Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 21:58:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8751221.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_SRR8751221 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8751221.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 21:58:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8751221.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,069,643
Mapped reads	6,954,978 / 98.38%
Unmapped reads	114,665 / 1.62%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	128,445 / 1.82%
Read min/max/mean length	30 / 101 / 101.75
Duplicated reads (estimated)	136,713 / 1.93%
Duplication rate	1.76%
Clipped reads	1,348,821 / 19.08%

2.2. ACGT Content

Number/percentage of A's	199,038,232 / 29.42%
Number/percentage of C's	139,765,938 / 20.66%
Number/percentage of T's	200,781,163 / 29.68%
Number/percentage of G's	136,838,773 / 20.23%
Number/percentage of N's	3,670 / 0%
GC Percentage	40.89%

2.3. Coverage

Mean	0.2186

Standard Deviation	0.6778

2.4. Mapping Quality

Mean Mapping Quality	51.66

2.5. Mismatches and indels

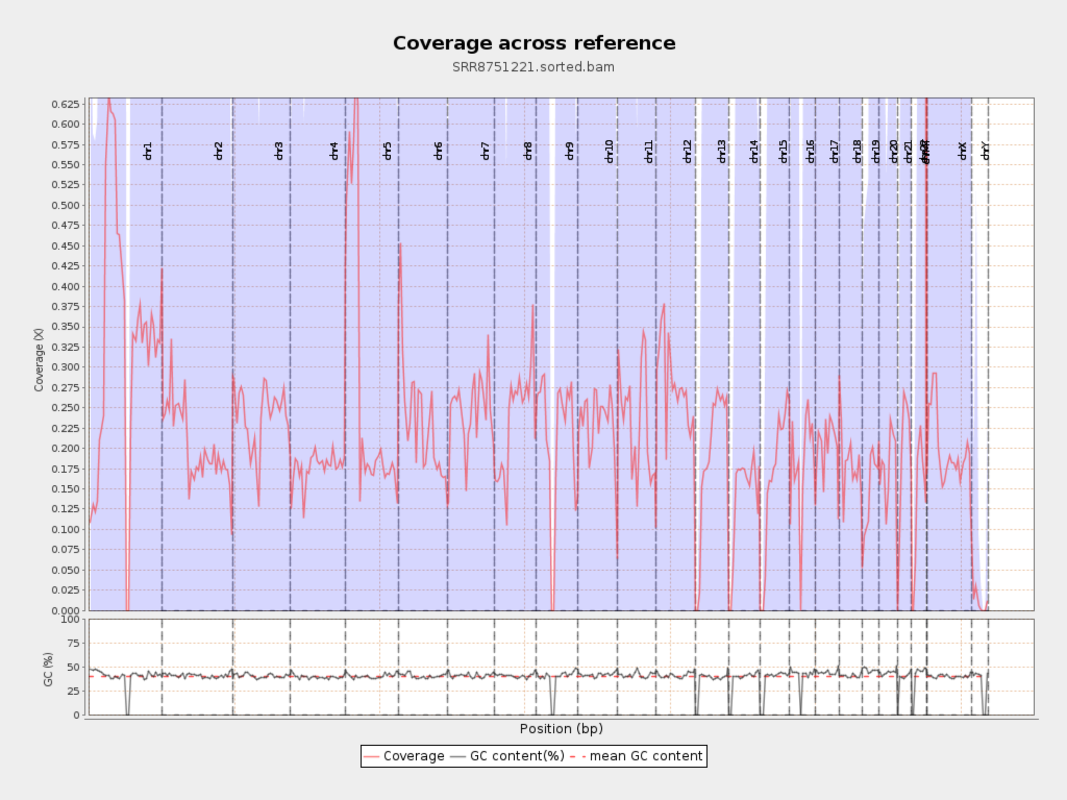
General error rate	0.29%
Mismatches	1,839,908
Insertions	71,306
Mapped reads with at least one insertion	1.01%
Deletions	75,135
Mapped reads with at least one deletion	1.06%
Homopolymer indels	46.29%

2.6. Chromosome stats

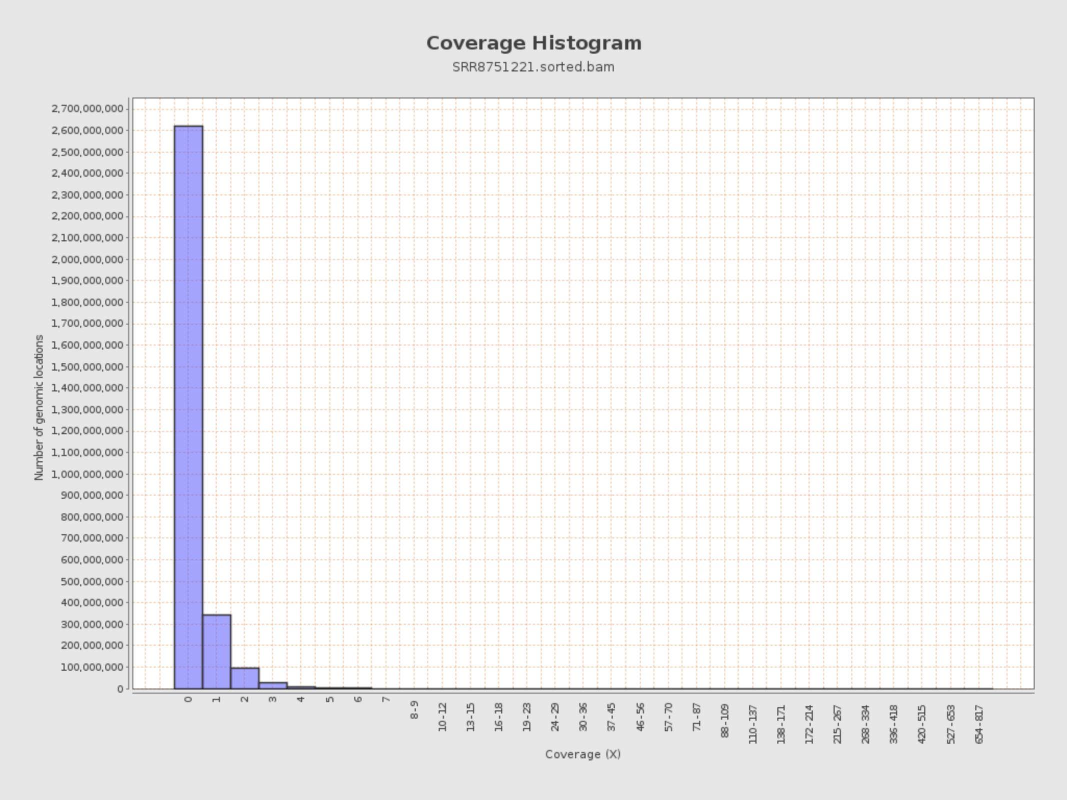
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	82686762	0.3317	1.0708
chr2	243199373	49515281	0.2036	0.5697
chr3	198022430	47422328	0.2395	0.6122
chr4	191154276	33807213	0.1769	0.5264
chr5	180915260	50608636	0.2797	0.6983
chr6	171115067	40225391	0.2351	0.6802
chr7	159138663	39408386	0.2476	0.6399

chr8	146364022	34752425	0.2374	0.6194
chr9	141213431	30091191	0.2131	0.5938
chr10	135534747	31924907	0.2355	0.7521
chr11	135006516	31182766	0.231	0.6294
chr12	133851895	37196750	0.2779	0.6676
chr13	115169878	21506511	0.1867	0.5472
chr14	107349540	14786098	0.1377	0.4679
chr15	102531392	16743792	0.1633	0.514
chr16	90354753	16226834	0.1796	0.5423
chr17	81195210	16404366	0.202	0.6161
chr18	78077248	14150222	0.1812	0.6146
chr19	59128983	8740409	0.1478	0.7726
chr20	63025520	11077396	0.1758	0.5316
chr21	48129895	8996719	0.1869	0.5625
chr22	51304566	6594950	0.1285	0.4616
chrMT	16571	1079603	65.1501	33.586
chrX	155270560	30715965	0.1978	0.5641
chrY	59373566	745308	0.0126	0.2225

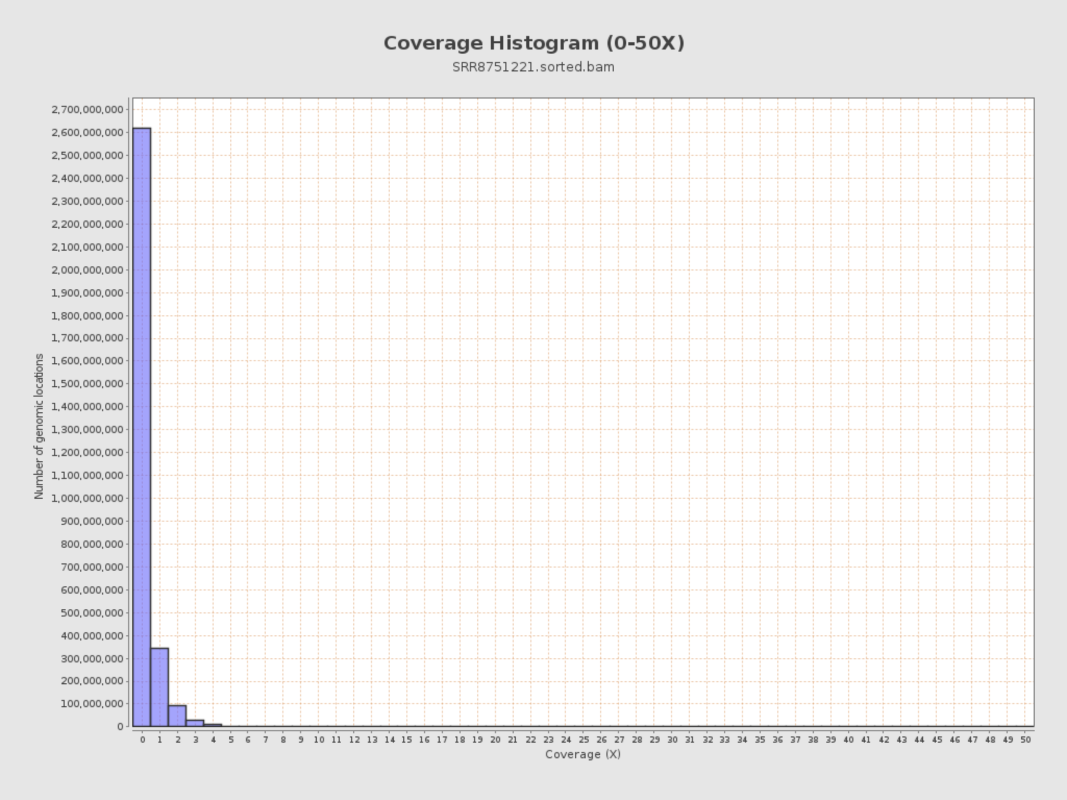
3. Results : Coverage across reference



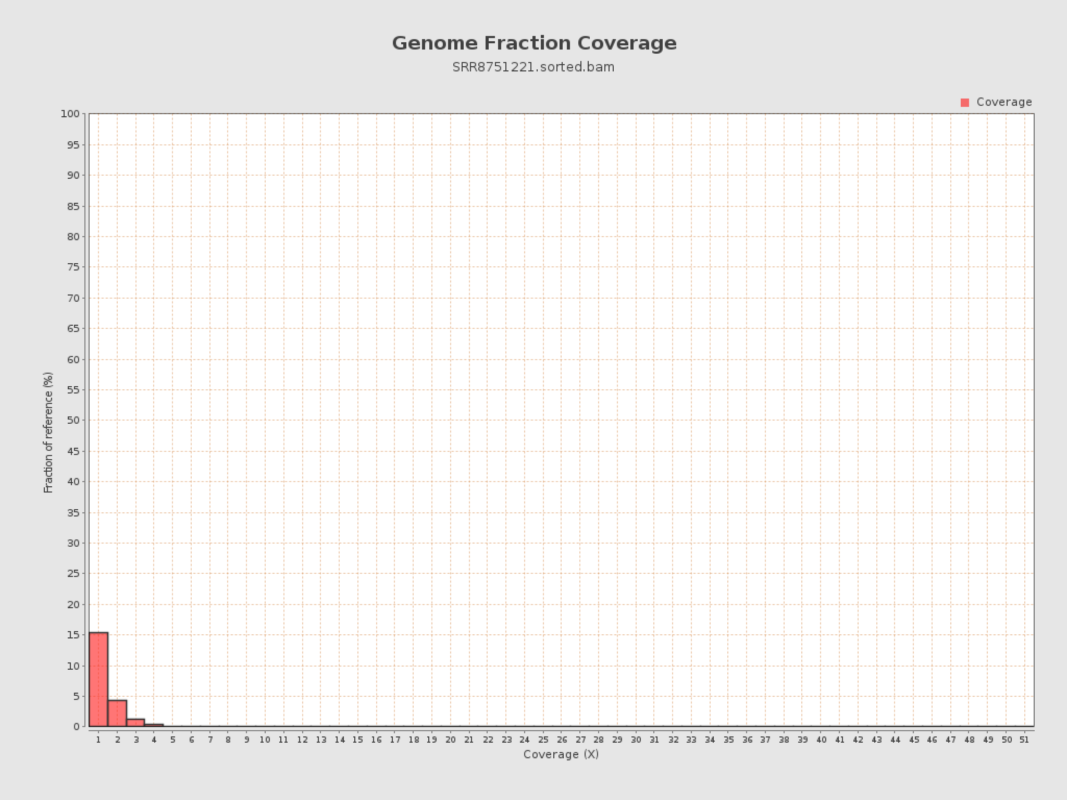
4. Results : Coverage Histogram



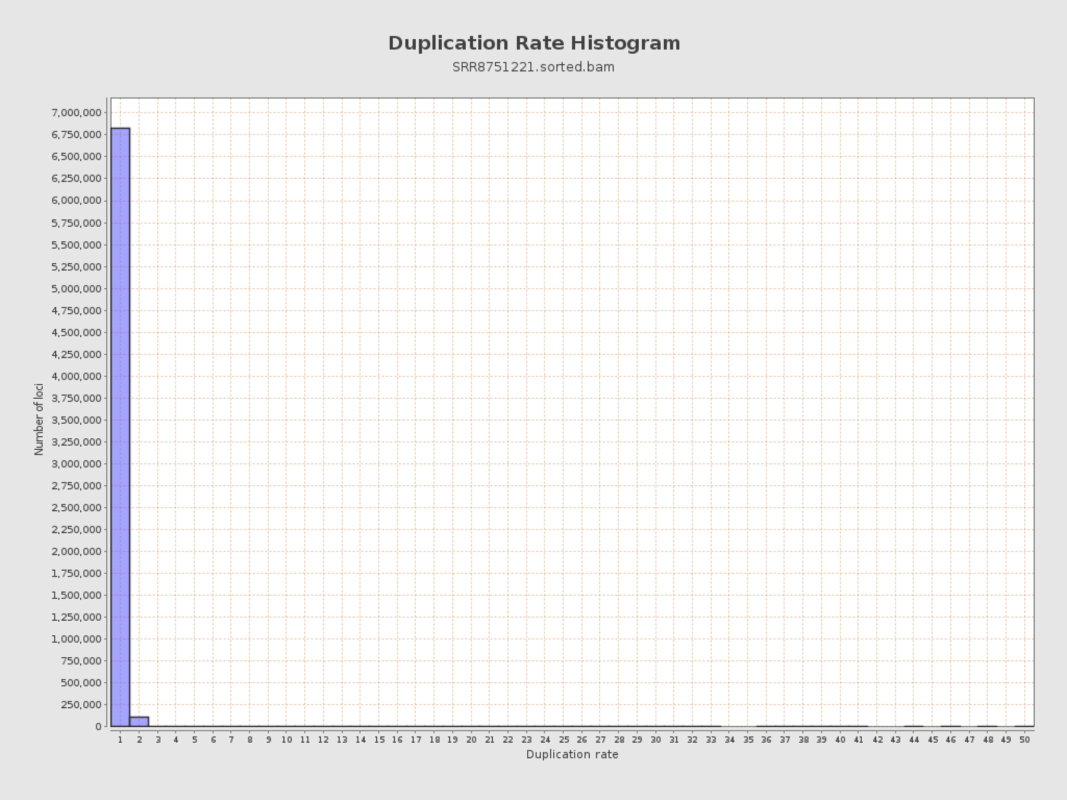
5. Results : Coverage Histogram (0-50X)



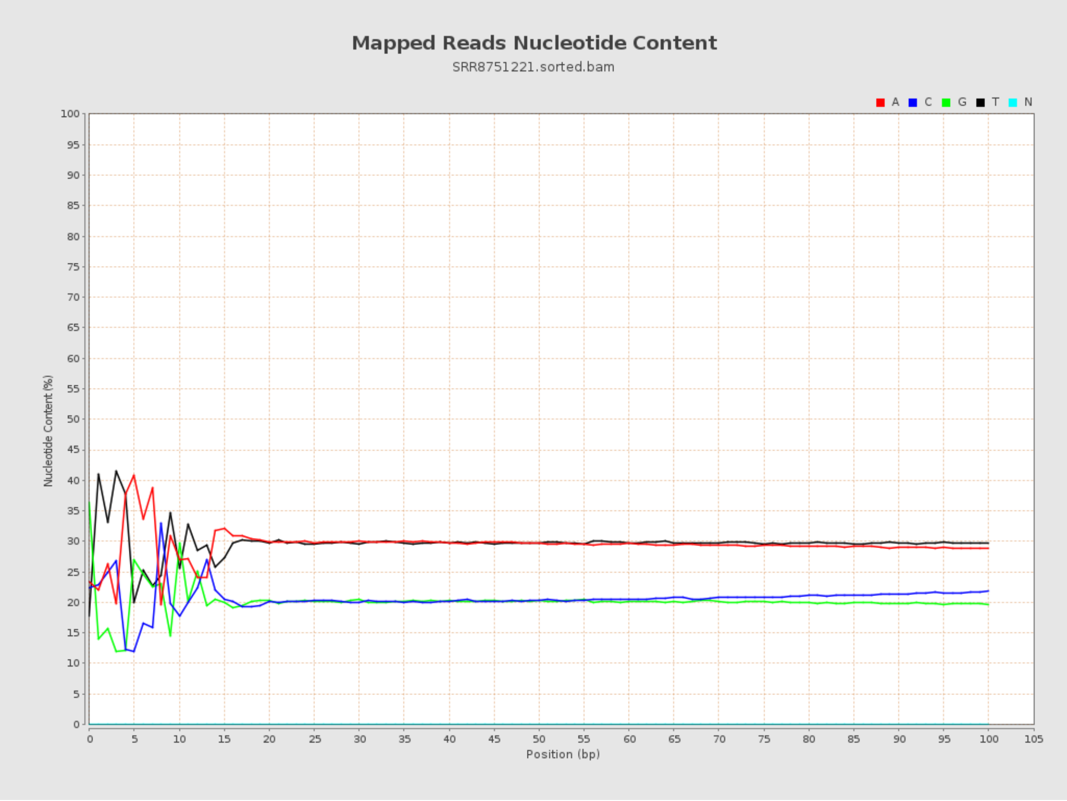
6. Results : Genome Fraction Coverage



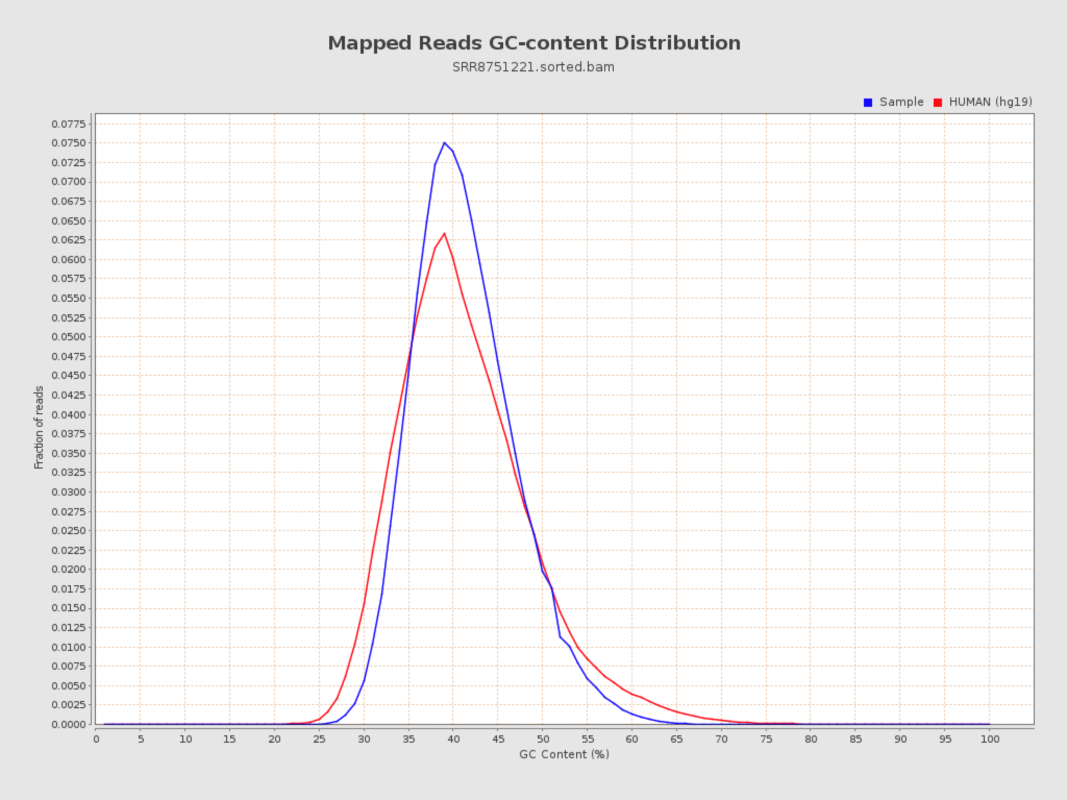
7. Results : Duplication Rate Histogram



8. Results : Mapped Reads Nucleotide Content

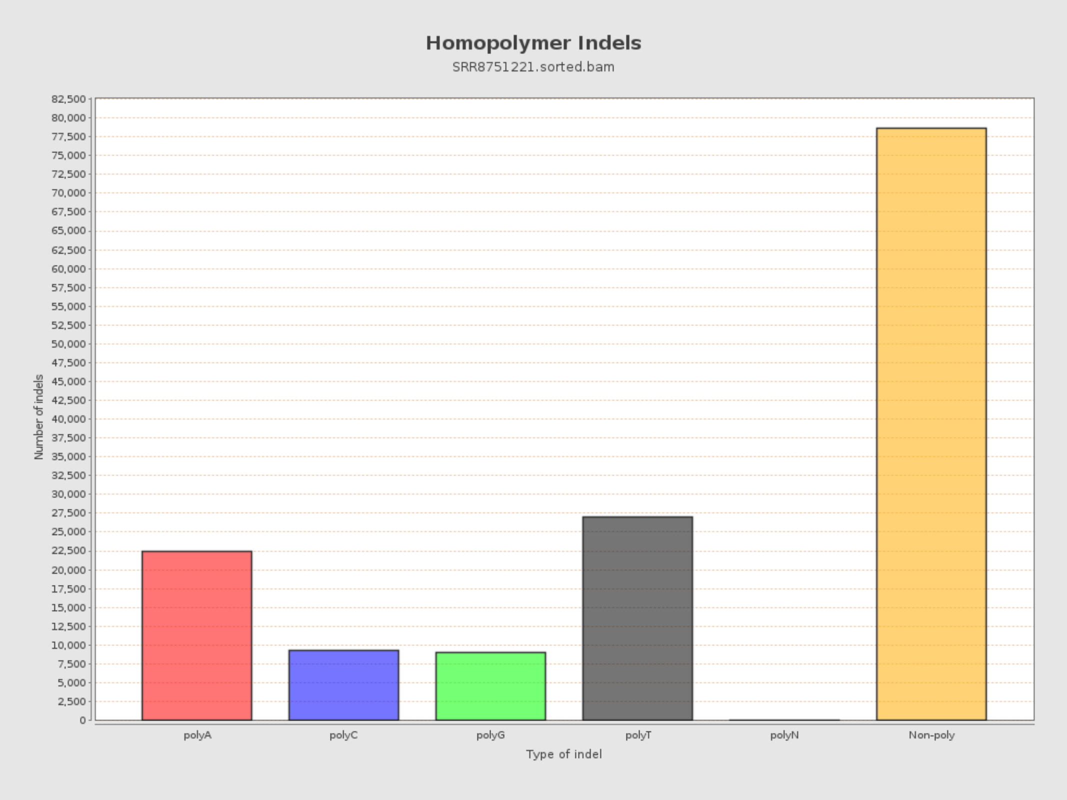


9. Results : Mapped Reads GC-content Distribution

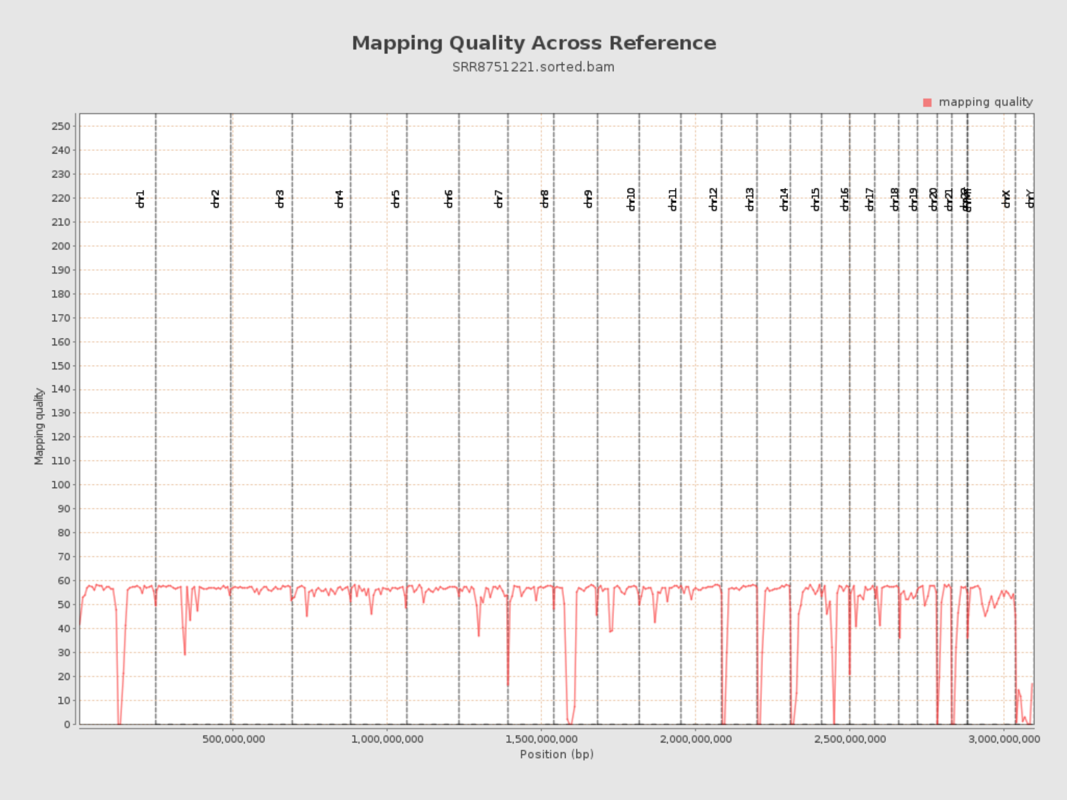


10. Results : Mapped Reads Clipping Profile

11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram