Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 21:02:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8751213.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_SRR8751213 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8751213.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 21:02:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8751213.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,255,322
Mapped reads	3,148,652 / 59.91%
Unmapped reads	2,106,670 / 40.09%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	190,663 / 3.63%
Read min/max/mean length	30 / 101 / 102.5
Duplicated reads (estimated)	129,610 / 2.47%
Duplication rate	1.94%
Clipped reads	816,500 / 15.54%

2.2. ACGT Content

Number/percentage of A's	91,764,805 / 29.71%
Number/percentage of C's	62,654,912 / 20.29%
Number/percentage of T's	92,230,755 / 29.86%
Number/percentage of G's	62,208,793 / 20.14%
Number/percentage of N's	2,208 / 0%
GC Percentage	40.43%

2.3. Coverage

Mean	0.0998

Standard Deviation	1.3999

2.4. Mapping Quality

Mean Mapping Quality	50.9

2.5. Mismatches and indels

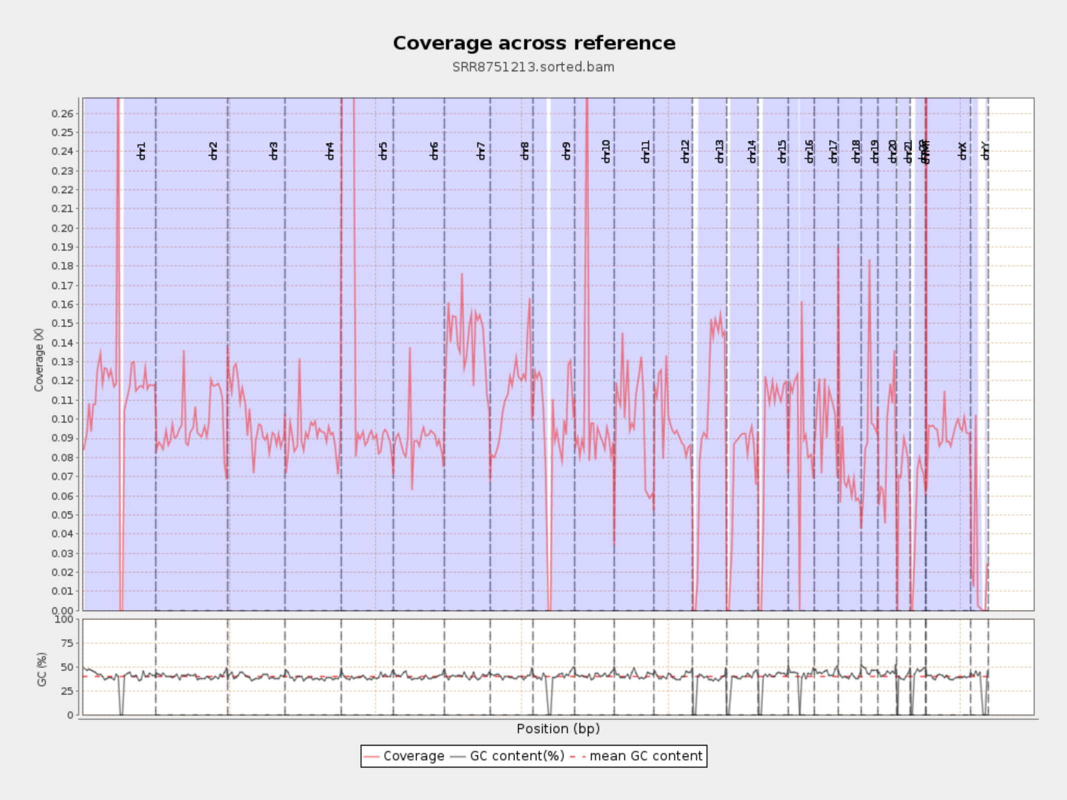
General error rate	0.51%
Mismatches	1,322,860
Insertions	189,467
Mapped reads with at least one insertion	5.79%
Deletions	49,693
Mapped reads with at least one deletion	1.54%
Homopolymer indels	51.65%

2.6. Chromosome stats

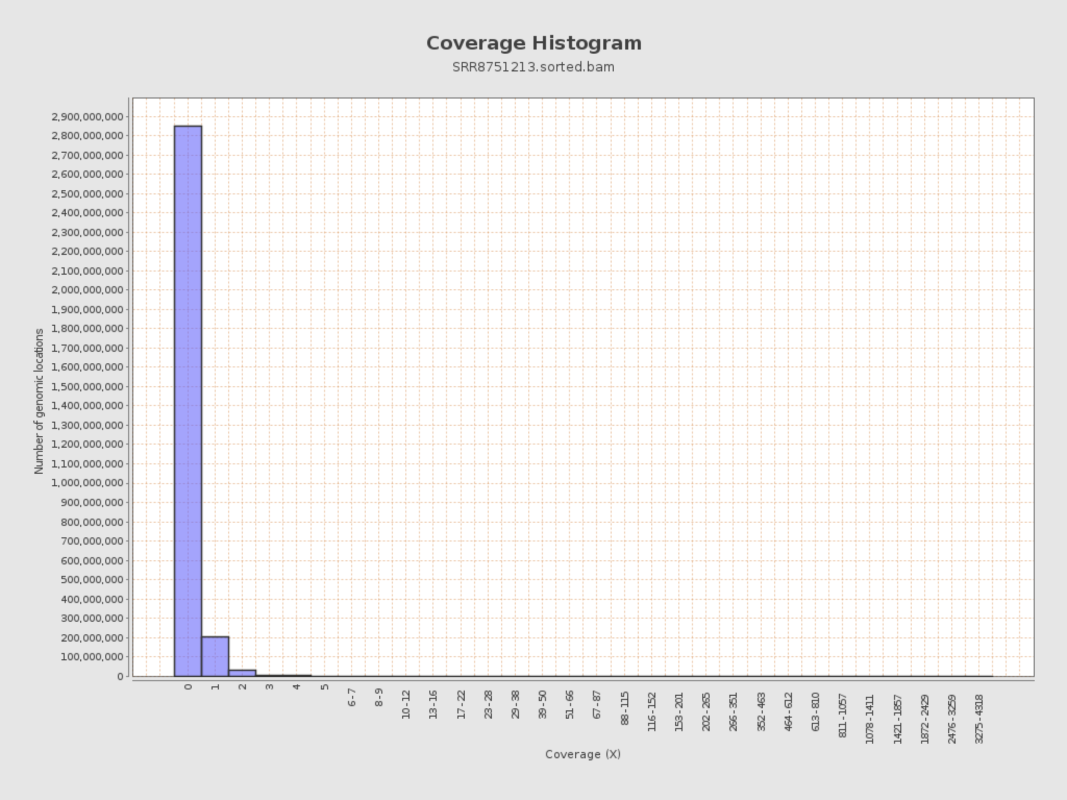
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	28649019	0.1149	4.0198
chr2	243199373	23635816	0.0972	0.5996
chr3	198022430	19828104	0.1001	0.4536
chr4	191154276	17471401	0.0914	0.4614
chr5	180915260	26543001	0.1467	0.5115
chr6	171115067	15379604	0.0899	0.5951
chr7	159138663	22380782	0.1406	0.9269

chr8	146364022	16535746	0.113	1.0487
chr9	141213431	13229191	0.0937	0.6659
chr10	135534747	13654281	0.1007	1.7997
chr11	135006516	13517386	0.1001	0.5792
chr12	133851895	13150323	0.0982	0.4006
chr13	115169878	11959766	0.1038	0.3799
chr14	107349540	7822068	0.0729	0.344
chr15	102531392	9552124	0.0932	0.3586
chr16	90354753	8504539	0.0941	0.7141
chr17	81195210	8344518	0.1028	0.5792
chr18	78077248	5579632	0.0715	1.6608
chr19	59128983	5781628	0.0978	2.7387
chr20	63025520	5515021	0.0875	0.3742
chr21	48129895	3344976	0.0695	0.3808
chr22	51304566	2623726	0.0511	0.2695
chrMT	16571	312244	18.8428	18.2252
chrX	155270560	14444293	0.093	0.4137
chrY	59373566	1217896	0.0205	1.0263

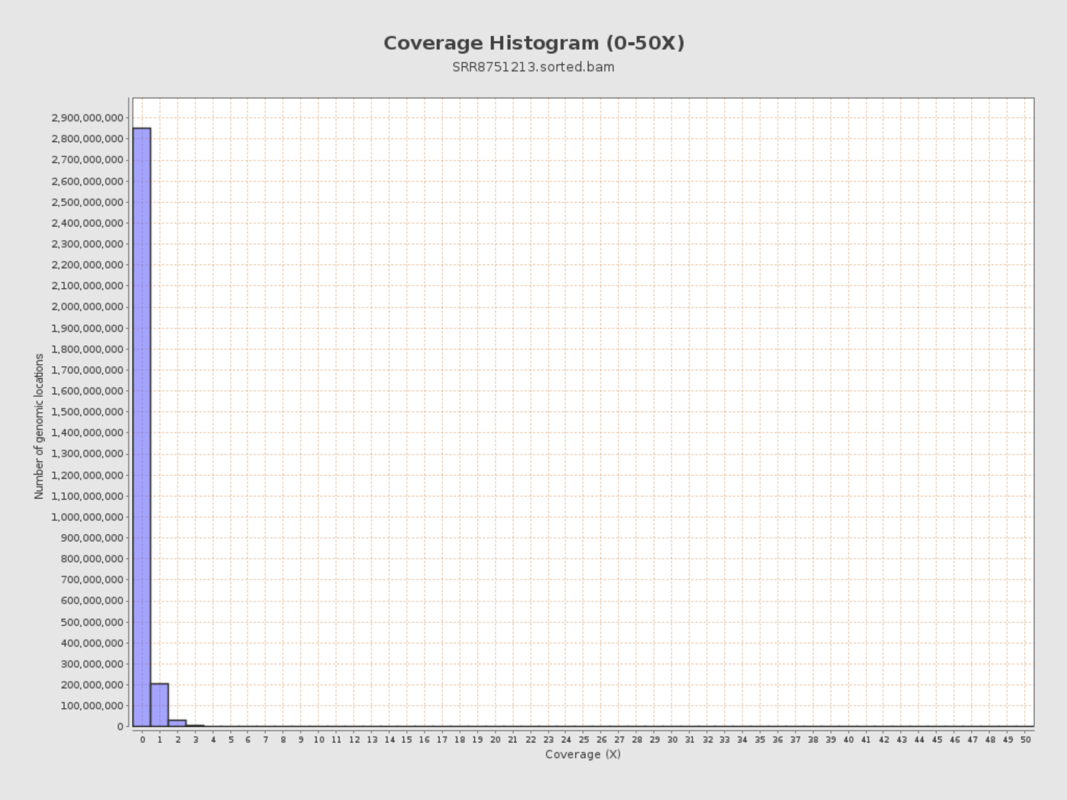
3. Results : Coverage across reference



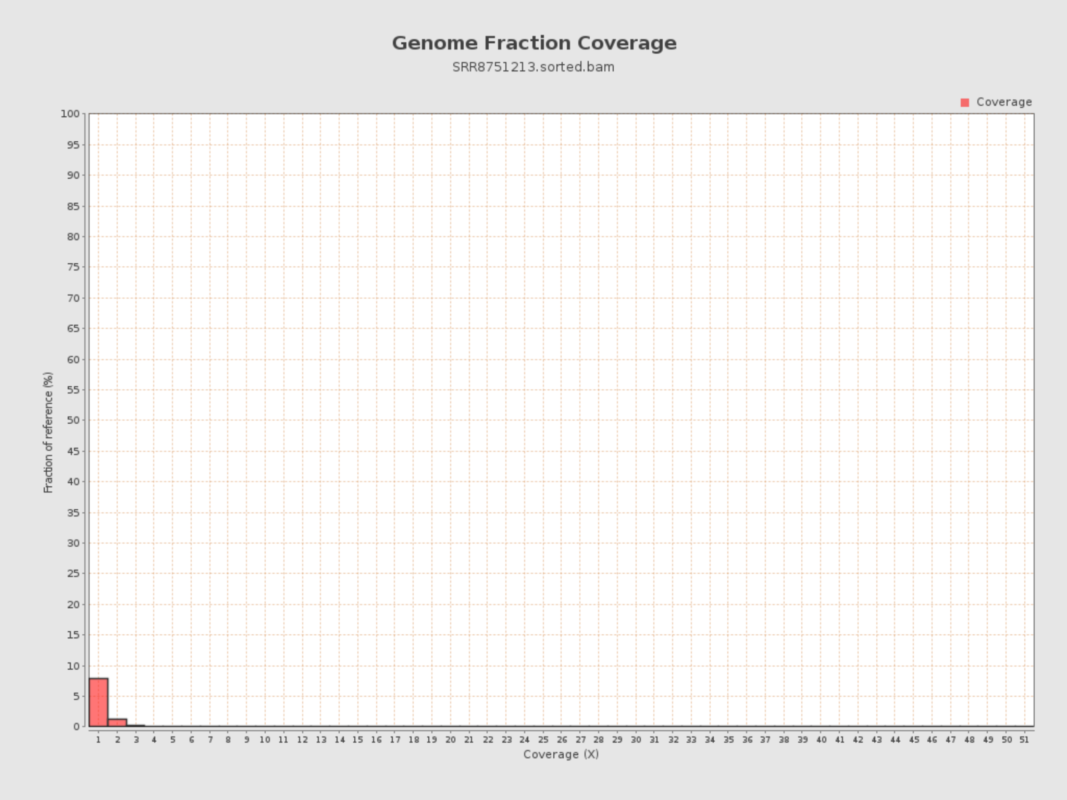
4. Results : Coverage Histogram



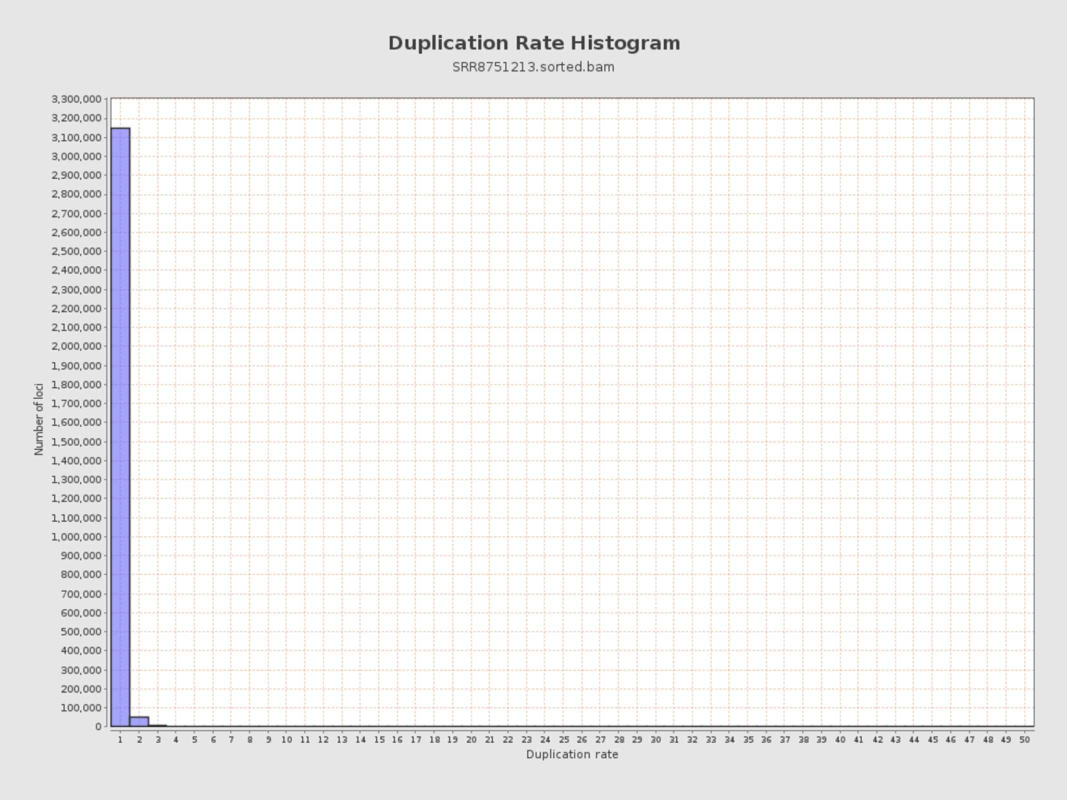
5. Results : Coverage Histogram (0-50X)



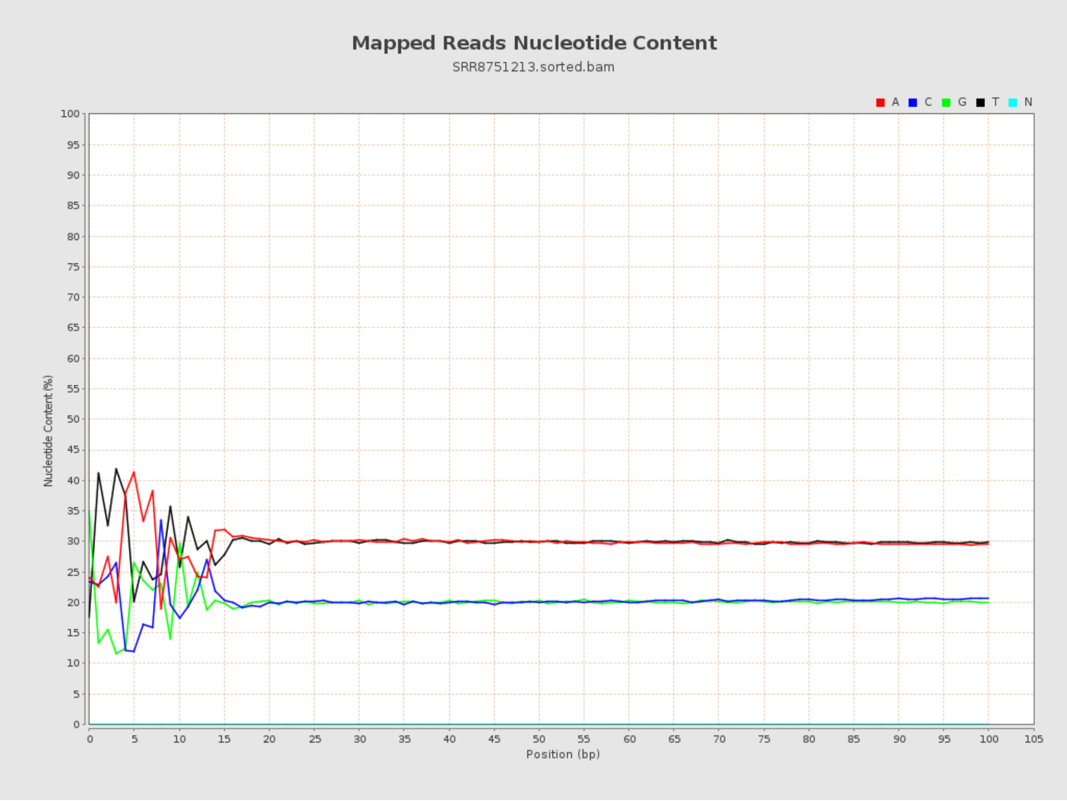
6. Results : Genome Fraction Coverage



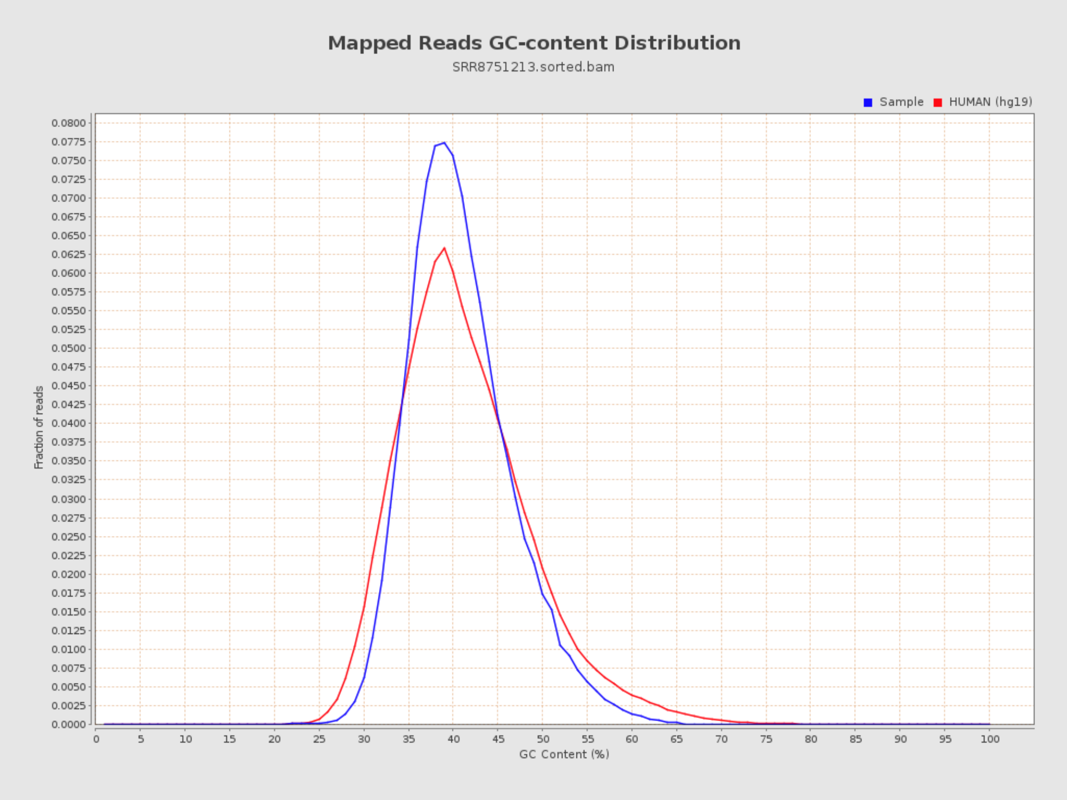
7. Results : Duplication Rate Histogram



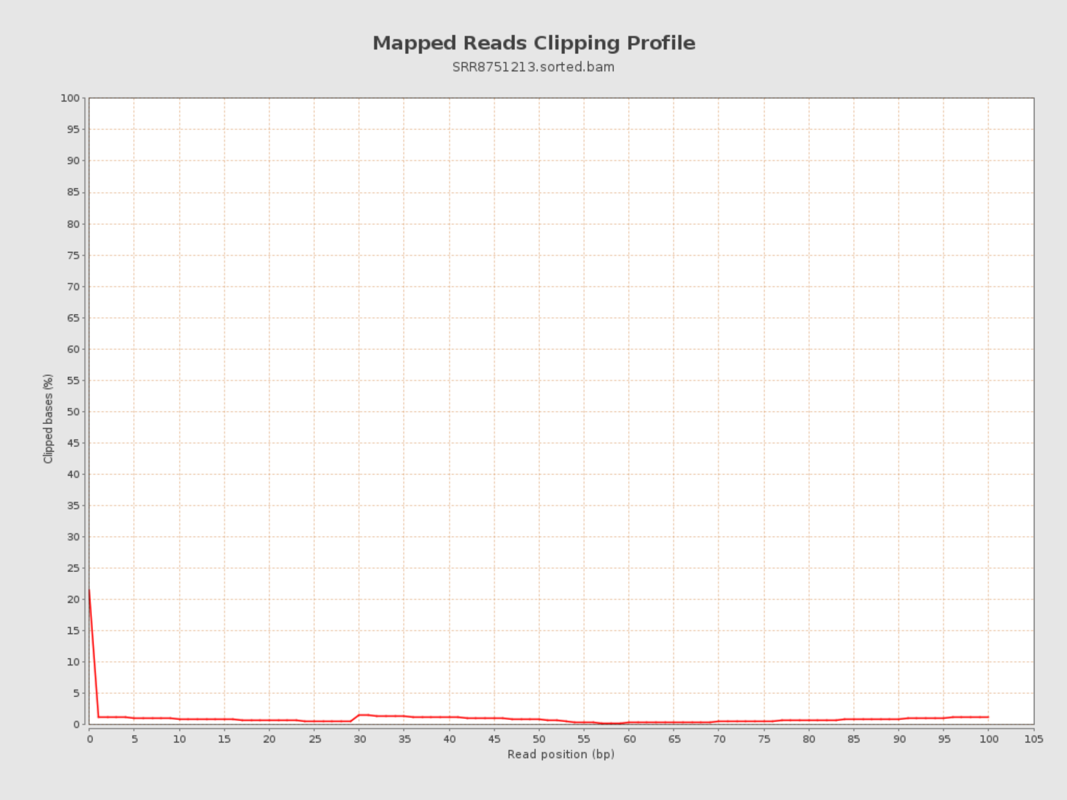
8. Results : Mapped Reads Nucleotide Content



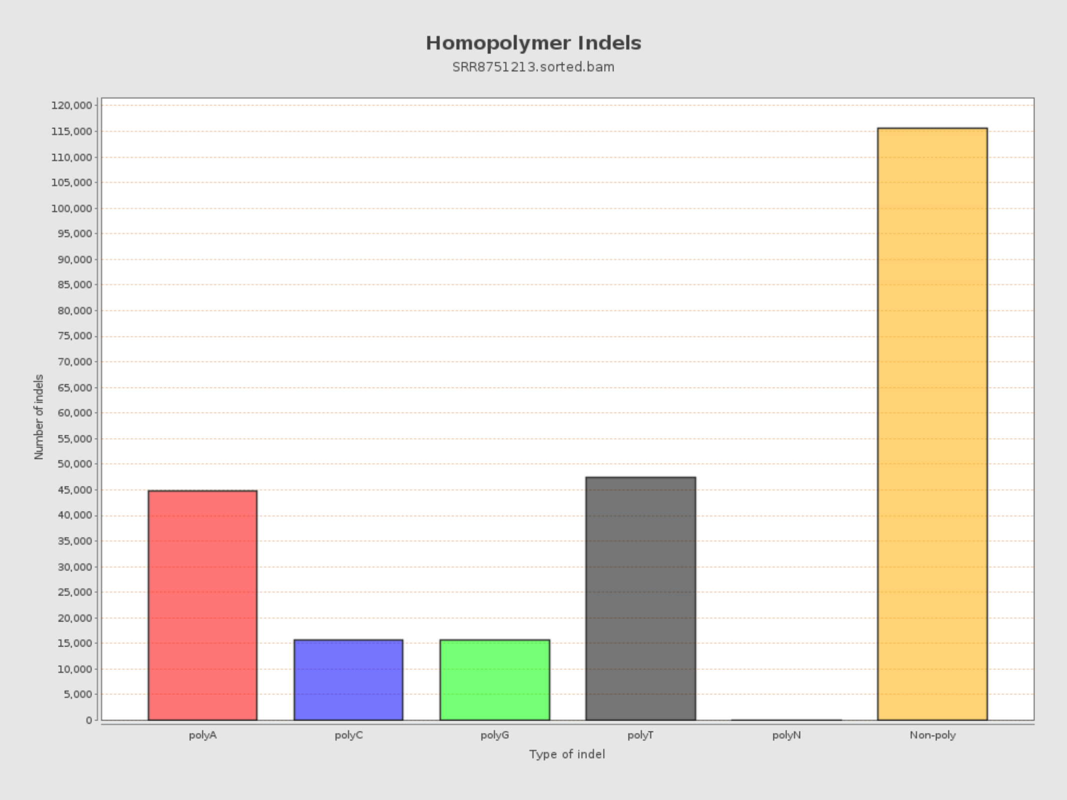
9. Results : Mapped Reads GC-content Distribution



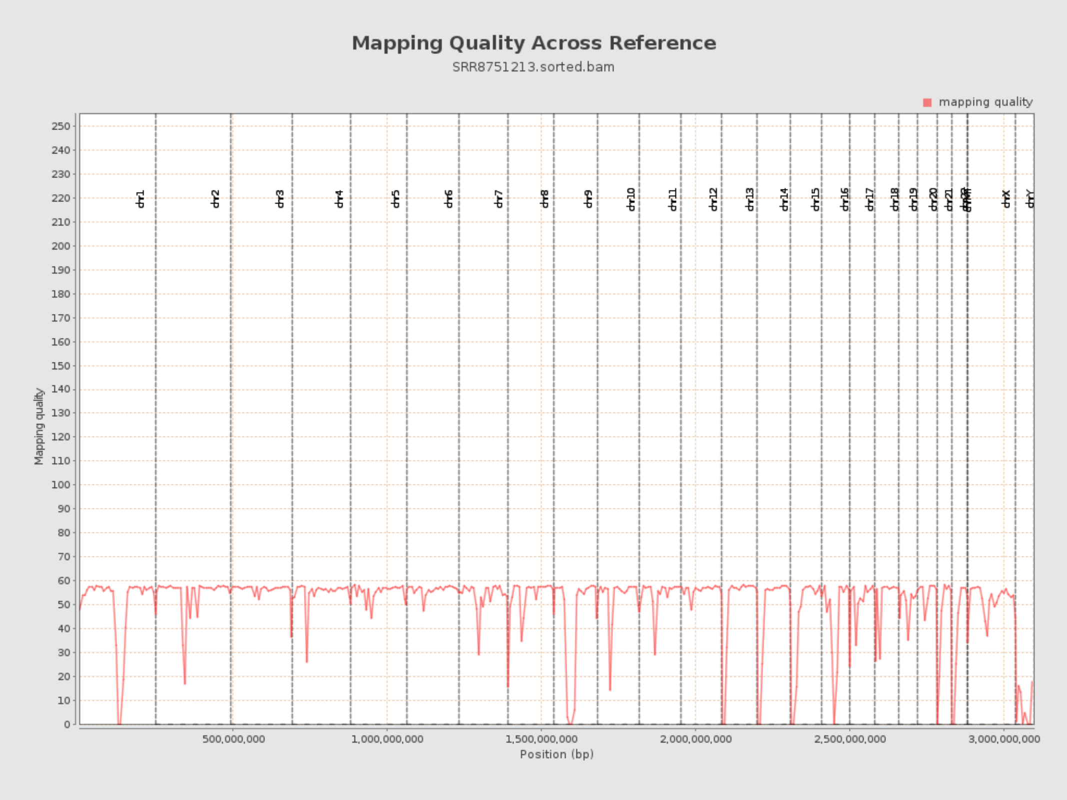
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram