Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 12:52:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716428.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_SRR9716428 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716428.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 12:52:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716428.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,540,215
Mapped reads	1,424,863 / 92.51%
Unmapped reads	115,352 / 7.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,069 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	66,252 / 4.3%
Duplication rate	3.54%
Clipped reads	1,429,955 / 92.84%

2.2. ACGT Content

Number/percentage of A's	21,216,048 / 25.39%
Number/percentage of C's	15,060,201 / 18.02%
Number/percentage of T's	26,097,824 / 31.23%
Number/percentage of G's	21,181,506 / 25.35%
Number/percentage of N's	1,722 / 0%
GC Percentage	43.37%

2.3. Coverage

Mean	0.027

Standard Deviation	0.2605

2.4. Mapping Quality

Mean Mapping Quality	45.11

2.5. Mismatches and indels

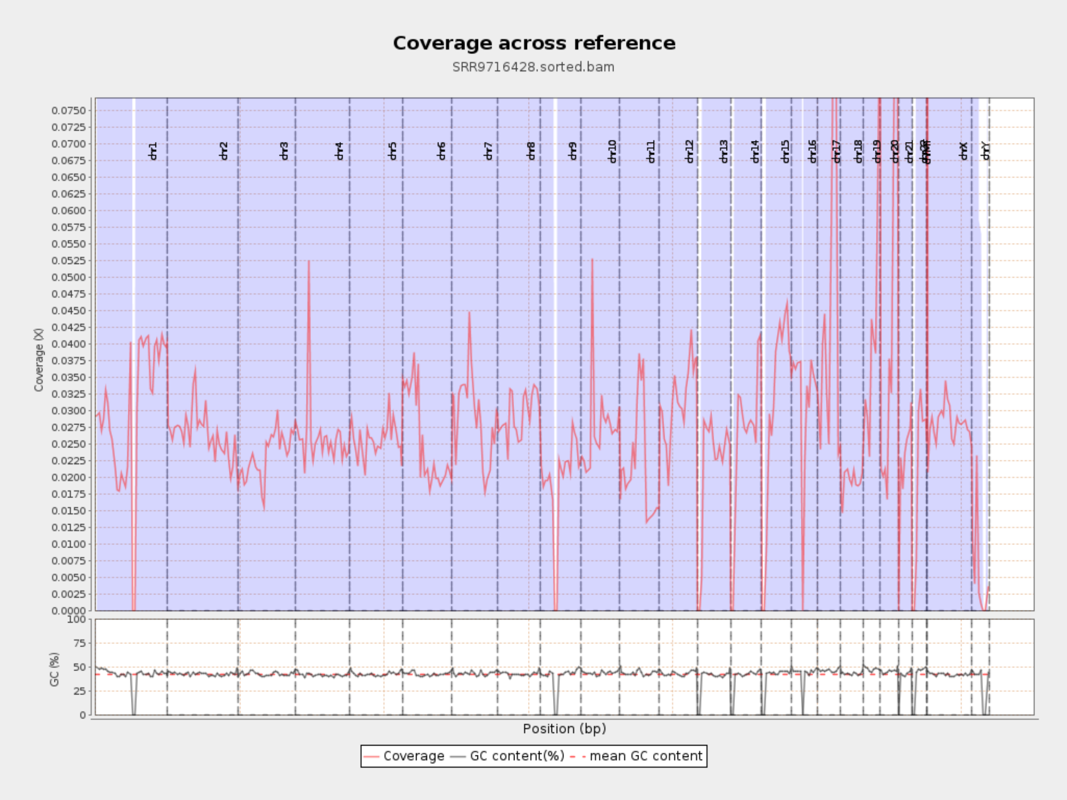
General error rate	0.49%
Mismatches	399,906
Insertions	5,483
Mapped reads with at least one insertion	0.38%
Deletions	14,913
Mapped reads with at least one deletion	1.04%
Homopolymer indels	44.7%

2.6. Chromosome stats

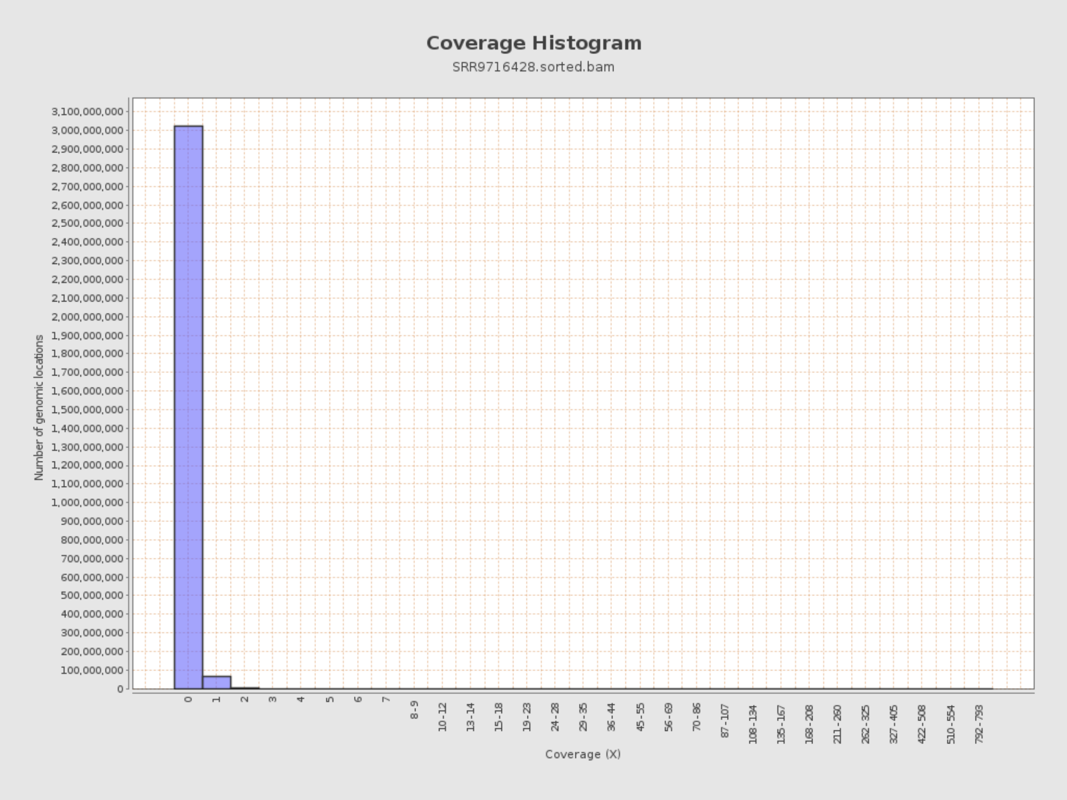
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7405438	0.0297	0.3986
chr2	243199373	6448102	0.0265	0.3723
chr3	198022430	4597930	0.0232	0.1675
chr4	191154276	5014797	0.0262	0.2211
chr5	180915260	4661995	0.0258	0.1762
chr6	171115067	4358083	0.0255	0.1977
chr7	159138663	4640003	0.0292	0.298

chr8	146364022	4306600	0.0294	0.3766
chr9	141213431	2741720	0.0194	0.1804
chr10	135534747	3729269	0.0275	0.2894
chr11	135006516	2952665	0.0219	0.1982
chr12	133851895	4175715	0.0312	0.1953
chr13	115169878	2465143	0.0214	0.1622
chr14	107349540	2764573	0.0258	0.1802
chr15	102531392	3118109	0.0304	0.1914
chr16	90354753	2828209	0.0313	0.2018
chr17	81195210	3720879	0.0458	0.2474
chr18	78077248	1496457	0.0192	0.2716
chr19	59128983	2543480	0.043	0.3298
chr20	63025520	2809637	0.0446	0.243
chr21	48129895	1064950	0.0221	0.2046
chr22	51304566	1041096	0.0203	0.1577
chrMT	16571	14731	0.889	1.1133
chrX	155270560	4360463	0.0281	0.1959
chrY	59373566	322064	0.0054	0.2605

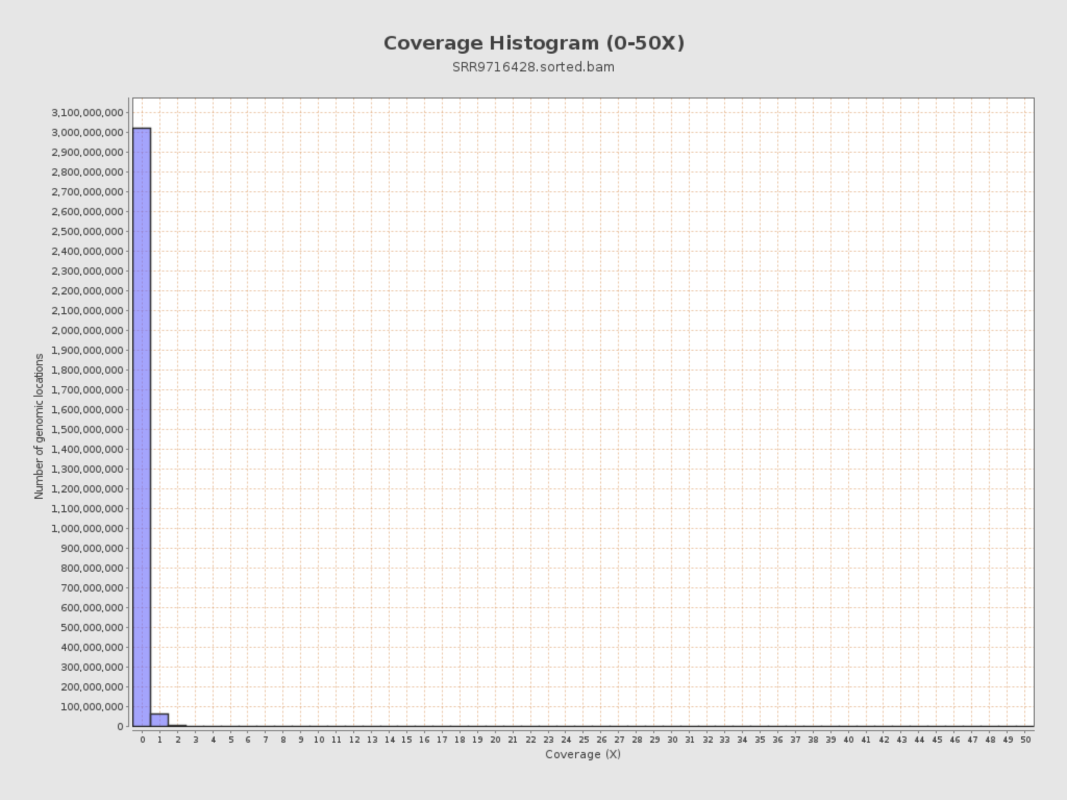
3. Results : Coverage across reference



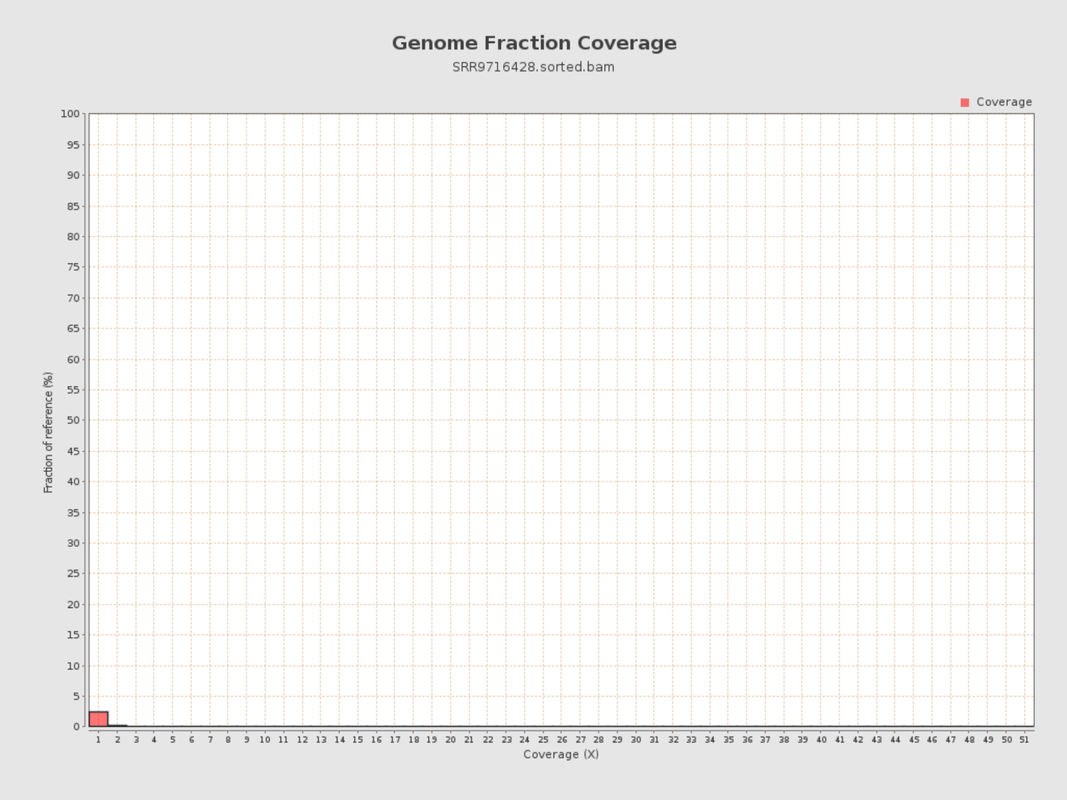
4. Results : Coverage Histogram



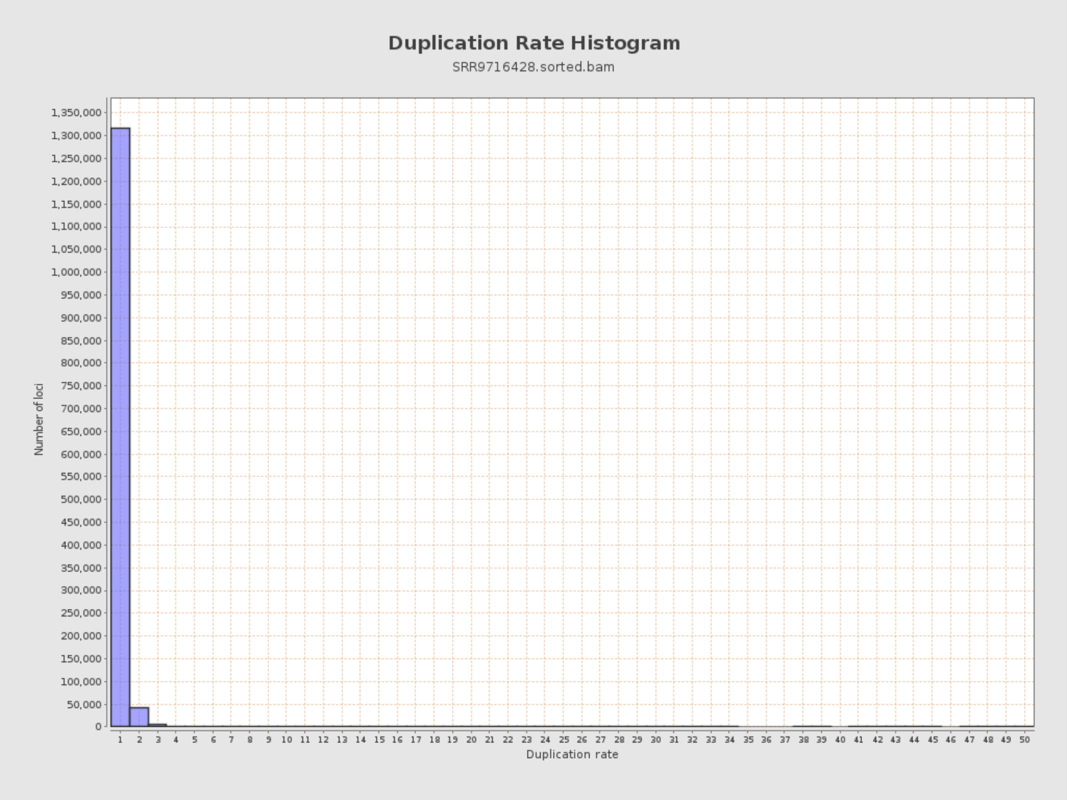
5. Results : Coverage Histogram (0-50X)



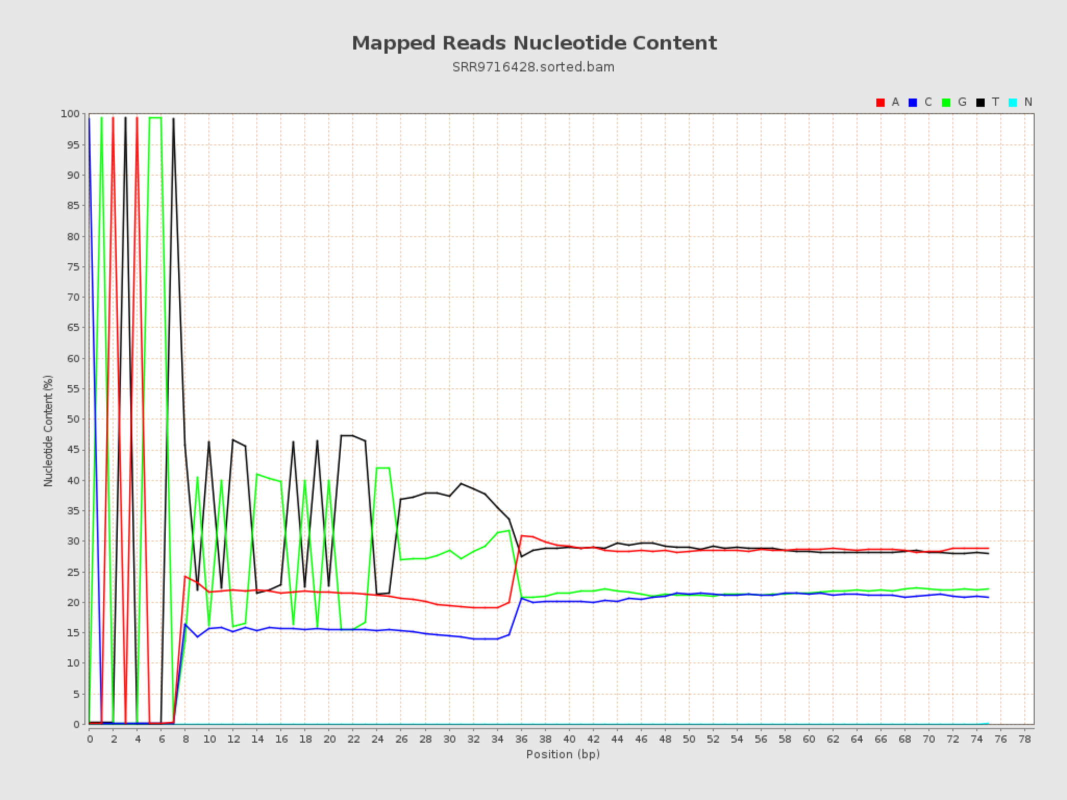
6. Results : Genome Fraction Coverage



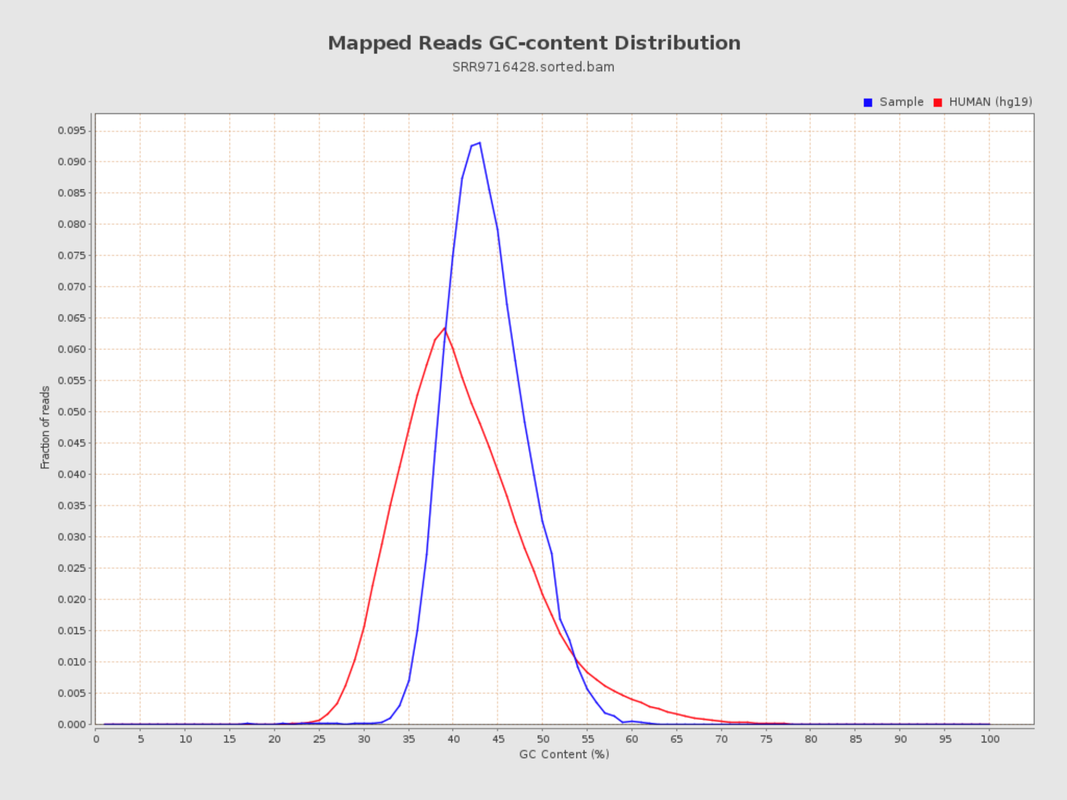
7. Results : Duplication Rate Histogram



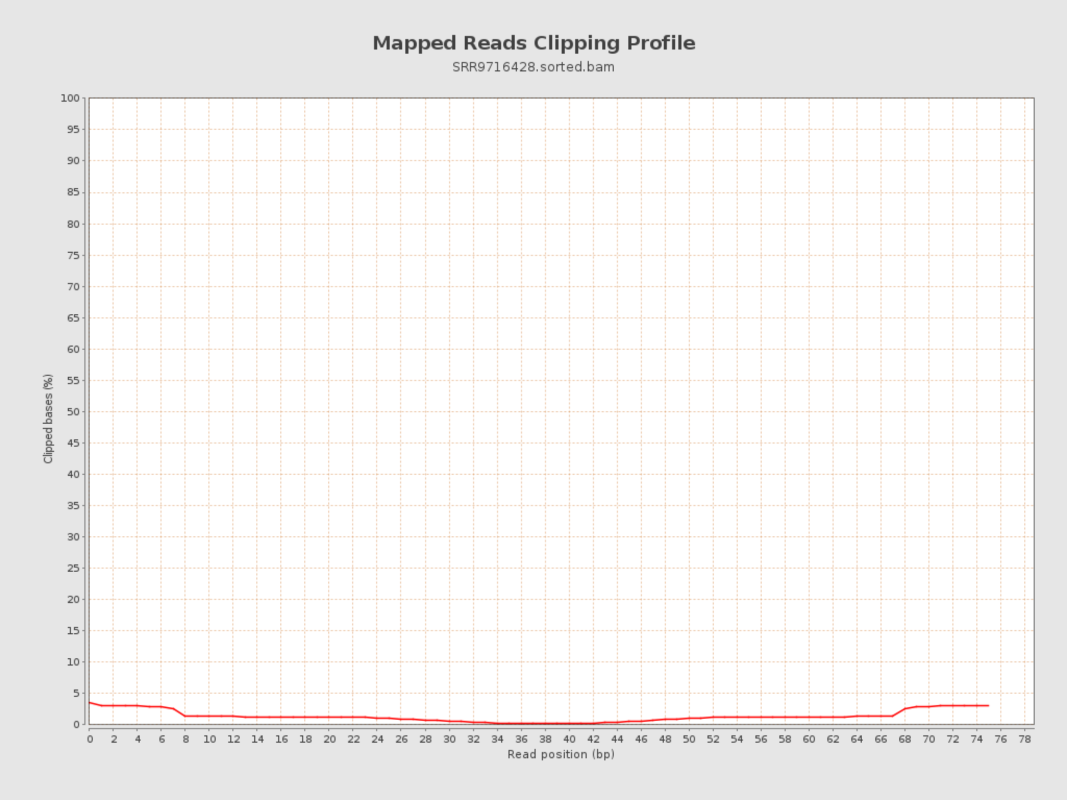
8. Results : Mapped Reads Nucleotide Content



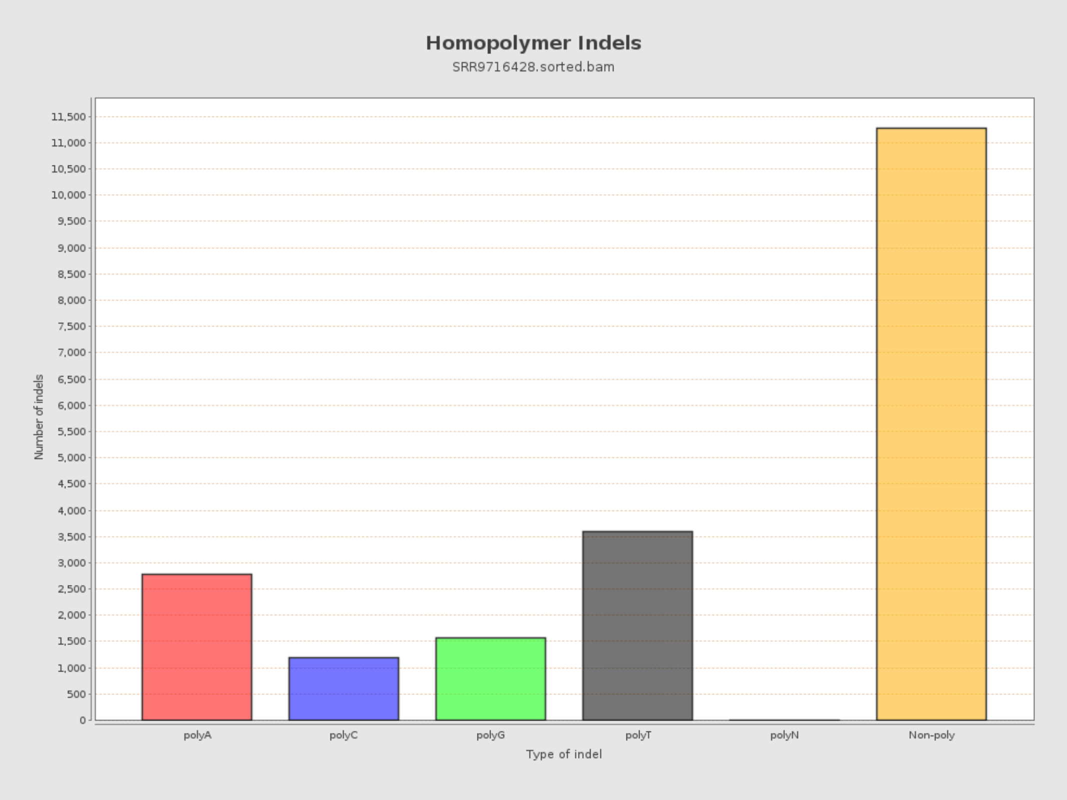
9. Results : Mapped Reads GC-content Distribution



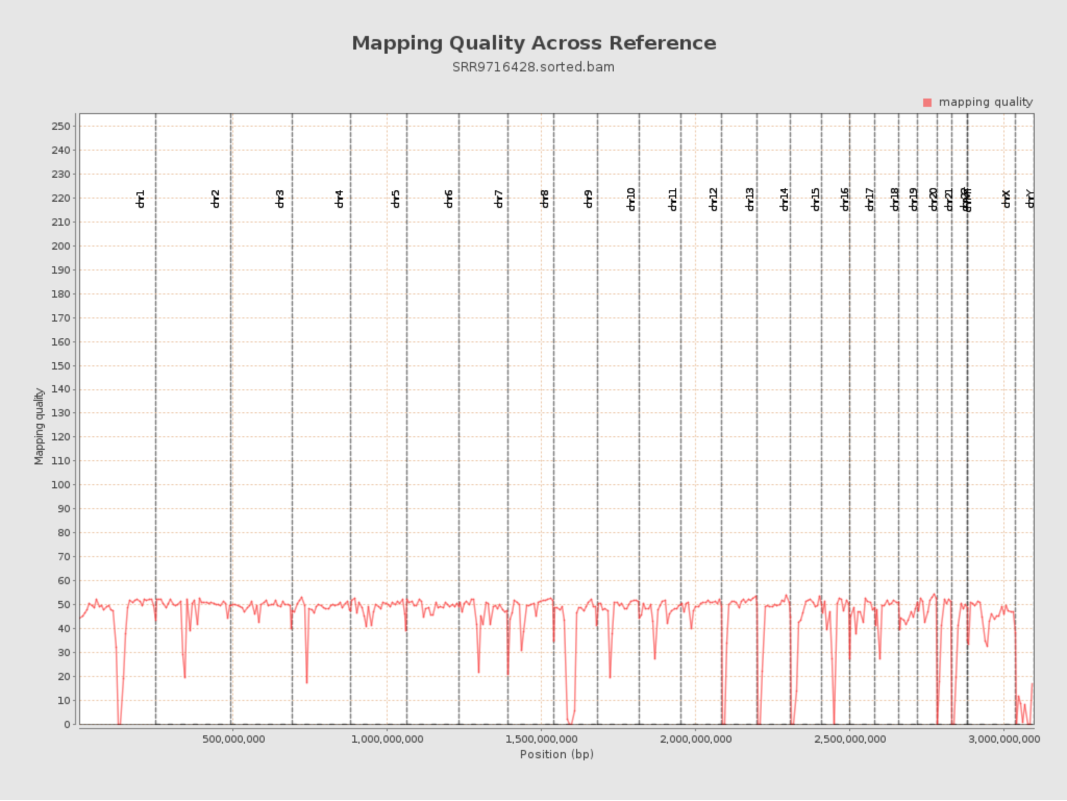
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram