Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 09:50:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716745.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_SRR9716745 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716745.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 09:50:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716745.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,227,059
Mapped reads	901,461 / 73.47%
Unmapped reads	325,598 / 26.53%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	939 / 0.08%
Read min/max/mean length	30 / 76 / 76.03
Duplicated reads (estimated)	77,400 / 6.31%
Duplication rate	7.41%
Clipped reads	901,869 / 73.5%

2.2. ACGT Content

Number/percentage of A's	9,931,955 / 21.18%
Number/percentage of C's	8,537,771 / 18.21%
Number/percentage of T's	15,376,169 / 32.79%
Number/percentage of G's	13,050,933 / 27.83%
Number/percentage of N's	869 / 0%
GC Percentage	46.03%

2.3. Coverage

Mean	0.0152

Standard Deviation	0.1634

2.4. Mapping Quality

Mean Mapping Quality	42.55

2.5. Mismatches and indels

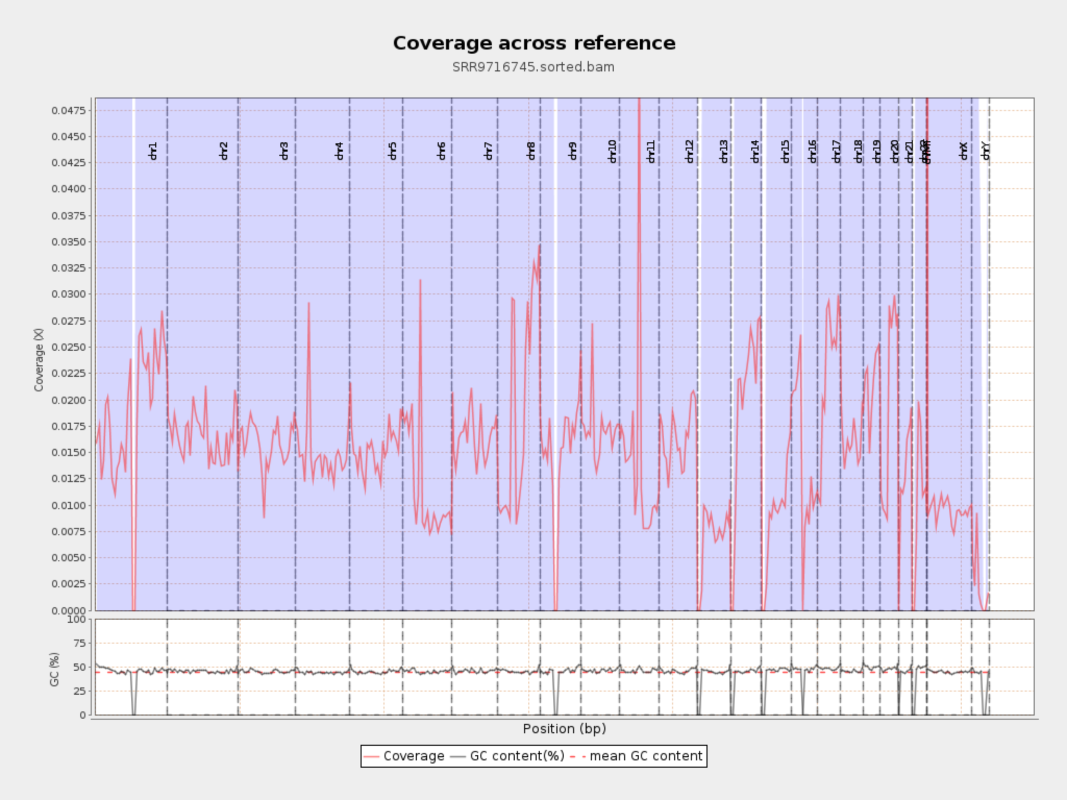
General error rate	0.69%
Mismatches	319,844
Insertions	2,382
Mapped reads with at least one insertion	0.26%
Deletions	6,894
Mapped reads with at least one deletion	0.76%
Homopolymer indels	39.86%

2.6. Chromosome stats

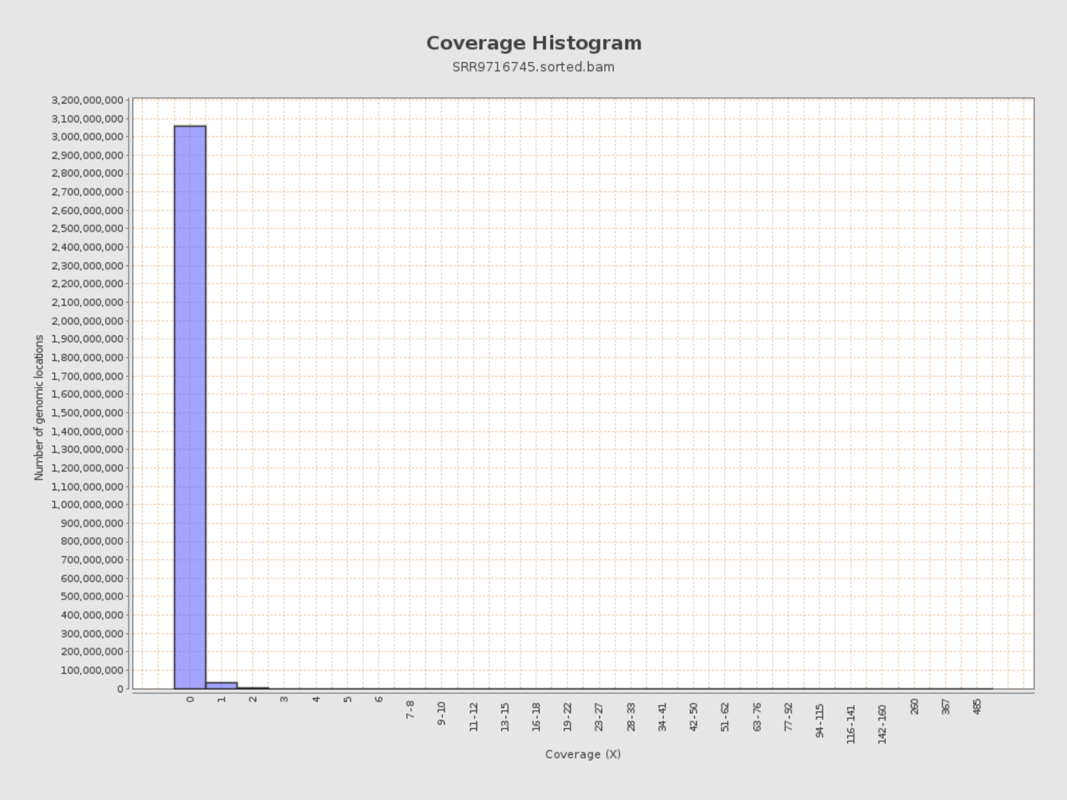
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4594670	0.0184	0.1894
chr2	243199373	4030633	0.0166	0.2464
chr3	198022430	3122396	0.0158	0.1468
chr4	191154276	2878720	0.0151	0.1502
chr5	180915260	2764299	0.0153	0.1427
chr6	171115067	2021353	0.0118	0.1453
chr7	159138663	2646992	0.0166	0.1707

chr8	146364022	2828621	0.0193	0.1658
chr9	141213431	2042657	0.0145	0.1471
chr10	135534747	2337274	0.0172	0.176
chr11	135006516	1954778	0.0145	0.1524
chr12	133851895	2210866	0.0165	0.1509
chr13	115169878	790303	0.0069	0.0957
chr14	107349540	2098025	0.0195	0.1651
chr15	102531392	906249	0.0088	0.1095
chr16	90354753	1261446	0.014	0.1528
chr17	81195210	1842112	0.0227	0.1836
chr18	78077248	1250309	0.016	0.1682
chr19	59128983	1270797	0.0215	0.203
chr20	63025520	1239802	0.0197	0.1714
chr21	48129895	629429	0.0131	0.1402
chr22	51304566	535563	0.0104	0.1228
chrMT	16571	31152	1.8799	1.9742
chrX	155270560	1475617	0.0095	0.1163
chrY	59373566	145480	0.0025	0.0795

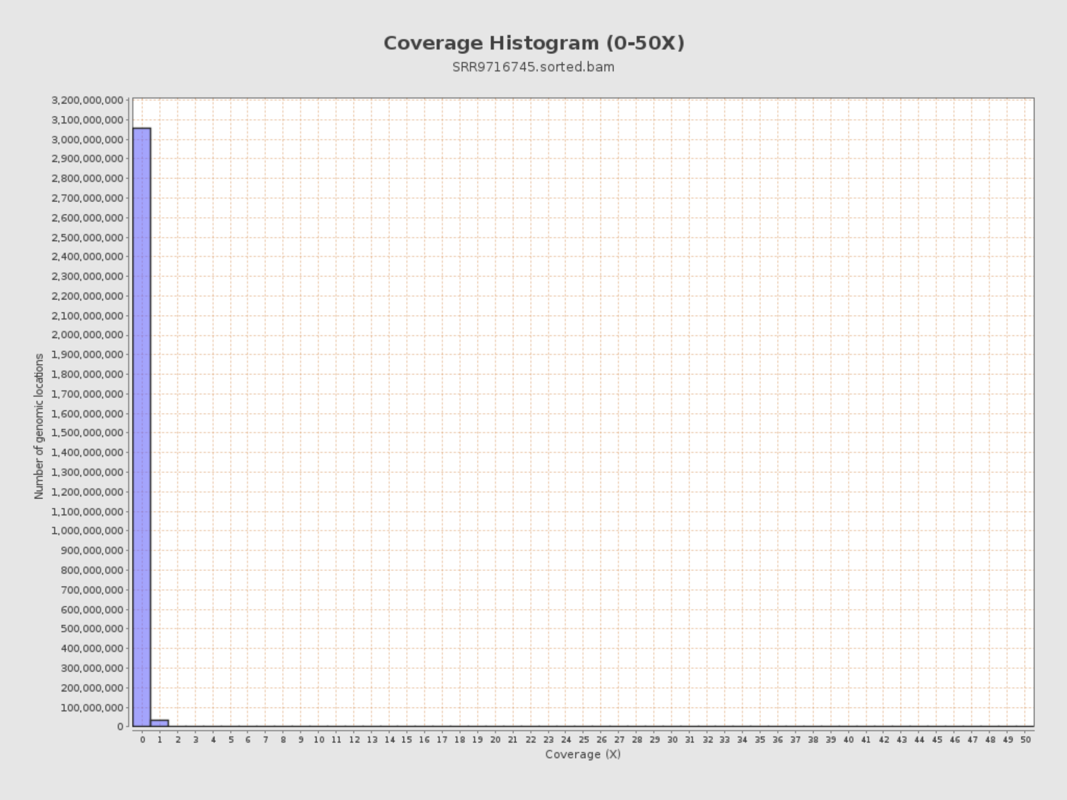
3. Results : Coverage across reference



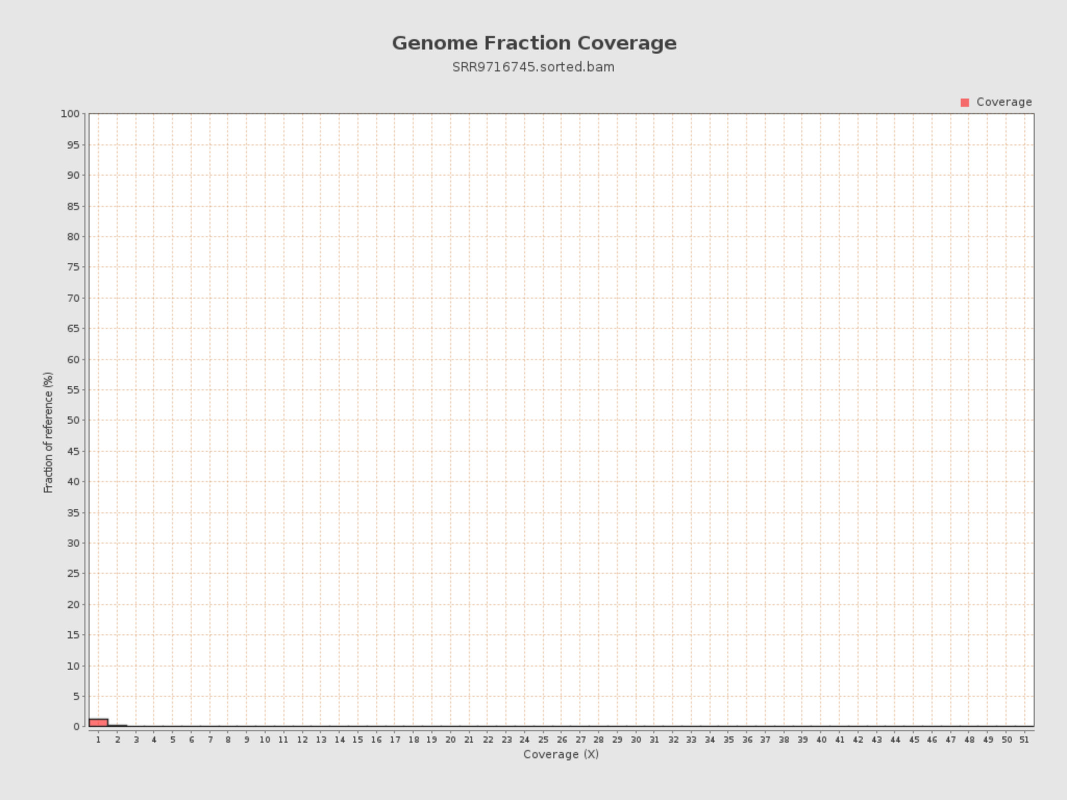
4. Results : Coverage Histogram



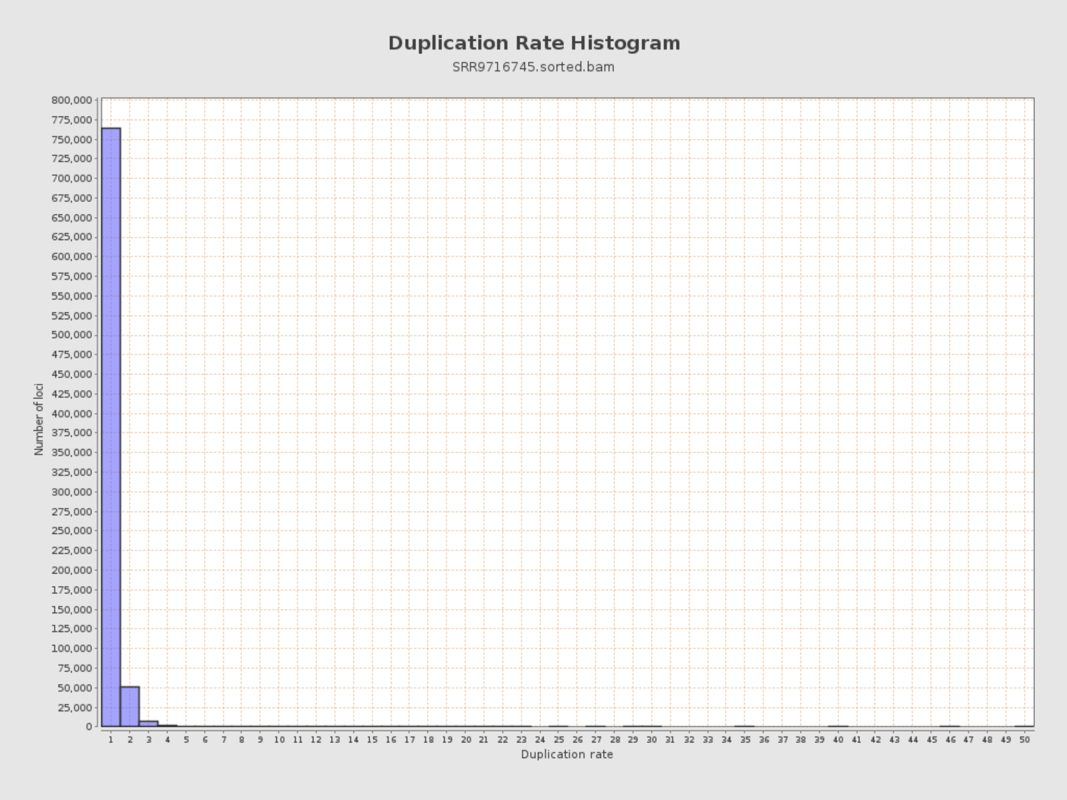
5. Results : Coverage Histogram (0-50X)



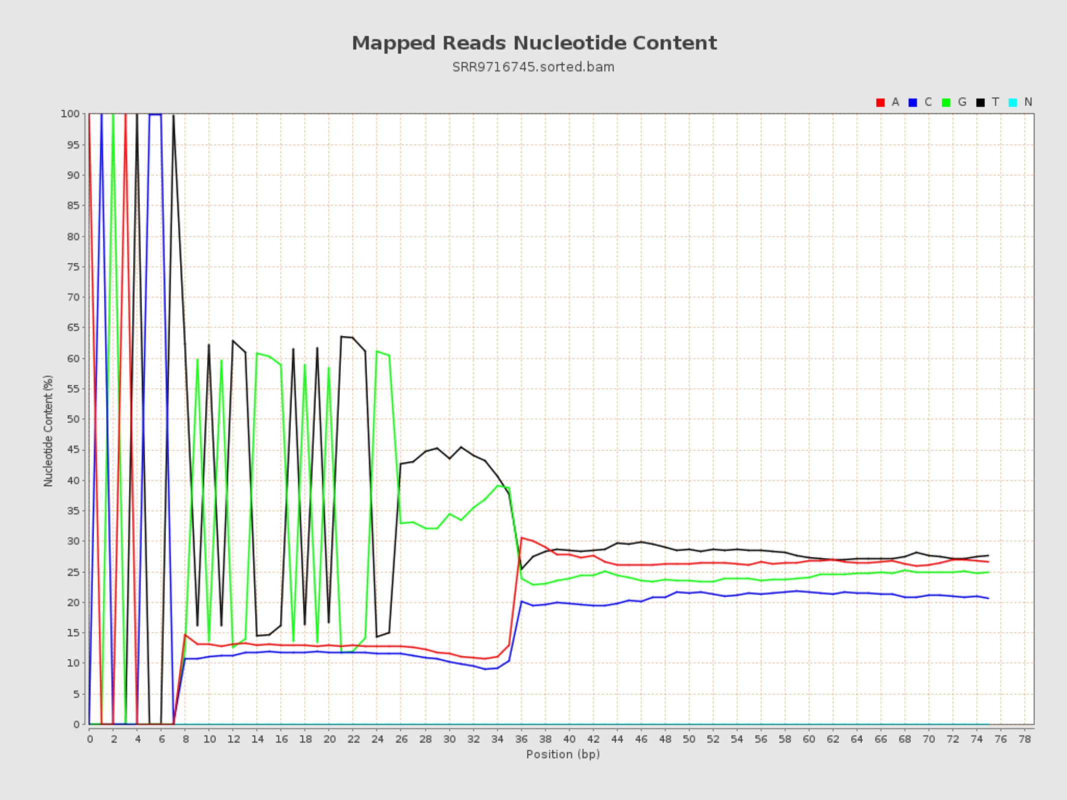
6. Results : Genome Fraction Coverage



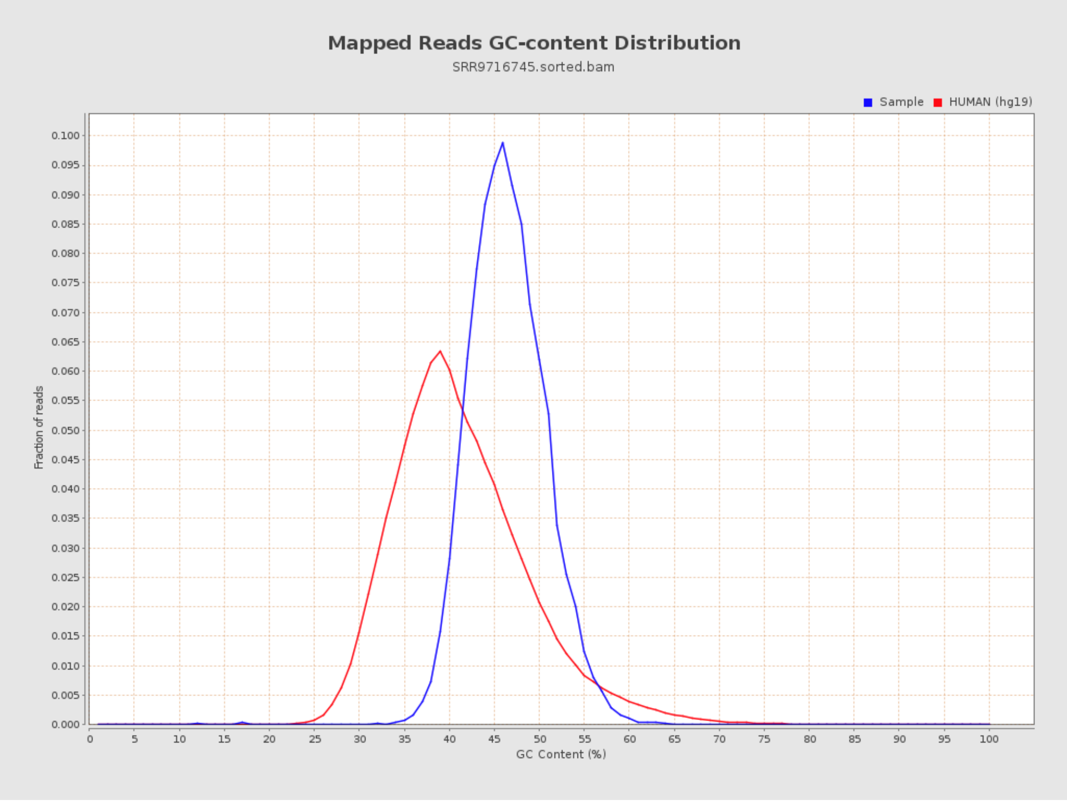
7. Results : Duplication Rate Histogram



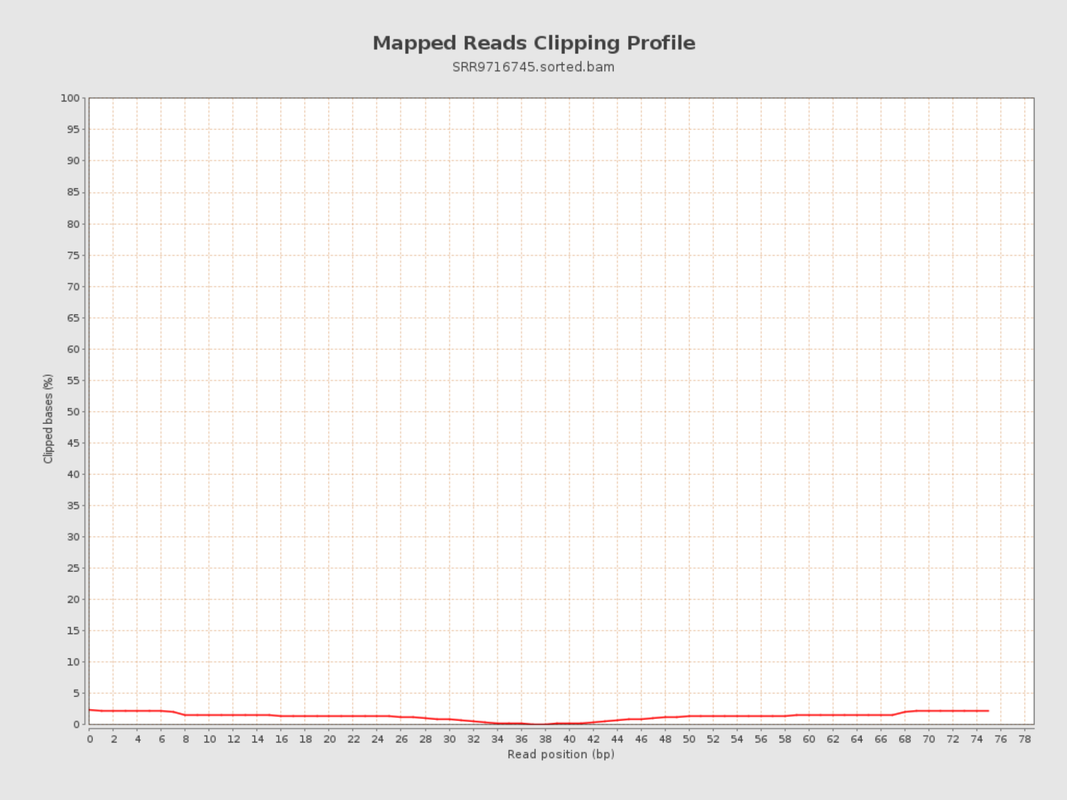
8. Results : Mapped Reads Nucleotide Content



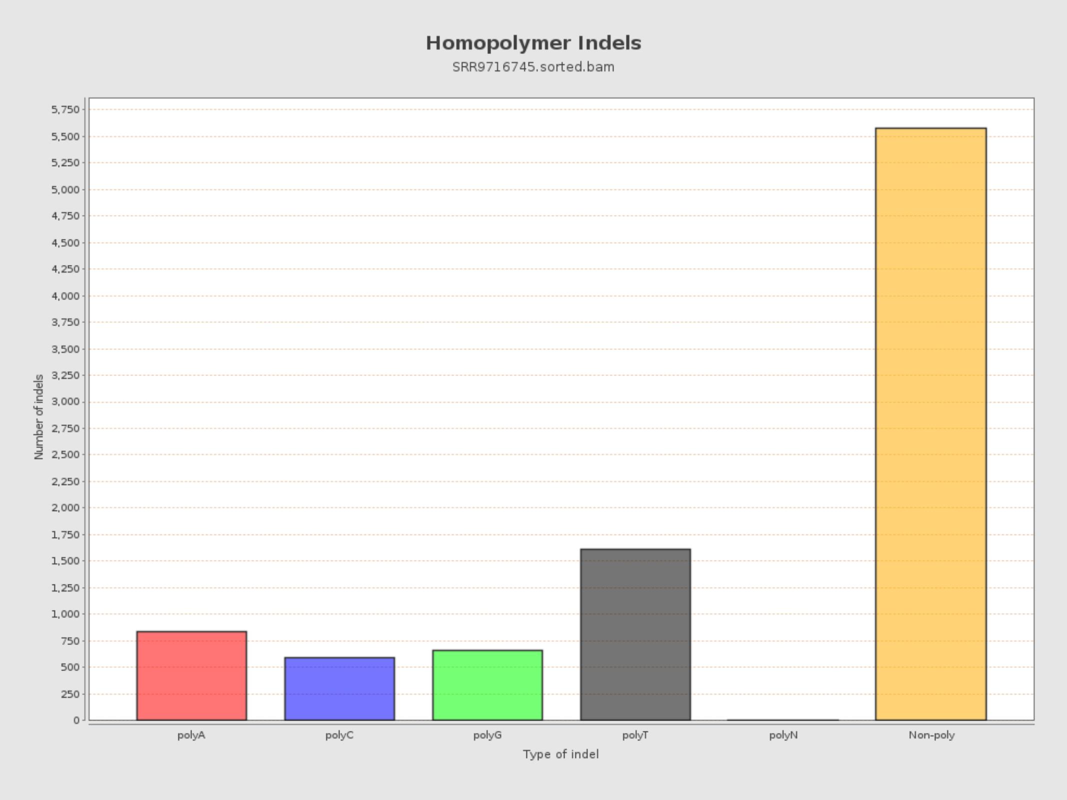
9. Results : Mapped Reads GC-content Distribution



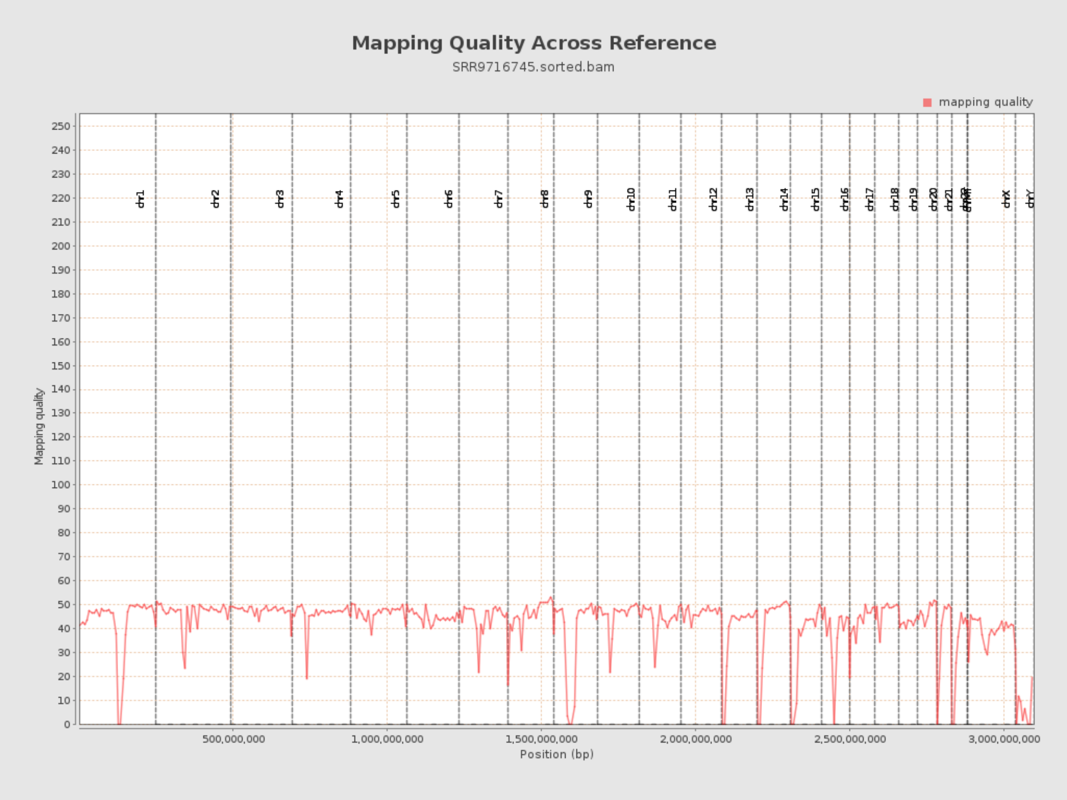
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram