Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 12:46:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068145.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_SRR6068145 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068145.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 12:46:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068145.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,268,914
Mapped reads	3,067,152 / 93.83%
Unmapped reads	201,762 / 6.17%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	26,173 / 0.8%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	306,615 / 9.38%
Duplication rate	8.56%
Clipped reads	1,616,594 / 49.45%

2.2. ACGT Content

Number/percentage of A's	52,446,359 / 26.55%
Number/percentage of C's	35,215,922 / 17.83%
Number/percentage of T's	64,442,449 / 32.63%
Number/percentage of G's	45,391,636 / 22.98%
Number/percentage of N's	22,687 / 0.01%
GC Percentage	40.81%

2.3. Coverage

Mean	0.0638

Standard Deviation	0.6478

2.4. Mapping Quality

Mean Mapping Quality	46.23

2.5. Mismatches and indels

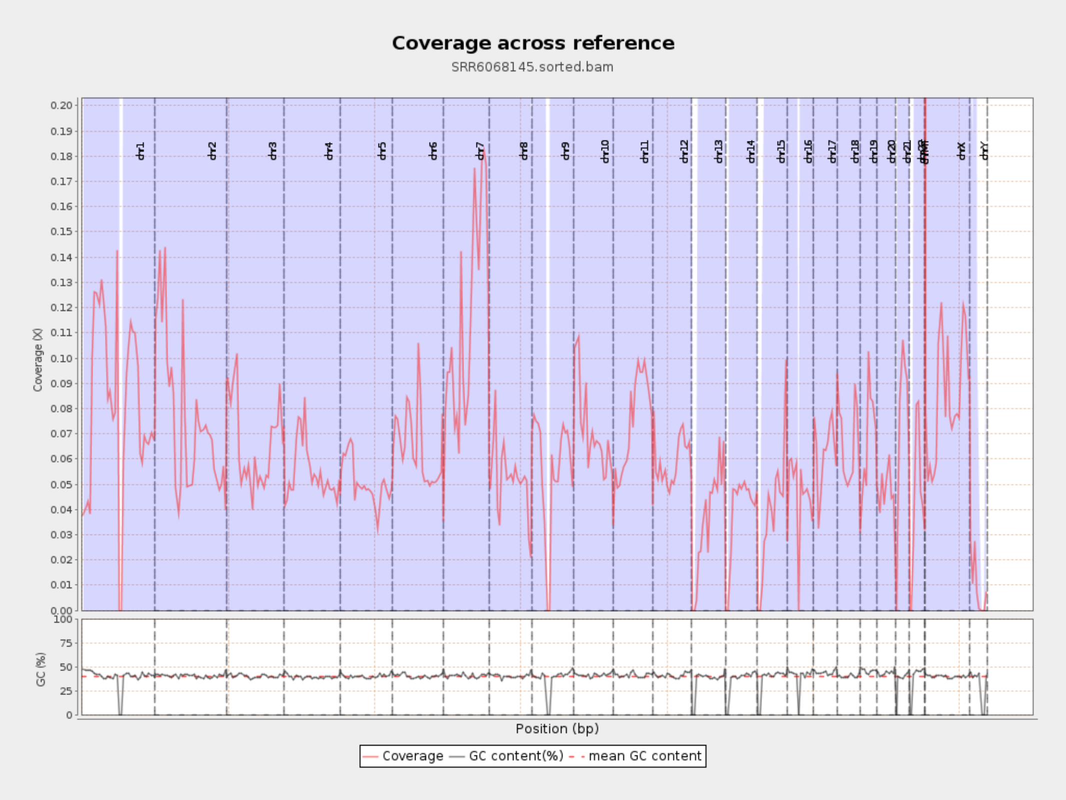
General error rate	0.58%
Mismatches	1,116,703
Insertions	12,778
Mapped reads with at least one insertion	0.41%
Deletions	49,064
Mapped reads with at least one deletion	1.58%
Homopolymer indels	45.01%

2.6. Chromosome stats

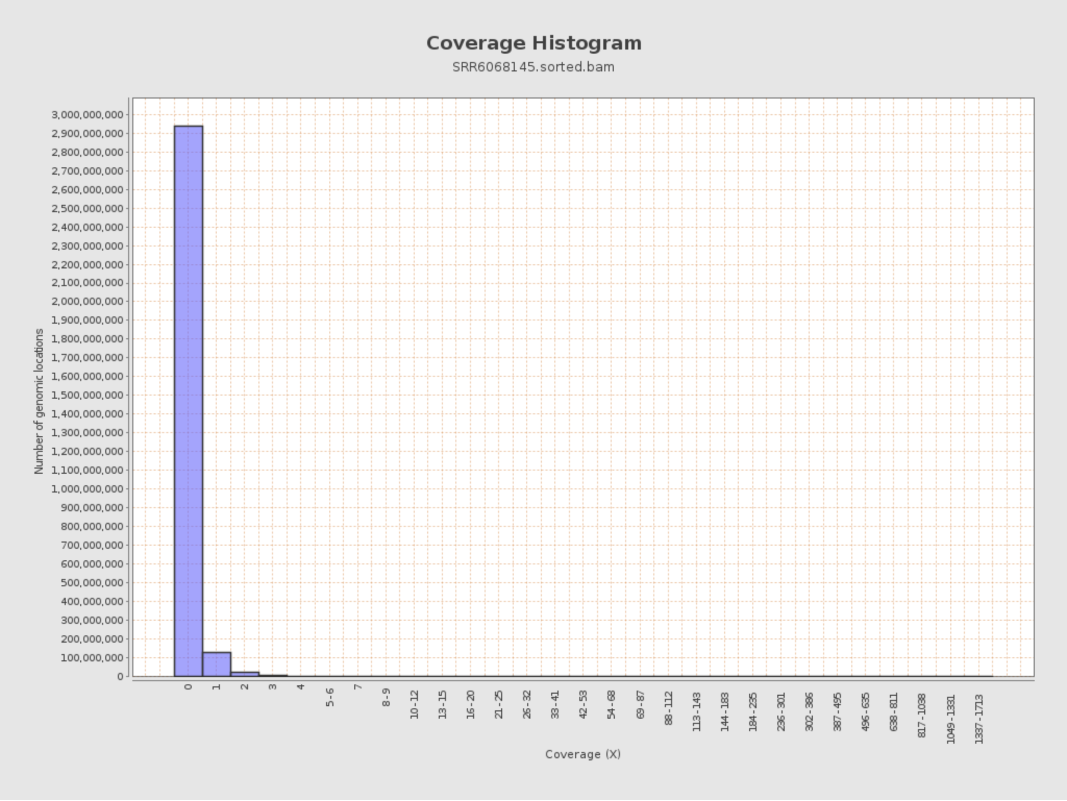
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	20394387	0.0818	1.4684
chr2	243199373	18572907	0.0764	0.8349
chr3	198022430	13118591	0.0662	0.3132
chr4	191154276	10491516	0.0549	0.3024
chr5	180915260	9167997	0.0507	0.2742
chr6	171115067	11187003	0.0654	0.3911
chr7	159138663	18377915	0.1155	0.9817

chr8	146364022	7576514	0.0518	0.7275
chr9	141213431	7842405	0.0555	0.4737
chr10	135534747	9748130	0.0719	0.4536
chr11	135006516	10051937	0.0745	0.417
chr12	133851895	7948567	0.0594	0.315
chr13	115169878	4198867	0.0365	0.2512
chr14	107349540	4212655	0.0392	0.2872
chr15	102531392	3938102	0.0384	0.2697
chr16	90354753	4076487	0.0451	0.2796
chr17	81195210	5126411	0.0631	0.3269
chr18	78077248	5180341	0.0663	0.8472
chr19	59128983	4006606	0.0678	0.8939
chr20	63025520	2981381	0.0473	0.2794
chr21	48129895	3484377	0.0724	0.3411
chr22	51304566	2216938	0.0432	0.2488
chrMT	16571	98558	5.9476	4.1379
chrX	155270560	13052139	0.0841	0.4112
chrY	59373566	553487	0.0093	0.2441

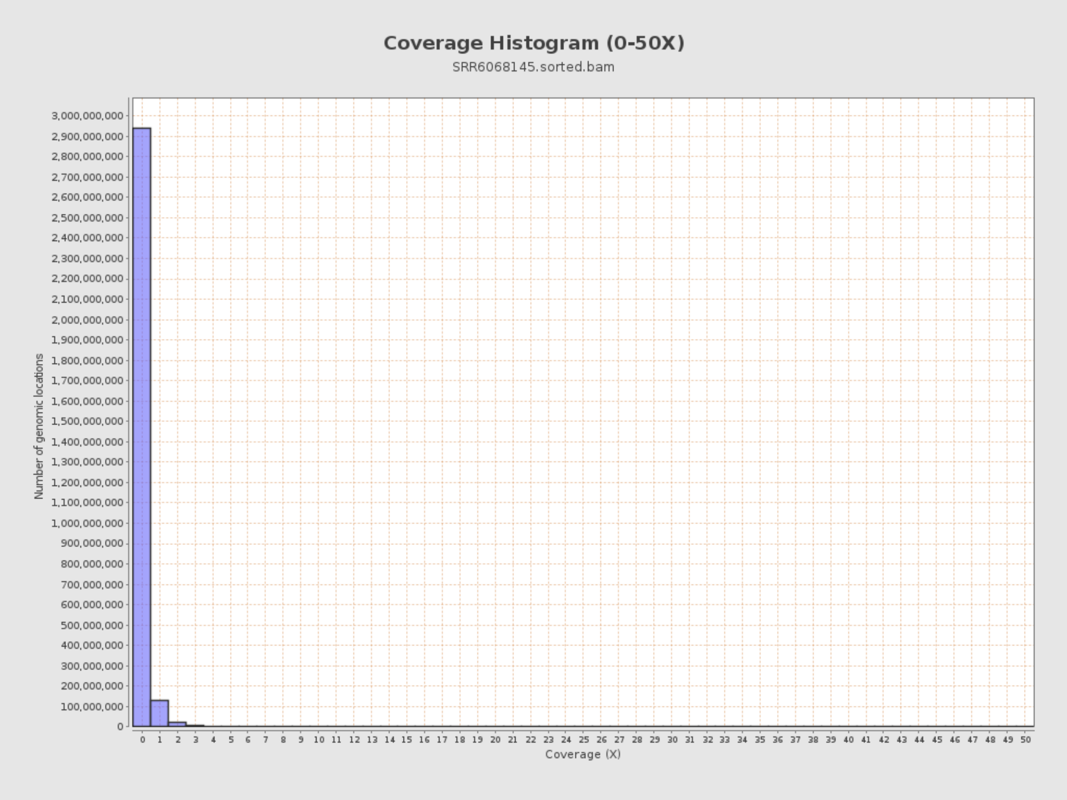
3. Results : Coverage across reference



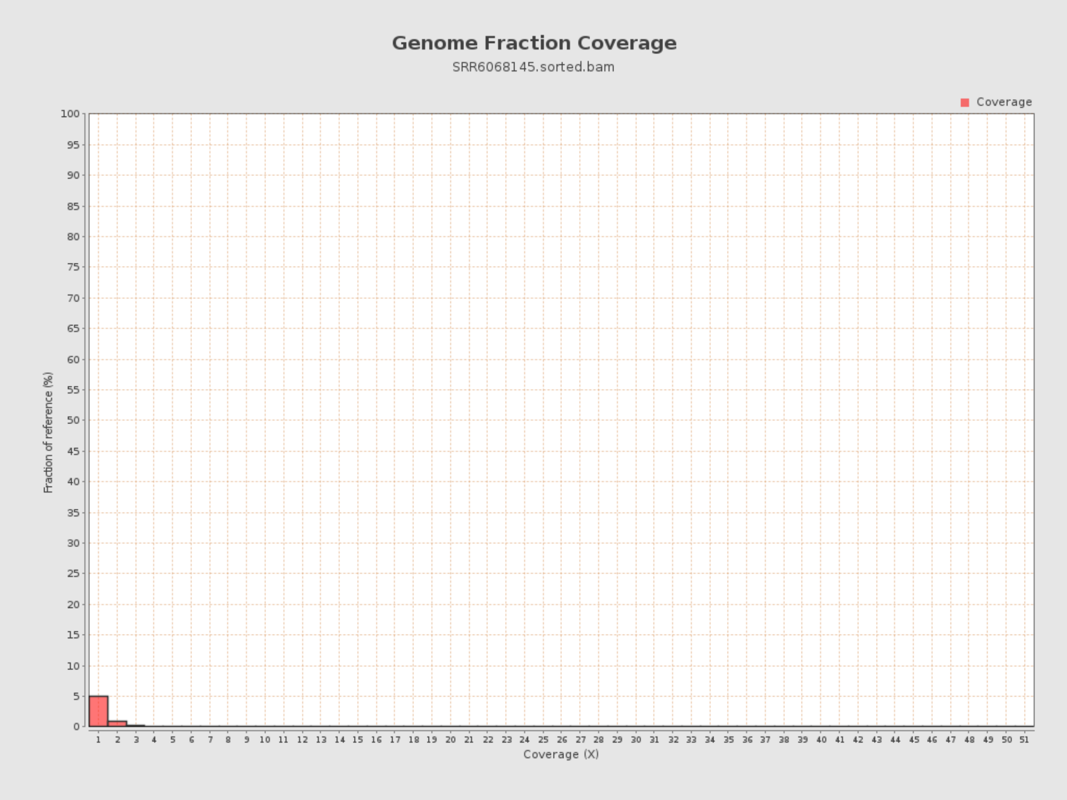
4. Results : Coverage Histogram



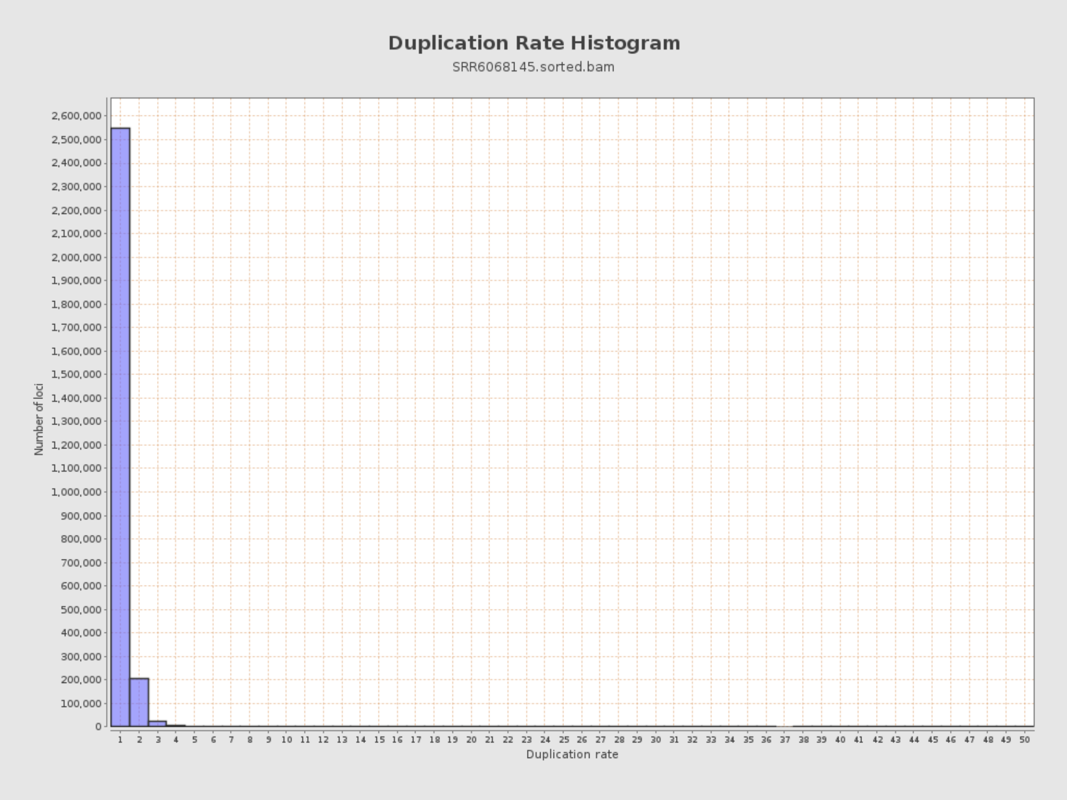
5. Results : Coverage Histogram (0-50X)



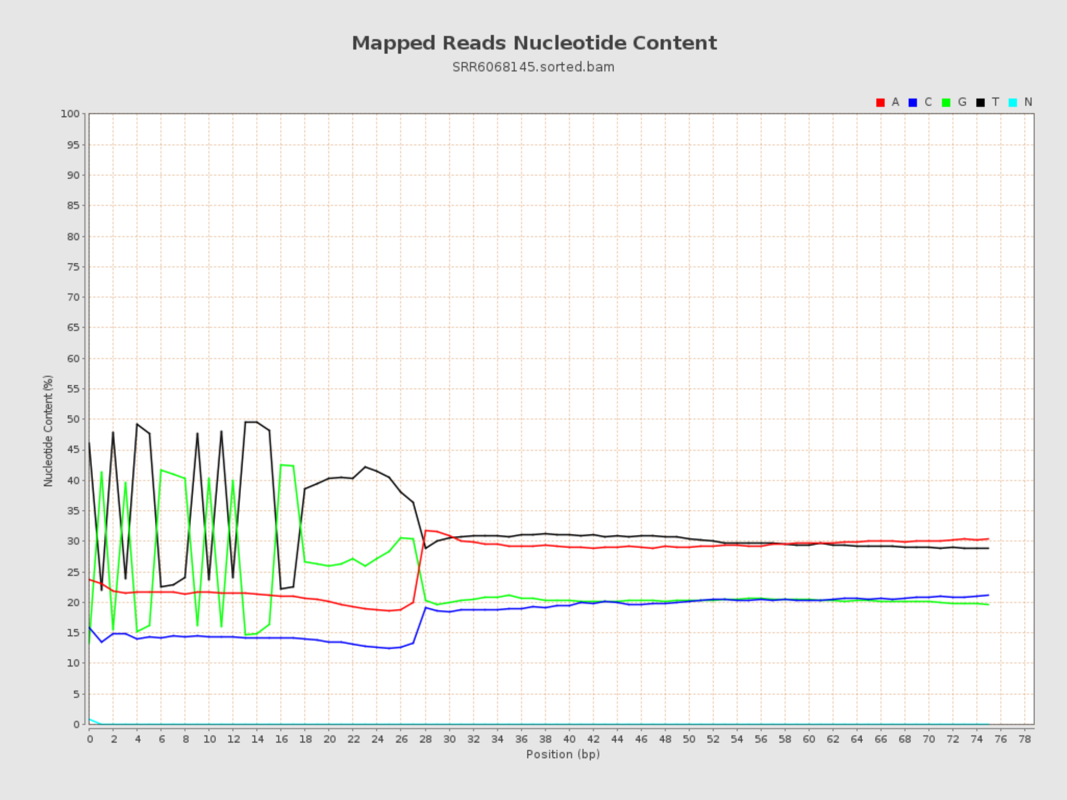
6. Results : Genome Fraction Coverage



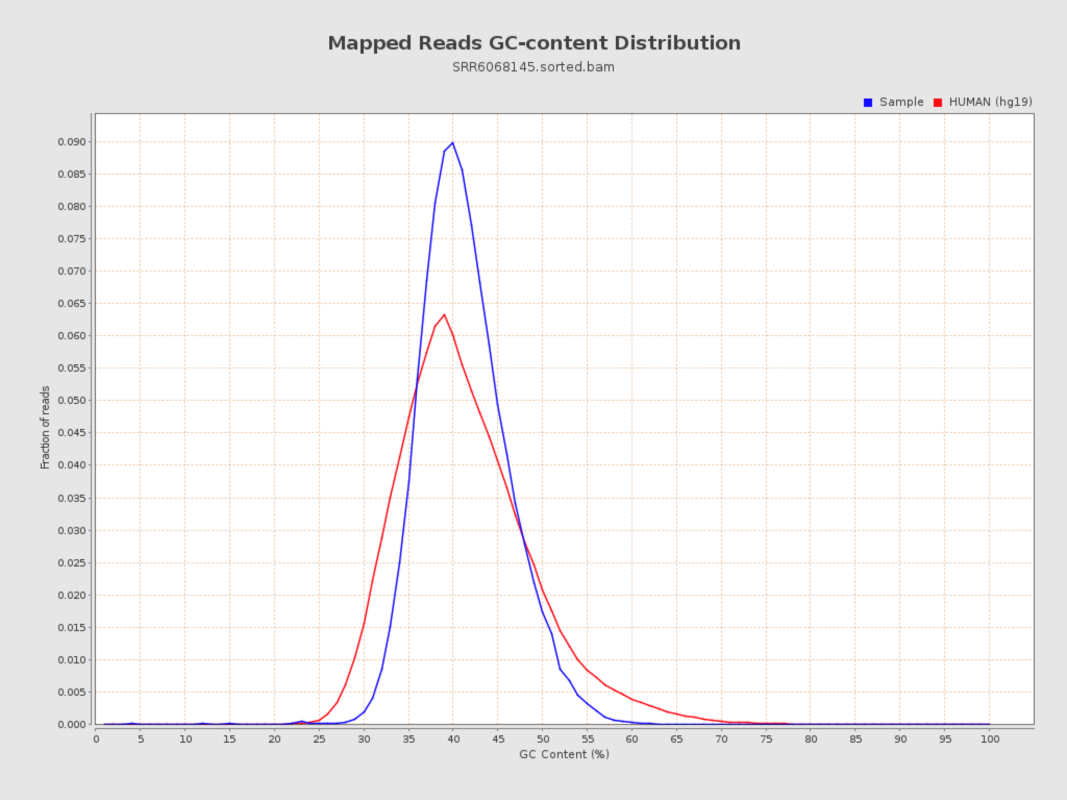
7. Results : Duplication Rate Histogram



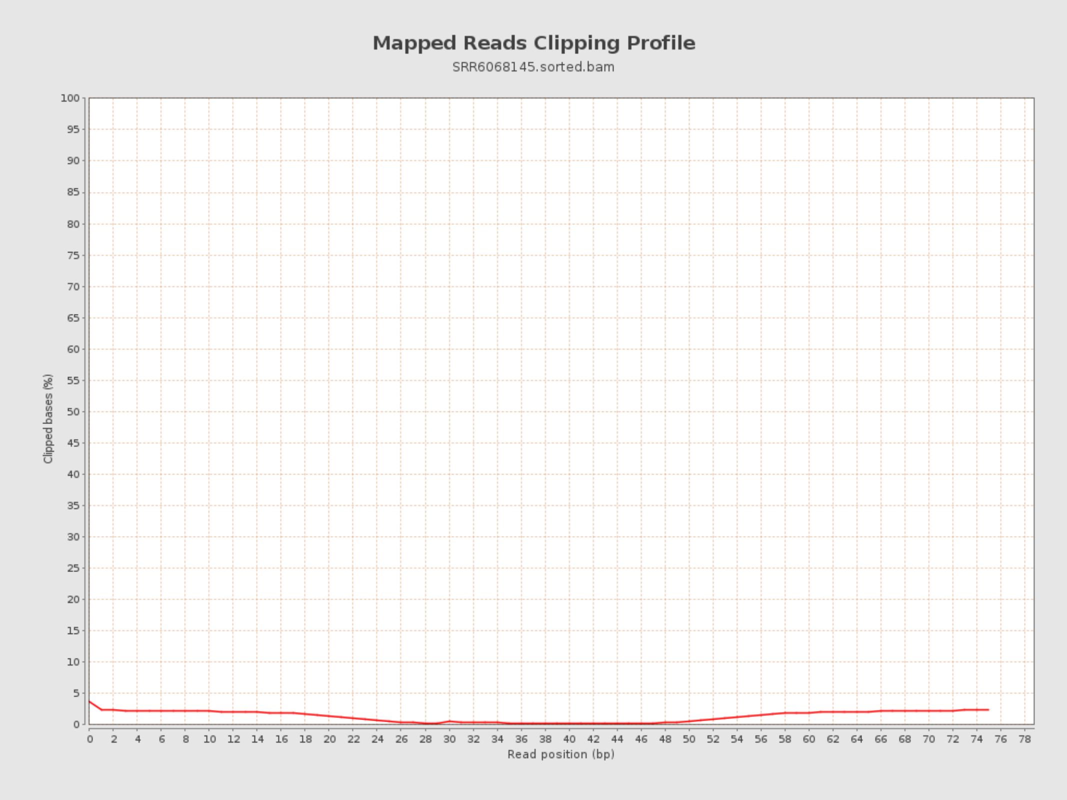
8. Results : Mapped Reads Nucleotide Content



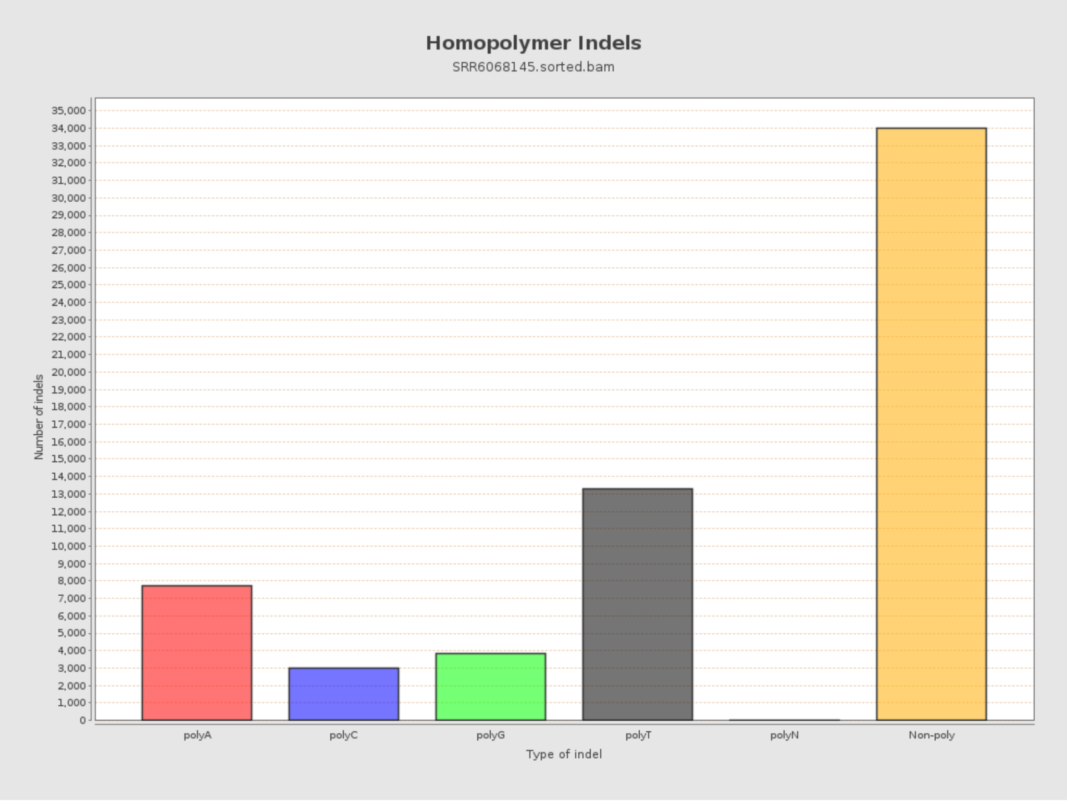
9. Results : Mapped Reads GC-content Distribution



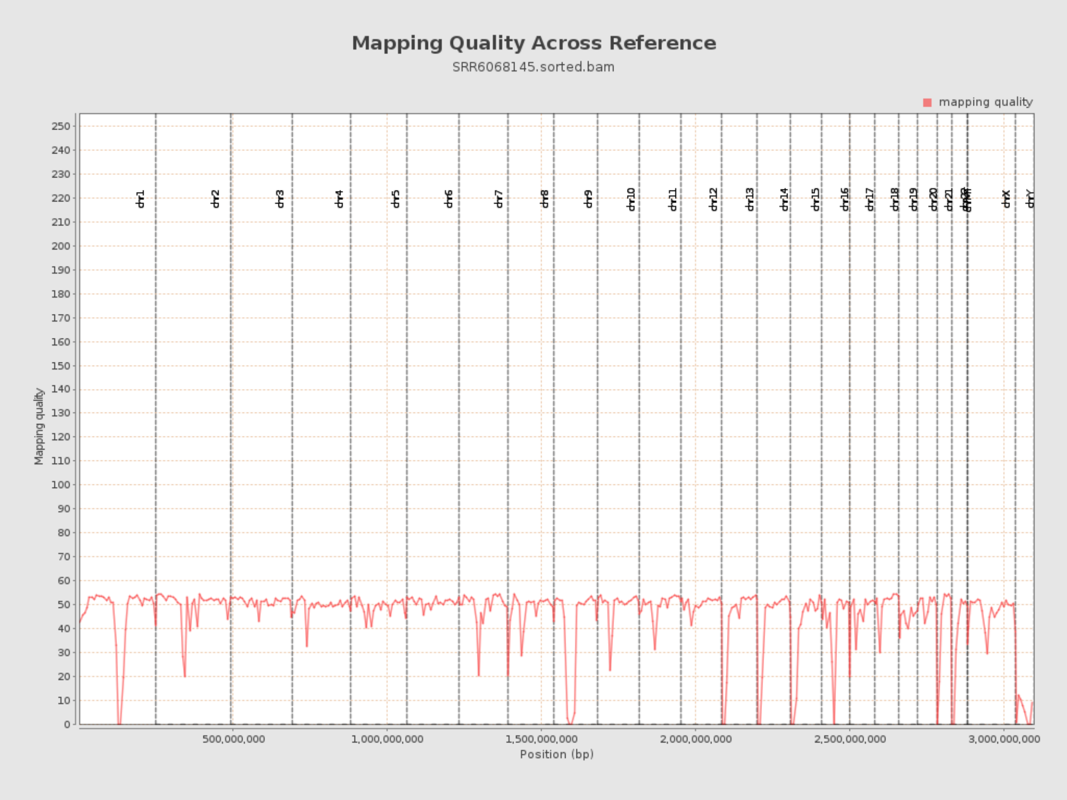
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram