Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 13:29:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068154.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_SRR6068154 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068154.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 13:29:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068154.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,984,320
Mapped reads	3,762,574 / 94.43%
Unmapped reads	221,746 / 5.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	29,152 / 0.73%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	1,297,601 / 32.57%
Duplication rate	20.04%
Clipped reads	1,997,117 / 50.12%

2.2. ACGT Content

Number/percentage of A's	63,258,876 / 26.12%
Number/percentage of C's	43,092,528 / 17.79%
Number/percentage of T's	79,628,301 / 32.88%
Number/percentage of G's	56,164,669 / 23.19%
Number/percentage of N's	27,331 / 0.01%
GC Percentage	40.99%

2.3. Coverage

Mean	0.0783

Standard Deviation	0.913

2.4. Mapping Quality

Mean Mapping Quality	45.63

2.5. Mismatches and indels

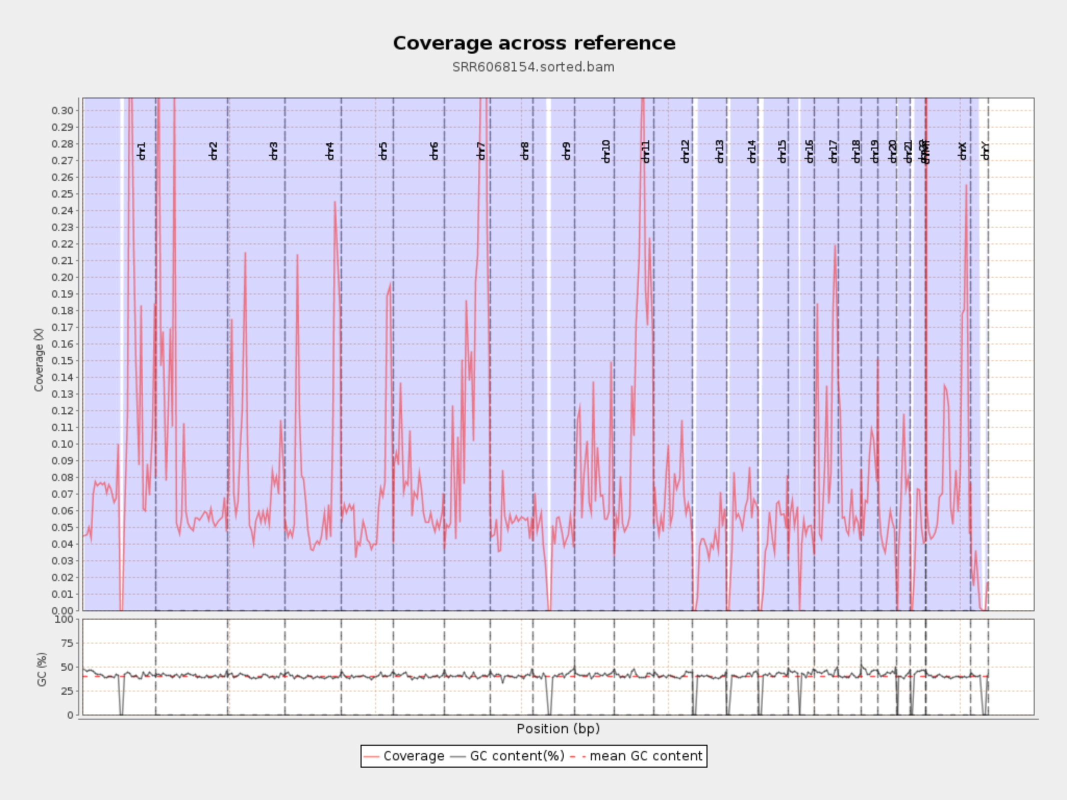
General error rate	0.55%
Mismatches	1,292,917
Insertions	15,429
Mapped reads with at least one insertion	0.41%
Deletions	59,275
Mapped reads with at least one deletion	1.56%
Homopolymer indels	47.24%

2.6. Chromosome stats

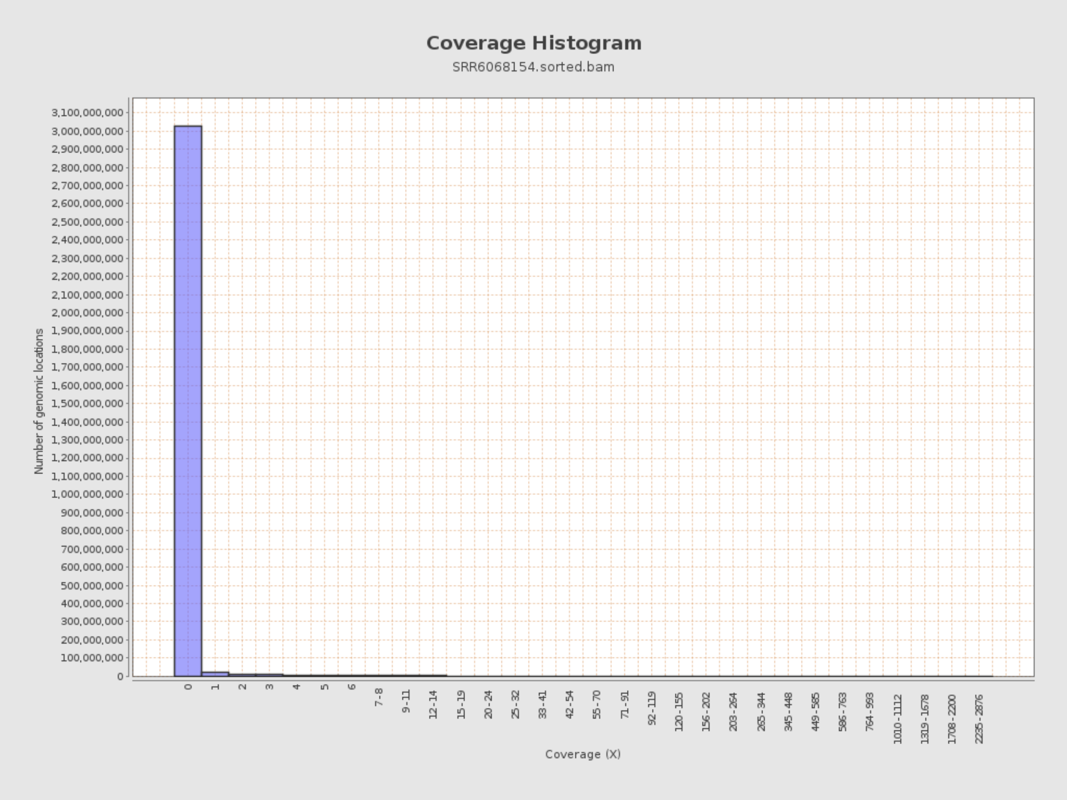
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	24353979	0.0977	1.1273
chr2	243199373	22685507	0.0933	1.2662
chr3	198022430	15851025	0.08	0.7403
chr4	191154276	15517862	0.0812	0.7406
chr5	180915260	12064533	0.0667	0.6679
chr6	171115067	12217043	0.0714	0.7683
chr7	159138663	25230873	0.1585	1.2105

chr8	146364022	7705354	0.0526	1.7174
chr9	141213431	6040623	0.0428	0.6116
chr10	135534747	11344324	0.0837	0.8023
chr11	135006516	18693706	0.1385	0.9761
chr12	133851895	9120708	0.0681	0.6948
chr13	115169878	4322905	0.0375	0.527
chr14	107349540	5778551	0.0538	0.6042
chr15	102531392	4238179	0.0413	0.5498
chr16	90354753	4165341	0.0461	0.5715
chr17	81195210	9472991	0.1167	0.8503
chr18	78077248	4997567	0.064	0.9255
chr19	59128983	4885000	0.0826	0.9015
chr20	63025520	2972100	0.0472	0.5769
chr21	48129895	3185895	0.0662	0.6874
chr22	51304566	2065224	0.0403	0.5399
chrMT	16571	396202	23.9094	17.6383
chrX	155270560	14160218	0.0912	0.7708
chrY	59373566	811771	0.0137	0.334

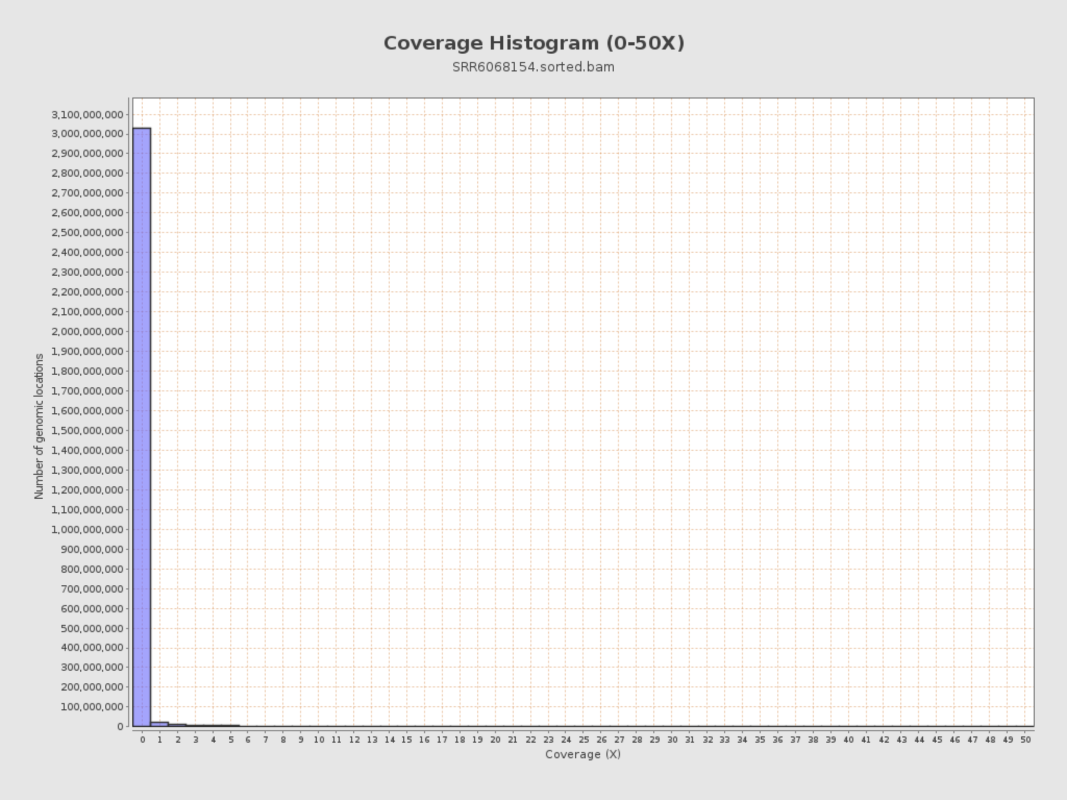
3. Results : Coverage across reference



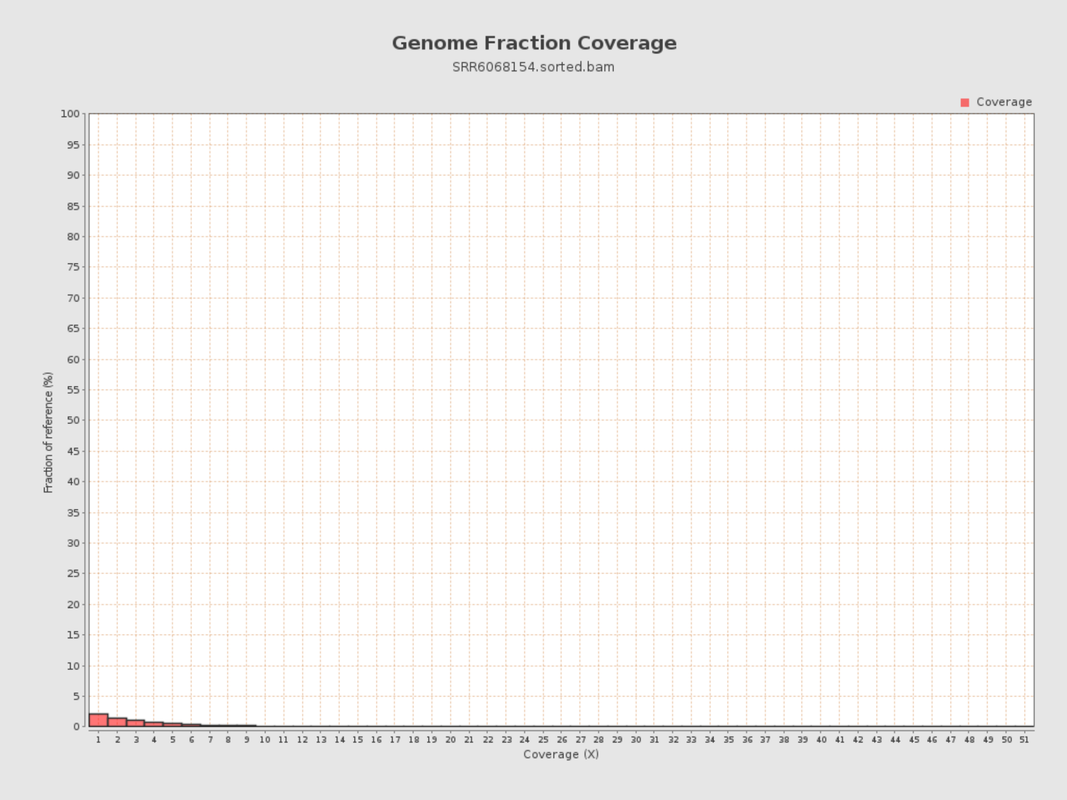
4. Results : Coverage Histogram



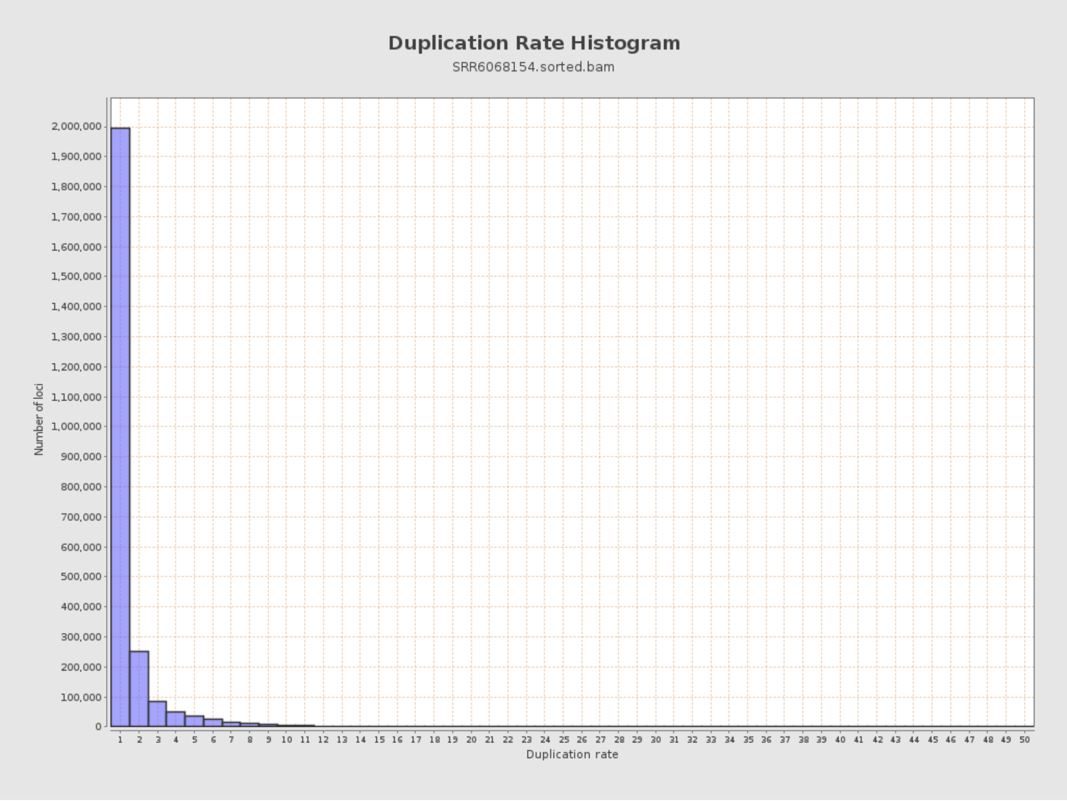
5. Results : Coverage Histogram (0-50X)



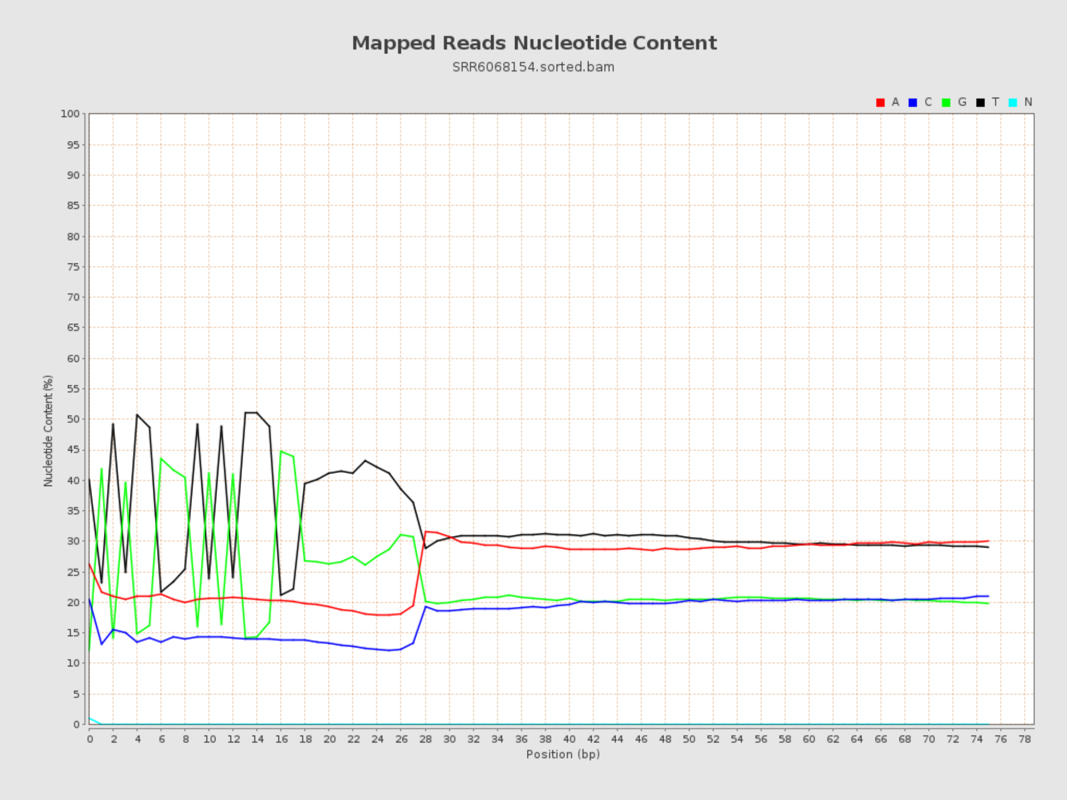
6. Results : Genome Fraction Coverage



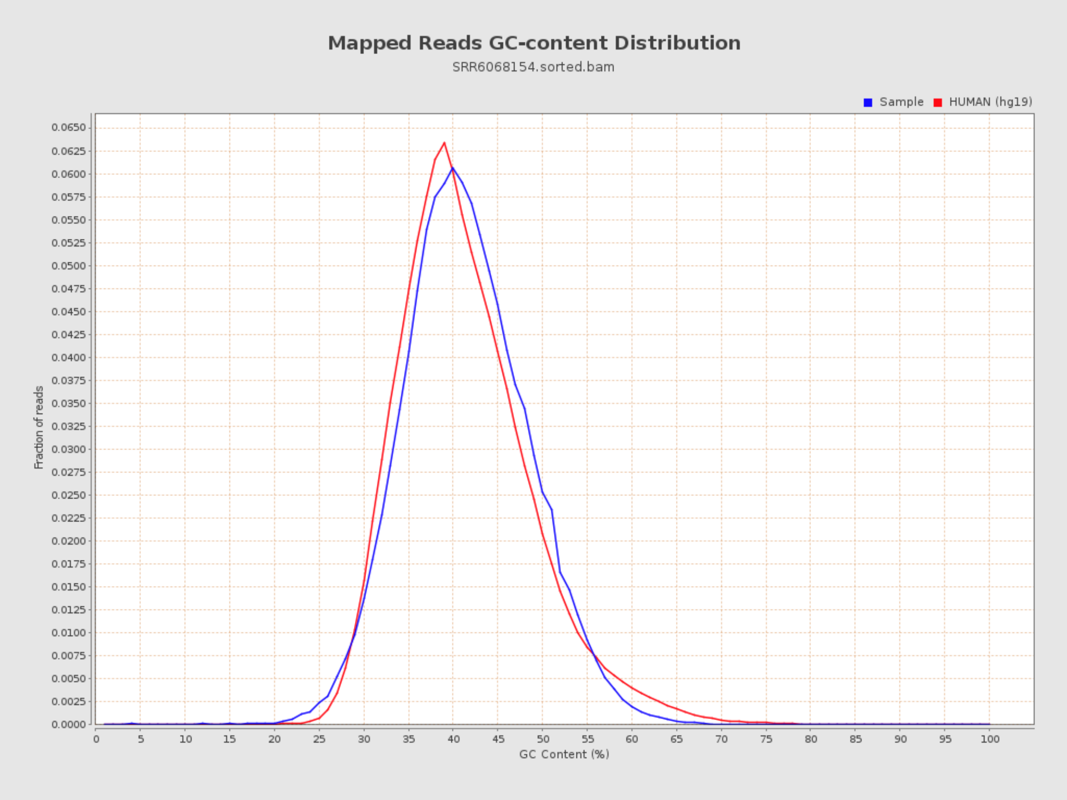
7. Results : Duplication Rate Histogram



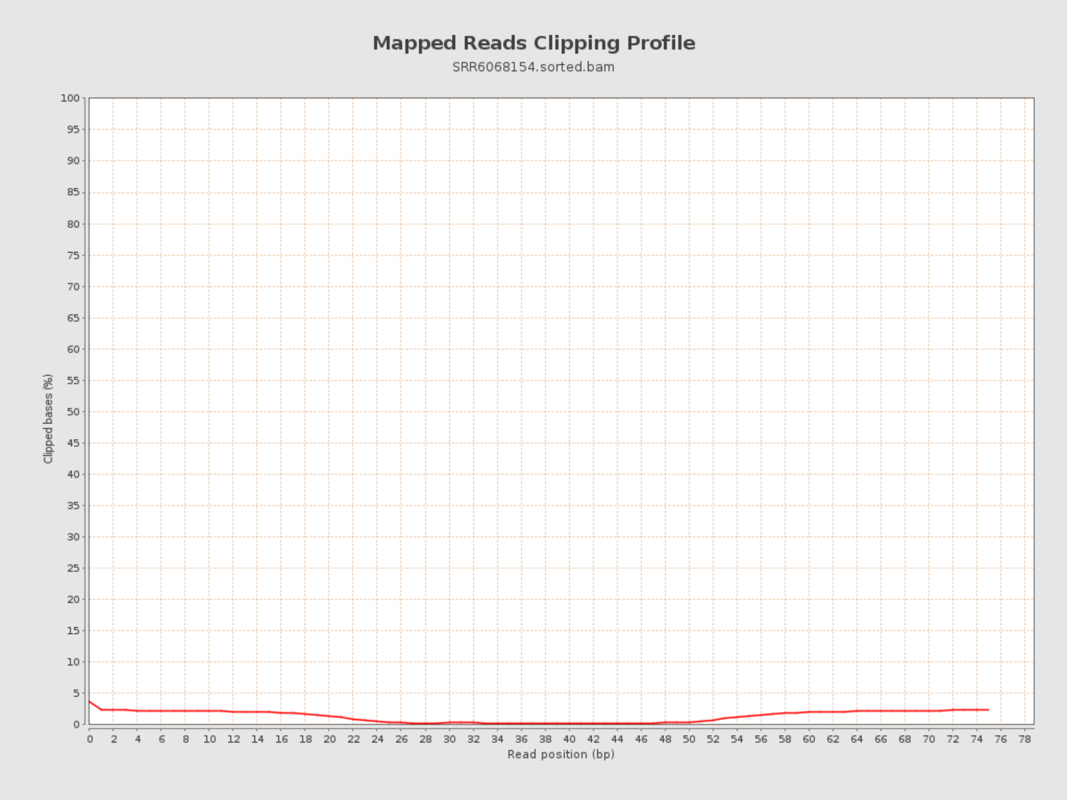
8. Results : Mapped Reads Nucleotide Content



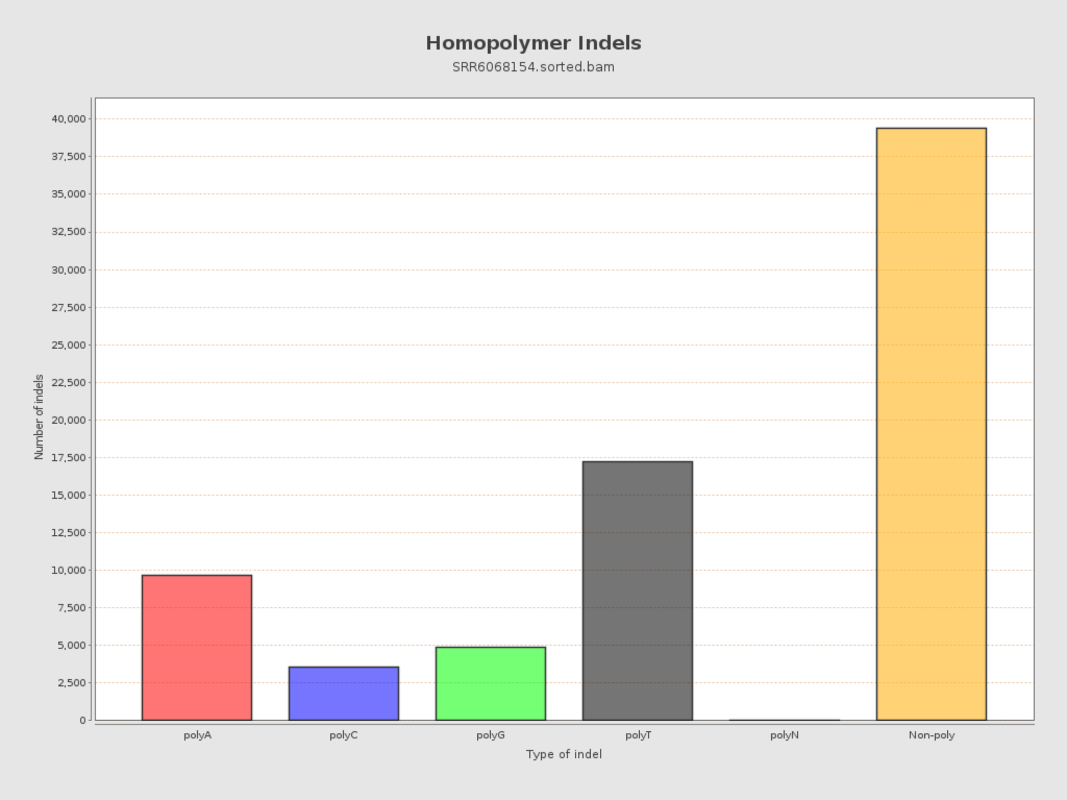
9. Results : Mapped Reads GC-content Distribution



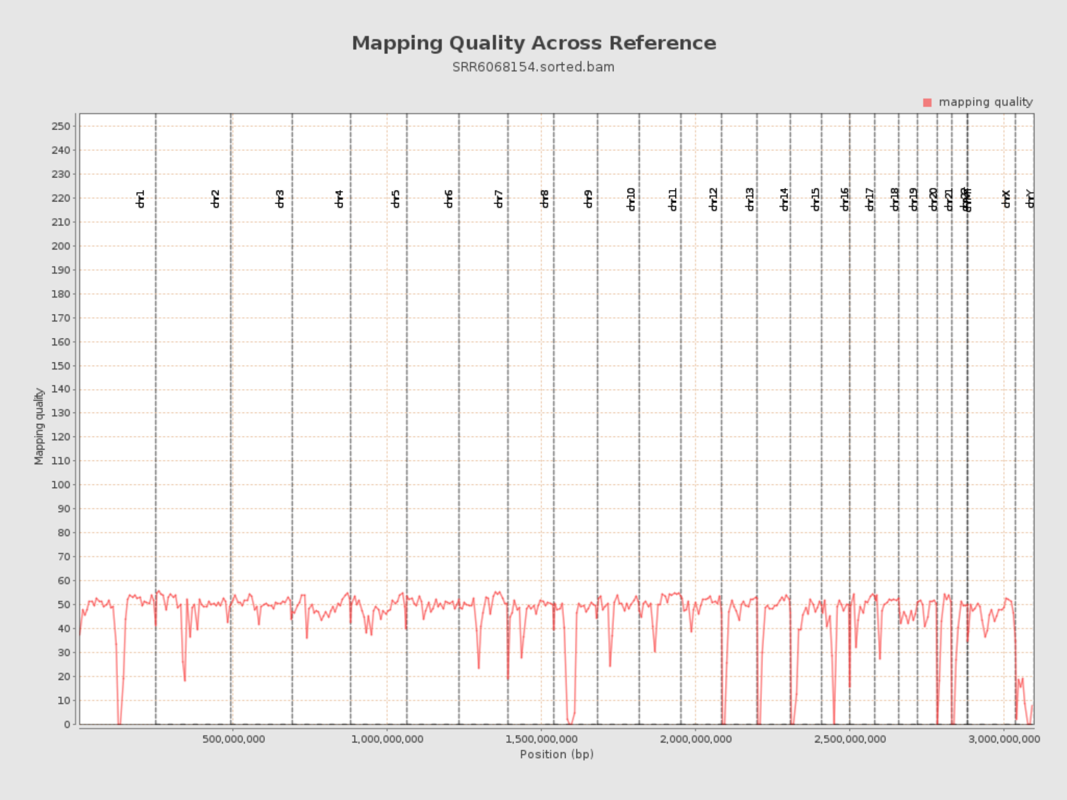
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram