Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 10:28:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008766.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_SRR6008766 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008766.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 10:28:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008766.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,455,931
Mapped reads	2,277,348 / 92.73%
Unmapped reads	178,583 / 7.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,912 / 0.73%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	112,893 / 4.6%
Duplication rate	3.82%
Clipped reads	1,168,225 / 47.57%

2.2. ACGT Content

Number/percentage of A's	39,448,788 / 26.75%
Number/percentage of C's	26,094,365 / 17.69%
Number/percentage of T's	47,558,020 / 32.25%
Number/percentage of G's	34,350,762 / 23.29%
Number/percentage of N's	28,095 / 0.02%
GC Percentage	40.99%

2.3. Coverage

Mean	0.0477

Standard Deviation	0.4281

2.4. Mapping Quality

Mean Mapping Quality	45.22

2.5. Mismatches and indels

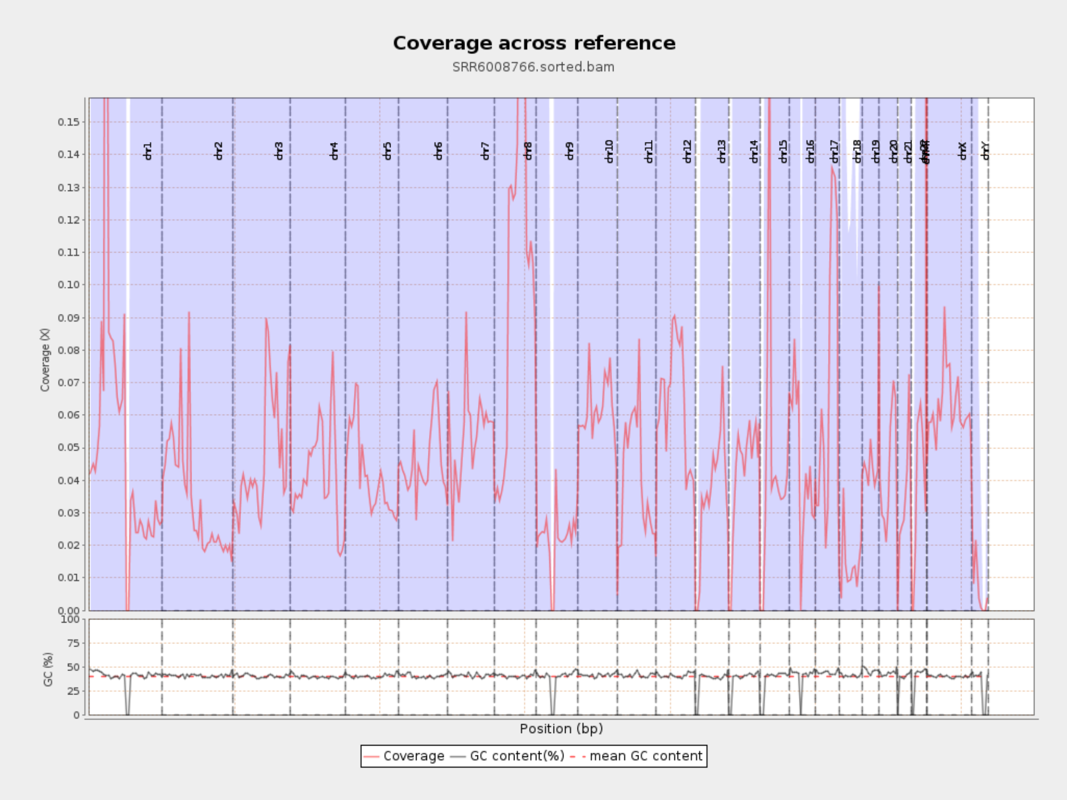
General error rate	0.71%
Mismatches	1,023,076
Insertions	11,409
Mapped reads with at least one insertion	0.5%
Deletions	38,137
Mapped reads with at least one deletion	1.66%
Homopolymer indels	47.42%

2.6. Chromosome stats

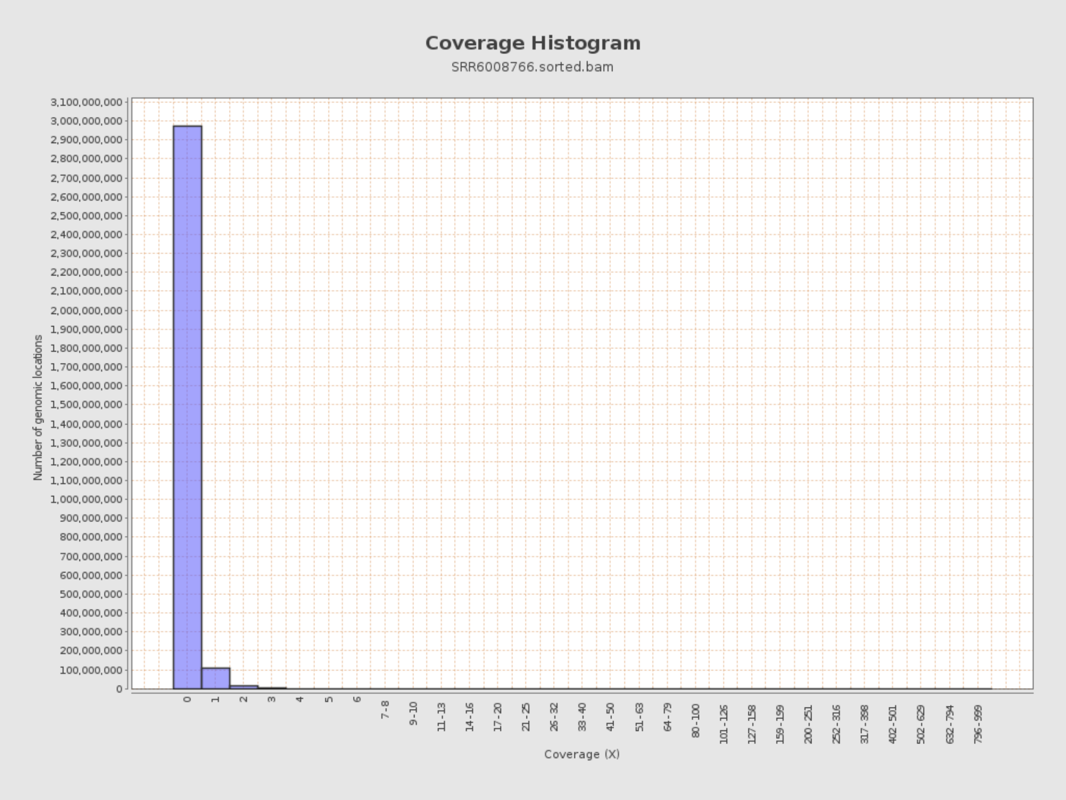
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13176762	0.0529	0.8526
chr2	243199373	8426279	0.0346	0.4704
chr3	198022430	9416879	0.0476	0.2489
chr4	191154276	7817028	0.0409	0.2412
chr5	180915260	7569773	0.0418	0.2357
chr6	171115067	7820622	0.0457	0.3009
chr7	159138663	8550049	0.0537	0.5284

chr8	146364022	15833448	0.1082	0.5164
chr9	141213431	3094091	0.0219	0.3616
chr10	135534747	8393853	0.0619	0.3933
chr11	135006516	5552059	0.0411	0.3658
chr12	133851895	8603819	0.0643	0.2936
chr13	115169878	4146964	0.036	0.2141
chr14	107349540	4501742	0.0419	0.2444
chr15	102531392	4731634	0.0461	0.2525
chr16	90354753	4051558	0.0448	0.2798
chr17	81195210	5693972	0.0701	0.3869
chr18	78077248	1094556	0.014	0.7407
chr19	59128983	2688557	0.0455	0.5742
chr20	63025520	2691110	0.0427	0.2528
chr21	48129895	1613167	0.0335	0.2215
chr22	51304566	1861361	0.0363	0.212
chrMT	16571	70034	4.2263	3.2358
chrX	155270560	9733185	0.0627	0.3382
chrY	59373566	409315	0.0069	0.2341

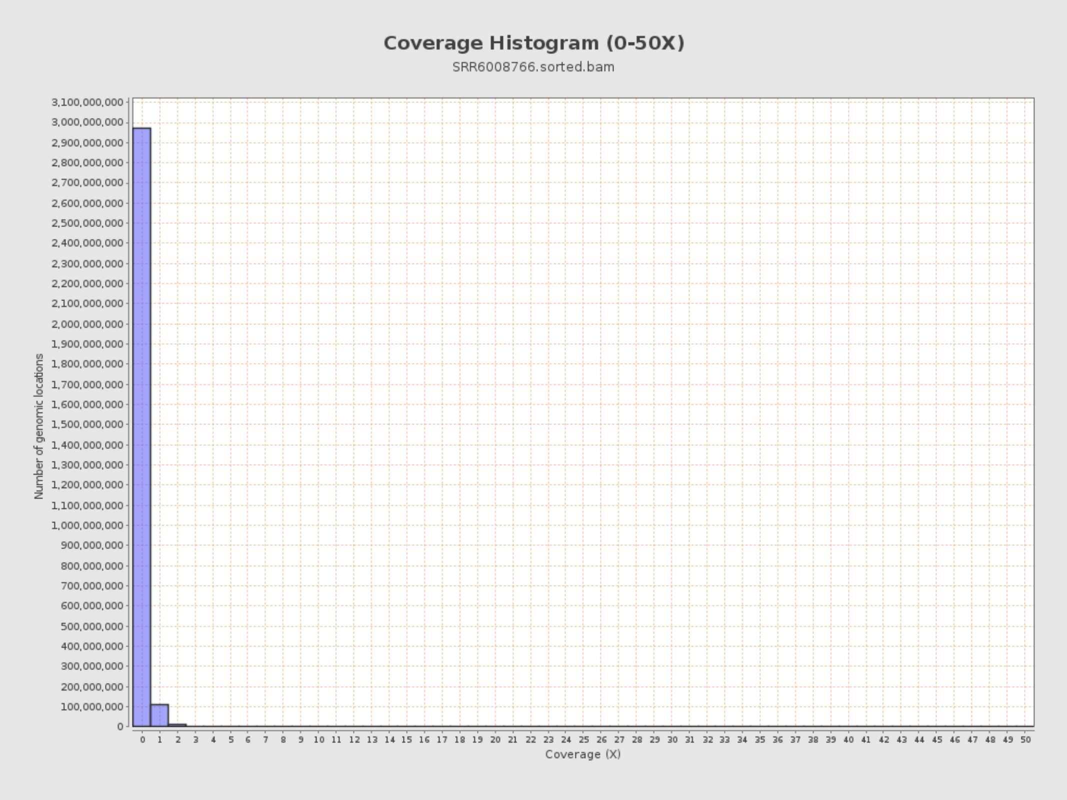
3. Results : Coverage across reference



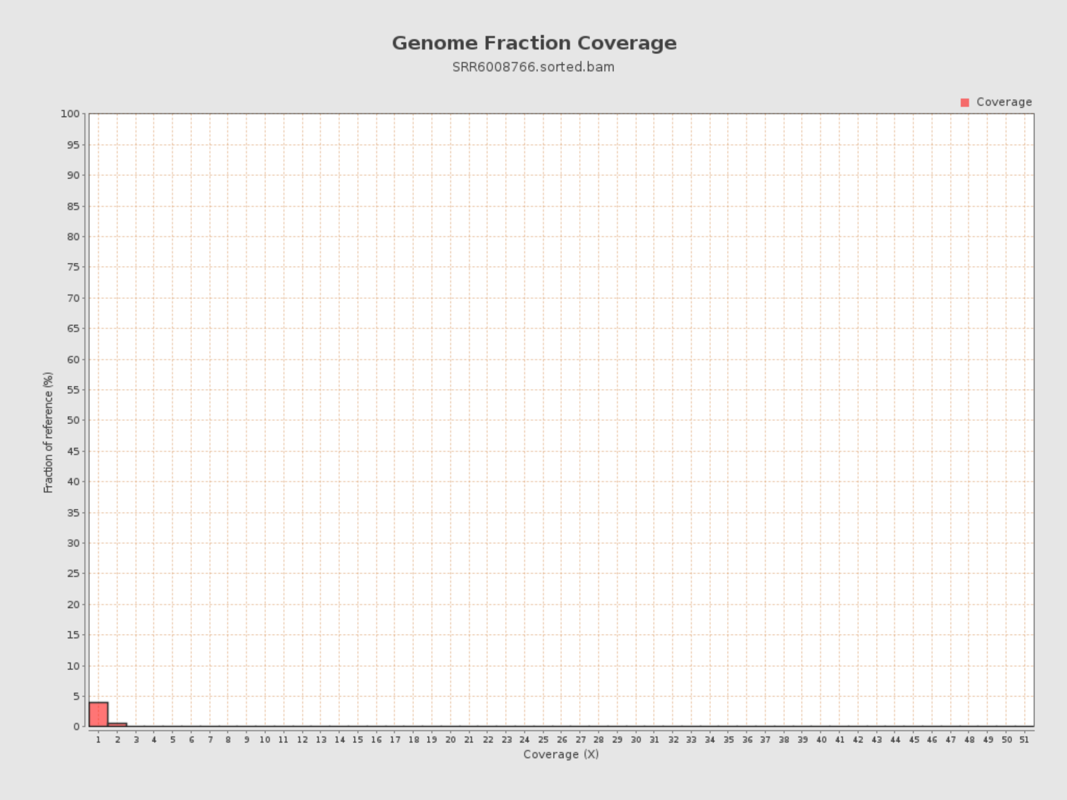
4. Results : Coverage Histogram



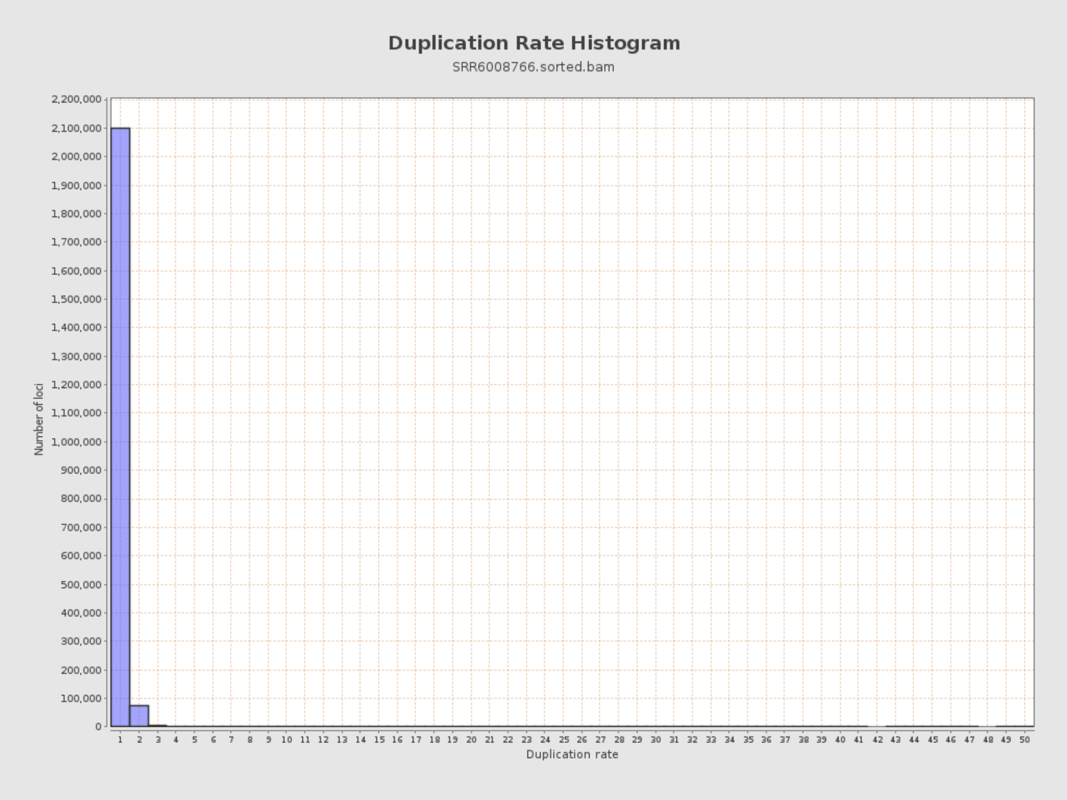
5. Results : Coverage Histogram (0-50X)



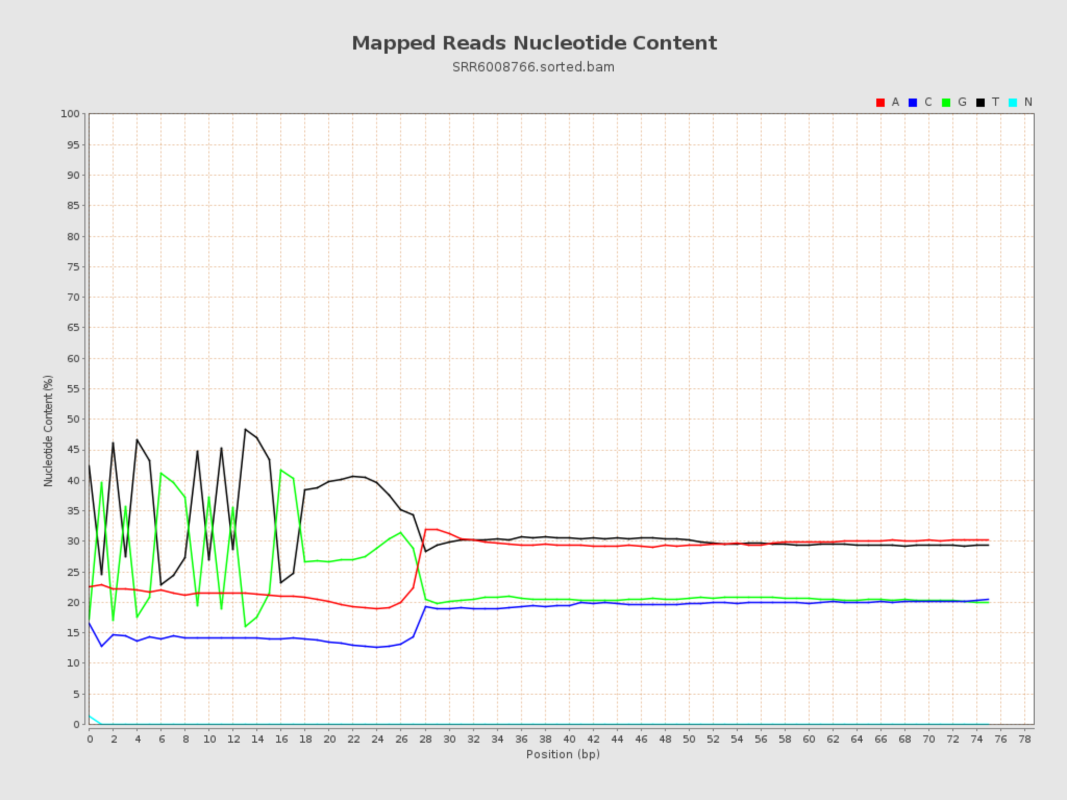
6. Results : Genome Fraction Coverage



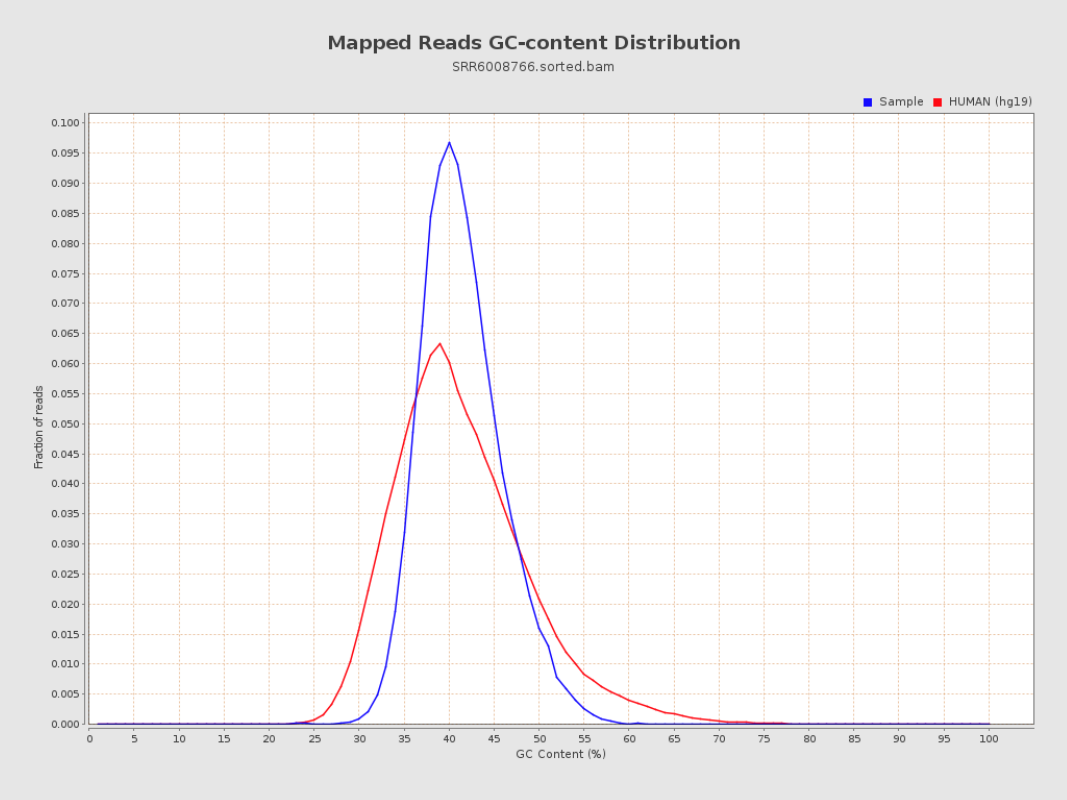
7. Results : Duplication Rate Histogram



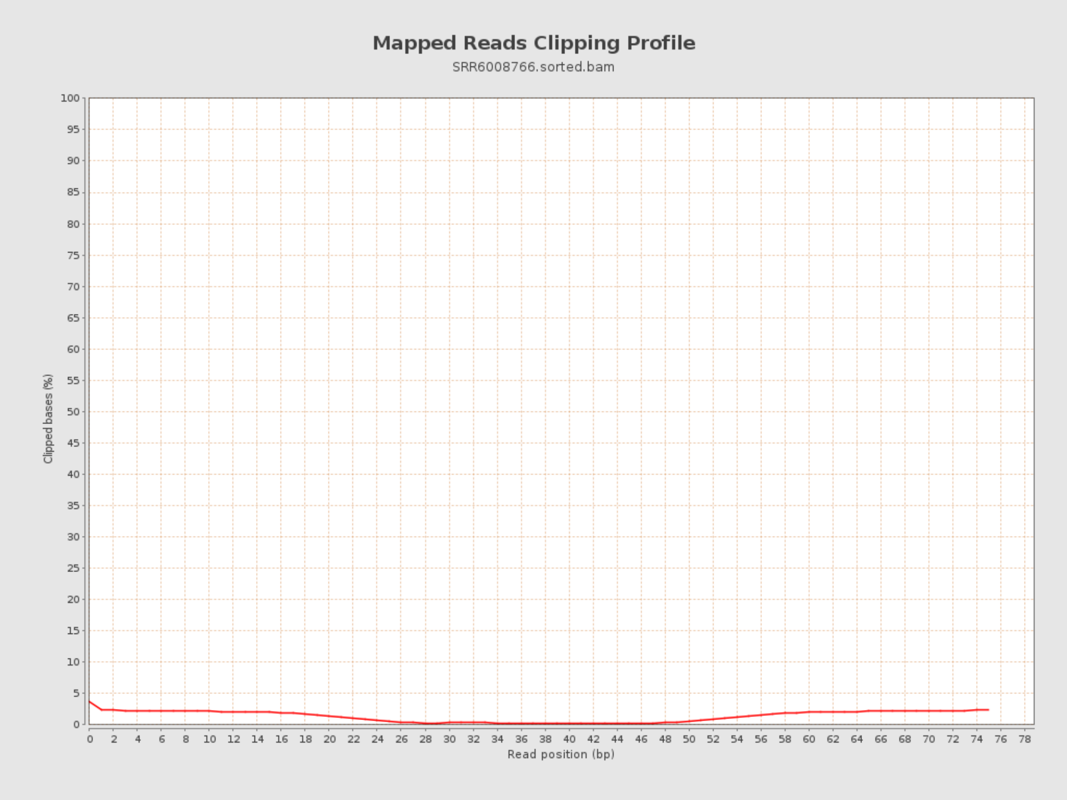
8. Results : Mapped Reads Nucleotide Content



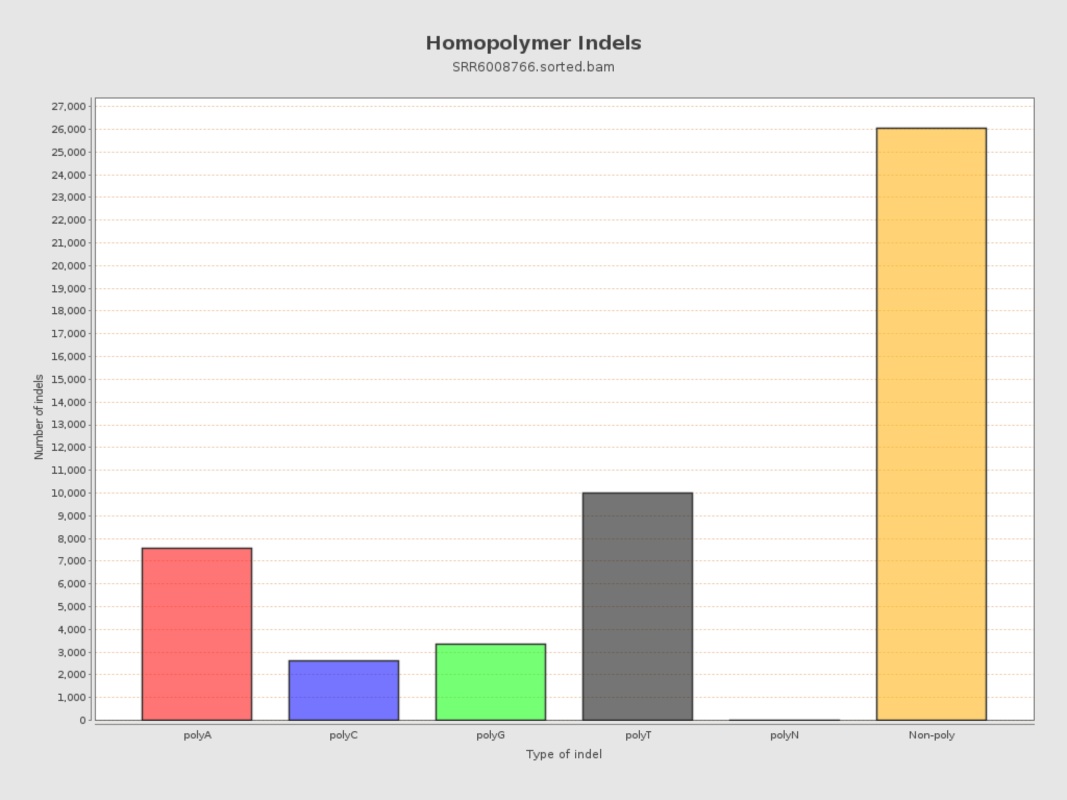
9. Results : Mapped Reads GC-content Distribution



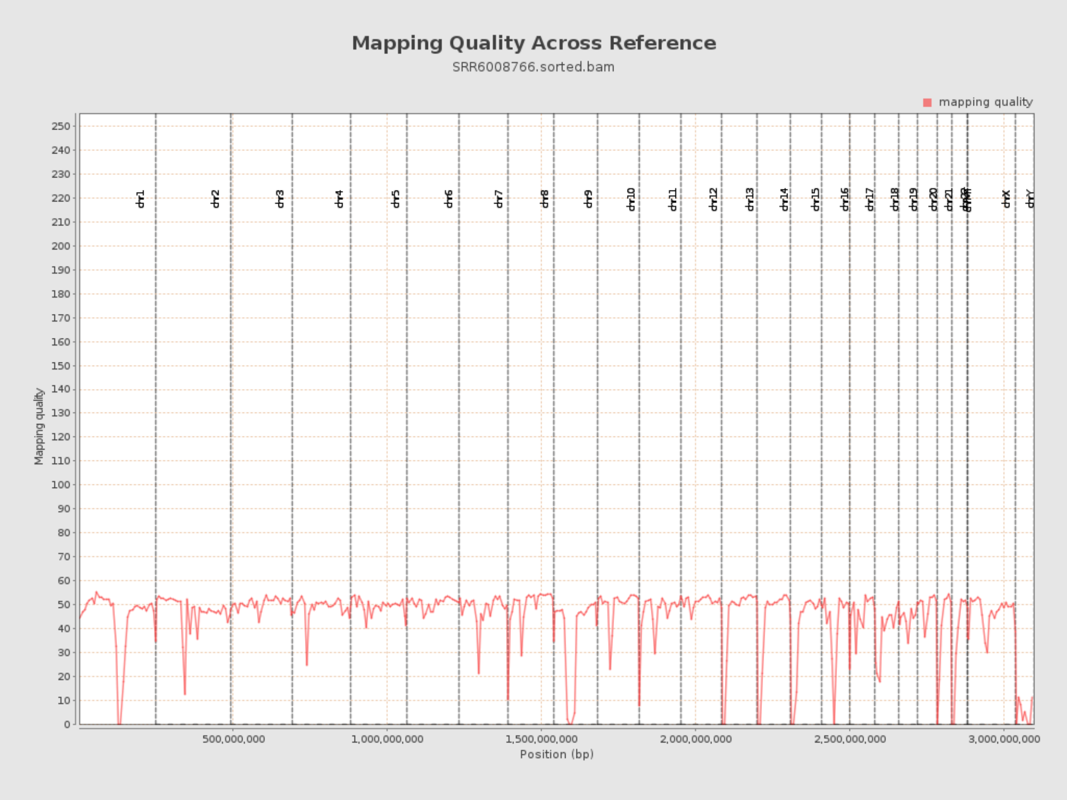
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram