

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 14:45:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234083.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_SRR6234083 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234083.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 14:45:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234083.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,644,608
Mapped reads	1,427,343 / 86.79%
Unmapped reads	217,265 / 13.21%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,130 / 0.62%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	40,205 / 2.44%
Duplication rate	1.8%
Clipped reads	672,242 / 40.88%

2.2. ACGT Content

Number/percentage of A's	26,166,005 / 27.77%
Number/percentage of C's	17,545,491 / 18.62%
Number/percentage of T's	29,119,516 / 30.9%
Number/percentage of G's	21,388,084 / 22.7%
Number/percentage of N's	17,327 / 0.02%
GC Percentage	41.31%

2.3. Coverage

Mean	0.0305

Standard Deviation	0.343
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2.4. Mapping Quality

Mean Mapping Quality	43.46
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2.5. Mismatches and indels

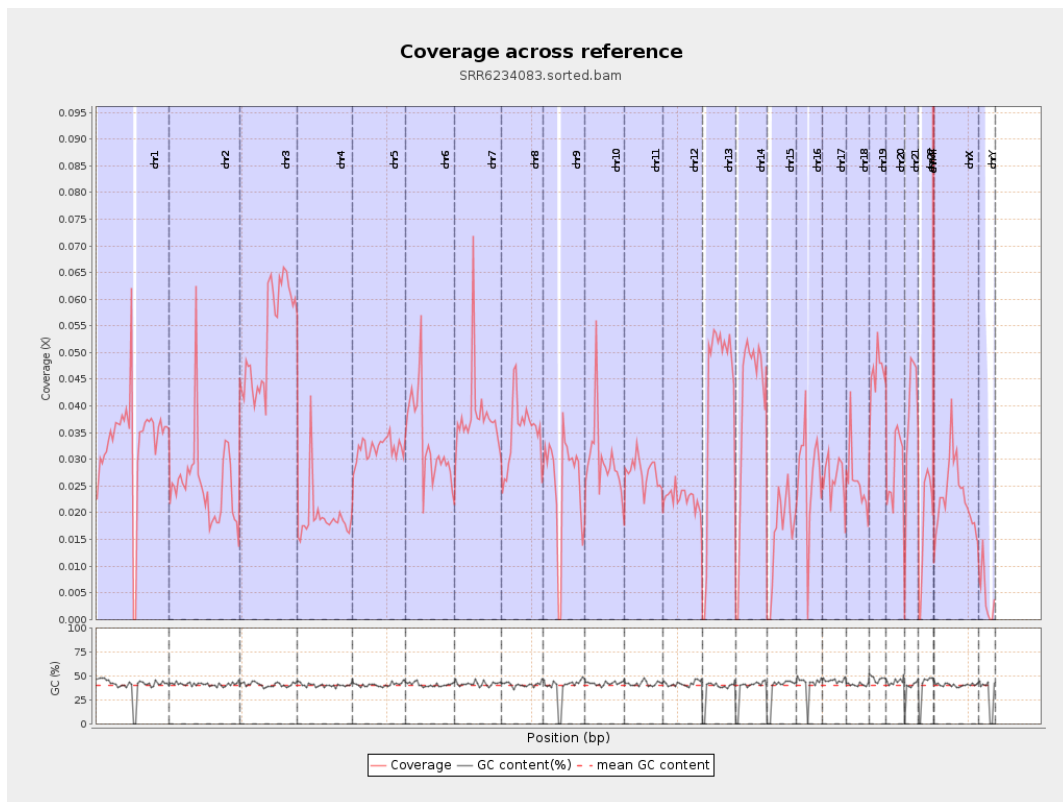
General error rate	0.87%
Mismatches	803,107
Insertions	7,934
Mapped reads with at least one insertion	0.55%
Deletions	30,808
Mapped reads with at least one deletion	2.13%
Homopolymer indels	45.03%

2.6. Chromosome stats

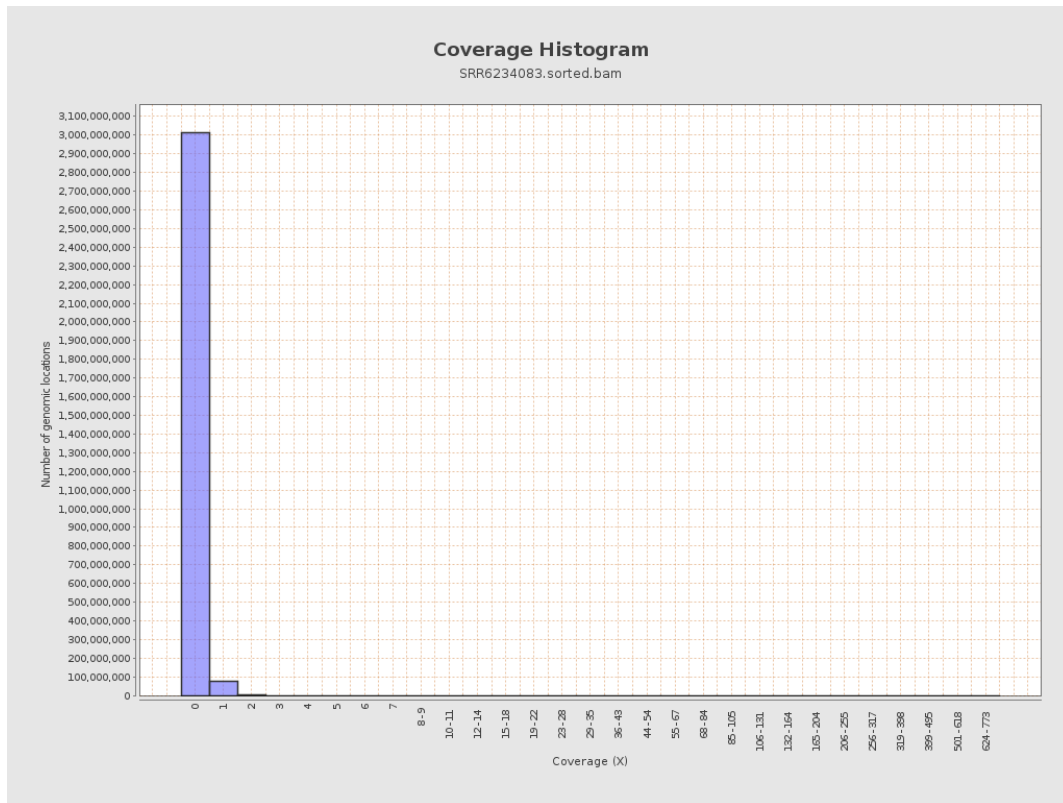
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	8313426	0.0334	0.6821
chr2	243199373	6147820	0.0253	0.3375
chr3	198022430	10502406	0.053	0.2484
chr4	191154276	3629725	0.019	0.1676
chr5	180915260	5801386	0.0321	0.1958
chr6	171115067	5686760	0.0332	0.2457
chr7	159138663	6107049	0.0384	0.5041

chr8	146364022	5096856	0.0348	0.4875
chr9	141213431	3650863	0.0259	0.2739
chr10	135534747	4042004	0.0298	0.2951
chr11	135006516	3703189	0.0274	0.2796
chr12	133851895	3039635	0.0227	0.1671
chr13	115169878	4865893	0.0422	0.2214
chr14	107349540	4298879	0.04	0.2396
chr15	102531392	1667886	0.0163	0.1433
chr16	90354753	2482357	0.0275	0.2222
chr17	81195210	2114709	0.026	0.1999
chr18	78077248	2030365	0.026	0.5942
chr19	59128983	2743553	0.0464	0.4457
chr20	63025520	1769836	0.0281	0.1958
chr21	48129895	1821440	0.0378	0.2223
chr22	51304566	929870	0.0181	0.1441
chrMT	16571	28897	1.7438	1.7229
chrX	155270560	3563085	0.0229	0.1944
chrY	59373566	252102	0.0042	0.1103

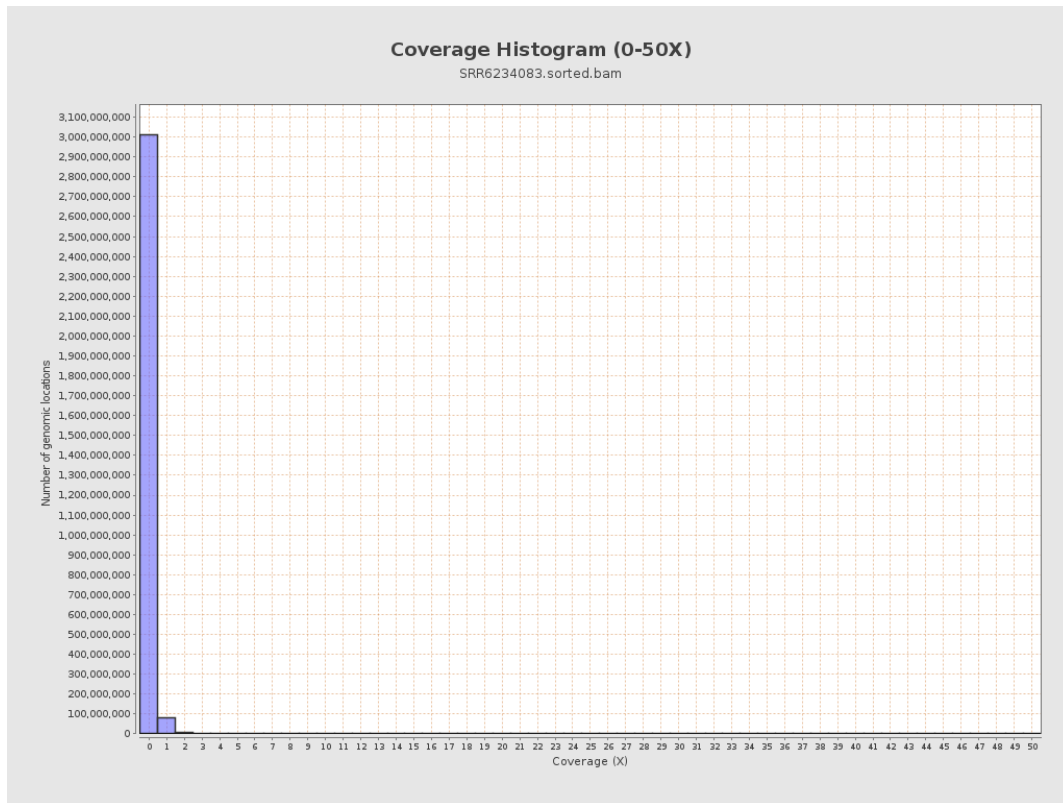
3. Results : Coverage across reference



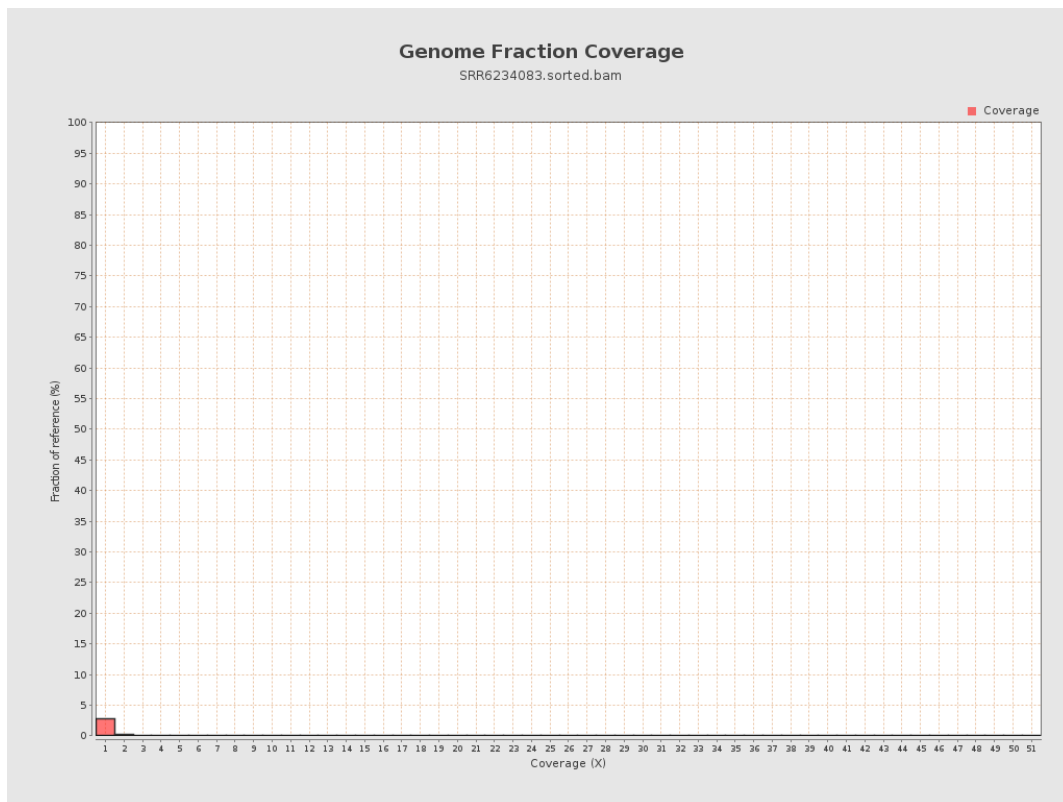
4. Results : Coverage Histogram



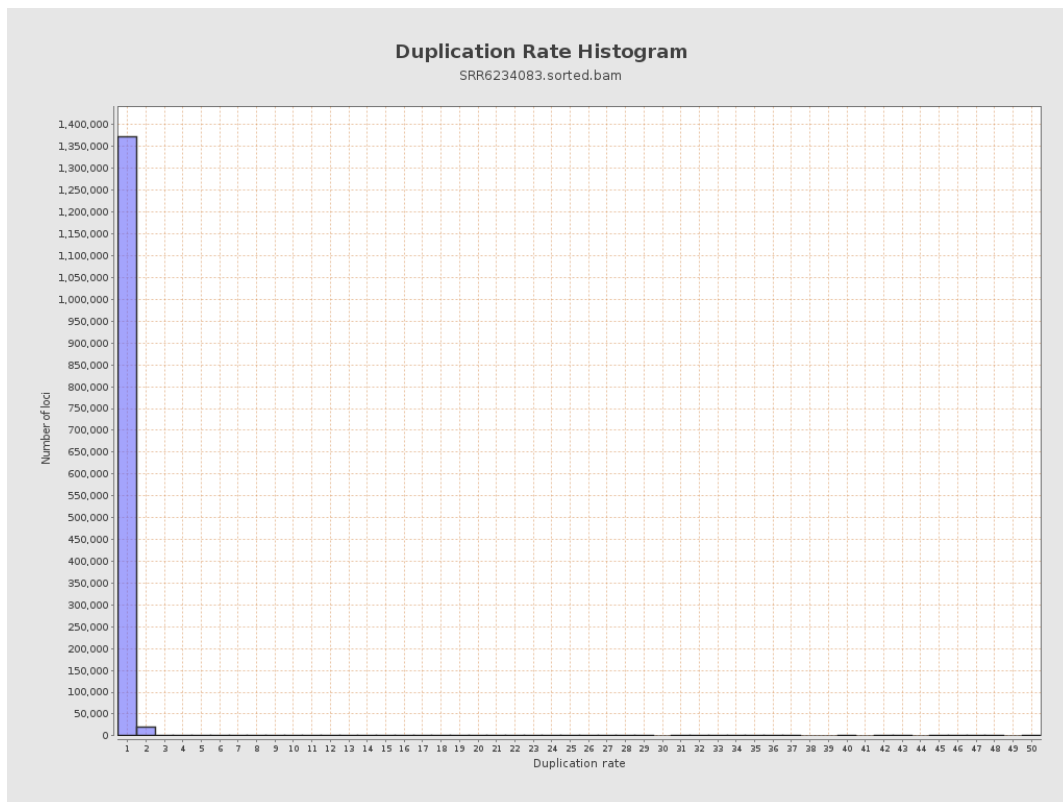
5. Results : Coverage Histogram (0-50X)



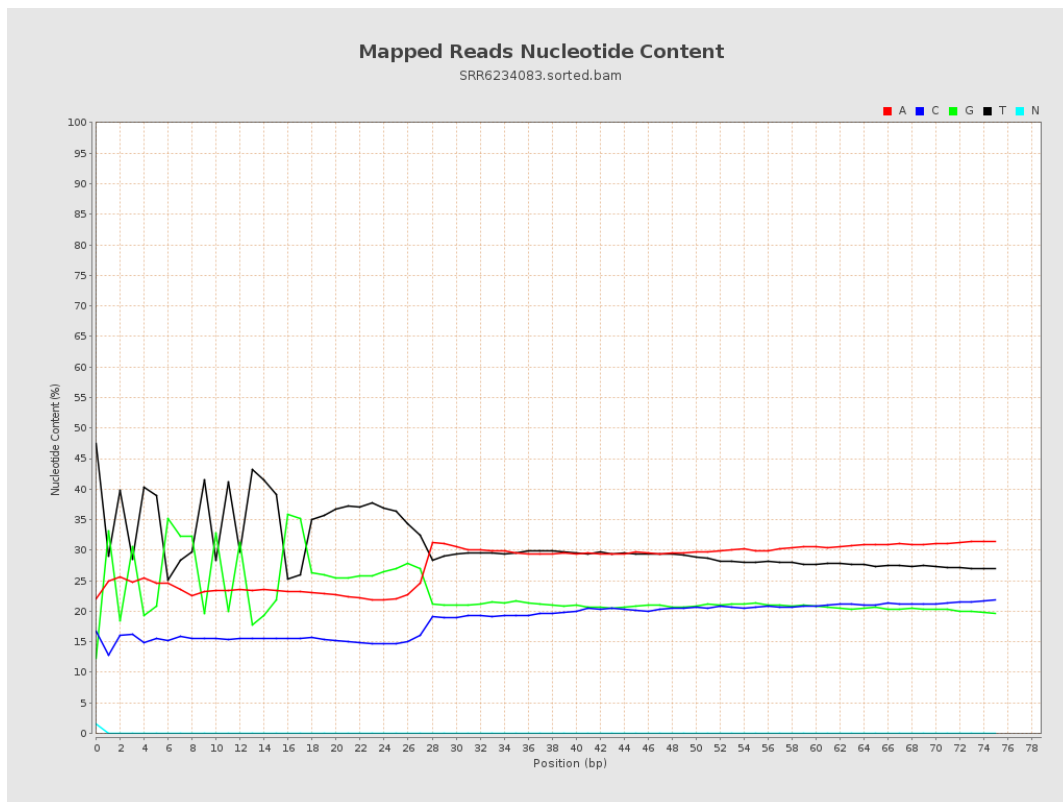
6. Results : Genome Fraction Coverage



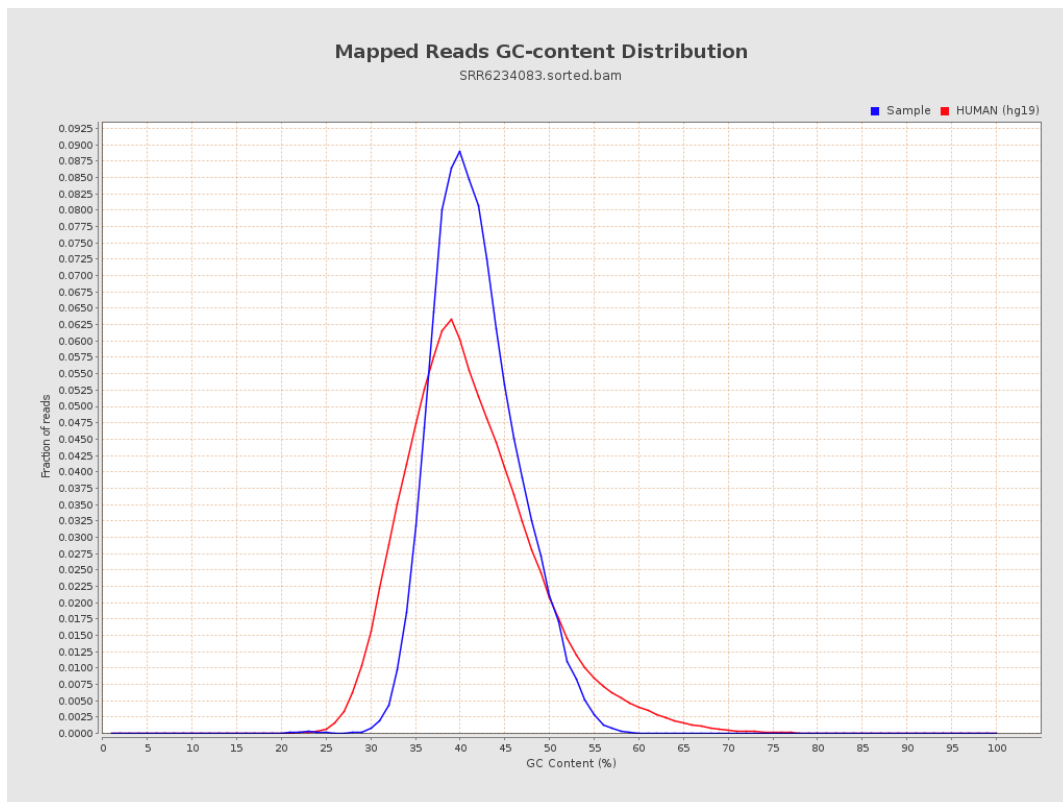
7. Results : Duplication Rate Histogram



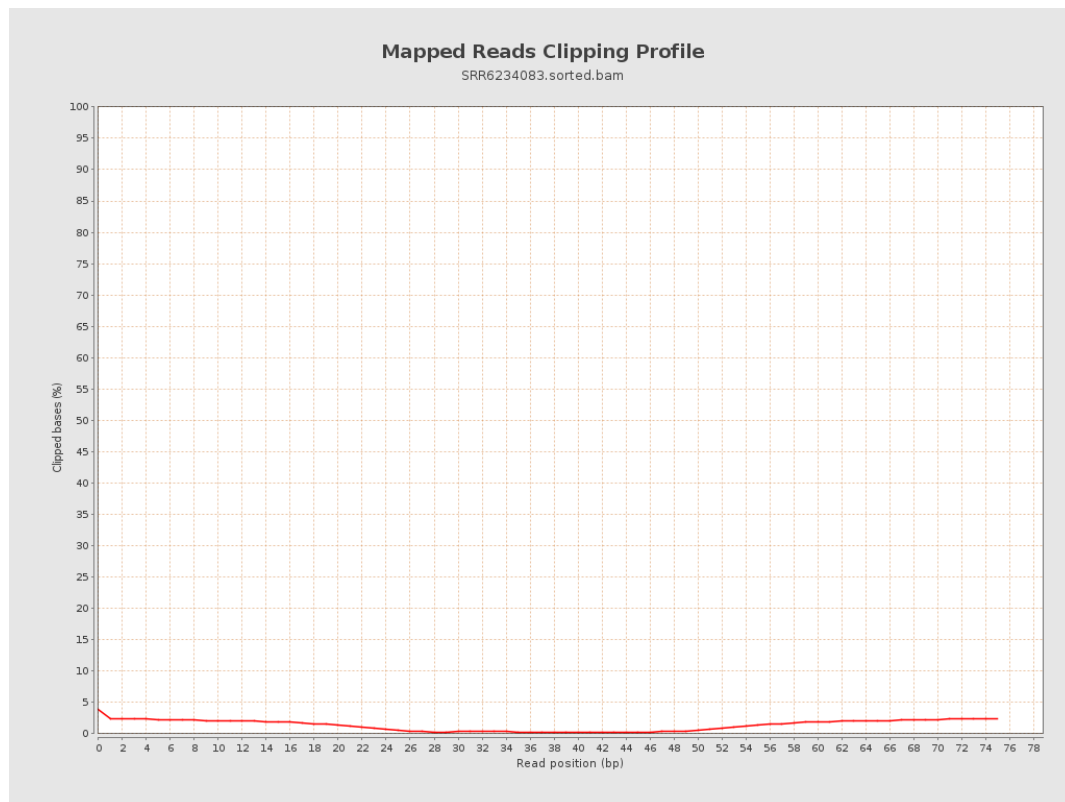
8. Results : Mapped Reads Nucleotide Content



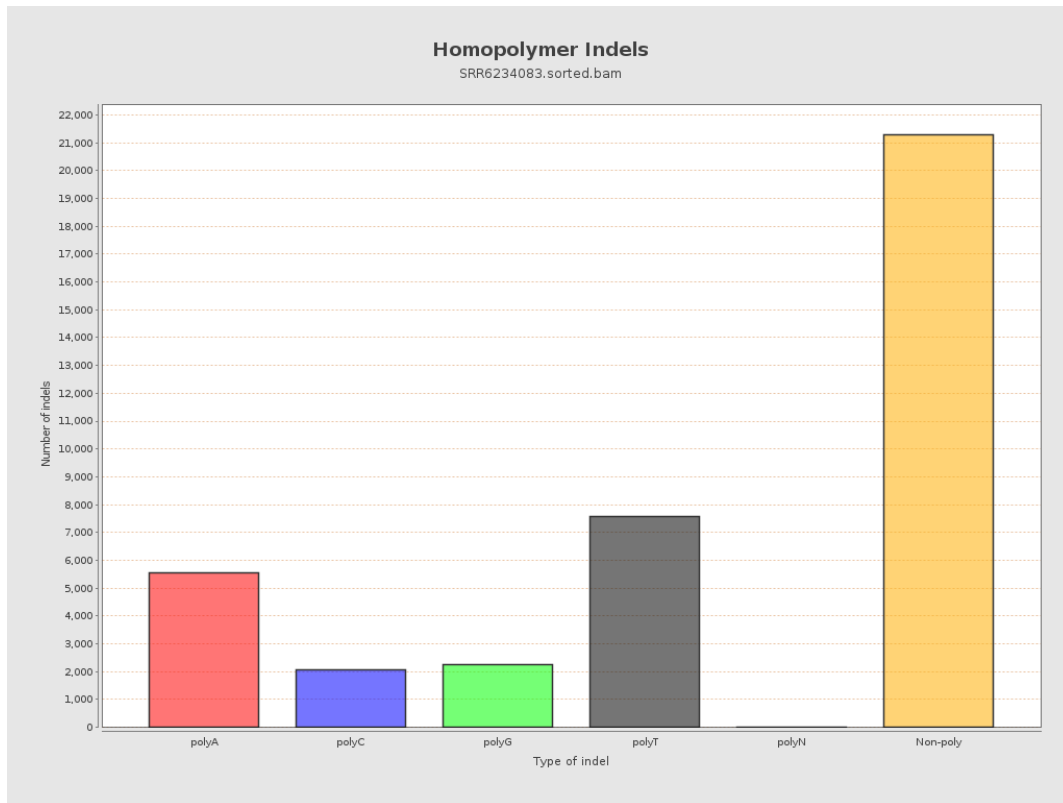
9. Results : Mapped Reads GC-content Distribution



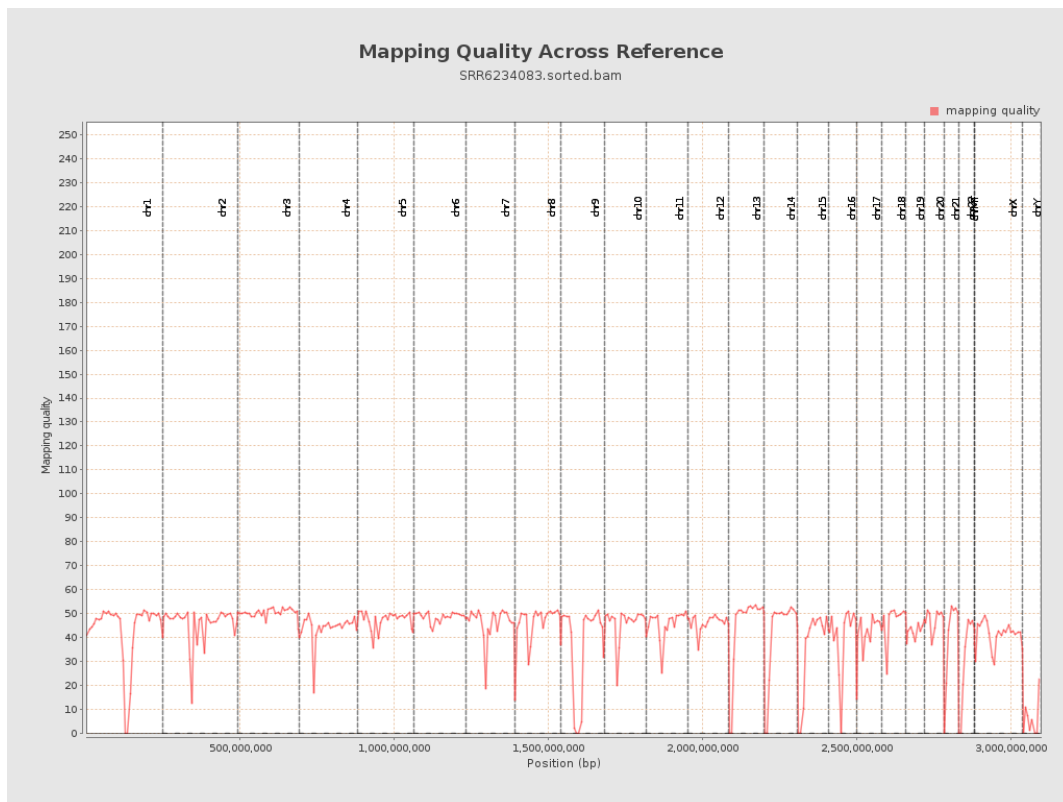
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

