Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 14:57:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716851.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_SRR9716851 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716851.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 14:57:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716851.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	876,892
Mapped reads	774,146 / 88.28%
Unmapped reads	102,746 / 11.72%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,458 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	16,336 / 1.86%
Duplication rate	1.51%
Clipped reads	774,771 / 88.35%

2.2. ACGT Content

Number/percentage of A's	10,660,856 / 23.91%
Number/percentage of C's	8,718,128 / 19.55%
Number/percentage of T's	14,629,582 / 32.81%
Number/percentage of G's	10,580,325 / 23.73%
Number/percentage of N's	275 / 0%
GC Percentage	43.28%

2.3. Coverage

Mean	0.0144

Standard Deviation	0.1594

2.4. Mapping Quality

Mean Mapping Quality	44.25

2.5. Mismatches and indels

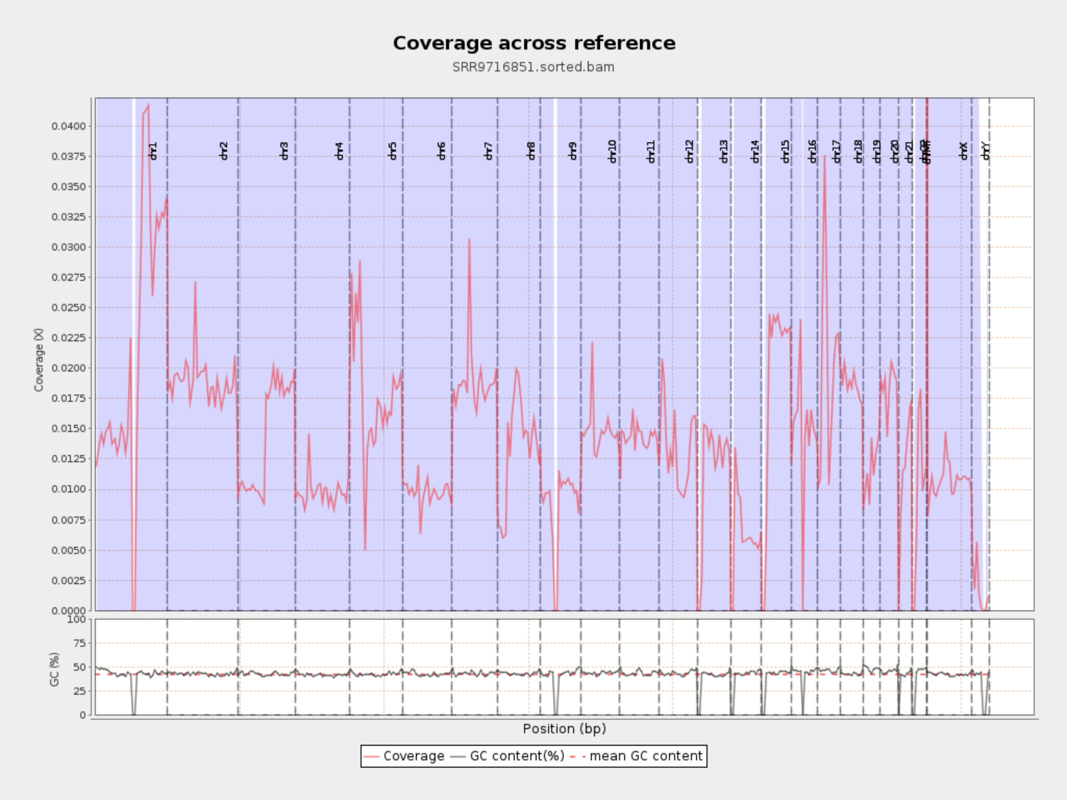
General error rate	0.52%
Mismatches	226,932
Insertions	3,325
Mapped reads with at least one insertion	0.43%
Deletions	8,461
Mapped reads with at least one deletion	1.09%
Homopolymer indels	41.74%

2.6. Chromosome stats

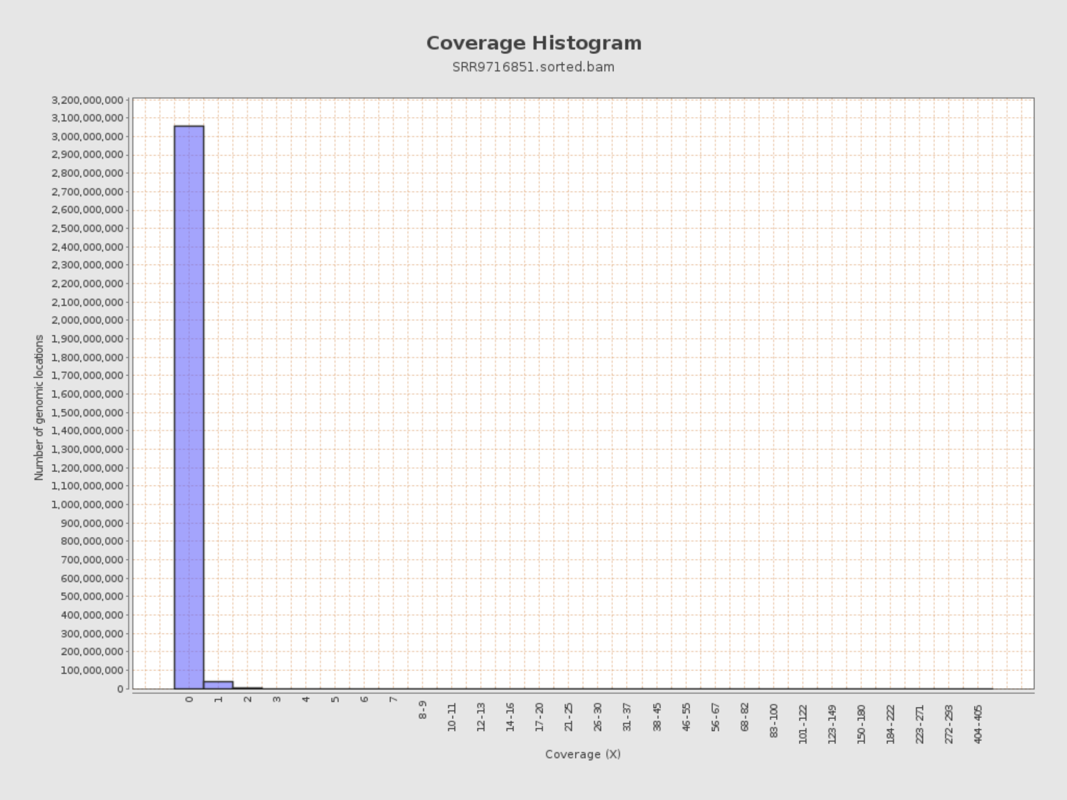
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5290381	0.0212	0.2401
chr2	243199373	4621474	0.019	0.2251
chr3	198022430	2850106	0.0144	0.1253
chr4	191154276	1873099	0.0098	0.1085
chr5	180915260	3246646	0.0179	0.1395
chr6	171115067	1667803	0.0097	0.1105
chr7	159138663	3031803	0.0191	0.24

chr8	146364022	1984519	0.0136	0.1361
chr9	141213431	1229847	0.0087	0.1176
chr10	135534747	2022730	0.0149	0.1445
chr11	135006516	1941348	0.0144	0.1519
chr12	133851895	1795656	0.0134	0.1214
chr13	115169878	1314589	0.0114	0.1116
chr14	107349540	653198	0.0061	0.0846
chr15	102531392	1936002	0.0189	0.1455
chr16	90354753	1321528	0.0146	0.1315
chr17	81195210	1664323	0.0205	0.1547
chr18	78077248	1457957	0.0187	0.2413
chr19	59128983	699913	0.0118	0.1825
chr20	63025520	1150683	0.0183	0.1411
chr21	48129895	564442	0.0117	0.1145
chr22	51304566	503753	0.0098	0.1025
chrMT	16571	2450	0.1478	0.4089
chrX	155270560	1677480	0.0108	0.1198
chrY	59373566	100852	0.0017	0.053

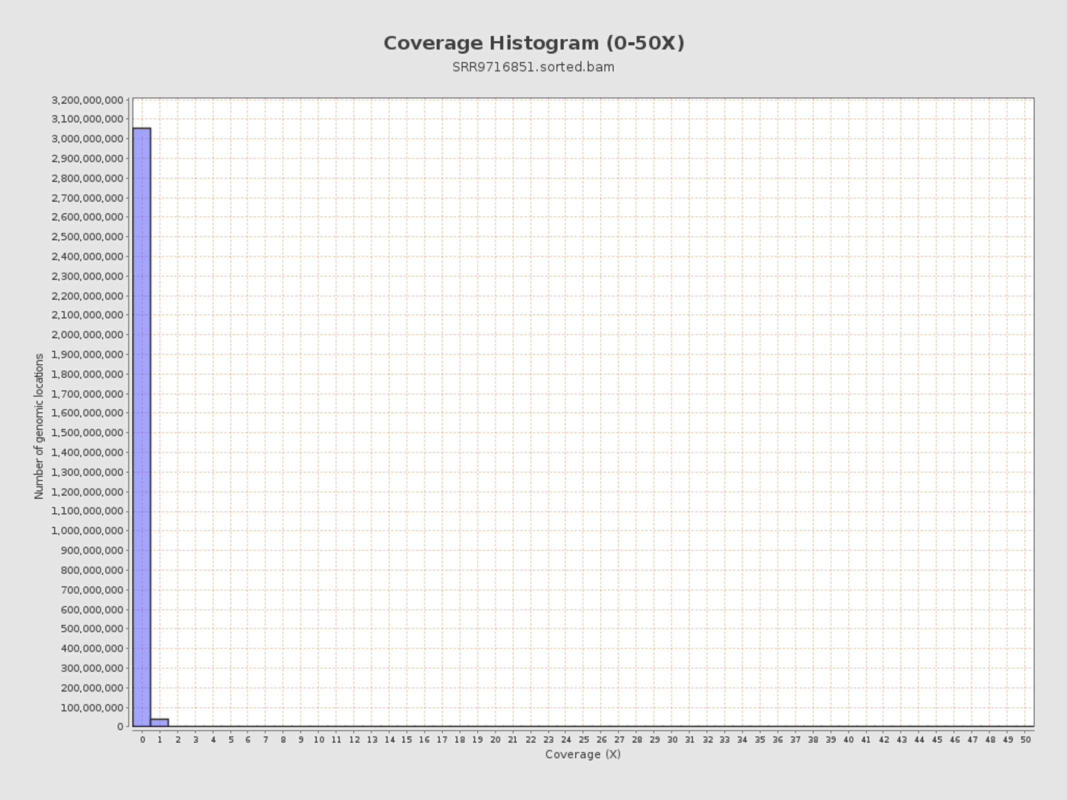
3. Results : Coverage across reference



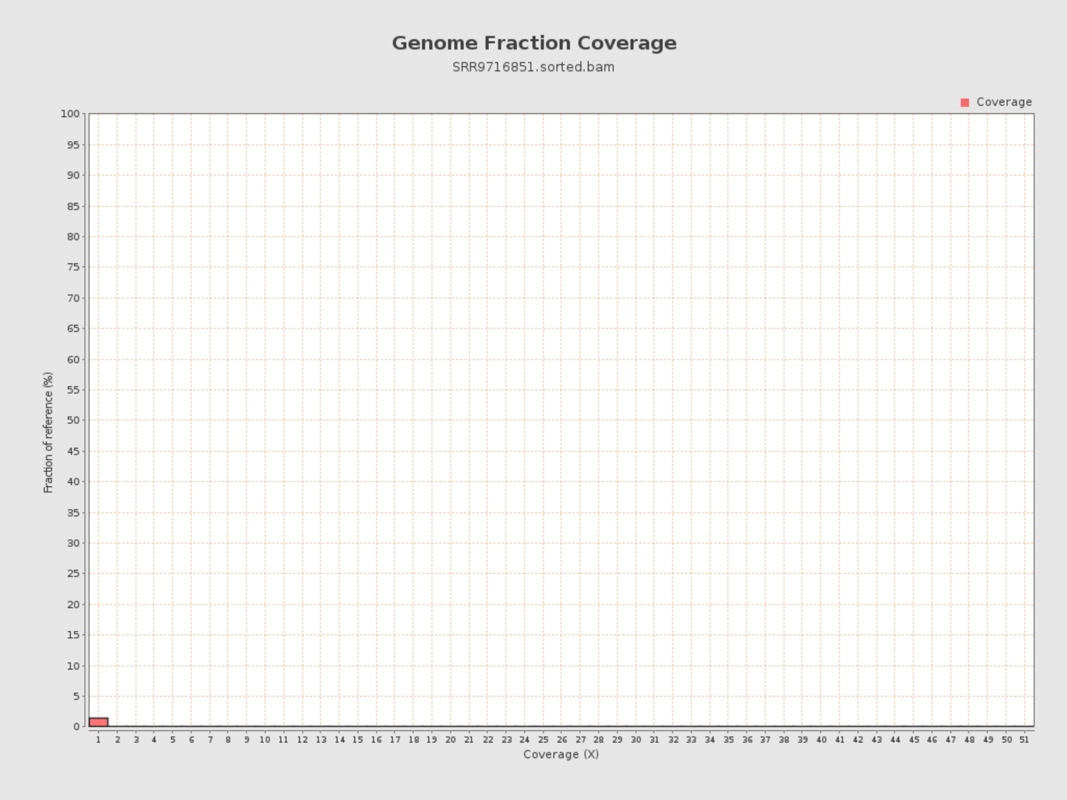
4. Results : Coverage Histogram



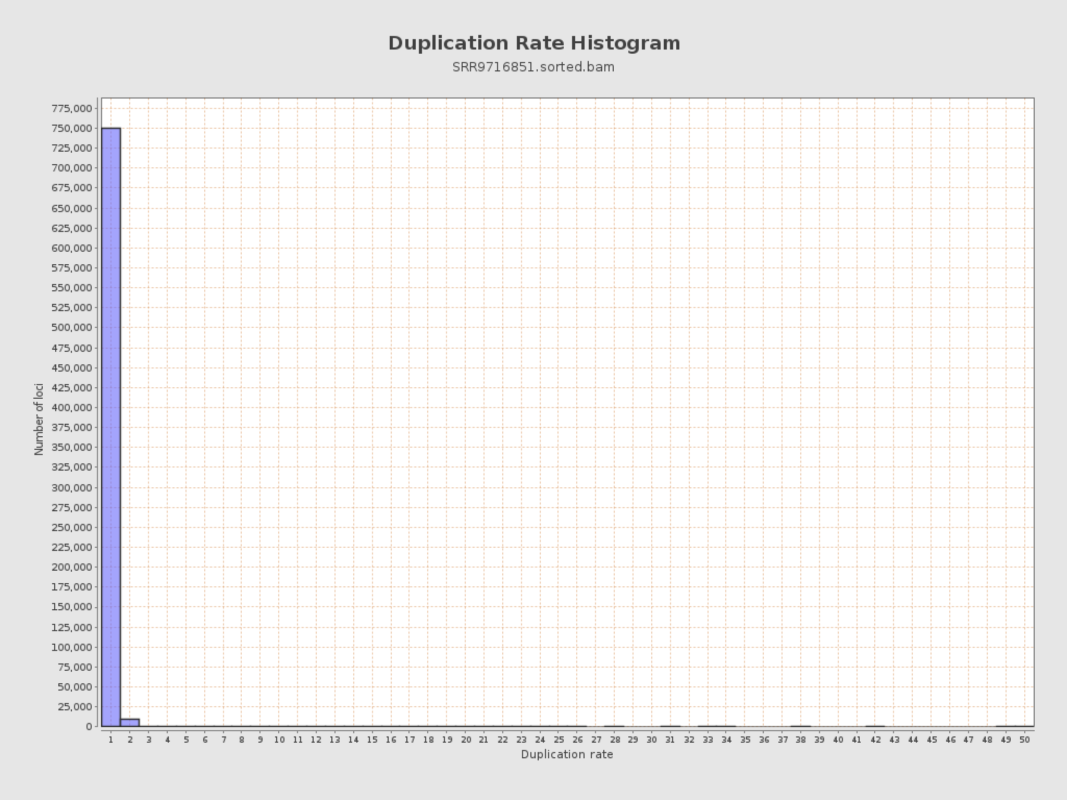
5. Results : Coverage Histogram (0-50X)



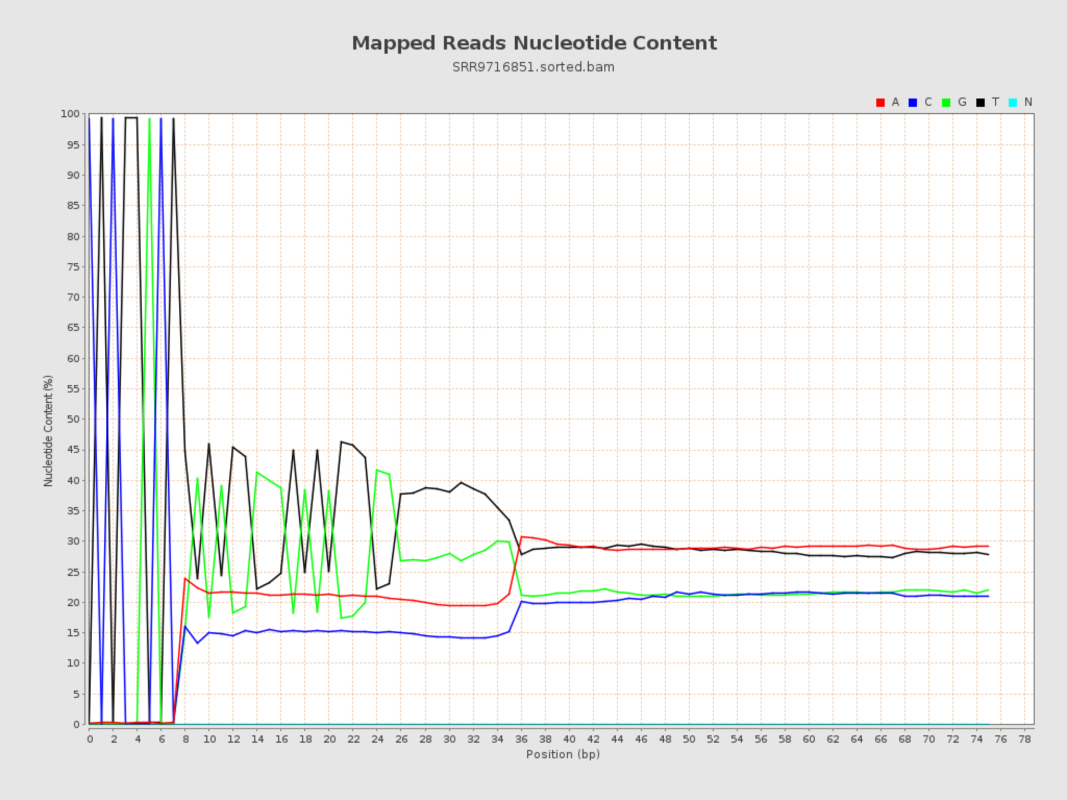
6. Results : Genome Fraction Coverage



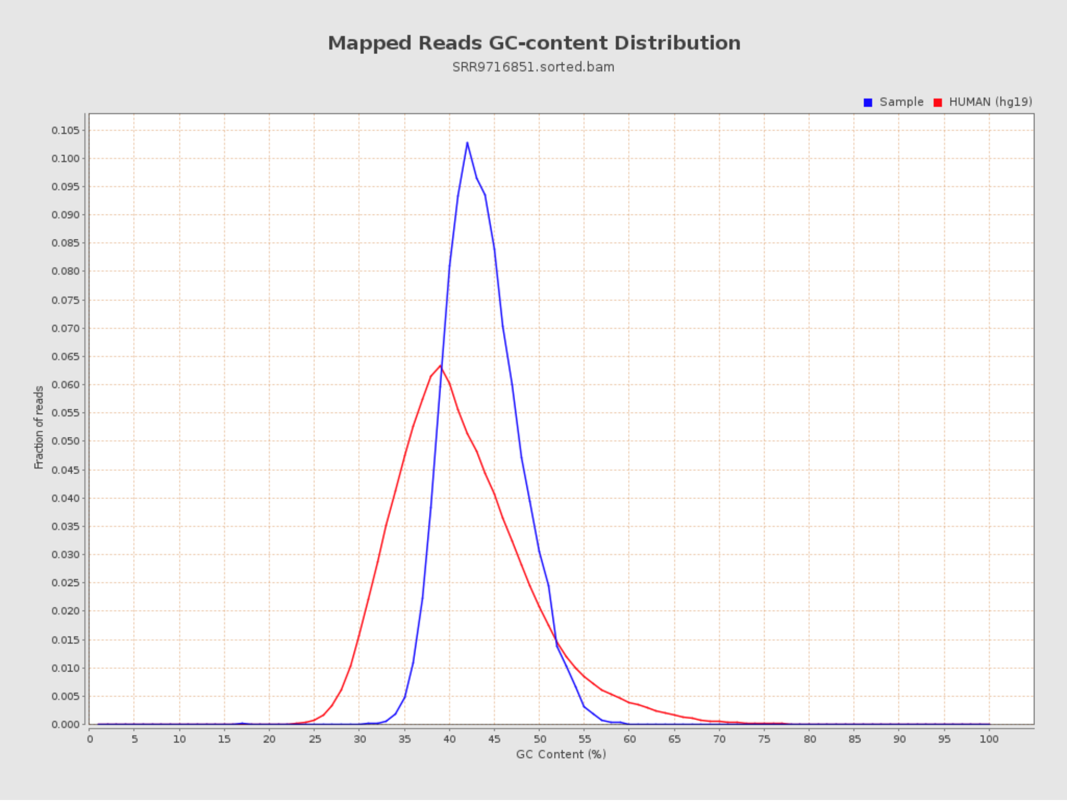
7. Results : Duplication Rate Histogram



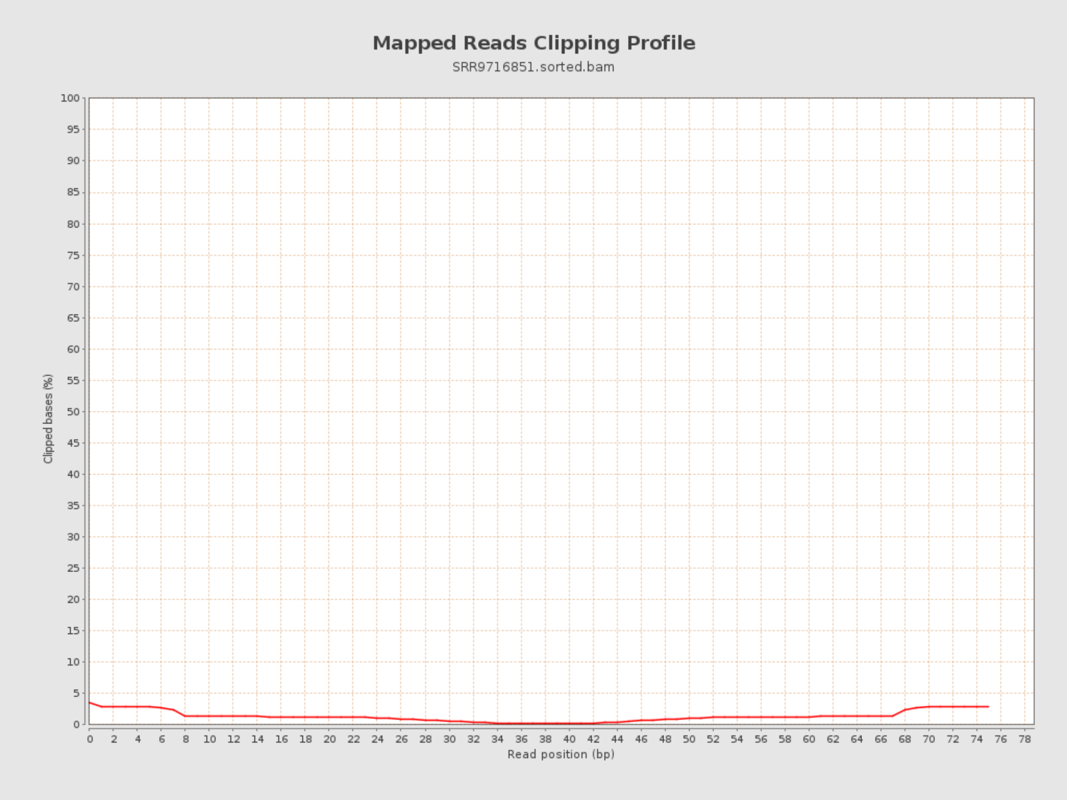
8. Results : Mapped Reads Nucleotide Content



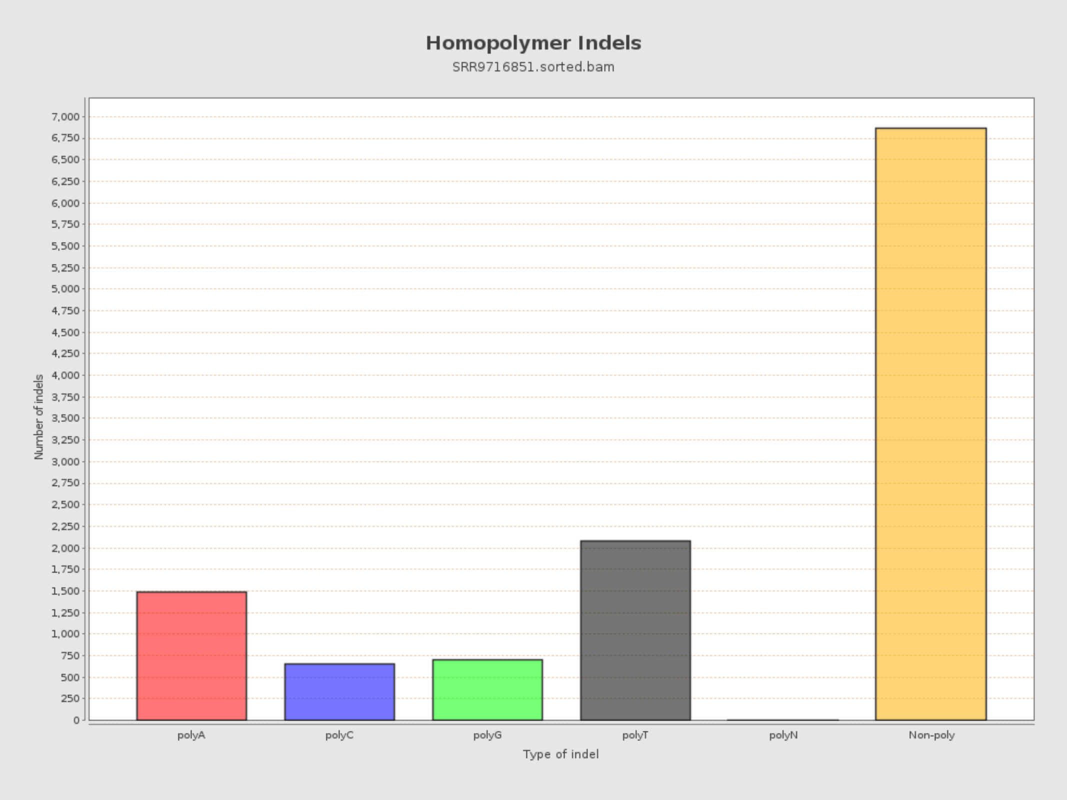
9. Results : Mapped Reads GC-content Distribution



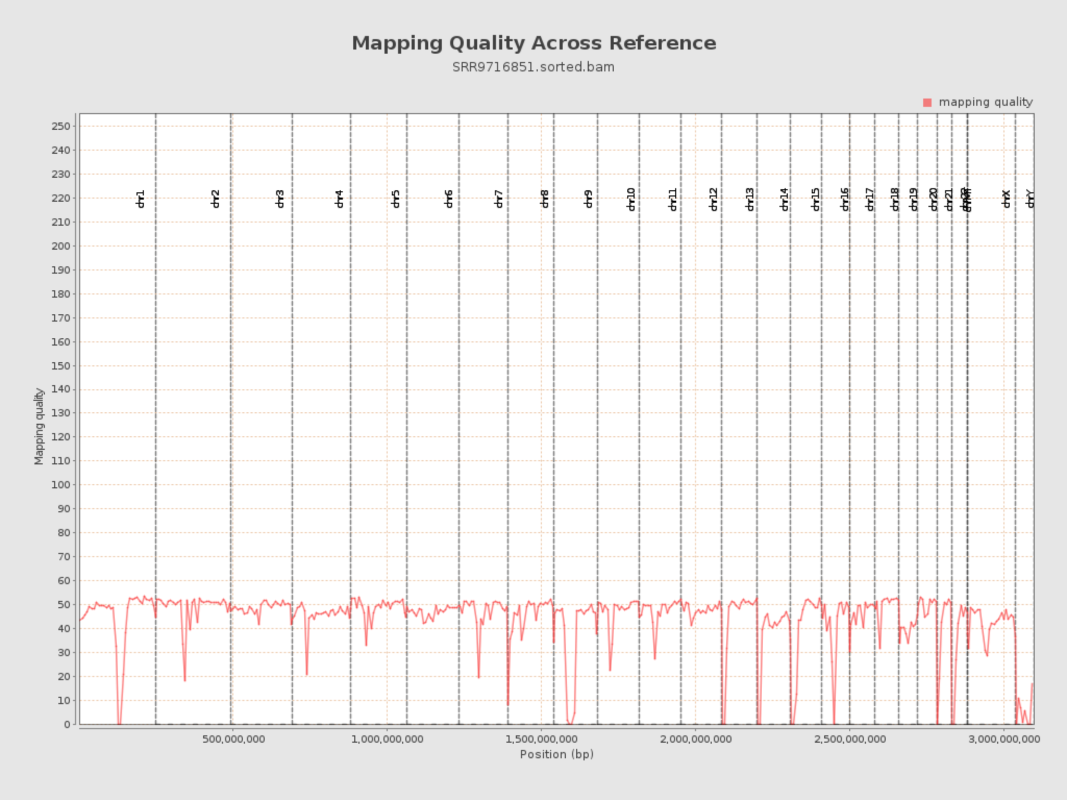
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram