Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 07:20:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081740.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_SRR3081740 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081740.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 07:20:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081740.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,072,534
Mapped reads	3,663,447 / 89.95%
Unmapped reads	409,087 / 10.05%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,346 / 0.55%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	180,873 / 4.44%
Duplication rate	3.69%
Clipped reads	1,611,328 / 39.57%

2.2. ACGT Content

Number/percentage of A's	67,077,593 / 27.45%
Number/percentage of C's	46,347,306 / 18.97%
Number/percentage of T's	75,890,175 / 31.05%
Number/percentage of G's	55,058,720 / 22.53%
Number/percentage of N's	2,755 / 0%
GC Percentage	41.5%

2.3. Coverage

Mean	0.079

Standard Deviation	0.6001

2.4. Mapping Quality

Mean Mapping Quality	45.19

2.5. Mismatches and indels

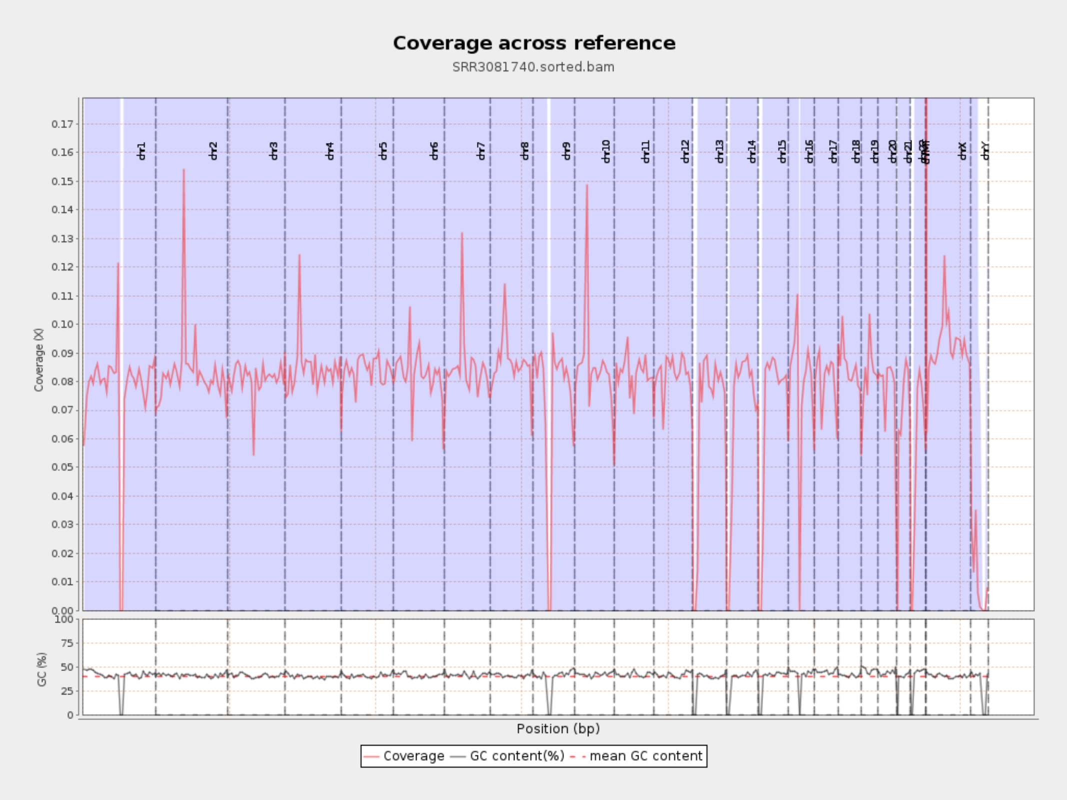
General error rate	0.84%
Mismatches	2,007,774
Insertions	18,143
Mapped reads with at least one insertion	0.49%
Deletions	52,237
Mapped reads with at least one deletion	1.41%
Homopolymer indels	46.93%

2.6. Chromosome stats

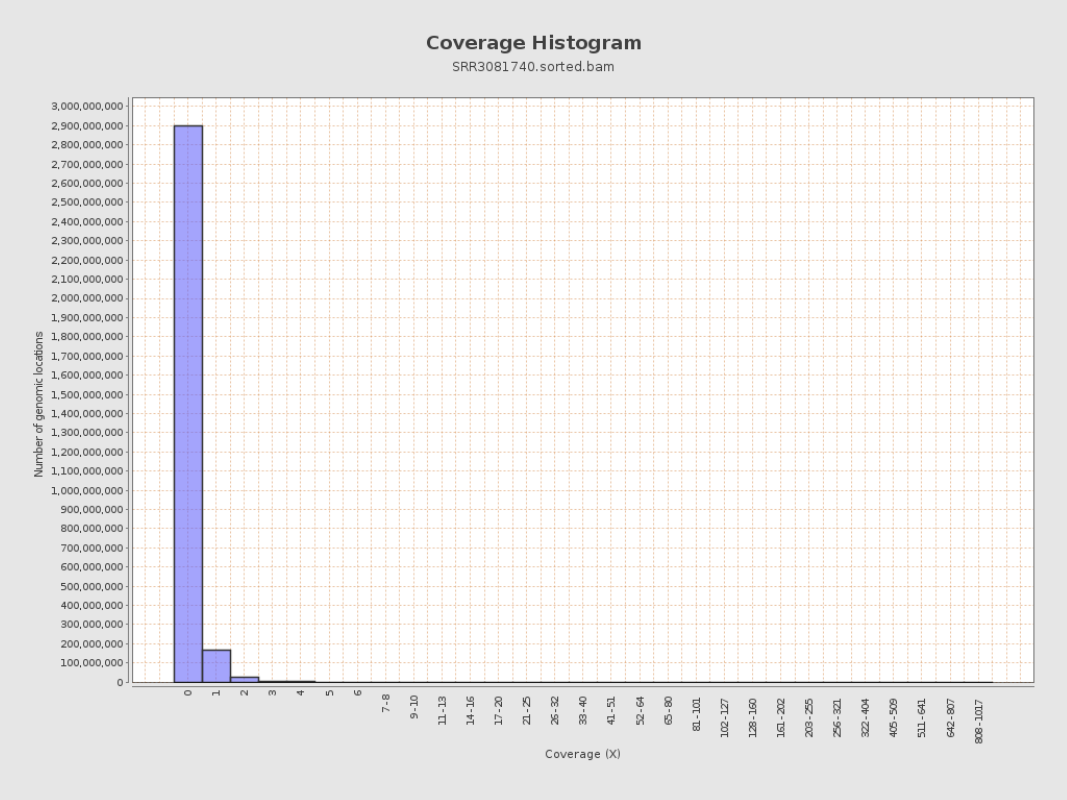
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	19068543	0.0765	0.9651
chr2	243199373	20318458	0.0835	0.7916
chr3	198022430	16046824	0.081	0.3419
chr4	191154276	16206711	0.0848	0.4082
chr5	180915260	15155570	0.0838	0.3476
chr6	171115067	14182221	0.0829	0.4468
chr7	159138663	13533264	0.085	0.8452

chr8	146364022	12649997	0.0864	0.7711
chr9	141213431	10383652	0.0735	0.5865
chr10	135534747	11667489	0.0861	0.7047
chr11	135006516	11119386	0.0824	0.5208
chr12	133851895	11072198	0.0827	0.3499
chr13	115169878	7749330	0.0673	0.3086
chr14	107349540	7371877	0.0687	0.3526
chr15	102531392	6935839	0.0676	0.3186
chr16	90354753	6916811	0.0766	0.4063
chr17	81195210	6582549	0.0811	0.3924
chr18	78077248	6681700	0.0856	1.1278
chr19	59128983	4895108	0.0828	0.7643
chr20	63025520	4947464	0.0785	0.3567
chr21	48129895	3242879	0.0674	0.3668
chr22	51304566	2721851	0.0531	0.2726
chrMT	16571	42553	2.5679	2.3207
chrX	155270560	14325142	0.0923	0.4397
chrY	59373566	651337	0.011	0.281

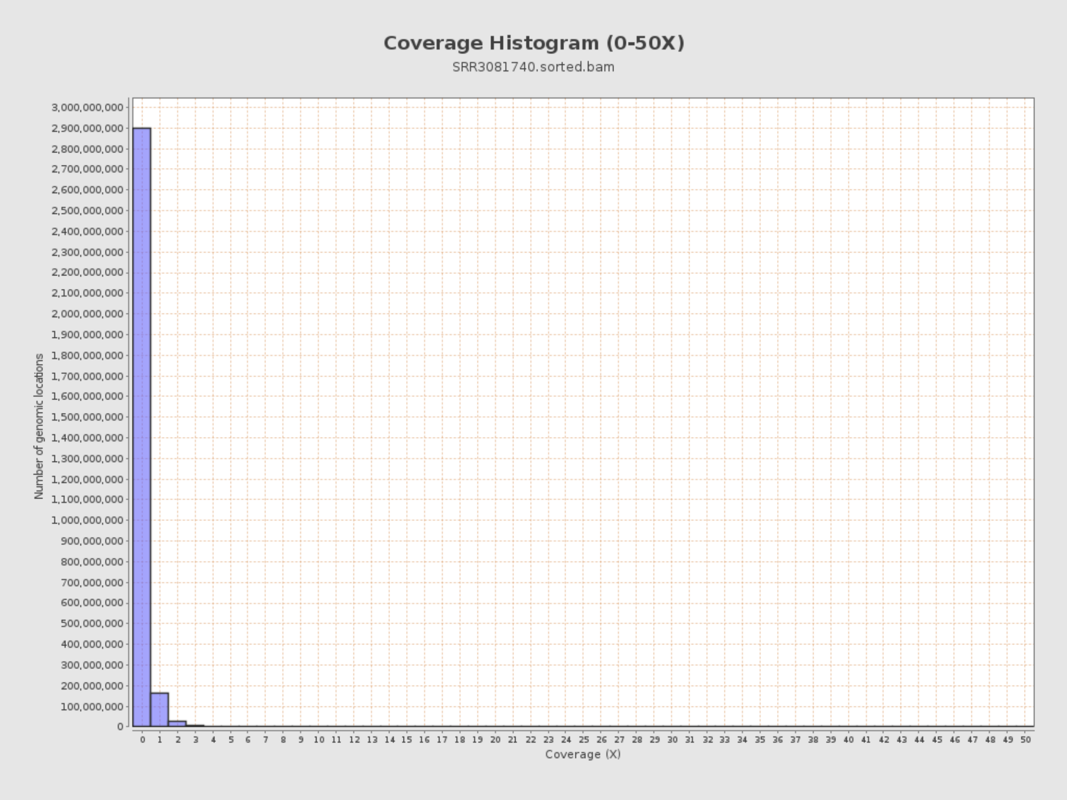
3. Results : Coverage across reference



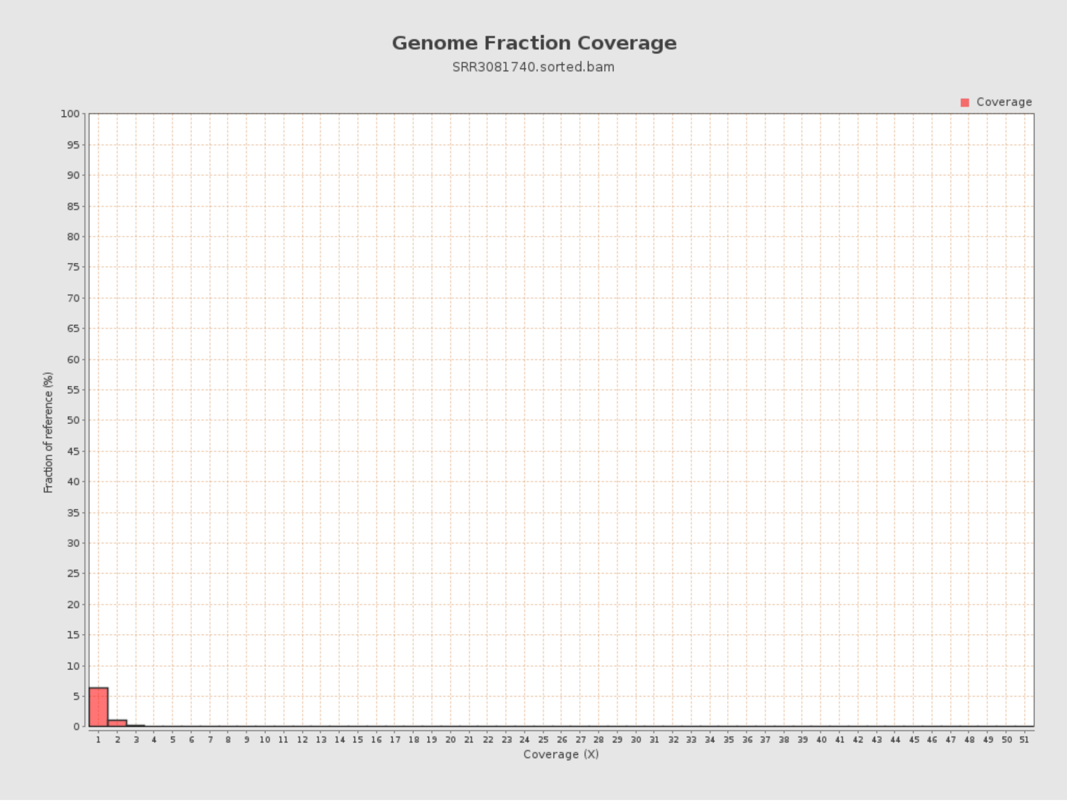
4. Results : Coverage Histogram



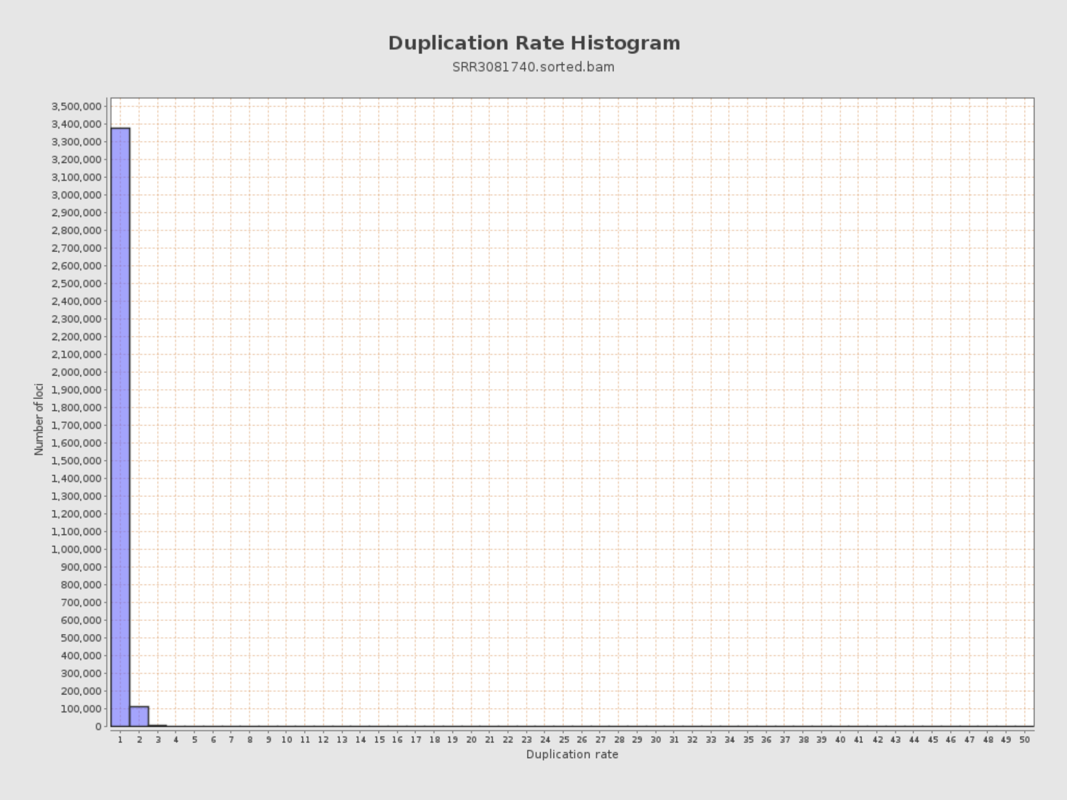
5. Results : Coverage Histogram (0-50X)



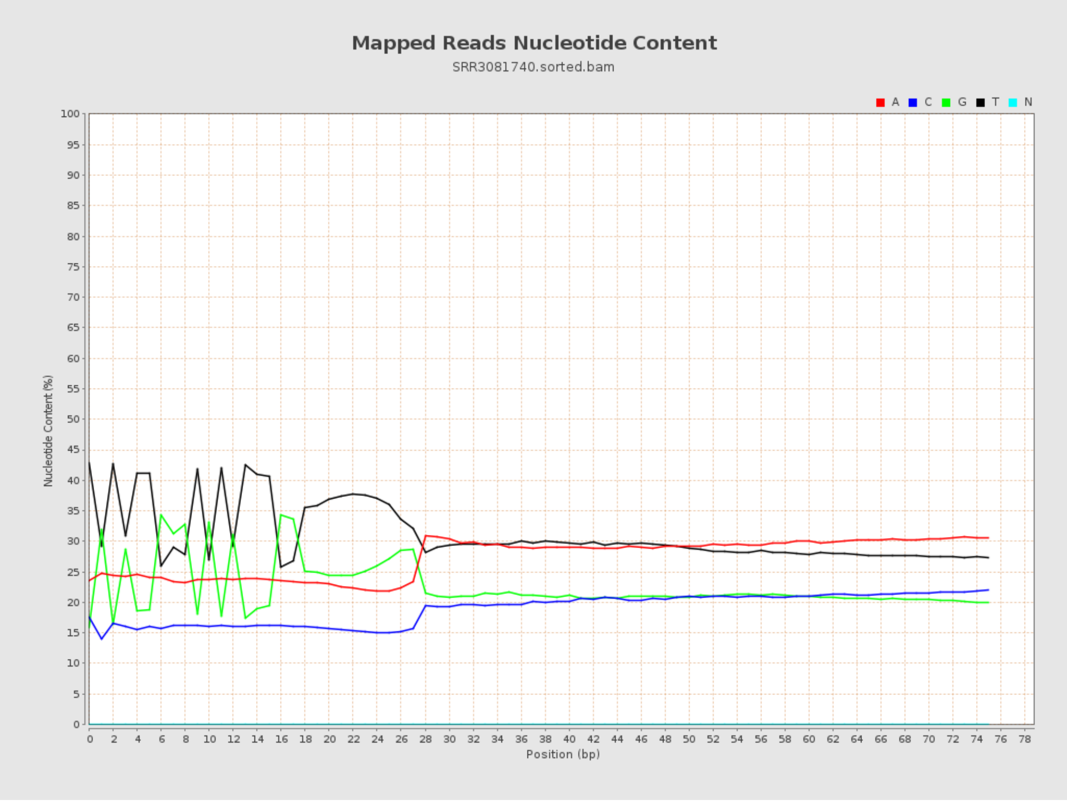
6. Results : Genome Fraction Coverage



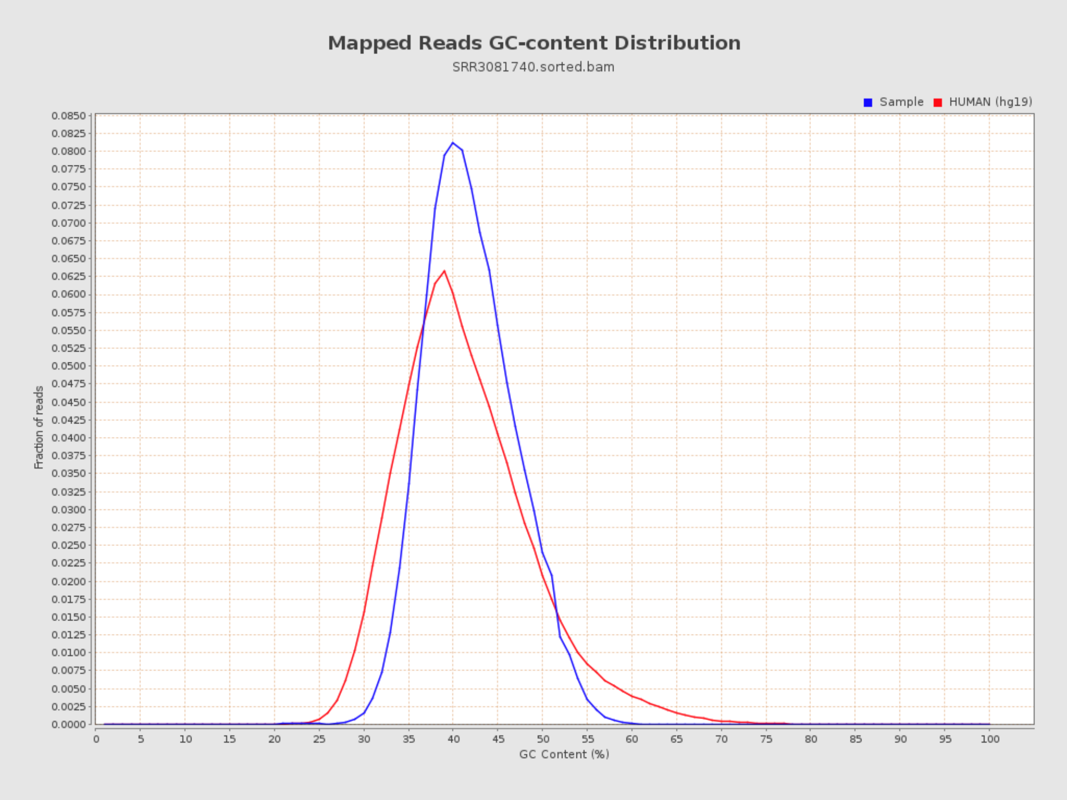
7. Results : Duplication Rate Histogram



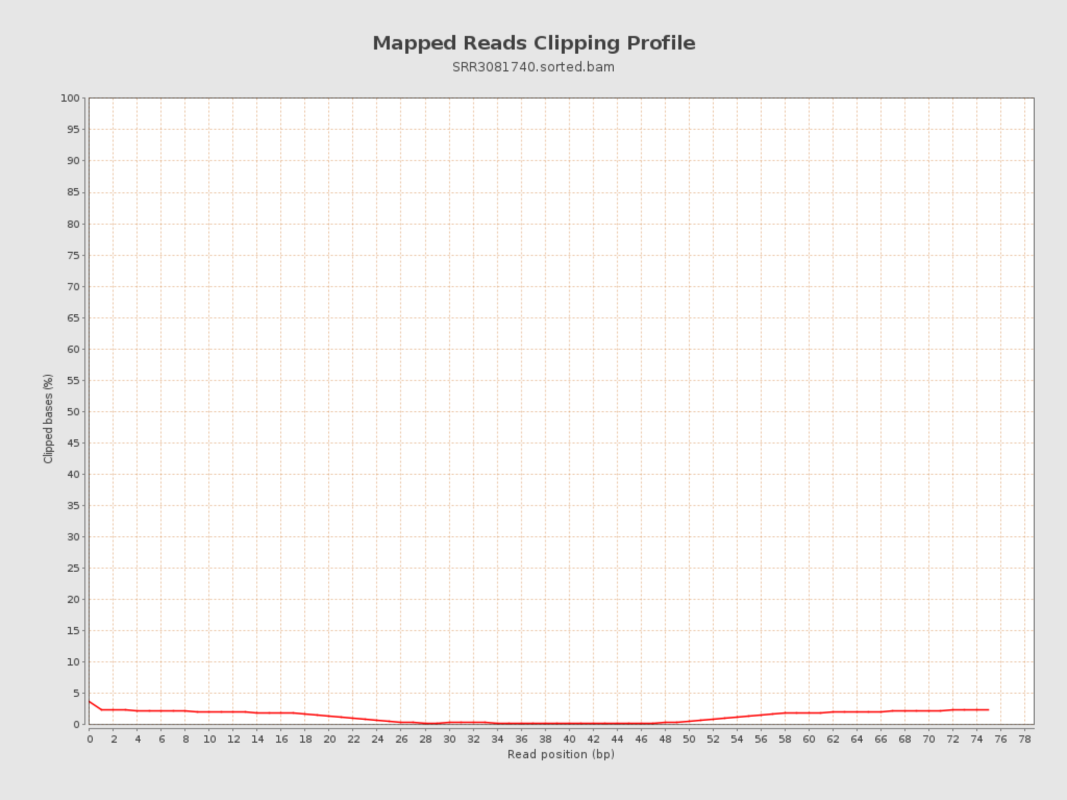
8. Results : Mapped Reads Nucleotide Content



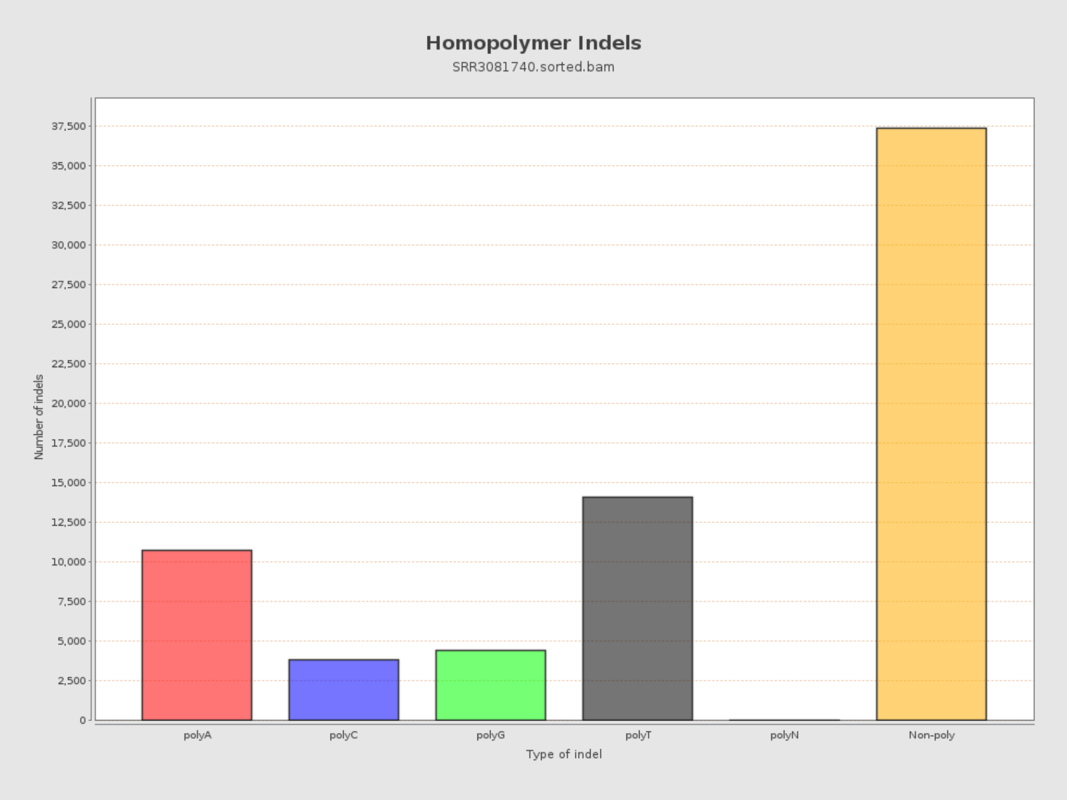
9. Results : Mapped Reads GC-content Distribution



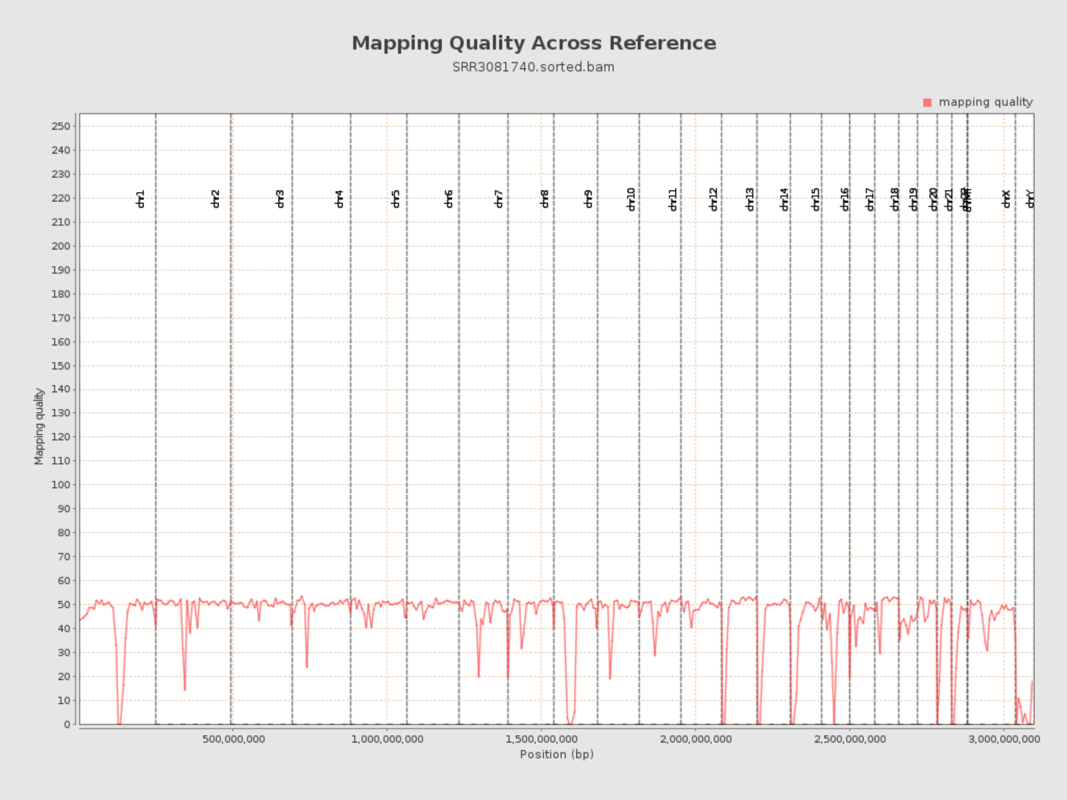
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram