

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 03:59:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004138.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_SRR6004138 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004138.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 03:59:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004138.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,687,240
Mapped reads	1,373,528 / 81.41%
Unmapped reads	313,712 / 18.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,342 / 1.03%
Read min/max/mean length	30 / 76 / 76.36
Duplicated reads (estimated)	76,068 / 4.51%
Duplication rate	4.54%
Clipped reads	720,670 / 42.71%

2.2. ACGT Content

Number/percentage of A's	24,733,807 / 27.74%
Number/percentage of C's	16,263,012 / 18.24%
Number/percentage of T's	28,430,260 / 31.89%
Number/percentage of G's	19,718,763 / 22.12%
Number/percentage of N's	14,570 / 0.02%
GC Percentage	40.36%

2.3. Coverage

Mean	0.0288

Standard Deviation	0.2948
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2.4. Mapping Quality

Mean Mapping Quality	46.27
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2.5. Mismatches and indels

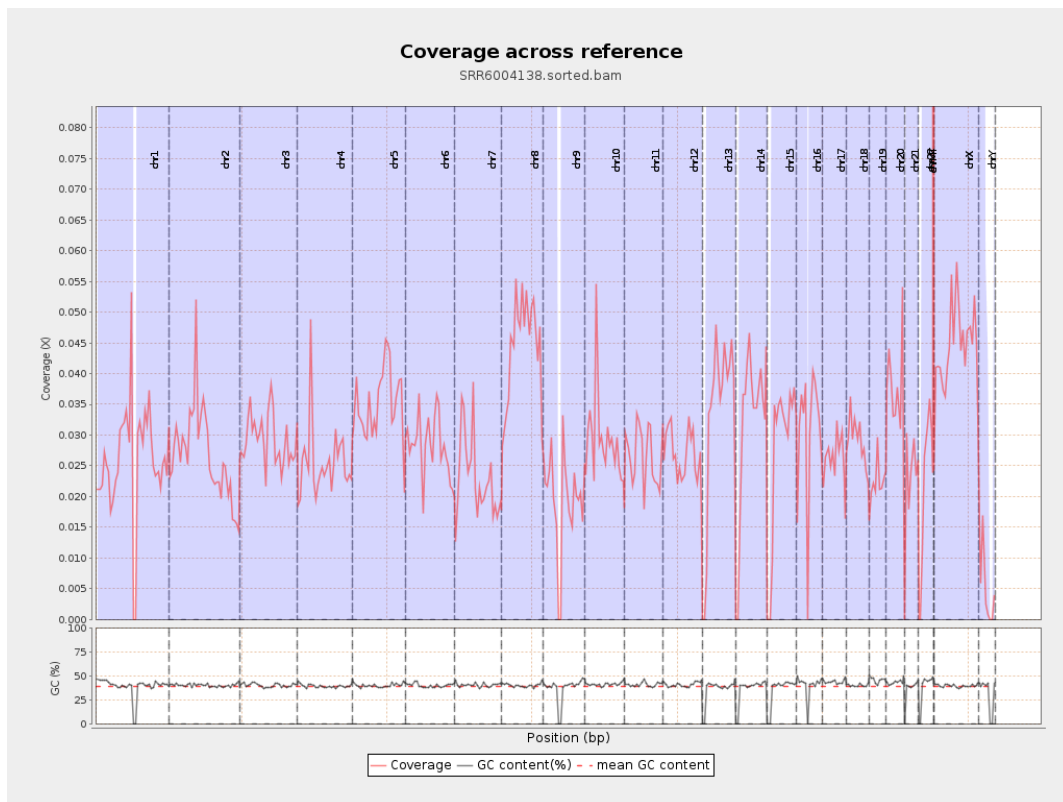
General error rate	0.94%
Mismatches	821,134
Insertions	6,644
Mapped reads with at least one insertion	0.48%
Deletions	22,539
Mapped reads with at least one deletion	1.62%
Homopolymer indels	46.43%

2.6. Chromosome stats

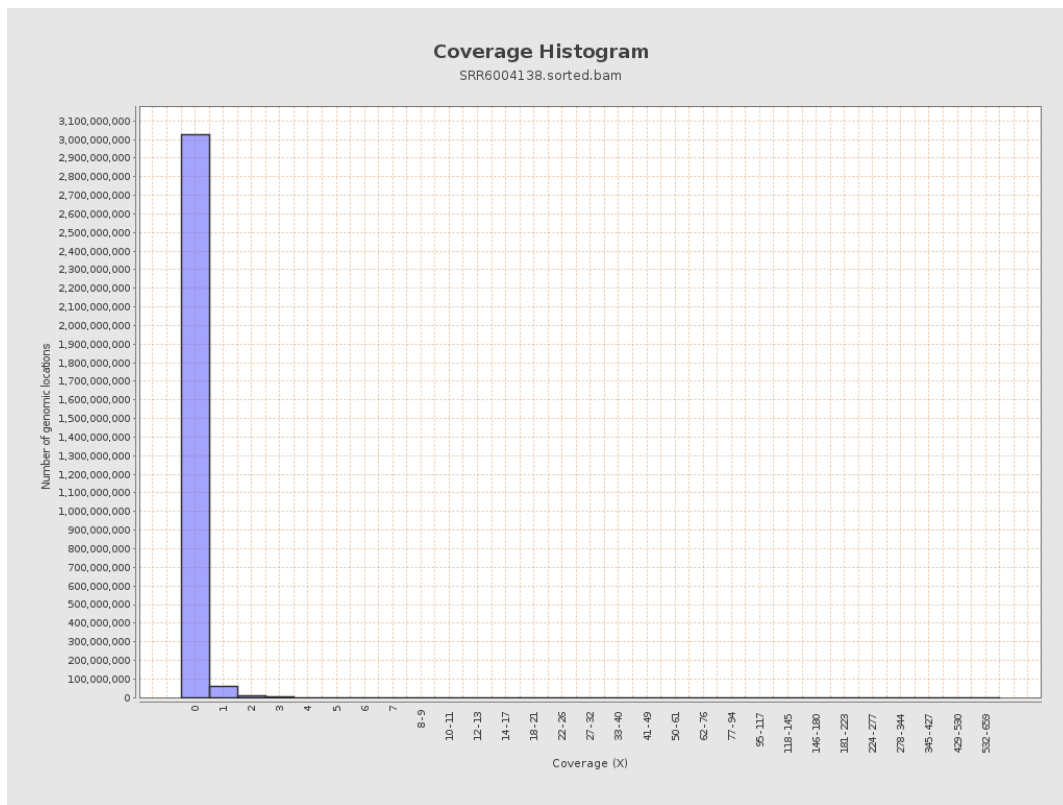
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6450508	0.0259	0.5511
chr2	243199373	6512458	0.0268	0.2749
chr3	198022430	5759226	0.0291	0.2023
chr4	191154276	4833302	0.0253	0.2028
chr5	180915260	6344800	0.0351	0.2245
chr6	171115067	4835937	0.0283	0.2094
chr7	159138663	3691376	0.0232	0.2862

chr8	146364022	6495481	0.0444	0.3798
chr9	141213431	2720475	0.0193	0.2634
chr10	135534747	3944551	0.0291	0.2767
chr11	135006516	3550675	0.0263	0.2858
chr12	133851895	3608060	0.027	0.1984
chr13	115169878	3831099	0.0333	0.2168
chr14	107349540	3394378	0.0316	0.2217
chr15	102531392	2814557	0.0275	0.1962
chr16	90354753	2760477	0.0306	0.2302
chr17	81195210	2114151	0.026	0.2169
chr18	78077248	2275061	0.0291	0.4887
chr19	59128983	1330234	0.0225	0.3882
chr20	63025520	2399564	0.0381	0.2432
chr21	48129895	1094447	0.0227	0.1924
chr22	51304566	1100815	0.0215	0.1735
chrMT	16571	126479	7.6326	5.2504
chrX	155270560	6902446	0.0445	0.2705
chrY	59373566	307618	0.0052	0.13

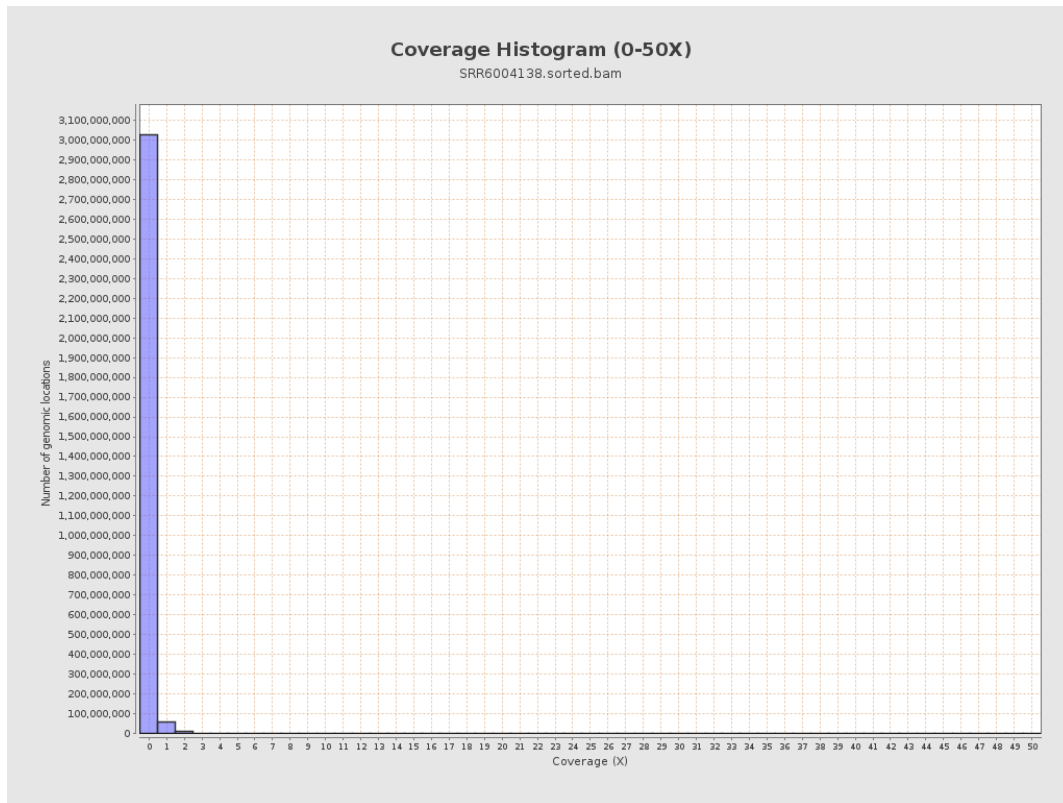
3. Results : Coverage across reference



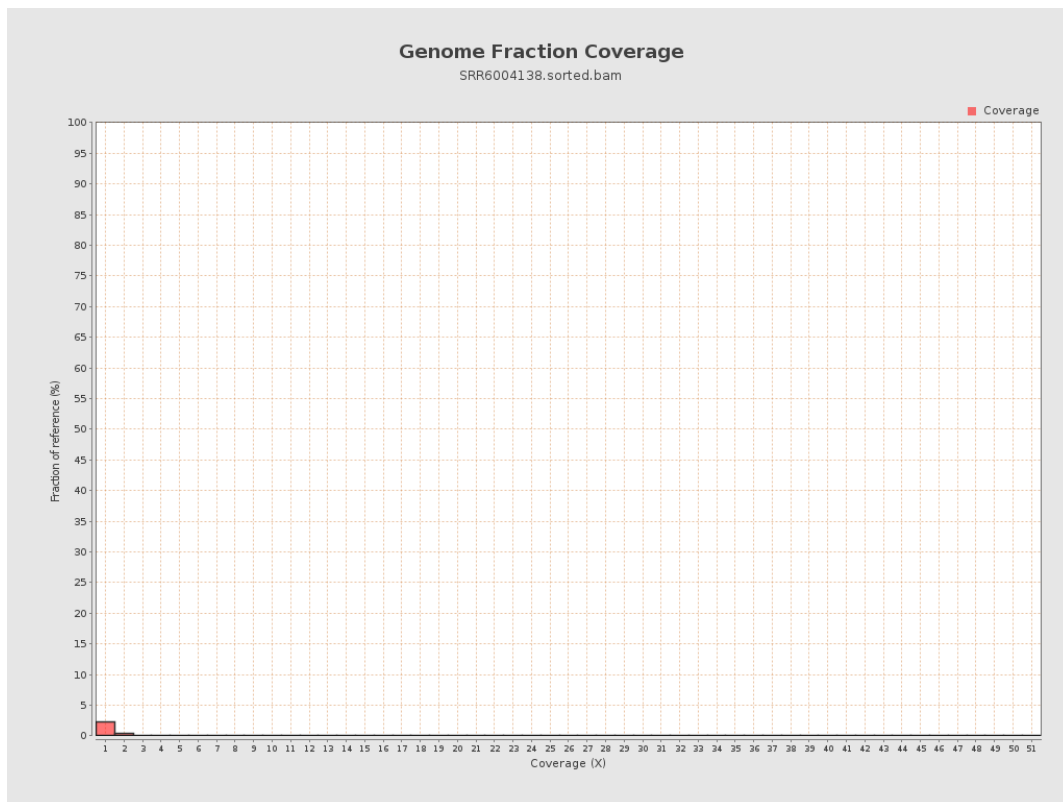
4. Results : Coverage Histogram



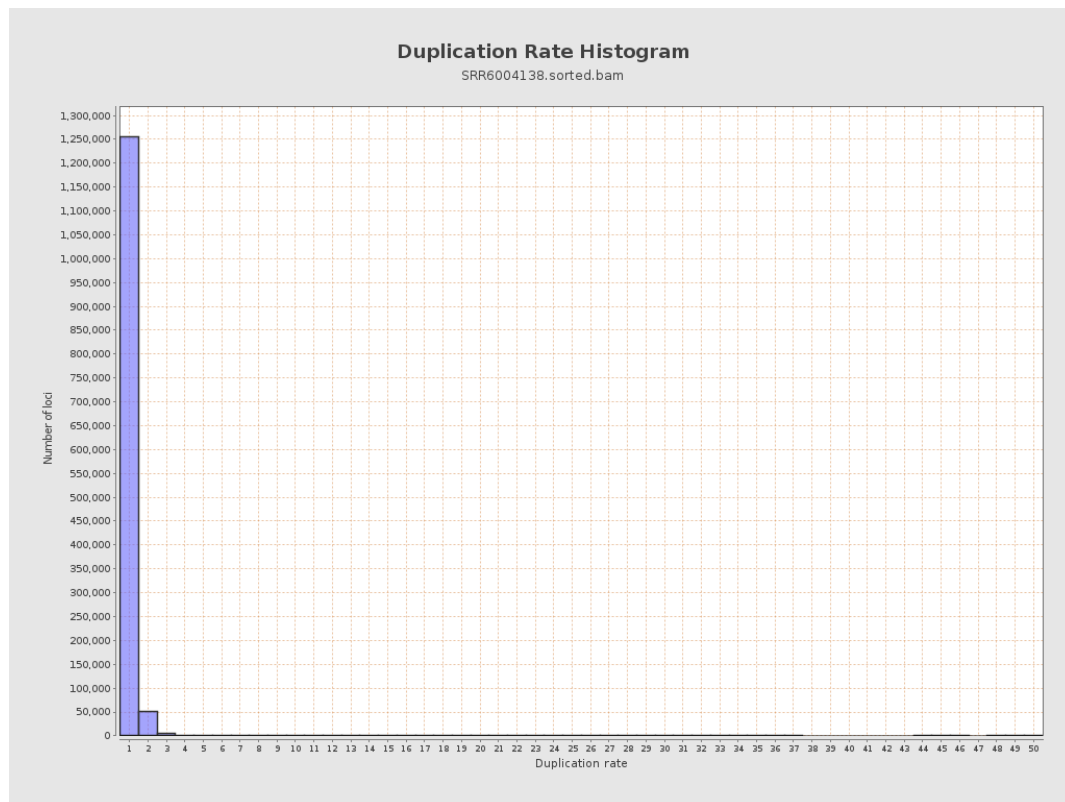
5. Results : Coverage Histogram (0-50X)



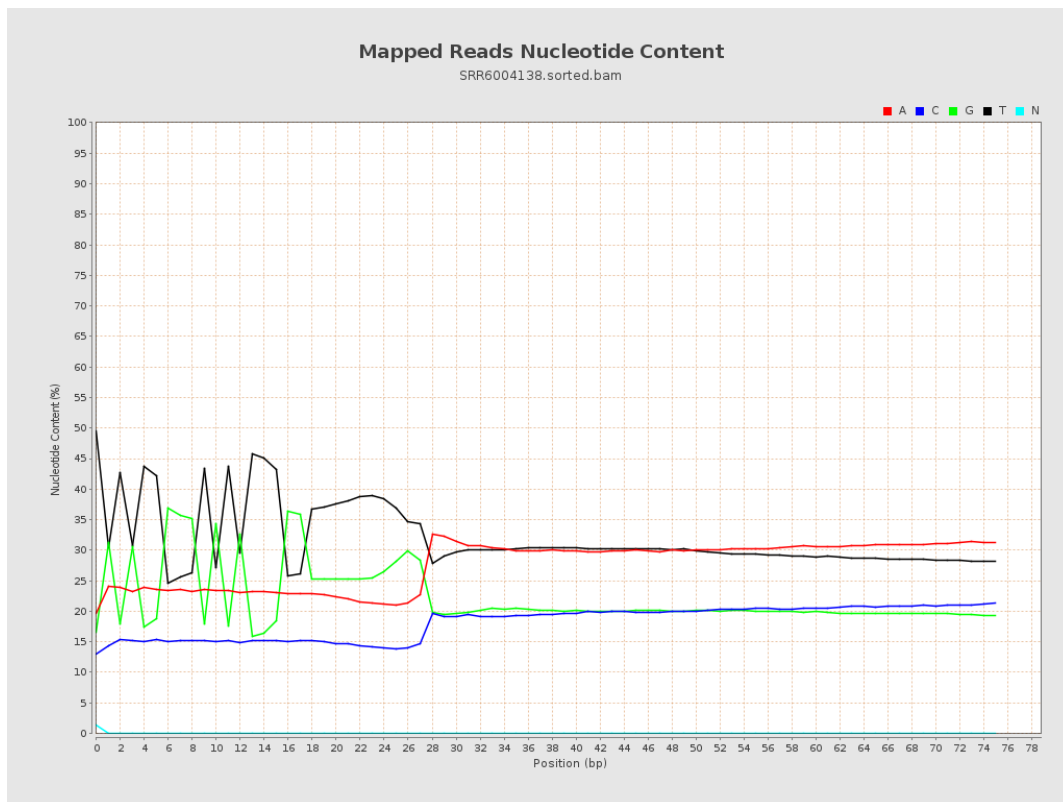
6. Results : Genome Fraction Coverage



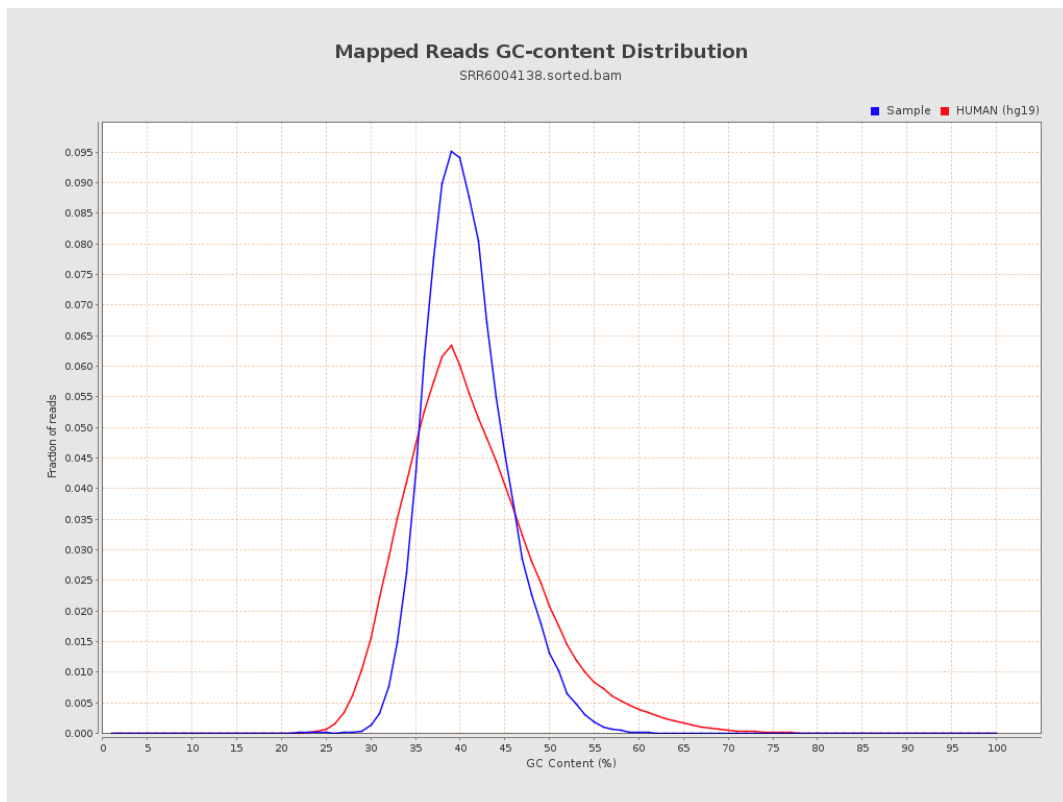
7. Results : Duplication Rate Histogram



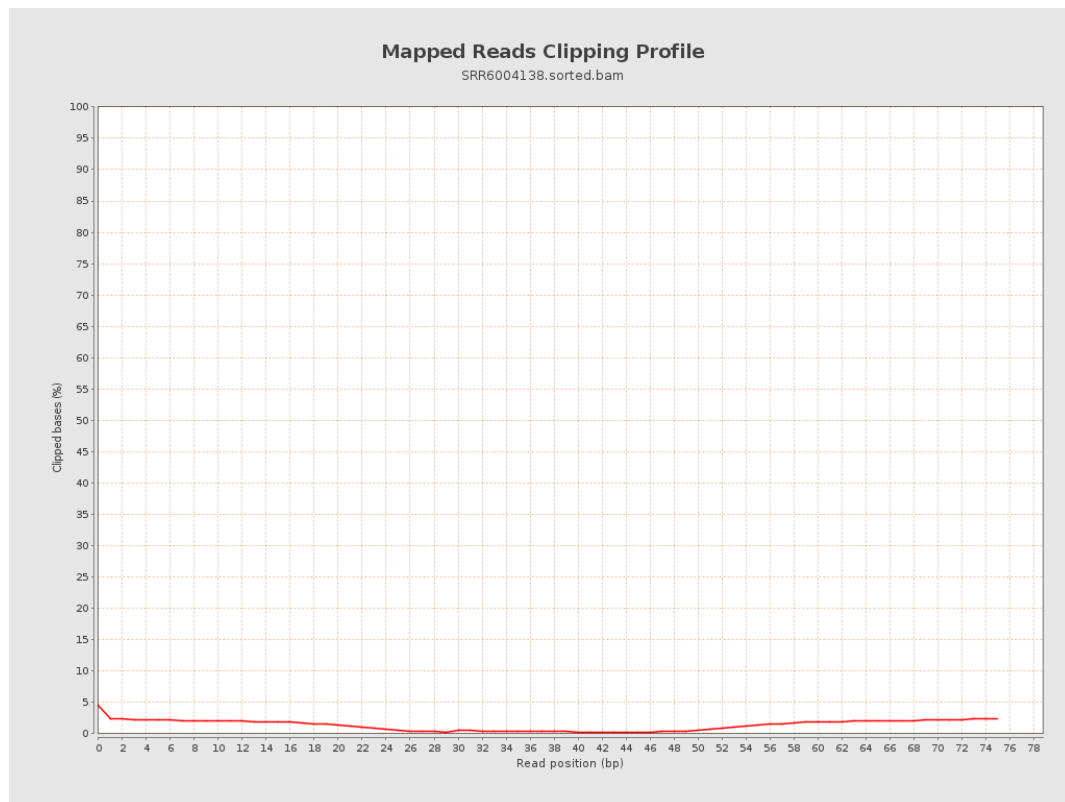
8. Results : Mapped Reads Nucleotide Content



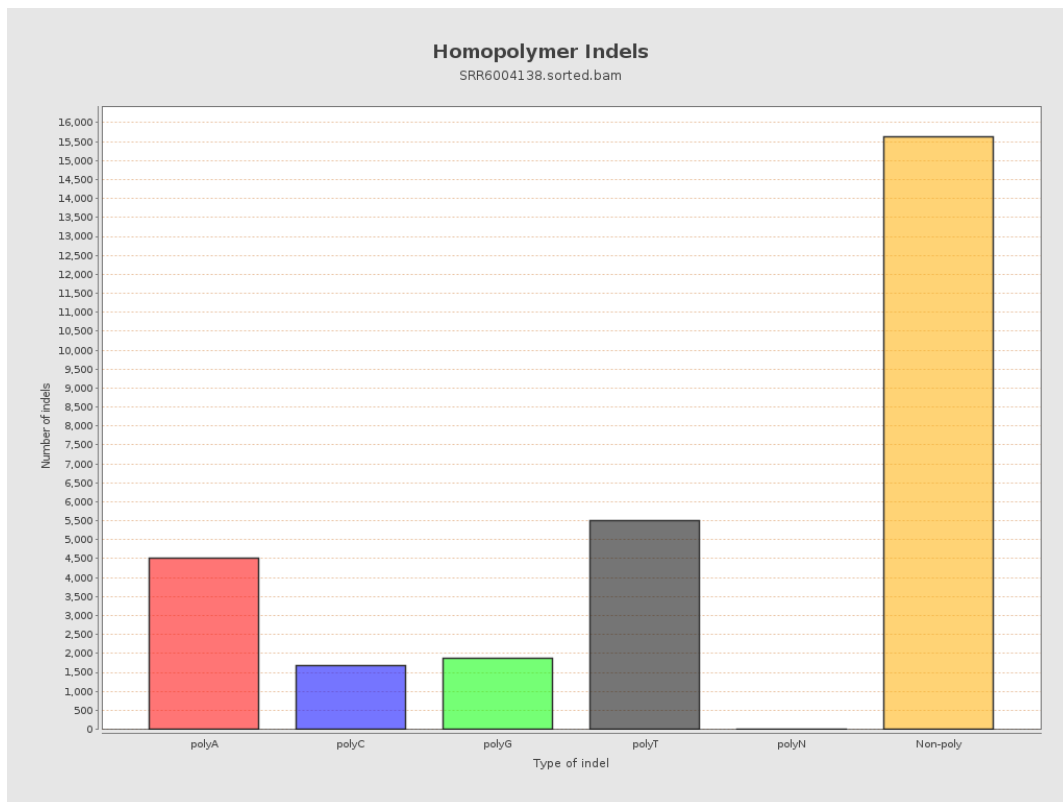
9. Results : Mapped Reads GC-content Distribution



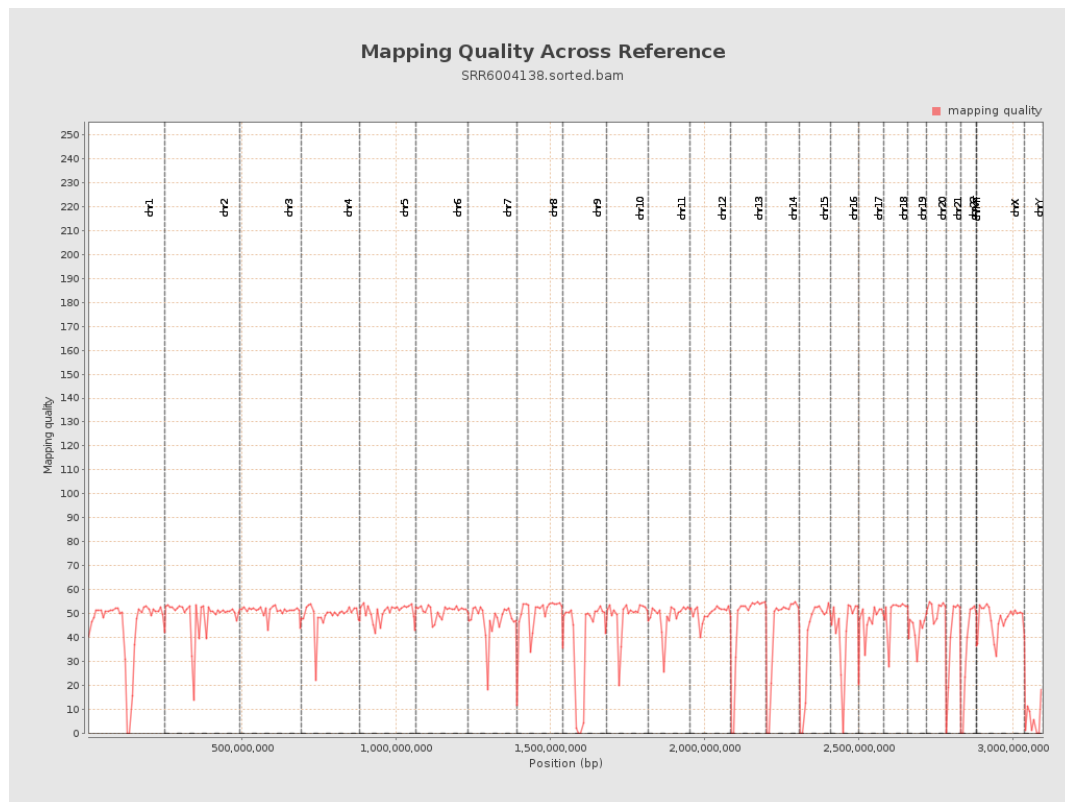
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

