Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 15:08:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082445.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_SRR3082445 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082445.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 15:08:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082445.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,291,331
Mapped reads	2,080,781 / 90.81%
Unmapped reads	210,550 / 9.19%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,691 / 0.77%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	68,538 / 2.99%
Duplication rate	2.27%
Clipped reads	743,977 / 32.47%

2.2. ACGT Content

Number/percentage of A's	42,612,585 / 29.52%
Number/percentage of C's	27,047,969 / 18.74%
Number/percentage of T's	44,050,596 / 30.51%
Number/percentage of G's	30,646,876 / 21.23%
Number/percentage of N's	2,962 / 0%
GC Percentage	39.97%

2.3. Coverage

Mean	0.0467

Standard Deviation	0.4503

2.4. Mapping Quality

Mean Mapping Quality	46.68

2.5. Mismatches and indels

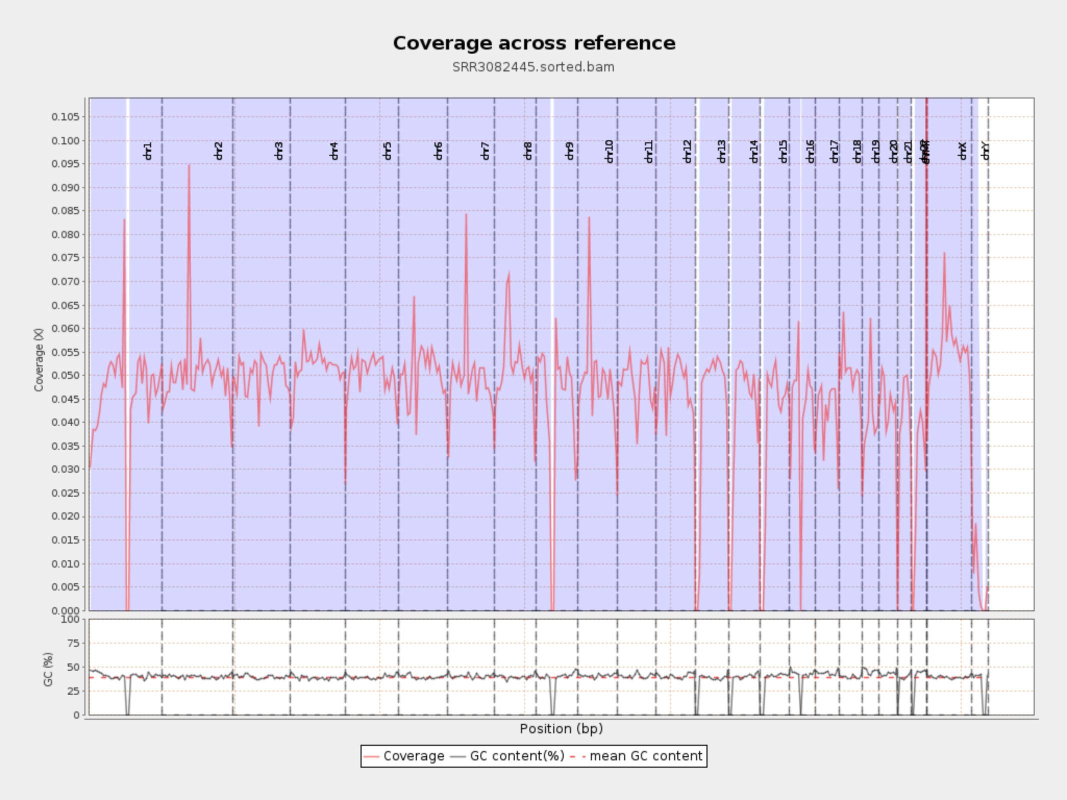
General error rate	0.88%
Mismatches	1,242,579
Insertions	12,338
Mapped reads with at least one insertion	0.59%
Deletions	33,967
Mapped reads with at least one deletion	1.61%
Homopolymer indels	47.21%

2.6. Chromosome stats

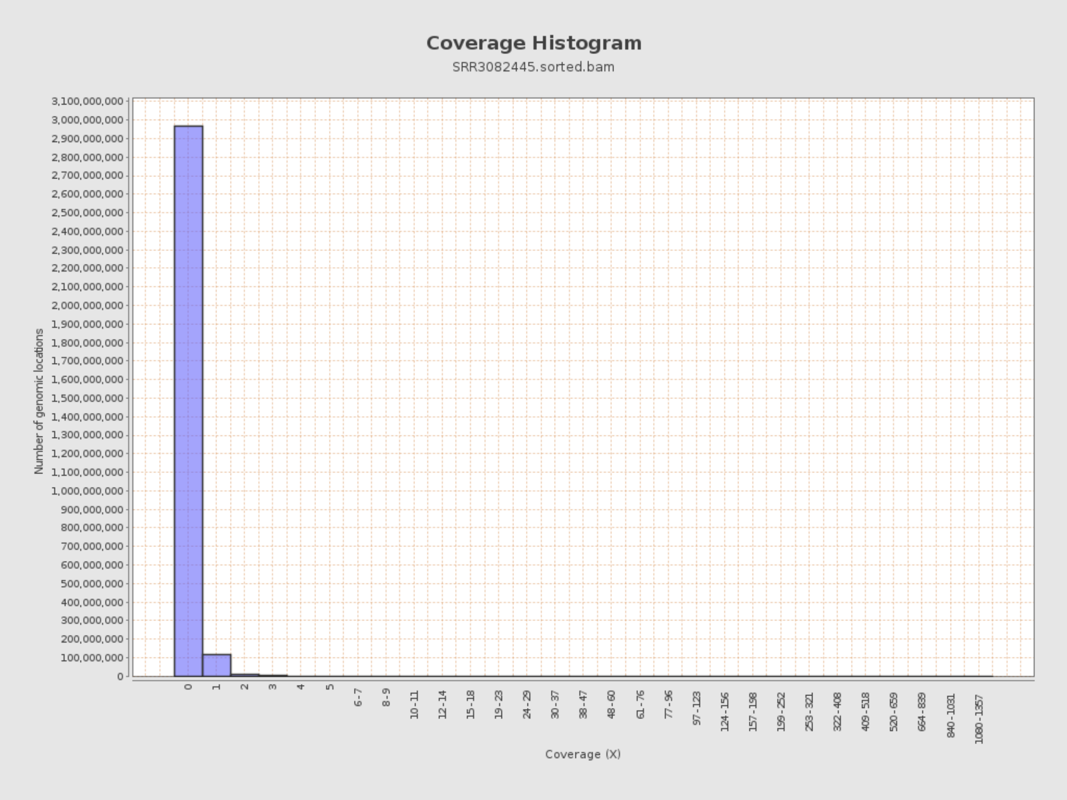
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11345498	0.0455	0.8265
chr2	243199373	12399096	0.051	0.4675
chr3	198022430	9930987	0.0502	0.2482
chr4	191154276	9891737	0.0517	0.2629
chr5	180915260	9162063	0.0506	0.2477
chr6	171115067	8654294	0.0506	0.2971
chr7	159138663	7990009	0.0502	0.5947

chr8	146364022	7558031	0.0516	0.8622
chr9	141213431	6094812	0.0432	0.4
chr10	135534747	6710719	0.0495	0.411
chr11	135006516	6513520	0.0482	0.3565
chr12	133851895	6481114	0.0484	0.2442
chr13	115169878	4825816	0.0419	0.2226
chr14	107349540	4333330	0.0404	0.2455
chr15	102531392	3947229	0.0385	0.2154
chr16	90354753	3815470	0.0422	0.2712
chr17	81195210	3386802	0.0417	0.2558
chr18	78077248	3991727	0.0511	0.733
chr19	59128983	2449773	0.0414	0.6364
chr20	63025520	2746002	0.0436	0.2362
chr21	48129895	1886757	0.0392	0.2384
chr22	51304566	1367902	0.0267	0.1763
chrMT	16571	4849	0.2926	0.5226
chrX	155270560	8568782	0.0552	0.2894
chrY	59373566	361017	0.0061	0.1442

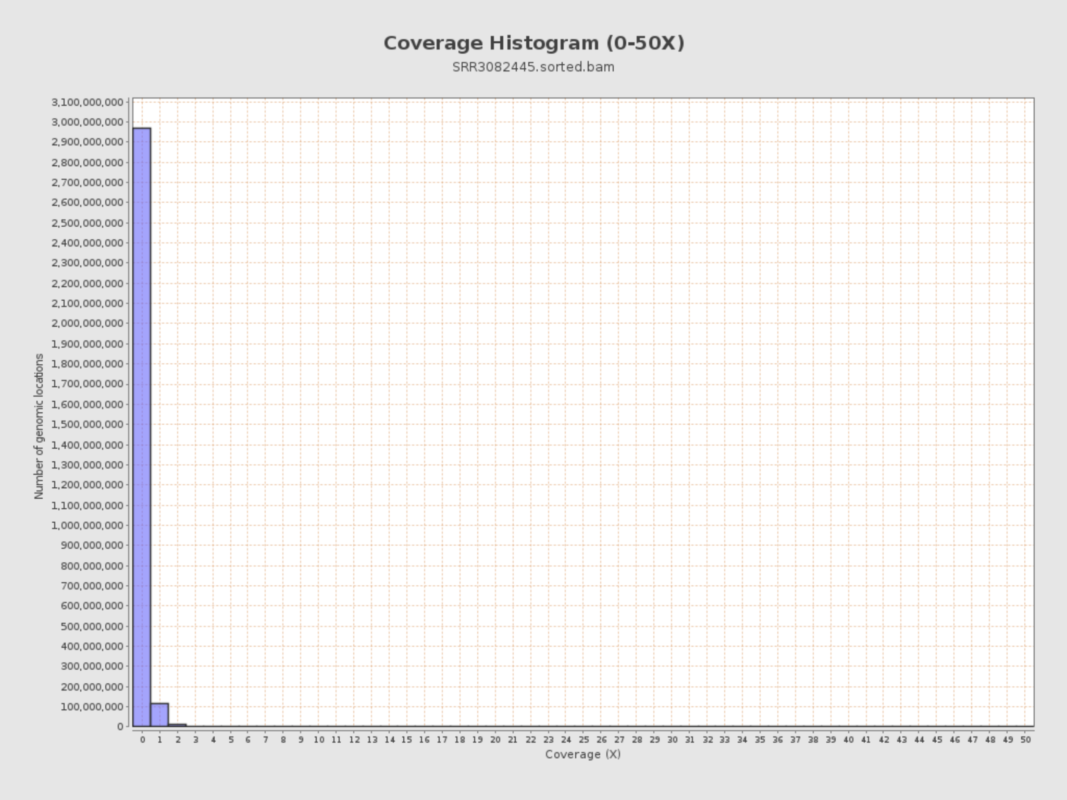
3. Results : Coverage across reference



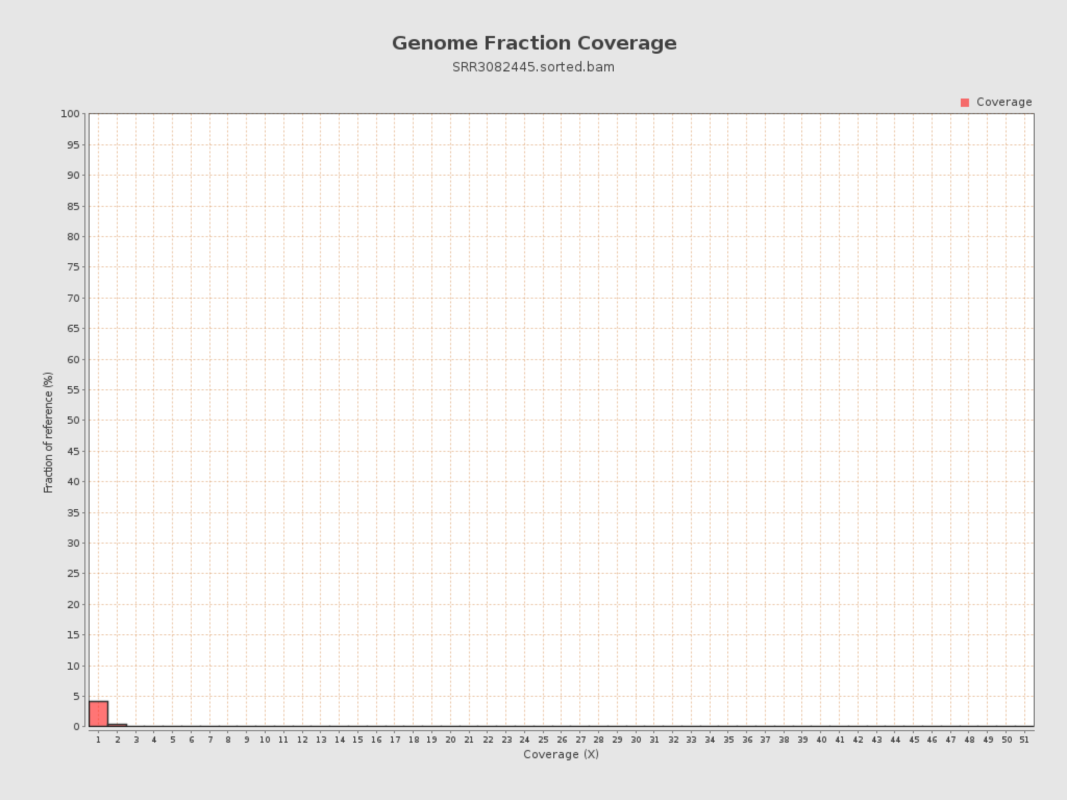
4. Results : Coverage Histogram



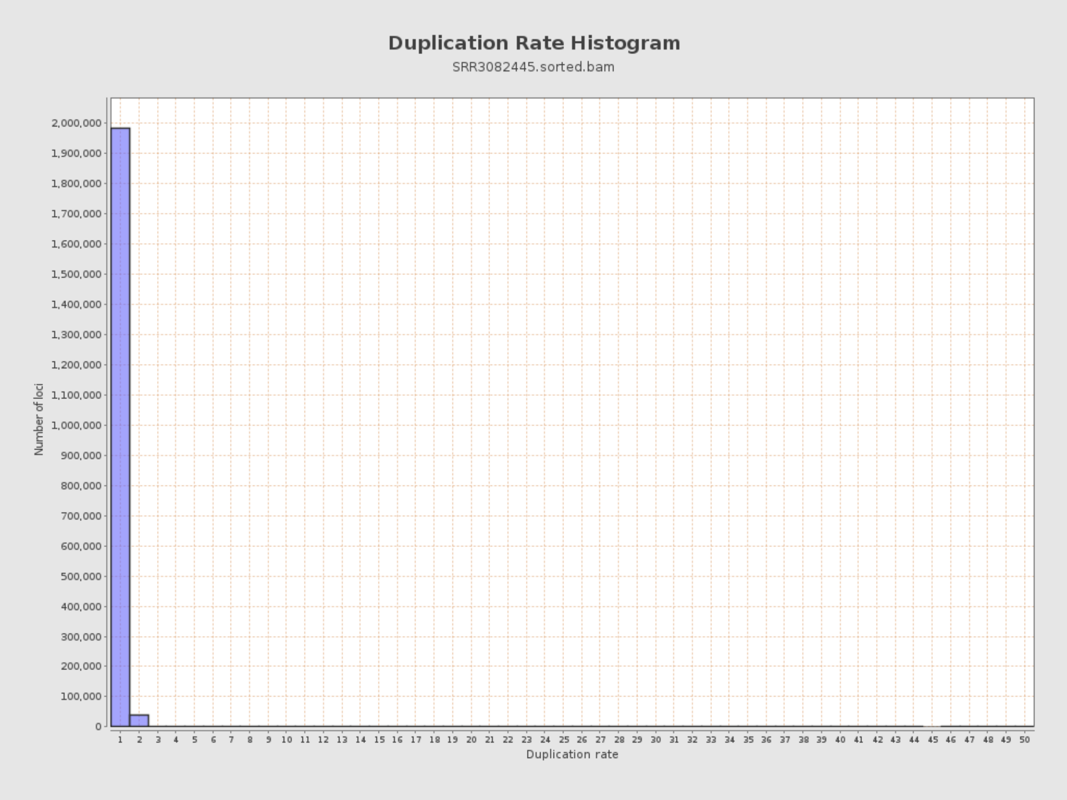
5. Results : Coverage Histogram (0-50X)



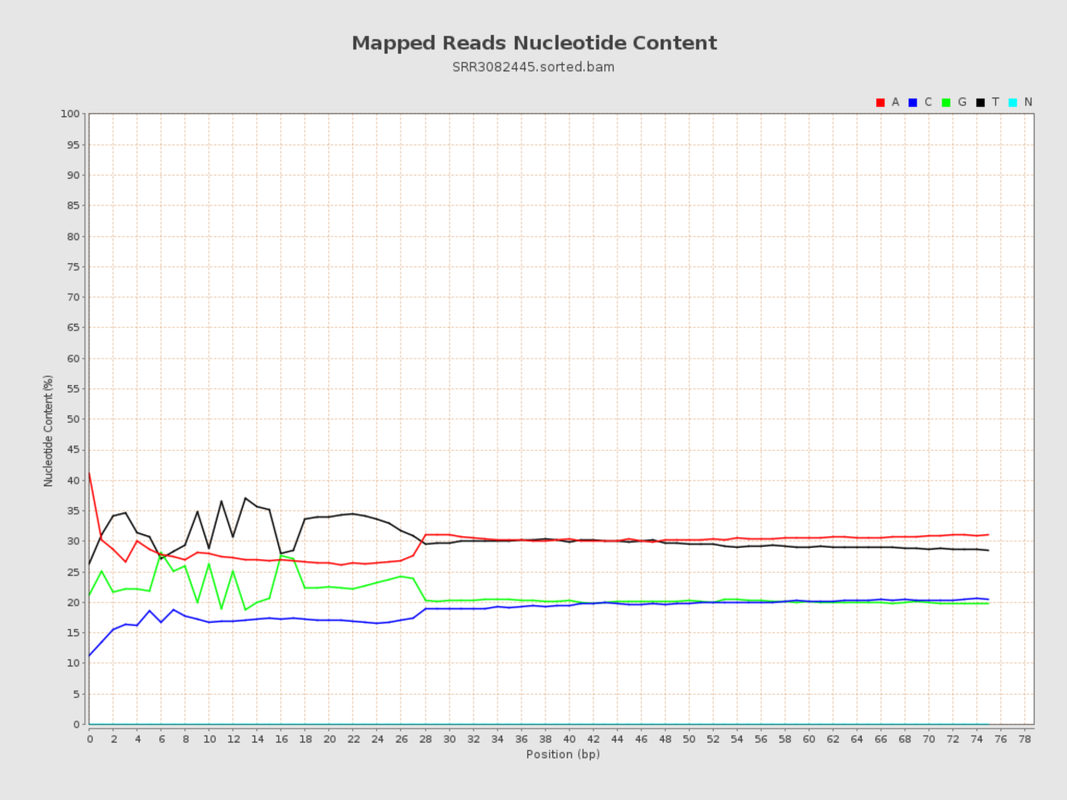
6. Results : Genome Fraction Coverage



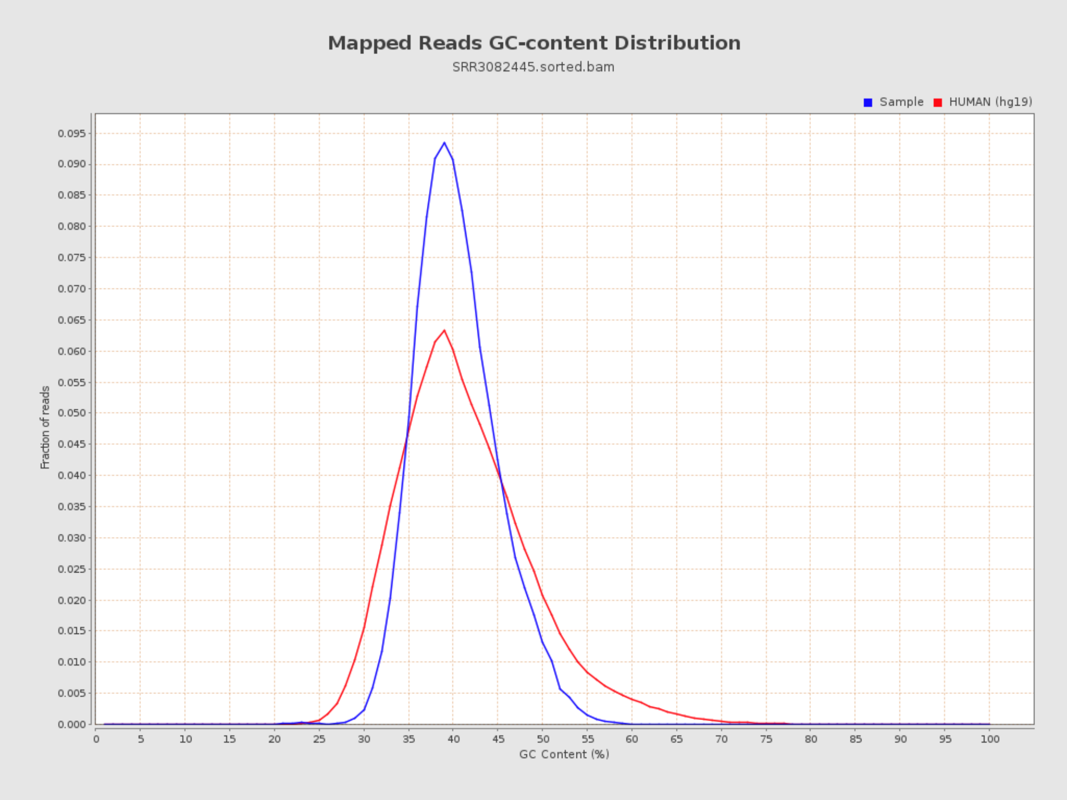
7. Results : Duplication Rate Histogram



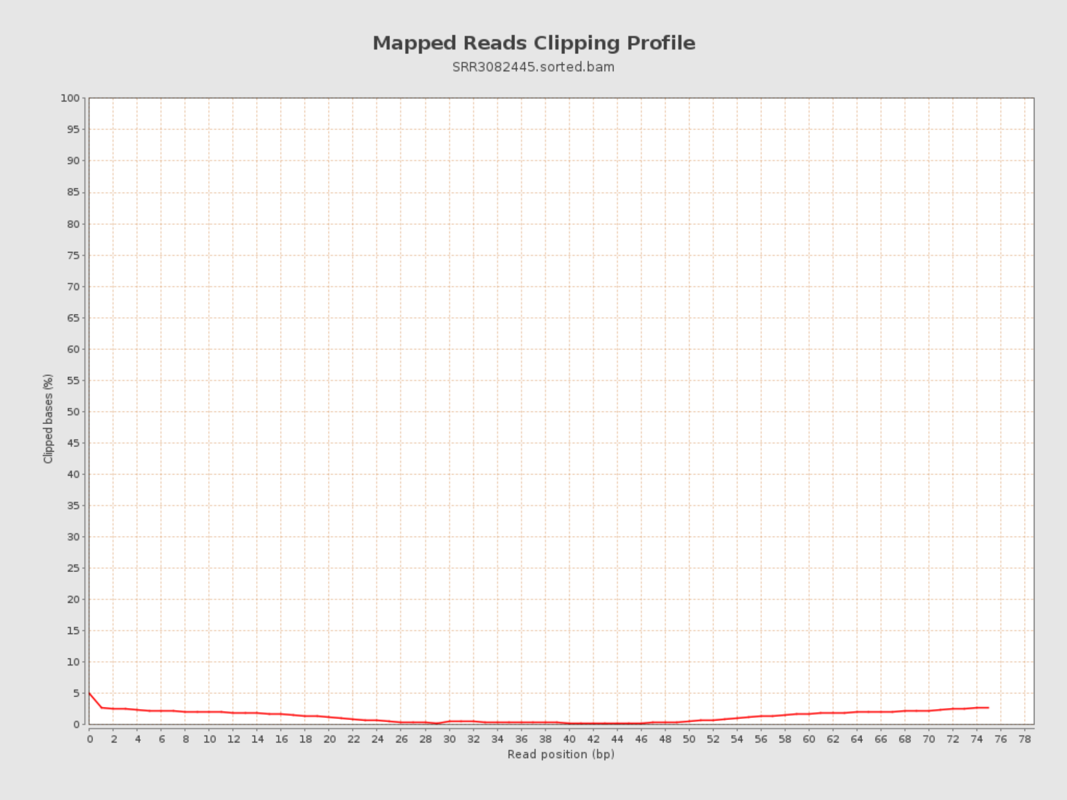
8. Results : Mapped Reads Nucleotide Content



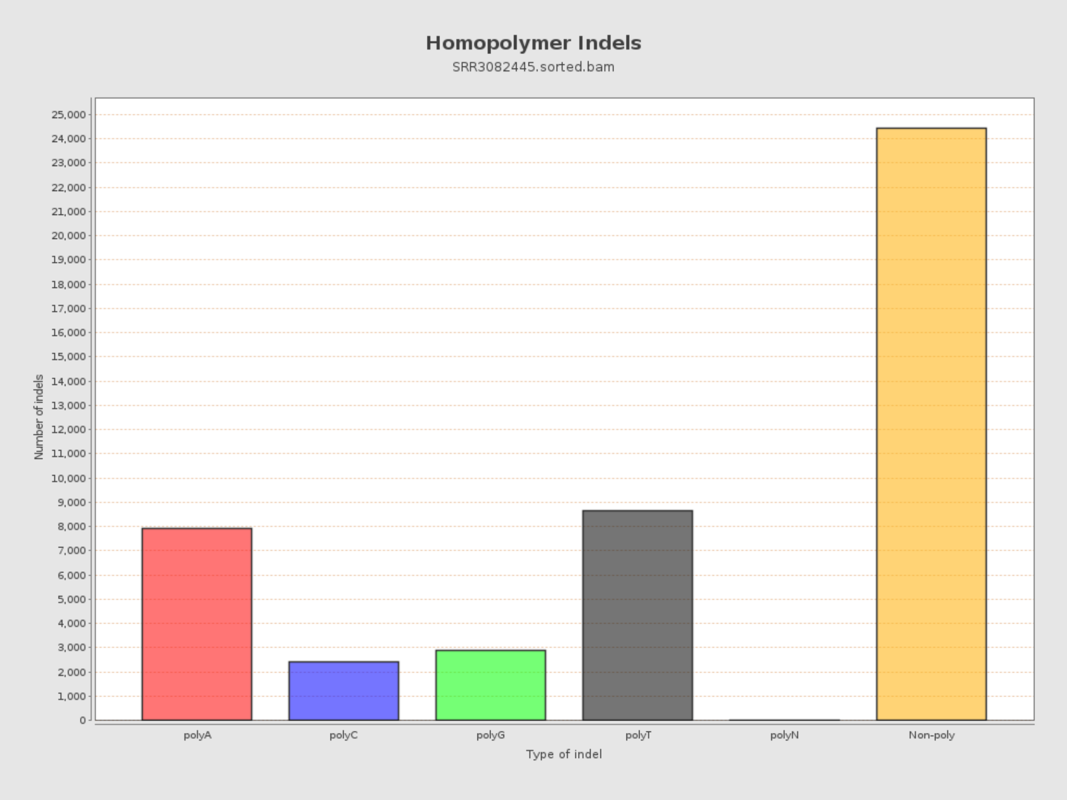
9. Results : Mapped Reads GC-content Distribution



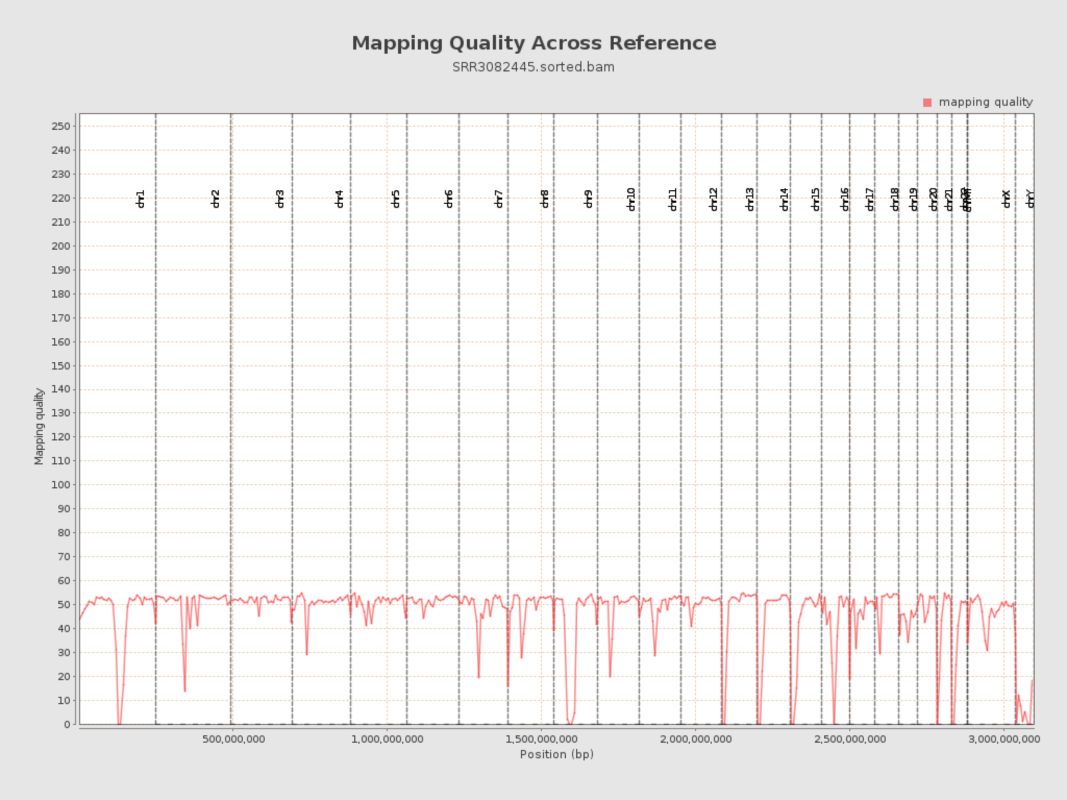
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram