Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 21:15:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8751215.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_SRR8751215 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8751215.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 21:15:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8751215.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,855,803
Mapped reads	3,996,709 / 82.31%
Unmapped reads	859,094 / 17.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	212,991 / 4.39%
Read min/max/mean length	30 / 101 / 102.81
Duplicated reads (estimated)	145,663 / 3%
Duplication rate	1.75%
Clipped reads	908,423 / 18.71%

2.2. ACGT Content

Number/percentage of A's	117,630,316 / 29.89%
Number/percentage of C's	79,071,212 / 20.09%
Number/percentage of T's	118,214,270 / 30.04%
Number/percentage of G's	78,635,452 / 19.98%
Number/percentage of N's	2,915 / 0%
GC Percentage	40.07%

2.3. Coverage

Mean	0.1272

Standard Deviation	1.5214

2.4. Mapping Quality

Mean Mapping Quality	51.03

2.5. Mismatches and indels

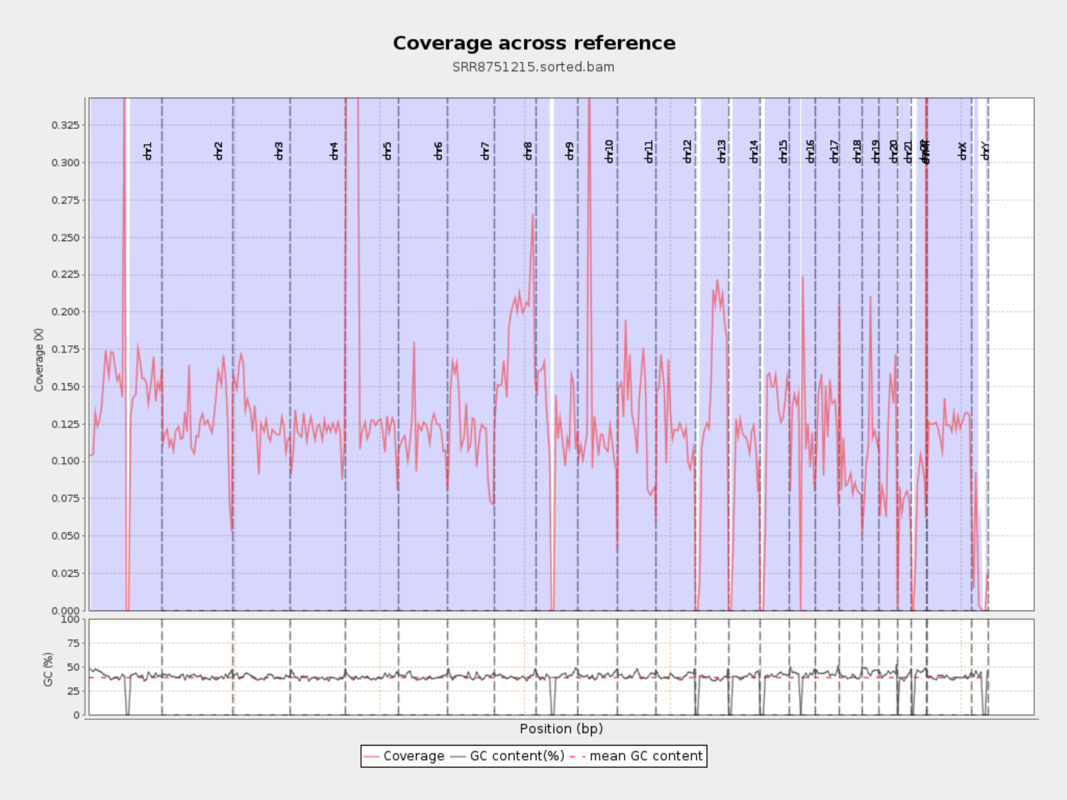
General error rate	0.47%
Mismatches	1,548,081
Insertions	223,019
Mapped reads with at least one insertion	5.39%
Deletions	58,940
Mapped reads with at least one deletion	1.44%
Homopolymer indels	52.33%

2.6. Chromosome stats

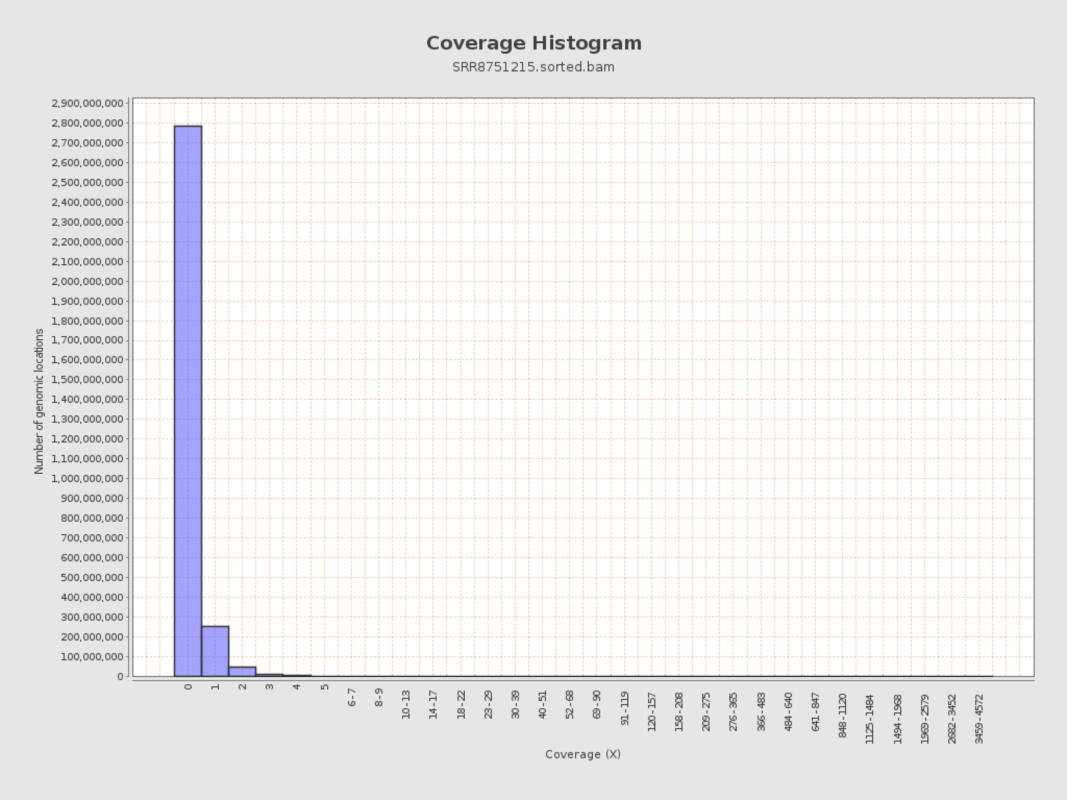
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	36464791	0.1463	4.2847
chr2	243199373	30191083	0.1241	0.6025
chr3	198022430	25692905	0.1297	0.5479
chr4	191154276	22717154	0.1188	0.4585
chr5	180915260	35207927	0.1946	0.5406
chr6	171115067	20418385	0.1193	0.7986
chr7	159138663	19306539	0.1213	0.7465

chr8	146364022	27626902	0.1888	0.9562
chr9	141213431	16771543	0.1188	0.7831
chr10	135534747	17156102	0.1266	2.4044
chr11	135006516	17538093	0.1299	0.6872
chr12	133851895	16898725	0.1262	0.424
chr13	115169878	16272496	0.1413	0.4379
chr14	107349540	10157855	0.0946	0.3786
chr15	102531392	12135953	0.1184	0.4001
chr16	90354753	10636919	0.1177	0.9513
chr17	81195210	10434449	0.1285	0.7492
chr18	78077248	7160169	0.0917	1.7386
chr19	59128983	6898926	0.1167	2.9739
chr20	63025520	6966648	0.1105	0.4031
chr21	48129895	3162750	0.0657	0.3521
chr22	51304566	3221112	0.0628	0.2932
chrMT	16571	263667	15.9114	9.6235
chrX	155270560	19151293	0.1233	0.482
chrY	59373566	1227255	0.0207	0.951

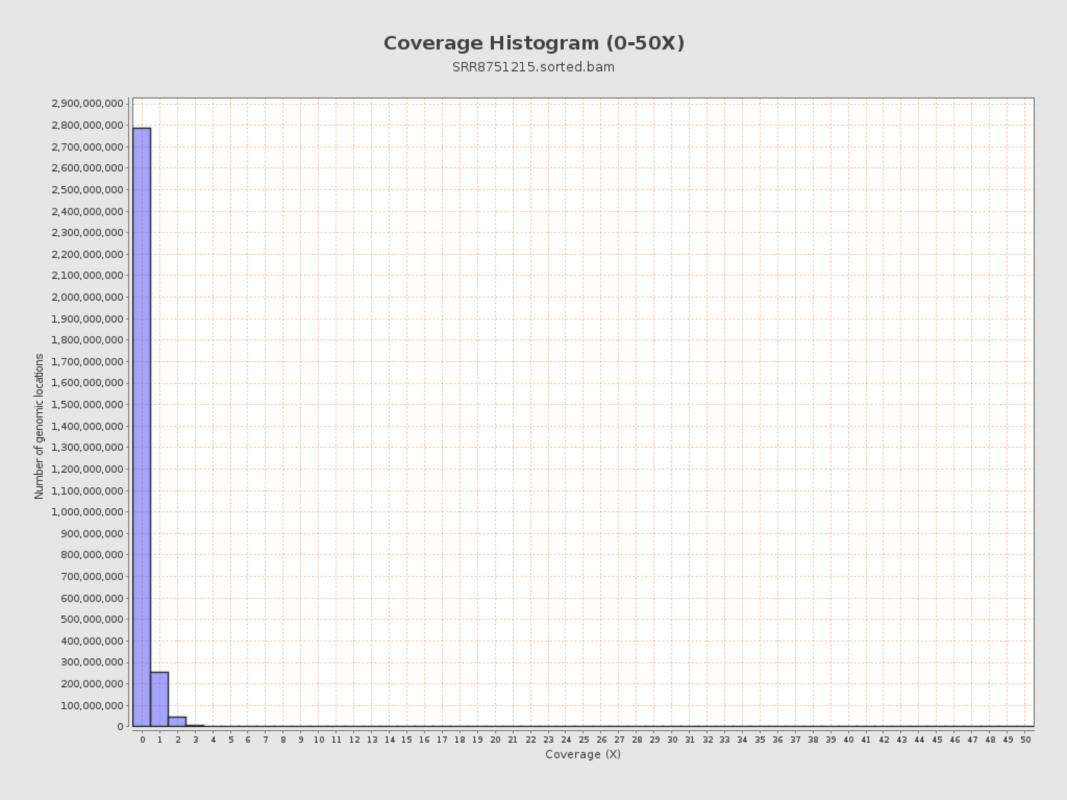
3. Results : Coverage across reference



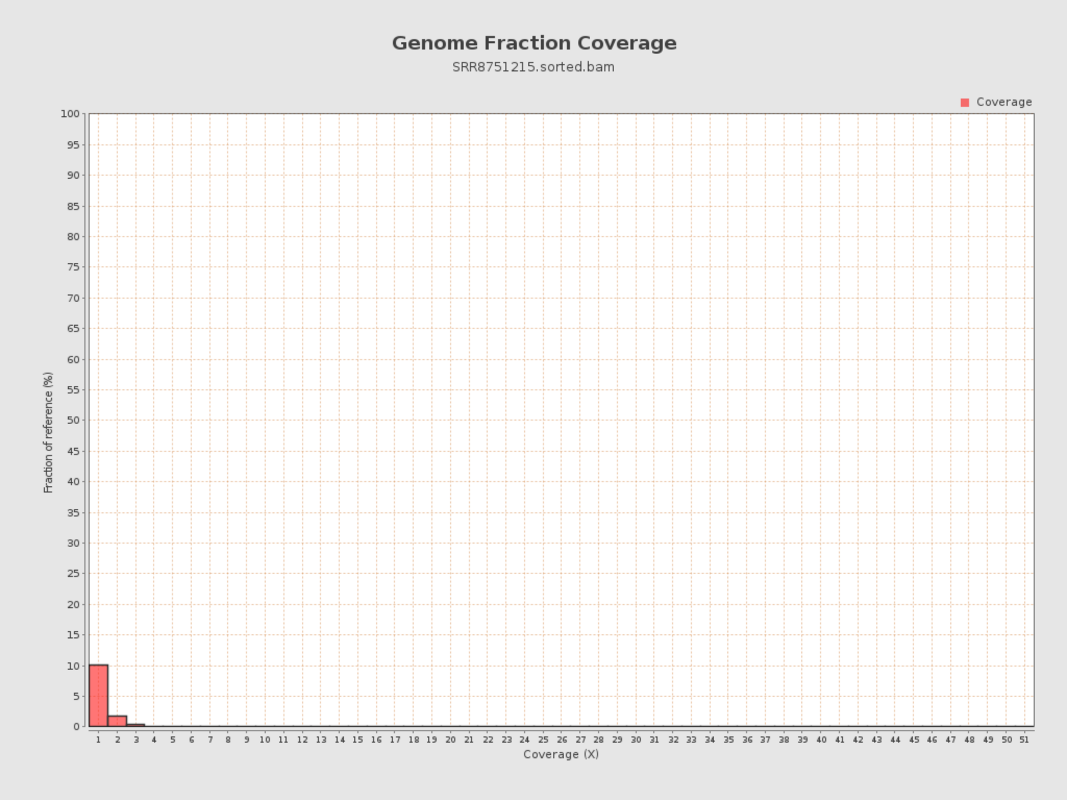
4. Results : Coverage Histogram



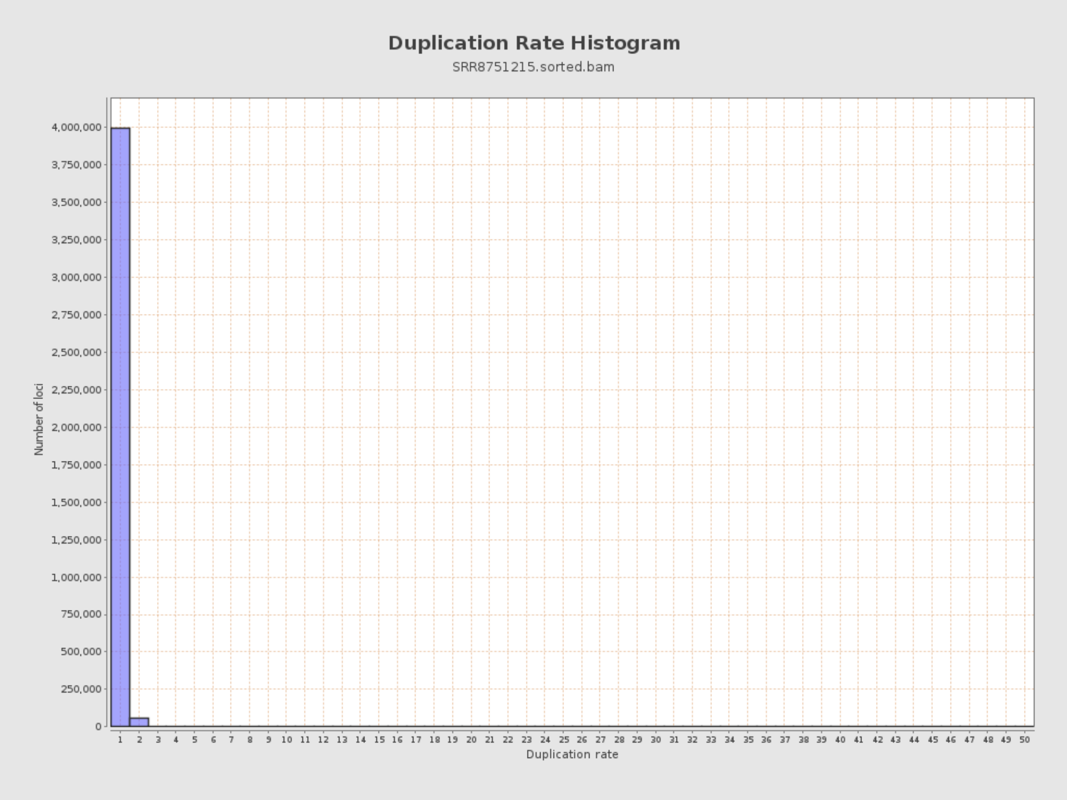
5. Results : Coverage Histogram (0-50X)



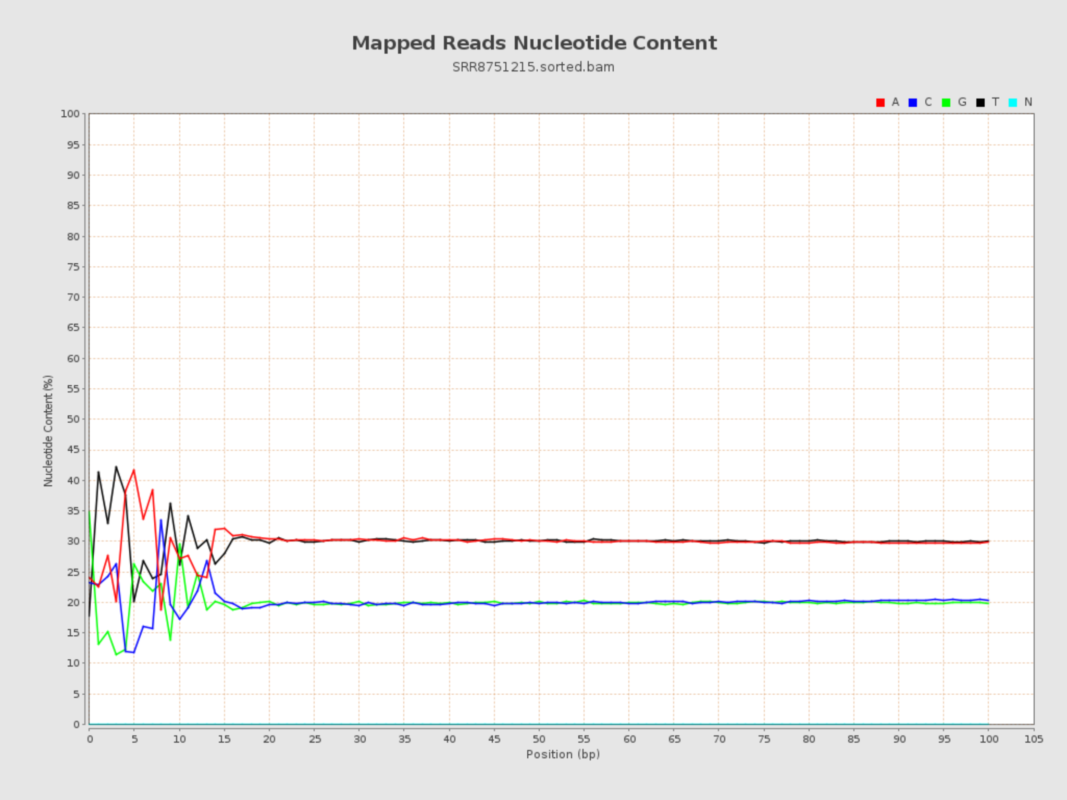
6. Results : Genome Fraction Coverage



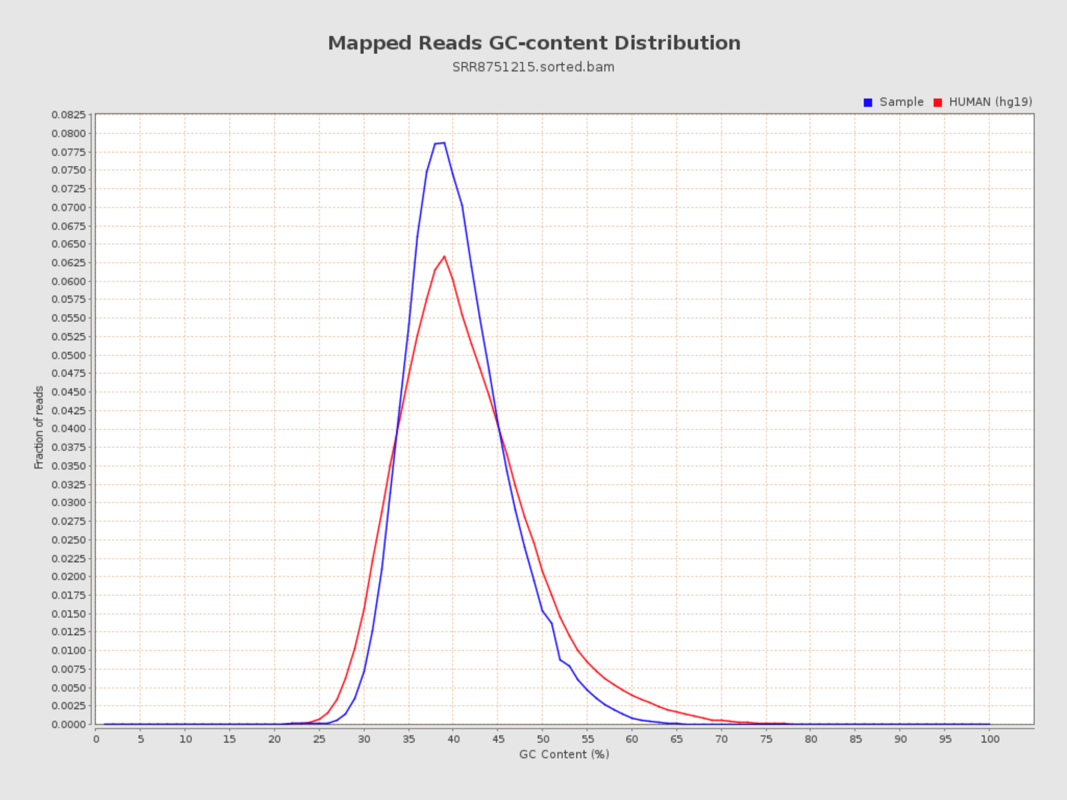
7. Results : Duplication Rate Histogram



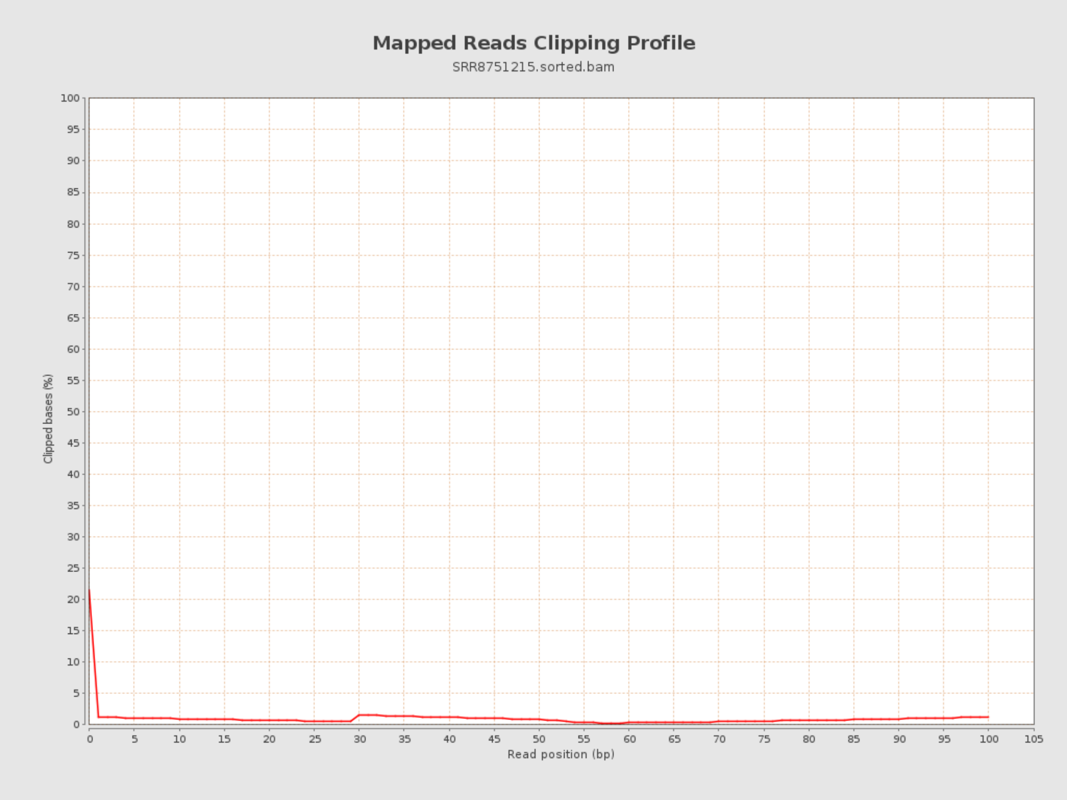
8. Results : Mapped Reads Nucleotide Content



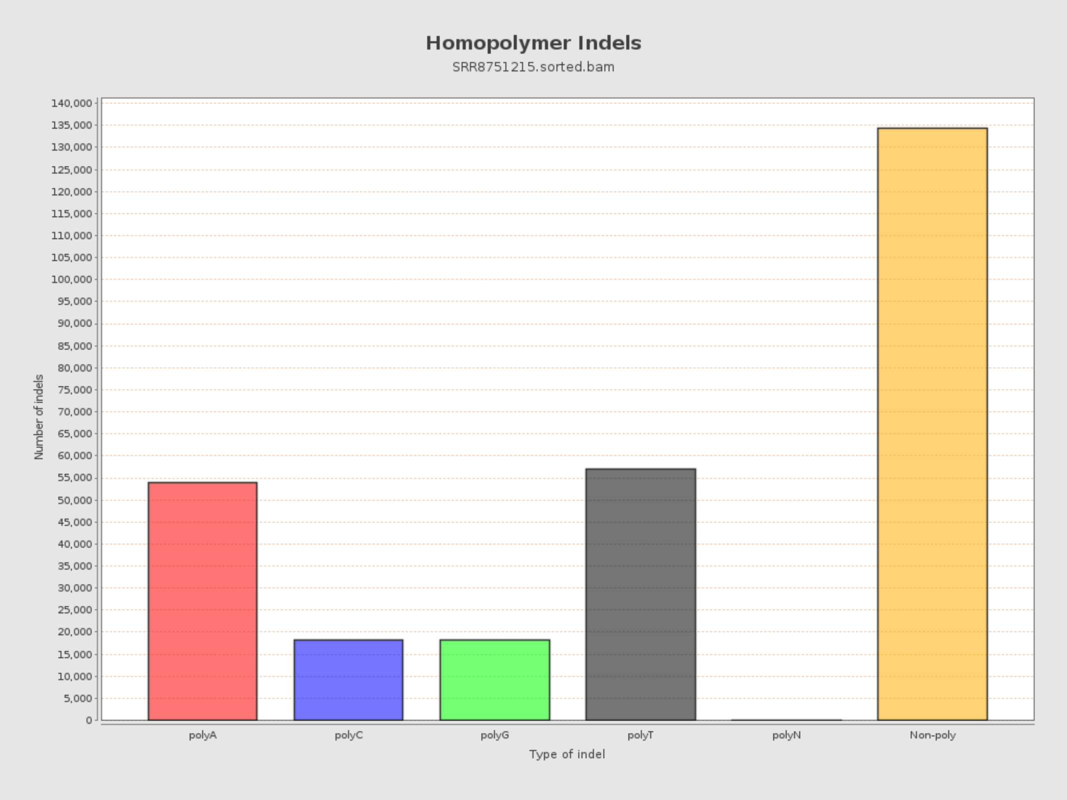
9. Results : Mapped Reads GC-content Distribution



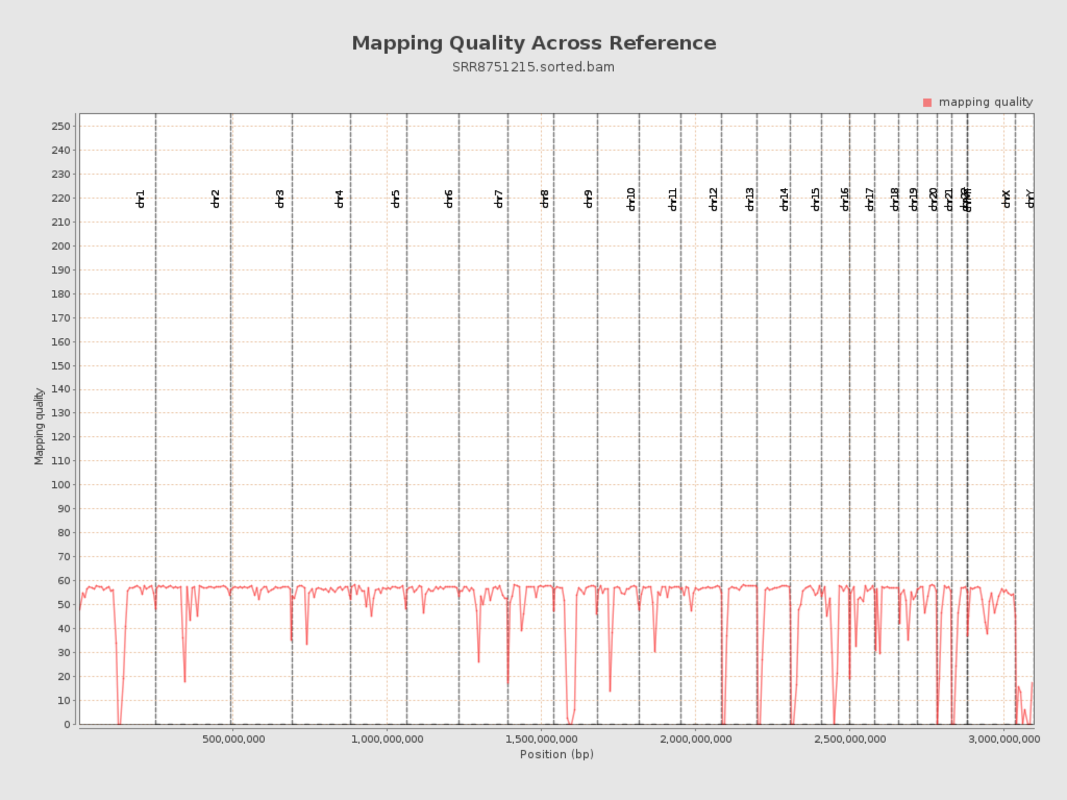
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram