

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 09:04:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708621.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_SRR1708621 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708621.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 09:04:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708621.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,315,477
Mapped reads	3,164,630 / 73.33%
Unmapped reads	1,150,847 / 26.67%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	957 / 0.02%
Read min/max/mean length	30 / 51 / 51.01
Duplicated reads (estimated)	129,976 / 3.01%
Duplication rate	2.76%
Clipped reads	488,820 / 11.33%

2.2. ACGT Content

Number/percentage of A's	45,401,812 / 29.46%
Number/percentage of C's	29,027,912 / 18.83%
Number/percentage of T's	48,707,333 / 31.6%
Number/percentage of G's	30,981,629 / 20.1%
Number/percentage of N's	13,246 / 0.01%
GC Percentage	38.93%

2.3. Coverage

Mean	0.0498

Standard Deviation	0.5079
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2.4. Mapping Quality

Mean Mapping Quality	43.18
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2.5. Mismatches and indels

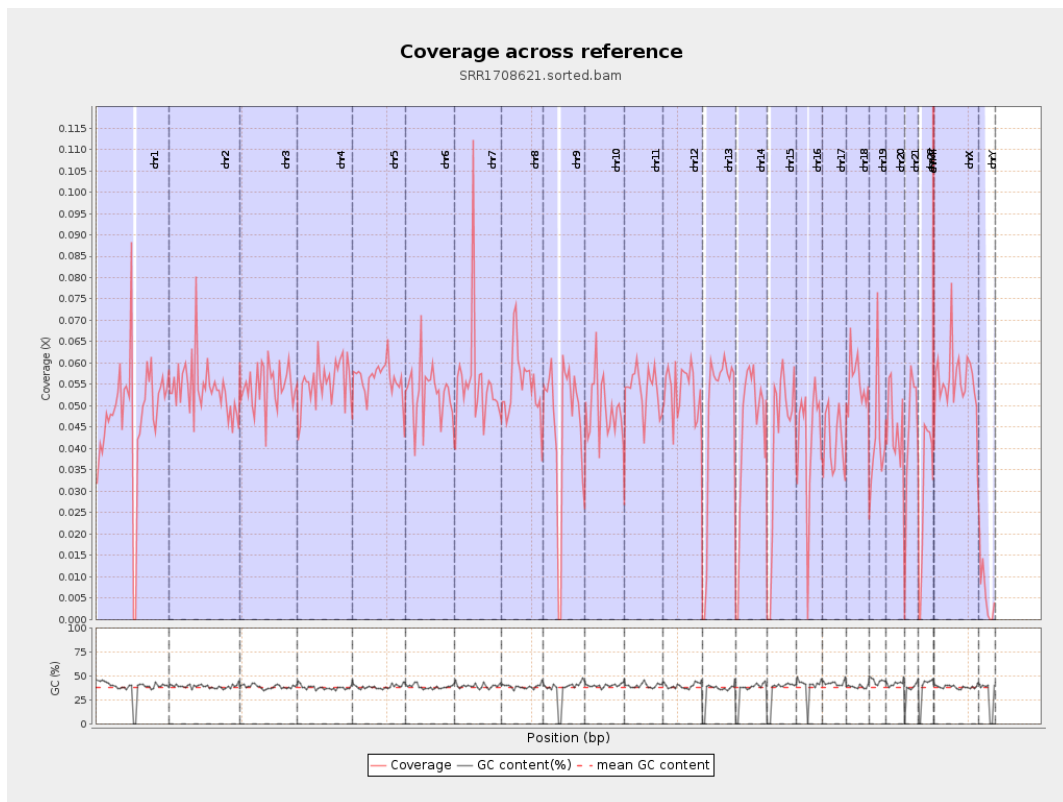
General error rate	0.65%
Mismatches	997,934
Insertions	7,404
Mapped reads with at least one insertion	0.23%
Deletions	19,372
Mapped reads with at least one deletion	0.61%
Homopolymer indels	48.11%

2.6. Chromosome stats

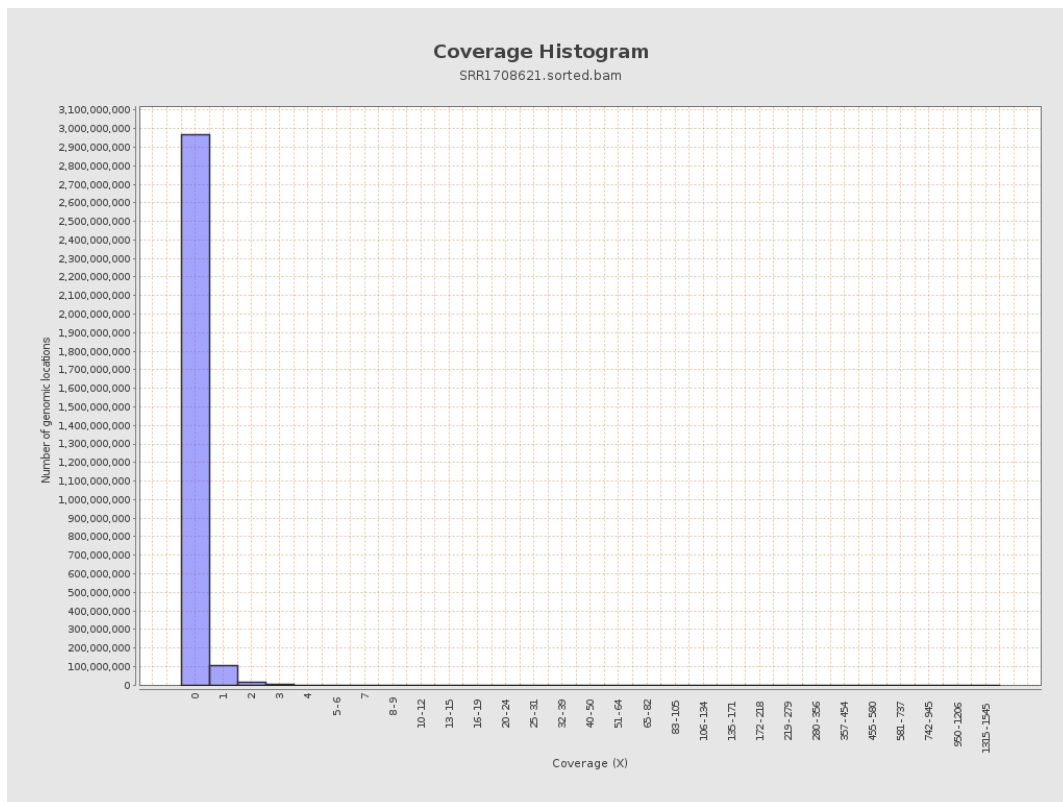
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	11913333	0.0478	0.9195
chr2	243199373	13089789	0.0538	0.5478
chr3	198022430	10810542	0.0546	0.2788
chr4	191154276	10586911	0.0554	0.2838
chr5	180915260	10183672	0.0563	0.2884
chr6	171115067	9085205	0.0531	0.3773
chr7	159138663	8883228	0.0558	0.7932

chr8	146364022	8013853	0.0548	0.8984
chr9	141213431	6530142	0.0462	0.4014
chr10	135534747	6686787	0.0493	0.4008
chr11	135006516	7197142	0.0533	0.4182
chr12	133851895	7159289	0.0535	0.2841
chr13	115169878	5471865	0.0475	0.2619
chr14	107349540	4723648	0.044	0.2778
chr15	102531392	4288330	0.0418	0.2407
chr16	90354753	3850786	0.0426	0.2645
chr17	81195210	3301915	0.0407	0.2878
chr18	78077248	4337941	0.0556	0.8412
chr19	59128983	2532554	0.0428	0.7094
chr20	63025520	2841024	0.0451	0.2635
chr21	48129895	2093727	0.0435	0.2707
chr22	51304566	1552179	0.0303	0.2018
chrMT	16571	8516	0.5139	0.8894
chrX	155270560	8664804	0.0558	0.3235
chrY	59373566	354240	0.006	0.1059

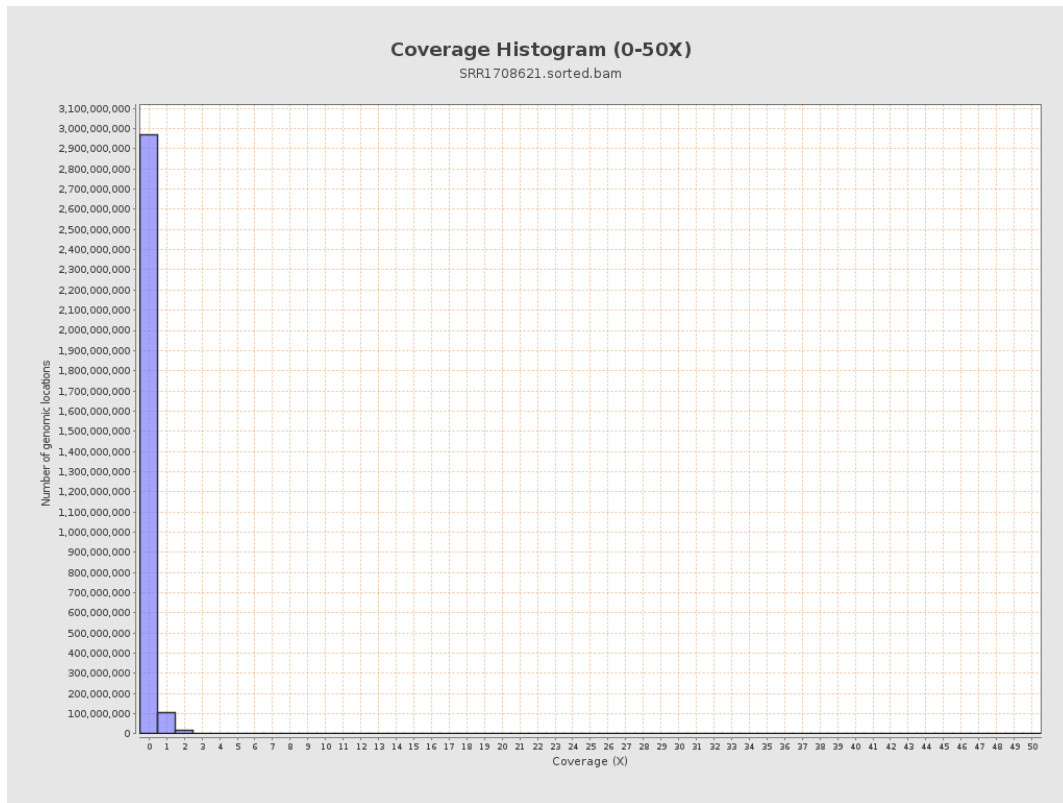
3. Results : Coverage across reference



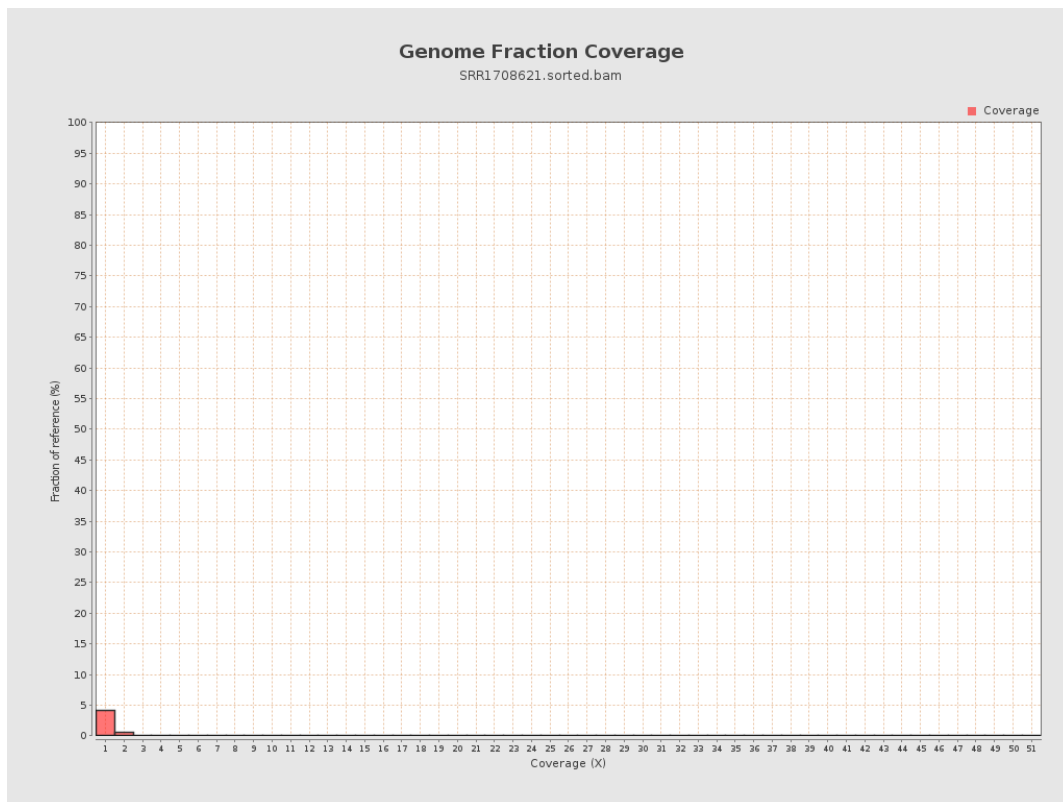
4. Results : Coverage Histogram



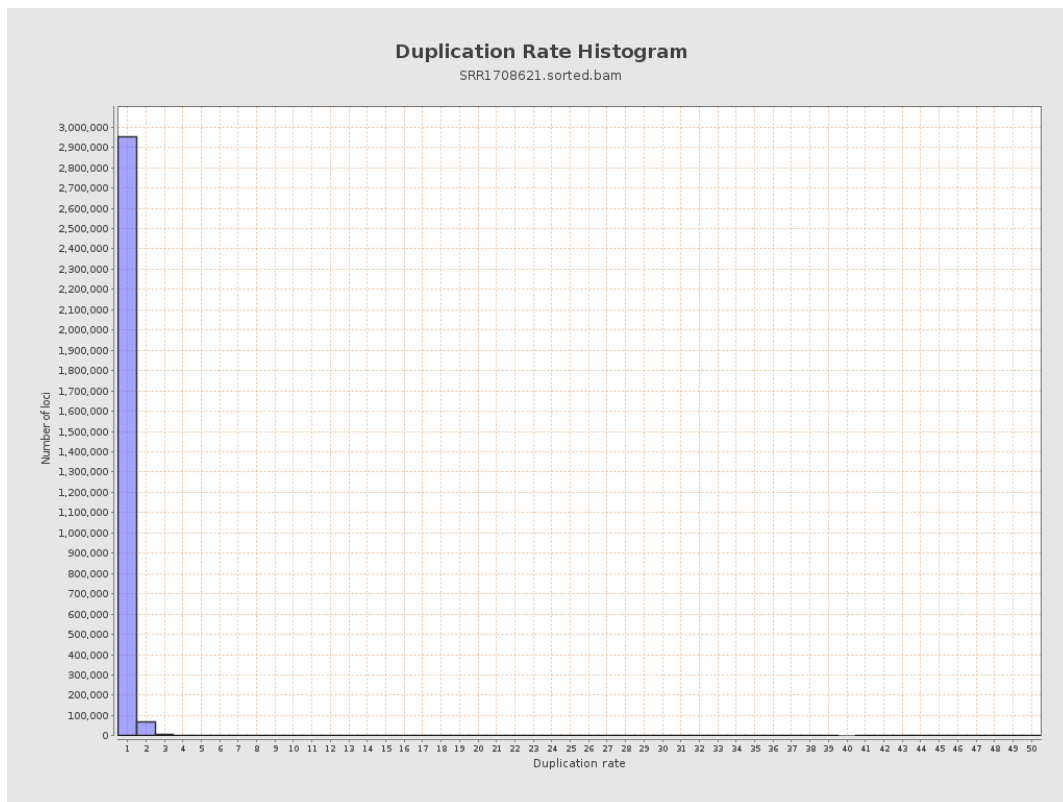
5. Results : Coverage Histogram (0-50X)



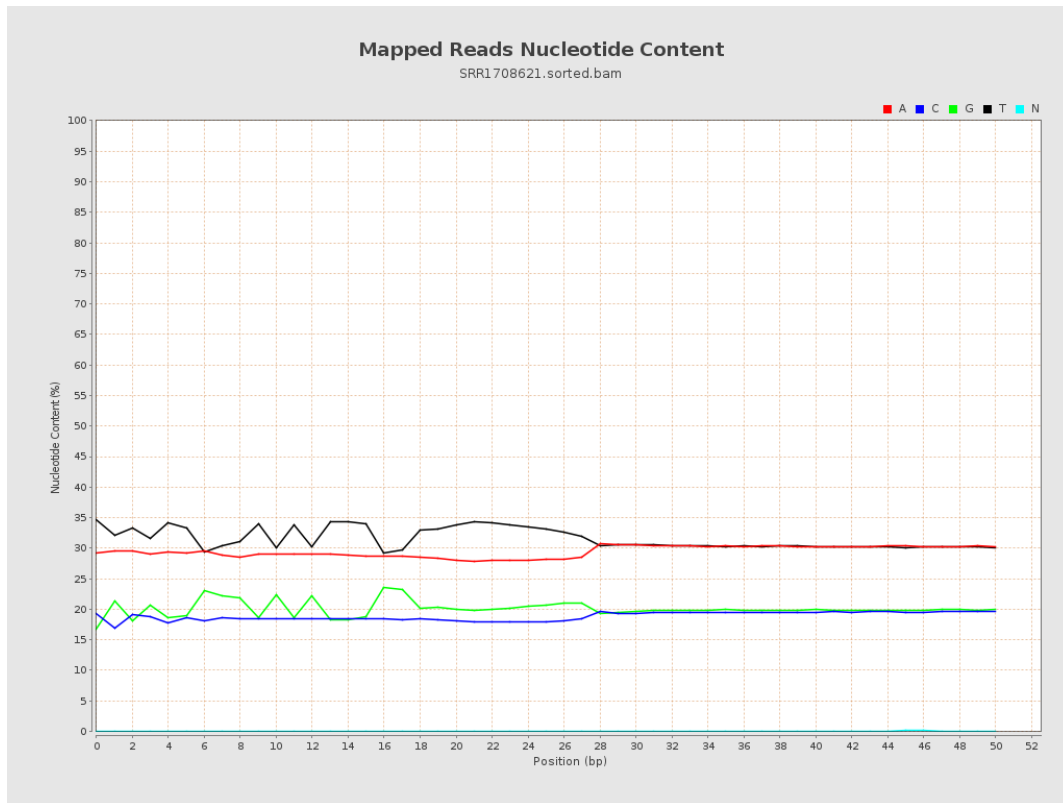
6. Results : Genome Fraction Coverage



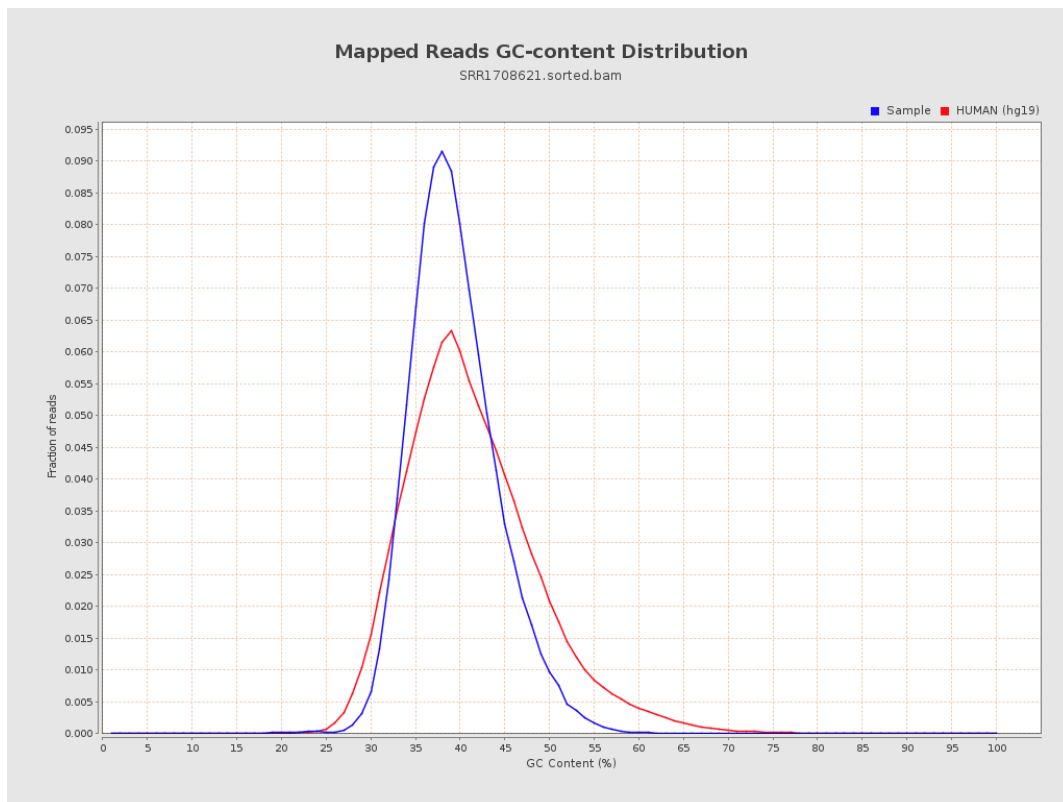
7. Results : Duplication Rate Histogram



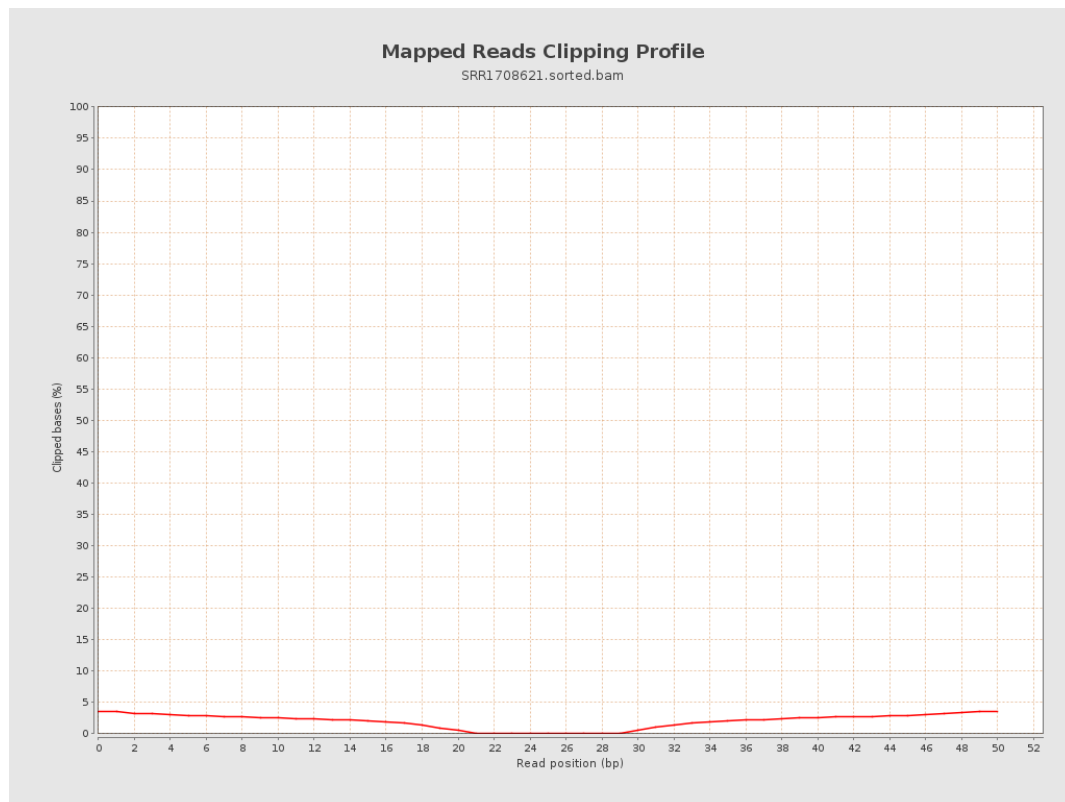
8. Results : Mapped Reads Nucleotide Content



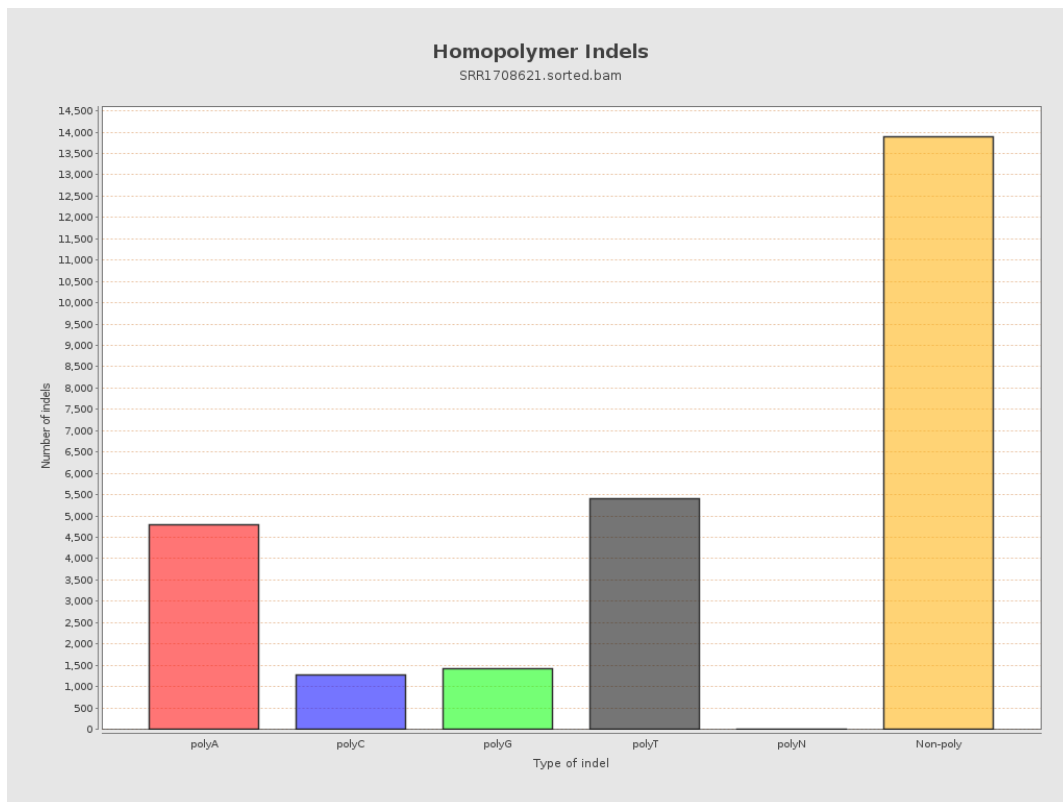
9. Results : Mapped Reads GC-content Distribution



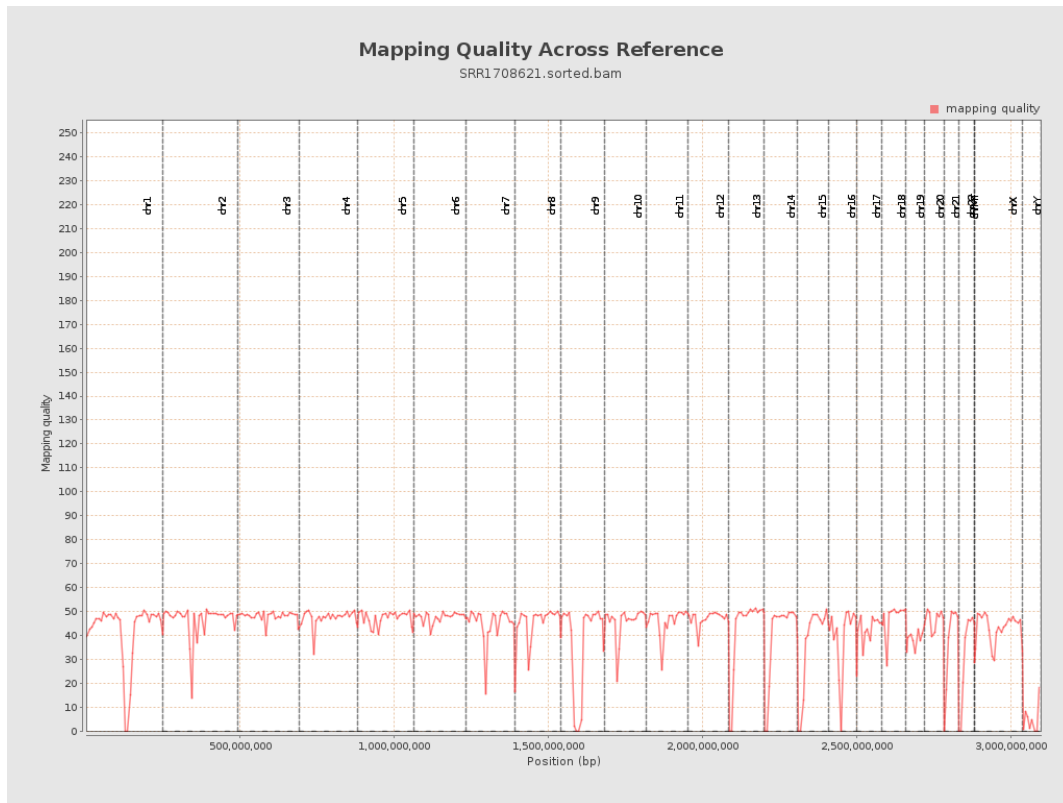
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

