Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 16:22:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716883.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_SRR9716883 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716883.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 16:22:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716883.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	539,605
Mapped reads	494,099 / 91.57%
Unmapped reads	45,506 / 8.43%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,306 / 0.43%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	8,846 / 1.64%
Duplication rate	1.31%
Clipped reads	496,135 / 91.94%

2.2. ACGT Content

Number/percentage of A's	7,298,160 / 25.28%
Number/percentage of C's	5,643,468 / 19.55%
Number/percentage of T's	9,012,105 / 31.22%
Number/percentage of G's	6,915,450 / 23.95%
Number/percentage of N's	789 / 0%
GC Percentage	43.5%

2.3. Coverage

Mean	0.0093

Standard Deviation	0.1187

2.4. Mapping Quality

Mean Mapping Quality	44.9

2.5. Mismatches and indels

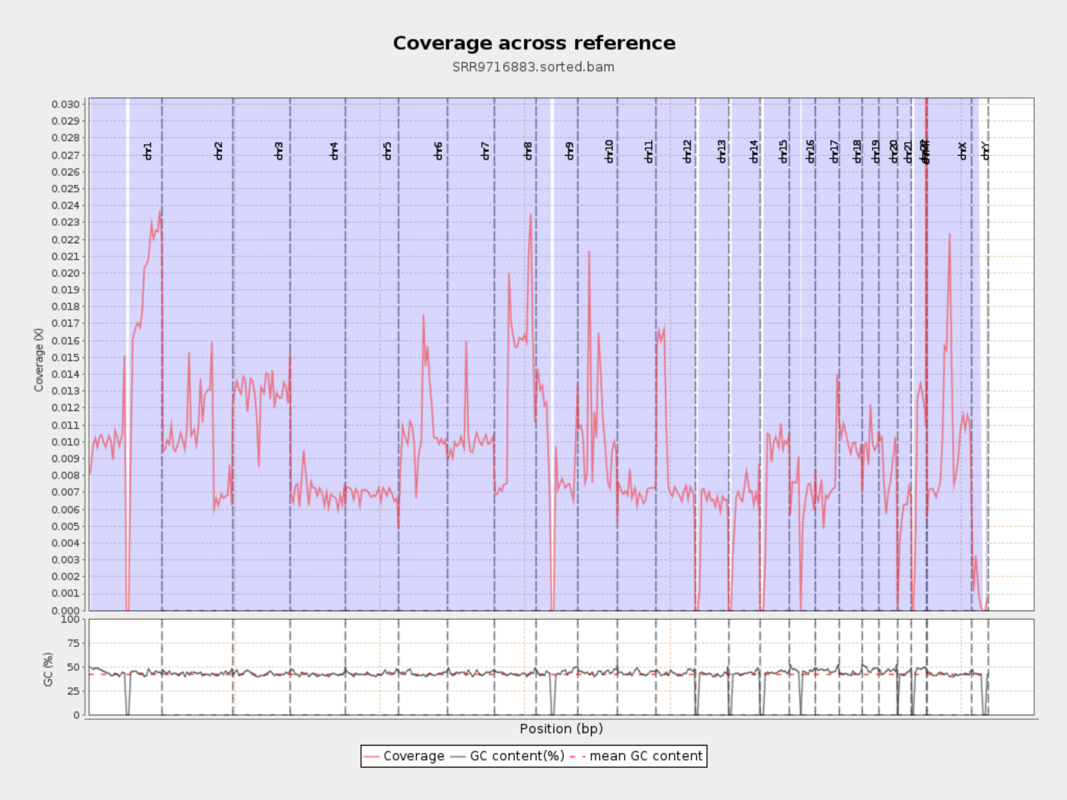
General error rate	0.5%
Mismatches	141,964
Insertions	1,539
Mapped reads with at least one insertion	0.31%
Deletions	5,220
Mapped reads with at least one deletion	1.05%
Homopolymer indels	44.41%

2.6. Chromosome stats

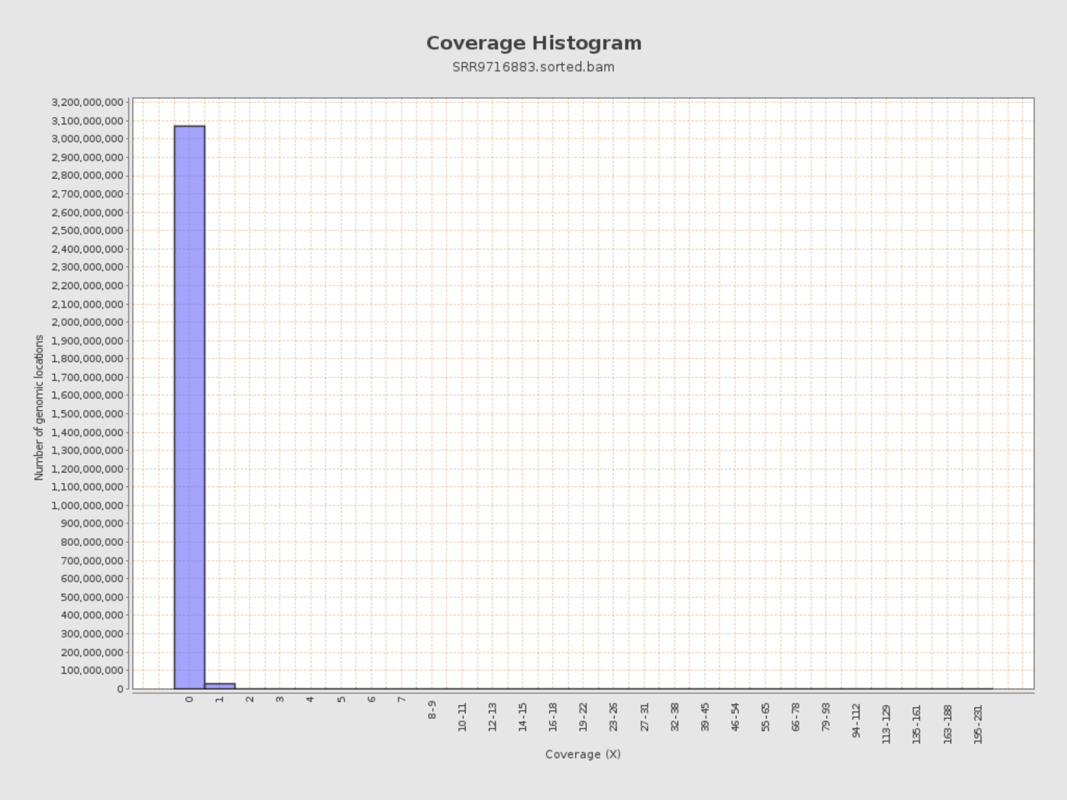
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3385809	0.0136	0.1843
chr2	243199373	2427083	0.01	0.1406
chr3	198022430	2552555	0.0129	0.1178
chr4	191154276	1334098	0.007	0.0881
chr5	180915260	1253118	0.0069	0.0867
chr6	171115067	1846251	0.0108	0.1136
chr7	159138663	1620490	0.0102	0.1373

chr8	146364022	2037578	0.0139	0.1298
chr9	141213431	1187954	0.0084	0.1086
chr10	135534747	1468966	0.0108	0.1346
chr11	135006516	945226	0.007	0.0969
chr12	133851895	1242270	0.0093	0.1006
chr13	115169878	637252	0.0055	0.0773
chr14	107349540	624121	0.0058	0.0836
chr15	102531392	827741	0.0081	0.0934
chr16	90354753	584609	0.0065	0.0894
chr17	81195210	631153	0.0078	0.0922
chr18	78077248	781034	0.01	0.1602
chr19	59128983	582339	0.0098	0.1427
chr20	63025520	528637	0.0084	0.0945
chr21	48129895	259839	0.0054	0.0783
chr22	51304566	441904	0.0086	0.0956
chrMT	16571	5362	0.3236	0.5951
chrX	155270560	1608360	0.0104	0.1121
chrY	59373566	64347	0.0011	0.0386

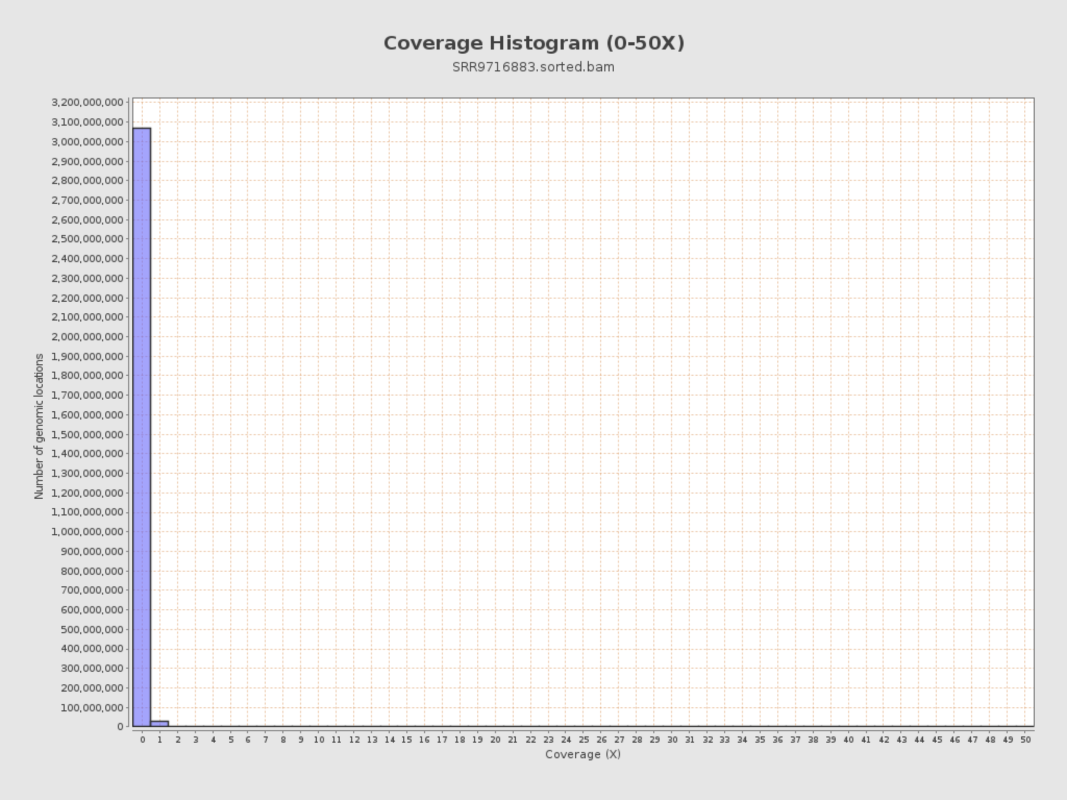
3. Results : Coverage across reference



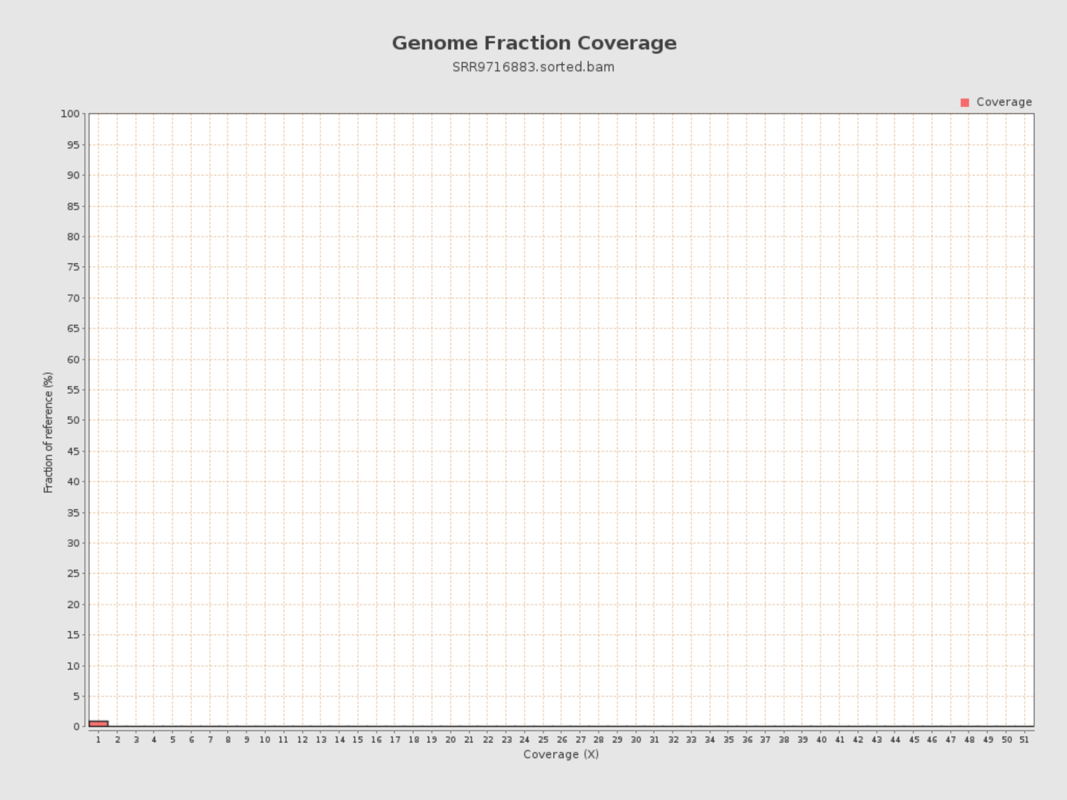
4. Results : Coverage Histogram



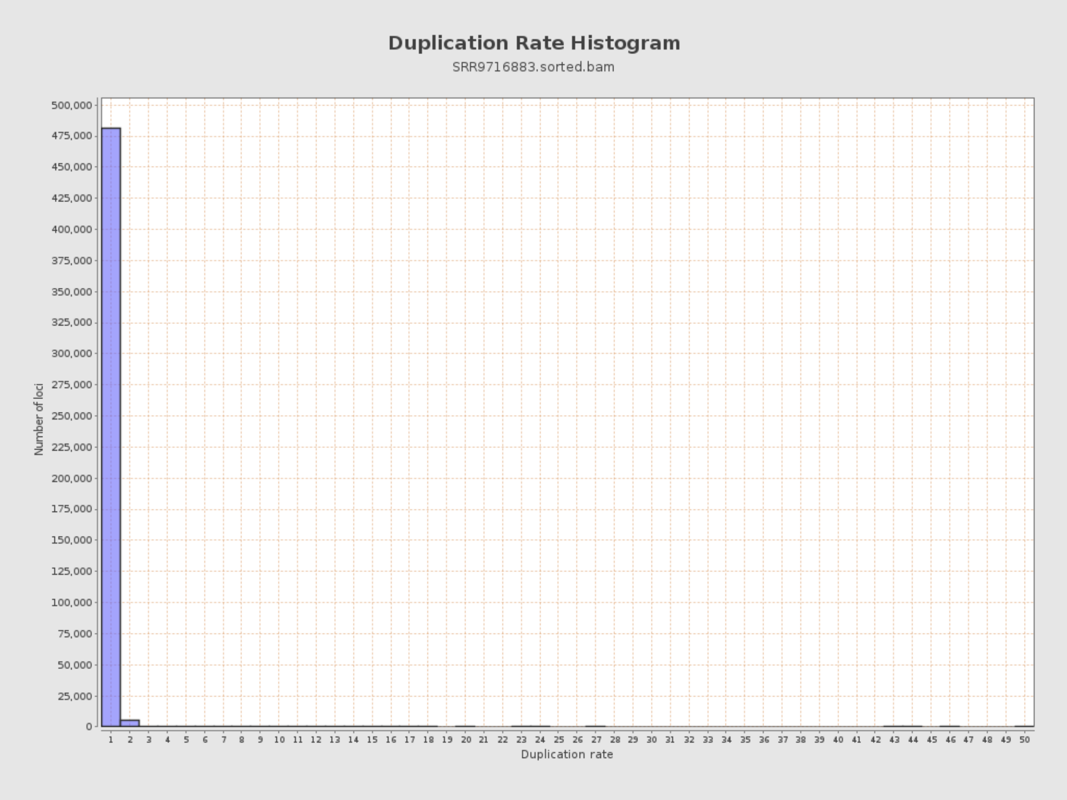
5. Results : Coverage Histogram (0-50X)



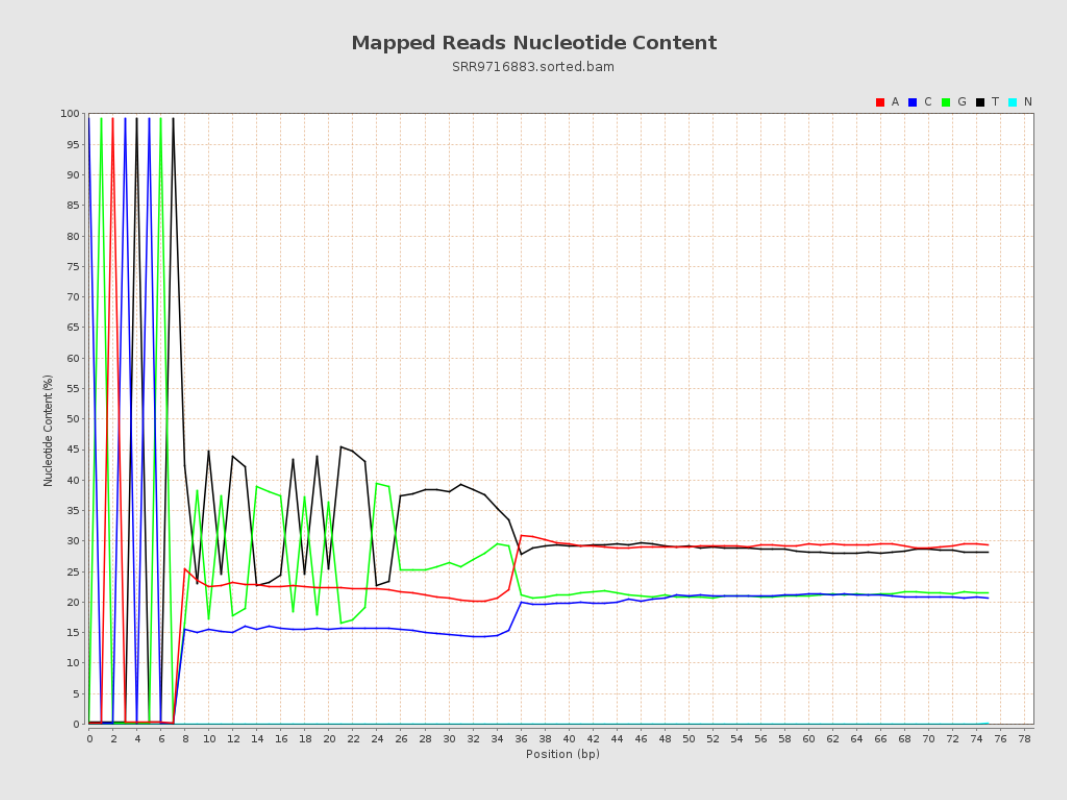
6. Results : Genome Fraction Coverage



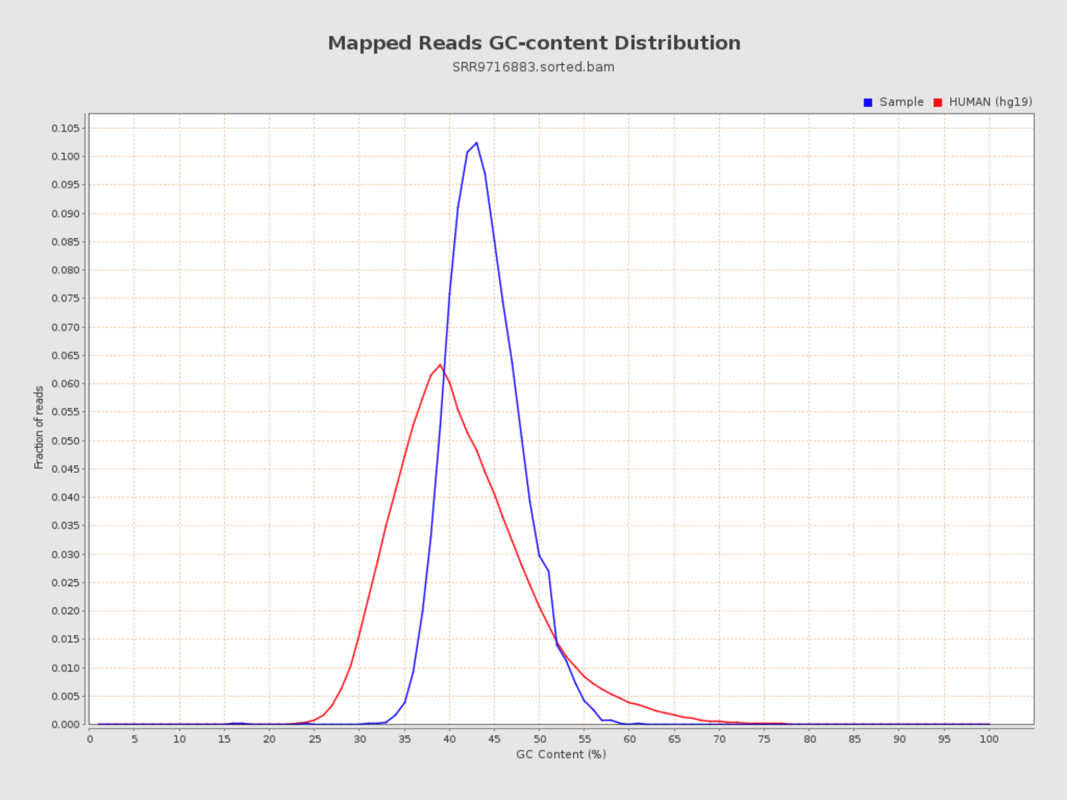
7. Results : Duplication Rate Histogram



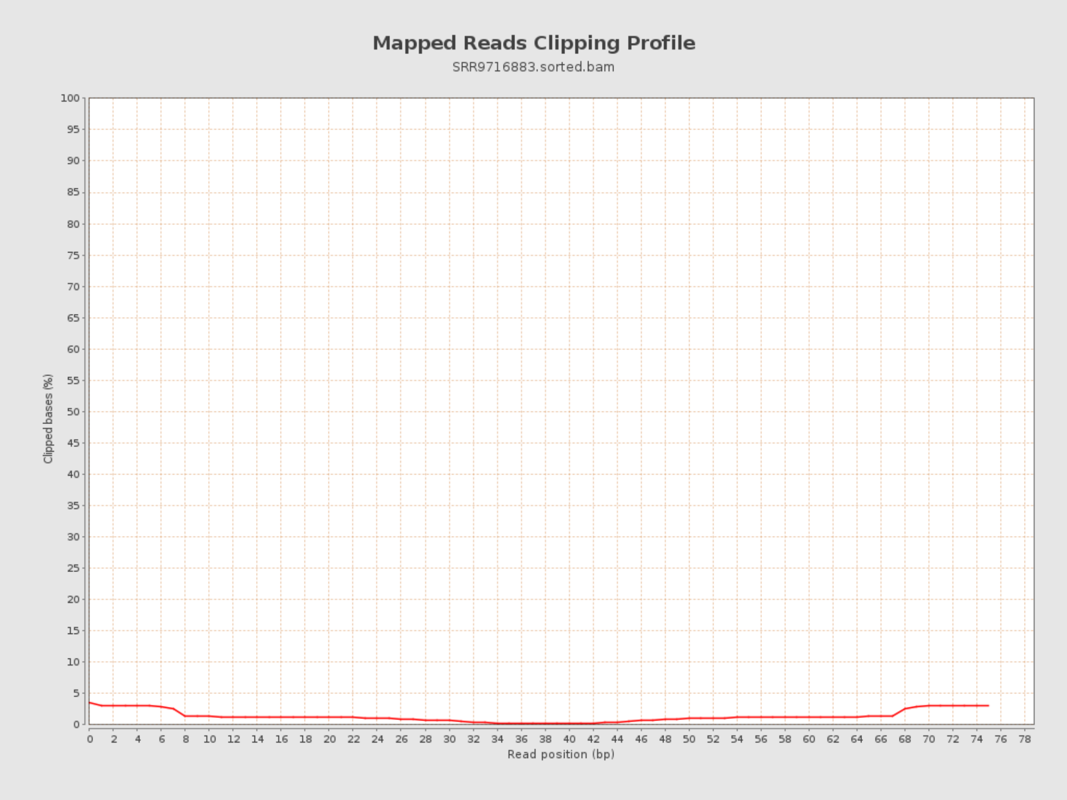
8. Results : Mapped Reads Nucleotide Content



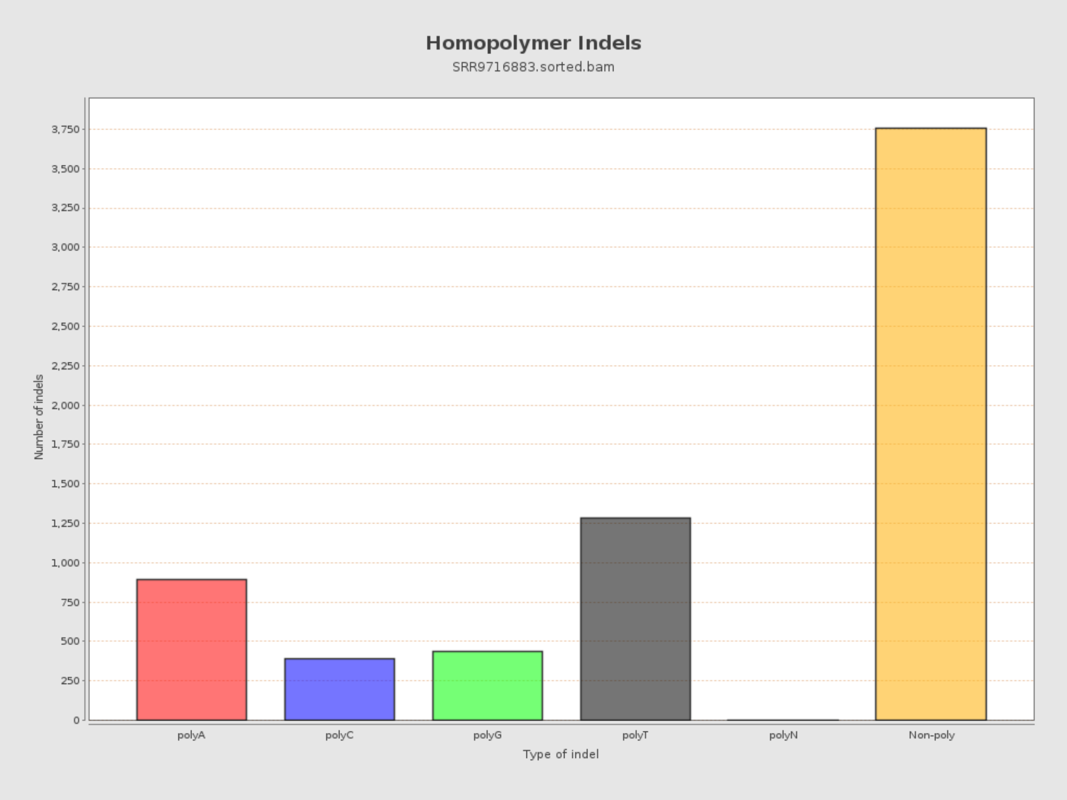
9. Results : Mapped Reads GC-content Distribution



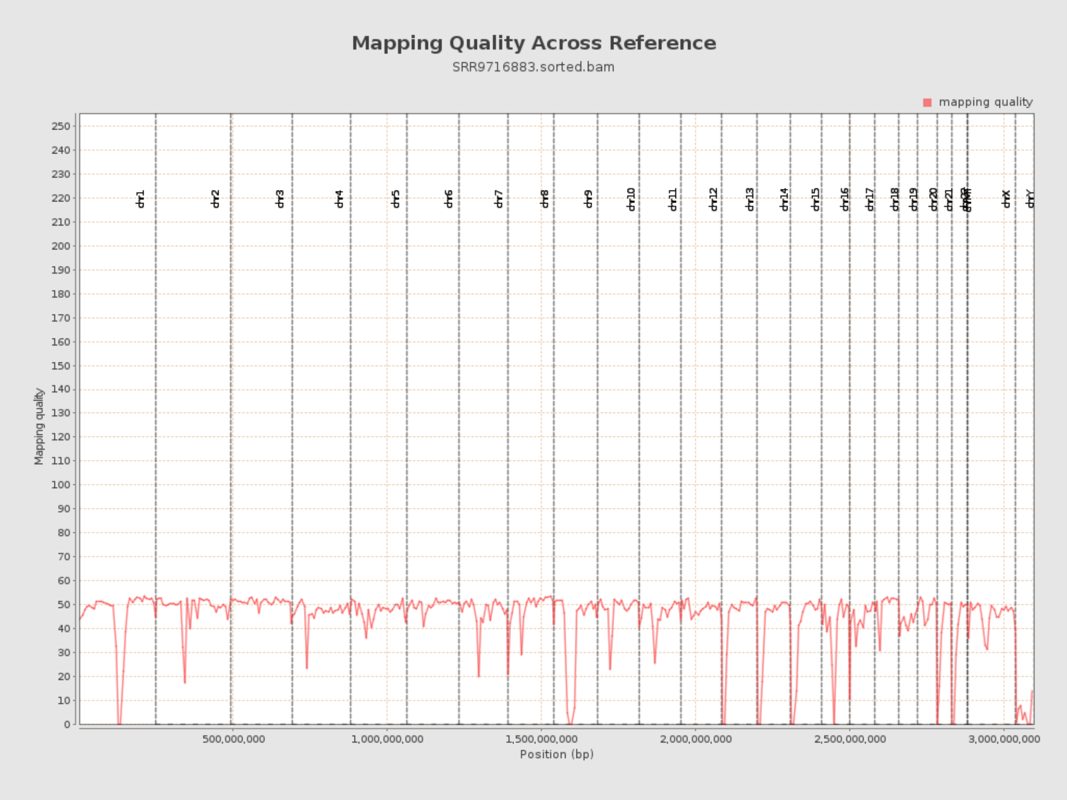
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram