Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 00:23:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716209.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_SRR9716209 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716209.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 00:23:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716209.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,633,724
Mapped reads	1,445,237 / 88.46%
Unmapped reads	188,487 / 11.54%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,413 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	35,627 / 2.18%
Duplication rate	1.72%
Clipped reads	1,446,540 / 88.54%

2.2. ACGT Content

Number/percentage of A's	19,912,189 / 24.35%
Number/percentage of C's	17,078,206 / 20.88%
Number/percentage of T's	25,892,828 / 31.66%
Number/percentage of G's	18,900,164 / 23.11%
Number/percentage of N's	586 / 0%
GC Percentage	43.99%

2.3. Coverage

Mean	0.0264

Standard Deviation	0.231

2.4. Mapping Quality

Mean Mapping Quality	42.02

2.5. Mismatches and indels

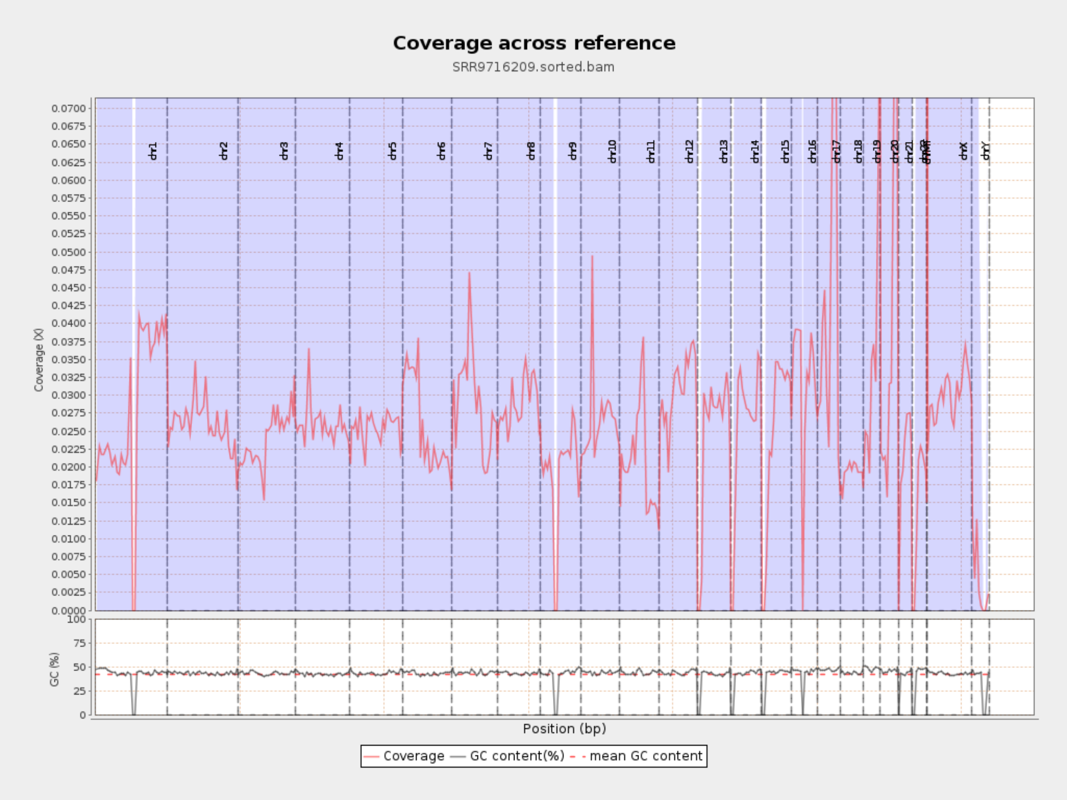
General error rate	0.54%
Mismatches	429,376
Insertions	6,401
Mapped reads with at least one insertion	0.44%
Deletions	16,072
Mapped reads with at least one deletion	1.1%
Homopolymer indels	40.44%

2.6. Chromosome stats

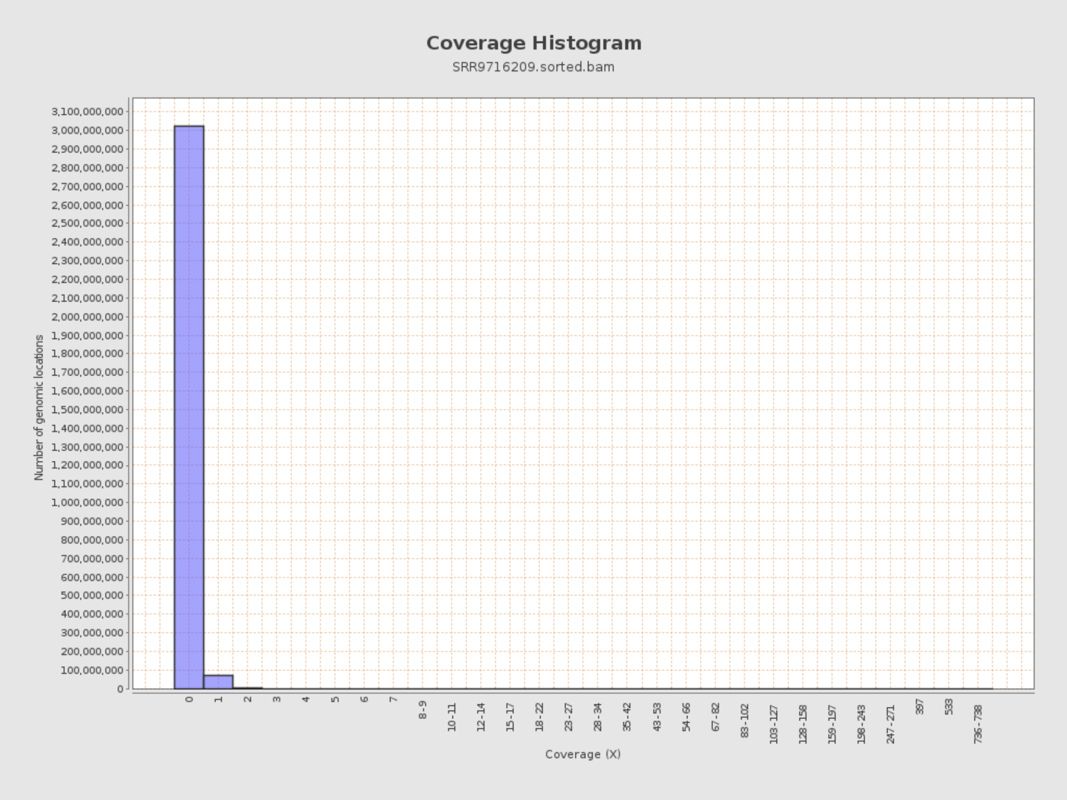
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6915051	0.0277	0.2887
chr2	243199373	6327668	0.026	0.3417
chr3	198022430	4714625	0.0238	0.1713
chr4	191154276	4987821	0.0261	0.1834
chr5	180915260	4637081	0.0256	0.1724
chr6	171115067	4416241	0.0258	0.2048
chr7	159138663	4683576	0.0294	0.3154

chr8	146364022	4241144	0.029	0.2267
chr9	141213431	2693787	0.0191	0.168
chr10	135534747	3609084	0.0266	0.2762
chr11	135006516	2840715	0.021	0.1901
chr12	133851895	4127525	0.0308	0.1918
chr13	115169878	2794815	0.0243	0.1685
chr14	107349540	2715286	0.0253	0.1779
chr15	102531392	2501466	0.0244	0.1715
chr16	90354753	2834636	0.0314	0.2008
chr17	81195210	3618473	0.0446	0.2389
chr18	78077248	1507940	0.0193	0.2573
chr19	59128983	2160927	0.0365	0.2849
chr20	63025520	2599652	0.0412	0.2288
chr21	48129895	1013935	0.0211	0.1674
chr22	51304566	759782	0.0148	0.1326
chrMT	16571	192425	11.6122	8.2426
chrX	155270560	4679306	0.0301	0.1987
chrY	59373566	236284	0.004	0.1049

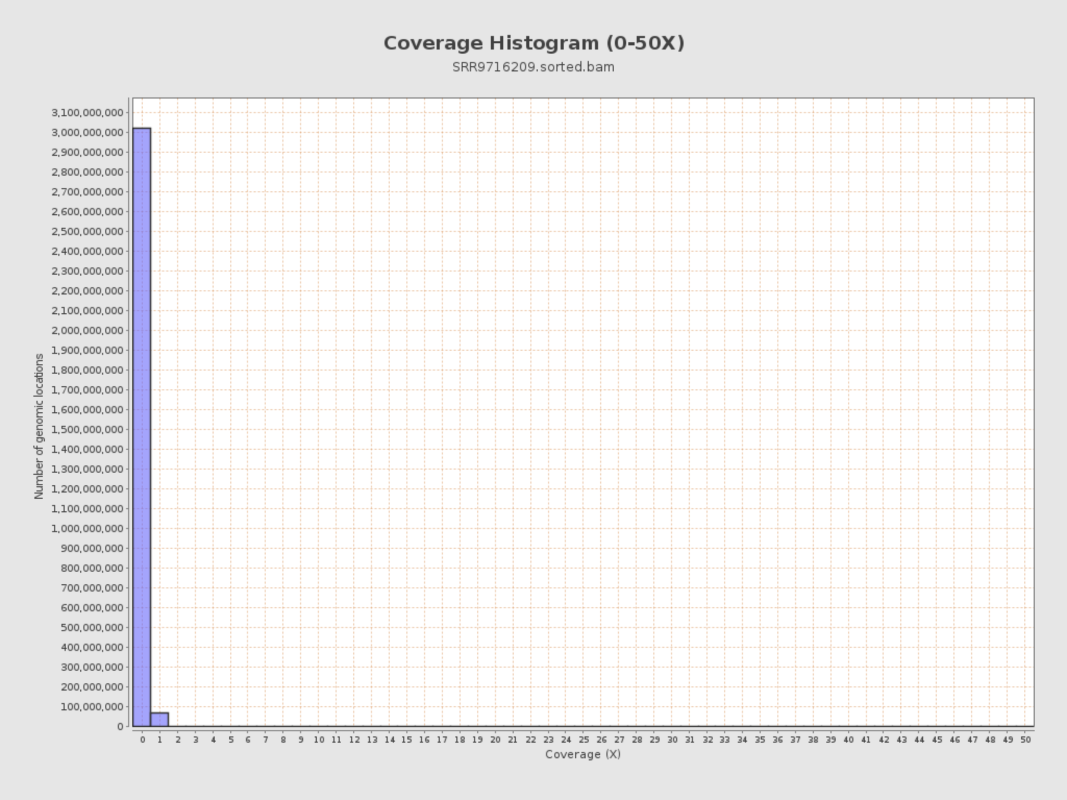
3. Results : Coverage across reference



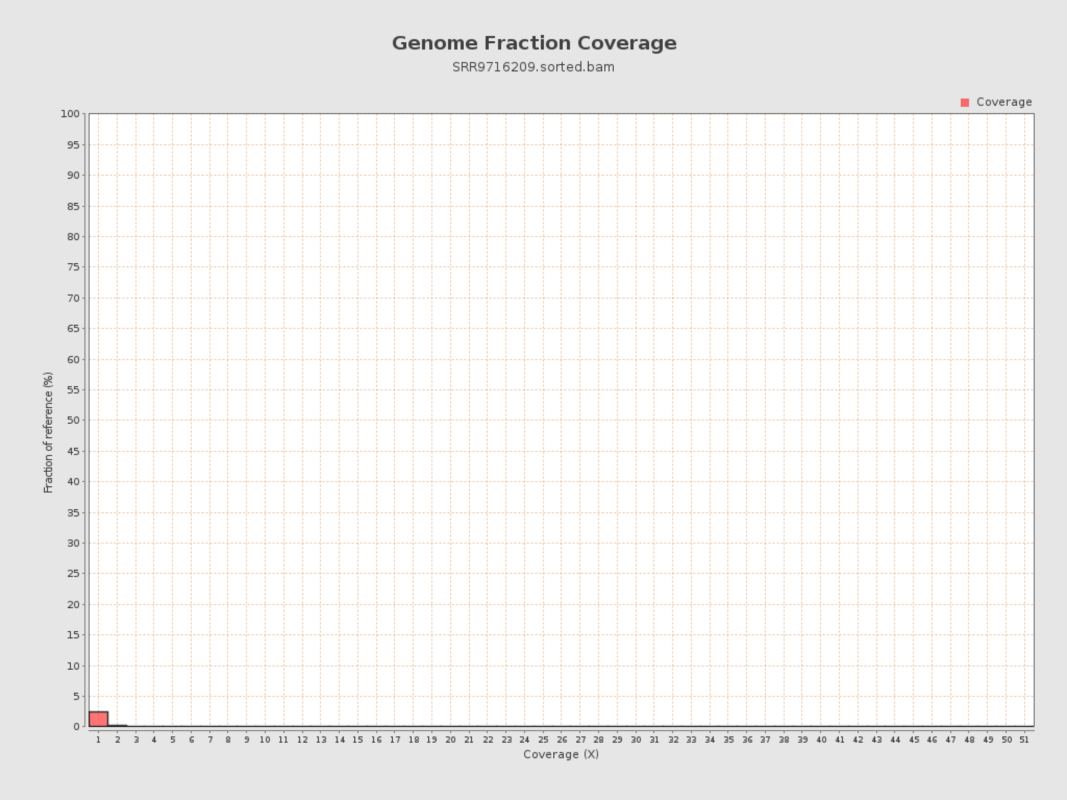
4. Results : Coverage Histogram



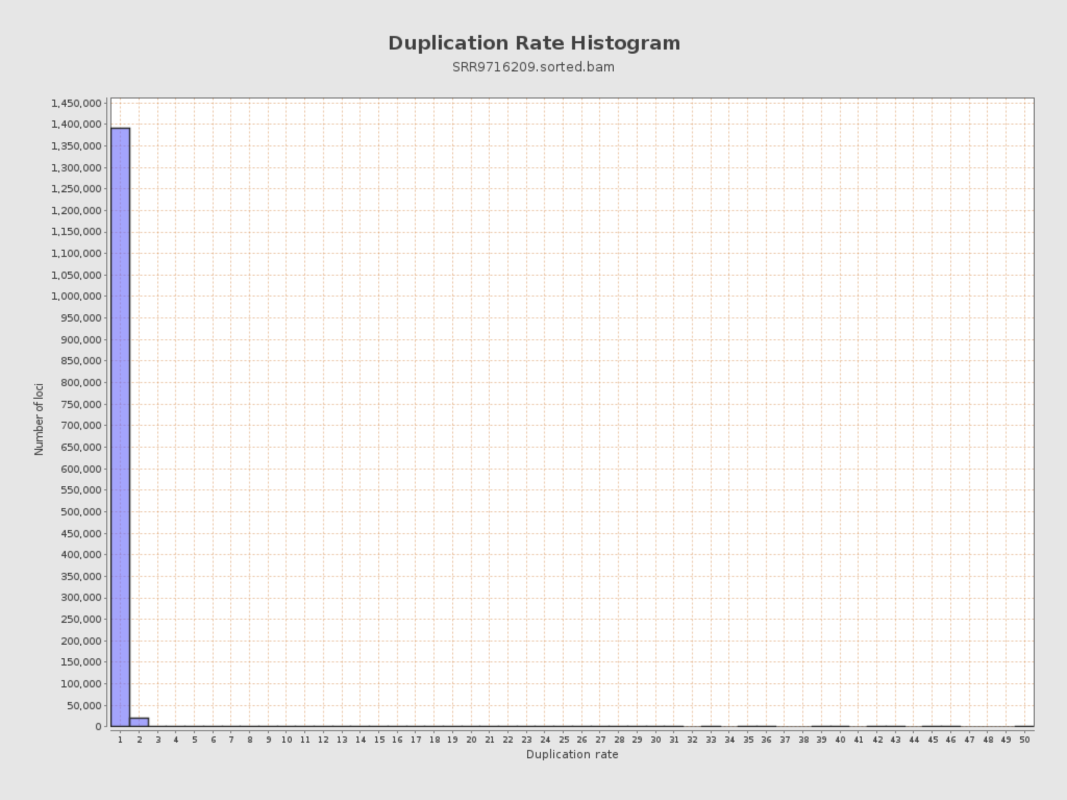
5. Results : Coverage Histogram (0-50X)



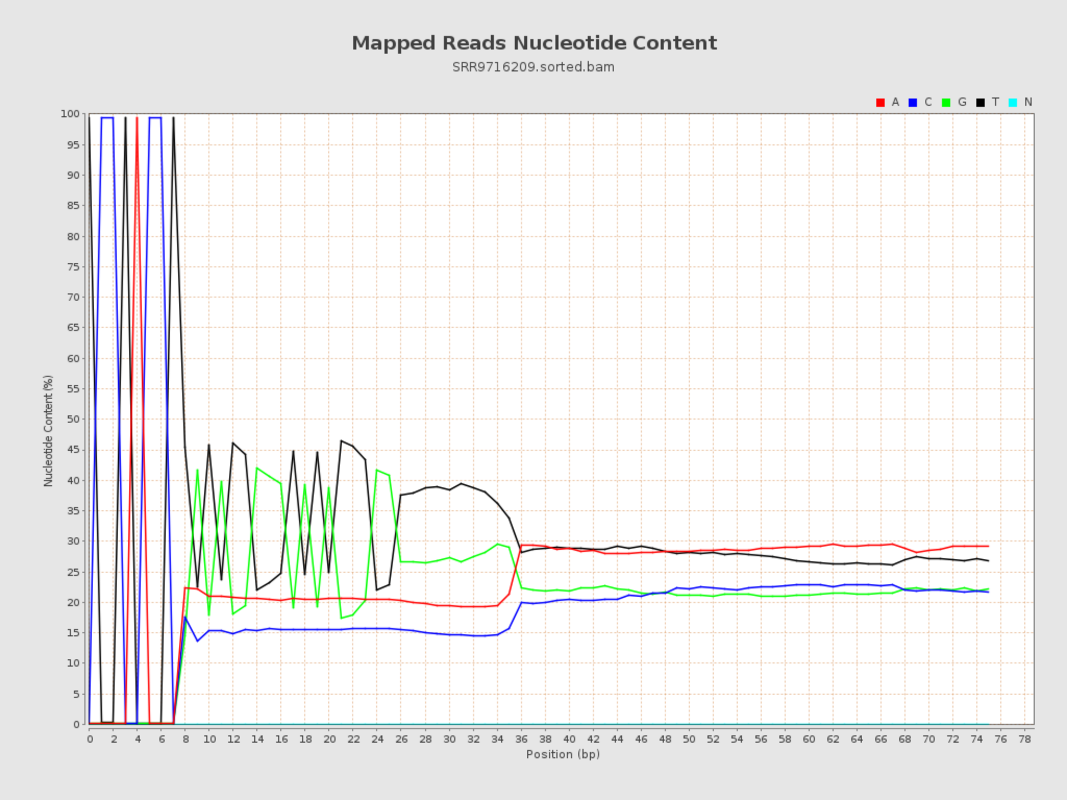
6. Results : Genome Fraction Coverage



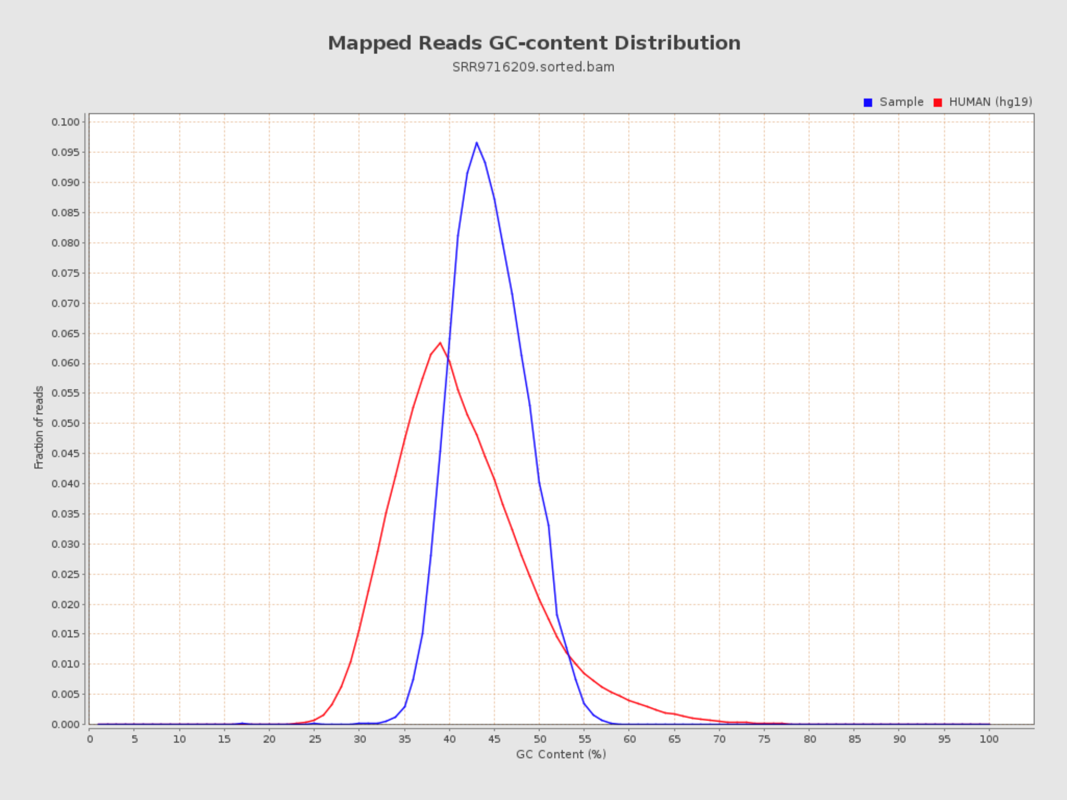
7. Results : Duplication Rate Histogram



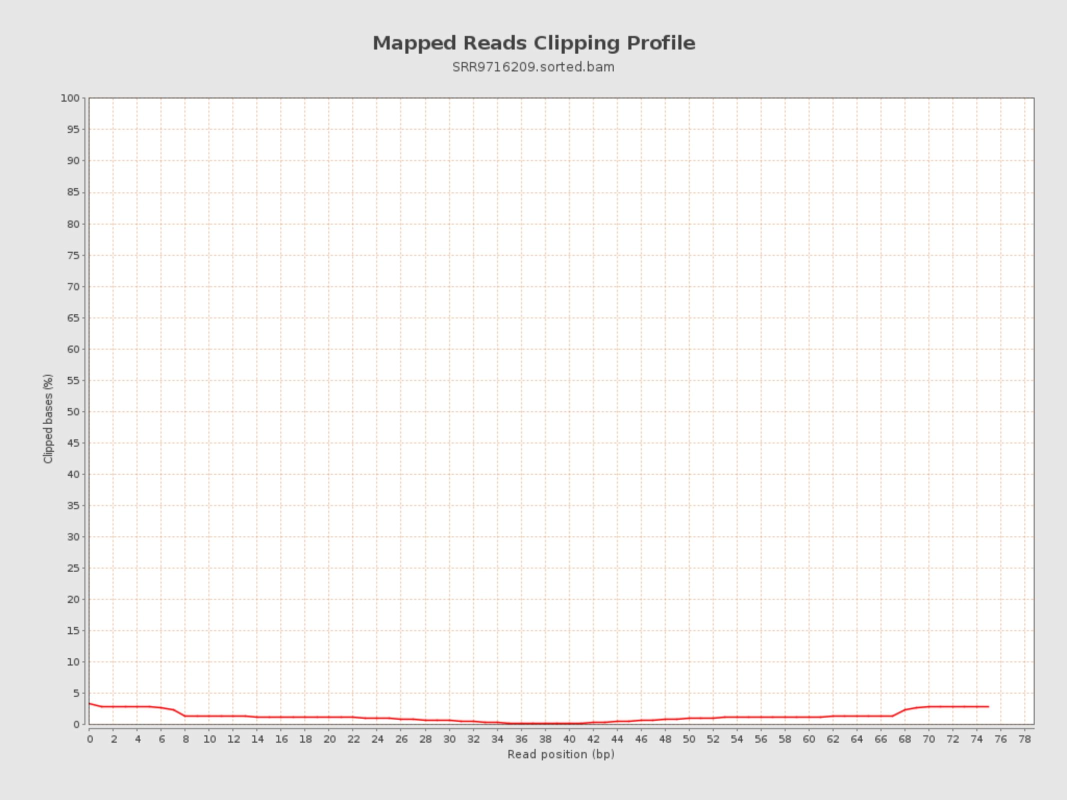
8. Results : Mapped Reads Nucleotide Content



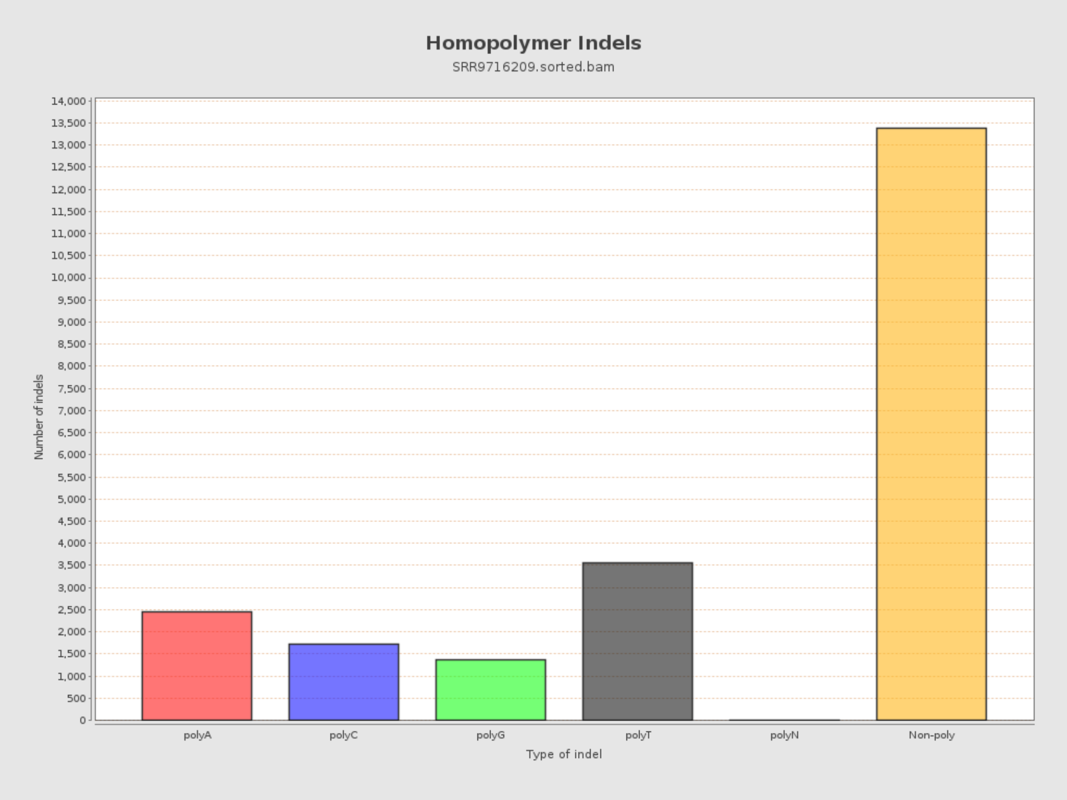
9. Results : Mapped Reads GC-content Distribution



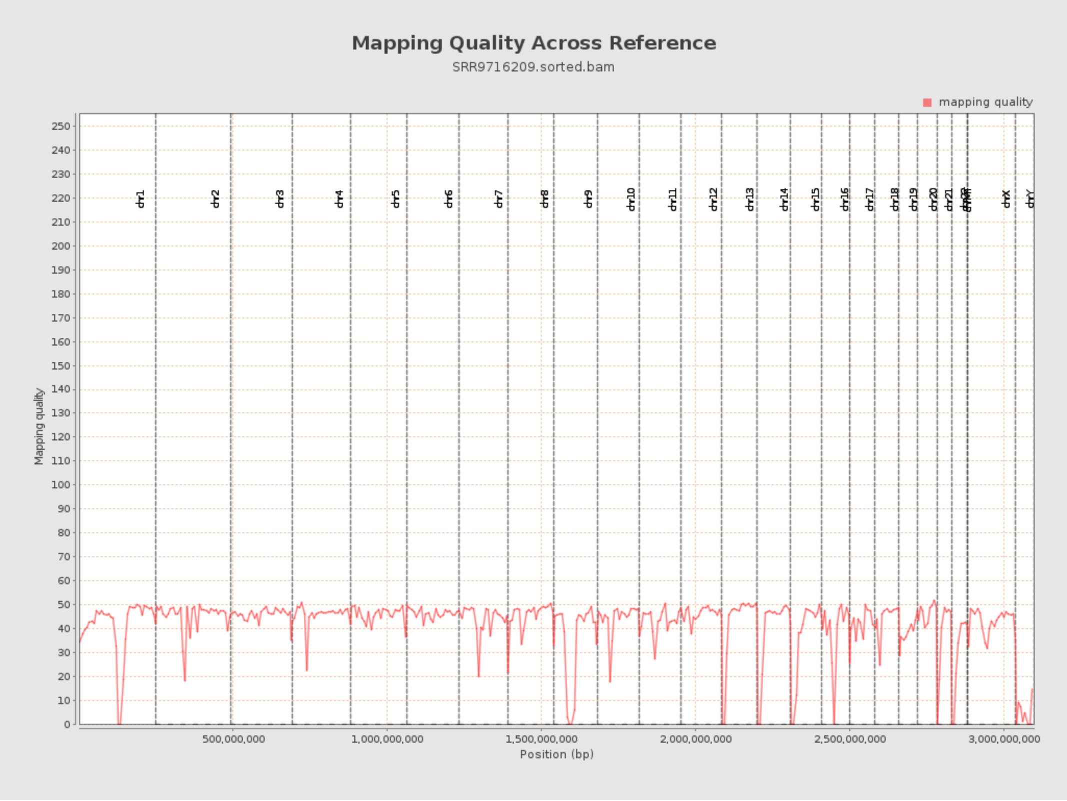
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram