Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 20:46:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082945.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_SRR3082945 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082945.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 20:46:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082945.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,789,066
Mapped reads	1,645,521 / 91.98%
Unmapped reads	143,545 / 8.02%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,624 / 0.87%
Read min/max/mean length	30 / 76 / 76.31
Duplicated reads (estimated)	76,643 / 4.28%
Duplication rate	3.78%
Clipped reads	700,945 / 39.18%

2.2. ACGT Content

Number/percentage of A's	30,629,785 / 27.76%
Number/percentage of C's	20,184,159 / 18.29%
Number/percentage of T's	35,310,744 / 32%
Number/percentage of G's	24,222,754 / 21.95%
Number/percentage of N's	5,826 / 0.01%
GC Percentage	40.24%

2.3. Coverage

Mean	0.0357

Standard Deviation	0.3288

2.4. Mapping Quality

Mean Mapping Quality	45.77

2.5. Mismatches and indels

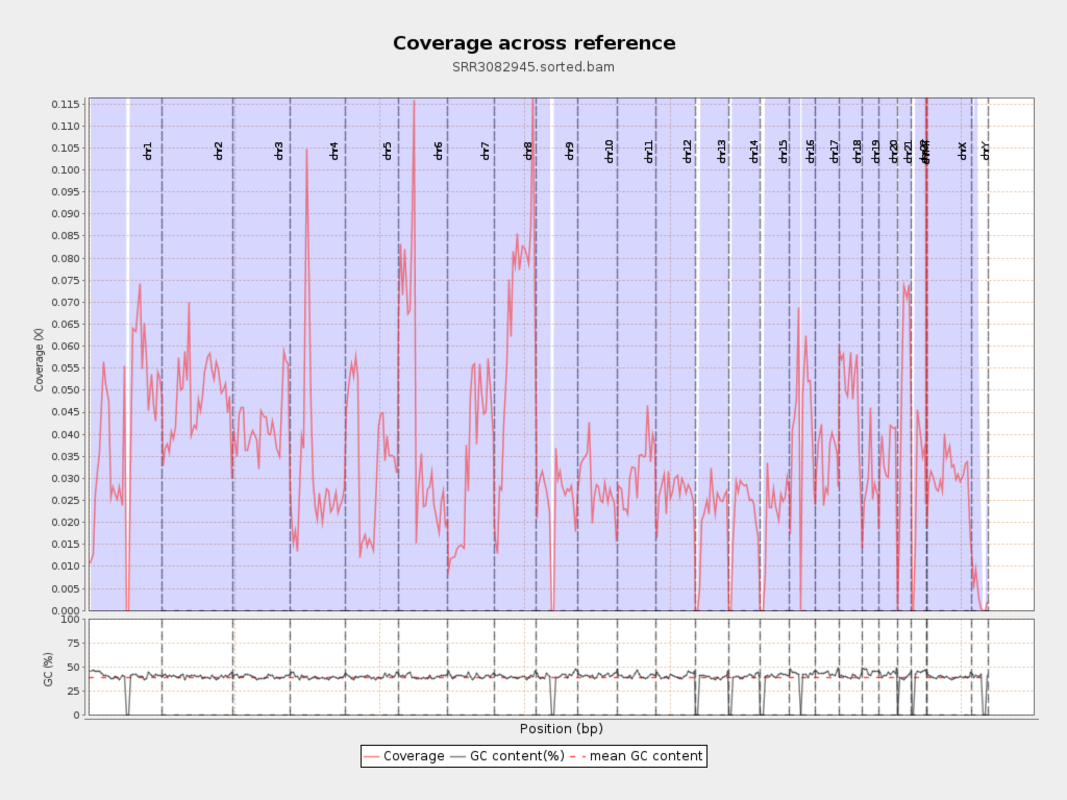
General error rate	0.73%
Mismatches	784,178
Insertions	9,311
Mapped reads with at least one insertion	0.56%
Deletions	25,618
Mapped reads with at least one deletion	1.54%
Homopolymer indels	48.4%

2.6. Chromosome stats

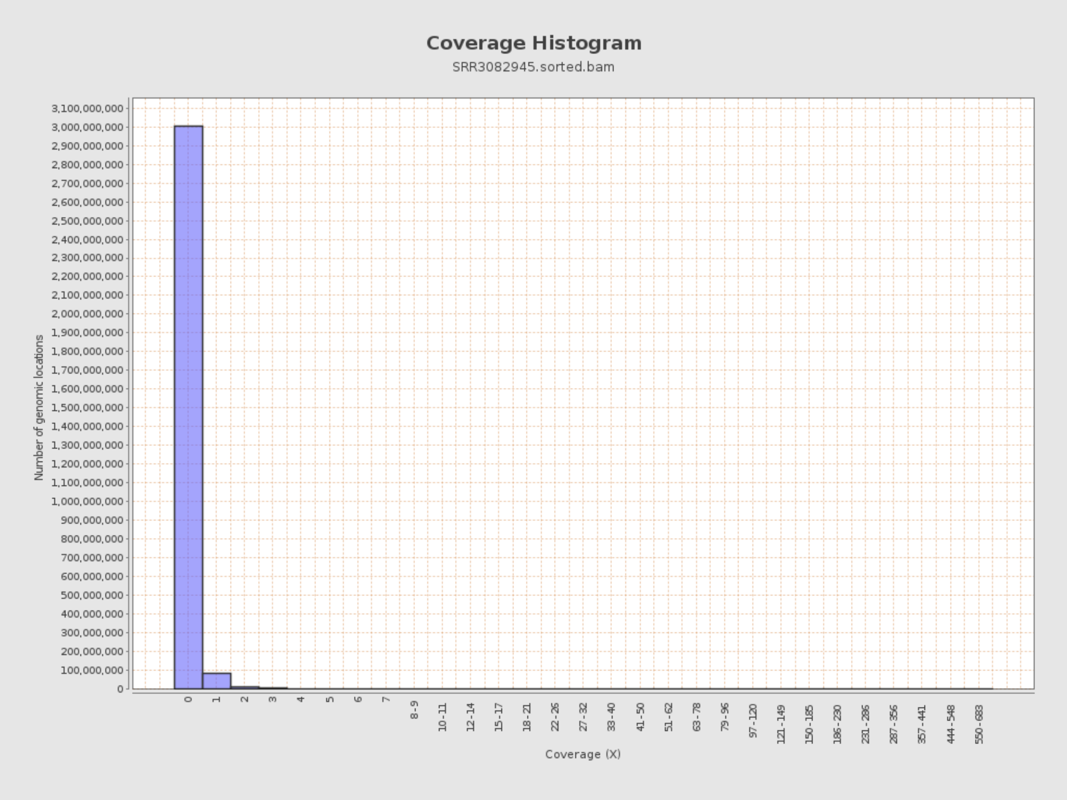
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10225040	0.041	0.6288
chr2	243199373	11716602	0.0482	0.4392
chr3	198022430	8377122	0.0423	0.234
chr4	191154276	5929350	0.031	0.2086
chr5	180915260	6199377	0.0343	0.2131
chr6	171115067	7562988	0.0442	0.3244
chr7	159138663	5434611	0.0342	0.2767

chr8	146364022	9544093	0.0652	0.4049
chr9	141213431	3497265	0.0248	0.2777
chr10	135534747	3867359	0.0285	0.2405
chr11	135006516	4262894	0.0316	0.2561
chr12	133851895	3606998	0.0269	0.191
chr13	115169878	2386100	0.0207	0.1668
chr14	107349540	2320952	0.0216	0.1874
chr15	102531392	2147592	0.0209	0.173
chr16	90354753	3845757	0.0426	0.2492
chr17	81195210	2752355	0.0339	0.2345
chr18	78077248	3954526	0.0506	0.6076
chr19	59128983	1693083	0.0286	0.3961
chr20	63025520	2242224	0.0356	0.2245
chr21	48129895	2480183	0.0515	0.2669
chr22	51304566	1376065	0.0268	0.1854
chrMT	16571	56581	3.4145	2.7399
chrX	155270560	4708610	0.0303	0.2179
chrY	59373566	207866	0.0035	0.0834

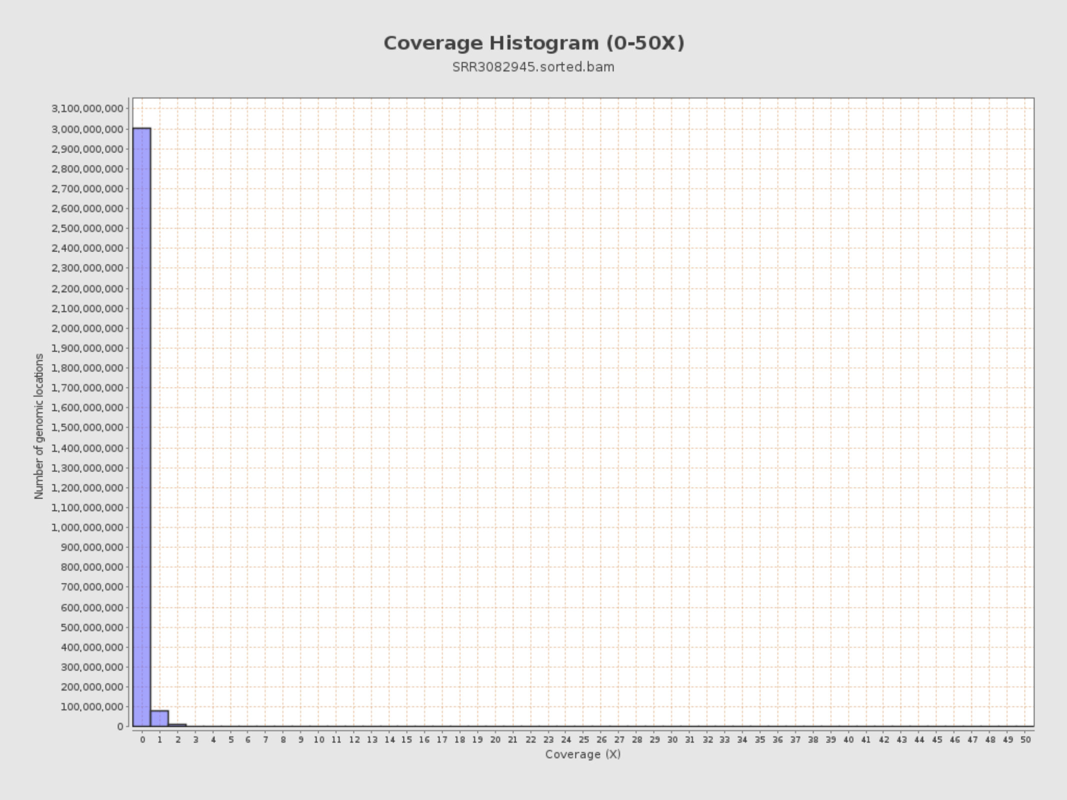
3. Results : Coverage across reference



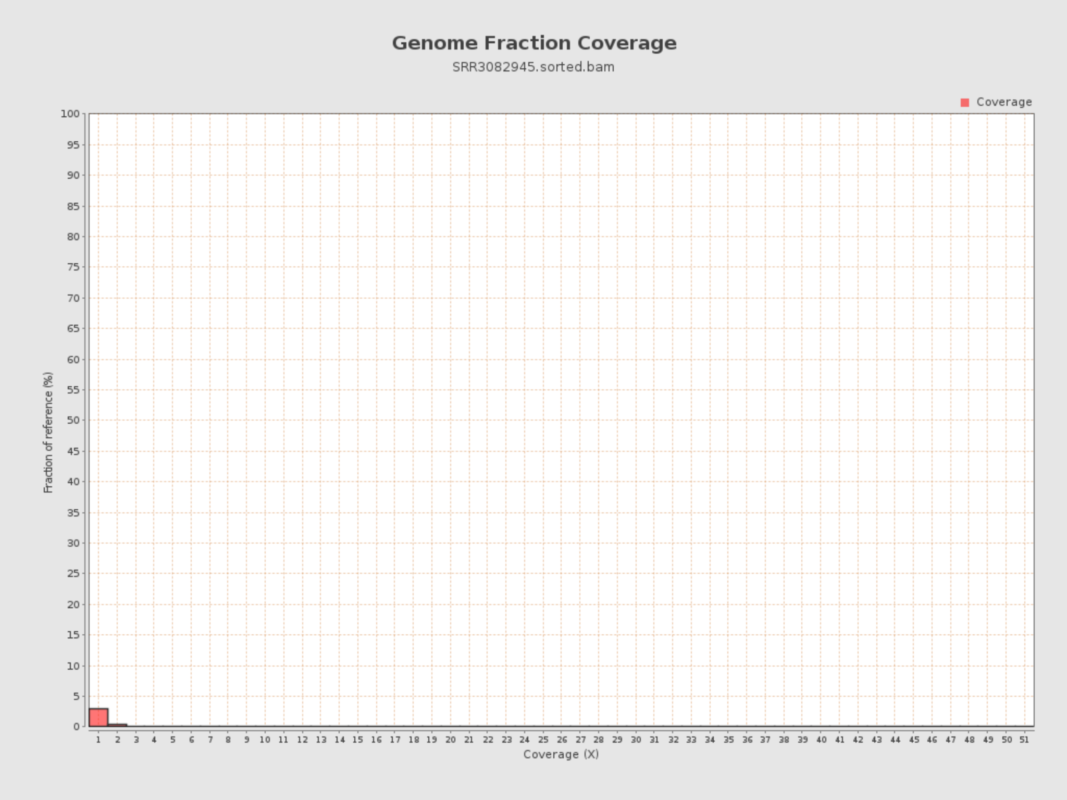
4. Results : Coverage Histogram



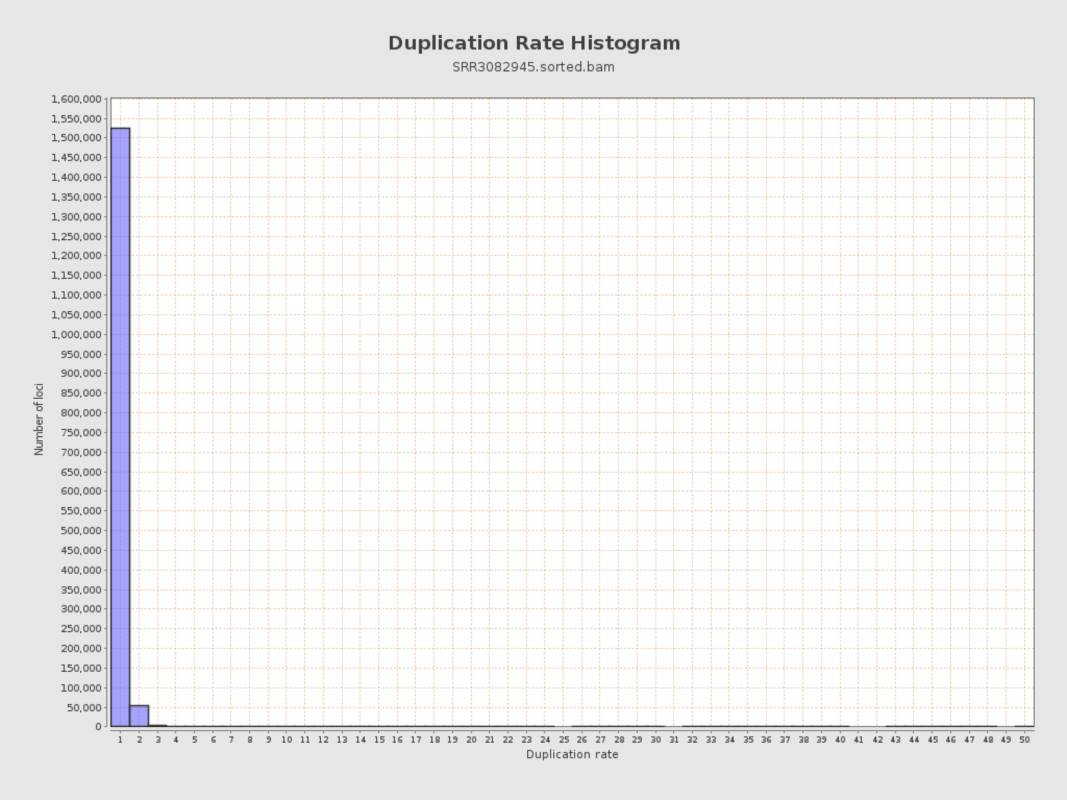
5. Results : Coverage Histogram (0-50X)



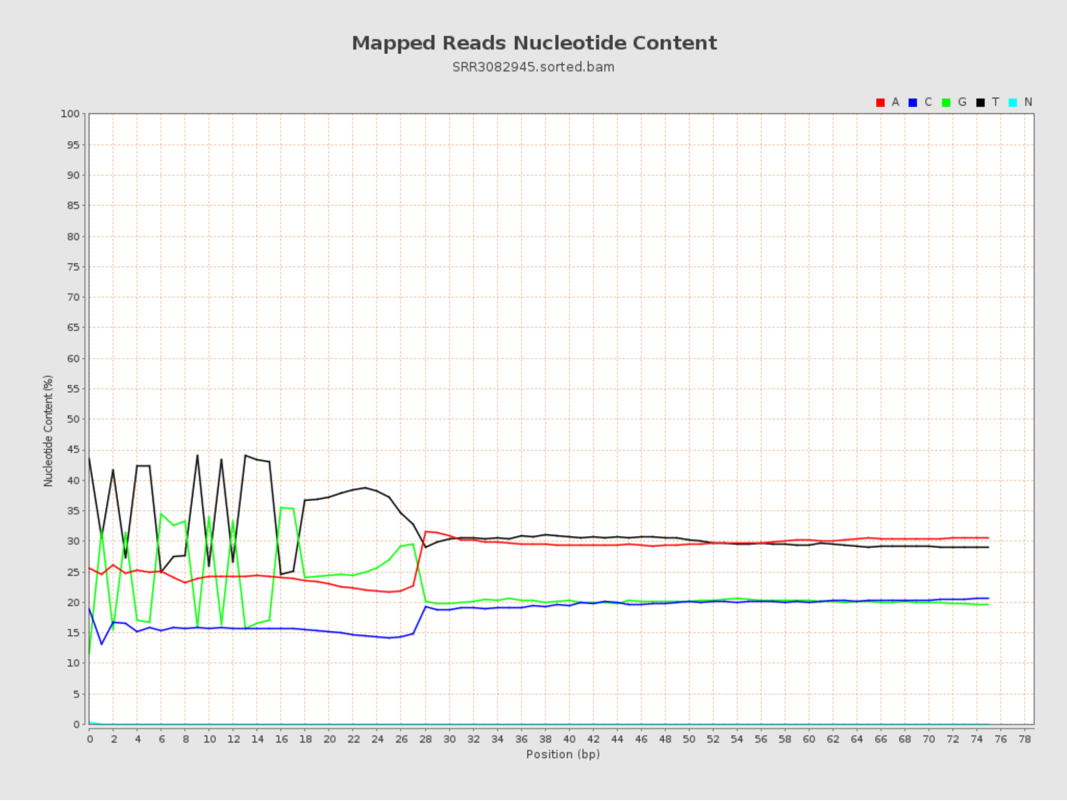
6. Results : Genome Fraction Coverage



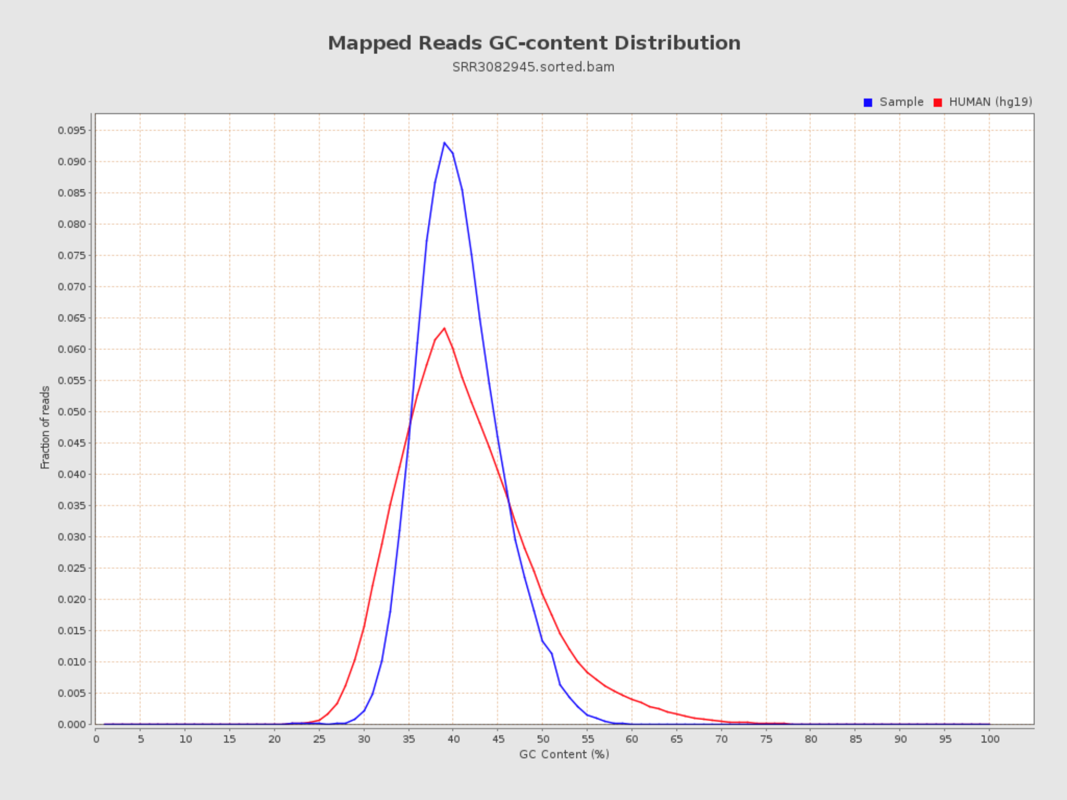
7. Results : Duplication Rate Histogram



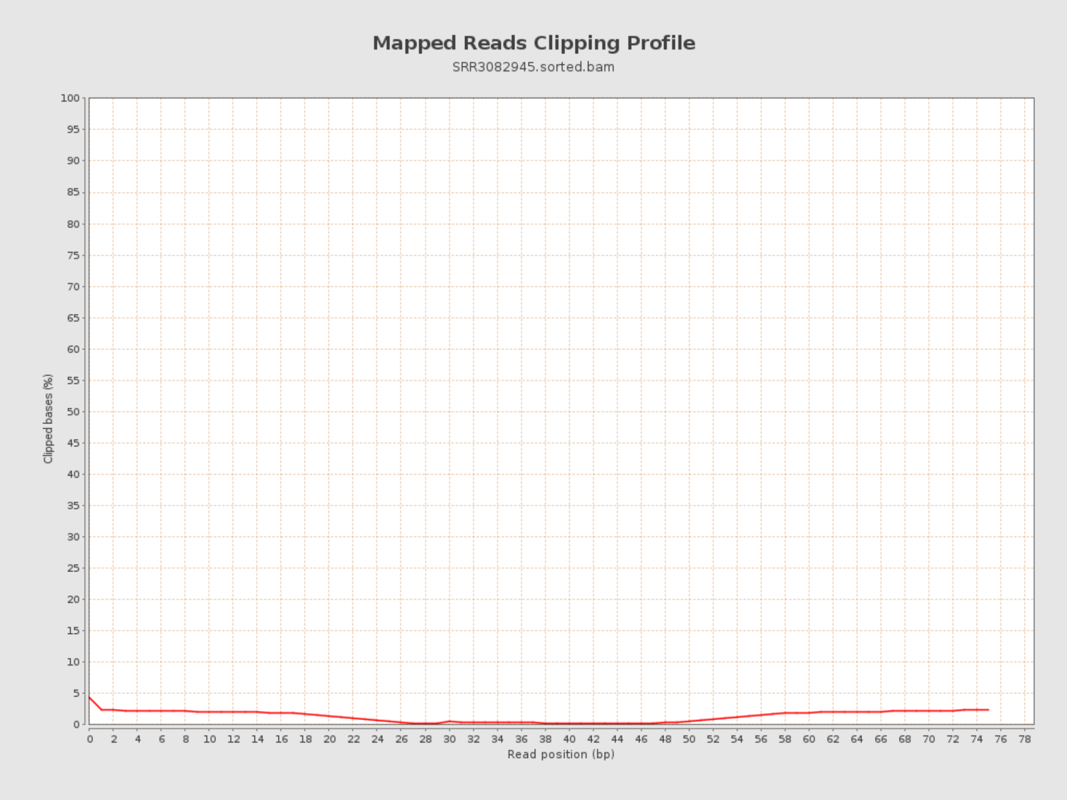
8. Results : Mapped Reads Nucleotide Content



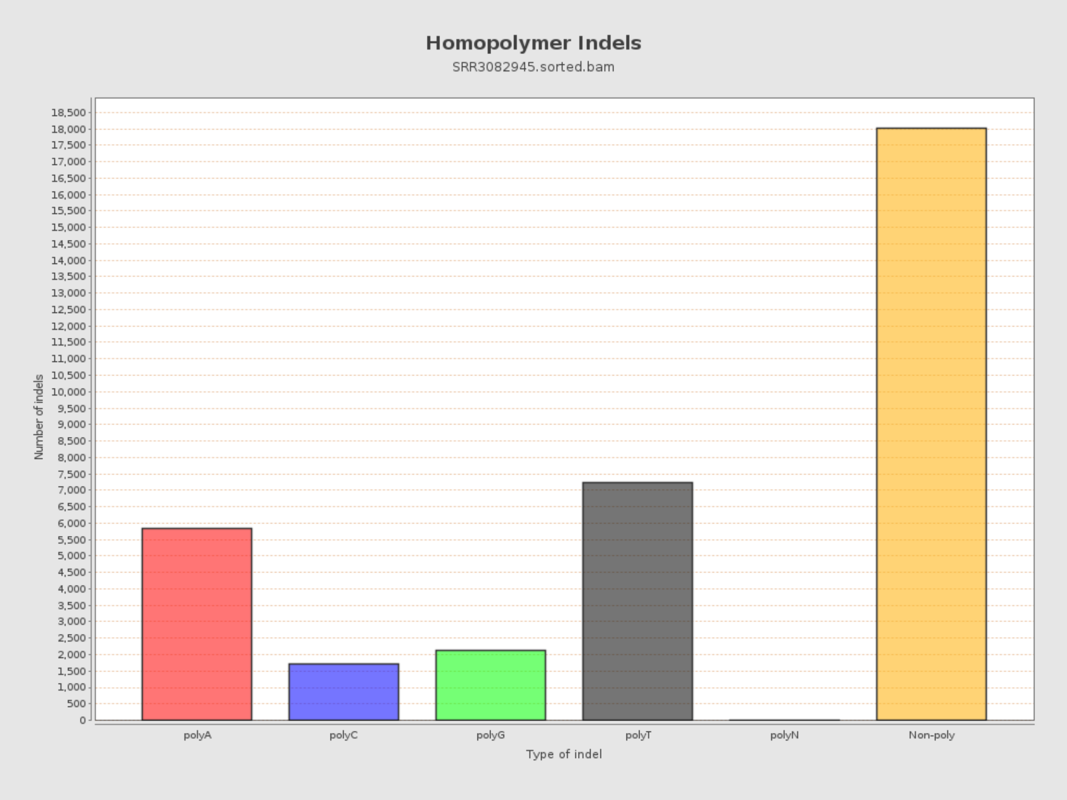
9. Results : Mapped Reads GC-content Distribution



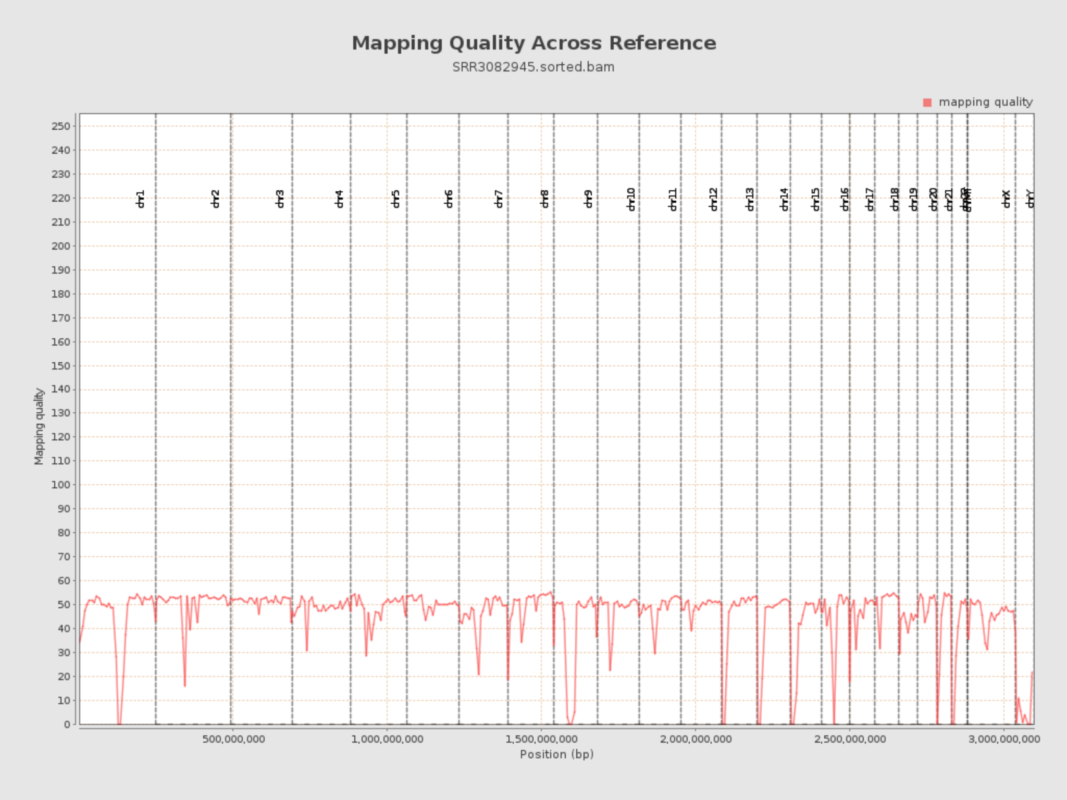
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram