Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 00:38:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716614.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_SRR9716614 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716614.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 00:38:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716614.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	884,758
Mapped reads	803,111 / 90.77%
Unmapped reads	81,647 / 9.23%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,629 / 0.18%
Read min/max/mean length	30 / 76 / 76.06
Duplicated reads (estimated)	17,705 / 2%
Duplication rate	1.6%
Clipped reads	803,676 / 90.84%

2.2. ACGT Content

Number/percentage of A's	11,905,595 / 25.47%
Number/percentage of C's	9,465,748 / 20.25%
Number/percentage of T's	14,321,962 / 30.64%
Number/percentage of G's	11,050,579 / 23.64%
Number/percentage of N's	516 / 0%
GC Percentage	43.89%

2.3. Coverage

Mean	0.0151

Standard Deviation	0.1616

2.4. Mapping Quality

Mean Mapping Quality	44.17

2.5. Mismatches and indels

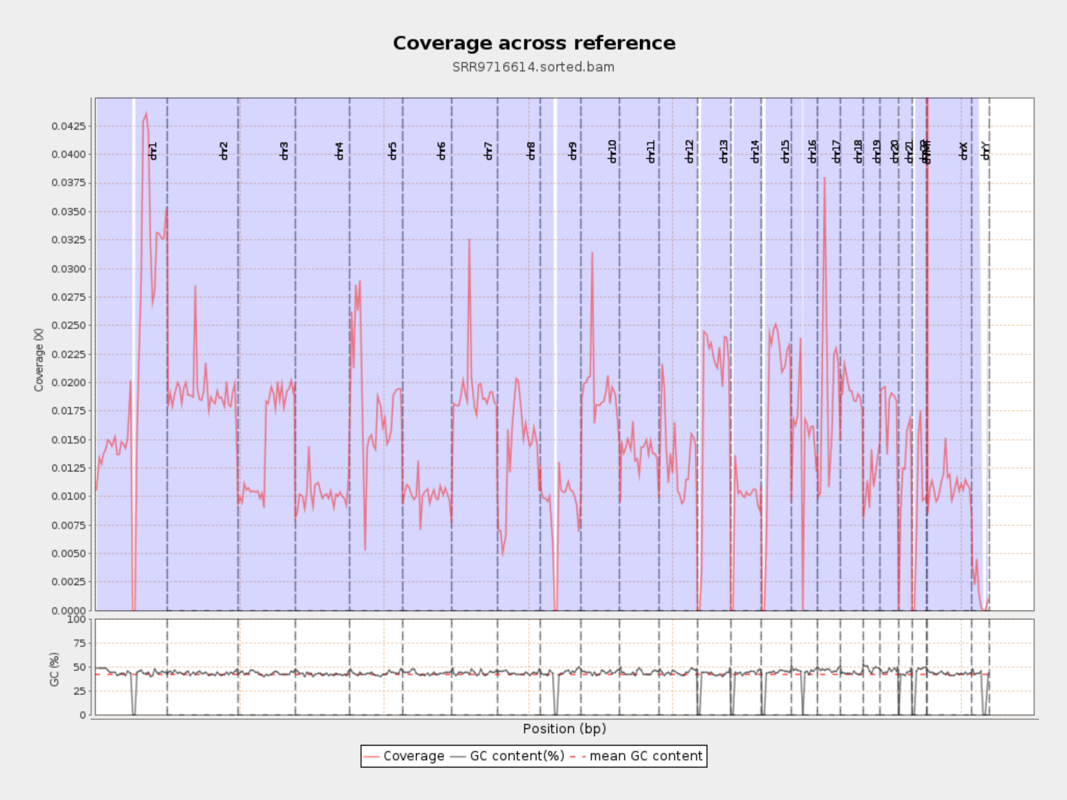
General error rate	0.48%
Mismatches	218,239
Insertions	2,836
Mapped reads with at least one insertion	0.35%
Deletions	8,691
Mapped reads with at least one deletion	1.08%
Homopolymer indels	44.28%

2.6. Chromosome stats

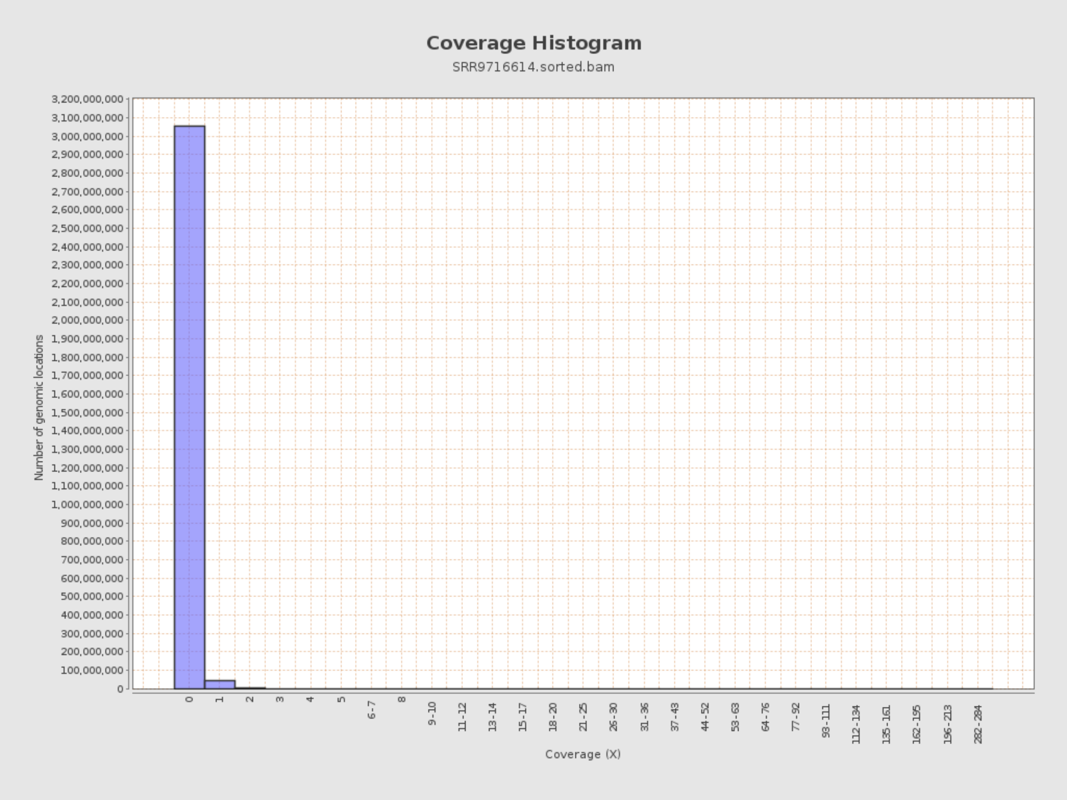
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5309018	0.0213	0.2042
chr2	243199373	4651529	0.0191	0.2098
chr3	198022430	2925106	0.0148	0.1293
chr4	191154276	1942617	0.0102	0.1078
chr5	180915260	3314088	0.0183	0.1427
chr6	171115067	1737221	0.0102	0.114
chr7	159138663	3069599	0.0193	0.2667

chr8	146364022	2027872	0.0139	0.1394
chr9	141213431	1251225	0.0089	0.1316
chr10	135534747	2635776	0.0194	0.196
chr11	135006516	1893640	0.014	0.1563
chr12	133851895	1810939	0.0135	0.1224
chr13	115169878	2170411	0.0188	0.1442
chr14	107349540	973039	0.0091	0.1044
chr15	102531392	1911944	0.0186	0.1445
chr16	90354753	1344818	0.0149	0.1374
chr17	81195210	1606230	0.0198	0.1541
chr18	78077248	1503838	0.0193	0.2578
chr19	59128983	684644	0.0116	0.1597
chr20	63025520	1128134	0.0179	0.1407
chr21	48129895	580759	0.0121	0.1171
chr22	51304566	474349	0.0092	0.1009
chrMT	16571	12153	0.7334	0.9583
chrX	155270560	1704366	0.011	0.1271
chrY	59373566	94645	0.0016	0.0472

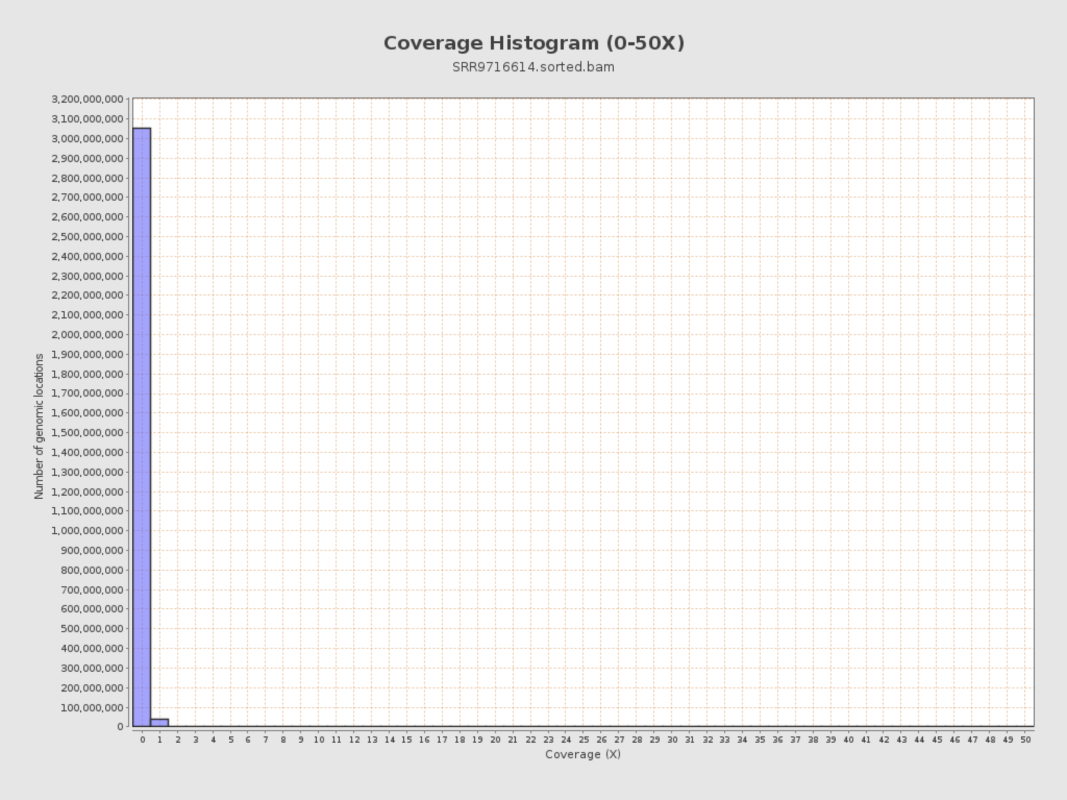
3. Results : Coverage across reference



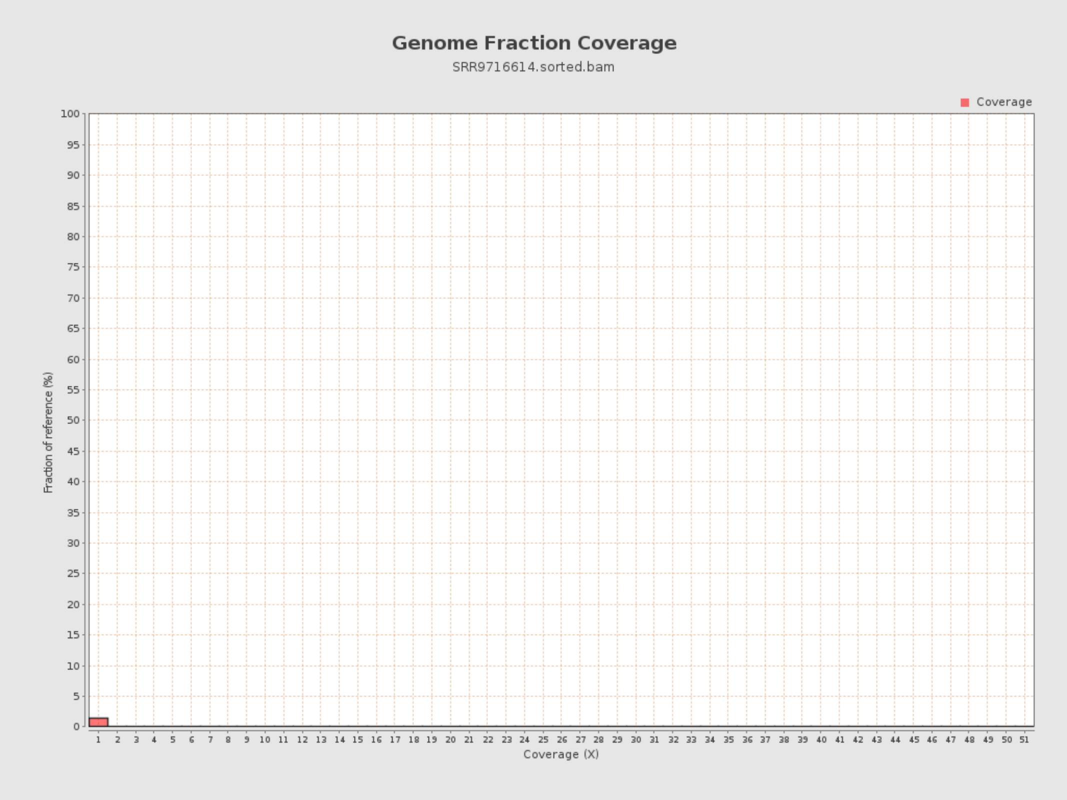
4. Results : Coverage Histogram



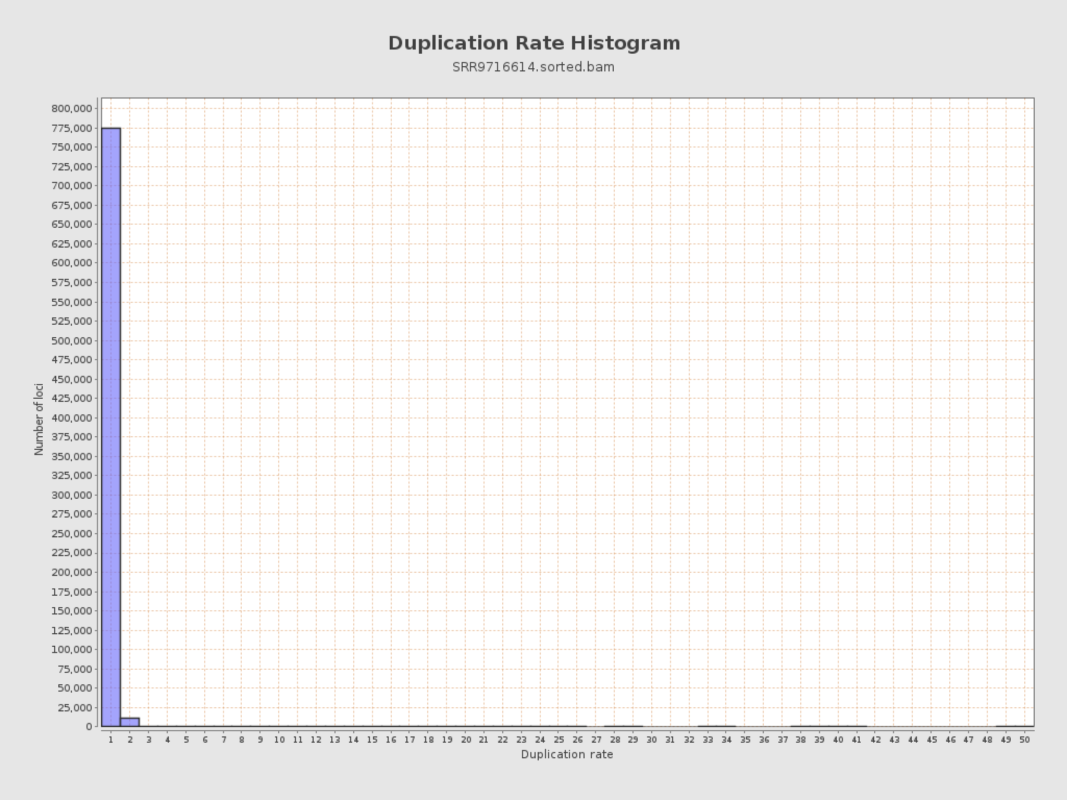
5. Results : Coverage Histogram (0-50X)



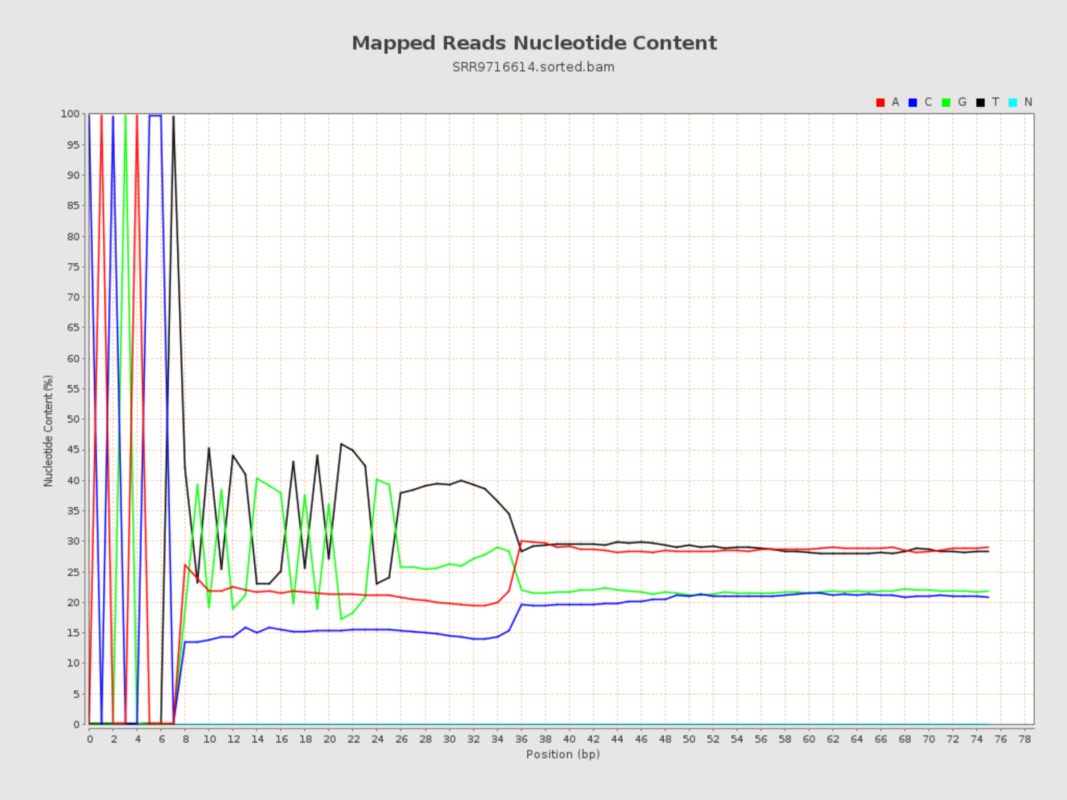
6. Results : Genome Fraction Coverage



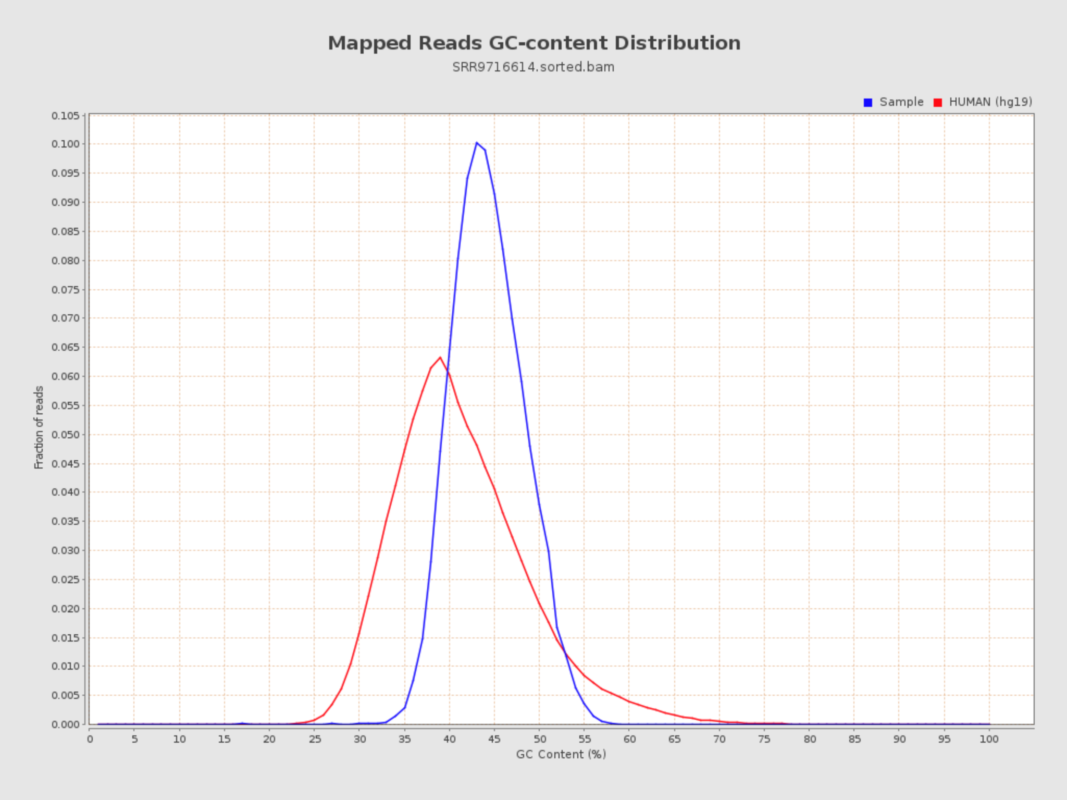
7. Results : Duplication Rate Histogram



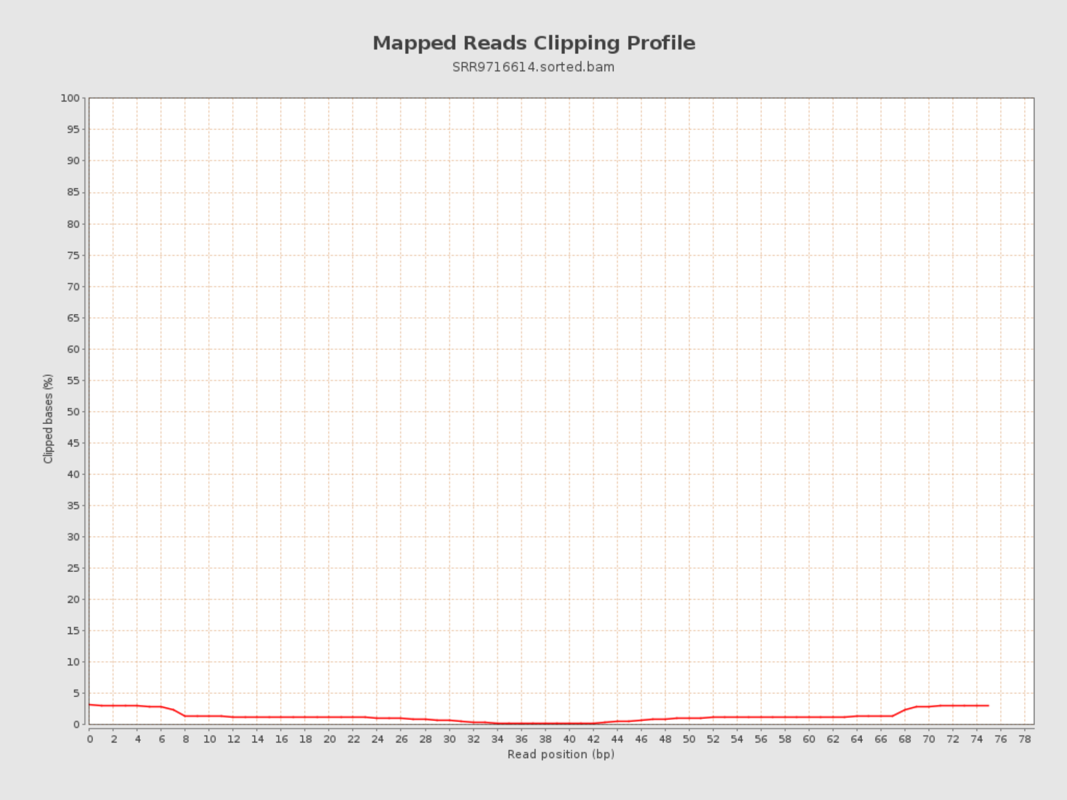
8. Results : Mapped Reads Nucleotide Content



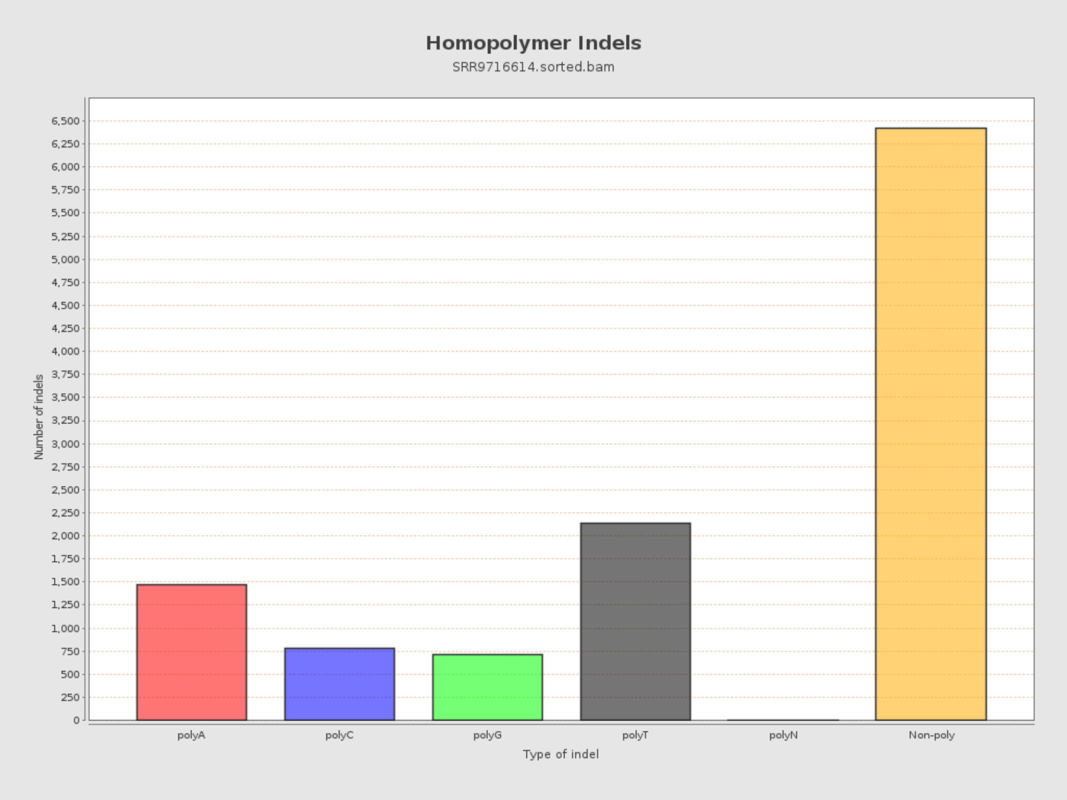
9. Results : Mapped Reads GC-content Distribution



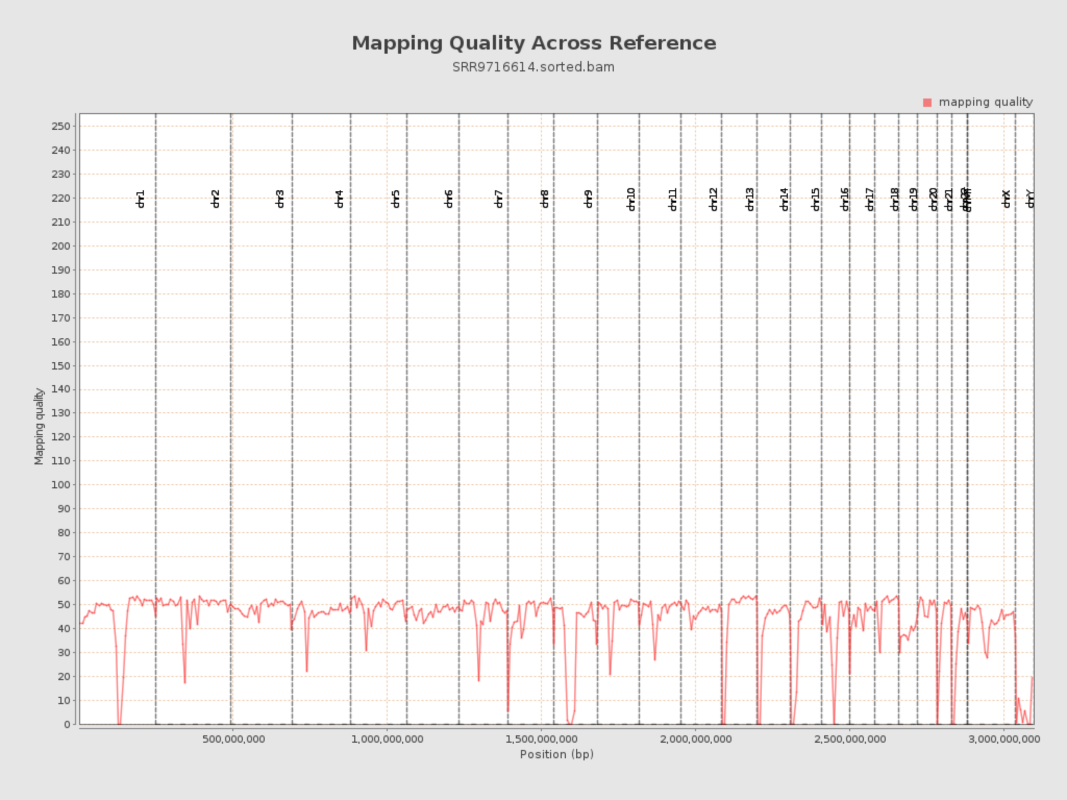
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram