Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 02:17:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716243.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_SRR9716243 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716243.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 02:17:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716243.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	788,948
Mapped reads	746,329 / 94.6%
Unmapped reads	42,619 / 5.4%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,452 / 1.58%
Read min/max/mean length	30 / 101 / 101.58
Duplicated reads (estimated)	24,092 / 3.05%
Duplication rate	1.76%
Clipped reads	758,093 / 96.09%

2.2. ACGT Content

Number/percentage of A's	15,502,814 / 25.76%
Number/percentage of C's	11,524,556 / 19.15%
Number/percentage of T's	18,277,257 / 30.37%
Number/percentage of G's	14,881,174 / 24.72%
Number/percentage of N's	3,690 / 0.01%
GC Percentage	43.87%

2.3. Coverage

Mean	0.0195

Standard Deviation	0.2693

2.4. Mapping Quality

Mean Mapping Quality	45.71

2.5. Mismatches and indels

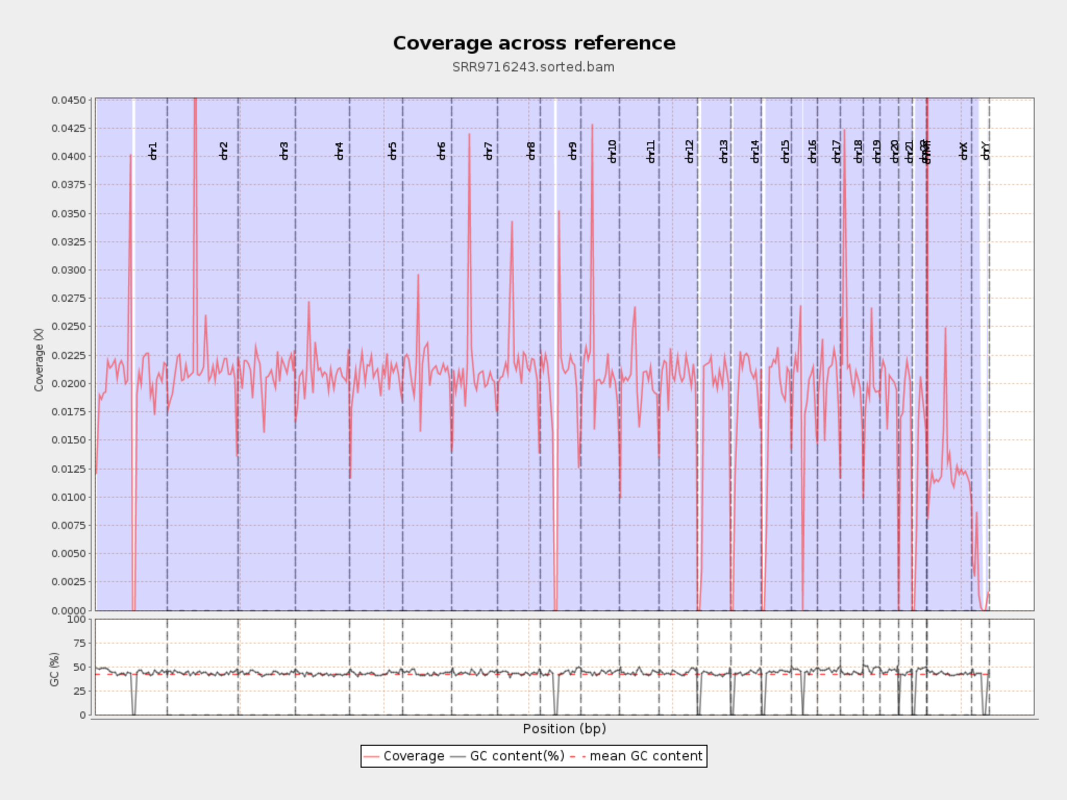
General error rate	0.81%
Mismatches	476,783
Insertions	5,258
Mapped reads with at least one insertion	0.69%
Deletions	15,228
Mapped reads with at least one deletion	2.01%
Homopolymer indels	44.83%

2.6. Chromosome stats

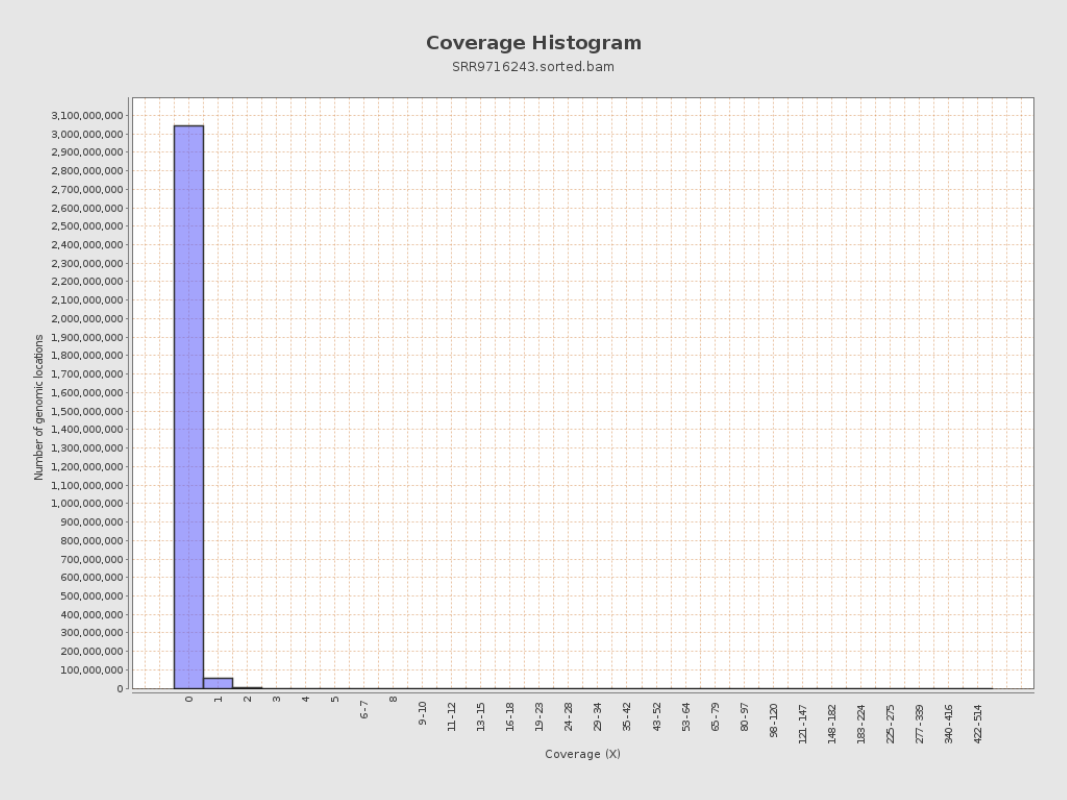
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4904361	0.0197	0.4285
chr2	243199373	5376677	0.0221	0.3665
chr3	198022430	4159769	0.021	0.1546
chr4	191154276	3984053	0.0208	0.1608
chr5	180915260	3750061	0.0207	0.155
chr6	171115067	3650232	0.0213	0.1795
chr7	159138663	3381678	0.0212	0.328

chr8	146364022	3226393	0.022	0.3803
chr9	141213431	2686936	0.019	0.3051
chr10	135534747	2929411	0.0216	0.2667
chr11	135006516	2744093	0.0203	0.2493
chr12	133851895	2773943	0.0207	0.156
chr13	115169878	1998714	0.0174	0.1379
chr14	107349540	1883047	0.0175	0.1853
chr15	102531392	1737497	0.0169	0.138
chr16	90354753	1659968	0.0184	0.1694
chr17	81195210	1630788	0.0201	0.1682
chr18	78077248	1778177	0.0228	0.5869
chr19	59128983	1161301	0.0196	0.3185
chr20	63025520	1237449	0.0196	0.1571
chr21	48129895	823304	0.0171	0.146
chr22	51304566	635441	0.0124	0.1171
chrMT	16571	11018	0.6649	0.8781
chrX	155270560	1954309	0.0126	0.1687
chrY	59373566	137482	0.0023	0.0822

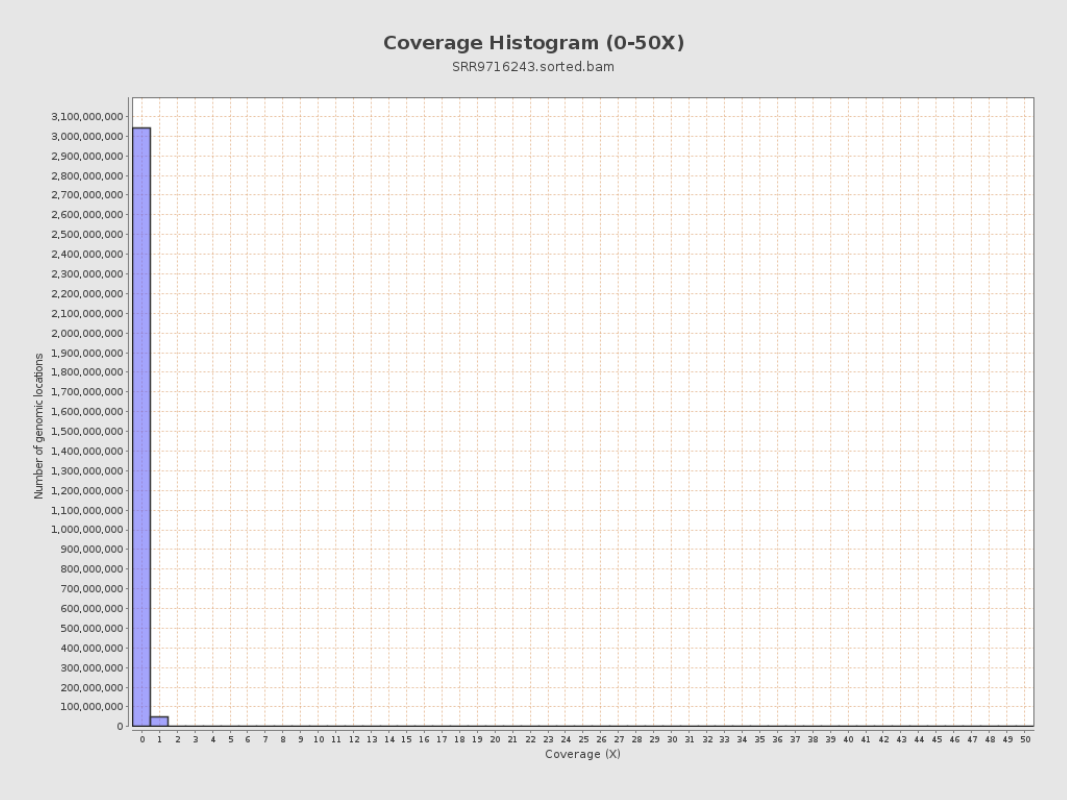
3. Results : Coverage across reference



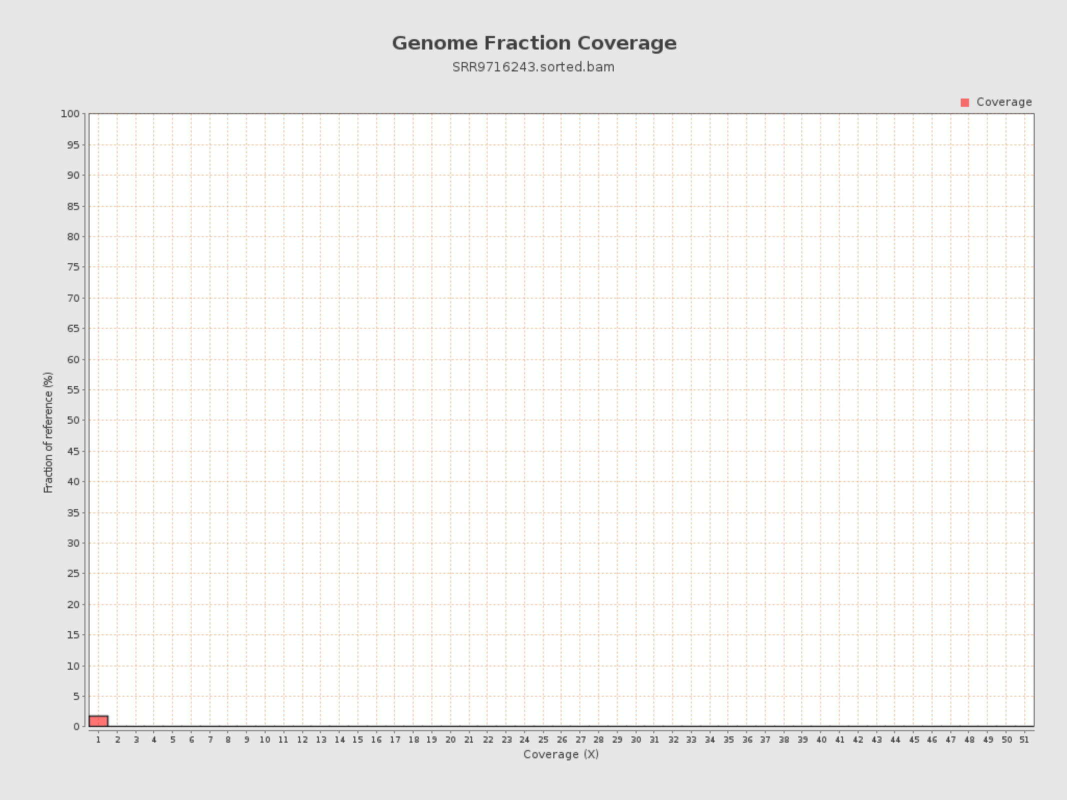
4. Results : Coverage Histogram



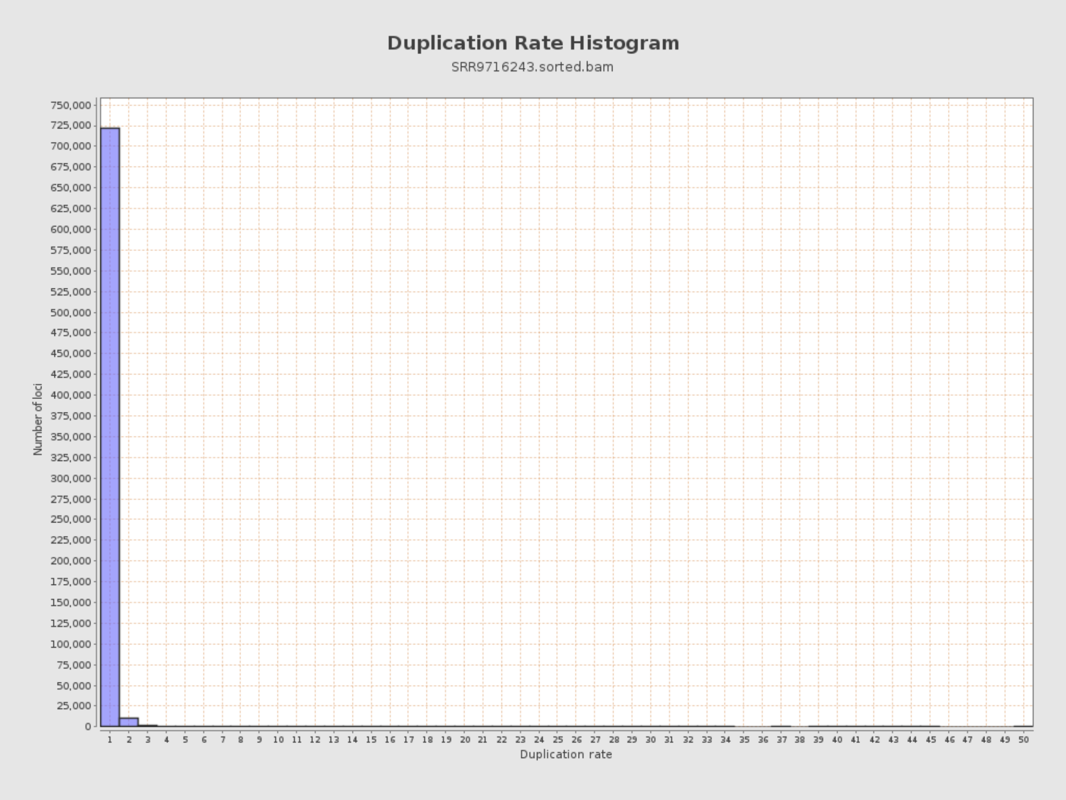
5. Results : Coverage Histogram (0-50X)



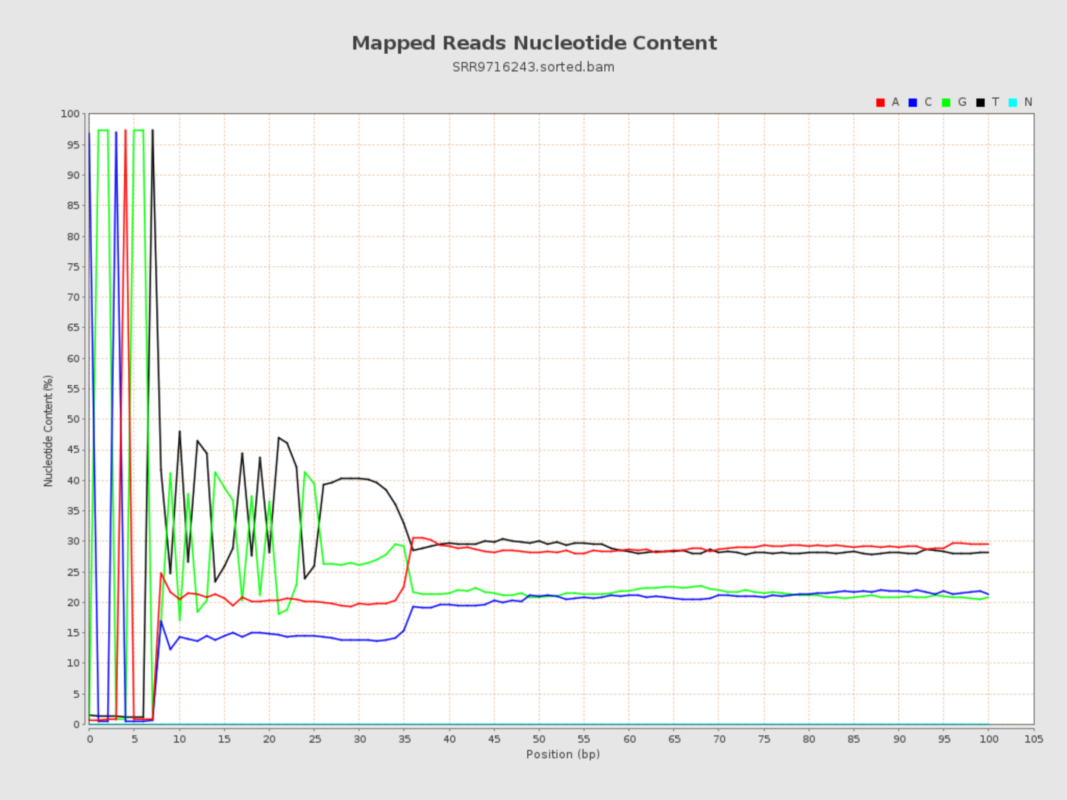
6. Results : Genome Fraction Coverage



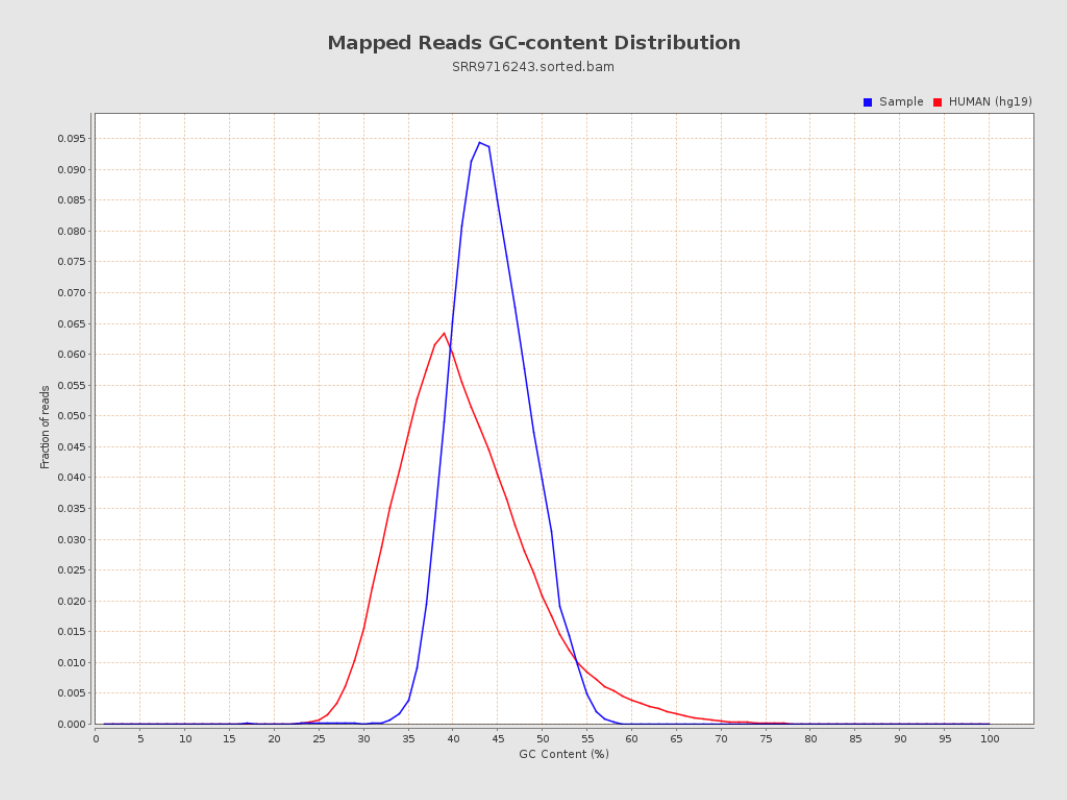
7. Results : Duplication Rate Histogram



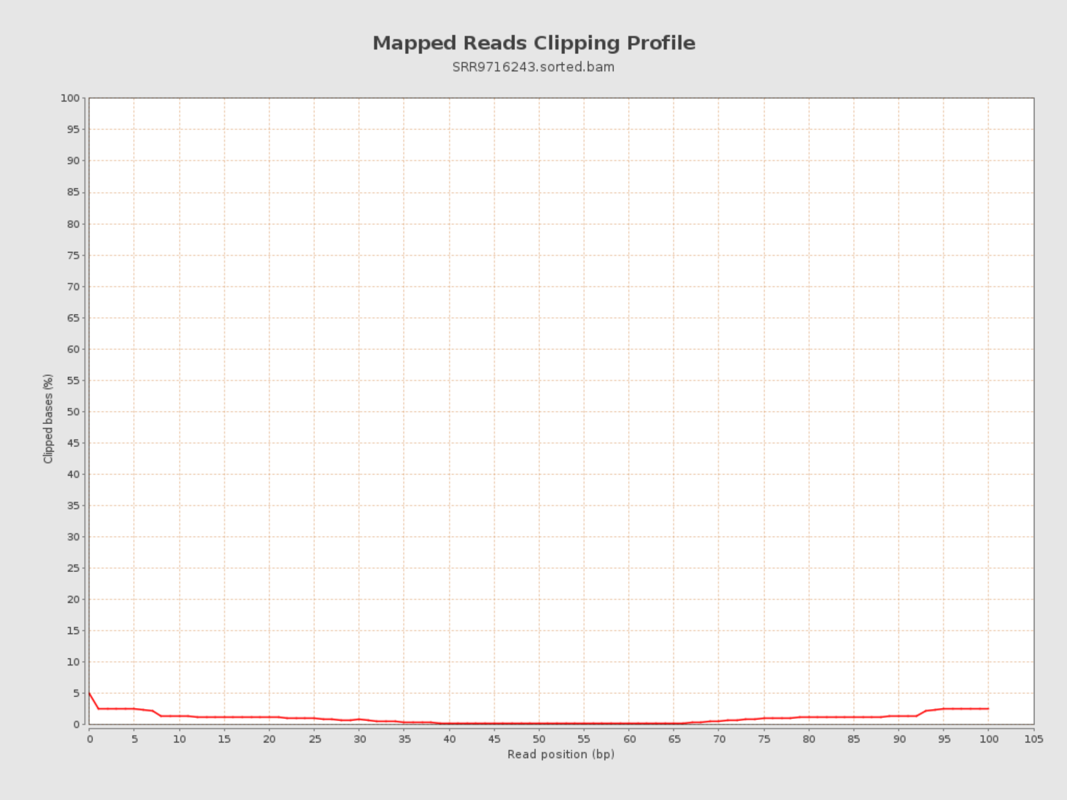
8. Results : Mapped Reads Nucleotide Content



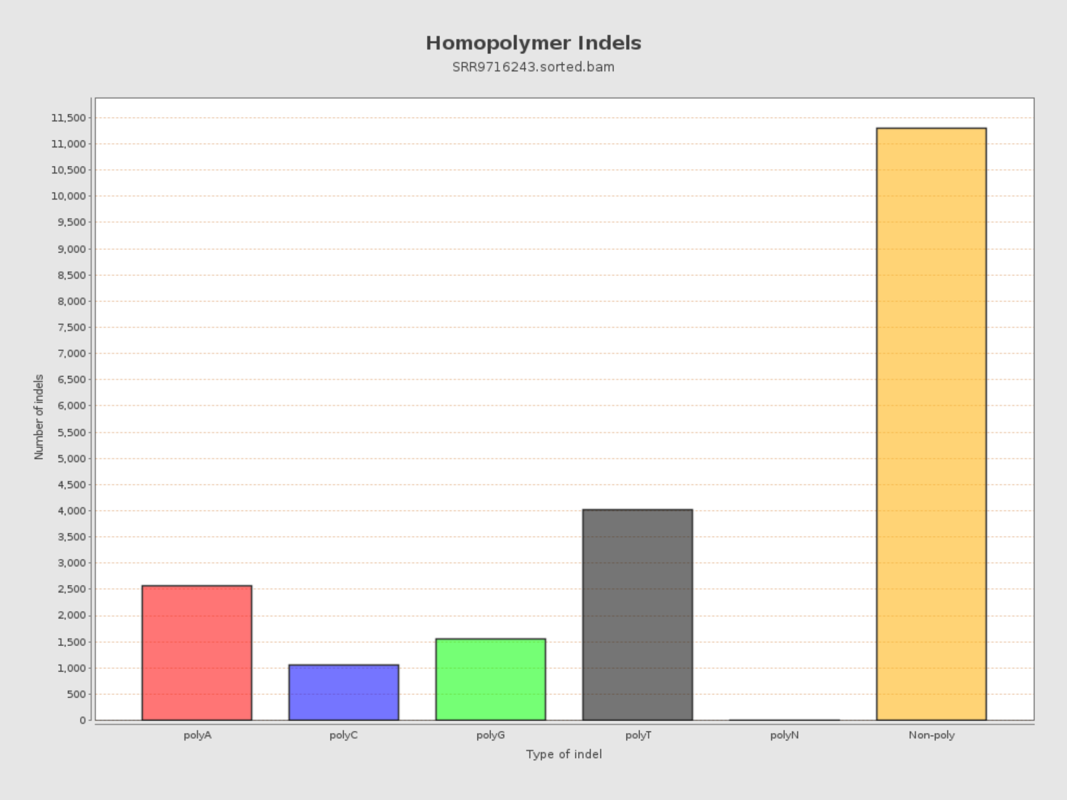
9. Results : Mapped Reads GC-content Distribution



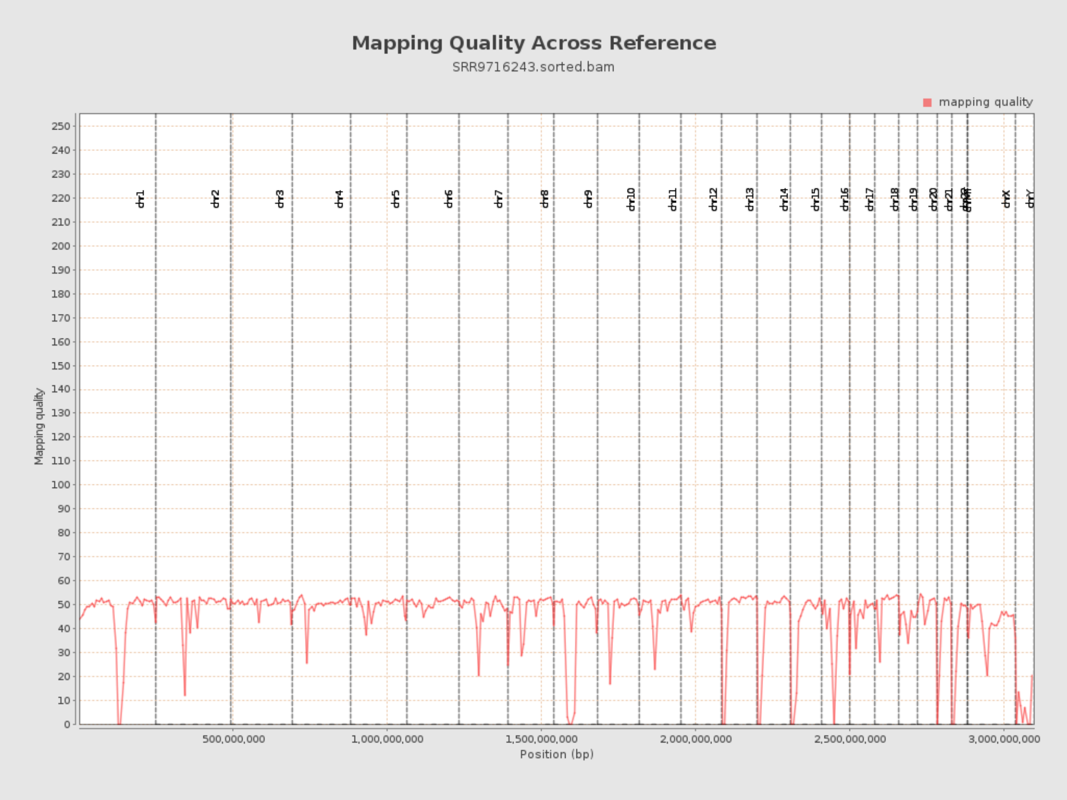
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram