Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 21:36:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8751218.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_SRR8751218 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8751218.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 21:36:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8751218.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,182,653
Mapped reads	4,995,816 / 80.8%
Unmapped reads	1,186,837 / 19.2%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	304,536 / 4.93%
Read min/max/mean length	30 / 101 / 103.03
Duplicated reads (estimated)	161,155 / 2.61%
Duplication rate	1.61%
Clipped reads	1,277,193 / 20.66%

2.2. ACGT Content

Number/percentage of A's	143,657,871 / 29.3%
Number/percentage of C's	101,339,422 / 20.67%
Number/percentage of T's	144,681,253 / 29.5%
Number/percentage of G's	100,694,637 / 20.53%
Number/percentage of N's	3,562 / 0%
GC Percentage	41.2%

2.3. Coverage

Mean	0.1585

Standard Deviation	1.4156

2.4. Mapping Quality

Mean Mapping Quality	50.85

2.5. Mismatches and indels

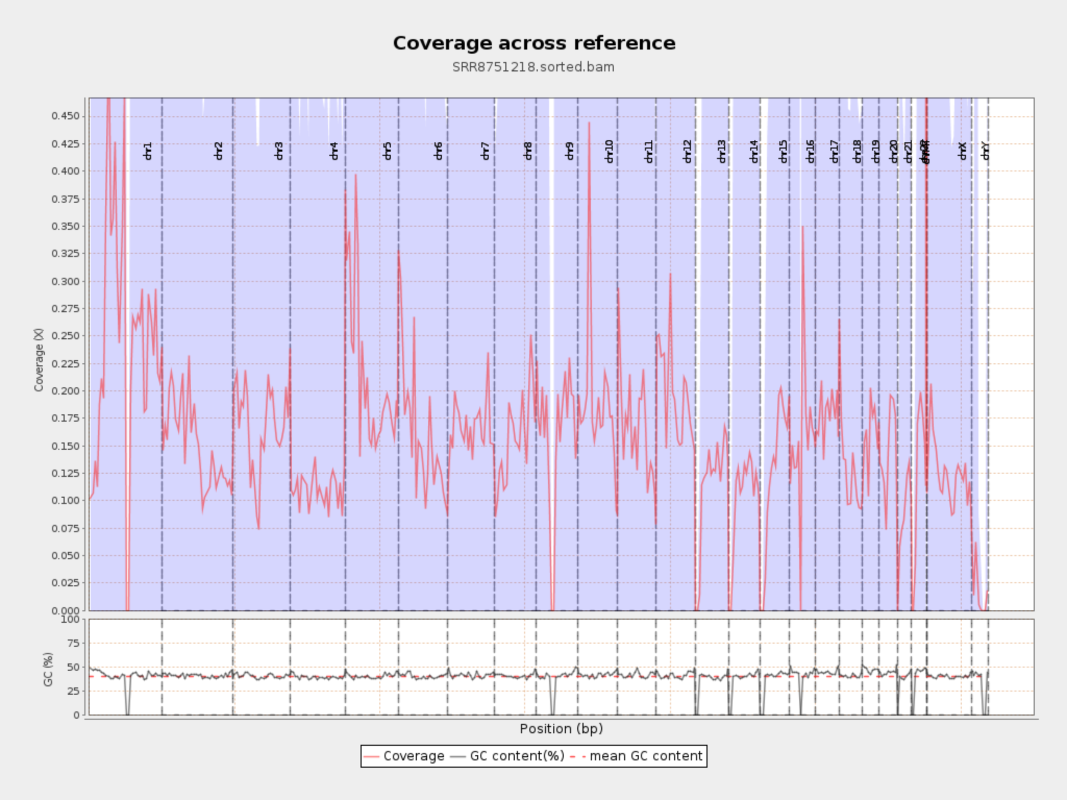
General error rate	0.48%
Mismatches	1,806,352
Insertions	427,727
Mapped reads with at least one insertion	8.16%
Deletions	76,270
Mapped reads with at least one deletion	1.5%
Homopolymer indels	53.95%

2.6. Chromosome stats

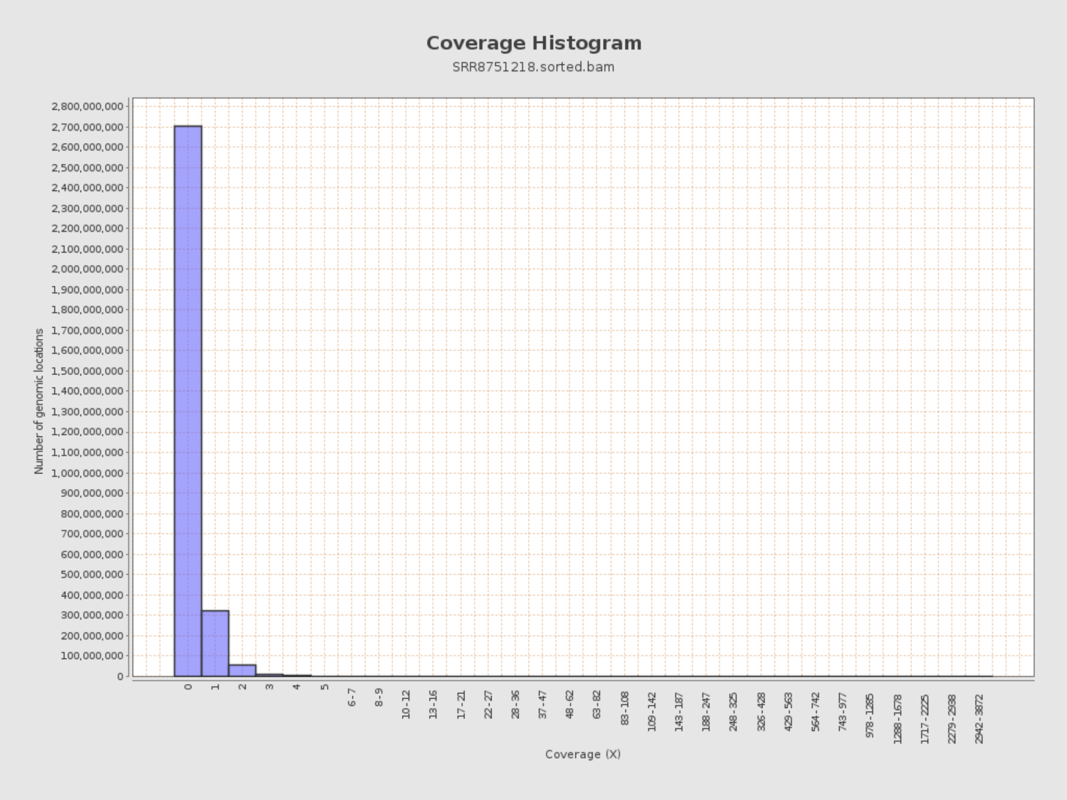
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	61058552	0.245	3.6161
chr2	243199373	36738614	0.1511	0.6876
chr3	198022430	33087304	0.1671	0.6307
chr4	191154276	21010641	0.1099	0.4436
chr5	180915260	38425293	0.2124	0.5428
chr6	171115067	27811271	0.1625	1.0378
chr7	159138663	26757925	0.1681	0.9123

chr8	146364022	23074583	0.1577	0.6169
chr9	141213431	22119349	0.1566	0.8493
chr10	135534747	25861606	0.1908	2.841
chr11	135006516	22522832	0.1668	0.7322
chr12	133851895	26784777	0.2001	0.5179
chr13	115169878	12961014	0.1125	0.3789
chr14	107349540	10871466	0.1013	0.3802
chr15	102531392	12648855	0.1234	0.3986
chr16	90354753	14159564	0.1567	1.3978
chr17	81195210	14497208	0.1785	0.7482
chr18	78077248	9972475	0.1277	1.4903
chr19	59128983	9429419	0.1595	2.5197
chr20	63025520	9088687	0.1442	0.442
chr21	48129895	4155021	0.0863	0.3812
chr22	51304566	5972069	0.1164	0.3917
chrMT	16571	1043885	62.9947	24.0495
chrX	155270560	19500511	0.1256	0.4825
chrY	59373566	986422	0.0166	0.574

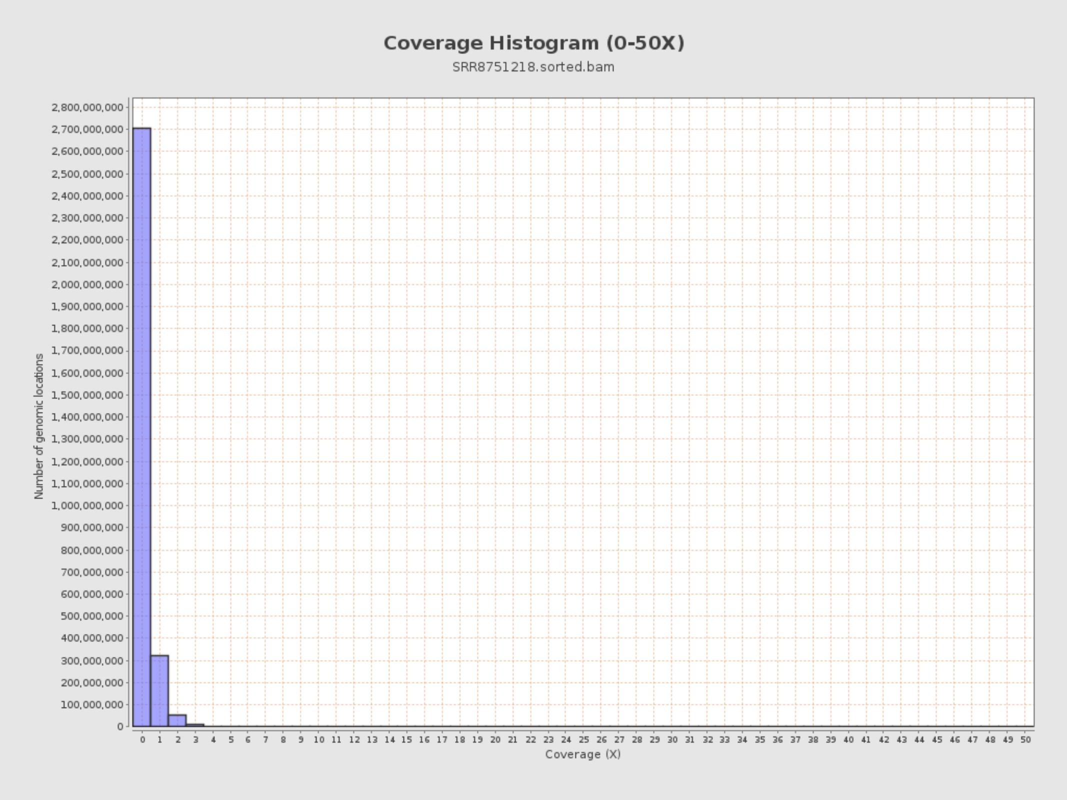
3. Results : Coverage across reference



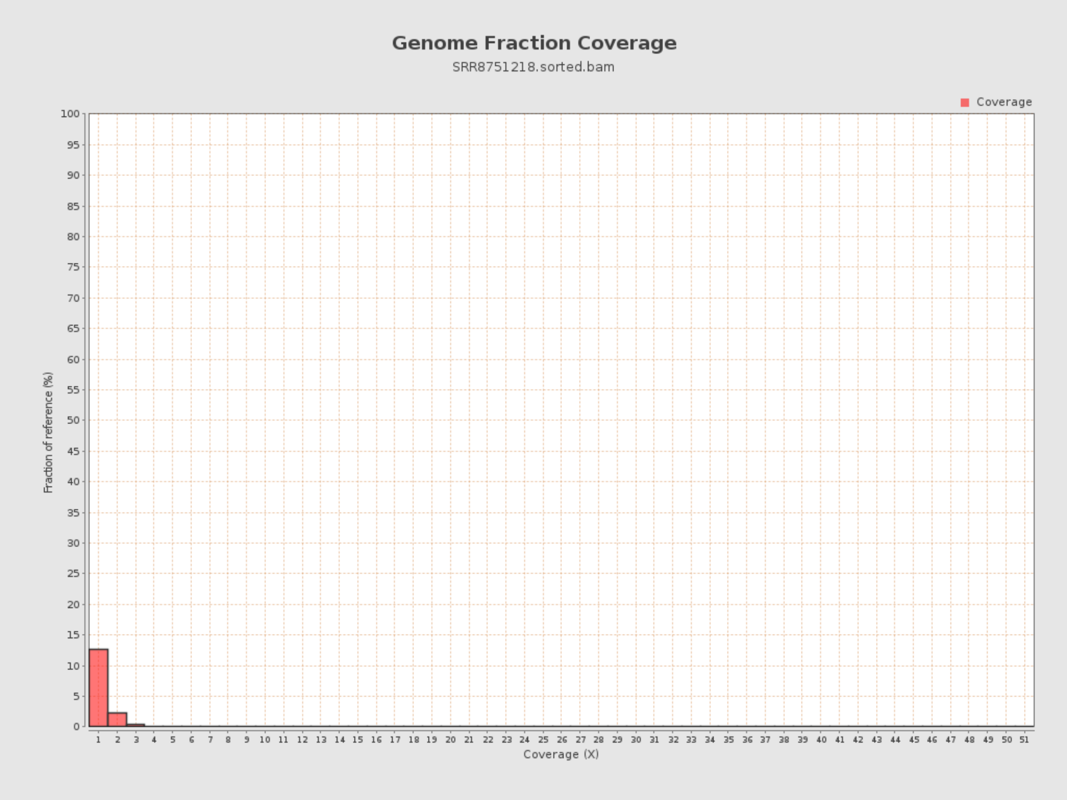
4. Results : Coverage Histogram



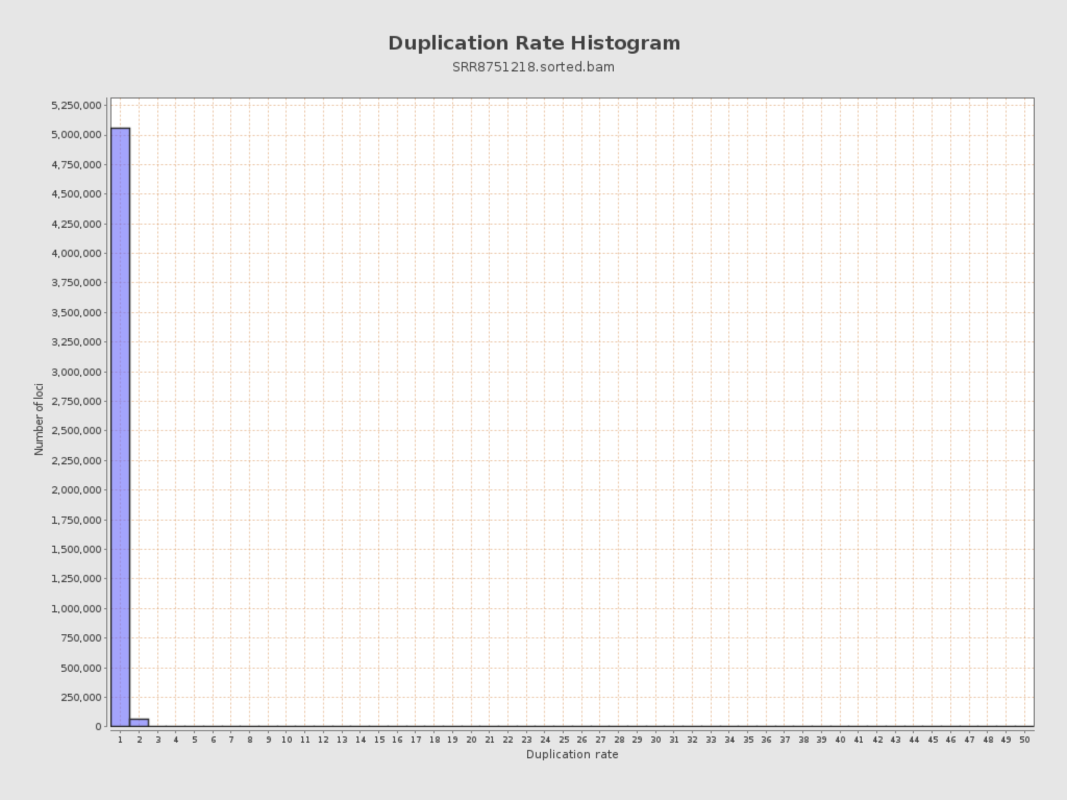
5. Results : Coverage Histogram (0-50X)



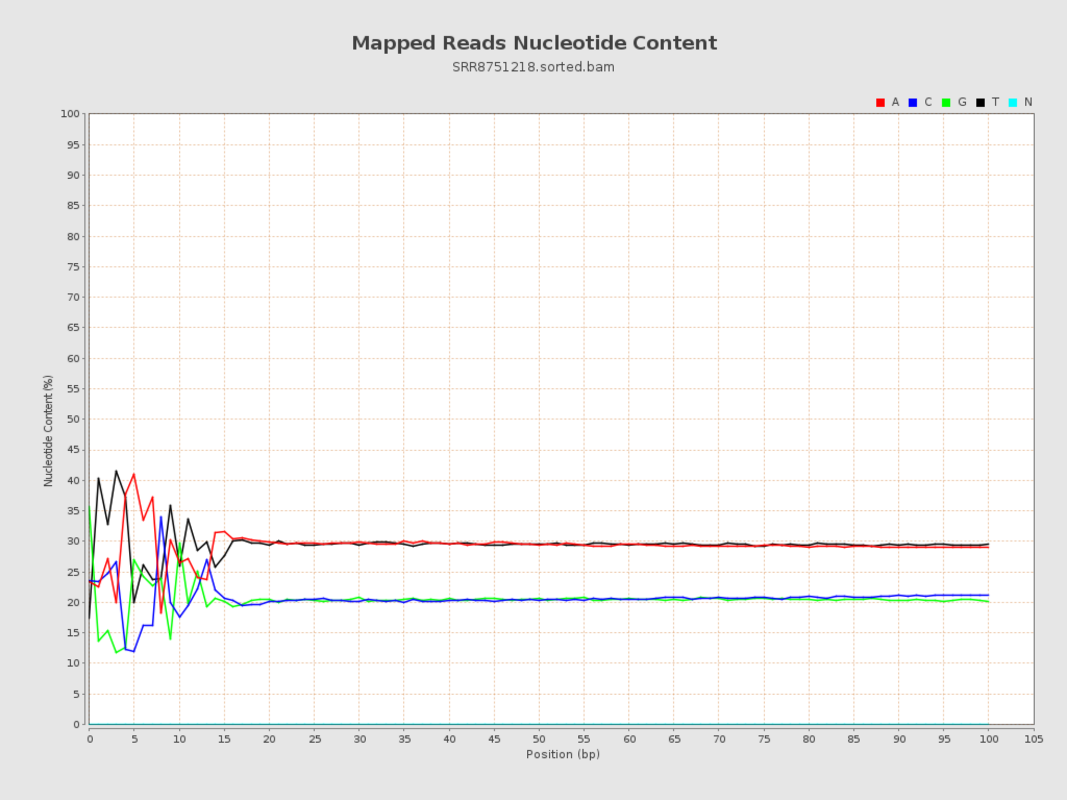
6. Results : Genome Fraction Coverage



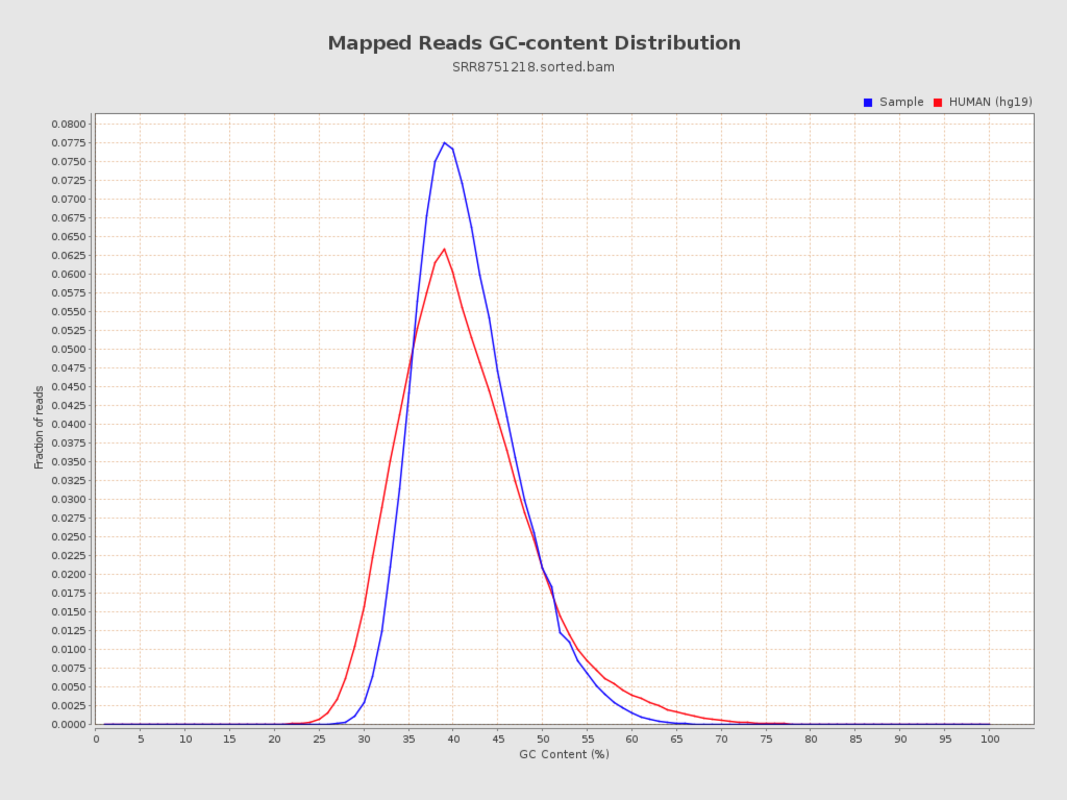
7. Results : Duplication Rate Histogram



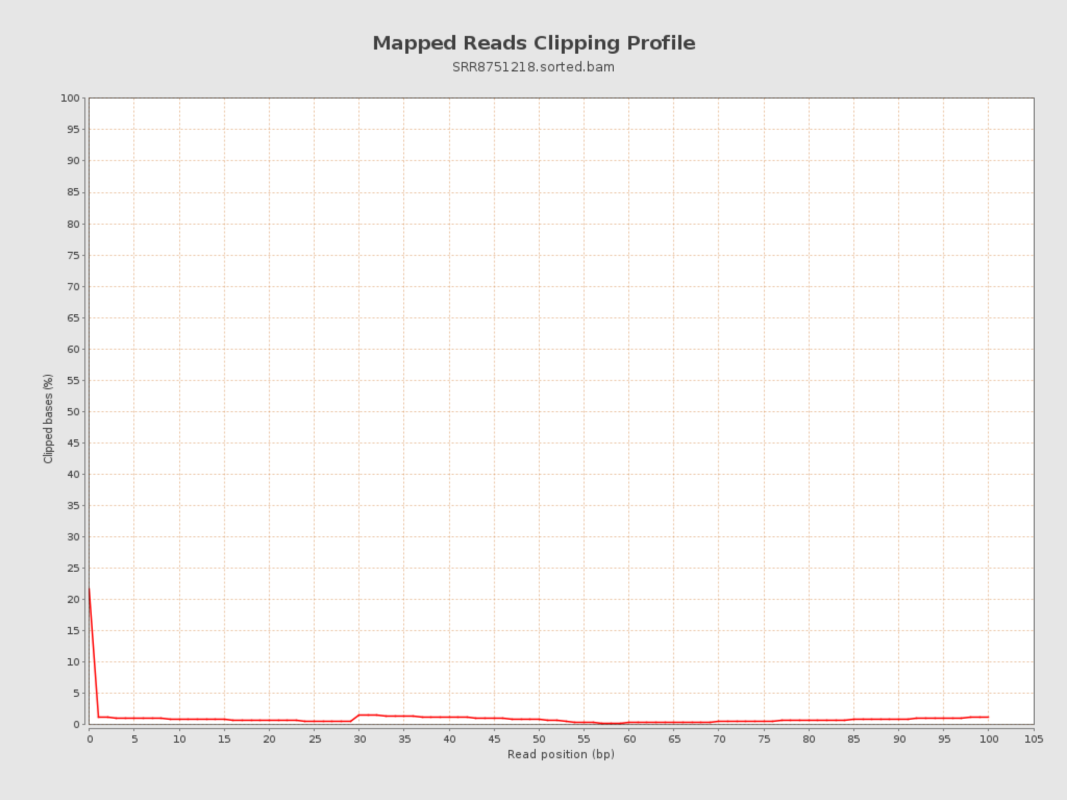
8. Results : Mapped Reads Nucleotide Content



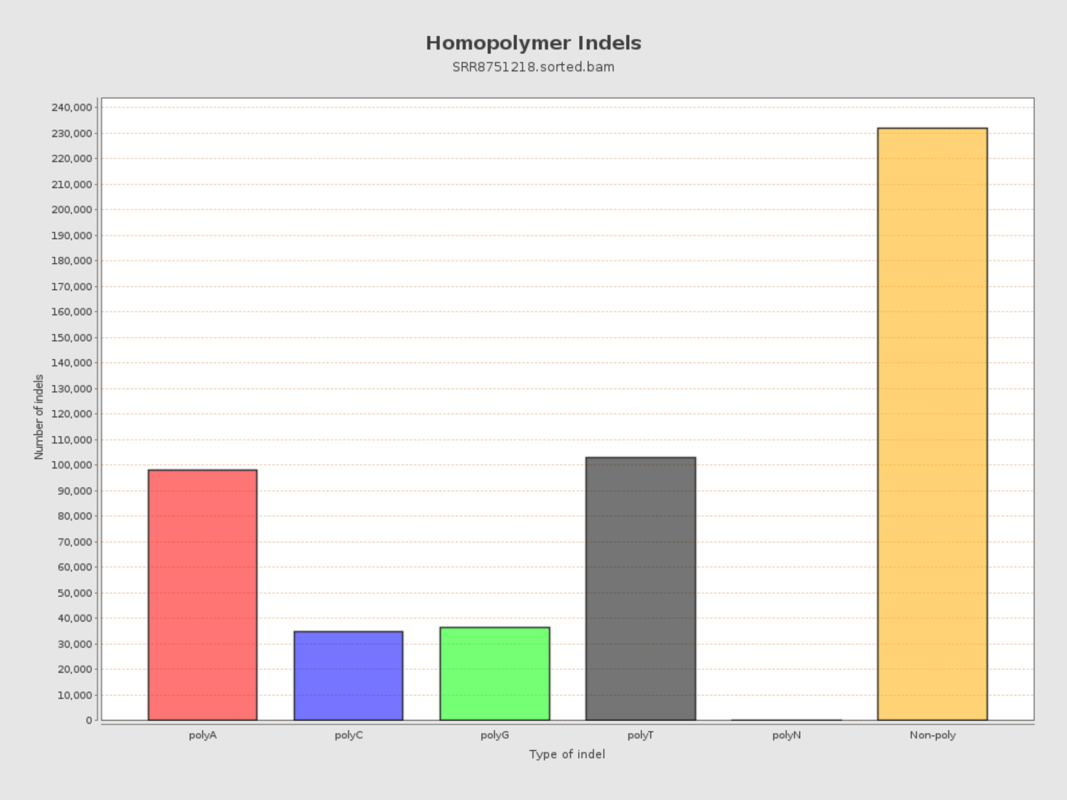
9. Results : Mapped Reads GC-content Distribution



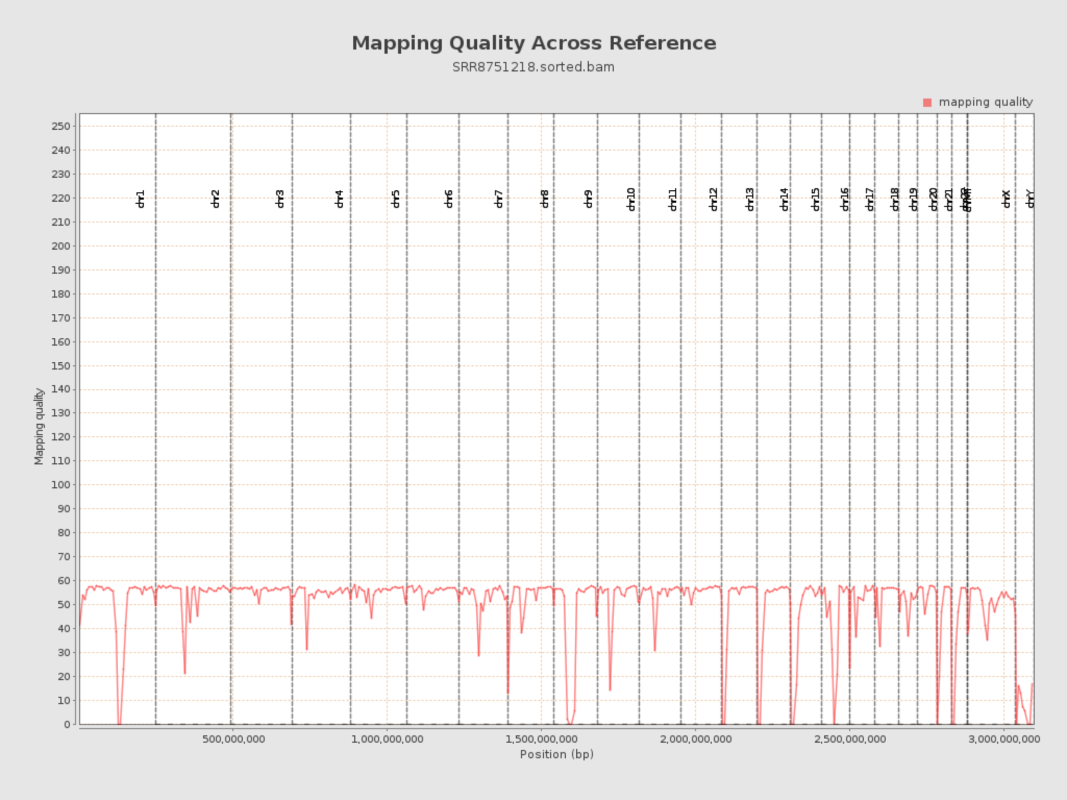
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram