Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 11:20:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716775.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_SRR9716775 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716775.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 11:20:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716775.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,014,608
Mapped reads	2,800,937 / 92.91%
Unmapped reads	213,671 / 7.09%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	66,127 / 2.19%
Read min/max/mean length	30 / 101 / 101.79
Duplicated reads (estimated)	174,594 / 5.79%
Duplication rate	4.76%
Clipped reads	2,861,191 / 94.91%

2.2. ACGT Content

Number/percentage of A's	53,761,979 / 25.11%
Number/percentage of C's	41,603,249 / 19.43%
Number/percentage of T's	64,109,384 / 29.94%
Number/percentage of G's	54,626,032 / 25.51%
Number/percentage of N's	8,723 / 0%
GC Percentage	44.94%

2.3. Coverage

Mean	0.0692

Standard Deviation	0.522

2.4. Mapping Quality

Mean Mapping Quality	45.86

2.5. Mismatches and indels

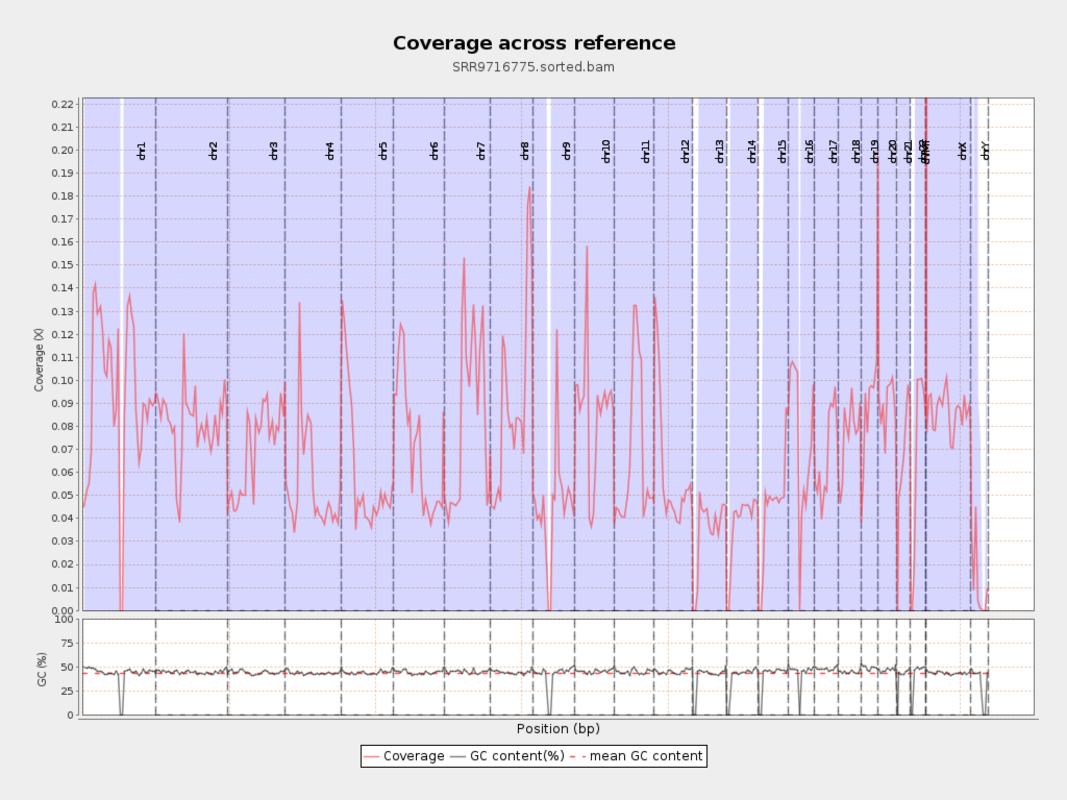
General error rate	0.68%
Mismatches	1,411,641
Insertions	18,642
Mapped reads with at least one insertion	0.65%
Deletions	39,758
Mapped reads with at least one deletion	1.4%
Homopolymer indels	39.24%

2.6. Chromosome stats

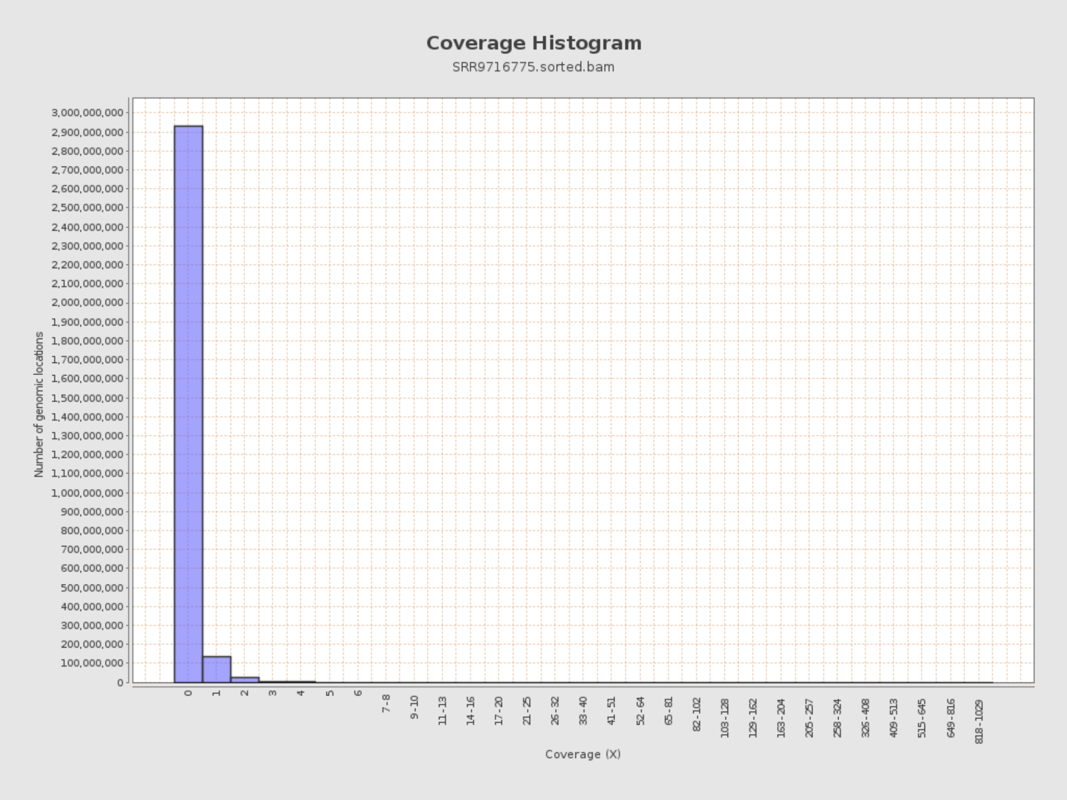
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	23153935	0.0929	0.9756
chr2	243199373	19849074	0.0816	0.5669
chr3	198022430	13796356	0.0697	0.3337
chr4	191154276	10464274	0.0547	0.4588
chr5	180915260	10968858	0.0606	0.3107
chr6	171115067	11994203	0.0701	0.3606
chr7	159138663	13242017	0.0832	0.7423

chr8	146364022	13248202	0.0905	0.5415
chr9	141213431	6428306	0.0455	0.3671
chr10	135534747	11552744	0.0852	0.7513
chr11	135006516	8988176	0.0666	0.4394
chr12	133851895	8287845	0.0619	0.3138
chr13	115169878	3973436	0.0345	0.2274
chr14	107349540	4027709	0.0375	0.2668
chr15	102531392	4438590	0.0433	0.2553
chr16	90354753	6555904	0.0726	0.3691
chr17	81195210	5520976	0.068	0.3752
chr18	78077248	5899054	0.0756	0.5647
chr19	59128983	5395759	0.0913	0.7057
chr20	63025520	5635839	0.0894	0.4101
chr21	48129895	3179857	0.0661	0.4178
chr22	51304566	3399596	0.0663	0.3414
chrMT	16571	36470	2.2008	2.151
chrX	155270560	13441286	0.0866	0.4037
chrY	59373566	713788	0.012	0.4275

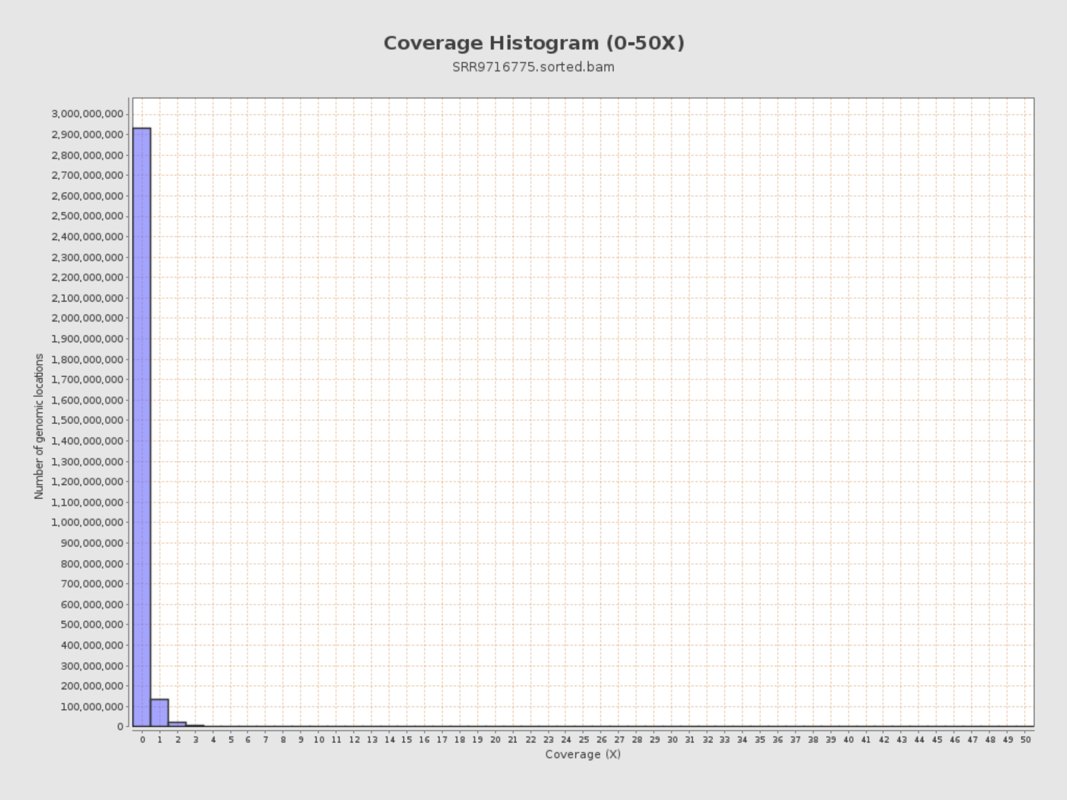
3. Results : Coverage across reference



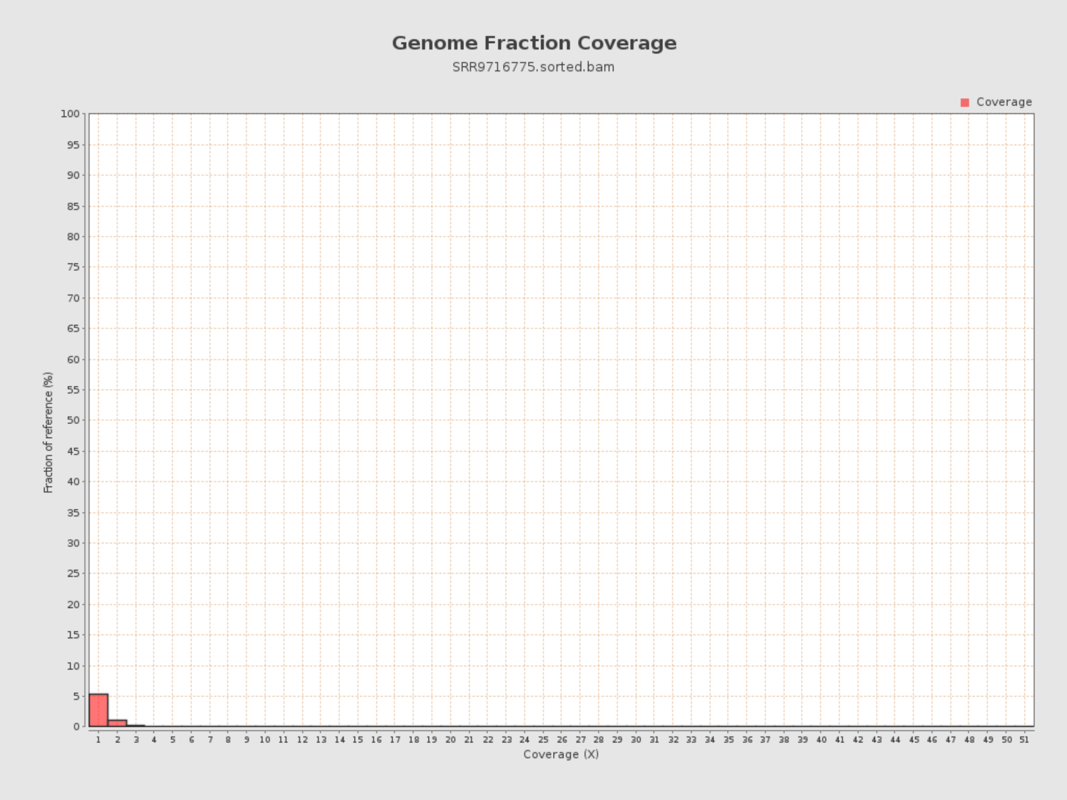
4. Results : Coverage Histogram



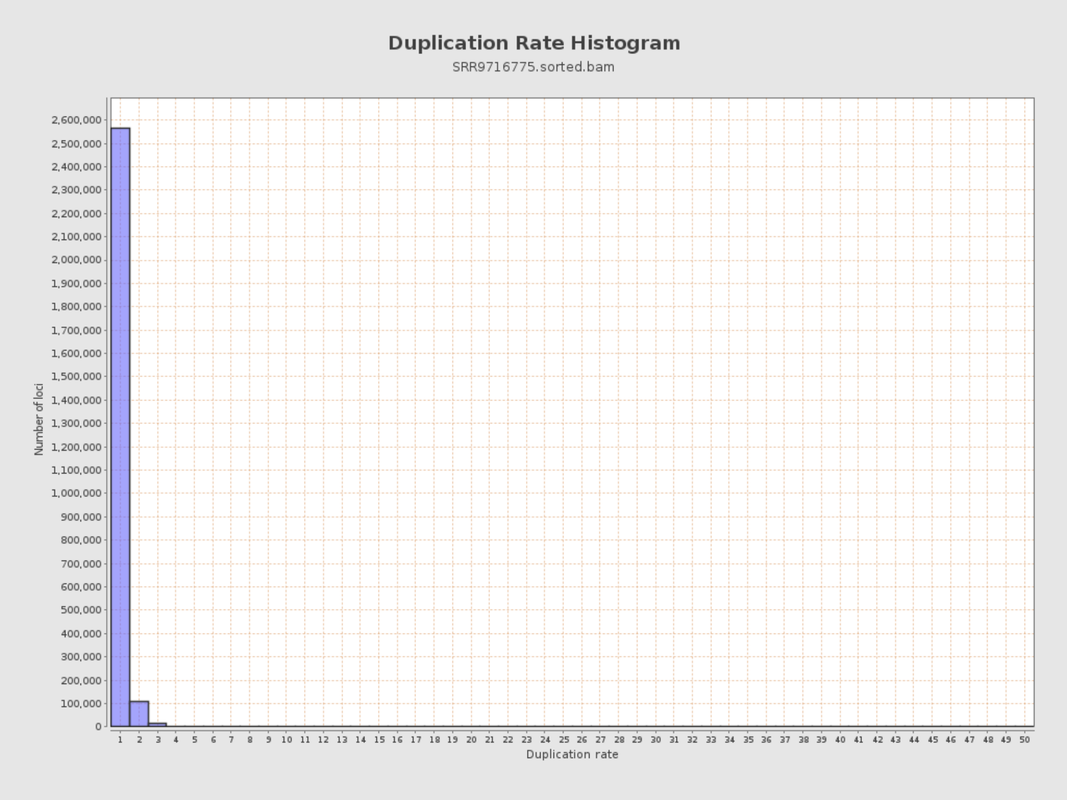
5. Results : Coverage Histogram (0-50X)



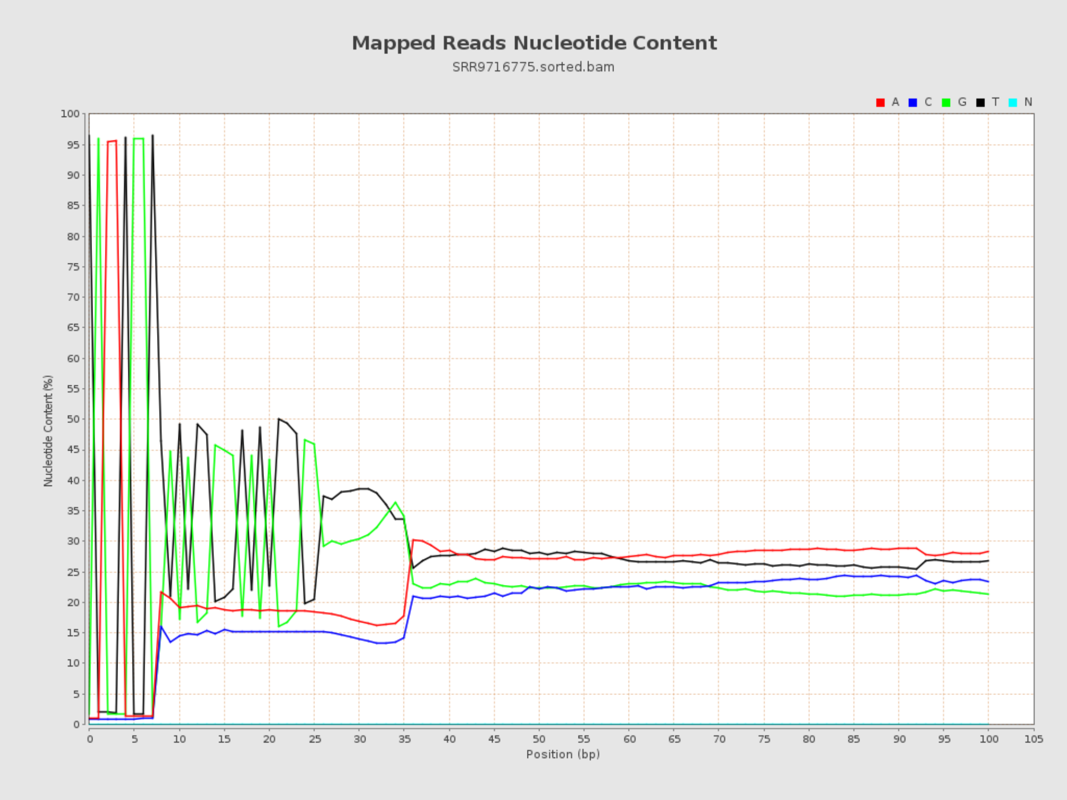
6. Results : Genome Fraction Coverage



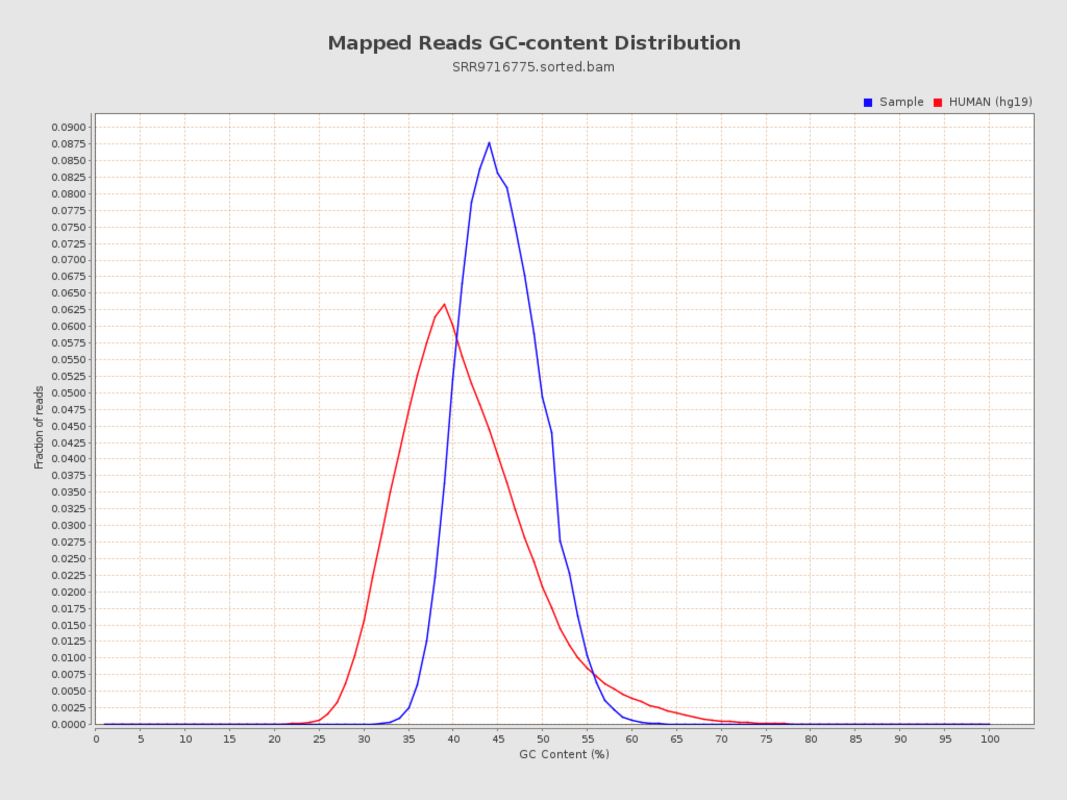
7. Results : Duplication Rate Histogram



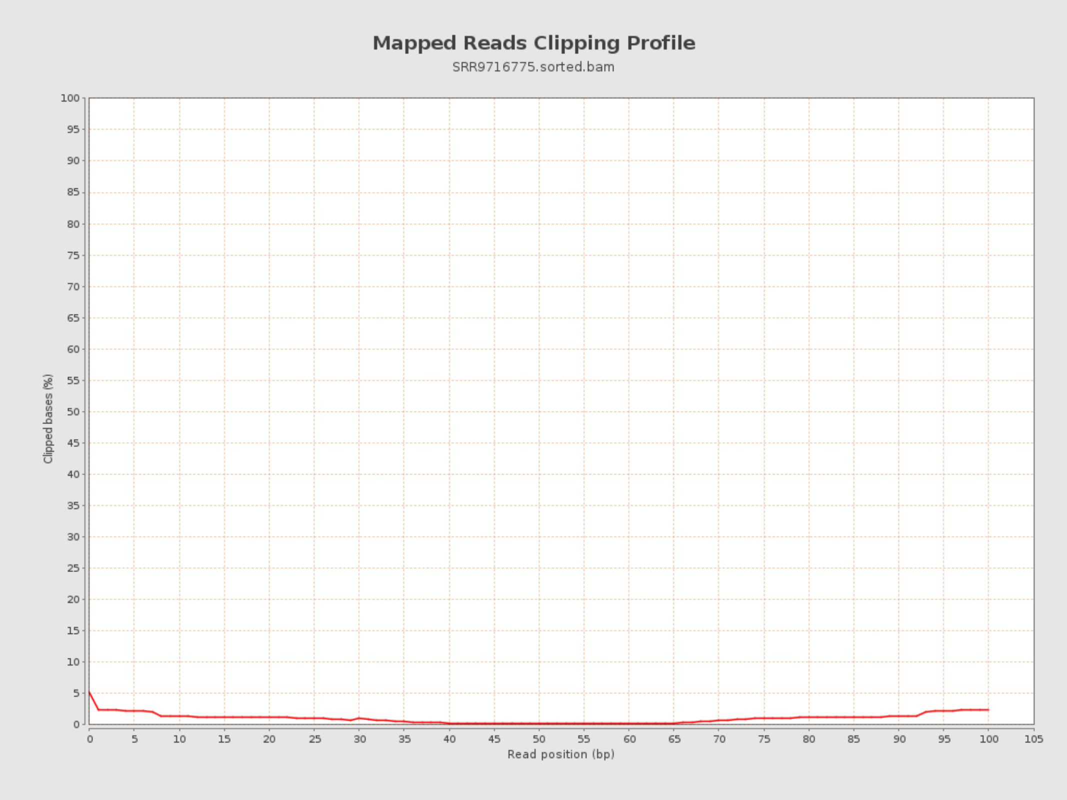
8. Results : Mapped Reads Nucleotide Content



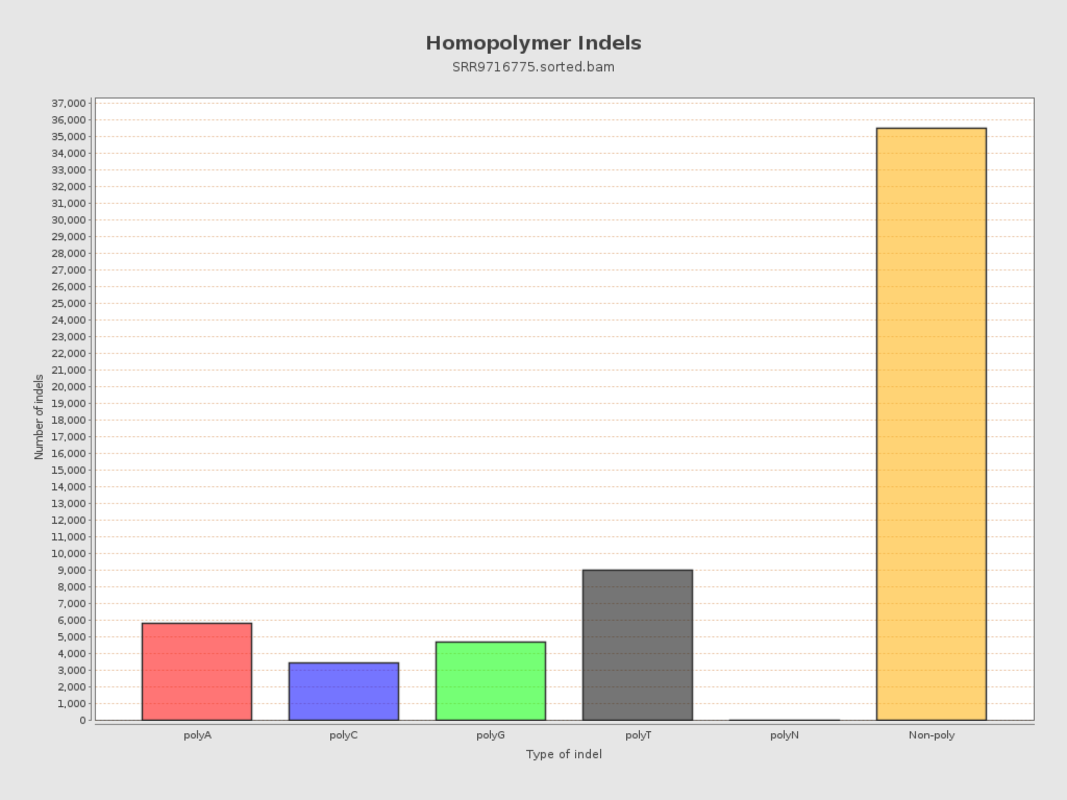
9. Results : Mapped Reads GC-content Distribution



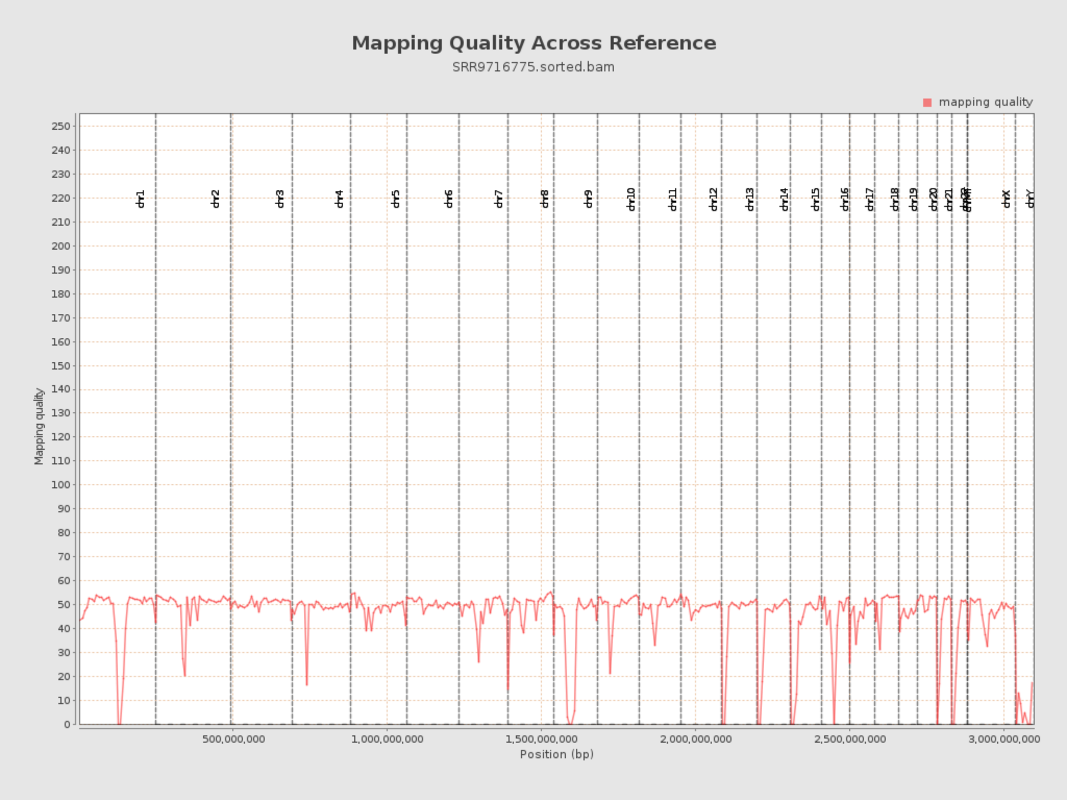
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram