Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 20:27:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8751208.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_SRR8751208 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8751208.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 20:27:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8751208.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,779,653
Mapped reads	5,390,986 / 93.28%
Unmapped reads	388,667 / 6.72%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	325,210 / 5.63%
Read min/max/mean length	30 / 101 / 103.31
Duplicated reads (estimated)	220,844 / 3.82%
Duplication rate	2.09%
Clipped reads	1,450,835 / 25.1%

2.2. ACGT Content

Number/percentage of A's	155,935,698 / 29.6%
Number/percentage of C's	107,198,338 / 20.35%
Number/percentage of T's	156,935,499 / 29.79%
Number/percentage of G's	106,811,473 / 20.27%
Number/percentage of N's	2,790 / 0%
GC Percentage	40.62%

2.3. Coverage

Mean	0.1703

Standard Deviation	1.7785

2.4. Mapping Quality

Mean Mapping Quality	50.9

2.5. Mismatches and indels

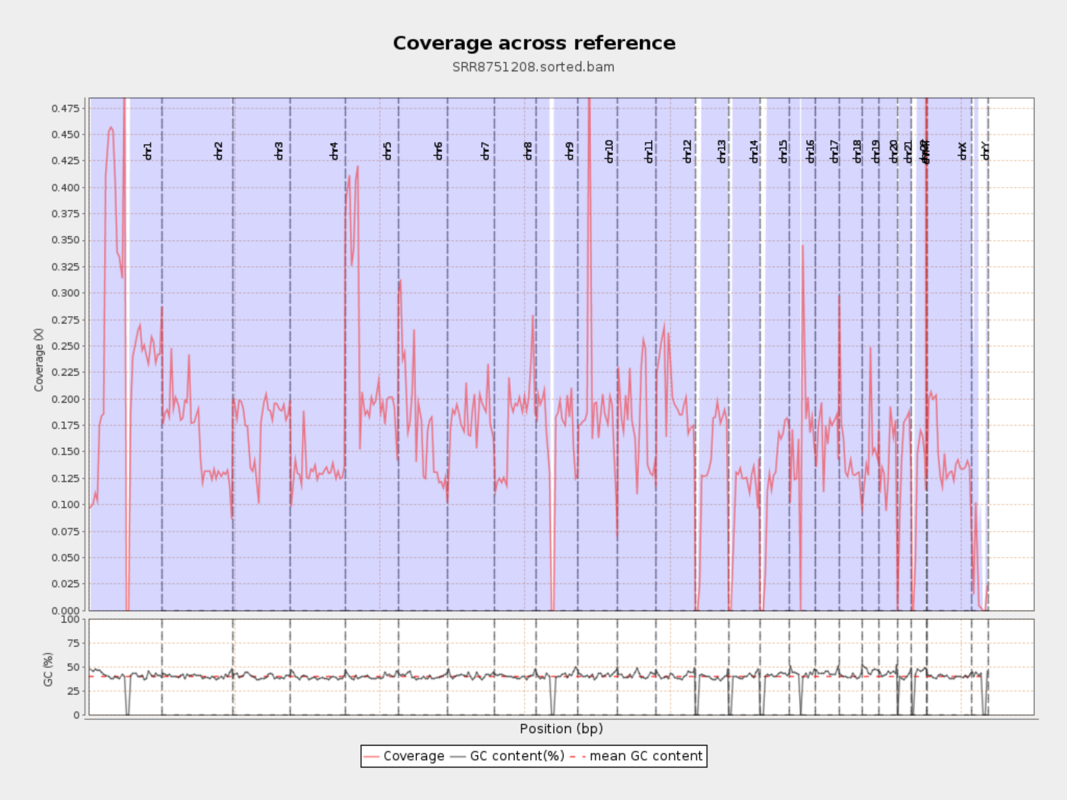
General error rate	0.56%
Mismatches	2,214,113
Insertions	520,758
Mapped reads with at least one insertion	9.16%
Deletions	87,030
Mapped reads with at least one deletion	1.58%
Homopolymer indels	54.38%

2.6. Chromosome stats

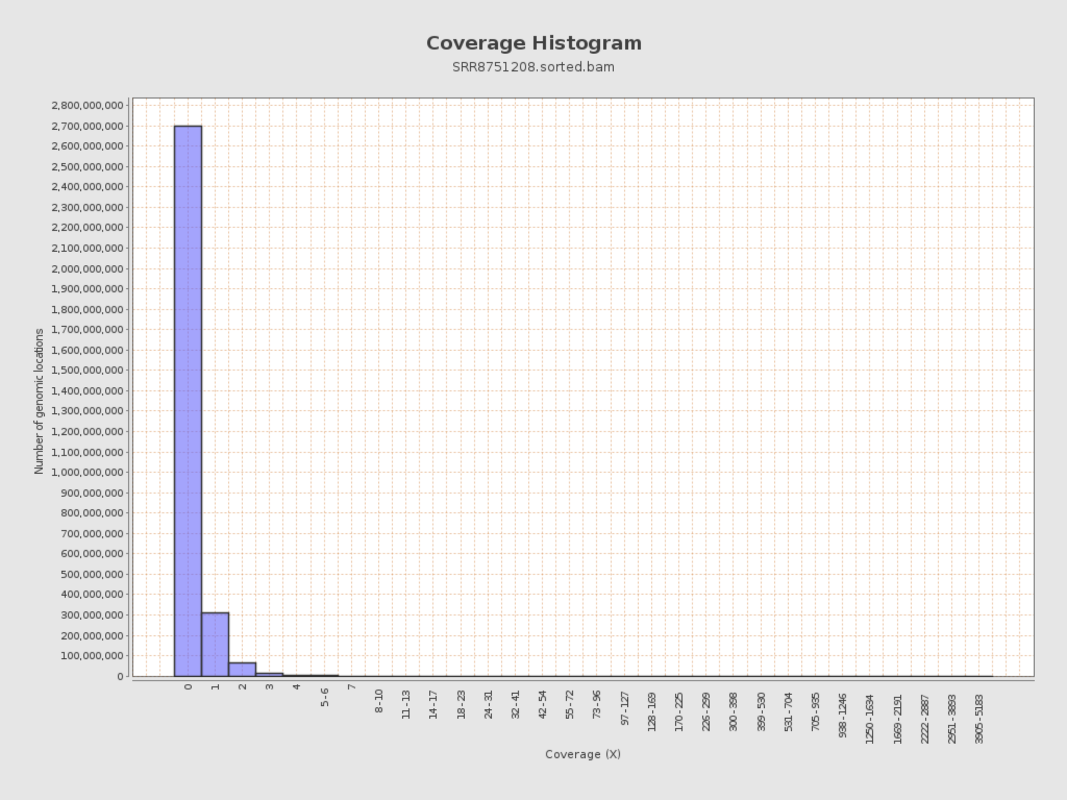
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	62914976	0.2524	4.8166
chr2	243199373	39706945	0.1633	0.8014
chr3	198022430	35080808	0.1772	0.6876
chr4	191154276	25085851	0.1312	0.6538
chr5	180915260	43432456	0.2401	0.5996
chr6	171115067	30274798	0.1769	1.2193
chr7	159138663	29353750	0.1845	1.0819

chr8	146364022	26157235	0.1787	0.6681
chr9	141213431	22797475	0.1614	0.9605
chr10	135534747	27168533	0.2005	3.2255
chr11	135006516	24109940	0.1786	0.8711
chr12	133851895	27448536	0.2051	0.554
chr13	115169878	15493669	0.1345	0.4406
chr14	107349540	11060550	0.103	0.4292
chr15	102531392	12173182	0.1187	0.41
chr16	90354753	14617853	0.1618	1.3277
chr17	81195210	13510191	0.1664	0.7823
chr18	78077248	11303364	0.1448	1.9552
chr19	59128983	8989912	0.152	3.2402
chr20	63025520	8853460	0.1405	0.4919
chr21	48129895	6704325	0.1393	0.5534
chr22	51304566	5470792	0.1066	0.3951
chrMT	16571	1162519	70.1538	22.6301
chrX	155270560	22833166	0.1471	0.5647
chrY	59373566	1366414	0.023	0.9351

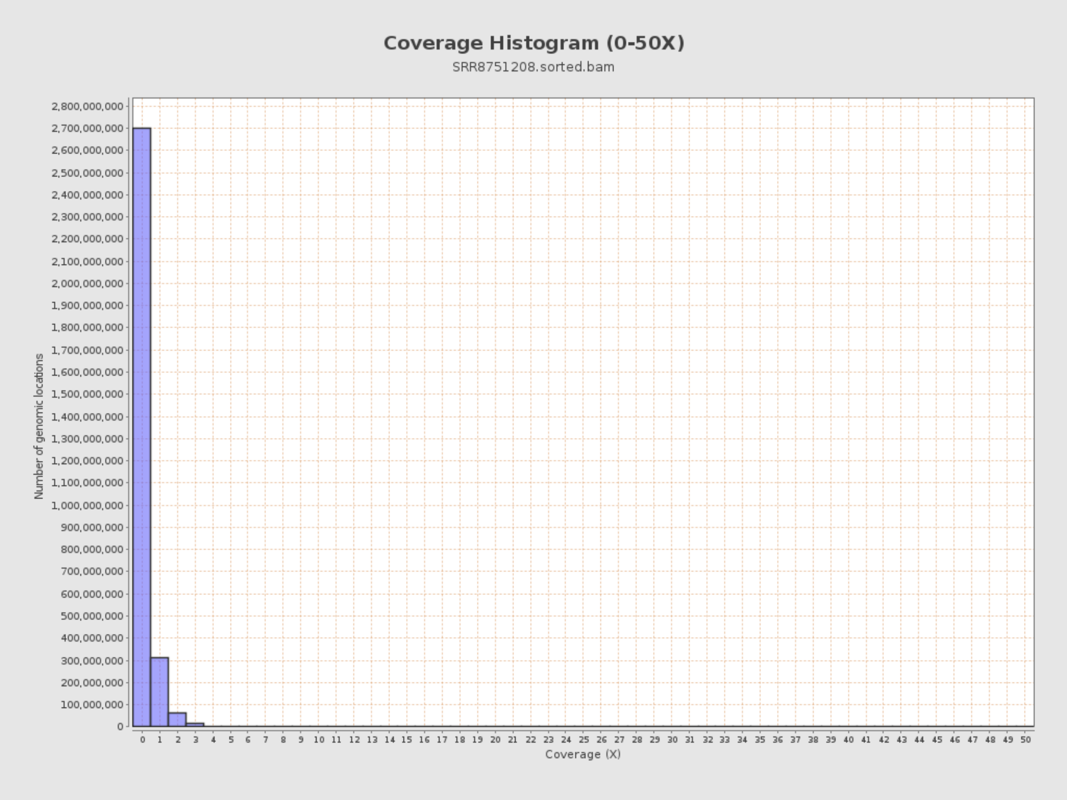
3. Results : Coverage across reference



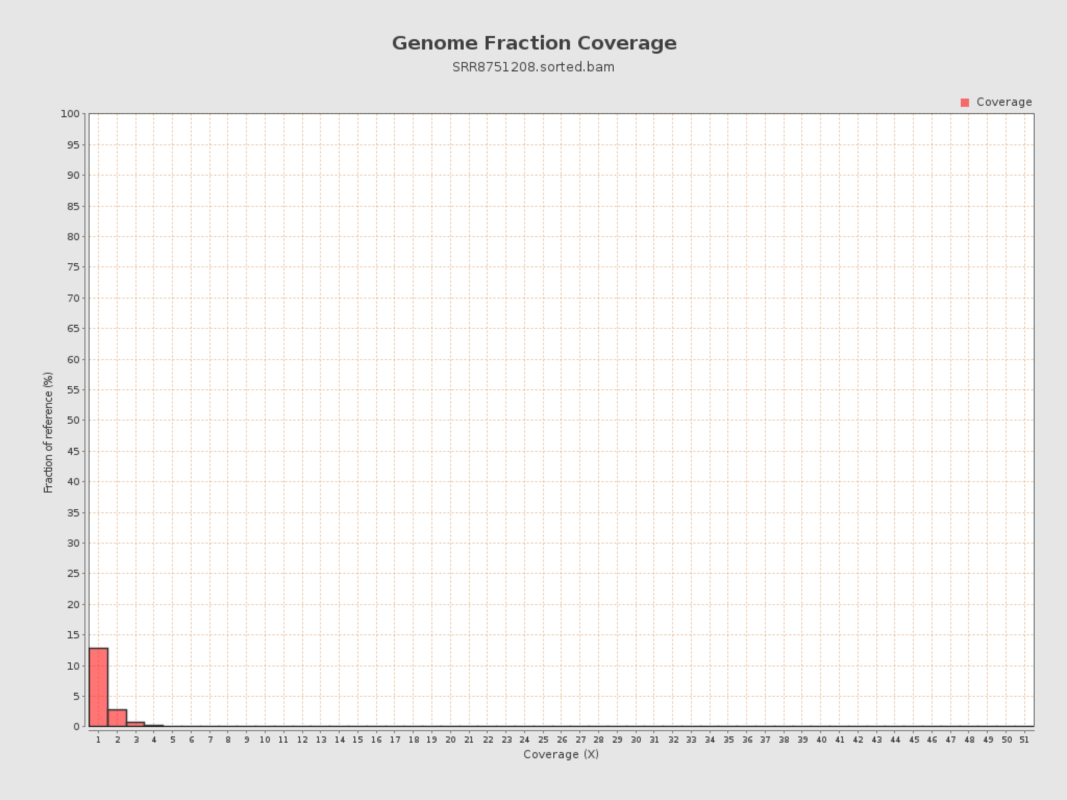
4. Results : Coverage Histogram



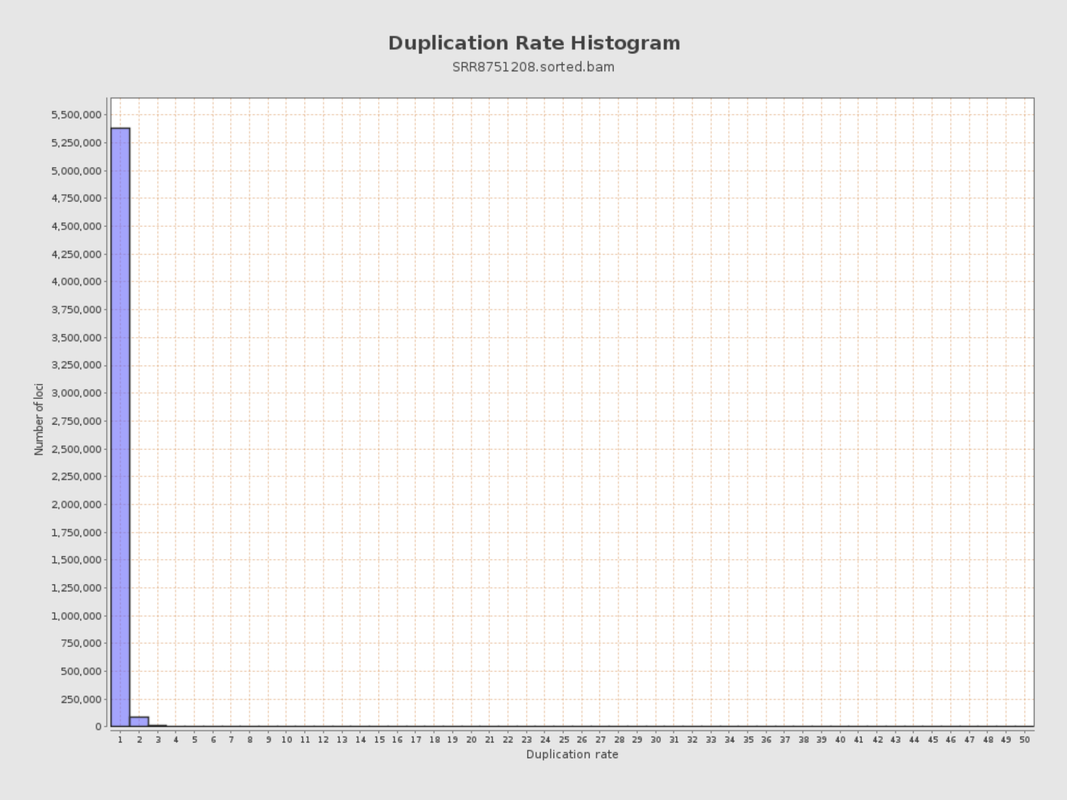
5. Results : Coverage Histogram (0-50X)



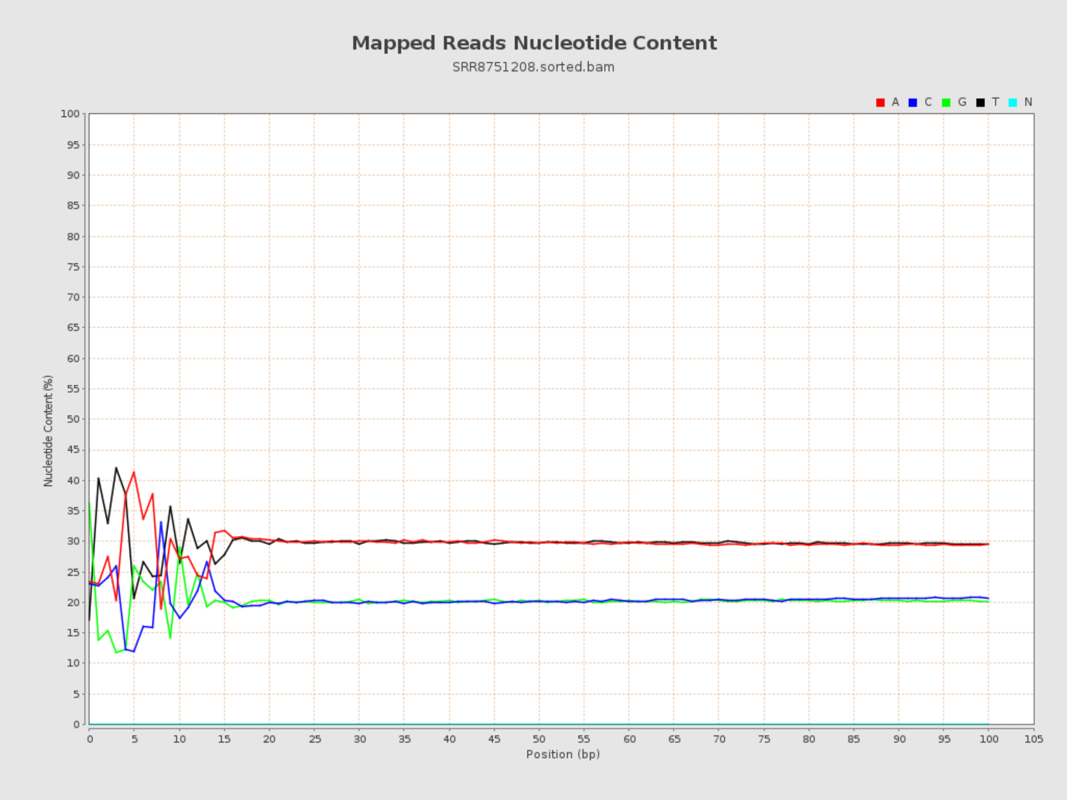
6. Results : Genome Fraction Coverage



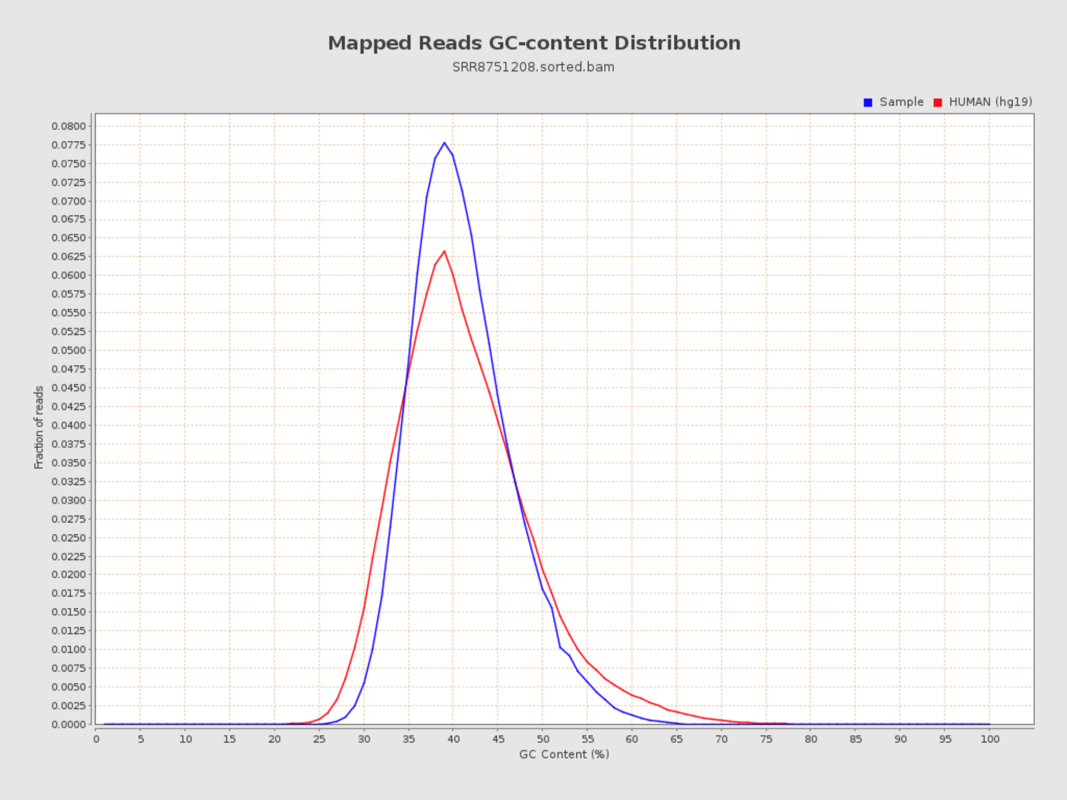
7. Results : Duplication Rate Histogram



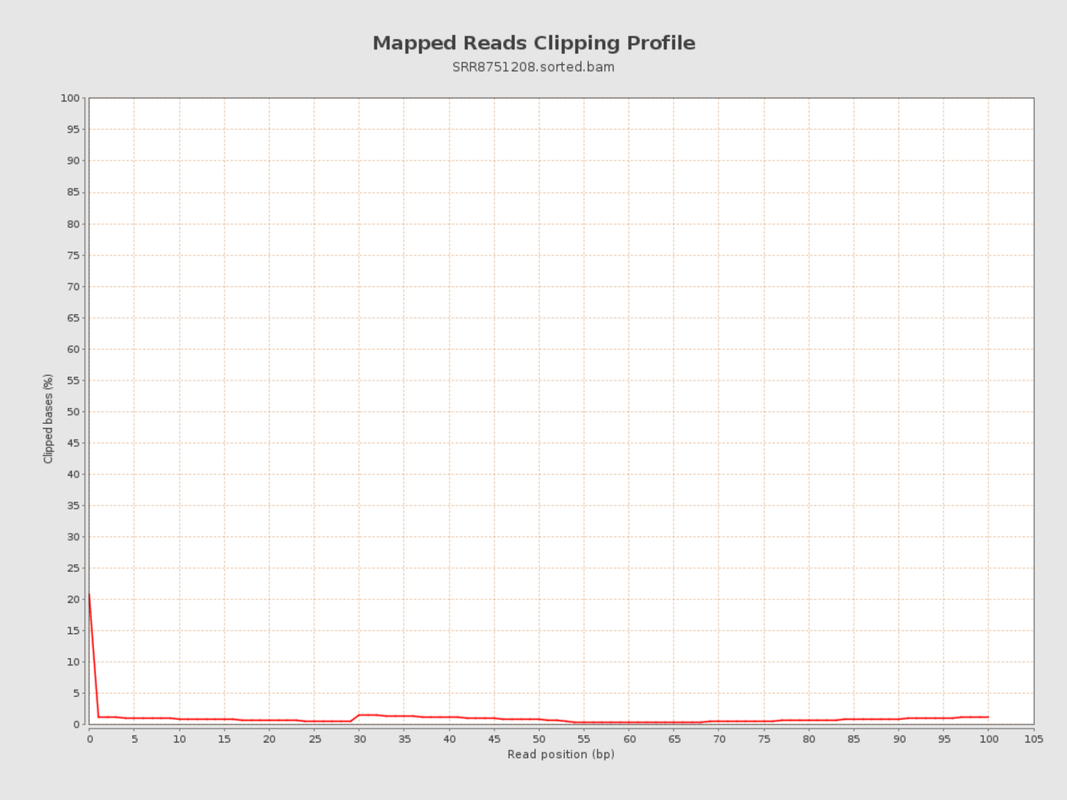
8. Results : Mapped Reads Nucleotide Content



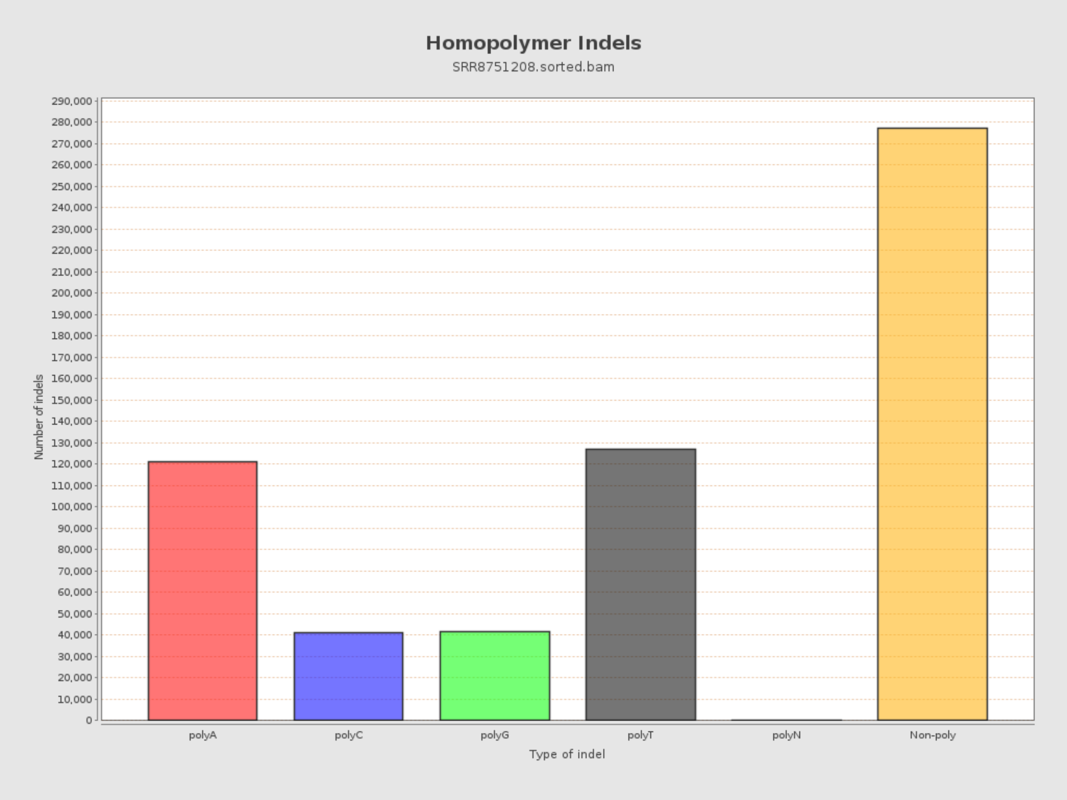
9. Results : Mapped Reads GC-content Distribution



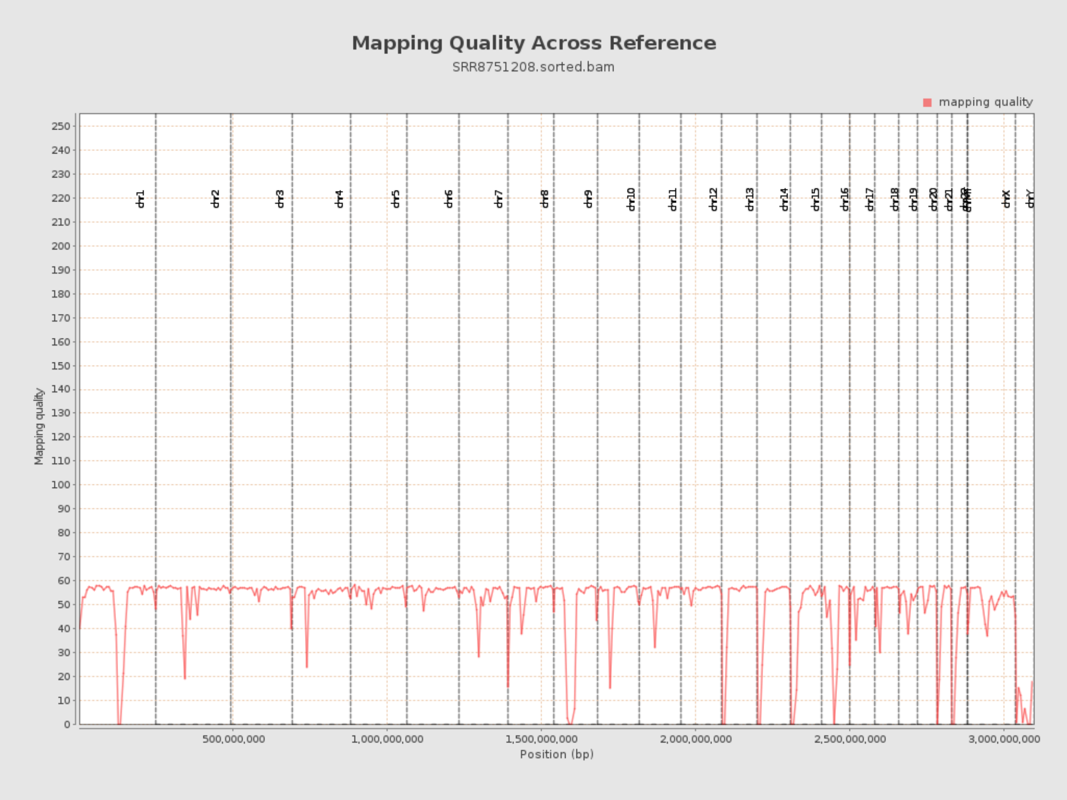
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram