Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 03:00:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716254.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_SRR9716254 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716254.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 03:00:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716254.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,609,939
Mapped reads	3,423,471 / 94.83%
Unmapped reads	186,468 / 5.17%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	73,310 / 2.03%
Read min/max/mean length	30 / 101 / 101.73
Duplicated reads (estimated)	268,672 / 7.44%
Duplication rate	6%
Clipped reads	3,495,327 / 96.83%

2.2. ACGT Content

Number/percentage of A's	63,459,742 / 23.89%
Number/percentage of C's	54,492,672 / 20.51%
Number/percentage of T's	79,400,014 / 29.89%
Number/percentage of G's	68,310,432 / 25.71%
Number/percentage of N's	10,457 / 0%
GC Percentage	46.22%

2.3. Coverage

Mean	0.0859

Standard Deviation	0.615

2.4. Mapping Quality

Mean Mapping Quality	46.43

2.5. Mismatches and indels

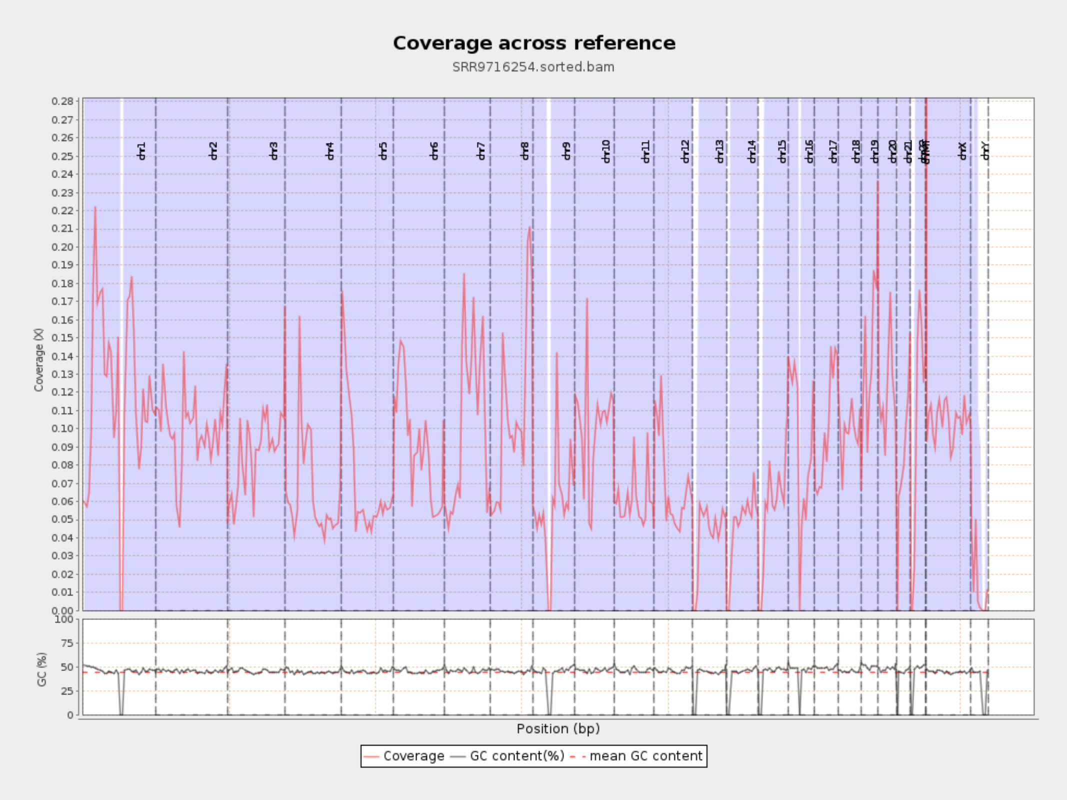
General error rate	0.64%
Mismatches	1,654,721
Insertions	19,985
Mapped reads with at least one insertion	0.57%
Deletions	46,975
Mapped reads with at least one deletion	1.35%
Homopolymer indels	40.25%

2.6. Chromosome stats

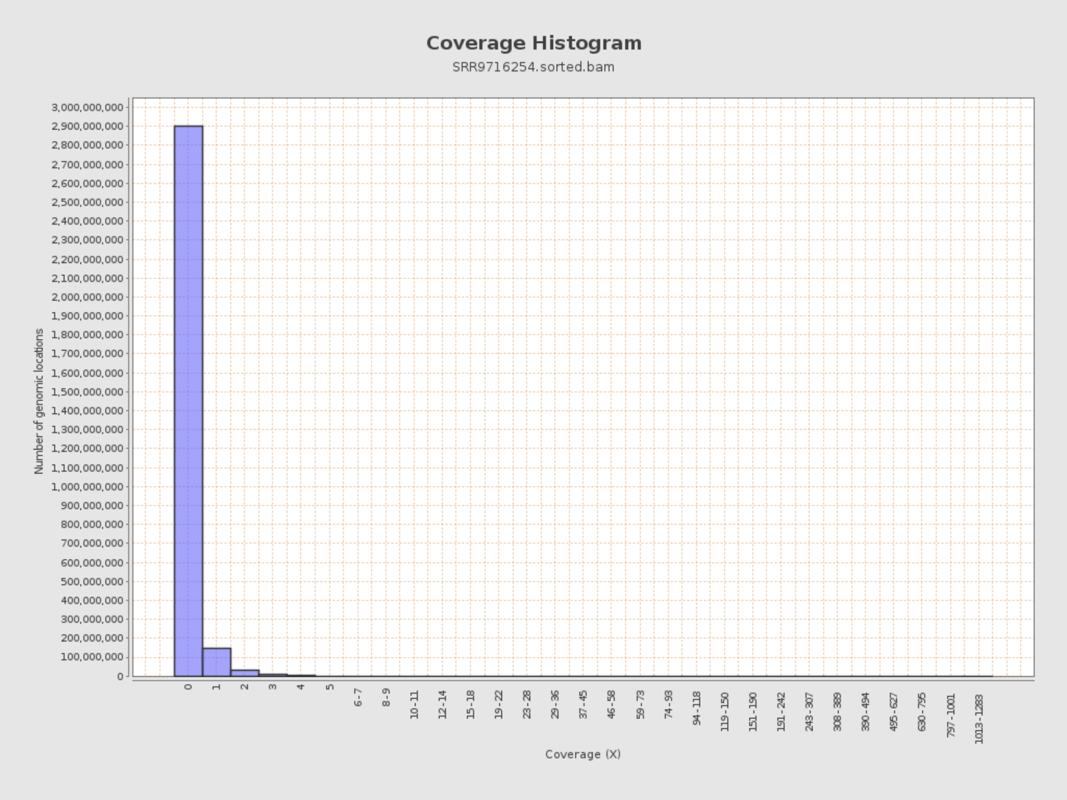
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	29970618	0.1202	1.1933
chr2	243199373	24400658	0.1003	0.6577
chr3	198022430	17032916	0.086	0.3844
chr4	191154276	12447383	0.0651	0.5038
chr5	180915260	13196967	0.0729	0.3603
chr6	171115067	15507558	0.0906	0.4318
chr7	159138663	16247765	0.1021	0.8344

chr8	146364022	15863023	0.1084	0.6541
chr9	141213431	8010479	0.0567	0.4352
chr10	135534747	13711207	0.1012	0.8431
chr11	135006516	8209308	0.0608	0.4666
chr12	133851895	9532727	0.0712	0.3521
chr13	115169878	4782290	0.0415	0.2616
chr14	107349540	5016556	0.0467	0.3194
chr15	102531392	5669623	0.0553	0.3029
chr16	90354753	8128156	0.09	0.4339
chr17	81195210	8058050	0.0992	0.4762
chr18	78077248	7680047	0.0984	0.6684
chr19	59128983	8316557	0.1407	0.9274
chr20	63025520	7521217	0.1193	0.494
chr21	48129895	4083317	0.0848	0.4879
chr22	51304566	5154689	0.1005	0.4438
chrMT	16571	159851	9.6464	7.7833
chrX	155270560	16226881	0.1045	0.4587
chrY	59373566	843408	0.0142	0.4435

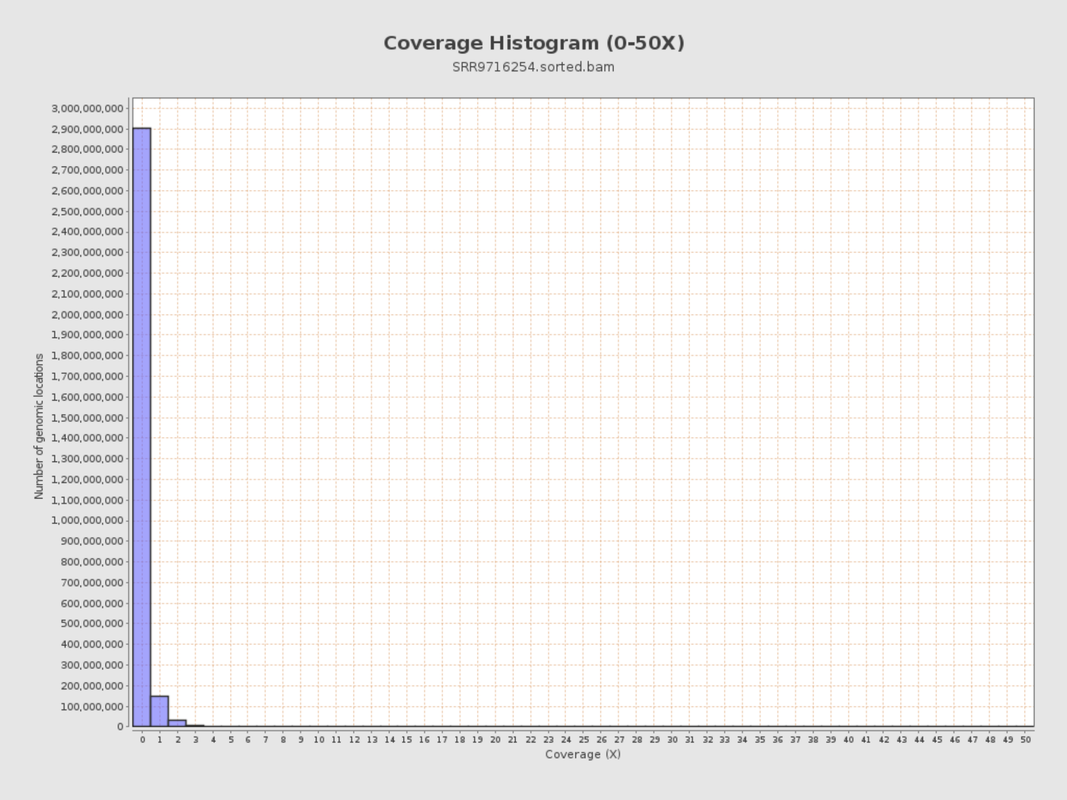
3. Results : Coverage across reference



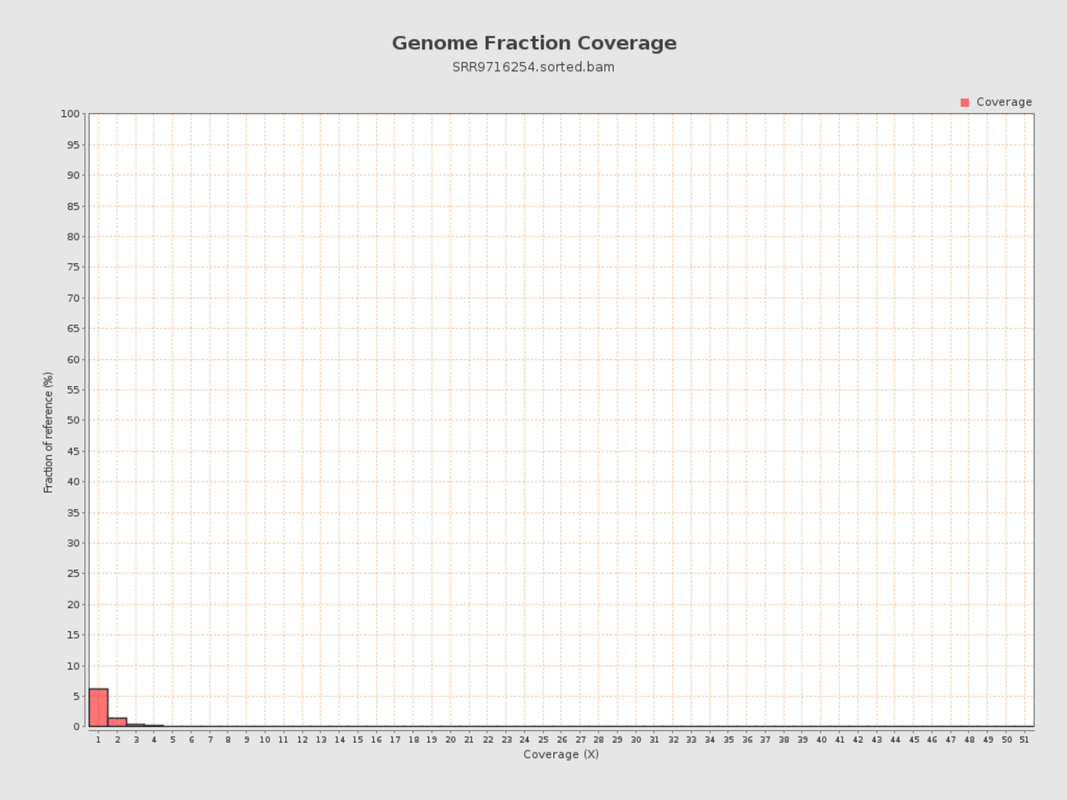
4. Results : Coverage Histogram



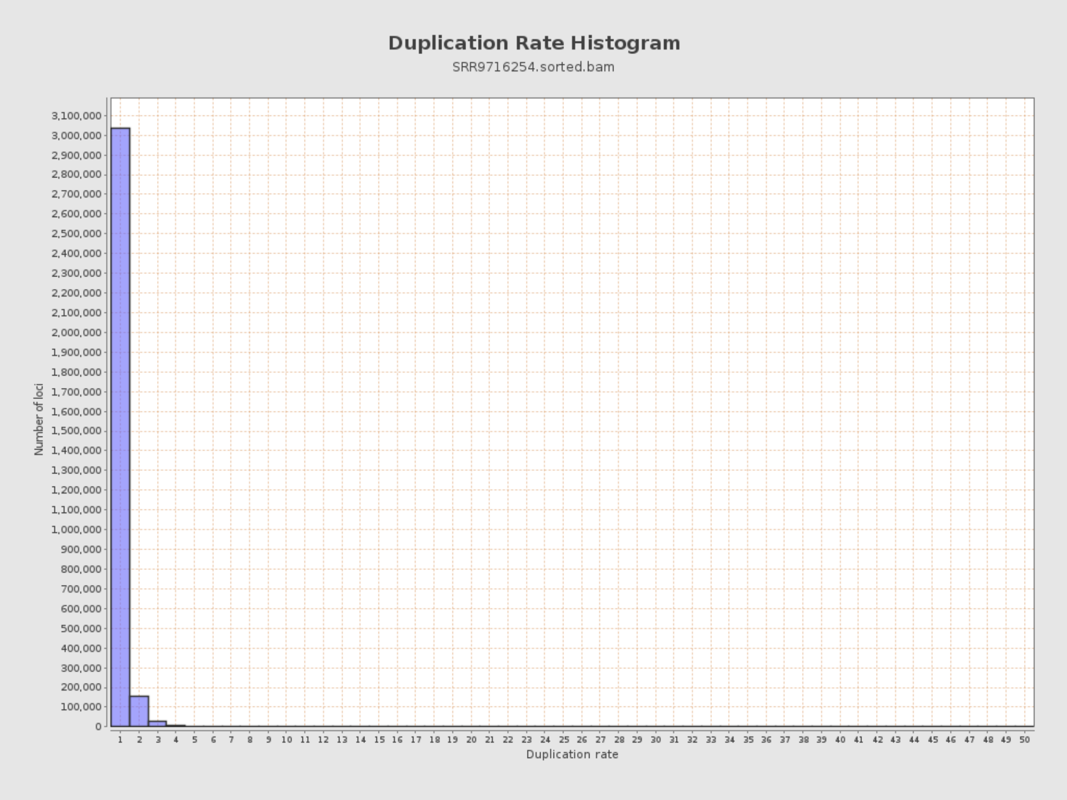
5. Results : Coverage Histogram (0-50X)



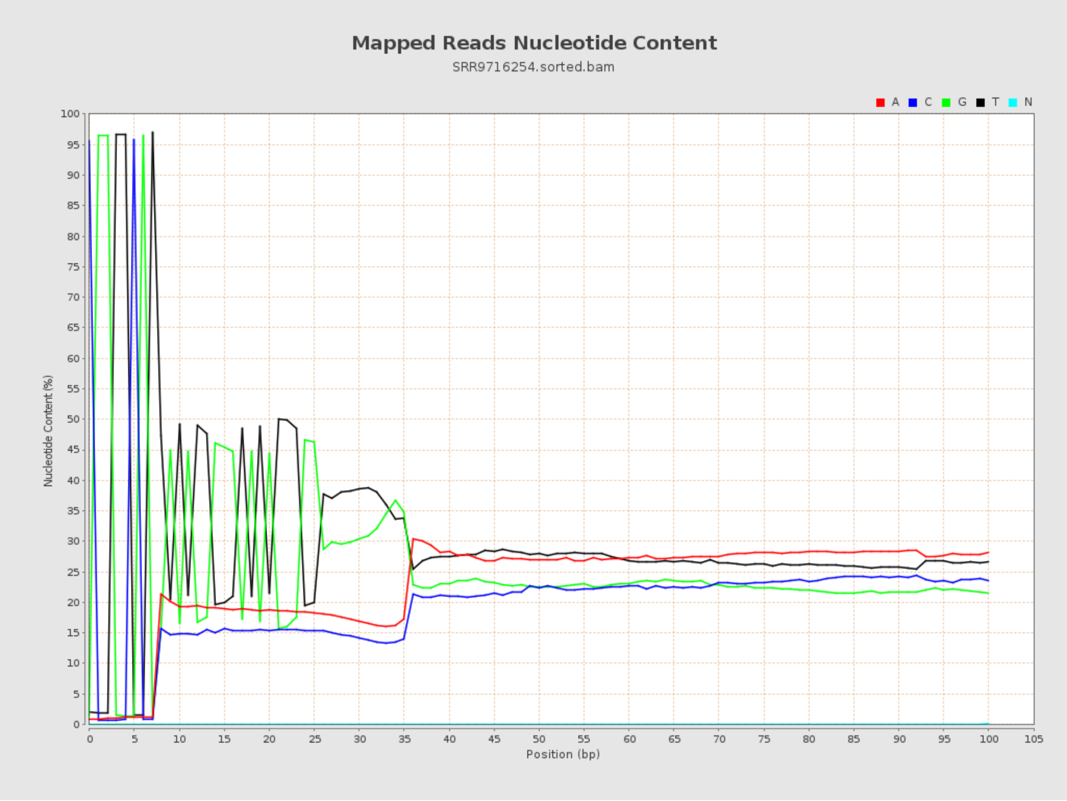
6. Results : Genome Fraction Coverage



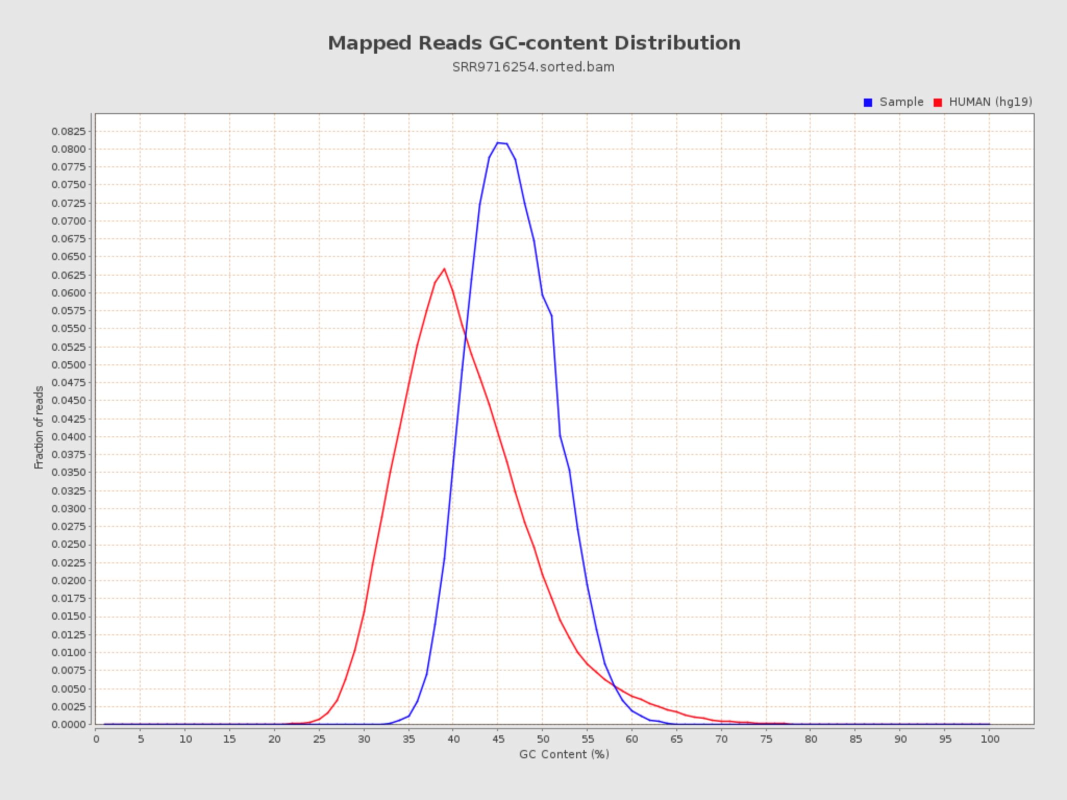
7. Results : Duplication Rate Histogram



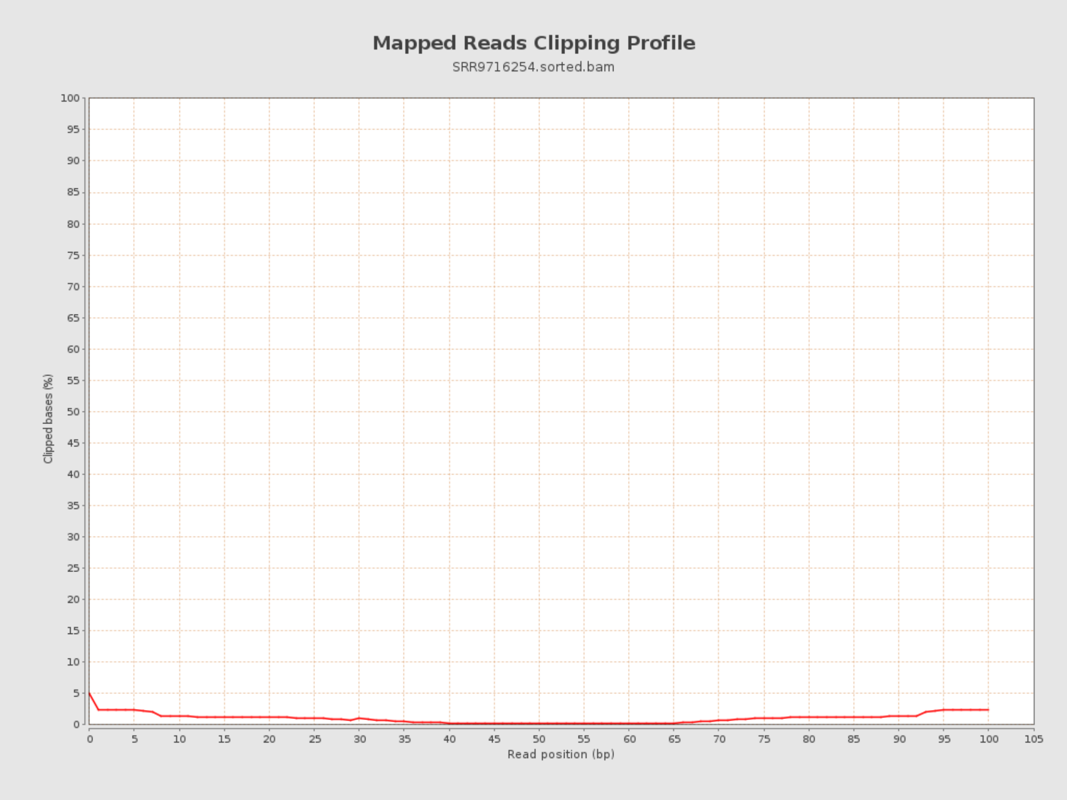
8. Results : Mapped Reads Nucleotide Content



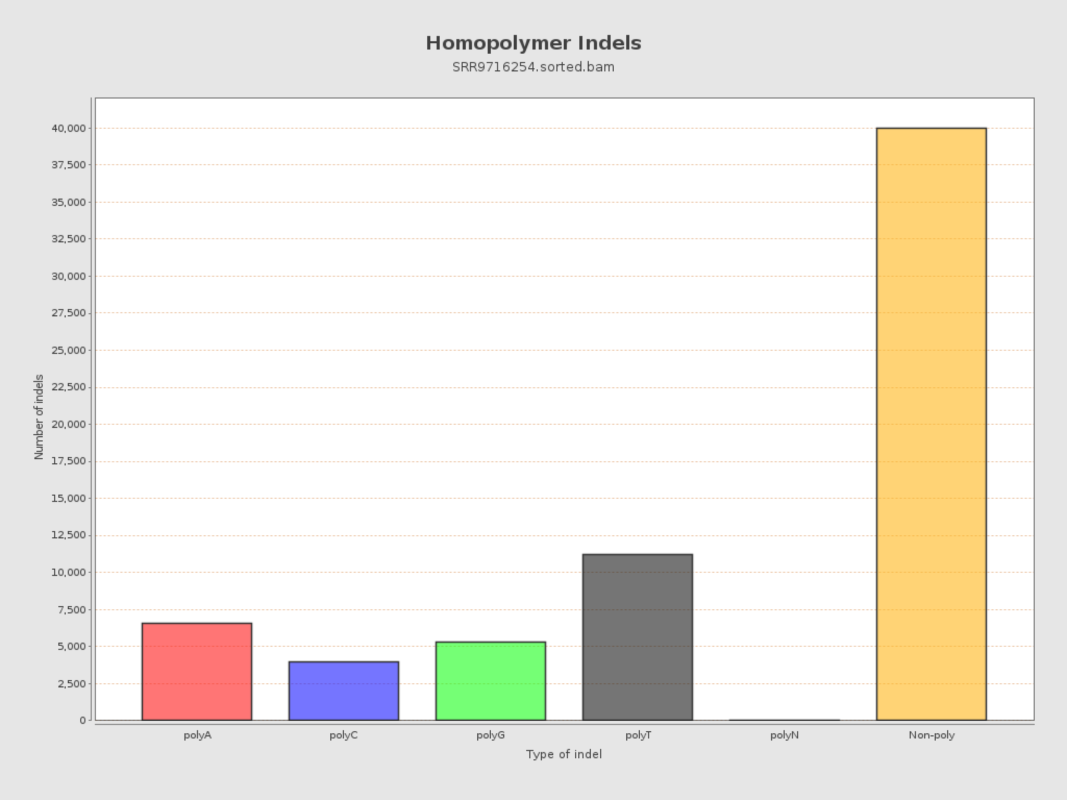
9. Results : Mapped Reads GC-content Distribution



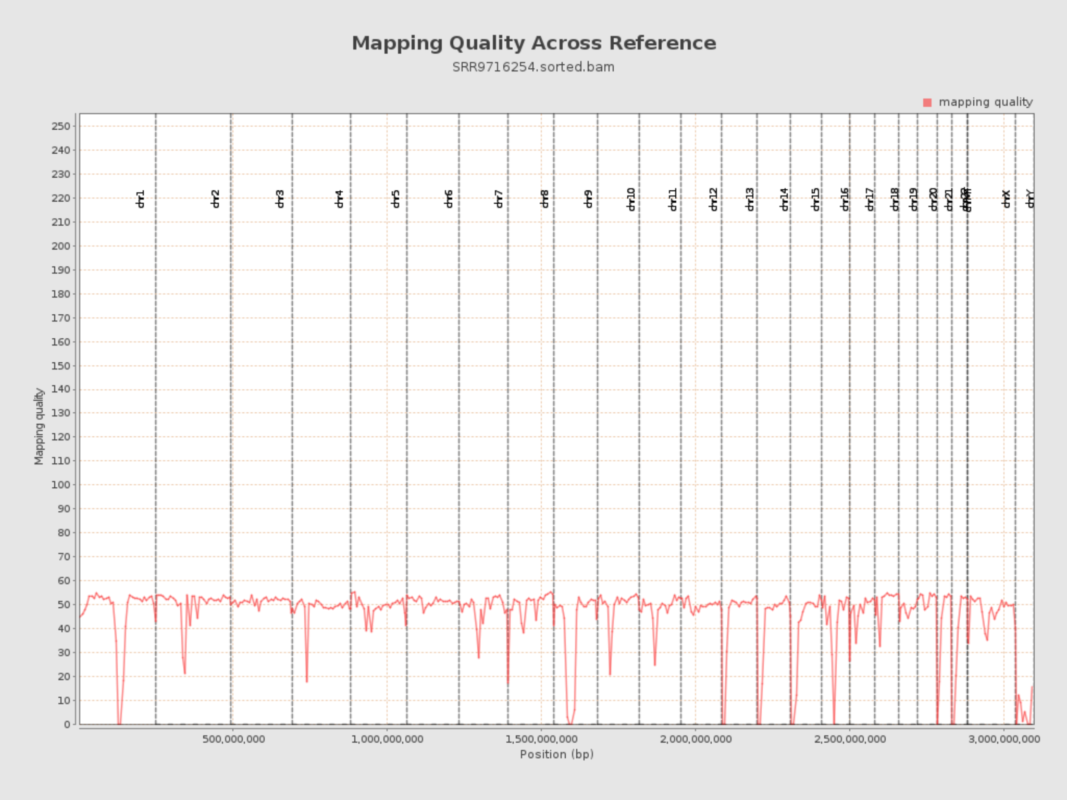
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram