Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 08:40:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008726.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_SRR6008726 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008726.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 08:40:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008726.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,583,514
Mapped reads	2,380,258 / 92.13%
Unmapped reads	203,256 / 7.87%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,098 / 0.62%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	88,643 / 3.43%
Duplication rate	2.48%
Clipped reads	957,031 / 37.04%

2.2. ACGT Content

Number/percentage of A's	45,385,724 / 28.2%
Number/percentage of C's	29,524,288 / 18.35%
Number/percentage of T's	50,966,620 / 31.67%
Number/percentage of G's	34,904,001 / 21.69%
Number/percentage of N's	143,442 / 0.09%
GC Percentage	40.04%

2.3. Coverage

Mean	0.052

Standard Deviation	0.5047

2.4. Mapping Quality

Mean Mapping Quality	45.42

2.5. Mismatches and indels

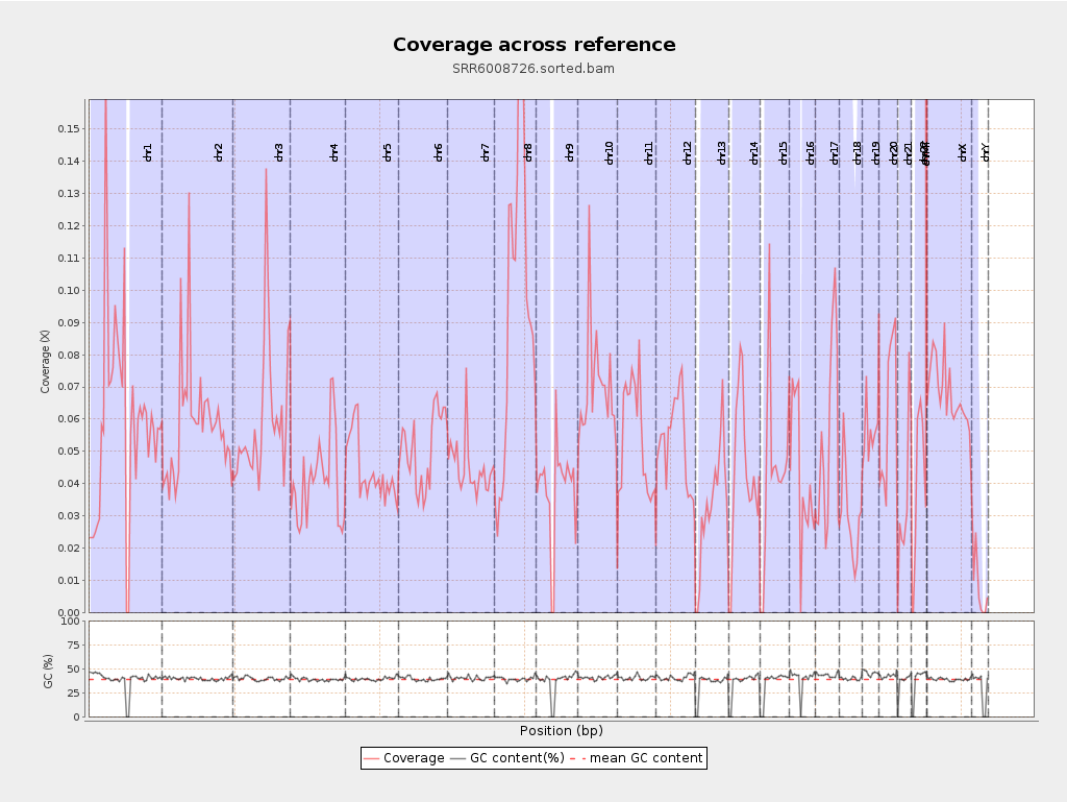
General error rate	0.92%
Mismatches	1,450,036
Insertions	13,725
Mapped reads with at least one insertion	0.57%
Deletions	59,065
Mapped reads with at least one deletion	2.45%
Homopolymer indels	45.52%

2.6. Chromosome stats

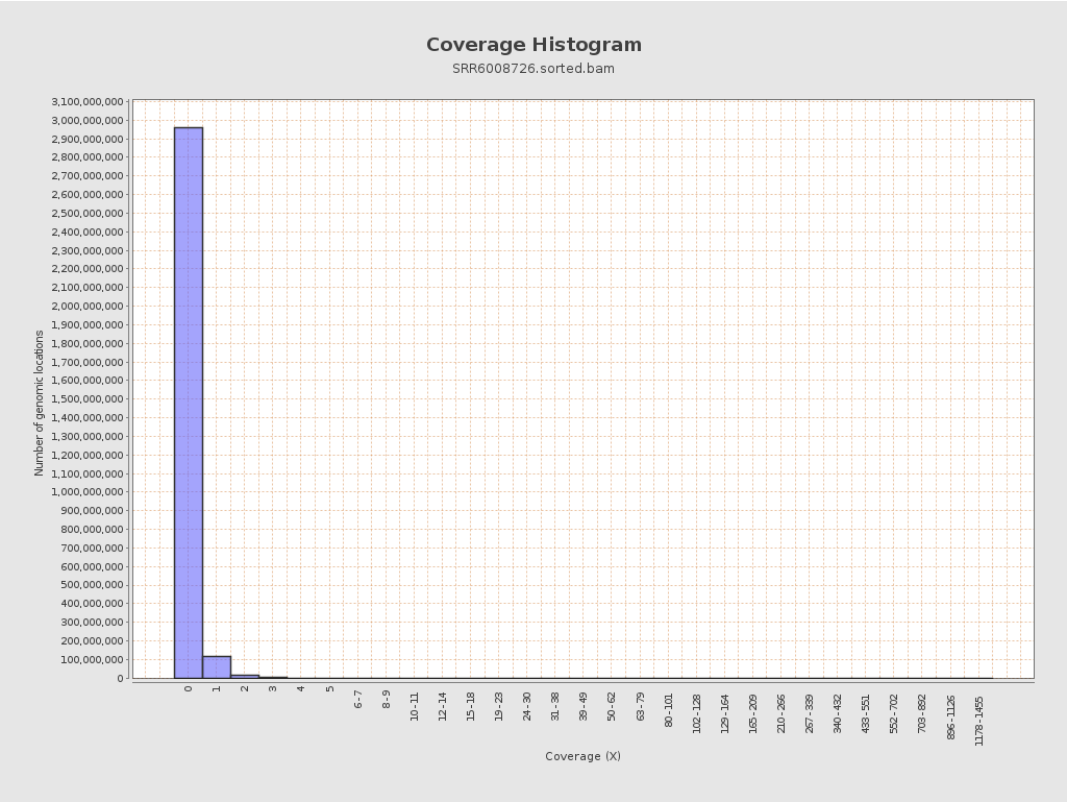
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	14635529	0.0587	0.9125
chr2	243199373	14195431	0.0584	0.6216
chr3	198022430	11867867	0.0599	0.2881
chr4	191154276	7732966	0.0405	0.2541
chr5	180915260	7967214	0.044	0.2406
chr6	171115067	8693239	0.0508	0.2947
chr7	159138663	7183707	0.0451	0.4994

chr8	146364022	13822640	0.0944	0.9565
chr9	141213431	5356852	0.0379	0.447
chr10	135534747	9482262	0.07	0.5365
chr11	135006516	7285974	0.054	0.5289
chr12	133851895	7116266	0.0532	0.2697
chr13	115169878	3808273	0.0331	0.2052
chr14	107349540	4676117	0.0436	0.2518
chr15	102531392	4495478	0.0438	0.2446
chr16	90354753	3860402	0.0427	0.2979
chr17	81195210	4391268	0.0541	0.3605
chr18	78077248	2320321	0.0297	0.818
chr19	59128983	3365987	0.0569	0.6035
chr20	63025520	3930972	0.0624	0.2941
chr21	48129895	1721587	0.0358	0.2384
chr22	51304566	1982357	0.0386	0.2196
chrMT	16571	115417	6.965	5.3876
chrX	155270560	10534940	0.0678	0.3446
chrY	59373566	479790	0.0081	0.2347

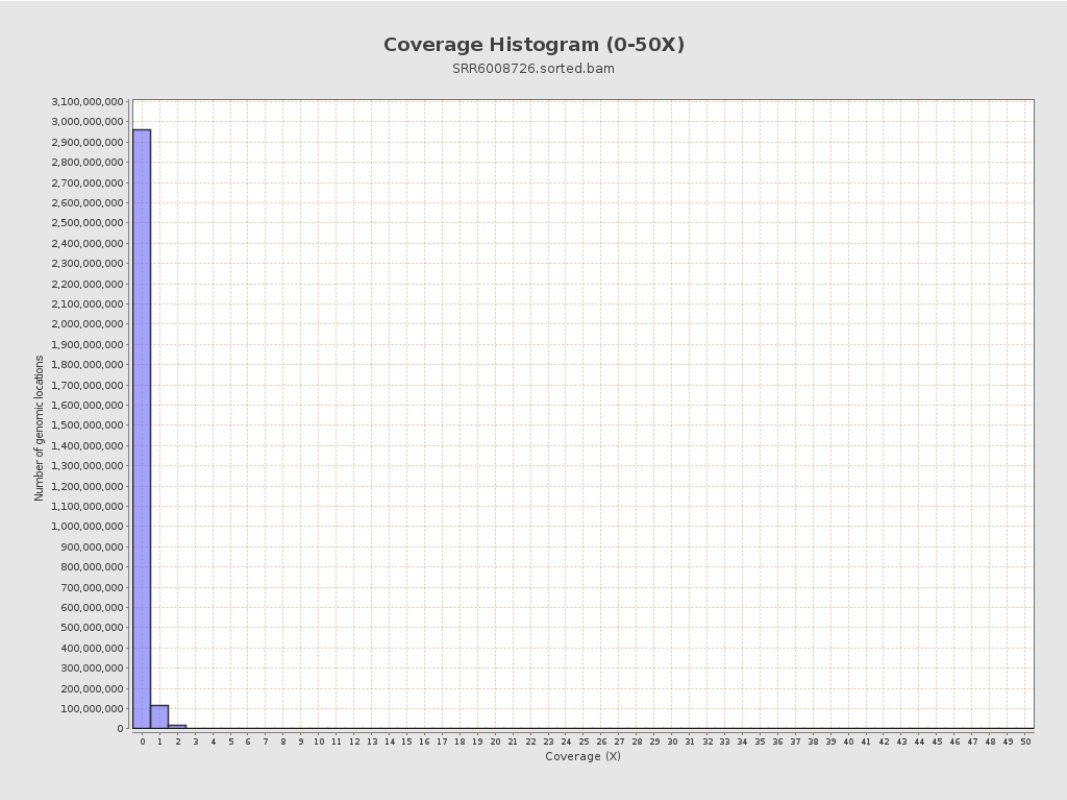
3. Results : Coverage across reference



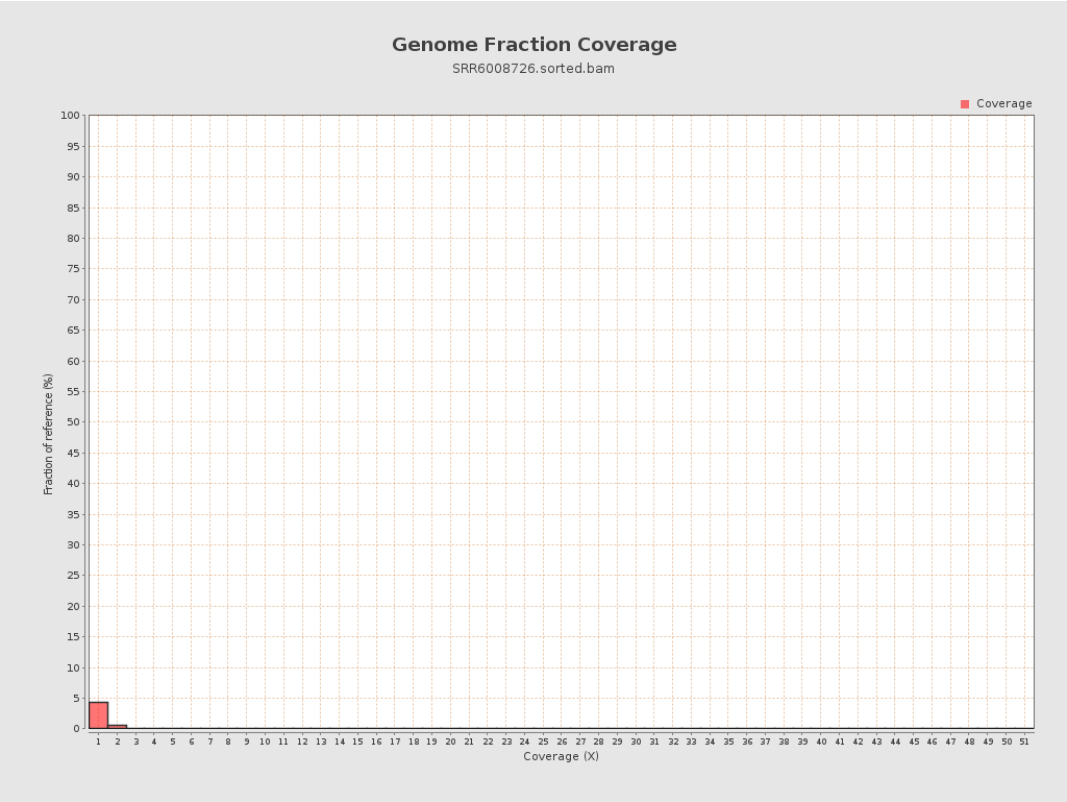
4. Results : Coverage Histogram



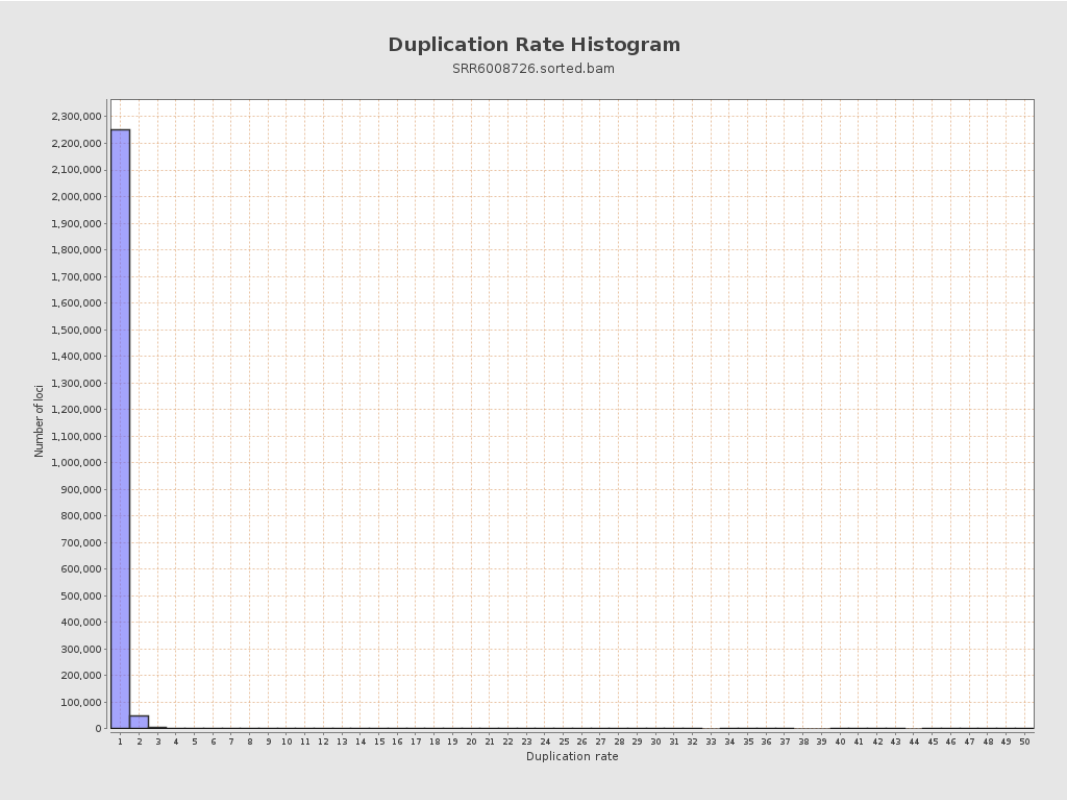
5. Results : Coverage Histogram (0-50X)



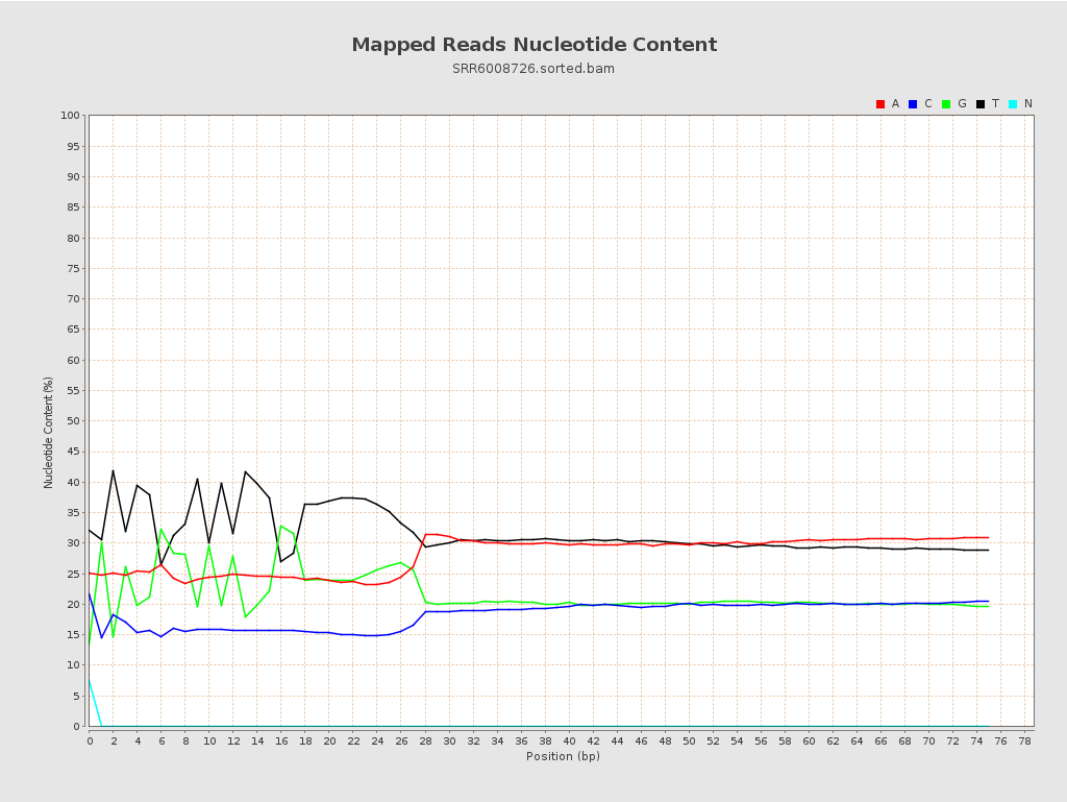
6. Results : Genome Fraction Coverage



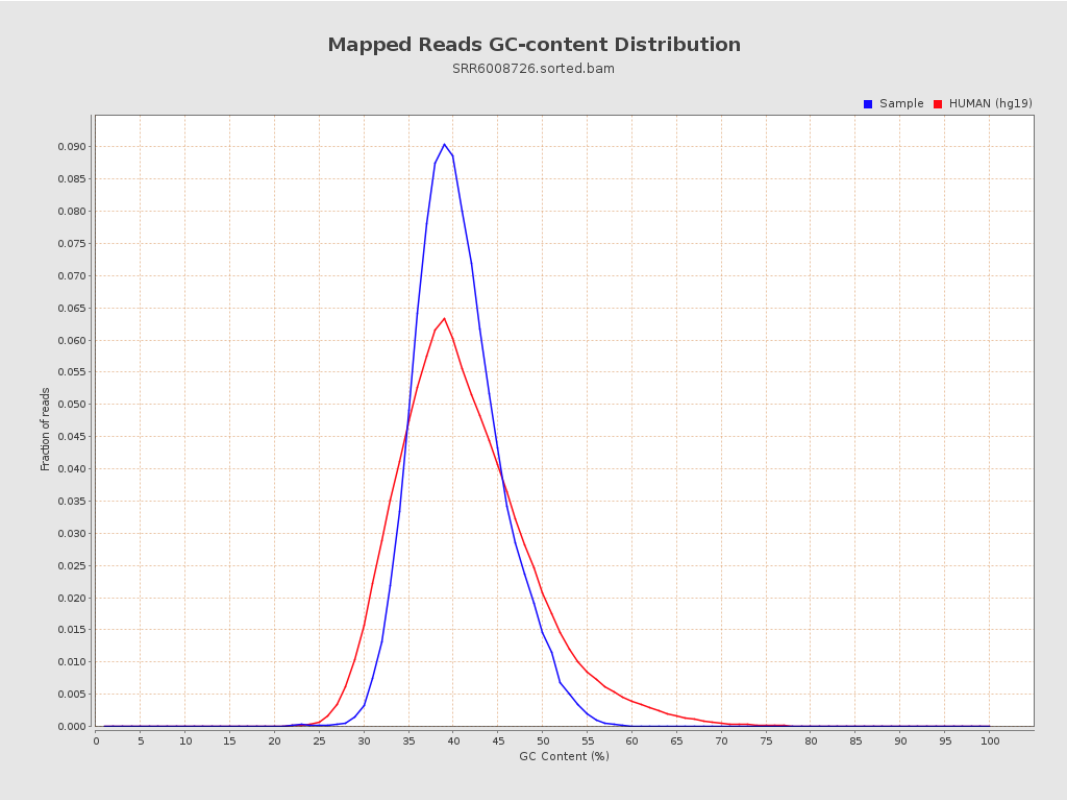
7. Results : Duplication Rate Histogram



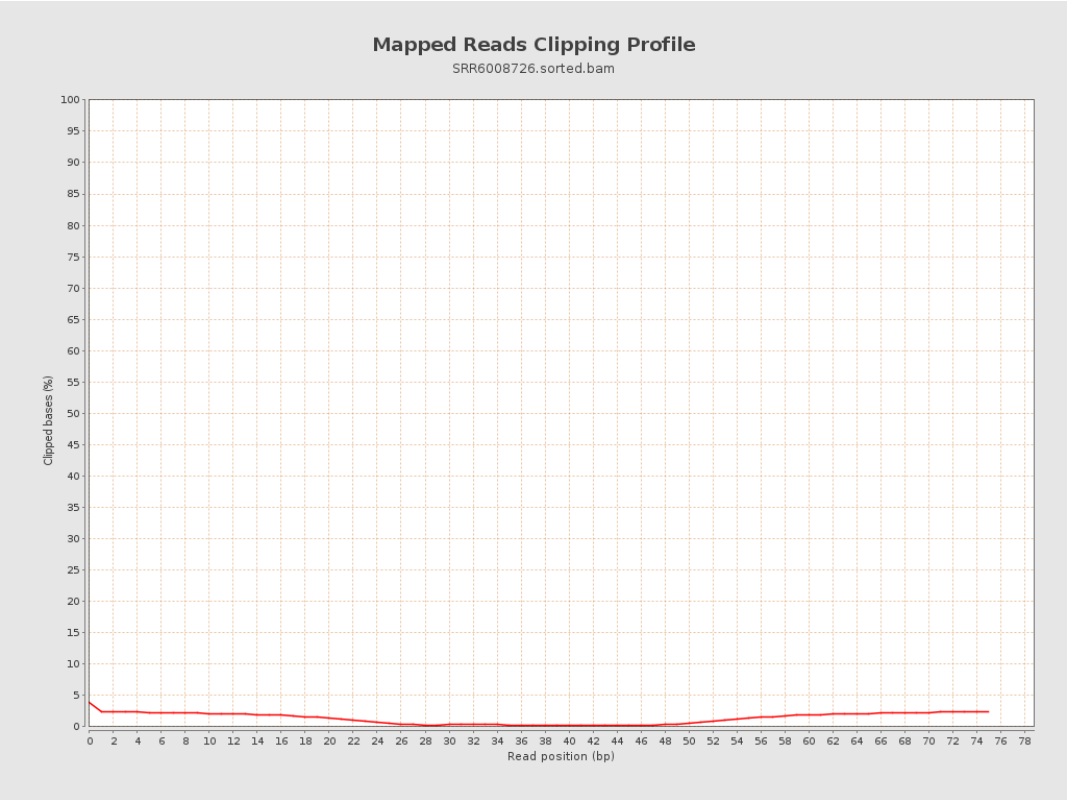
8. Results : Mapped Reads Nucleotide Content



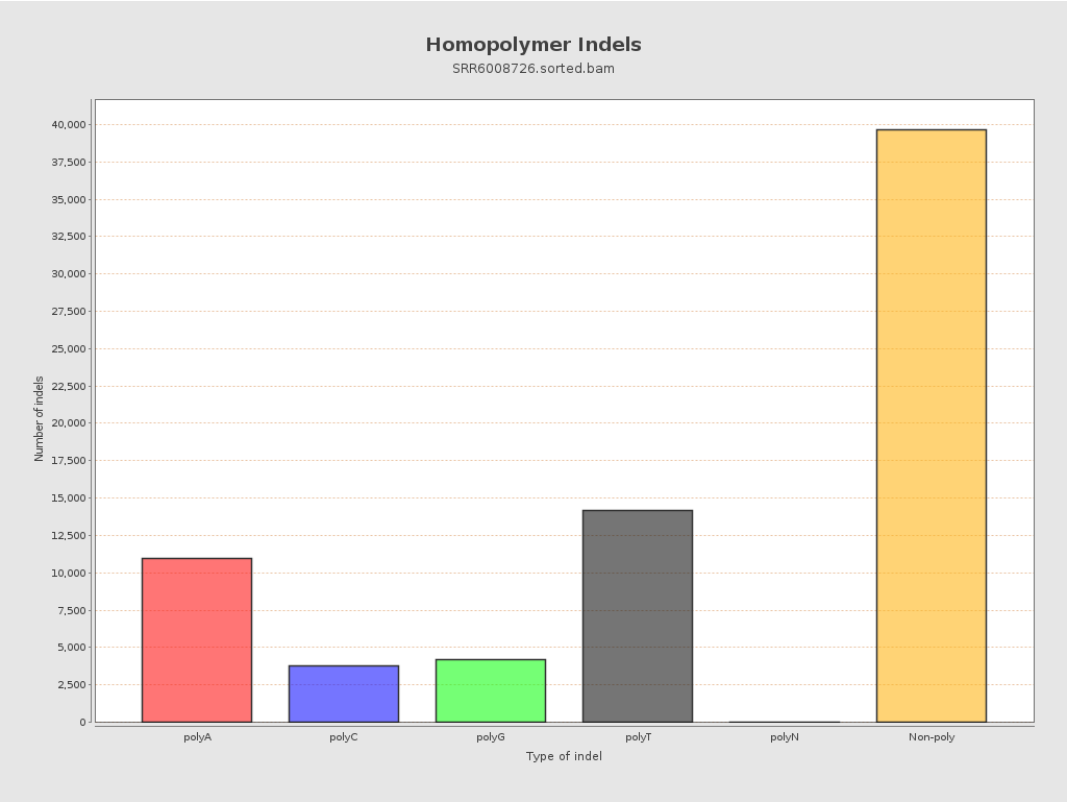
9. Results : Mapped Reads GC-content Distribution



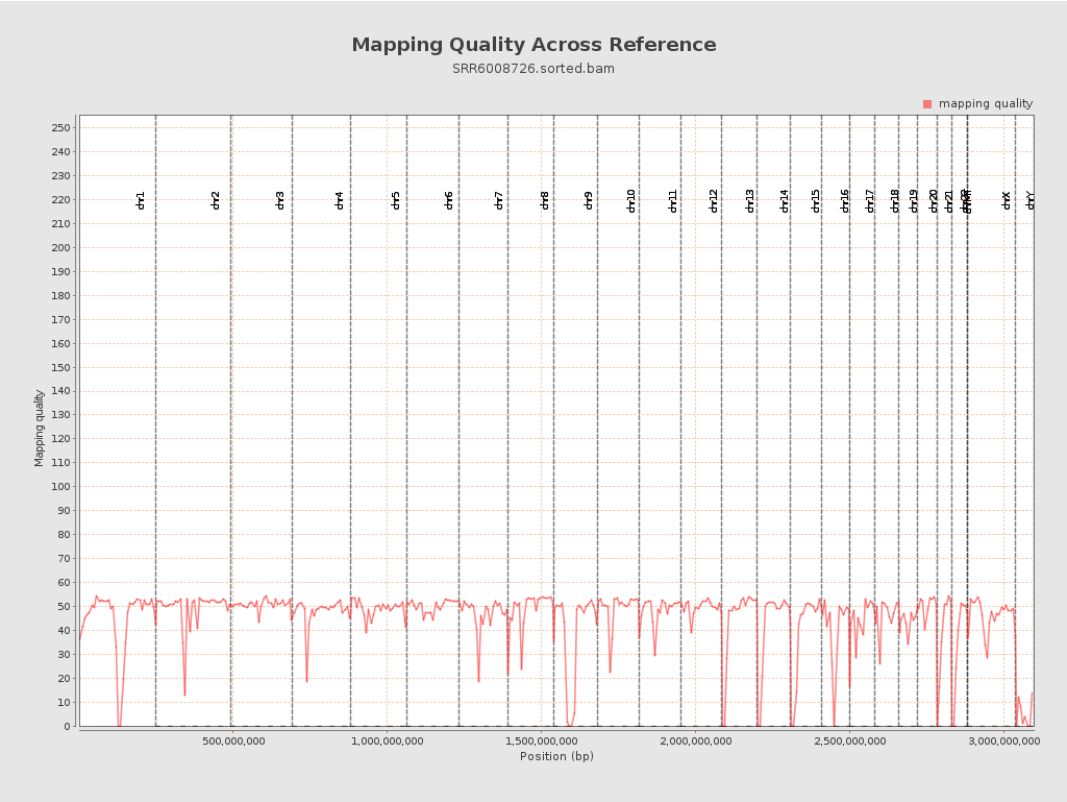
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram