Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 10:20:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716376.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_SRR9716376 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716376.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 10:20:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716376.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,862,380
Mapped reads	1,736,453 / 93.24%
Unmapped reads	125,927 / 6.76%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	35,371 / 1.9%
Read min/max/mean length	30 / 101 / 101.68
Duplicated reads (estimated)	67,957 / 3.65%
Duplication rate	2.75%
Clipped reads	1,769,415 / 95.01%

2.2. ACGT Content

Number/percentage of A's	35,187,610 / 25.63%
Number/percentage of C's	26,537,631 / 19.33%
Number/percentage of T's	42,608,827 / 31.03%
Number/percentage of G's	32,960,286 / 24.01%
Number/percentage of N's	9,929 / 0.01%
GC Percentage	43.33%

2.3. Coverage

Mean	0.0444

Standard Deviation	0.4242

2.4. Mapping Quality

Mean Mapping Quality	47.45

2.5. Mismatches and indels

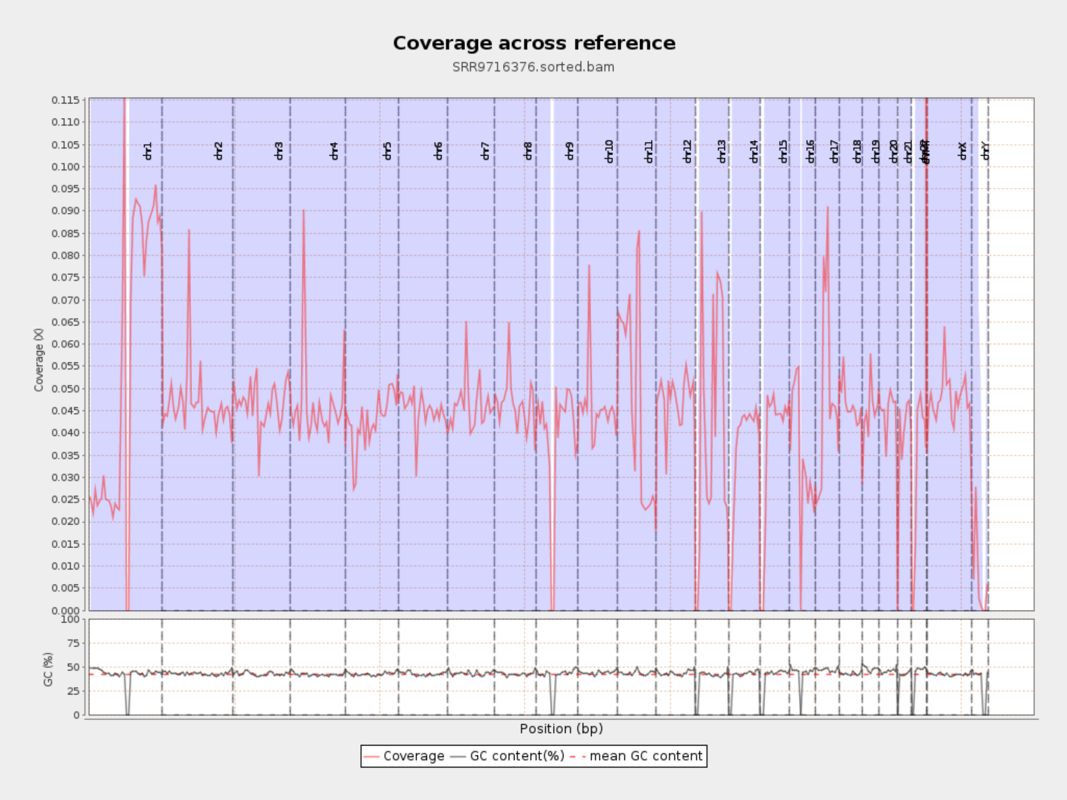
General error rate	0.68%
Mismatches	915,884
Insertions	10,948
Mapped reads with at least one insertion	0.62%
Deletions	33,531
Mapped reads with at least one deletion	1.9%
Homopolymer indels	42.9%

2.6. Chromosome stats

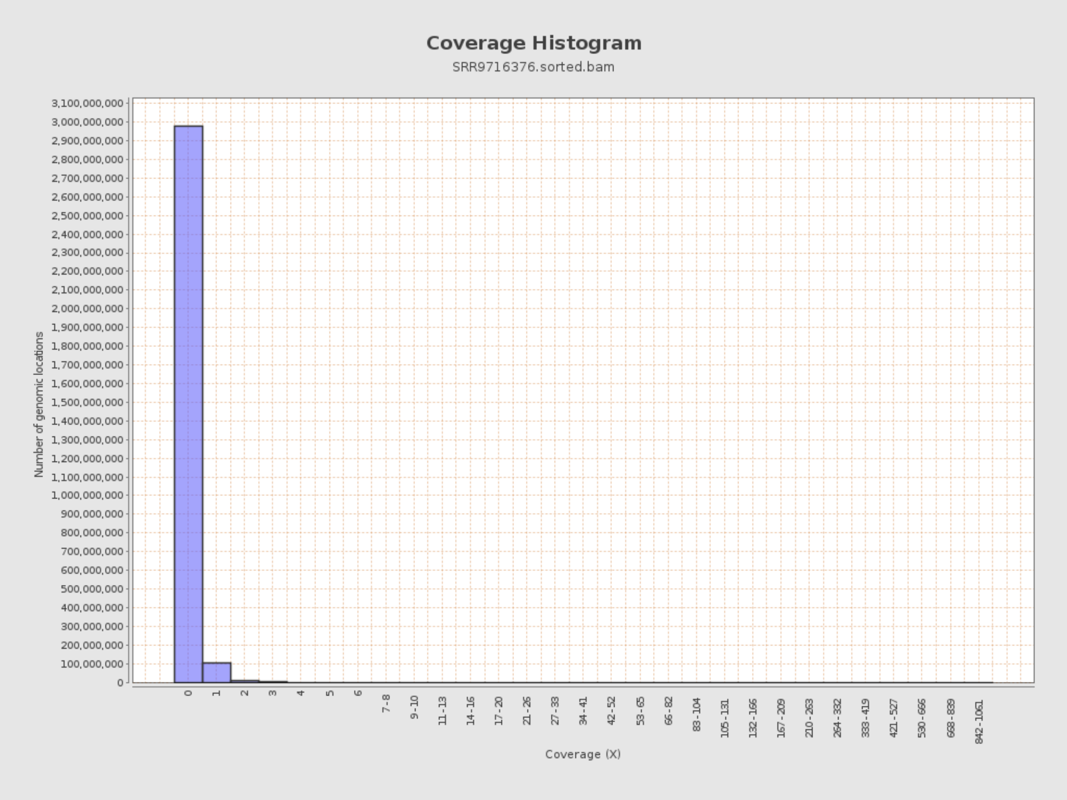
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13667503	0.0548	0.9355
chr2	243199373	11389198	0.0468	0.4298
chr3	198022430	9251970	0.0467	0.2398
chr4	191154276	8820640	0.0461	0.3039
chr5	180915260	7726742	0.0427	0.2317
chr6	171115067	7734813	0.0452	0.2557
chr7	159138663	7354113	0.0462	0.4689

chr8	146364022	6823909	0.0466	0.4953
chr9	141213431	5529129	0.0392	0.3328
chr10	135534747	6223176	0.0459	0.3844
chr11	135006516	6394348	0.0474	0.3841
chr12	133851895	6397717	0.0478	0.2448
chr13	115169878	4740874	0.0412	0.2276
chr14	107349540	3793816	0.0353	0.227
chr15	102531392	3799217	0.0371	0.2141
chr16	90354753	3098291	0.0343	0.2323
chr17	81195210	3996759	0.0492	0.2875
chr18	78077248	3646179	0.0467	0.6211
chr19	59128983	2675874	0.0453	0.6105
chr20	63025520	2812735	0.0446	0.2535
chr21	48129895	1853789	0.0385	0.2617
chr22	51304566	1580699	0.0308	0.196
chrMT	16571	230906	13.9343	8.1781
chrX	155270560	7408760	0.0477	0.2845
chrY	59373566	418027	0.007	0.2383

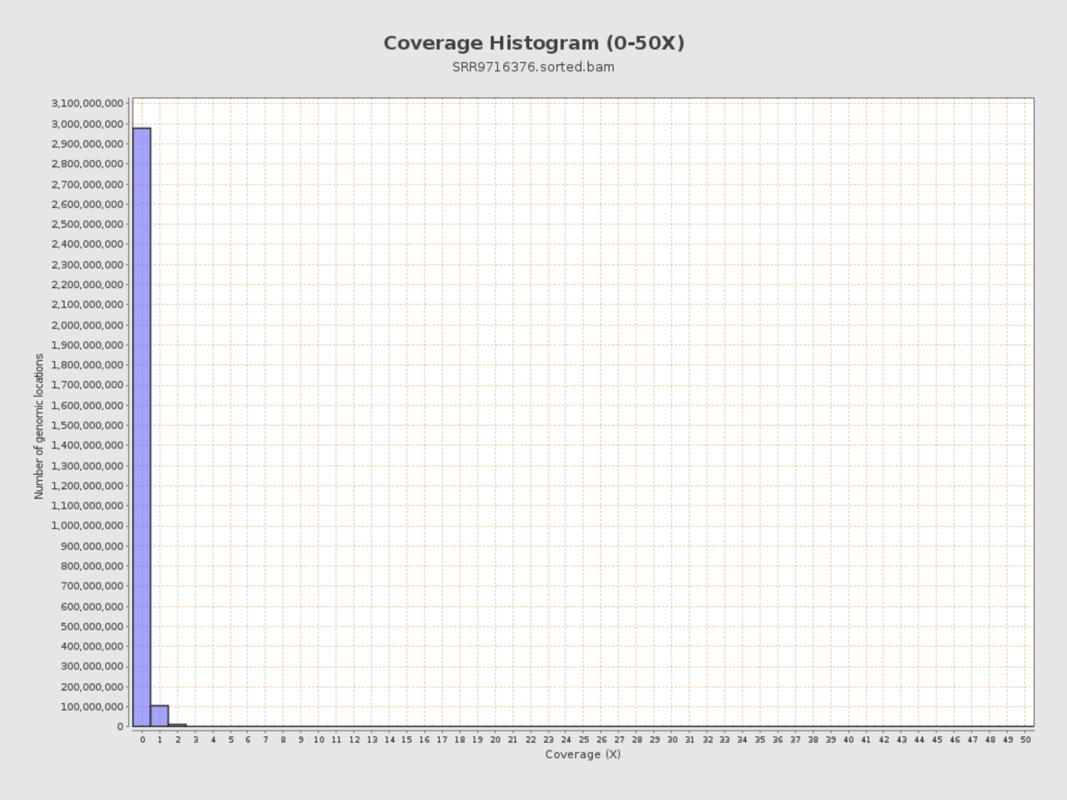
3. Results : Coverage across reference



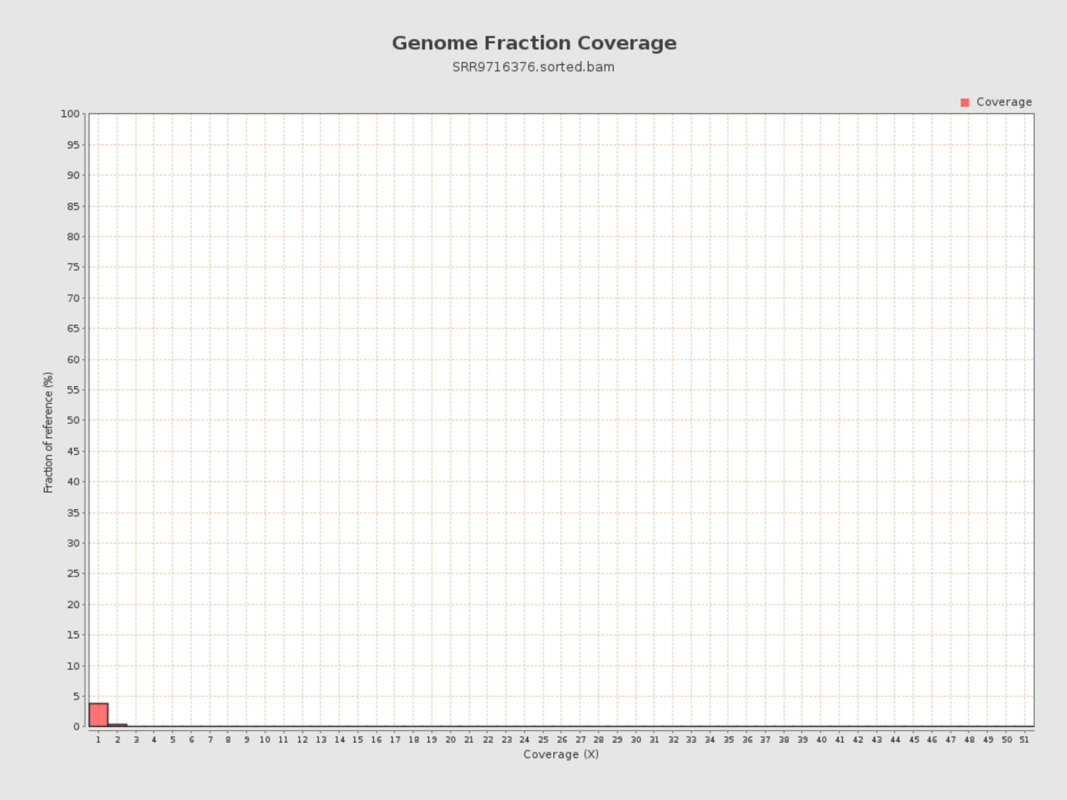
4. Results : Coverage Histogram



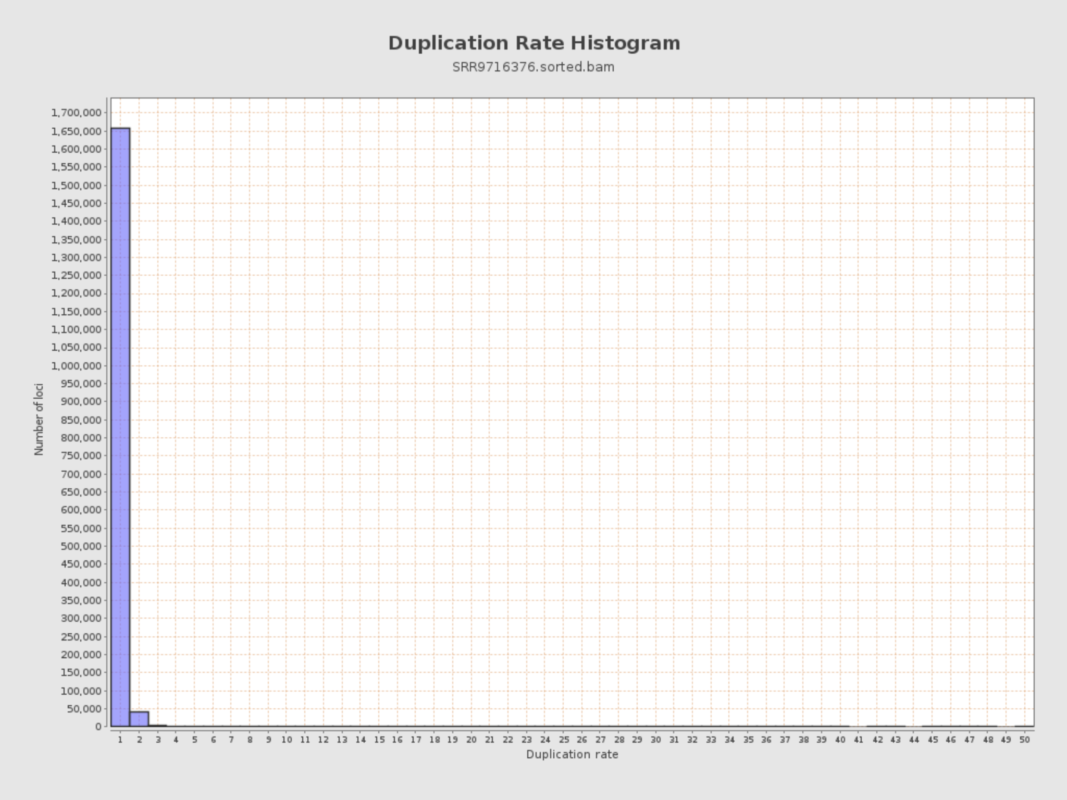
5. Results : Coverage Histogram (0-50X)



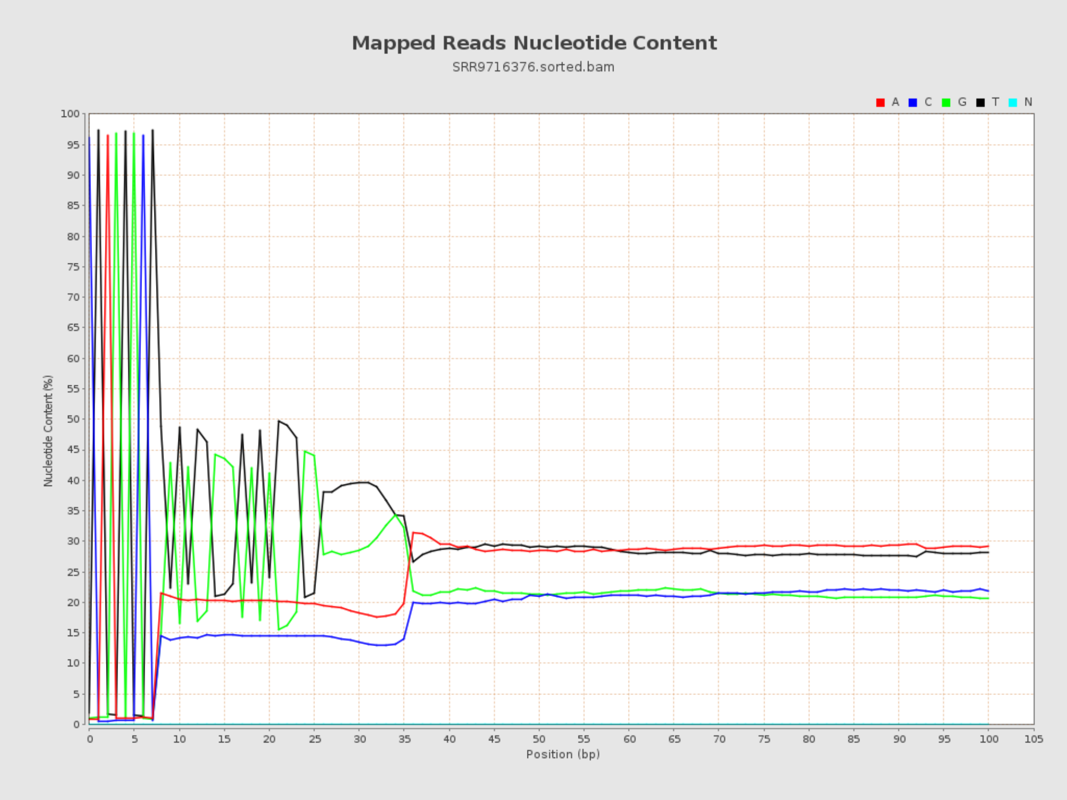
6. Results : Genome Fraction Coverage



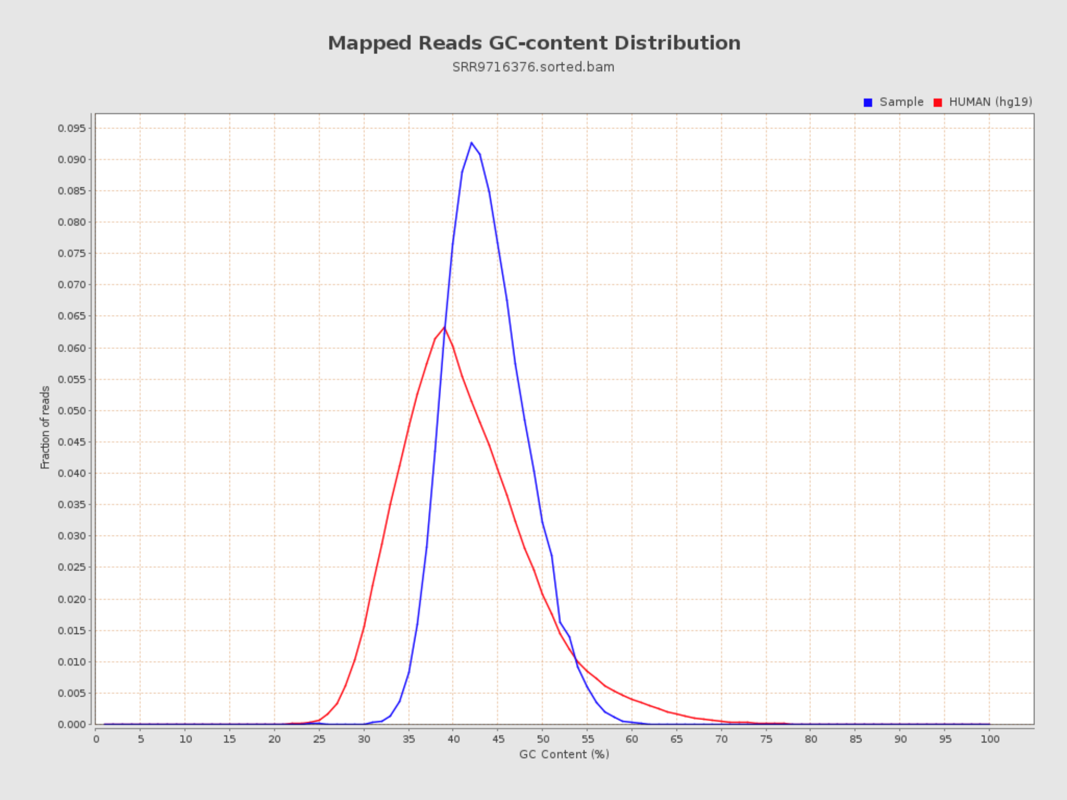
7. Results : Duplication Rate Histogram



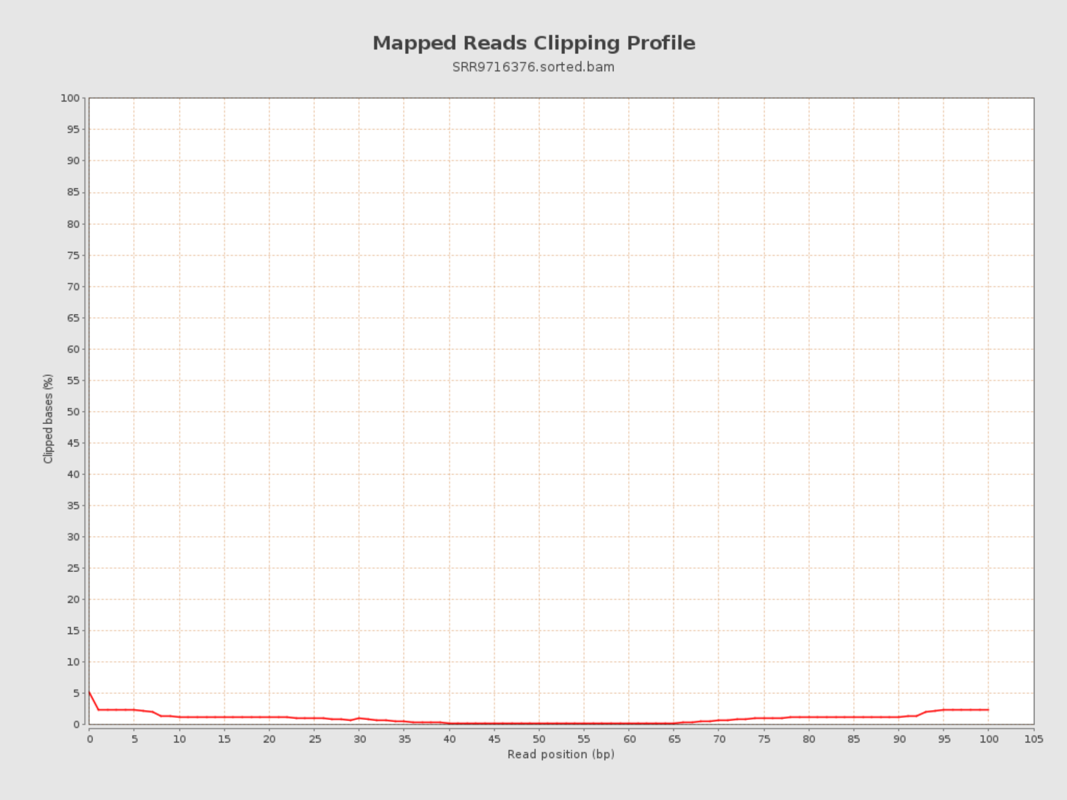
8. Results : Mapped Reads Nucleotide Content



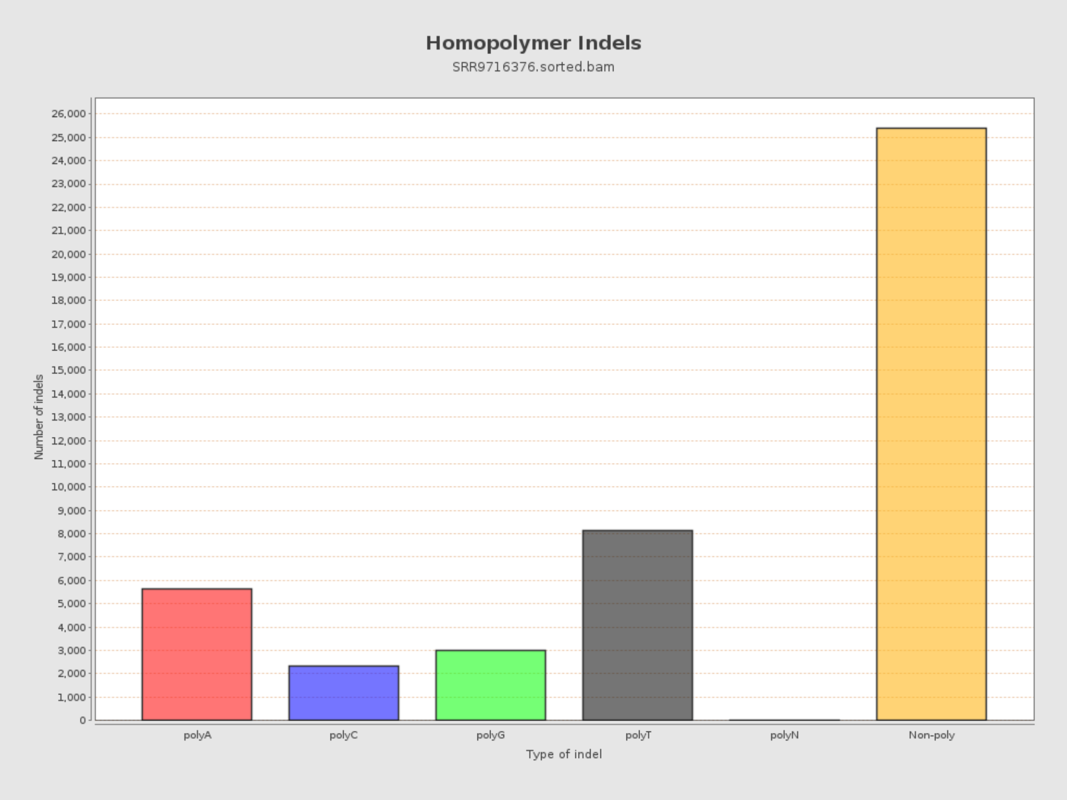
9. Results : Mapped Reads GC-content Distribution



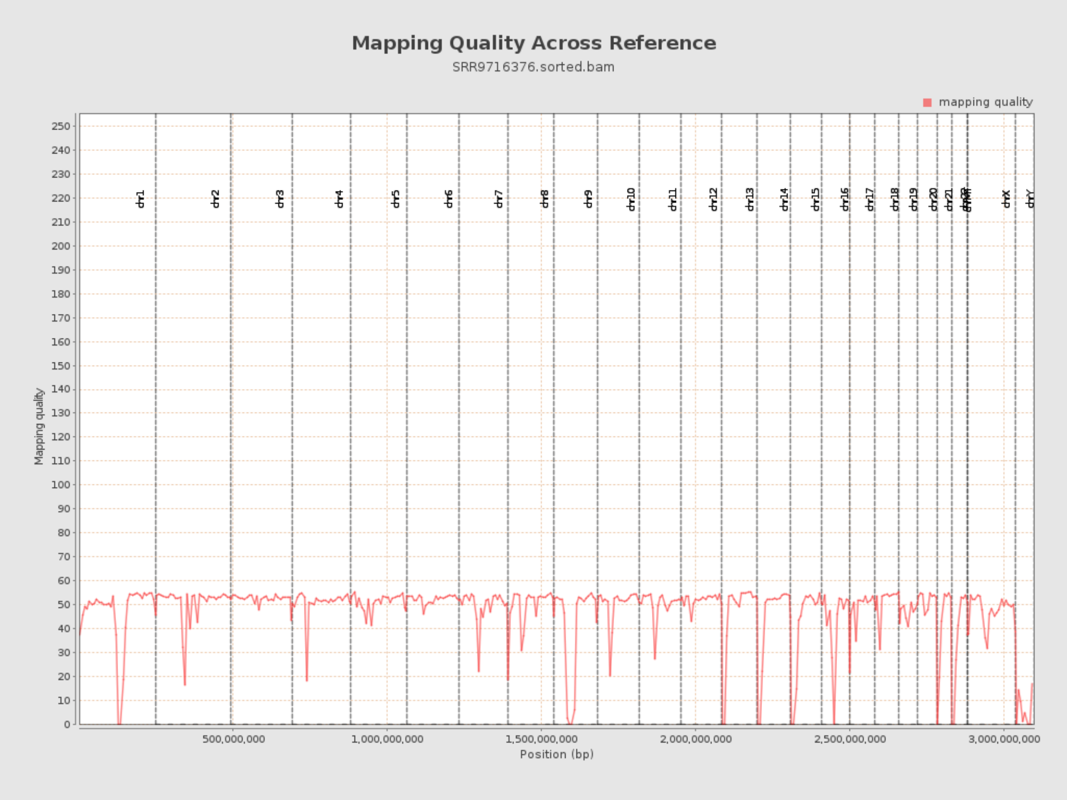
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram