Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 08:35:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068076.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_SRR6068076 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068076.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 08:35:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068076.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,439,925
Mapped reads	4,171,147 / 93.95%
Unmapped reads	268,778 / 6.05%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	30,426 / 0.69%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	570,762 / 12.86%
Duplication rate	11.31%
Clipped reads	2,228,543 / 50.19%

2.2. ACGT Content

Number/percentage of A's	69,074,169 / 25.84%
Number/percentage of C's	47,699,820 / 17.84%
Number/percentage of T's	87,681,861 / 32.8%
Number/percentage of G's	62,830,037 / 23.5%
Number/percentage of N's	29,621 / 0.01%
GC Percentage	41.35%

2.3. Coverage

Mean	0.0864

Standard Deviation	0.9684

2.4. Mapping Quality

Mean Mapping Quality	45.61

2.5. Mismatches and indels

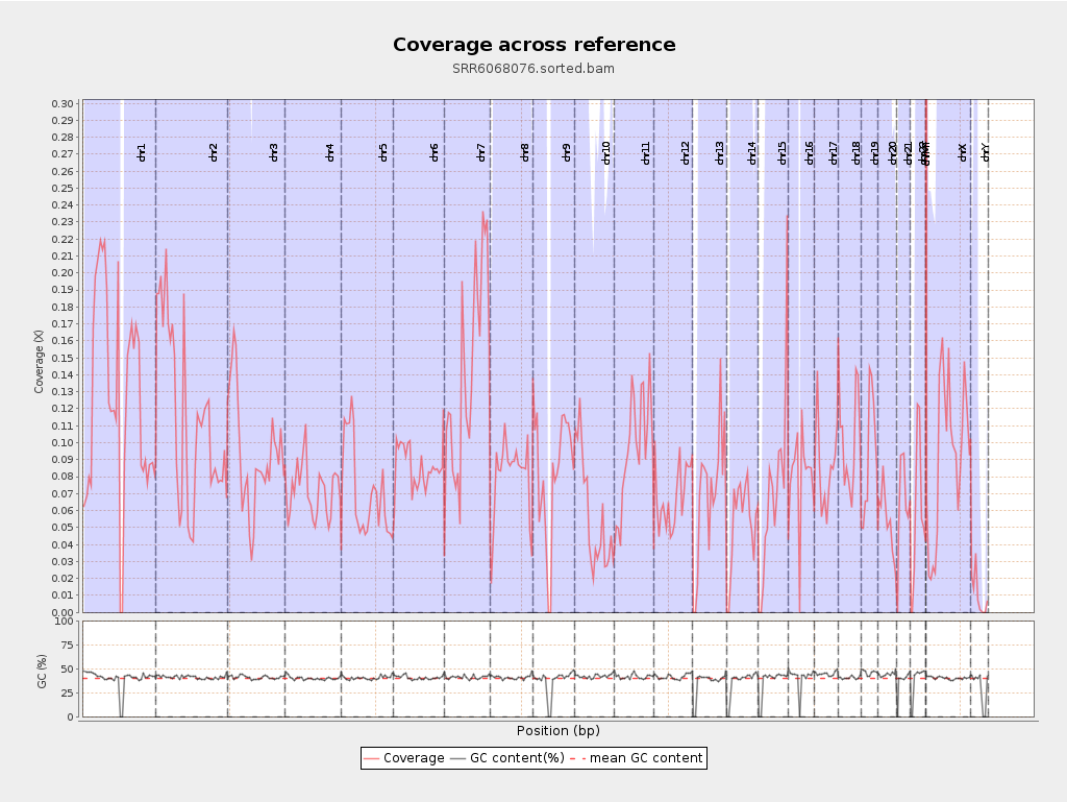
General error rate	0.58%
Mismatches	1,518,200
Insertions	16,606
Mapped reads with at least one insertion	0.39%
Deletions	63,108
Mapped reads with at least one deletion	1.5%
Homopolymer indels	44.3%

2.6. Chromosome stats

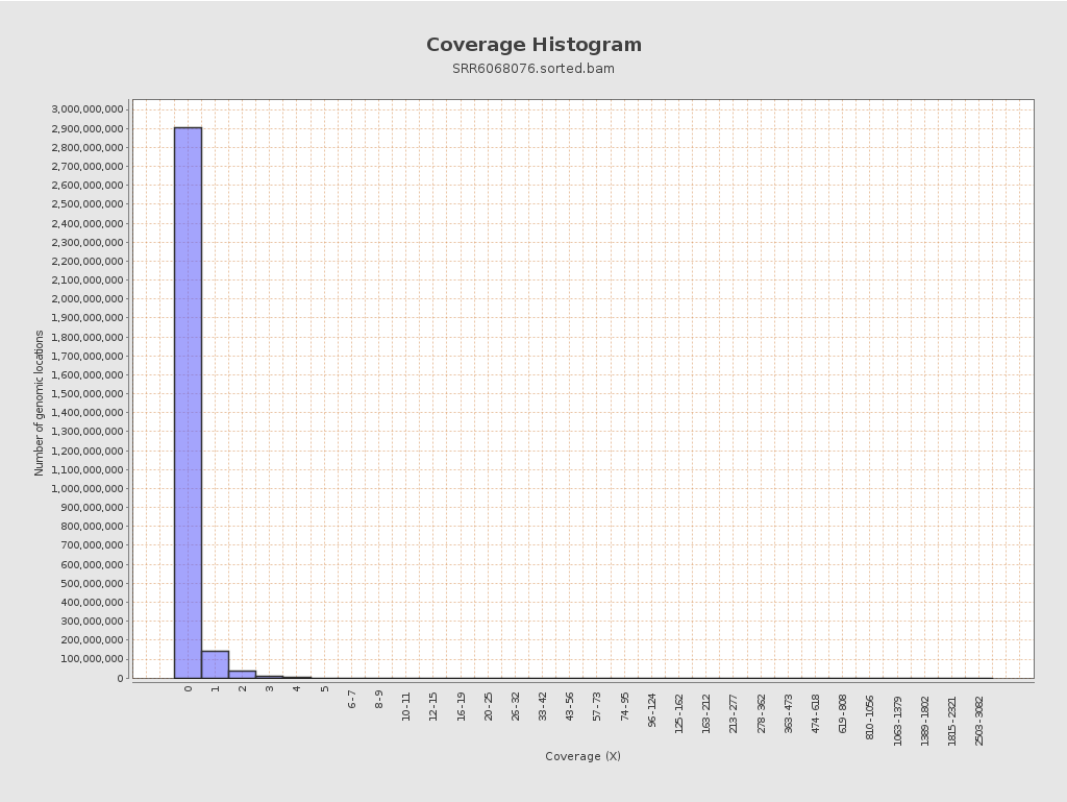
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	31335619	0.1257	2.228
chr2	243199373	27973731	0.115	1.522
chr3	198022430	18379244	0.0928	0.4063
chr4	191154276	13719384	0.0718	0.3787
chr5	180915260	12754465	0.0705	0.3582
chr6	171115067	14734964	0.0861	0.5645
chr7	159138663	22707852	0.1427	1.4076

chr8	146364022	11742234	0.0802	0.7844
chr9	141213431	11452360	0.0811	0.6294
chr10	135534747	7677098	0.0566	0.5048
chr11	135006516	13036381	0.0966	0.6089
chr12	133851895	9107791	0.068	0.3831
chr13	115169878	8087693	0.0702	0.4029
chr14	107349540	5692897	0.053	0.36
chr15	102531392	7006244	0.0683	0.3892
chr16	90354753	7159562	0.0792	0.417
chr17	81195210	6934911	0.0854	0.438
chr18	78077248	7930356	0.1016	1.203
chr19	59128983	5469416	0.0925	1.4857
chr20	63025520	3409271	0.0541	0.3475
chr21	48129895	3055454	0.0635	0.3577
chr22	51304566	2980965	0.0581	0.3136
chrMT	16571	270138	16.3019	9.3542
chrX	155270560	14197345	0.0914	0.5209
chrY	59373566	611059	0.0103	0.3542

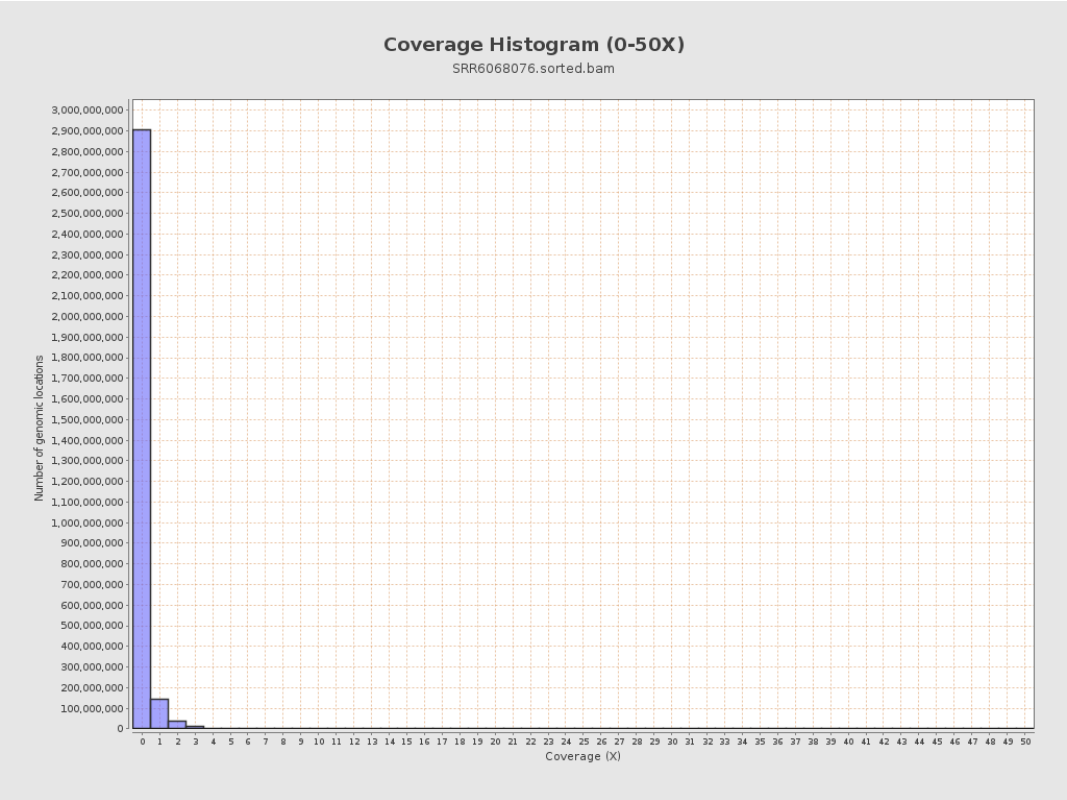
3. Results : Coverage across reference



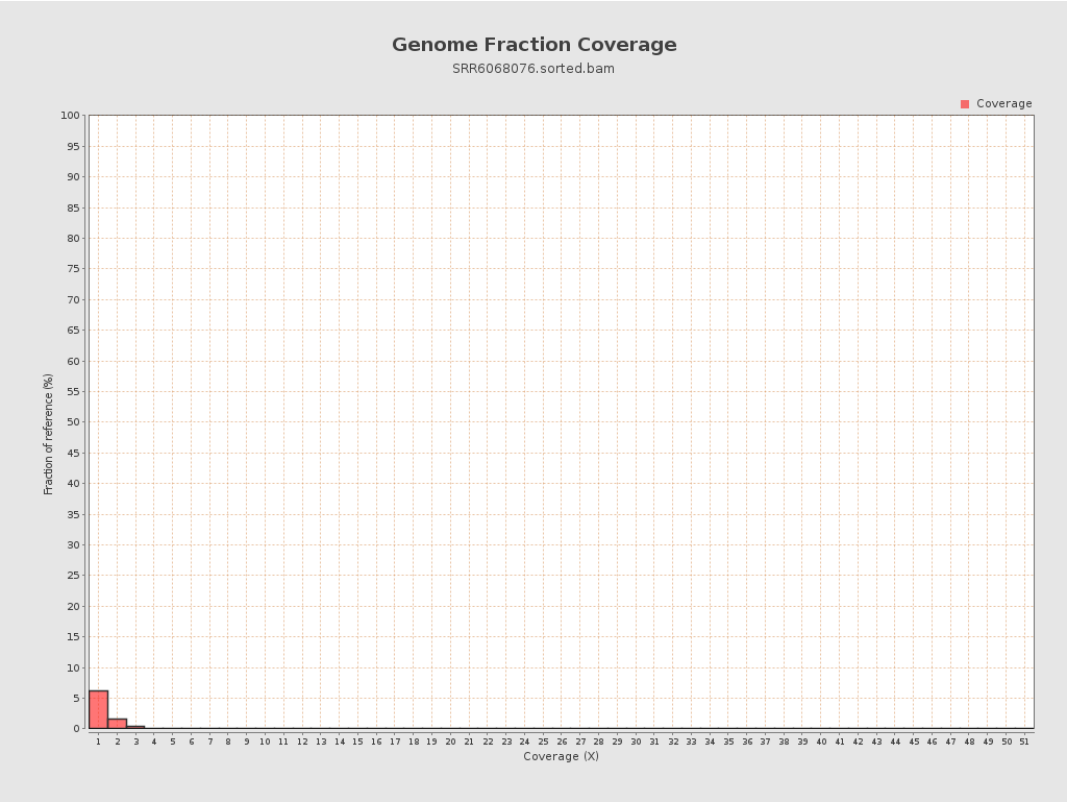
4. Results : Coverage Histogram



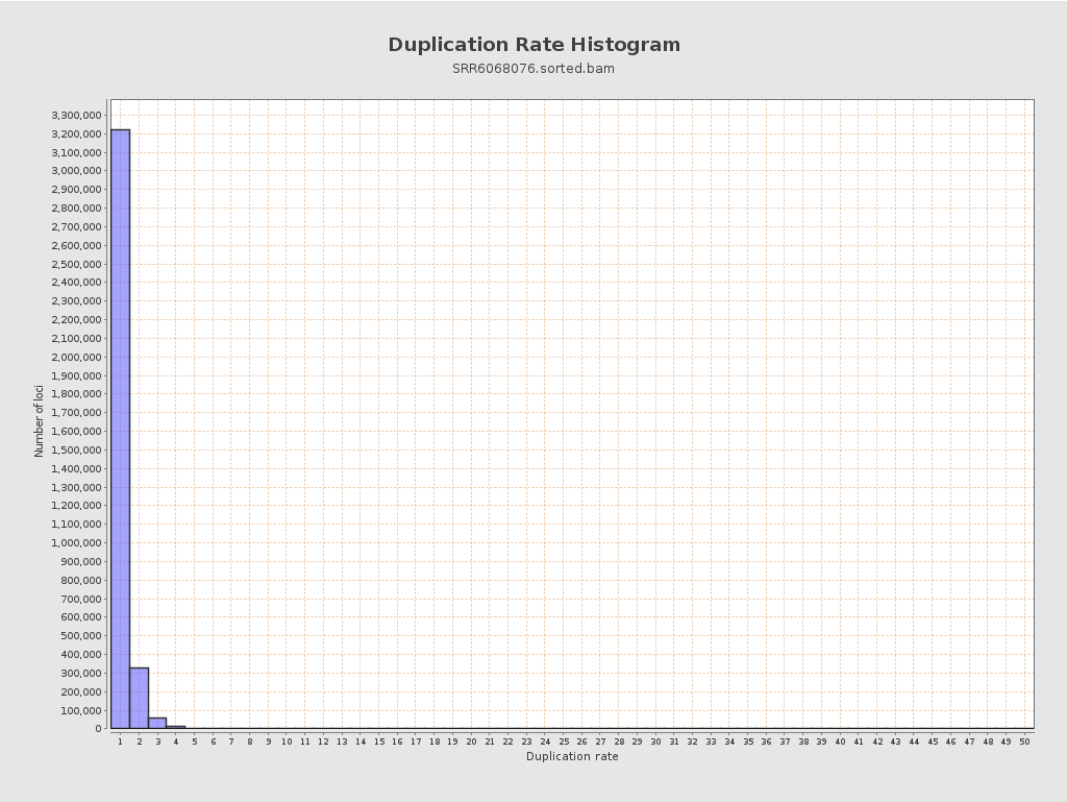
5. Results : Coverage Histogram (0-50X)



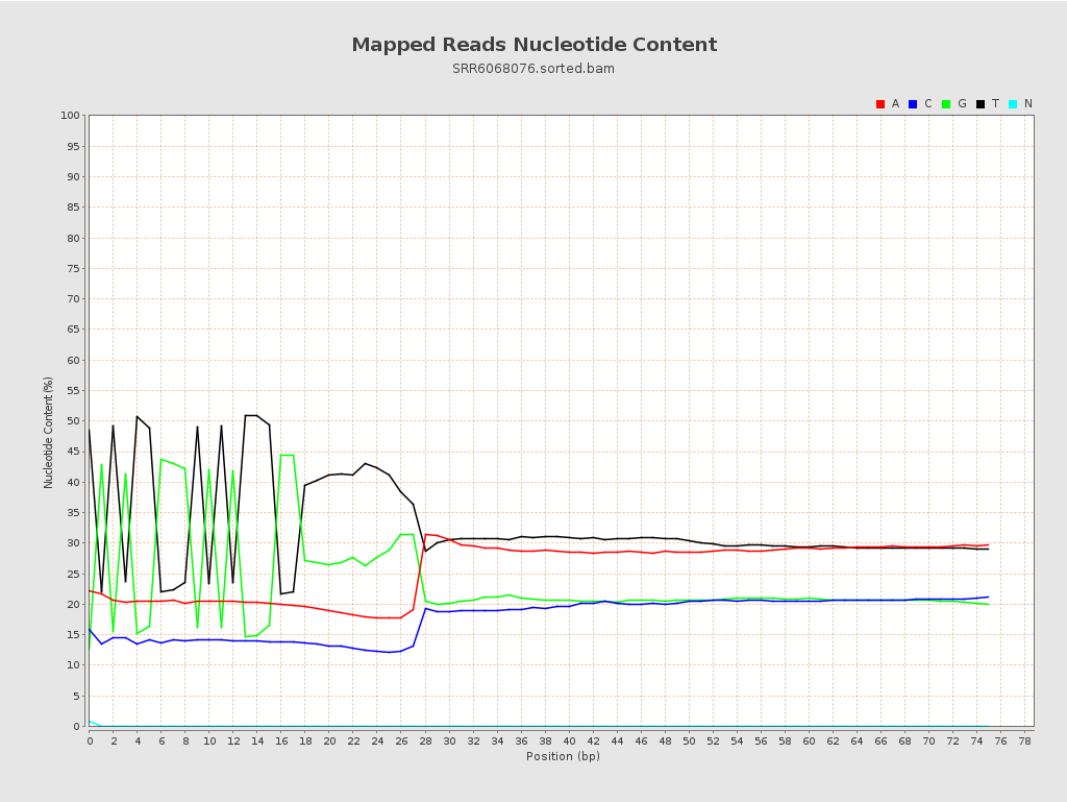
6. Results : Genome Fraction Coverage



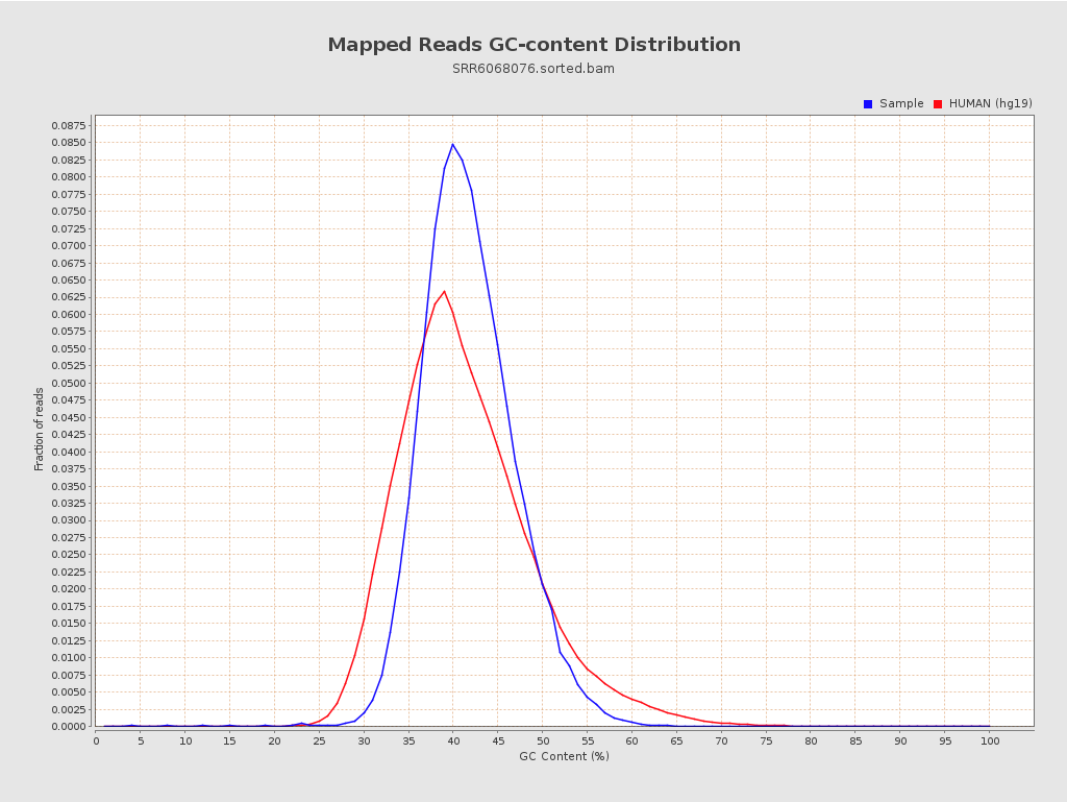
7. Results : Duplication Rate Histogram



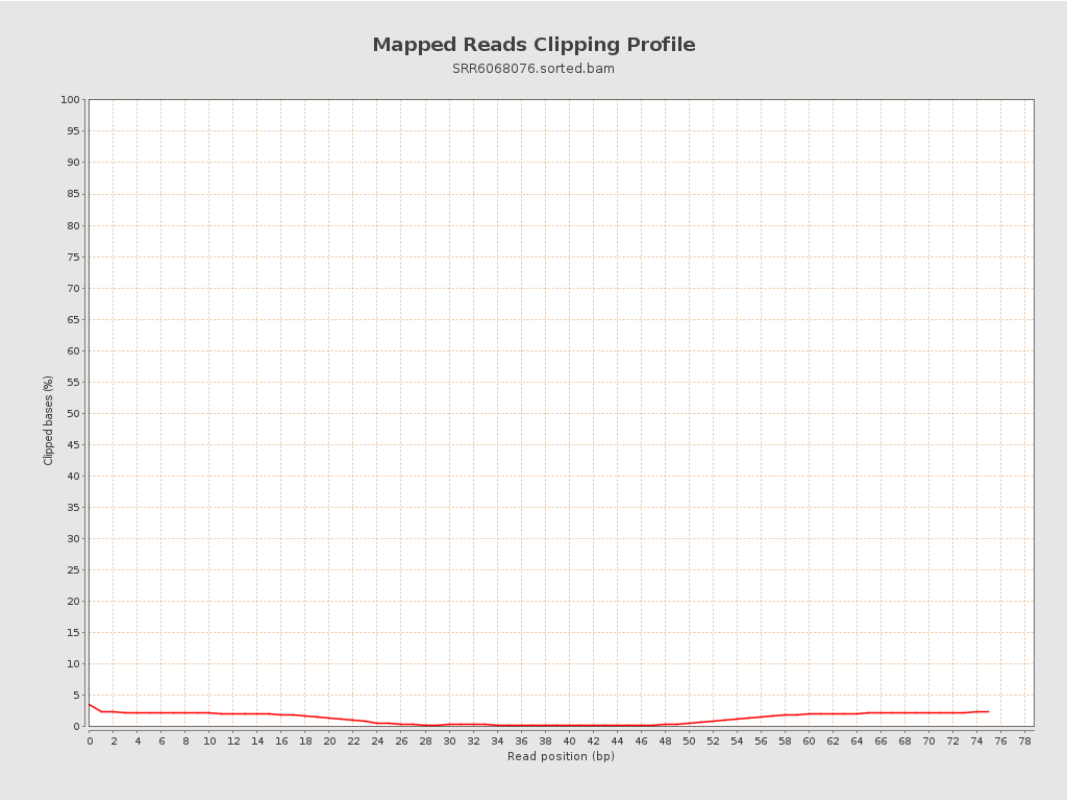
8. Results : Mapped Reads Nucleotide Content



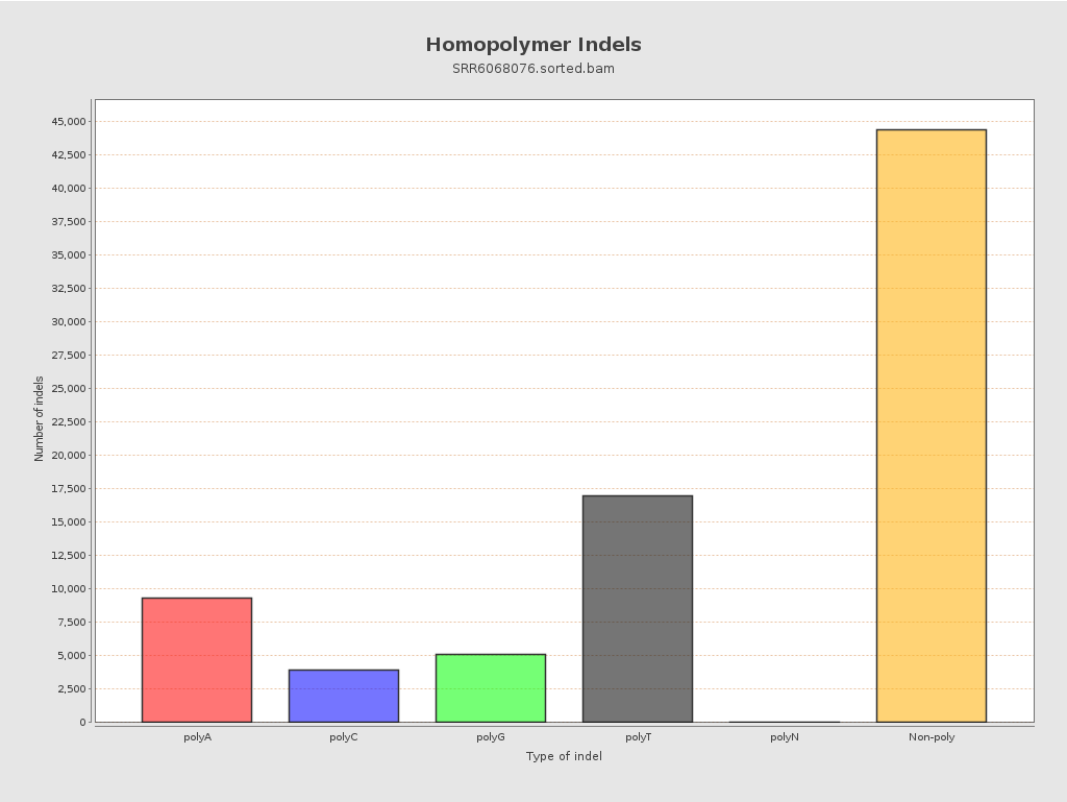
9. Results : Mapped Reads GC-content Distribution



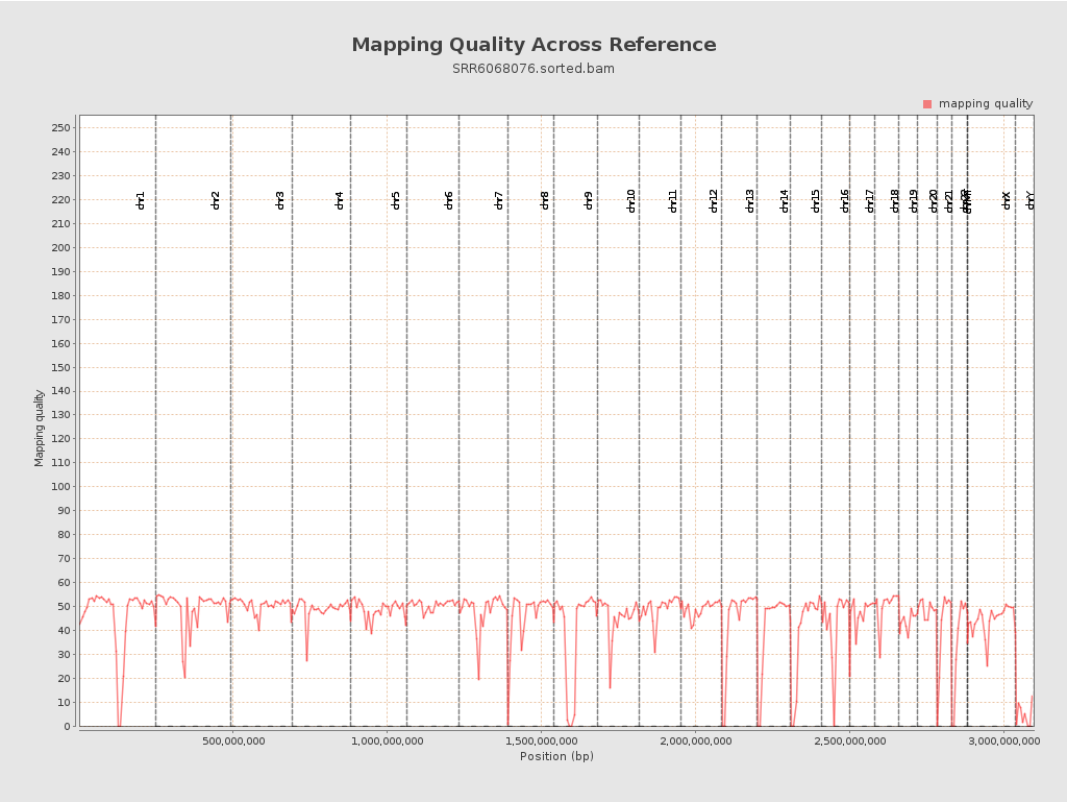
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram