Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 23:34:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716998.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_SRR9716998 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716998.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 23:34:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716998.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,102,986
Mapped reads	5,564,563 / 91.18%
Unmapped reads	538,423 / 8.82%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	30,053 / 0.49%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	484,576 / 7.94%
Duplication rate	6.57%
Clipped reads	5,576,495 / 91.37%

2.2. ACGT Content

Number/percentage of A's	85,897,175 / 26.71%
Number/percentage of C's	59,079,431 / 18.37%
Number/percentage of T's	98,717,847 / 30.69%
Number/percentage of G's	77,937,302 / 24.23%
Number/percentage of N's	4,988 / 0%
GC Percentage	42.6%

2.3. Coverage

Mean	0.1039

Standard Deviation	0.8711

2.4. Mapping Quality

Mean Mapping Quality	45.69

2.5. Mismatches and indels

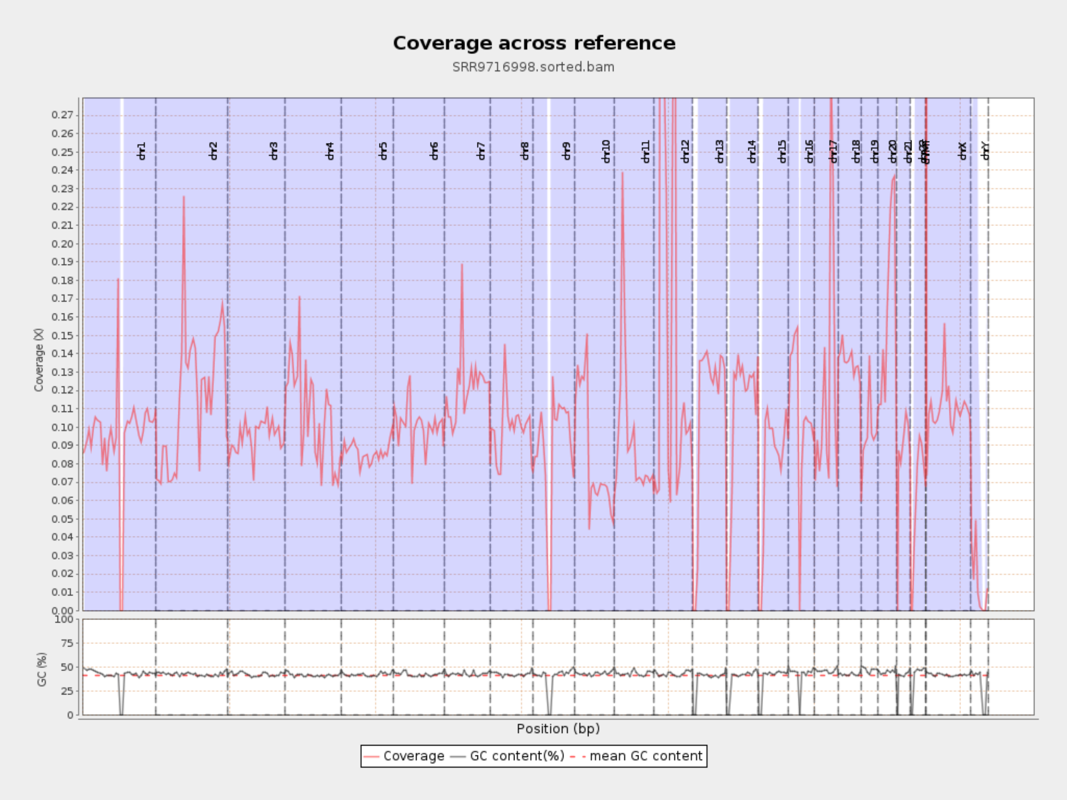
General error rate	0.55%
Mismatches	1,713,359
Insertions	25,255
Mapped reads with at least one insertion	0.45%
Deletions	53,345
Mapped reads with at least one deletion	0.95%
Homopolymer indels	43.04%

2.6. Chromosome stats

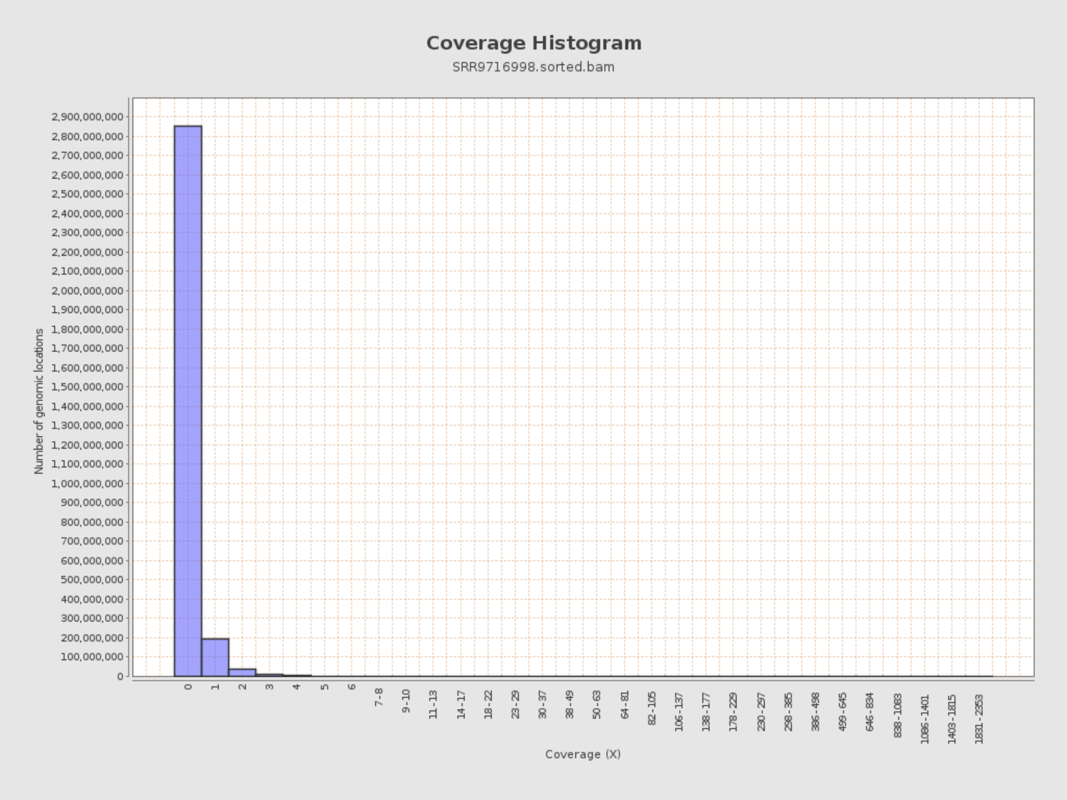
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	23530278	0.0944	1.8283
chr2	243199373	28432465	0.1169	0.9774
chr3	198022430	18849050	0.0952	0.3849
chr4	191154276	20534046	0.1074	0.5125
chr5	180915260	15658397	0.0866	0.3882
chr6	171115067	17288480	0.101	0.5163
chr7	159138663	19417693	0.122	1.0815

chr8	146364022	14507380	0.0991	0.9241
chr9	141213431	12463429	0.0883	0.8645
chr10	135534747	11533460	0.0851	0.7993
chr11	135006516	12892932	0.0955	0.6695
chr12	133851895	22540409	0.1684	0.6747
chr13	115169878	12722434	0.1105	0.4166
chr14	107349540	11378999	0.106	0.4815
chr15	102531392	7930871	0.0774	0.3496
chr16	90354753	9556465	0.1058	0.4741
chr17	81195210	10089843	0.1243	0.4943
chr18	78077248	10644580	0.1363	1.6682
chr19	59128983	5799421	0.0981	1.254
chr20	63025520	10612234	0.1684	0.5578
chr21	48129895	4089129	0.085	0.4619
chr22	51304566	3113290	0.0607	0.2992
chrMT	16571	176113	10.6278	6.3653
chrX	155270560	17082616	0.11	0.5921
chrY	59373566	881286	0.0148	0.3023

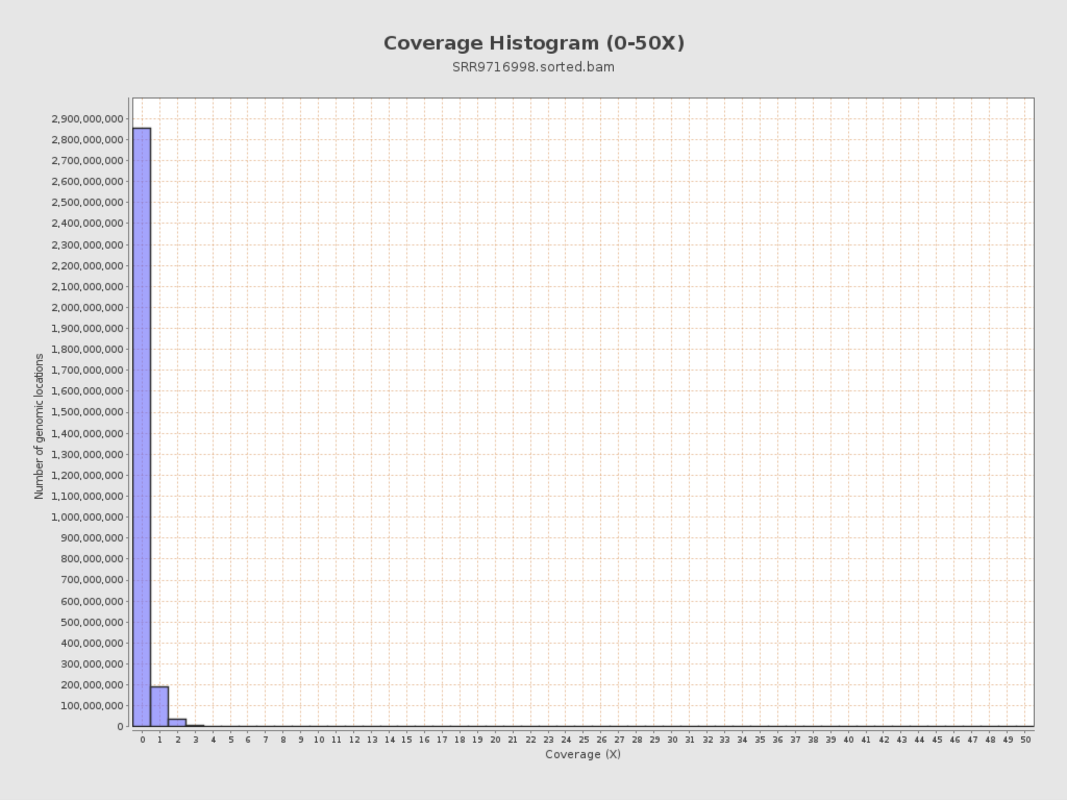
3. Results : Coverage across reference



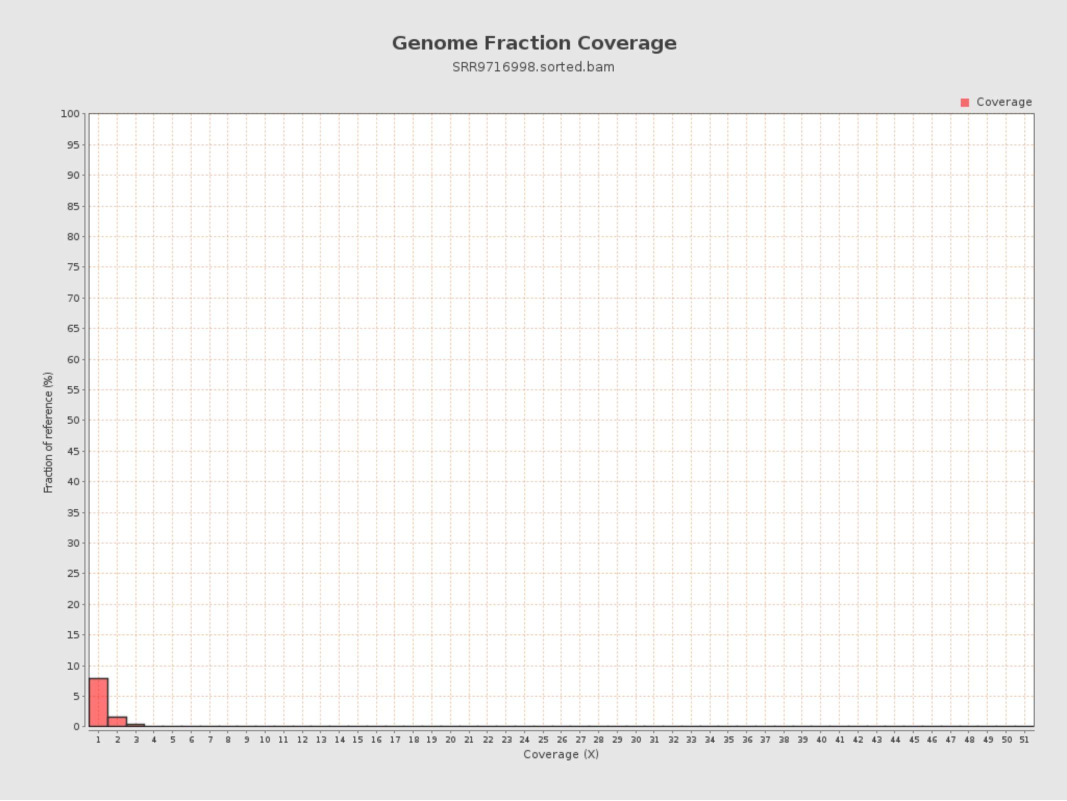
4. Results : Coverage Histogram



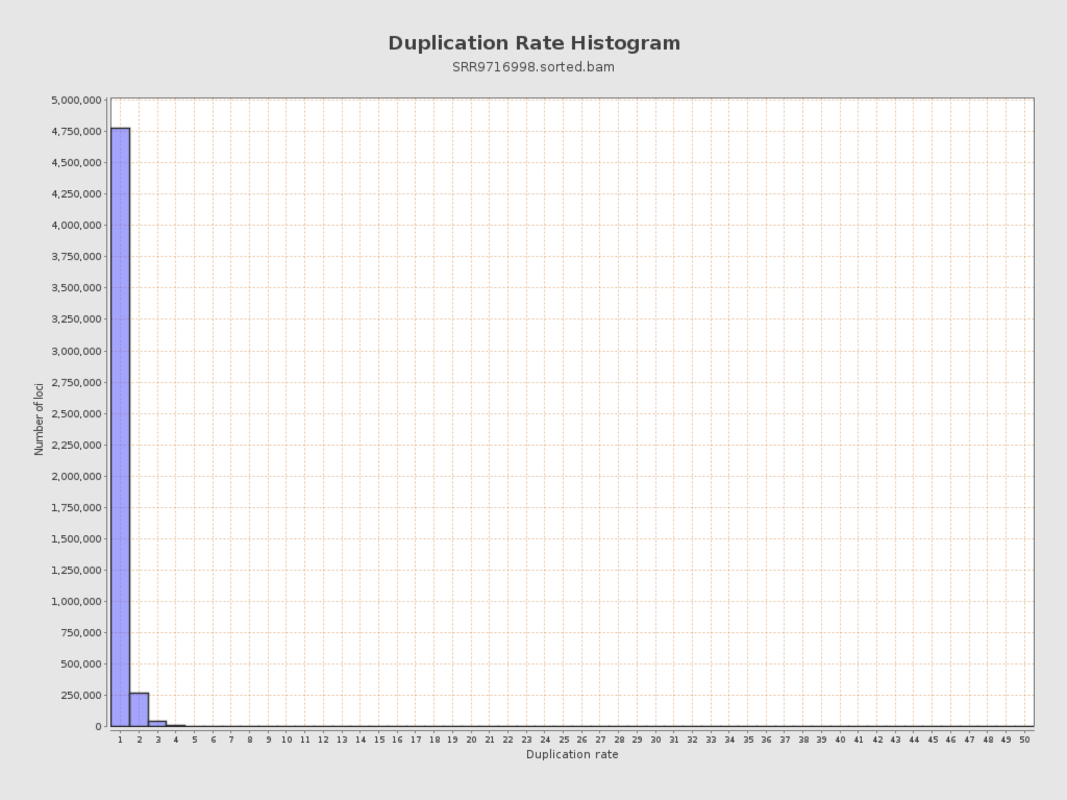
5. Results : Coverage Histogram (0-50X)



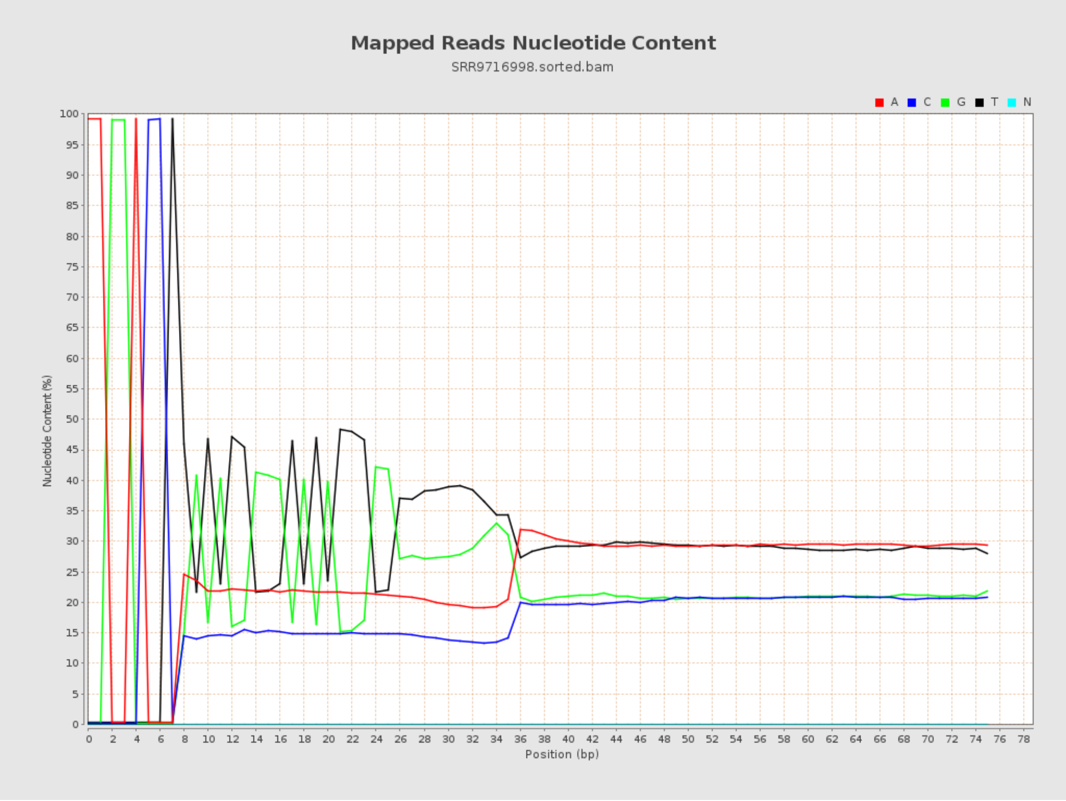
6. Results : Genome Fraction Coverage



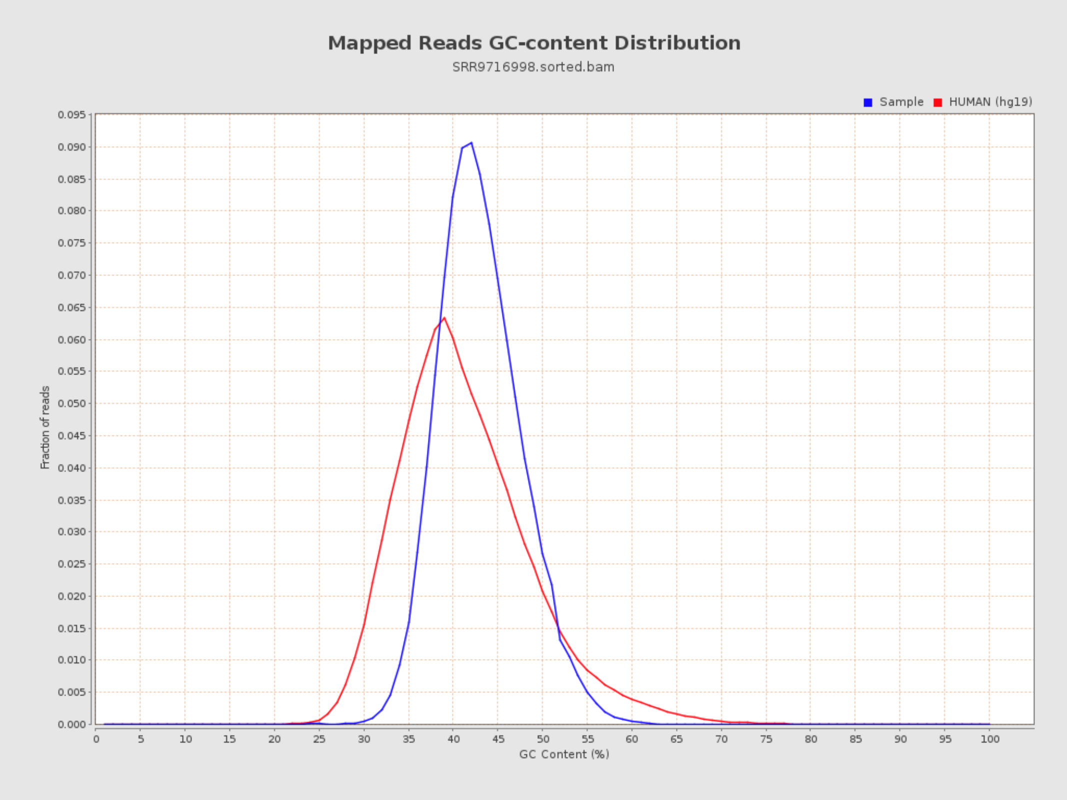
7. Results : Duplication Rate Histogram



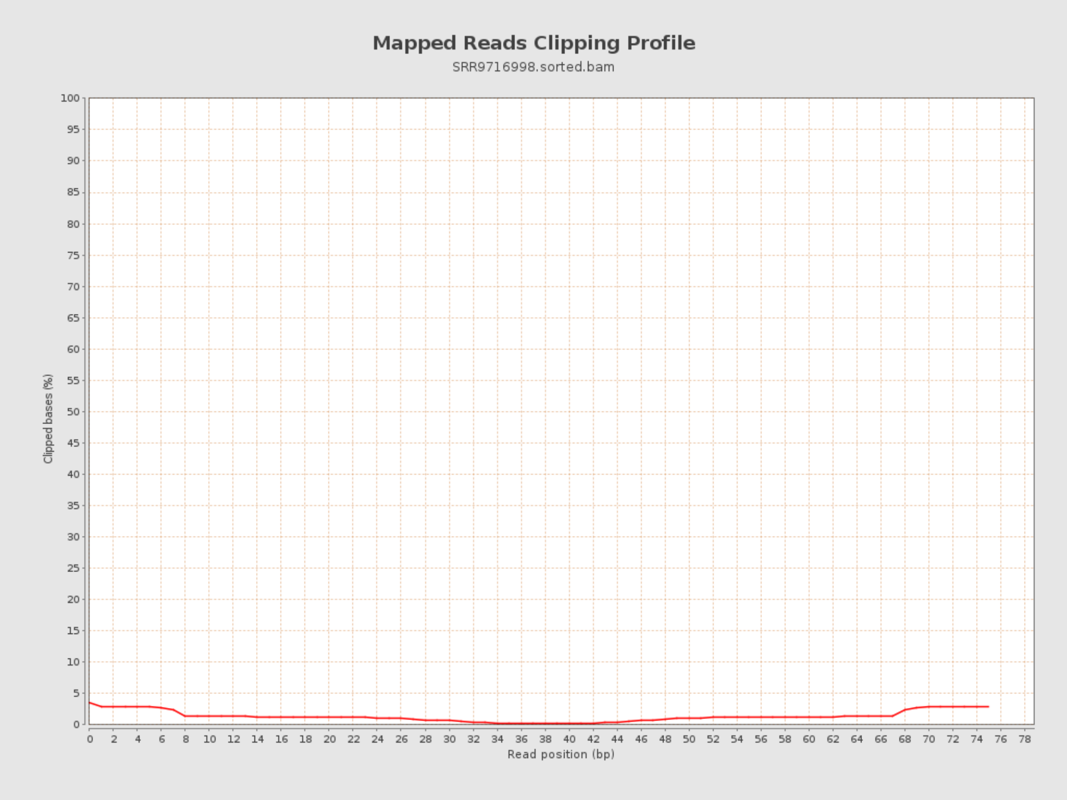
8. Results : Mapped Reads Nucleotide Content



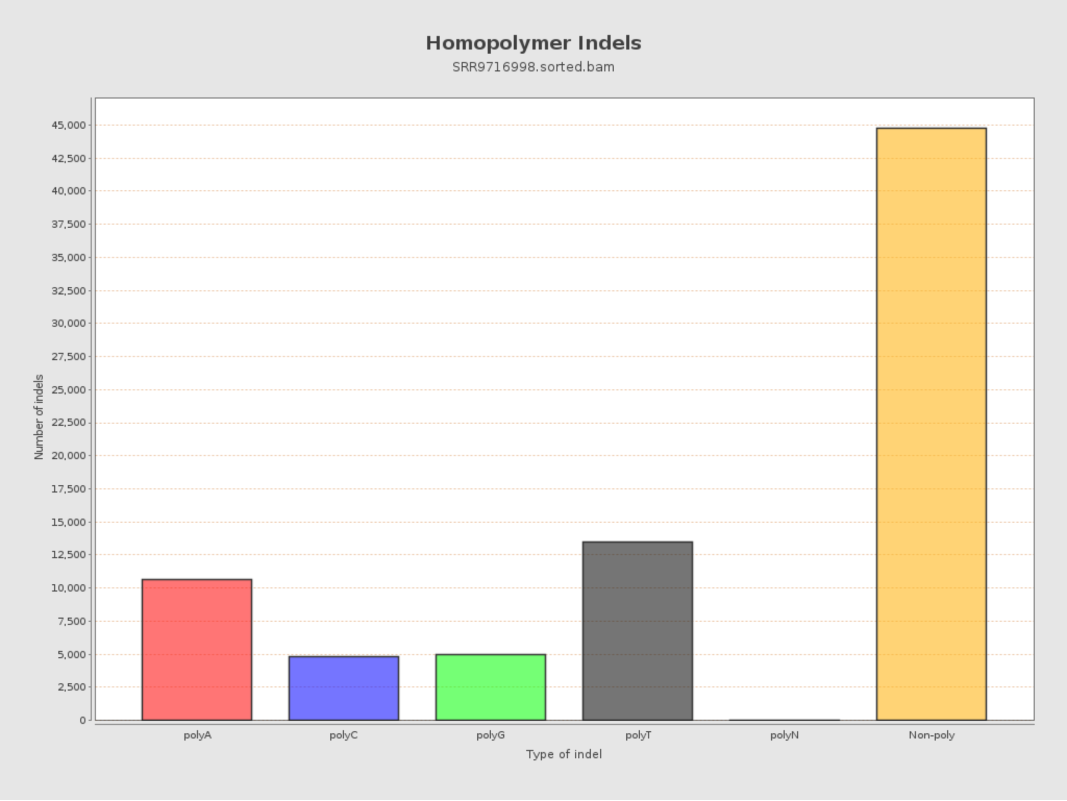
9. Results : Mapped Reads GC-content Distribution



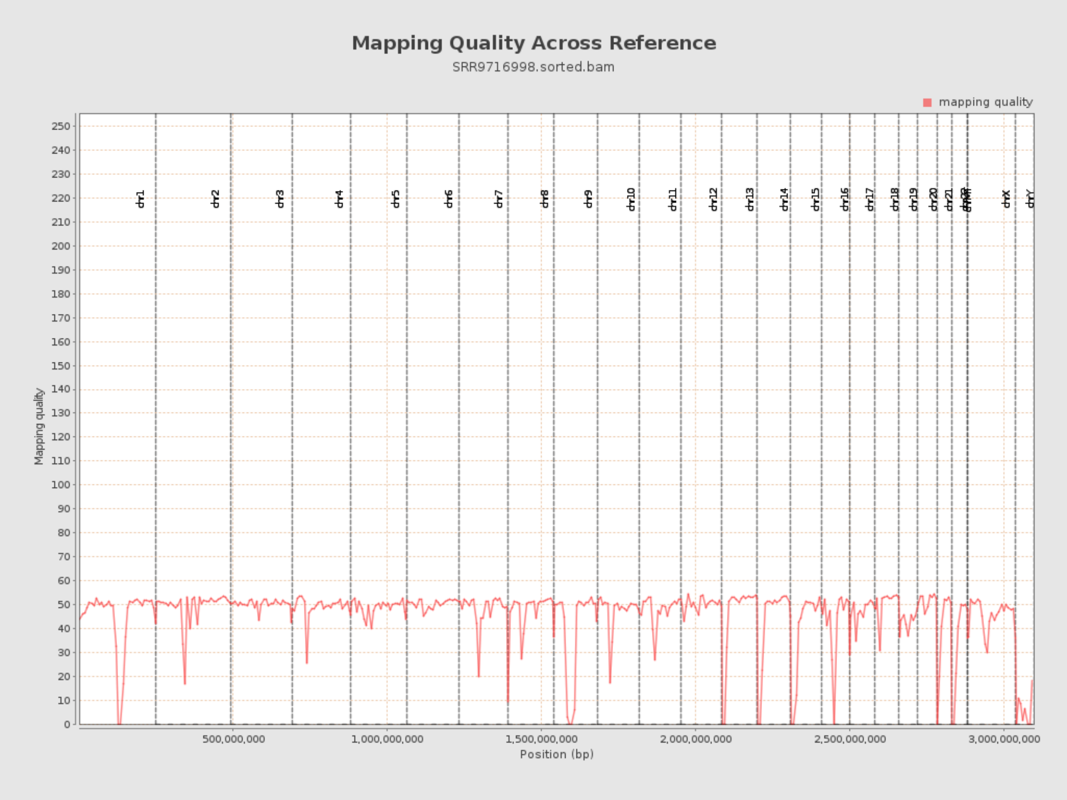
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram