Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 07:08:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716318.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_SRR9716318 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716318.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 07:08:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716318.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,456,164
Mapped reads	1,318,762 / 90.56%
Unmapped reads	137,402 / 9.44%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,732 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	31,008 / 2.13%
Duplication rate	1.77%
Clipped reads	1,321,088 / 90.72%

2.2. ACGT Content

Number/percentage of A's	18,914,608 / 25.15%
Number/percentage of C's	13,977,945 / 18.59%
Number/percentage of T's	23,058,659 / 30.66%
Number/percentage of G's	19,253,076 / 25.6%
Number/percentage of N's	1,692 / 0%
GC Percentage	44.19%

2.3. Coverage

Mean	0.0243

Standard Deviation	0.2015

2.4. Mapping Quality

Mean Mapping Quality	43.92

2.5. Mismatches and indels

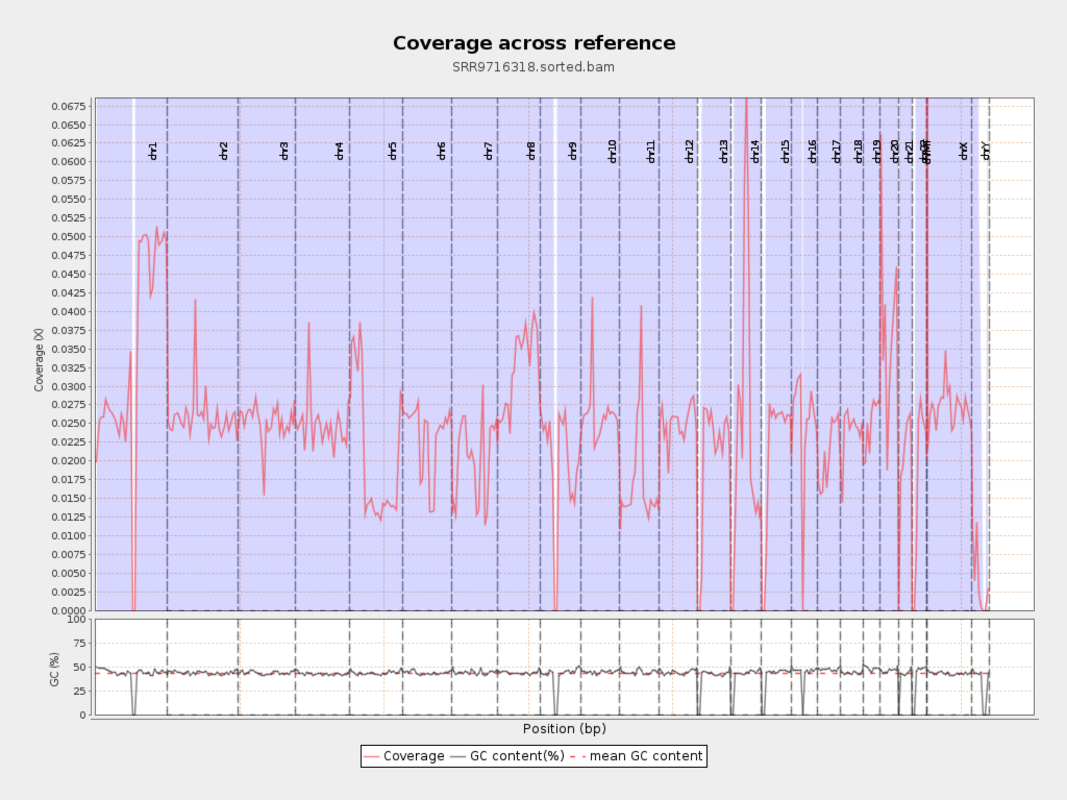
General error rate	0.5%
Mismatches	363,671
Insertions	4,853
Mapped reads with at least one insertion	0.37%
Deletions	11,757
Mapped reads with at least one deletion	0.88%
Homopolymer indels	40.36%

2.6. Chromosome stats

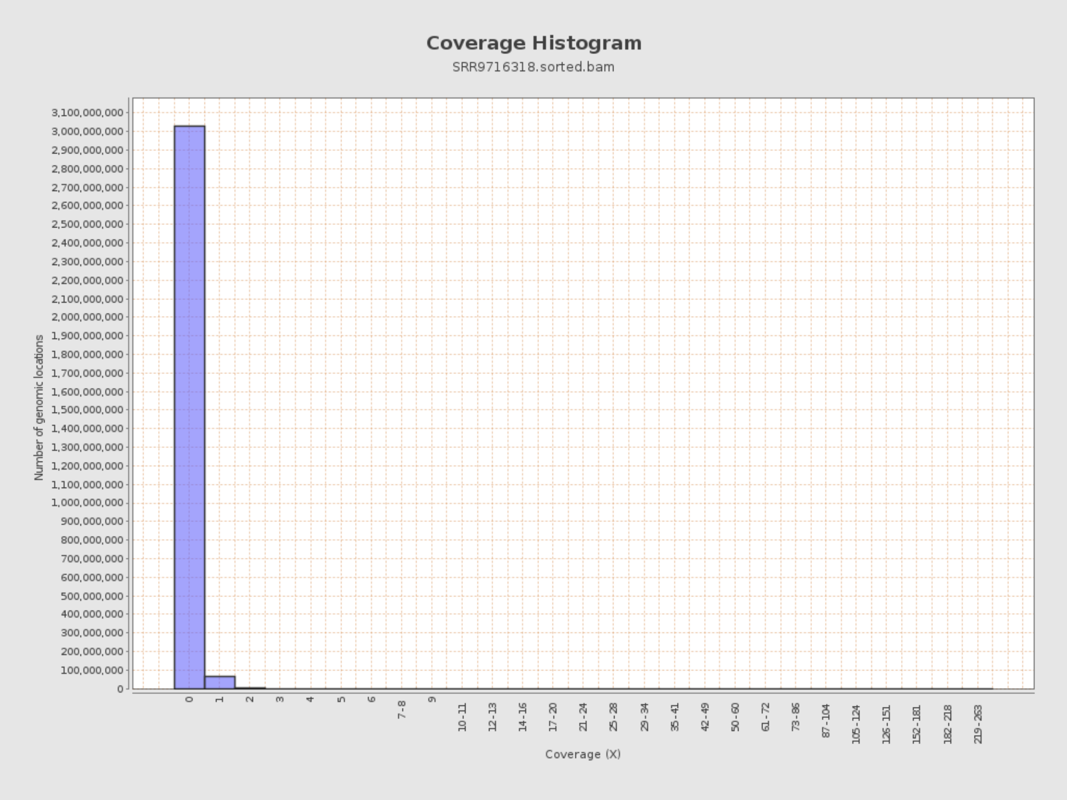
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8420625	0.0338	0.284
chr2	243199373	6301728	0.0259	0.2279
chr3	198022430	4978823	0.0251	0.1699
chr4	191154276	4754547	0.0249	0.1809
chr5	180915260	3714873	0.0205	0.1554
chr6	171115067	3980649	0.0233	0.172
chr7	159138663	3228440	0.0203	0.176

chr8	146364022	4744754	0.0324	0.214
chr9	141213431	2731716	0.0193	0.2058
chr10	135534747	3554347	0.0262	0.2276
chr11	135006516	2366666	0.0175	0.1871
chr12	133851895	3362606	0.0251	0.1717
chr13	115169878	2339585	0.0203	0.1519
chr14	107349540	2651247	0.0247	0.1779
chr15	102531392	2171517	0.0212	0.1569
chr16	90354753	2226409	0.0246	0.182
chr17	81195210	1694191	0.0209	0.1594
chr18	78077248	1842080	0.0236	0.3501
chr19	59128983	1475920	0.025	0.2366
chr20	63025520	2352755	0.0373	0.213
chr21	48129895	973364	0.0202	0.1683
chr22	51304566	908507	0.0177	0.1423
chrMT	16571	3614	0.2181	0.4667
chrX	155270560	4224405	0.0272	0.1957
chrY	59373566	222631	0.0037	0.0912

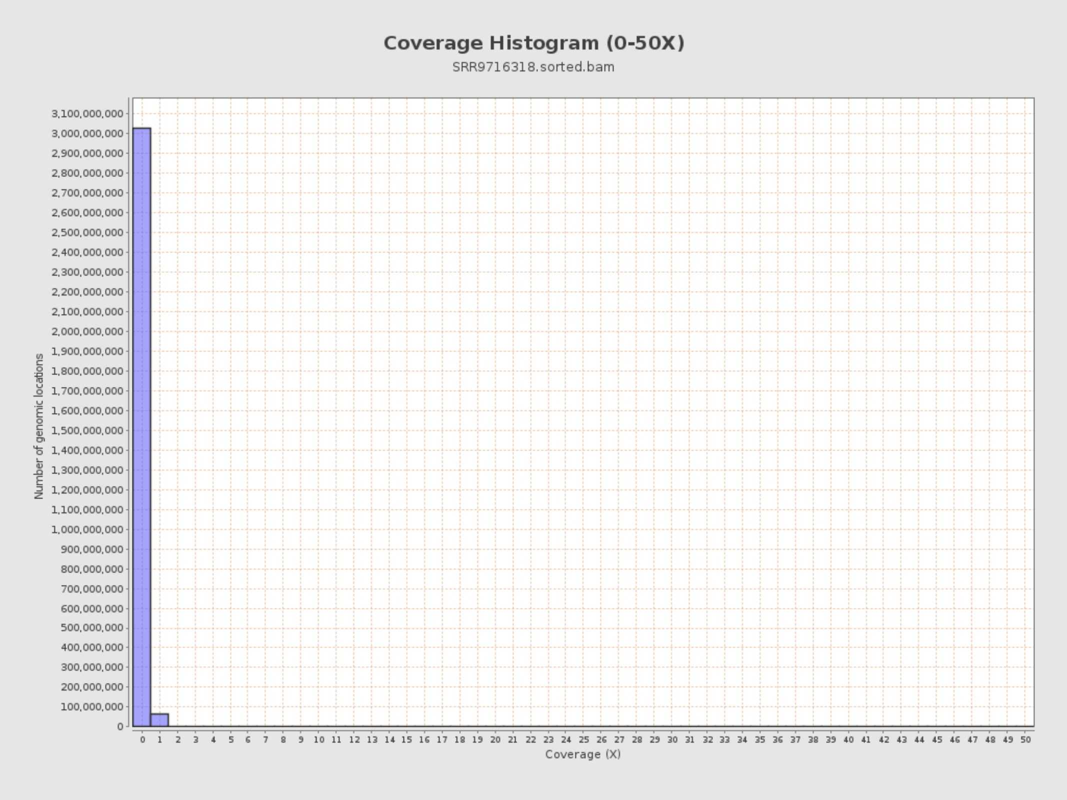
3. Results : Coverage across reference



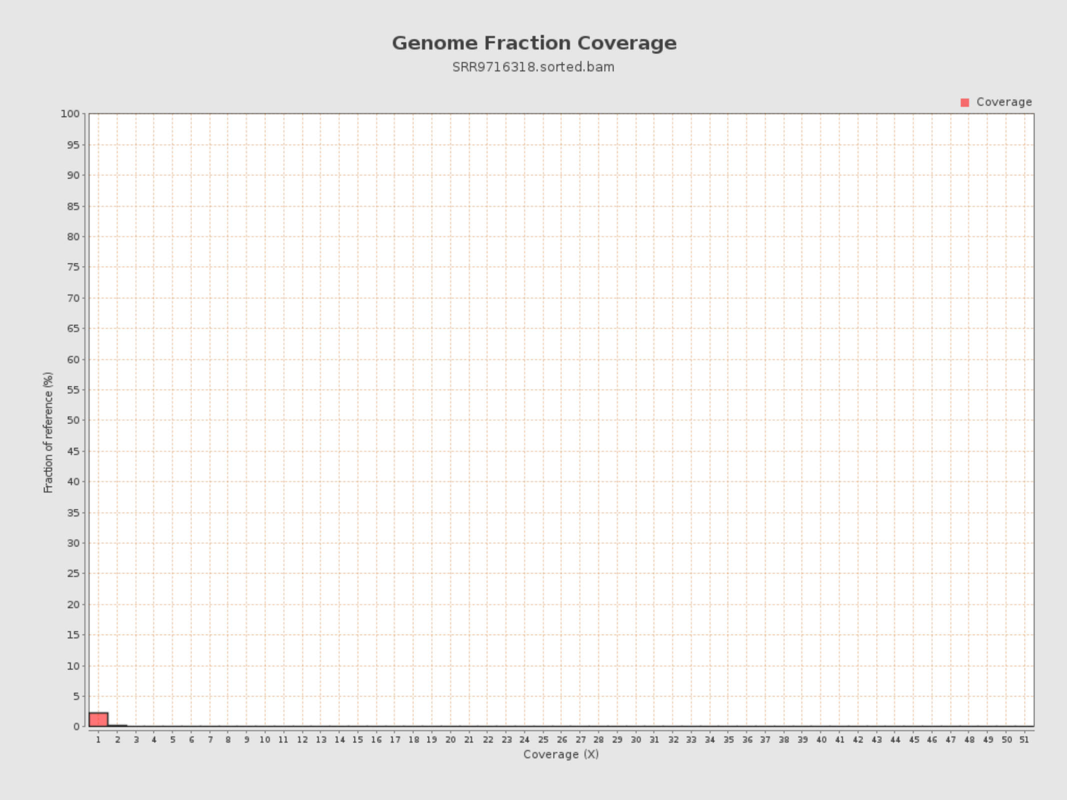
4. Results : Coverage Histogram



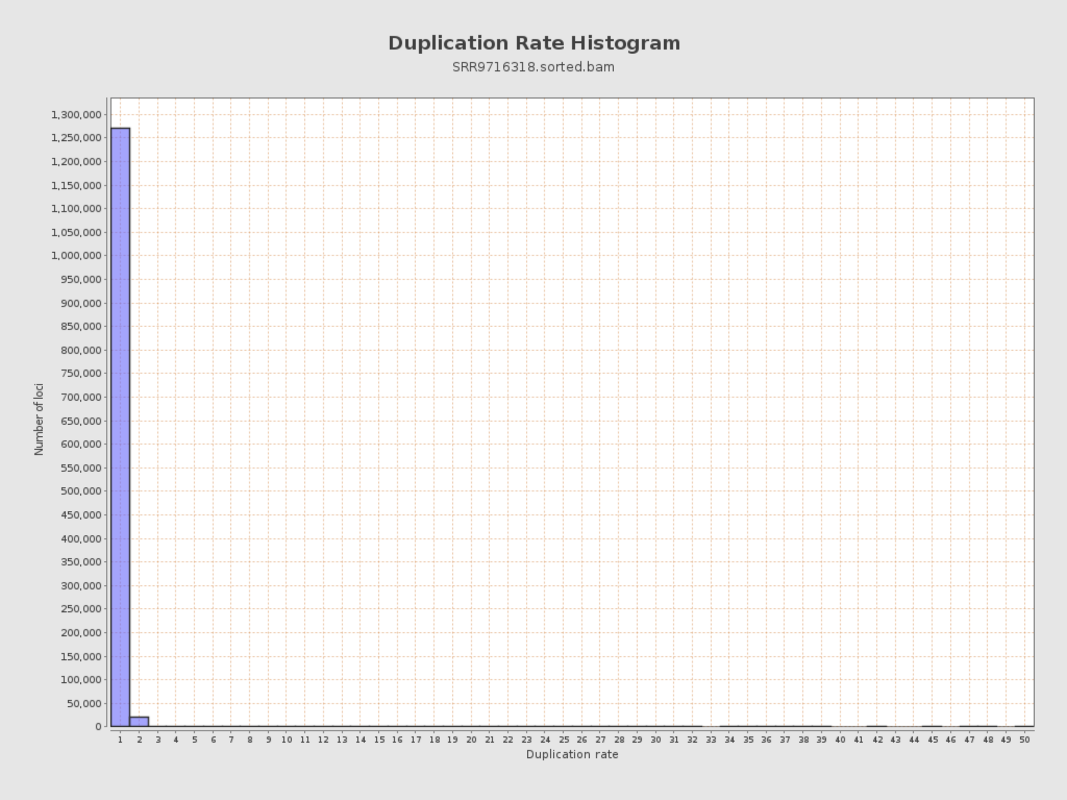
5. Results : Coverage Histogram (0-50X)



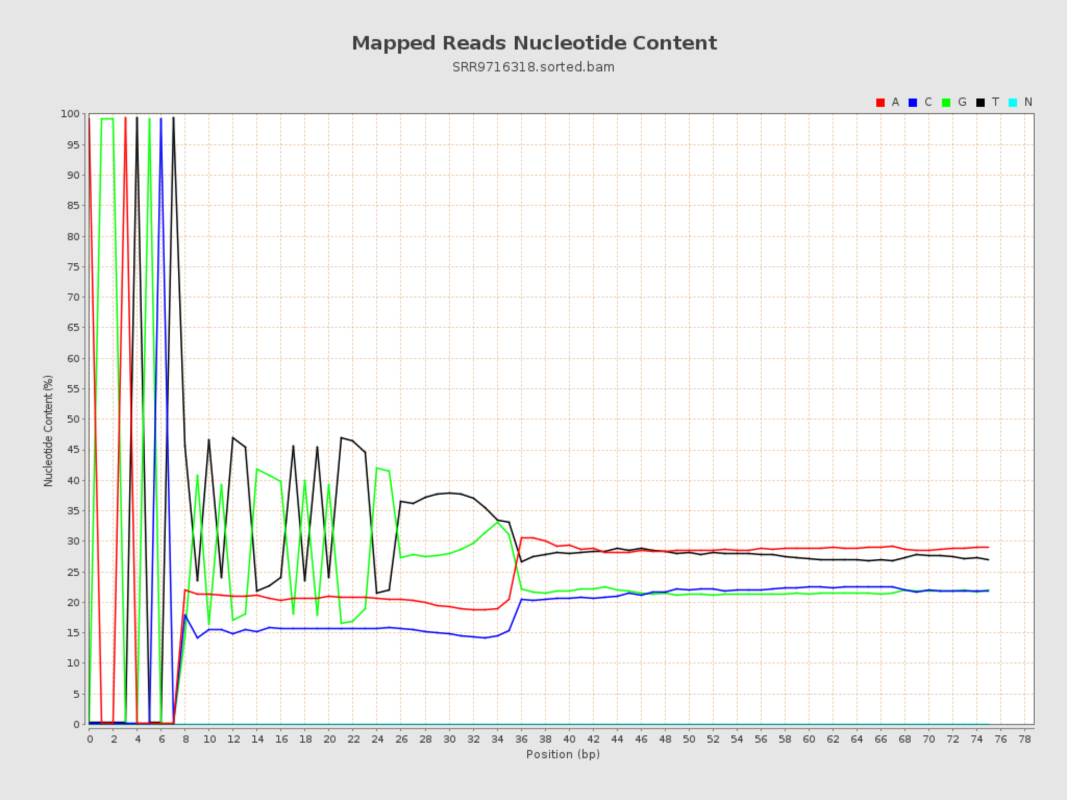
6. Results : Genome Fraction Coverage



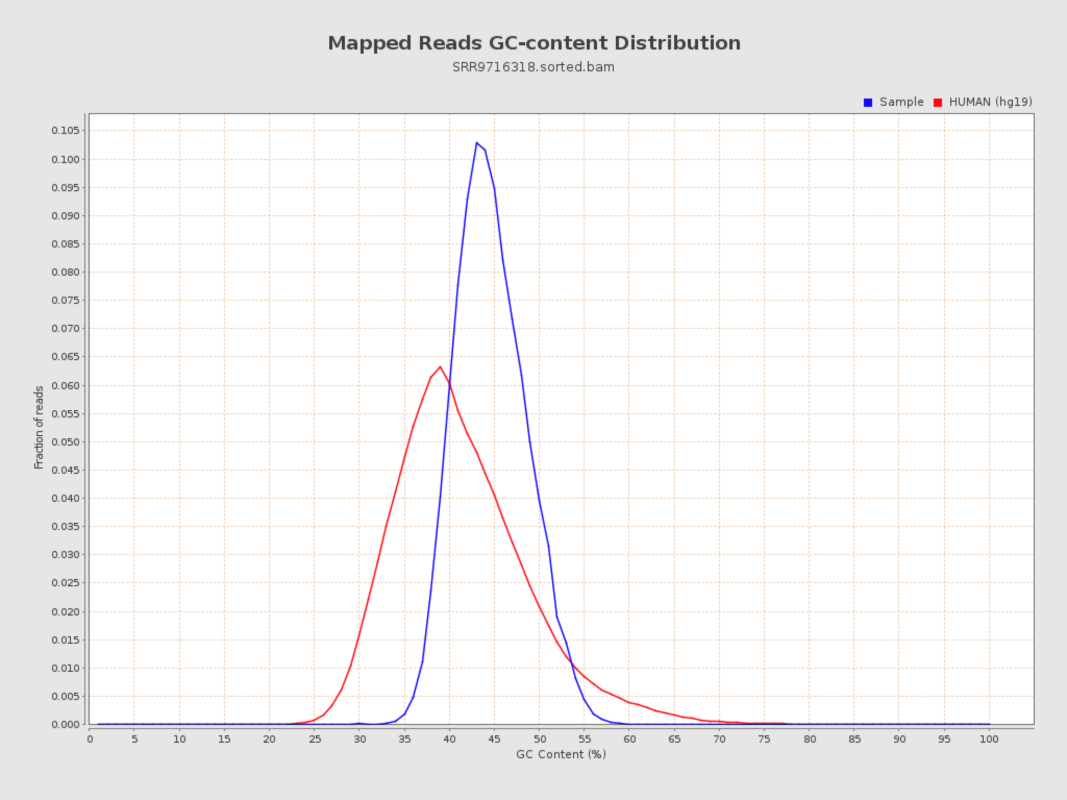
7. Results : Duplication Rate Histogram



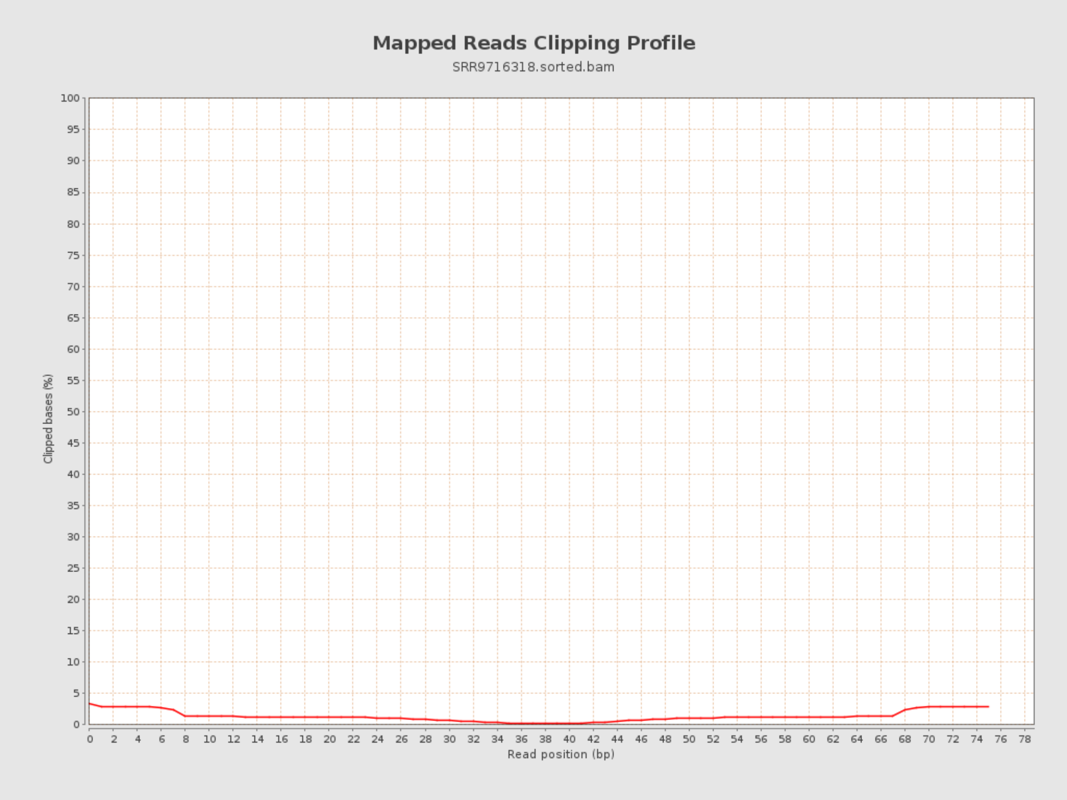
8. Results : Mapped Reads Nucleotide Content



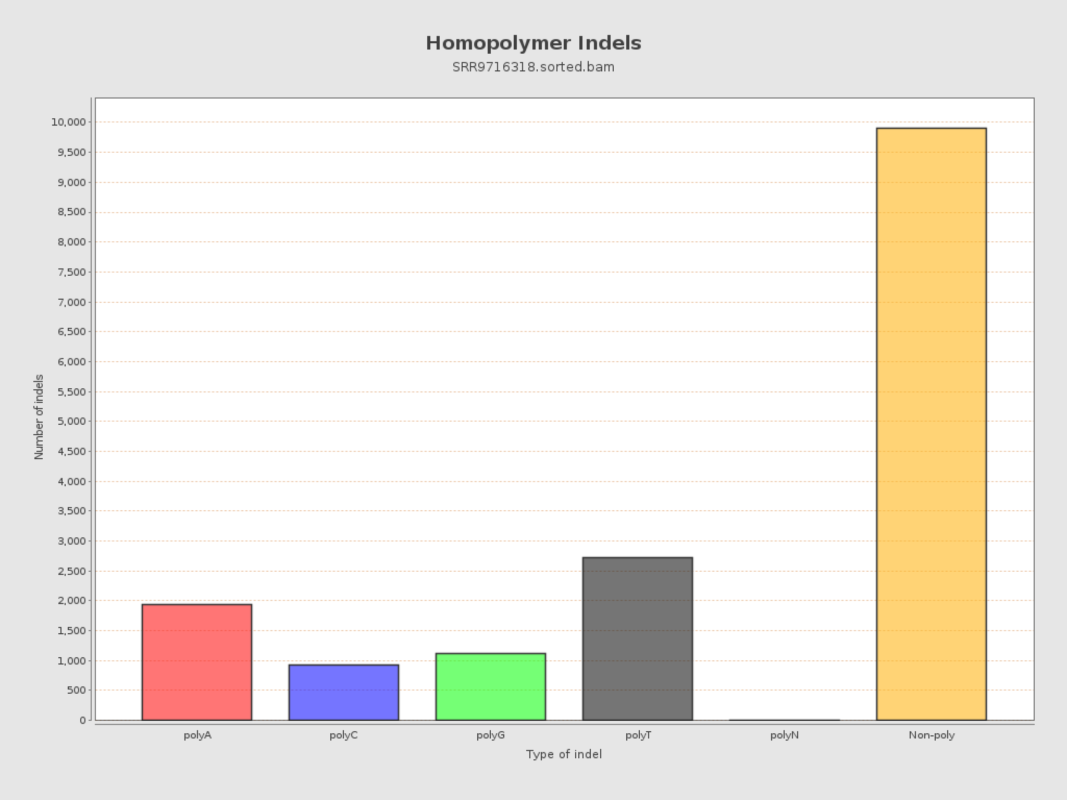
9. Results : Mapped Reads GC-content Distribution



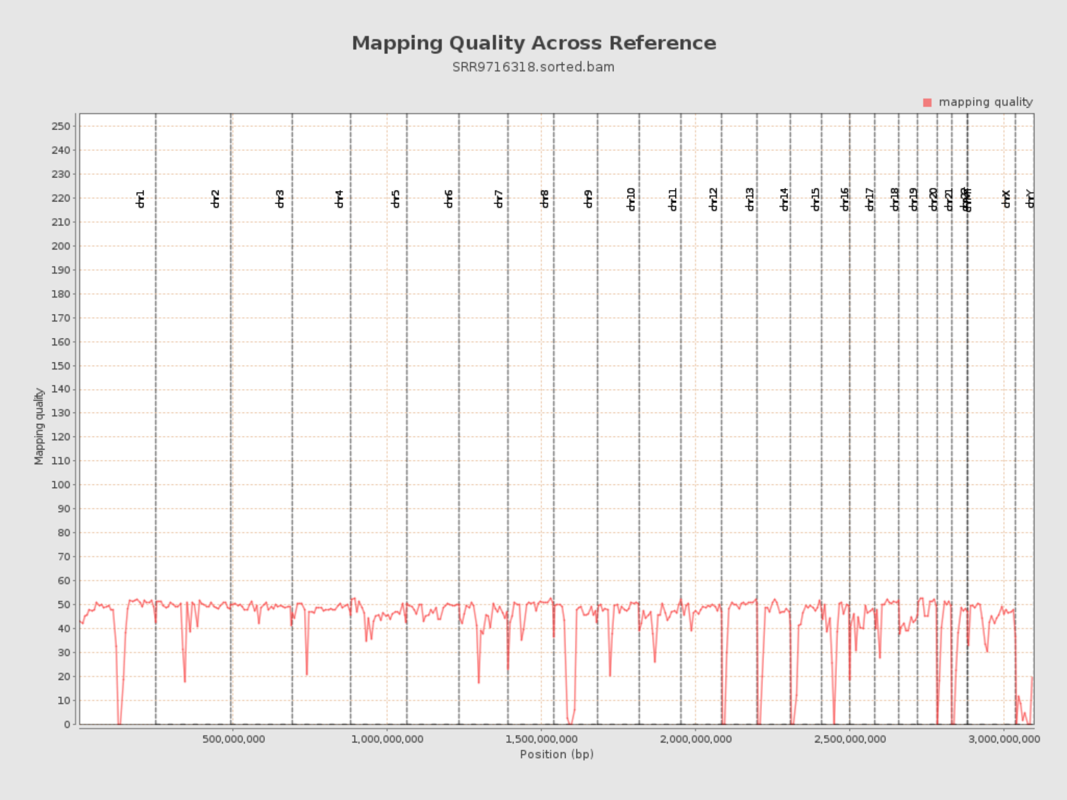
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram