Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 13:32:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716818.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_SRR9716818 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716818.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 13:32:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716818.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	686,394
Mapped reads	544,515 / 79.33%
Unmapped reads	141,879 / 20.67%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,611 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	13,317 / 1.94%
Duplication rate	1.95%
Clipped reads	545,540 / 79.48%

2.2. ACGT Content

Number/percentage of A's	8,114,634 / 25.69%
Number/percentage of C's	5,506,223 / 17.43%
Number/percentage of T's	10,004,315 / 31.67%
Number/percentage of G's	7,965,398 / 25.21%
Number/percentage of N's	195 / 0%
GC Percentage	42.64%

2.3. Coverage

Mean	0.0102

Standard Deviation	0.1265

2.4. Mapping Quality

Mean Mapping Quality	44.69

2.5. Mismatches and indels

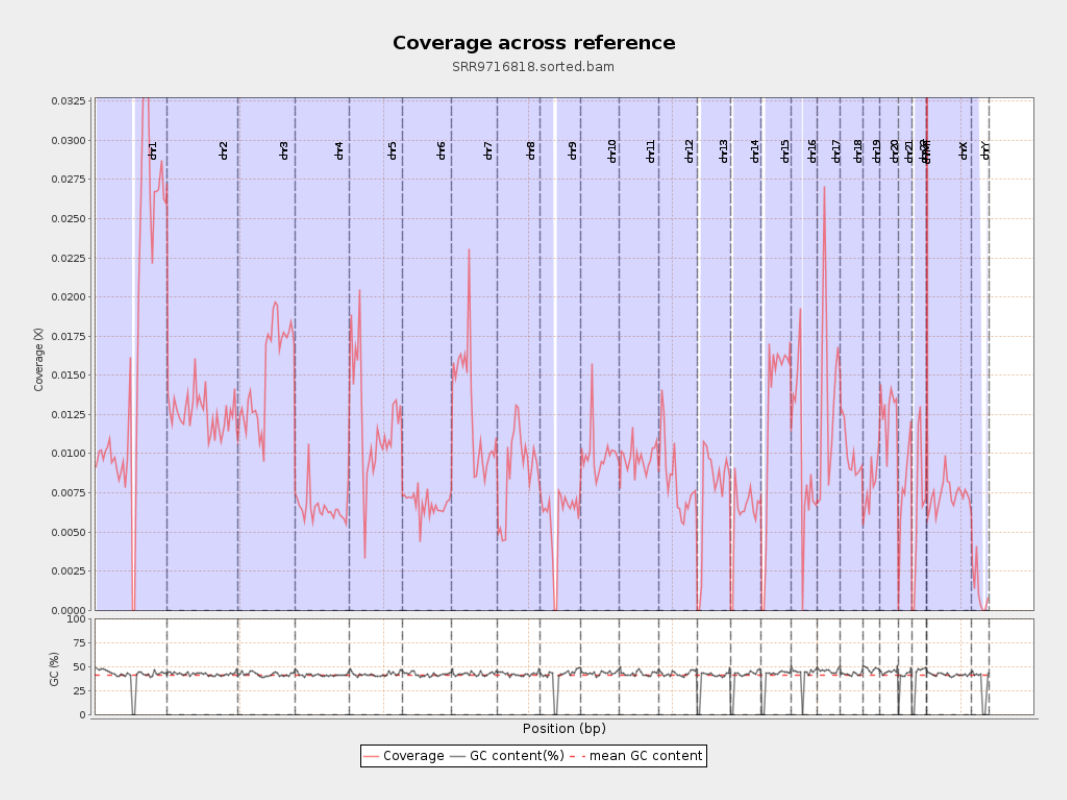
General error rate	0.5%
Mismatches	153,118
Insertions	2,230
Mapped reads with at least one insertion	0.41%
Deletions	5,396
Mapped reads with at least one deletion	0.98%
Homopolymer indels	43.4%

2.6. Chromosome stats

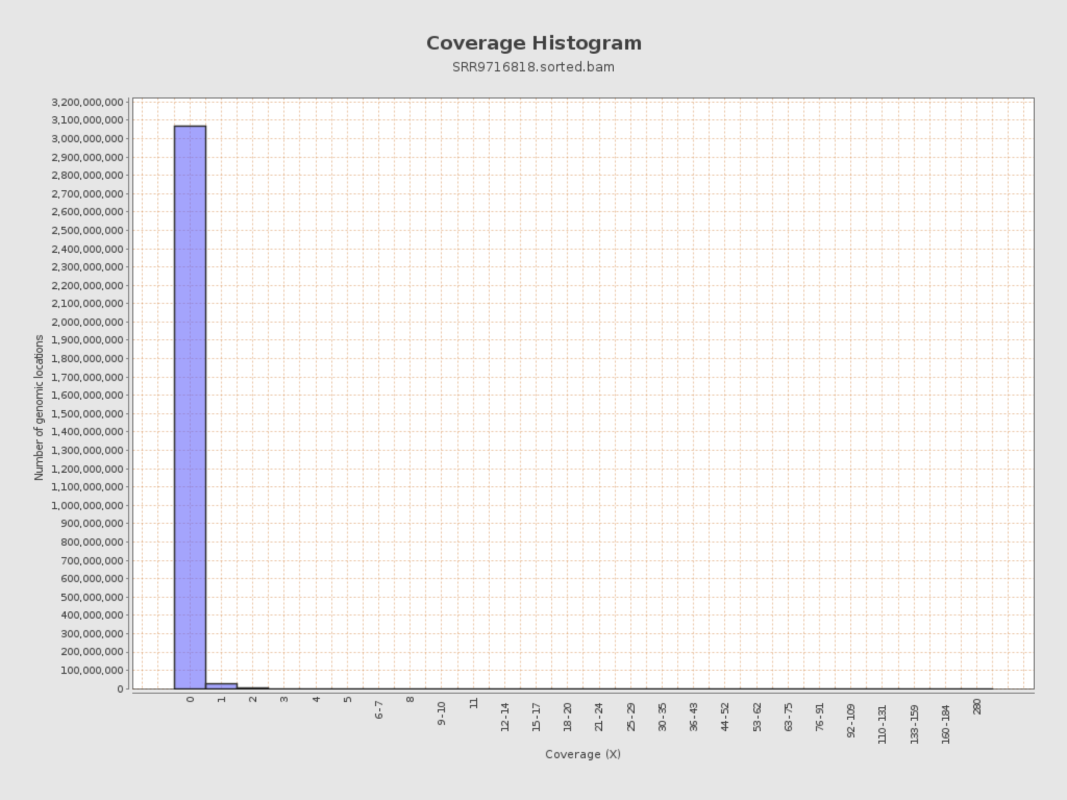
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4130916	0.0166	0.1927
chr2	243199373	3065420	0.0126	0.1633
chr3	198022430	2989309	0.0151	0.1284
chr4	191154276	1261712	0.0066	0.0903
chr5	180915260	2176506	0.012	0.115
chr6	171115067	1160697	0.0068	0.0917
chr7	159138663	2019462	0.0127	0.1859

chr8	146364022	1321099	0.009	0.1126
chr9	141213431	830850	0.0059	0.0909
chr10	135534747	1357146	0.01	0.1167
chr11	135006516	1313820	0.0097	0.1161
chr12	133851895	1105430	0.0083	0.096
chr13	115169878	872629	0.0076	0.0911
chr14	107349540	641839	0.006	0.0822
chr15	102531392	1312310	0.0128	0.1188
chr16	90354753	869571	0.0096	0.1051
chr17	81195210	1155184	0.0142	0.1289
chr18	78077248	780353	0.01	0.1572
chr19	59128983	477298	0.0081	0.1378
chr20	63025520	798525	0.0127	0.1182
chr21	48129895	380907	0.0079	0.0954
chr22	51304566	354521	0.0069	0.0872
chrMT	16571	2906	0.1754	0.4257
chrX	155270560	1146650	0.0074	0.0938
chrY	59373566	74055	0.0012	0.0435

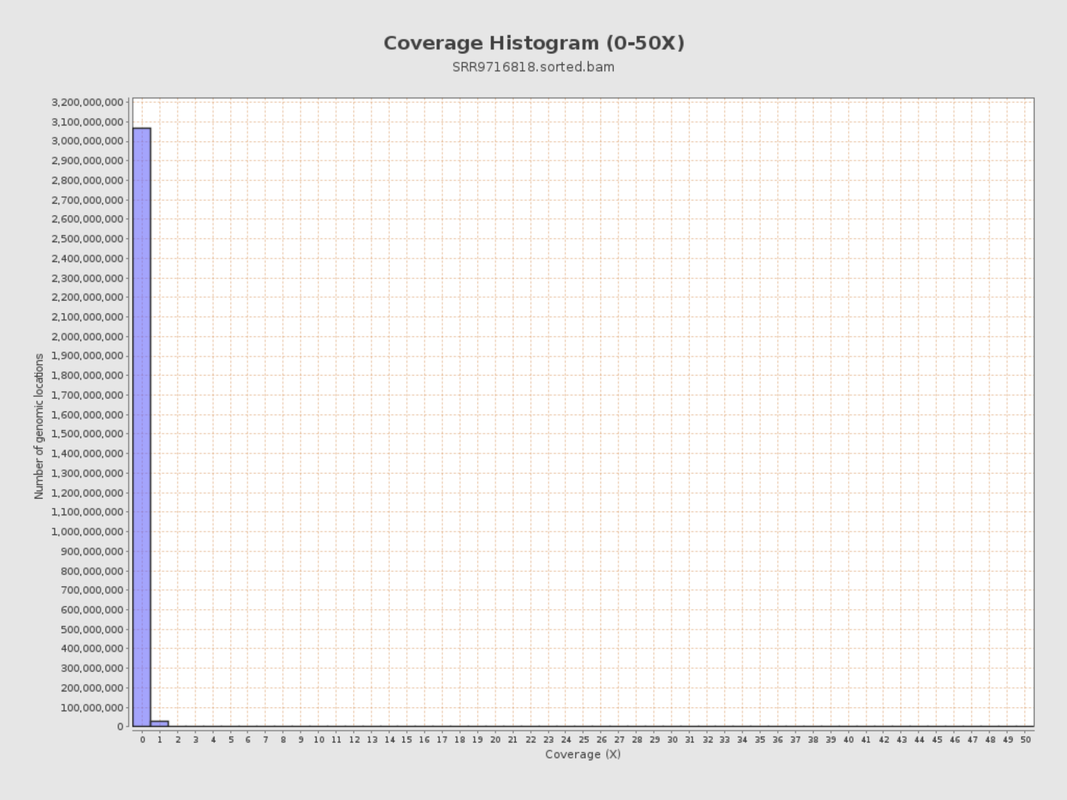
3. Results : Coverage across reference



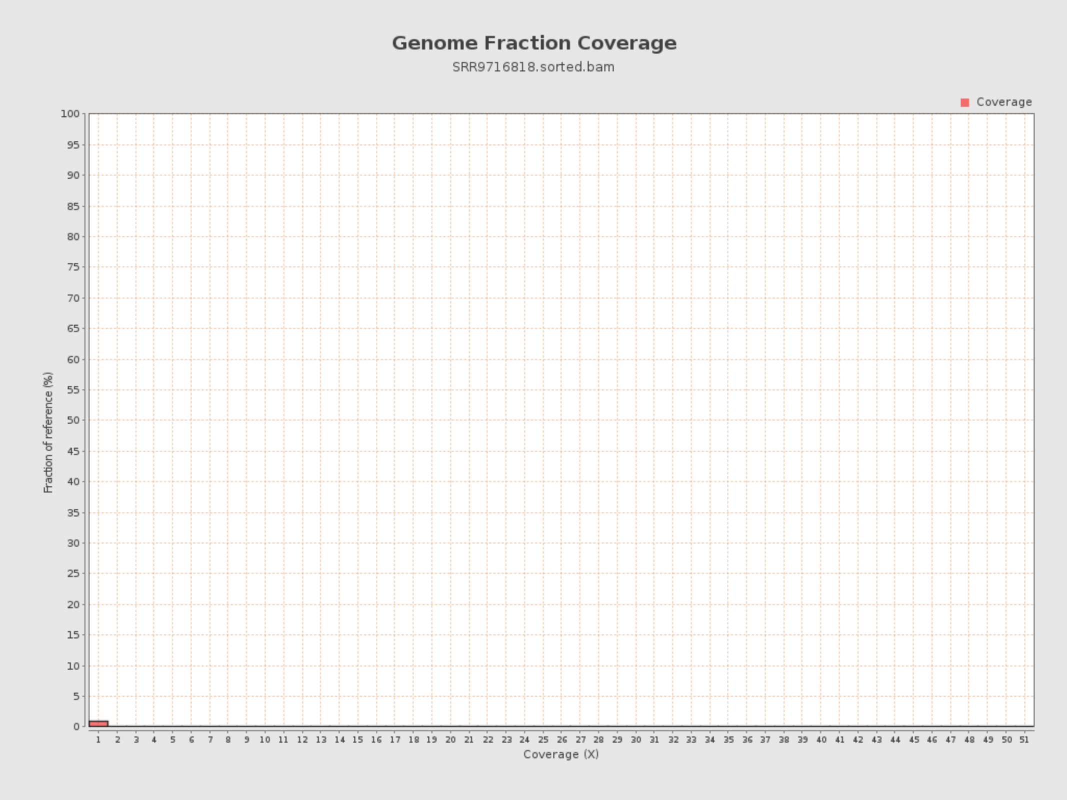
4. Results : Coverage Histogram



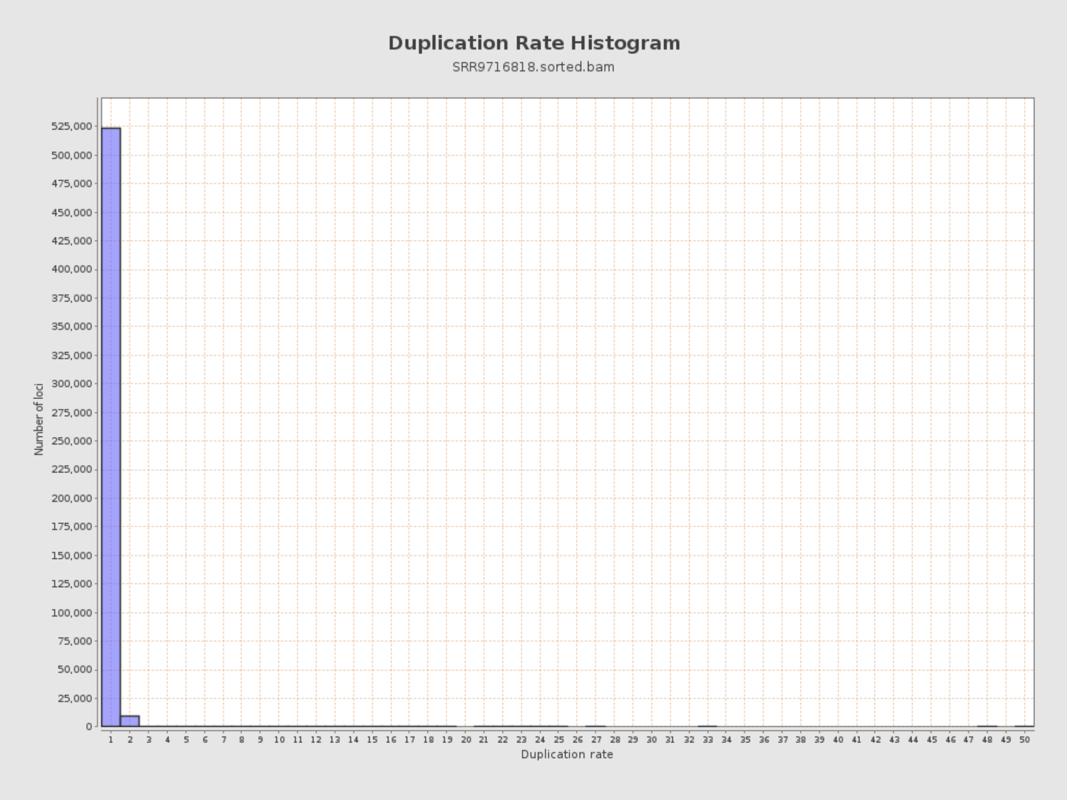
5. Results : Coverage Histogram (0-50X)



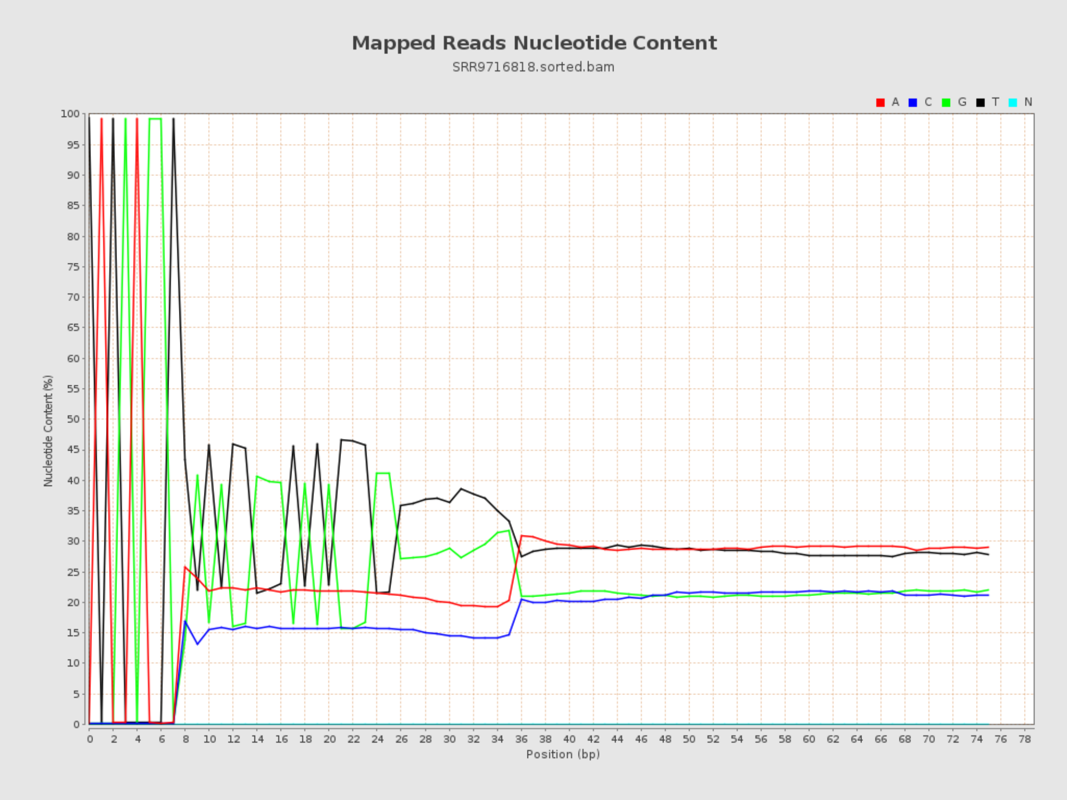
6. Results : Genome Fraction Coverage



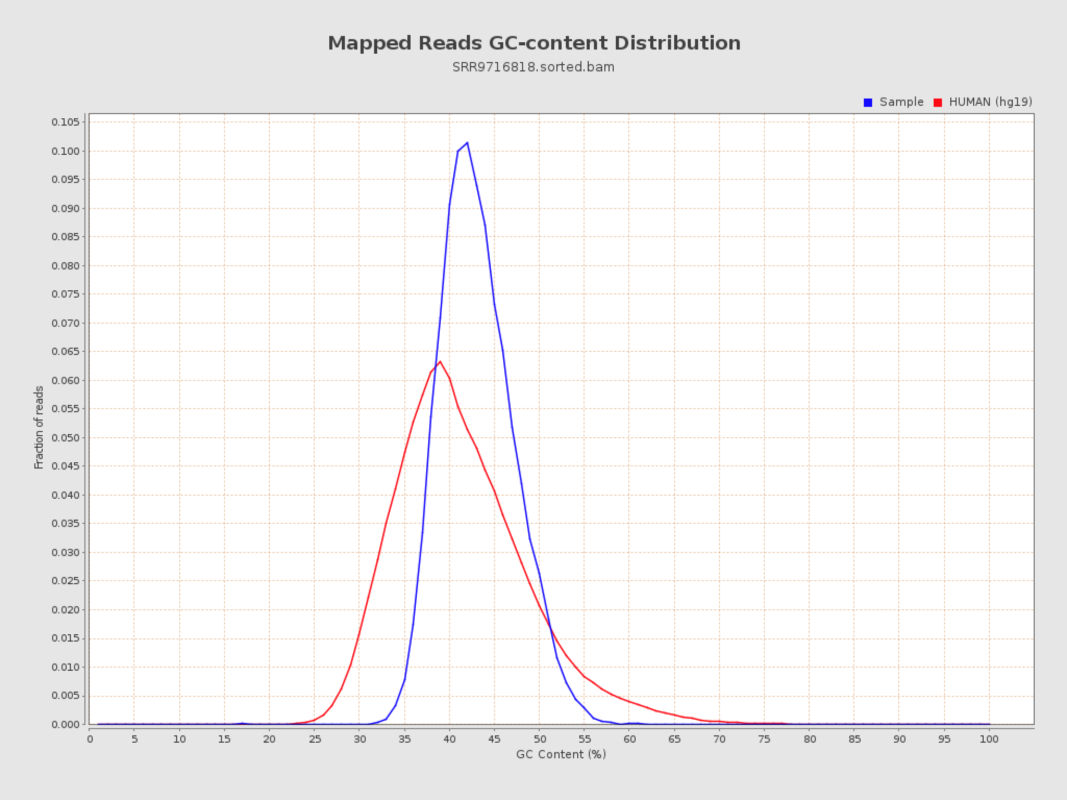
7. Results : Duplication Rate Histogram



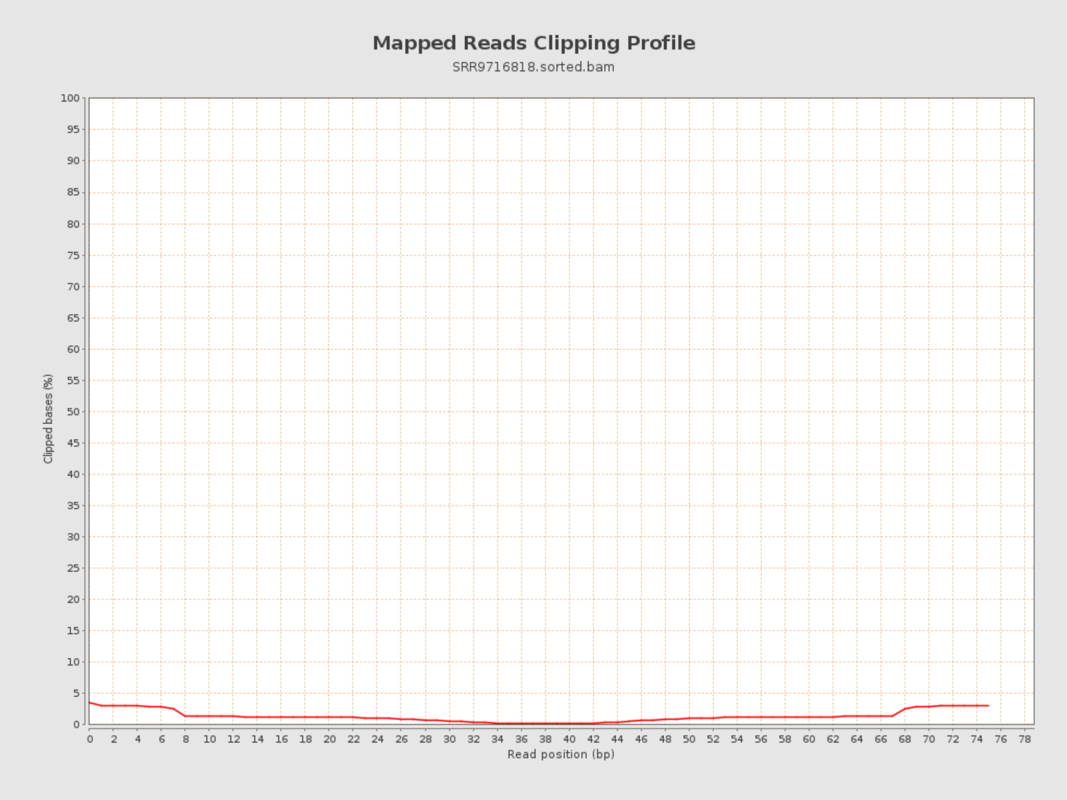
8. Results : Mapped Reads Nucleotide Content



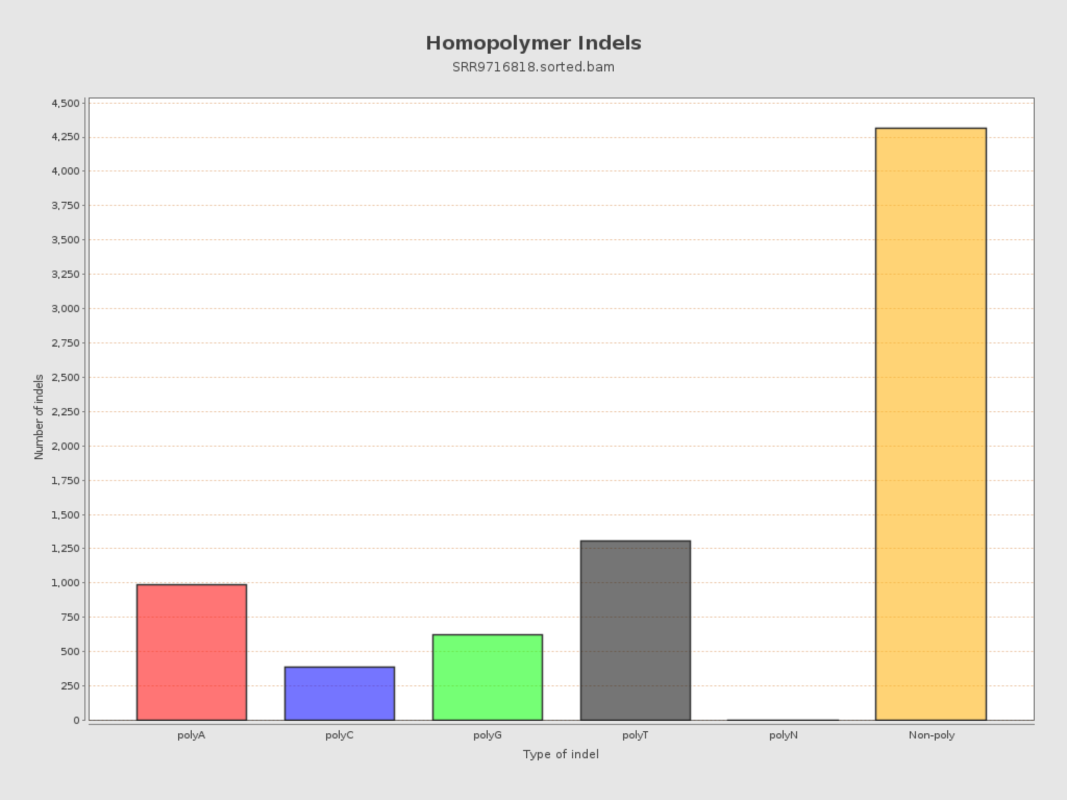
9. Results : Mapped Reads GC-content Distribution



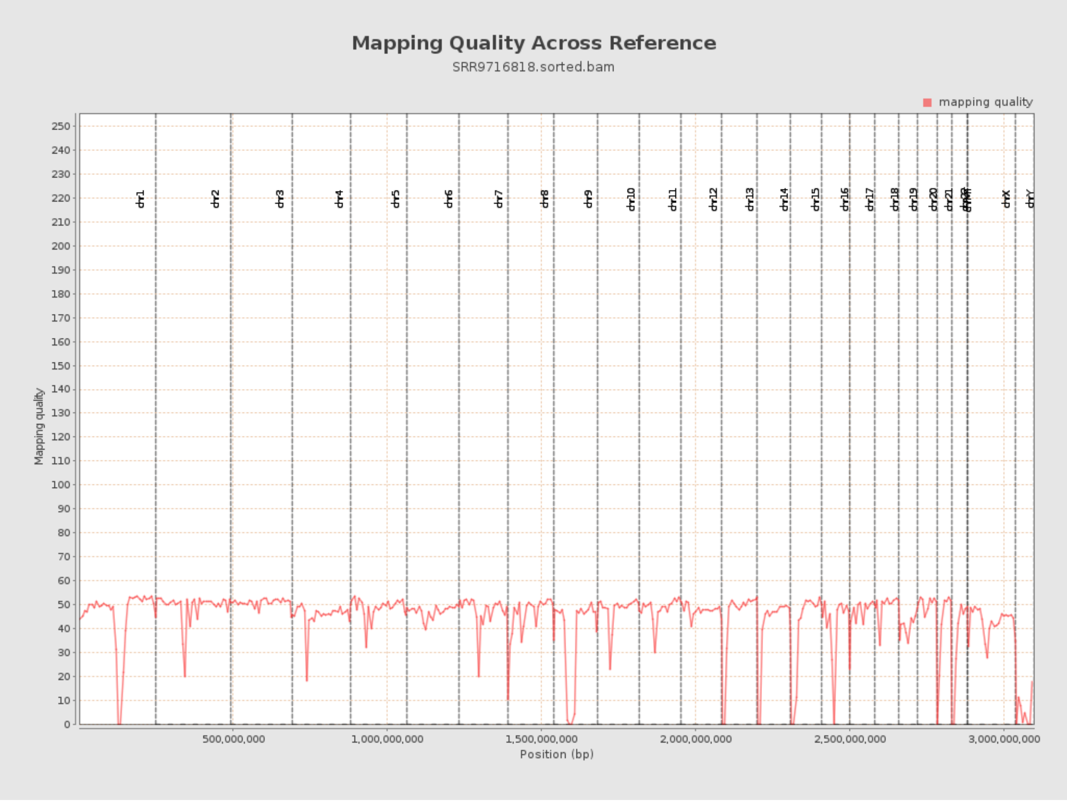
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram