Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 07:45:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716325.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_SRR9716325 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716325.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 07:45:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716325.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,594,440
Mapped reads	3,289,861 / 91.53%
Unmapped reads	304,579 / 8.47%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,721 / 0.47%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	180,764 / 5.03%
Duplication rate	4.01%
Clipped reads	3,304,091 / 91.92%

2.2. ACGT Content

Number/percentage of A's	46,763,206 / 24.37%
Number/percentage of C's	37,578,799 / 19.59%
Number/percentage of T's	59,844,353 / 31.19%
Number/percentage of G's	47,670,420 / 24.85%
Number/percentage of N's	5,600 / 0%
GC Percentage	44.43%

2.3. Coverage

Mean	0.062

Standard Deviation	0.5344

2.4. Mapping Quality

Mean Mapping Quality	44.94

2.5. Mismatches and indels

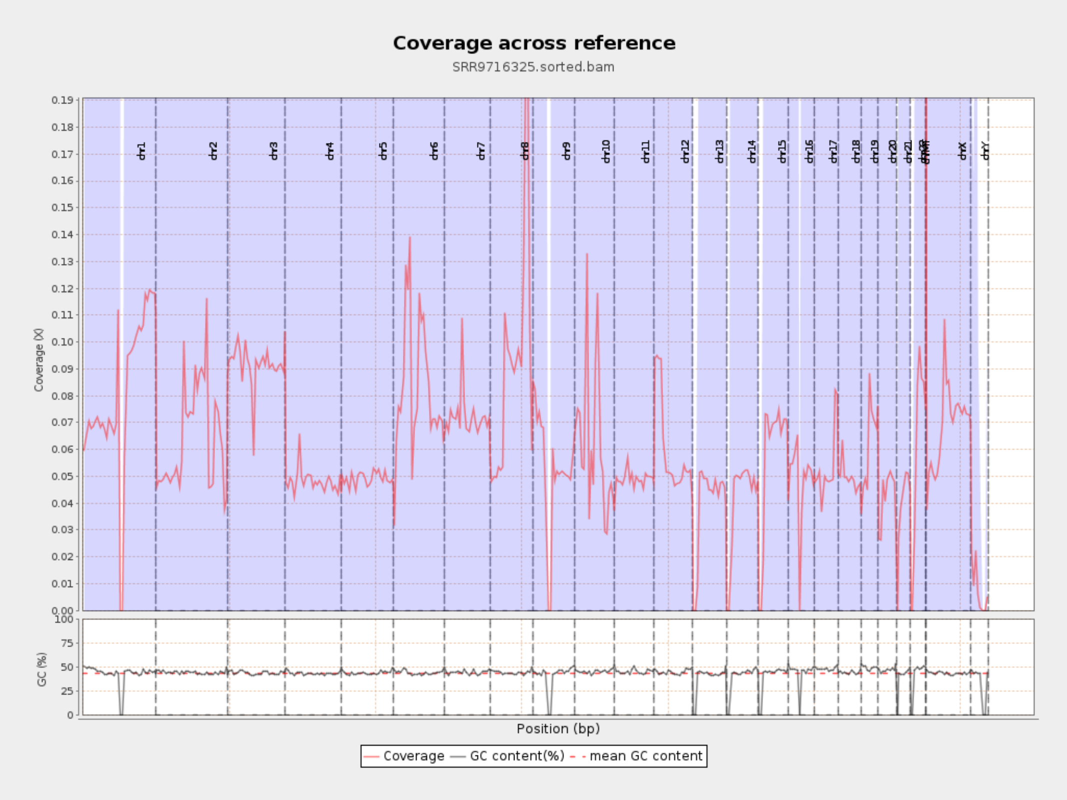
General error rate	0.5%
Mismatches	933,933
Insertions	10,797
Mapped reads with at least one insertion	0.33%
Deletions	35,010
Mapped reads with at least one deletion	1.06%
Homopolymer indels	43.7%

2.6. Chromosome stats

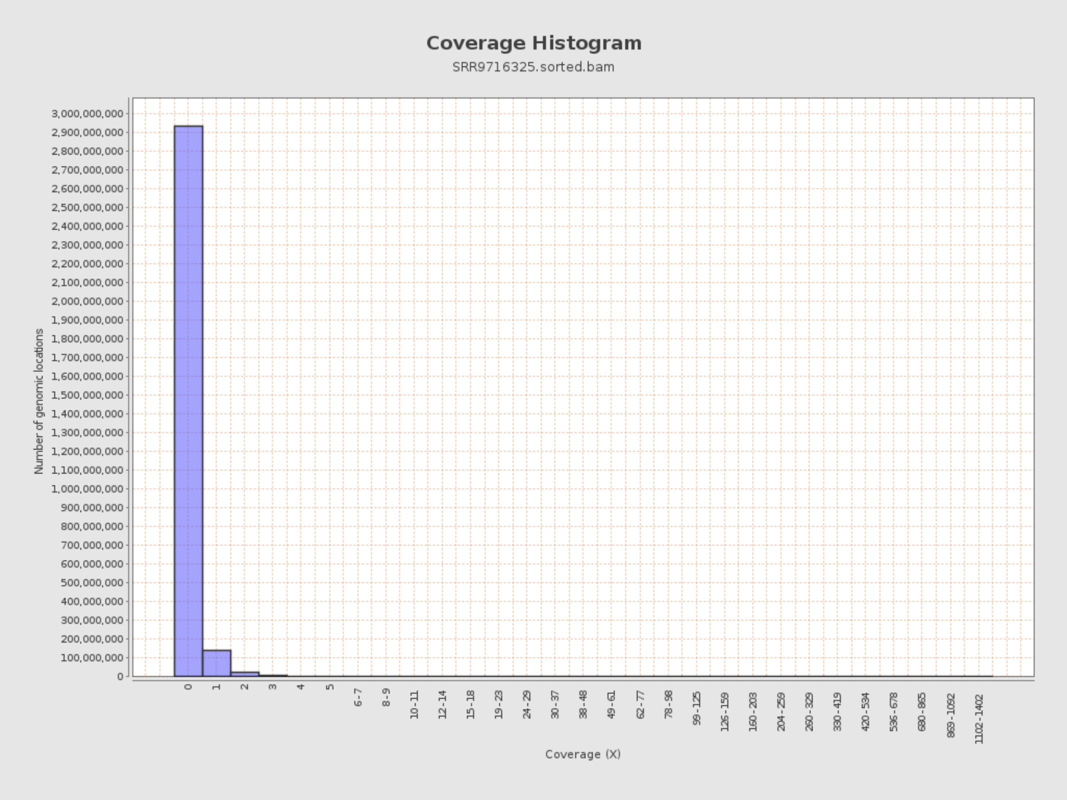
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	20183641	0.081	1.0592
chr2	243199373	15595117	0.0641	0.6558
chr3	198022430	18102796	0.0914	0.3614
chr4	191154276	9239211	0.0483	0.277
chr5	180915260	8877354	0.0491	0.2631
chr6	171115067	14454028	0.0845	0.6281
chr7	159138663	11546709	0.0726	0.7023

chr8	146364022	13703327	0.0936	0.4415
chr9	141213431	7353354	0.0521	0.4446
chr10	135534747	8393436	0.0619	0.5643
chr11	135006516	6601743	0.0489	0.4112
chr12	133851895	8153328	0.0609	0.3046
chr13	115169878	4546024	0.0395	0.235
chr14	107349540	4437864	0.0413	0.2782
chr15	102531392	5794519	0.0565	0.284
chr16	90354753	4273520	0.0473	0.3183
chr17	81195210	4281097	0.0527	0.2868
chr18	78077248	3882580	0.0497	0.8684
chr19	59128983	3682579	0.0623	0.7279
chr20	63025520	2695080	0.0428	0.2466
chr21	48129895	1883401	0.0391	0.2756
chr22	51304566	3090066	0.0602	0.2885
chrMT	16571	10207	0.616	0.9408
chrX	155270560	10681549	0.0688	0.3835
chrY	59373566	455011	0.0077	0.1526

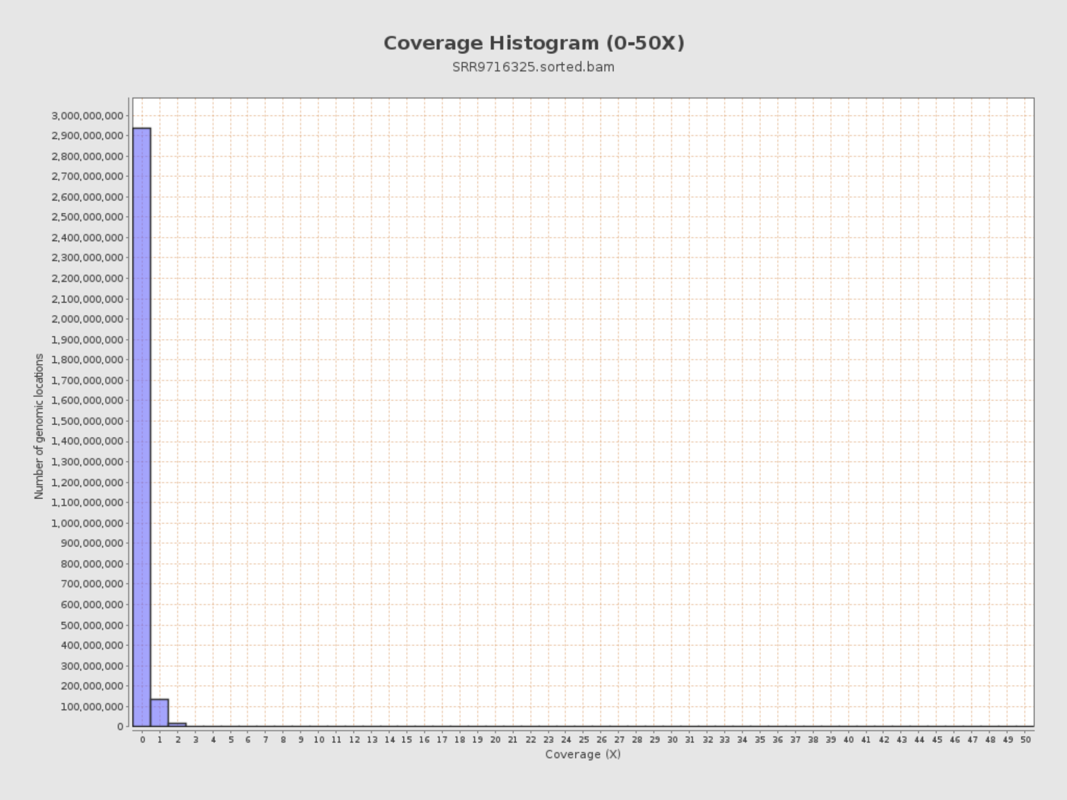
3. Results : Coverage across reference



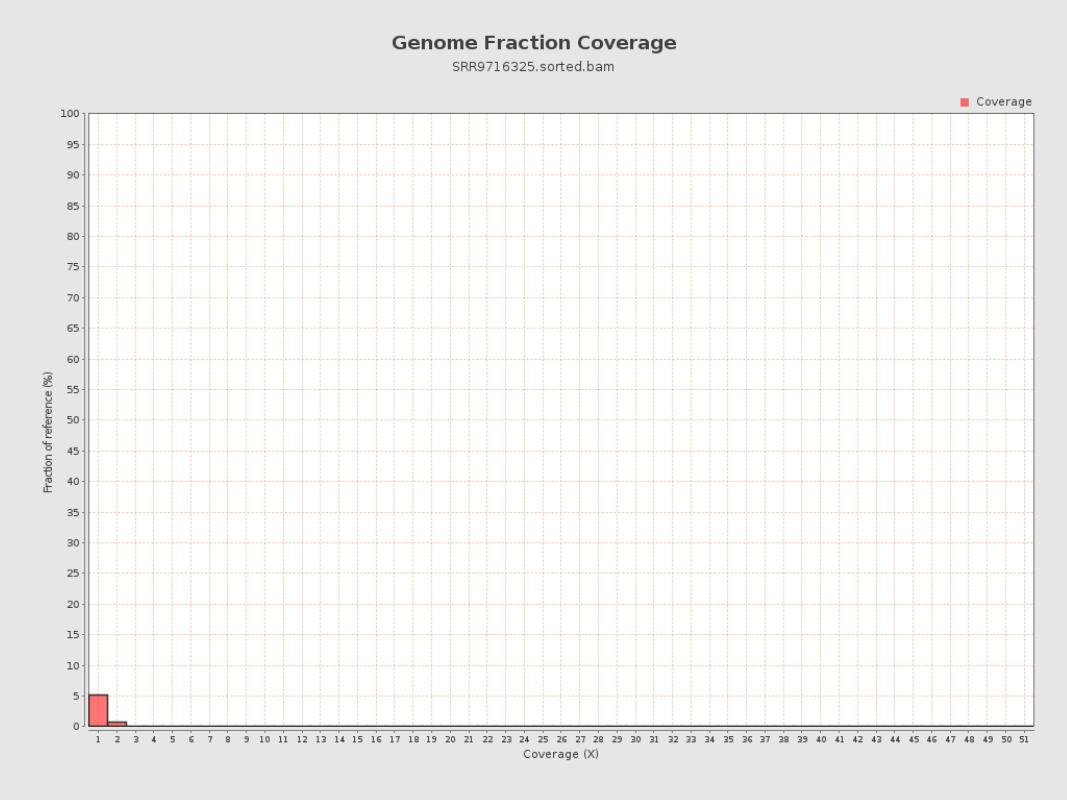
4. Results : Coverage Histogram



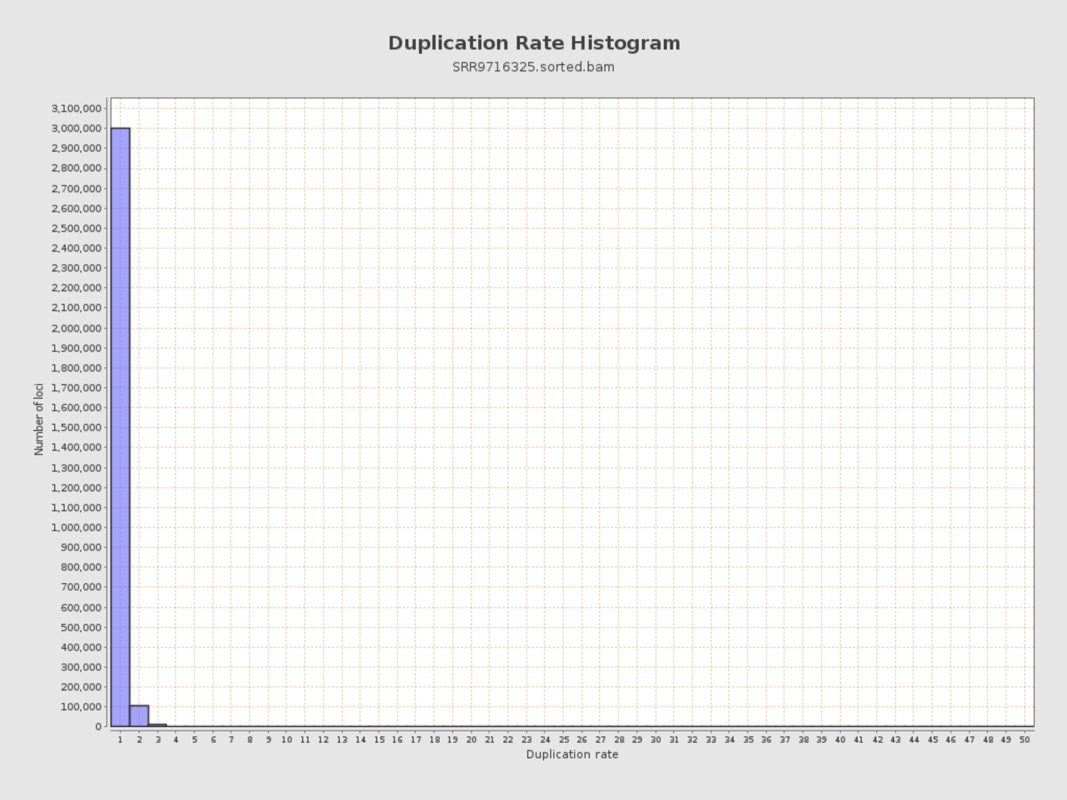
5. Results : Coverage Histogram (0-50X)



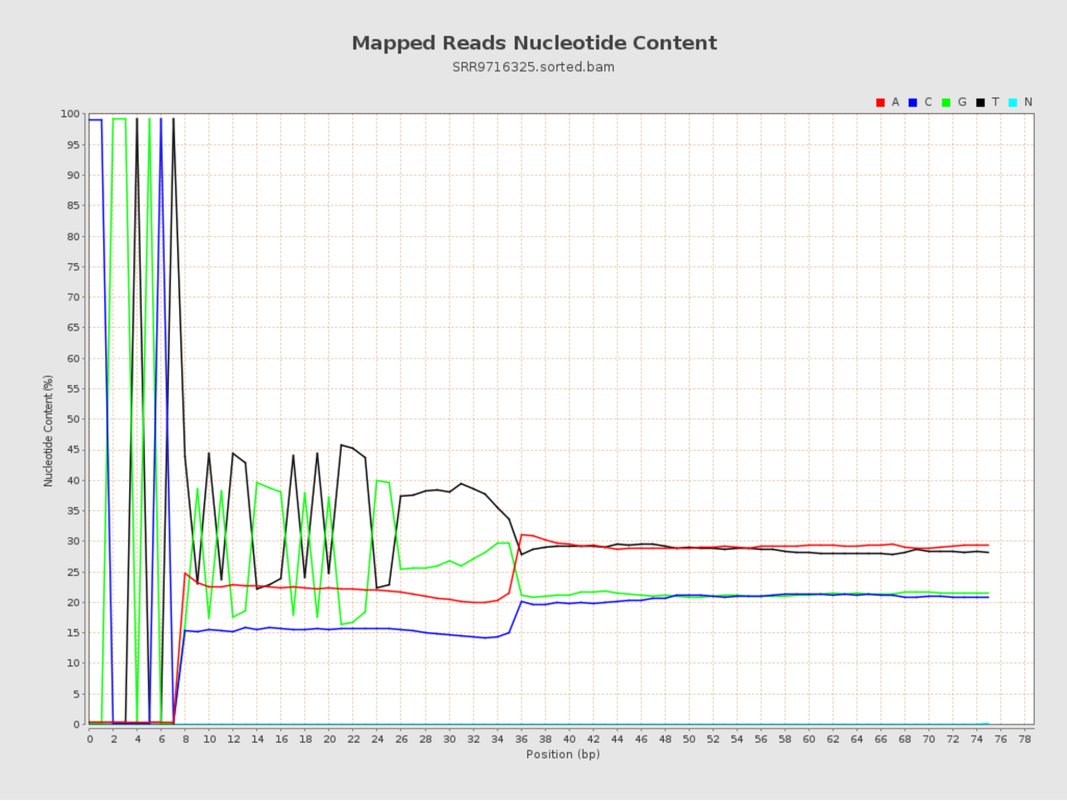
6. Results : Genome Fraction Coverage



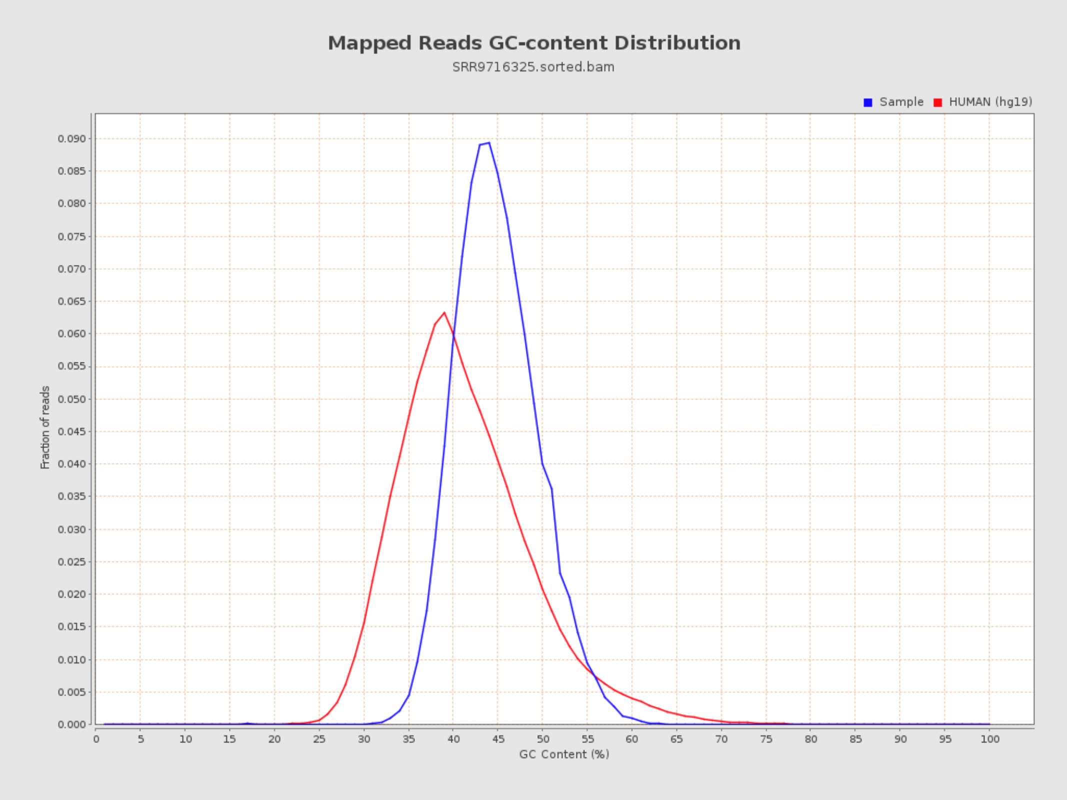
7. Results : Duplication Rate Histogram



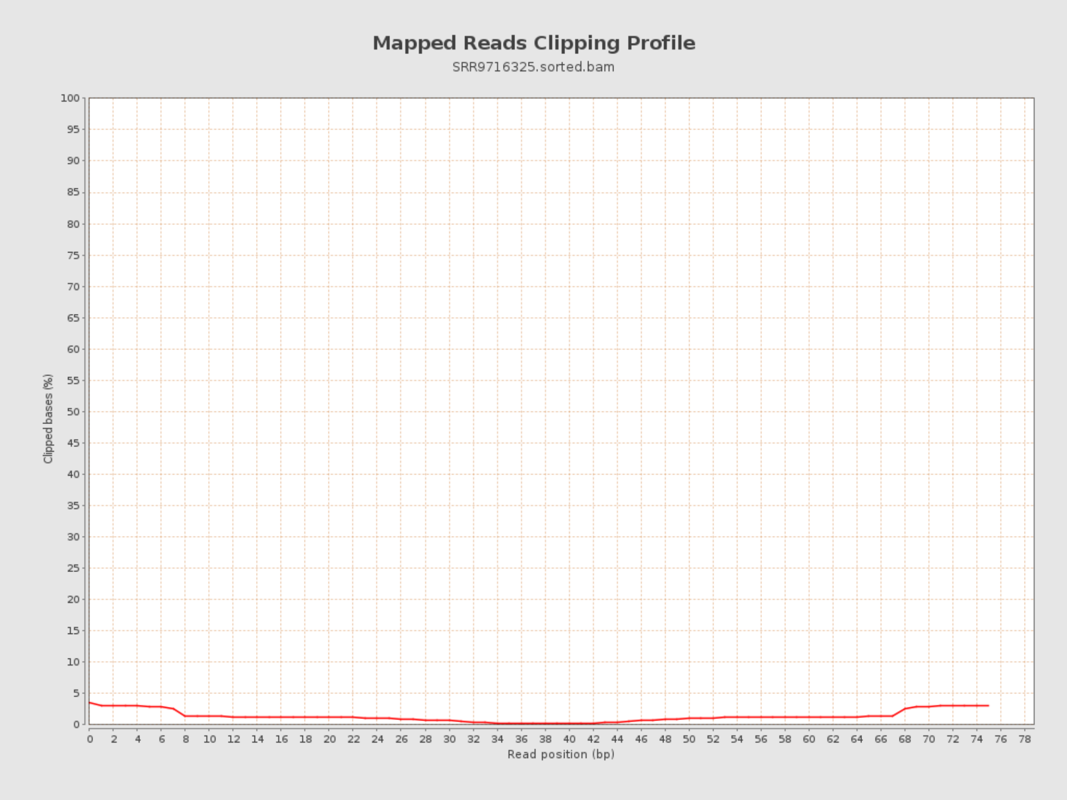
8. Results : Mapped Reads Nucleotide Content



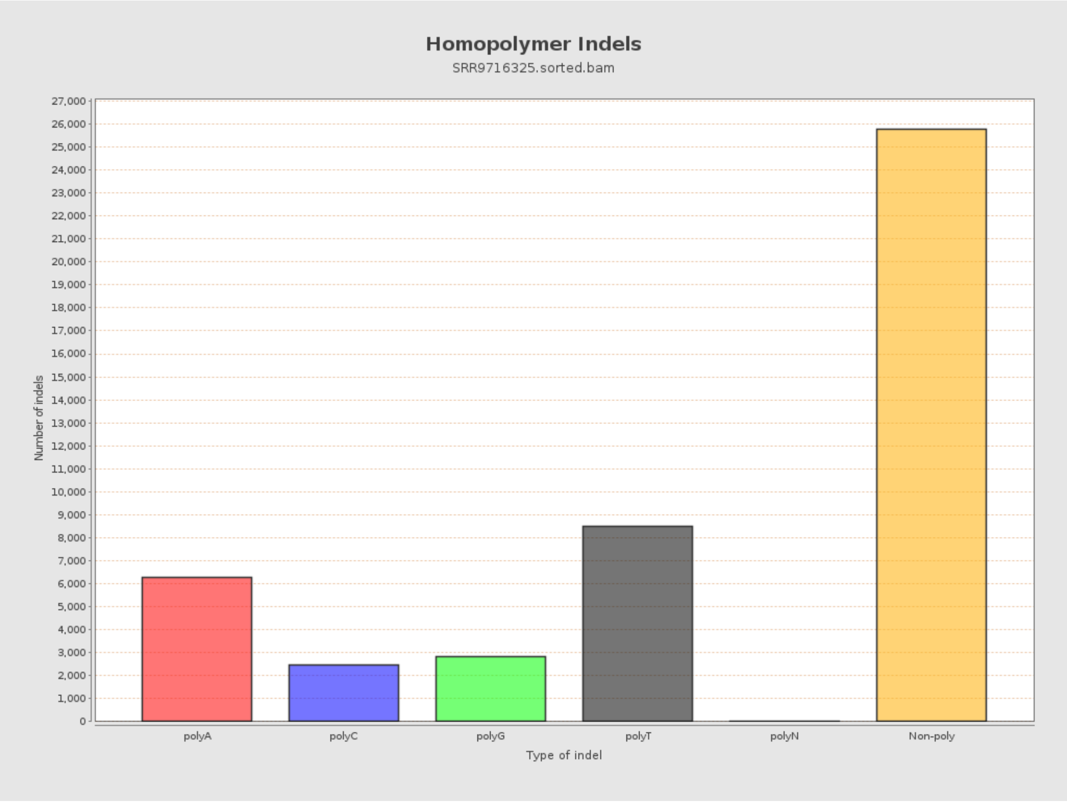
9. Results : Mapped Reads GC-content Distribution



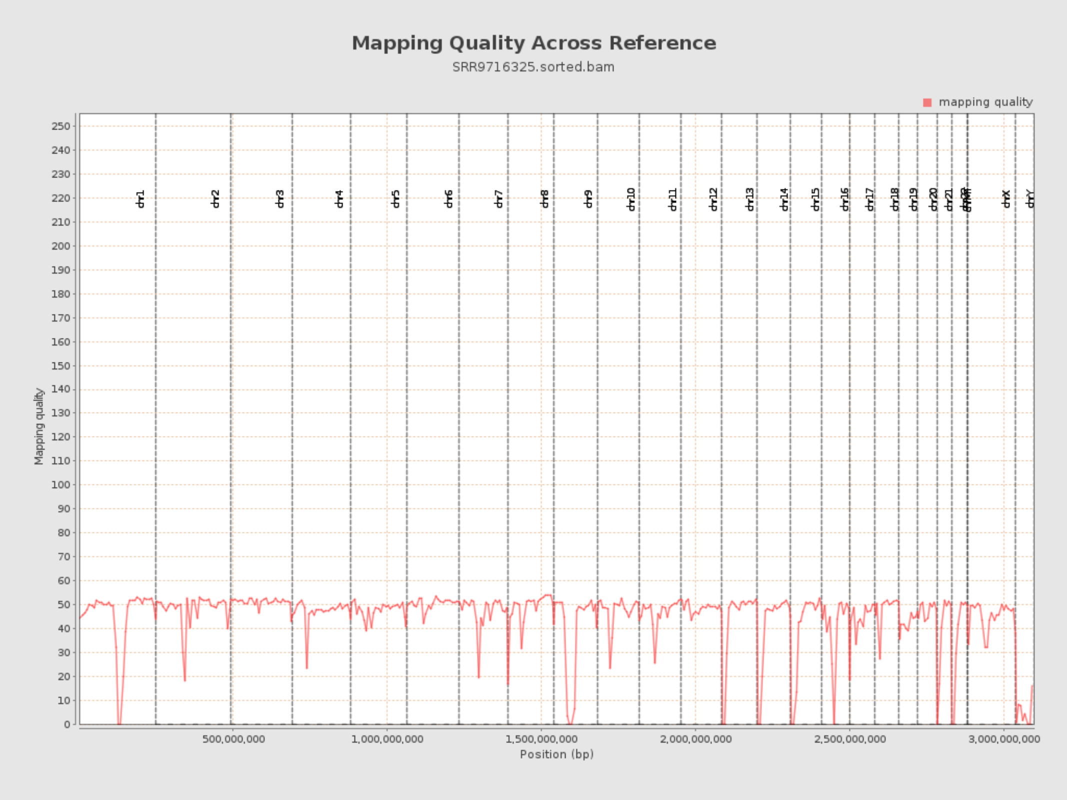
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram