Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 08:11:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008715.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_SRR6008715 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008715.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 08:11:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008715.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,493,486
Mapped reads	1,082,182 / 72.46%
Unmapped reads	411,304 / 27.54%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,160 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	15,973 / 1.07%
Duplication rate	1.21%
Clipped reads	428,713 / 28.71%

2.2. ACGT Content

Number/percentage of A's	22,488,206 / 30.62%
Number/percentage of C's	12,978,130 / 17.67%
Number/percentage of T's	21,400,617 / 29.13%
Number/percentage of G's	16,574,854 / 22.57%
Number/percentage of N's	11,591 / 0.02%
GC Percentage	40.23%

2.3. Coverage

Mean	0.0237

Standard Deviation	0.1848

2.4. Mapping Quality

Mean Mapping Quality	48.76

2.5. Mismatches and indels

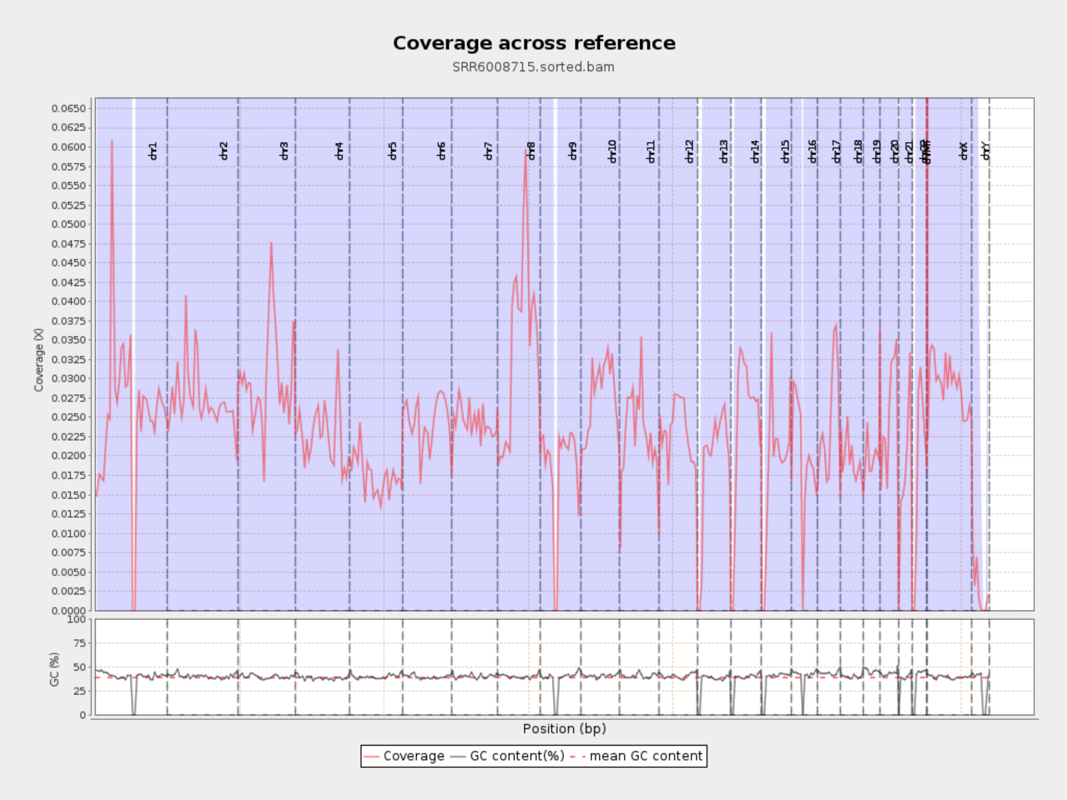
General error rate	0.93%
Mismatches	673,402
Insertions	5,068
Mapped reads with at least one insertion	0.46%
Deletions	19,391
Mapped reads with at least one deletion	1.77%
Homopolymer indels	47.14%

2.6. Chromosome stats

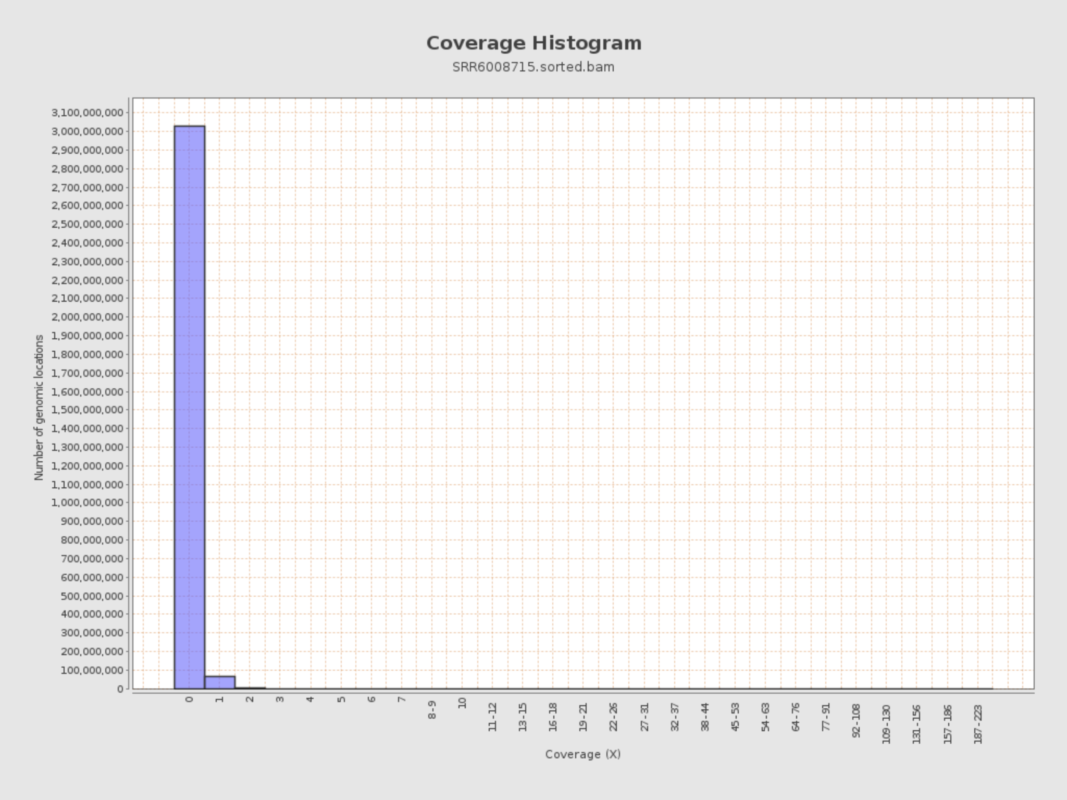
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6304585	0.0253	0.2441
chr2	243199373	6648203	0.0273	0.2401
chr3	198022430	5946856	0.03	0.18
chr4	191154276	4345121	0.0227	0.1573
chr5	180915260	3162752	0.0175	0.1366
chr6	171115067	4203842	0.0246	0.1707
chr7	159138663	3876537	0.0244	0.1919

chr8	146364022	5125167	0.035	0.238
chr9	141213431	2576799	0.0182	0.1558
chr10	135534747	3753521	0.0277	0.1963
chr11	135006516	3152303	0.0233	0.1743
chr12	133851895	3115757	0.0233	0.1582
chr13	115169878	2160782	0.0188	0.1416
chr14	107349540	2589617	0.0241	0.1648
chr15	102531392	1890837	0.0184	0.1415
chr16	90354753	1770975	0.0196	0.1531
chr17	81195210	2005089	0.0247	0.1687
chr18	78077248	1519583	0.0195	0.2327
chr19	59128983	1201712	0.0203	0.1725
chr20	63025520	1601319	0.0254	0.1668
chr21	48129895	881785	0.0183	0.1446
chr22	51304566	941218	0.0183	0.1408
chrMT	16571	14682	0.886	1.2159
chrX	155270560	4537718	0.0292	0.1835
chrY	59373566	157484	0.0027	0.0652

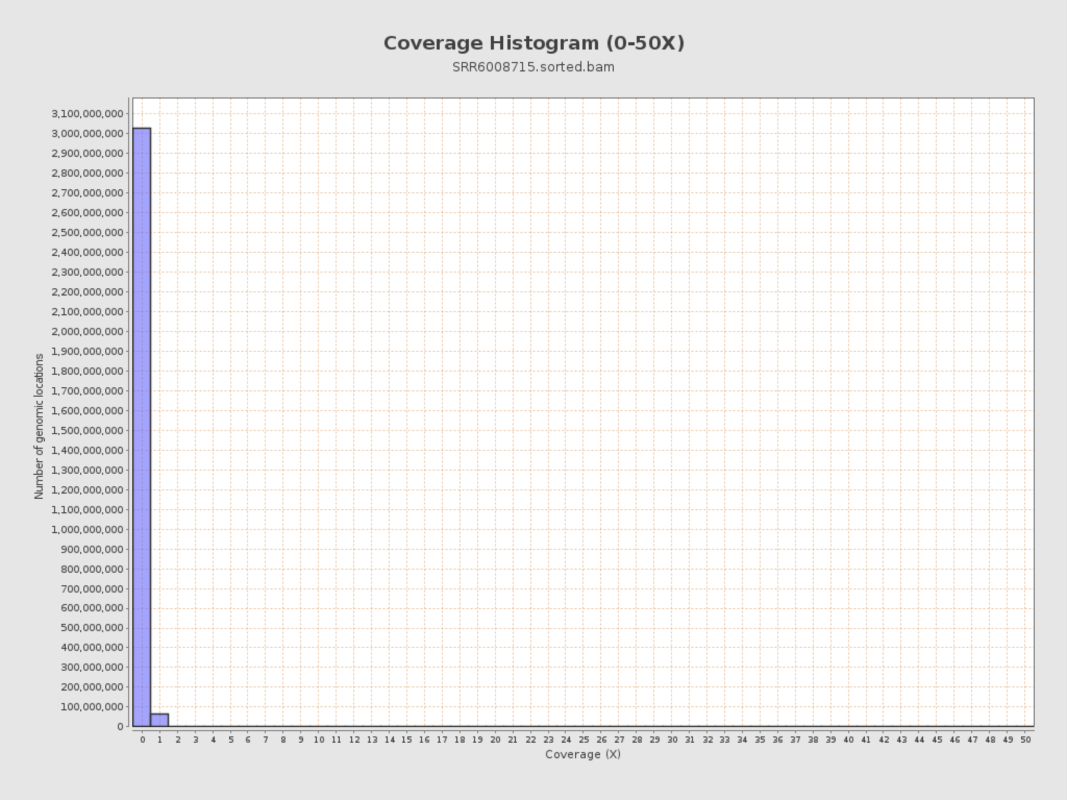
3. Results : Coverage across reference



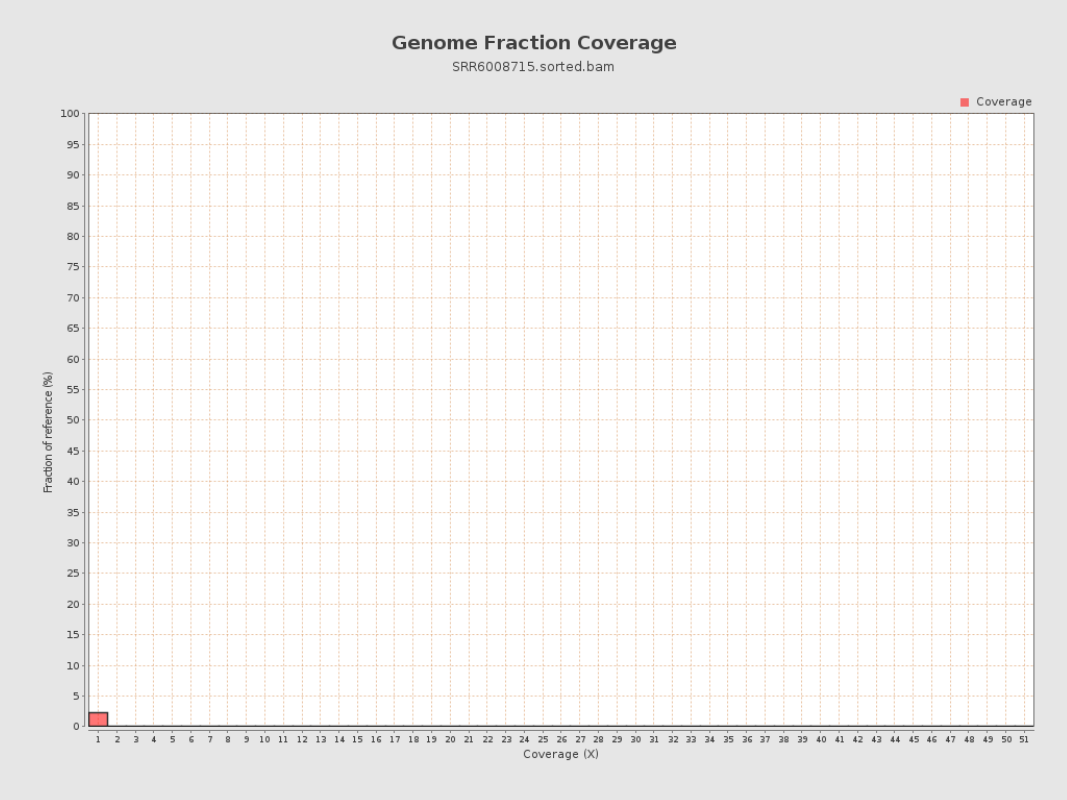
4. Results : Coverage Histogram



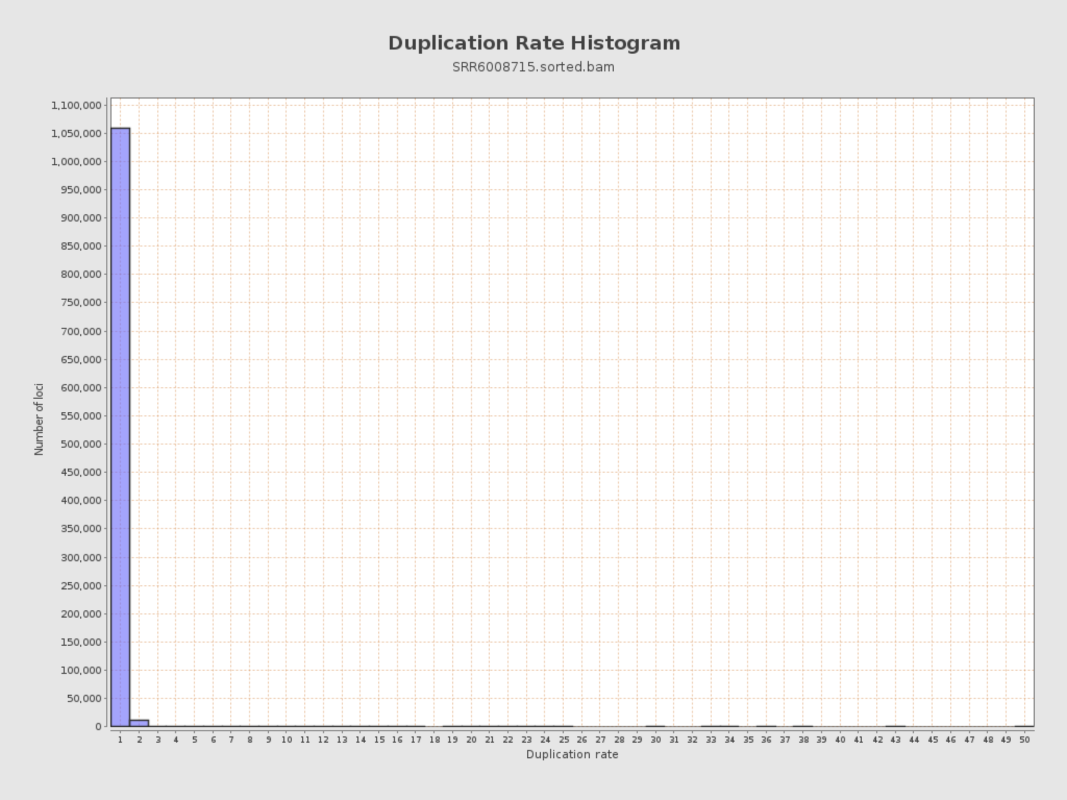
5. Results : Coverage Histogram (0-50X)



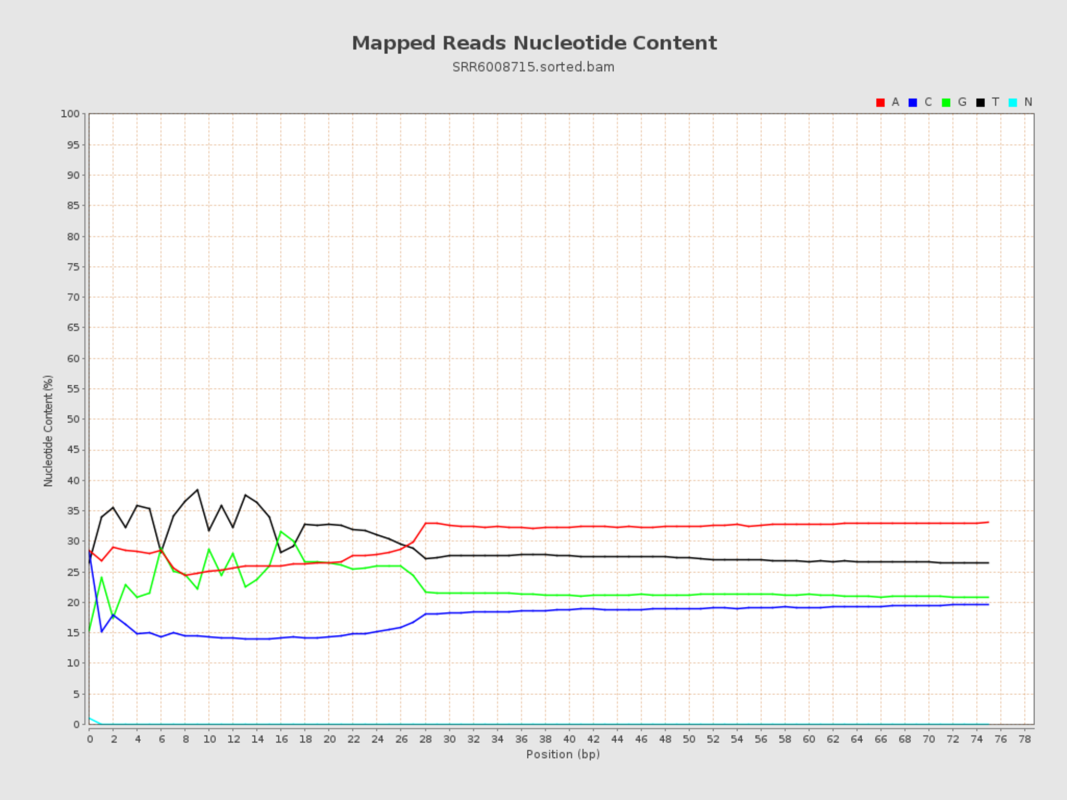
6. Results : Genome Fraction Coverage



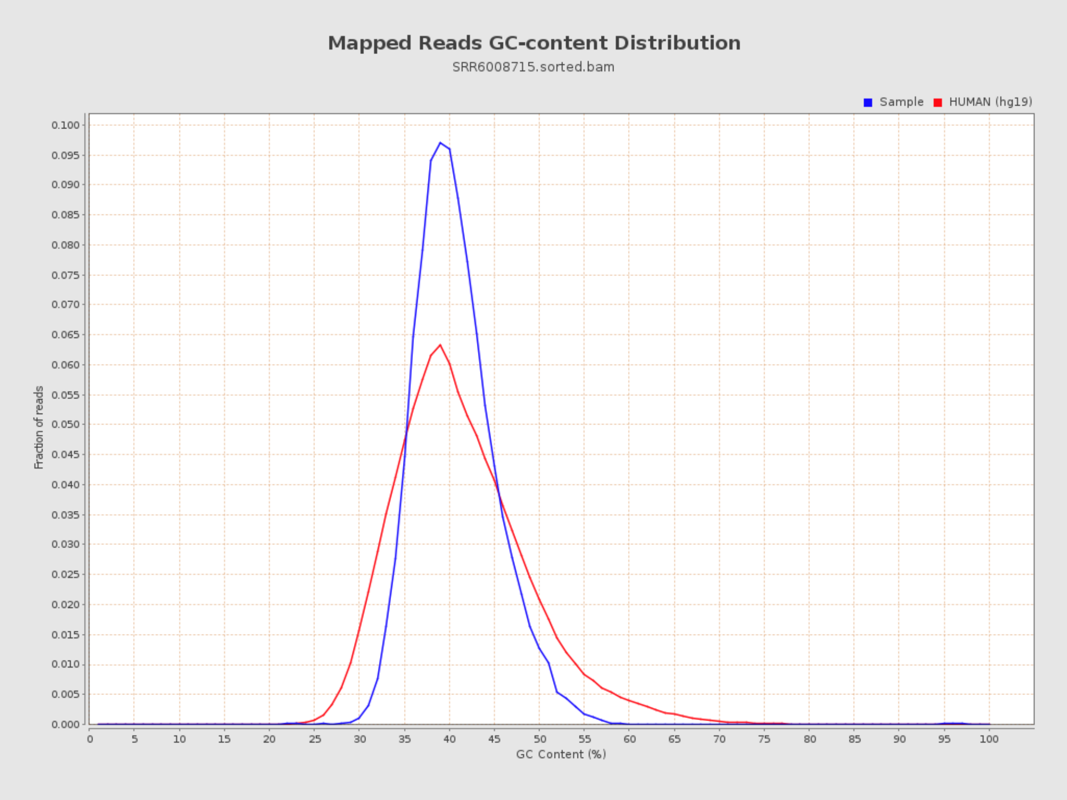
7. Results : Duplication Rate Histogram



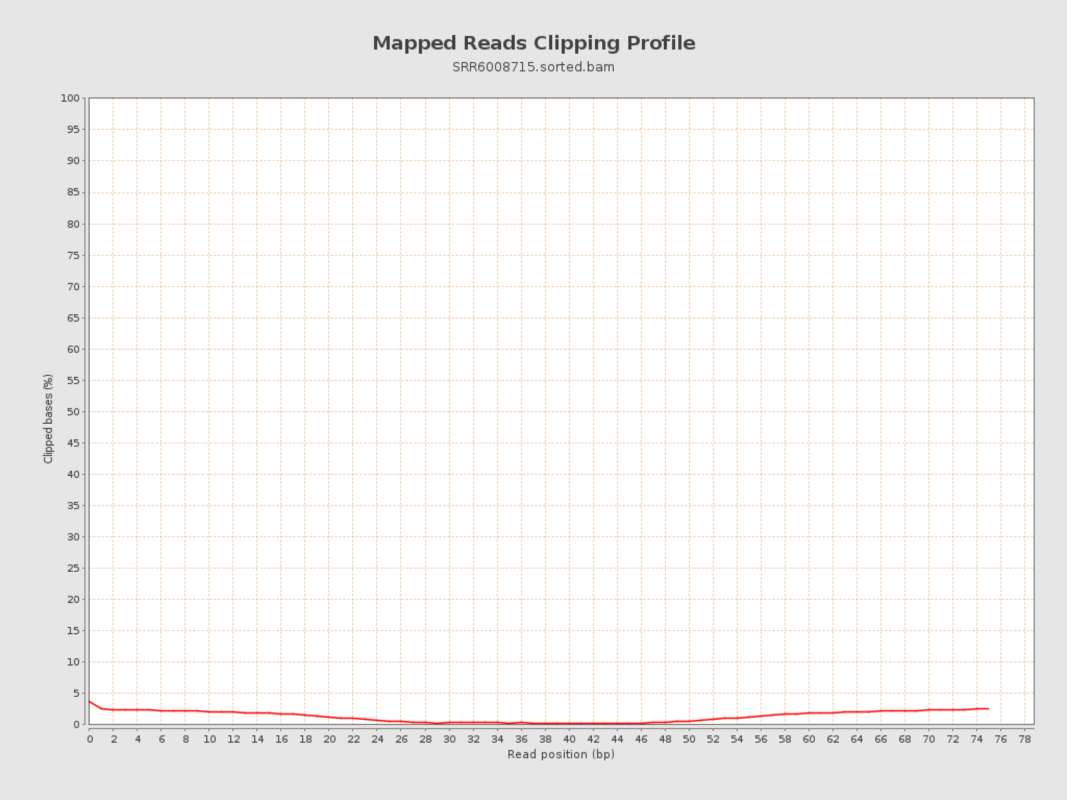
8. Results : Mapped Reads Nucleotide Content



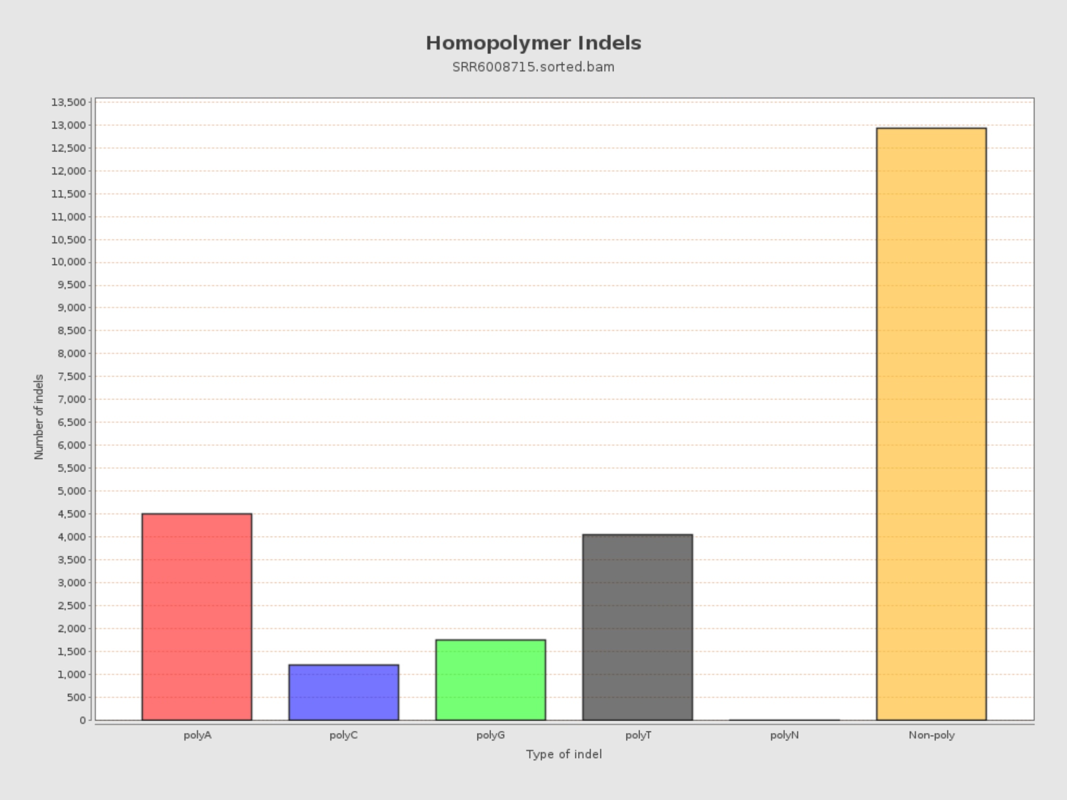
9. Results : Mapped Reads GC-content Distribution



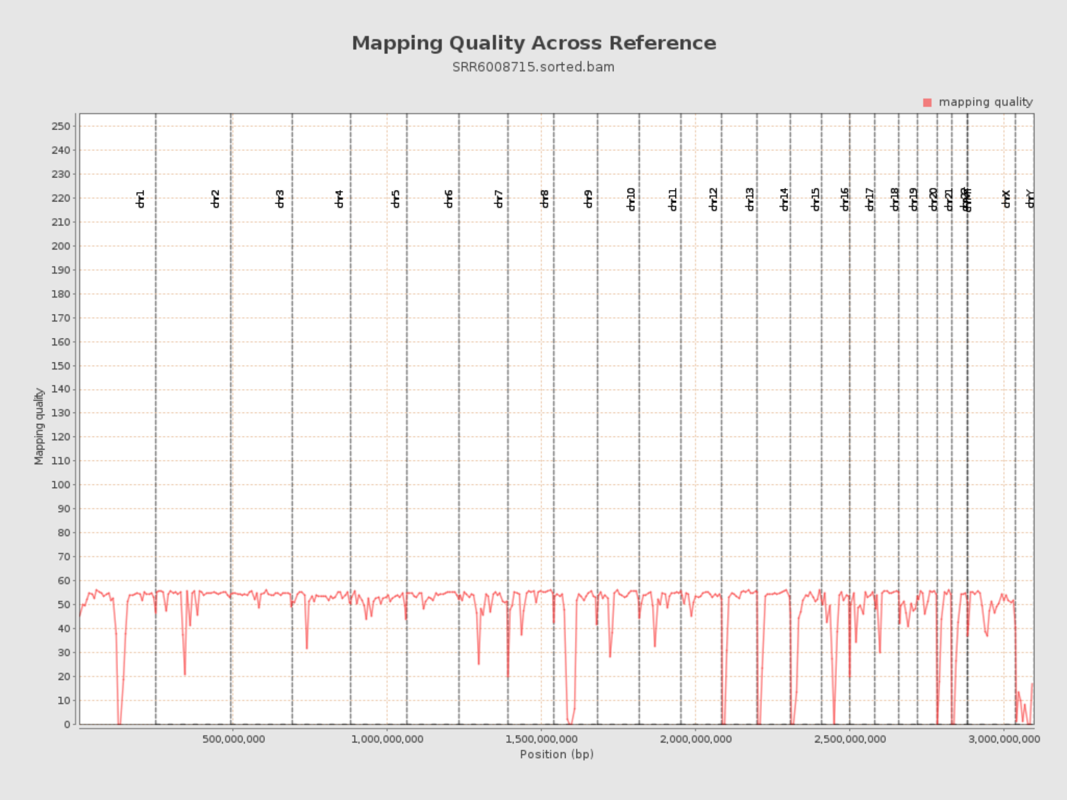
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram