Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 03:31:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819151.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_SRR1819151 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819151.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 03:31:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819151.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	21,337,406
Mapped reads	20,898,728 / 97.94%
Unmapped reads	438,678 / 2.06%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,546 / 0.05%
Read min/max/mean length	30 / 76 / 76.02
Duplicated reads (estimated)	1,118,721 / 5.24%
Duplication rate	1.98%
Clipped reads	20,812,277 / 97.54%

2.2. ACGT Content

Number/percentage of A's	401,208,997 / 28.3%
Number/percentage of C's	297,799,518 / 21.01%
Number/percentage of T's	417,007,026 / 29.42%
Number/percentage of G's	301,408,441 / 21.26%
Number/percentage of N's	89,184 / 0.01%
GC Percentage	42.27%

2.3. Coverage

Mean	0.458

Standard Deviation	4.9285

2.4. Mapping Quality

Mean Mapping Quality	48.79

2.5. Mismatches and indels

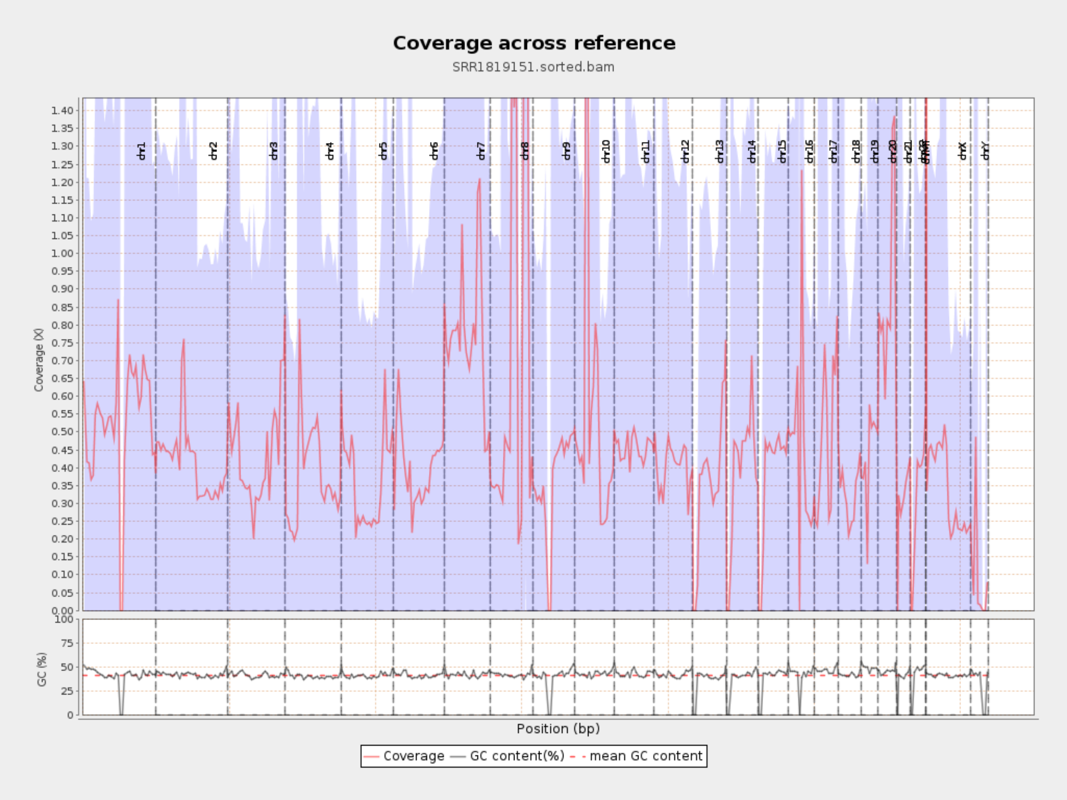
General error rate	0.31%
Mismatches	4,180,589
Insertions	111,654
Mapped reads with at least one insertion	0.53%
Deletions	113,223
Mapped reads with at least one deletion	0.54%
Homopolymer indels	36.64%

2.6. Chromosome stats

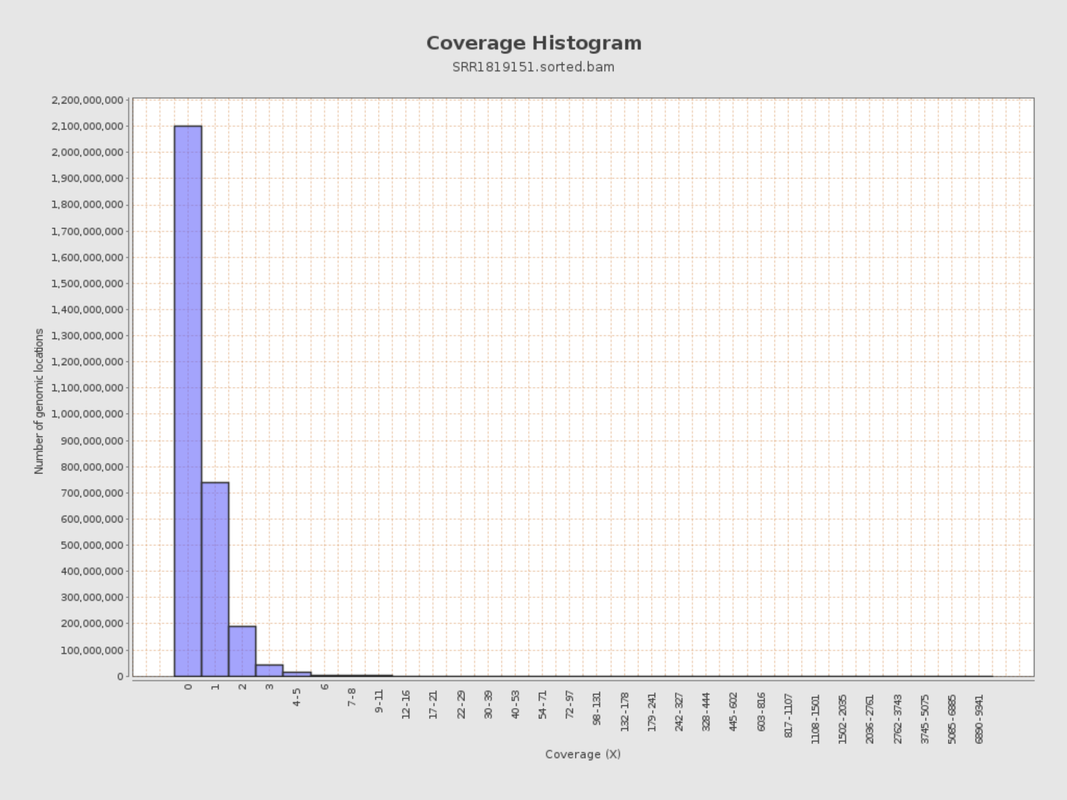
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	132187435	0.5303	7.7624
chr2	243199373	101450925	0.4172	3.3926
chr3	198022430	86175821	0.4352	2.8036
chr4	191154276	73378670	0.3839	2.8905
chr5	180915260	65794311	0.3637	0.7213
chr6	171115067	68229670	0.3987	1.2129
chr7	159138663	122638163	0.7706	6.8671

chr8	146364022	125450124	0.8571	2.5028
chr9	141213431	50619269	0.3585	1.8729
chr10	135534747	74926119	0.5528	16.4421
chr11	135006516	61457463	0.4552	1.8977
chr12	133851895	54300430	0.4057	0.7867
chr13	115169878	41274522	0.3584	0.6545
chr14	107349540	42832878	0.399	0.8759
chr15	102531392	38281584	0.3734	0.6772
chr16	90354753	40769973	0.4512	5.0915
chr17	81195210	38655294	0.4761	1.8755
chr18	78077248	25758638	0.3299	3.8818
chr19	59128983	25695762	0.4346	4.9197
chr20	63025520	57866789	0.9181	1.4462
chr21	48129895	14970215	0.311	2.6646
chr22	51304566	15232377	0.2969	0.8399
chrMT	16571	1350461	81.4954	25.6652
chrX	155270560	52663648	0.3392	1.1401
chrY	59373566	5786595	0.0975	4.9068

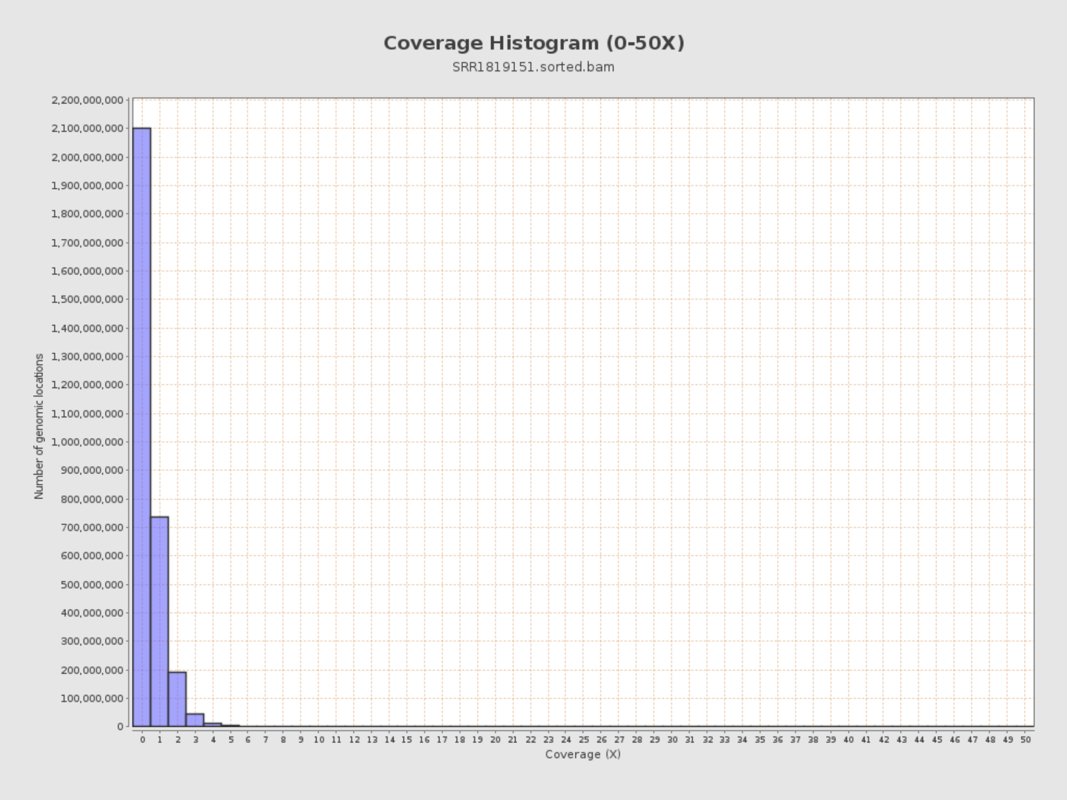
3. Results : Coverage across reference



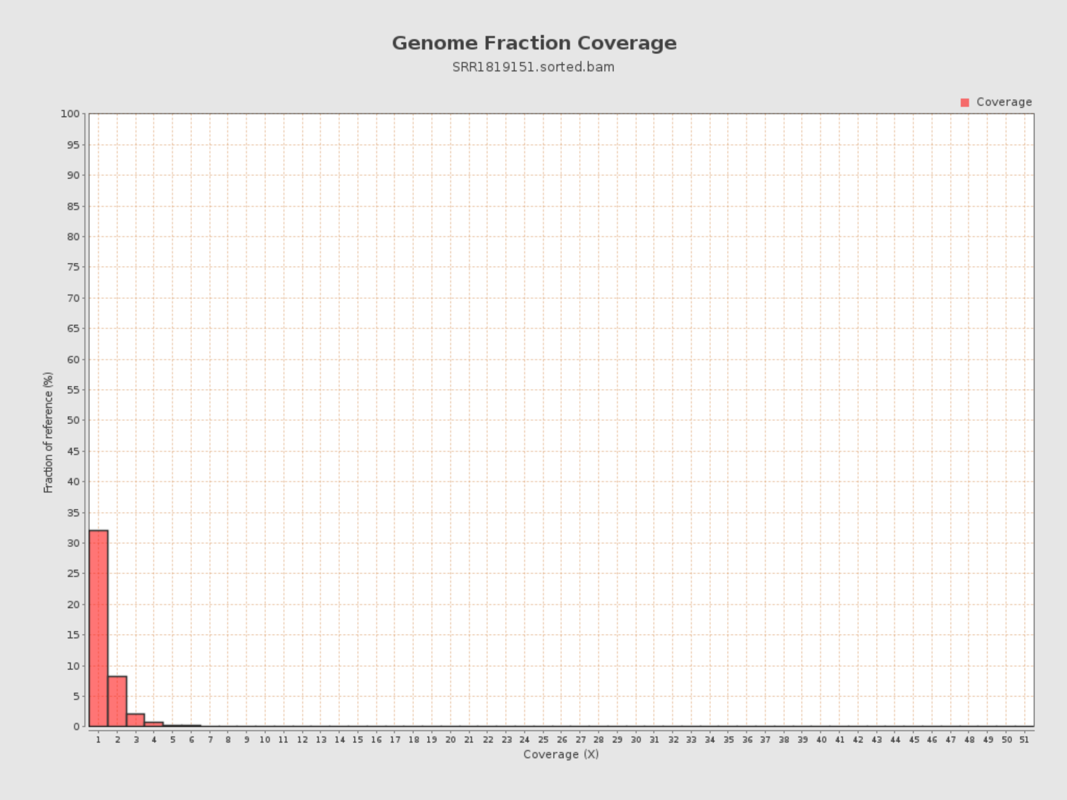
4. Results : Coverage Histogram



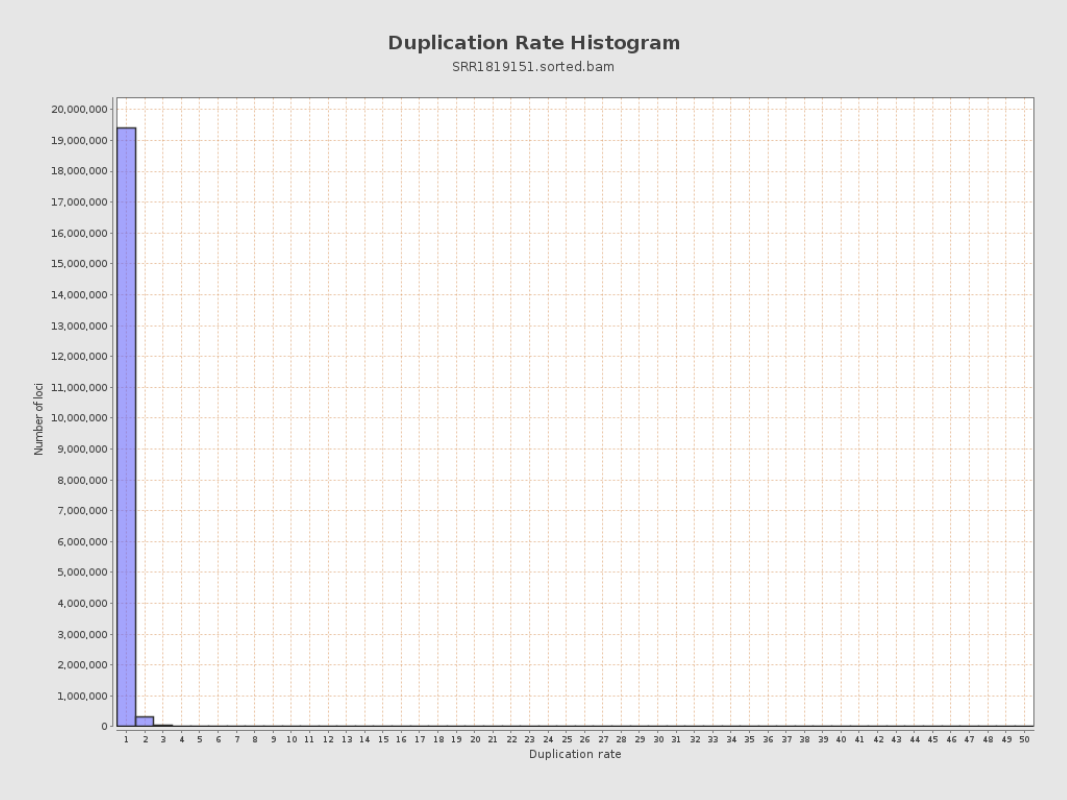
5. Results : Coverage Histogram (0-50X)



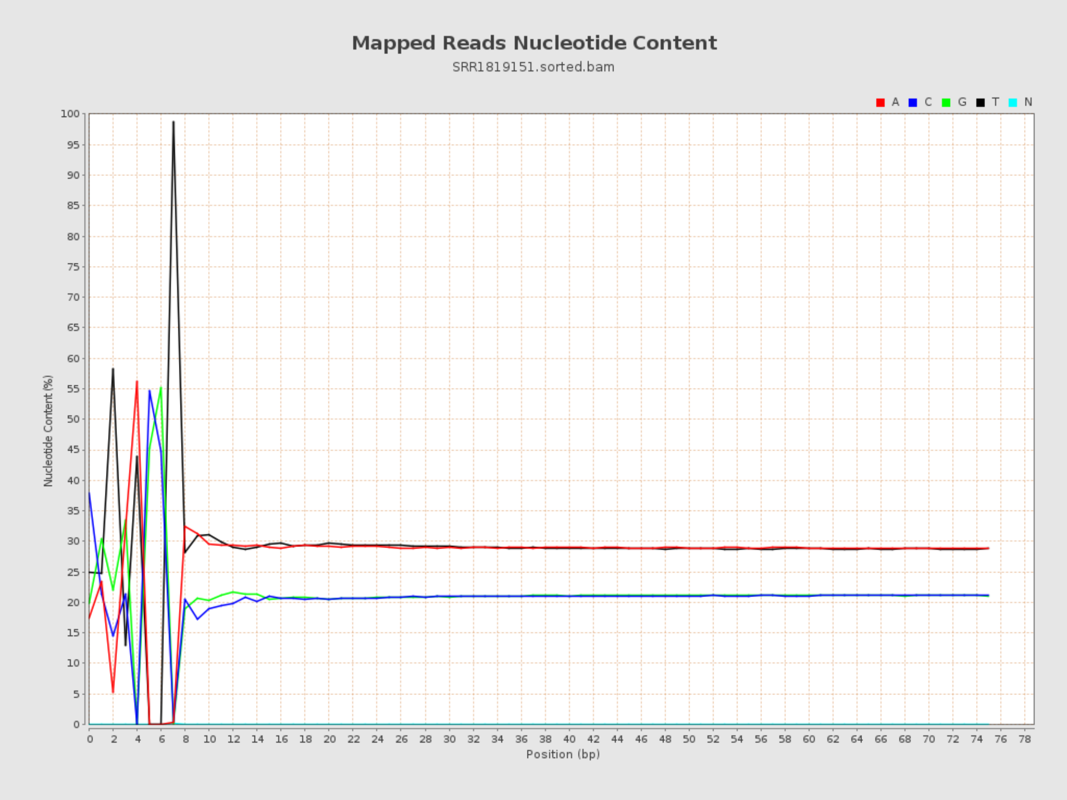
6. Results : Genome Fraction Coverage



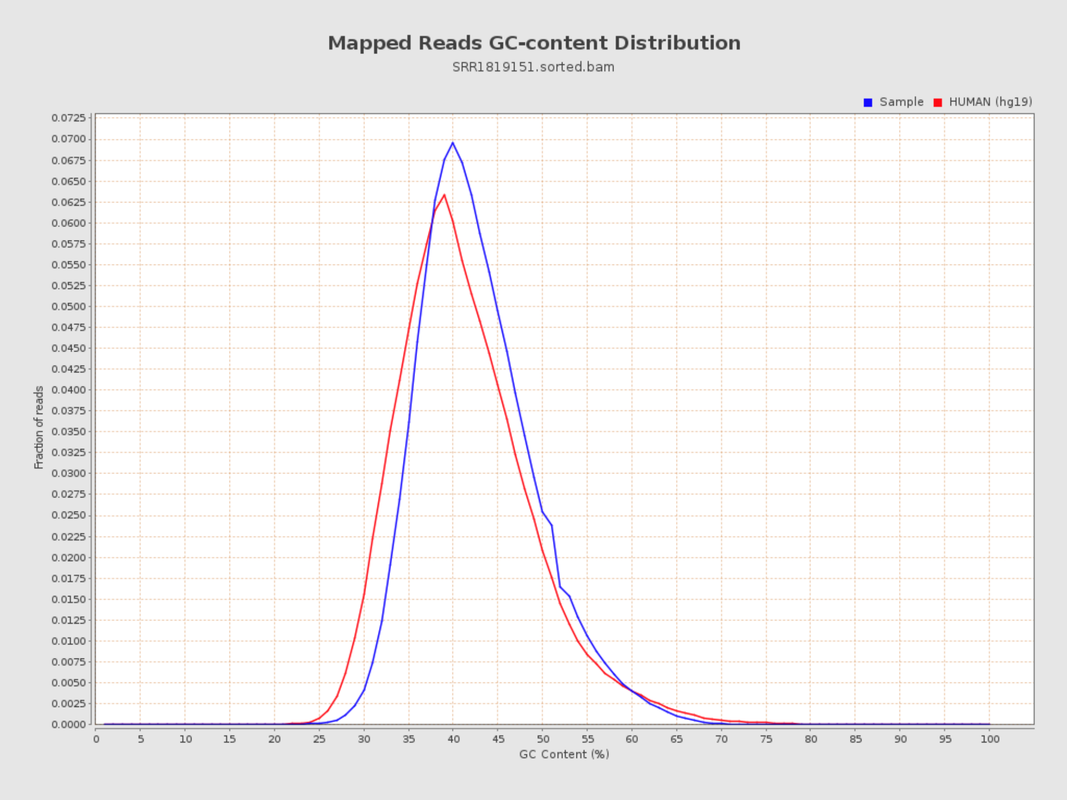
7. Results : Duplication Rate Histogram



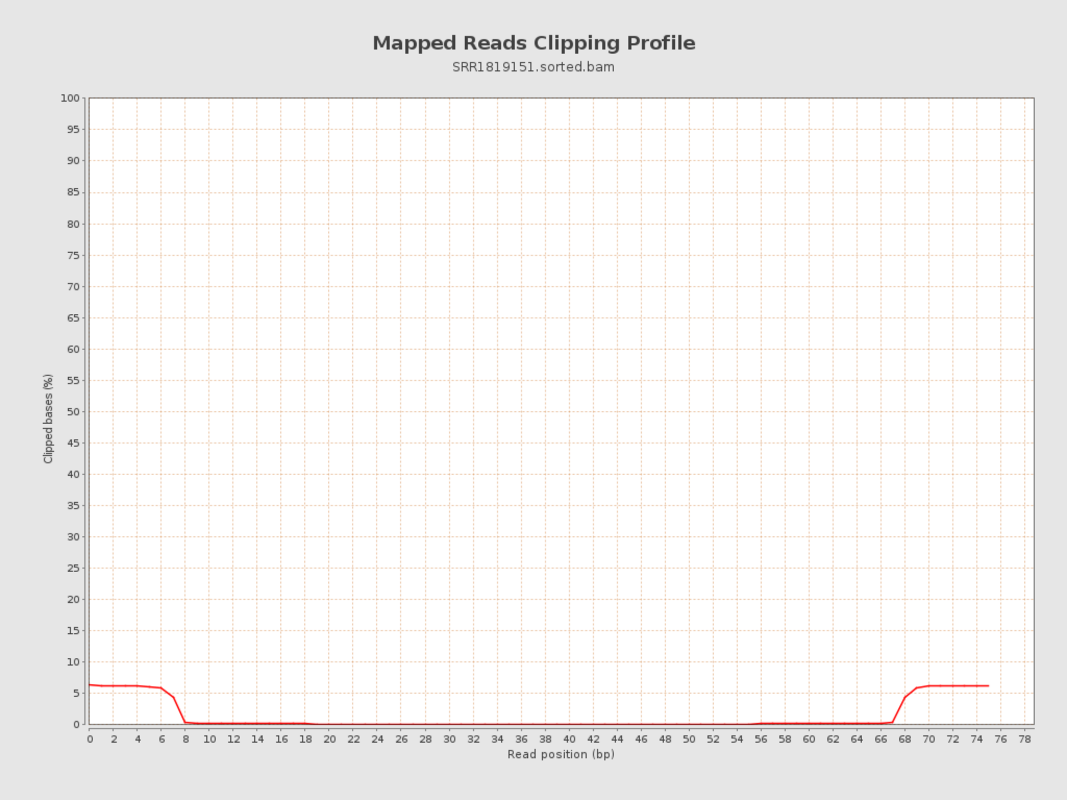
8. Results : Mapped Reads Nucleotide Content



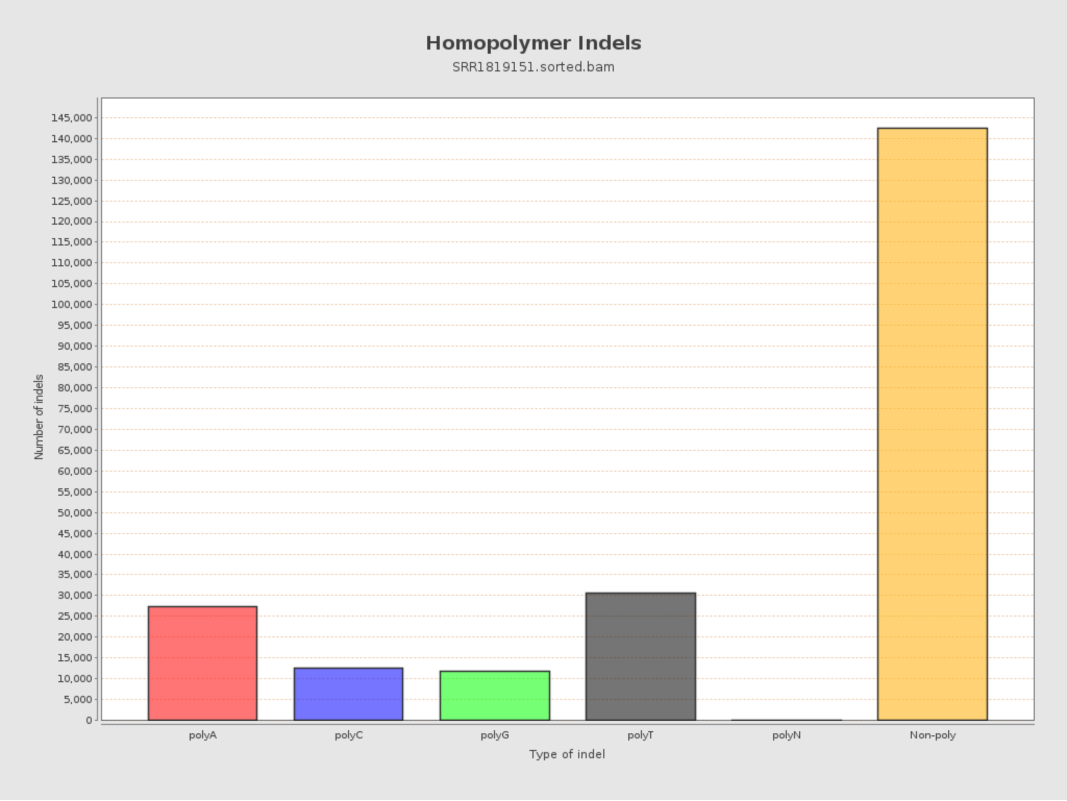
9. Results : Mapped Reads GC-content Distribution



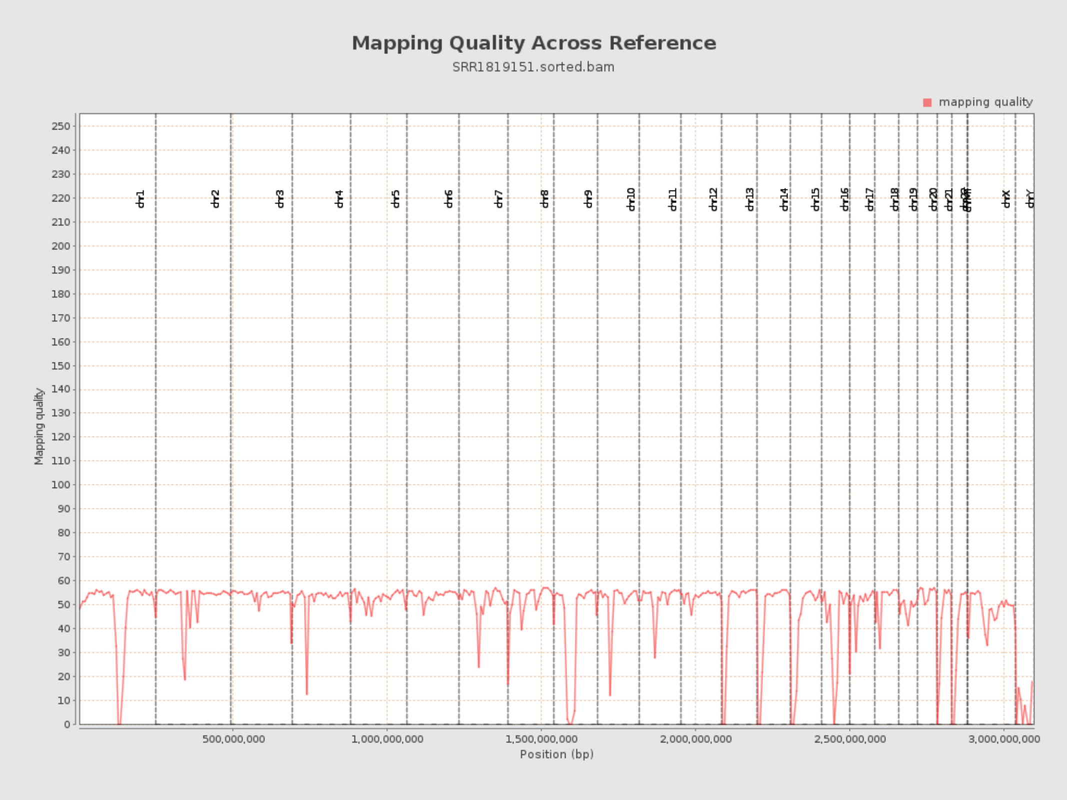
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram