Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 01:07:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716218.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_SRR9716218 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716218.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 01:07:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716218.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,764,694
Mapped reads	1,593,883 / 90.32%
Unmapped reads	170,811 / 9.68%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,482 / 0.54%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	64,606 / 3.66%
Duplication rate	2.98%
Clipped reads	1,597,855 / 90.55%

2.2. ACGT Content

Number/percentage of A's	22,929,882 / 24.67%
Number/percentage of C's	19,406,530 / 20.88%
Number/percentage of T's	29,244,521 / 31.47%
Number/percentage of G's	21,349,303 / 22.97%
Number/percentage of N's	1,133 / 0%
GC Percentage	43.86%

2.3. Coverage

Mean	0.03

Standard Deviation	0.2842

2.4. Mapping Quality

Mean Mapping Quality	44.49

2.5. Mismatches and indels

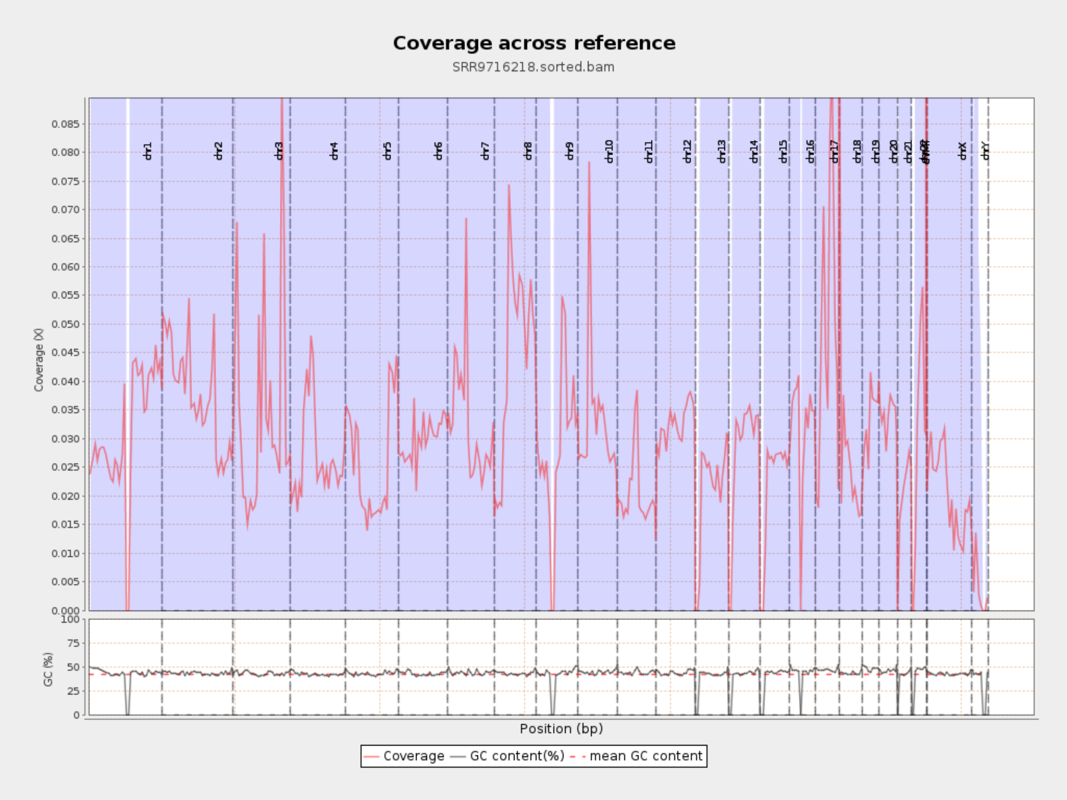
General error rate	0.51%
Mismatches	457,253
Insertions	7,716
Mapped reads with at least one insertion	0.48%
Deletions	17,034
Mapped reads with at least one deletion	1.06%
Homopolymer indels	39.78%

2.6. Chromosome stats

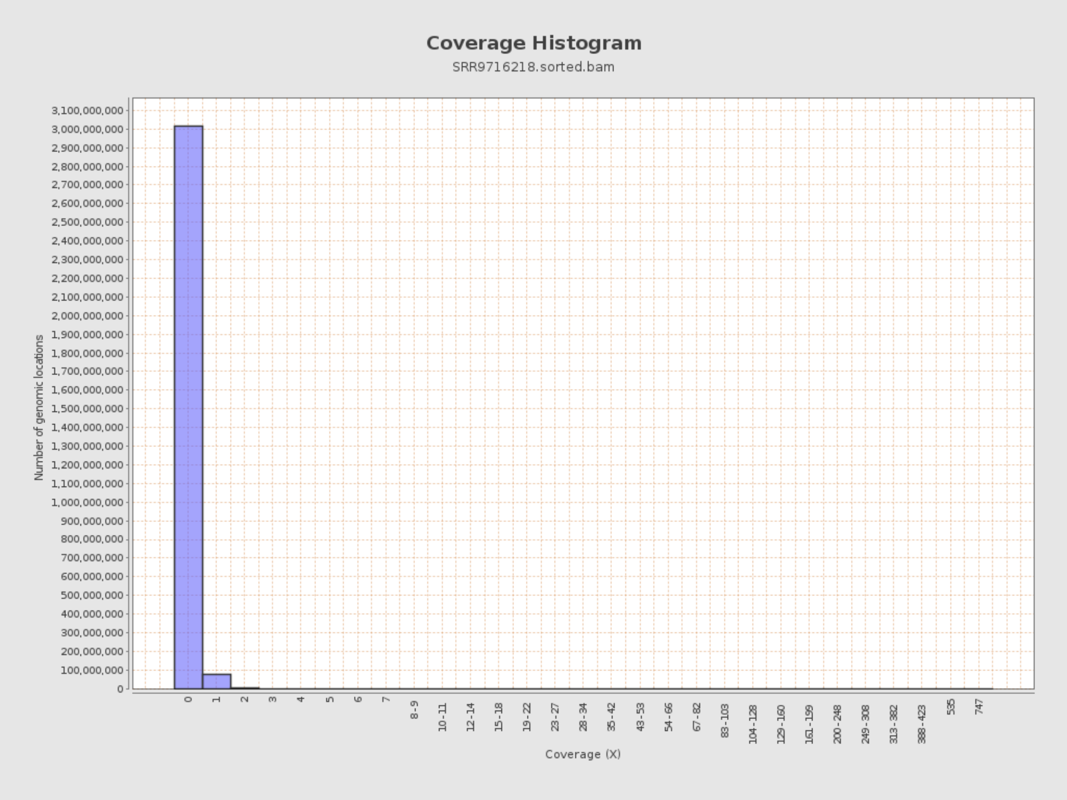
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7751614	0.0311	0.3823
chr2	243199373	9234882	0.038	0.3782
chr3	198022430	6870067	0.0347	0.2179
chr4	191154276	5173390	0.0271	0.2077
chr5	180915260	4663505	0.0258	0.178
chr6	171115067	5135954	0.03	0.2083
chr7	159138663	5209554	0.0327	0.5497

chr8	146364022	6637478	0.0453	0.3193
chr9	141213431	3921898	0.0278	0.2124
chr10	135534747	4466489	0.033	0.3843
chr11	135006516	2767354	0.0205	0.1966
chr12	133851895	4361208	0.0326	0.2187
chr13	115169878	2400954	0.0208	0.1599
chr14	107349540	2963844	0.0276	0.1855
chr15	102531392	2241252	0.0219	0.1638
chr16	90354753	2887235	0.032	0.2064
chr17	81195210	4011726	0.0494	0.2578
chr18	78077248	2151946	0.0276	0.3309
chr19	59128983	1977198	0.0334	0.3503
chr20	63025520	2145692	0.034	0.2136
chr21	48129895	969590	0.0201	0.1784
chr22	51304566	1487091	0.029	0.1882
chrMT	16571	45334	2.7357	2.2902
chrX	155270560	3254287	0.021	0.181
chrY	59373566	228688	0.0039	0.117

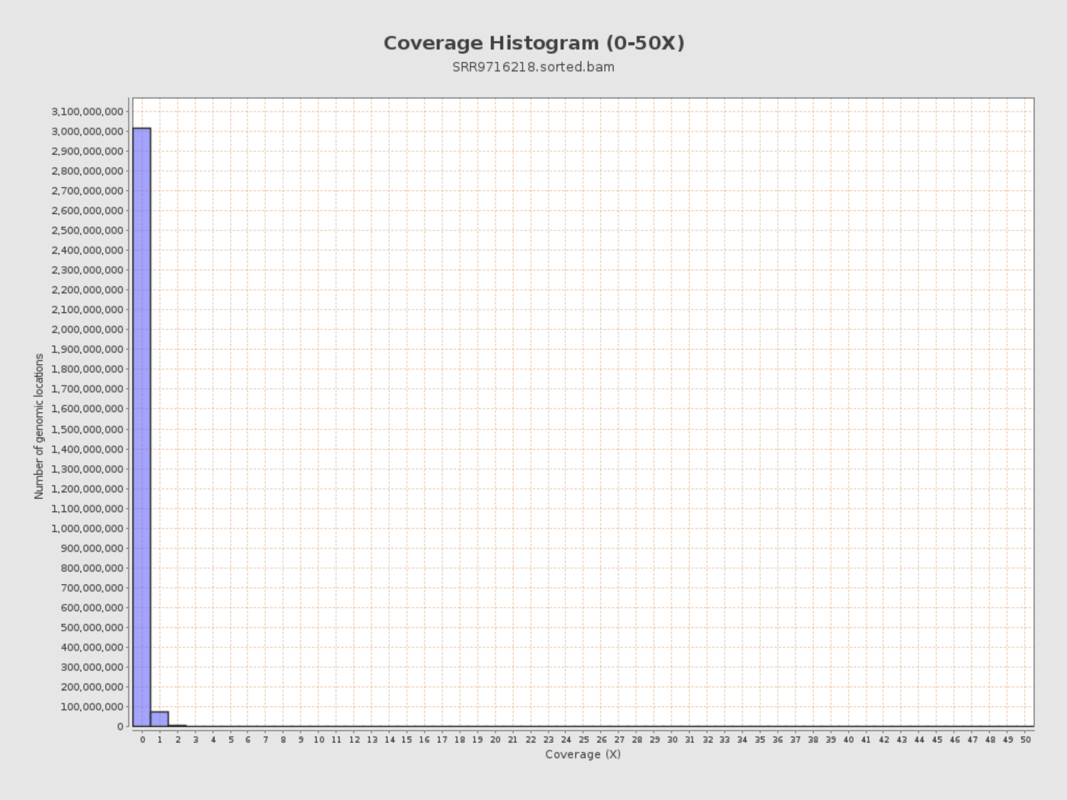
3. Results : Coverage across reference



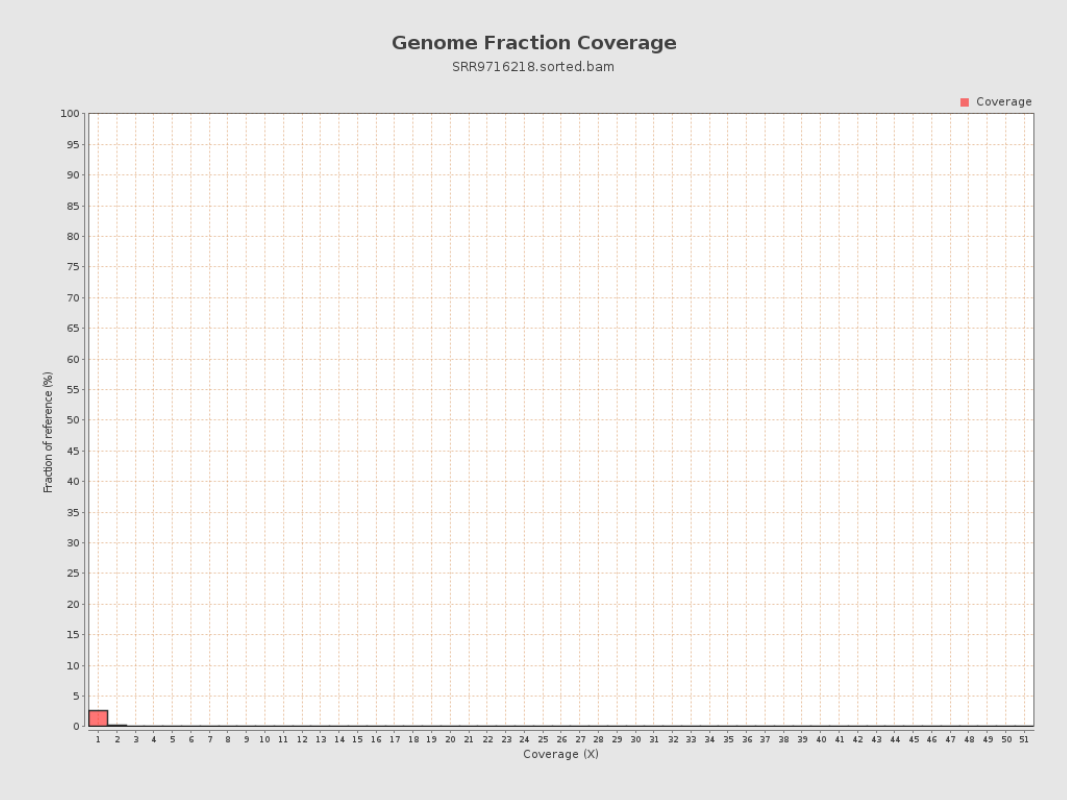
4. Results : Coverage Histogram



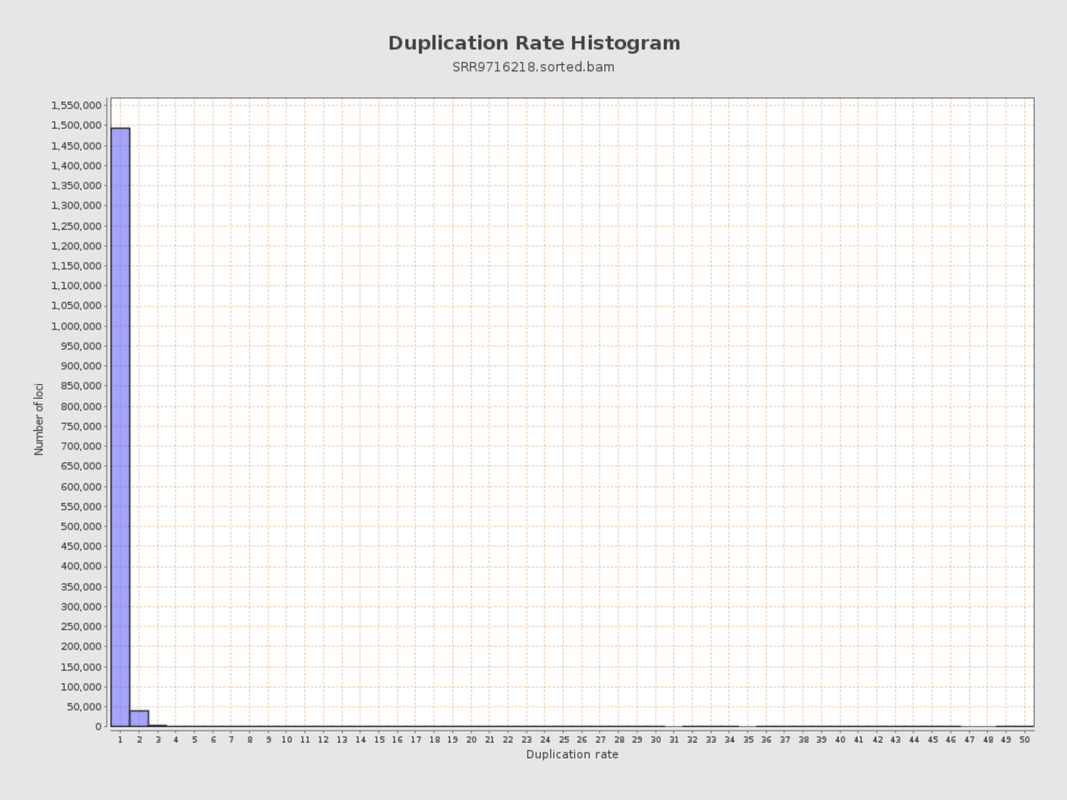
5. Results : Coverage Histogram (0-50X)



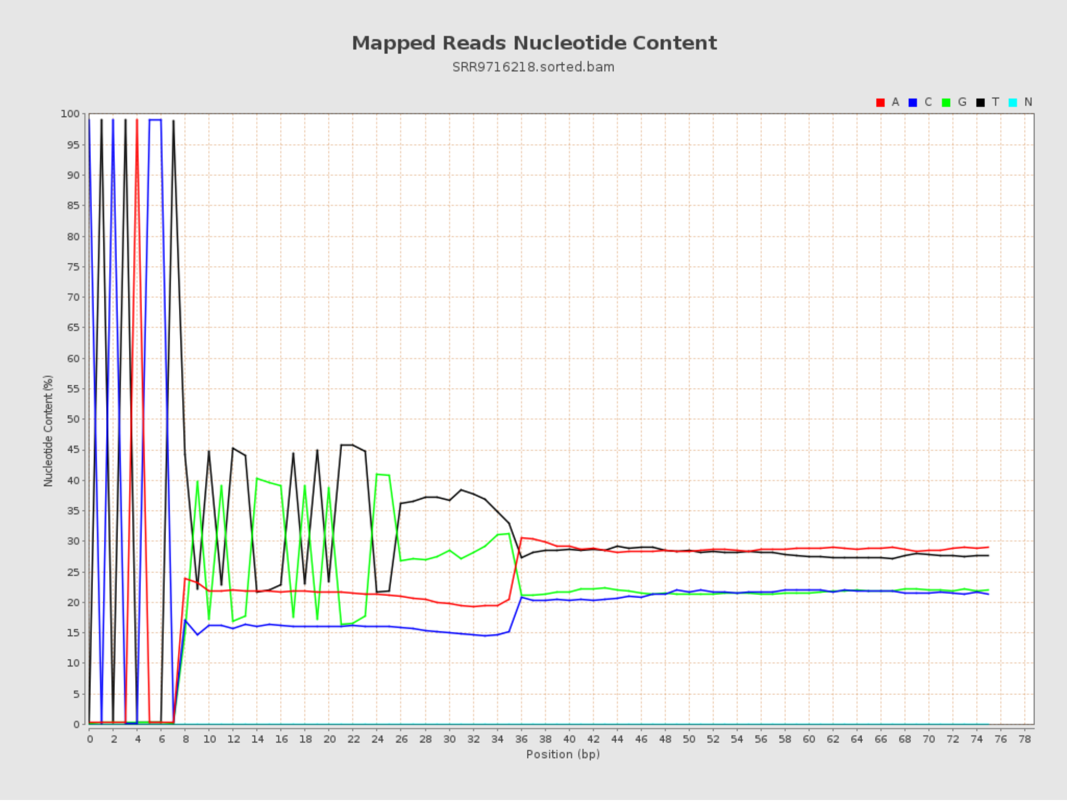
6. Results : Genome Fraction Coverage



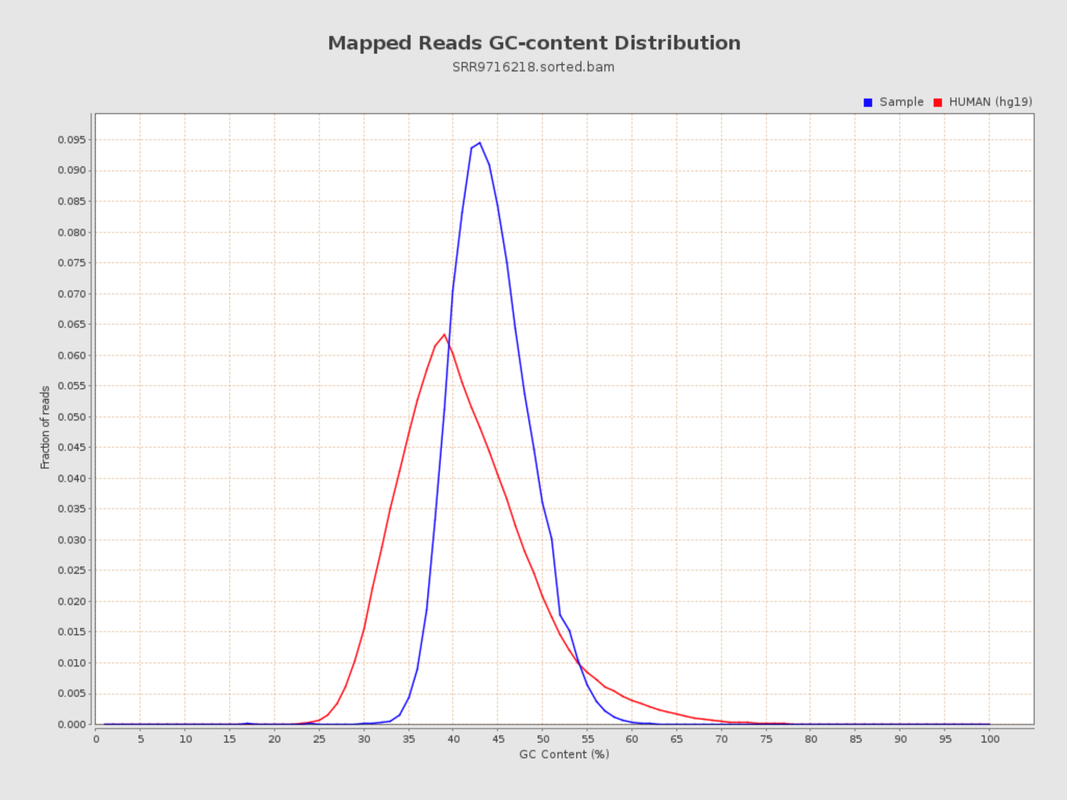
7. Results : Duplication Rate Histogram



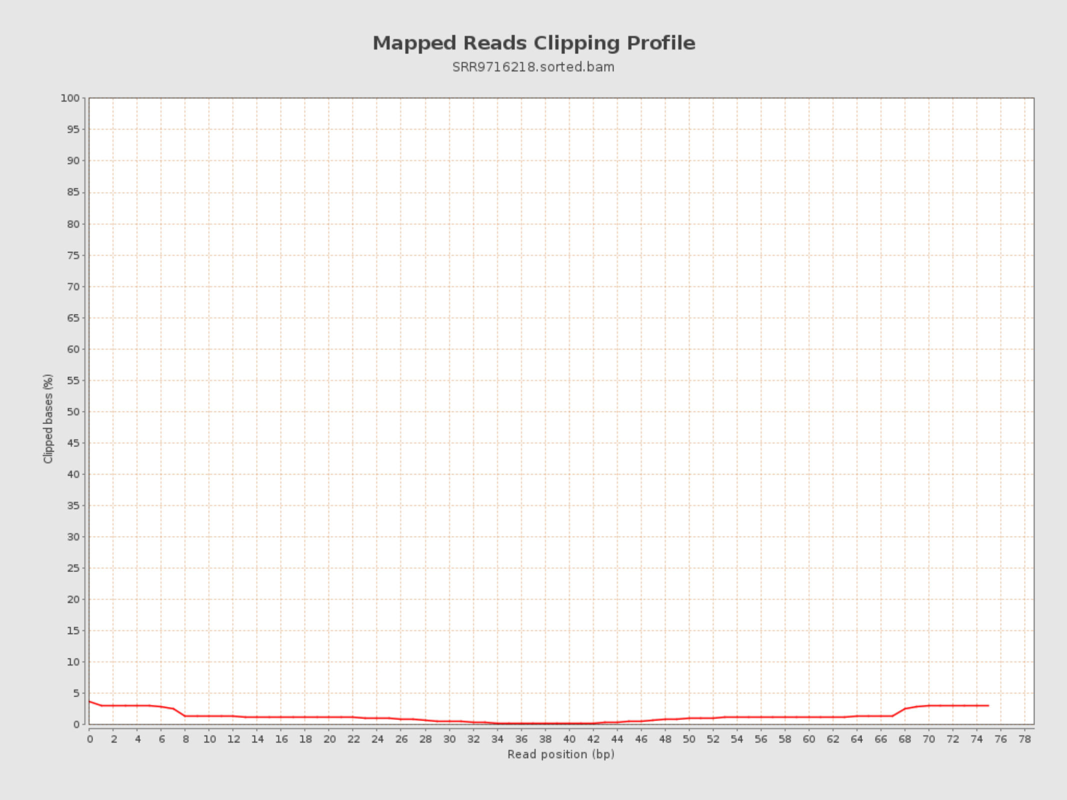
8. Results : Mapped Reads Nucleotide Content



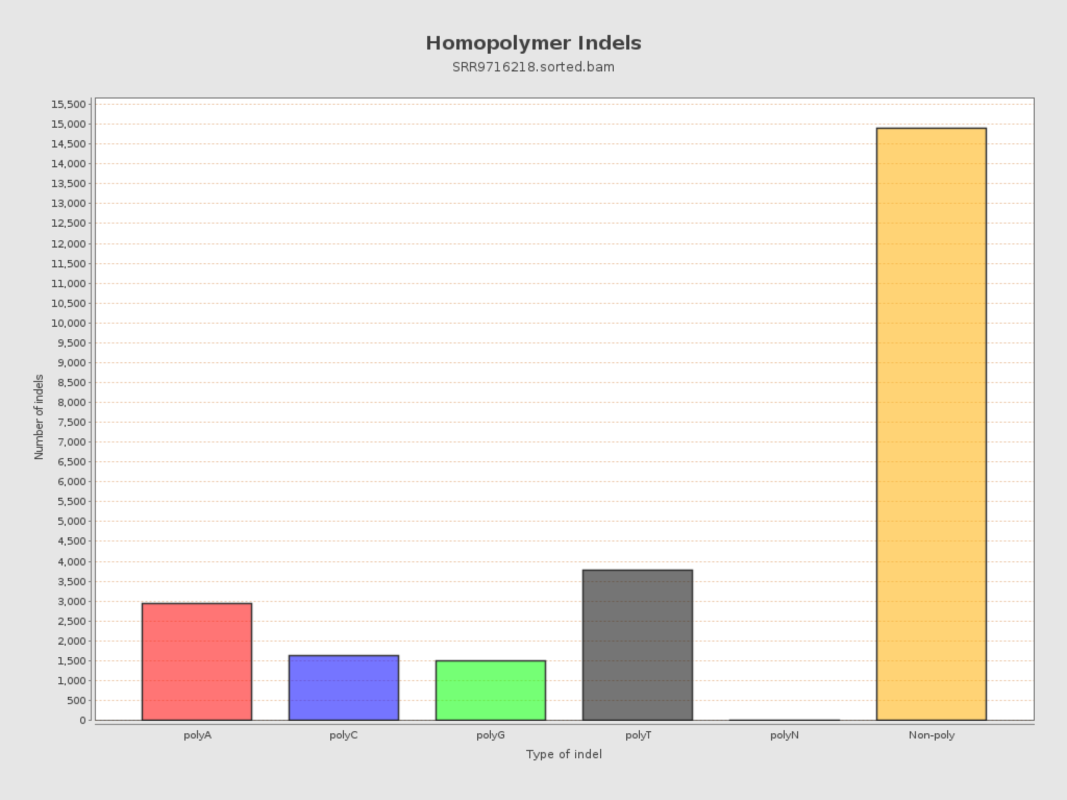
9. Results : Mapped Reads GC-content Distribution



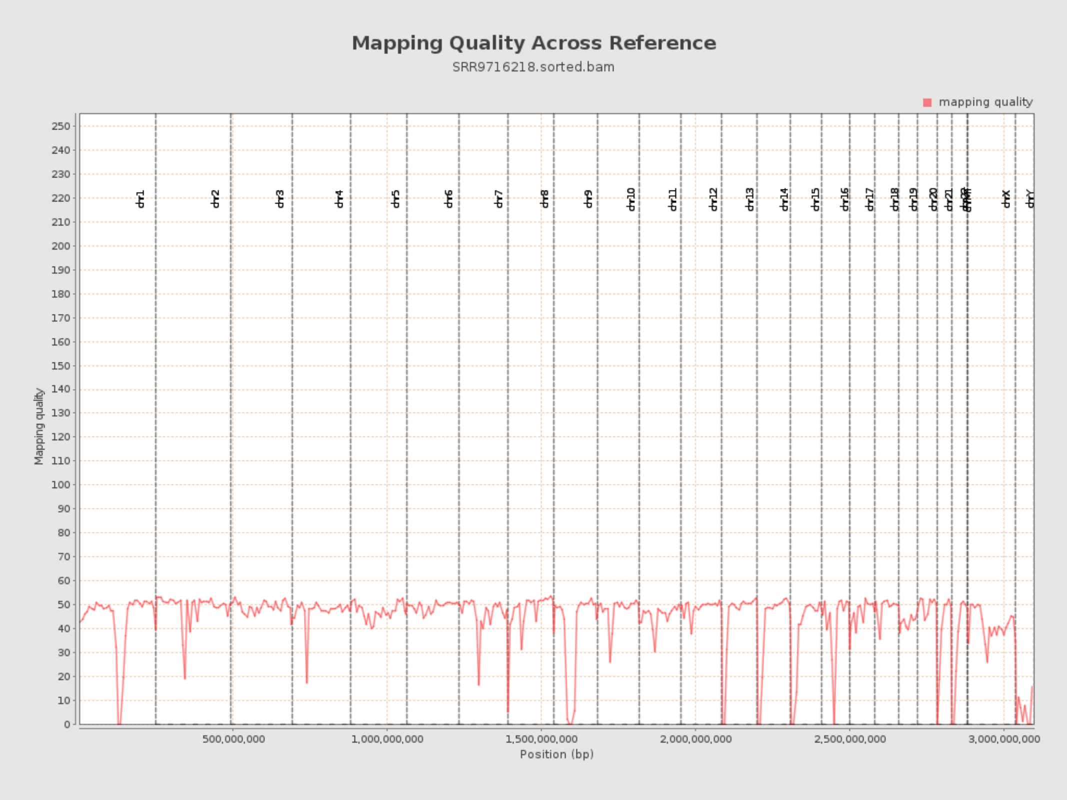
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram