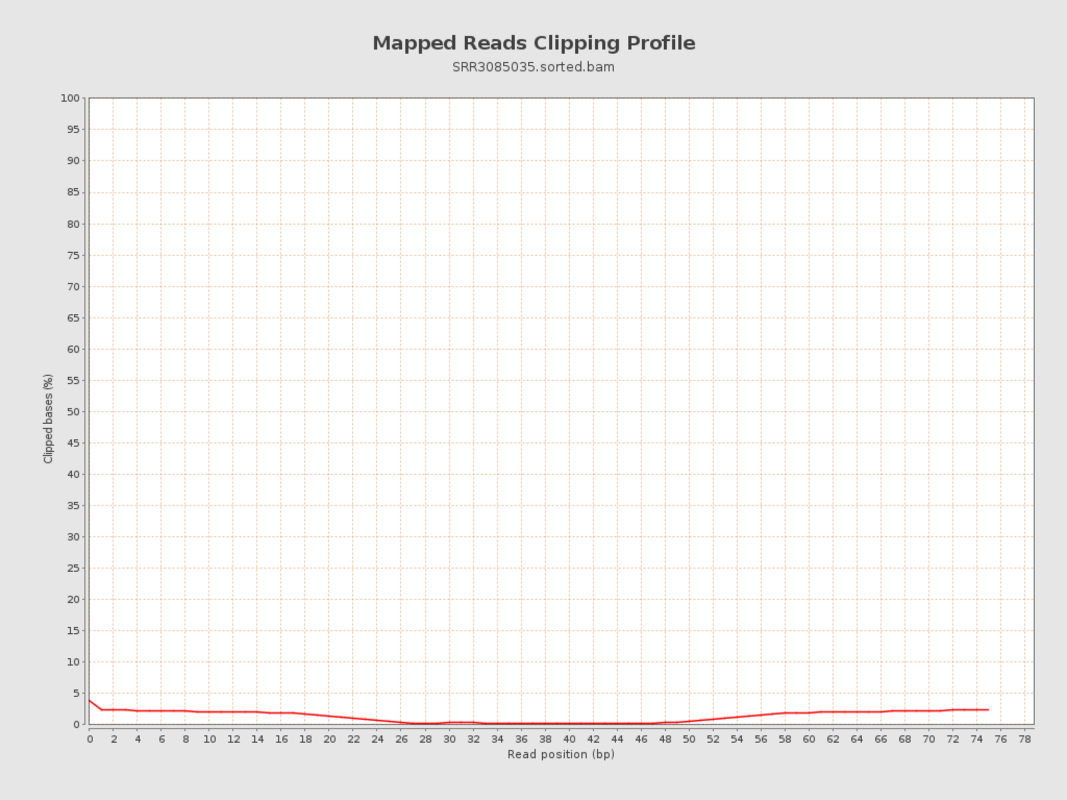
8. Results : Mapped Reads Nucleotide Content



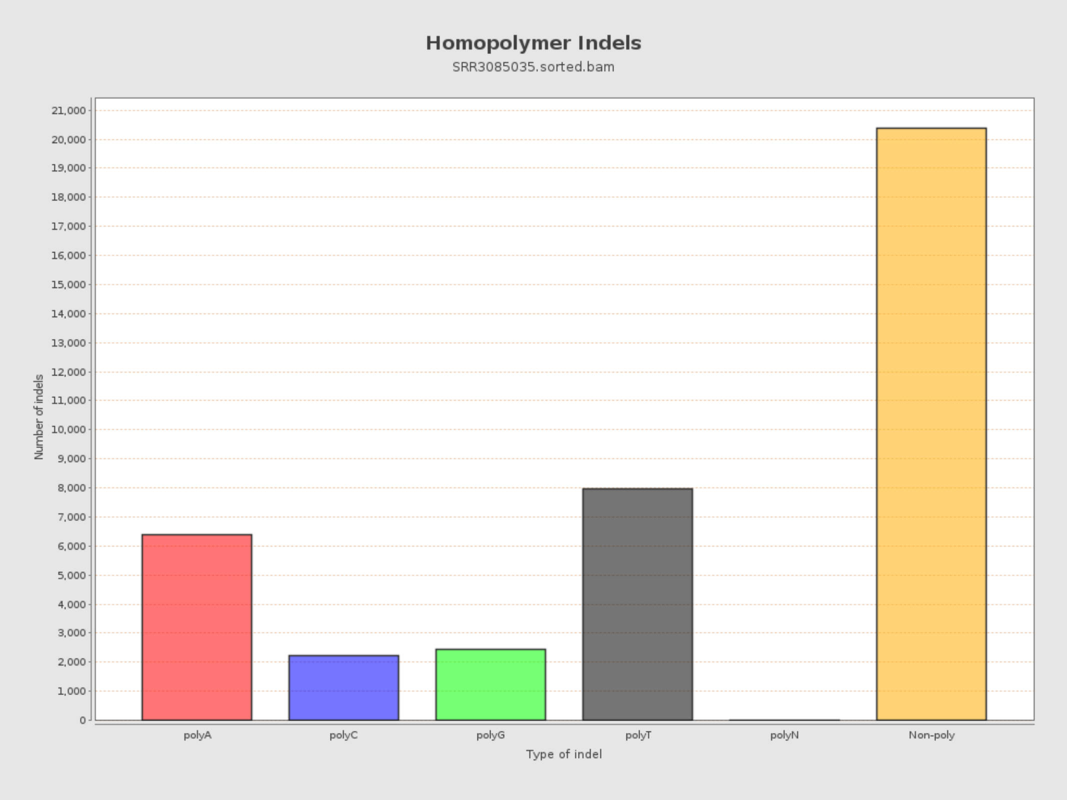
9. Results : Mapped Reads GC-content Distribution



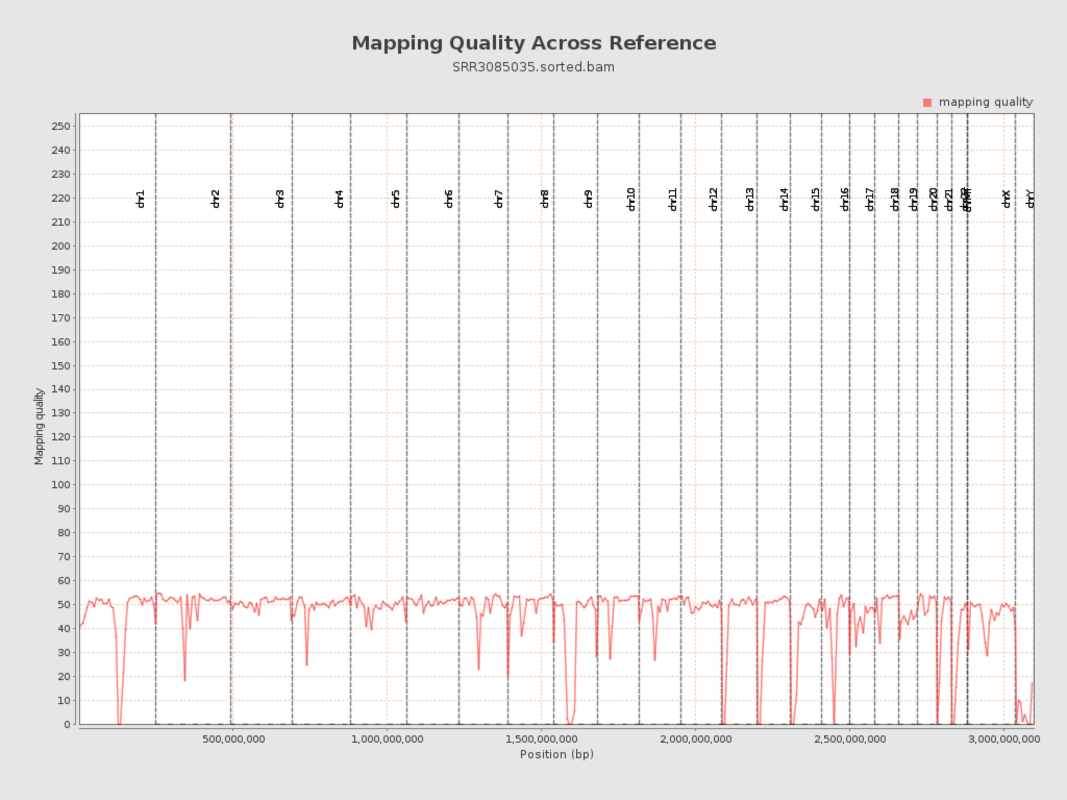
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram