Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 19:59:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8751204.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_SRR8751204 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8751204.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 19:59:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8751204.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,439,056
Mapped reads	4,065,149 / 91.58%
Unmapped reads	373,907 / 8.42%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	153,405 / 3.46%
Read min/max/mean length	30 / 101 / 102.43
Duplicated reads (estimated)	131,038 / 2.95%
Duplication rate	1.62%
Clipped reads	782,678 / 17.63%

2.2. ACGT Content

Number/percentage of A's	116,912,531 / 29.23%
Number/percentage of C's	82,957,998 / 20.74%
Number/percentage of T's	117,560,331 / 29.39%
Number/percentage of G's	82,556,501 / 20.64%
Number/percentage of N's	2,253 / 0%
GC Percentage	41.38%

2.3. Coverage

Mean	0.1292

Standard Deviation	1.4066

2.4. Mapping Quality

Mean Mapping Quality	51.1

2.5. Mismatches and indels

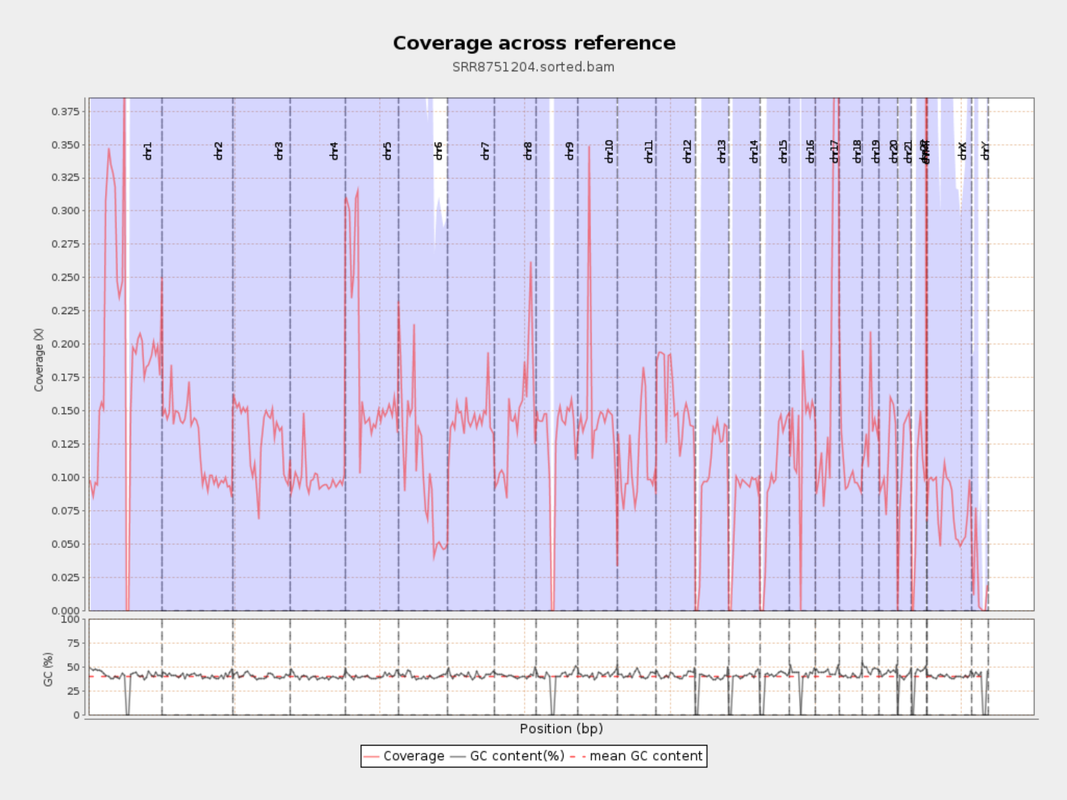
General error rate	0.45%
Mismatches	1,597,186
Insertions	152,433
Mapped reads with at least one insertion	3.65%
Deletions	57,958
Mapped reads with at least one deletion	1.4%
Homopolymer indels	50.68%

2.6. Chromosome stats

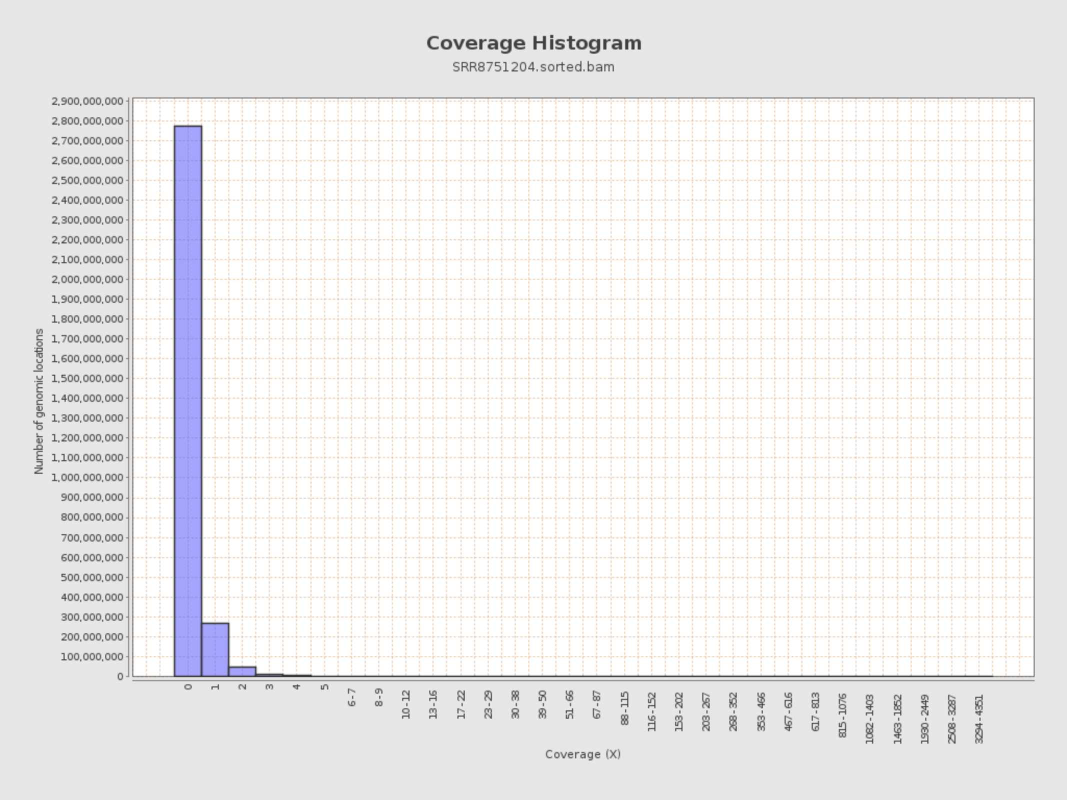
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	48910113	0.1962	4.0516
chr2	243199373	30368890	0.1249	0.5744
chr3	198022430	25763033	0.1301	0.4667
chr4	191154276	18773694	0.0982	0.4961
chr5	180915260	32744001	0.181	0.4897
chr6	171115067	18285679	0.1069	0.7932
chr7	159138663	23045833	0.1448	0.8013

chr8	146364022	21228982	0.145	0.5397
chr9	141213431	17665477	0.1251	0.6628
chr10	135534747	20310415	0.1499	1.8634
chr11	135006516	15086987	0.1118	0.5934
chr12	133851895	21239448	0.1587	0.459
chr13	115169878	11538163	0.1002	0.3596
chr14	107349540	8623773	0.0803	0.3462
chr15	102531392	9846948	0.096	0.3524
chr16	90354753	11931829	0.1321	0.8543
chr17	81195210	16698169	0.2057	0.7224
chr18	78077248	8317585	0.1065	1.311
chr19	59128983	8183182	0.1384	2.7649
chr20	63025520	7285637	0.1156	0.4074
chr21	48129895	5353313	0.1112	0.4673
chr22	51304566	4262287	0.0831	0.3319
chrMT	16571	1440385	86.922	30.4392
chrX	155270560	12220440	0.0787	0.3832
chrY	59373566	992388	0.0167	0.7046

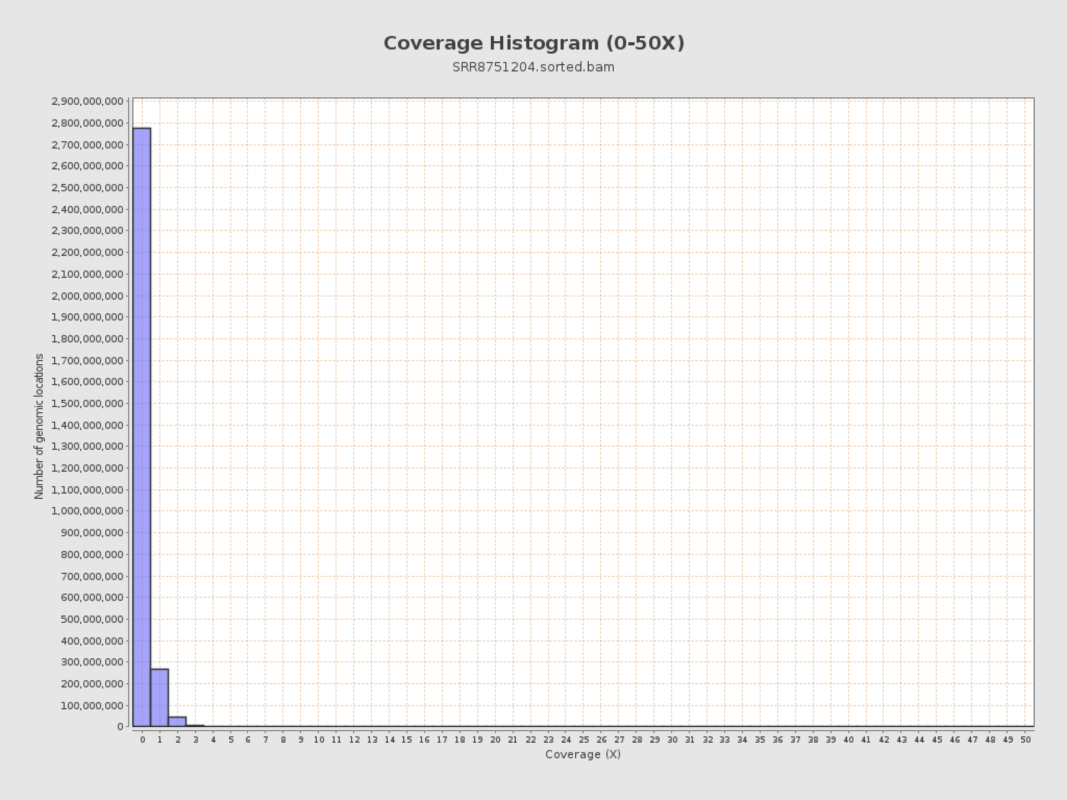
3. Results : Coverage across reference



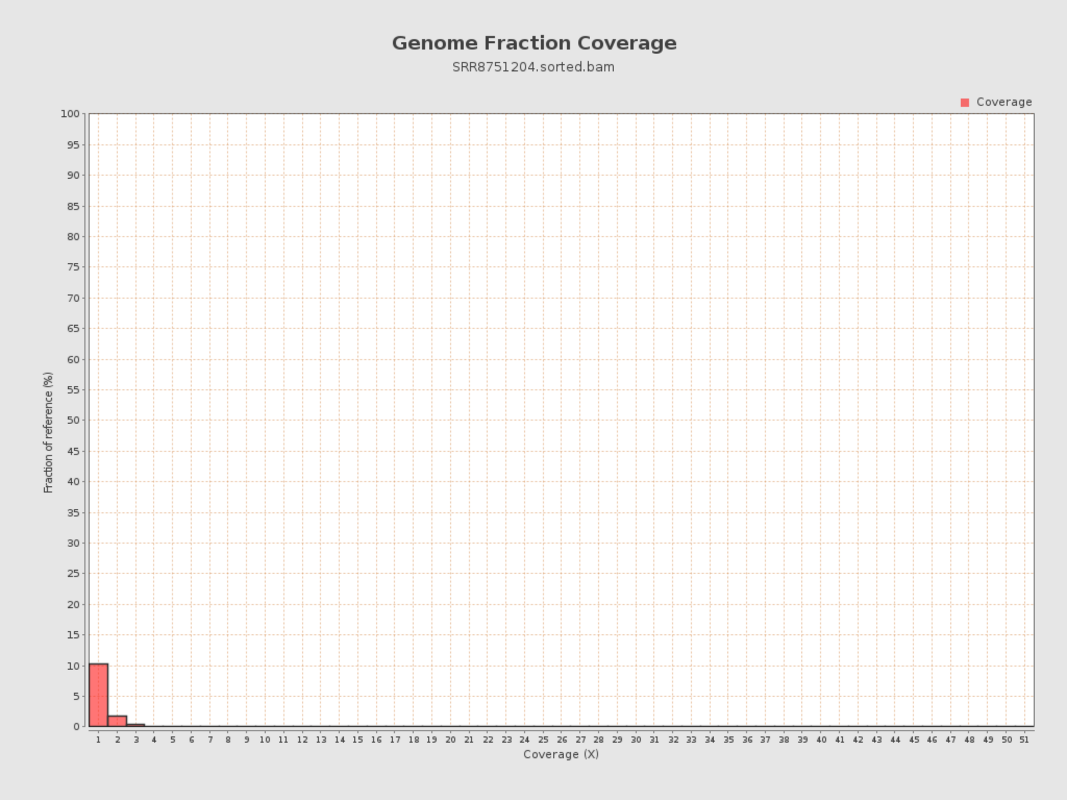
4. Results : Coverage Histogram



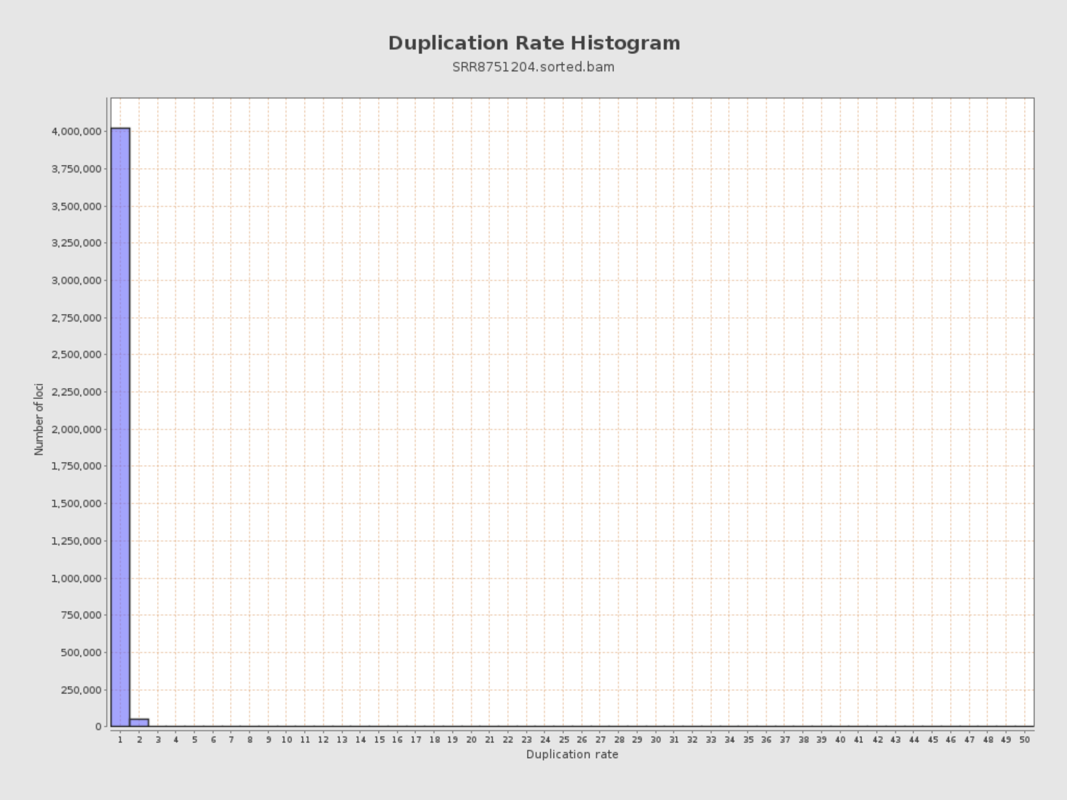
5. Results : Coverage Histogram (0-50X)



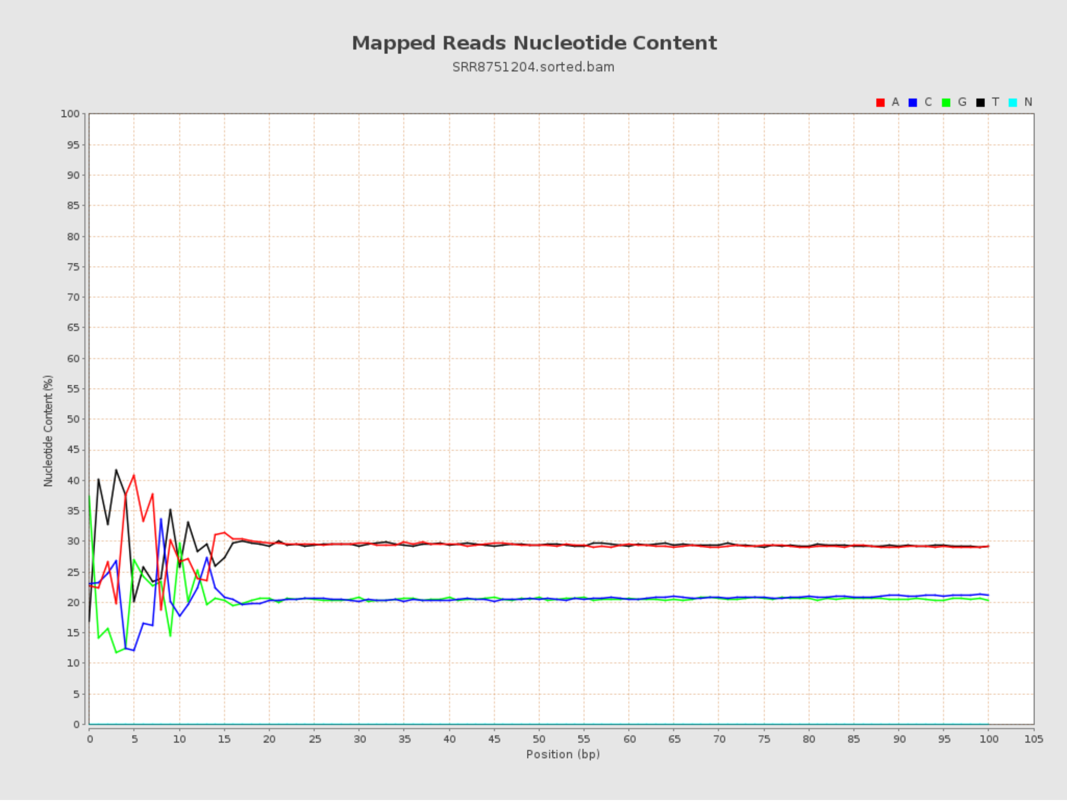
6. Results : Genome Fraction Coverage



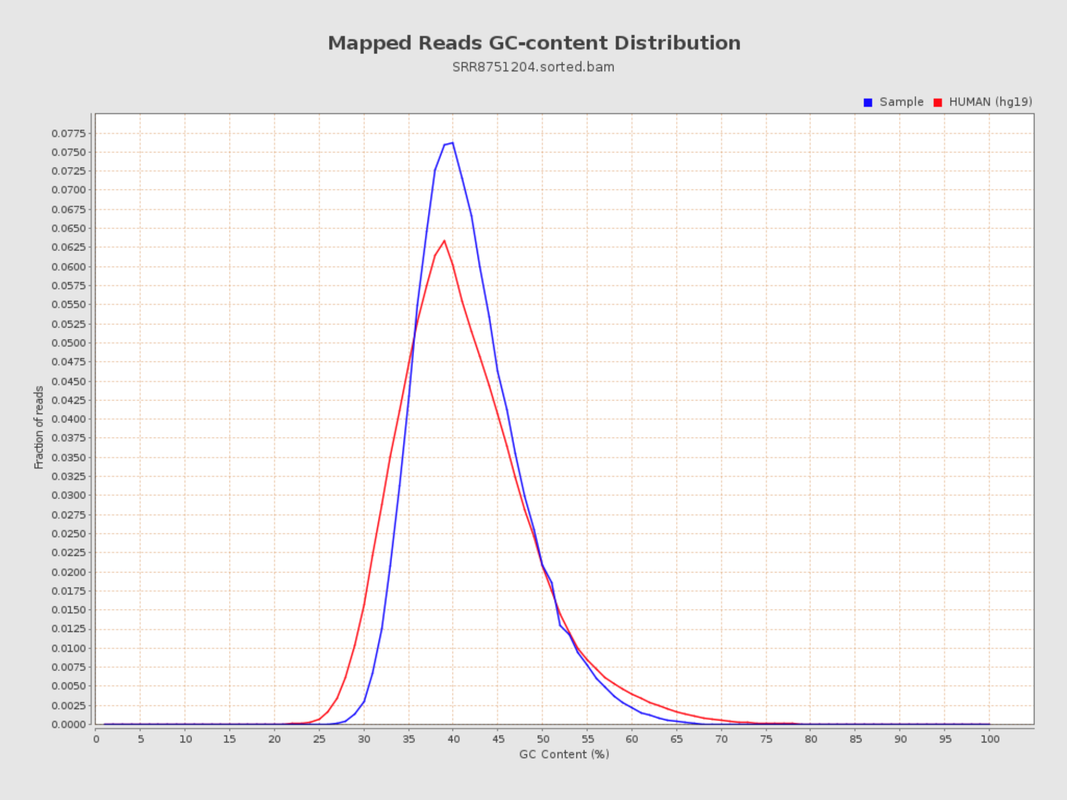
7. Results : Duplication Rate Histogram



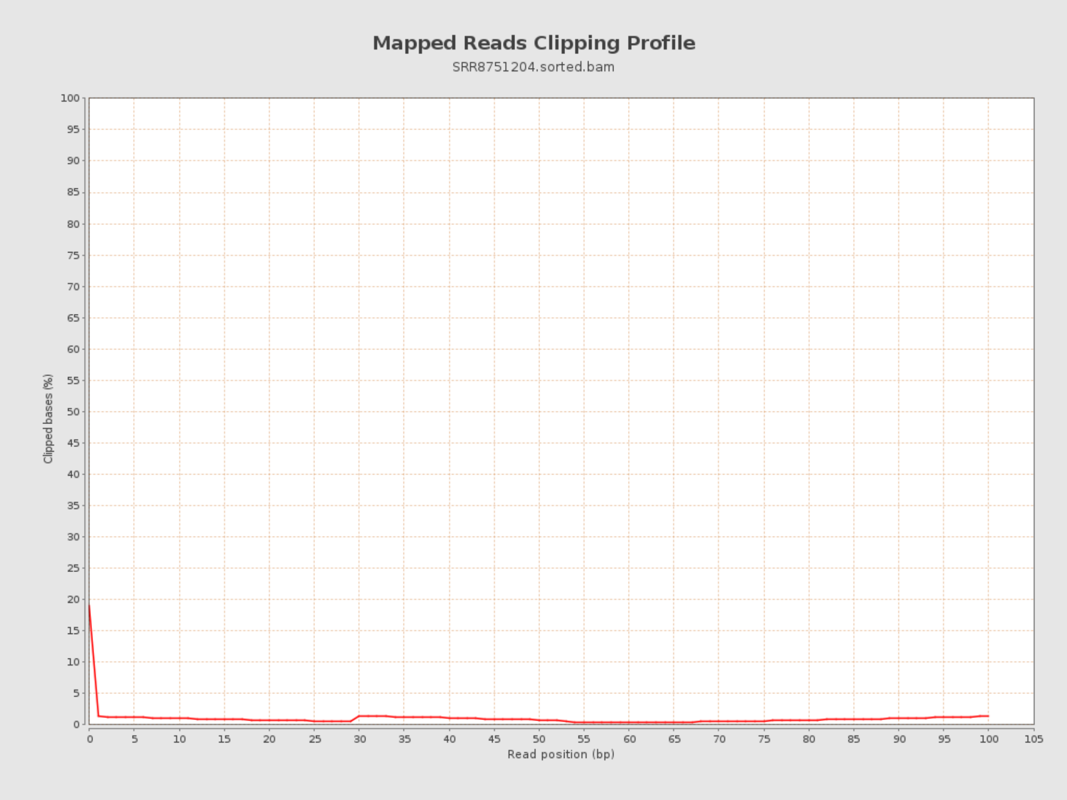
8. Results : Mapped Reads Nucleotide Content



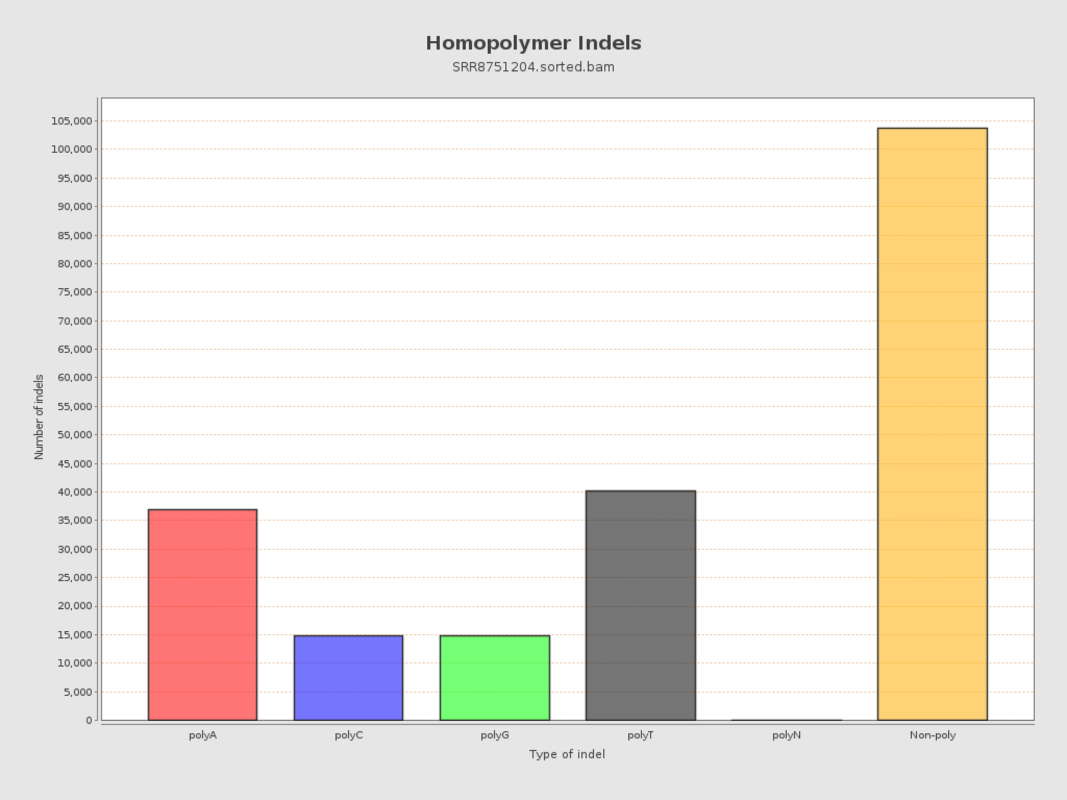
9. Results : Mapped Reads GC-content Distribution



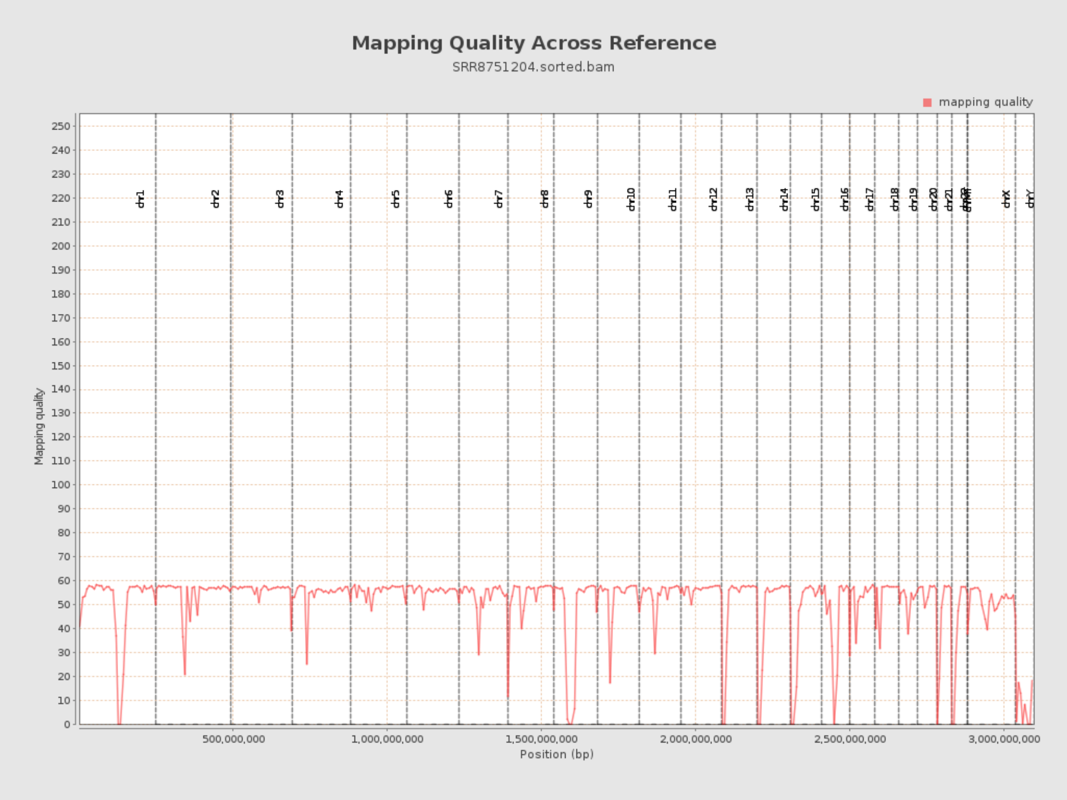
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram