Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 08:38:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716718.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_SRR9716718 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716718.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 08:38:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716718.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,591,713
Mapped reads	1,468,359 / 92.25%
Unmapped reads	123,354 / 7.75%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	27,827 / 1.75%
Read min/max/mean length	30 / 101 / 101.64
Duplicated reads (estimated)	93,487 / 5.87%
Duplication rate	5.22%
Clipped reads	1,493,346 / 93.82%

2.2. ACGT Content

Number/percentage of A's	28,508,082 / 25.04%
Number/percentage of C's	22,290,273 / 19.58%
Number/percentage of T's	33,926,887 / 29.8%
Number/percentage of G's	29,133,251 / 25.59%
Number/percentage of N's	4,505 / 0%
GC Percentage	45.16%

2.3. Coverage

Mean	0.0368

Standard Deviation	0.3079

2.4. Mapping Quality

Mean Mapping Quality	46.56

2.5. Mismatches and indels

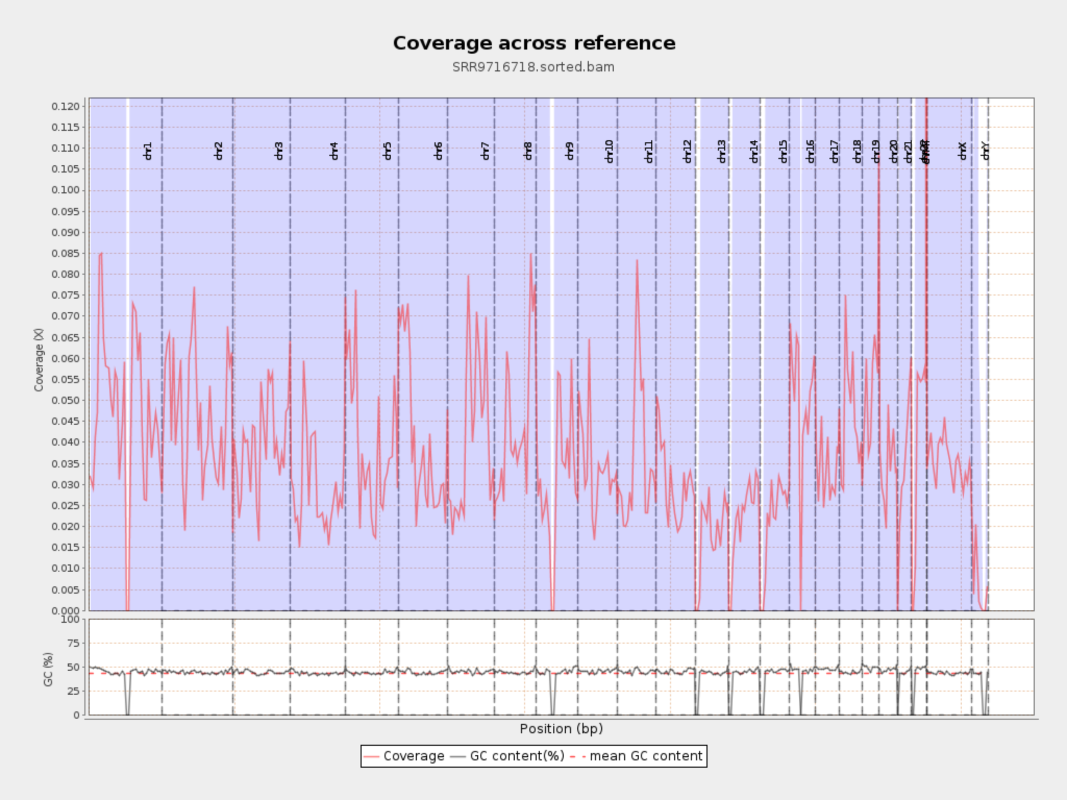
General error rate	0.67%
Mismatches	744,080
Insertions	9,488
Mapped reads with at least one insertion	0.64%
Deletions	20,673
Mapped reads with at least one deletion	1.38%
Homopolymer indels	38.68%

2.6. Chromosome stats

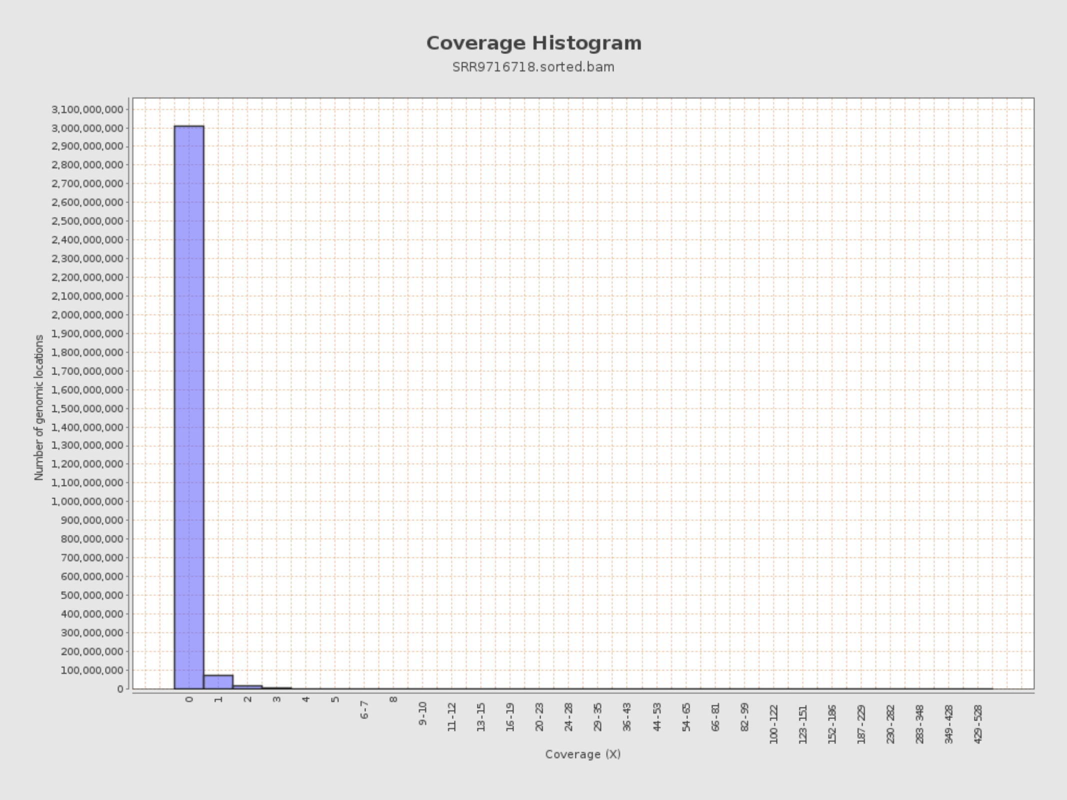
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11695500	0.0469	0.5335
chr2	243199373	11428598	0.047	0.3385
chr3	198022430	7754498	0.0392	0.2451
chr4	191154276	5450742	0.0285	0.27
chr5	180915260	7048295	0.039	0.2464
chr6	171115067	6929930	0.0405	0.2591
chr7	159138663	6677859	0.042	0.3578

chr8	146364022	6501938	0.0444	0.3135
chr9	141213431	4376519	0.031	0.2395
chr10	135534747	4678359	0.0345	0.3544
chr11	135006516	4961945	0.0368	0.269
chr12	133851895	4072717	0.0304	0.2147
chr13	115169878	2059837	0.0179	0.1643
chr14	107349540	2334290	0.0217	0.1857
chr15	102531392	2161381	0.0211	0.1772
chr16	90354753	4496231	0.0498	0.2987
chr17	81195210	2700899	0.0333	0.2419
chr18	78077248	3628875	0.0465	0.329
chr19	59128983	3116600	0.0527	0.4413
chr20	63025520	2126836	0.0337	0.2379
chr21	48129895	1663192	0.0346	0.2755
chr22	51304566	1924104	0.0375	0.2499
chrMT	16571	248195	14.9777	11.2316
chrX	155270560	5531521	0.0356	0.2383
chrY	59373566	336668	0.0057	0.2053

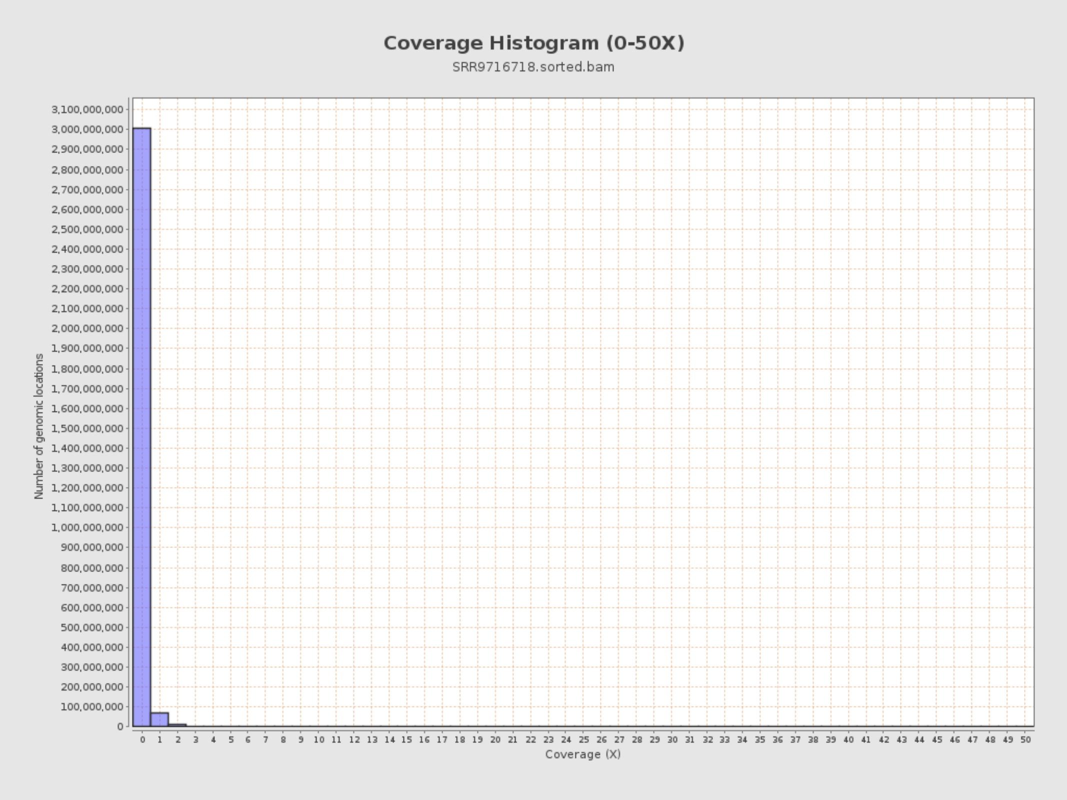
3. Results : Coverage across reference



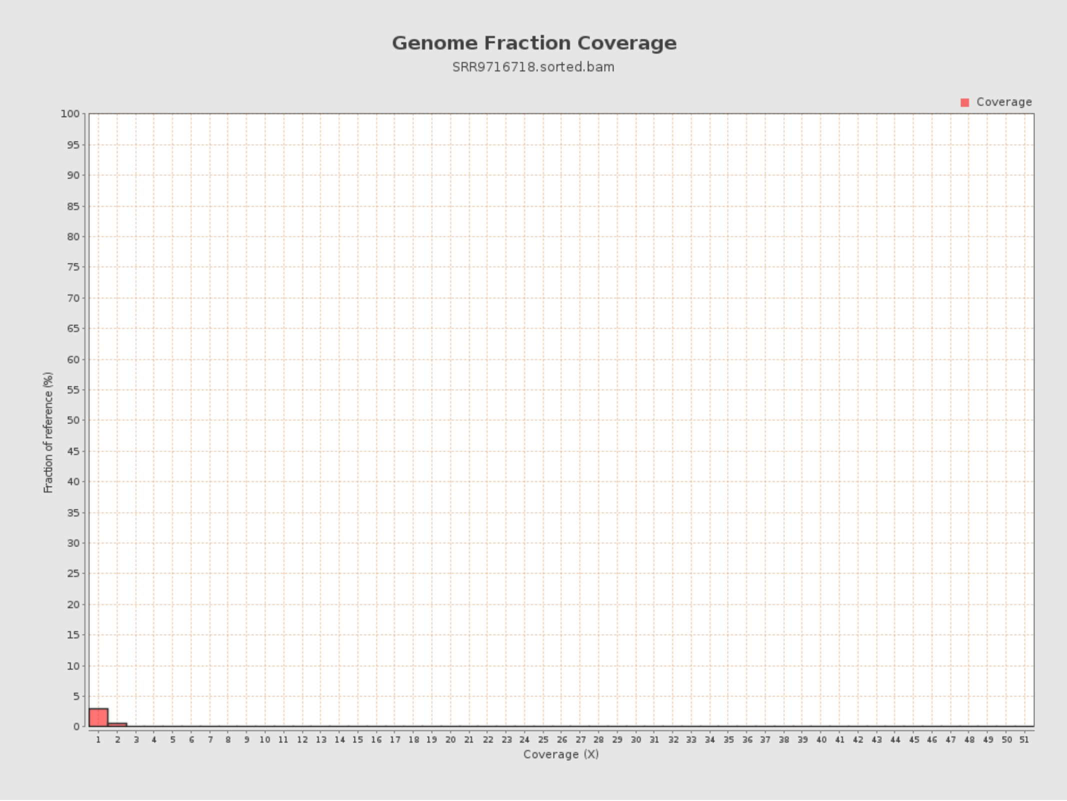
4. Results : Coverage Histogram



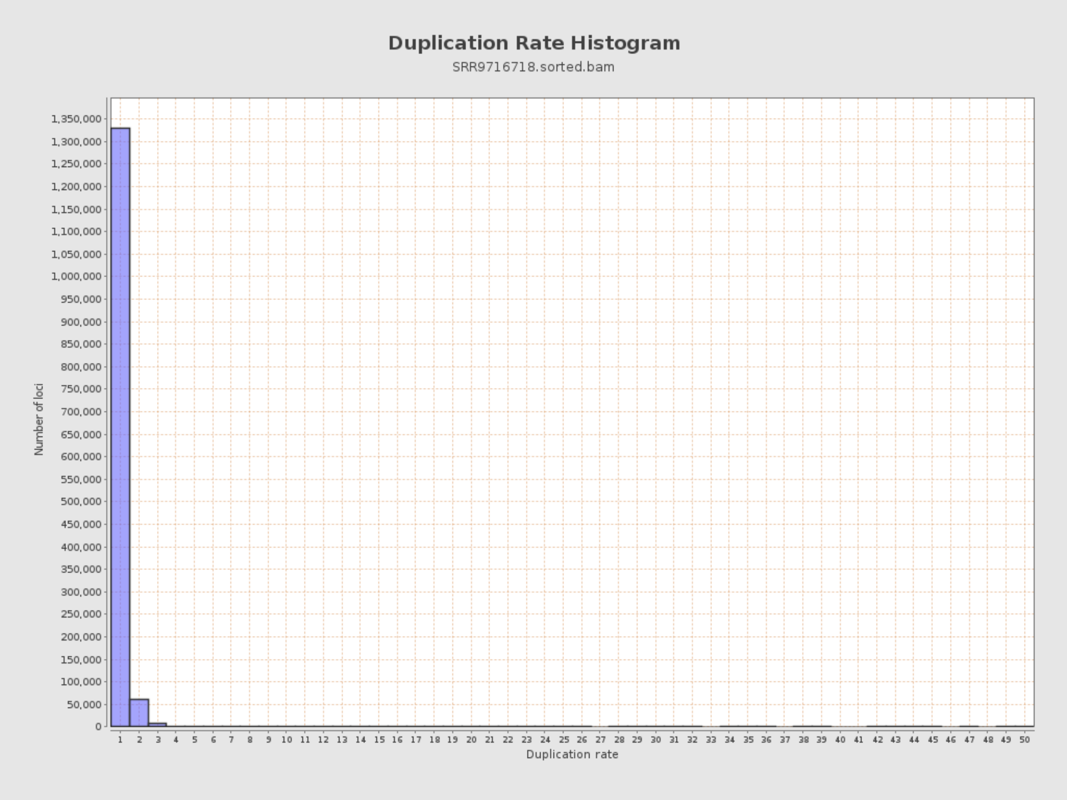
5. Results : Coverage Histogram (0-50X)



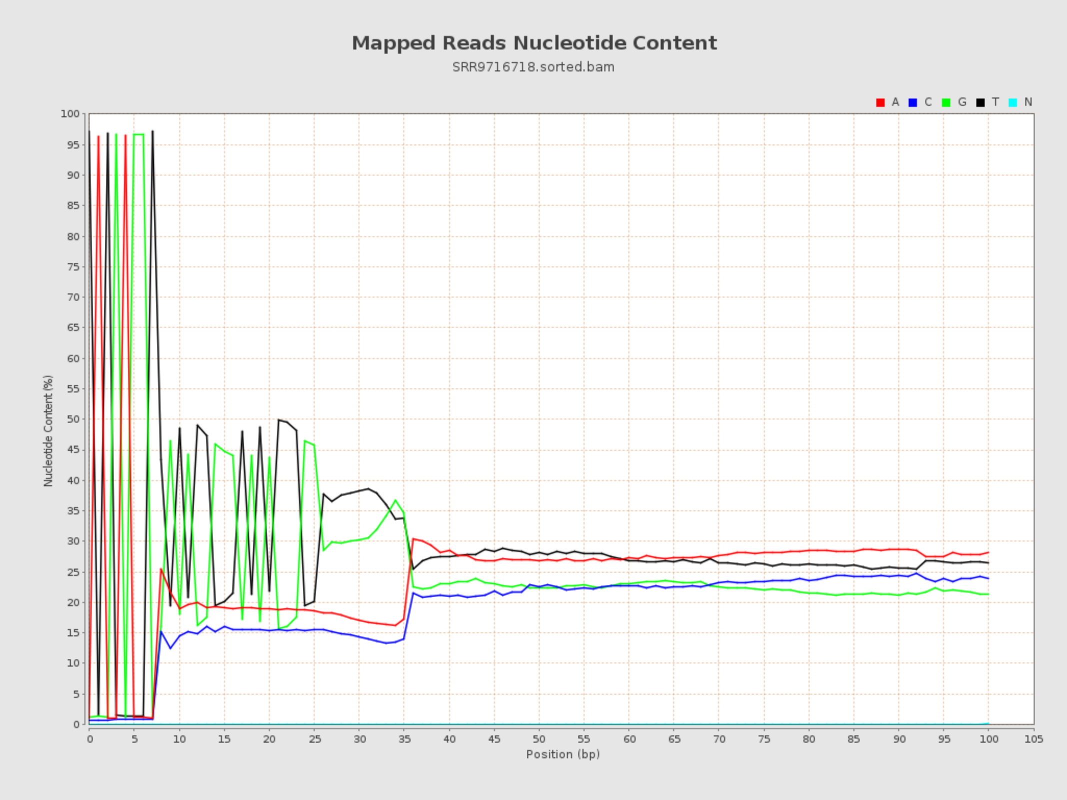
6. Results : Genome Fraction Coverage



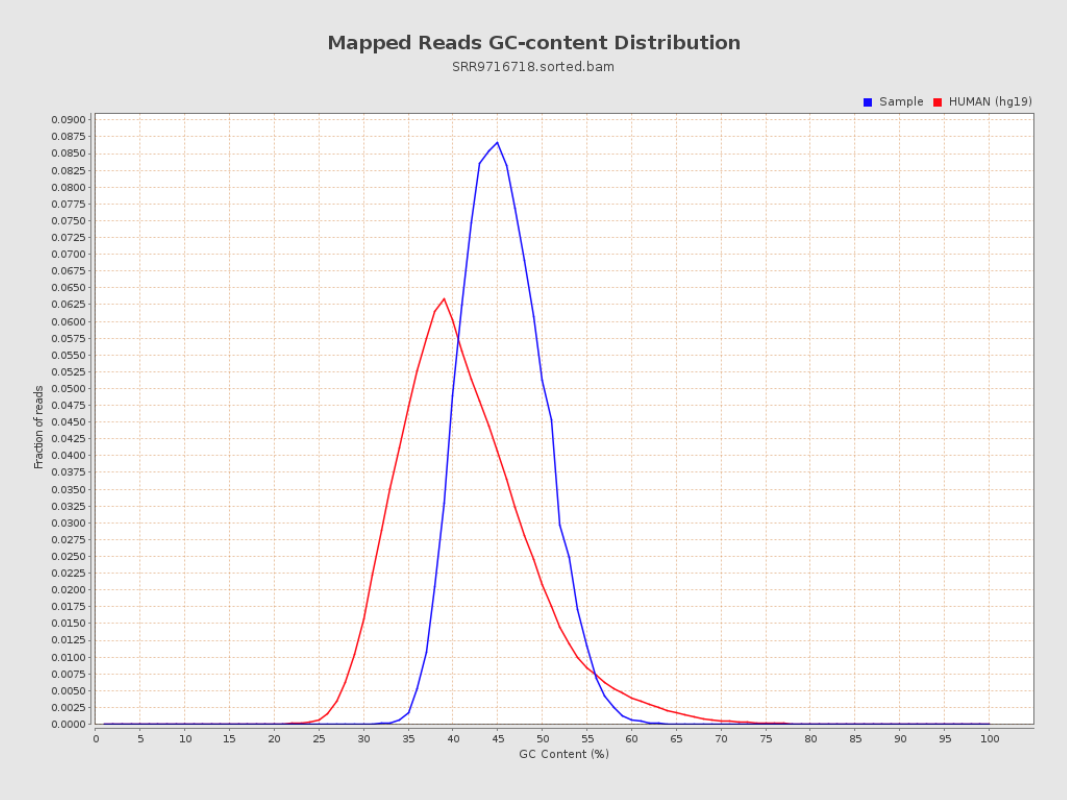
7. Results : Duplication Rate Histogram



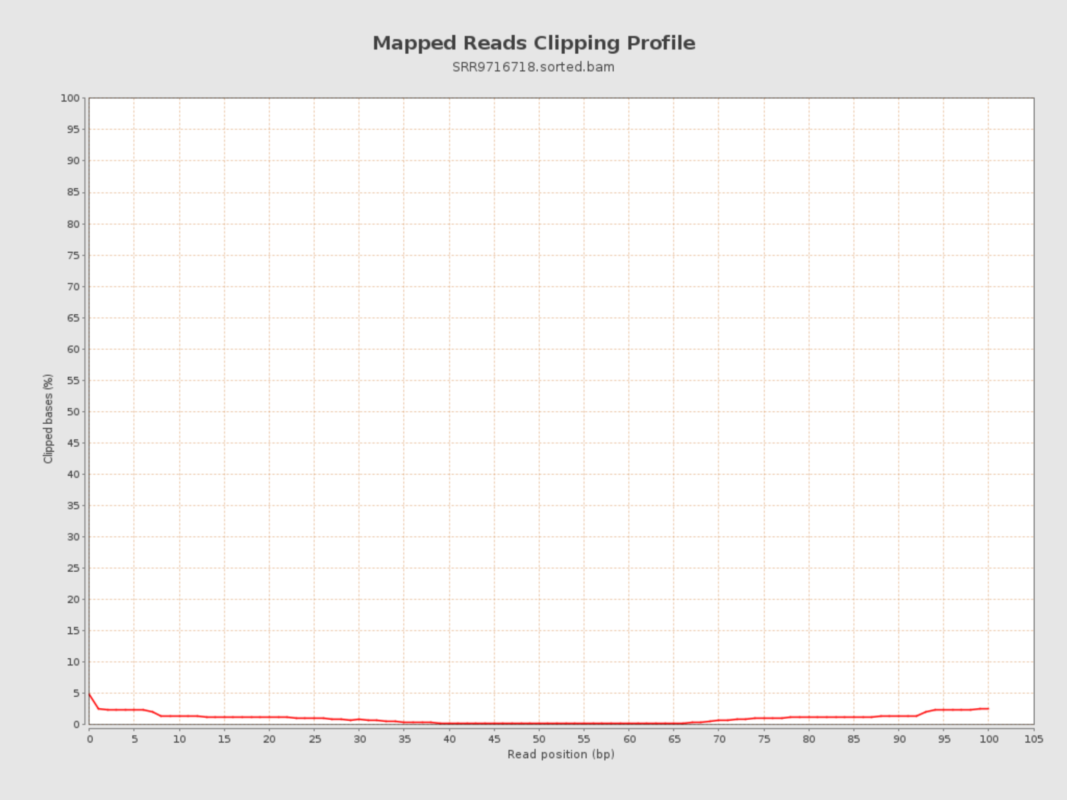
8. Results : Mapped Reads Nucleotide Content



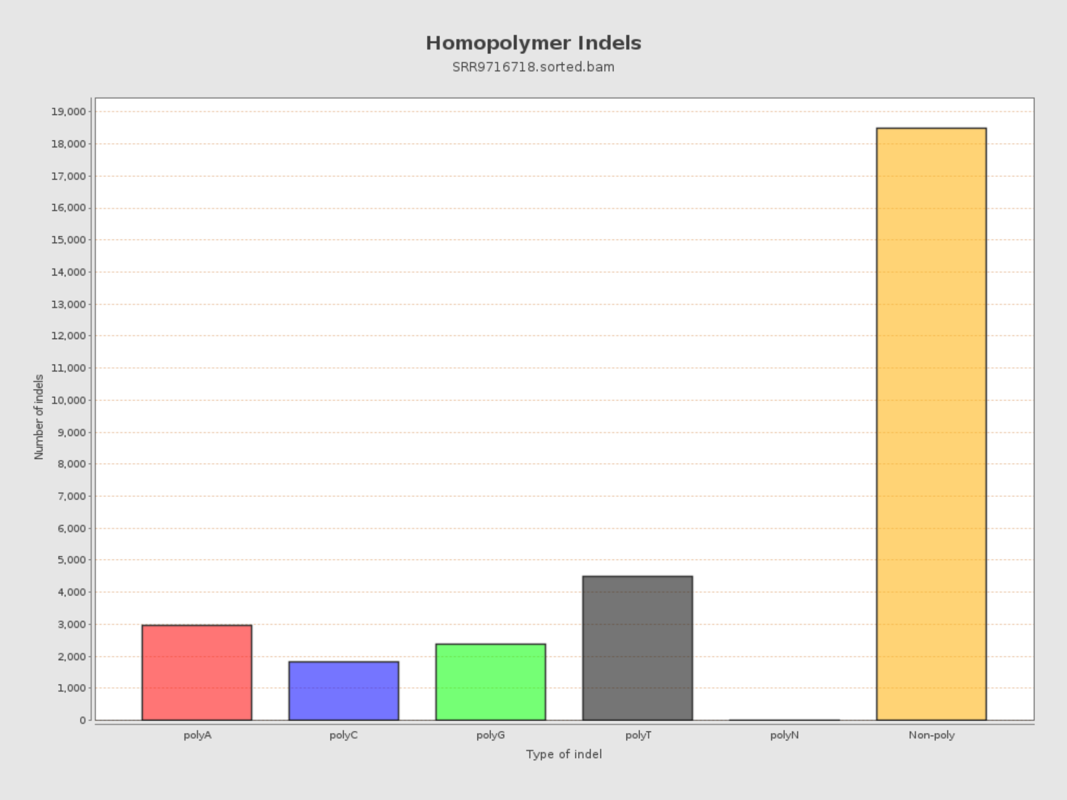
9. Results : Mapped Reads GC-content Distribution



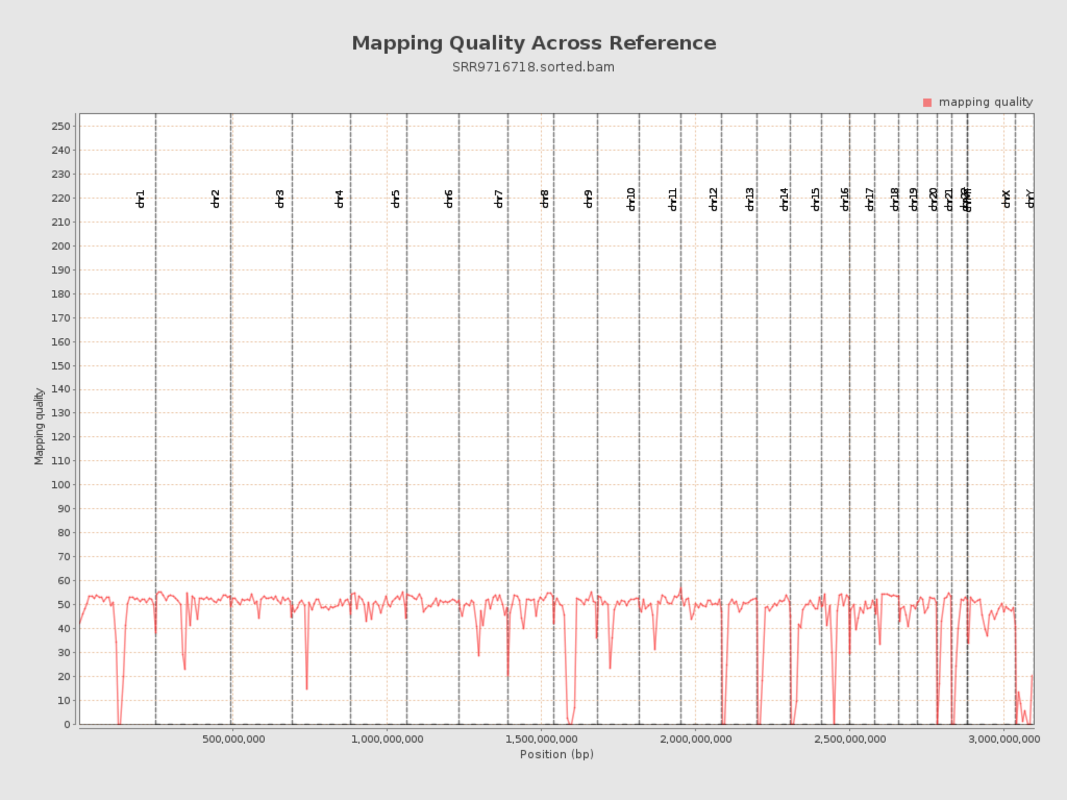
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram