Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 18:27:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716111.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_SRR9716111 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716111.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 18:27:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716111.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,432,866
Mapped reads	2,056,472 / 84.53%
Unmapped reads	376,394 / 15.47%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,057 / 0.29%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	62,440 / 2.57%
Duplication rate	2.11%
Clipped reads	2,059,882 / 84.67%

2.2. ACGT Content

Number/percentage of A's	28,927,689 / 24.93%
Number/percentage of C's	22,439,079 / 19.33%
Number/percentage of T's	36,768,857 / 31.68%
Number/percentage of G's	27,918,183 / 24.06%
Number/percentage of N's	895 / 0%
GC Percentage	43.39%

2.3. Coverage

Mean	0.0375

Standard Deviation	0.305

2.4. Mapping Quality

Mean Mapping Quality	41.87

2.5. Mismatches and indels

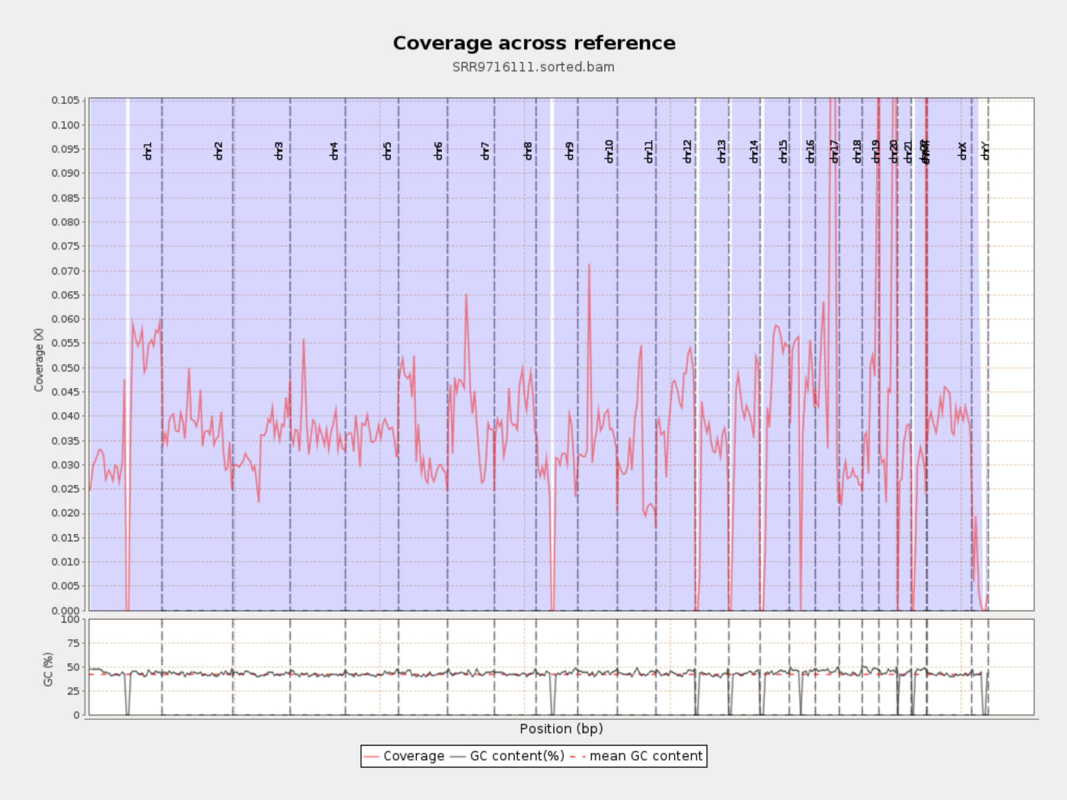
General error rate	0.54%
Mismatches	609,119
Insertions	7,459
Mapped reads with at least one insertion	0.36%
Deletions	21,931
Mapped reads with at least one deletion	1.06%
Homopolymer indels	41.16%

2.6. Chromosome stats

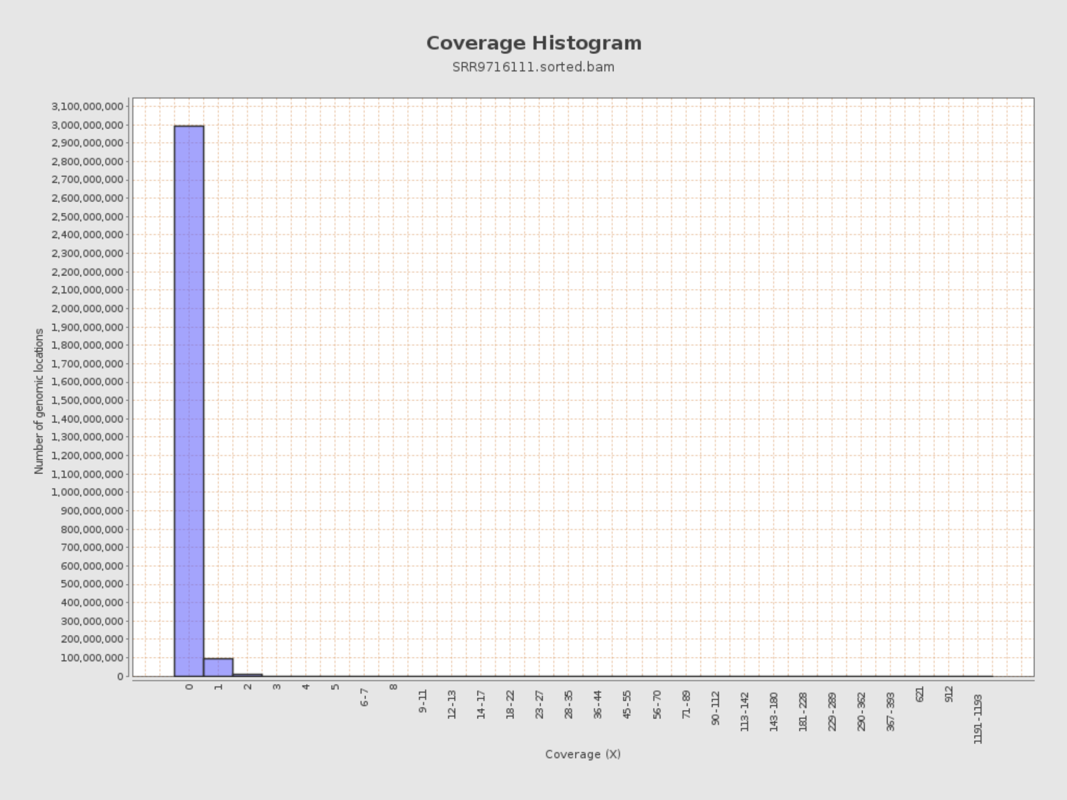
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9758340	0.0392	0.3729
chr2	243199373	9068311	0.0373	0.5132
chr3	198022430	6747731	0.0341	0.2103
chr4	191154276	7064790	0.037	0.2328
chr5	180915260	6584928	0.0364	0.2111
chr6	171115067	6190796	0.0362	0.2602
chr7	159138663	6611120	0.0415	0.4295

chr8	146364022	5976044	0.0408	0.2781
chr9	141213431	3864755	0.0274	0.2201
chr10	135534747	5106457	0.0377	0.3731
chr11	135006516	4121661	0.0305	0.2578
chr12	133851895	5787895	0.0432	0.2326
chr13	115169878	3458604	0.03	0.1939
chr14	107349540	3908937	0.0364	0.2263
chr15	102531392	4273393	0.0417	0.2314
chr16	90354753	4064897	0.045	0.2556
chr17	81195210	5218415	0.0643	0.3027
chr18	78077248	2115422	0.0271	0.3463
chr19	59128983	3153650	0.0533	0.3636
chr20	63025520	3718201	0.059	0.2849
chr21	48129895	1434006	0.0298	0.2116
chr22	51304566	1103486	0.0215	0.1636
chrMT	16571	155017	9.3547	6.7581
chrX	155270560	6251787	0.0403	0.2457
chrY	59373566	350924	0.0059	0.1639

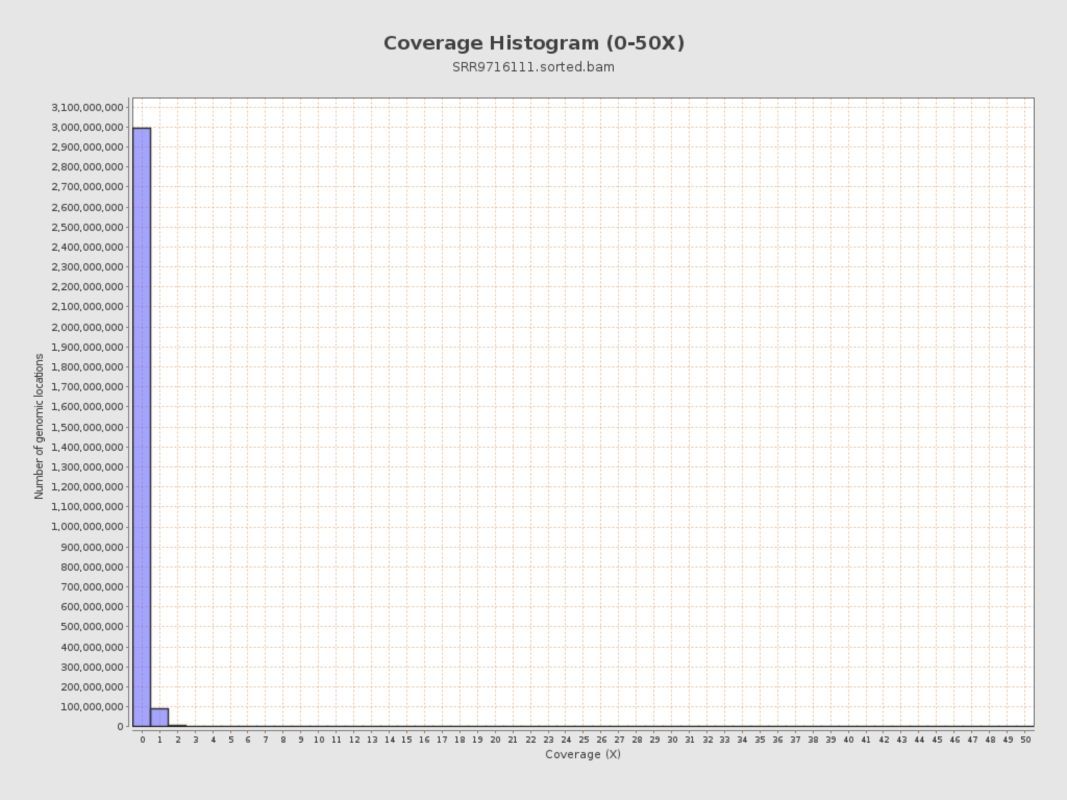
3. Results : Coverage across reference



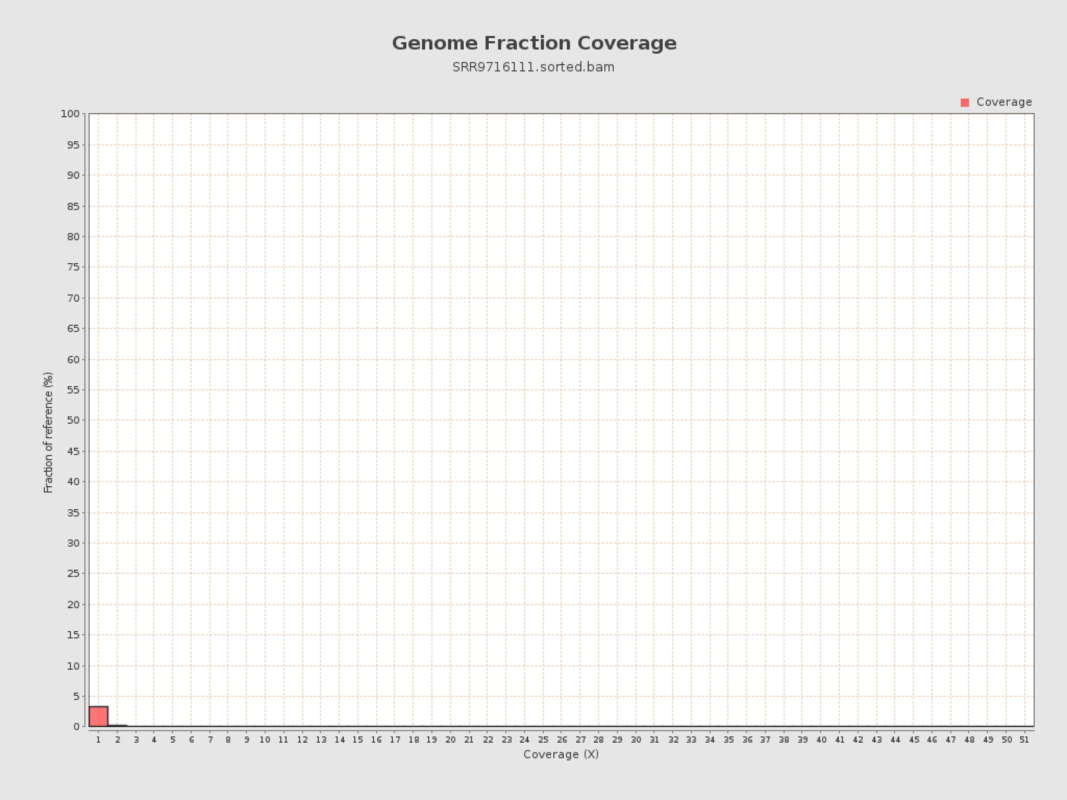
4. Results : Coverage Histogram



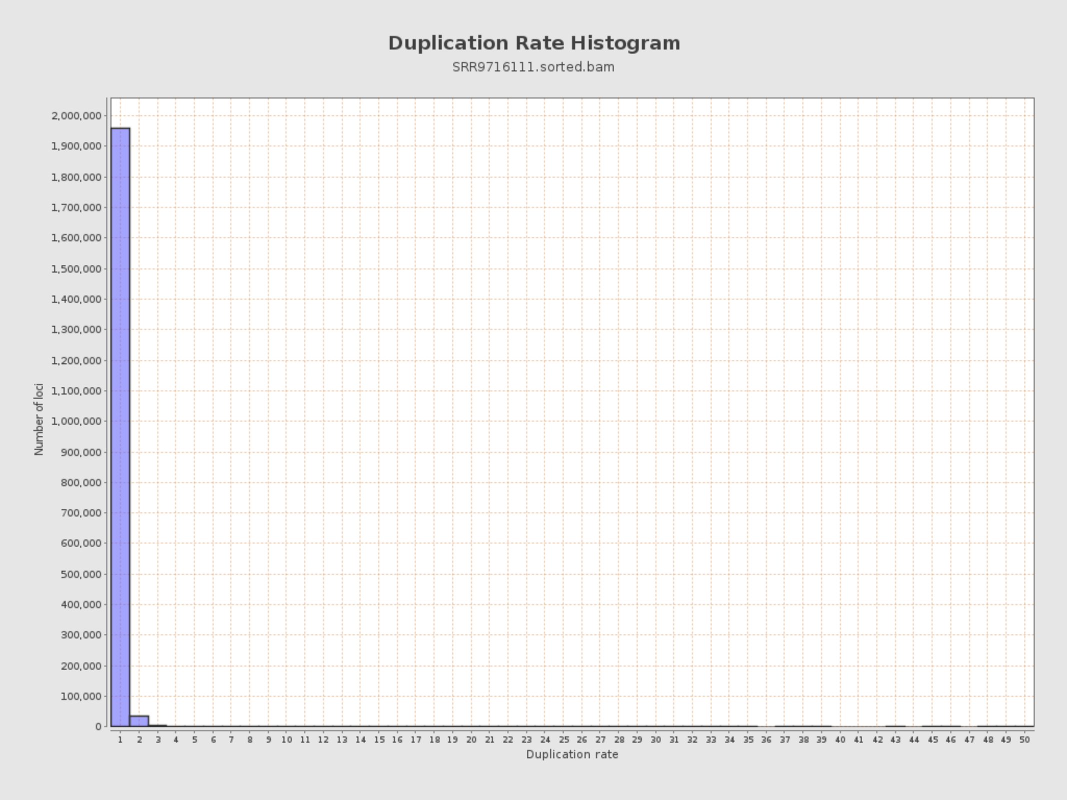
5. Results : Coverage Histogram (0-50X)



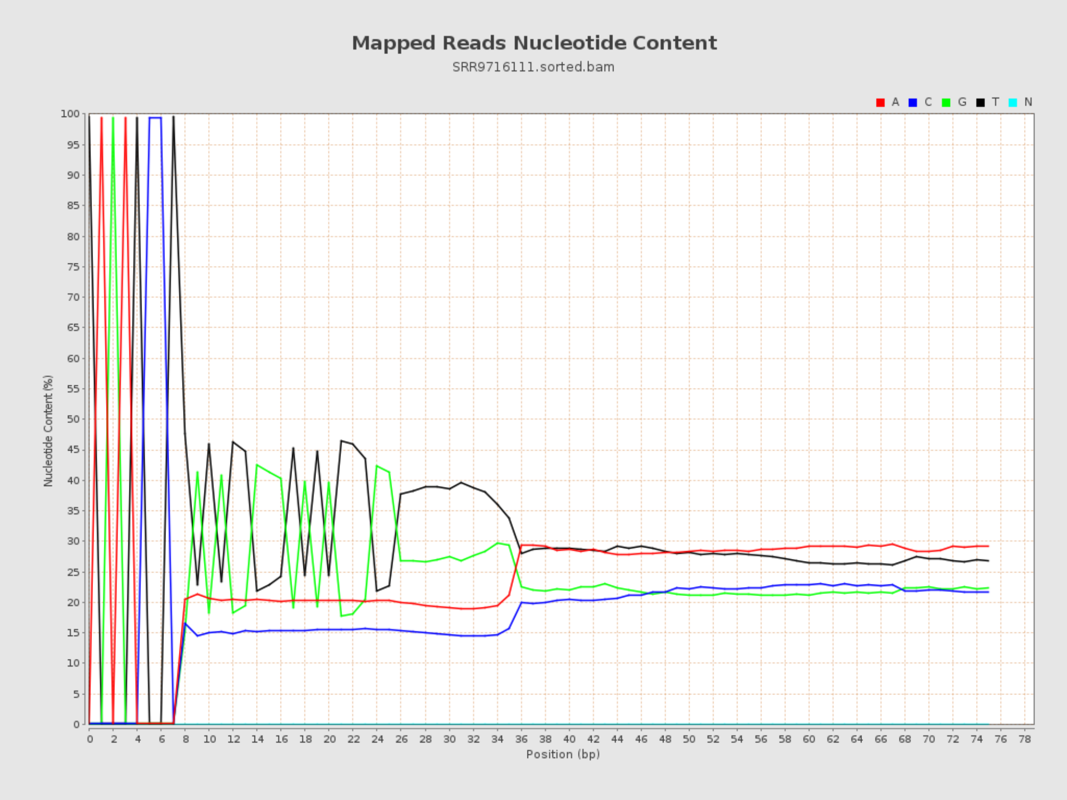
6. Results : Genome Fraction Coverage



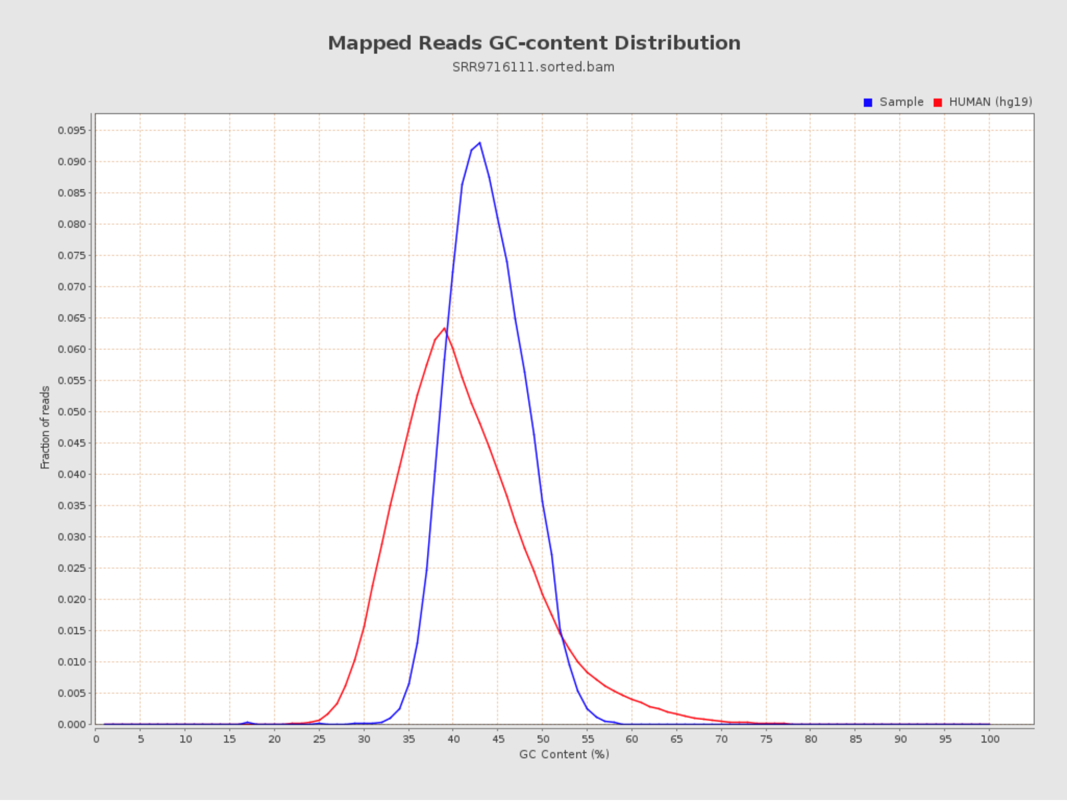
7. Results : Duplication Rate Histogram



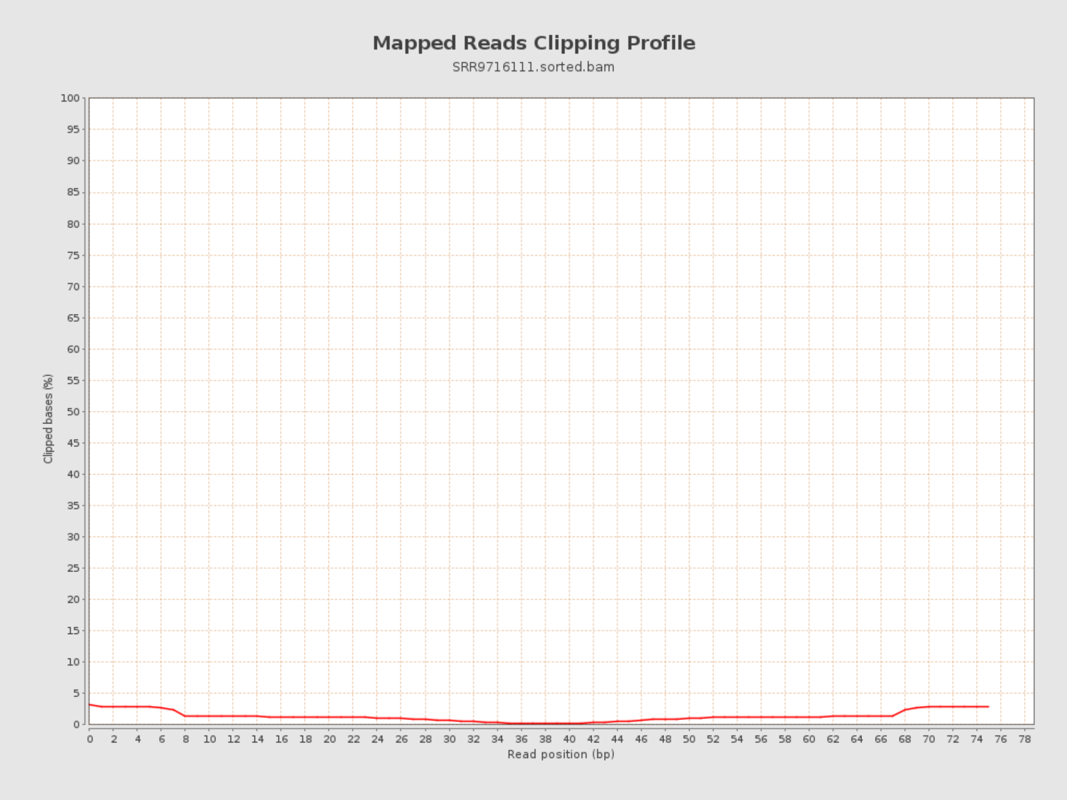
8. Results : Mapped Reads Nucleotide Content



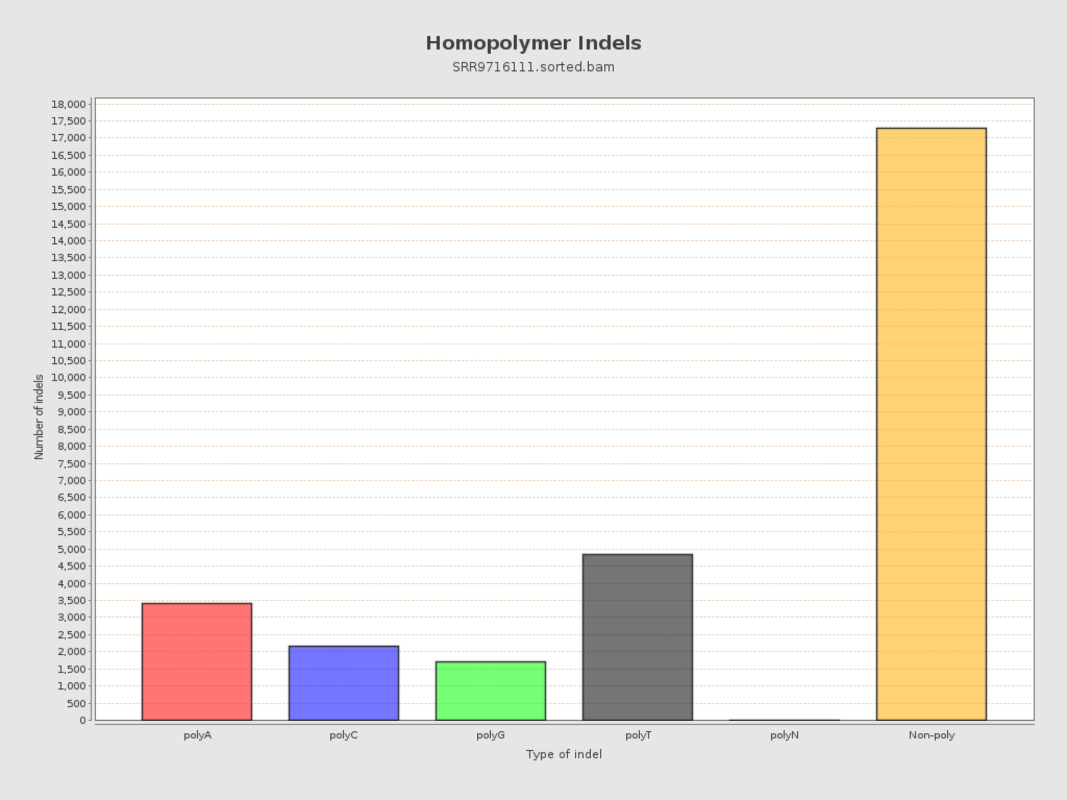
9. Results : Mapped Reads GC-content Distribution



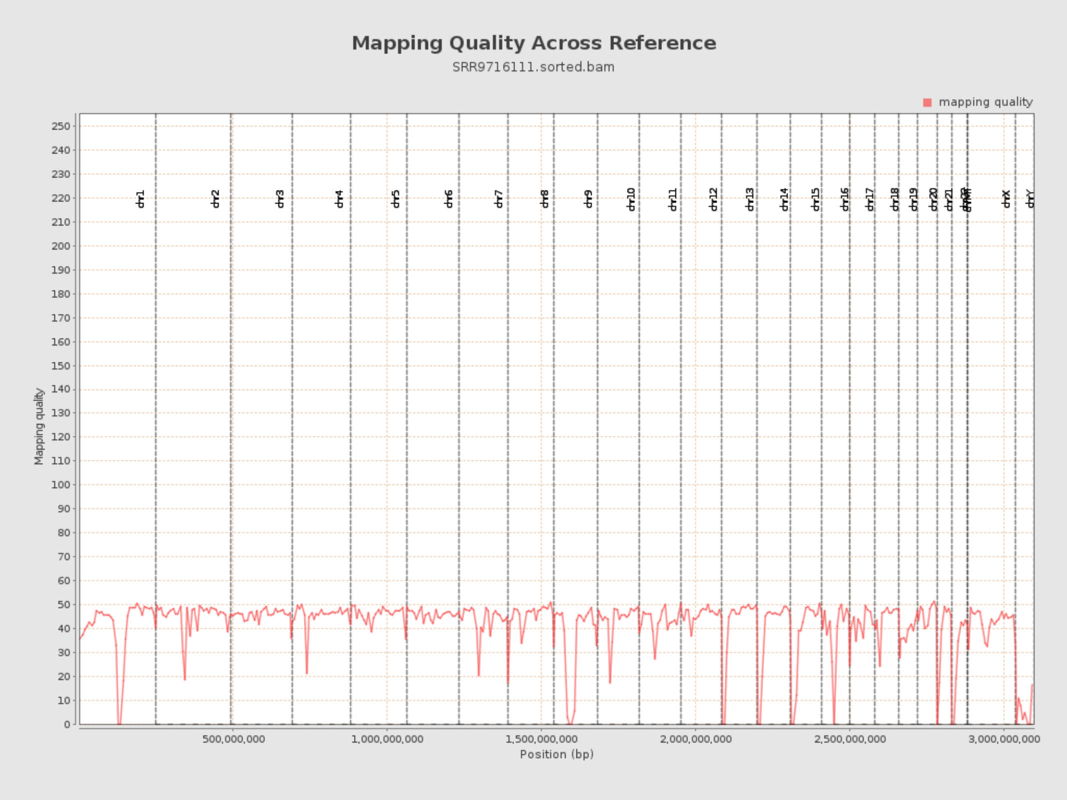
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram