Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 19:05:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819071.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_SRR1819071 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819071.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 19:05:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819071.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,654,663
Mapped reads	2,398,061 / 90.33%
Unmapped reads	256,602 / 9.67%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,263 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	126,819 / 4.78%
Duplication rate	4.29%
Clipped reads	2,400,756 / 90.44%

2.2. ACGT Content

Number/percentage of A's	34,176,741 / 24.65%
Number/percentage of C's	24,164,734 / 17.43%
Number/percentage of T's	43,867,066 / 31.64%
Number/percentage of G's	36,448,848 / 26.29%
Number/percentage of N's	3,132 / 0%
GC Percentage	43.71%

2.3. Coverage

Mean	0.0448

Standard Deviation	0.3101

2.4. Mapping Quality

Mean Mapping Quality	45.53

2.5. Mismatches and indels

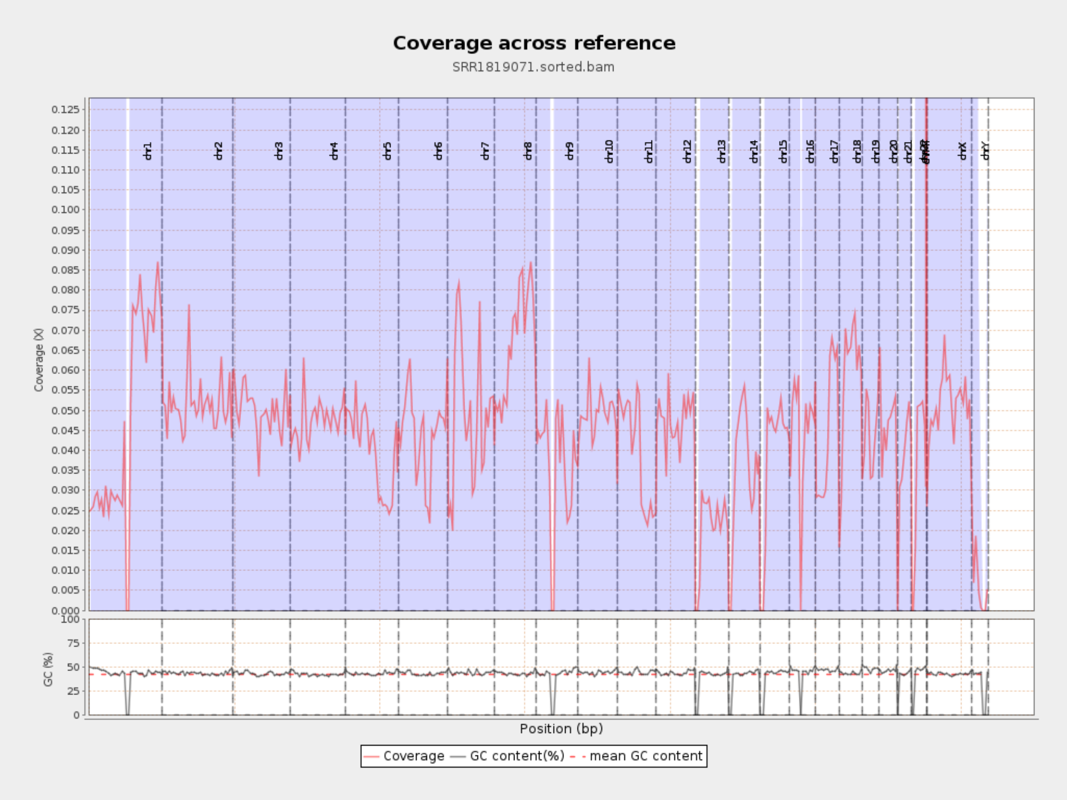
General error rate	0.48%
Mismatches	643,257
Insertions	8,206
Mapped reads with at least one insertion	0.34%
Deletions	20,465
Mapped reads with at least one deletion	0.85%
Homopolymer indels	43.32%

2.6. Chromosome stats

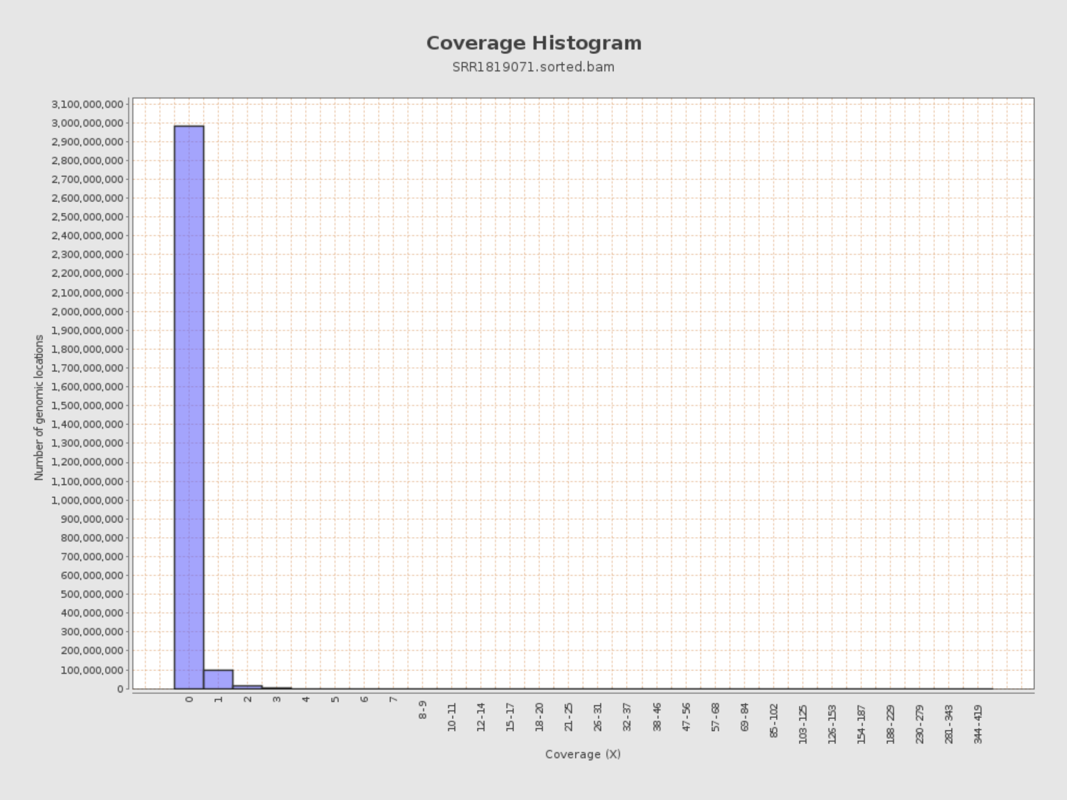
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11659455	0.0468	0.4102
chr2	243199373	12508496	0.0514	0.3819
chr3	198022430	9918659	0.0501	0.2606
chr4	191154276	9059152	0.0474	0.2706
chr5	180915260	7236698	0.04	0.2363
chr6	171115067	7570514	0.0442	0.2595
chr7	159138663	7762120	0.0488	0.3346

chr8	146364022	9854863	0.0673	0.3681
chr9	141213431	5001750	0.0354	0.3233
chr10	135534747	6697660	0.0494	0.3136
chr11	135006516	5329649	0.0395	0.3142
chr12	133851895	6368974	0.0476	0.258
chr13	115169878	2376441	0.0206	0.166
chr14	107349540	3717073	0.0346	0.2255
chr15	102531392	3922006	0.0383	0.228
chr16	90354753	4046849	0.0448	0.2629
chr17	81195210	3620327	0.0446	0.257
chr18	78077248	4633902	0.0594	0.5712
chr19	59128983	2594950	0.0439	0.3463
chr20	63025520	2954283	0.0469	0.2661
chr21	48129895	1771152	0.0368	0.2445
chr22	51304566	1733247	0.0338	0.2155
chrMT	16571	46934	2.8323	2.3954
chrX	155270560	7938653	0.0511	0.2982
chrY	59373566	371470	0.0063	0.1241

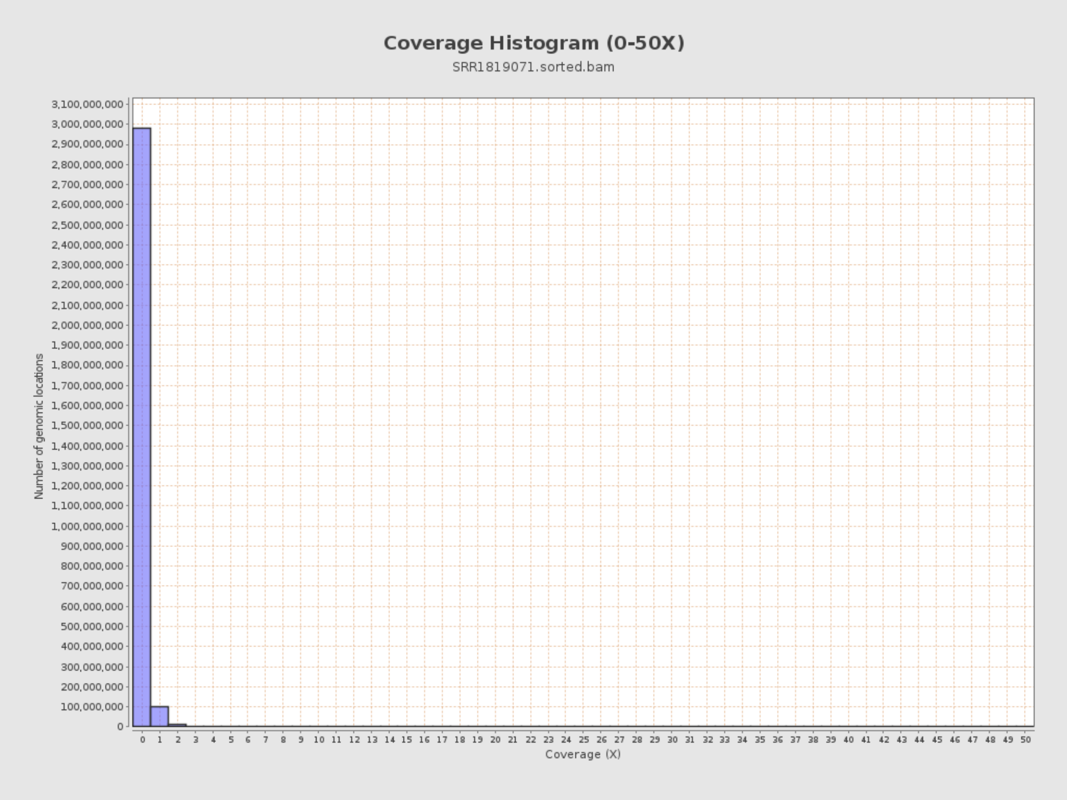
3. Results : Coverage across reference



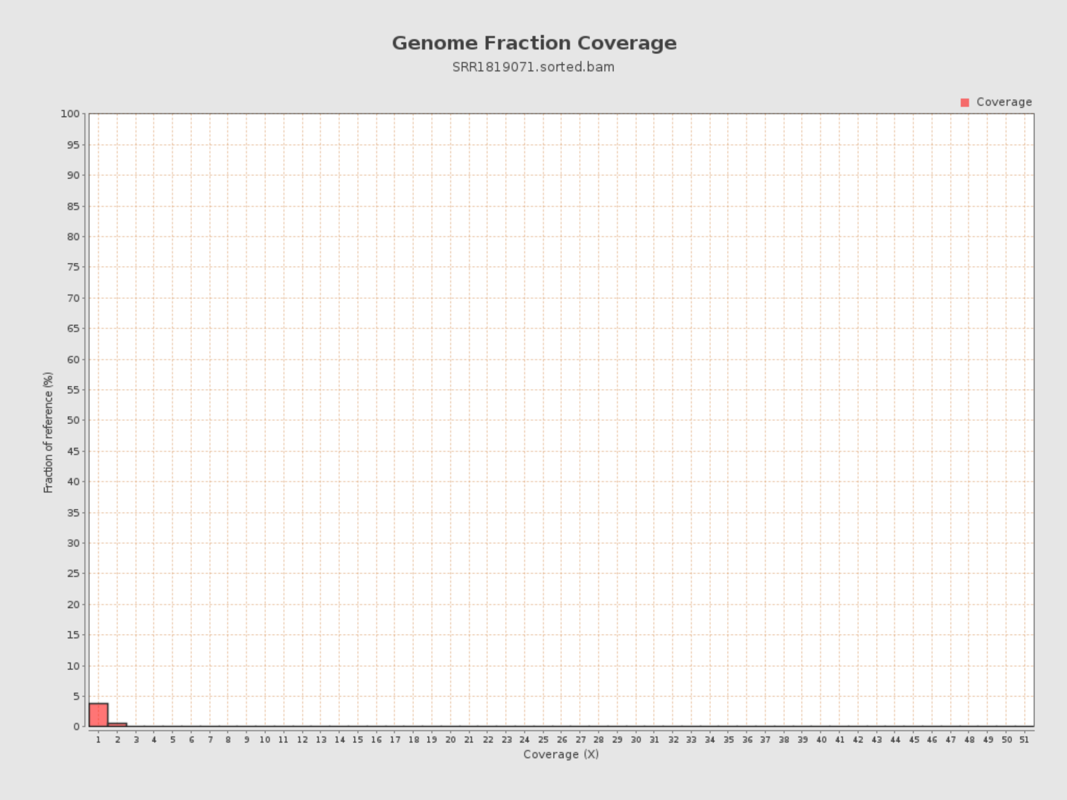
4. Results : Coverage Histogram



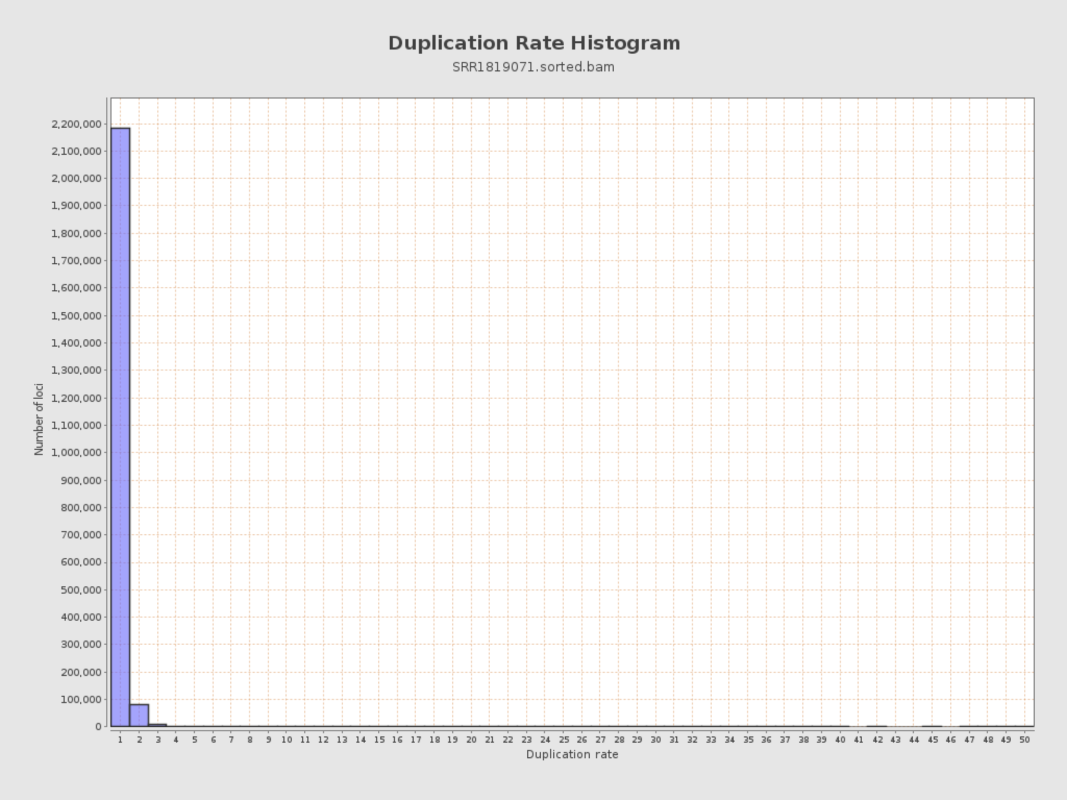
5. Results : Coverage Histogram (0-50X)



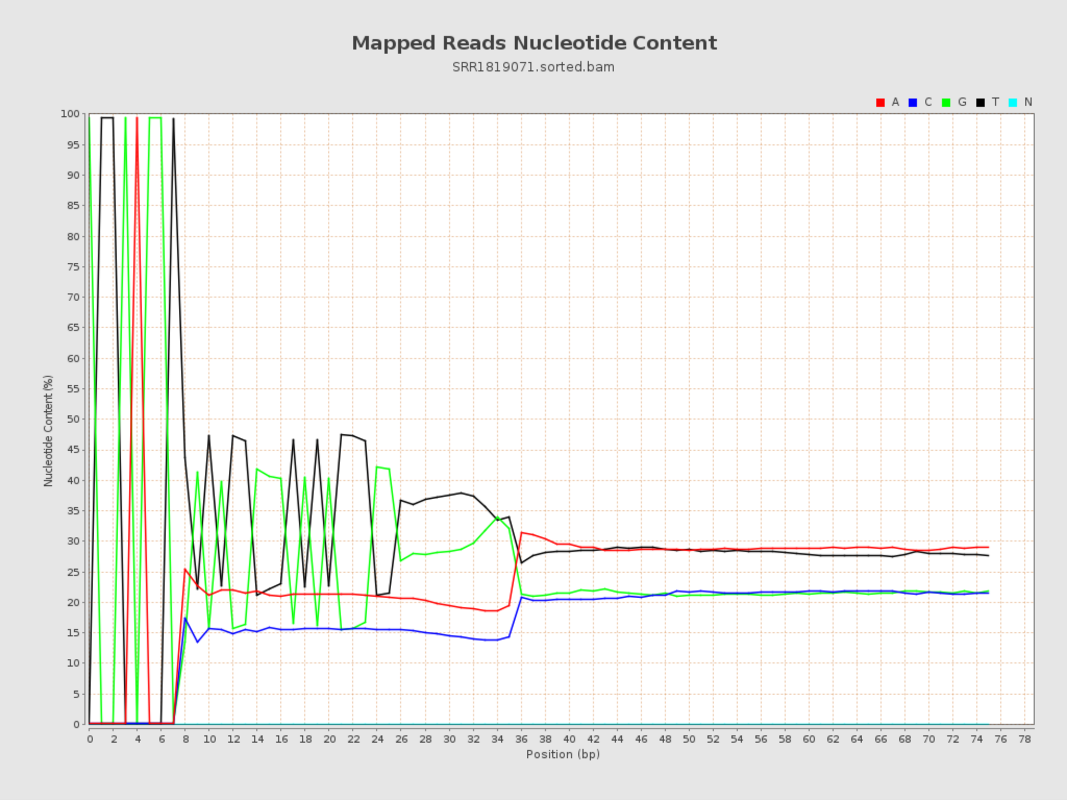
6. Results : Genome Fraction Coverage



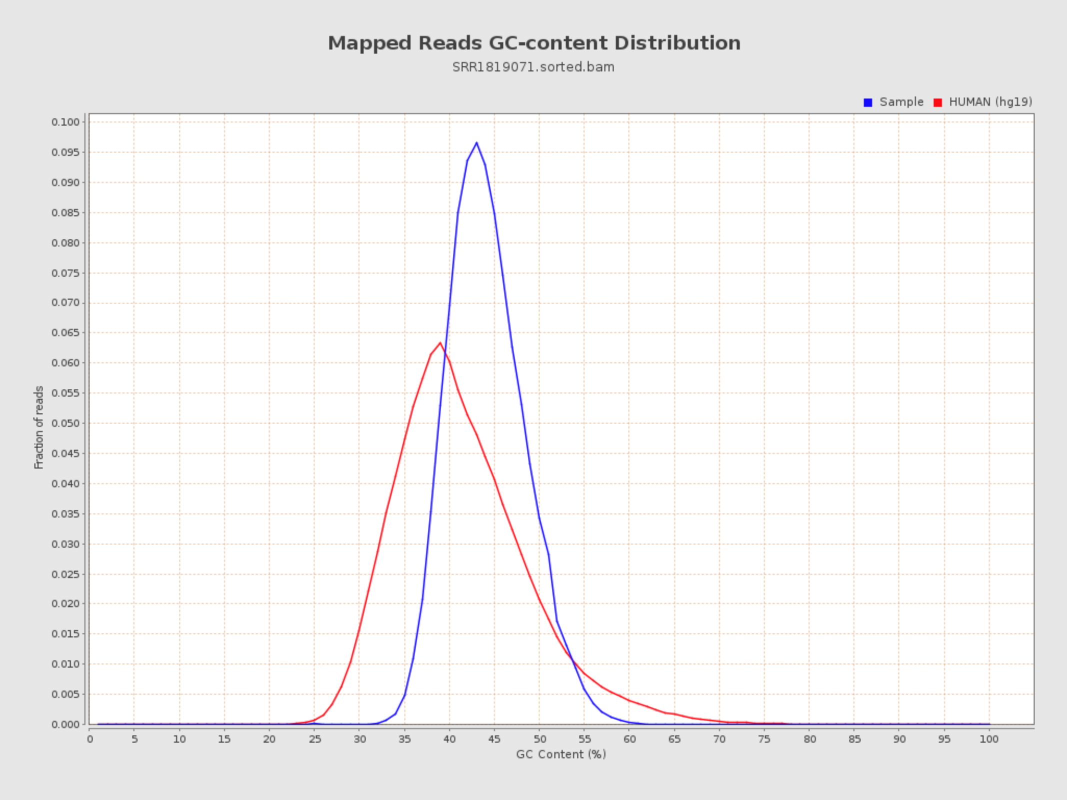
7. Results : Duplication Rate Histogram



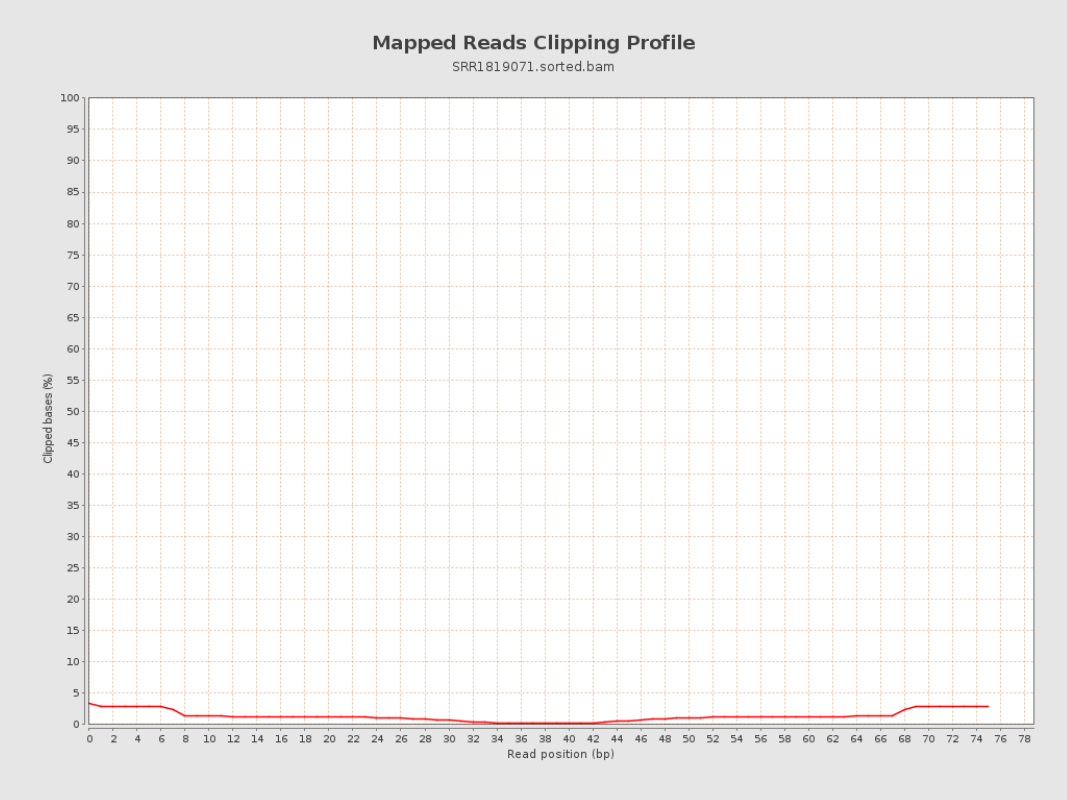
8. Results : Mapped Reads Nucleotide Content



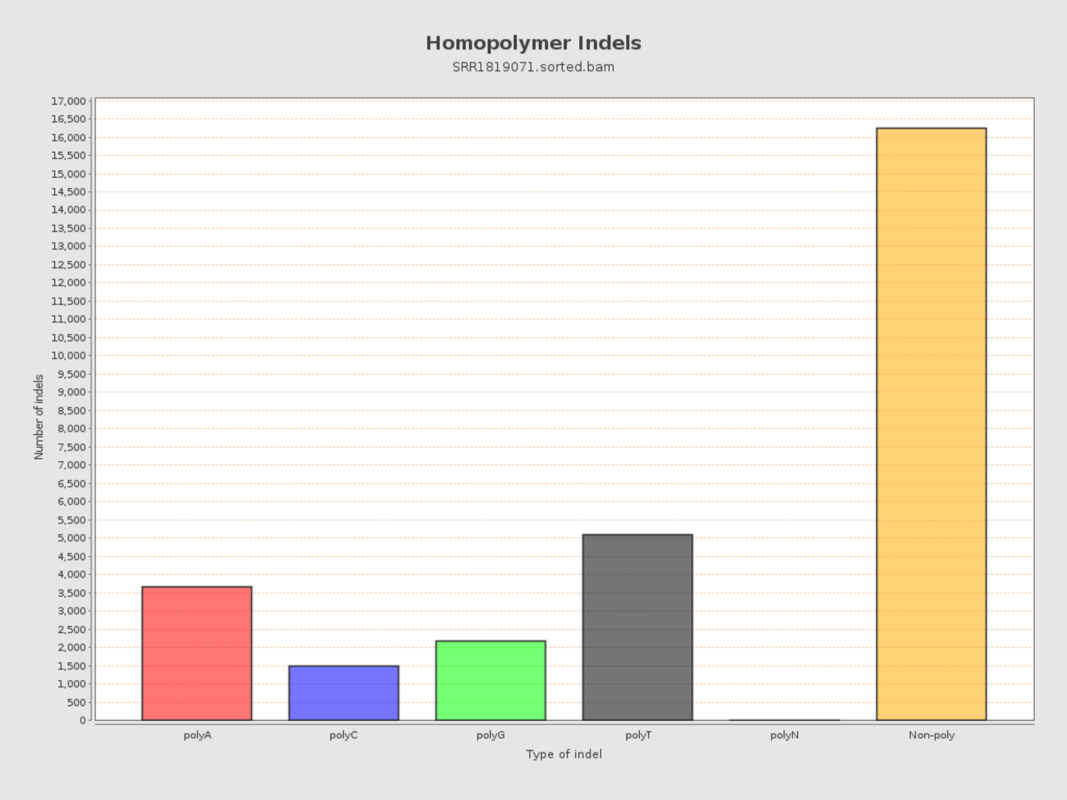
9. Results : Mapped Reads GC-content Distribution



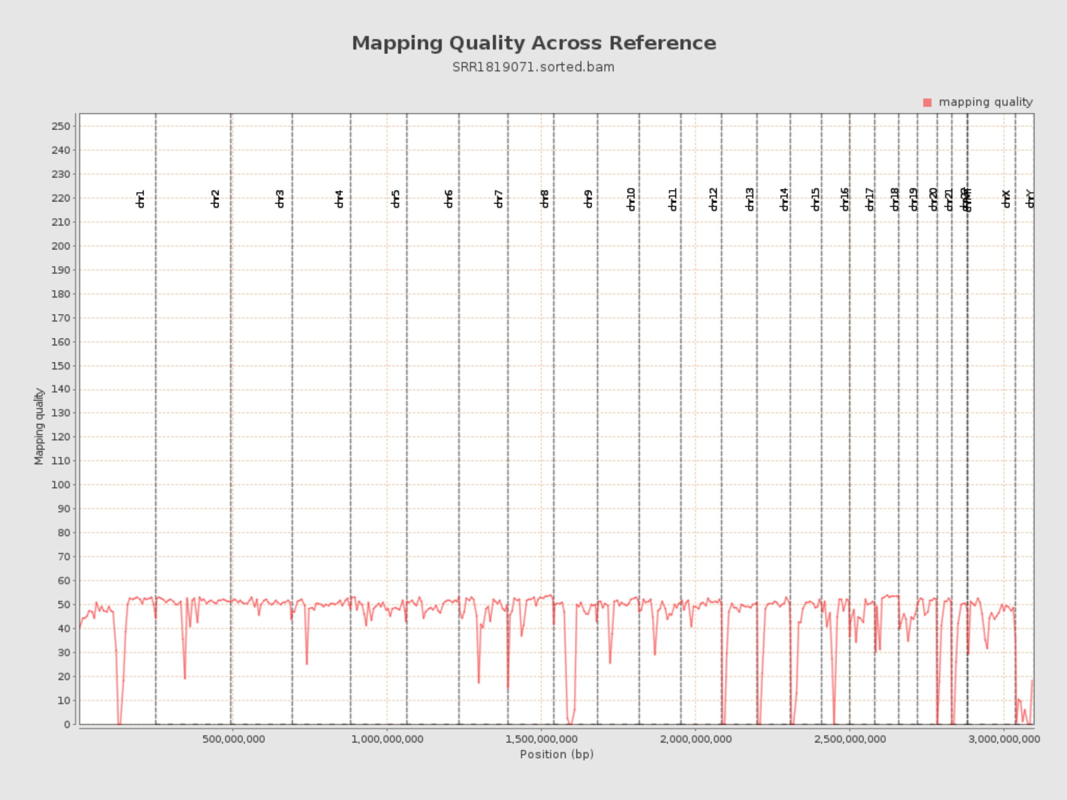
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram