Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 17:21:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716502.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_SRR9716502 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716502.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 17:21:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716502.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,167,196
Mapped reads	1,075,140 / 92.11%
Unmapped reads	92,056 / 7.89%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,658 / 0.31%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	32,016 / 2.74%
Duplication rate	2.1%
Clipped reads	1,076,006 / 92.19%

2.2. ACGT Content

Number/percentage of A's	15,765,465 / 25.35%
Number/percentage of C's	12,025,862 / 19.34%
Number/percentage of T's	19,682,721 / 31.65%
Number/percentage of G's	14,718,250 / 23.67%
Number/percentage of N's	1,171 / 0%
GC Percentage	43%

2.3. Coverage

Mean	0.0201

Standard Deviation	0.2075

2.4. Mapping Quality

Mean Mapping Quality	44.43

2.5. Mismatches and indels

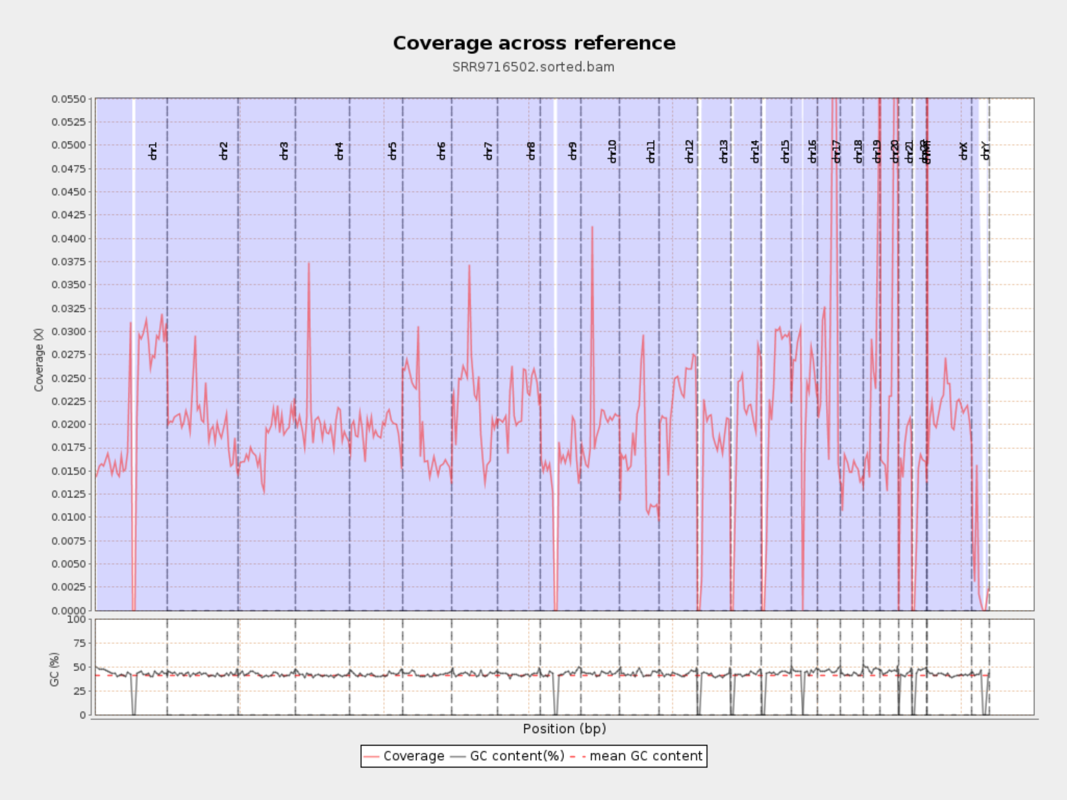
General error rate	0.52%
Mismatches	314,667
Insertions	4,355
Mapped reads with at least one insertion	0.4%
Deletions	12,382
Mapped reads with at least one deletion	1.14%
Homopolymer indels	42.71%

2.6. Chromosome stats

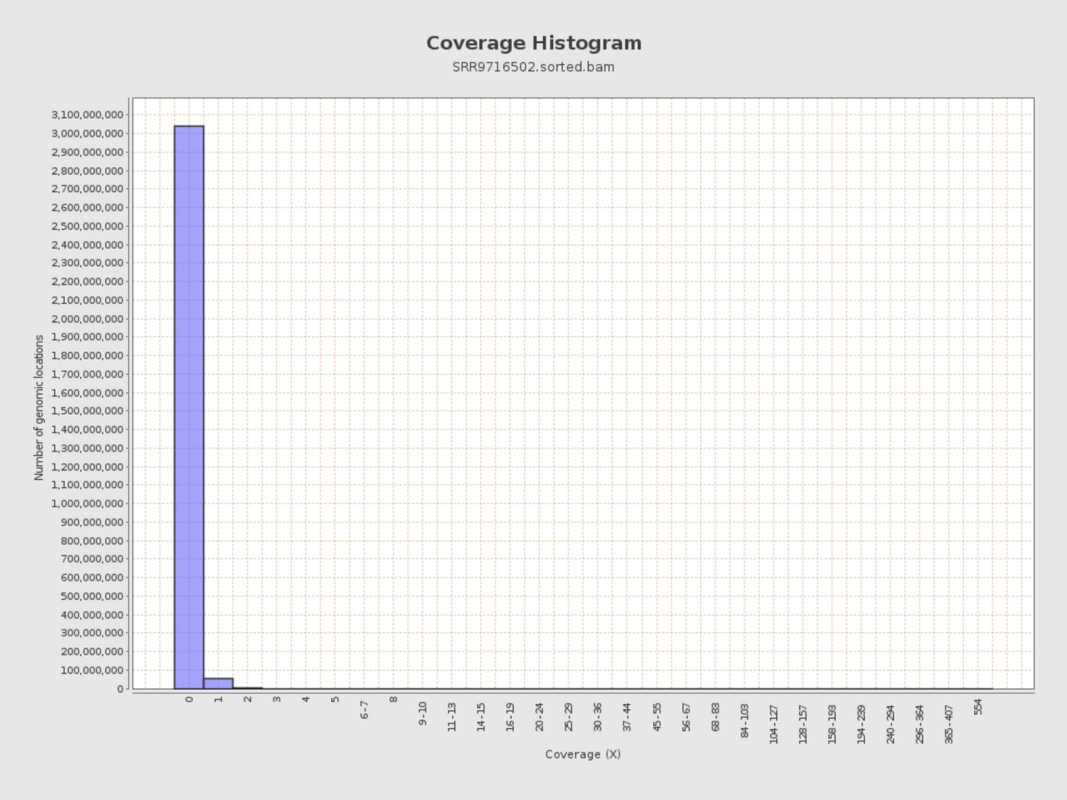
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5195993	0.0208	0.313
chr2	243199373	4921137	0.0202	0.2752
chr3	198022430	3590642	0.0181	0.1436
chr4	191154276	3895500	0.0204	0.1732
chr5	180915260	3530953	0.0195	0.1485
chr6	171115067	3325036	0.0194	0.1665
chr7	159138663	3543243	0.0223	0.2651

chr8	146364022	3283561	0.0224	0.2791
chr9	141213431	2059720	0.0146	0.1535
chr10	135534747	2776902	0.0205	0.2209
chr11	135006516	2224821	0.0165	0.164
chr12	133851895	3092589	0.0231	0.1618
chr13	115169878	1874286	0.0163	0.1357
chr14	107349540	2097652	0.0195	0.1502
chr15	102531392	2268939	0.0221	0.1589
chr16	90354753	2106126	0.0233	0.1689
chr17	81195210	2699000	0.0332	0.1991
chr18	78077248	1153935	0.0148	0.2375
chr19	59128983	1587444	0.0268	0.2684
chr20	63025520	1998051	0.0317	0.1949
chr21	48129895	784607	0.0163	0.1573
chr22	51304566	576494	0.0112	0.1124
chrMT	16571	40276	2.4305	2.1608
chrX	155270560	3364202	0.0217	0.1683
chrY	59373566	222156	0.0037	0.1756

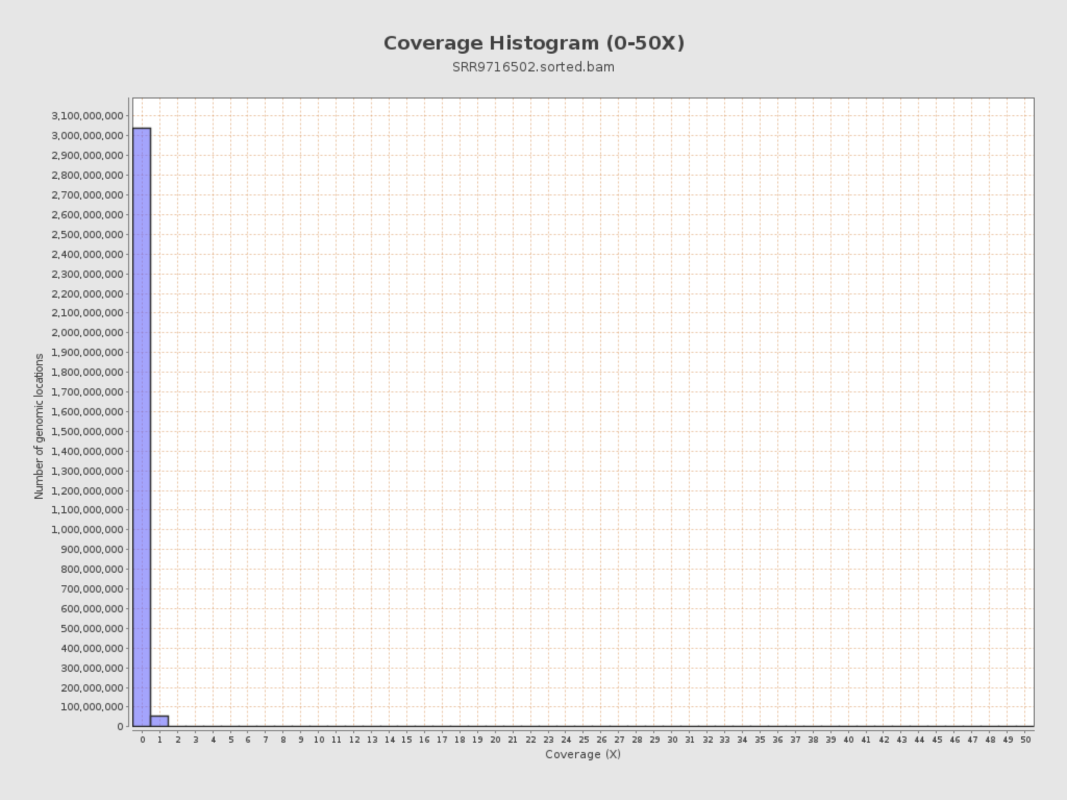
3. Results : Coverage across reference



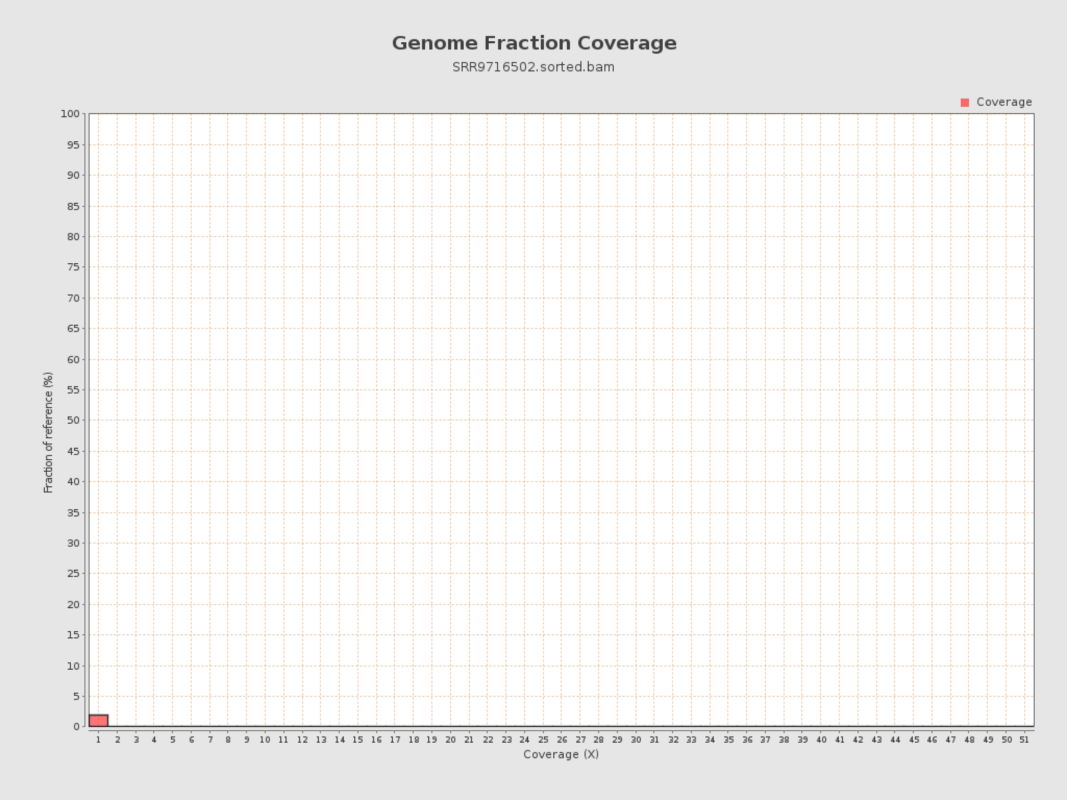
4. Results : Coverage Histogram



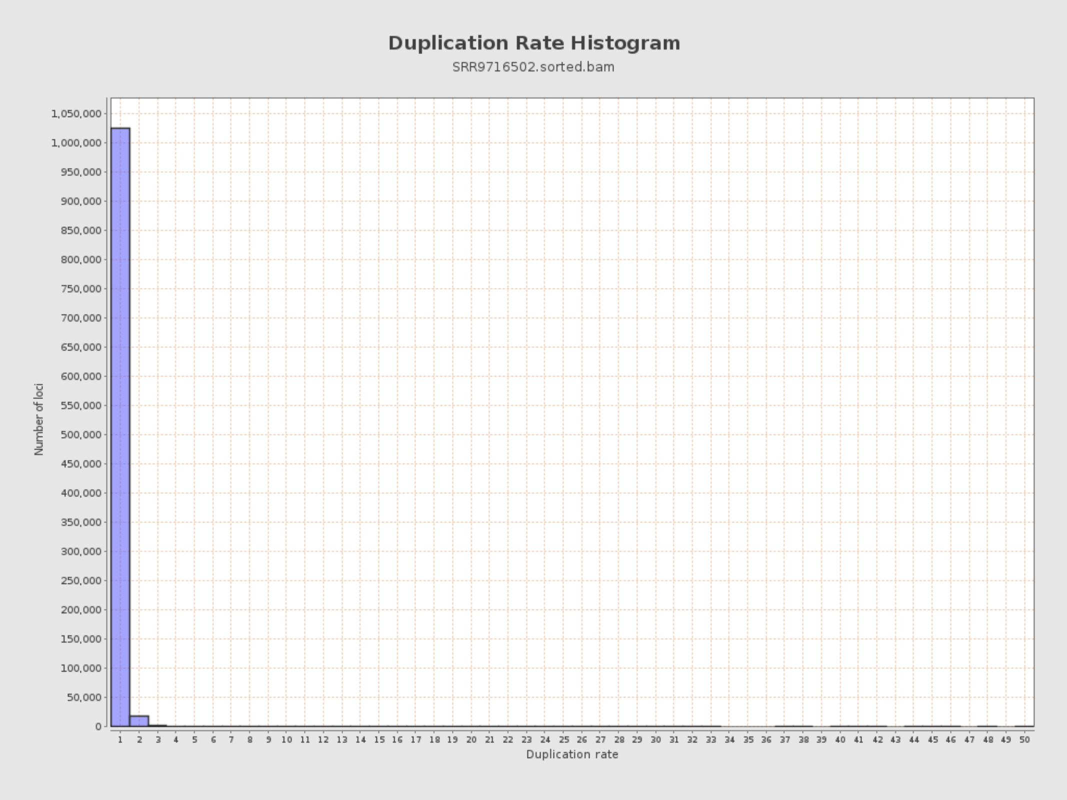
5. Results : Coverage Histogram (0-50X)



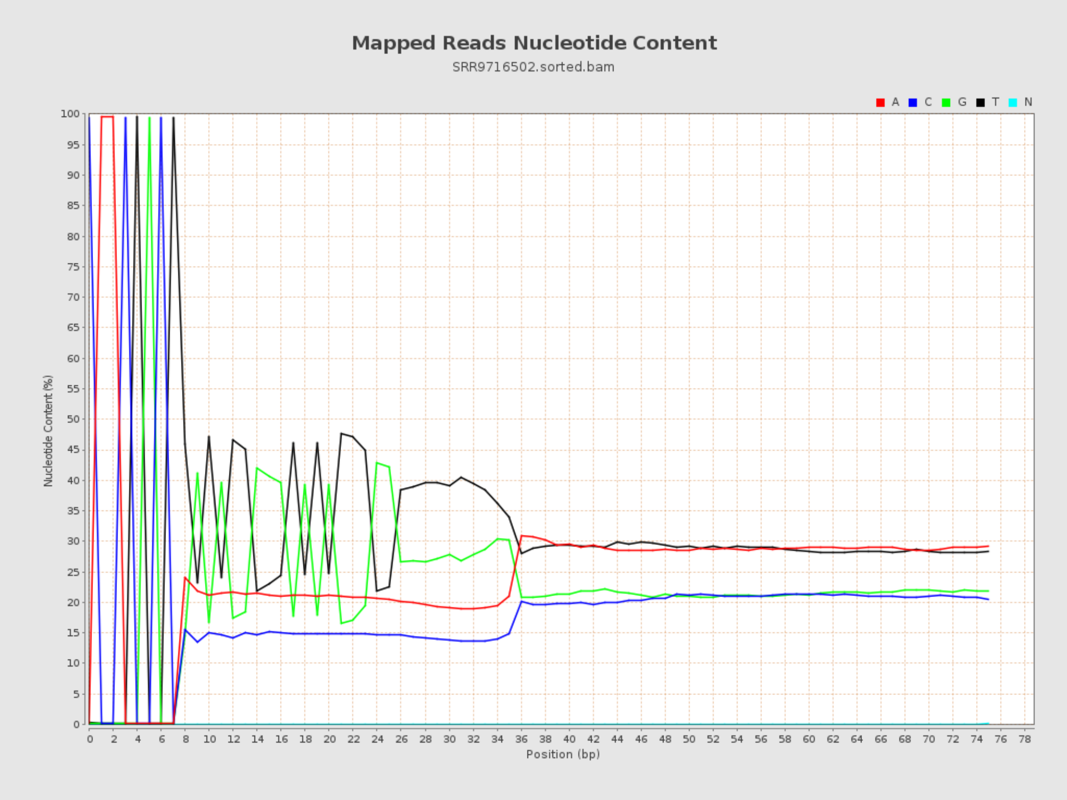
6. Results : Genome Fraction Coverage



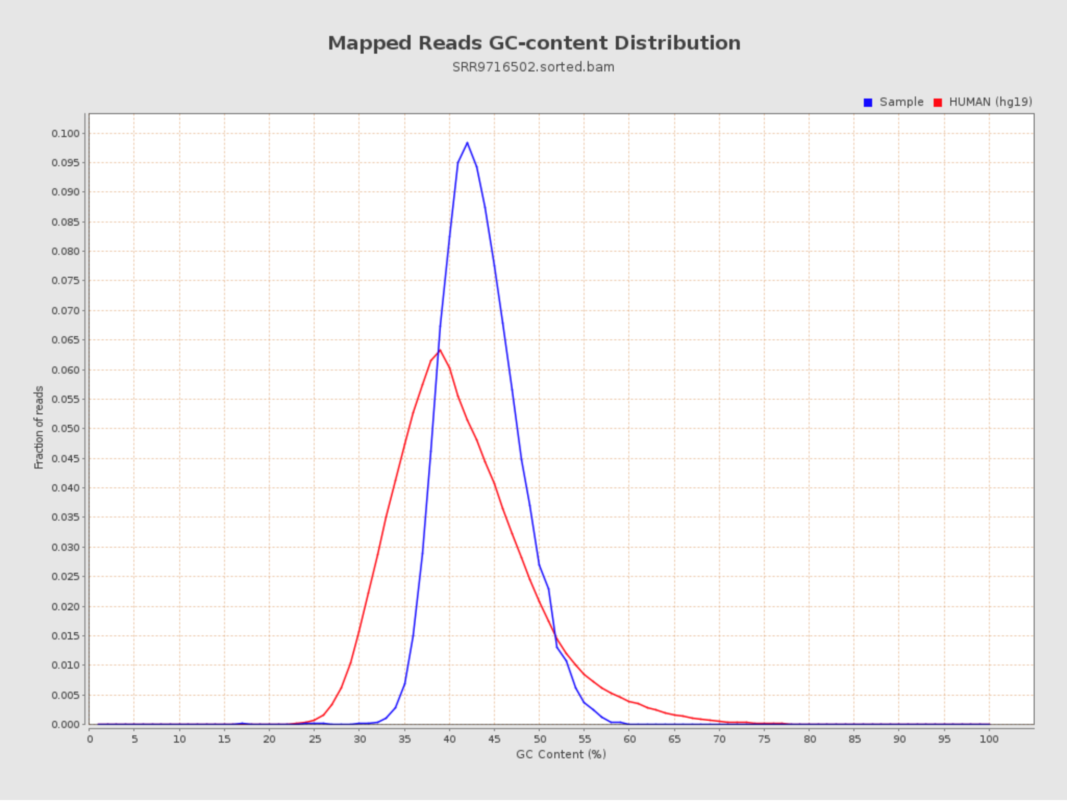
7. Results : Duplication Rate Histogram



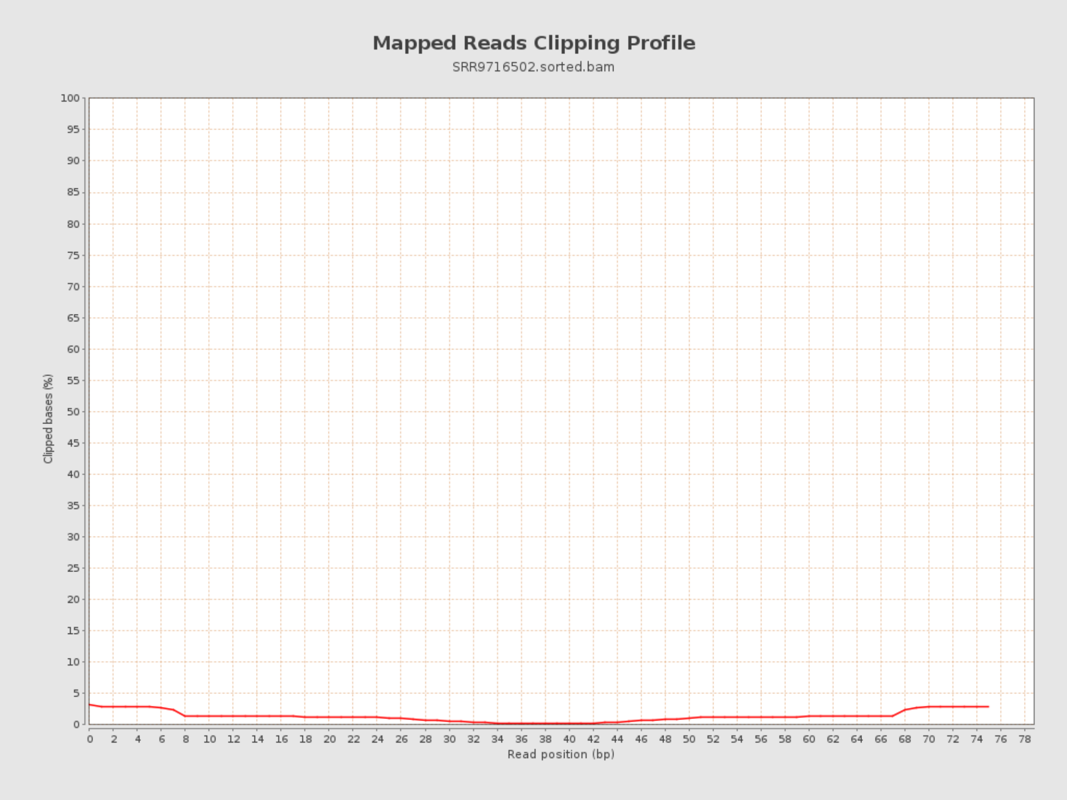
8. Results : Mapped Reads Nucleotide Content



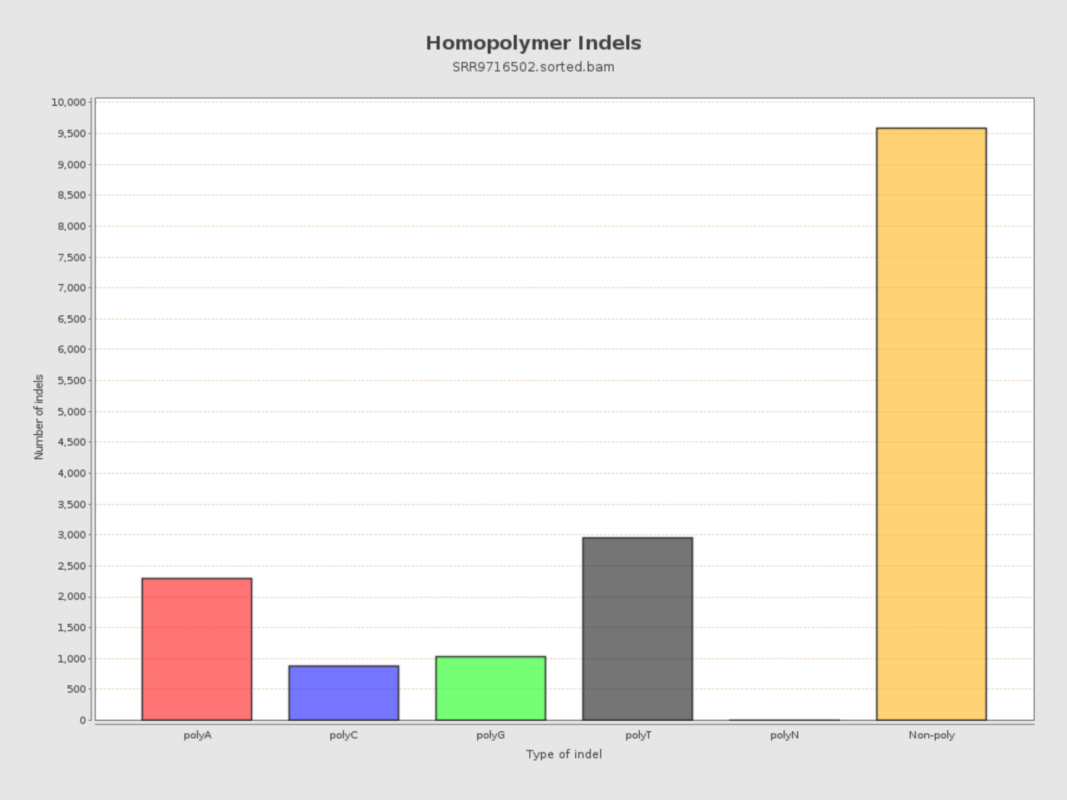
9. Results : Mapped Reads GC-content Distribution



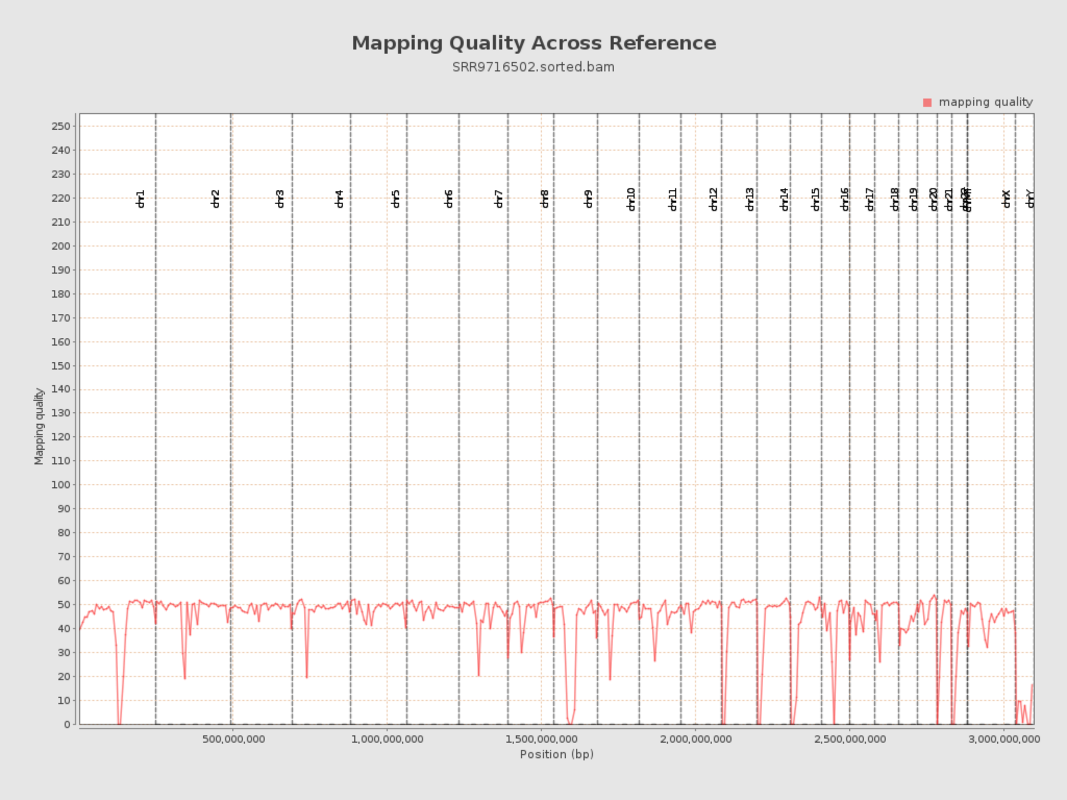
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram