Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 21:27:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716158.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_SRR9716158 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716158.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 21:27:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716158.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,658,455
Mapped reads	1,504,105 / 90.69%
Unmapped reads	154,350 / 9.31%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,020 / 0.3%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	45,802 / 2.76%
Duplication rate	2.37%
Clipped reads	1,507,474 / 90.9%

2.2. ACGT Content

Number/percentage of A's	20,178,804 / 23.47%
Number/percentage of C's	17,824,878 / 20.73%
Number/percentage of T's	27,123,961 / 31.55%
Number/percentage of G's	20,850,211 / 24.25%
Number/percentage of N's	1,741 / 0%
GC Percentage	44.98%

2.3. Coverage

Mean	0.0278

Standard Deviation	0.2225

2.4. Mapping Quality

Mean Mapping Quality	44.58

2.5. Mismatches and indels

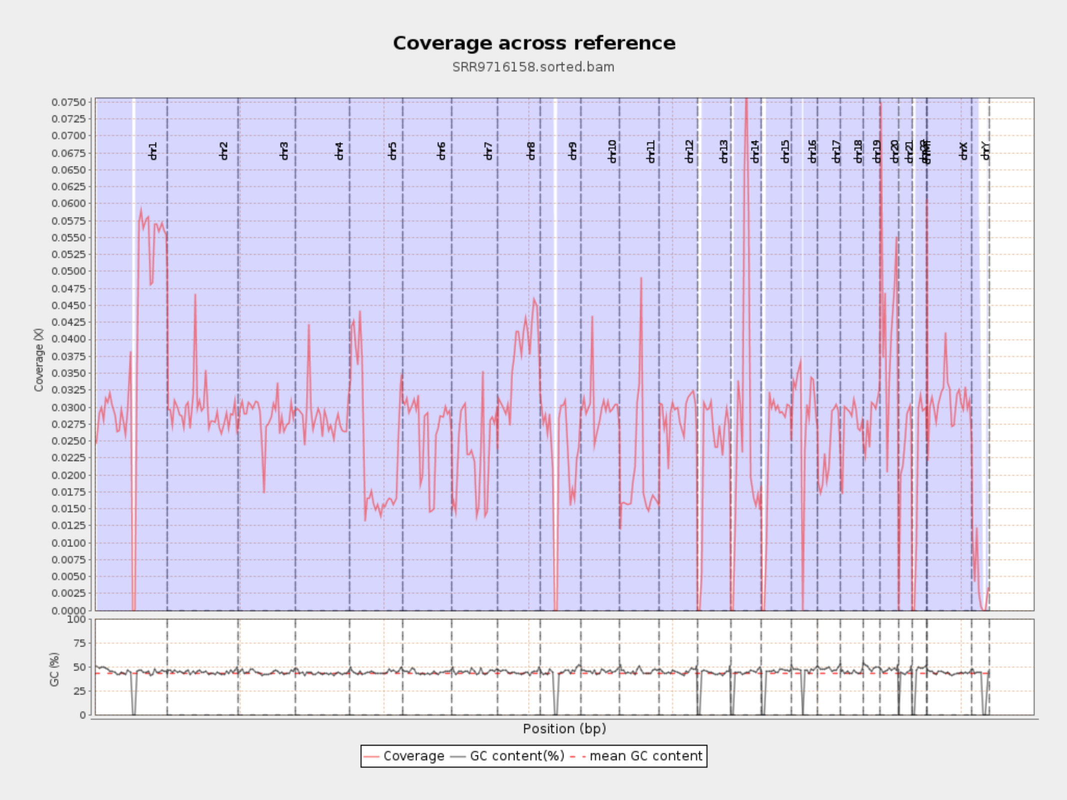
General error rate	0.5%
Mismatches	419,189
Insertions	4,472
Mapped reads with at least one insertion	0.3%
Deletions	13,017
Mapped reads with at least one deletion	0.86%
Homopolymer indels	43.69%

2.6. Chromosome stats

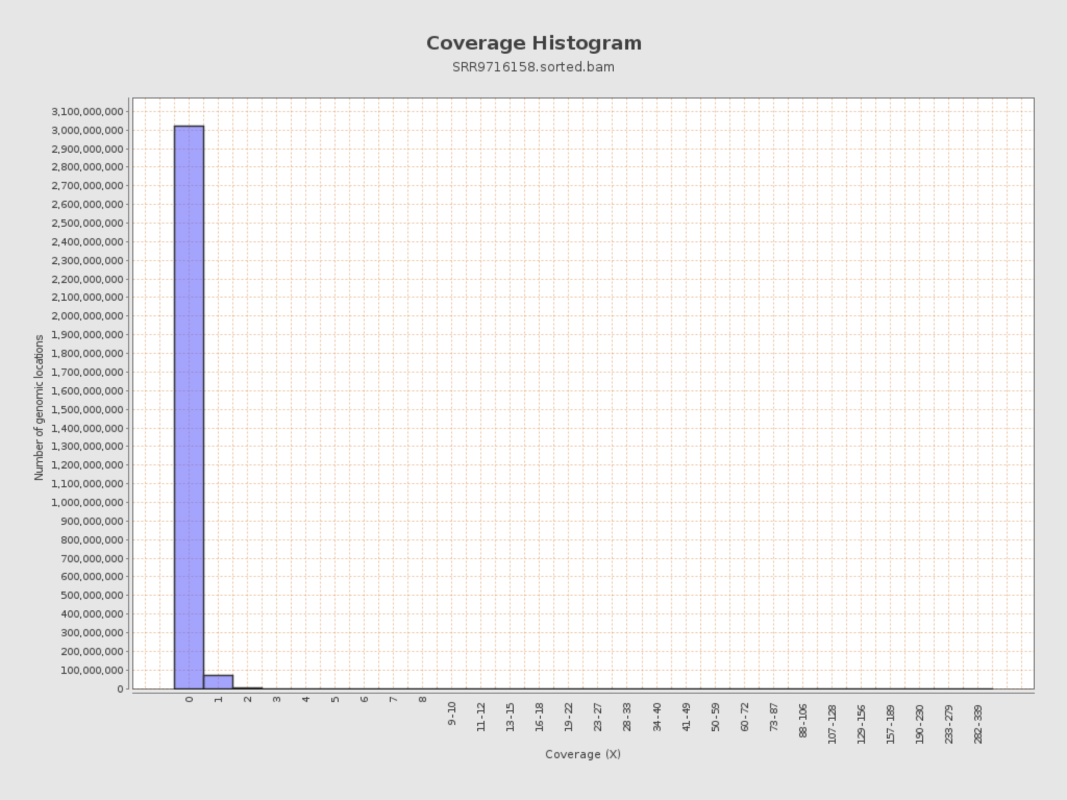
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9584549	0.0385	0.3209
chr2	243199373	7197944	0.0296	0.2579
chr3	198022430	5654000	0.0286	0.1838
chr4	191154276	5462309	0.0286	0.1971
chr5	180915260	4257922	0.0235	0.1693
chr6	171115067	4527552	0.0265	0.1896
chr7	159138663	3686366	0.0232	0.1987

chr8	146364022	5430419	0.0371	0.2415
chr9	141213431	3164156	0.0224	0.2262
chr10	135534747	4075433	0.0301	0.2298
chr11	135006516	2715343	0.0201	0.2058
chr12	133851895	3877047	0.029	0.1888
chr13	115169878	2644592	0.023	0.1644
chr14	107349540	3001675	0.028	0.1932
chr15	102531392	2481981	0.0242	0.1694
chr16	90354753	2589204	0.0287	0.199
chr17	81195210	1925375	0.0237	0.1721
chr18	78077248	2130938	0.0273	0.3966
chr19	59128983	1676867	0.0284	0.2579
chr20	63025520	2722261	0.0432	0.2344
chr21	48129895	1103308	0.0229	0.1767
chr22	51304566	1059391	0.0206	0.1569
chrMT	16571	1005	0.0606	0.2767
chrX	155270560	4796044	0.0309	0.2137
chrY	59373566	236054	0.004	0.0932

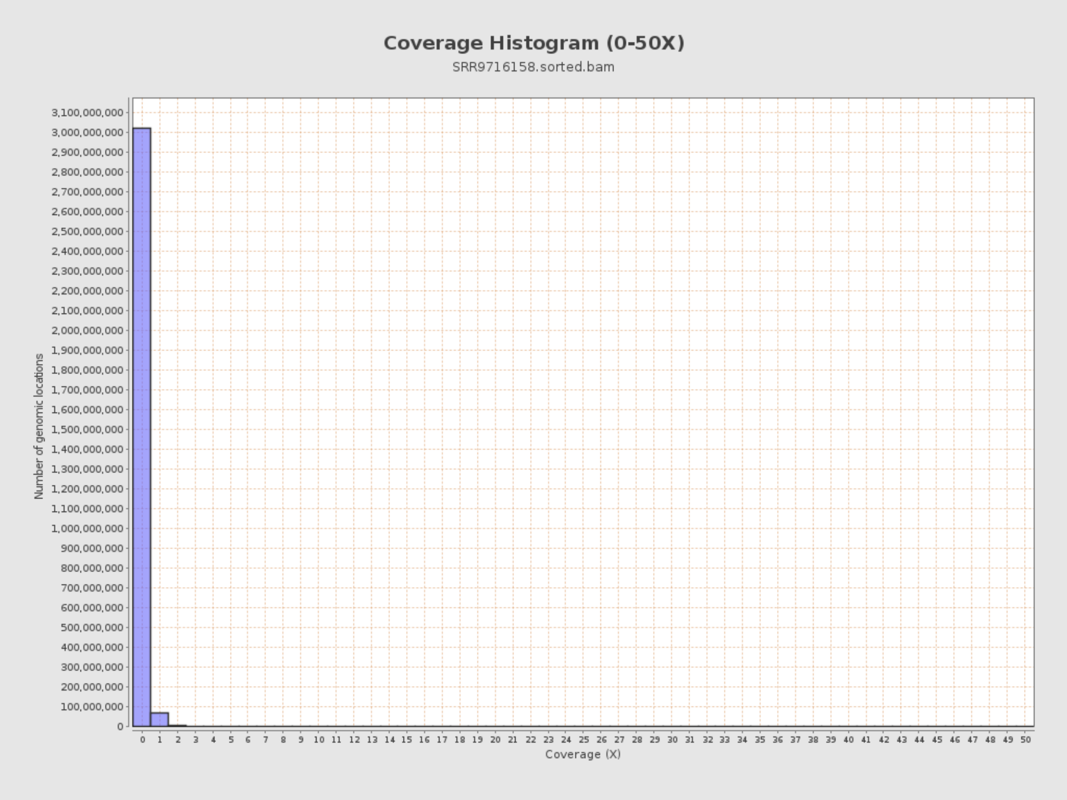
3. Results : Coverage across reference



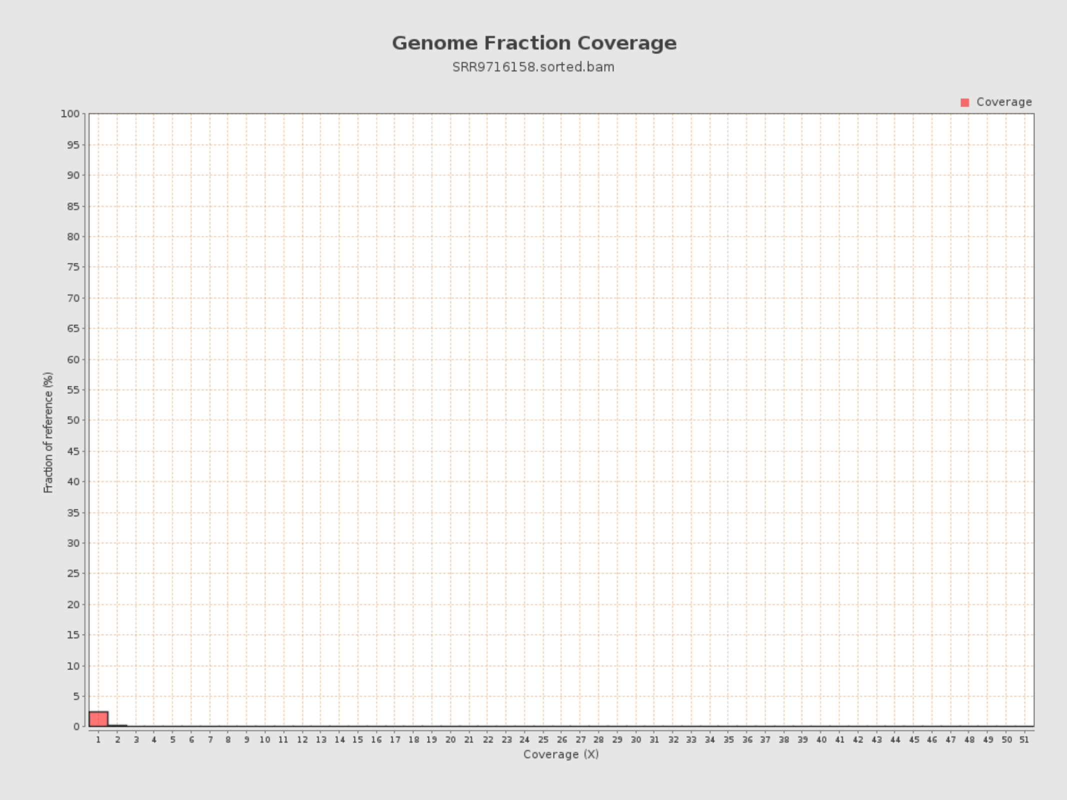
4. Results : Coverage Histogram



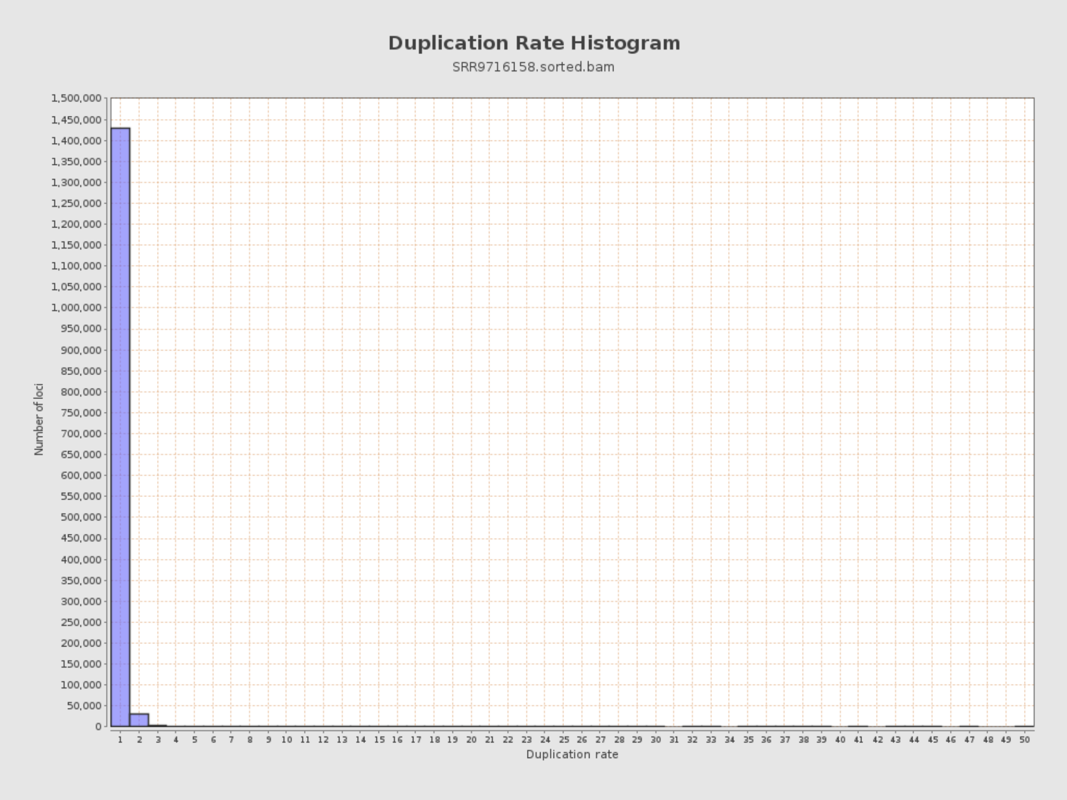
5. Results : Coverage Histogram (0-50X)



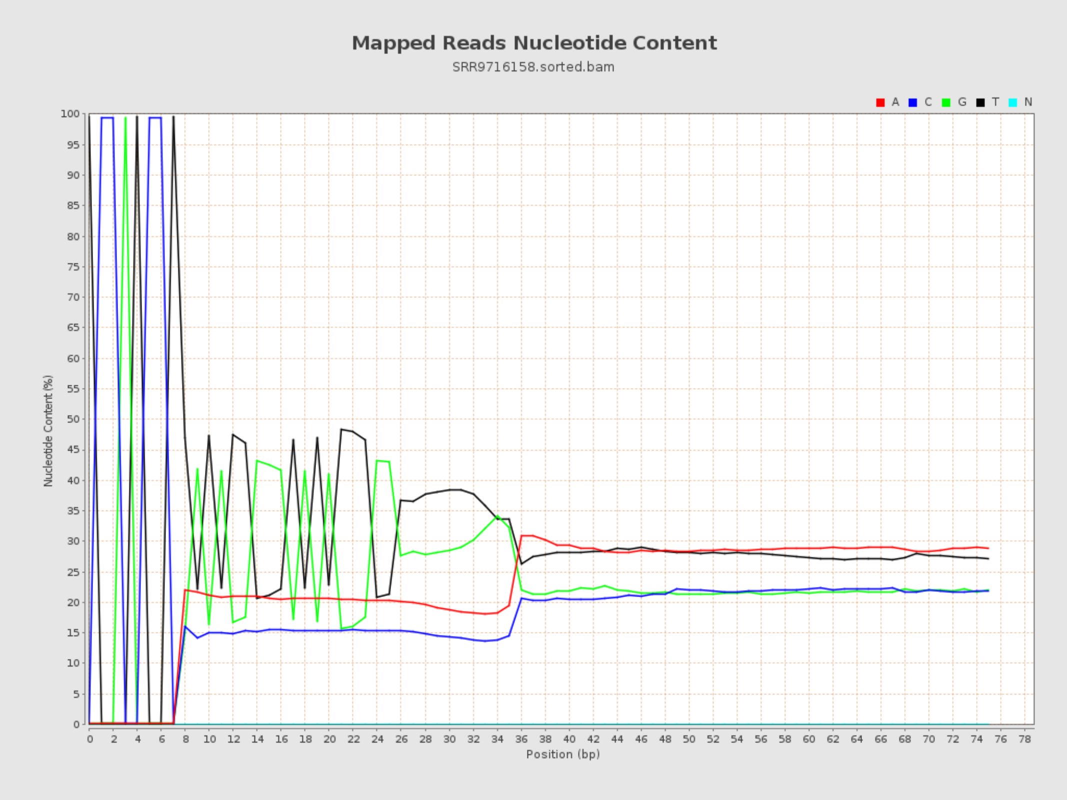
6. Results : Genome Fraction Coverage



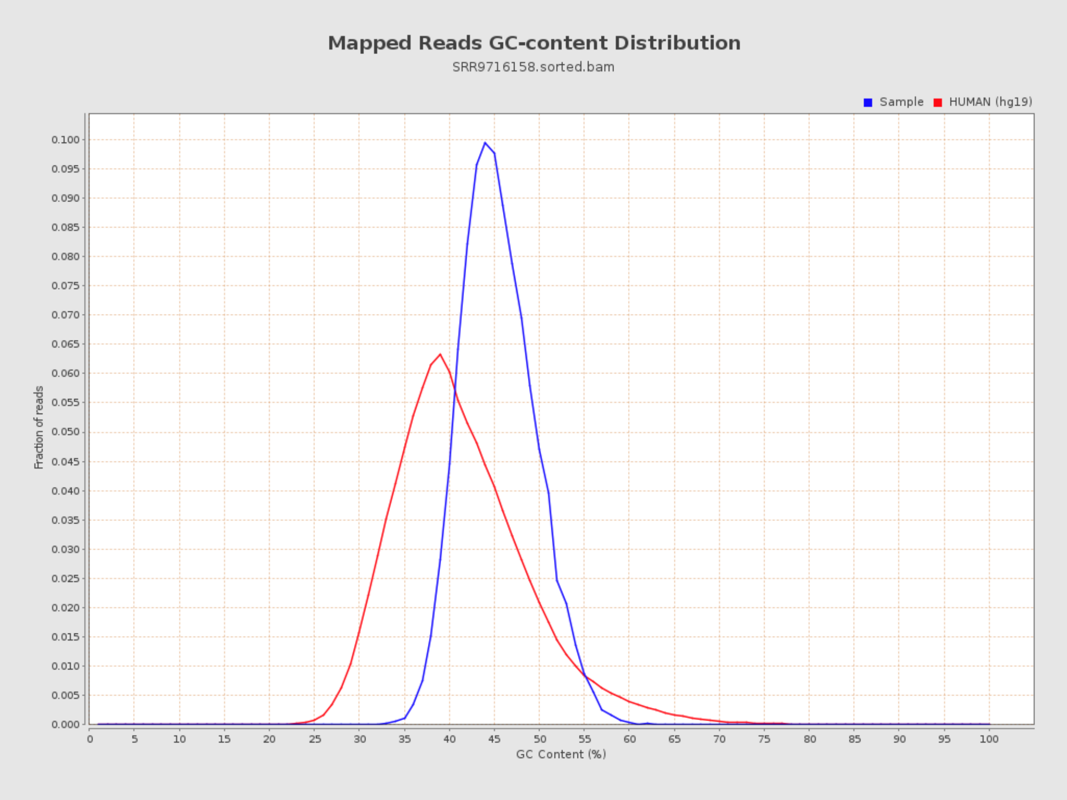
7. Results : Duplication Rate Histogram



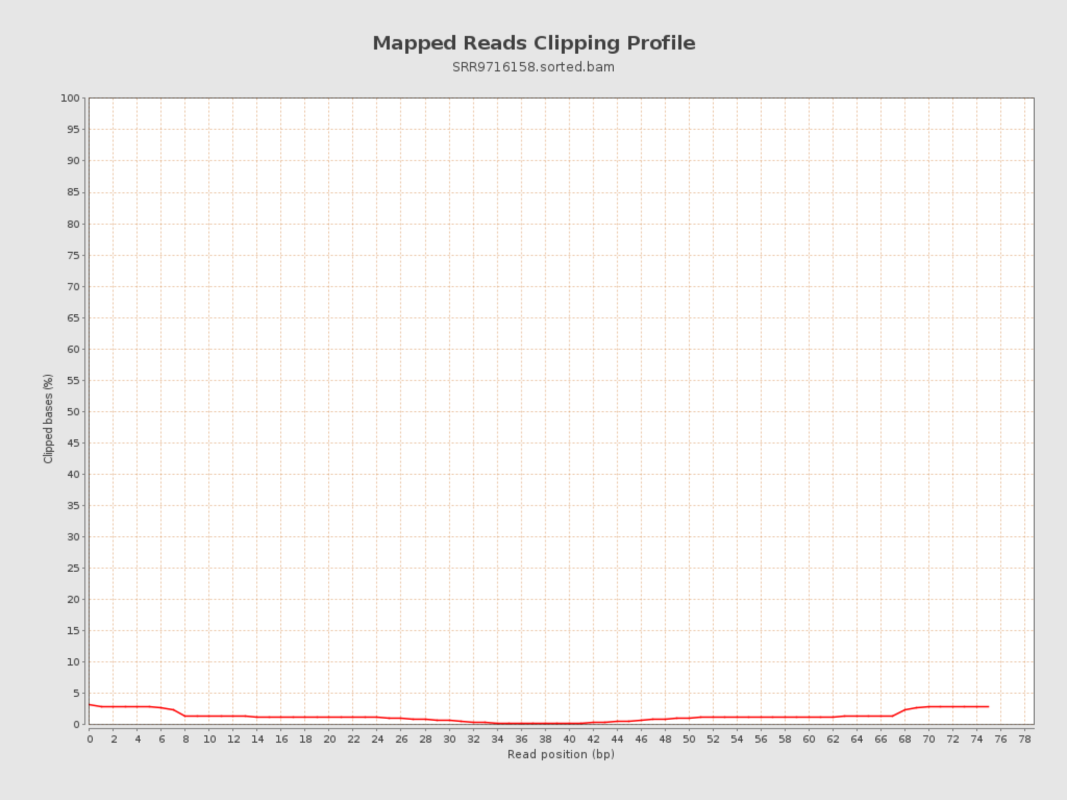
8. Results : Mapped Reads Nucleotide Content



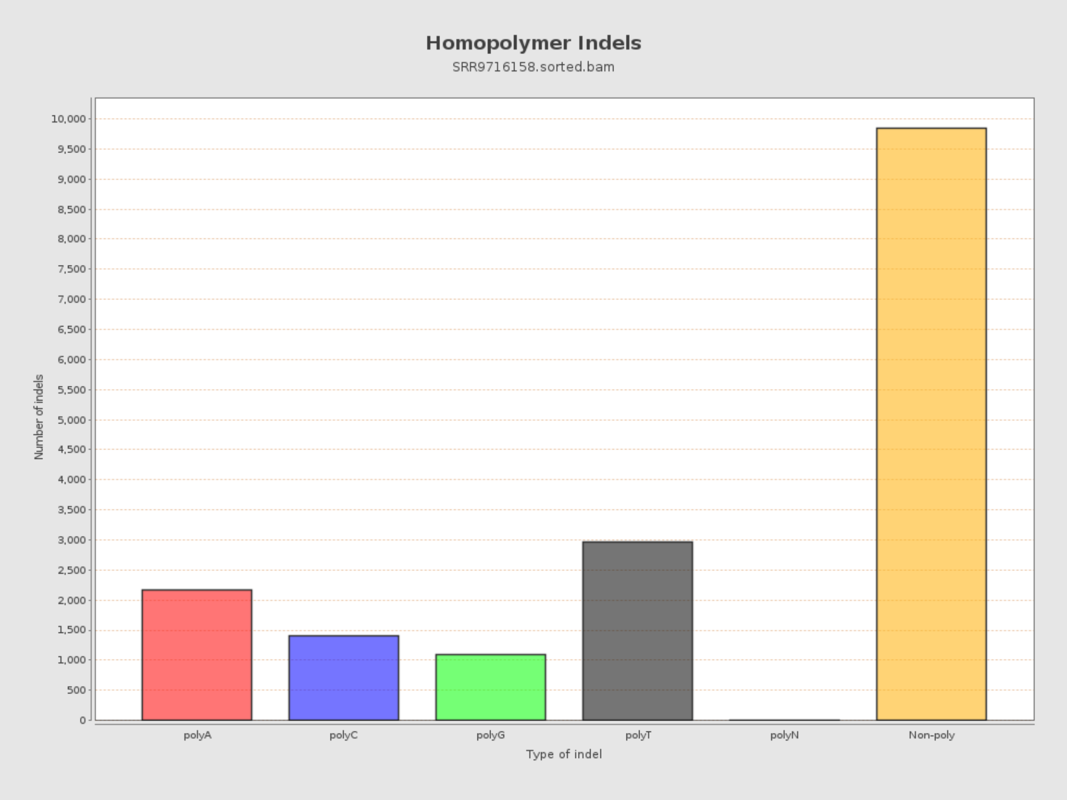
9. Results : Mapped Reads GC-content Distribution



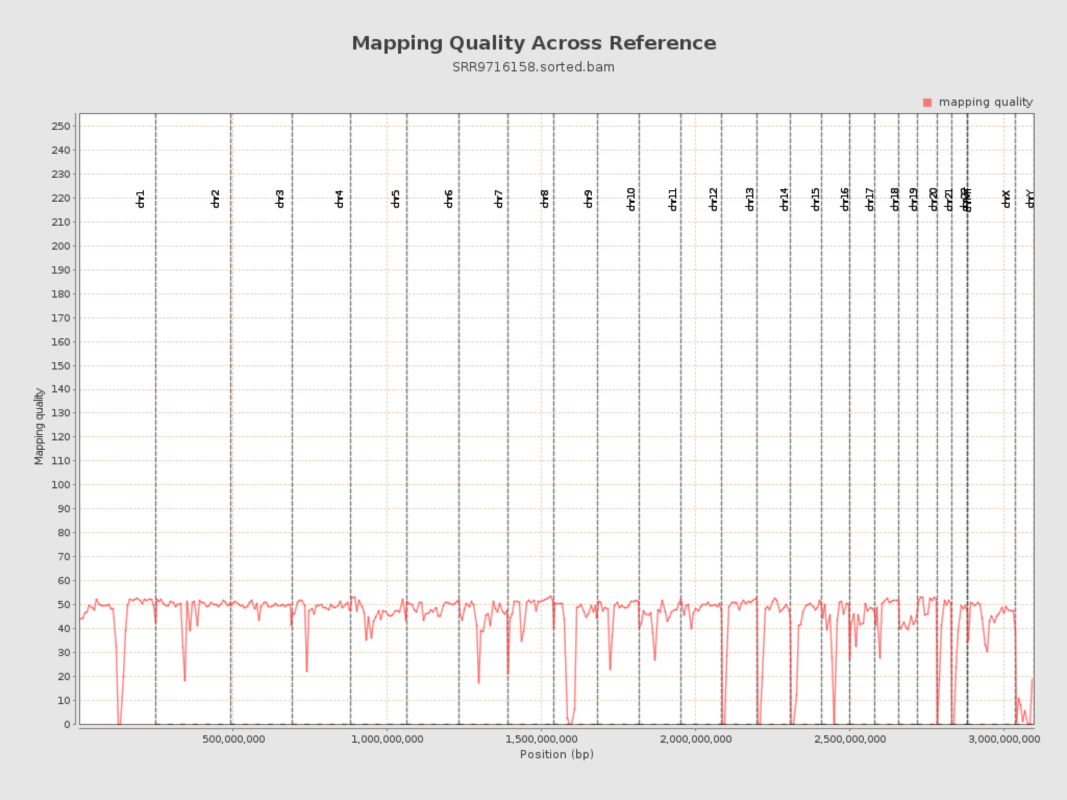
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram