Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 21:25:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085009.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_SRR3085009 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085009.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 21:25:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085009.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,695,634
Mapped reads	1,526,900 / 90.05%
Unmapped reads	168,734 / 9.95%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	37,183 / 2.19%
Read min/max/mean length	30 / 76 / 76.77
Duplicated reads (estimated)	54,821 / 3.23%
Duplication rate	2.05%
Clipped reads	601,599 / 35.48%

2.2. ACGT Content

Number/percentage of A's	31,937,502 / 30.14%
Number/percentage of C's	19,733,909 / 18.63%
Number/percentage of T's	31,832,128 / 30.04%
Number/percentage of G's	22,432,919 / 21.17%
Number/percentage of N's	14,975 / 0.01%
GC Percentage	39.8%

2.3. Coverage

Mean	0.0342

Standard Deviation	0.4795

2.4. Mapping Quality

Mean Mapping Quality	45.17

2.5. Mismatches and indels

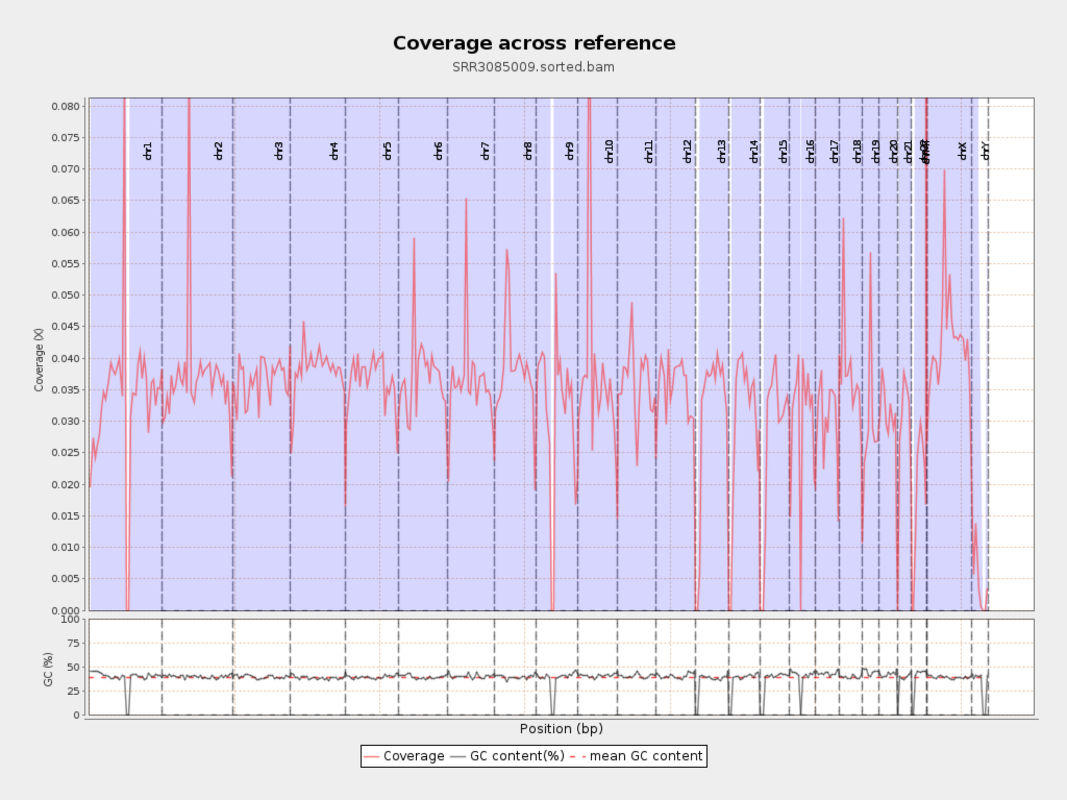
General error rate	0.87%
Mismatches	905,872
Insertions	10,008
Mapped reads with at least one insertion	0.65%
Deletions	21,863
Mapped reads with at least one deletion	1.42%
Homopolymer indels	44.53%

2.6. Chromosome stats

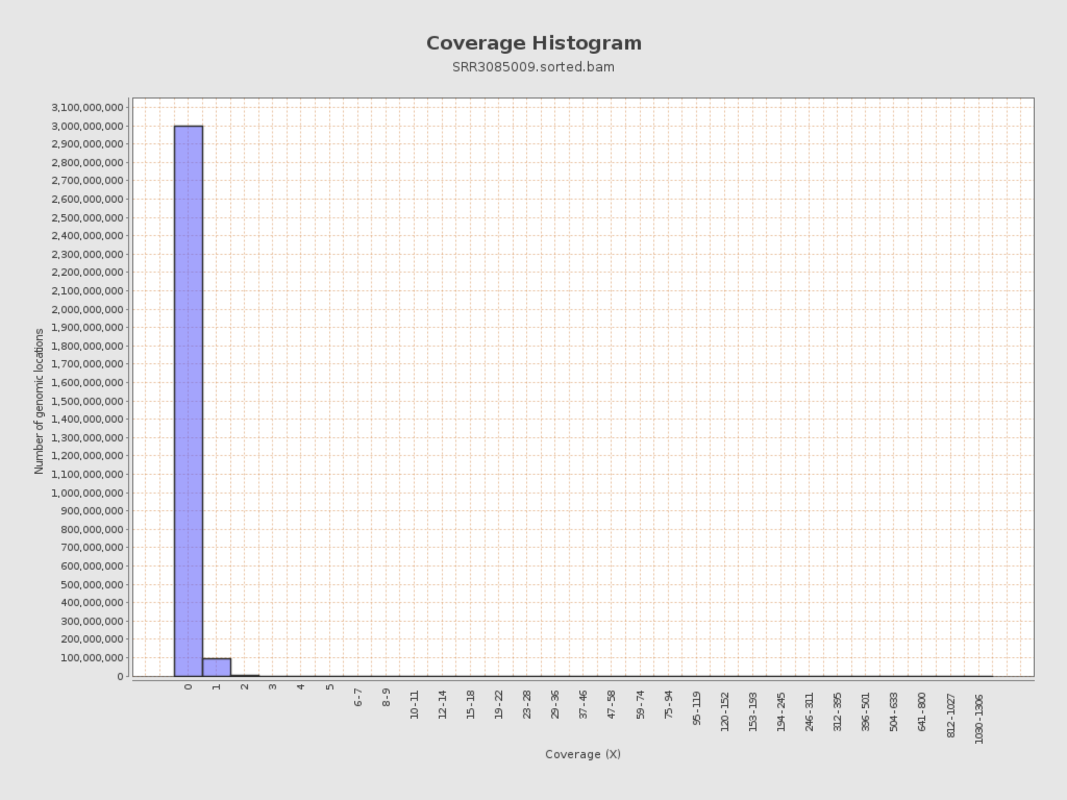
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8368619	0.0336	1.0383
chr2	243199373	9067210	0.0373	0.4422
chr3	198022430	7229324	0.0365	0.2268
chr4	191154276	7276486	0.0381	0.2121
chr5	180915260	6611127	0.0365	0.2032
chr6	171115067	6341930	0.0371	0.3011
chr7	159138663	5831730	0.0366	0.4057

chr8	146364022	5561781	0.038	0.7551
chr9	141213431	4442209	0.0315	0.396
chr10	135534747	5181330	0.0382	0.645
chr11	135006516	4830332	0.0358	0.3988
chr12	133851895	4718271	0.0352	0.2069
chr13	115169878	3484134	0.0303	0.1797
chr14	107349540	3175442	0.0296	0.2366
chr15	102531392	2820898	0.0275	0.1734
chr16	90354753	2716576	0.0301	0.2678
chr17	81195210	2436119	0.03	0.2498
chr18	78077248	2979601	0.0382	0.9146
chr19	59128983	1770268	0.0299	0.7186
chr20	63025520	1949745	0.0309	0.1989
chr21	48129895	1362285	0.0283	0.2082
chr22	51304566	923251	0.018	0.1392
chrMT	16571	30949	1.8677	1.7514
chrX	155270560	6605162	0.0425	0.2734
chrY	59373566	273597	0.0046	0.1076

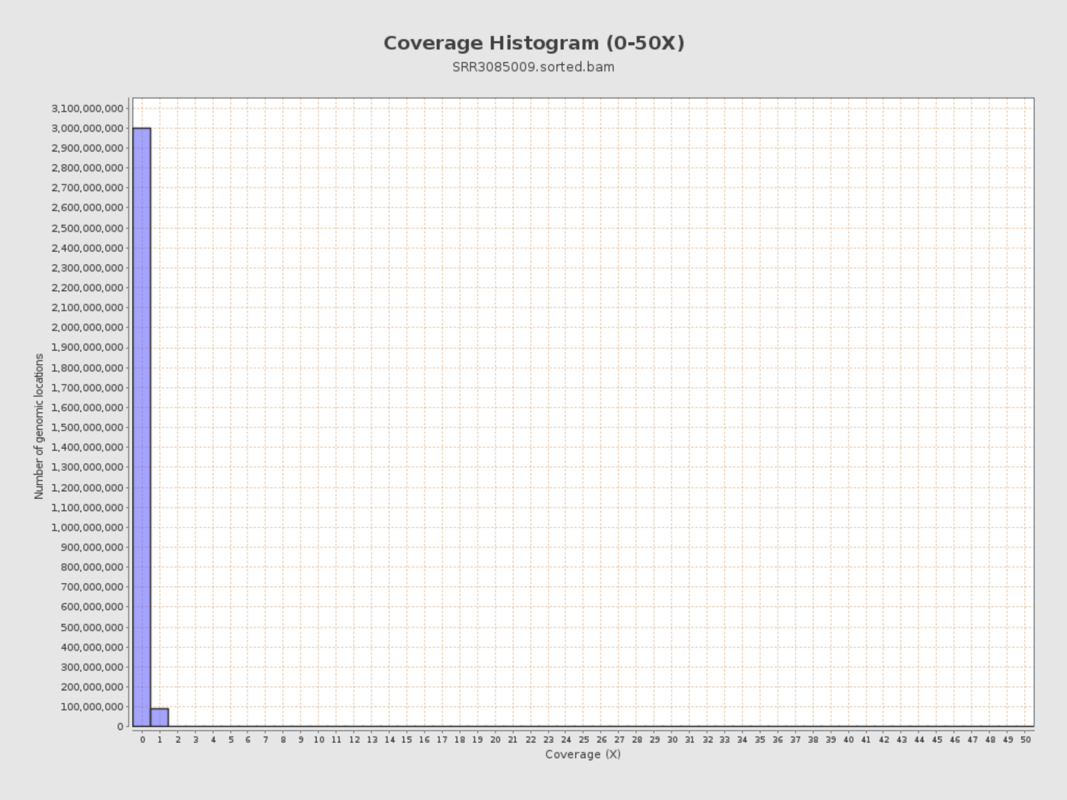
3. Results : Coverage across reference



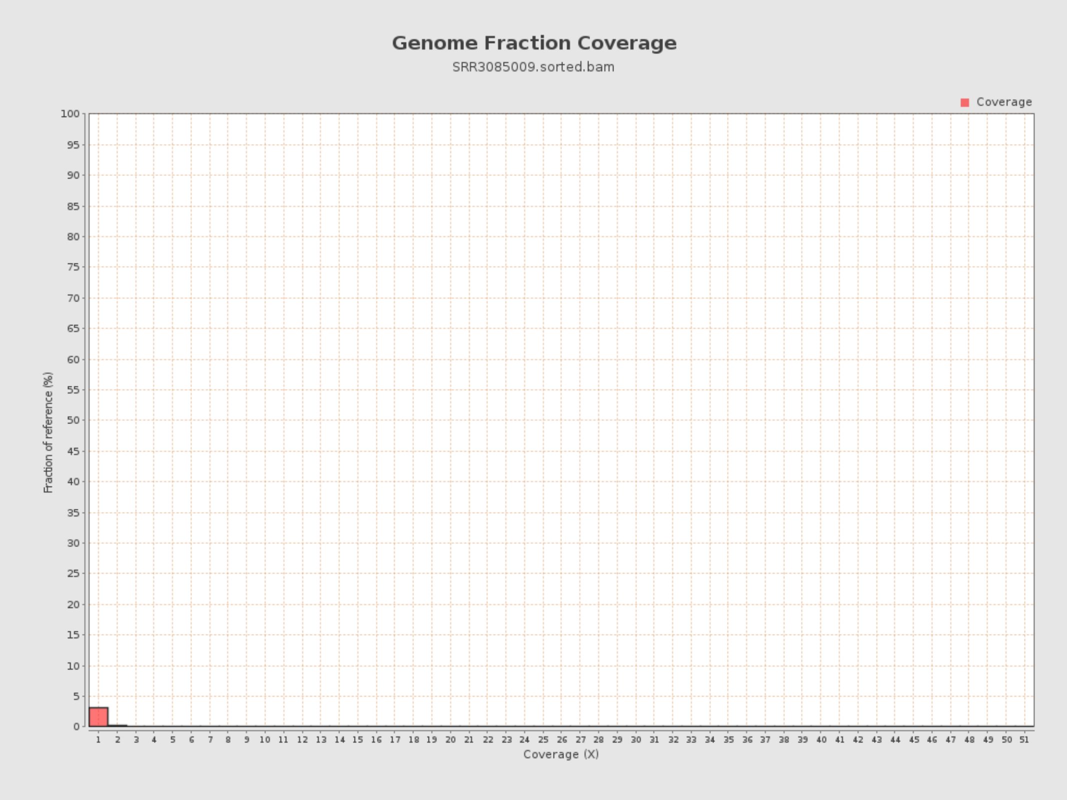
4. Results : Coverage Histogram



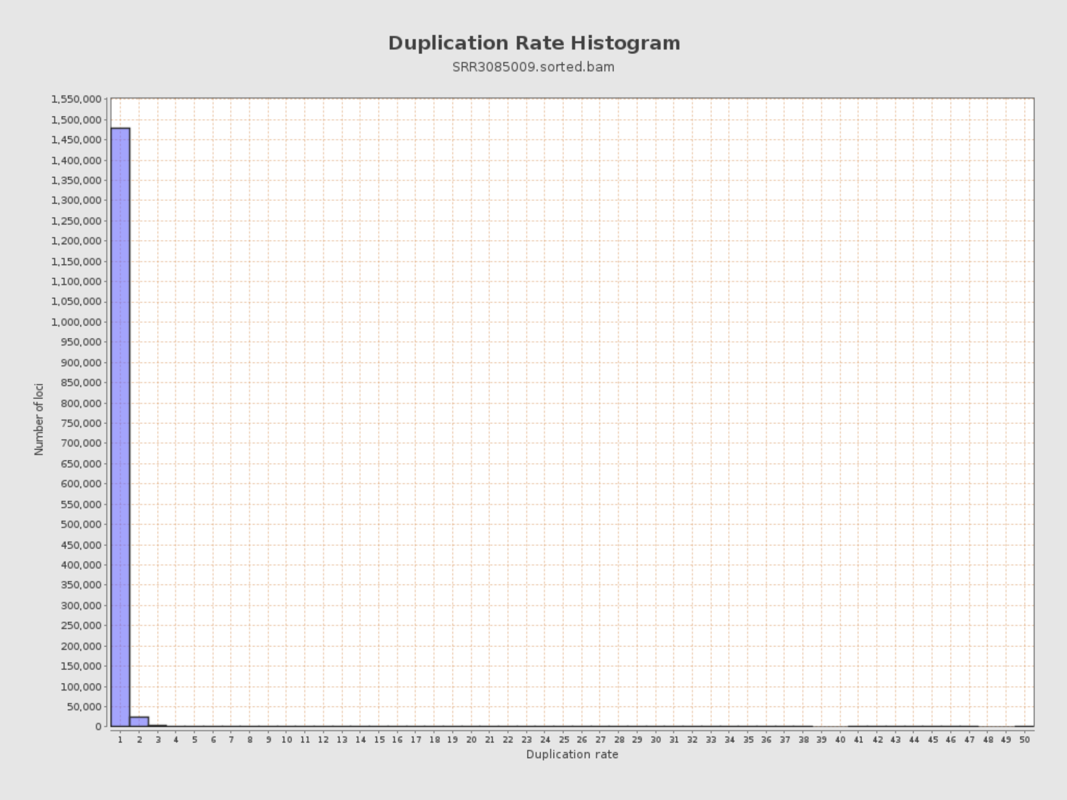
5. Results : Coverage Histogram (0-50X)



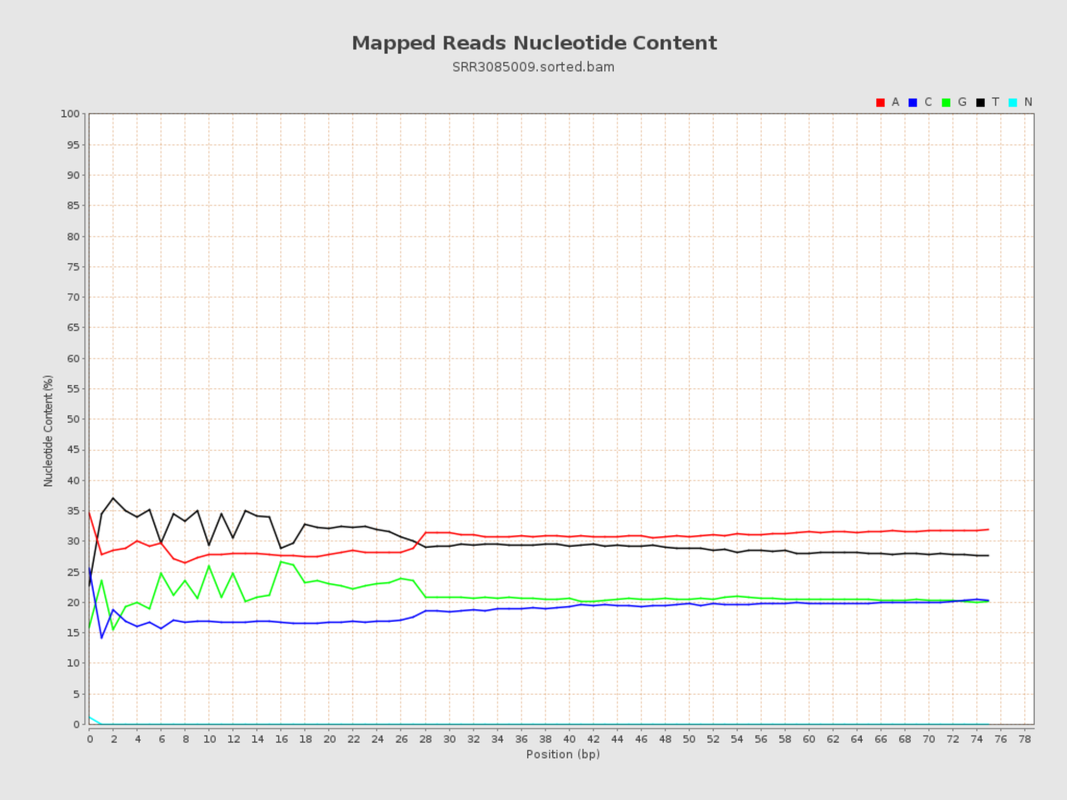
6. Results : Genome Fraction Coverage



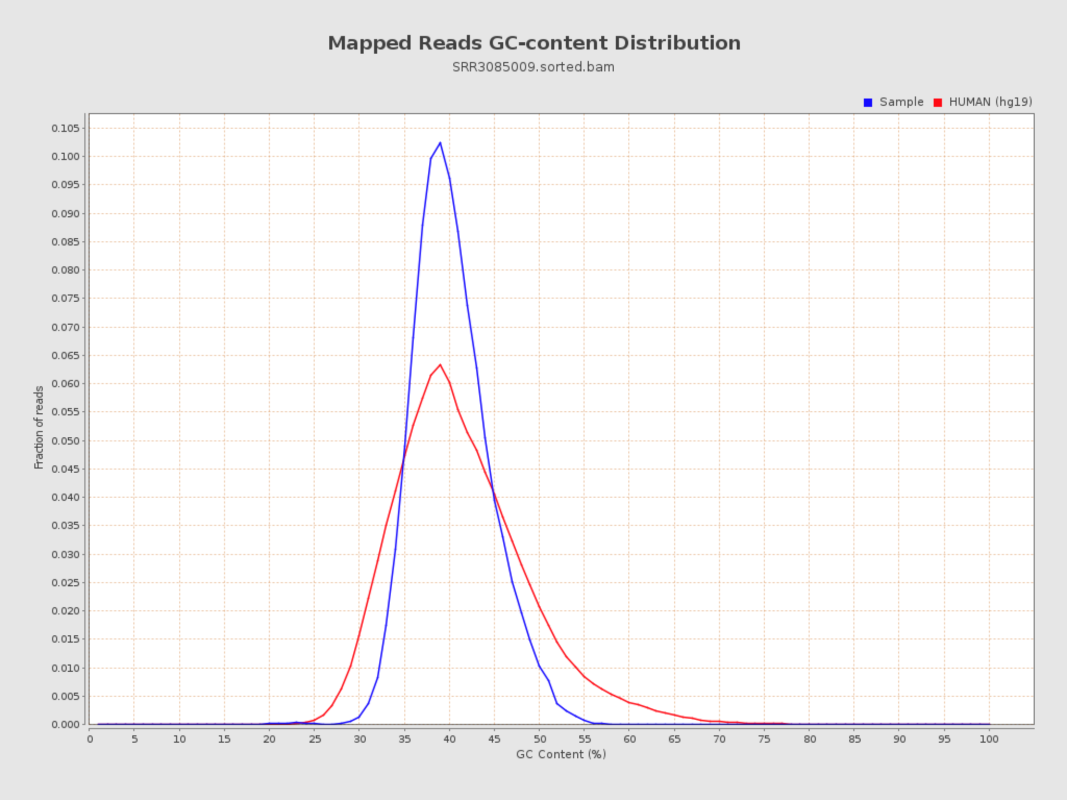
7. Results : Duplication Rate Histogram



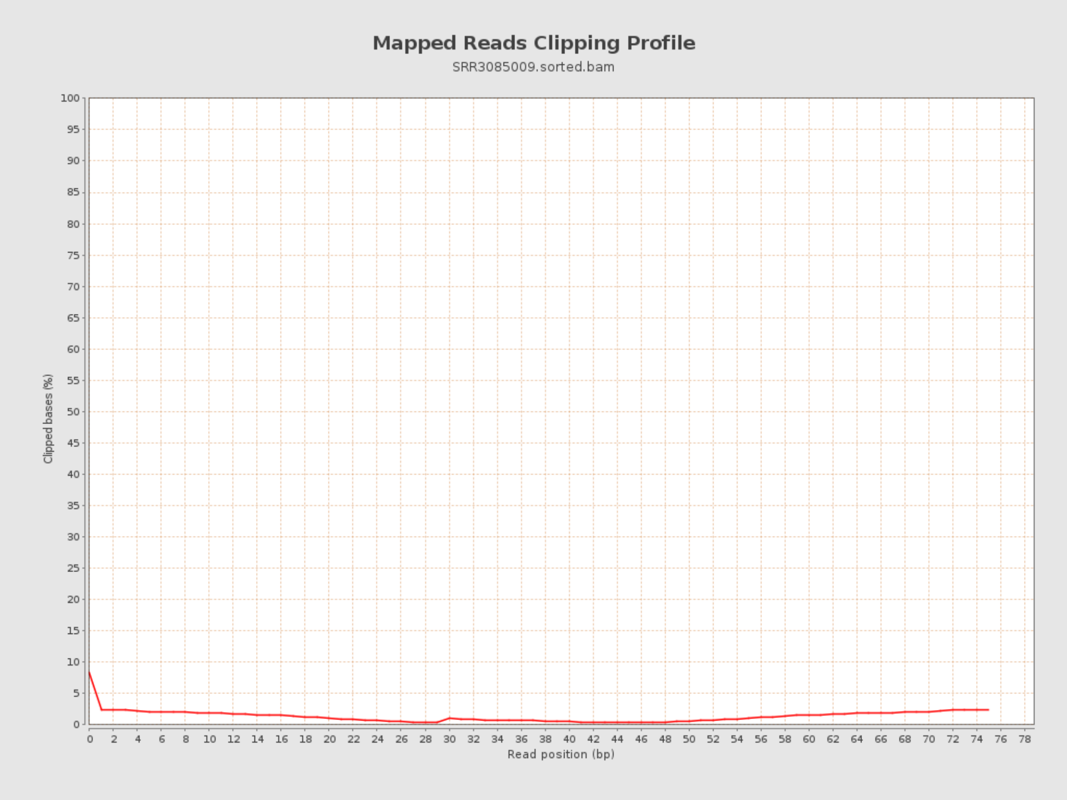
8. Results : Mapped Reads Nucleotide Content



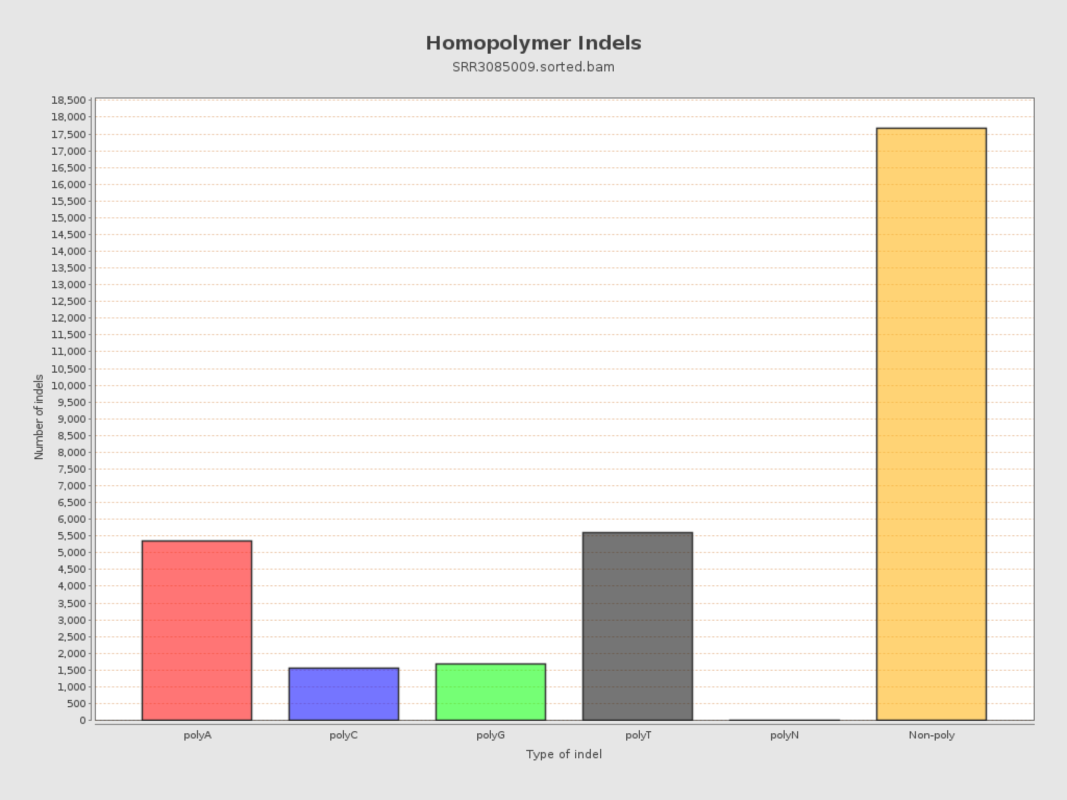
9. Results : Mapped Reads GC-content Distribution



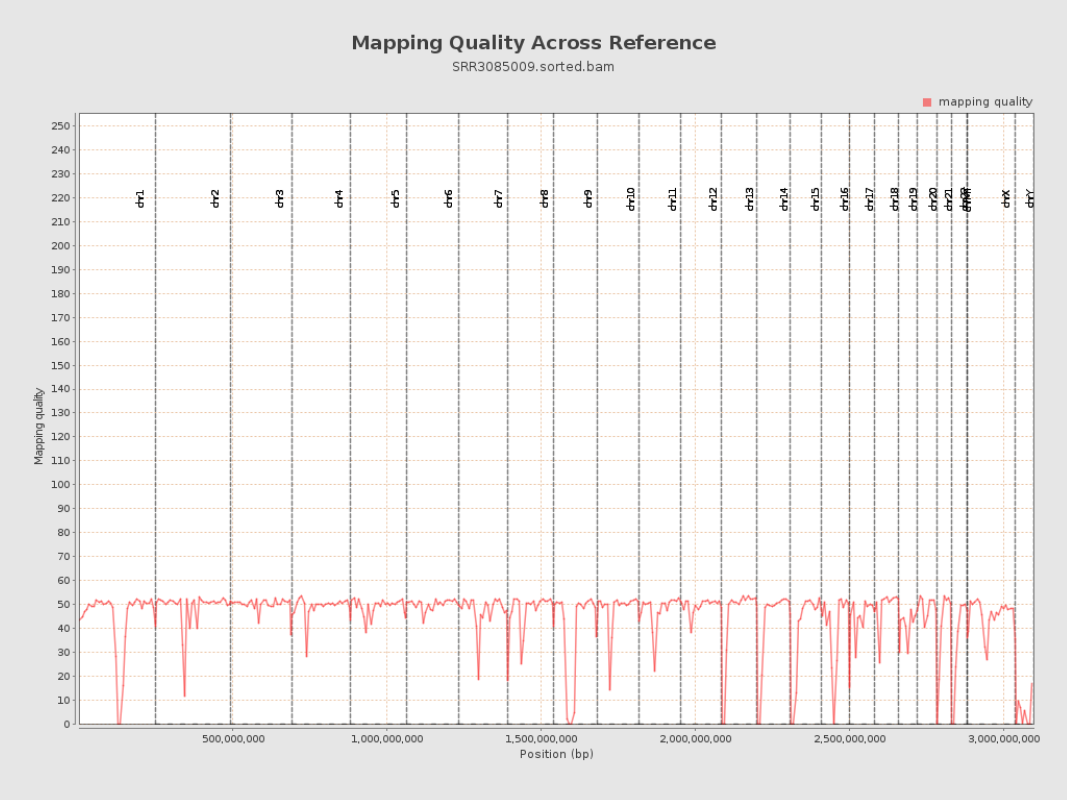
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram