Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 20:20:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8751207.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_SRR8751207 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8751207.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 20:20:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8751207.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,062,167
Mapped reads	3,025,580 / 59.77%
Unmapped reads	2,036,587 / 40.23%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	175,462 / 3.47%
Read min/max/mean length	30 / 101 / 102.43
Duplicated reads (estimated)	117,629 / 2.32%
Duplication rate	1.85%
Clipped reads	782,626 / 15.46%

2.2. ACGT Content

Number/percentage of A's	87,682,030 / 29.63%
Number/percentage of C's	60,341,480 / 20.39%
Number/percentage of T's	88,336,762 / 29.85%
Number/percentage of G's	59,584,514 / 20.13%
Number/percentage of N's	2,175 / 0%
GC Percentage	40.52%

2.3. Coverage

Mean	0.0956

Standard Deviation	1.3168

2.4. Mapping Quality

Mean Mapping Quality	50.93

2.5. Mismatches and indels

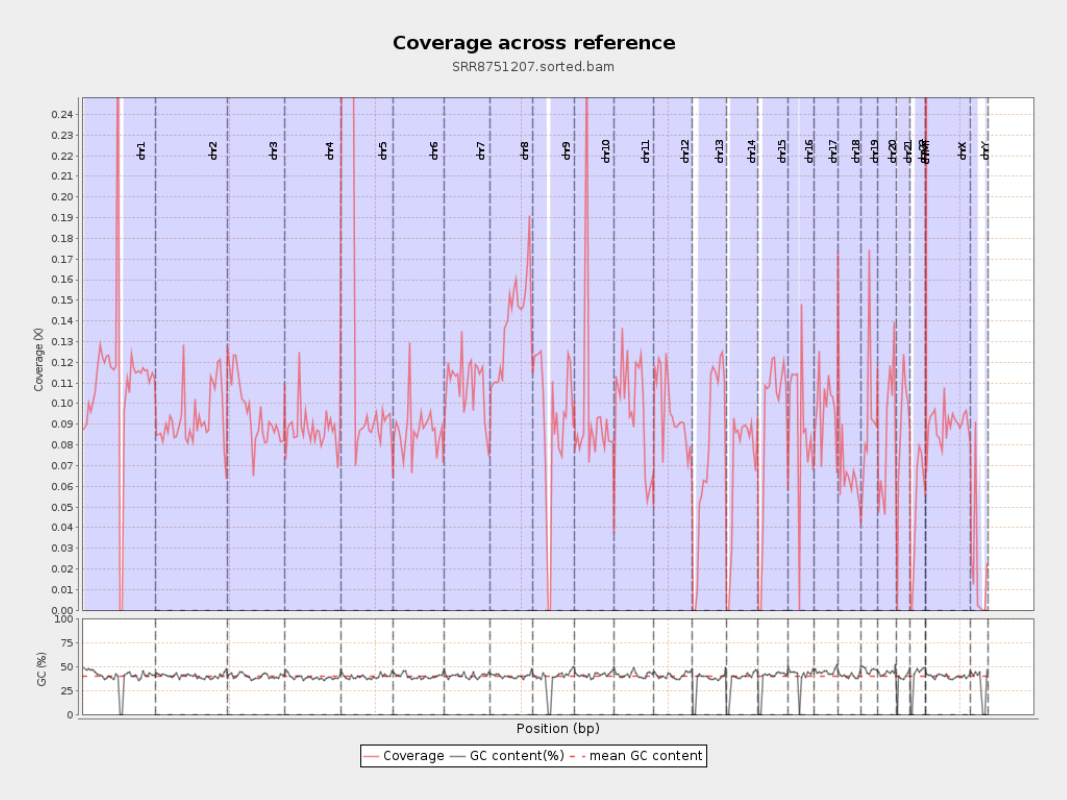
General error rate	0.5%
Mismatches	1,233,820
Insertions	170,820
Mapped reads with at least one insertion	5.44%
Deletions	45,793
Mapped reads with at least one deletion	1.48%
Homopolymer indels	51.6%

2.6. Chromosome stats

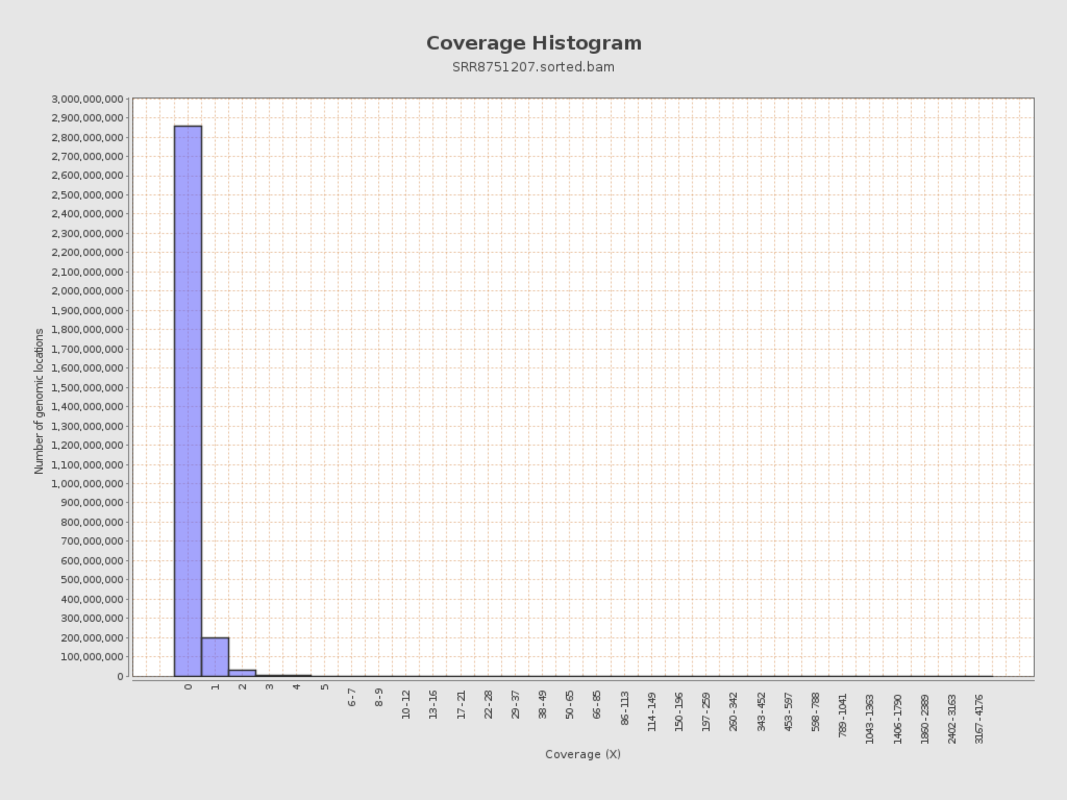
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	27698417	0.1111	3.8087
chr2	243199373	22642790	0.0931	0.5695
chr3	198022430	18955800	0.0957	0.4311
chr4	191154276	16801907	0.0879	0.4468
chr5	180915260	25678381	0.1419	0.4887
chr6	171115067	14969526	0.0875	0.5874
chr7	159138663	17176759	0.1079	0.7596

chr8	146364022	20324207	0.1389	0.9185
chr9	141213431	12950745	0.0917	0.6551
chr10	135534747	12850362	0.0948	1.6308
chr11	135006516	13081590	0.0969	0.5643
chr12	133851895	12882106	0.0962	0.3907
chr13	115169878	8933873	0.0776	0.3239
chr14	107349540	7549621	0.0703	0.3282
chr15	102531392	9200969	0.0897	0.3472
chr16	90354753	8023671	0.0888	0.6723
chr17	81195210	8019013	0.0988	0.5612
chr18	78077248	5382580	0.0689	1.4795
chr19	59128983	5523990	0.0934	2.6571
chr20	63025520	5362843	0.0851	0.3587
chr21	48129895	4159283	0.0864	0.4055
chr22	51304566	2547111	0.0496	0.2599
chrMT	16571	241539	14.576	15.541
chrX	155270560	13954705	0.0899	0.4021
chrY	59373566	1138724	0.0192	0.9339

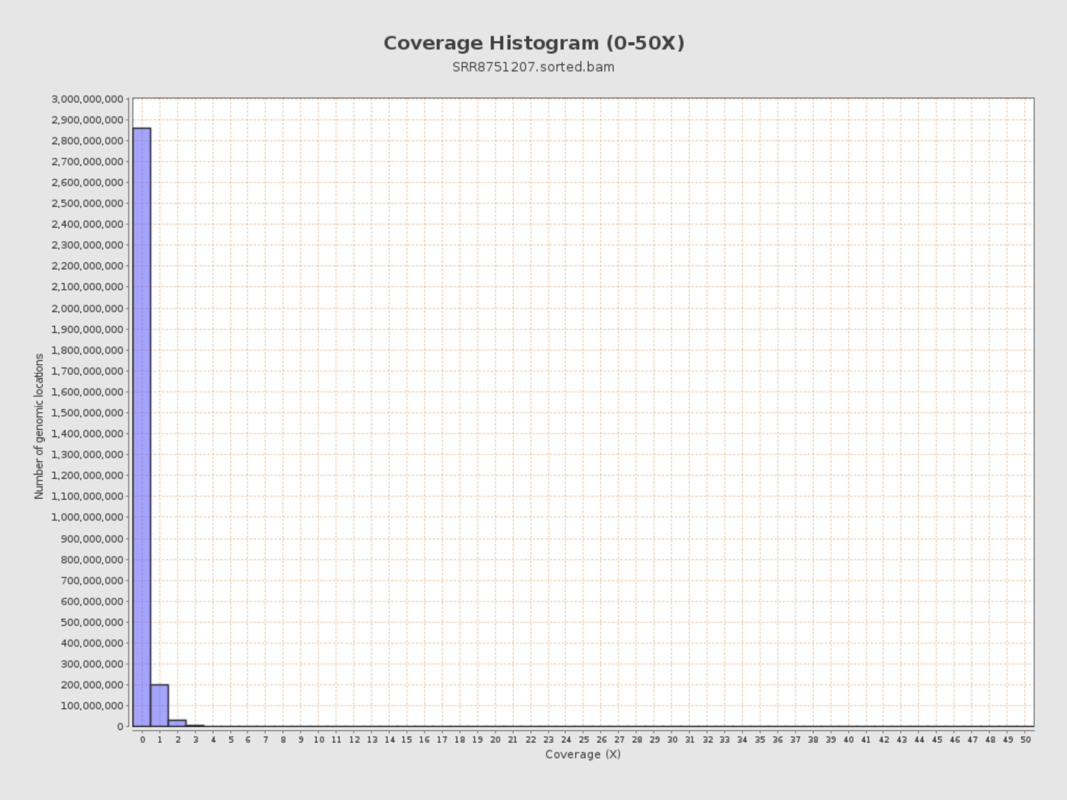
3. Results : Coverage across reference



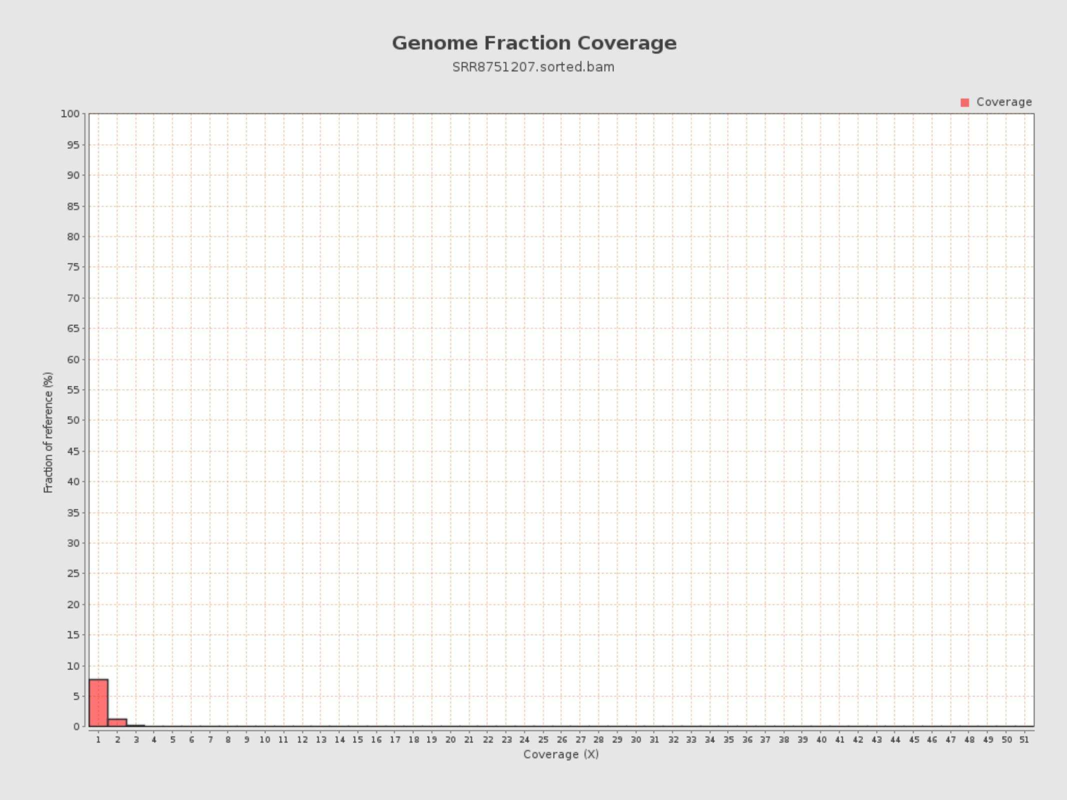
4. Results : Coverage Histogram



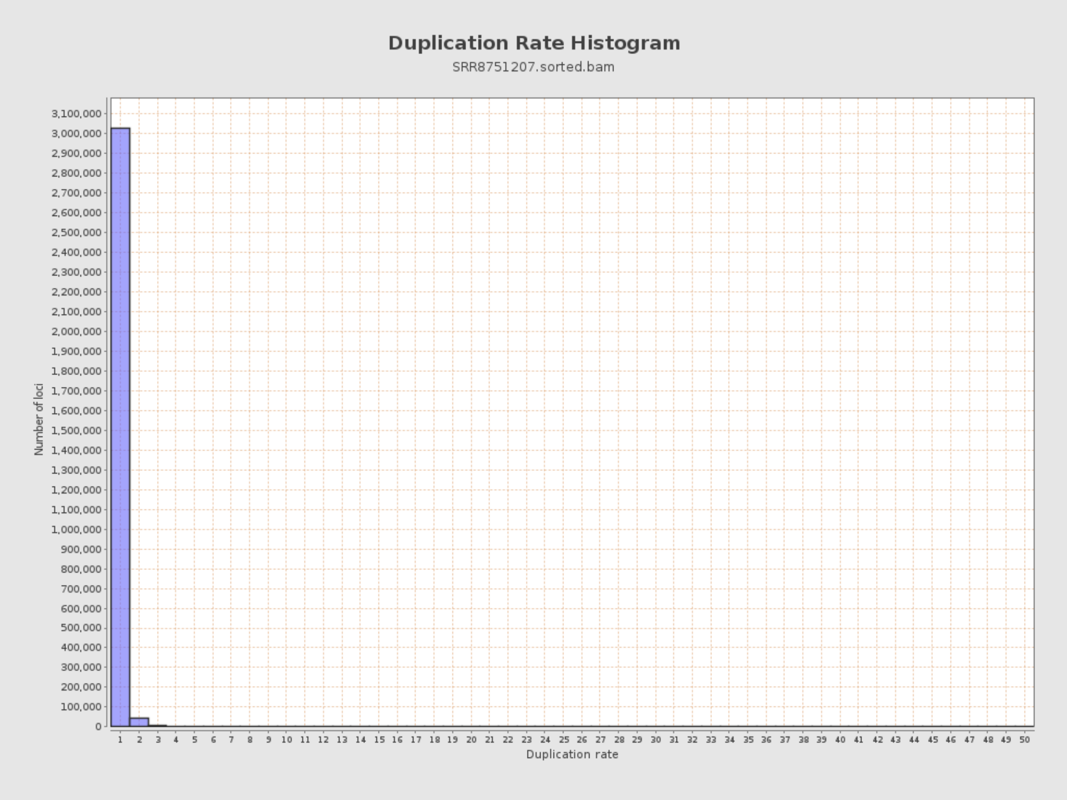
5. Results : Coverage Histogram (0-50X)



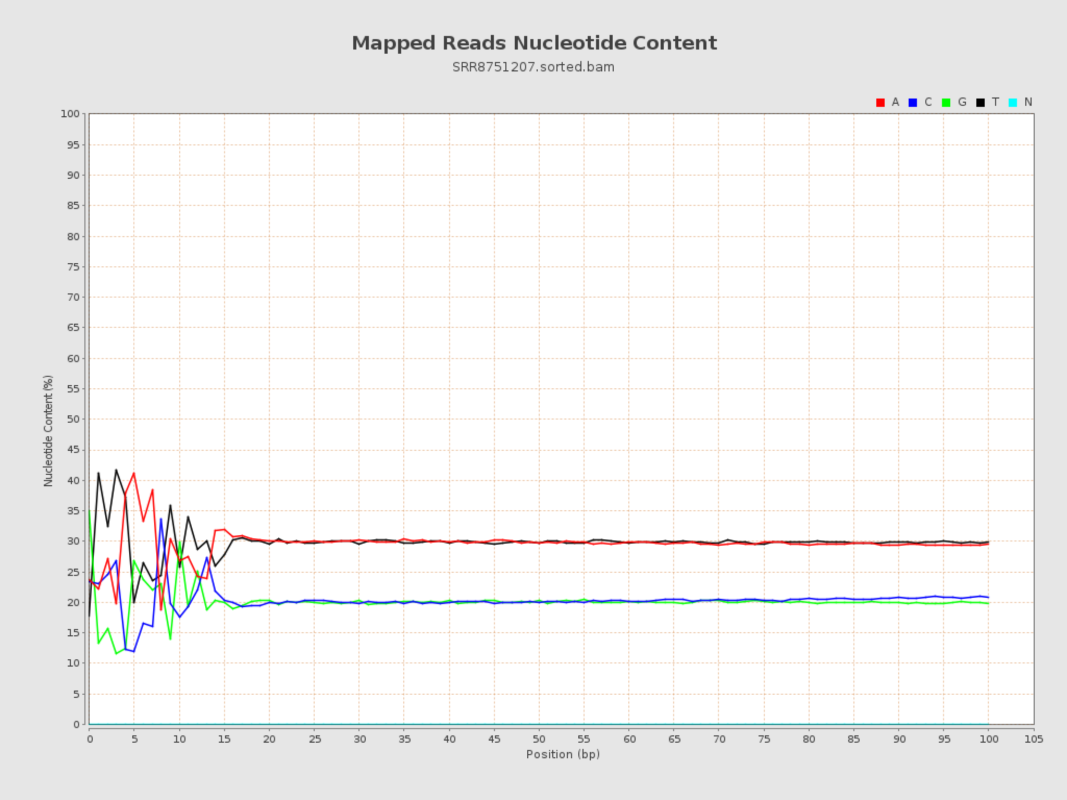
6. Results : Genome Fraction Coverage



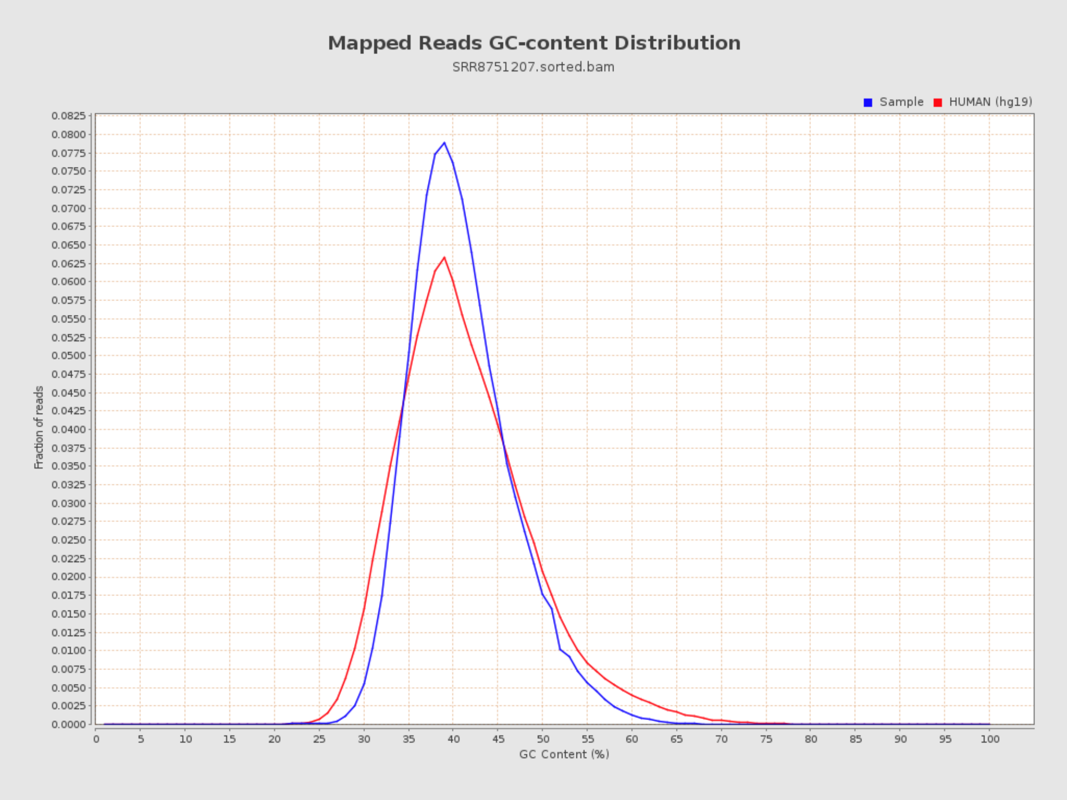
7. Results : Duplication Rate Histogram



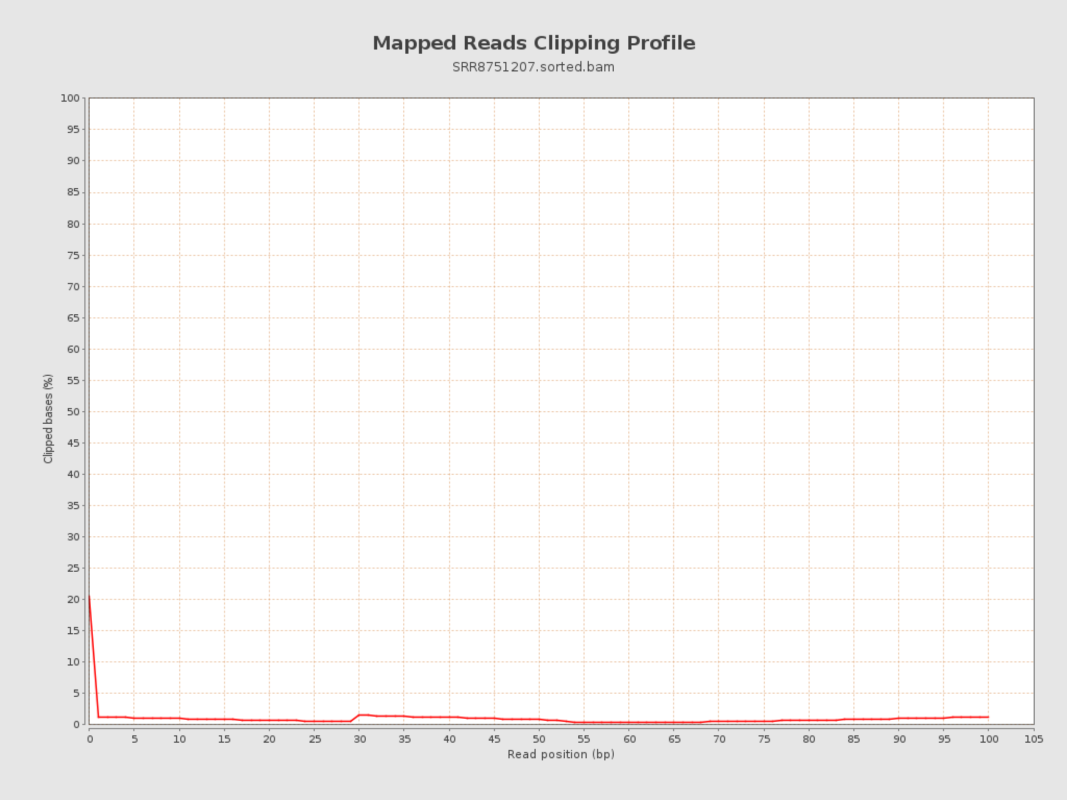
8. Results : Mapped Reads Nucleotide Content



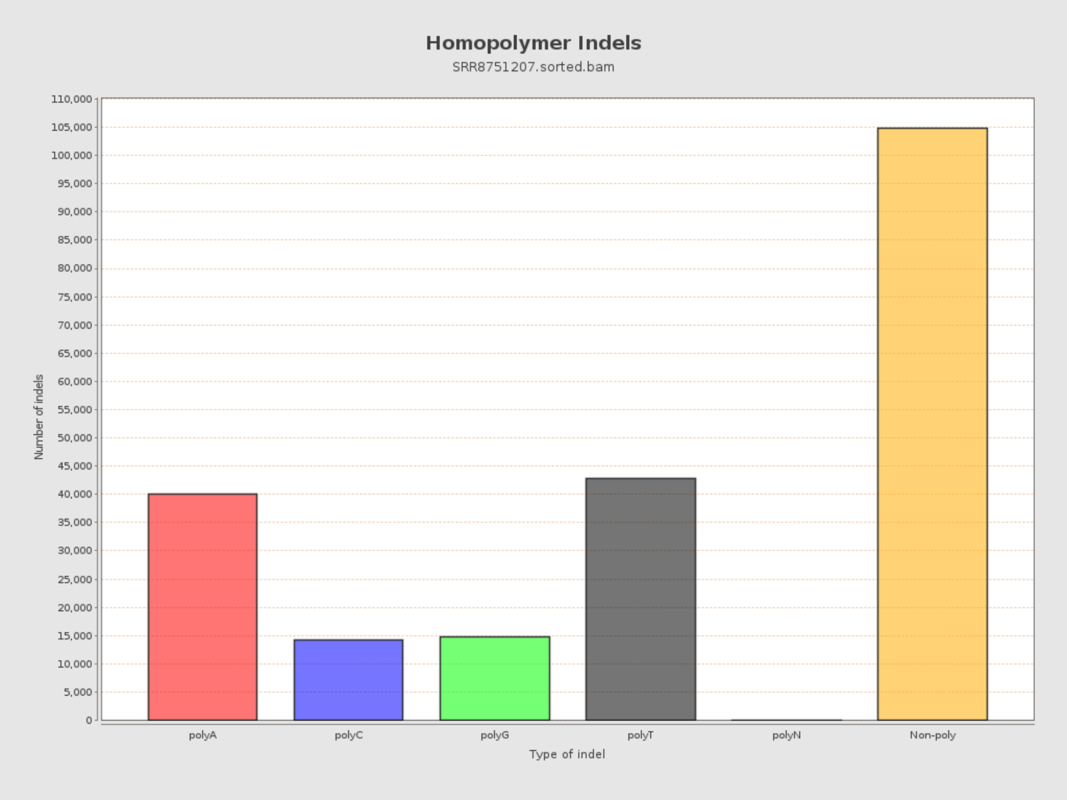
9. Results : Mapped Reads GC-content Distribution



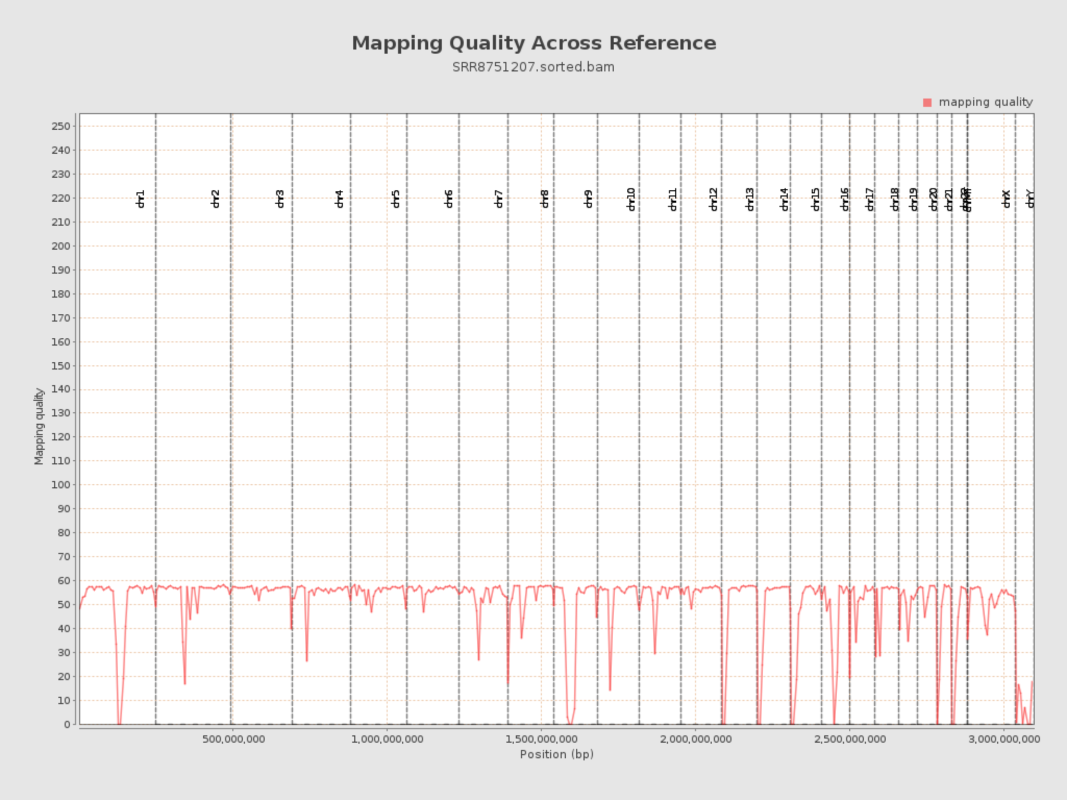
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram