Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 22:35:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716180.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_SRR9716180 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716180.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 22:35:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716180.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,198,523
Mapped reads	1,024,212 / 85.46%
Unmapped reads	174,311 / 14.54%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,954 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	24,823 / 2.07%
Duplication rate	1.84%
Clipped reads	1,024,394 / 85.47%

2.2. ACGT Content

Number/percentage of A's	16,040,096 / 26.89%
Number/percentage of C's	11,180,058 / 18.74%
Number/percentage of T's	18,237,861 / 30.57%
Number/percentage of G's	14,200,914 / 23.8%
Number/percentage of N's	463 / 0%
GC Percentage	42.54%

2.3. Coverage

Mean	0.0193

Standard Deviation	0.1796

2.4. Mapping Quality

Mean Mapping Quality	44.73

2.5. Mismatches and indels

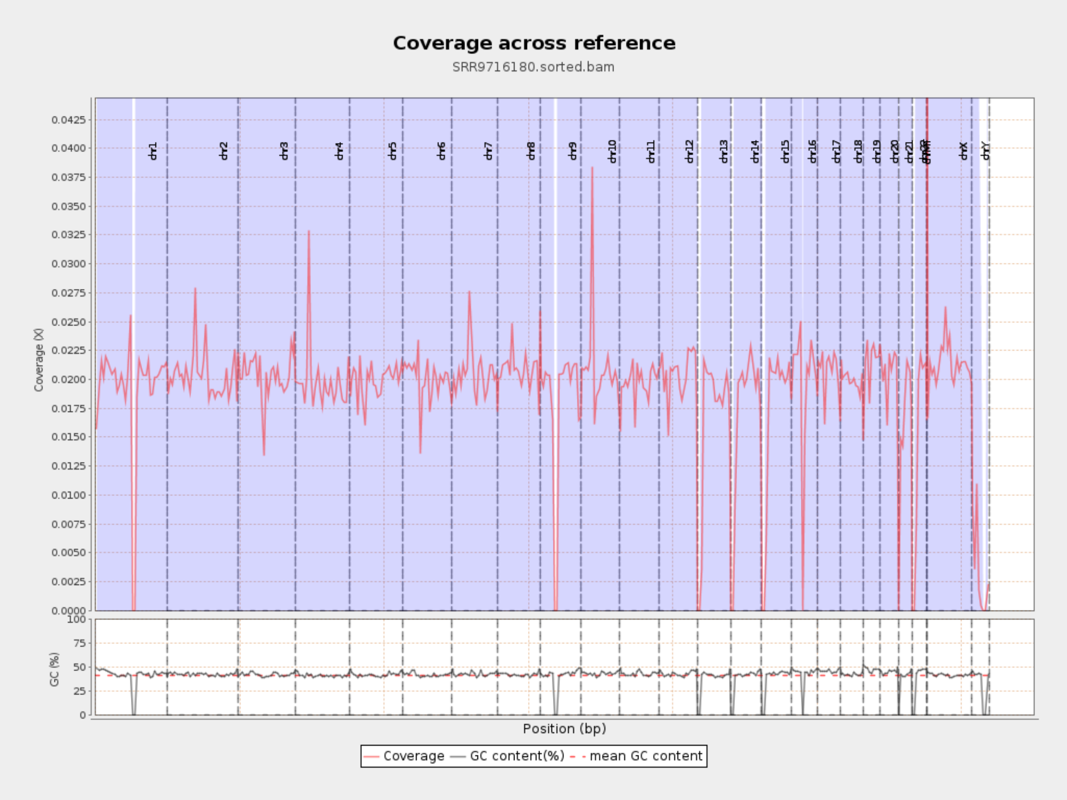
General error rate	0.52%
Mismatches	301,903
Insertions	4,895
Mapped reads with at least one insertion	0.48%
Deletions	10,967
Mapped reads with at least one deletion	1.06%
Homopolymer indels	40.3%

2.6. Chromosome stats

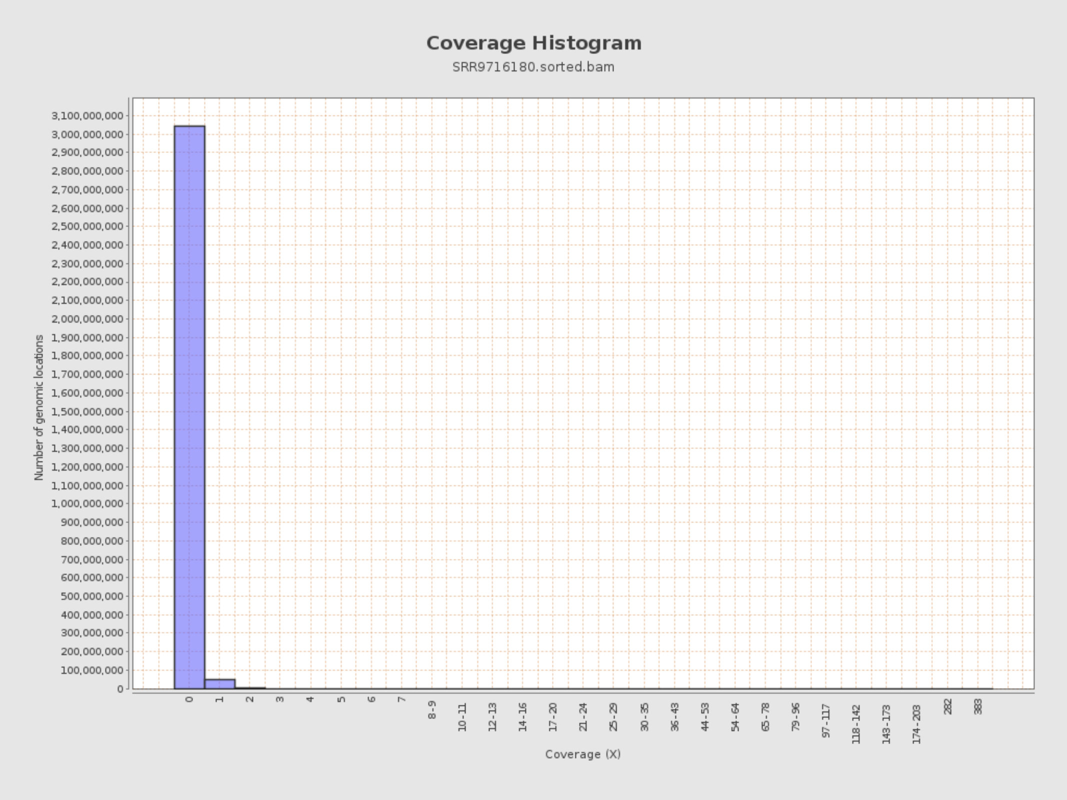
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4763435	0.0191	0.2225
chr2	243199373	4942219	0.0203	0.2324
chr3	198022430	4022613	0.0203	0.1527
chr4	191154276	3792958	0.0198	0.1632
chr5	180915260	3616585	0.02	0.1511
chr6	171115067	3422135	0.02	0.1618
chr7	159138663	3283496	0.0206	0.2153

chr8	146364022	3043709	0.0208	0.193
chr9	141213431	2529422	0.0179	0.1616
chr10	135534747	2868499	0.0212	0.2143
chr11	135006516	2667412	0.0198	0.1715
chr12	133851895	2740501	0.0205	0.1546
chr13	115169878	1872708	0.0163	0.1372
chr14	107349540	1811722	0.0169	0.1444
chr15	102531392	1716280	0.0167	0.1403
chr16	90354753	1751144	0.0194	0.1572
chr17	81195210	1678731	0.0207	0.1579
chr18	78077248	1553690	0.0199	0.2438
chr19	59128983	1270922	0.0215	0.2101
chr20	63025520	1288214	0.0204	0.1553
chr21	48129895	783574	0.0163	0.1451
chr22	51304566	744801	0.0145	0.1298
chrMT	16571	2032	0.1226	0.4291
chrX	155270560	3317568	0.0214	0.1628
chrY	59373566	192528	0.0032	0.1032

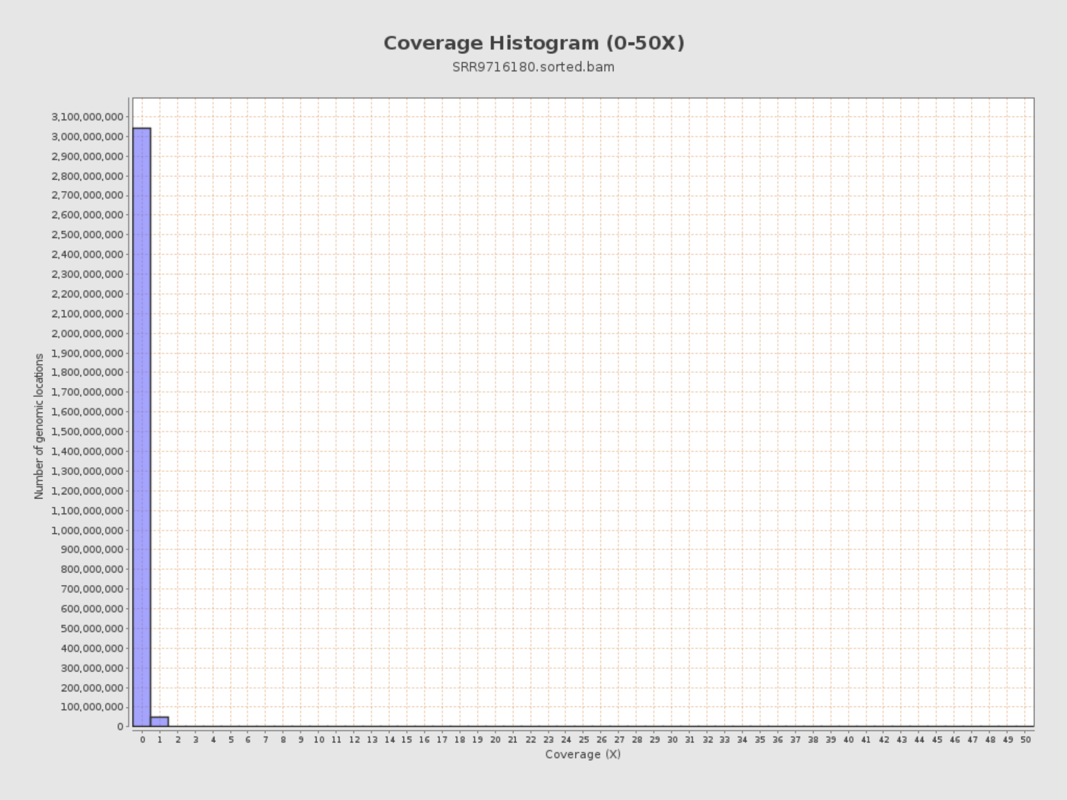
3. Results : Coverage across reference



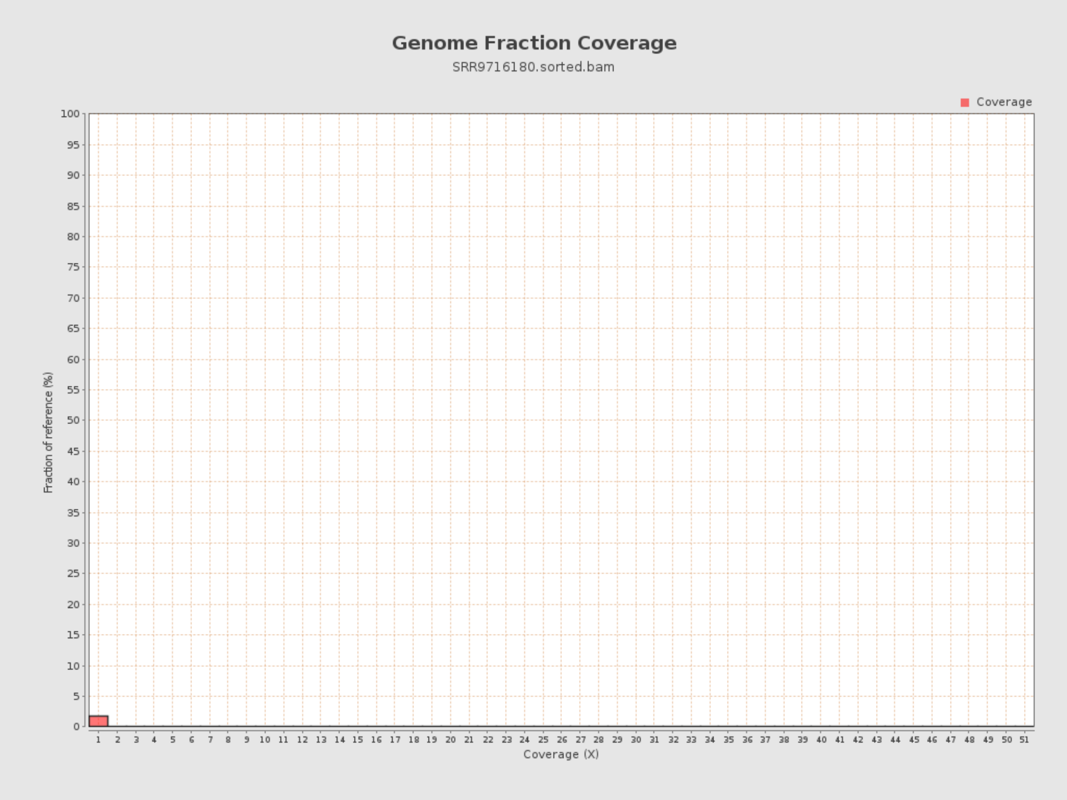
4. Results : Coverage Histogram



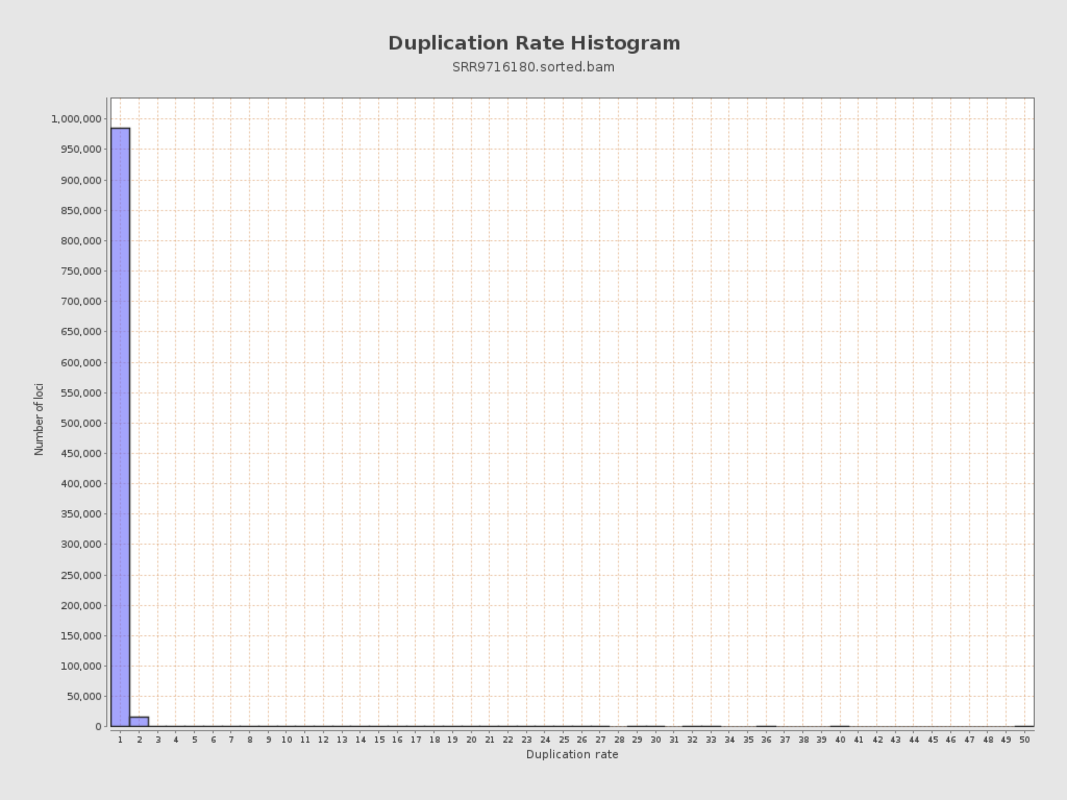
5. Results : Coverage Histogram (0-50X)



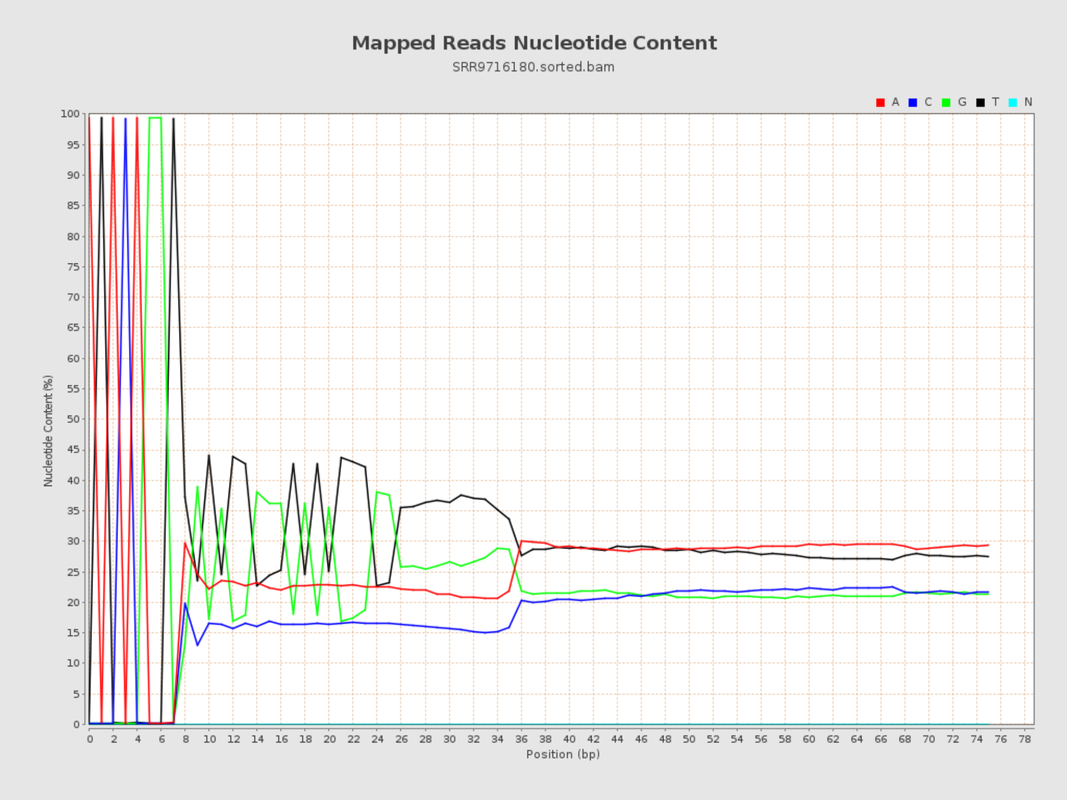
6. Results : Genome Fraction Coverage



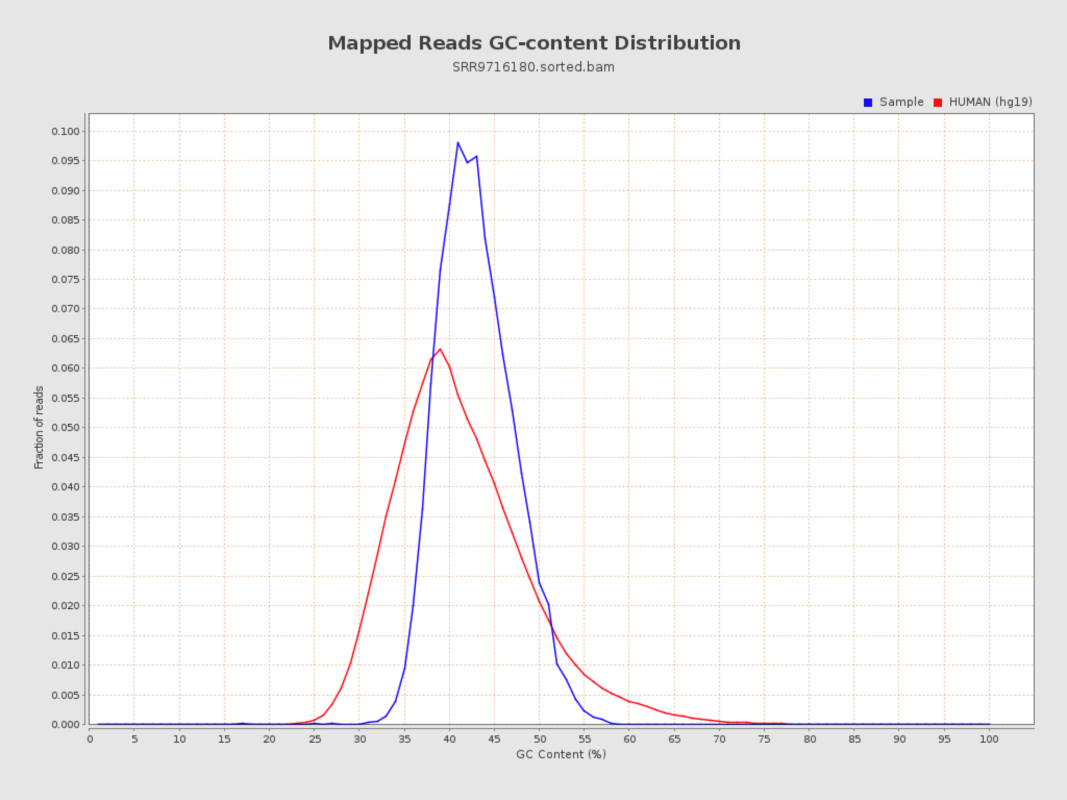
7. Results : Duplication Rate Histogram



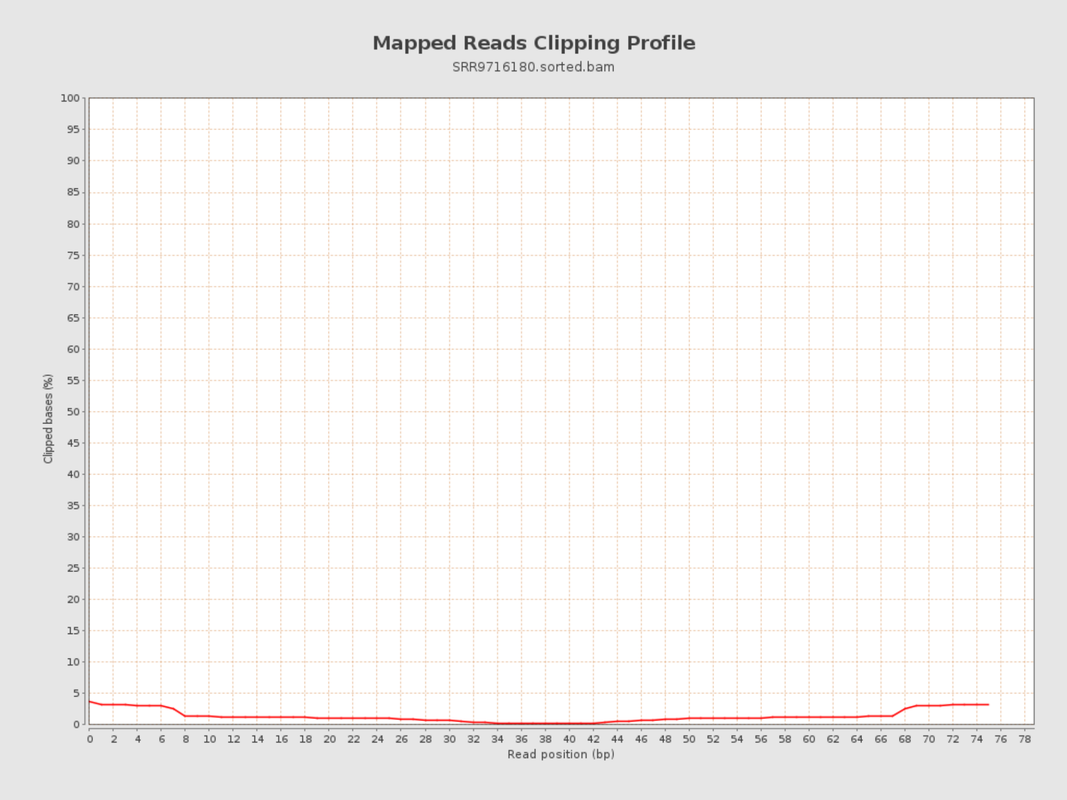
8. Results : Mapped Reads Nucleotide Content



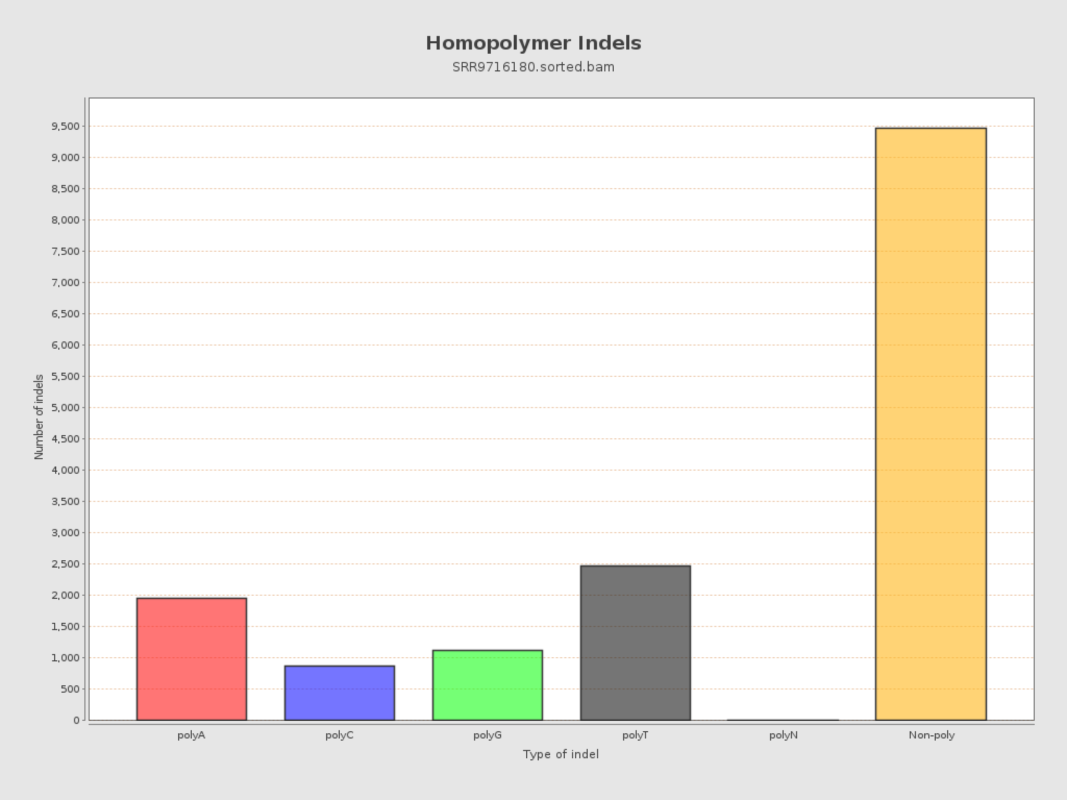
9. Results : Mapped Reads GC-content Distribution



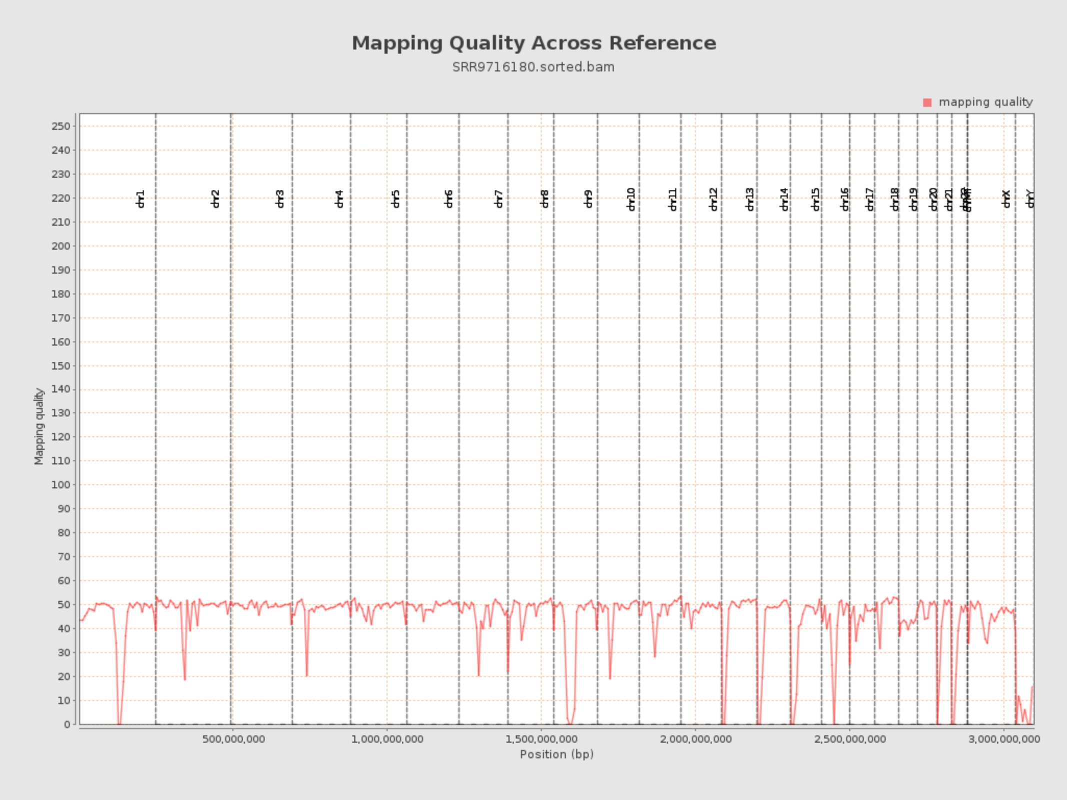
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram