

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 22:01:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004038.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_SRR6004038 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004038.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 22:01:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004038.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,079,193
Mapped reads	2,664,442 / 86.53%
Unmapped reads	414,751 / 13.47%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	31,370 / 1.02%
Read min/max/mean length	30 / 76 / 76.36
Duplicated reads (estimated)	225,082 / 7.31%
Duplication rate	6.74%
Clipped reads	1,301,040 / 42.25%

2.2. ACGT Content

Number/percentage of A's	49,861,595 / 28.5%
Number/percentage of C's	30,954,886 / 17.69%
Number/percentage of T's	56,705,658 / 32.41%
Number/percentage of G's	37,340,585 / 21.34%
Number/percentage of N's	78,441 / 0.04%
GC Percentage	39.04%

2.3. Coverage

Mean	0.0565

Standard Deviation	0.5087
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2.4. Mapping Quality

Mean Mapping Quality	46.58
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2.5. Mismatches and indels

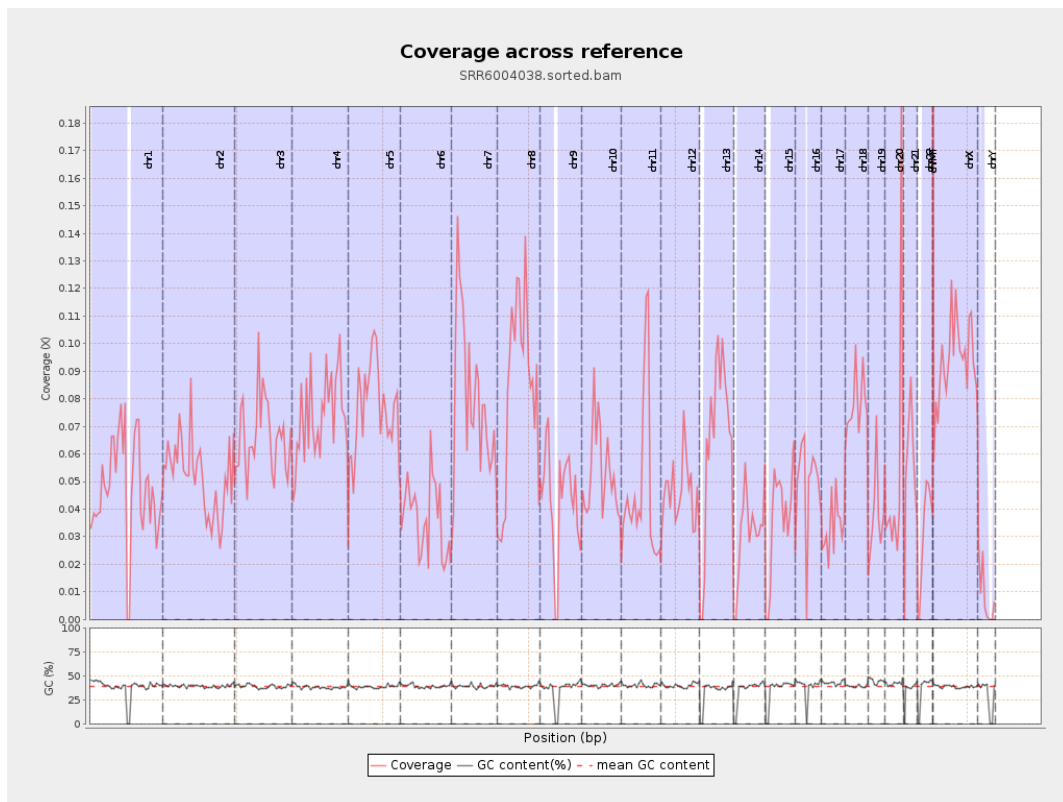
General error rate	0.87%
Mismatches	1,493,615
Insertions	12,747
Mapped reads with at least one insertion	0.47%
Deletions	59,059
Mapped reads with at least one deletion	2.19%
Homopolymer indels	44.56%

2.6. Chromosome stats

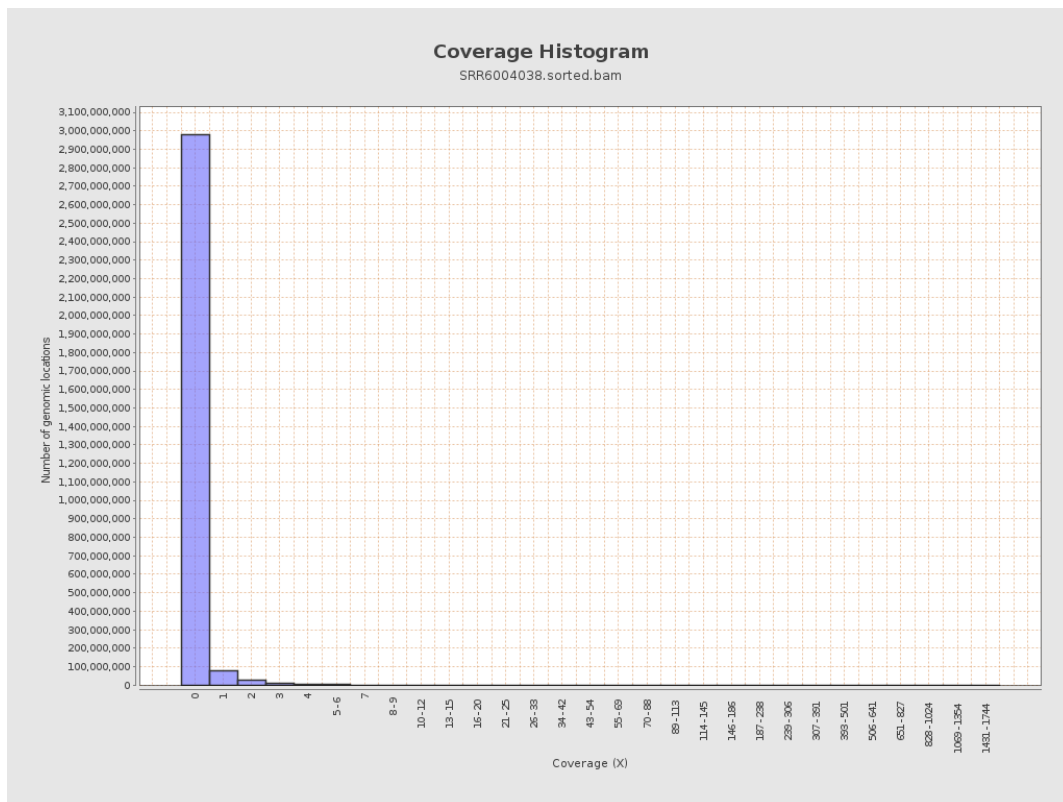
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	11790288	0.0473	0.776
chr2	243199373	12620739	0.0519	0.5026
chr3	198022430	13069716	0.066	0.3622
chr4	191154276	14124205	0.0739	0.4034
chr5	180915260	13811097	0.0763	0.3911
chr6	171115067	6288194	0.0367	0.2857
chr7	159138663	12577994	0.079	0.623

chr8	146364022	12139544	0.0829	1.0867
chr9	141213431	6140193	0.0435	0.4149
chr10	135534747	7177155	0.053	0.4803
chr11	135006516	6194383	0.0459	0.3484
chr12	133851895	6119743	0.0457	0.3084
chr13	115169878	7532477	0.0654	0.3644
chr14	107349540	3327082	0.031	0.281
chr15	102531392	3724861	0.0363	0.27
chr16	90354753	4402907	0.0487	0.3533
chr17	81195210	2692015	0.0332	0.2665
chr18	78077248	6115115	0.0783	0.7976
chr19	59128983	2311186	0.0391	0.5588
chr20	63025520	3520174	0.0559	0.3591
chr21	48129895	2610406	0.0542	0.3466
chr22	51304566	1620782	0.0316	0.2418
chrMT	16571	6902	0.4165	0.8938
chrX	155270560	14623581	0.0942	0.4743
chrY	59373566	499946	0.0084	0.1871

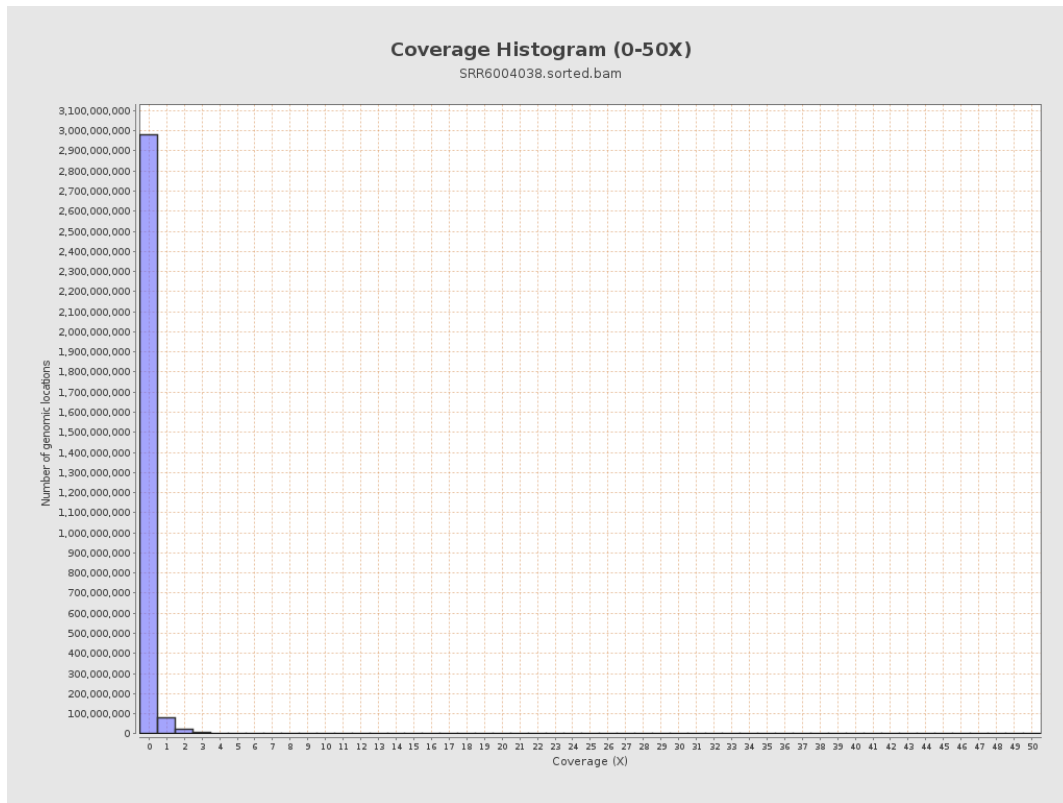
3. Results : Coverage across reference



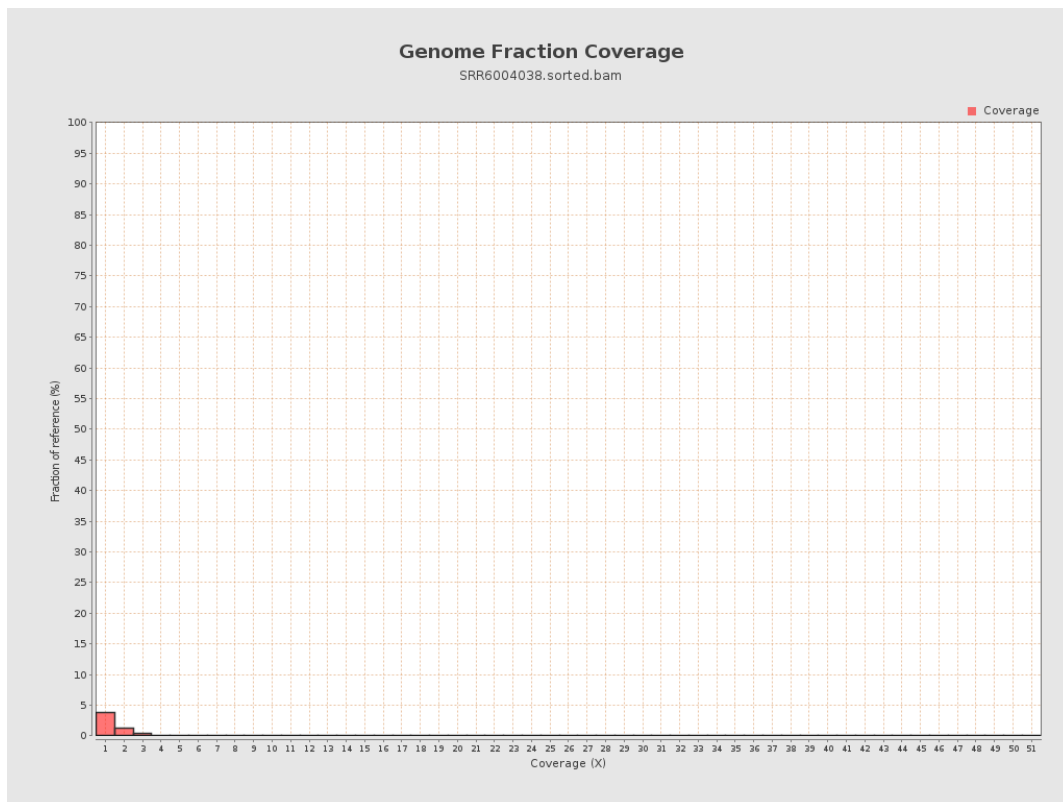
4. Results : Coverage Histogram



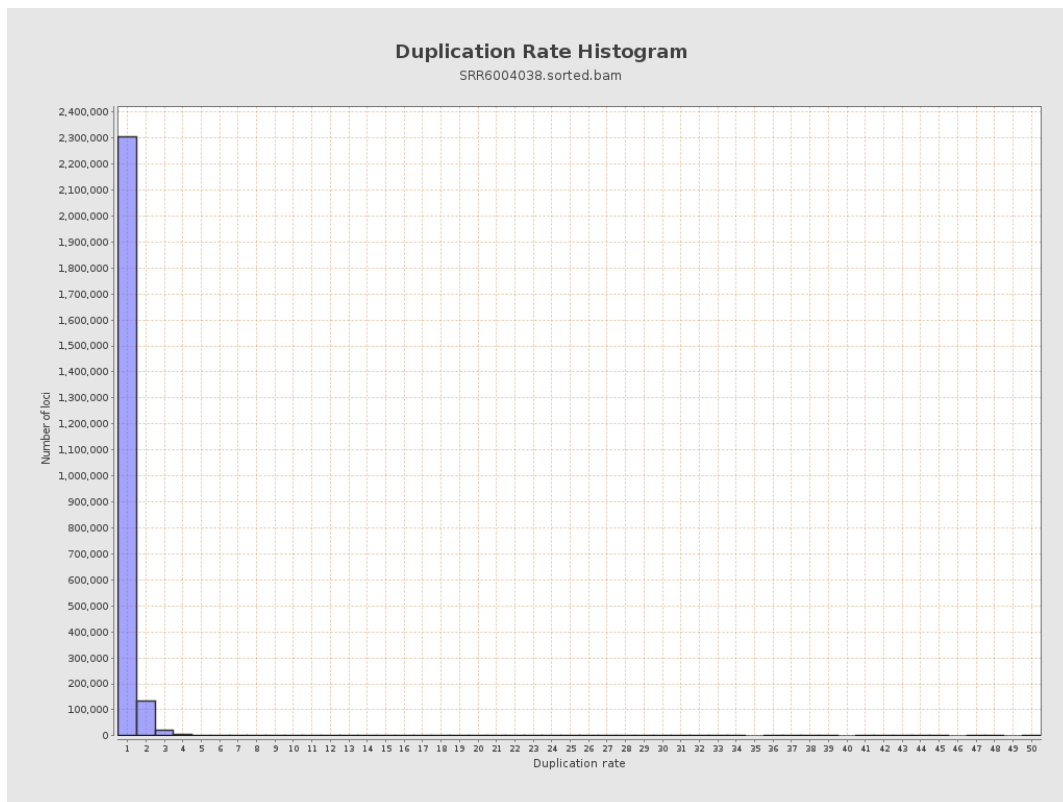
5. Results : Coverage Histogram (0-50X)



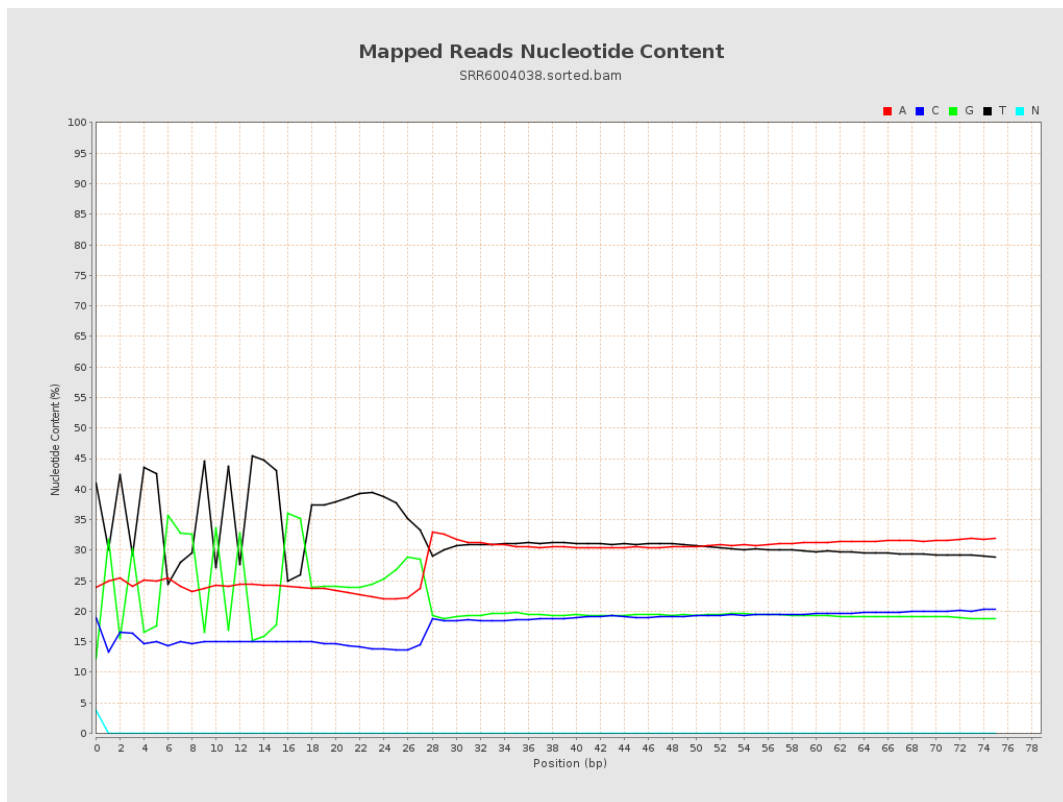
6. Results : Genome Fraction Coverage



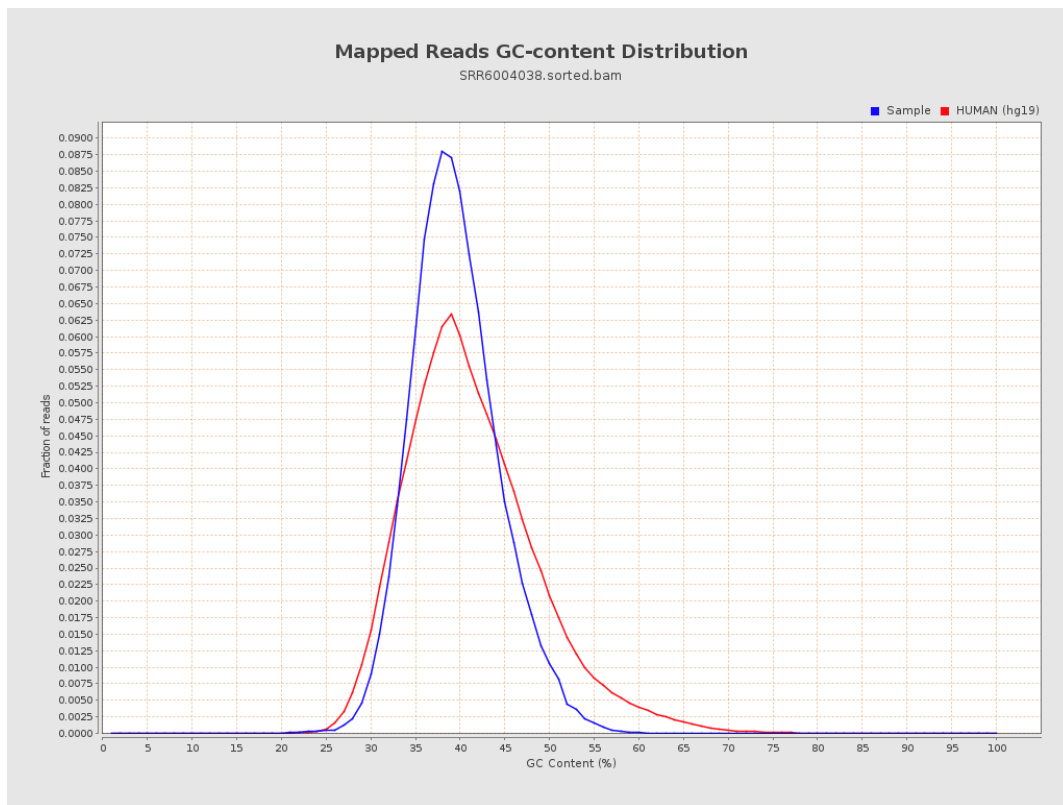
7. Results : Duplication Rate Histogram



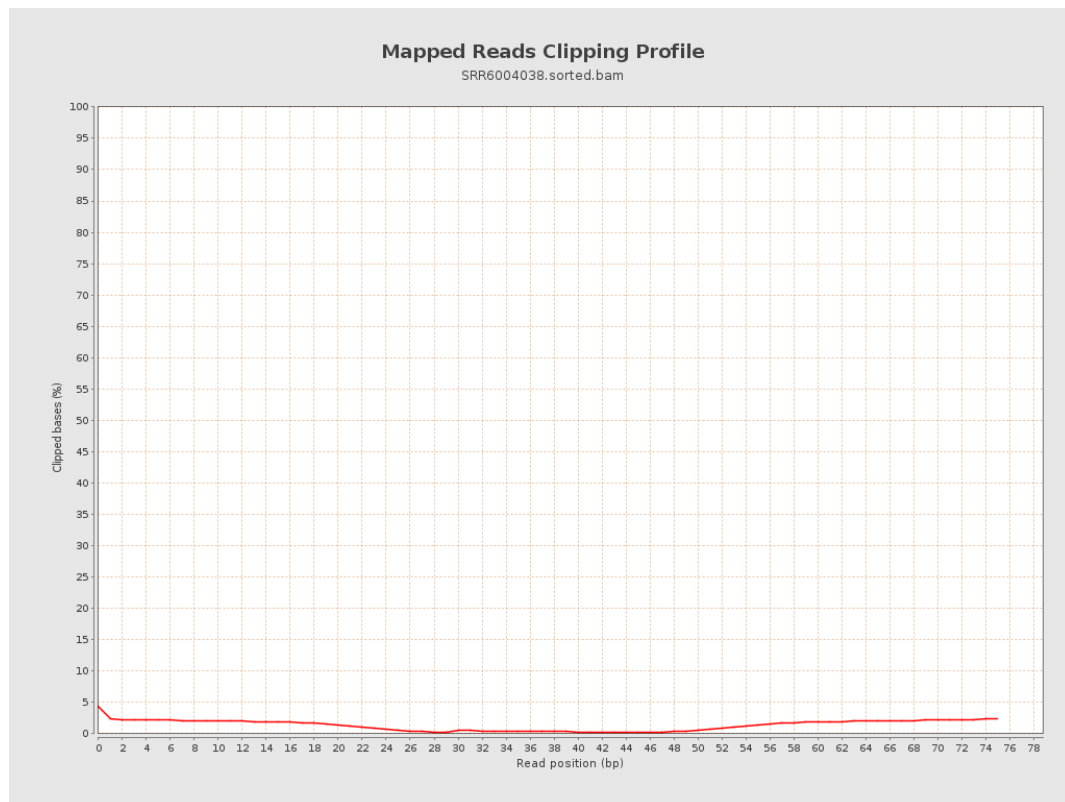
8. Results : Mapped Reads Nucleotide Content



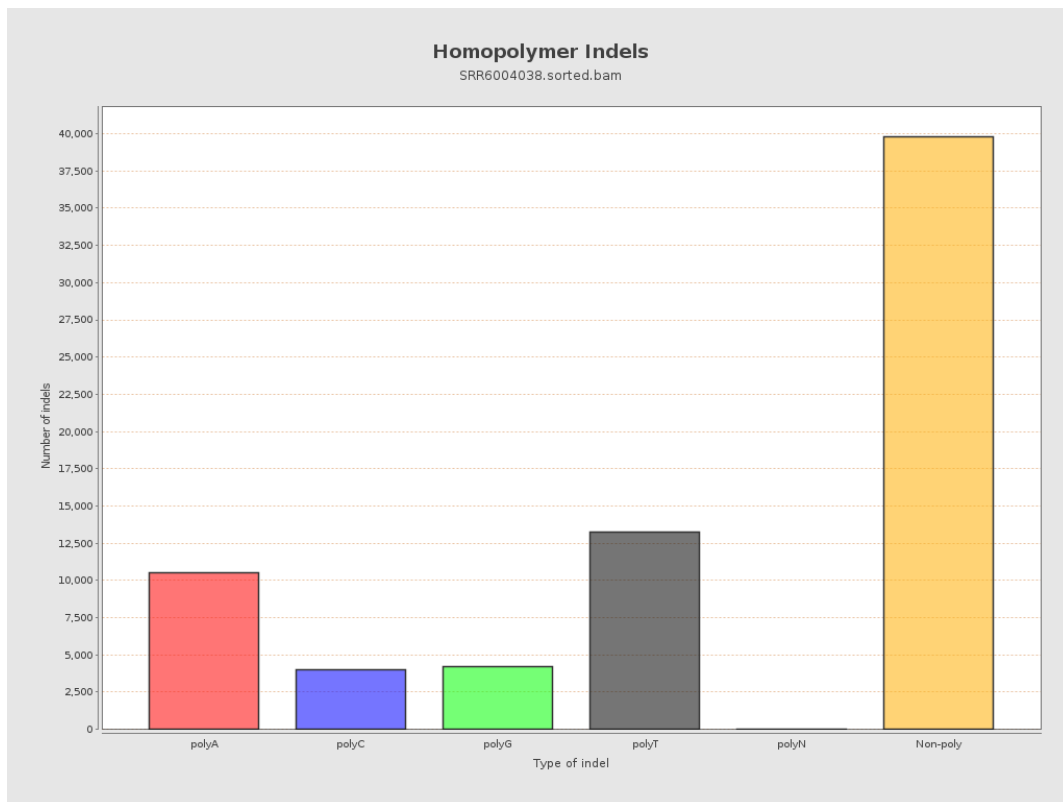
9. Results : Mapped Reads GC-content Distribution



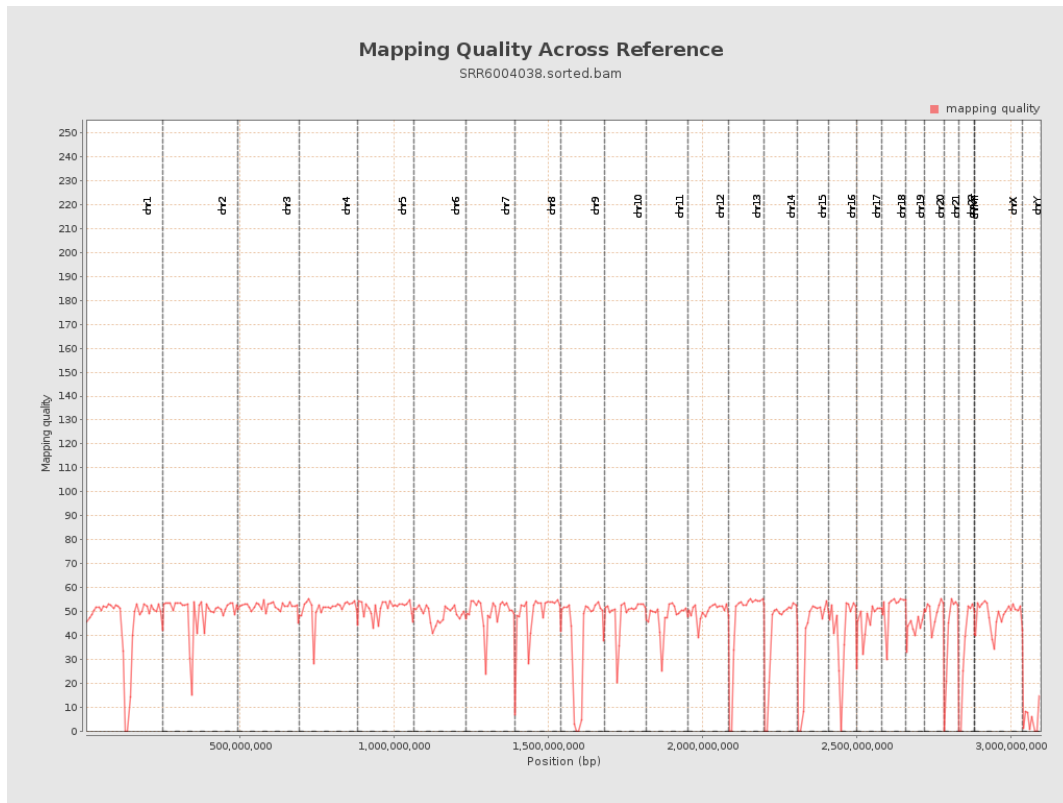
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

