Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 14:33:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716844.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_SRR9716844 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716844.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 14:33:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716844.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,325,715
Mapped reads	1,164,688 / 87.85%
Unmapped reads	161,027 / 12.15%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,884 / 1.5%
Read min/max/mean length	30 / 101 / 101.55
Duplicated reads (estimated)	43,122 / 3.25%
Duplication rate	2.16%
Clipped reads	1,181,230 / 89.1%

2.2. ACGT Content

Number/percentage of A's	23,357,506 / 25.53%
Number/percentage of C's	17,329,802 / 18.94%
Number/percentage of T's	28,839,115 / 31.53%
Number/percentage of G's	21,946,802 / 23.99%
Number/percentage of N's	5,365 / 0.01%
GC Percentage	42.94%

2.3. Coverage

Mean	0.0296

Standard Deviation	0.3564

2.4. Mapping Quality

Mean Mapping Quality	44.9

2.5. Mismatches and indels

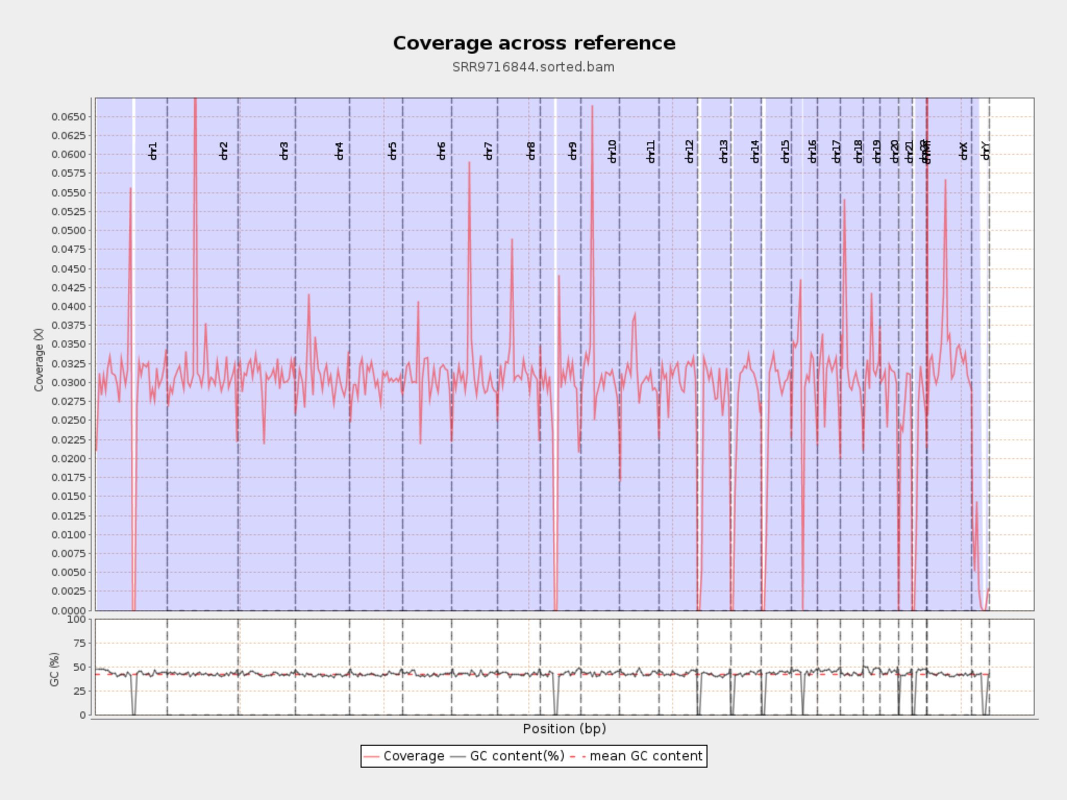
General error rate	0.86%
Mismatches	765,835
Insertions	9,284
Mapped reads with at least one insertion	0.79%
Deletions	23,385
Mapped reads with at least one deletion	1.98%
Homopolymer indels	43.51%

2.6. Chromosome stats

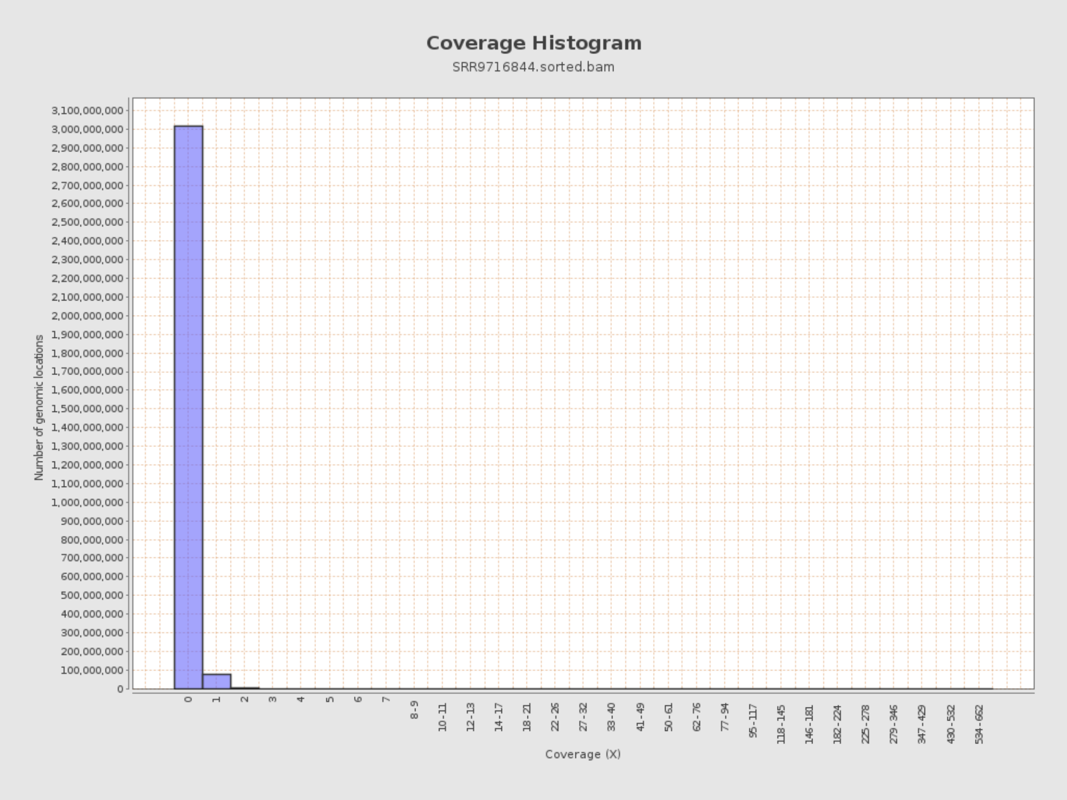
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7303917	0.0293	0.5615
chr2	243199373	7854497	0.0323	0.5314
chr3	198022430	6116091	0.0309	0.1923
chr4	191154276	5889166	0.0308	0.2055
chr5	180915260	5491622	0.0304	0.1939
chr6	171115067	5248363	0.0307	0.2294
chr7	159138663	5040918	0.0317	0.4538

chr8	146364022	4648499	0.0318	0.4616
chr9	141213431	3820101	0.0271	0.3784
chr10	135534747	4377774	0.0323	0.3709
chr11	135006516	4168304	0.0309	0.3507
chr12	133851895	4098255	0.0306	0.1935
chr13	115169878	2852970	0.0248	0.1688
chr14	107349540	2759591	0.0257	0.238
chr15	102531392	2573404	0.0251	0.1728
chr16	90354753	2684587	0.0297	0.2179
chr17	81195210	2510891	0.0309	0.216
chr18	78077248	2551653	0.0327	0.715
chr19	59128983	1915973	0.0324	0.4415
chr20	63025520	1858467	0.0295	0.202
chr21	48129895	1184568	0.0246	0.1853
chr22	51304566	1016164	0.0198	0.1521
chrMT	16571	2380	0.1436	0.4437
chrX	155270560	5293151	0.0341	0.2781
chrY	59373566	257766	0.0043	0.1258

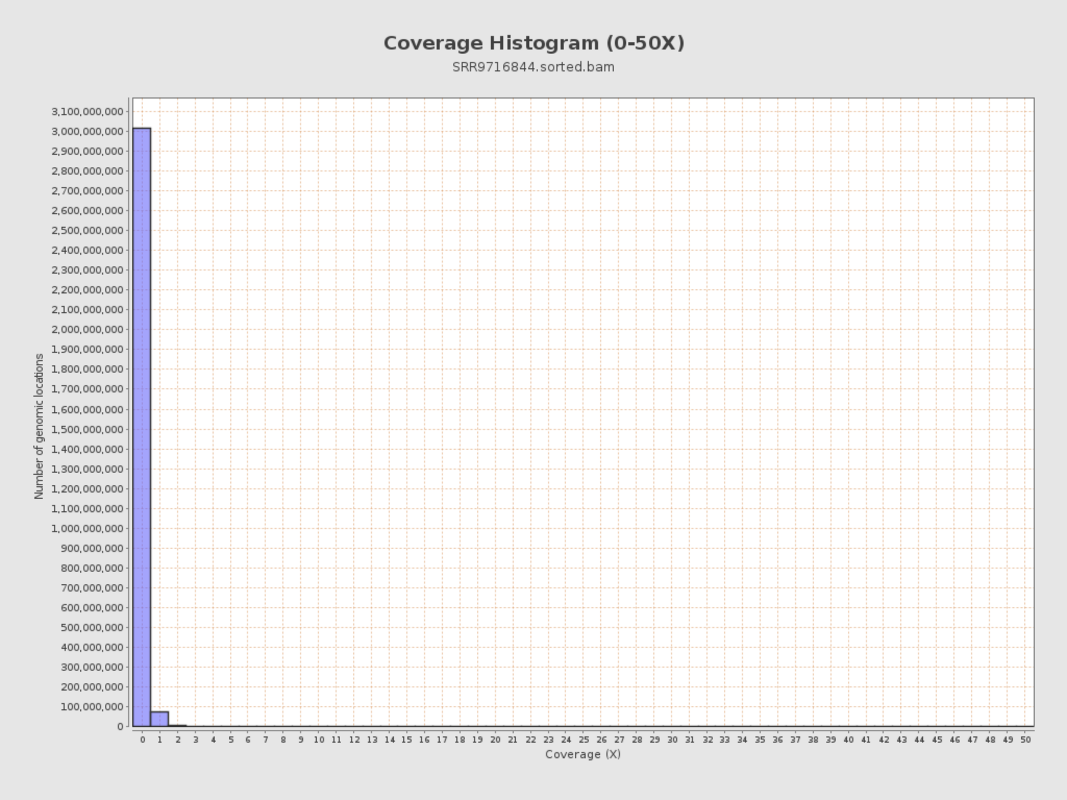
3. Results : Coverage across reference



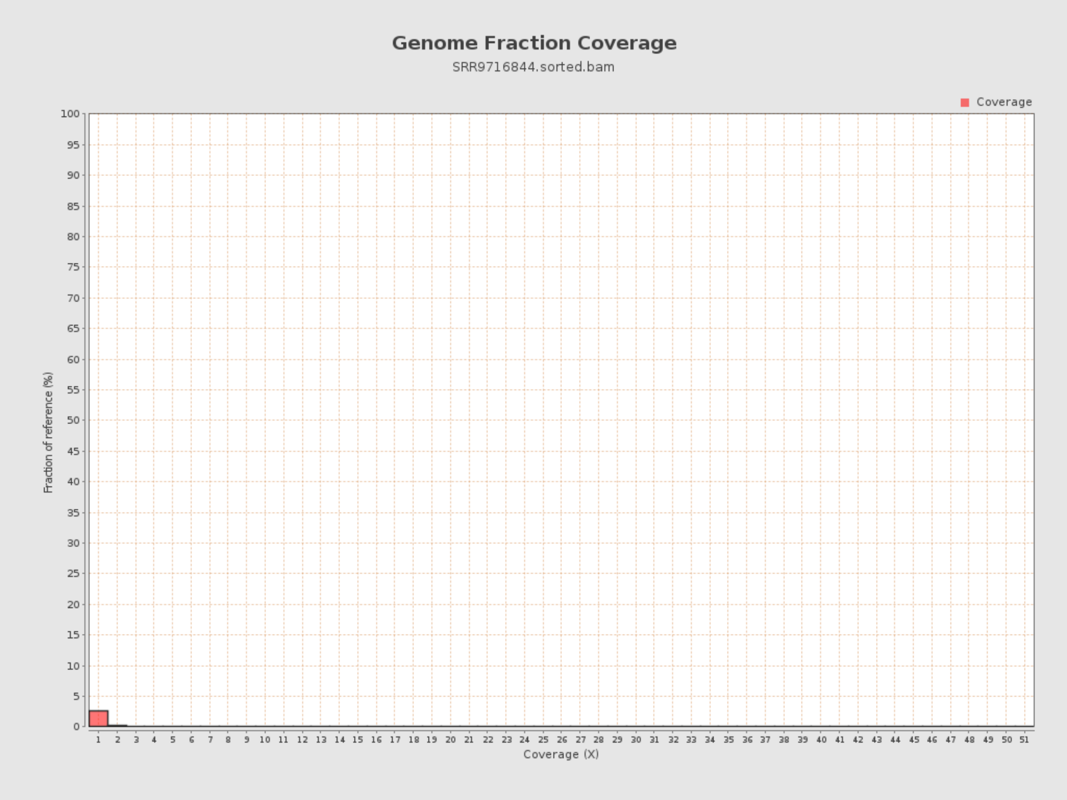
4. Results : Coverage Histogram



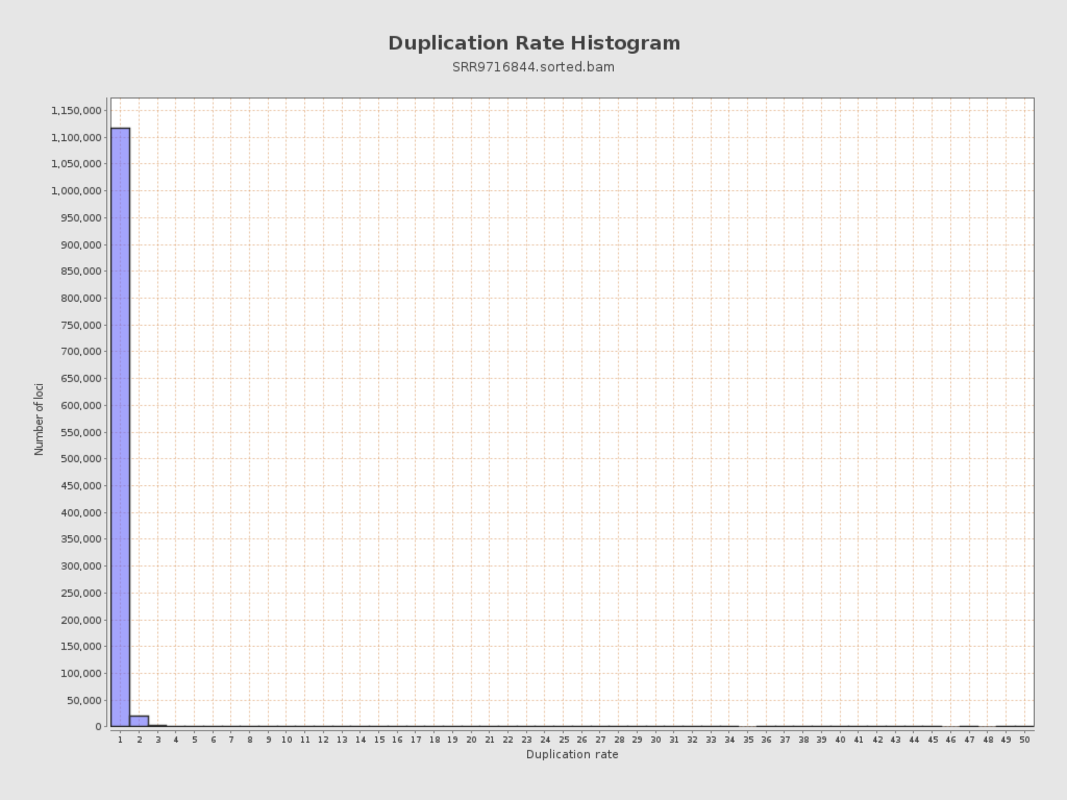
5. Results : Coverage Histogram (0-50X)



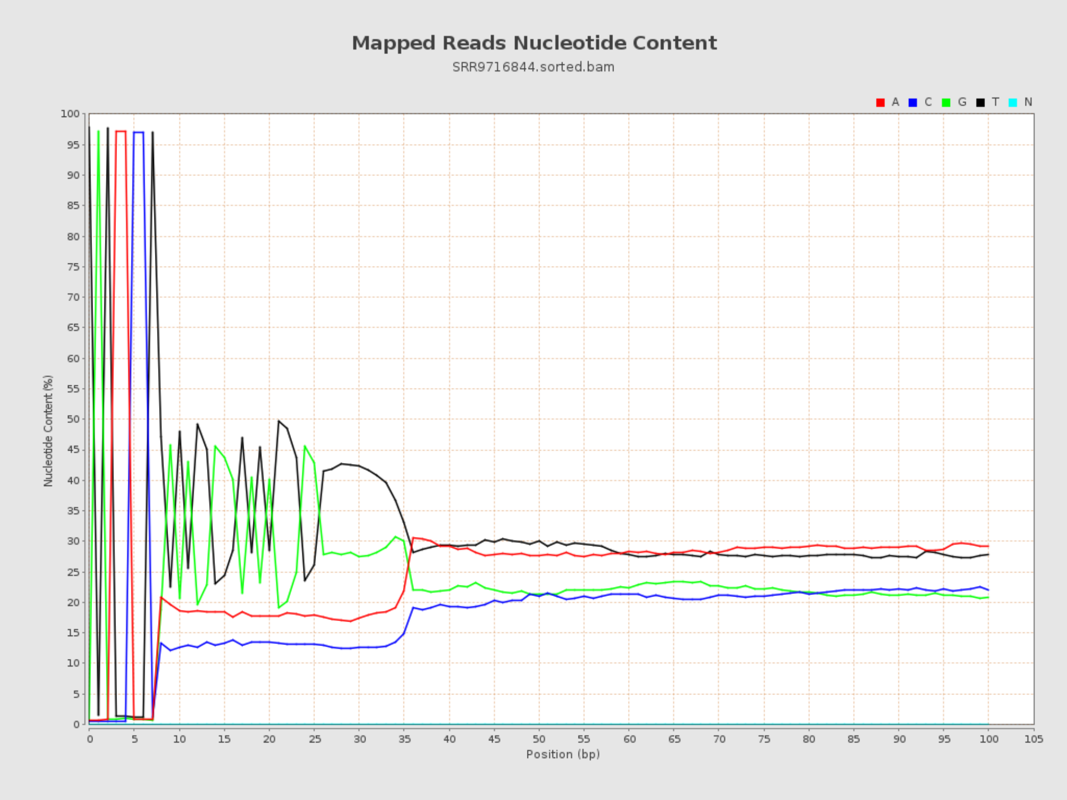
6. Results : Genome Fraction Coverage



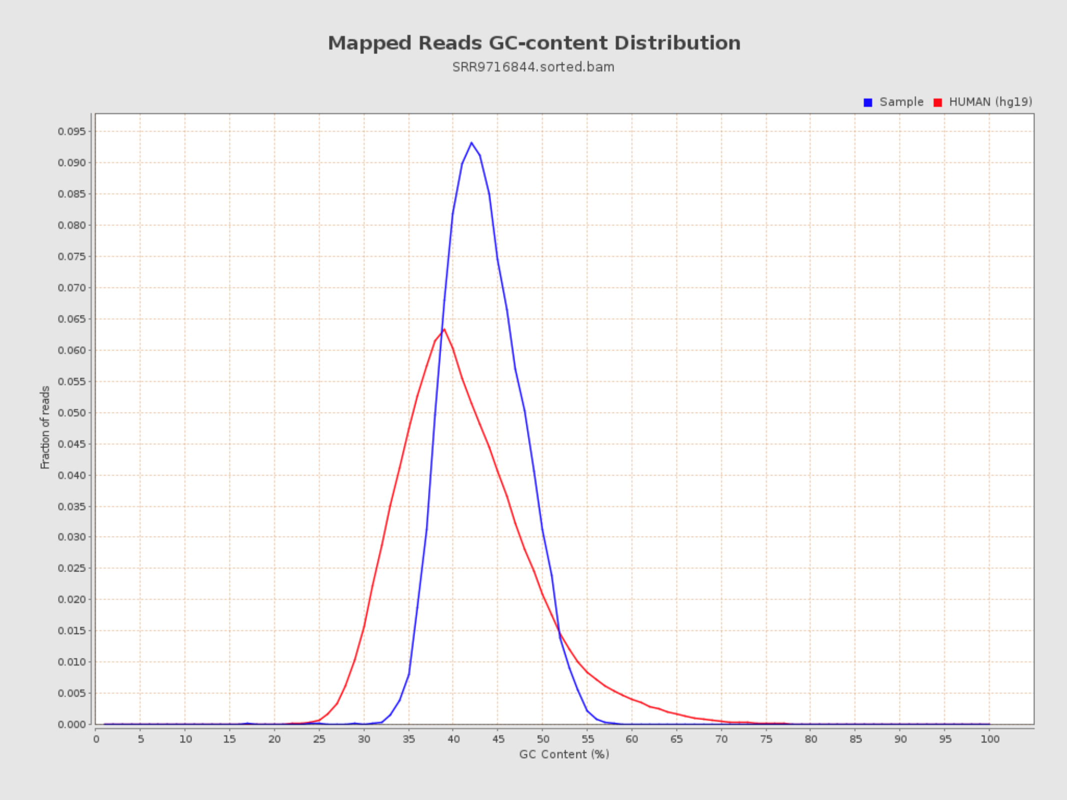
7. Results : Duplication Rate Histogram



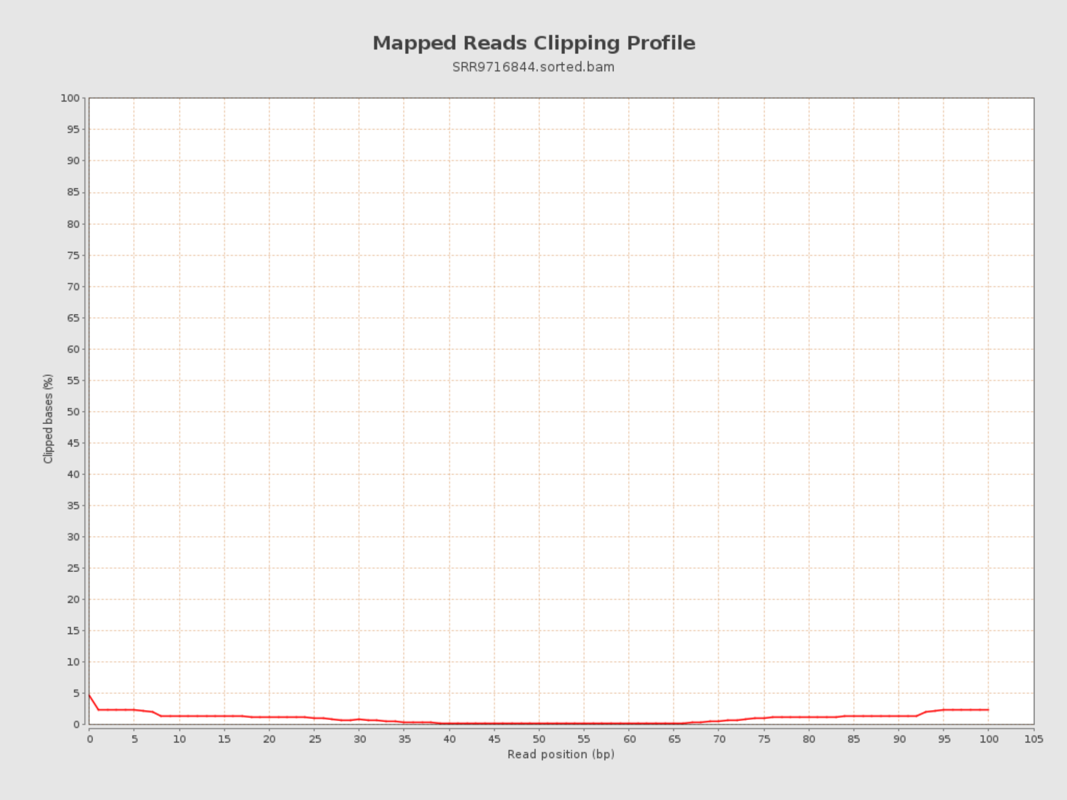
8. Results : Mapped Reads Nucleotide Content



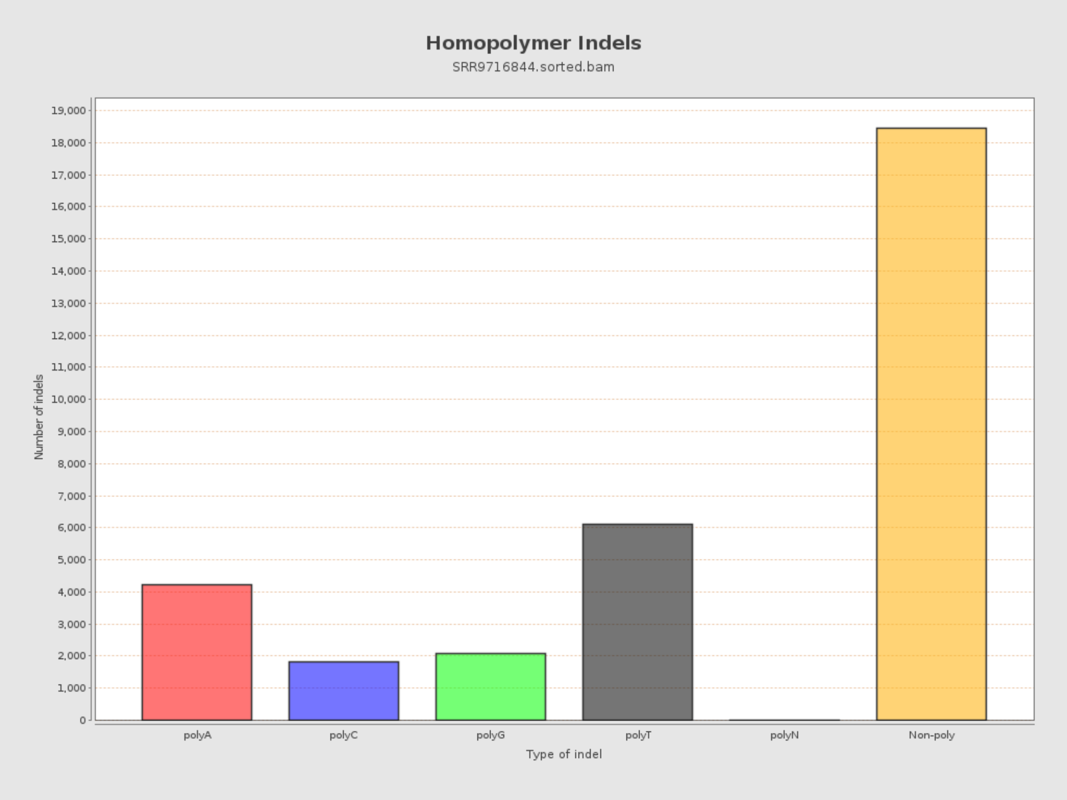
9. Results : Mapped Reads GC-content Distribution



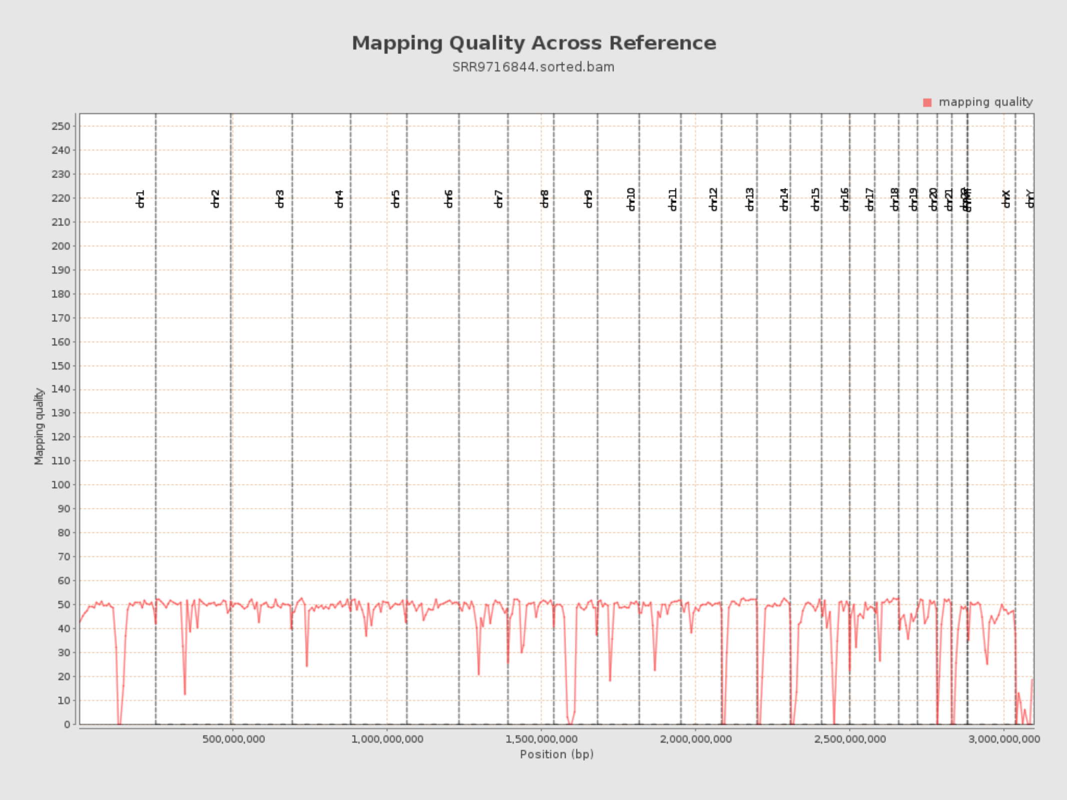
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram