Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 04:41:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081241.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_SRR3081241 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081241.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 04:41:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081241.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,318,062
Mapped reads	2,047,604 / 88.33%
Unmapped reads	270,458 / 11.67%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,163 / 0.96%
Read min/max/mean length	30 / 76 / 76.33
Duplicated reads (estimated)	84,810 / 3.66%
Duplication rate	3.27%
Clipped reads	1,203,296 / 51.91%

2.2. ACGT Content

Number/percentage of A's	38,003,226 / 29.05%
Number/percentage of C's	24,783,104 / 18.95%
Number/percentage of T's	40,366,298 / 30.86%
Number/percentage of G's	27,633,008 / 21.13%
Number/percentage of N's	15,946 / 0.01%
GC Percentage	40.07%

2.3. Coverage

Mean	0.0423

Standard Deviation	0.3673

2.4. Mapping Quality

Mean Mapping Quality	45.21

2.5. Mismatches and indels

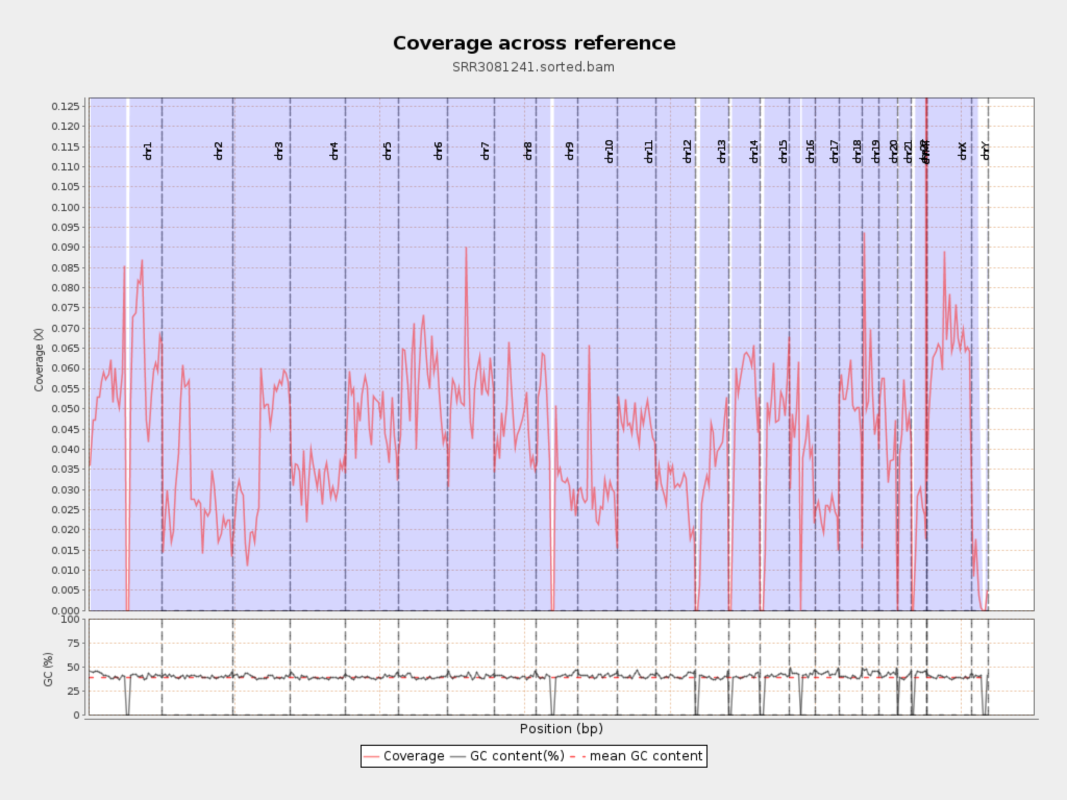
General error rate	0.93%
Mismatches	1,203,035
Insertions	10,025
Mapped reads with at least one insertion	0.49%
Deletions	30,215
Mapped reads with at least one deletion	1.46%
Homopolymer indels	47.37%

2.6. Chromosome stats

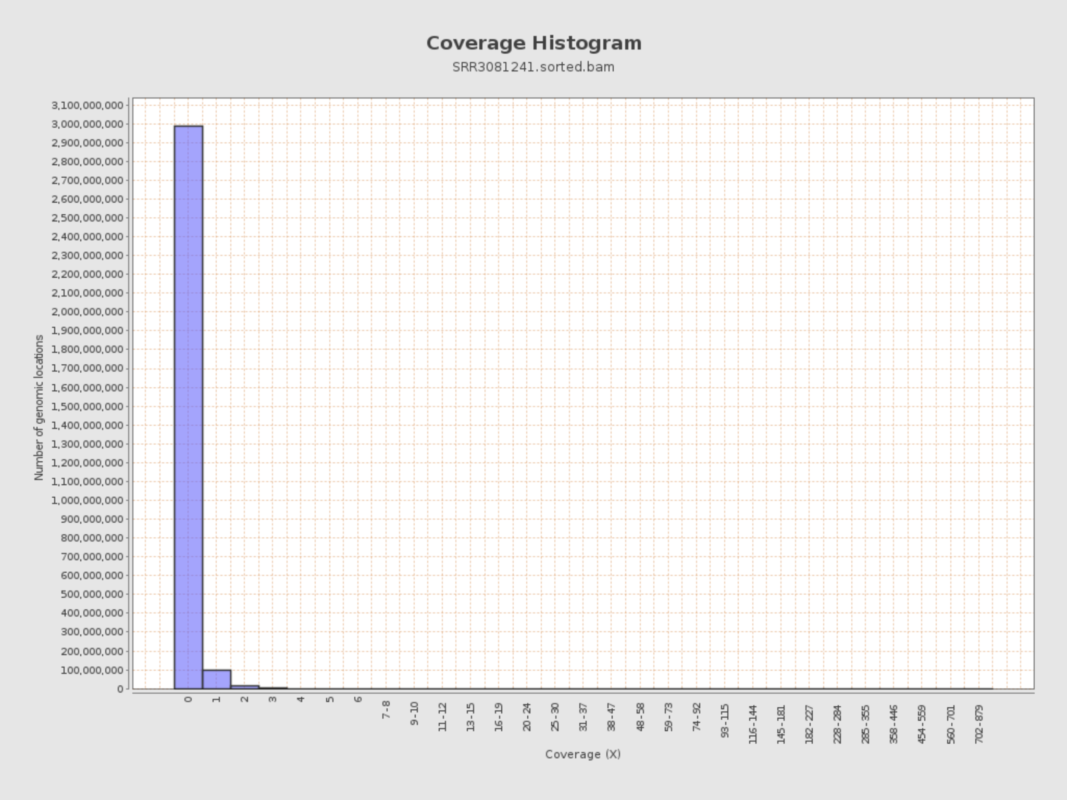
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13999262	0.0562	0.7417
chr2	243199373	7128599	0.0293	0.3559
chr3	198022430	7708784	0.0389	0.2284
chr4	191154276	6309072	0.033	0.2181
chr5	180915260	8739637	0.0483	0.2531
chr6	171115067	9664575	0.0565	0.3158
chr7	159138663	8865712	0.0557	0.5089

chr8	146364022	6677626	0.0456	0.4136
chr9	141213431	5123810	0.0363	0.2992
chr10	135534747	4015097	0.0296	0.3543
chr11	135006516	6239711	0.0462	0.3181
chr12	133851895	3999505	0.0299	0.2022
chr13	115169878	3747393	0.0325	0.2056
chr14	107349540	5232104	0.0487	0.2648
chr15	102531392	4327421	0.0422	0.2399
chr16	90354753	3499079	0.0387	0.2475
chr17	81195210	1958879	0.0241	0.1889
chr18	78077248	4129666	0.0529	0.5013
chr19	59128983	3309724	0.056	0.5146
chr20	63025520	2766822	0.0439	0.242
chr21	48129895	2006286	0.0417	0.244
chr22	51304566	967716	0.0189	0.1535
chrMT	16571	12278	0.7409	0.9529
chrX	155270560	10057240	0.0648	0.3161
chrY	59373566	364476	0.0061	0.1213

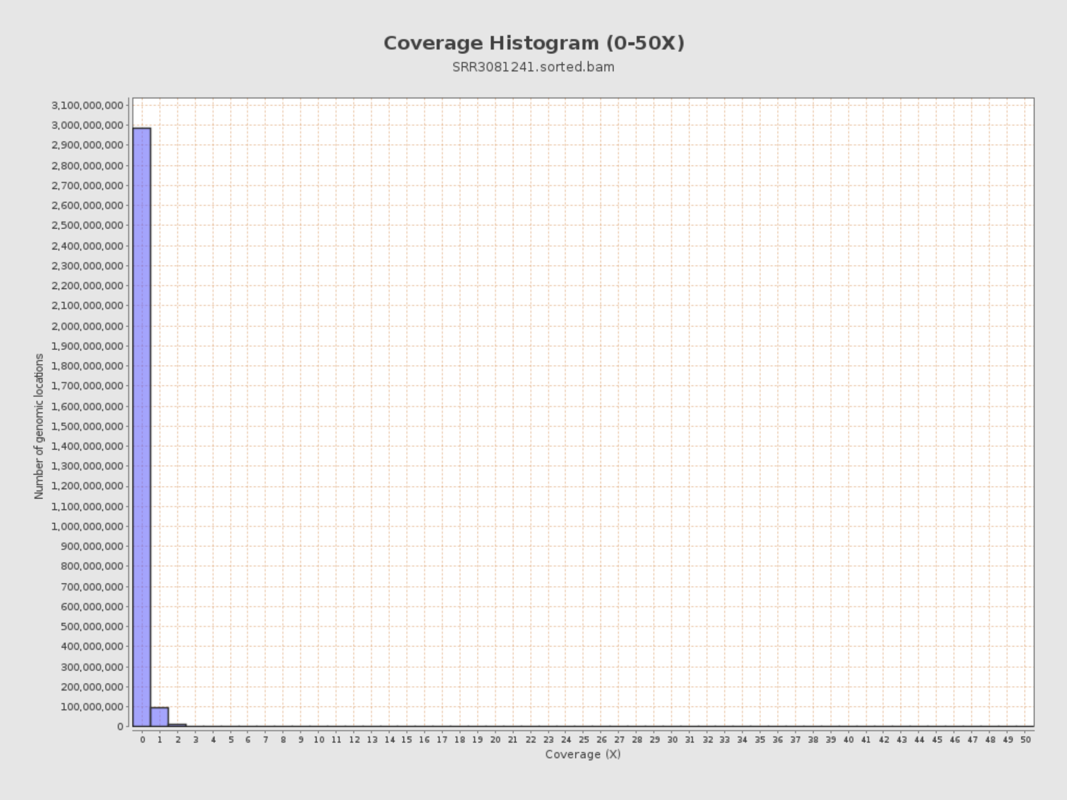
3. Results : Coverage across reference



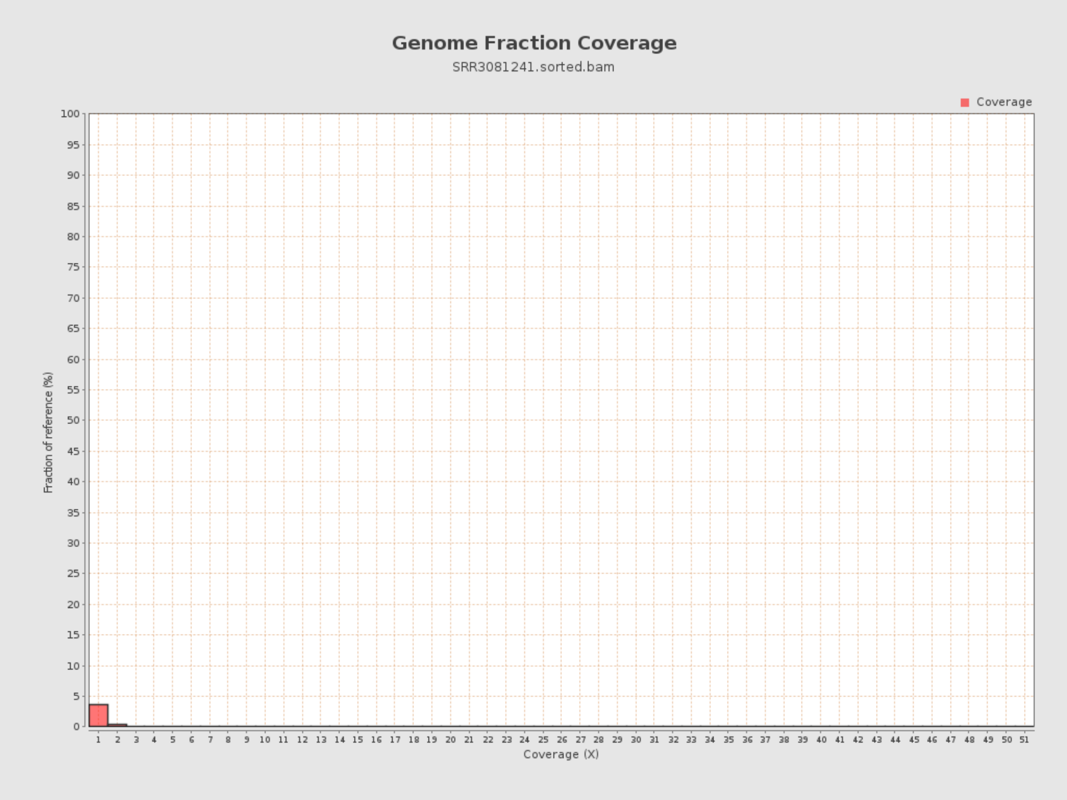
4. Results : Coverage Histogram



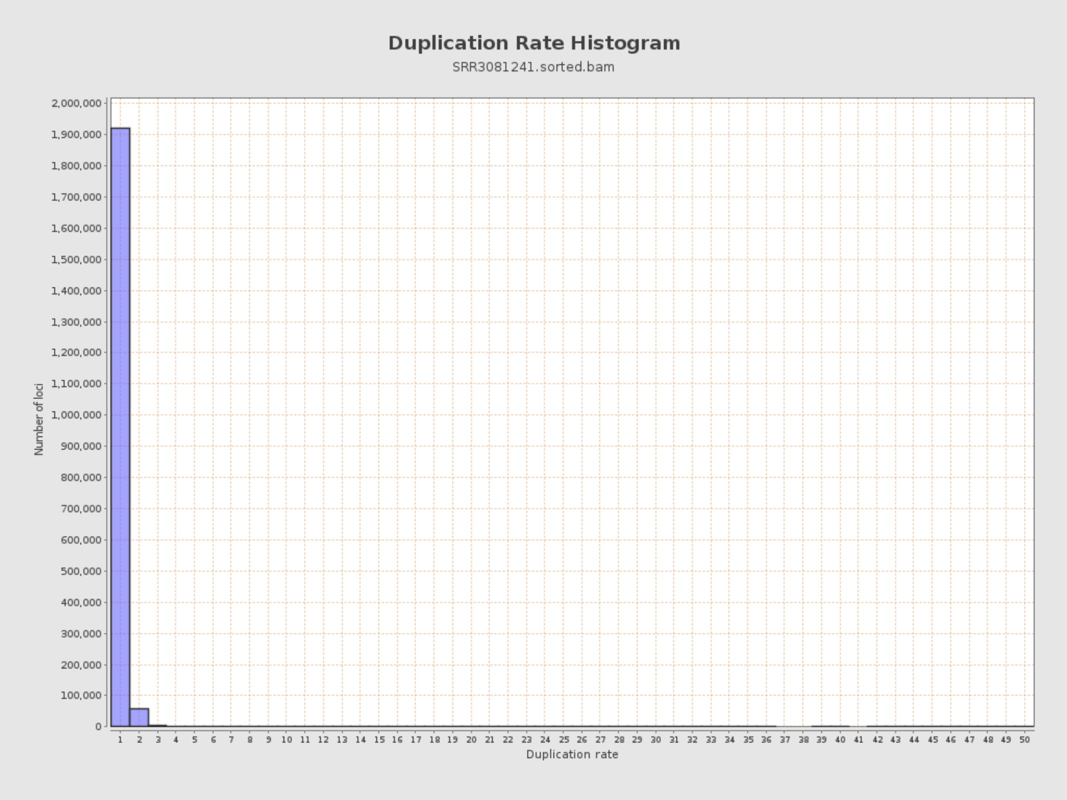
5. Results : Coverage Histogram (0-50X)



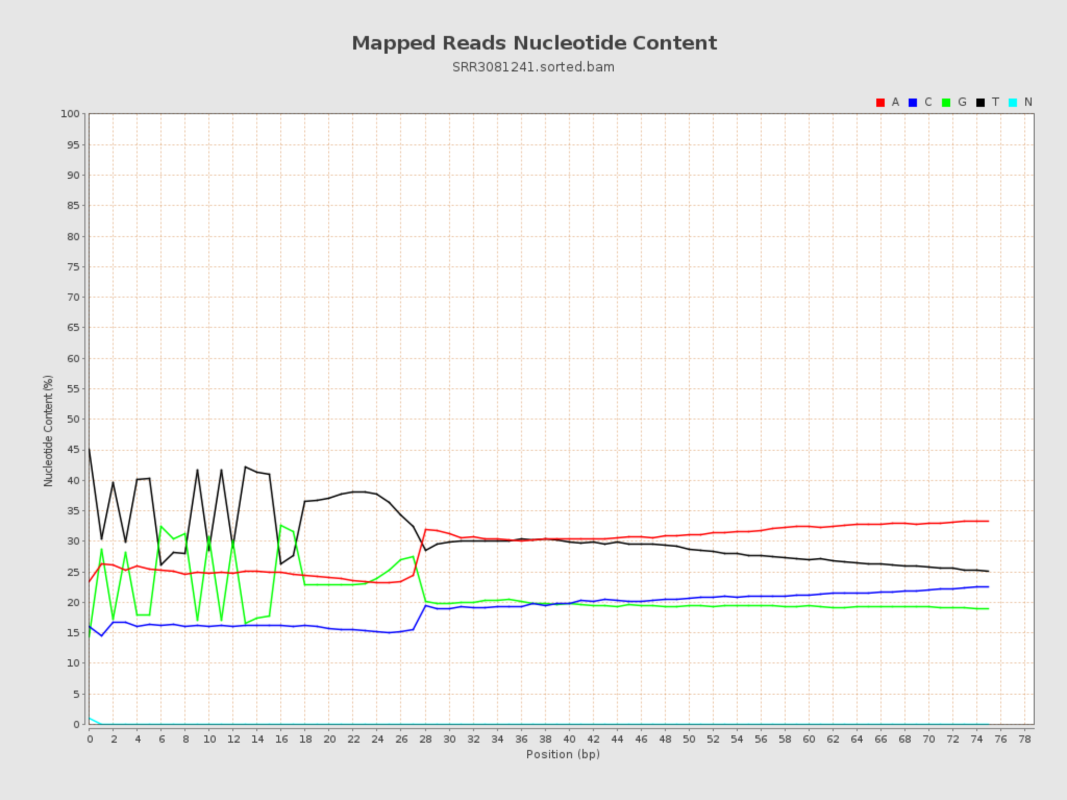
6. Results : Genome Fraction Coverage



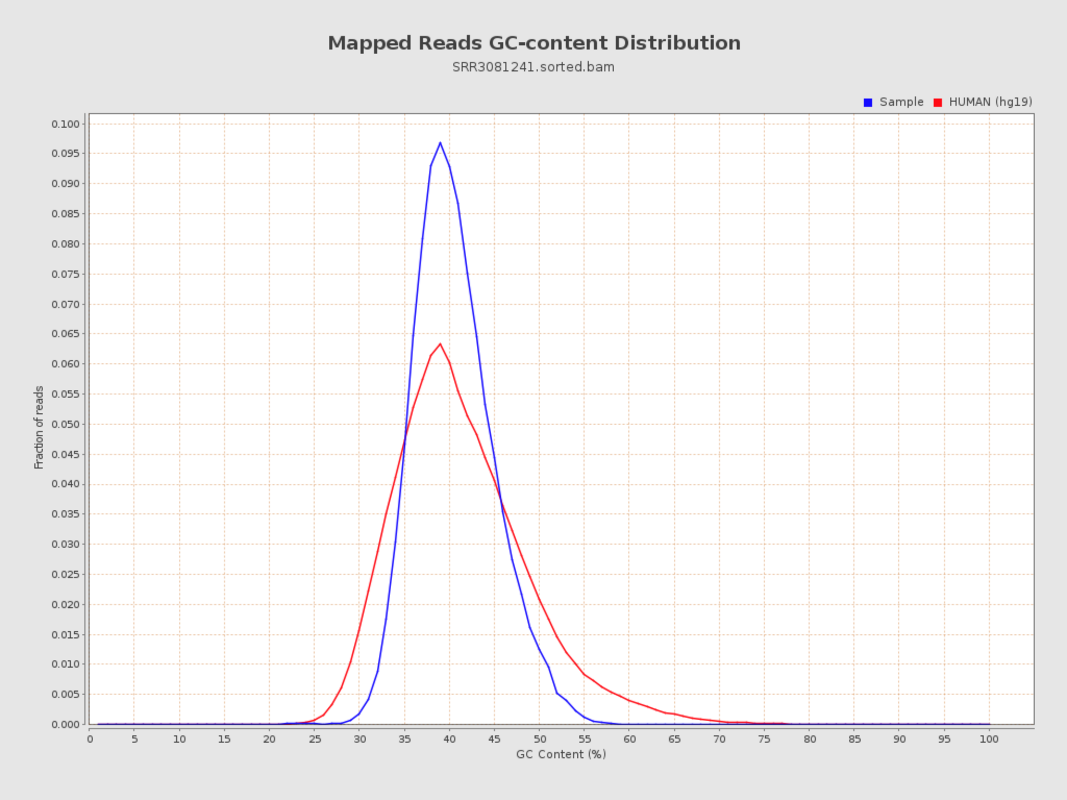
7. Results : Duplication Rate Histogram



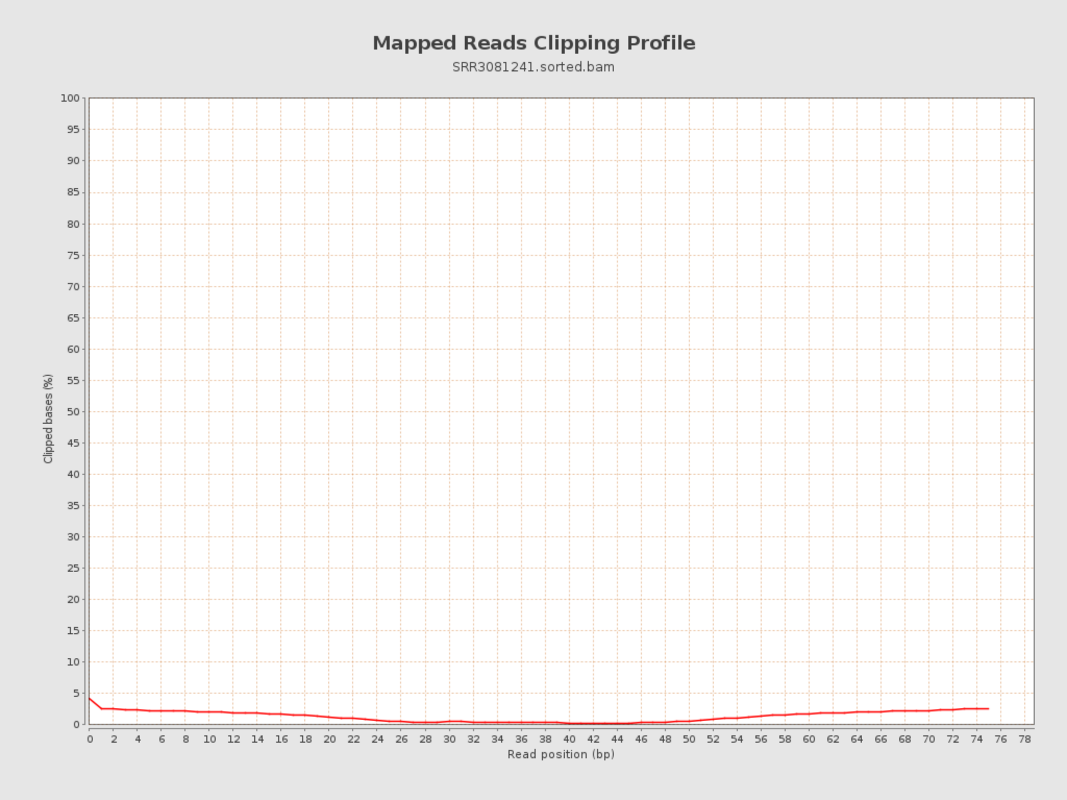
8. Results : Mapped Reads Nucleotide Content



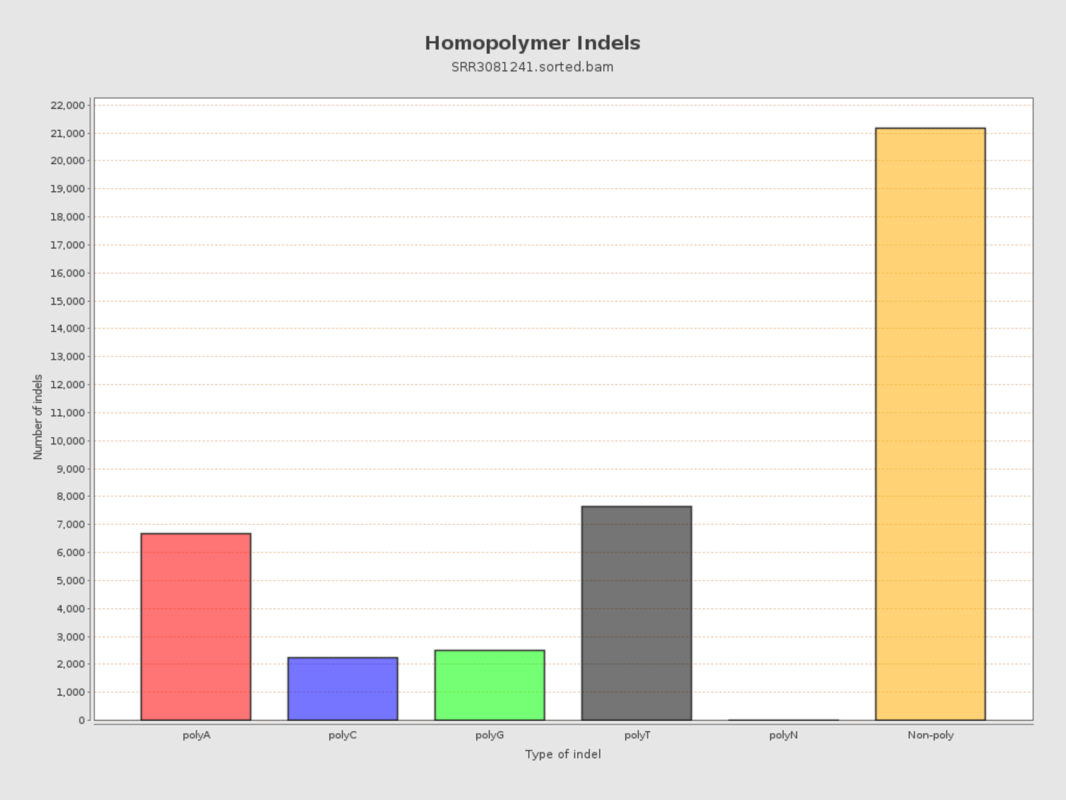
9. Results : Mapped Reads GC-content Distribution



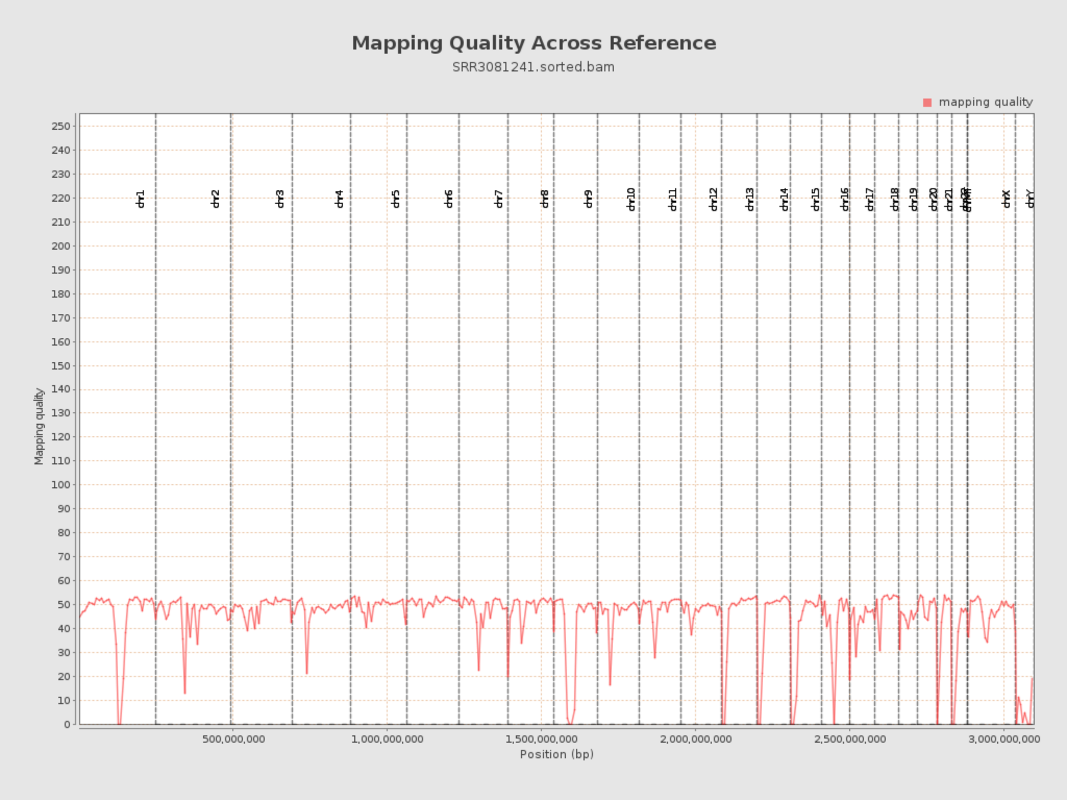
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram