

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 10:17:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238038.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_SRR6238038 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238038.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 10:17:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238038.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,791,883
Mapped reads	2,557,118 / 91.59%
Unmapped reads	234,765 / 8.41%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,993 / 0.86%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	118,978 / 4.26%
Duplication rate	3.53%
Clipped reads	1,080,987 / 38.72%

2.2. ACGT Content

Number/percentage of A's	49,711,832 / 28.86%
Number/percentage of C's	32,026,365 / 18.59%
Number/percentage of T's	53,956,350 / 31.32%
Number/percentage of G's	36,222,489 / 21.03%
Number/percentage of N's	347,986 / 0.2%
GC Percentage	39.62%

2.3. Coverage

Mean	0.0557

Standard Deviation	0.5433
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2.4. Mapping Quality

Mean Mapping Quality	47.4
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2.5. Mismatches and indels

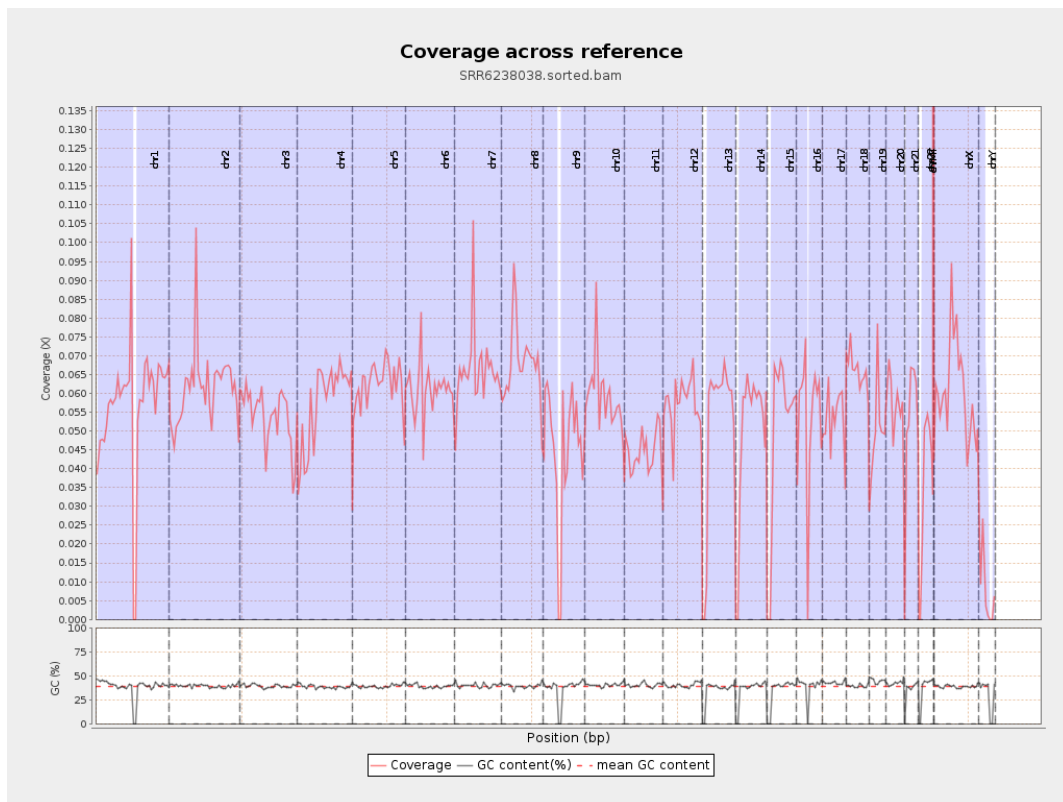
General error rate	0.94%
Mismatches	1,595,758
Insertions	14,680
Mapped reads with at least one insertion	0.57%
Deletions	59,050
Mapped reads with at least one deletion	2.28%
Homopolymer indels	45.72%

2.6. Chromosome stats

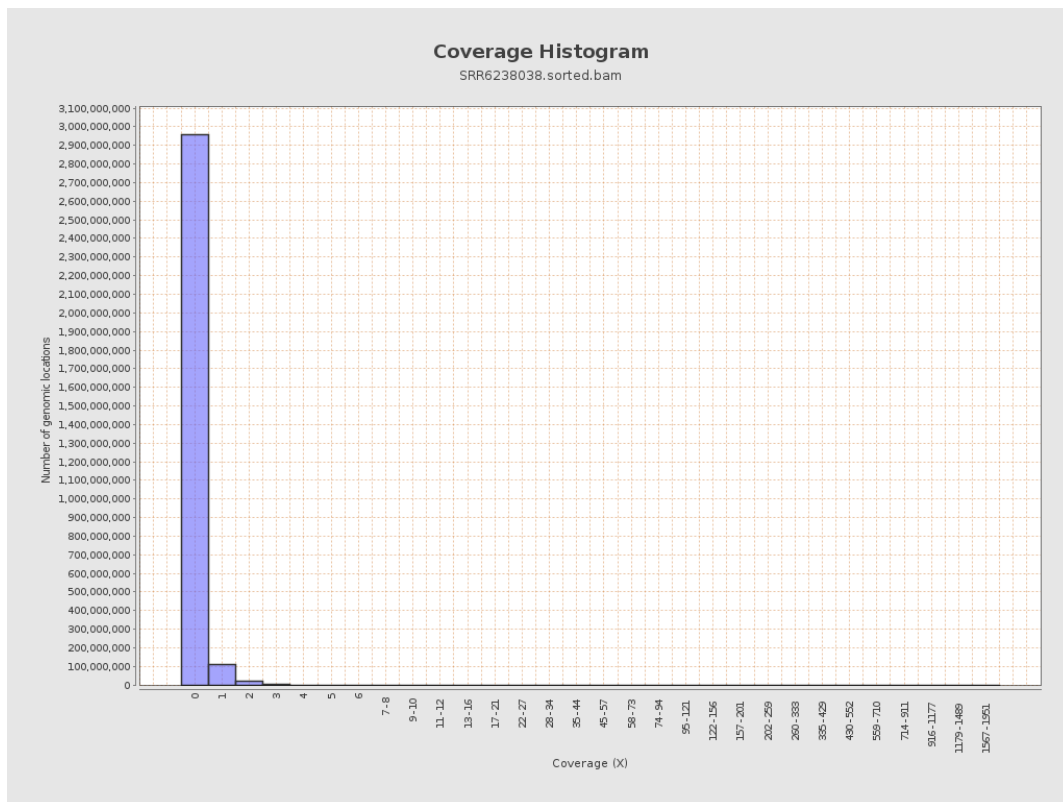
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	14175840	0.0569	1.0092
chr2	243199373	14941928	0.0614	0.5278
chr3	198022430	10680622	0.0539	0.2773
chr4	191154276	10949064	0.0573	0.3131
chr5	180915260	11279636	0.0623	0.3018
chr6	171115067	10423833	0.0609	0.3587
chr7	159138663	10586936	0.0665	0.7226

chr8	146364022	9913175	0.0677	1.2193
chr9	141213431	6351325	0.045	0.4044
chr10	135534747	8038531	0.0593	0.4212
chr11	135006516	5958065	0.0441	0.3361
chr12	133851895	7692515	0.0575	0.2906
chr13	115169878	5843264	0.0507	0.2715
chr14	107349540	5292525	0.0493	0.2796
chr15	102531392	5178569	0.0505	0.2688
chr16	90354753	4822574	0.0534	0.3032
chr17	81195210	4267162	0.0526	0.32
chr18	78077248	5172441	0.0662	0.7916
chr19	59128983	2995081	0.0507	0.6139
chr20	63025520	3595925	0.0571	0.2955
chr21	48129895	2529704	0.0526	0.2963
chr22	51304566	1778835	0.0347	0.2185
chrMT	16571	37168	2.243	1.9212
chrX	155270560	9392137	0.0605	0.3366
chrY	59373566	466977	0.0079	0.2214

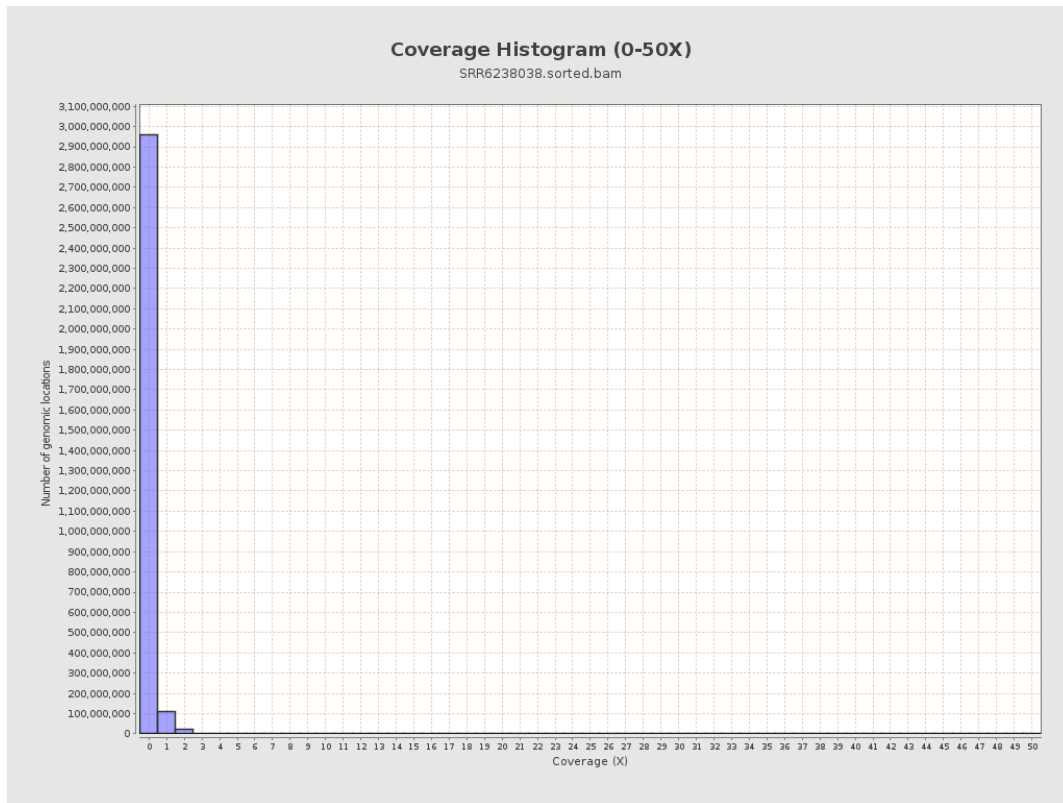
3. Results : Coverage across reference



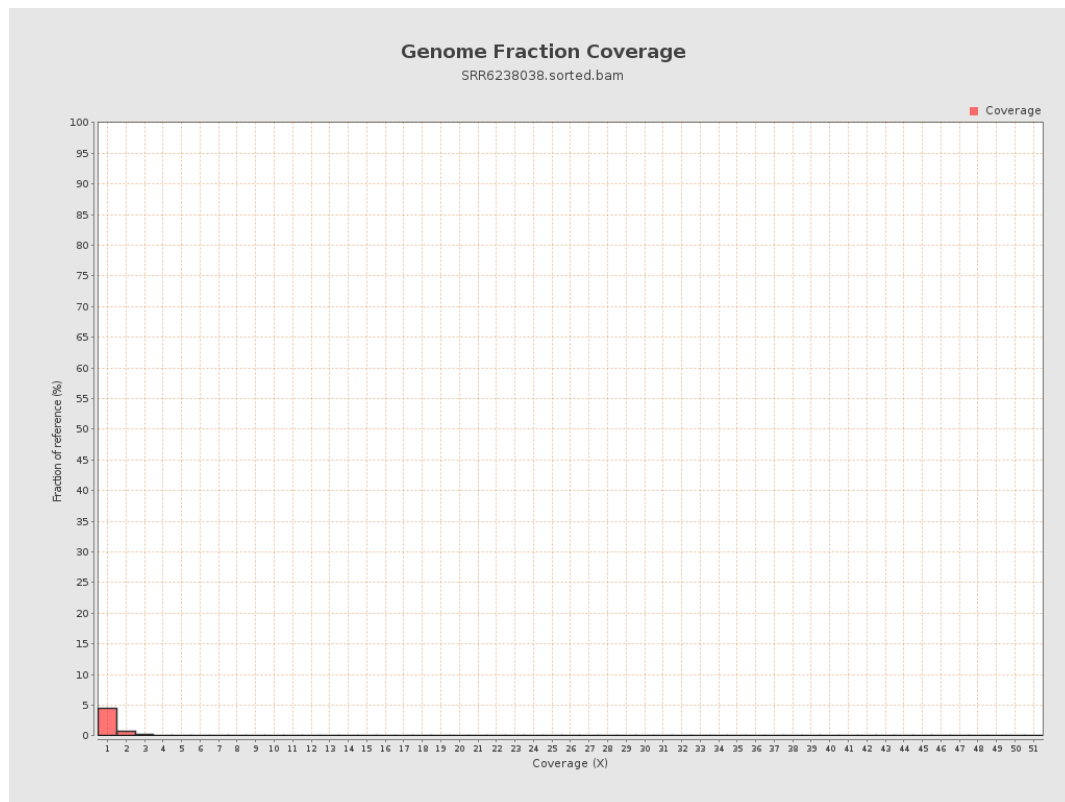
4. Results : Coverage Histogram



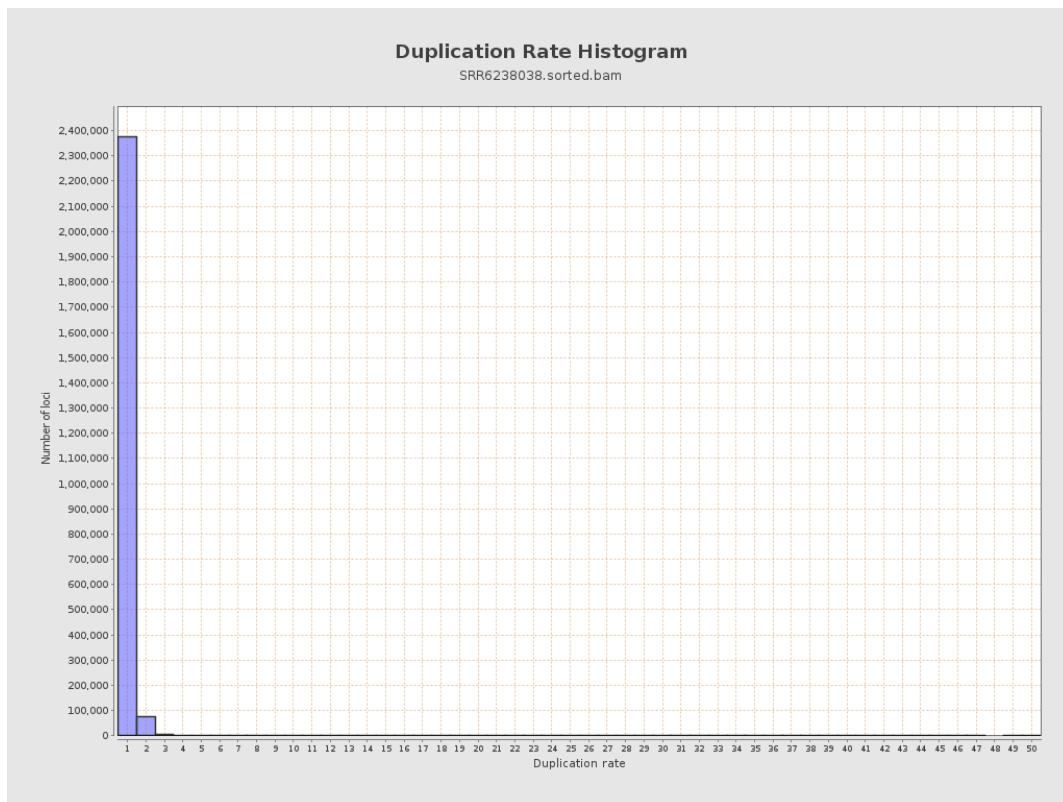
5. Results : Coverage Histogram (0-50X)



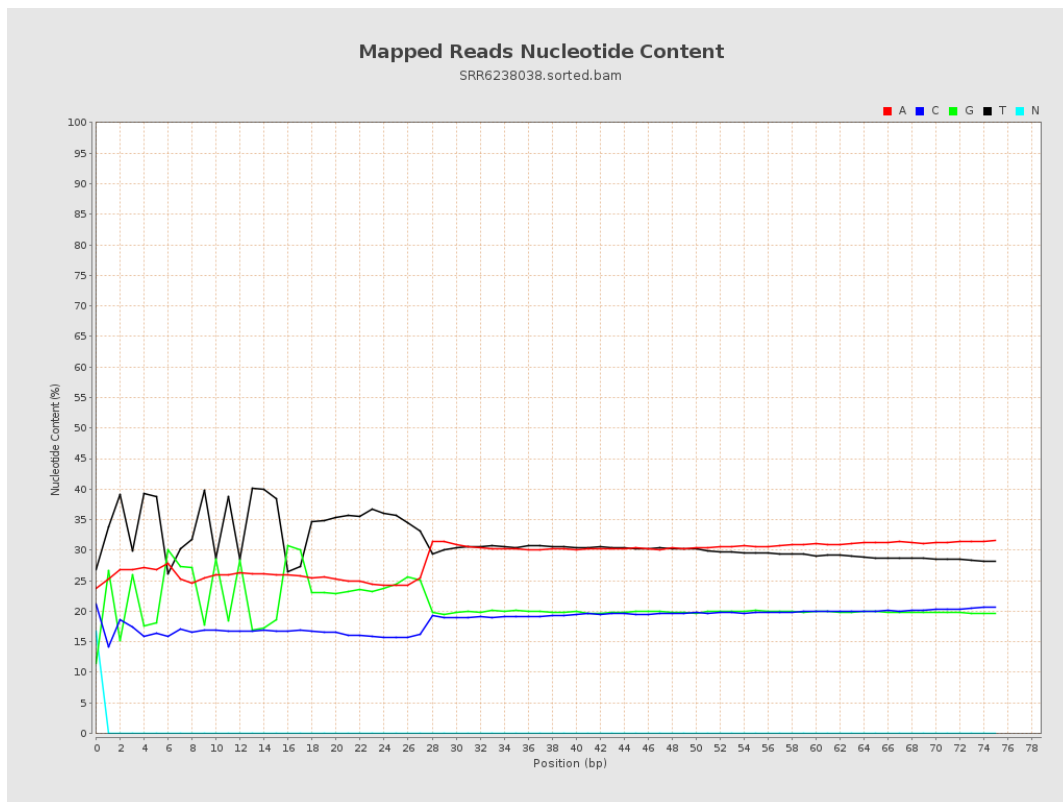
6. Results : Genome Fraction Coverage



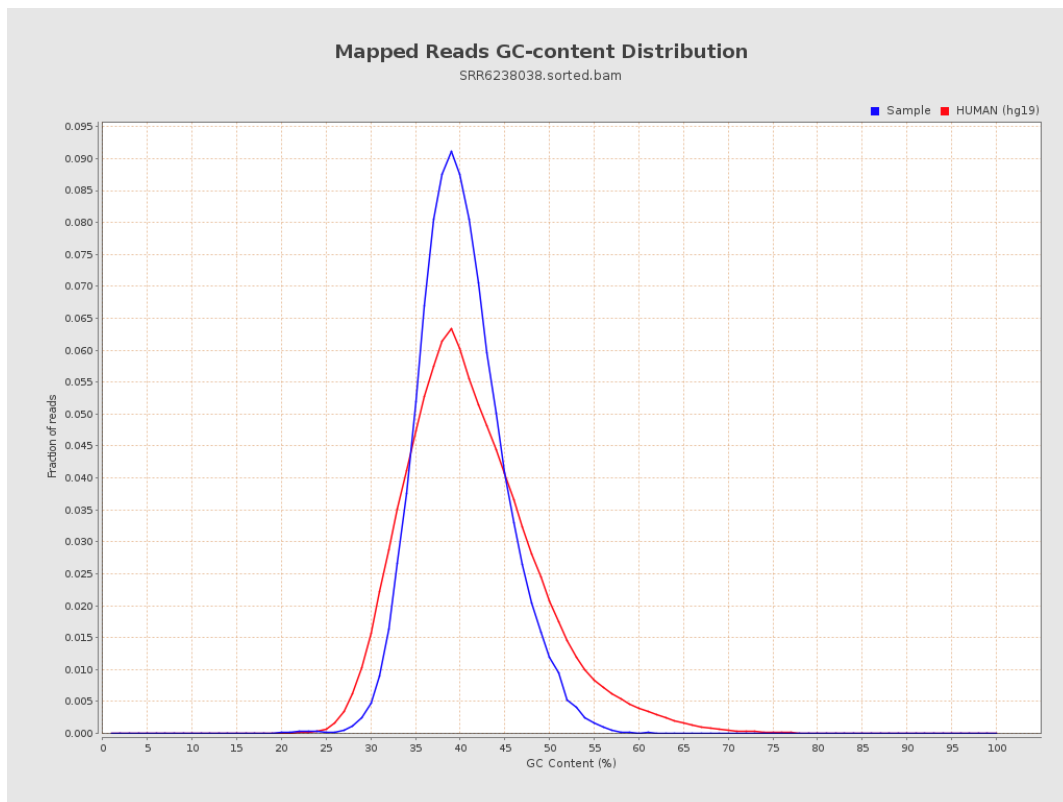
7. Results : Duplication Rate Histogram



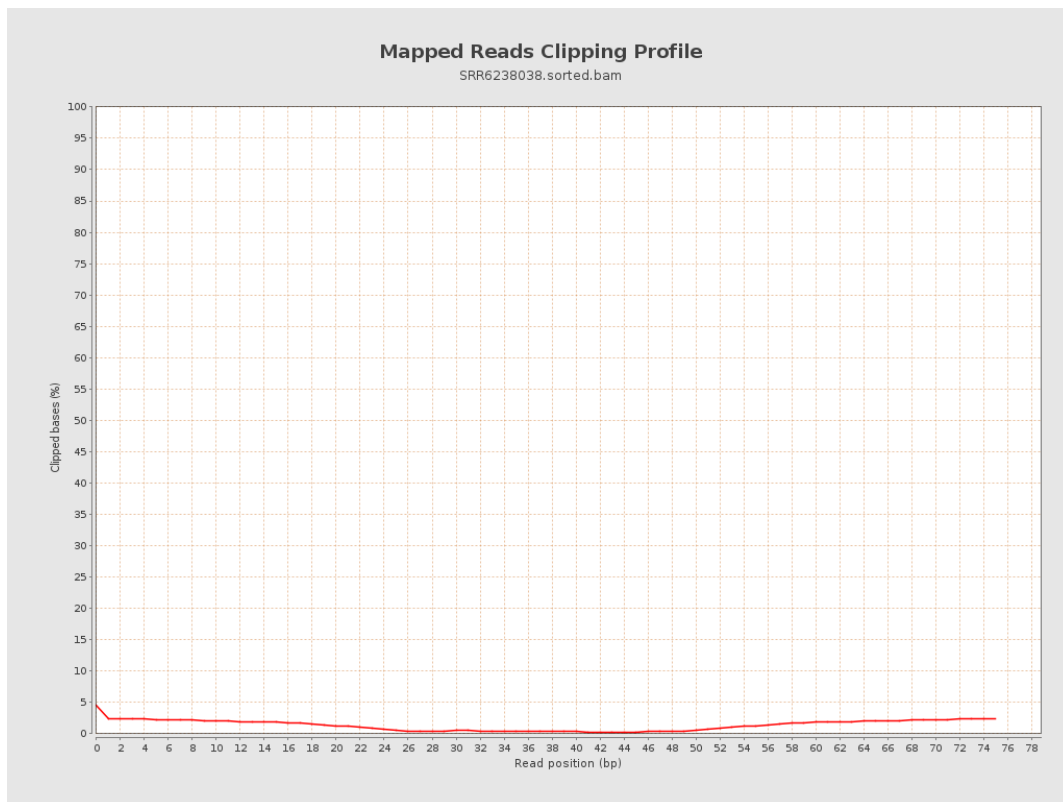
8. Results : Mapped Reads Nucleotide Content



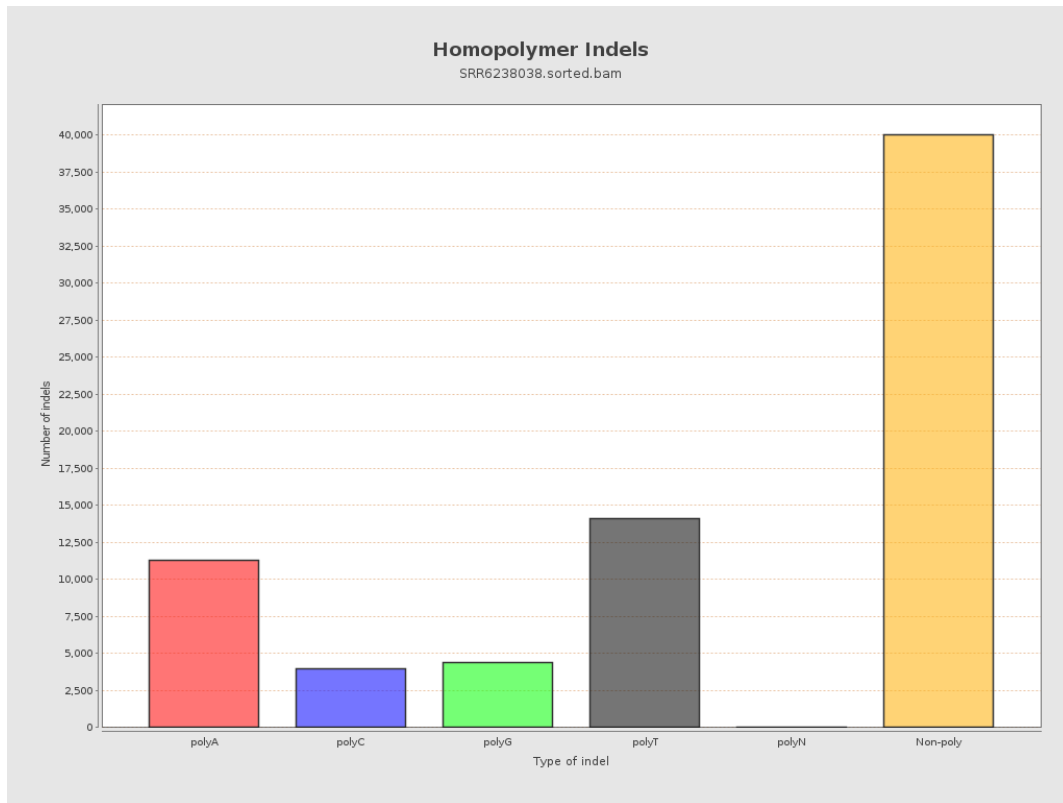
9. Results : Mapped Reads GC-content Distribution



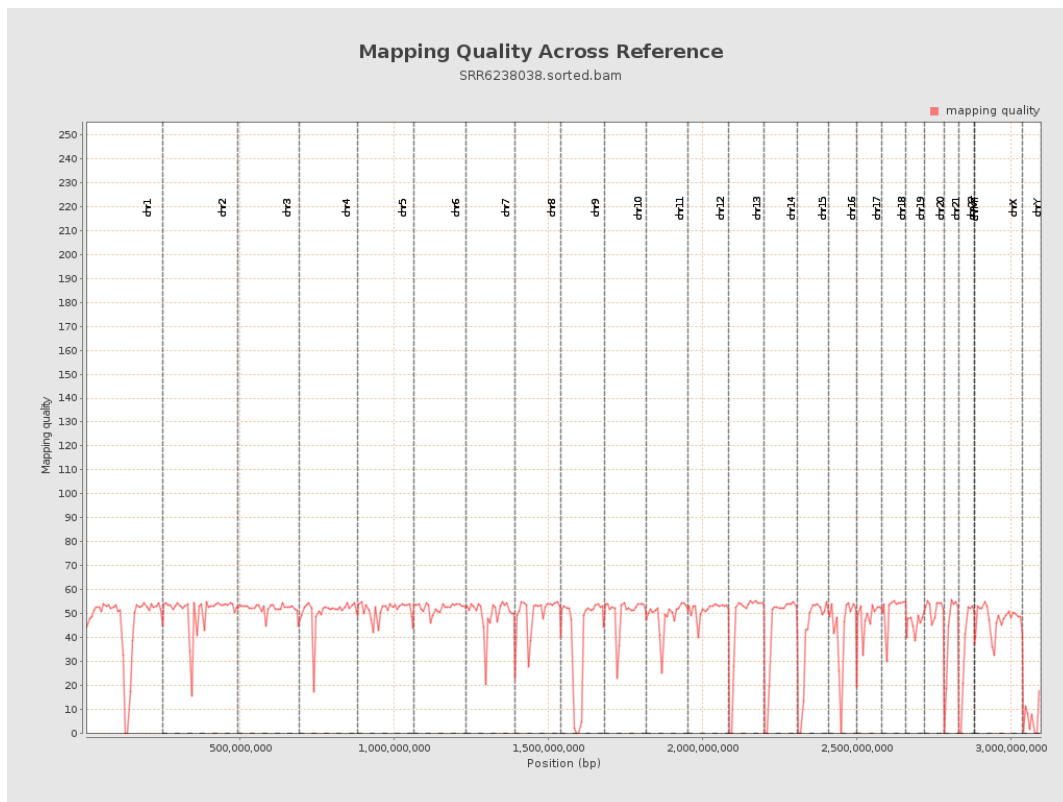
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

