Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 15:20:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716858.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_SRR9716858 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716858.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 15:20:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716858.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,090,936
Mapped reads	1,971,715 / 94.3%
Unmapped reads	119,221 / 5.7%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	41,490 / 1.98%
Read min/max/mean length	30 / 101 / 101.72
Duplicated reads (estimated)	110,459 / 5.28%
Duplication rate	4.4%
Clipped reads	2,008,664 / 96.07%

2.2. ACGT Content

Number/percentage of A's	38,316,119 / 25.17%
Number/percentage of C's	31,758,371 / 20.86%
Number/percentage of T's	44,987,992 / 29.55%
Number/percentage of G's	37,156,722 / 24.41%
Number/percentage of N's	5,735 / 0%
GC Percentage	45.27%

2.3. Coverage

Mean	0.0492

Standard Deviation	0.3878

2.4. Mapping Quality

Mean Mapping Quality	46.58

2.5. Mismatches and indels

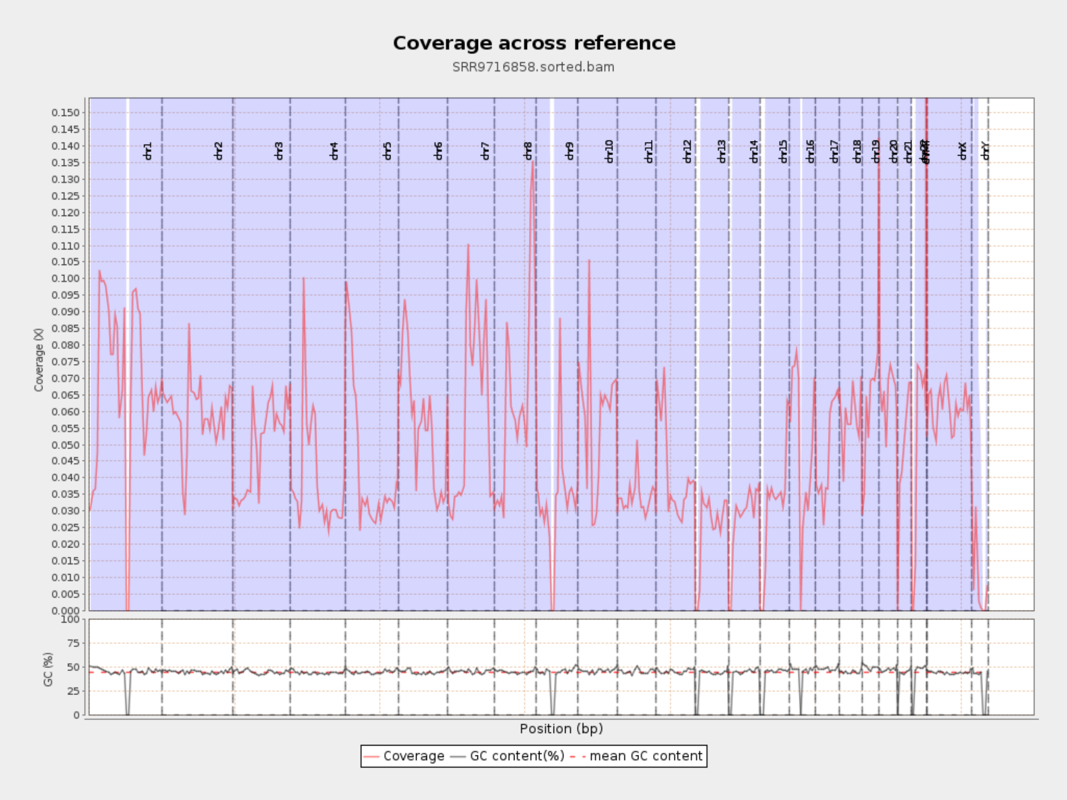
General error rate	0.66%
Mismatches	968,887
Insertions	14,190
Mapped reads with at least one insertion	0.71%
Deletions	28,219
Mapped reads with at least one deletion	1.4%
Homopolymer indels	37.62%

2.6. Chromosome stats

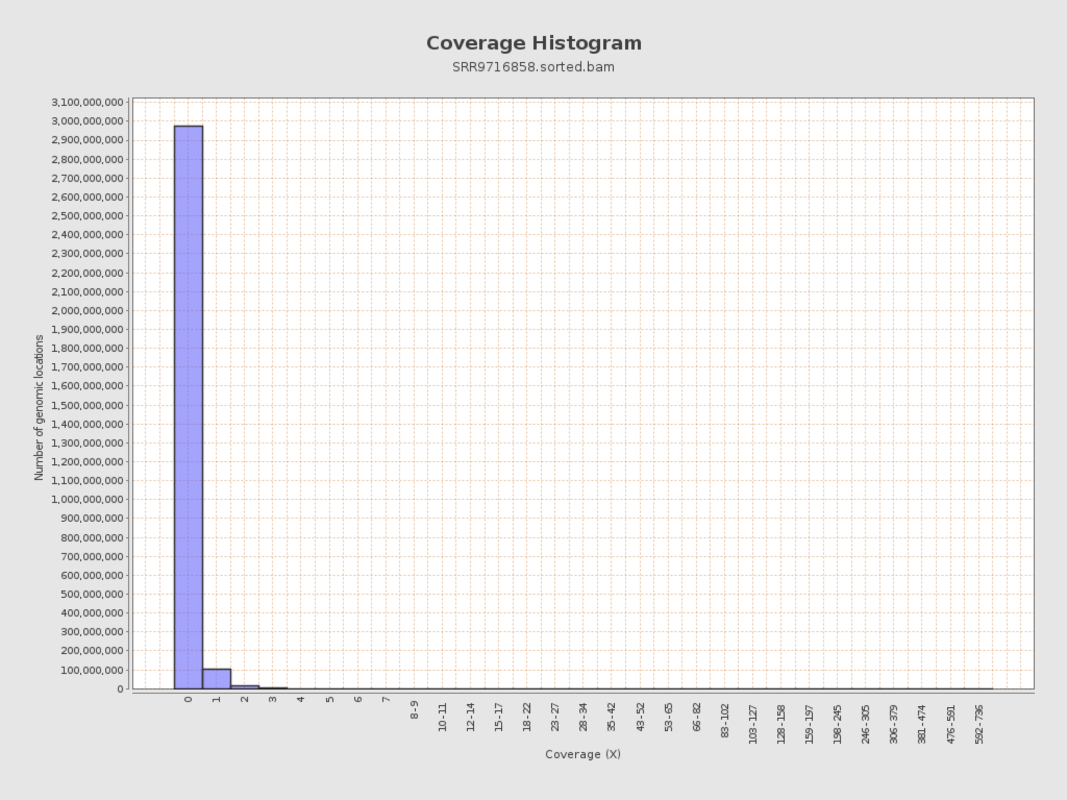
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16923786	0.0679	0.719
chr2	243199373	14422930	0.0593	0.4193
chr3	198022430	9831867	0.0497	0.2669
chr4	191154276	7450063	0.039	0.3397
chr5	180915260	7766034	0.0429	0.249
chr6	171115067	9613223	0.0562	0.2996
chr7	159138663	9632065	0.0605	0.5248

chr8	146364022	9408571	0.0643	0.4133
chr9	141213431	4574267	0.0324	0.2711
chr10	135534747	7866037	0.058	0.5291
chr11	135006516	4621044	0.0342	0.3035
chr12	133851895	5611600	0.0419	0.2442
chr13	115169878	2878165	0.025	0.1848
chr14	107349540	2919777	0.0272	0.2128
chr15	102531392	3184842	0.0311	0.2077
chr16	90354753	4510662	0.0499	0.2839
chr17	81195210	3848639	0.0474	0.2856
chr18	78077248	4519586	0.0579	0.4045
chr19	59128983	3774964	0.0638	0.5314
chr20	63025520	4117029	0.0653	0.3228
chr21	48129895	2344803	0.0487	0.3358
chr22	51304566	2433944	0.0474	0.2785
chrMT	16571	21666	1.3075	1.5196
chrX	155270560	9510803	0.0613	0.3124
chrY	59373566	497545	0.0084	0.2979

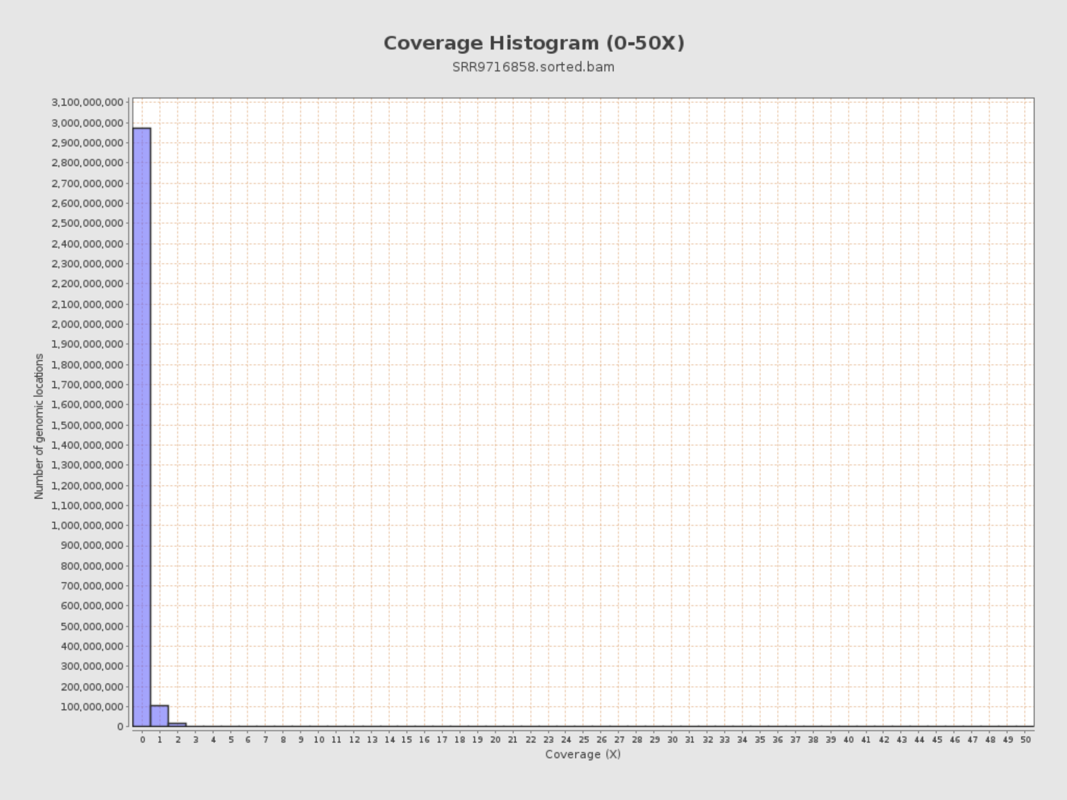
3. Results : Coverage across reference



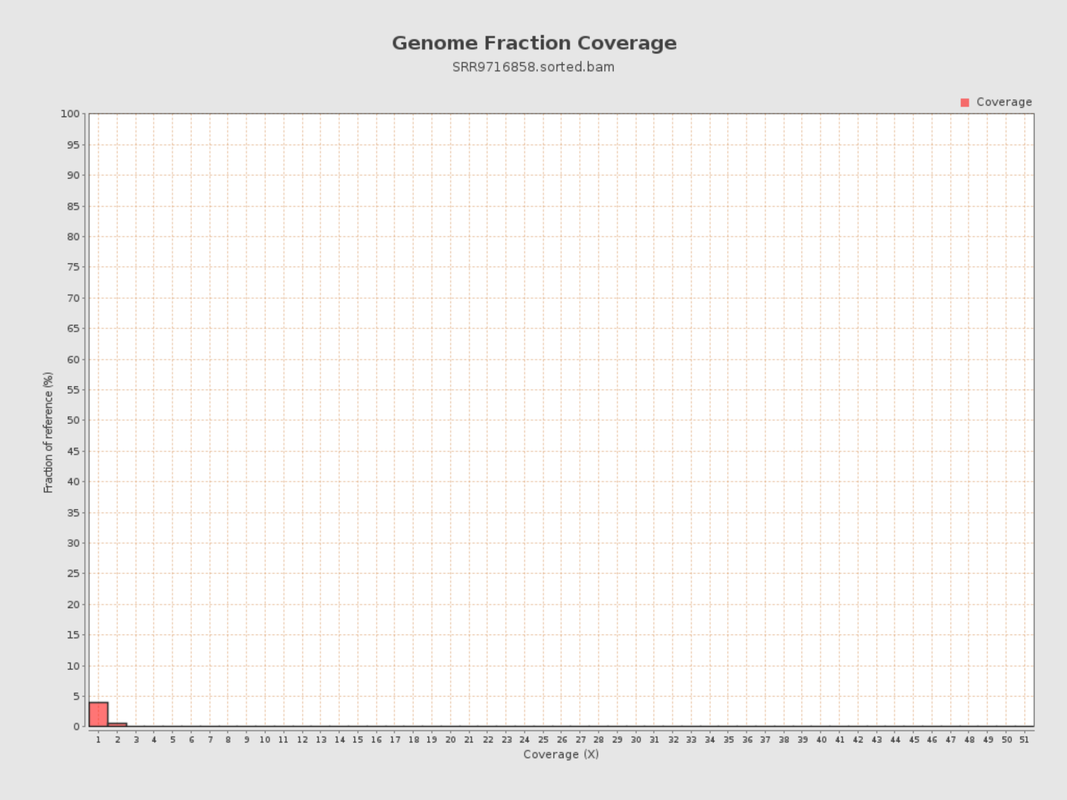
4. Results : Coverage Histogram



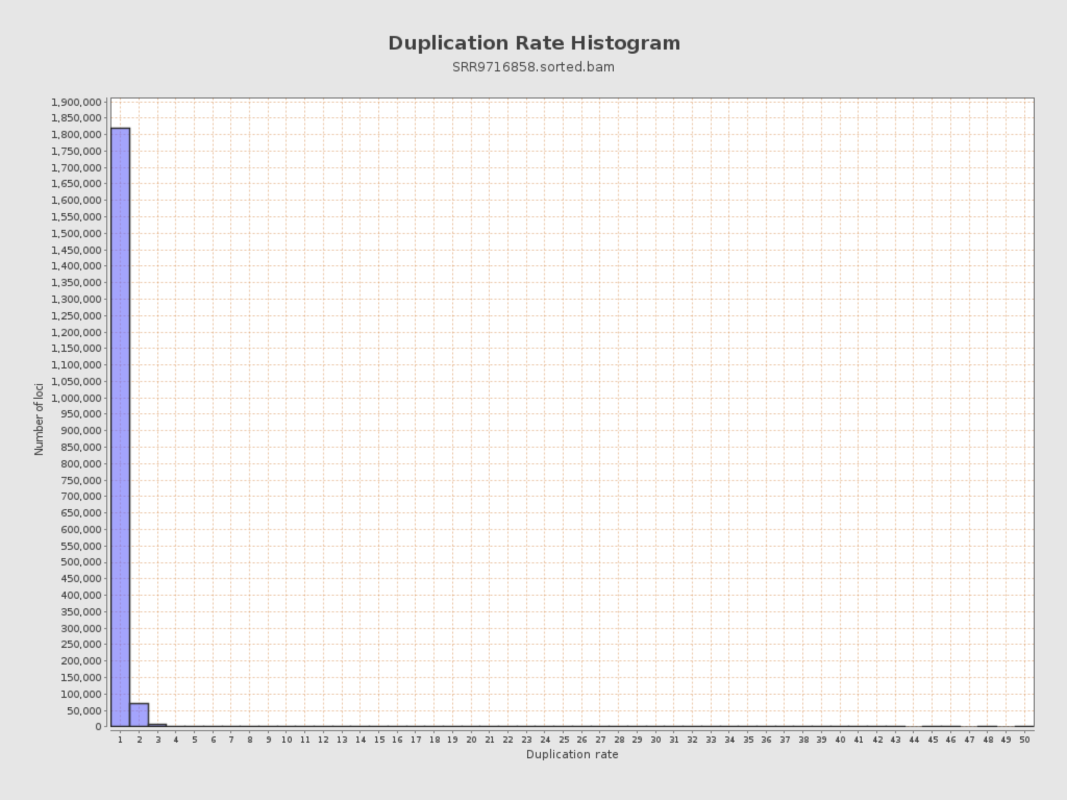
5. Results : Coverage Histogram (0-50X)



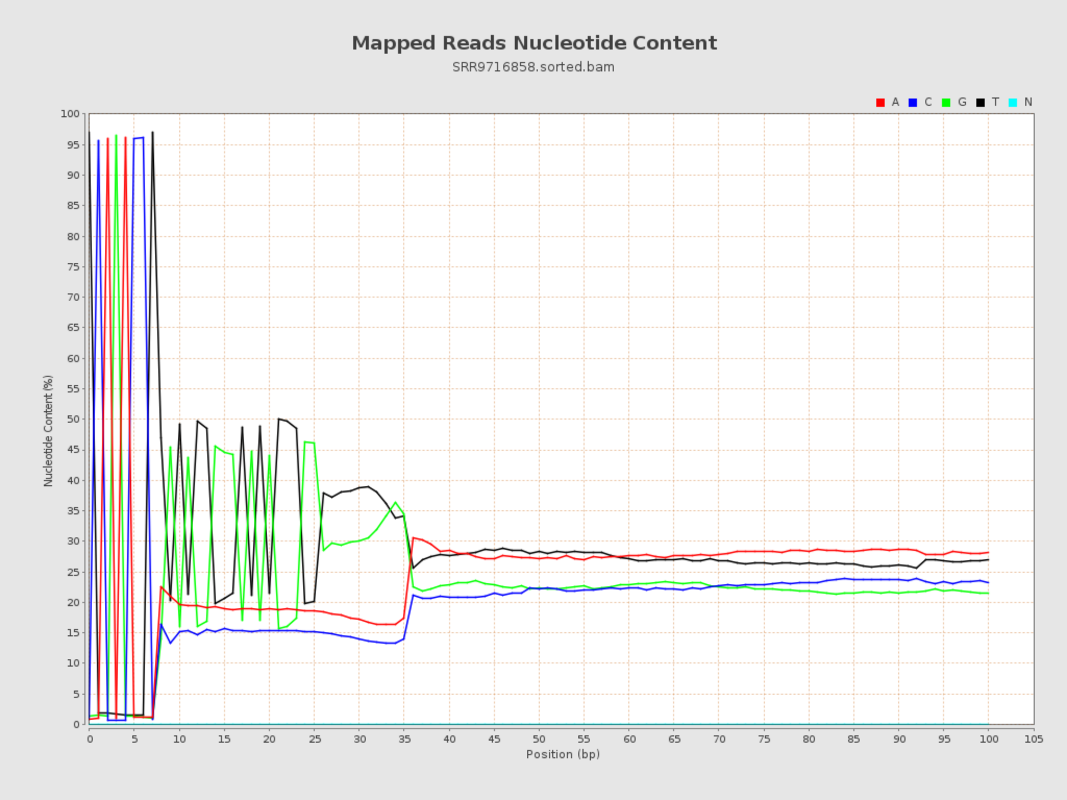
6. Results : Genome Fraction Coverage



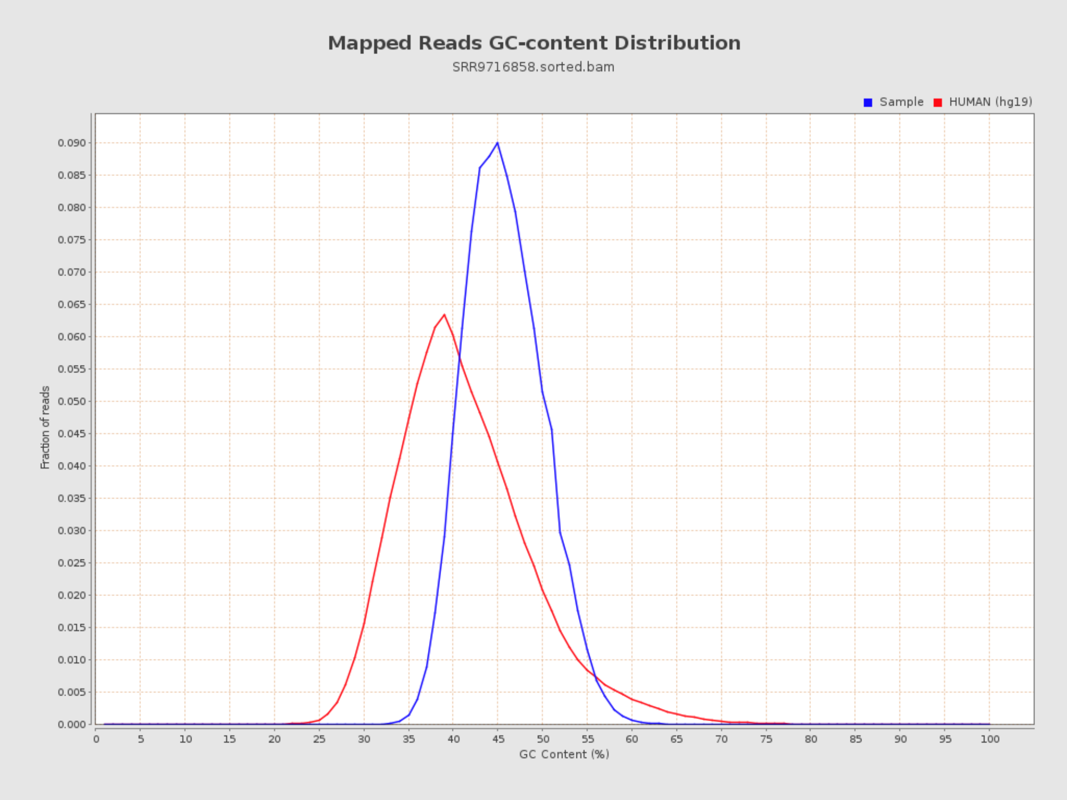
7. Results : Duplication Rate Histogram



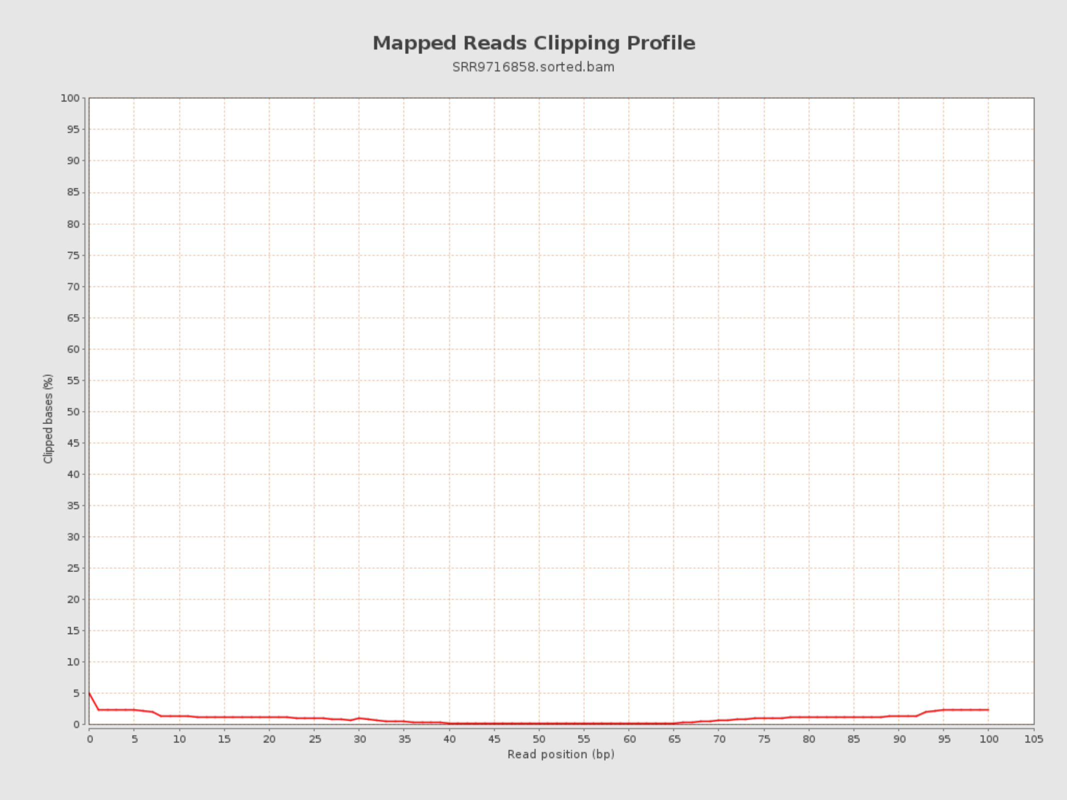
8. Results : Mapped Reads Nucleotide Content



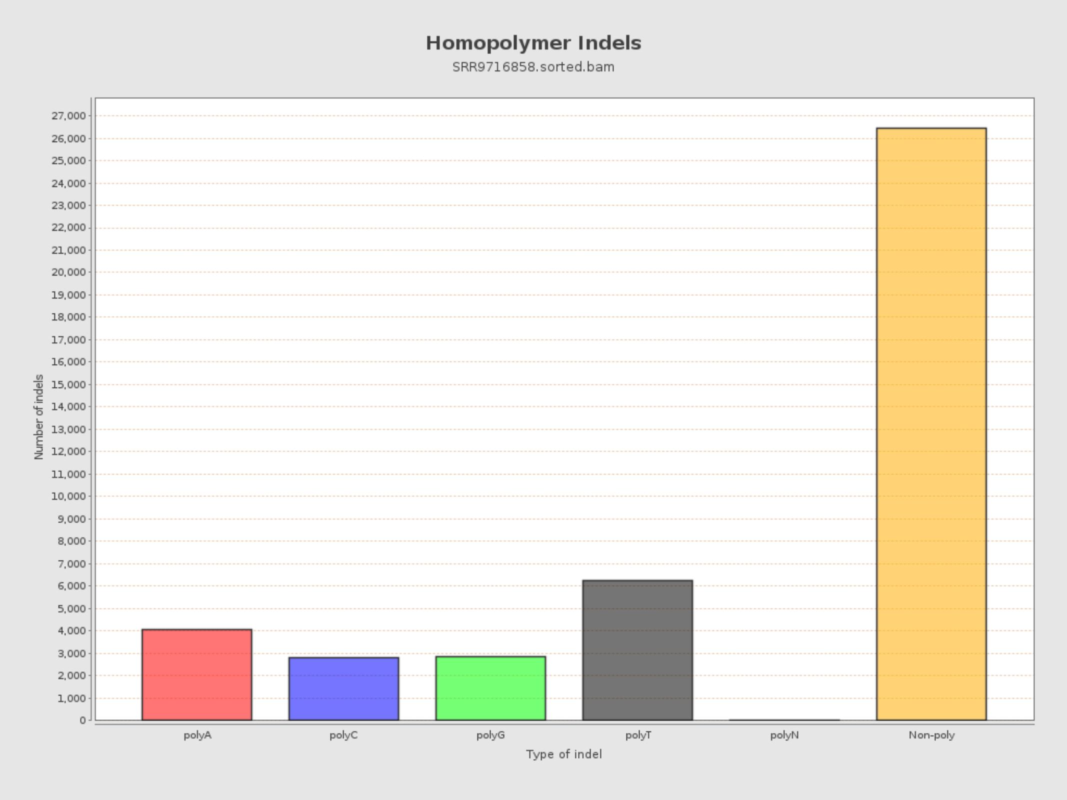
9. Results : Mapped Reads GC-content Distribution



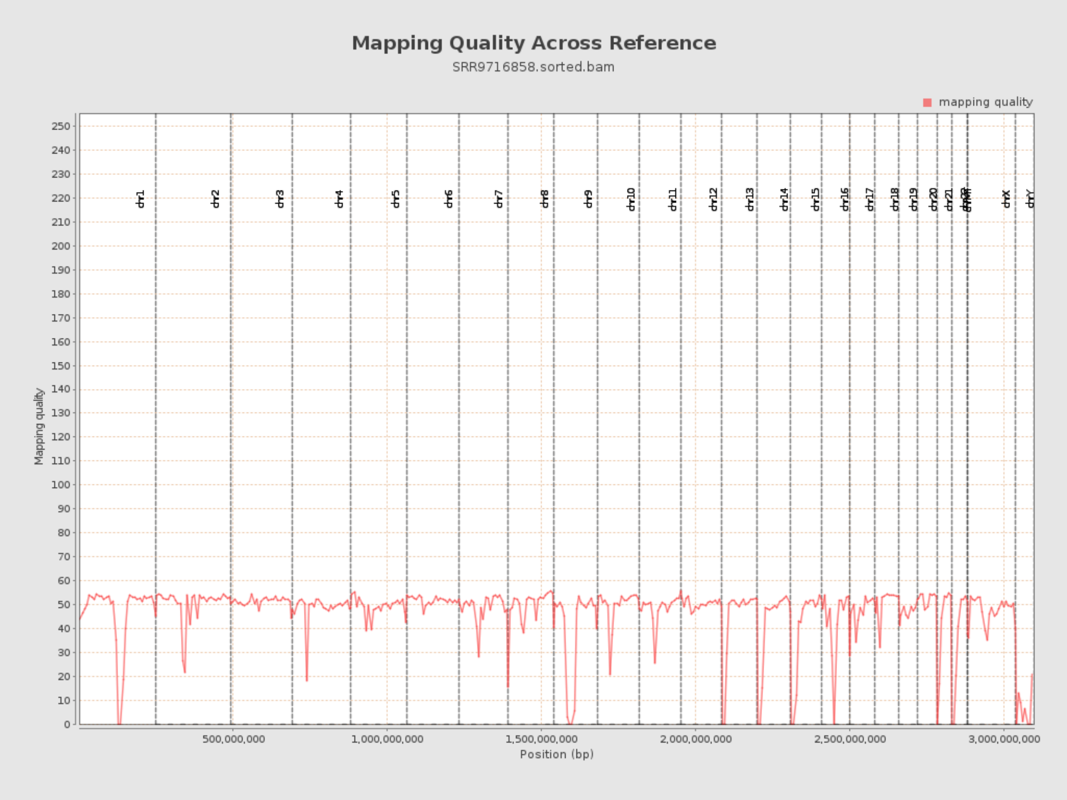
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram