Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 11:40:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008790.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_SRR6008790 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008790.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 11:40:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008790.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,734,122
Mapped reads	1,364,919 / 78.71%
Unmapped reads	369,203 / 21.29%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,154 / 0.59%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	72,414 / 4.18%
Duplication rate	4.21%
Clipped reads	780,800 / 45.03%

2.2. ACGT Content

Number/percentage of A's	23,249,905 / 26.86%
Number/percentage of C's	15,700,202 / 18.14%
Number/percentage of T's	27,678,947 / 31.98%
Number/percentage of G's	19,894,904 / 22.98%
Number/percentage of N's	34,829 / 0.04%
GC Percentage	41.12%

2.3. Coverage

Mean	0.028

Standard Deviation	0.305

2.4. Mapping Quality

Mean Mapping Quality	45.3

2.5. Mismatches and indels

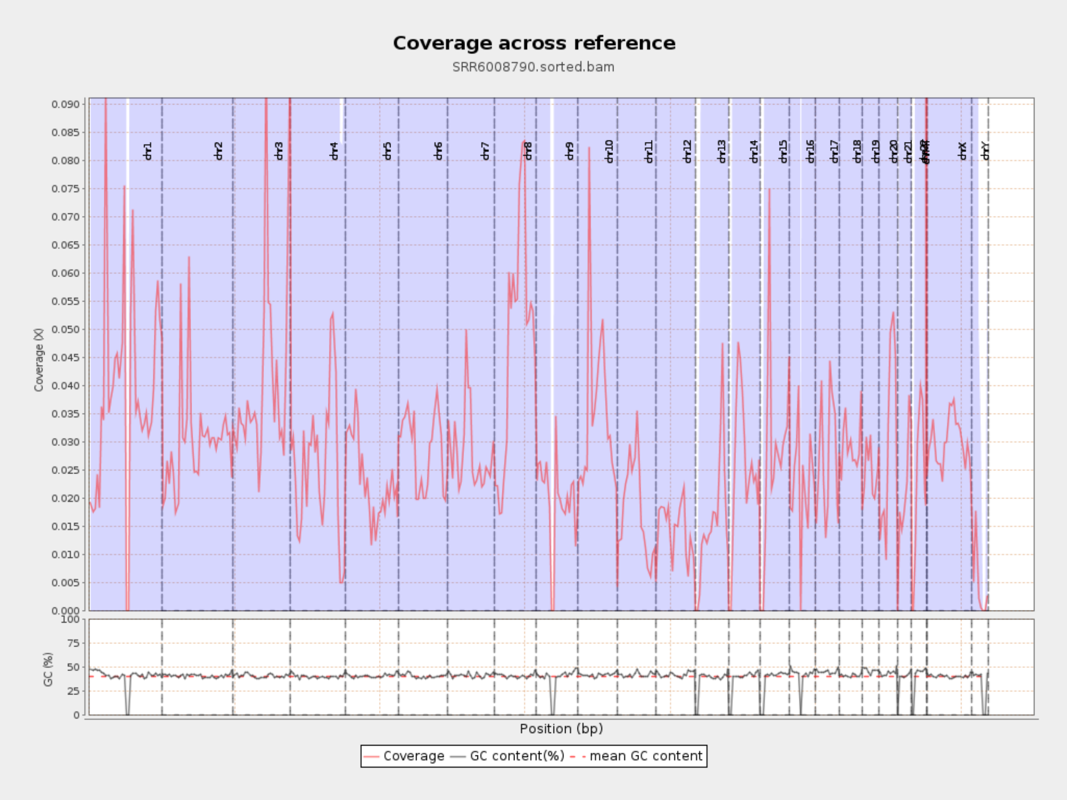
General error rate	0.89%
Mismatches	755,400
Insertions	5,882
Mapped reads with at least one insertion	0.43%
Deletions	27,768
Mapped reads with at least one deletion	2.01%
Homopolymer indels	43.4%

2.6. Chromosome stats

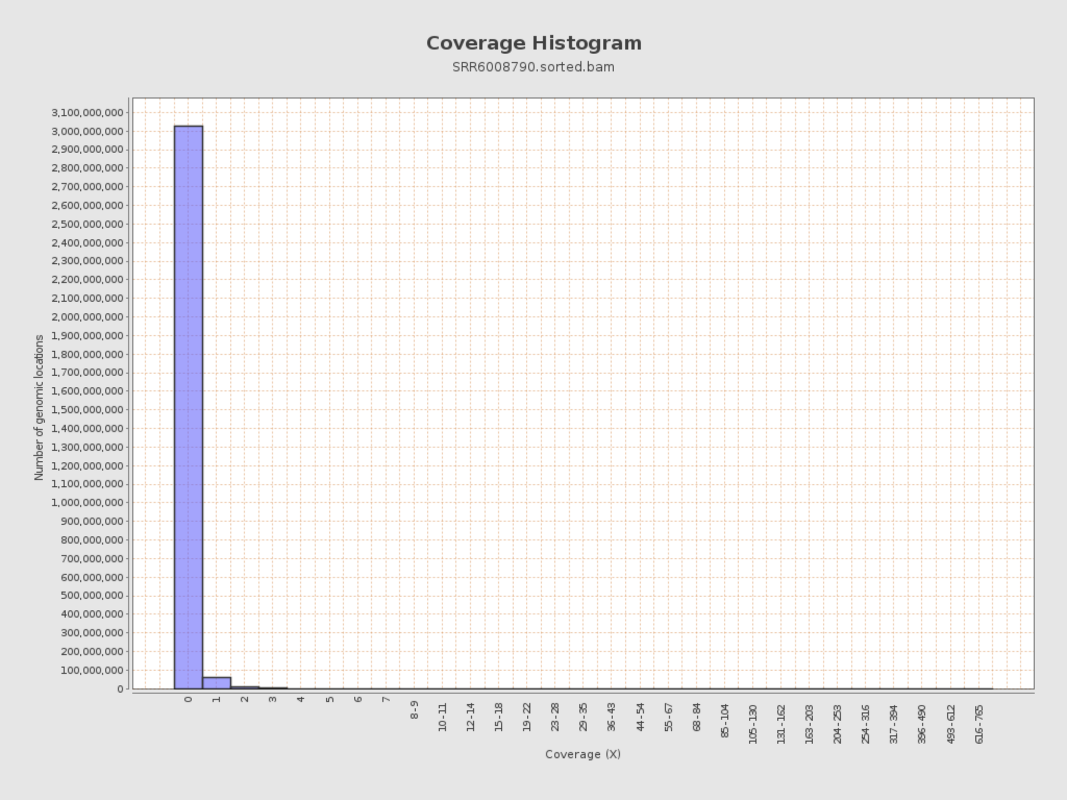
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9577473	0.0384	0.6125
chr2	243199373	7359033	0.0303	0.3275
chr3	198022430	8040144	0.0406	0.2458
chr4	191154276	4857231	0.0254	0.1962
chr5	180915260	4204842	0.0232	0.1785
chr6	171115067	4890767	0.0286	0.2215
chr7	159138663	4510576	0.0283	0.3037

chr8	146364022	7031506	0.048	0.3547
chr9	141213431	2729096	0.0193	0.2328
chr10	135534747	4789606	0.0353	0.4567
chr11	135006516	2409432	0.0178	0.2082
chr12	133851895	1926622	0.0144	0.1417
chr13	115169878	1841773	0.016	0.1459
chr14	107349540	2714391	0.0253	0.191
chr15	102531392	2808328	0.0274	0.1936
chr16	90354753	2045240	0.0226	0.2074
chr17	81195210	2155212	0.0265	0.2368
chr18	78077248	2272712	0.0291	0.4308
chr19	59128983	1476722	0.025	0.3897
chr20	63025520	1894353	0.0301	0.2059
chr21	48129895	1015102	0.0211	0.1795
chr22	51304566	1118454	0.0218	0.1706
chrMT	16571	13269	0.8007	1.2641
chrX	155270560	4642064	0.0299	0.2165
chrY	59373566	282930	0.0048	0.1809

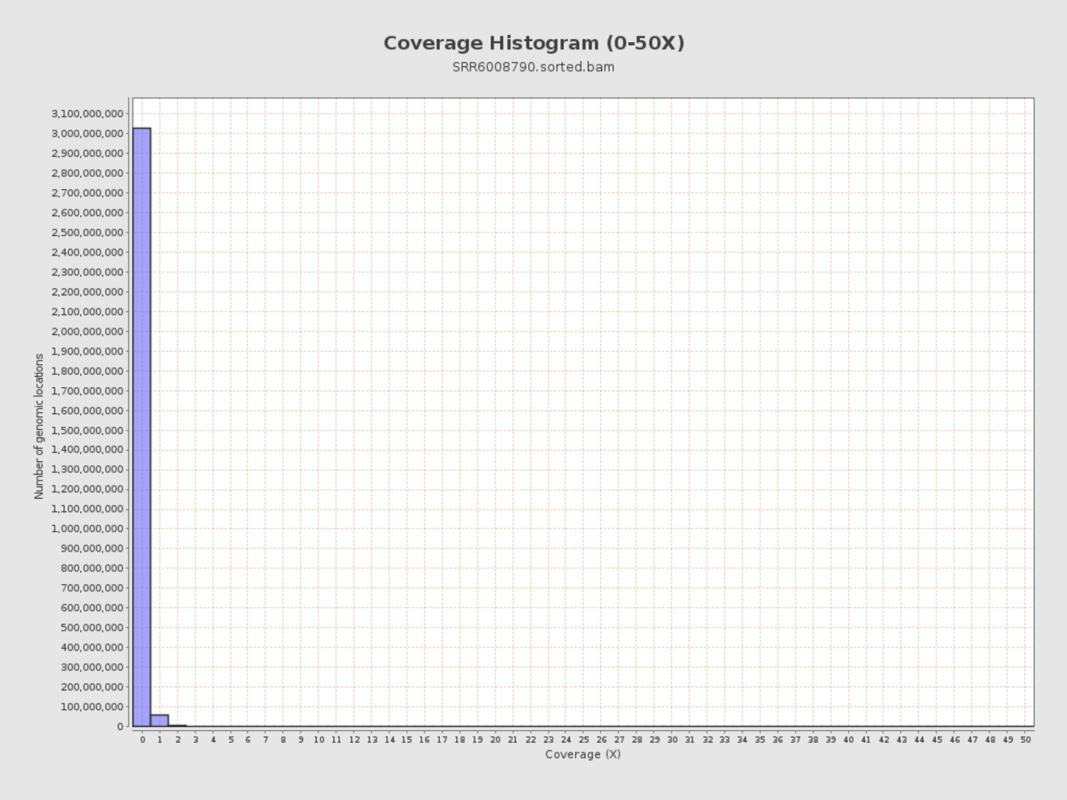
3. Results : Coverage across reference



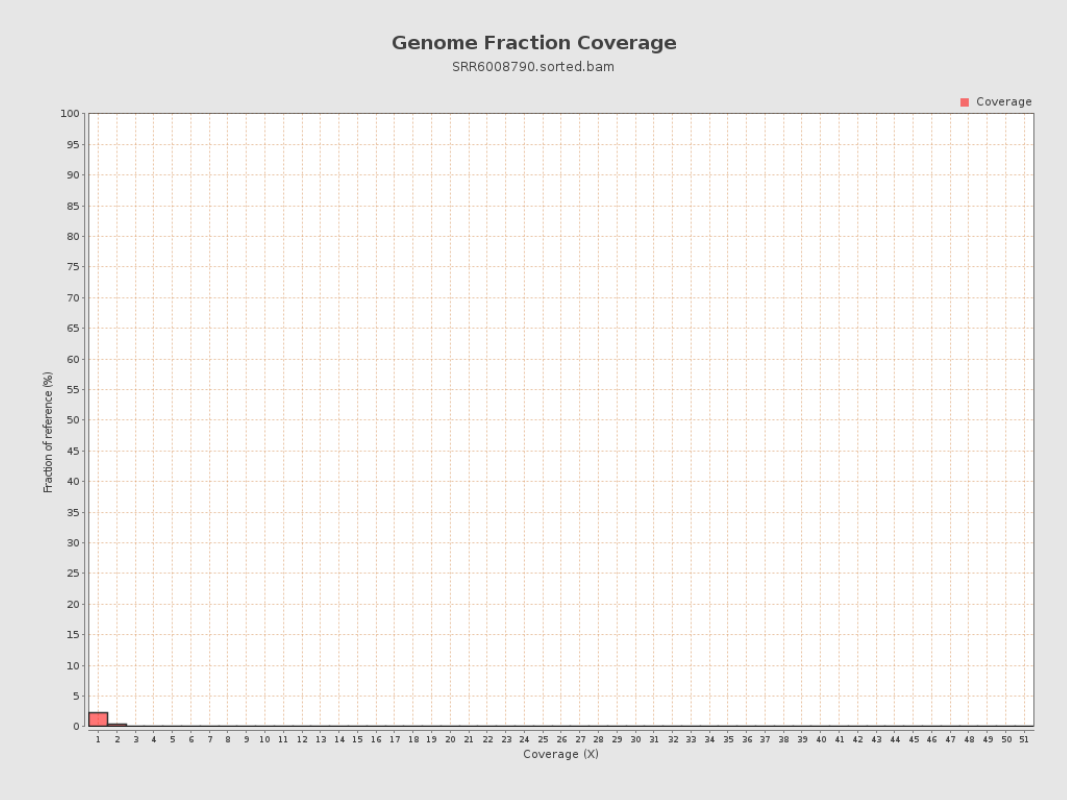
4. Results : Coverage Histogram



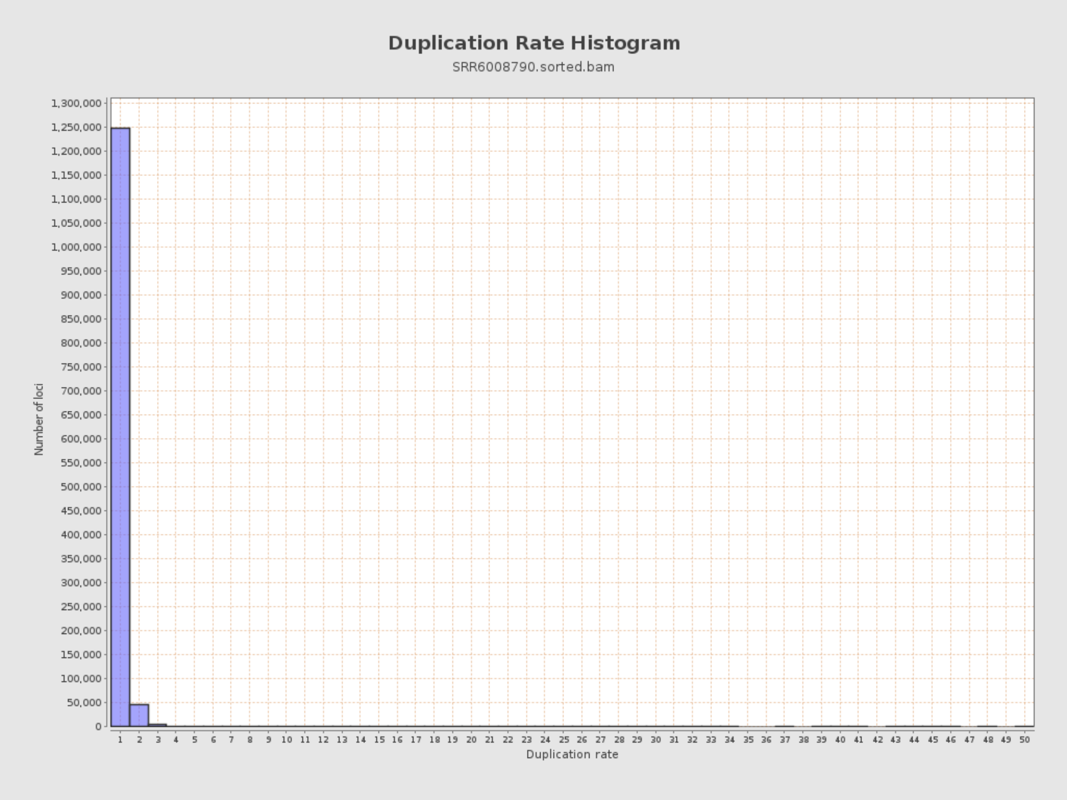
5. Results : Coverage Histogram (0-50X)



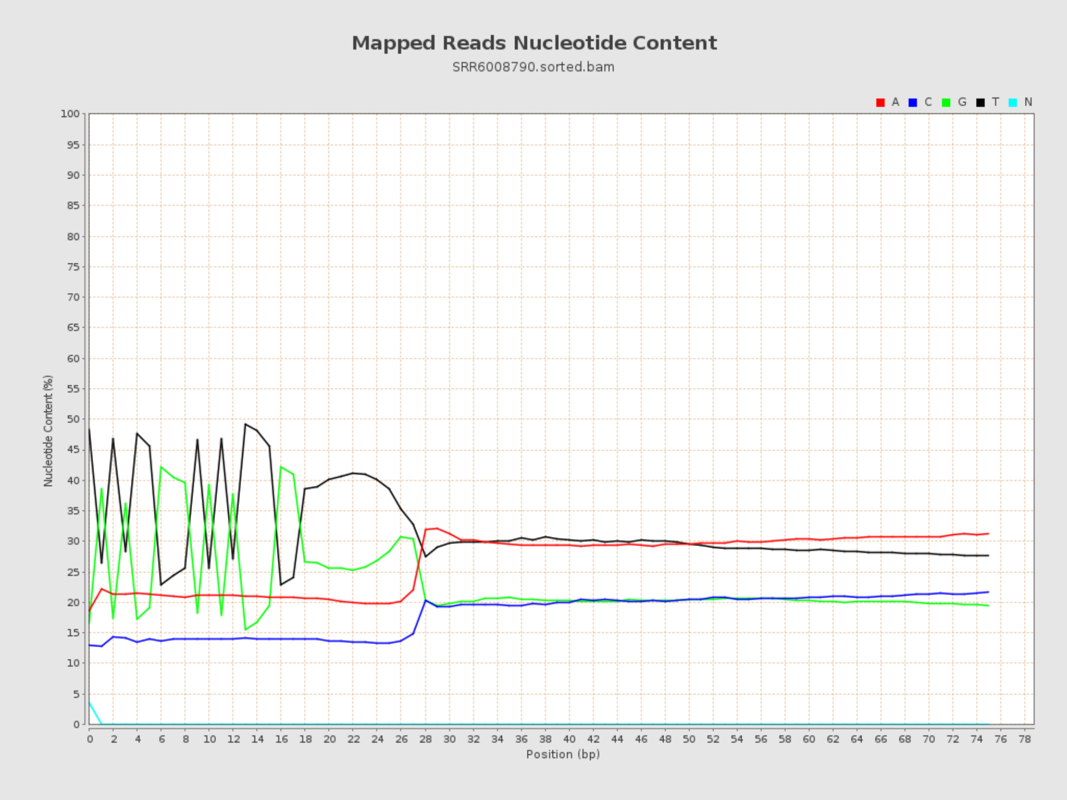
6. Results : Genome Fraction Coverage



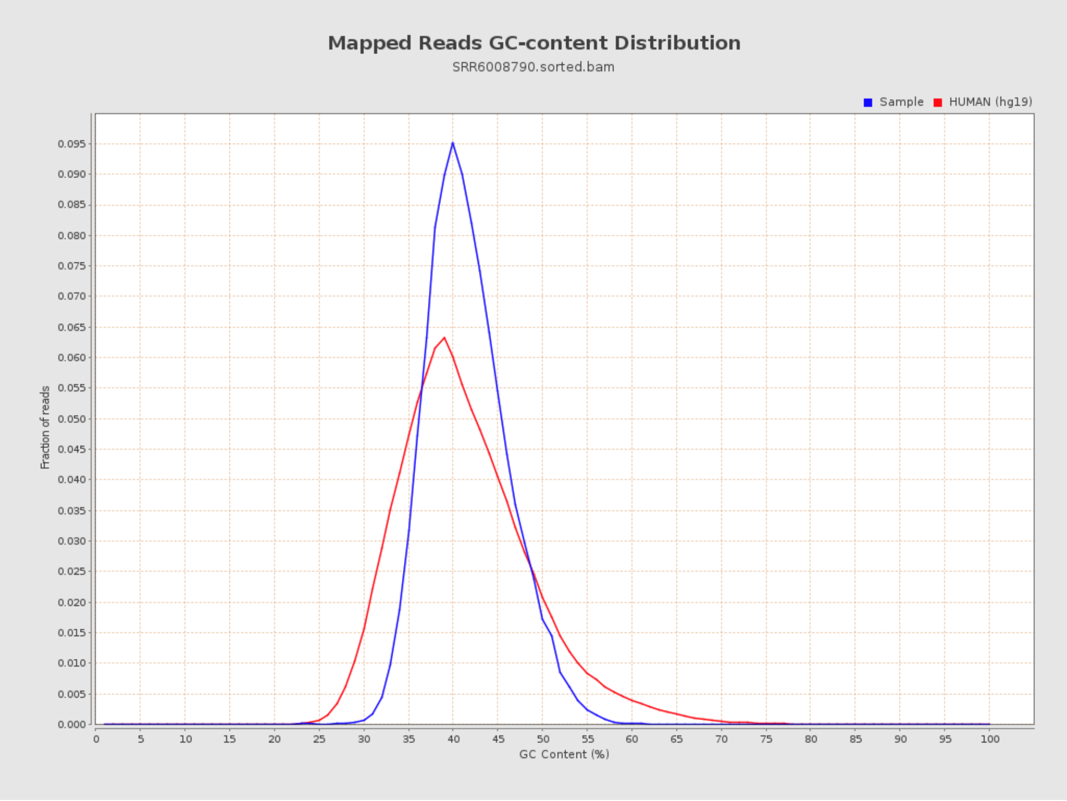
7. Results : Duplication Rate Histogram



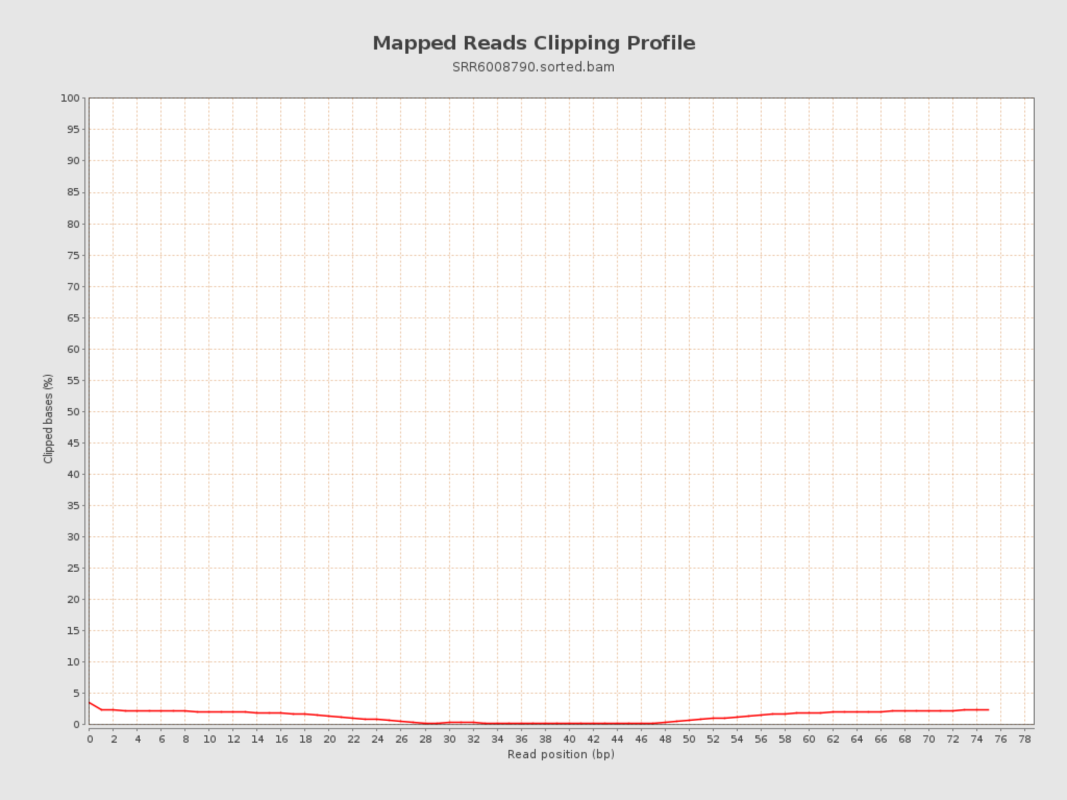
8. Results : Mapped Reads Nucleotide Content



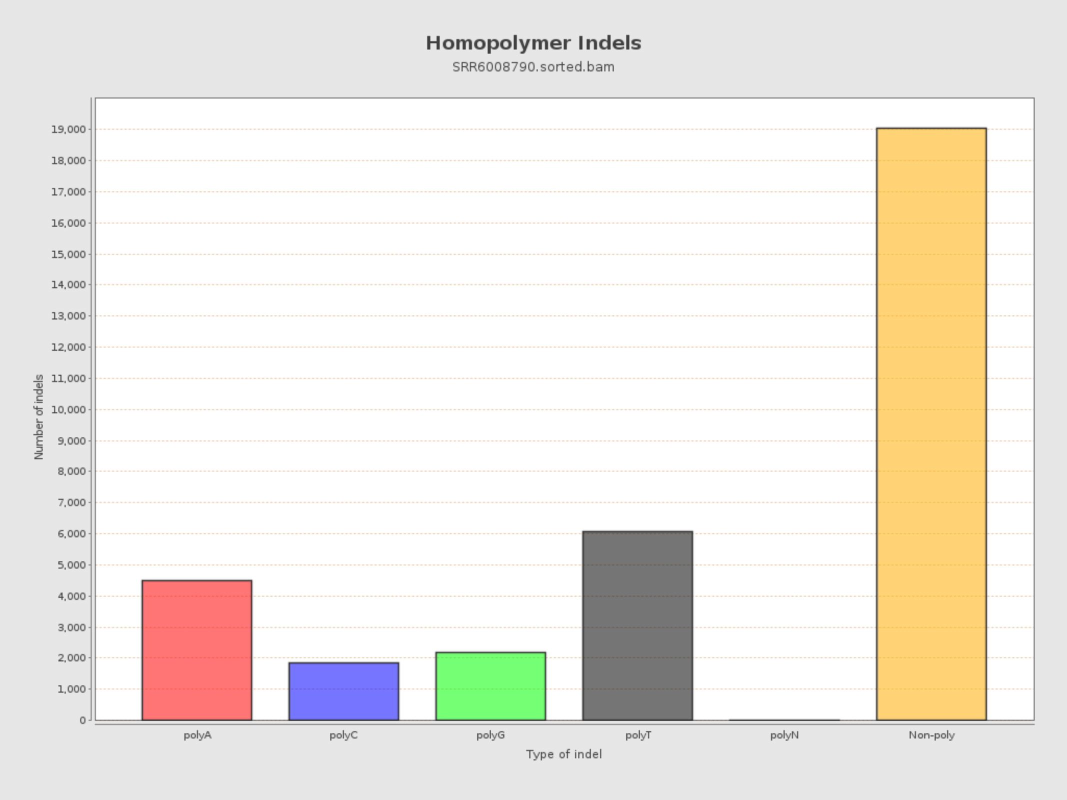
9. Results : Mapped Reads GC-content Distribution



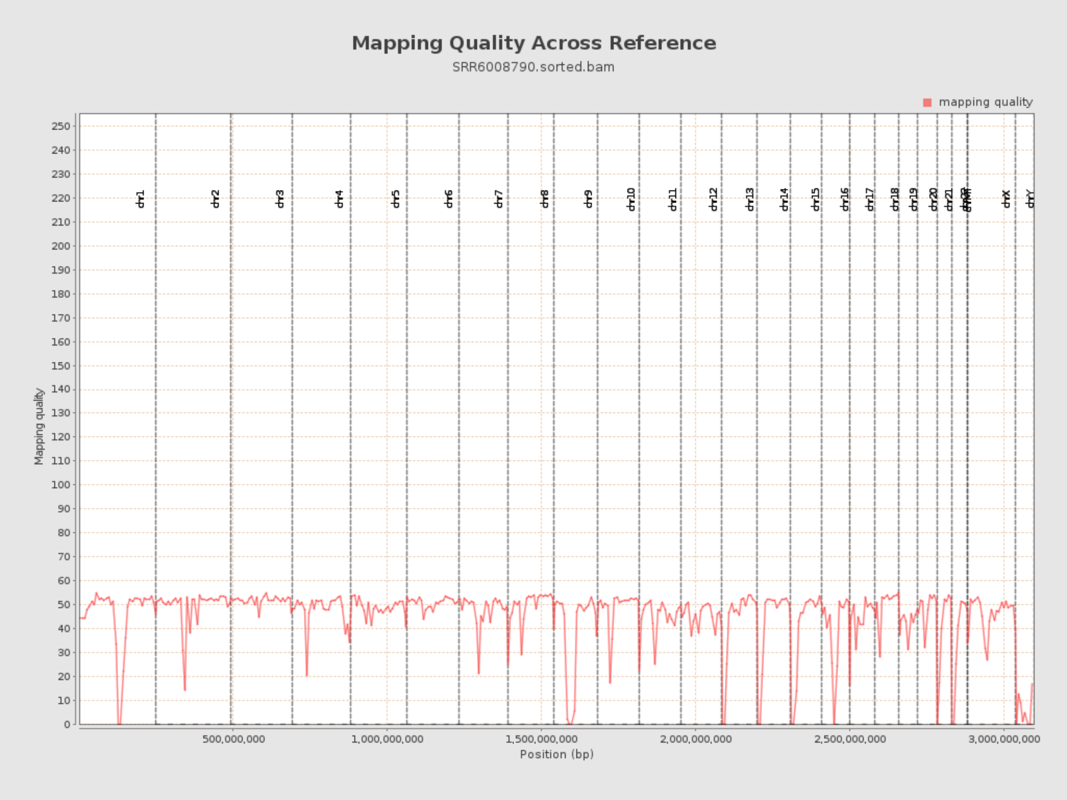
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram