Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 00:01:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717006.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_SRR9717006 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717006.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 00:01:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717006.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,771,838
Mapped reads	1,603,541 / 90.5%
Unmapped reads	168,297 / 9.5%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,592 / 0.43%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	61,795 / 3.49%
Duplication rate	3%
Clipped reads	1,607,234 / 90.71%

2.2. ACGT Content

Number/percentage of A's	23,840,099 / 25.61%
Number/percentage of C's	17,129,326 / 18.4%
Number/percentage of T's	28,578,113 / 30.7%
Number/percentage of G's	23,551,527 / 25.3%
Number/percentage of N's	2,187 / 0%
GC Percentage	43.7%

2.3. Coverage

Mean	0.0301

Standard Deviation	0.2633

2.4. Mapping Quality

Mean Mapping Quality	45.98

2.5. Mismatches and indels

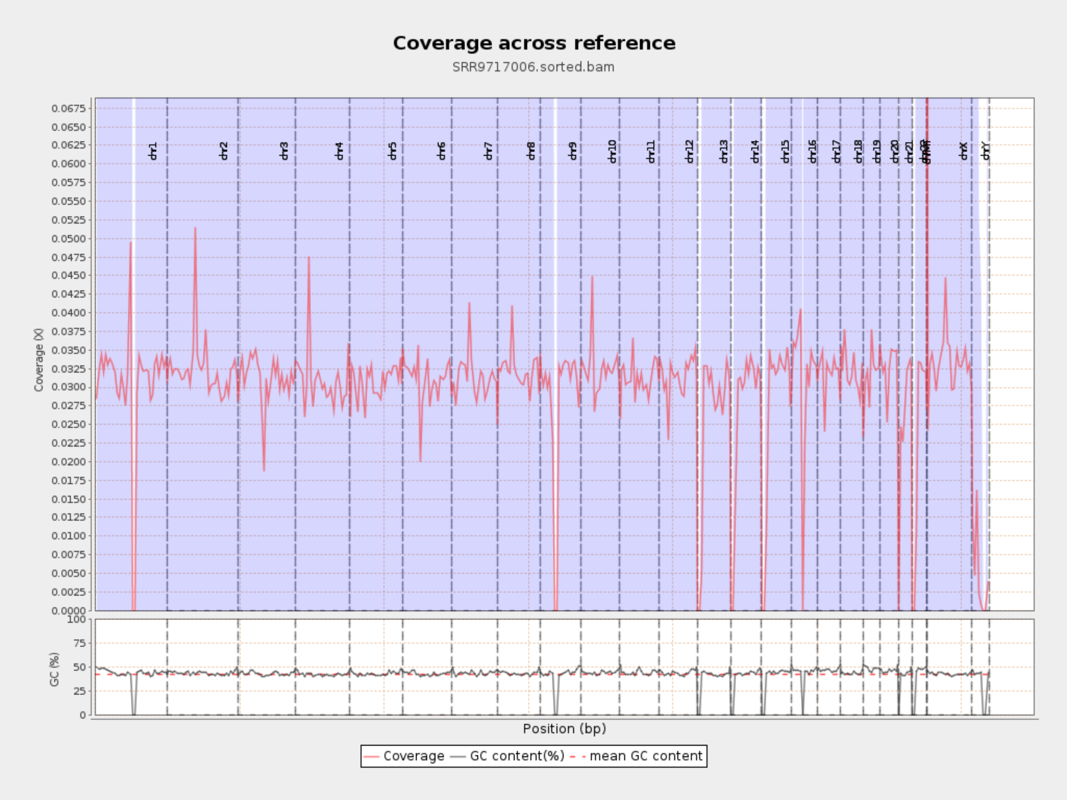
General error rate	0.5%
Mismatches	456,160
Insertions	5,816
Mapped reads with at least one insertion	0.36%
Deletions	15,206
Mapped reads with at least one deletion	0.94%
Homopolymer indels	40.23%

2.6. Chromosome stats

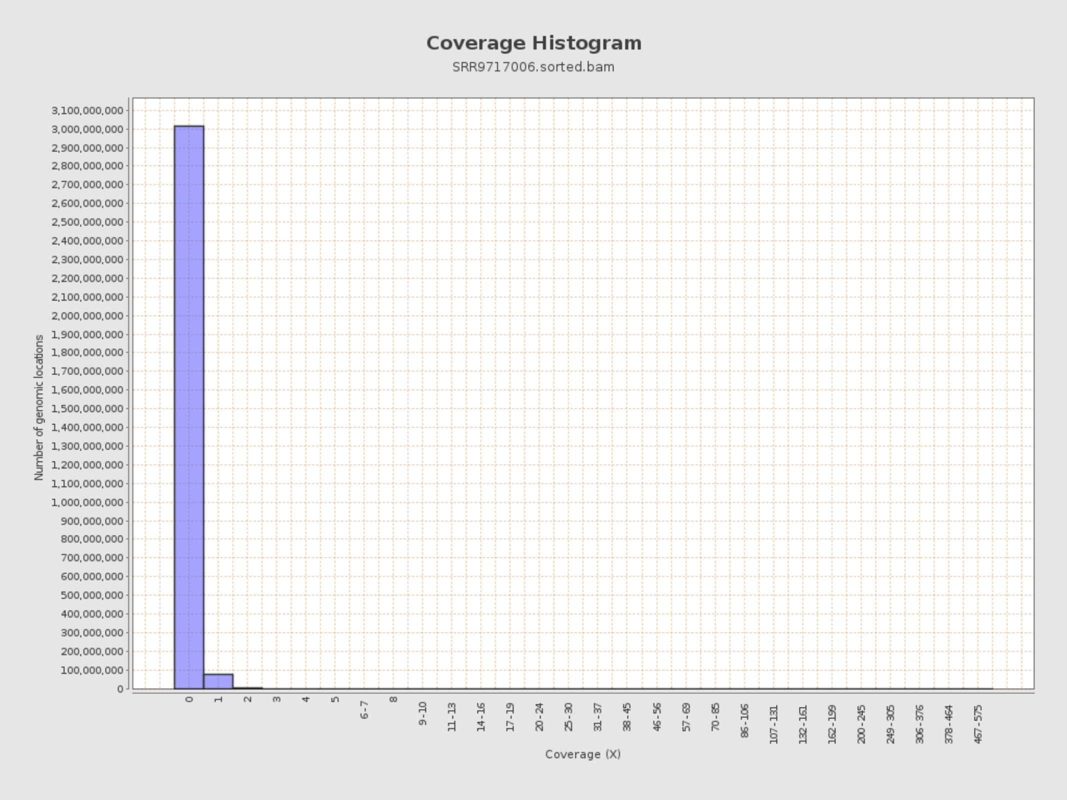
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7579296	0.0304	0.4841
chr2	243199373	7891772	0.0324	0.2773
chr3	198022430	6160838	0.0311	0.1931
chr4	191154276	5926167	0.031	0.21
chr5	180915260	5601507	0.031	0.1942
chr6	171115067	5301624	0.031	0.205
chr7	159138663	5016000	0.0315	0.2695

chr8	146364022	4724924	0.0323	0.2585
chr9	141213431	3930699	0.0278	0.2475
chr10	135534747	4417630	0.0326	0.2456
chr11	135006516	4230838	0.0313	0.2464
chr12	133851895	4212591	0.0315	0.1982
chr13	115169878	2915678	0.0253	0.173
chr14	107349540	2825414	0.0263	0.1846
chr15	102531392	2729910	0.0266	0.1783
chr16	90354753	2758432	0.0305	0.2082
chr17	81195210	2589625	0.0319	0.2068
chr18	78077248	2504132	0.0321	0.4721
chr19	59128983	1889708	0.032	0.321
chr20	63025520	2040727	0.0324	0.2031
chr21	48129895	1247700	0.0259	0.1933
chr22	51304566	1150039	0.0224	0.1638
chrMT	16571	9389	0.5666	0.9098
chrX	155270560	5193846	0.0335	0.2291
chrY	59373566	278366	0.0047	0.1166

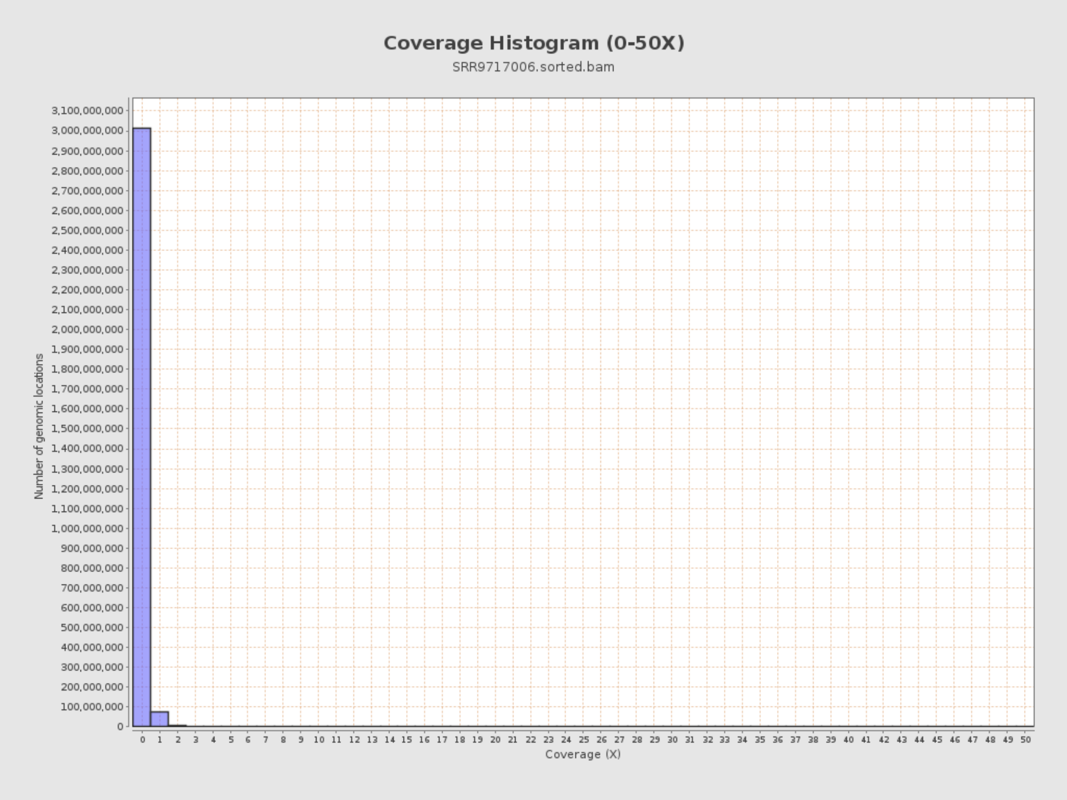
3. Results : Coverage across reference



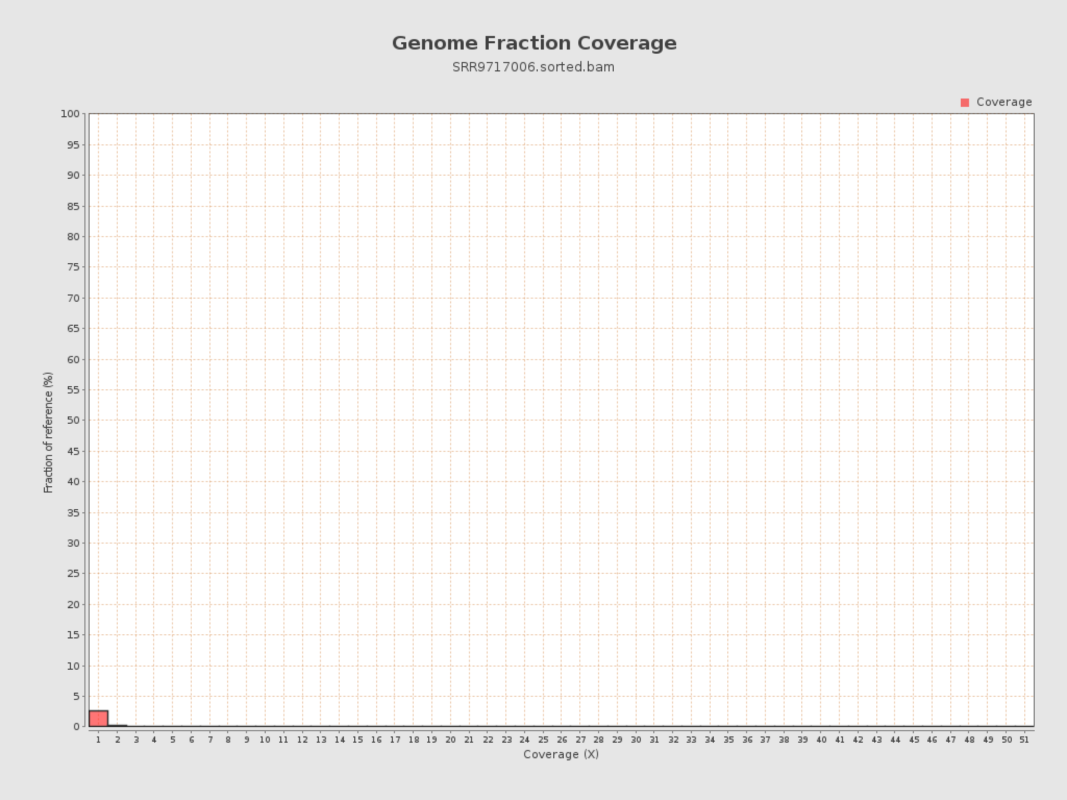
4. Results : Coverage Histogram



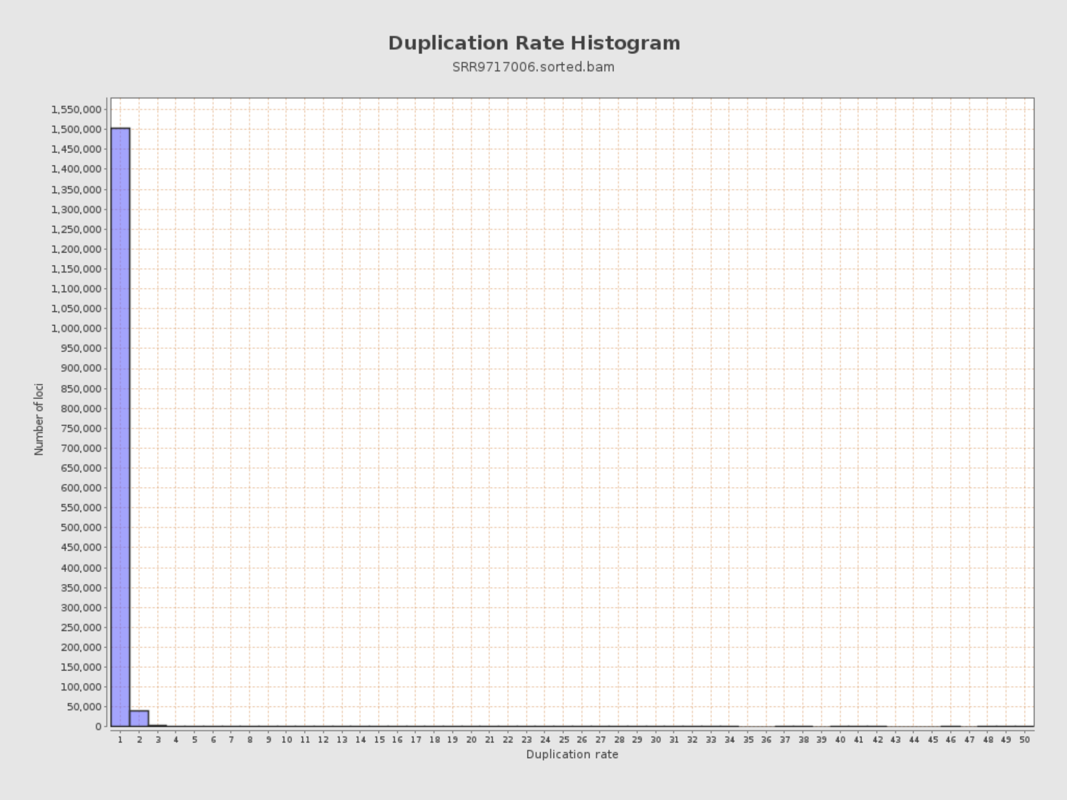
5. Results : Coverage Histogram (0-50X)



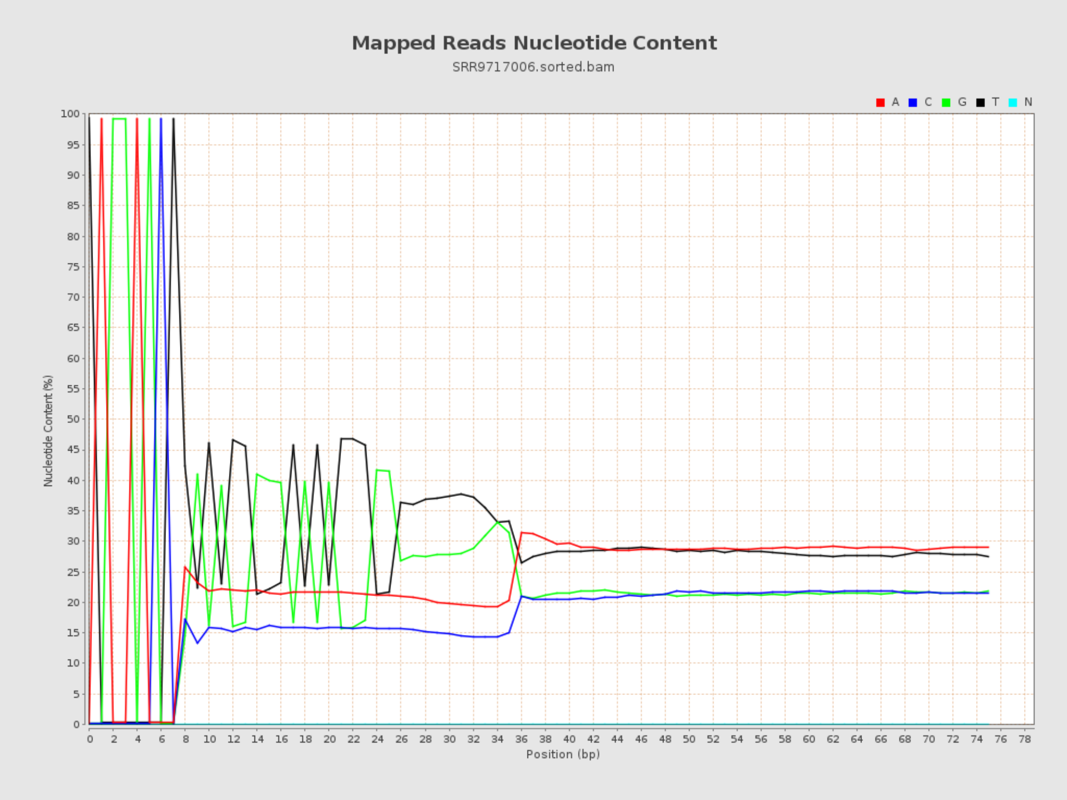
6. Results : Genome Fraction Coverage



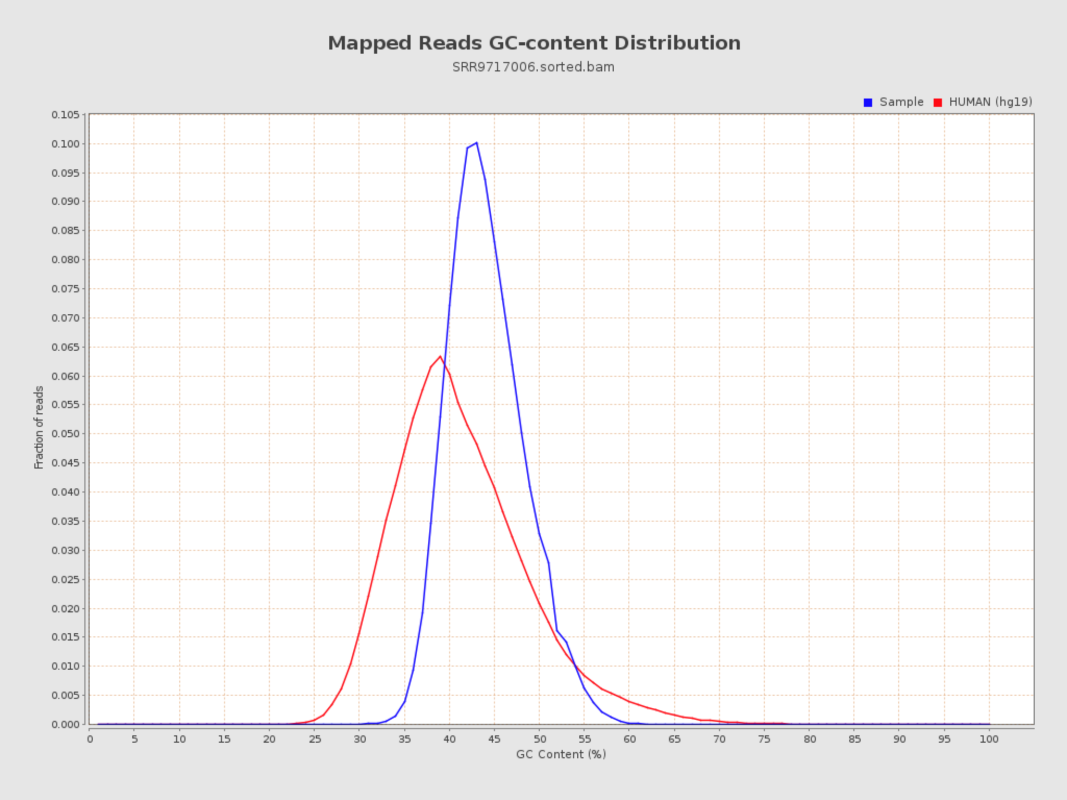
7. Results : Duplication Rate Histogram



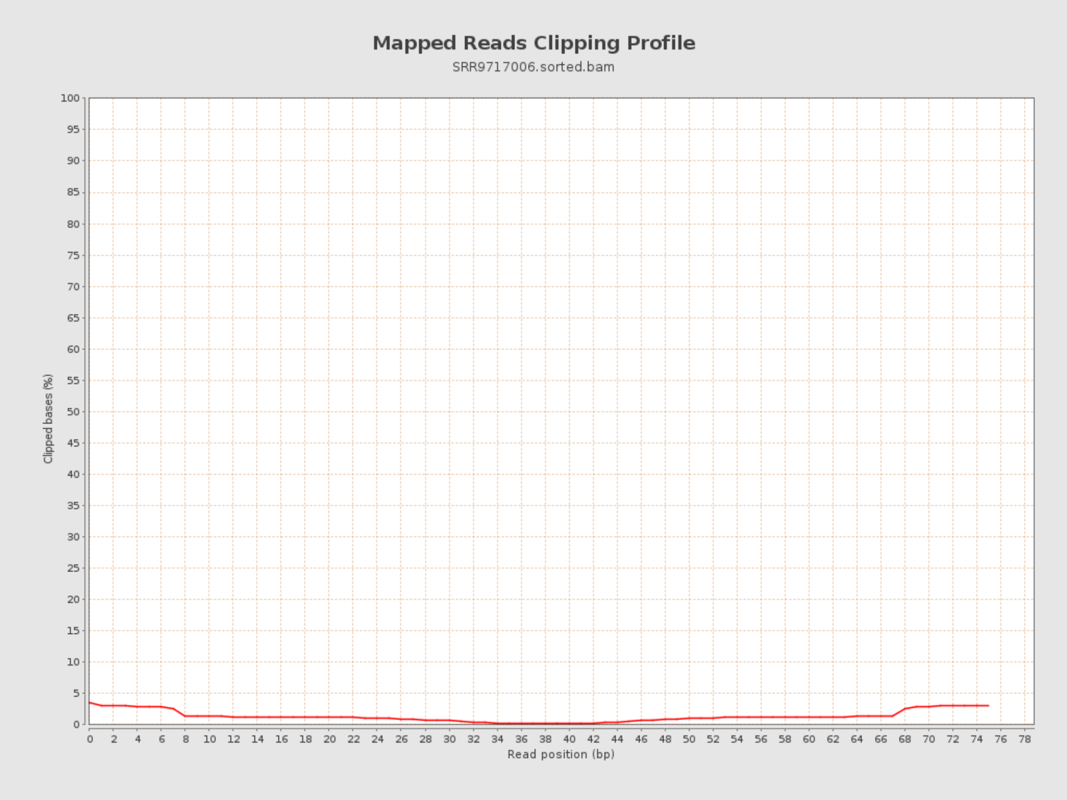
8. Results : Mapped Reads Nucleotide Content



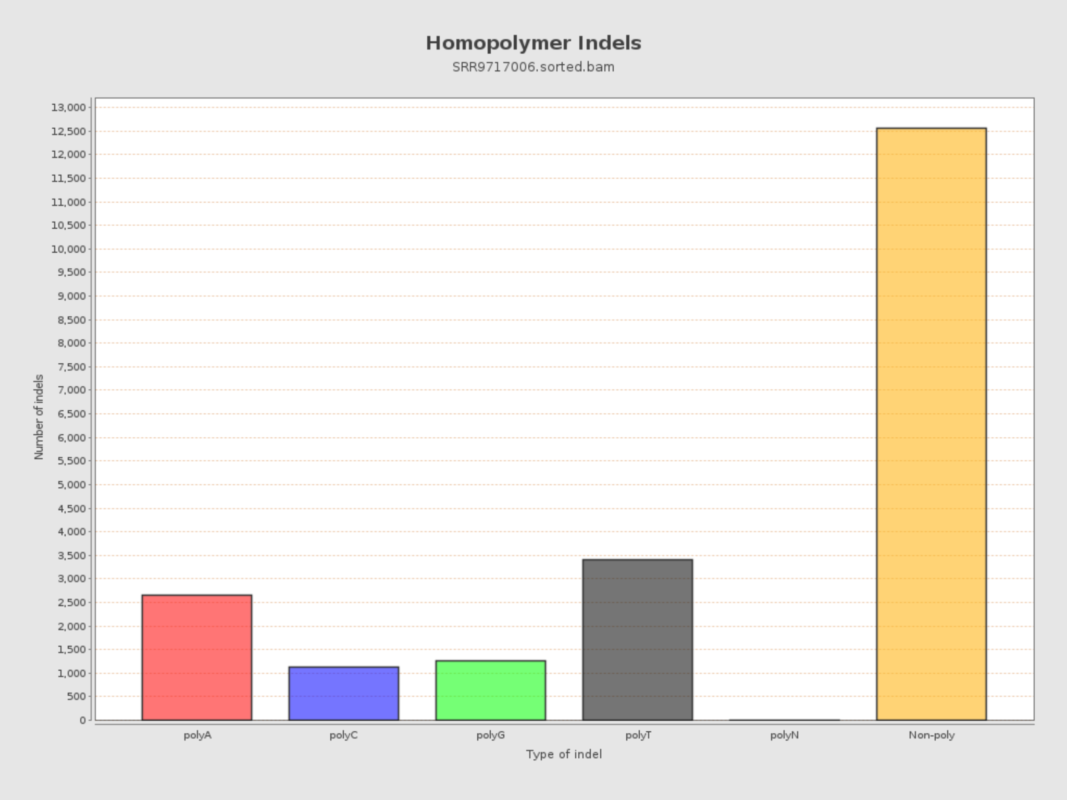
9. Results : Mapped Reads GC-content Distribution



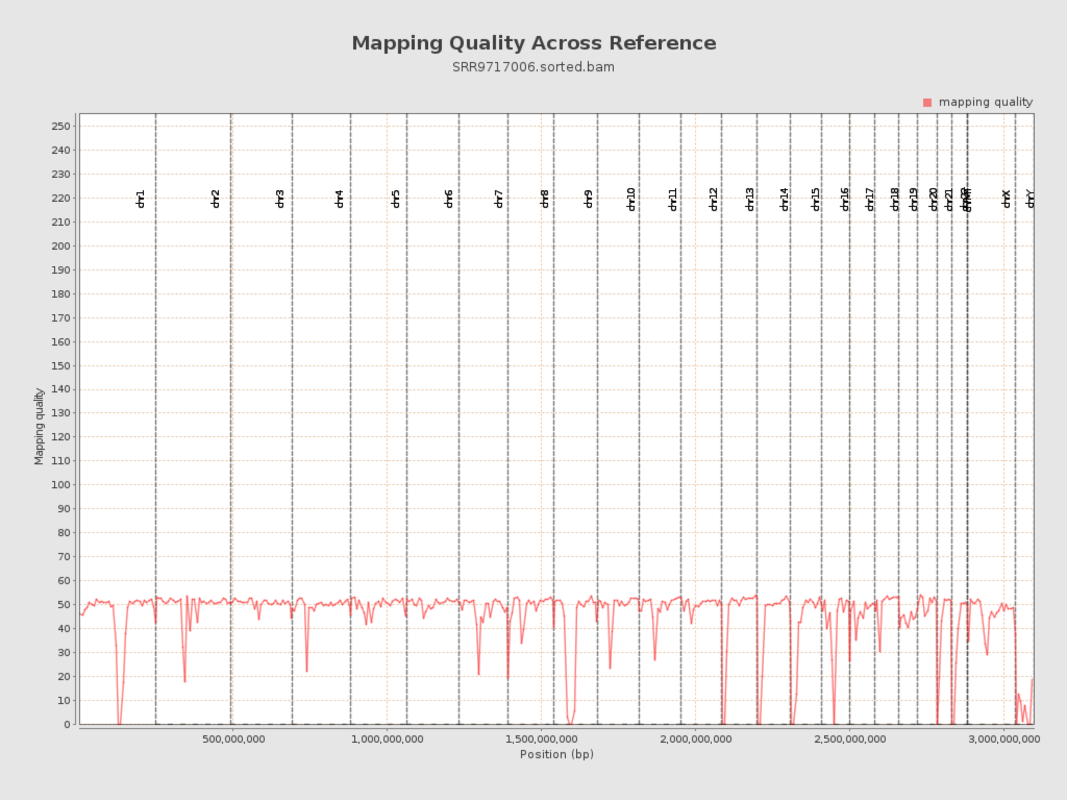
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram