Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 09:10:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081907.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_SRR3081907 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081907.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 09:10:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081907.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,258,131
Mapped reads	2,974,135 / 91.28%
Unmapped reads	283,996 / 8.72%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,695 / 0.76%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	128,633 / 3.95%
Duplication rate	3.46%
Clipped reads	1,328,641 / 40.78%

2.2. ACGT Content

Number/percentage of A's	55,710,656 / 27.99%
Number/percentage of C's	38,527,755 / 19.36%
Number/percentage of T's	60,826,912 / 30.56%
Number/percentage of G's	43,944,922 / 22.08%
Number/percentage of N's	2,215 / 0%
GC Percentage	41.44%

2.3. Coverage

Mean	0.0643

Standard Deviation	0.4438

2.4. Mapping Quality

Mean Mapping Quality	45.77

2.5. Mismatches and indels

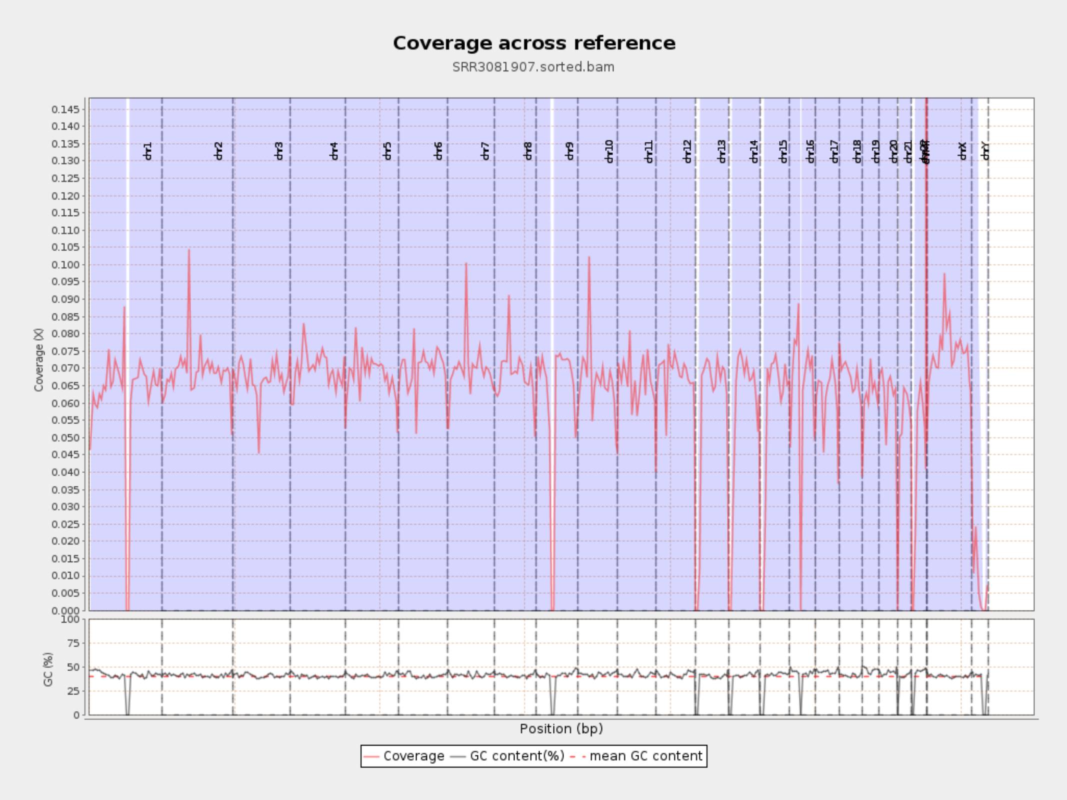
General error rate	0.83%
Mismatches	1,617,528
Insertions	13,652
Mapped reads with at least one insertion	0.45%
Deletions	37,812
Mapped reads with at least one deletion	1.26%
Homopolymer indels	46.86%

2.6. Chromosome stats

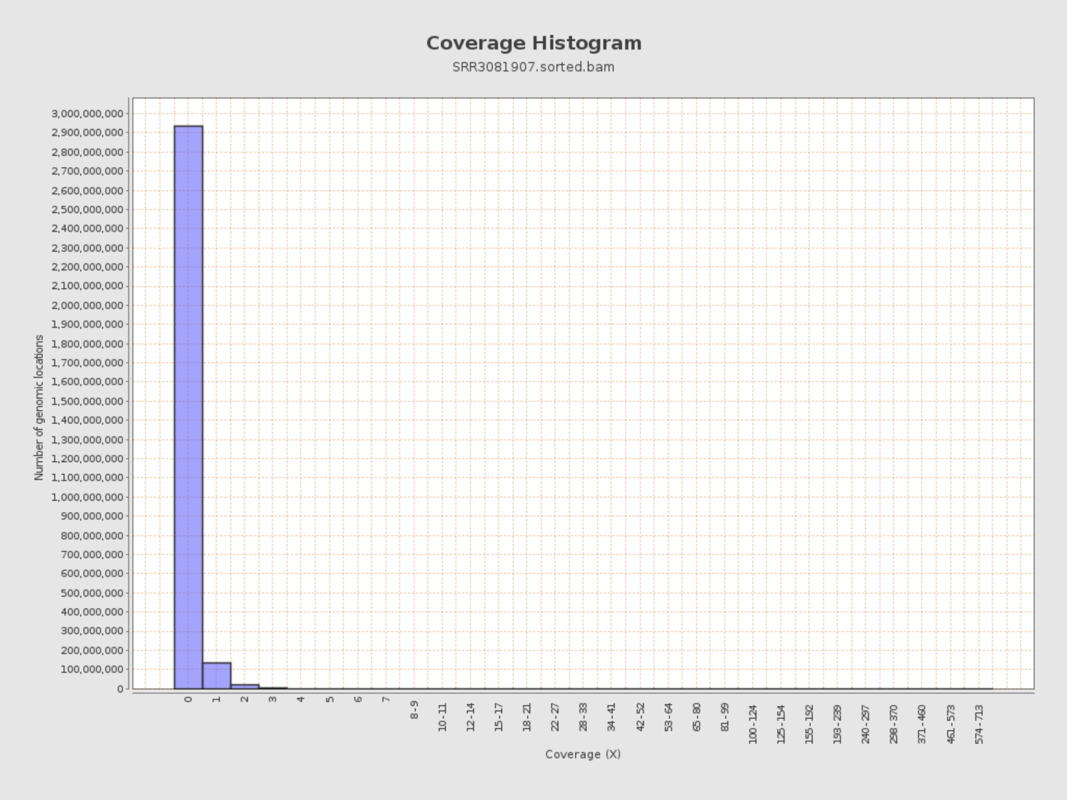
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15475935	0.0621	0.6935
chr2	243199373	16940169	0.0697	0.5347
chr3	198022430	13250081	0.0669	0.3035
chr4	191154276	13350742	0.0698	0.3307
chr5	180915260	12400387	0.0685	0.3103
chr6	171115067	11957859	0.0699	0.3585
chr7	159138663	11204775	0.0704	0.6092

chr8	146364022	10007008	0.0684	0.5494
chr9	141213431	8639463	0.0612	0.4273
chr10	135534747	9141221	0.0674	0.479
chr11	135006516	8960440	0.0664	0.3892
chr12	133851895	9160107	0.0684	0.3111
chr13	115169878	6521172	0.0566	0.2801
chr14	107349540	6056928	0.0564	0.2939
chr15	102531392	5660253	0.0552	0.2823
chr16	90354753	5794022	0.0641	0.3363
chr17	81195210	5015415	0.0618	0.3104
chr18	78077248	5292205	0.0678	0.7842
chr19	59128983	3693510	0.0625	0.5914
chr20	63025520	3923362	0.0623	0.3017
chr21	48129895	2486794	0.0517	0.2885
chr22	51304566	2081422	0.0406	0.2361
chrMT	16571	14634	0.8831	1.1631
chrX	155270560	11557628	0.0744	0.3617
chrY	59373566	494376	0.0083	0.1779

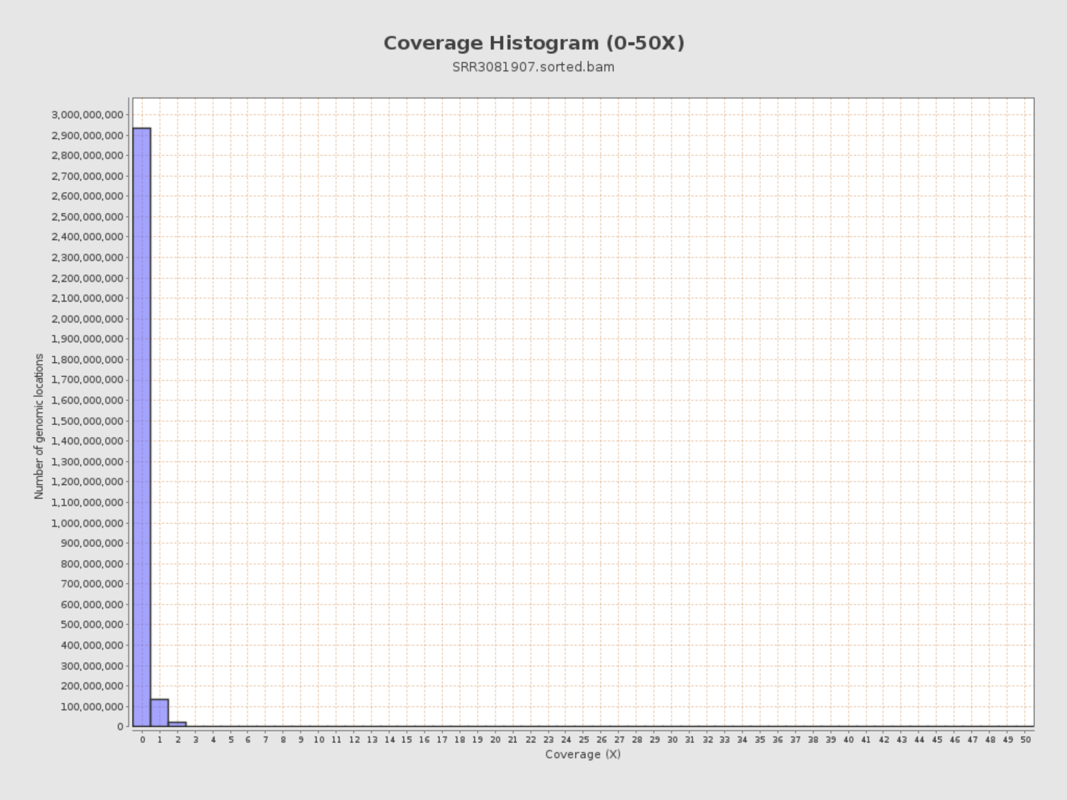
3. Results : Coverage across reference



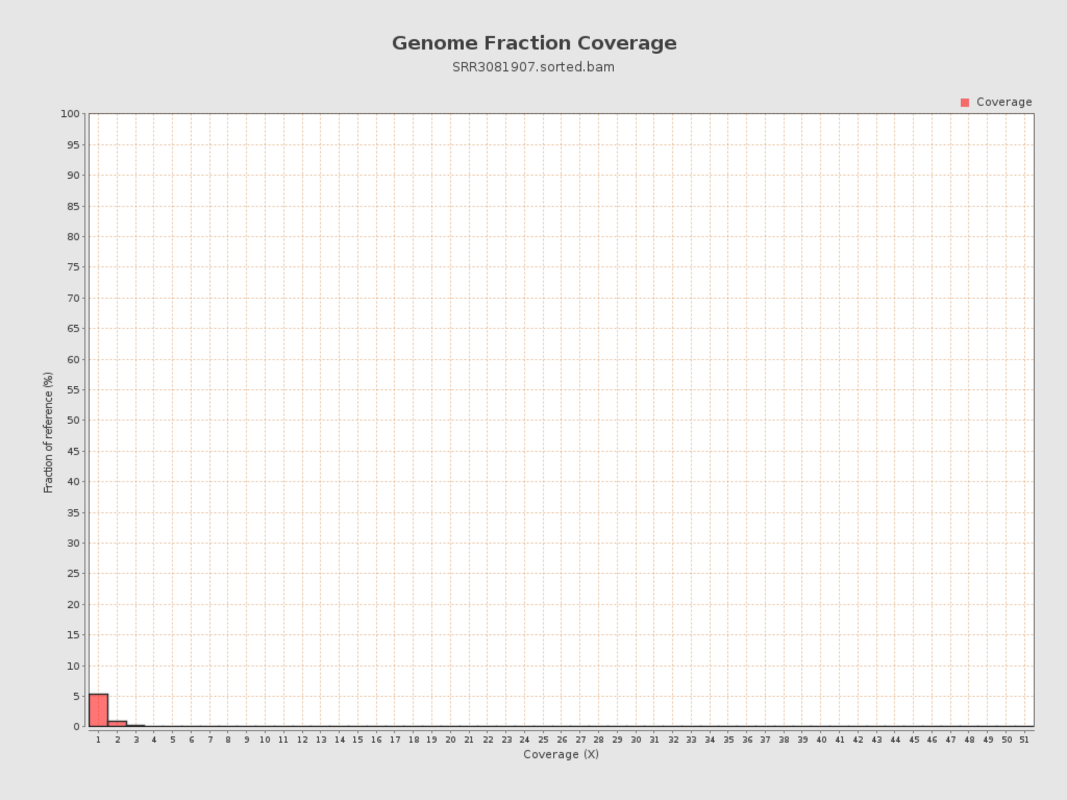
4. Results : Coverage Histogram



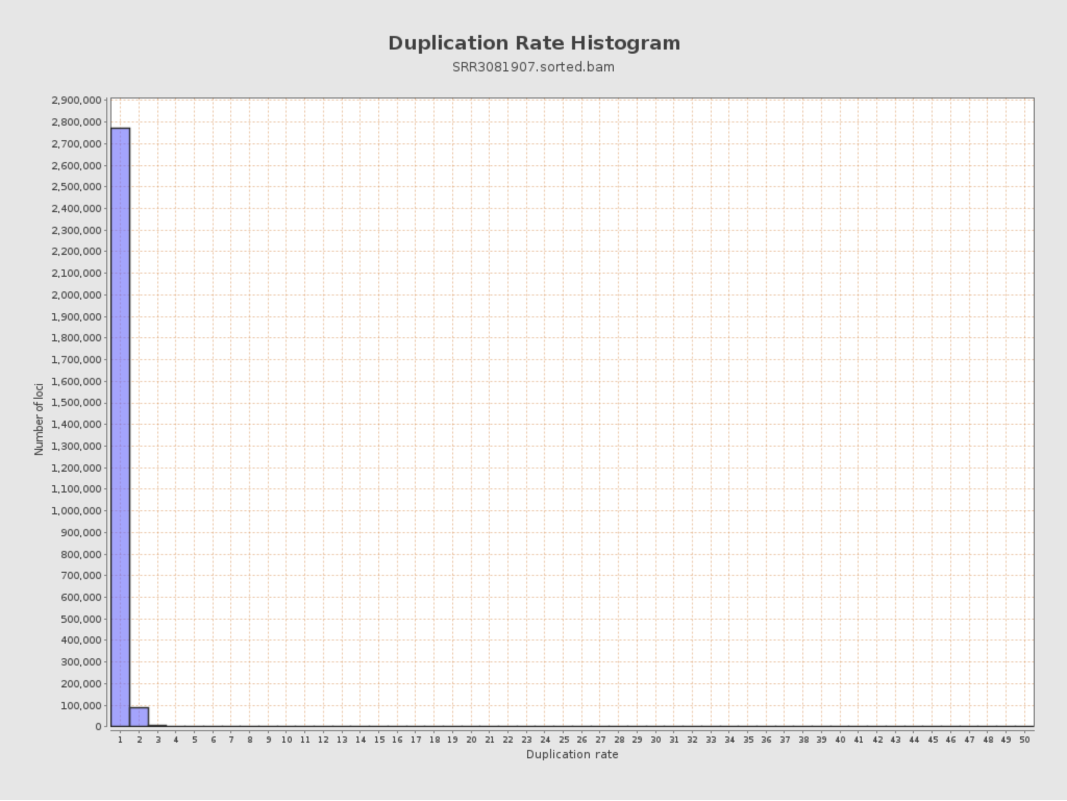
5. Results : Coverage Histogram (0-50X)



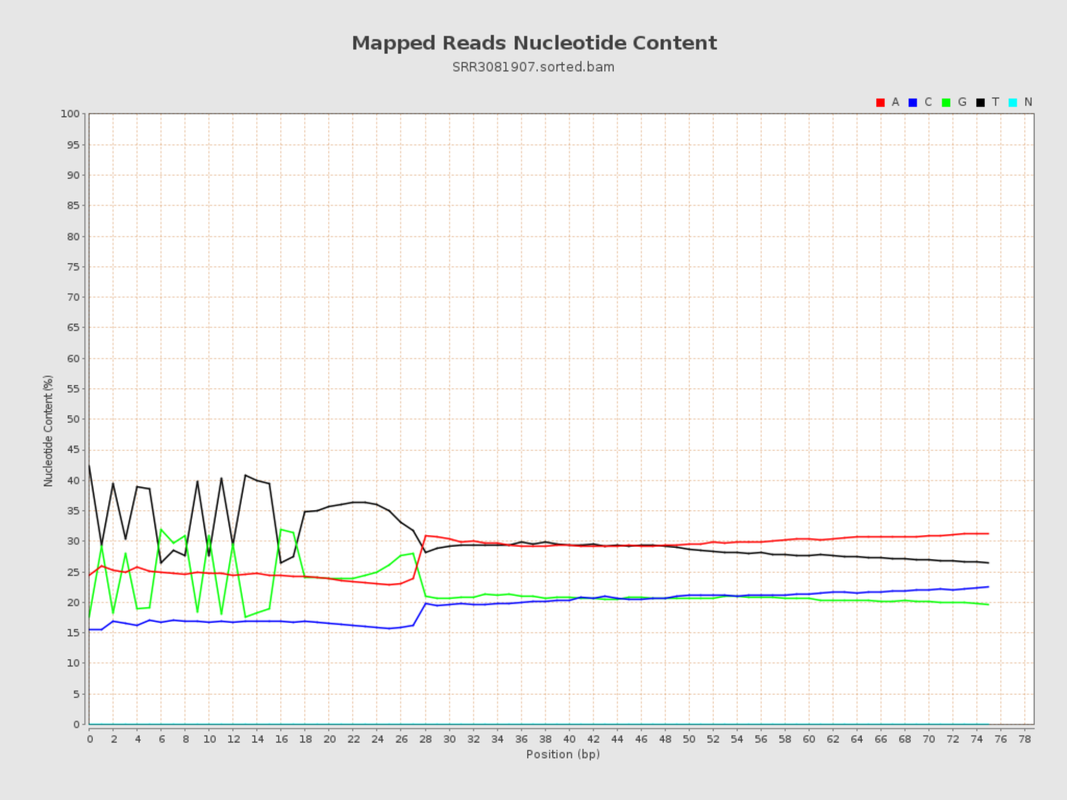
6. Results : Genome Fraction Coverage



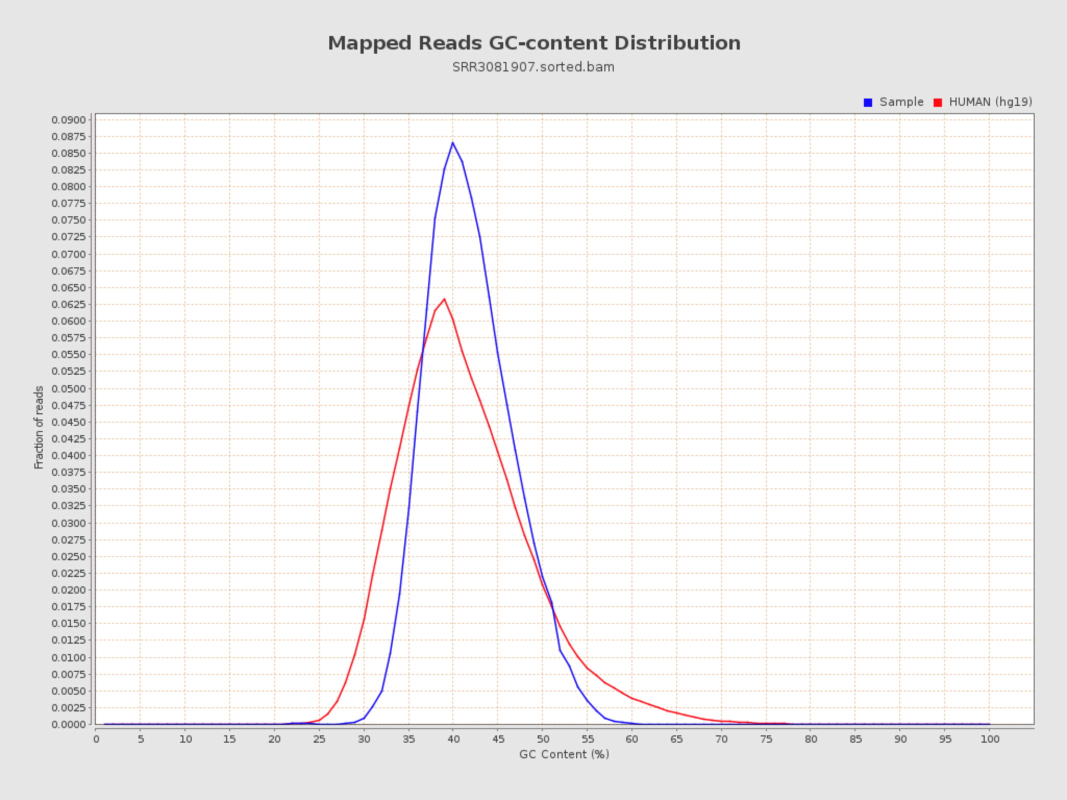
7. Results : Duplication Rate Histogram



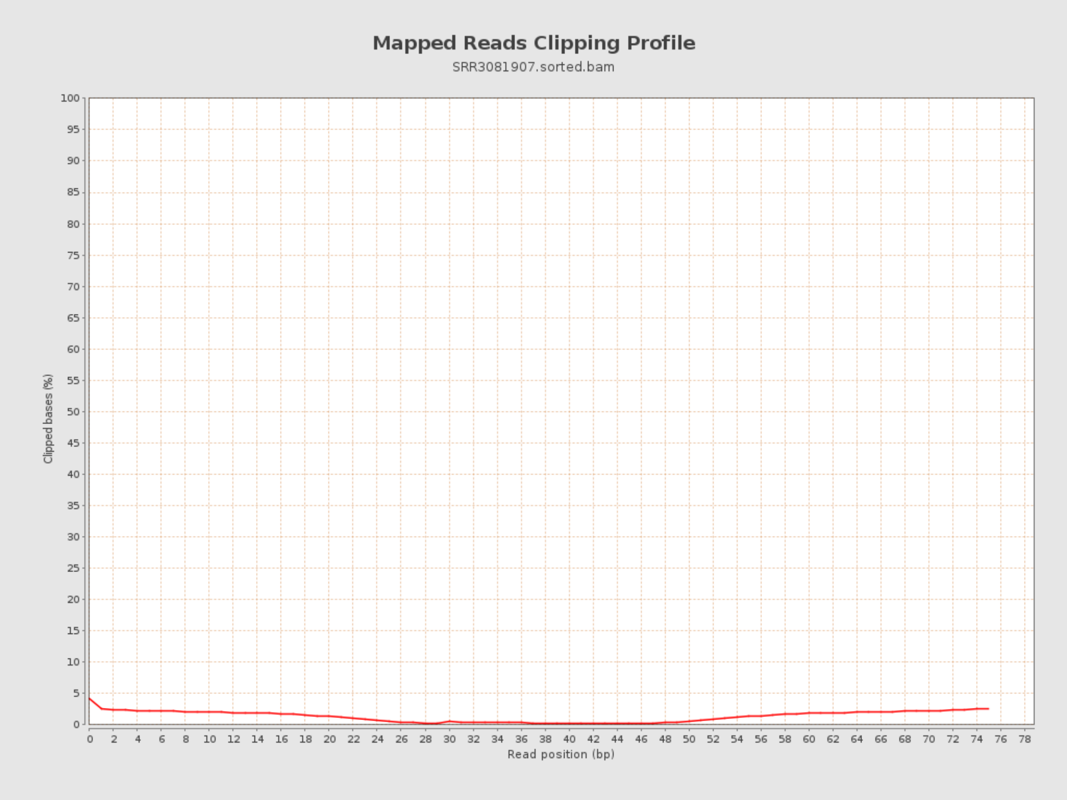
8. Results : Mapped Reads Nucleotide Content



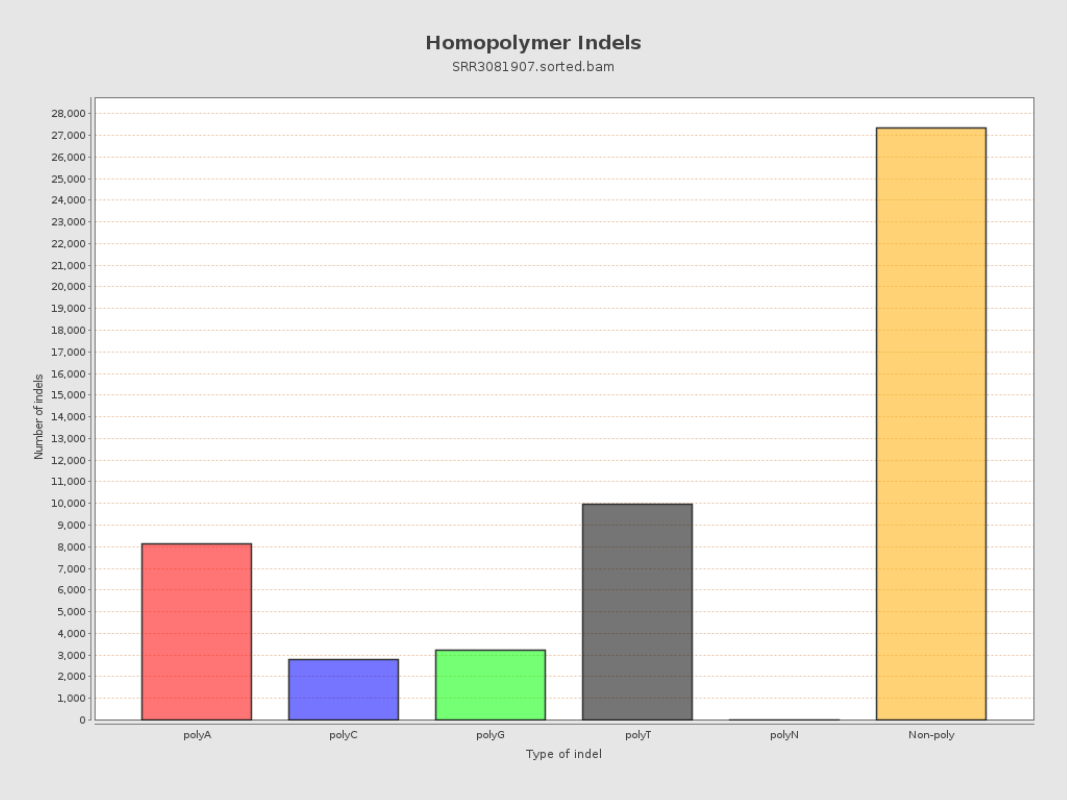
9. Results : Mapped Reads GC-content Distribution



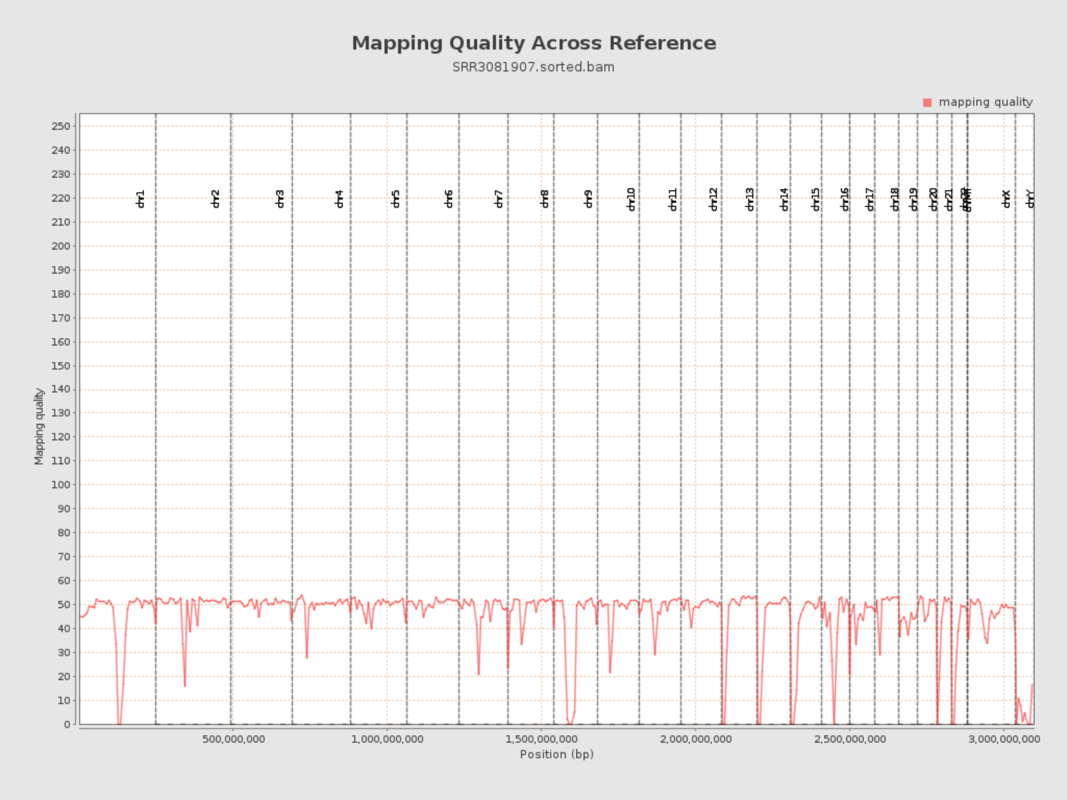
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram