Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 16:01:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068932.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_SRR6068932 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068932.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 16:01:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068932.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,864,569
Mapped reads	2,460,668 / 85.9%
Unmapped reads	403,901 / 14.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,694 / 0.48%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	93,956 / 3.28%
Duplication rate	2.28%
Clipped reads	1,229,182 / 42.91%

2.2. ACGT Content

Number/percentage of A's	42,978,004 / 26.67%
Number/percentage of C's	28,157,359 / 17.47%
Number/percentage of T's	52,757,698 / 32.74%
Number/percentage of G's	36,853,544 / 22.87%
Number/percentage of N's	391,772 / 0.24%
GC Percentage	40.34%

2.3. Coverage

Mean	0.0521

Standard Deviation	0.5782

2.4. Mapping Quality

Mean Mapping Quality	44.17

2.5. Mismatches and indels

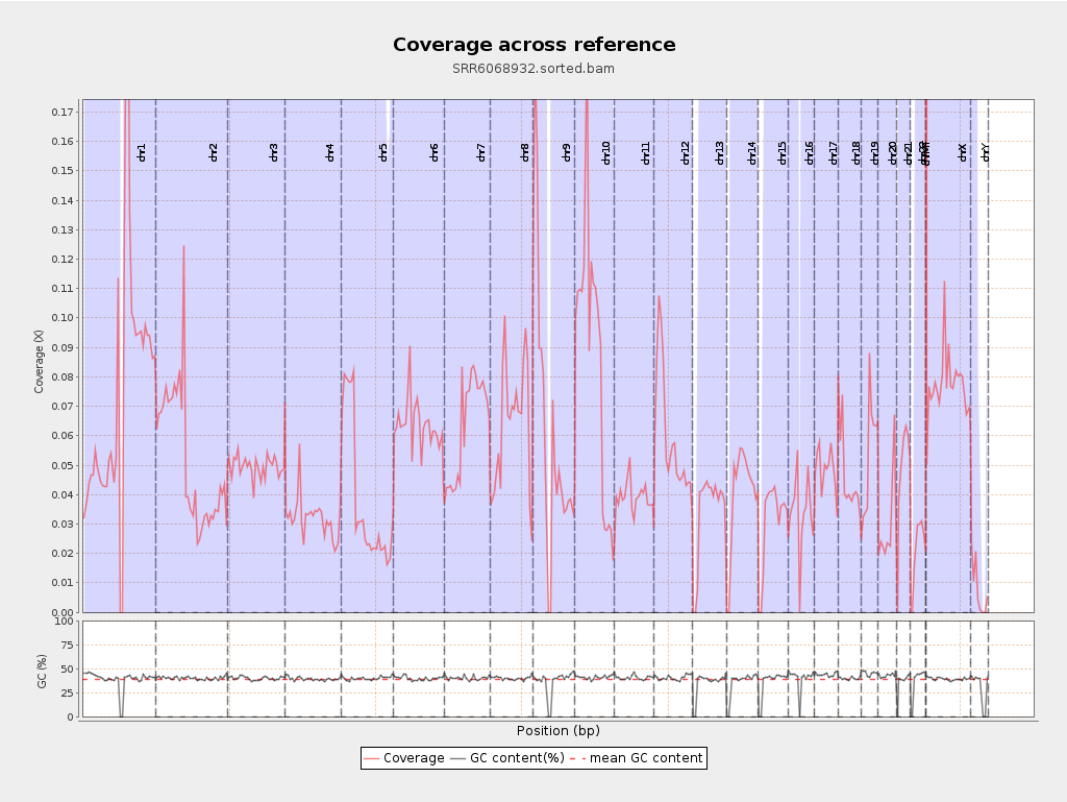
General error rate	0.98%
Mismatches	1,557,978
Insertions	15,467
Mapped reads with at least one insertion	0.62%
Deletions	44,043
Mapped reads with at least one deletion	1.77%
Homopolymer indels	47.63%

2.6. Chromosome stats

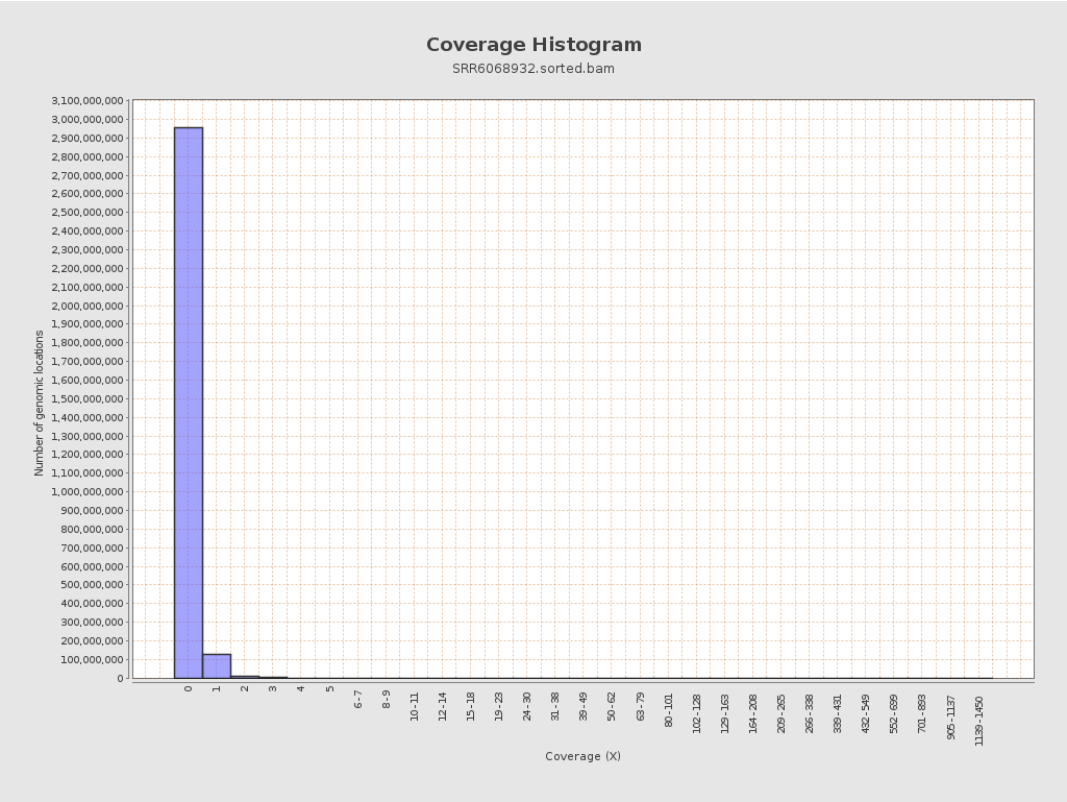
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	18496597	0.0742	1.2195
chr2	243199373	12499696	0.0514	0.5254
chr3	198022430	9836810	0.0497	0.3464
chr4	191154276	6135988	0.0321	0.2385
chr5	180915260	6922601	0.0383	0.2211
chr6	171115067	10885789	0.0636	0.4171
chr7	159138663	10086458	0.0634	0.55

chr8	146364022	9419303	0.0644	0.6484
chr9	141213431	8534416	0.0604	0.5363
chr10	135534747	11718254	0.0865	1.0972
chr11	135006516	5295818	0.0392	0.4302
chr12	133851895	8006889	0.0598	0.2867
chr13	115169878	3929938	0.0341	0.2005
chr14	107349540	4377211	0.0408	0.2908
chr15	102531392	3131791	0.0305	0.1933
chr16	90354753	2984227	0.033	0.2951
chr17	81195210	3999771	0.0493	0.2966
chr18	78077248	3614334	0.0463	0.9484
chr19	59128983	3180944	0.0538	0.7109
chr20	63025520	1990317	0.0316	0.2333
chr21	48129895	2342390	0.0487	0.2928
chr22	51304566	1076258	0.021	0.1661
chrMT	16571	277881	16.7691	12.6257
chrX	155270560	12015513	0.0774	0.3868
chrY	59373566	452909	0.0076	0.159

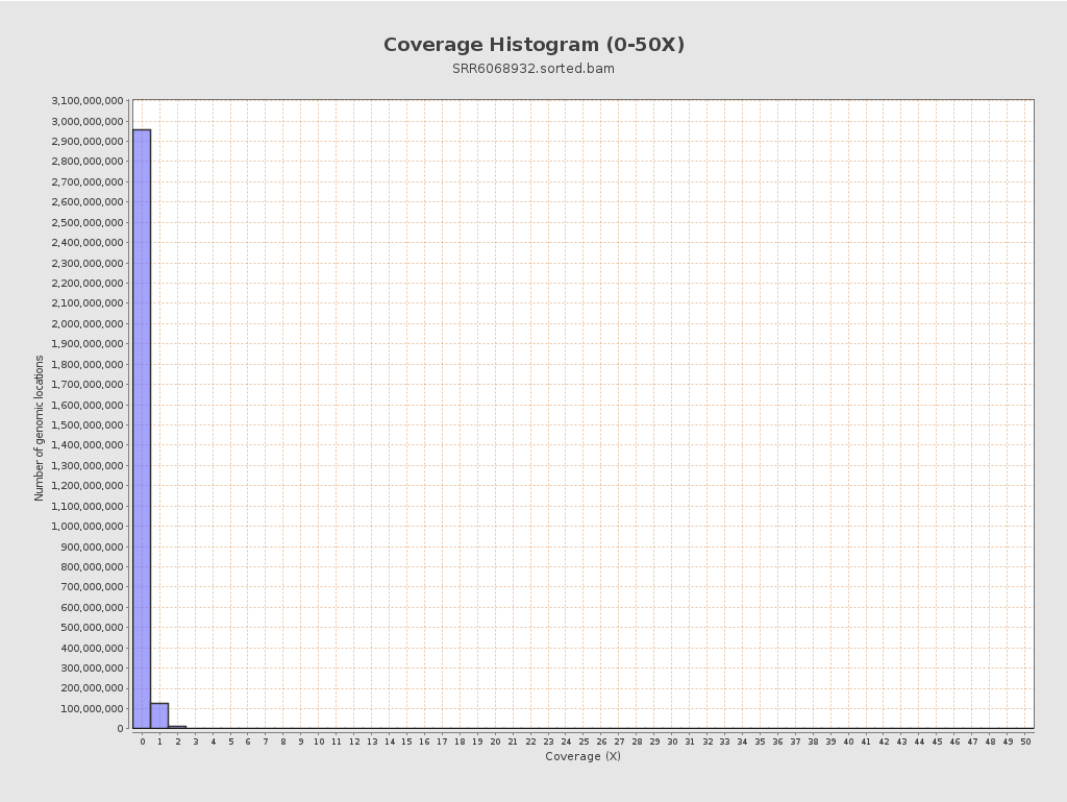
3. Results : Coverage across reference



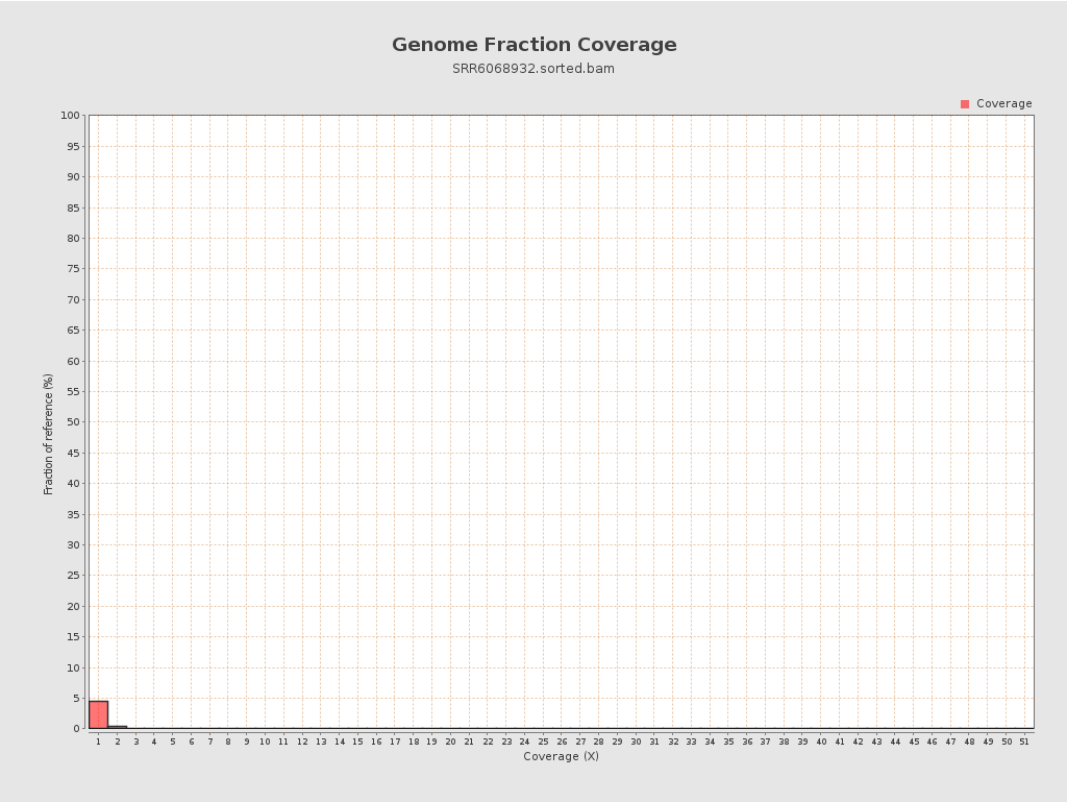
4. Results : Coverage Histogram



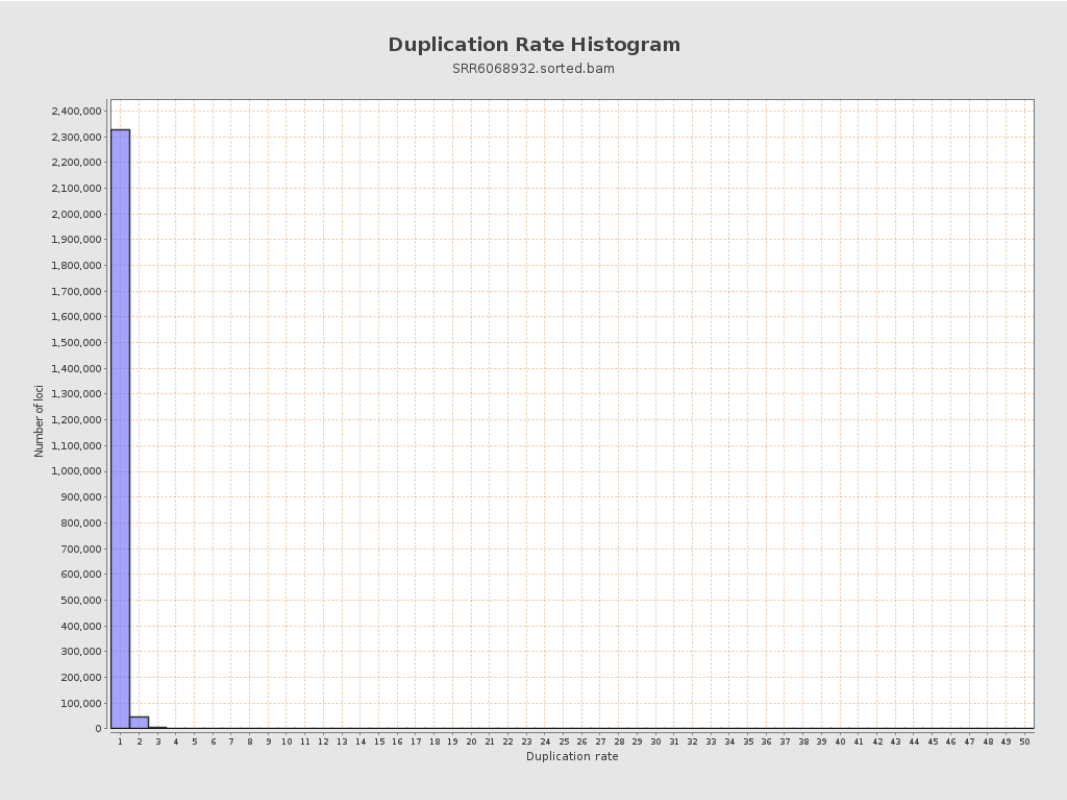
5. Results : Coverage Histogram (0-50X)



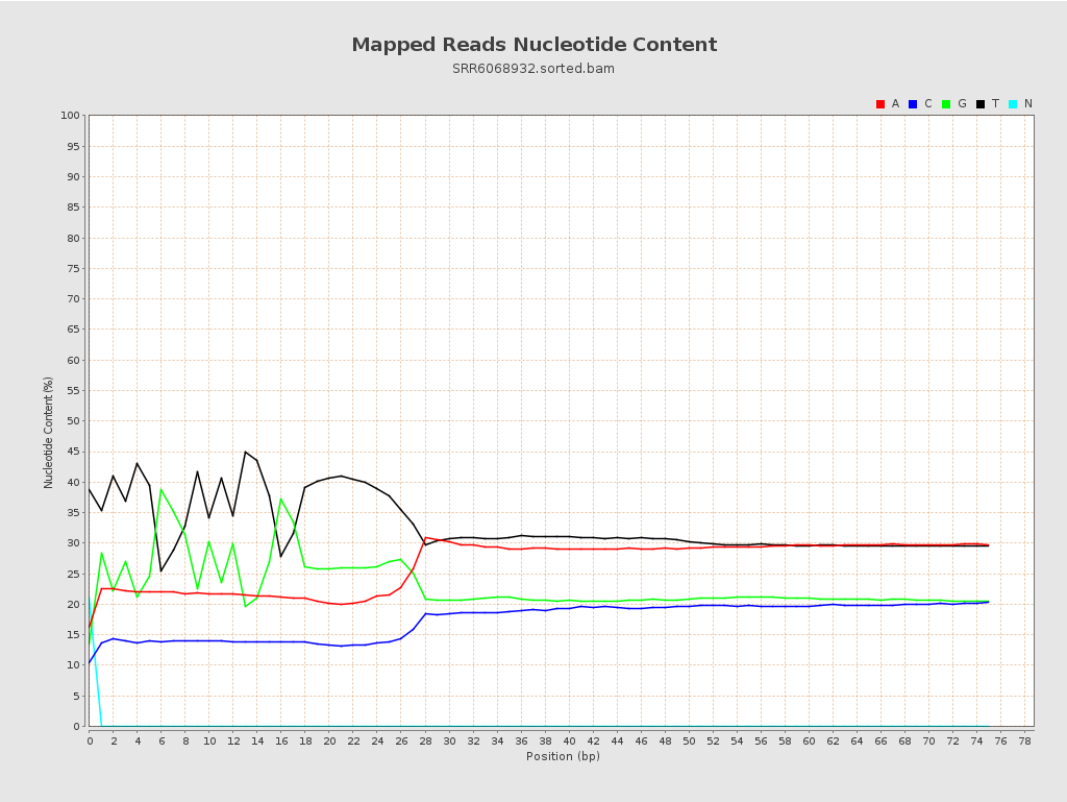
6. Results : Genome Fraction Coverage



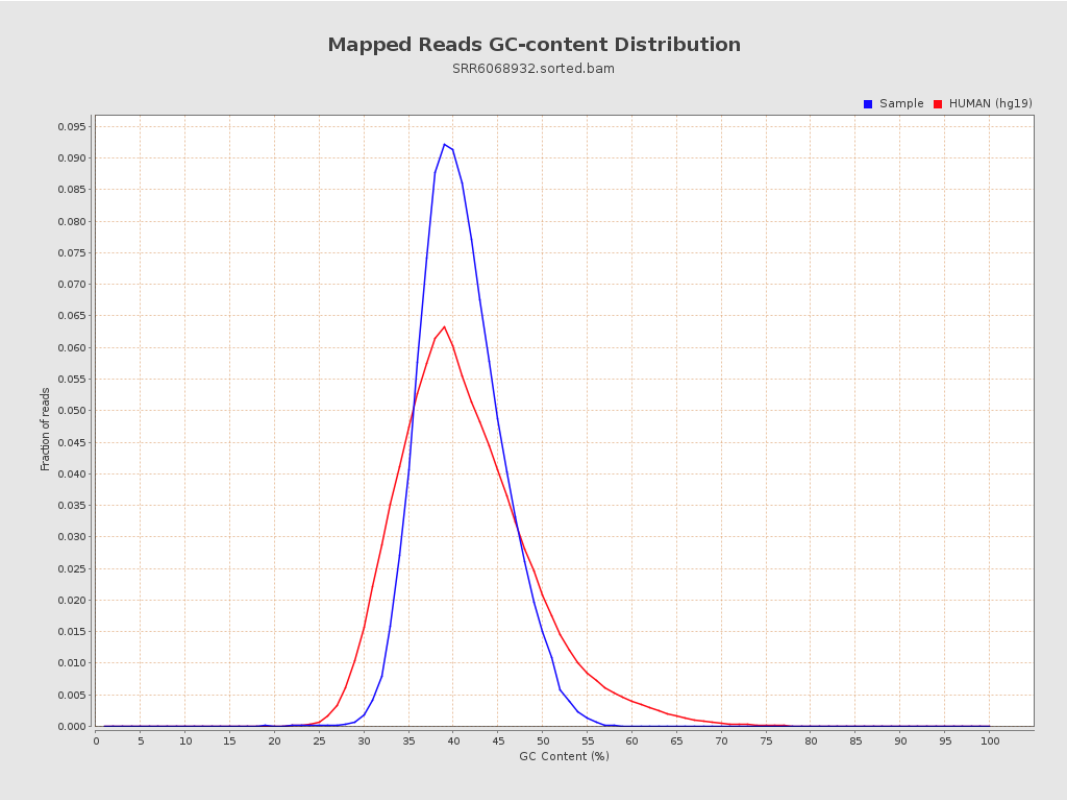
7. Results : Duplication Rate Histogram



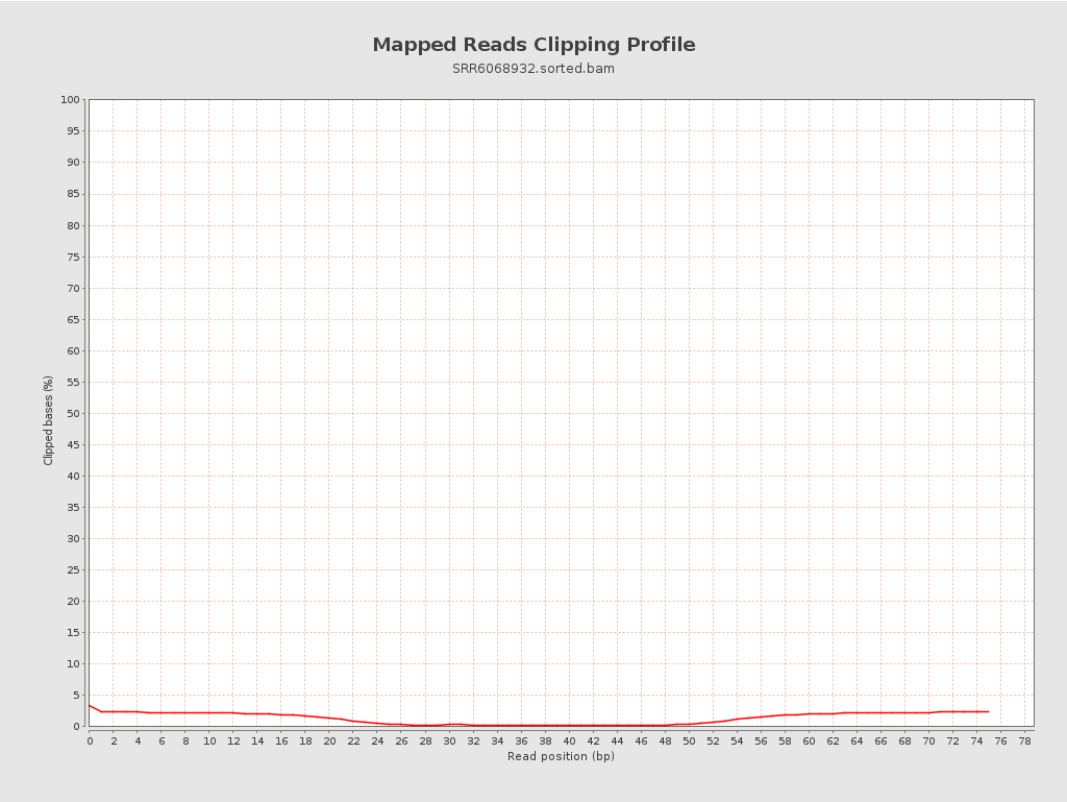
8. Results : Mapped Reads Nucleotide Content



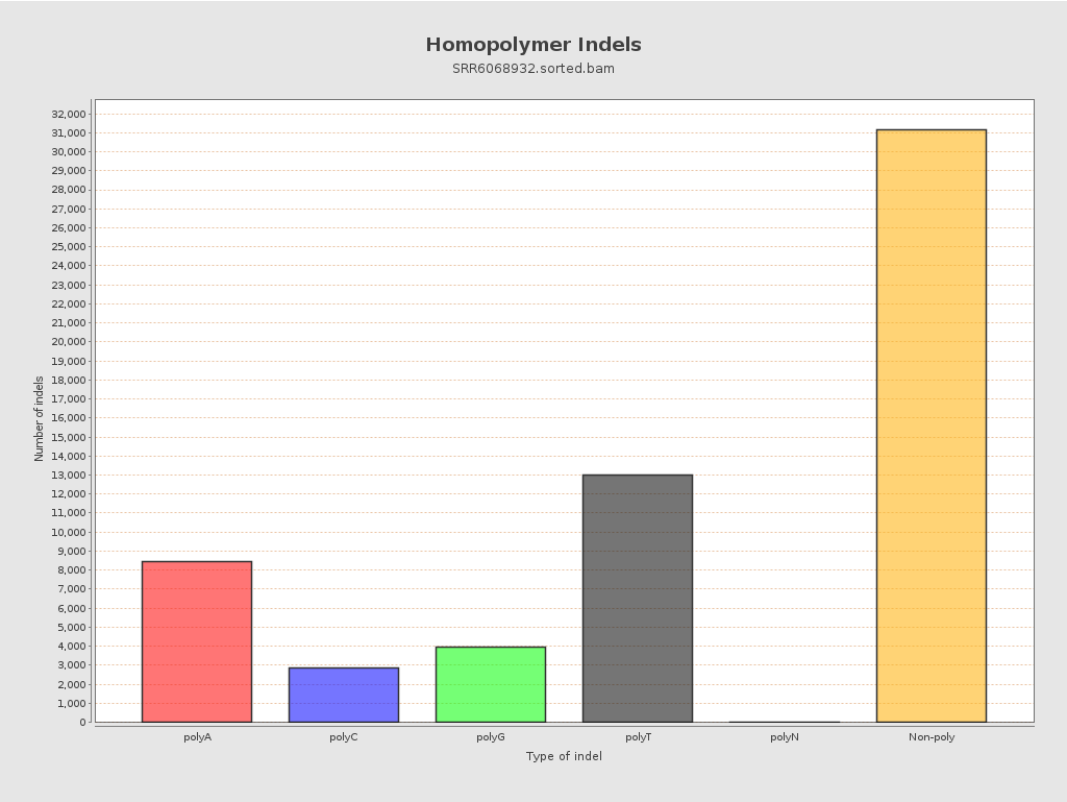
9. Results : Mapped Reads GC-content Distribution



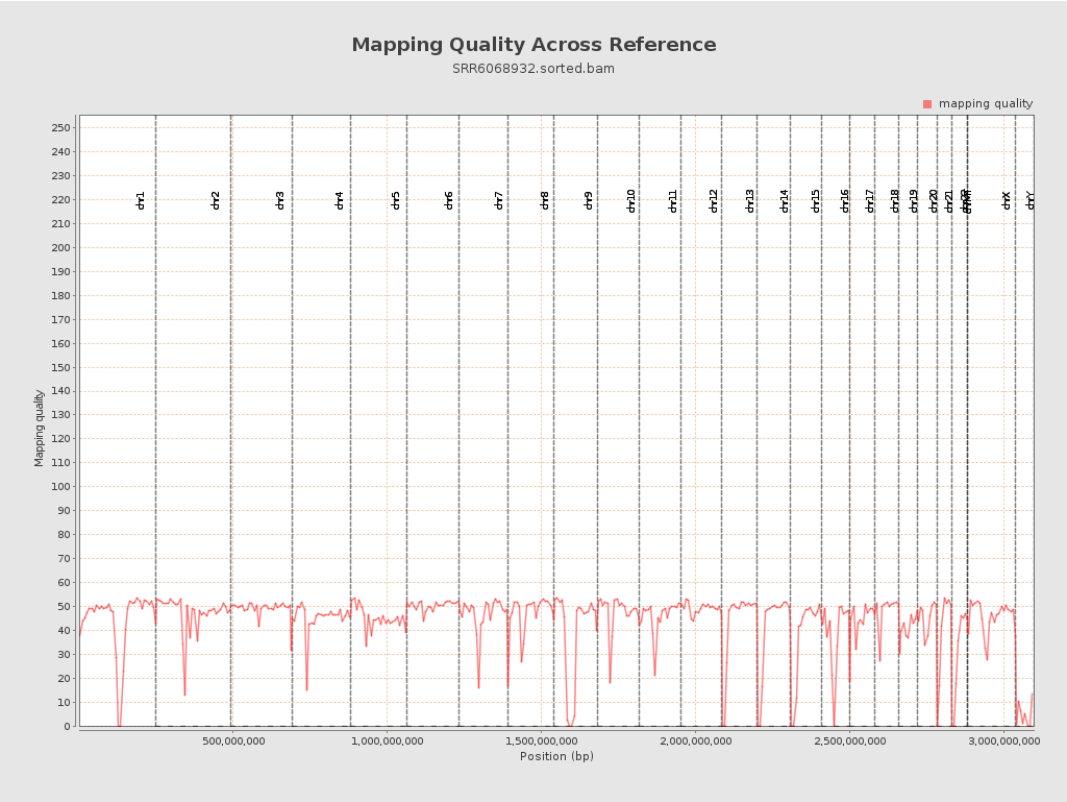
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram