

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 04:38:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237591.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_SRR6237591 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237591.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 04:38:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237591.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	427,677
Mapped reads	285,430 / 66.74%
Unmapped reads	142,247 / 33.26%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,683 / 0.39%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	5,125 / 1.2%
Duplication rate	1.47%
Clipped reads	160,710 / 37.58%

2.2. ACGT Content

Number/percentage of A's	5,206,825 / 28.67%
Number/percentage of C's	3,306,638 / 18.21%
Number/percentage of T's	5,425,644 / 29.88%
Number/percentage of G's	4,190,914 / 23.08%
Number/percentage of N's	30,036 / 0.17%
GC Percentage	41.29%

2.3. Coverage

Mean	0.0059

Standard Deviation	0.0883
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2.4. Mapping Quality

Mean Mapping Quality	43.63
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2.5. Mismatches and indels

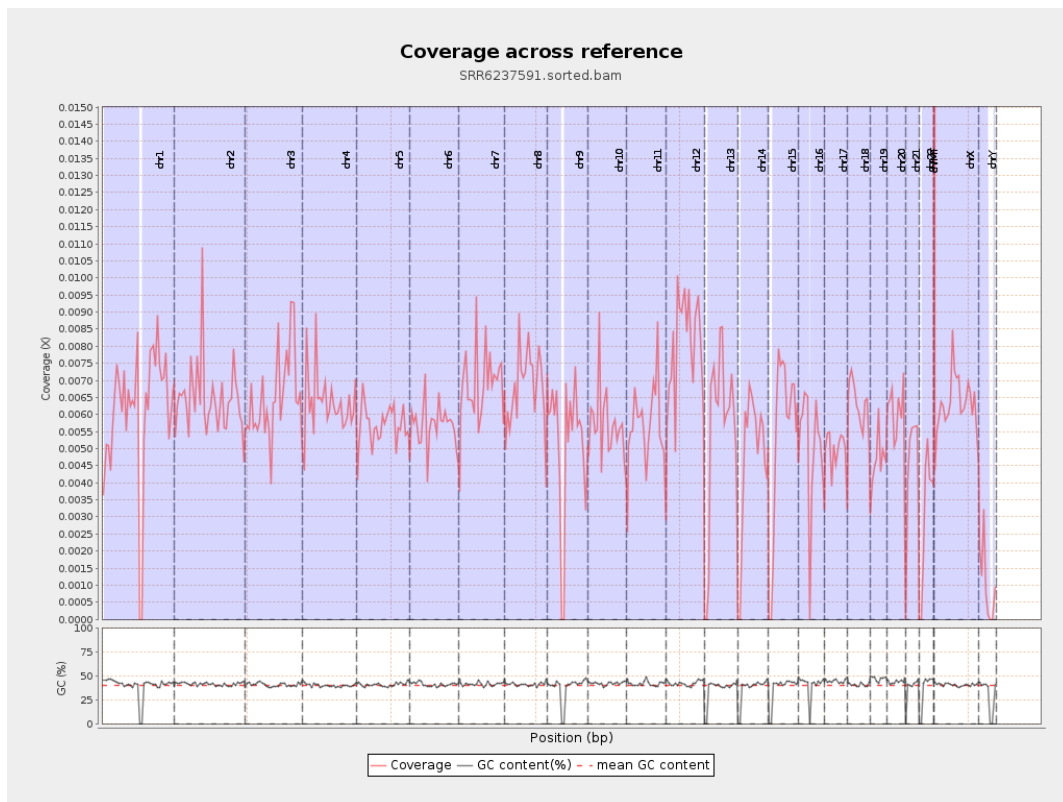
General error rate	1.18%
Mismatches	212,181
Insertions	1,702
Mapped reads with at least one insertion	0.59%
Deletions	6,319
Mapped reads with at least one deletion	2.18%
Homopolymer indels	46.09%

2.6. Chromosome stats

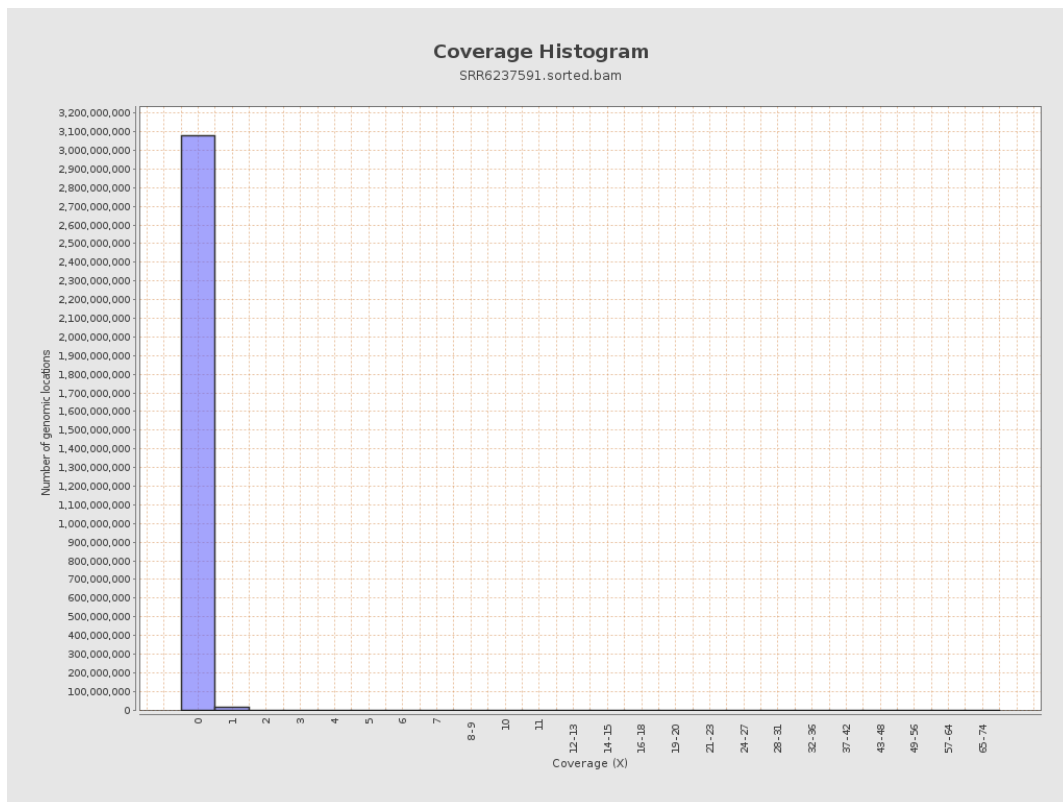
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	1525248	0.0061	0.1
chr2	243199373	1571625	0.0065	0.0981
chr3	198022430	1286669	0.0065	0.0861
chr4	191154276	1204571	0.0063	0.0849
chr5	180915260	1037685	0.0057	0.0795
chr6	171115067	971969	0.0057	0.081
chr7	159138663	1091618	0.0069	0.1082

chr8	146364022	991350	0.0068	0.0955
chr9	141213431	724043	0.0051	0.0856
chr10	135534747	766073	0.0057	0.0852
chr11	135006516	775364	0.0057	0.0938
chr12	133851895	1077049	0.008	0.096
chr13	115169878	638521	0.0055	0.0788
chr14	107349540	507857	0.0047	0.0748
chr15	102531392	556540	0.0054	0.0788
chr16	90354753	449555	0.005	0.078
chr17	81195210	402193	0.005	0.0755
chr18	78077248	491504	0.0063	0.1164
chr19	59128983	279058	0.0047	0.0829
chr20	63025520	379092	0.006	0.0829
chr21	48129895	222674	0.0046	0.0728
chr22	51304566	160145	0.0031	0.0588
chrMT	16571	12590	0.7598	1.1057
chrX	155270560	986784	0.0064	0.0863
chrY	59373566	60405	0.001	0.0366

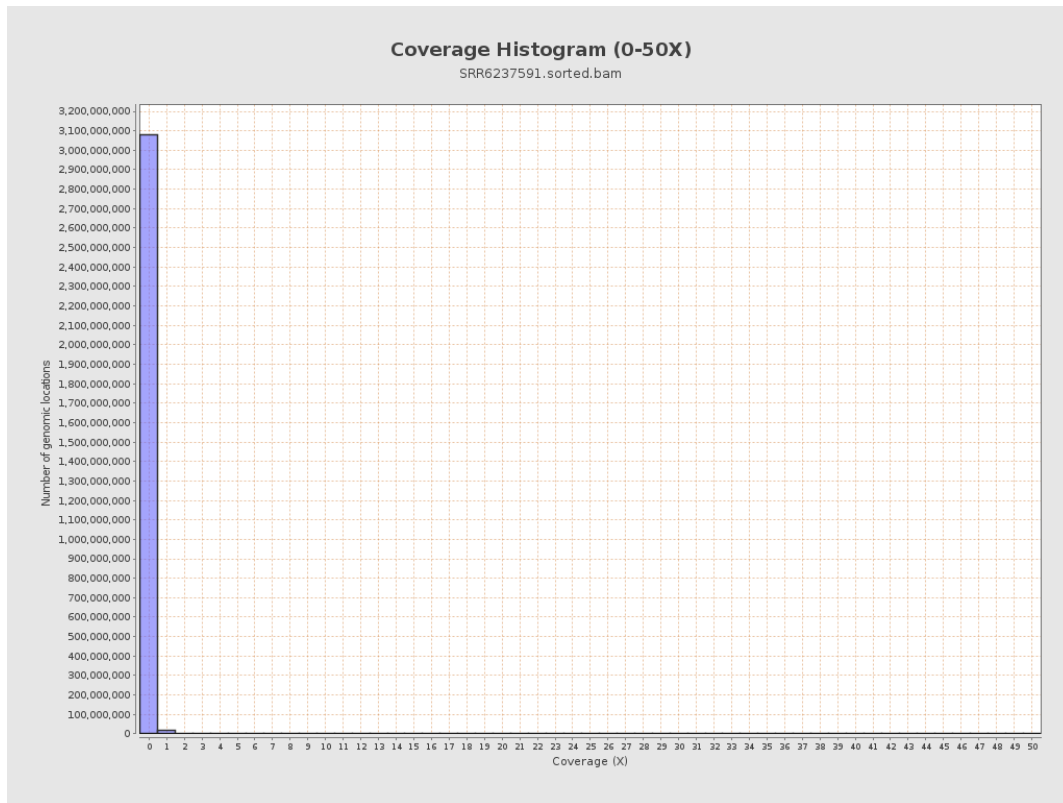
3. Results : Coverage across reference



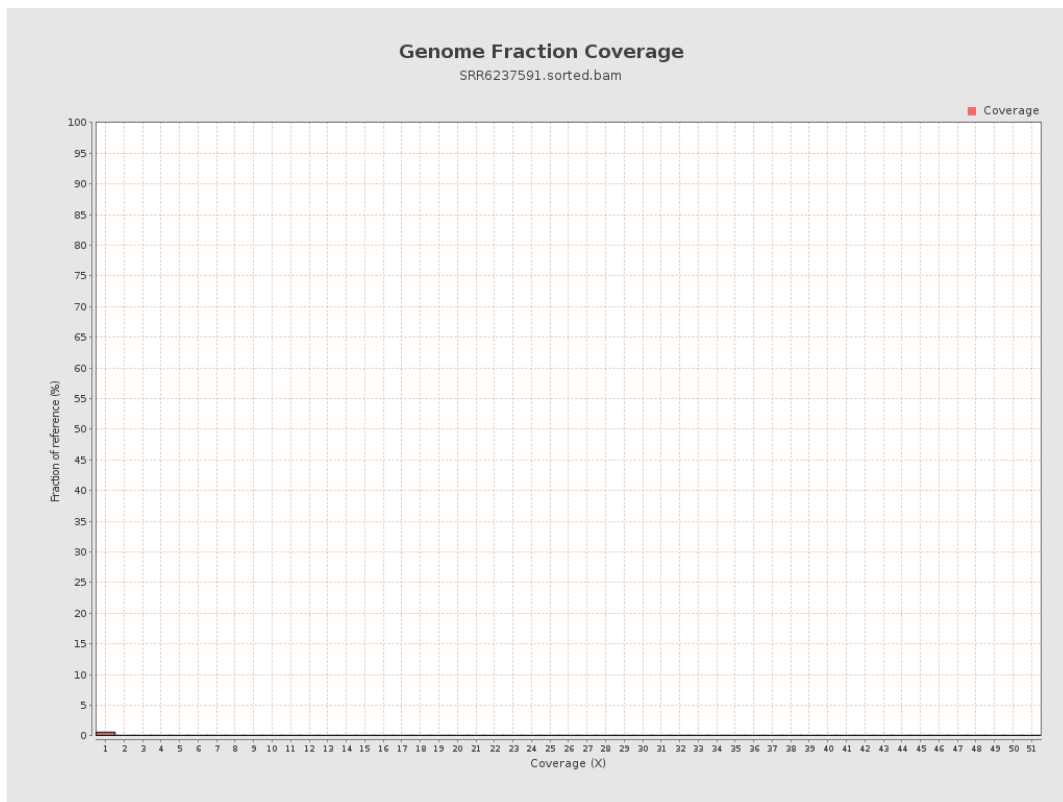
4. Results : Coverage Histogram



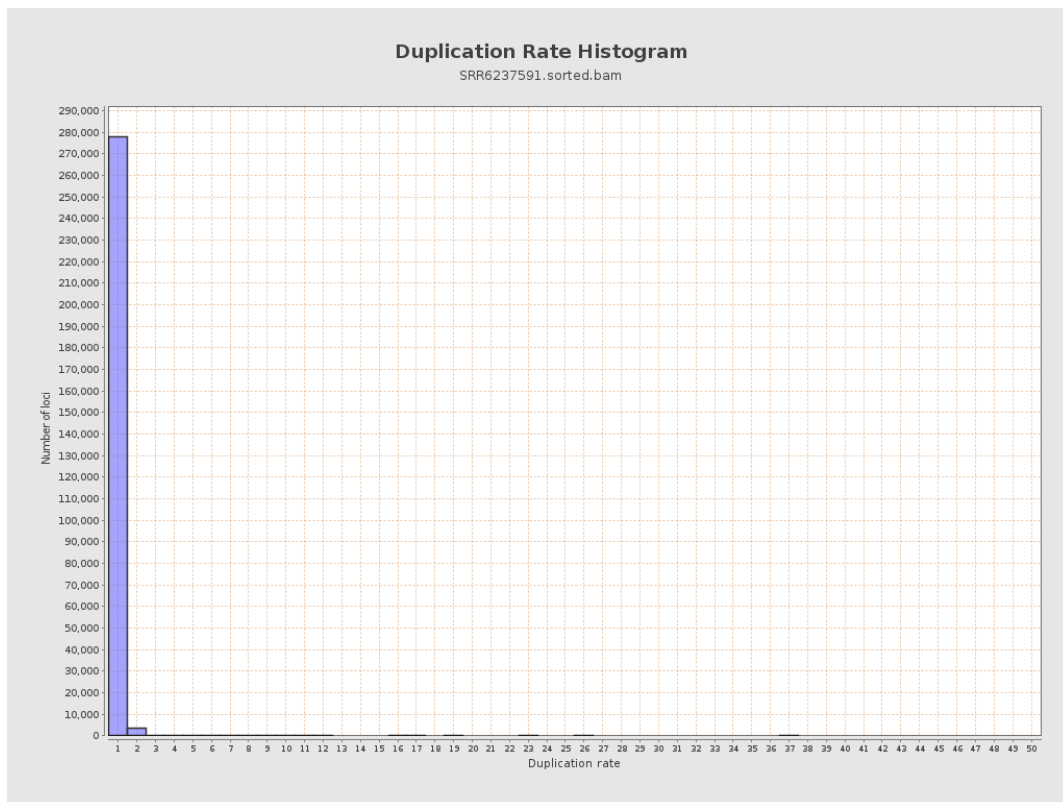
5. Results : Coverage Histogram (0-50X)



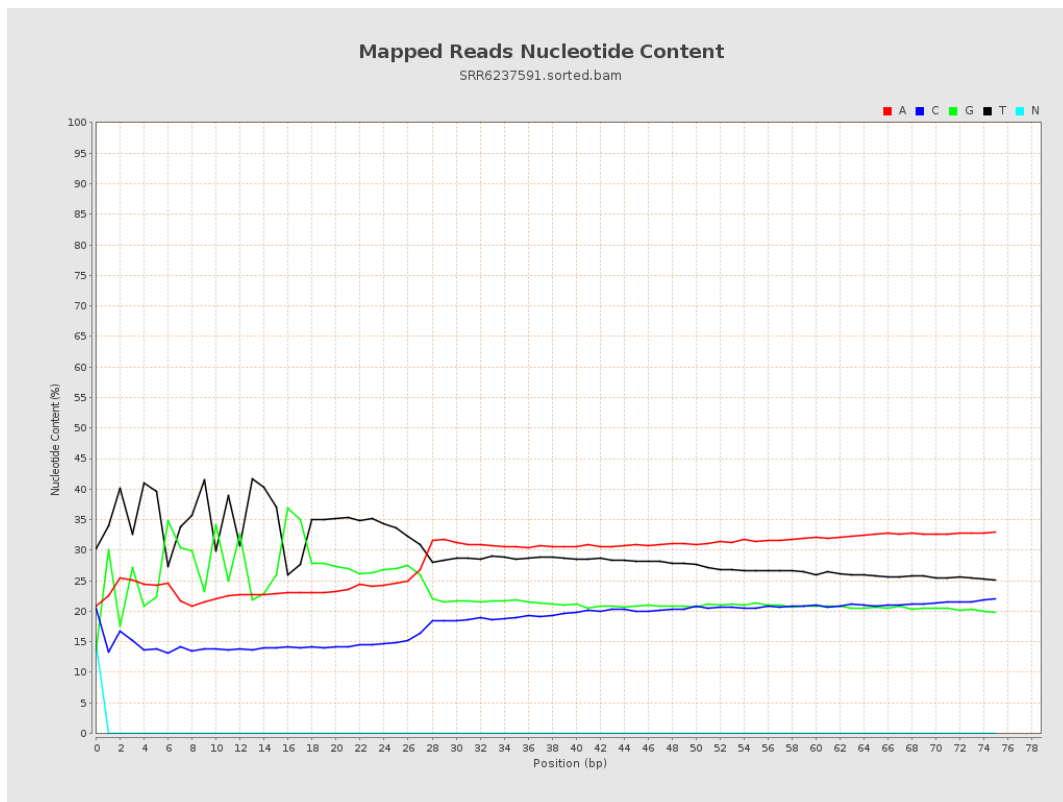
6. Results : Genome Fraction Coverage



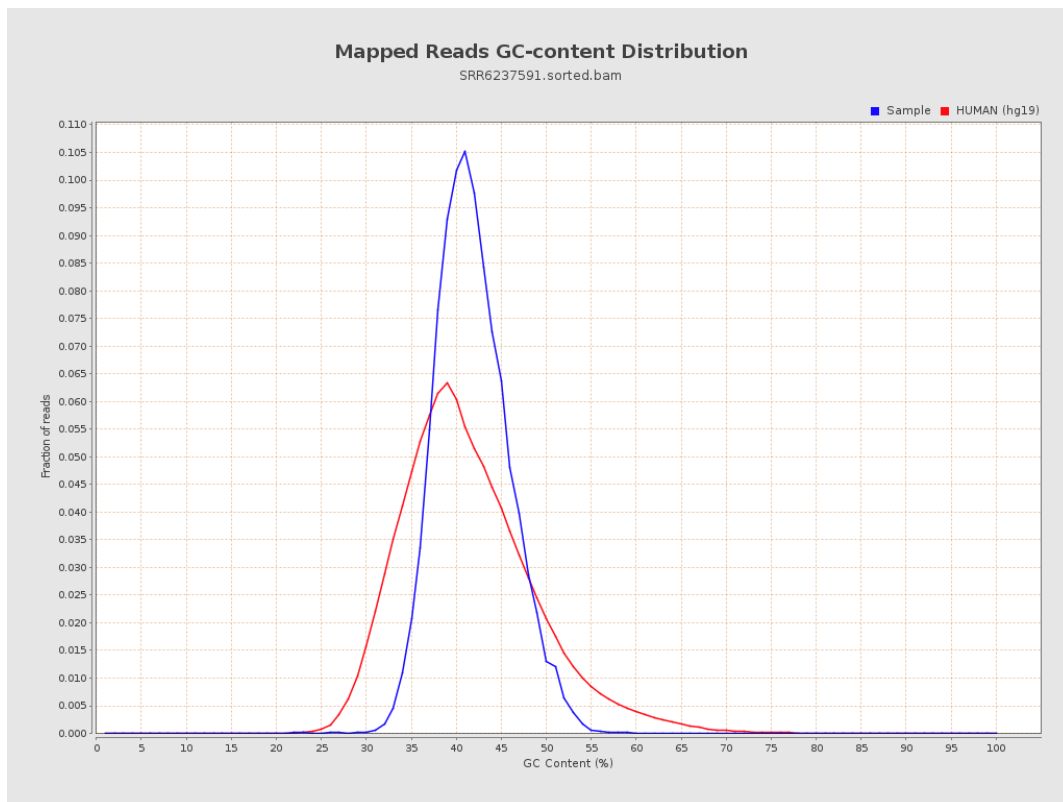
7. Results : Duplication Rate Histogram



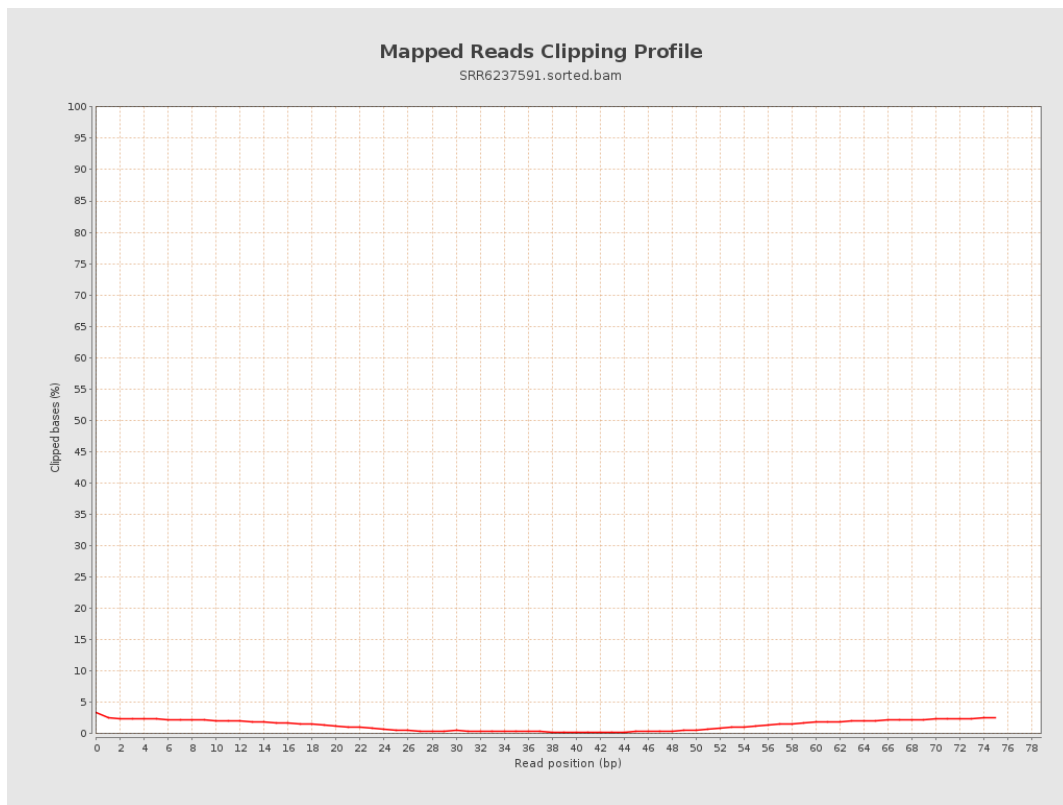
8. Results : Mapped Reads Nucleotide Content



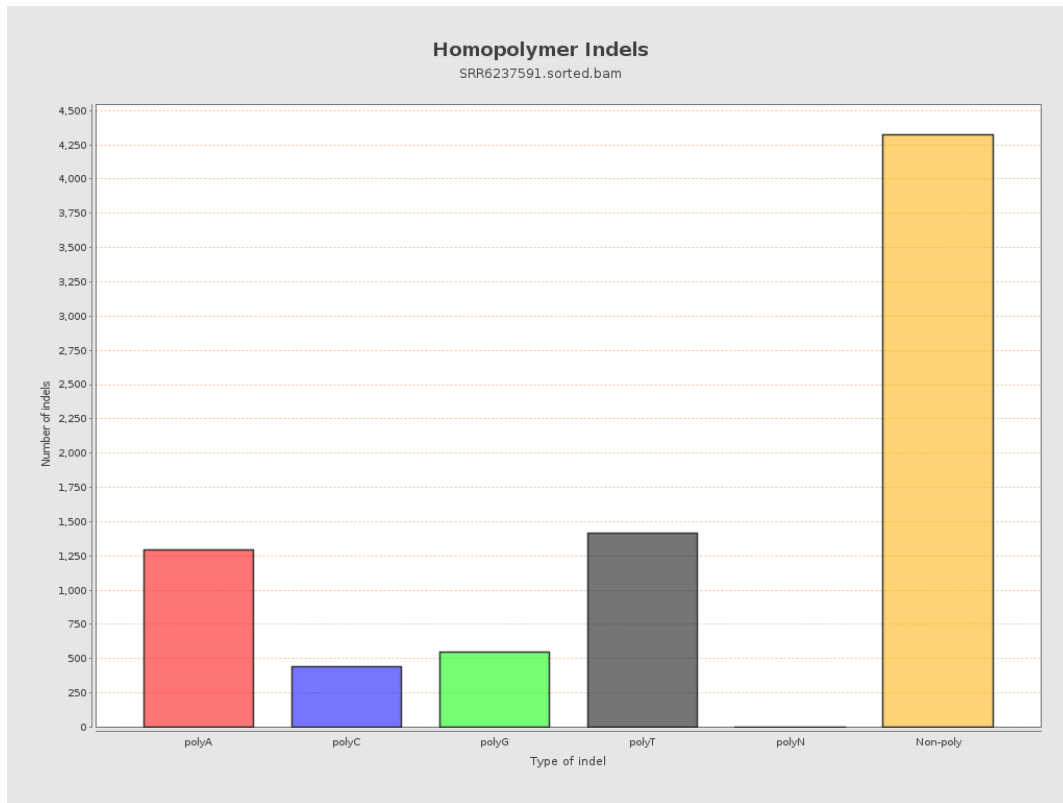
9. Results : Mapped Reads GC-content Distribution



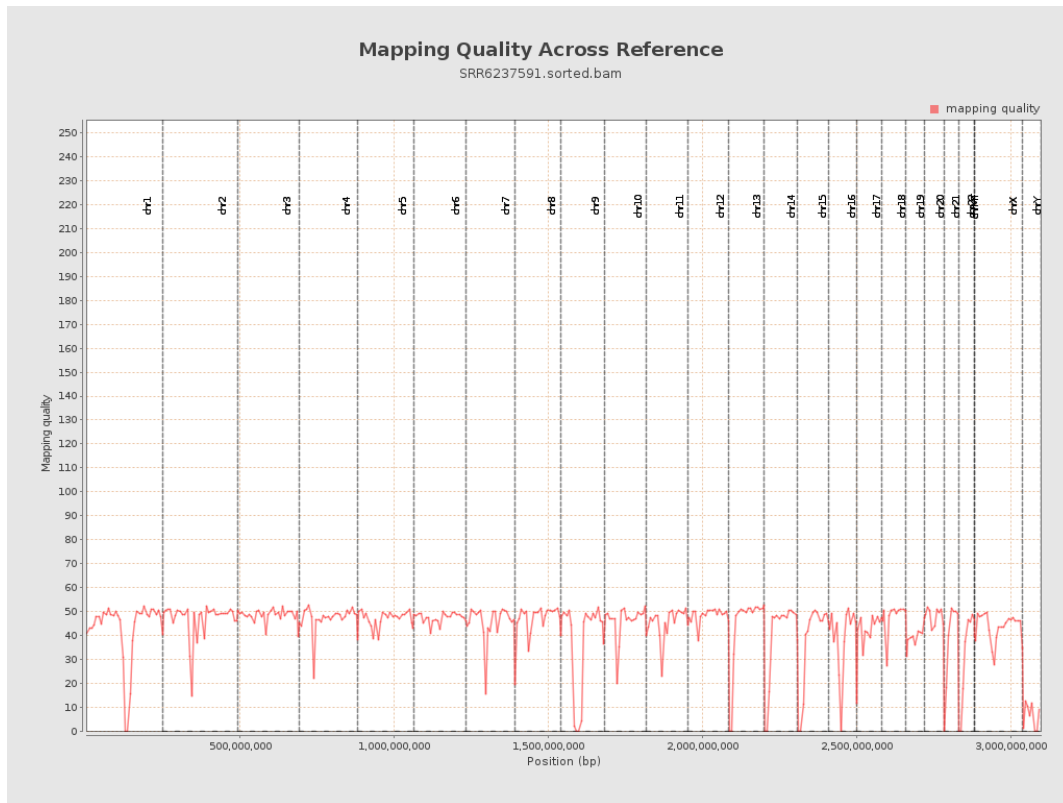
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

