Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 04:46:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081242.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_SRR3081242 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081242.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 04:46:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081242.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,192,467
Mapped reads	2,795,693 / 87.57%
Unmapped reads	396,774 / 12.43%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	30,121 / 0.94%
Read min/max/mean length	30 / 76 / 76.33
Duplicated reads (estimated)	145,908 / 4.57%
Duplication rate	4.2%
Clipped reads	1,632,750 / 51.14%

2.2. ACGT Content

Number/percentage of A's	52,004,992 / 29.09%
Number/percentage of C's	34,117,093 / 19.08%
Number/percentage of T's	55,007,757 / 30.77%
Number/percentage of G's	37,646,649 / 21.06%
Number/percentage of N's	22,035 / 0.01%
GC Percentage	40.14%

2.3. Coverage

Mean	0.0578

Standard Deviation	0.4555

2.4. Mapping Quality

Mean Mapping Quality	45.32

2.5. Mismatches and indels

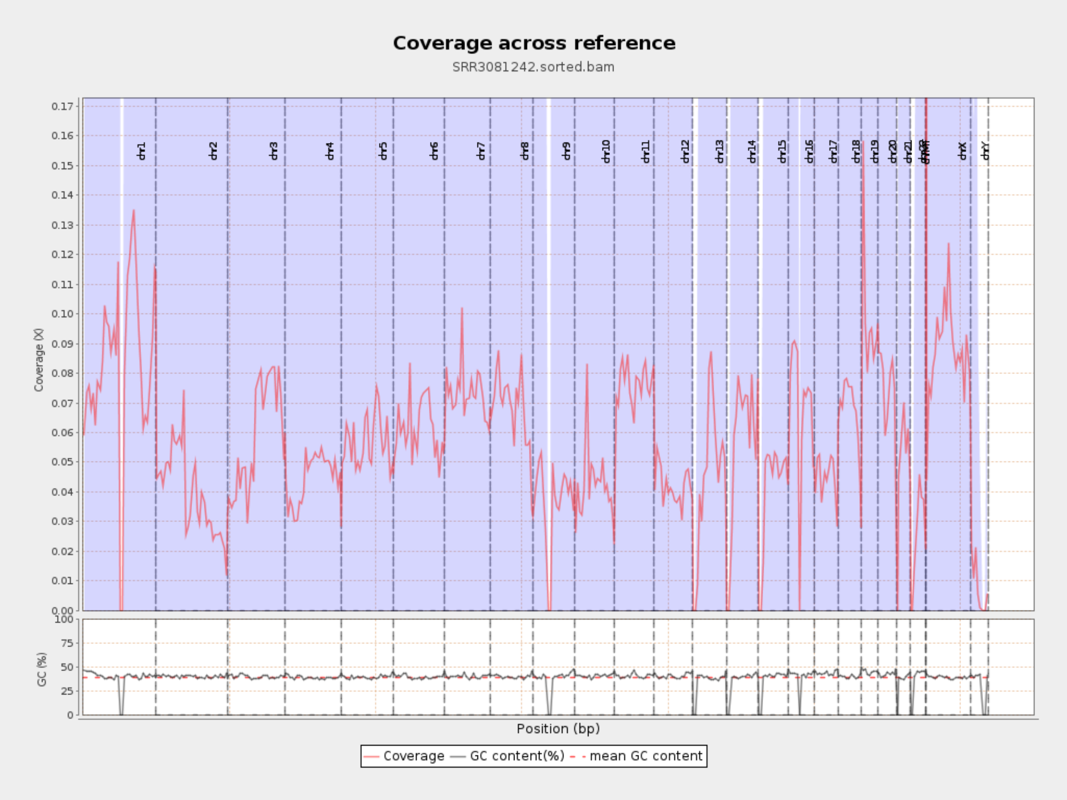
General error rate	0.94%
Mismatches	1,652,030
Insertions	13,600
Mapped reads with at least one insertion	0.48%
Deletions	40,721
Mapped reads with at least one deletion	1.44%
Homopolymer indels	47.02%

2.6. Chromosome stats

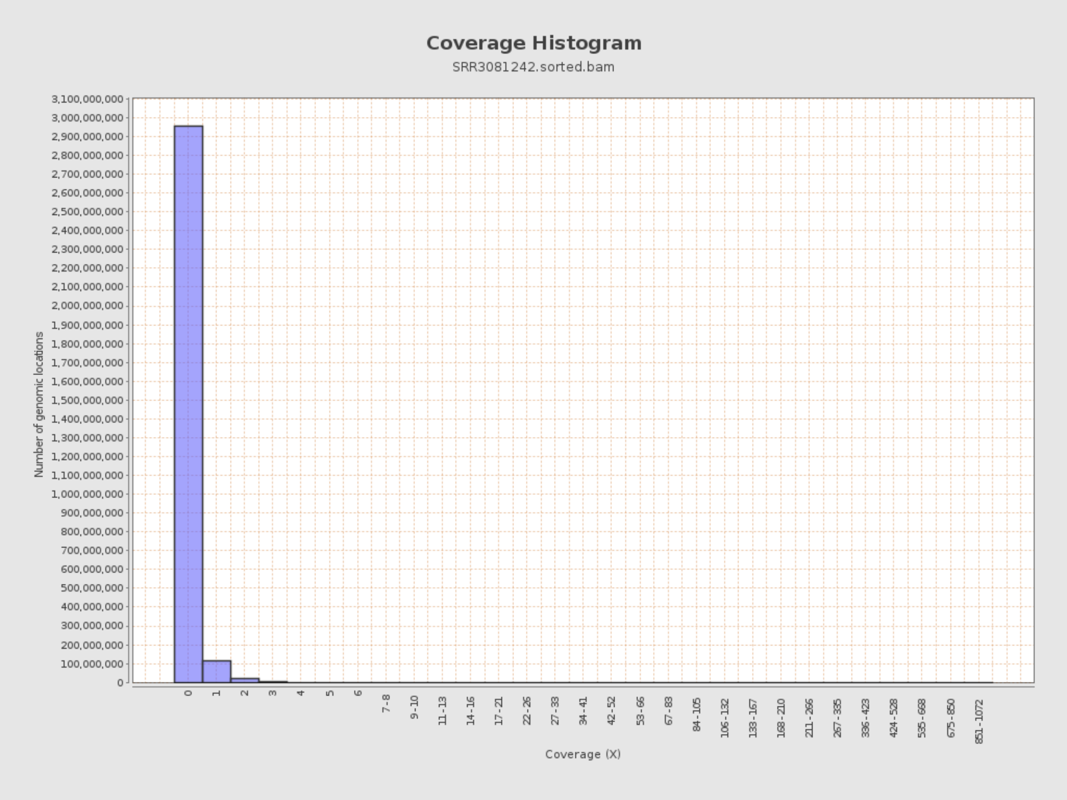
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	20839006	0.0836	0.9362
chr2	243199373	9632890	0.0396	0.4602
chr3	198022430	11584024	0.0585	0.2992
chr4	191154276	8572999	0.0448	0.2633
chr5	180915260	10242433	0.0566	0.2911
chr6	171115067	10604735	0.062	0.3518
chr7	159138663	11651470	0.0732	0.5672

chr8	146364022	10036593	0.0686	0.5264
chr9	141213431	5205640	0.0369	0.323
chr10	135534747	5784894	0.0427	0.474
chr11	135006516	10184033	0.0754	0.4806
chr12	133851895	5651000	0.0422	0.2554
chr13	115169878	5325786	0.0462	0.2655
chr14	107349540	5999701	0.0559	0.3013
chr15	102531392	4120041	0.0402	0.2633
chr16	90354753	6018923	0.0666	0.3312
chr17	81195210	3685777	0.0454	0.2945
chr18	78077248	5396676	0.0691	0.5122
chr19	59128983	5707241	0.0965	0.6598
chr20	63025520	4750968	0.0754	0.3409
chr21	48129895	2424866	0.0504	0.2877
chr22	51304566	1340132	0.0261	0.1919
chrMT	16571	30704	1.8529	1.9273
chrX	155270560	13621136	0.0877	0.3968
chrY	59373566	452910	0.0076	0.1348

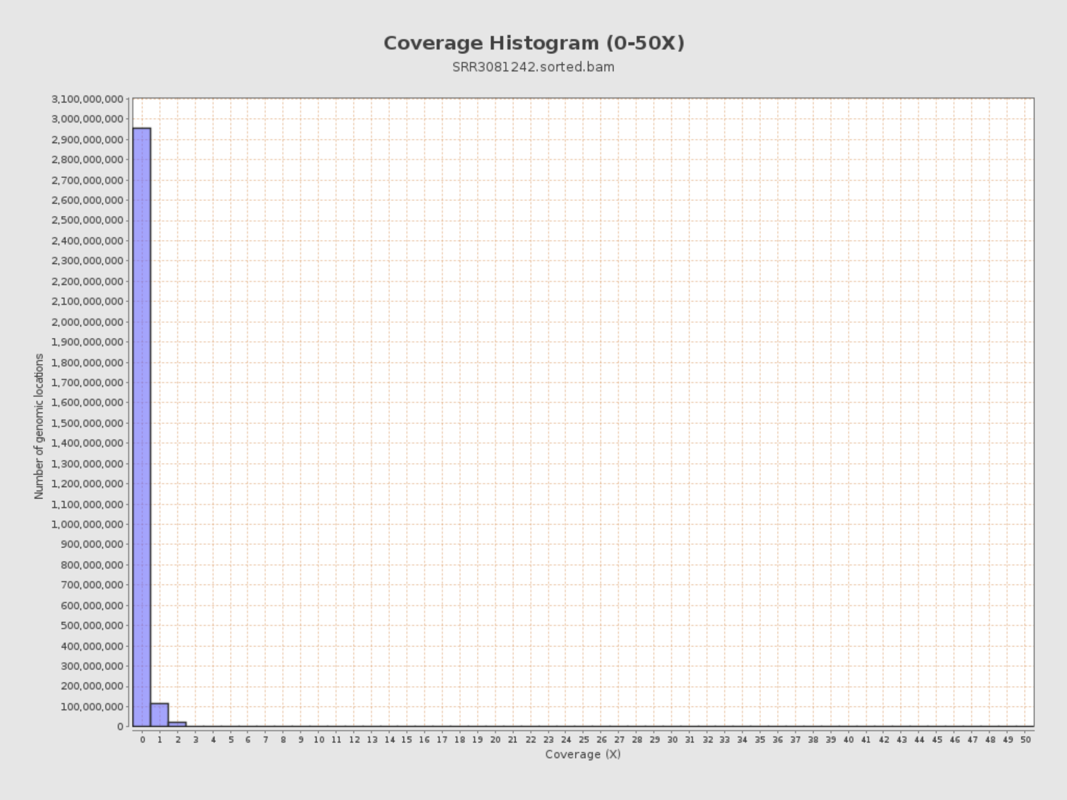
3. Results : Coverage across reference



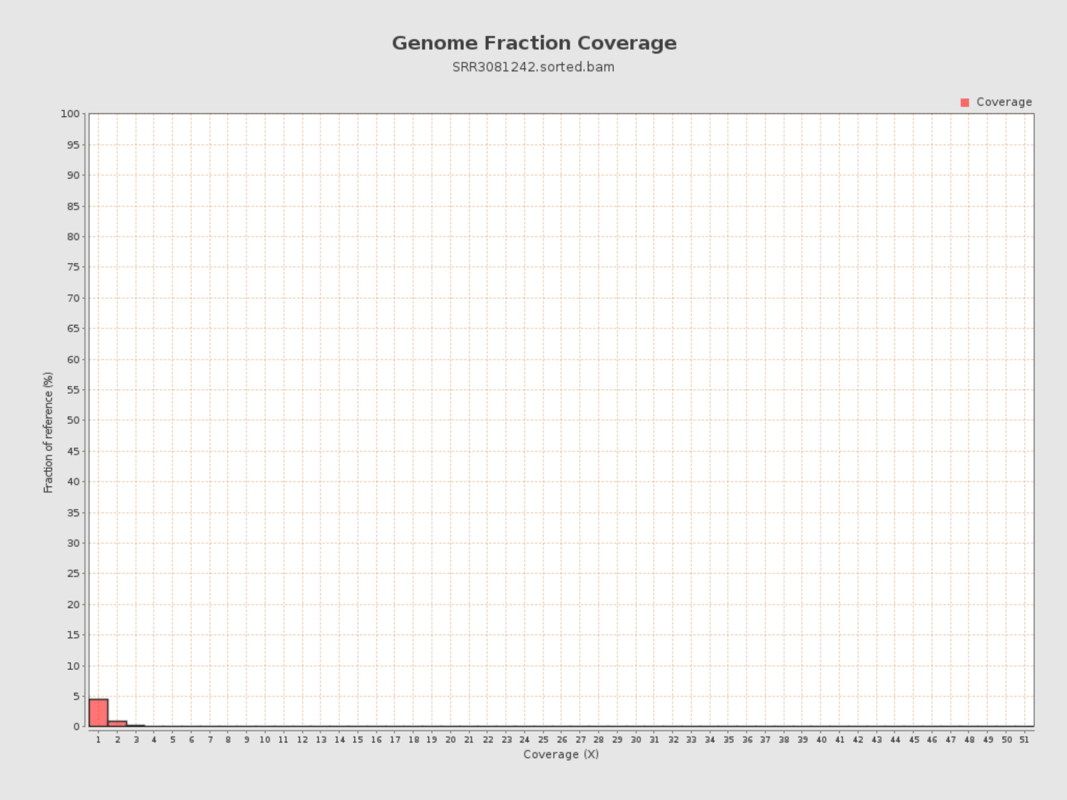
4. Results : Coverage Histogram



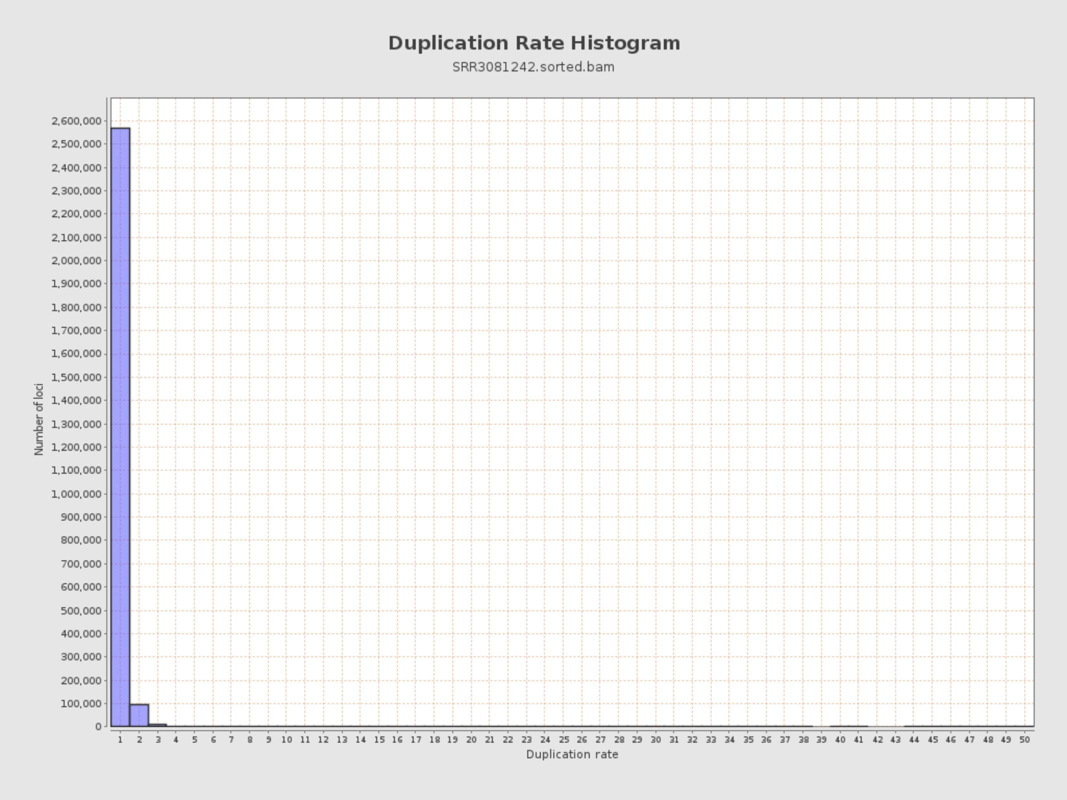
5. Results : Coverage Histogram (0-50X)



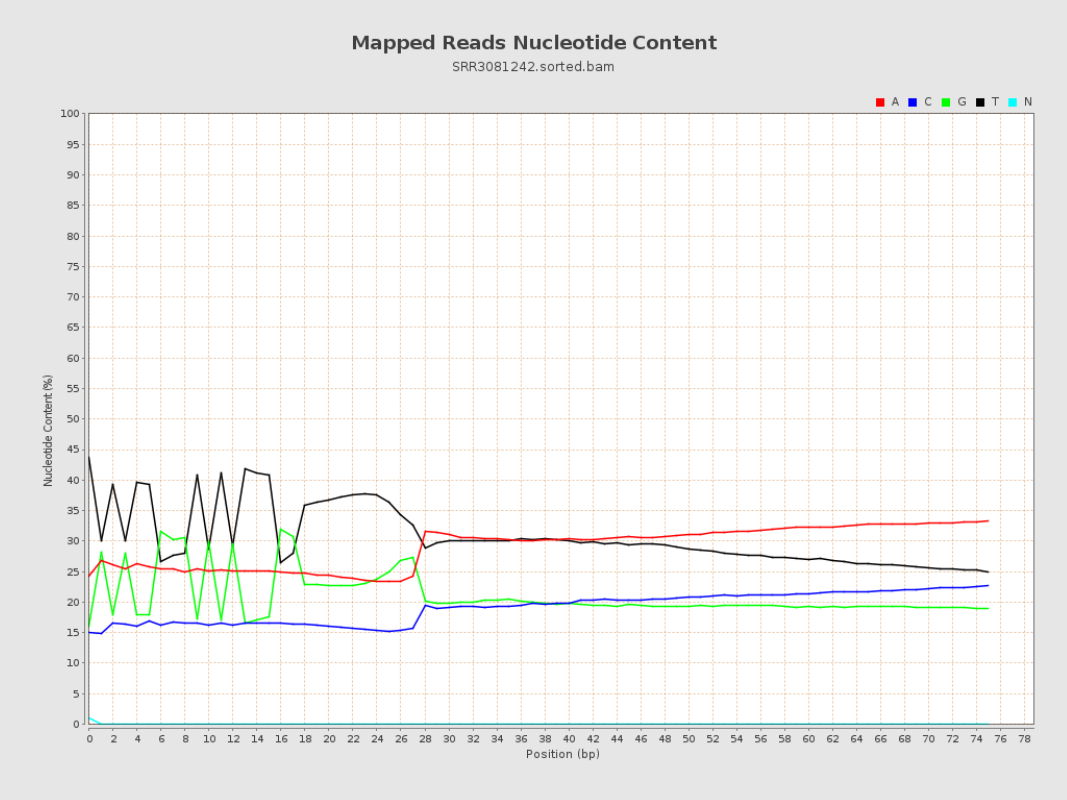
6. Results : Genome Fraction Coverage



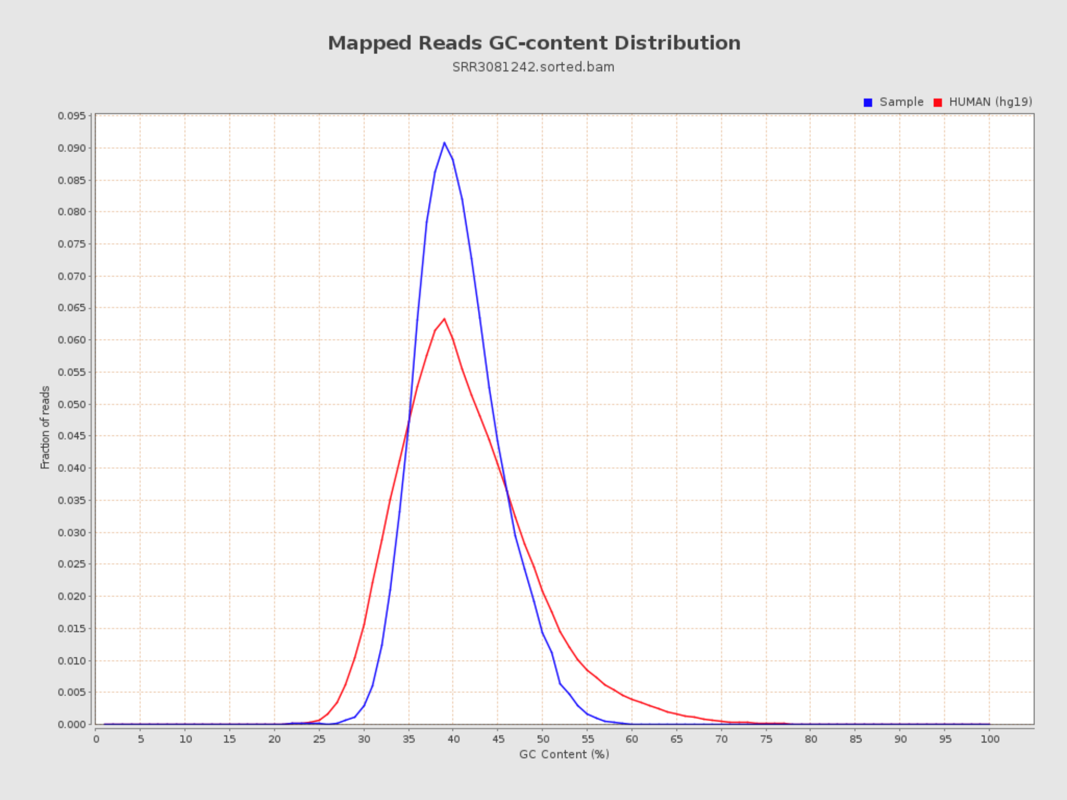
7. Results : Duplication Rate Histogram



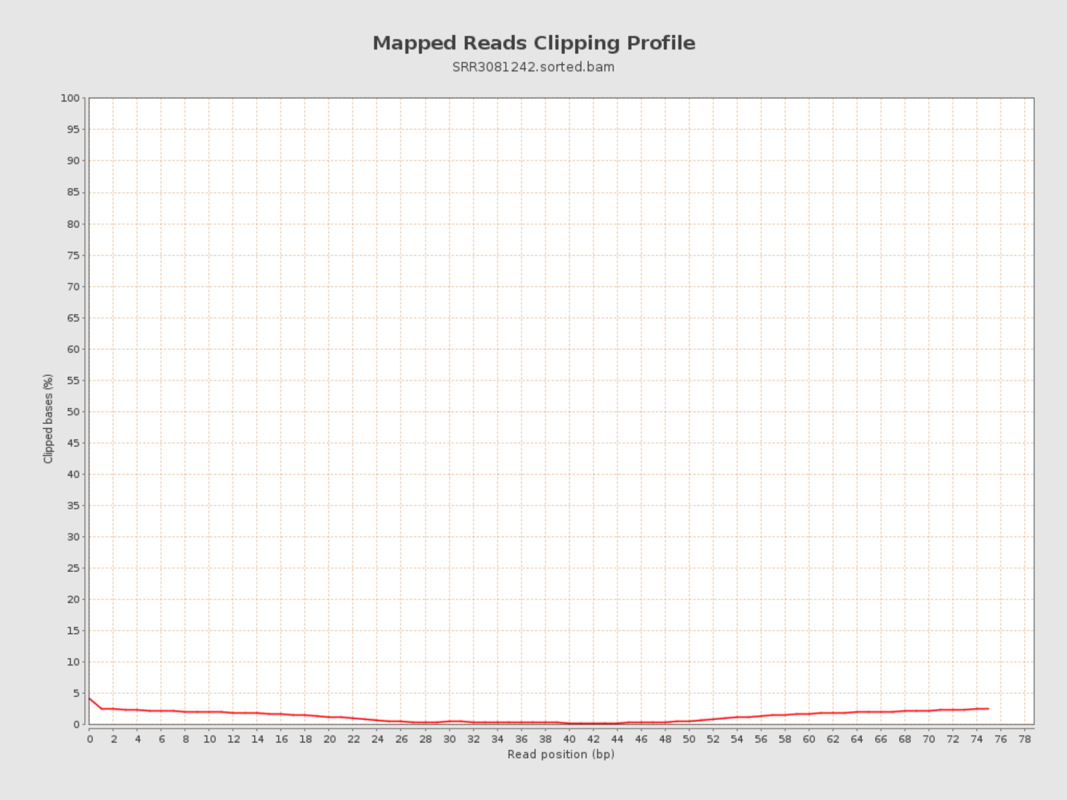
8. Results : Mapped Reads Nucleotide Content



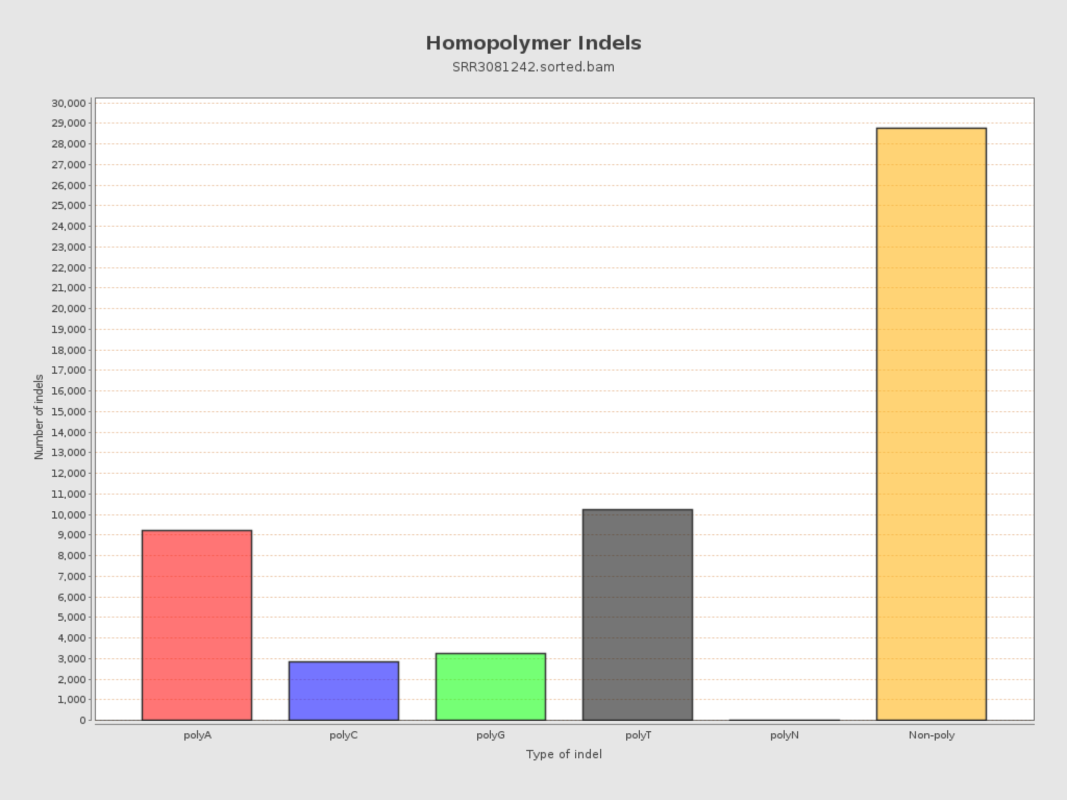
9. Results : Mapped Reads GC-content Distribution



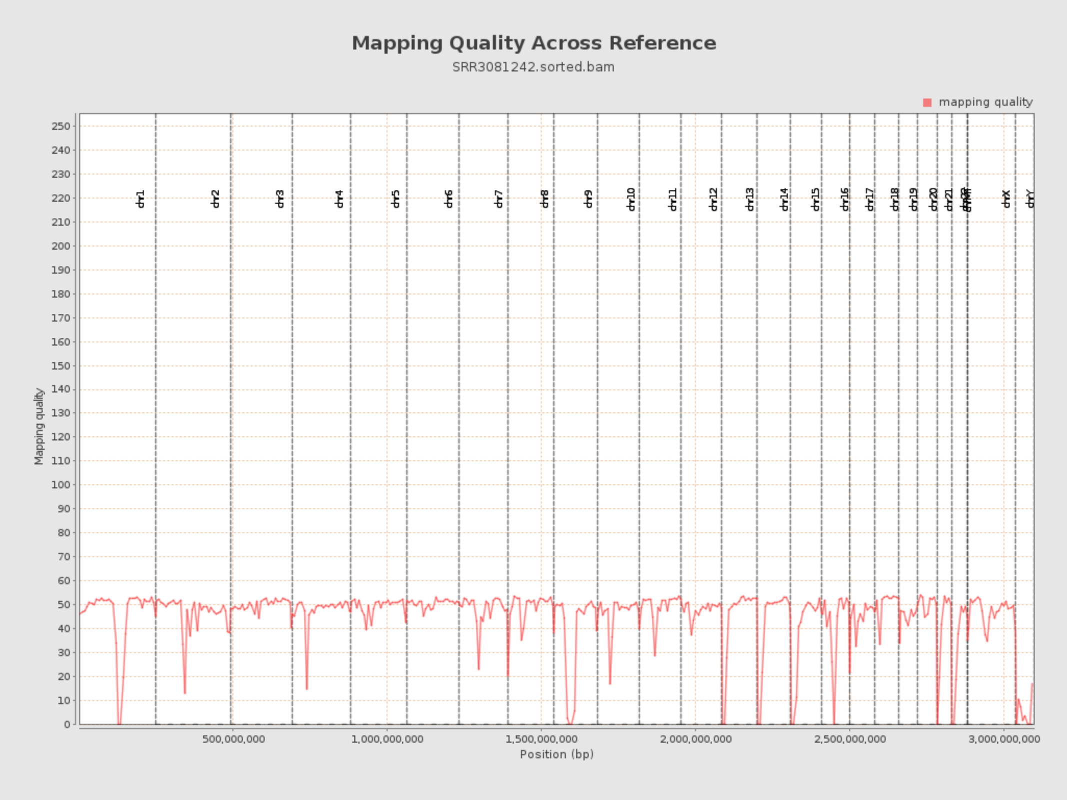
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram