Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 18:18:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716520.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_SRR9716520 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716520.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 18:18:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716520.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,196,222
Mapped reads	1,079,525 / 90.24%
Unmapped reads	116,697 / 9.76%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,182 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	37,285 / 3.12%
Duplication rate	2.71%
Clipped reads	1,080,442 / 90.32%

2.2. ACGT Content

Number/percentage of A's	16,116,895 / 25.74%
Number/percentage of C's	11,702,511 / 18.69%
Number/percentage of T's	20,164,627 / 32.21%
Number/percentage of G's	14,626,706 / 23.36%
Number/percentage of N's	1,728 / 0%
GC Percentage	42.05%

2.3. Coverage

Mean	0.0202

Standard Deviation	0.204

2.4. Mapping Quality

Mean Mapping Quality	45.35

2.5. Mismatches and indels

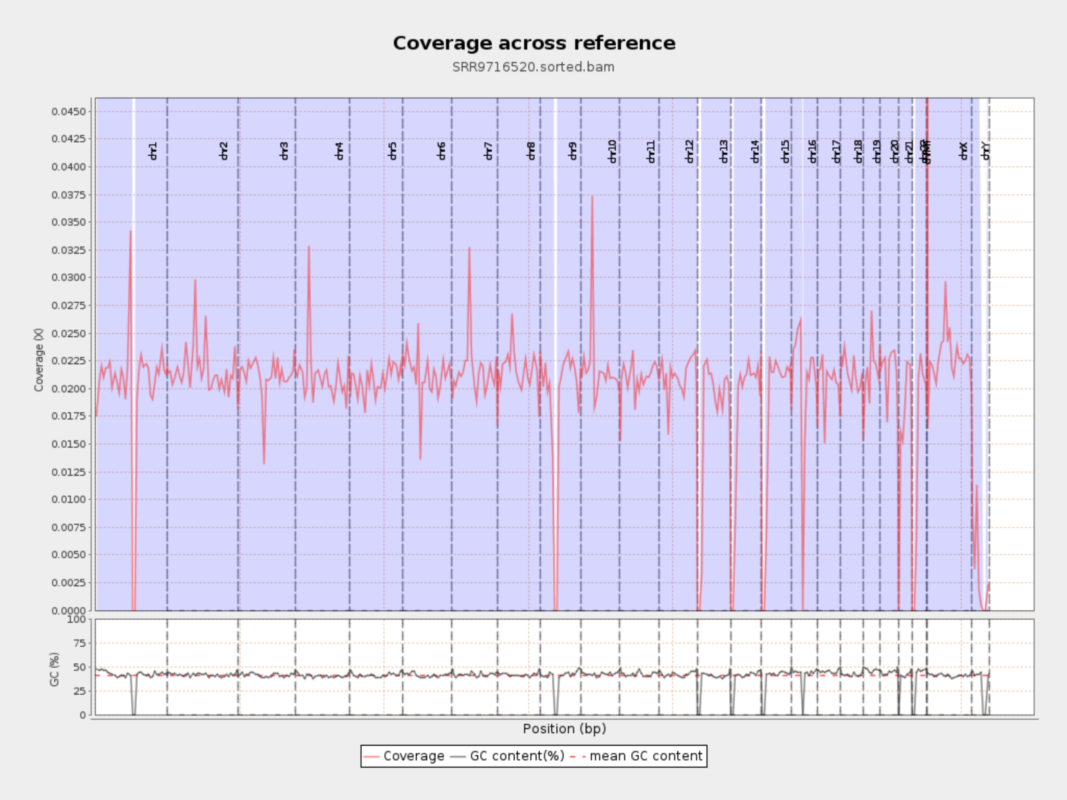
General error rate	0.52%
Mismatches	318,243
Insertions	4,441
Mapped reads with at least one insertion	0.41%
Deletions	11,915
Mapped reads with at least one deletion	1.1%
Homopolymer indels	42.35%

2.6. Chromosome stats

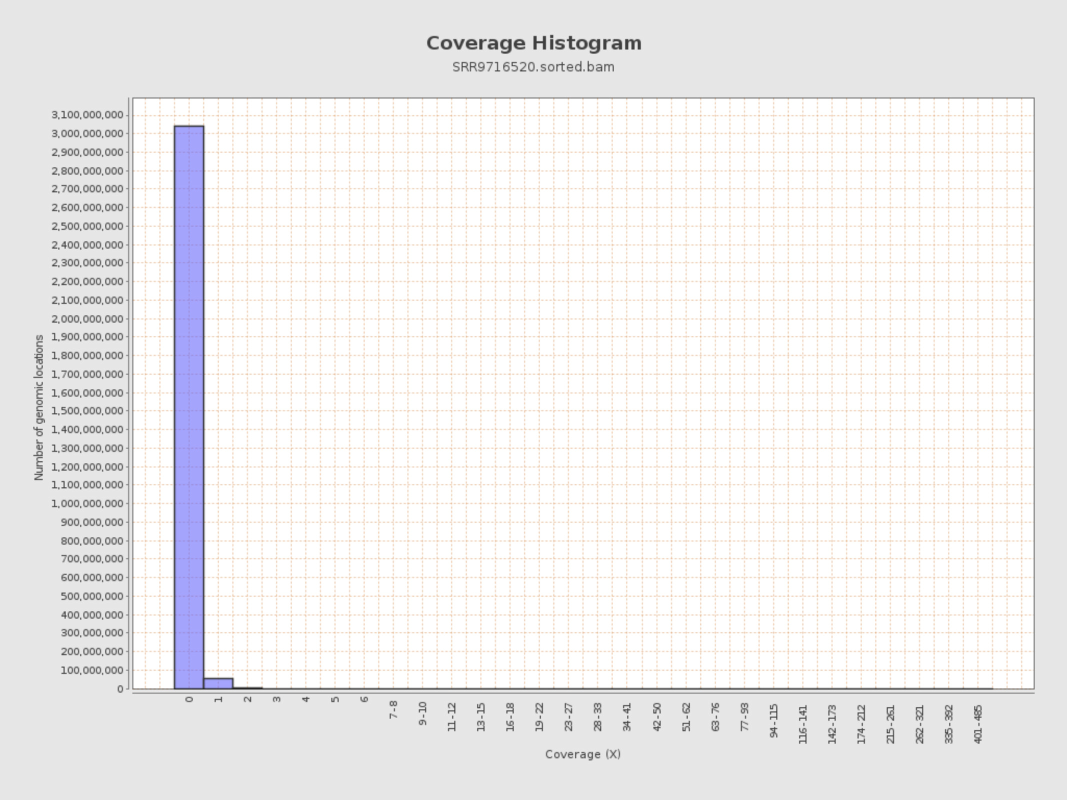
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5034858	0.0202	0.3487
chr2	243199373	5285174	0.0217	0.2604
chr3	198022430	4173854	0.0211	0.1564
chr4	191154276	4055657	0.0212	0.168
chr5	180915260	3773889	0.0209	0.1568
chr6	171115067	3635826	0.0212	0.1748
chr7	159138663	3465153	0.0218	0.2359

chr8	146364022	3183936	0.0218	0.1967
chr9	141213431	2623207	0.0186	0.1726
chr10	135534747	2980074	0.022	0.2067
chr11	135006516	2844212	0.0211	0.1824
chr12	133851895	2829275	0.0211	0.1581
chr13	115169878	1953776	0.017	0.1396
chr14	107349540	1871416	0.0174	0.145
chr15	102531392	1799153	0.0175	0.1428
chr16	90354753	1816327	0.0201	0.1592
chr17	81195210	1673228	0.0206	0.1597
chr18	78077248	1668070	0.0214	0.28
chr19	59128983	1283361	0.0217	0.2501
chr20	63025520	1363547	0.0216	0.1623
chr21	48129895	823572	0.0171	0.1512
chr22	51304566	748481	0.0146	0.1298
chrMT	16571	5191	0.3133	0.6188
chrX	155270560	3544080	0.0228	0.1761
chrY	59373566	196000	0.0033	0.0963

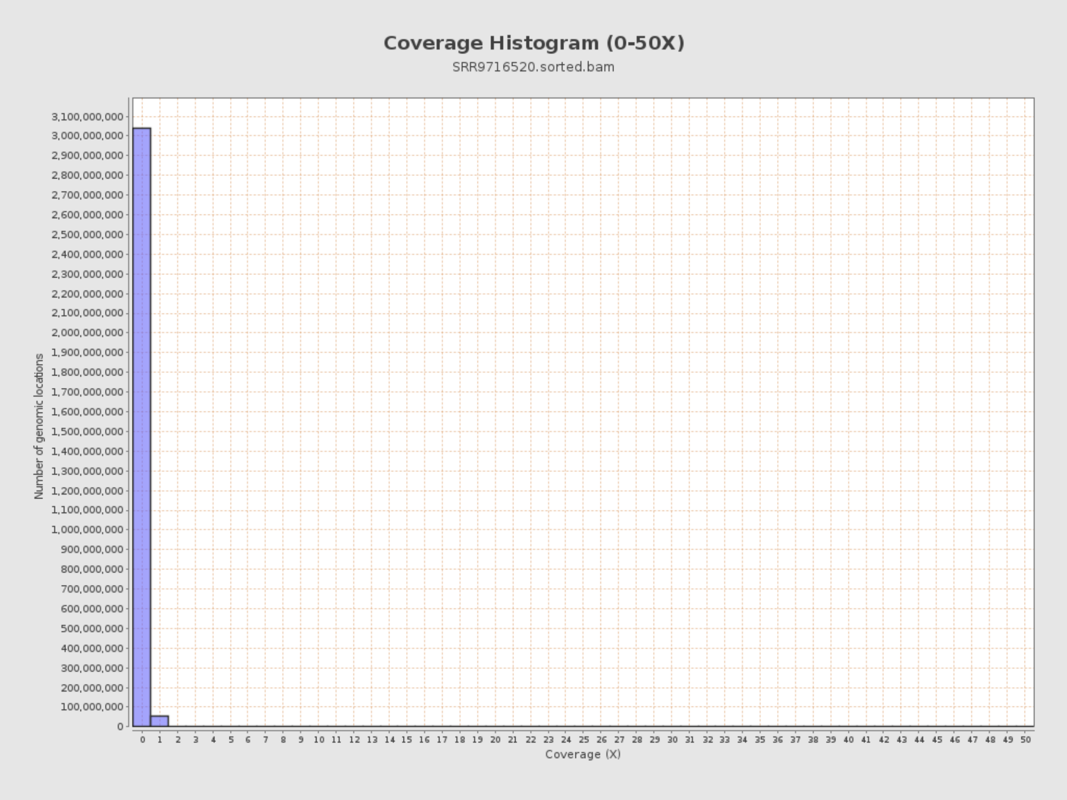
3. Results : Coverage across reference



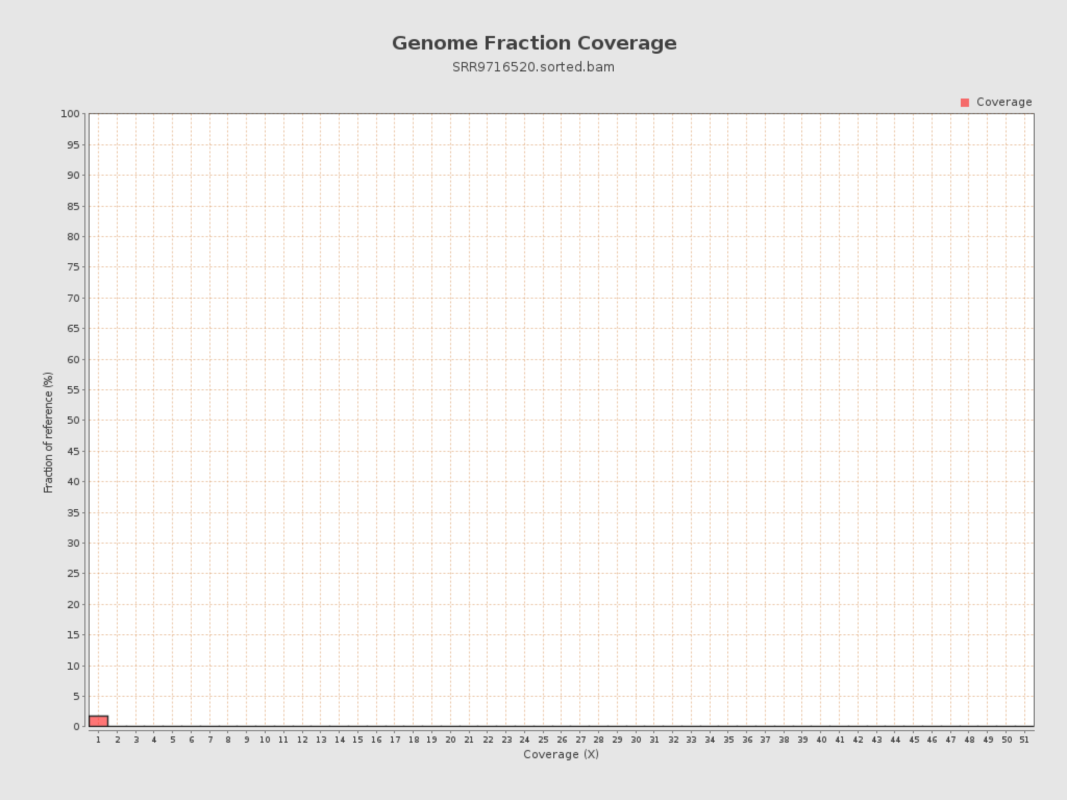
4. Results : Coverage Histogram



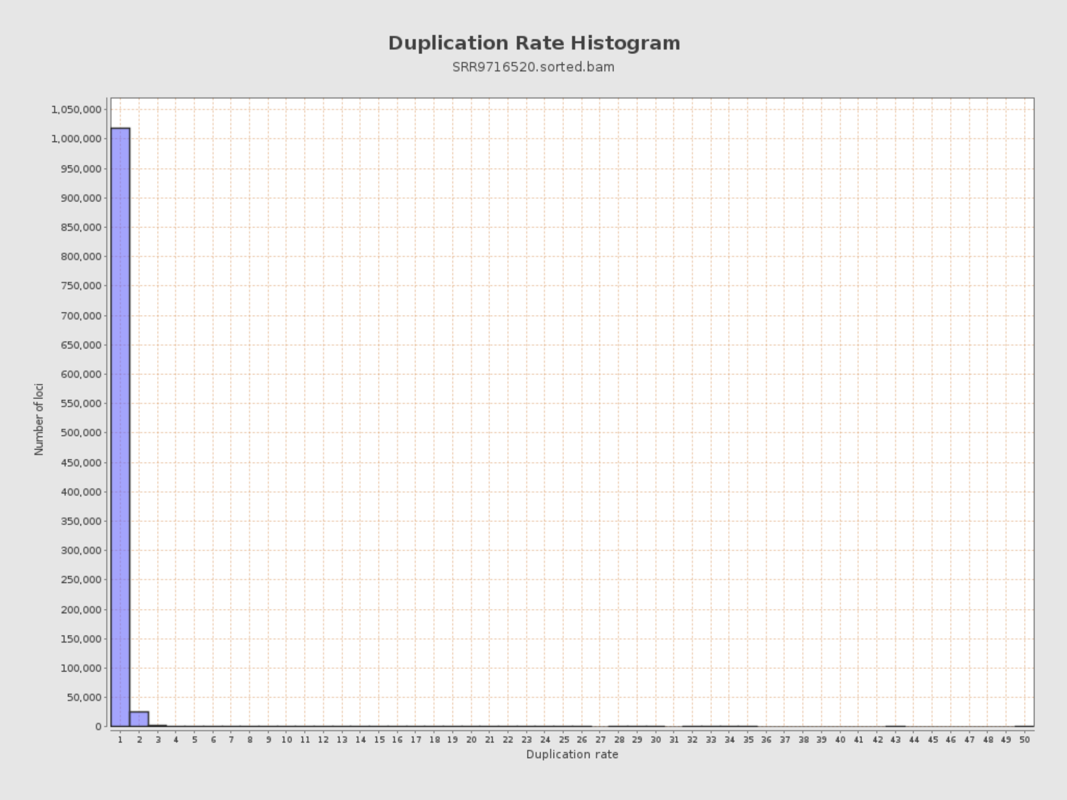
5. Results : Coverage Histogram (0-50X)



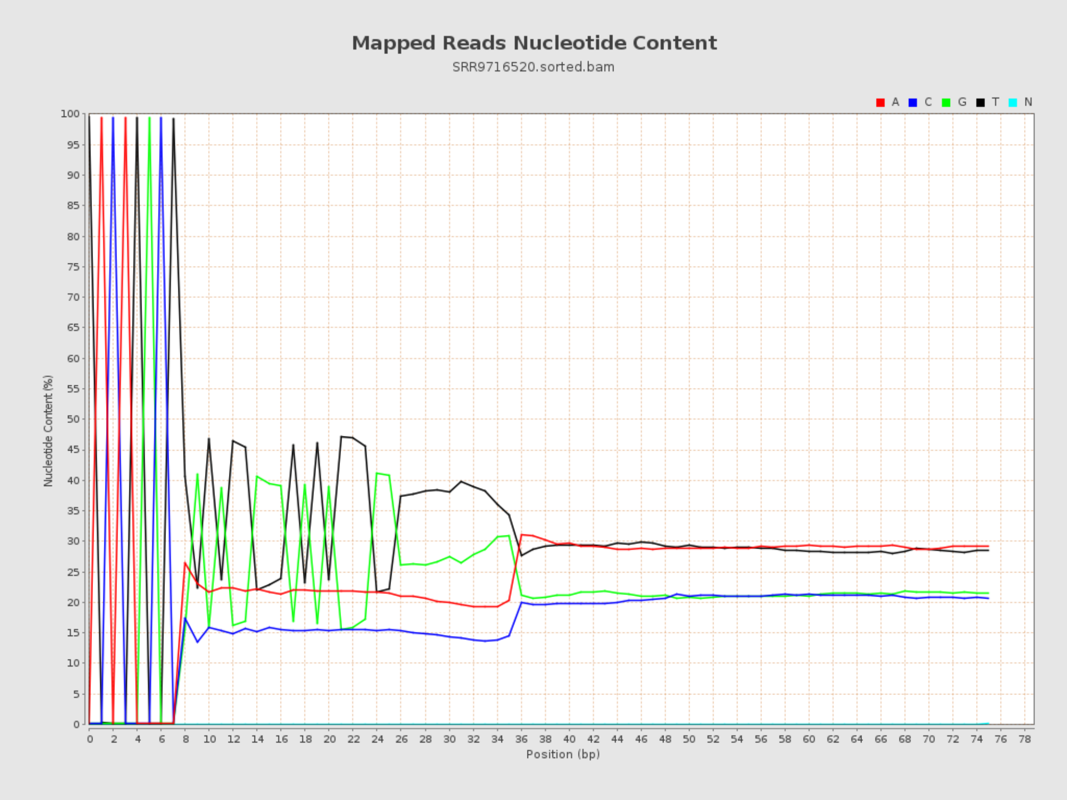
6. Results : Genome Fraction Coverage



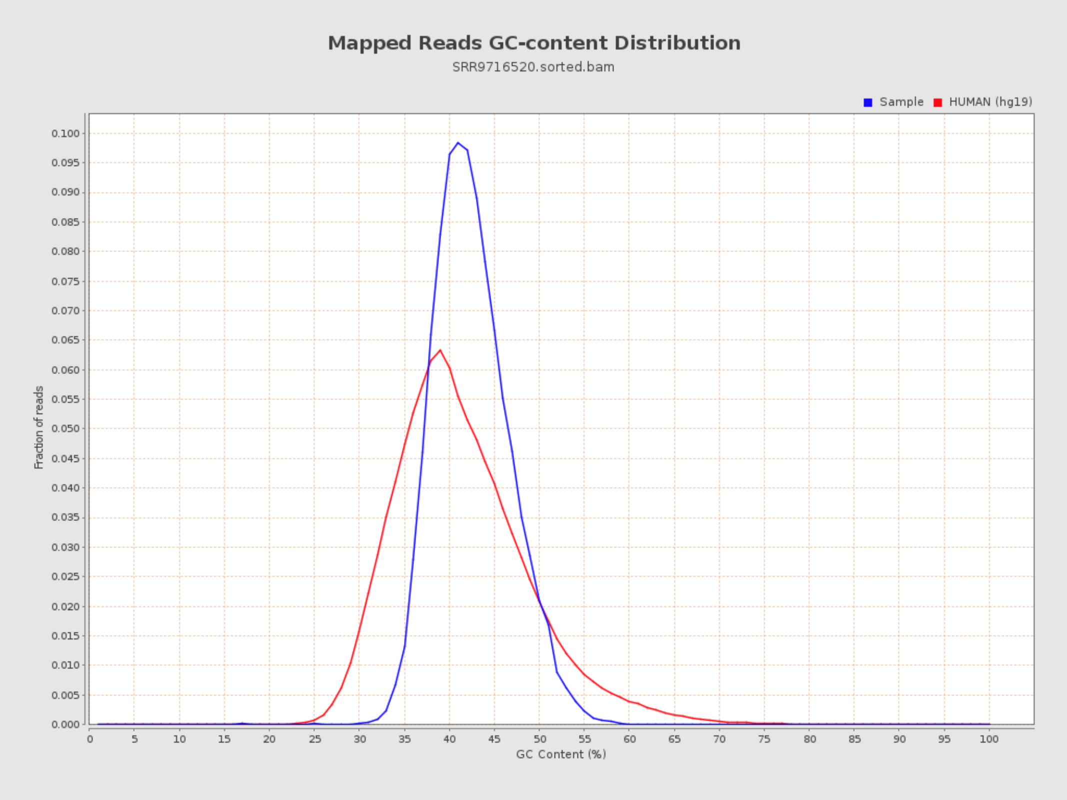
7. Results : Duplication Rate Histogram



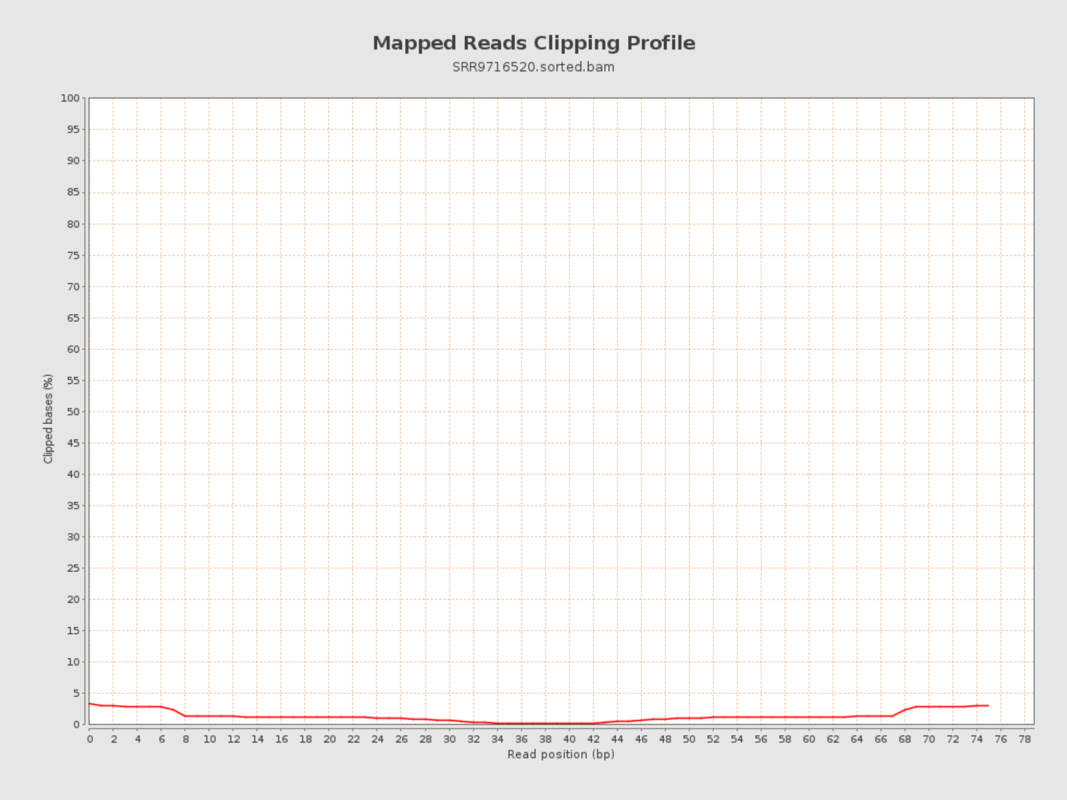
8. Results : Mapped Reads Nucleotide Content



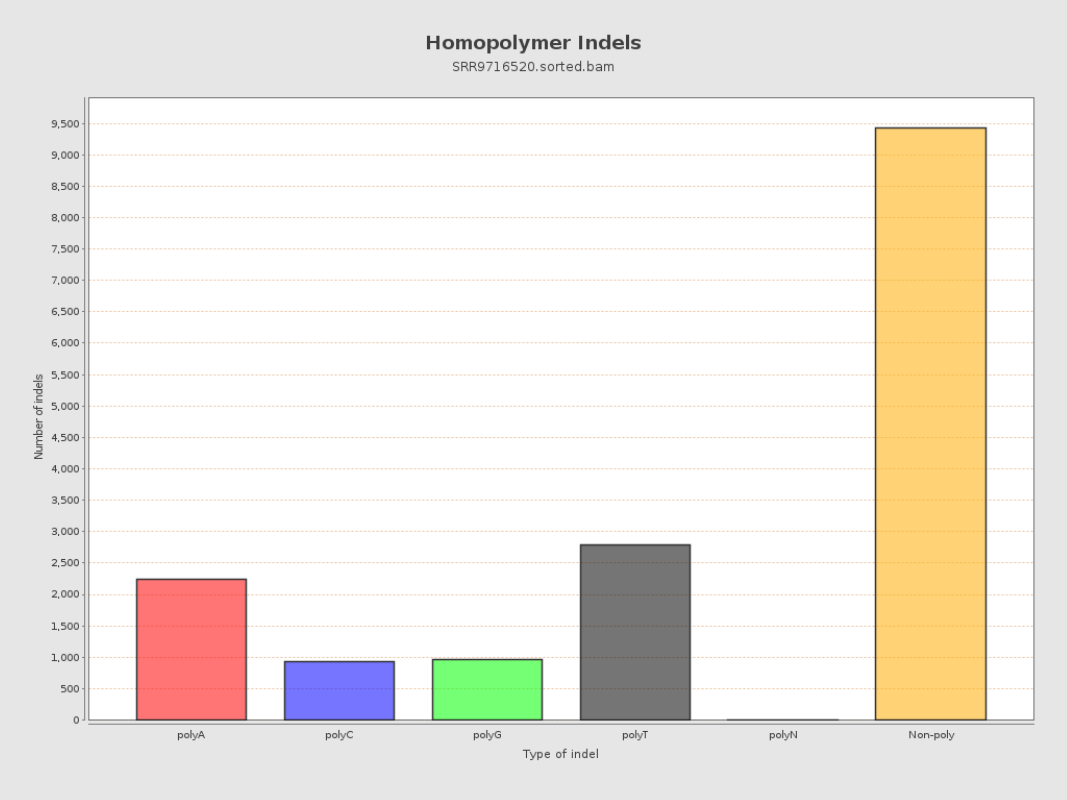
9. Results : Mapped Reads GC-content Distribution



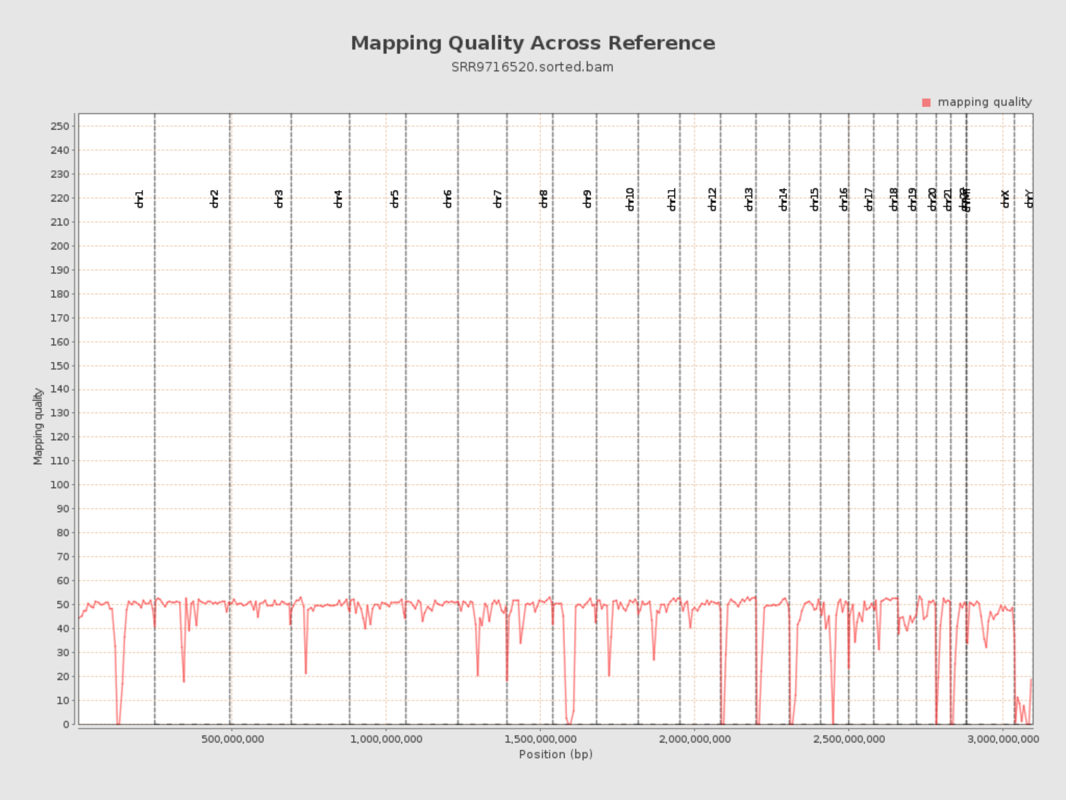
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram