Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 10:34:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716380.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_SRR9716380 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716380.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 10:34:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716380.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,485,138
Mapped reads	1,303,146 / 87.75%
Unmapped reads	181,992 / 12.25%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,955 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	29,440 / 1.98%
Duplication rate	1.57%
Clipped reads	1,305,257 / 87.89%

2.2. ACGT Content

Number/percentage of A's	18,606,134 / 25.13%
Number/percentage of C's	14,307,046 / 19.32%
Number/percentage of T's	23,425,423 / 31.64%
Number/percentage of G's	17,700,103 / 23.91%
Number/percentage of N's	555 / 0%
GC Percentage	43.23%

2.3. Coverage

Mean	0.0239

Standard Deviation	0.2111

2.4. Mapping Quality

Mean Mapping Quality	42.22

2.5. Mismatches and indels

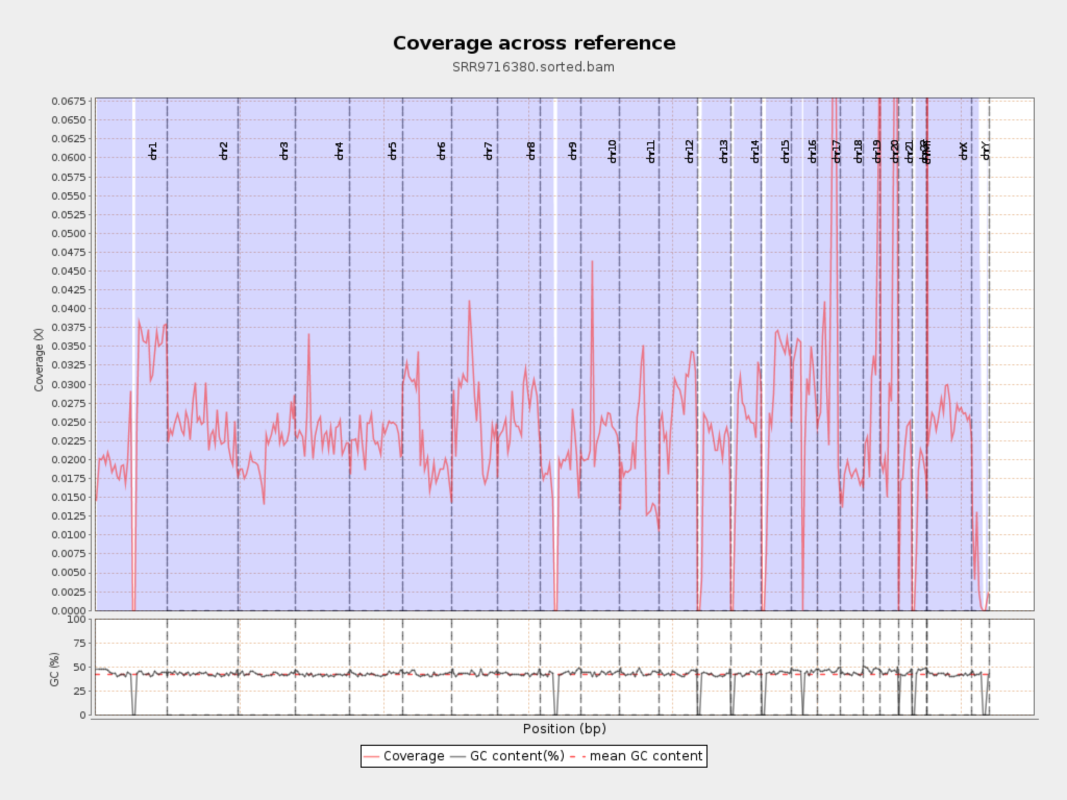
General error rate	0.53%
Mismatches	379,341
Insertions	5,676
Mapped reads with at least one insertion	0.43%
Deletions	13,798
Mapped reads with at least one deletion	1.05%
Homopolymer indels	40.83%

2.6. Chromosome stats

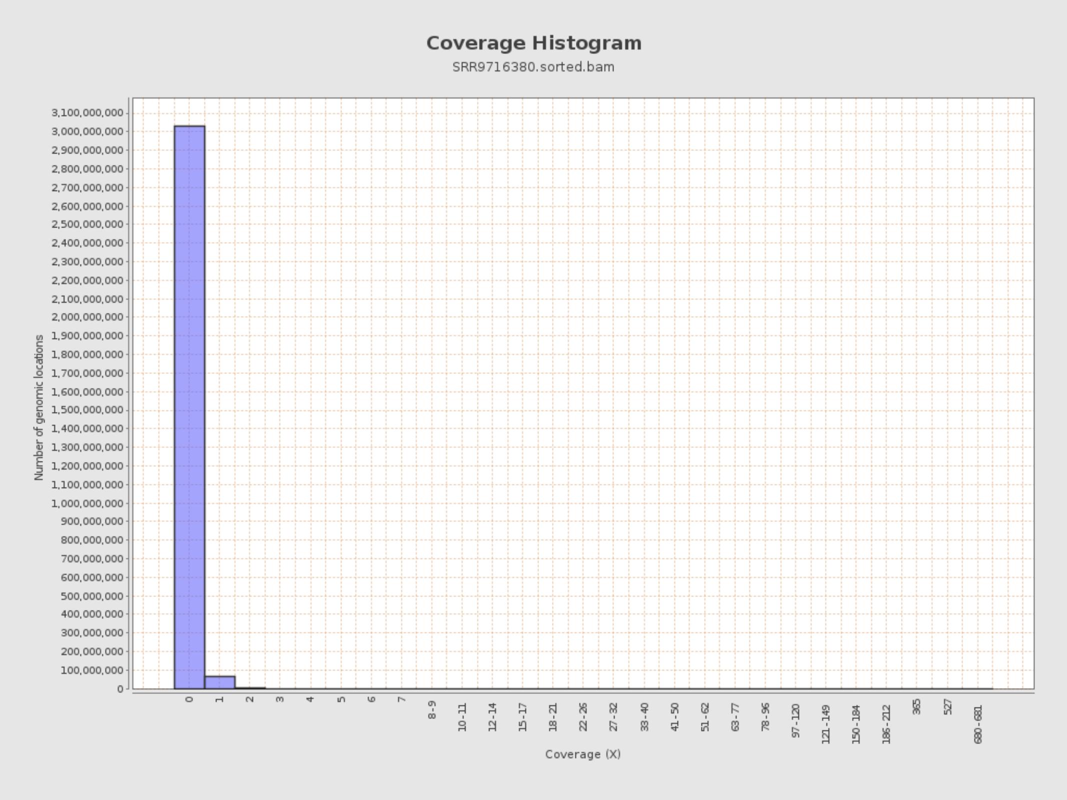
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6249634	0.0251	0.2449
chr2	243199373	5883079	0.0242	0.3238
chr3	198022430	4207620	0.0212	0.1584
chr4	191154276	4510524	0.0236	0.1768
chr5	180915260	4201501	0.0232	0.163
chr6	171115067	3946291	0.0231	0.1899
chr7	159138663	4242095	0.0267	0.2856

chr8	146364022	3817527	0.0261	0.2011
chr9	141213431	2453557	0.0174	0.1622
chr10	135534747	3267834	0.0241	0.2565
chr11	135006516	2635056	0.0195	0.1805
chr12	133851895	3711130	0.0277	0.1792
chr13	115169878	2229411	0.0194	0.1492
chr14	107349540	2466119	0.023	0.1677
chr15	102531392	2704076	0.0264	0.178
chr16	90354753	2563481	0.0284	0.1903
chr17	81195210	3320599	0.0409	0.2264
chr18	78077248	1371259	0.0176	0.2349
chr19	59128983	1998018	0.0338	0.2488
chr20	63025520	2391868	0.038	0.2185
chr21	48129895	918908	0.0191	0.158
chr22	51304566	695733	0.0136	0.1258
chrMT	16571	5010	0.3023	0.6565
chrX	155270560	4035293	0.026	0.1838
chrY	59373566	235771	0.004	0.1165

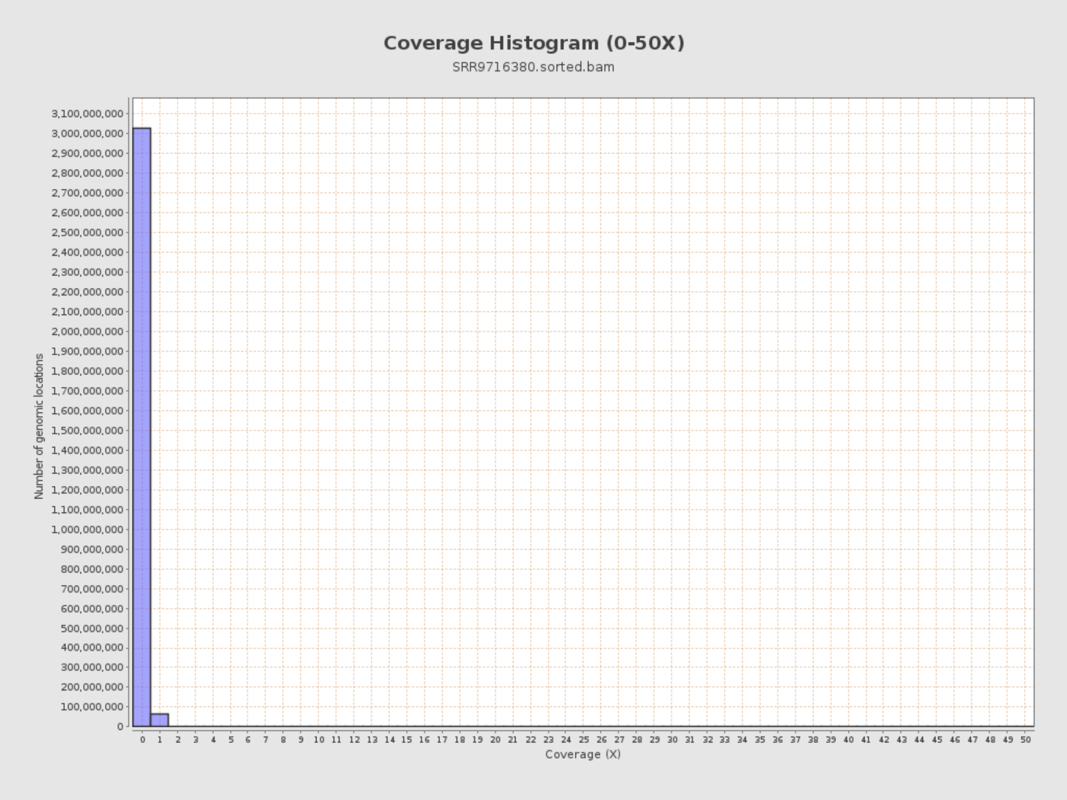
3. Results : Coverage across reference



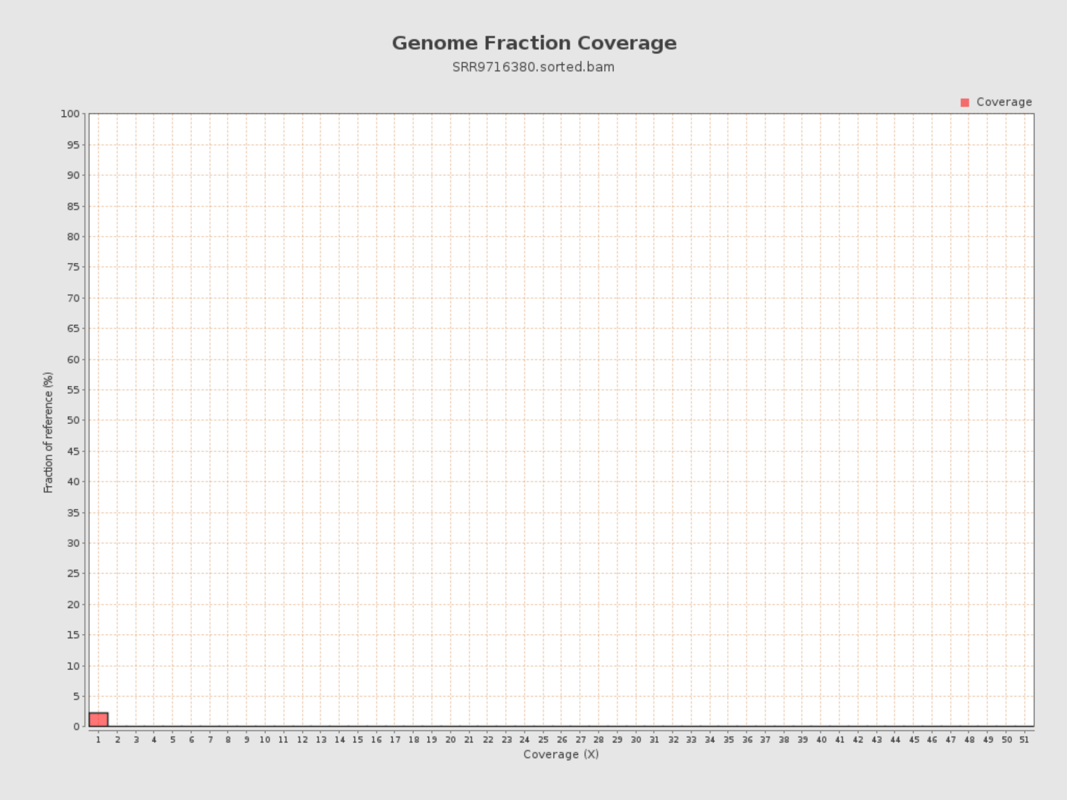
4. Results : Coverage Histogram



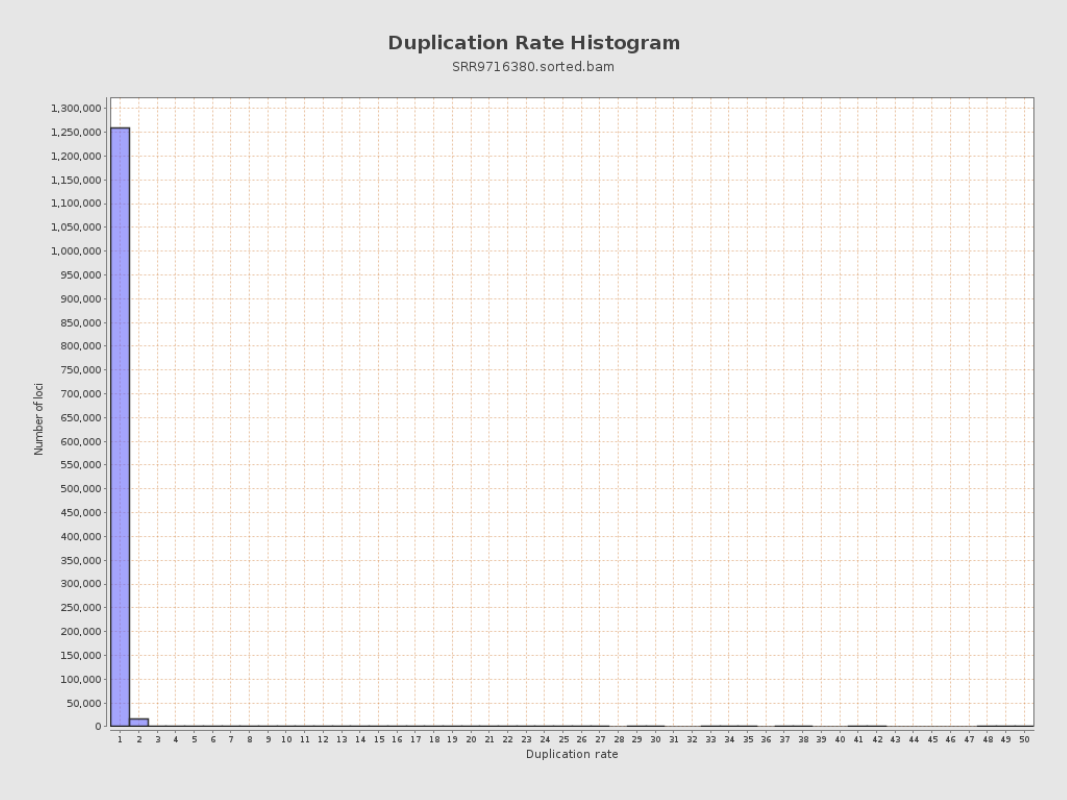
5. Results : Coverage Histogram (0-50X)



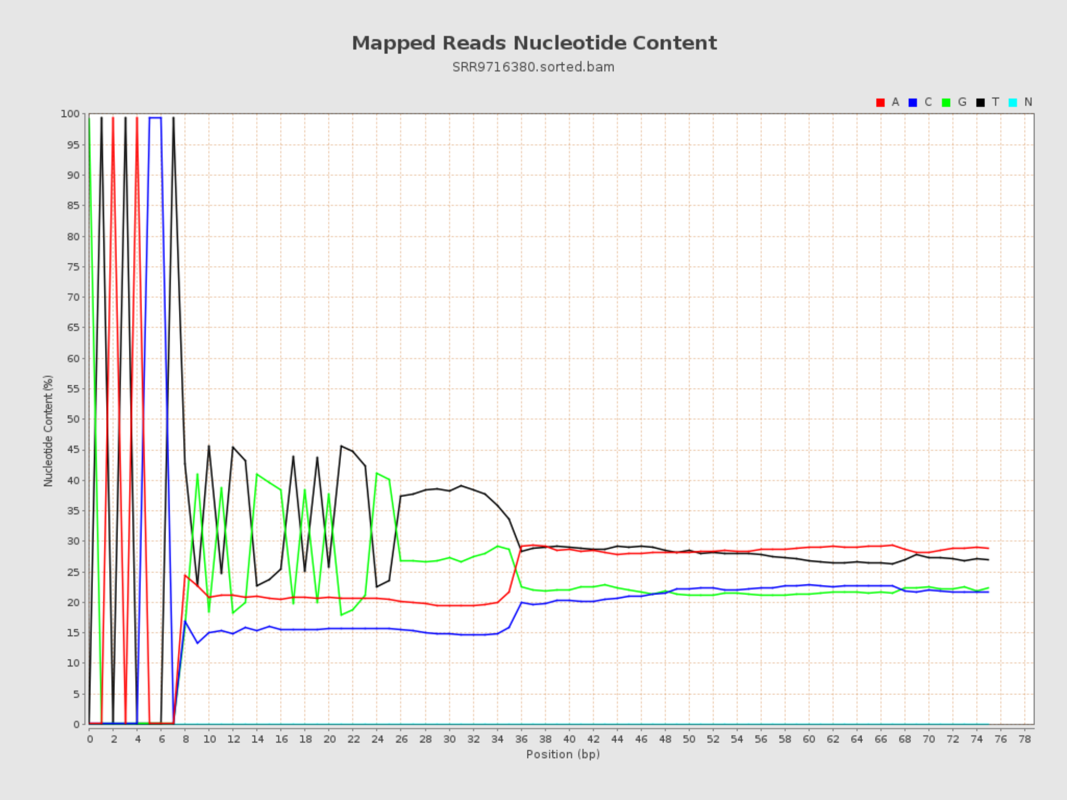
6. Results : Genome Fraction Coverage



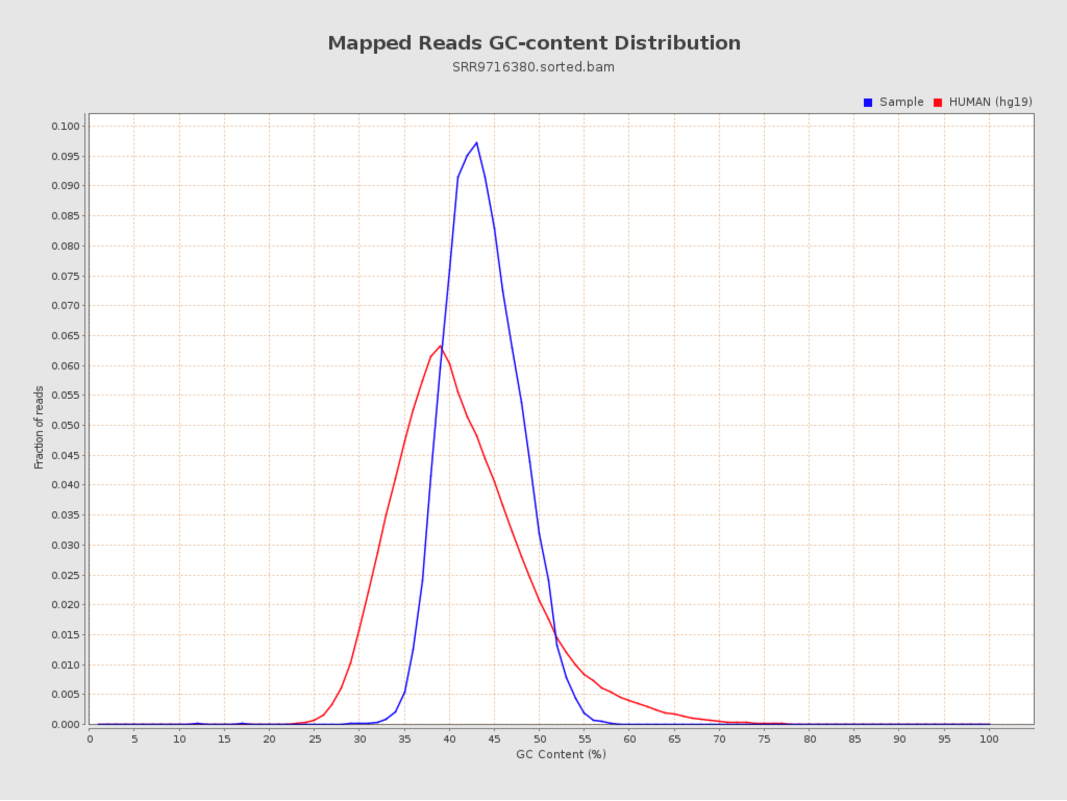
7. Results : Duplication Rate Histogram



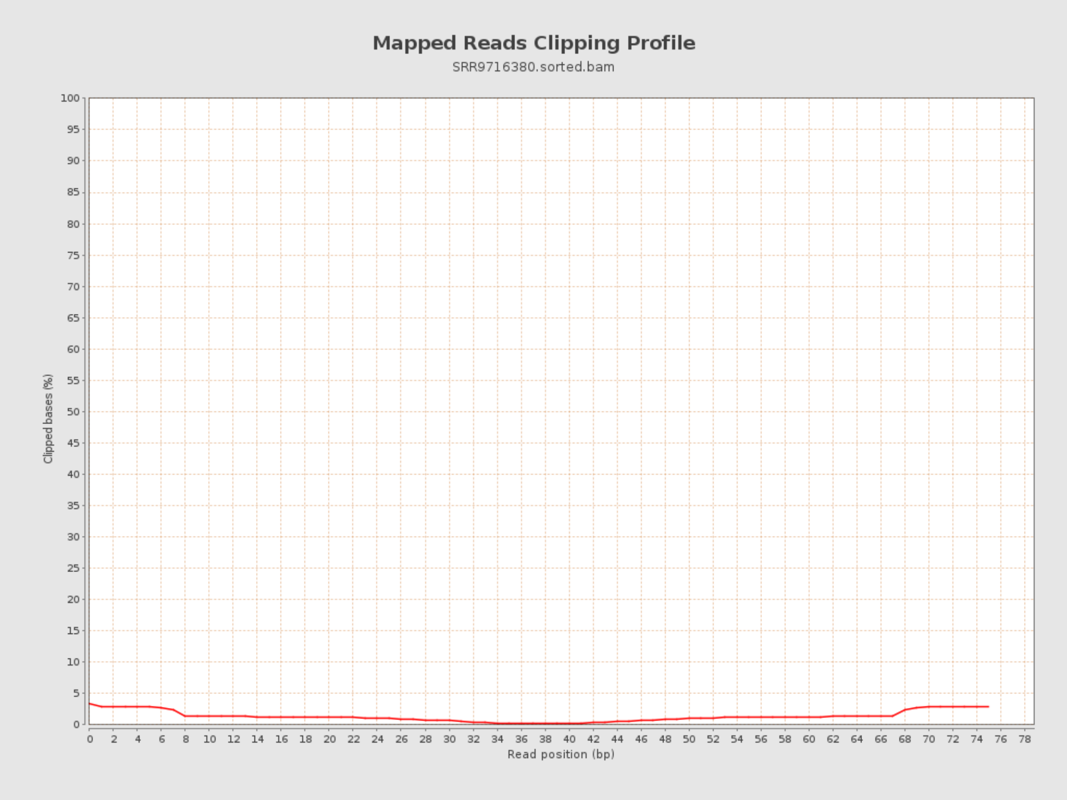
8. Results : Mapped Reads Nucleotide Content



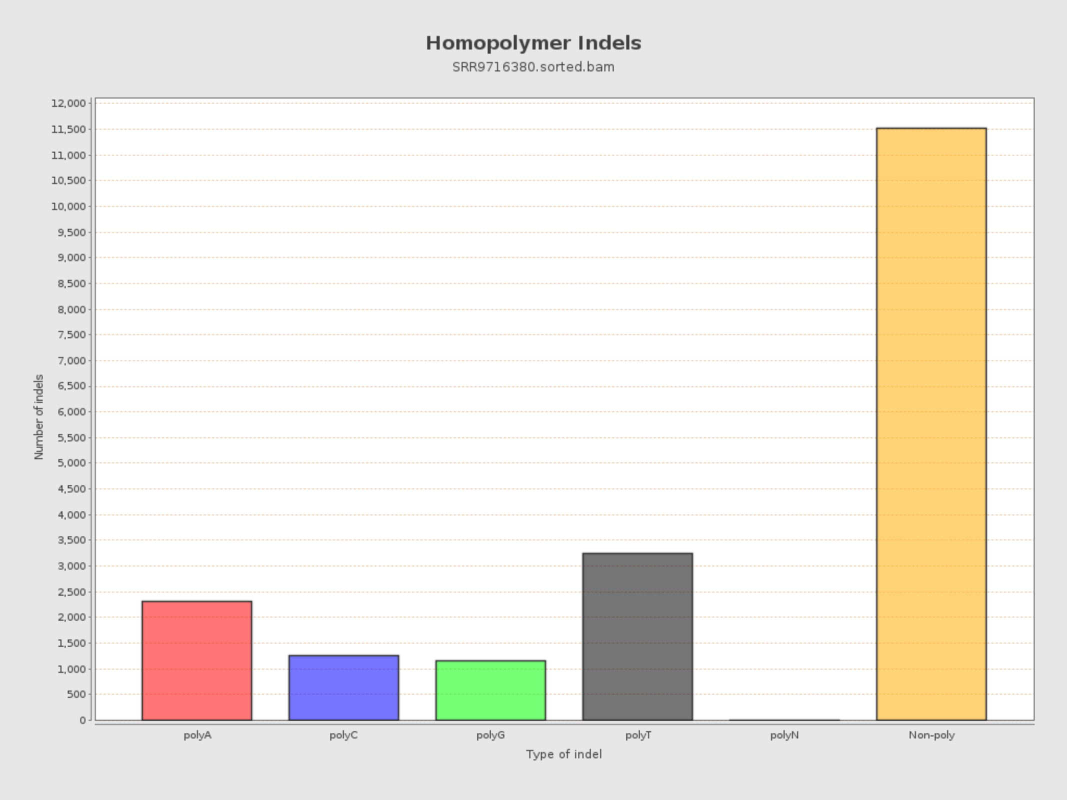
9. Results : Mapped Reads GC-content Distribution



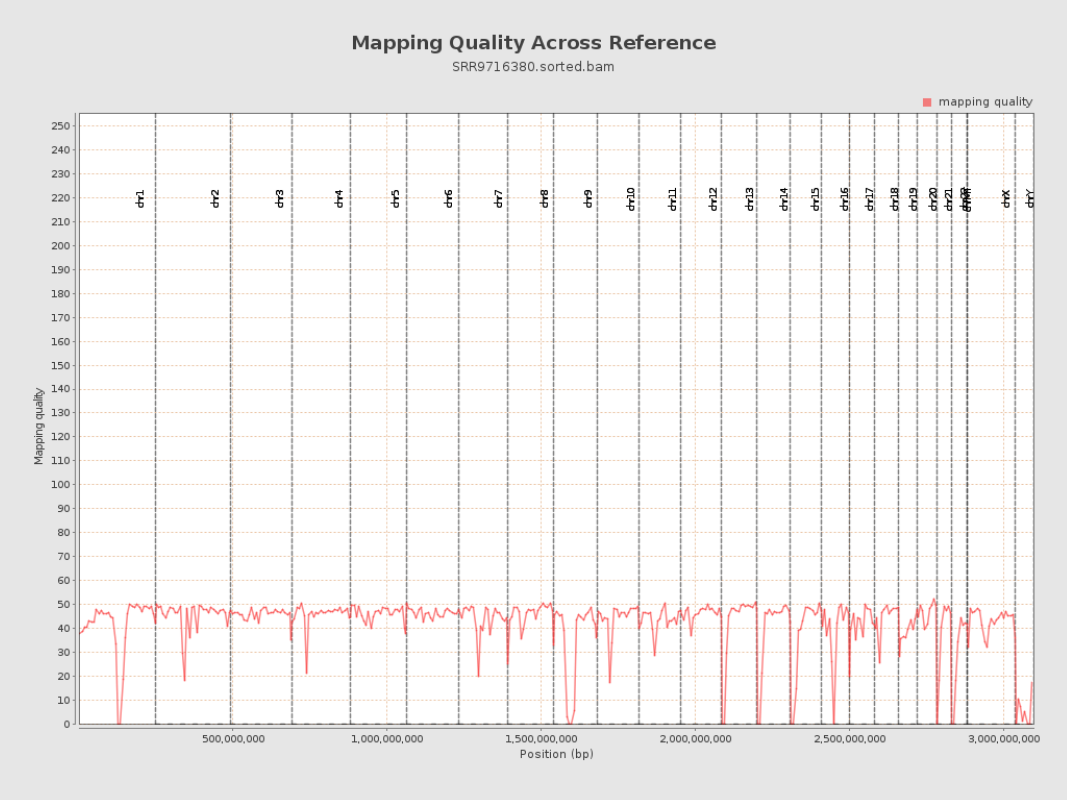
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram