Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 01:12:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716626.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_SRR9716626 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716626.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 01:12:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716626.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,246,863
Mapped reads	1,132,635 / 90.84%
Unmapped reads	114,228 / 9.16%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,545 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	28,269 / 2.27%
Duplication rate	1.88%
Clipped reads	1,133,646 / 90.92%

2.2. ACGT Content

Number/percentage of A's	16,809,147 / 25.94%
Number/percentage of C's	12,434,104 / 19.19%
Number/percentage of T's	19,387,497 / 29.92%
Number/percentage of G's	16,166,778 / 24.95%
Number/percentage of N's	1,532 / 0%
GC Percentage	44.14%

2.3. Coverage

Mean	0.0209

Standard Deviation	0.1922

2.4. Mapping Quality

Mean Mapping Quality	44.59

2.5. Mismatches and indels

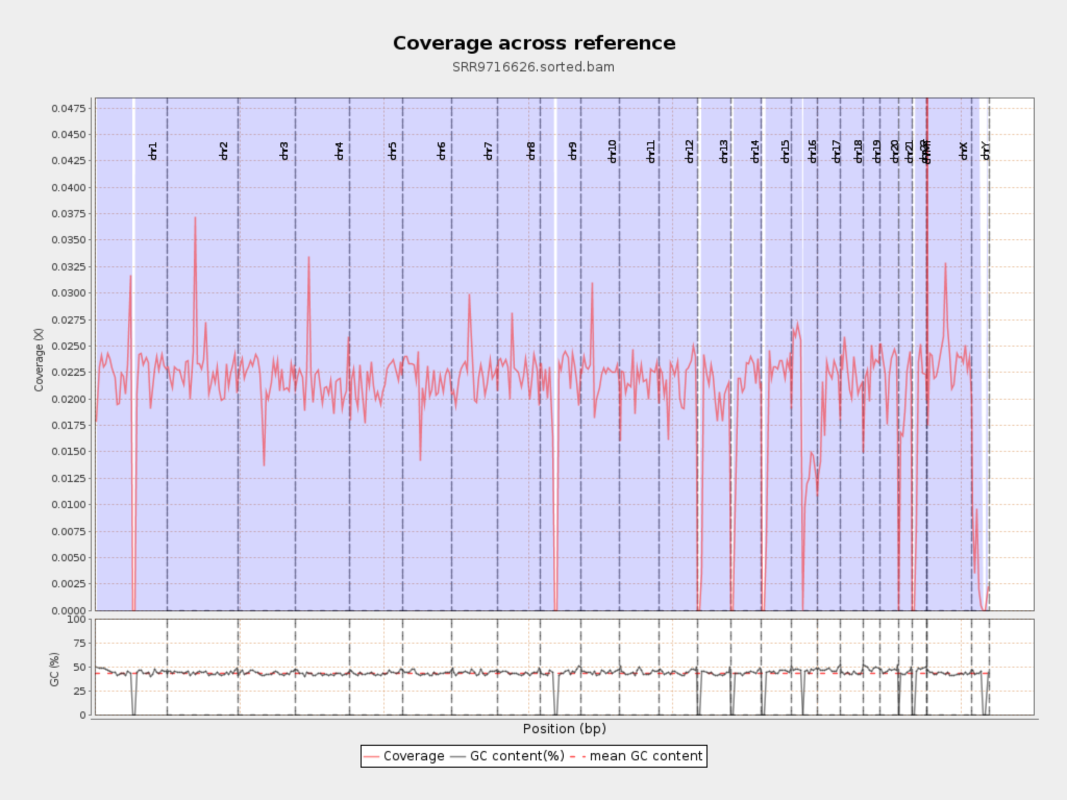
General error rate	0.5%
Mismatches	316,477
Insertions	4,880
Mapped reads with at least one insertion	0.43%
Deletions	10,481
Mapped reads with at least one deletion	0.92%
Homopolymer indels	40.9%

2.6. Chromosome stats

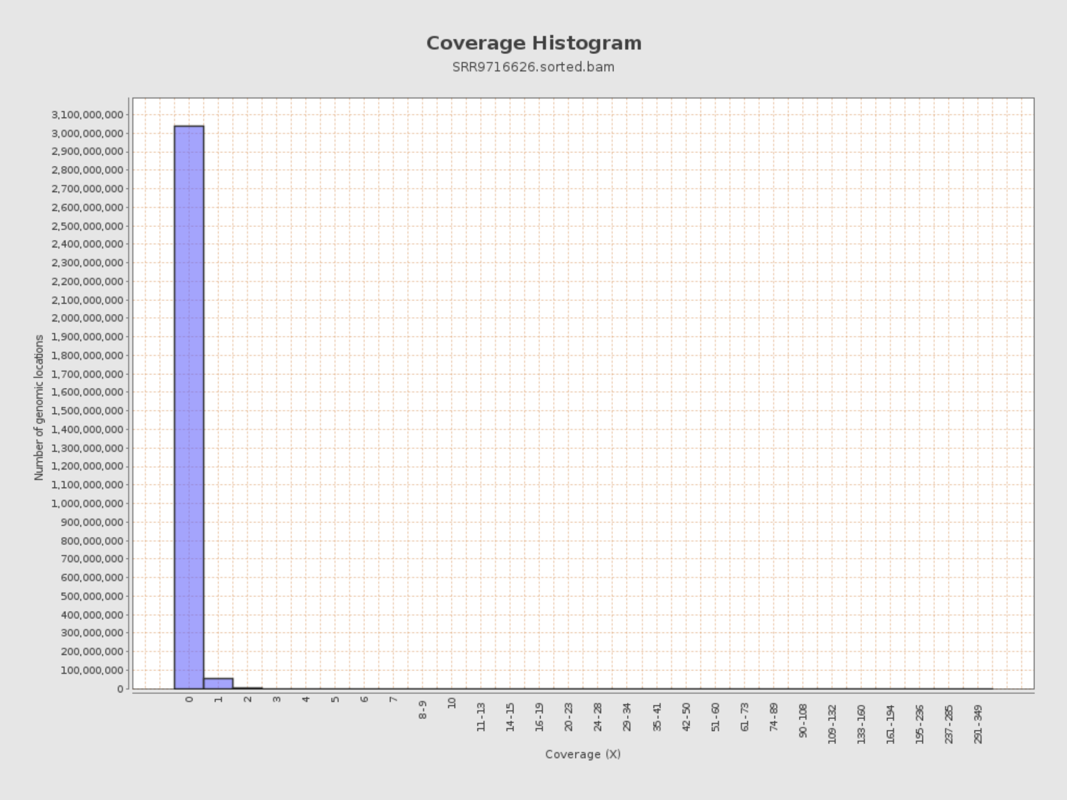
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5320127	0.0213	0.2919
chr2	243199373	5565228	0.0229	0.2178
chr3	198022430	4341234	0.0219	0.1574
chr4	191154276	4166779	0.0218	0.1662
chr5	180915260	3914202	0.0216	0.158
chr6	171115067	3729738	0.0218	0.1654
chr7	159138663	3567941	0.0224	0.2122

chr8	146364022	3323316	0.0227	0.18
chr9	141213431	2788561	0.0197	0.1997
chr10	135534747	3082768	0.0227	0.1851
chr11	135006516	2954308	0.0219	0.1936
chr12	133851895	2918921	0.0218	0.1592
chr13	115169878	2011493	0.0175	0.1399
chr14	107349540	1998395	0.0186	0.151
chr15	102531392	1909774	0.0186	0.1451
chr16	90354753	1500854	0.0166	0.1466
chr17	81195210	1633103	0.0201	0.1565
chr18	78077248	1740369	0.0223	0.3377
chr19	59128983	1332399	0.0225	0.2133
chr20	63025520	1421801	0.0226	0.1633
chr21	48129895	872338	0.0181	0.1552
chr22	51304566	824747	0.0161	0.1347
chrMT	16571	2715	0.1638	0.417
chrX	155270560	3709182	0.0239	0.1803
chrY	59373566	186339	0.0031	0.0787

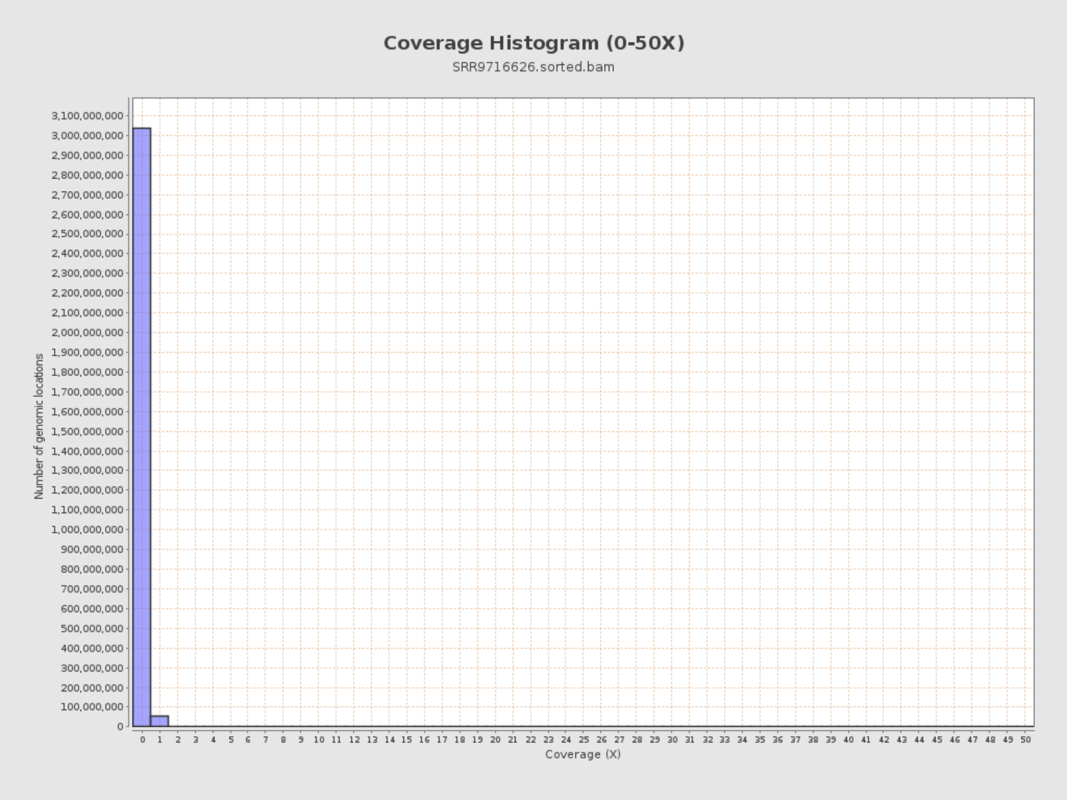
3. Results : Coverage across reference



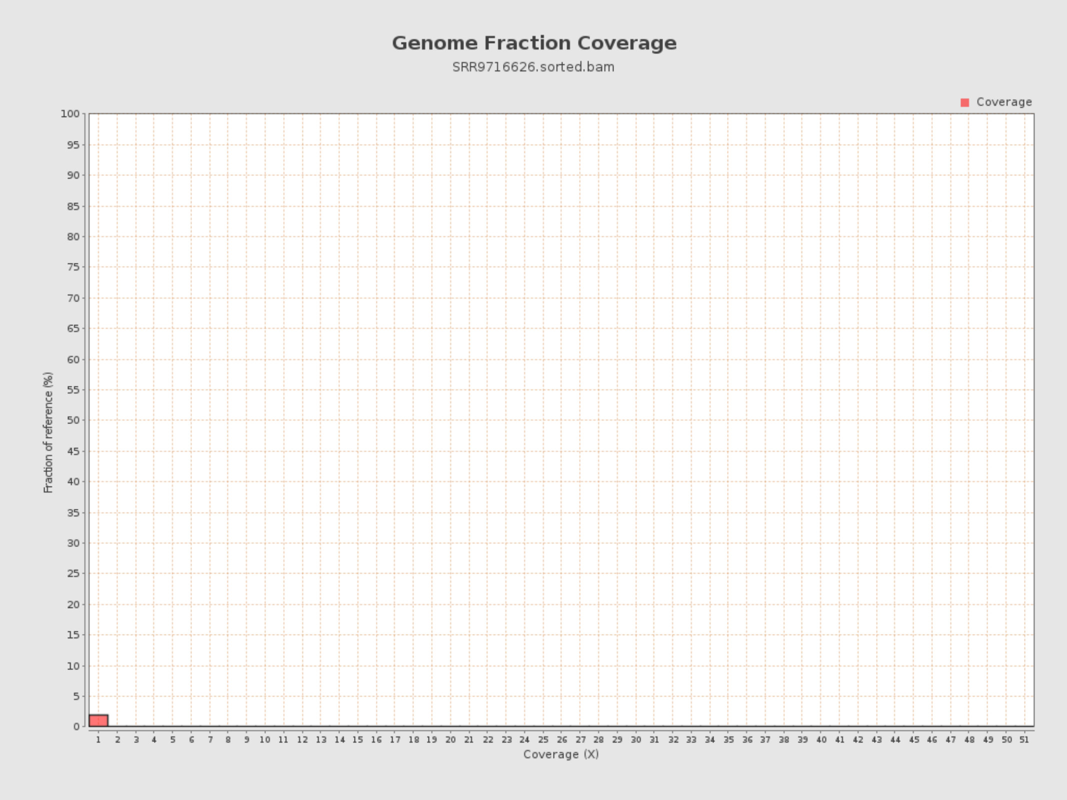
4. Results : Coverage Histogram



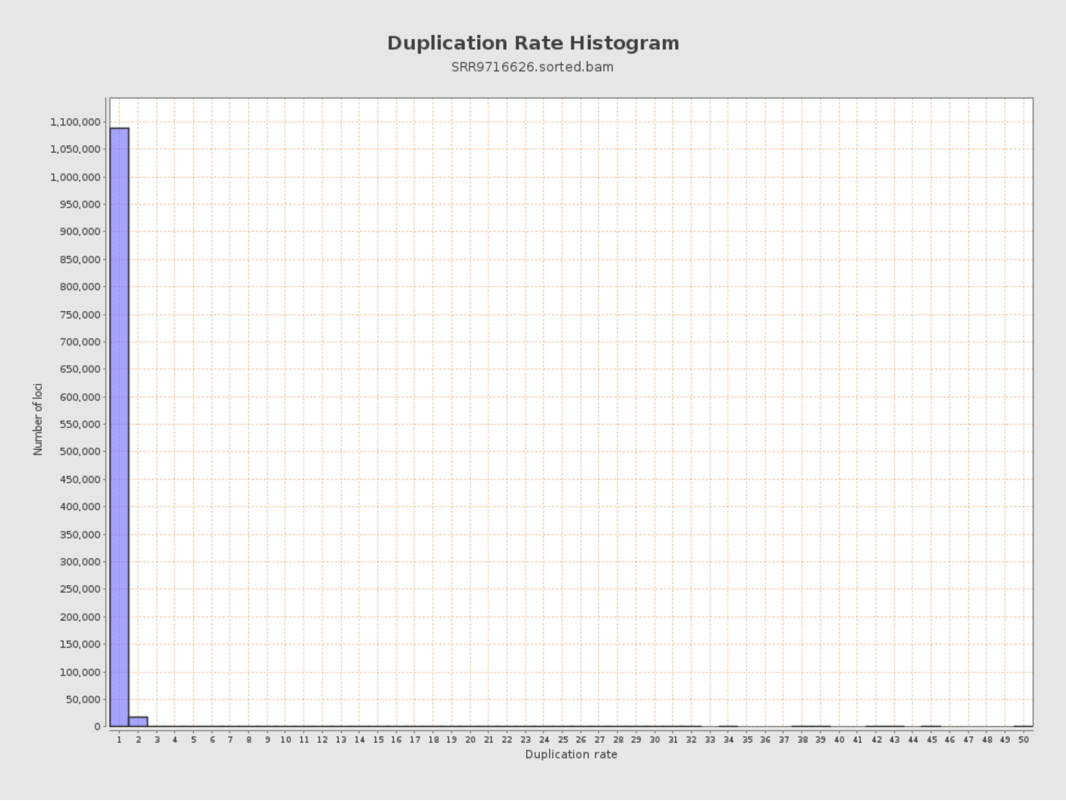
5. Results : Coverage Histogram (0-50X)



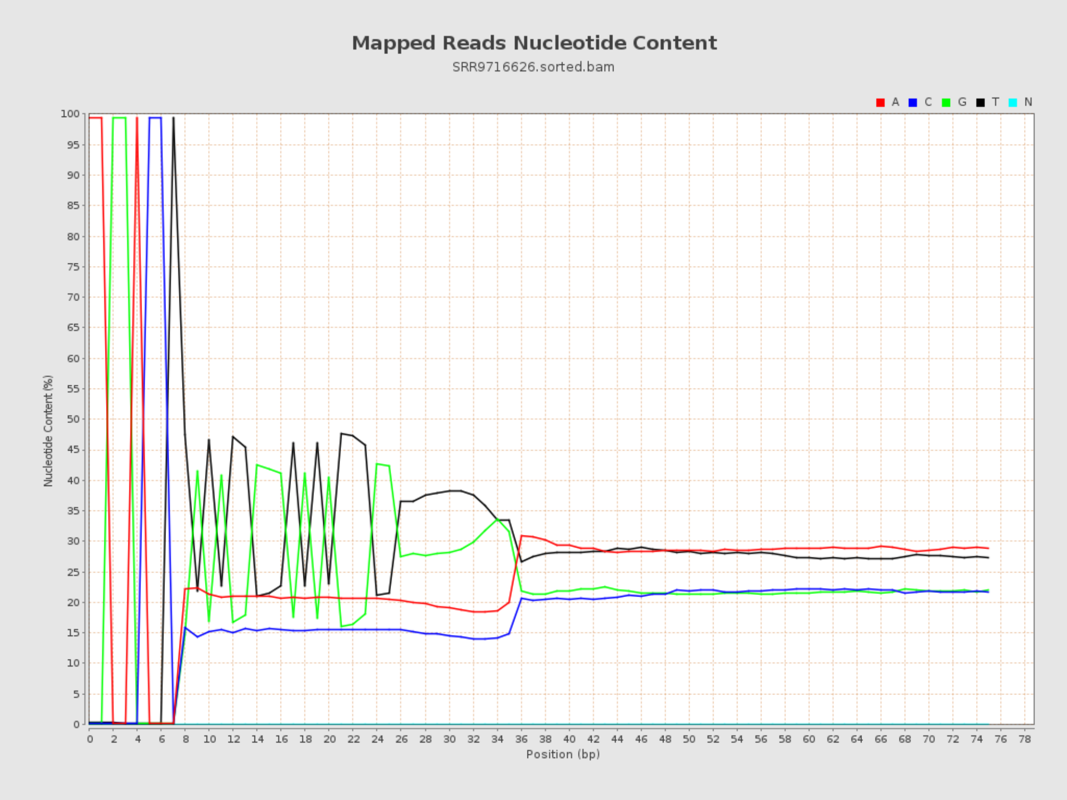
6. Results : Genome Fraction Coverage



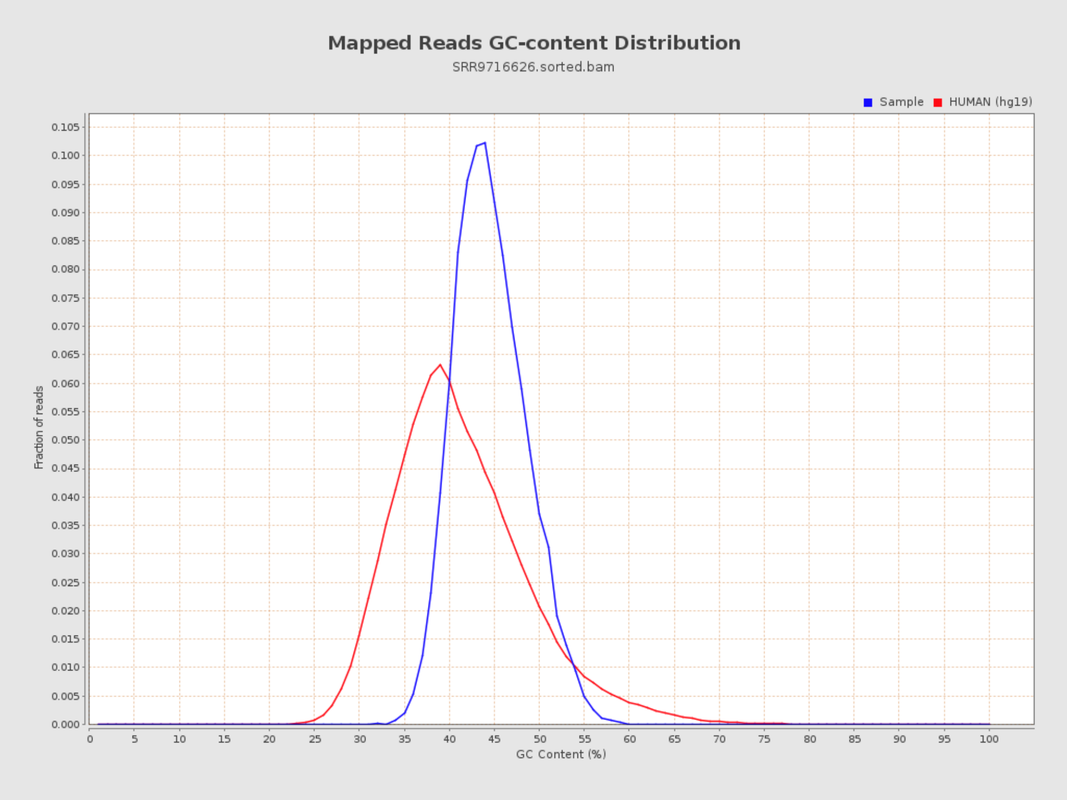
7. Results : Duplication Rate Histogram



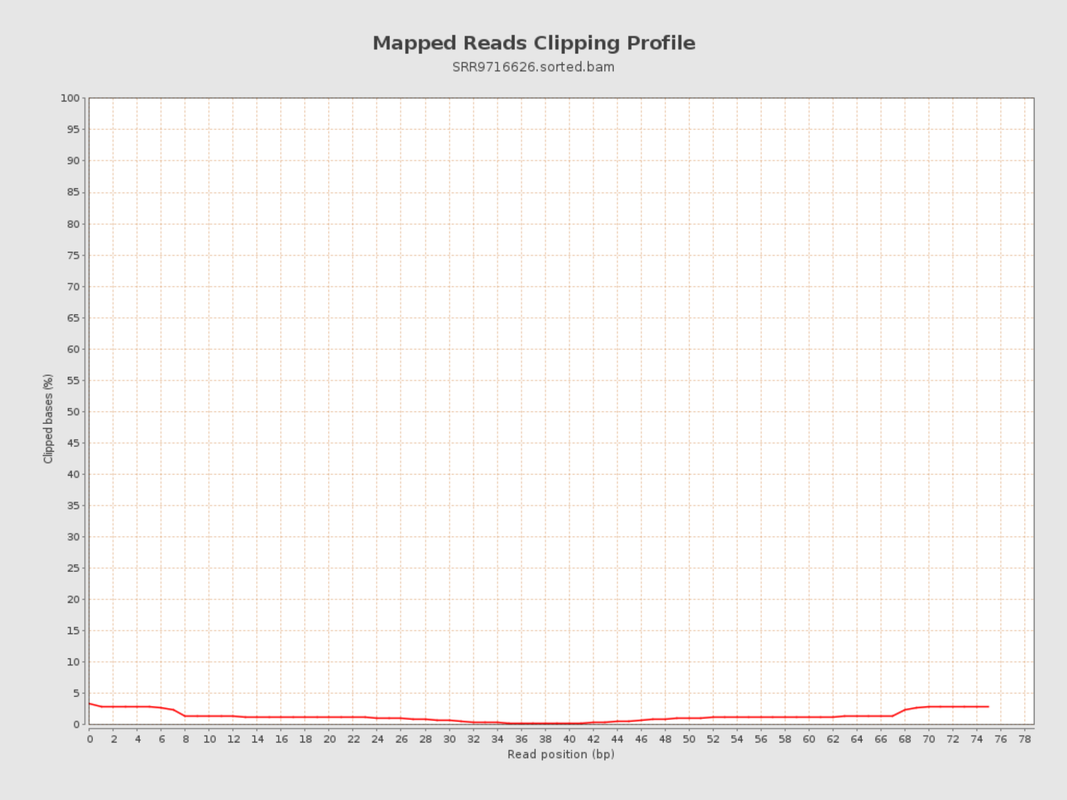
8. Results : Mapped Reads Nucleotide Content



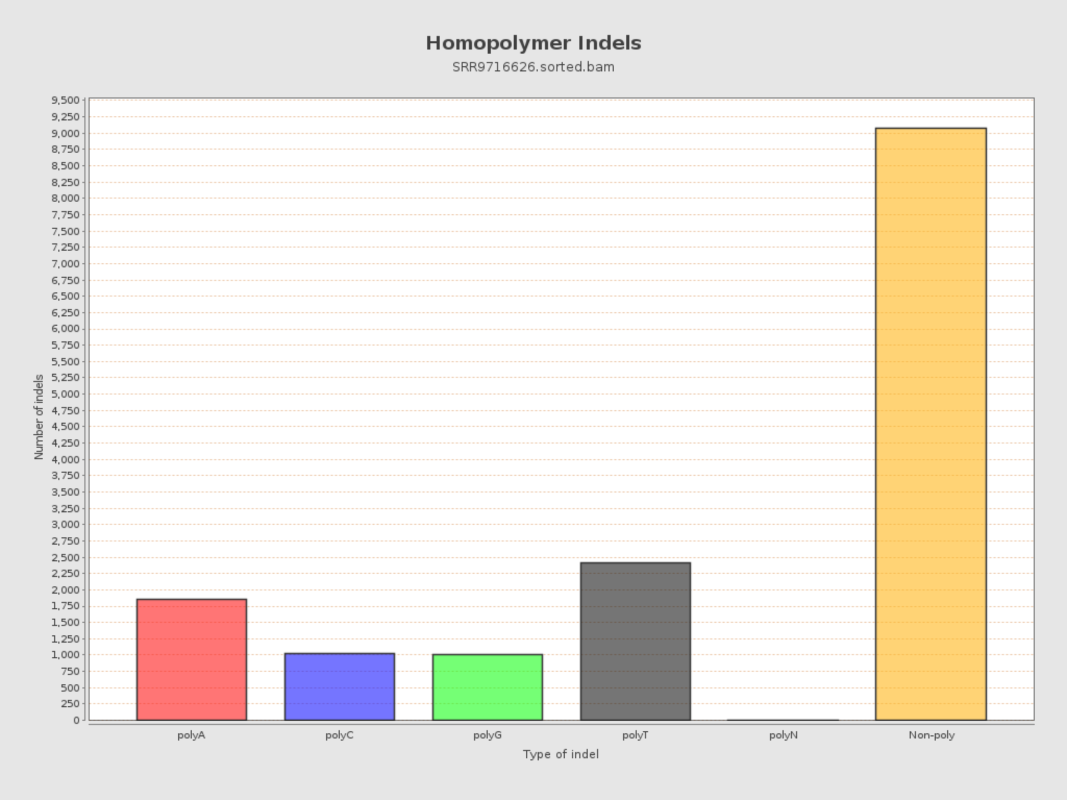
9. Results : Mapped Reads GC-content Distribution



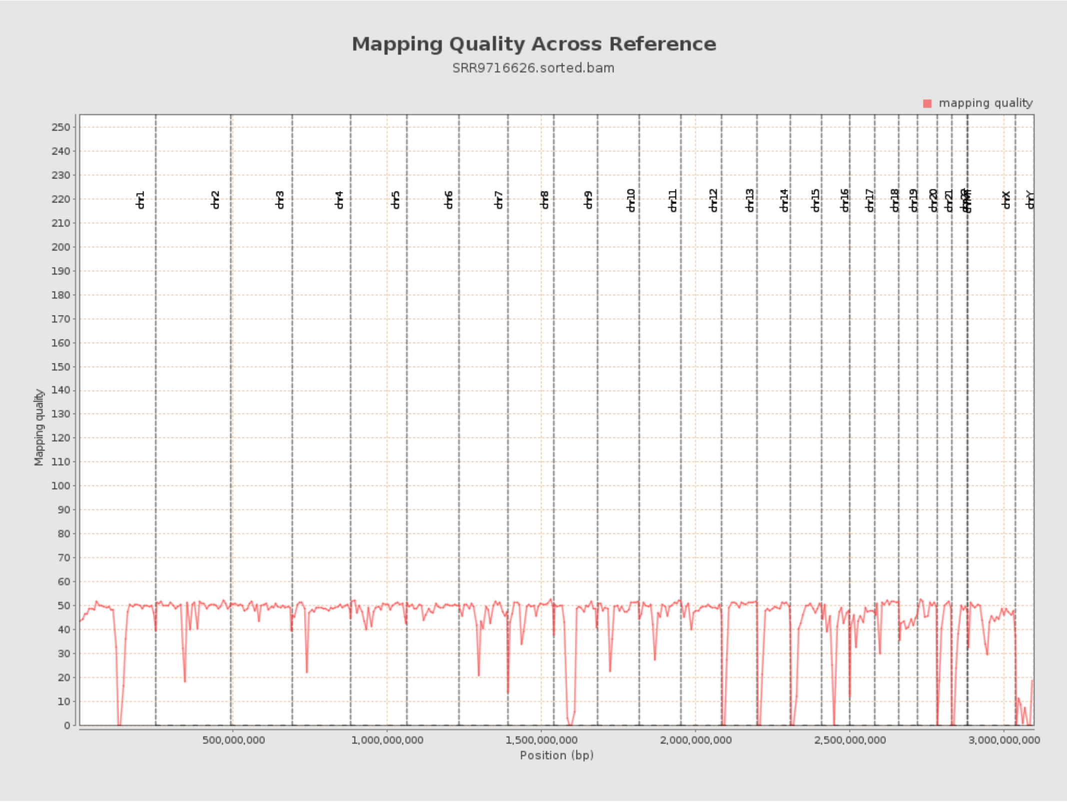
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram