Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 22:53:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716580.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_SRR9716580 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716580.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 22:53:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716580.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,207,614
Mapped reads	1,077,718 / 89.24%
Unmapped reads	129,896 / 10.76%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,909 / 0.49%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	30,776 / 2.55%
Duplication rate	2%
Clipped reads	1,080,797 / 89.5%

2.2. ACGT Content

Number/percentage of A's	16,110,565 / 25.68%
Number/percentage of C's	12,005,221 / 19.13%
Number/percentage of T's	19,866,192 / 31.66%
Number/percentage of G's	14,757,210 / 23.52%
Number/percentage of N's	839 / 0%
GC Percentage	42.66%

2.3. Coverage

Mean	0.0203

Standard Deviation	0.2207

2.4. Mapping Quality

Mean Mapping Quality	44.5

2.5. Mismatches and indels

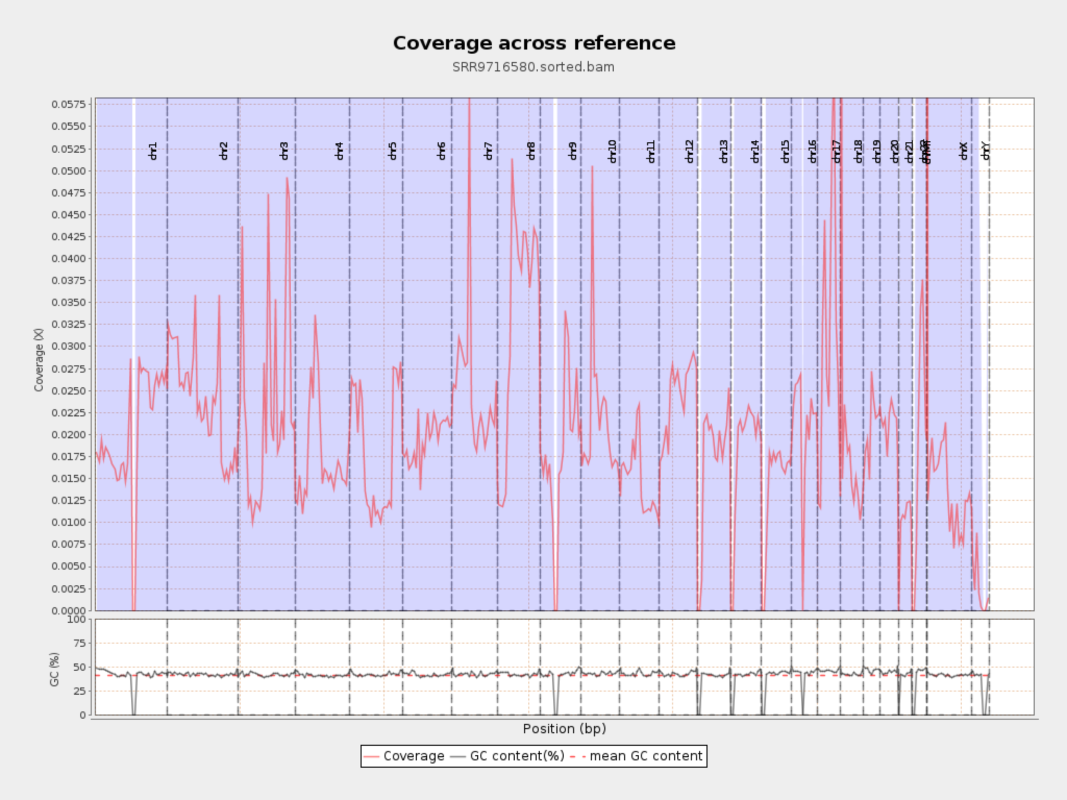
General error rate	0.51%
Mismatches	309,849
Insertions	4,898
Mapped reads with at least one insertion	0.45%
Deletions	11,826
Mapped reads with at least one deletion	1.09%
Homopolymer indels	41.26%

2.6. Chromosome stats

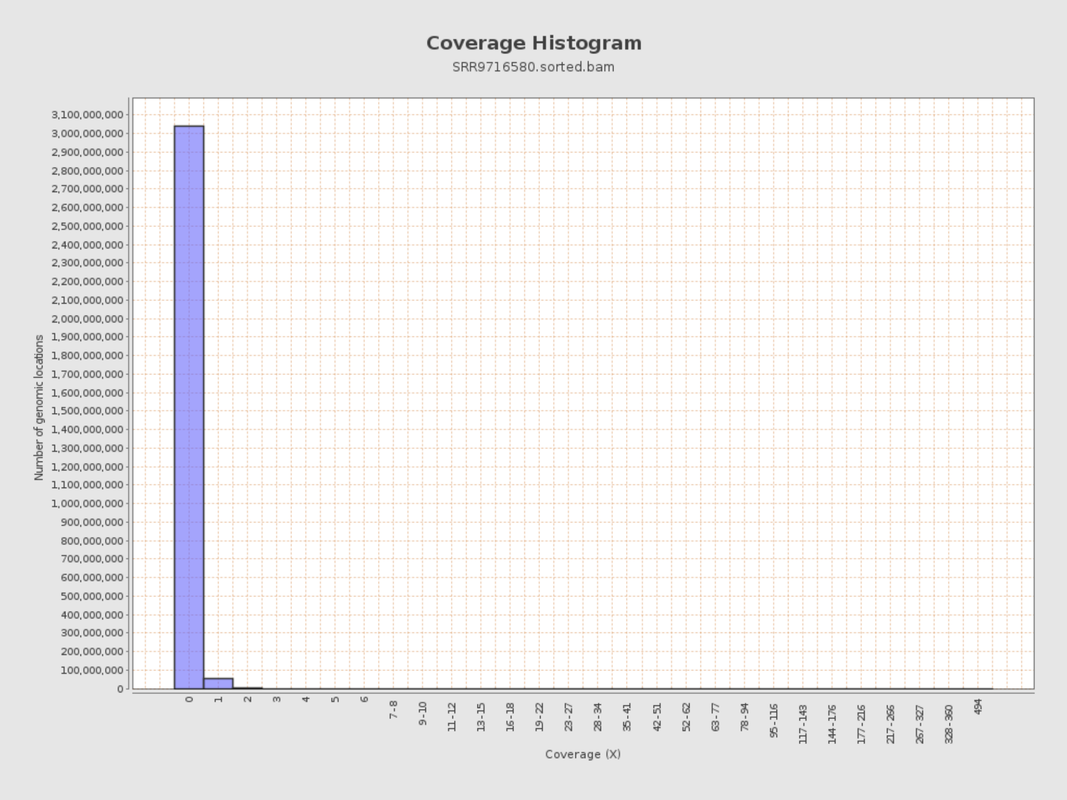
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4992340	0.02	0.295
chr2	243199373	5852437	0.0241	0.2658
chr3	198022430	4602979	0.0232	0.1649
chr4	191154276	3344050	0.0175	0.1553
chr5	180915260	3237660	0.0179	0.1421
chr6	171115067	3328670	0.0195	0.1556
chr7	159138663	4060219	0.0255	0.4913

chr8	146364022	4985676	0.0341	0.2407
chr9	141213431	2502496	0.0177	0.1549
chr10	135534747	2919985	0.0215	0.2565
chr11	135006516	2032337	0.0151	0.1498
chr12	133851895	3257640	0.0243	0.1732
chr13	115169878	1951541	0.0169	0.1377
chr14	107349540	1929650	0.018	0.1432
chr15	102531392	1428522	0.0139	0.1261
chr16	90354753	1865952	0.0207	0.1571
chr17	81195210	2566428	0.0316	0.1955
chr18	78077248	1442832	0.0185	0.2277
chr19	59128983	1231519	0.0208	0.2621
chr20	63025520	1346523	0.0214	0.1598
chr21	48129895	485979	0.0101	0.1171
chr22	51304566	980556	0.0191	0.1464
chrMT	16571	143755	8.6751	5.5326
chrX	155270560	2121276	0.0137	0.1358
chrY	59373566	147853	0.0025	0.083

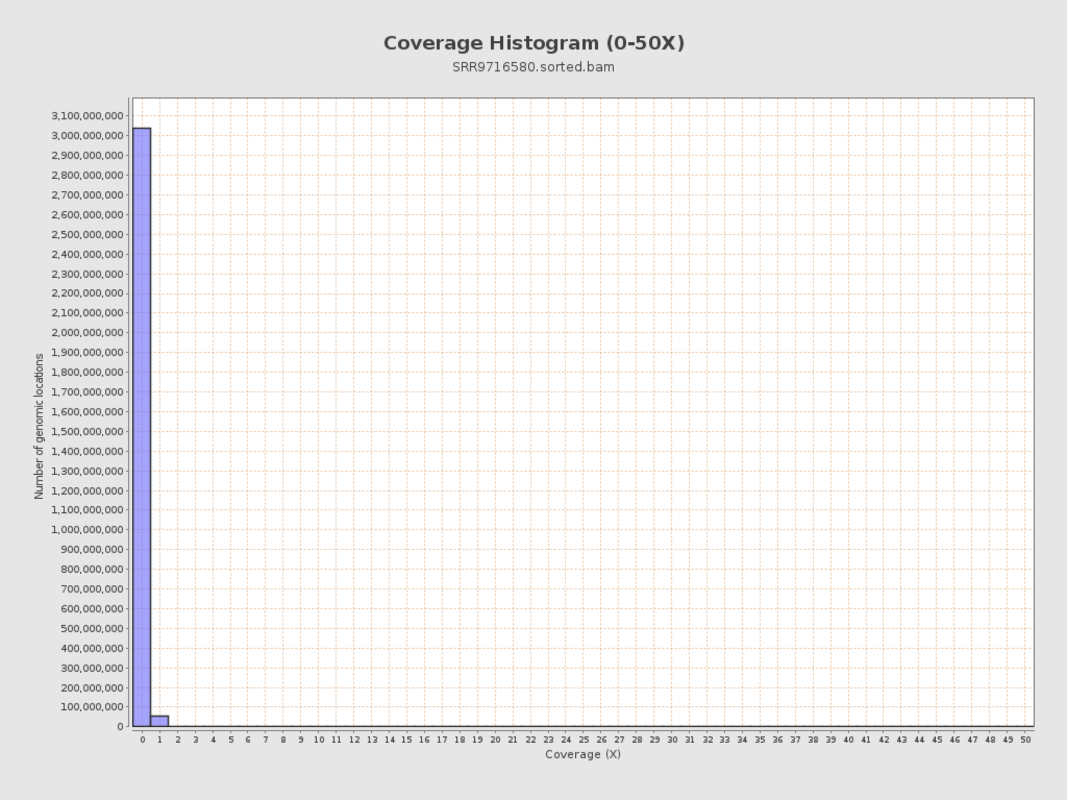
3. Results : Coverage across reference



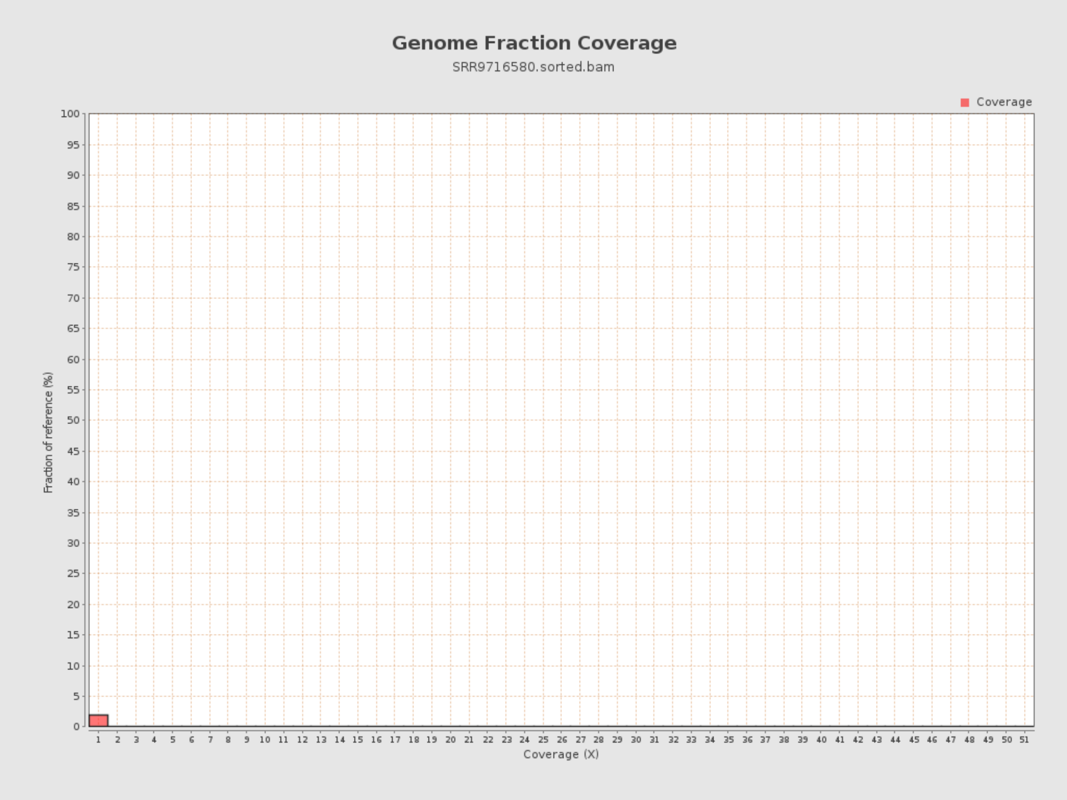
4. Results : Coverage Histogram



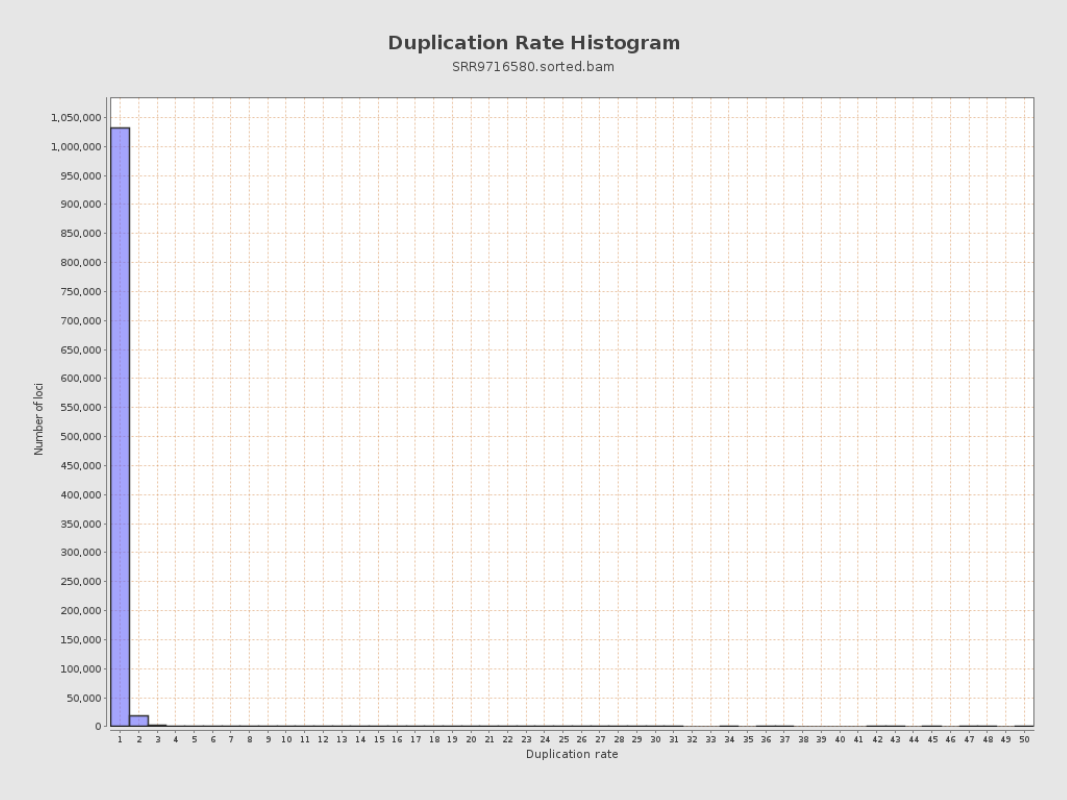
5. Results : Coverage Histogram (0-50X)



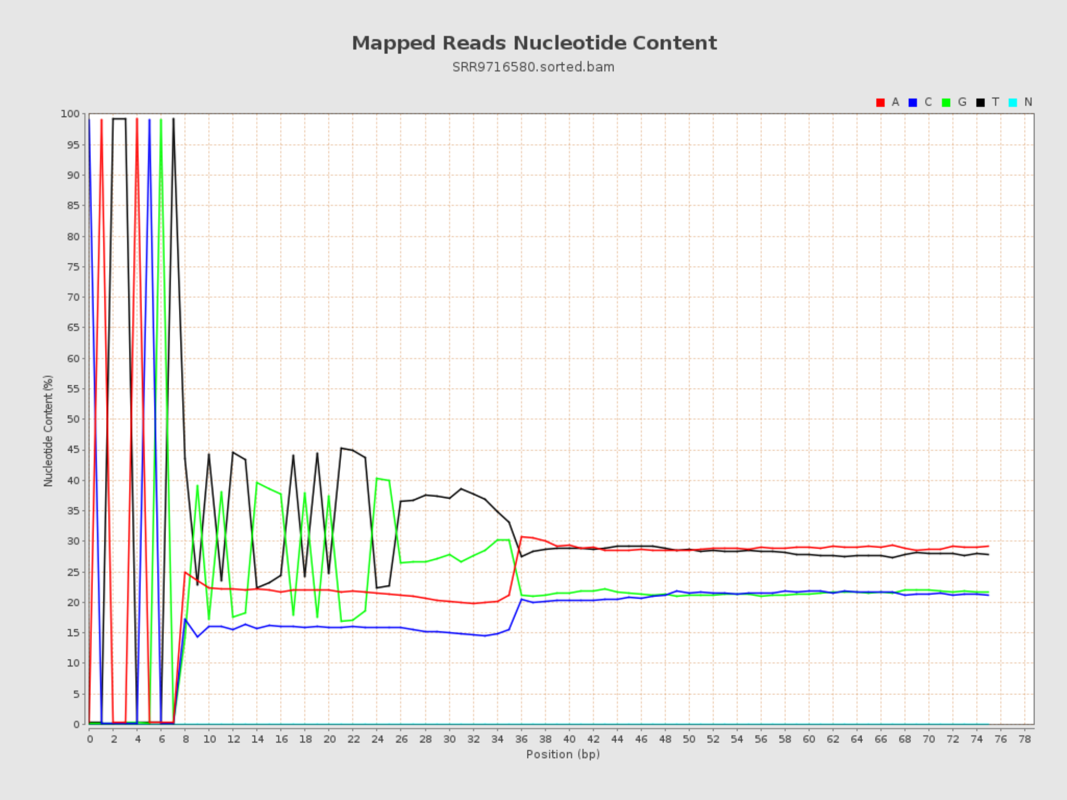
6. Results : Genome Fraction Coverage



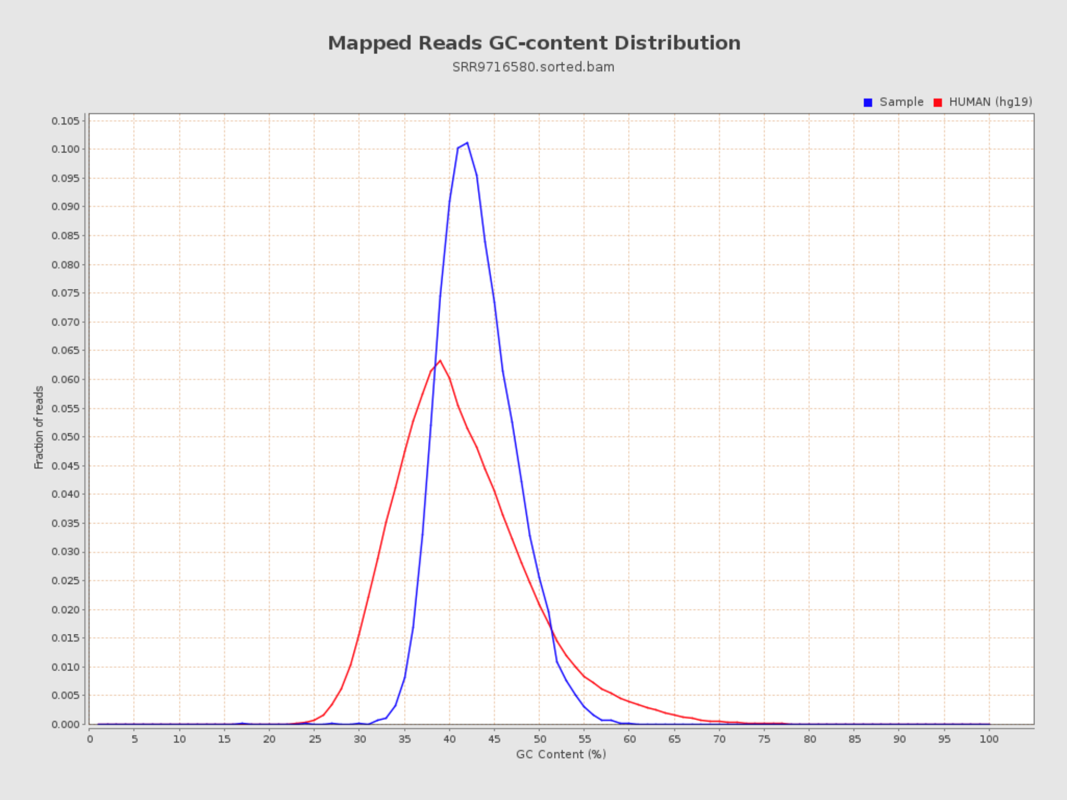
7. Results : Duplication Rate Histogram



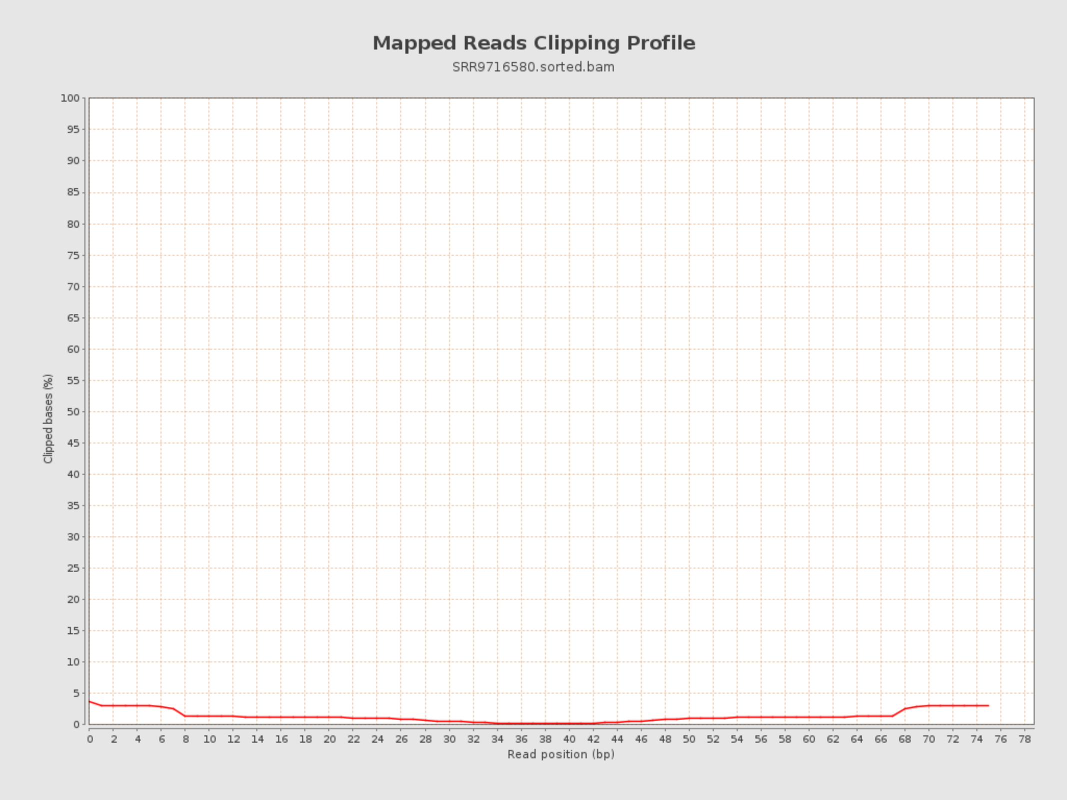
8. Results : Mapped Reads Nucleotide Content



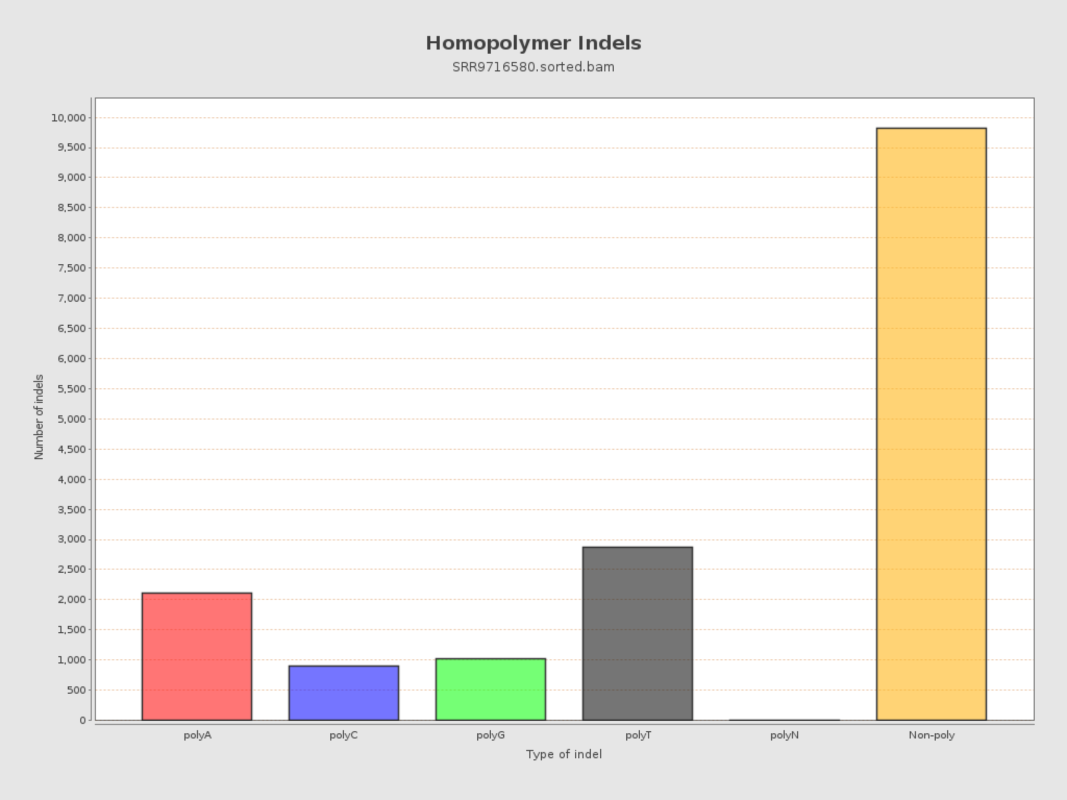
9. Results : Mapped Reads GC-content Distribution



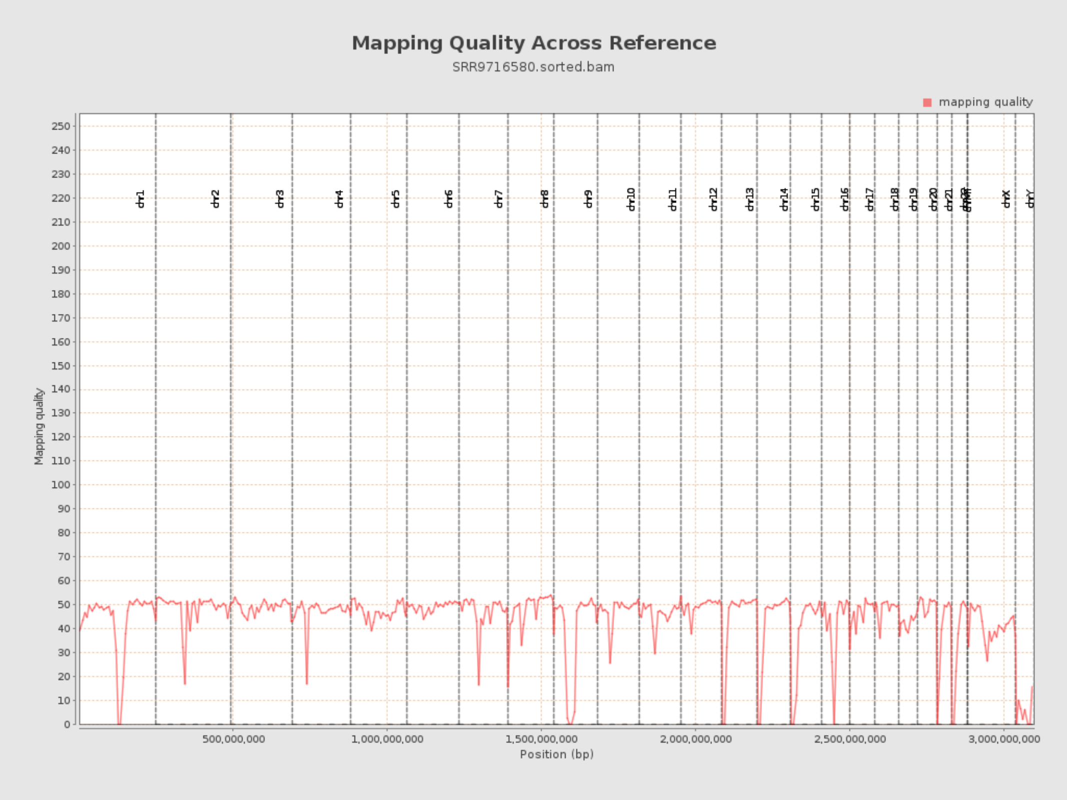
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram