Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 13:20:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068152.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_SRR6068152 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068152.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 13:20:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068152.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,132,915
Mapped reads	2,896,757 / 92.46%
Unmapped reads	236,158 / 7.54%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,614 / 0.79%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	721,041 / 23.02%
Duplication rate	17.14%
Clipped reads	1,679,772 / 53.62%

2.2. ACGT Content

Number/percentage of A's	46,587,356 / 25.44%
Number/percentage of C's	32,885,606 / 17.96%
Number/percentage of T's	59,889,992 / 32.71%
Number/percentage of G's	43,714,507 / 23.88%
Number/percentage of N's	19,897 / 0.01%
GC Percentage	41.84%

2.3. Coverage

Mean	0.0592

Standard Deviation	0.711

2.4. Mapping Quality

Mean Mapping Quality	45.49

2.5. Mismatches and indels

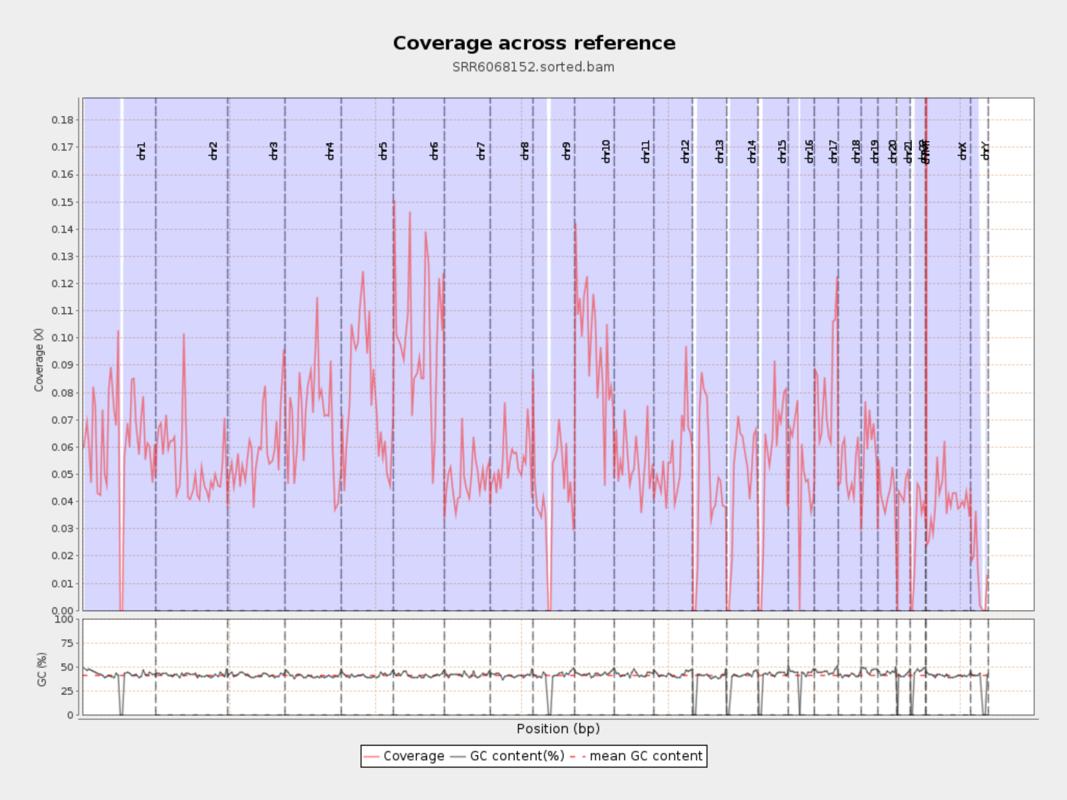
General error rate	0.63%
Mismatches	1,129,637
Insertions	11,762
Mapped reads with at least one insertion	0.4%
Deletions	42,538
Mapped reads with at least one deletion	1.46%
Homopolymer indels	44.15%

2.6. Chromosome stats

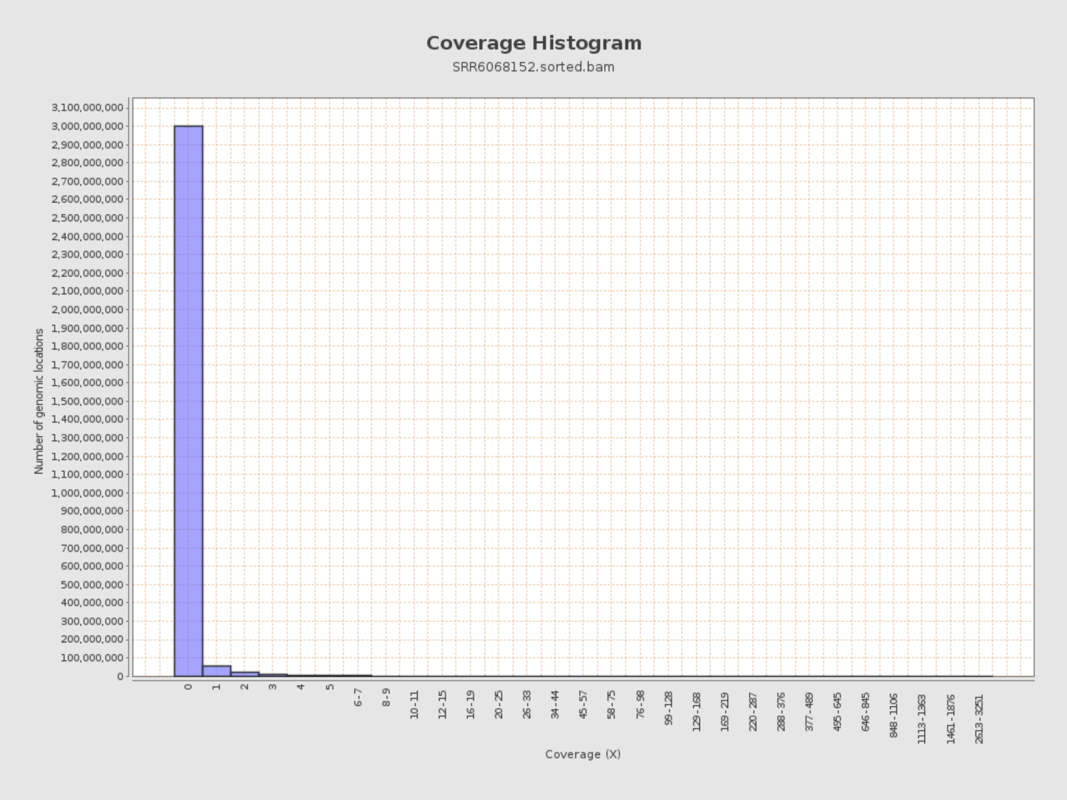
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15411753	0.0618	1.0421
chr2	243199373	13234206	0.0544	1.5252
chr3	198022430	11619787	0.0587	0.4376
chr4	191154276	13522877	0.0707	0.4748
chr5	180915260	14417596	0.0797	0.4928
chr6	171115067	16936083	0.099	0.7322
chr7	159138663	7744437	0.0487	0.5484

chr8	146364022	7981778	0.0545	0.7427
chr9	141213431	5947392	0.0421	0.4619
chr10	135534747	13260949	0.0978	0.6323
chr11	135006516	7315469	0.0542	0.4902
chr12	133851895	7454580	0.0557	0.4231
chr13	115169878	5325257	0.0462	0.4241
chr14	107349540	5199767	0.0484	0.4092
chr15	102531392	5652179	0.0551	0.4565
chr16	90354753	4553941	0.0504	0.4187
chr17	81195210	6638671	0.0818	0.5323
chr18	78077248	4008390	0.0513	0.8173
chr19	59128983	3569892	0.0604	0.7614
chr20	63025520	2732651	0.0434	0.4017
chr21	48129895	1936983	0.0402	0.3727
chr22	51304566	1451958	0.0283	0.3036
chrMT	16571	295577	17.837	13.7782
chrX	155270560	6196265	0.0399	0.3846
chrY	59373566	762513	0.0128	0.2364

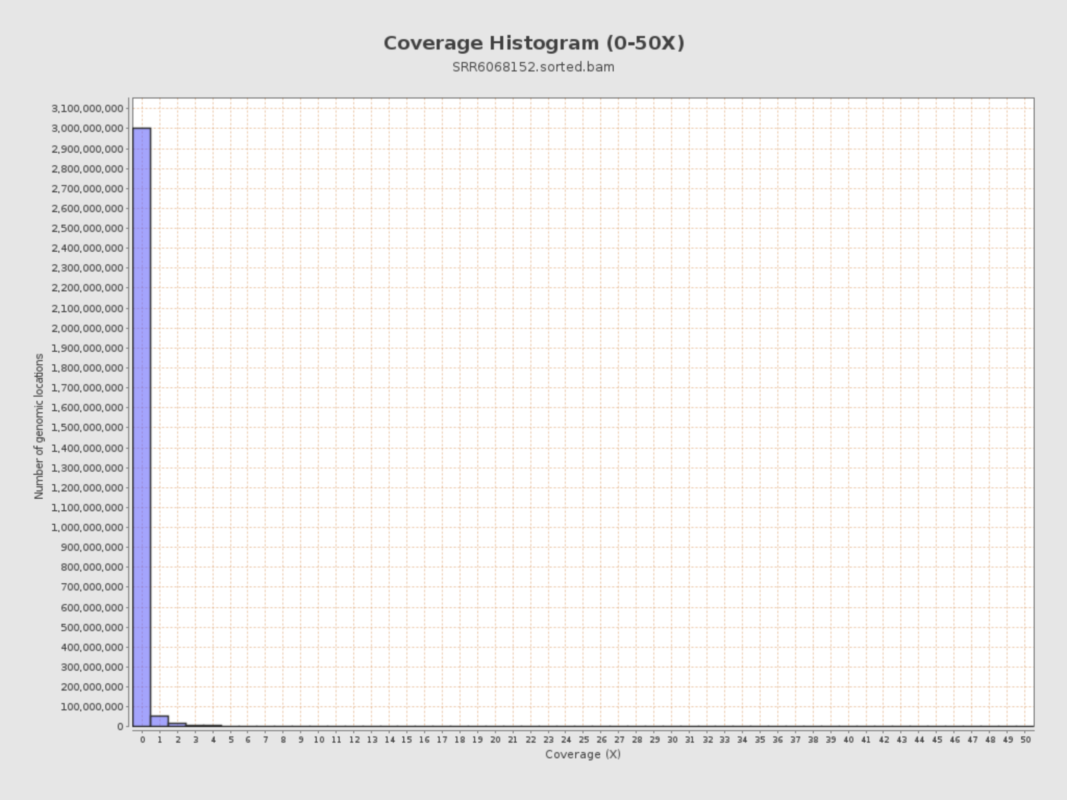
3. Results : Coverage across reference



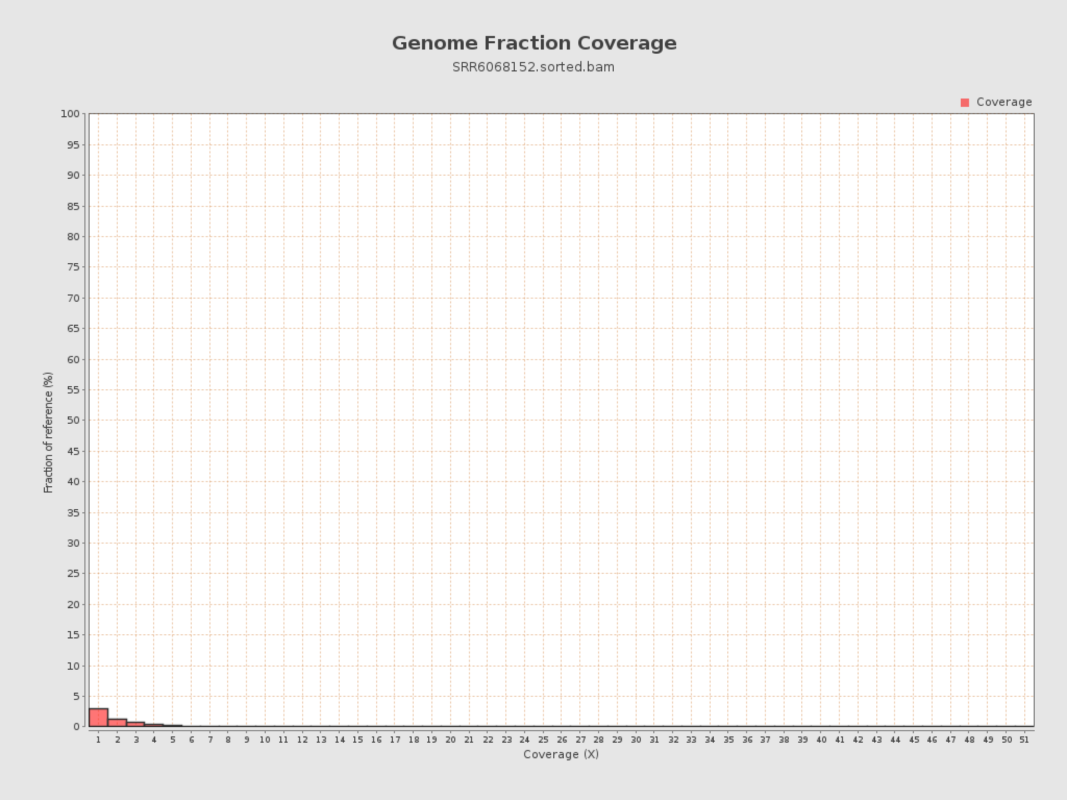
4. Results : Coverage Histogram



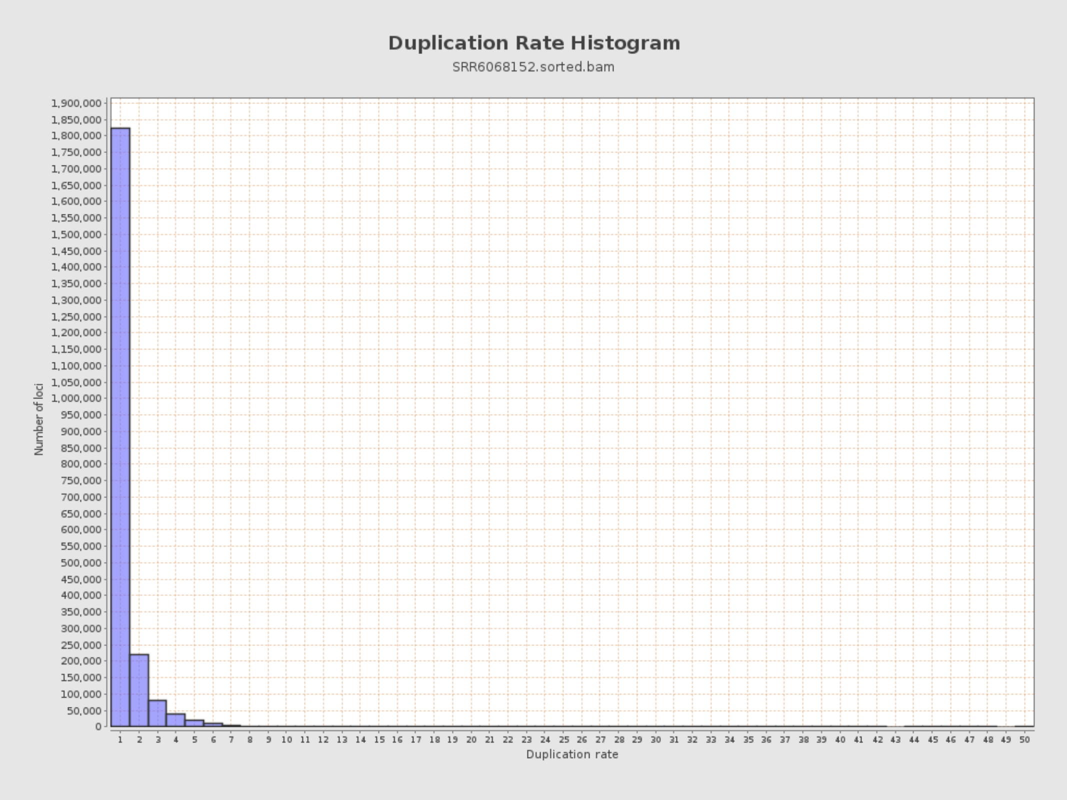
5. Results : Coverage Histogram (0-50X)



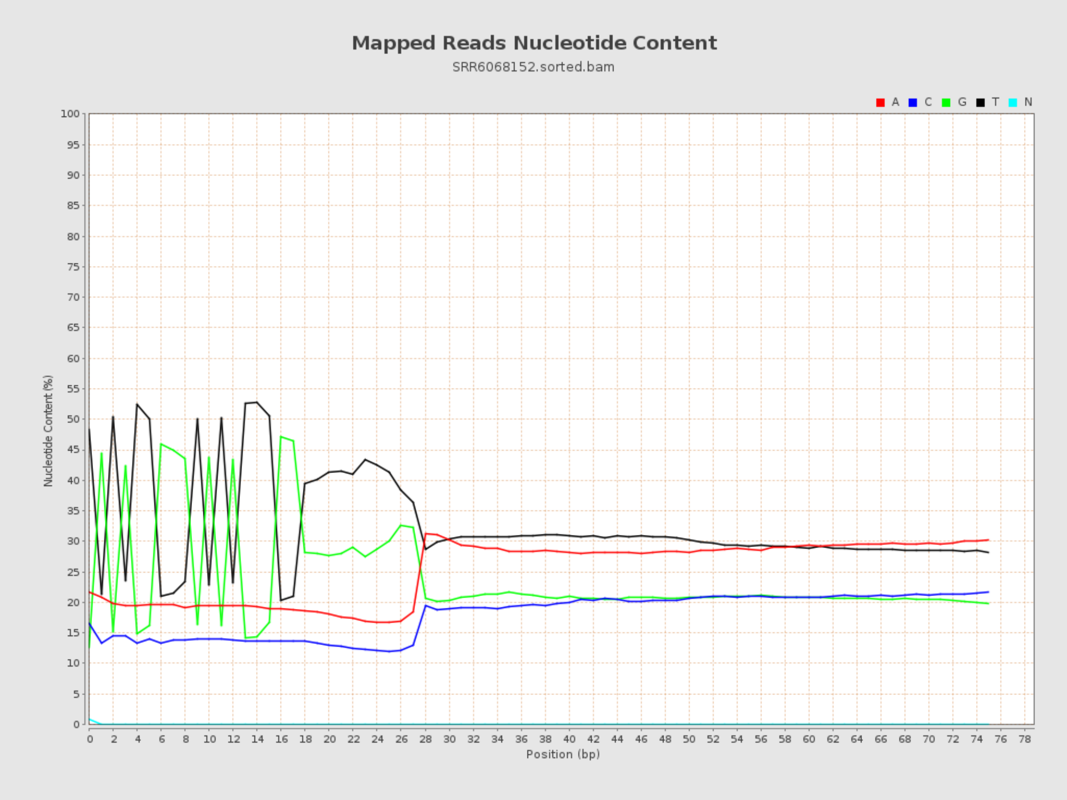
6. Results : Genome Fraction Coverage



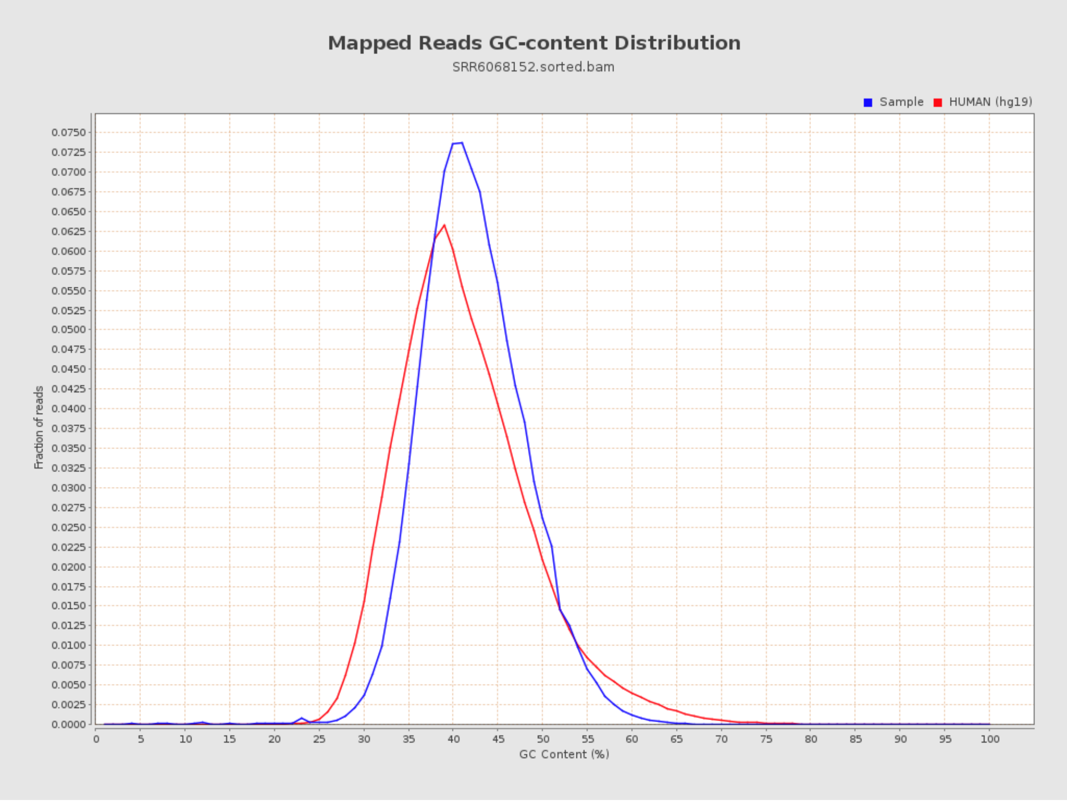
7. Results : Duplication Rate Histogram



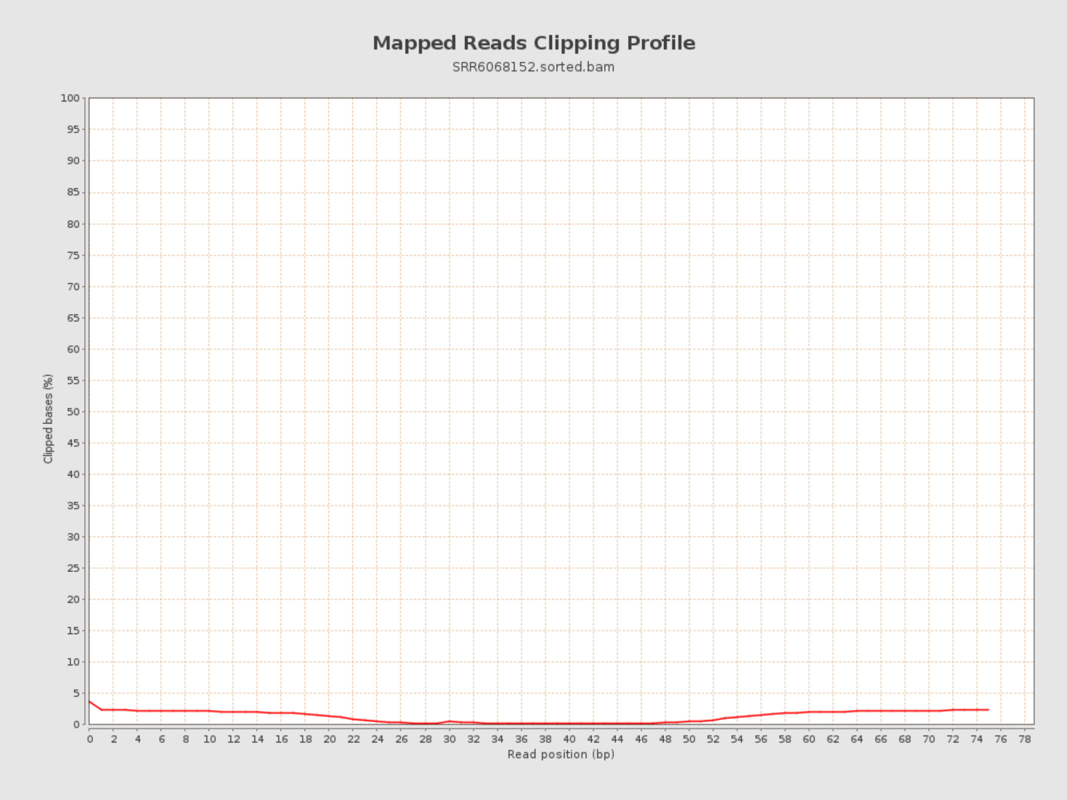
8. Results : Mapped Reads Nucleotide Content



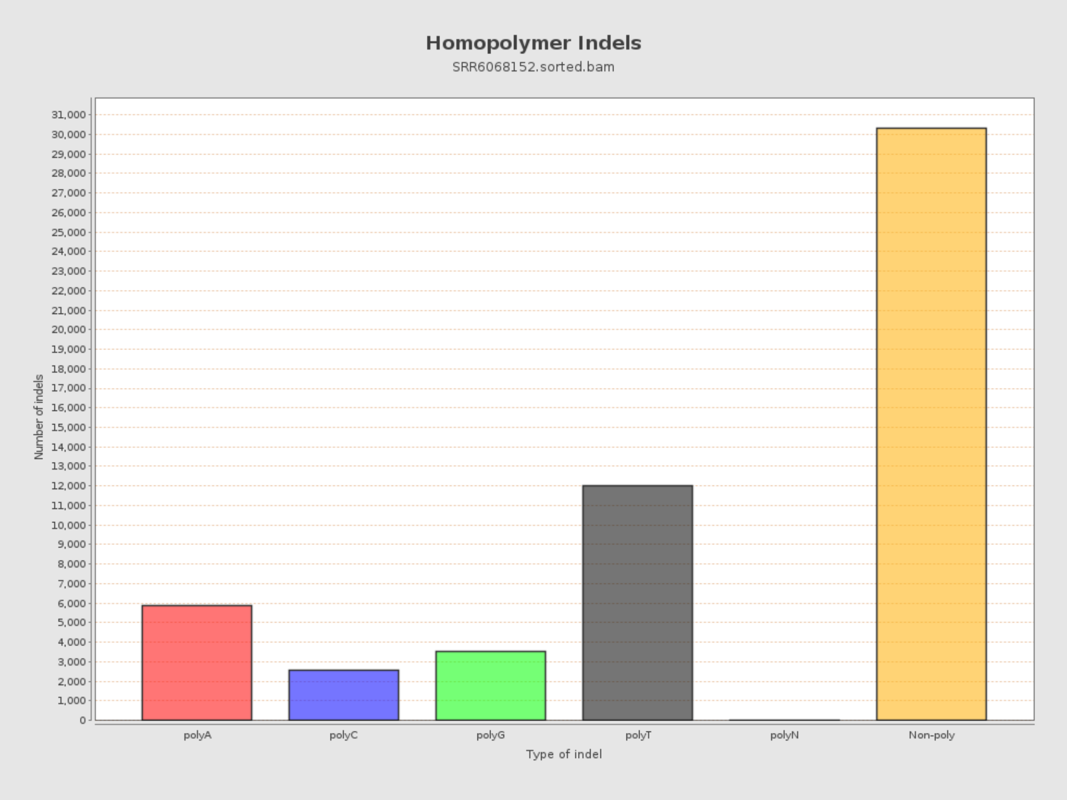
9. Results : Mapped Reads GC-content Distribution



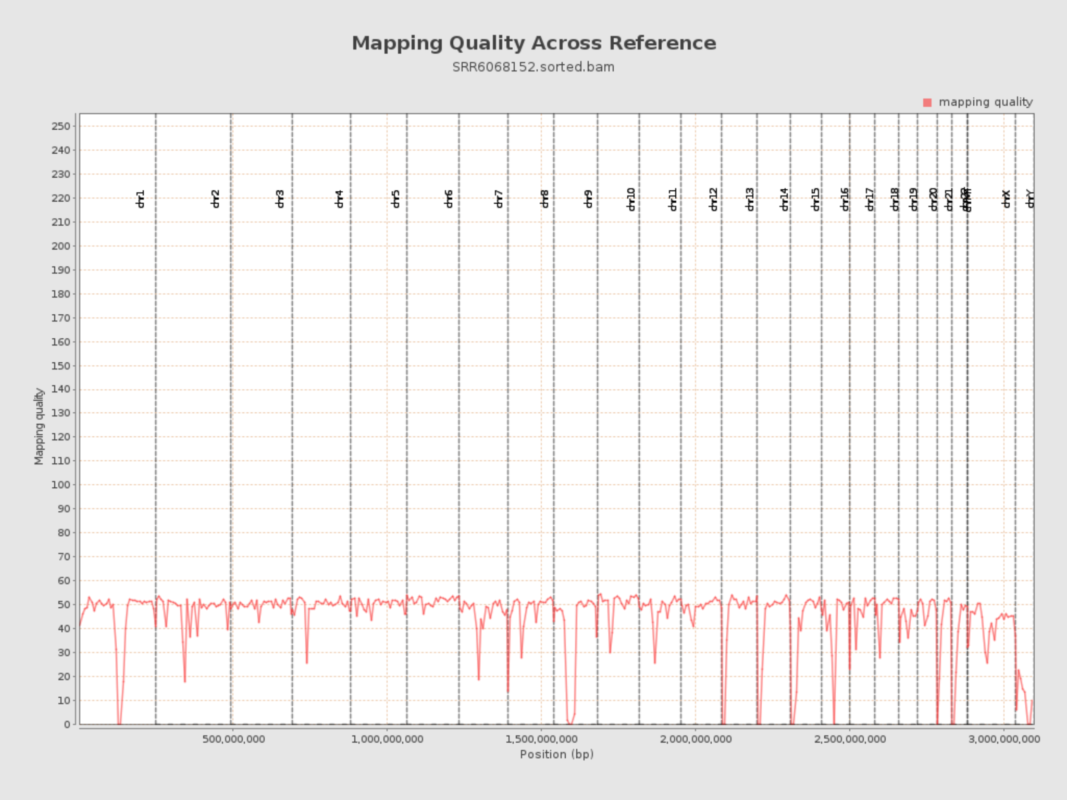
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram