Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 19:51:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8751203.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_SRR8751203 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8751203.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 19:51:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8751203.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,635,749
Mapped reads	4,517,083 / 97.44%
Unmapped reads	118,666 / 2.56%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	35,883 / 0.77%
Read min/max/mean length	30 / 151 / 151.37
Duplicated reads (estimated)	540,387 / 11.66%
Duplication rate	8.86%
Clipped reads	825,613 / 17.81%

2.2. ACGT Content

Number/percentage of A's	186,653,461 / 28.75%
Number/percentage of C's	137,790,137 / 21.23%
Number/percentage of T's	188,970,773 / 29.11%
Number/percentage of G's	135,703,274 / 20.91%
Number/percentage of N's	19,764 / 0%
GC Percentage	42.13%

2.3. Coverage

Mean	0.2098

Standard Deviation	3.3183

2.4. Mapping Quality

Mean Mapping Quality	52.25

2.5. Mismatches and indels

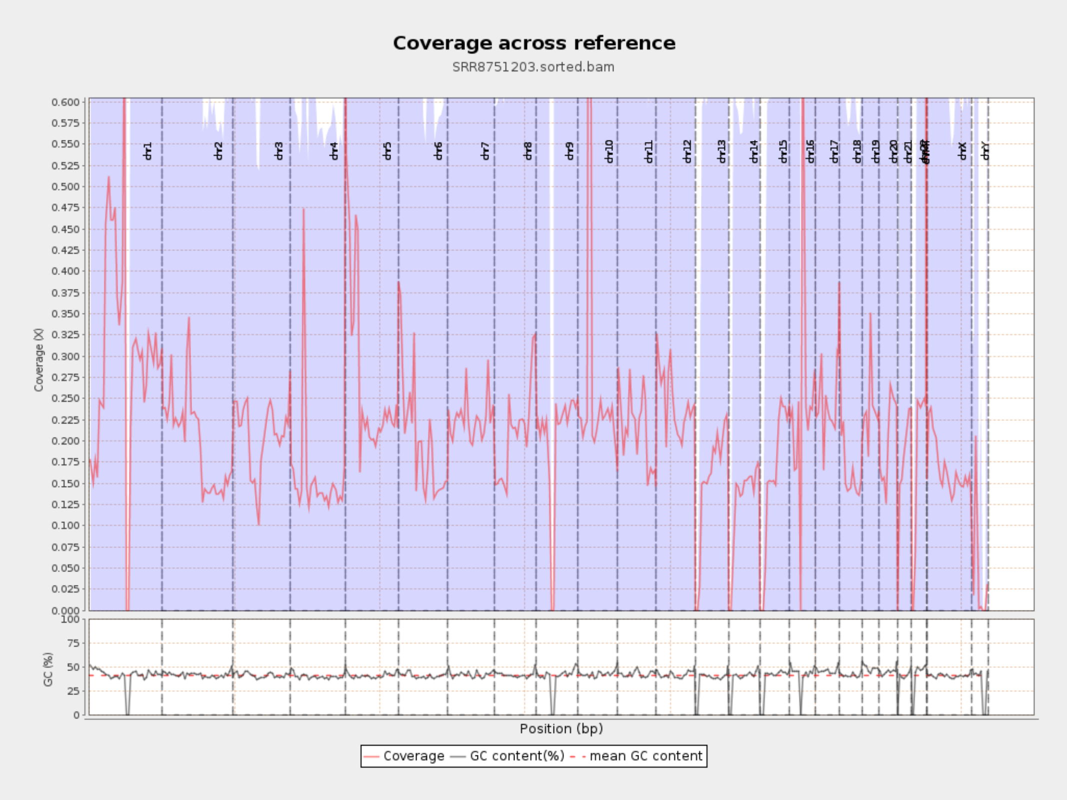
General error rate	0.76%
Mismatches	4,598,759
Insertions	89,370
Mapped reads with at least one insertion	1.84%
Deletions	91,118
Mapped reads with at least one deletion	1.91%
Homopolymer indels	41.27%

2.6. Chromosome stats

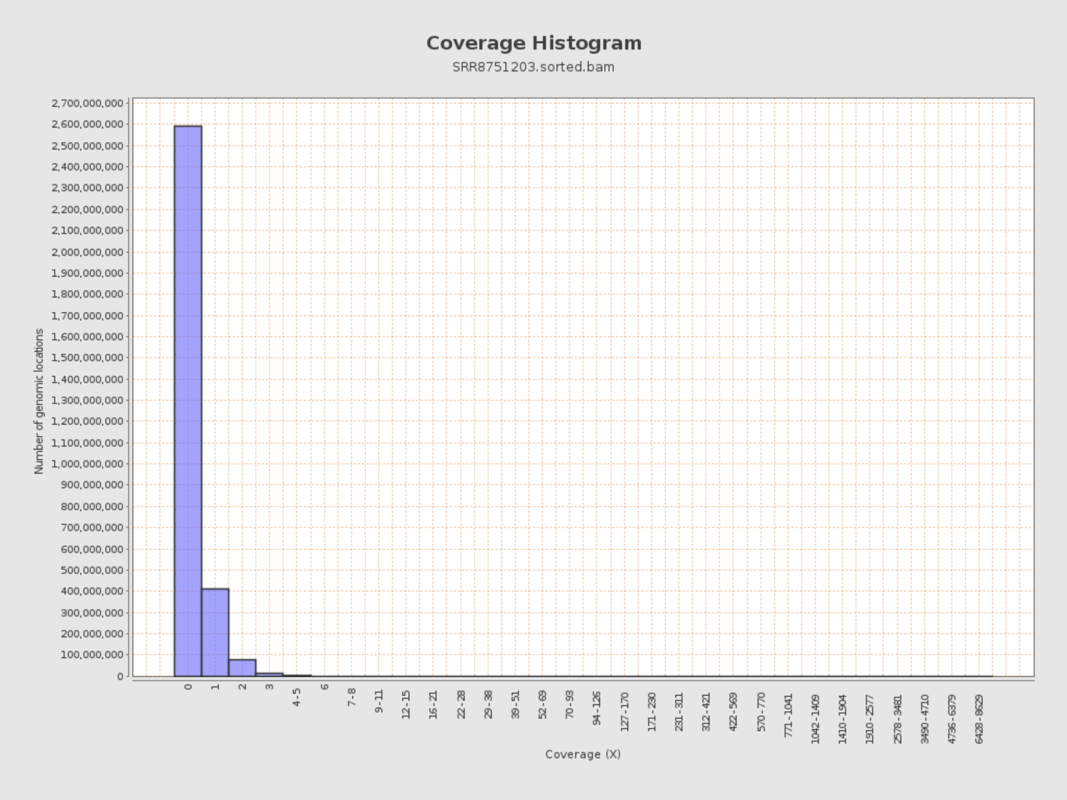
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	75328286	0.3022	7.8565
chr2	243199373	48355936	0.1988	1.3178
chr3	198022430	40824876	0.2062	0.8089
chr4	191154276	29668320	0.1552	2.1242
chr5	180915260	49274504	0.2724	0.6025
chr6	171115067	34864274	0.2037	1.3592
chr7	159138663	35990537	0.2262	1.6229

chr8	146364022	30862630	0.2109	0.6983
chr9	141213431	28213004	0.1998	1.68
chr10	135534747	37853181	0.2793	9.3834
chr11	135006516	29032241	0.215	1.3281
chr12	133851895	33092360	0.2472	0.6382
chr13	115169878	17620848	0.153	0.4352
chr14	107349540	13537980	0.1261	0.4191
chr15	102531392	16110430	0.1571	0.4818
chr16	90354753	22425541	0.2482	3.2133
chr17	81195210	19670810	0.2423	1.1617
chr18	78077248	13368488	0.1712	2.6041
chr19	59128983	14221765	0.2405	4.9747
chr20	63025520	12615004	0.2002	0.9611
chr21	48129895	8440007	0.1754	1.4207
chr22	51304566	8612526	0.1679	0.4662
chrMT	16571	1134035	68.4349	15.5067
chrX	155270560	25988270	0.1674	0.5929
chrY	59373566	2304990	0.0388	2.5315

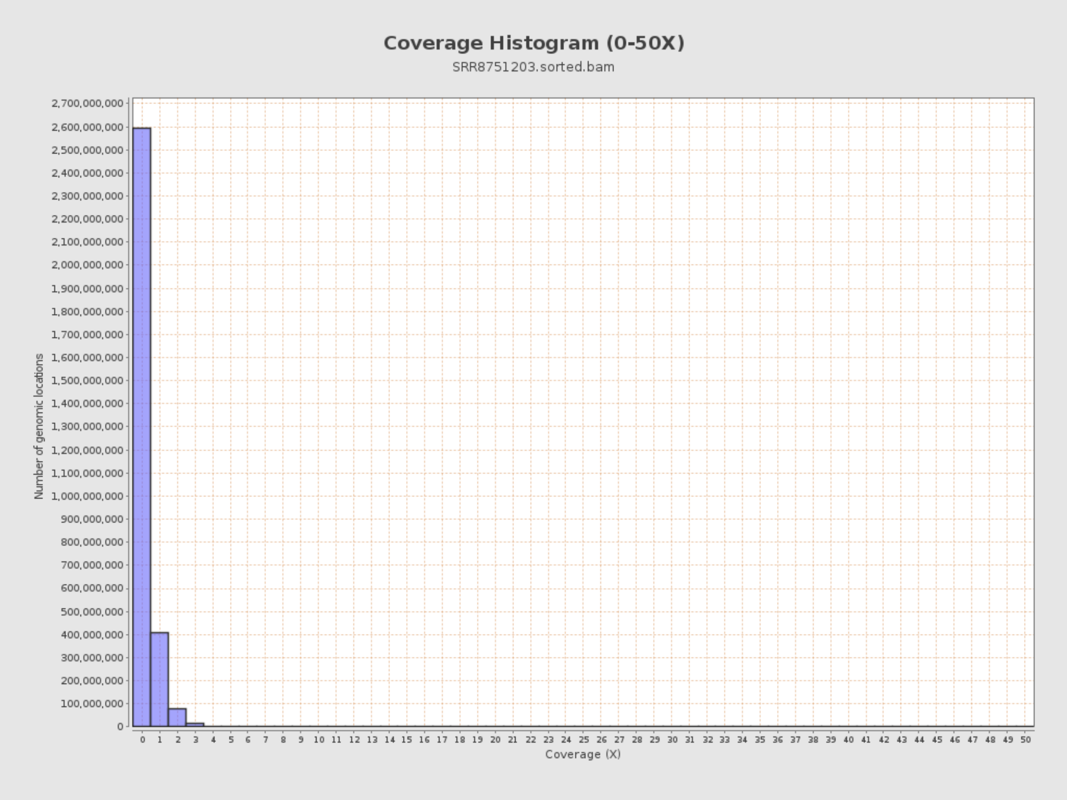
3. Results : Coverage across reference



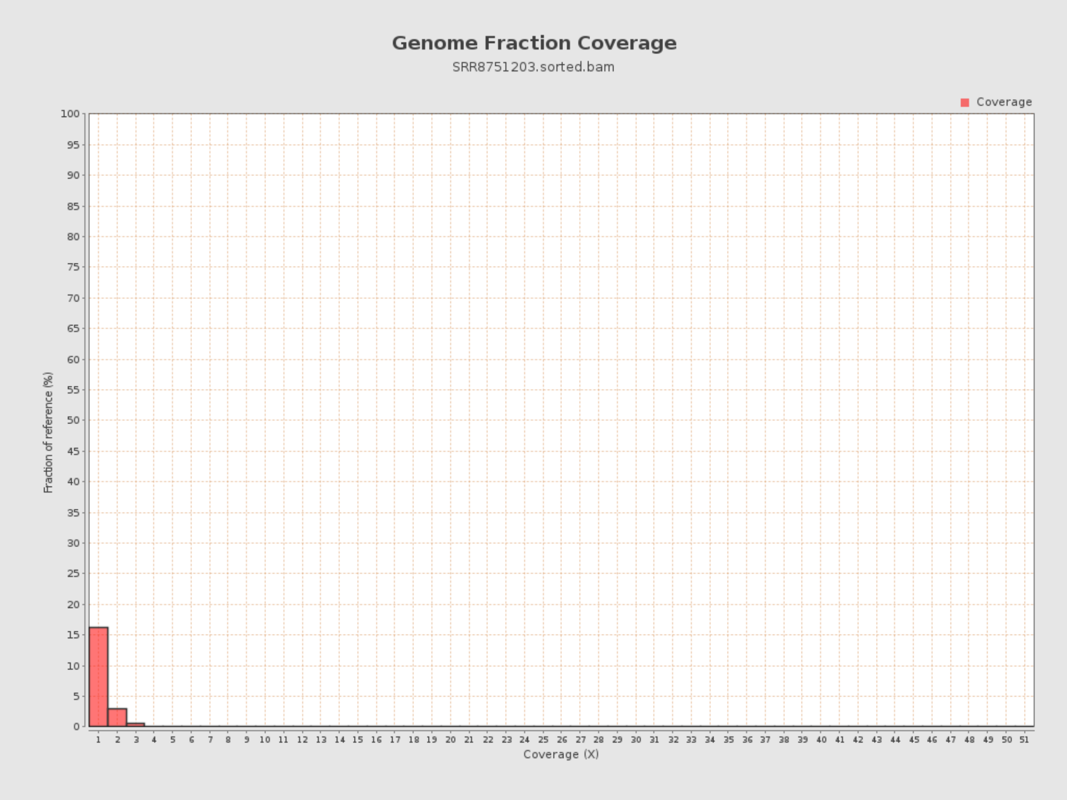
4. Results : Coverage Histogram



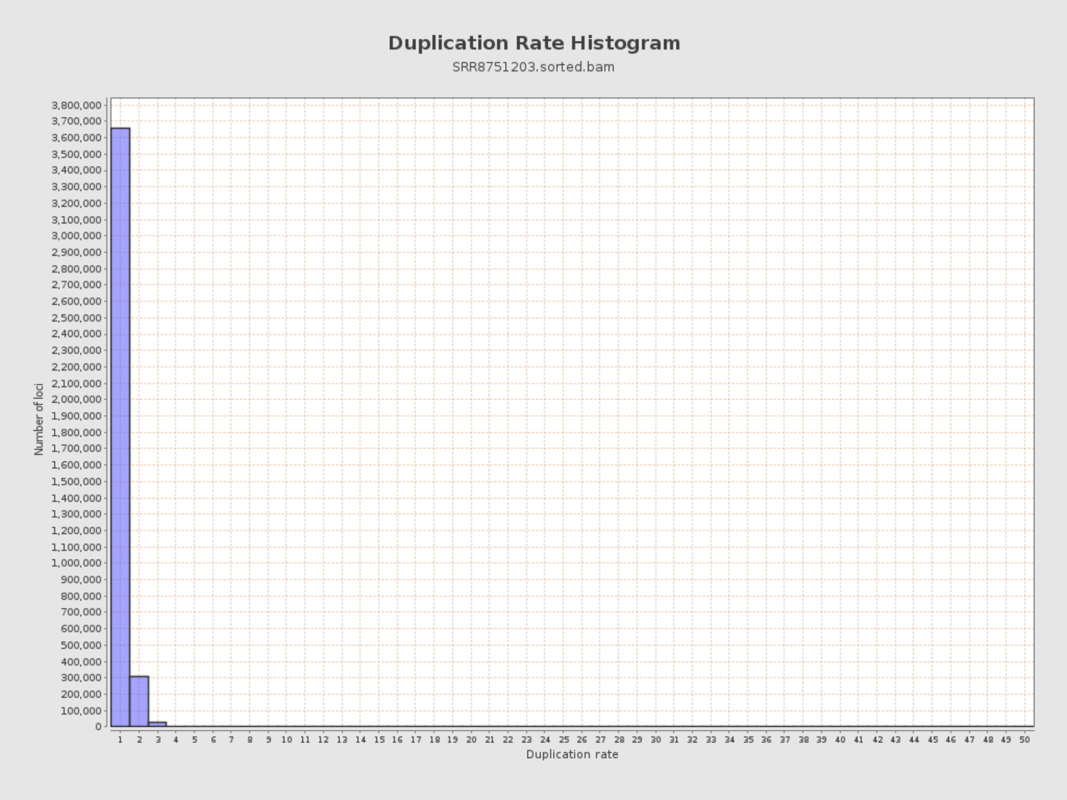
5. Results : Coverage Histogram (0-50X)



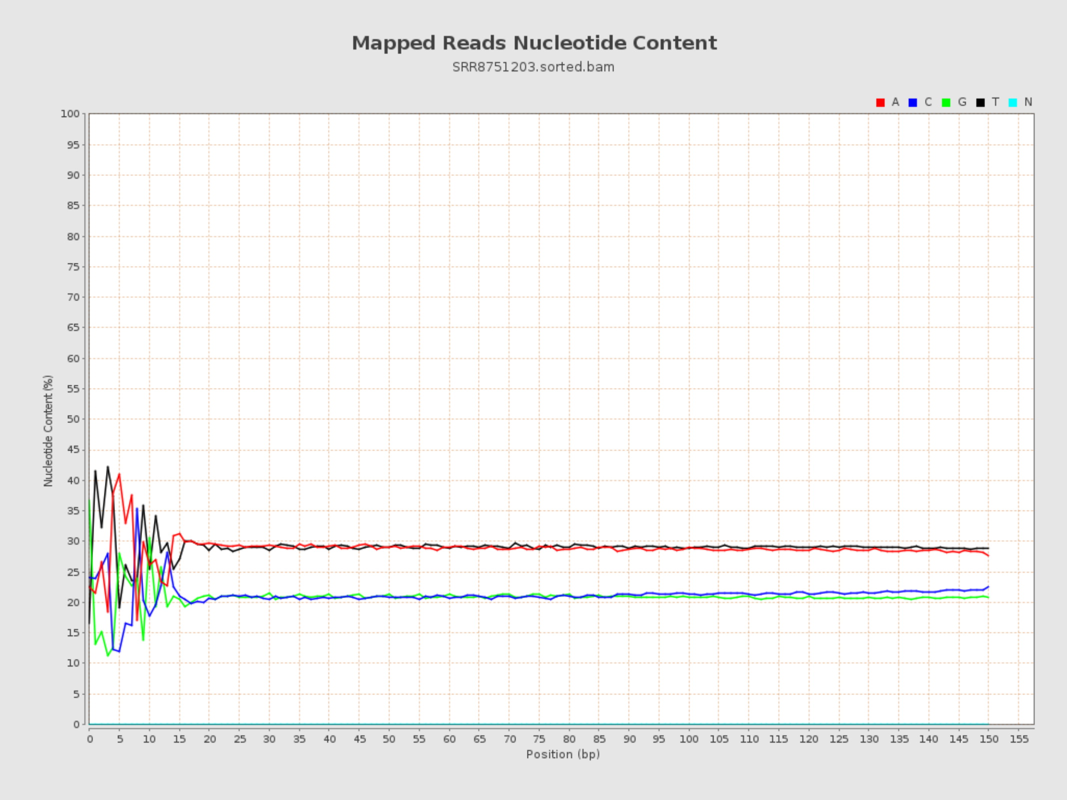
6. Results : Genome Fraction Coverage



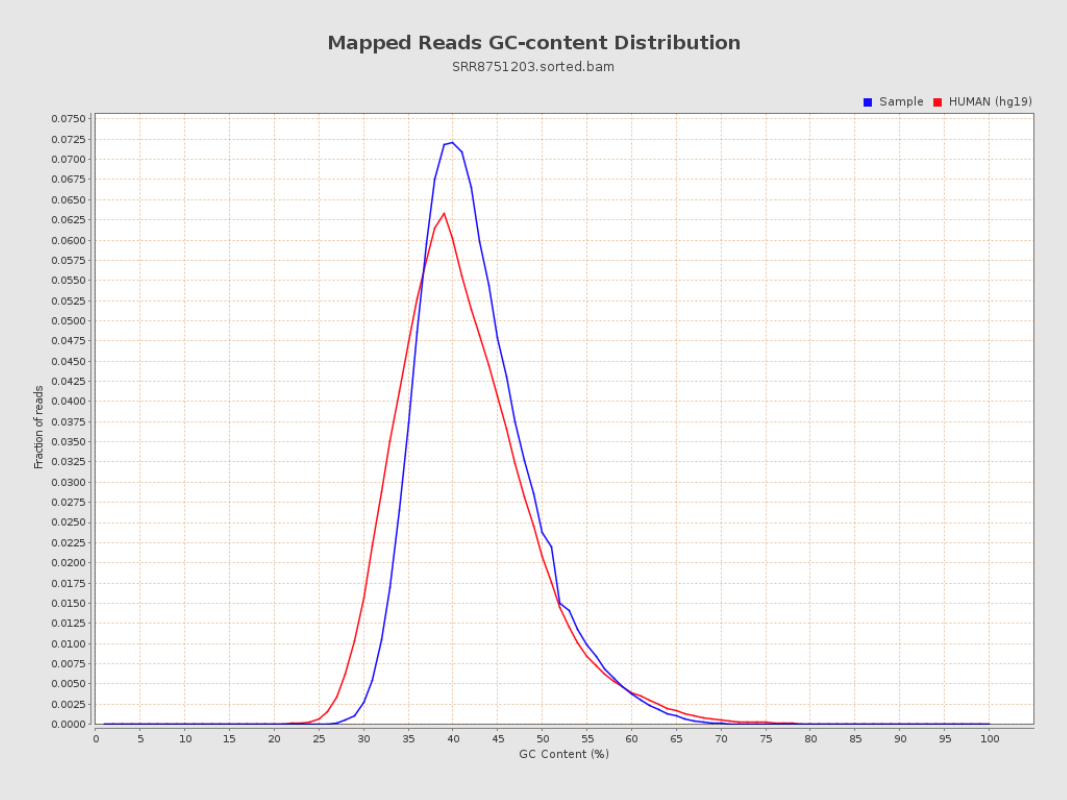
7. Results : Duplication Rate Histogram



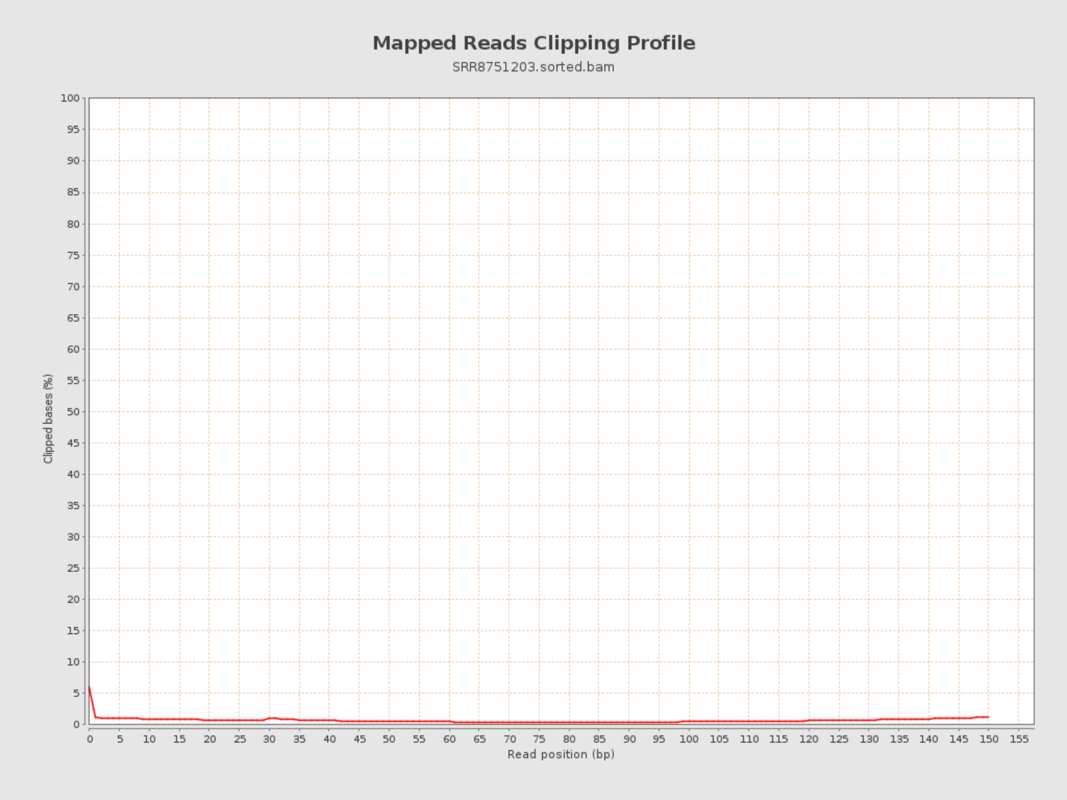
8. Results : Mapped Reads Nucleotide Content



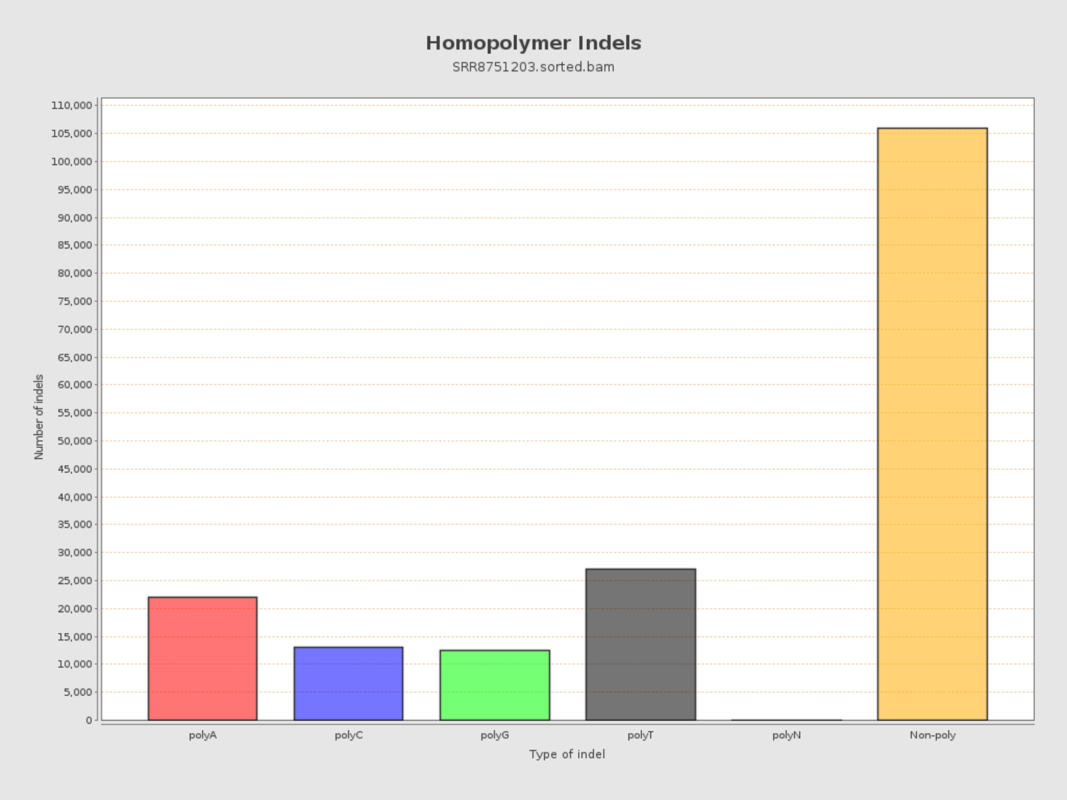
9. Results : Mapped Reads GC-content Distribution



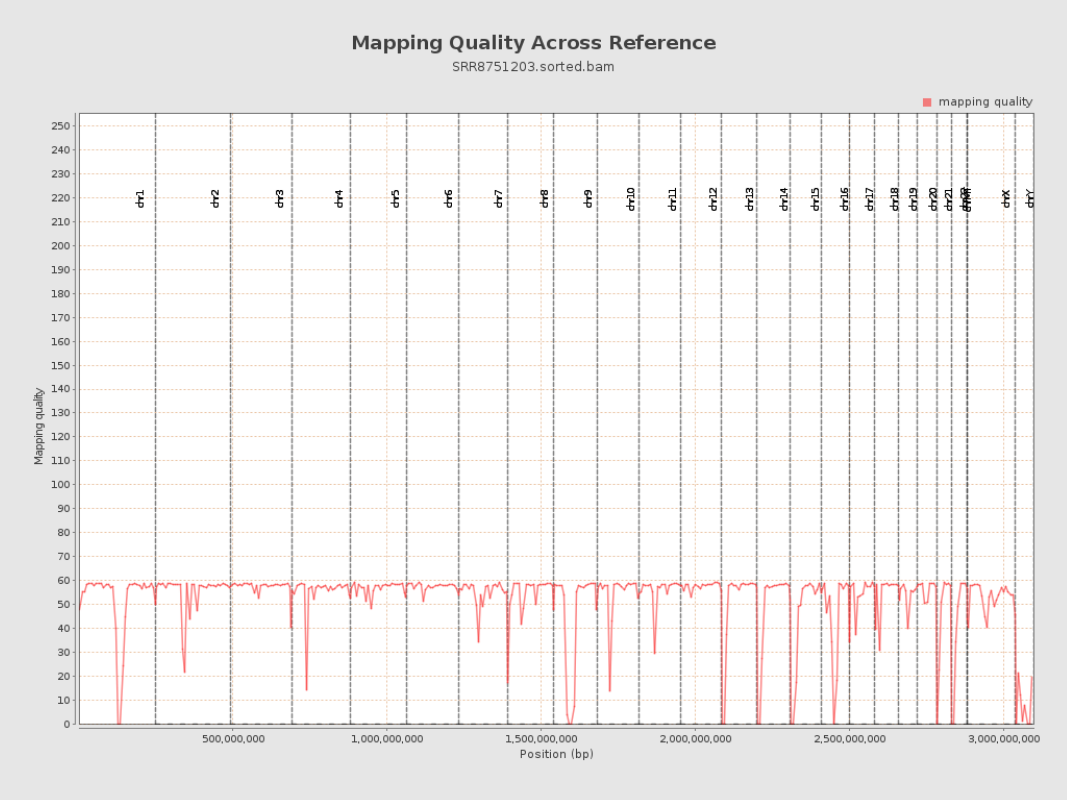
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram