

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 13:01:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234061.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_SRR6234061 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234061.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 13:01:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234061.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,270,566
Mapped reads	4,960,921 / 94.13%
Unmapped reads	309,645 / 5.87%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	52,287 / 0.99%
Read min/max/mean length	30 / 76 / 76.35
Duplicated reads (estimated)	850,409 / 16.14%
Duplication rate	6.43%
Clipped reads	1,756,147 / 33.32%

2.2. ACGT Content

Number/percentage of A's	86,751,895 / 25.37%
Number/percentage of C's	58,969,046 / 17.24%
Number/percentage of T's	93,627,934 / 27.38%
Number/percentage of G's	102,554,939 / 29.99%
Number/percentage of N's	74,905 / 0.02%
GC Percentage	47.23%

2.3. Coverage

Mean	0.1105

Standard Deviation	72.6298
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2.4. Mapping Quality

Mean Mapping Quality	43.87
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2.5. Mismatches and indels

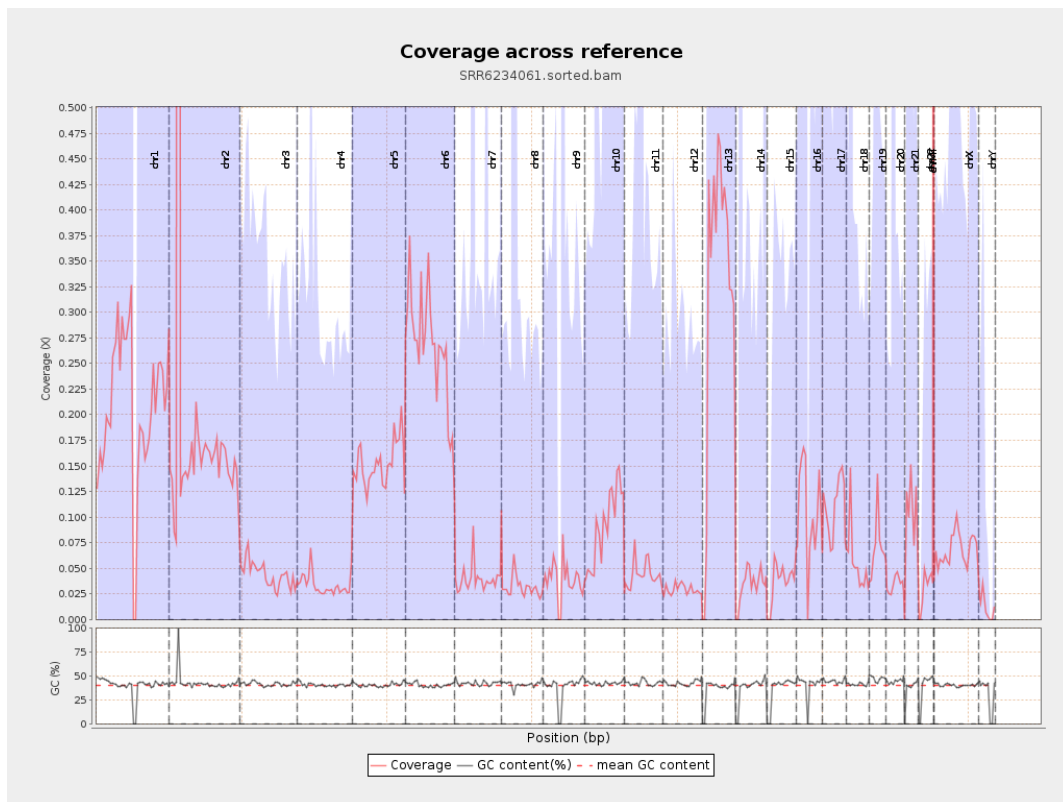
General error rate	0.61%
Mismatches	2,047,233
Insertions	22,130
Mapped reads with at least one insertion	0.44%
Deletions	65,166
Mapped reads with at least one deletion	1.3%
Homopolymer indels	47.57%

2.6. Chromosome stats

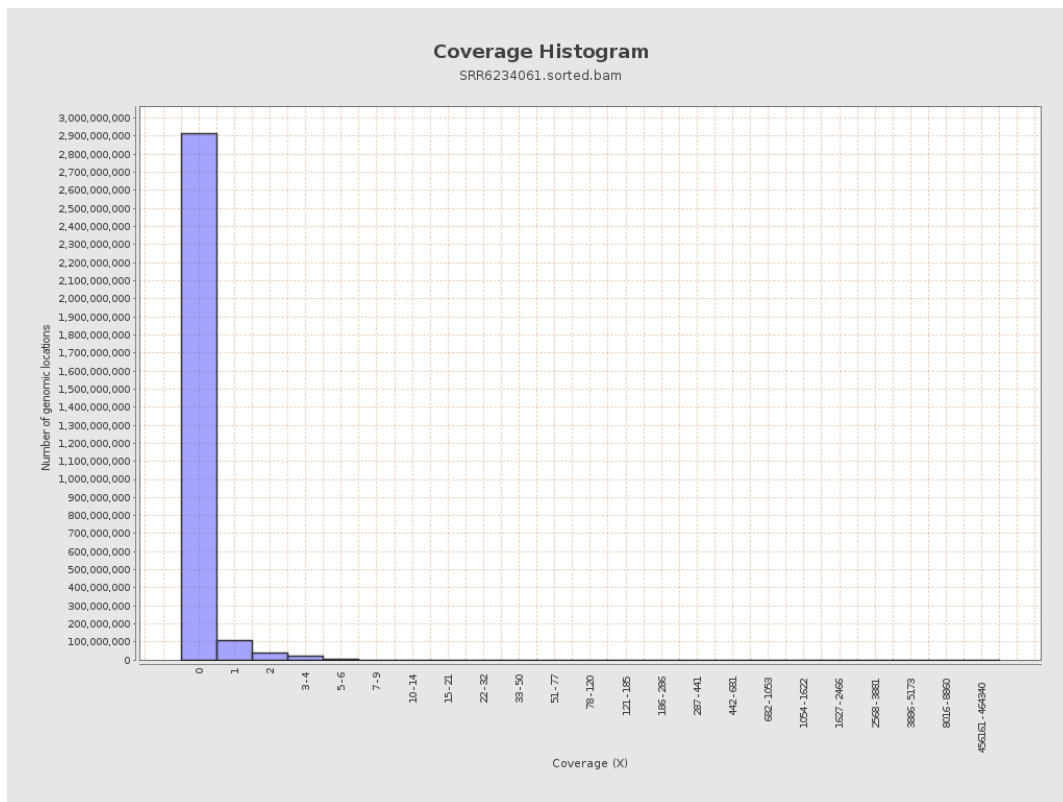
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	51337484	0.206	2.0513
chr2	243199373	72082956	0.2964	259.1049
chr3	198022430	8728139	0.0441	0.3154
chr4	191154276	6396746	0.0335	0.2935
chr5	180915260	27689145	0.1531	0.5988
chr6	171115067	45561466	0.2663	1.1247
chr7	159138663	6283610	0.0395	0.6295

chr8	146364022	4558648	0.0311	1.2935
chr9	141213431	5449719	0.0386	0.4993
chr10	135534747	12261913	0.0905	0.5902
chr11	135006516	5908245	0.0438	0.5033
chr12	133851895	3941236	0.0294	0.2665
chr13	115169878	37380081	0.3246	0.9122
chr14	107349540	3656444	0.0341	0.6901
chr15	102531392	3881280	0.0379	0.2898
chr16	90354753	9710986	0.1075	0.7817
chr17	81195210	8950286	0.1102	0.564
chr18	78077248	4416667	0.0566	2.5073
chr19	59128983	4278865	0.0724	1.5049
chr20	63025520	2147449	0.0341	0.6603
chr21	48129895	4690134	0.0974	0.5024
chr22	51304566	1511676	0.0295	0.2487
chrMT	16571	46094	2.7816	2.7988
chrX	155270560	10535917	0.0679	0.5398
chrY	59373566	680222	0.0115	0.2095

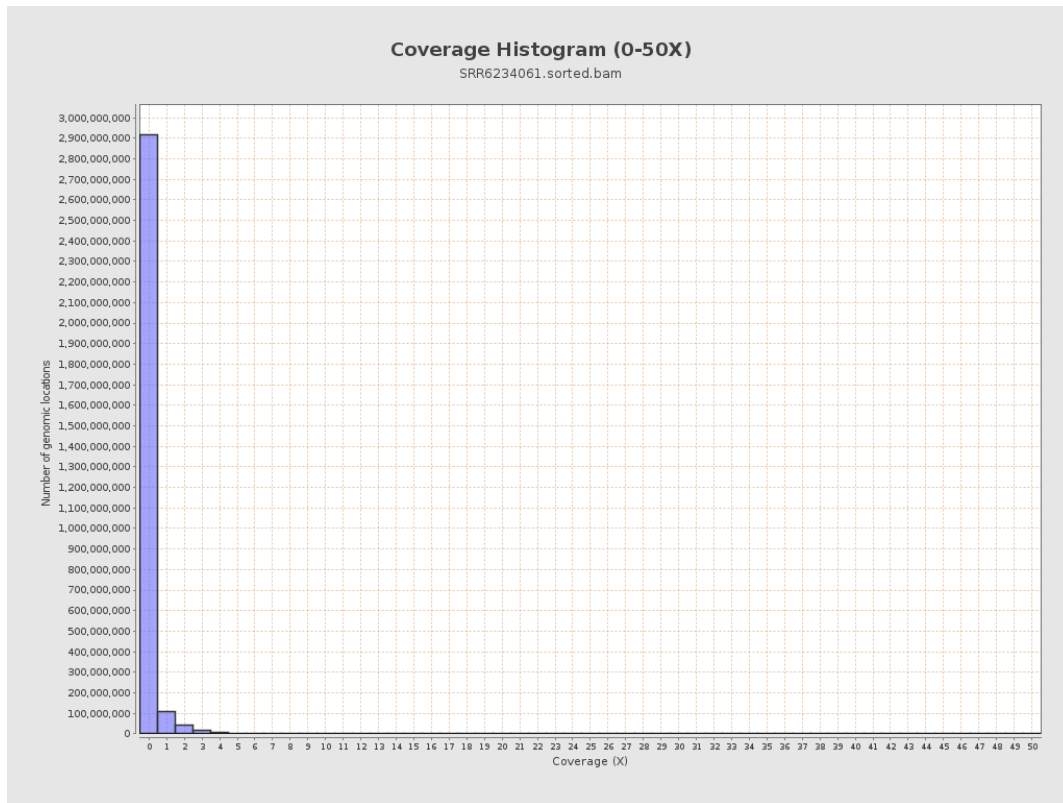
3. Results : Coverage across reference



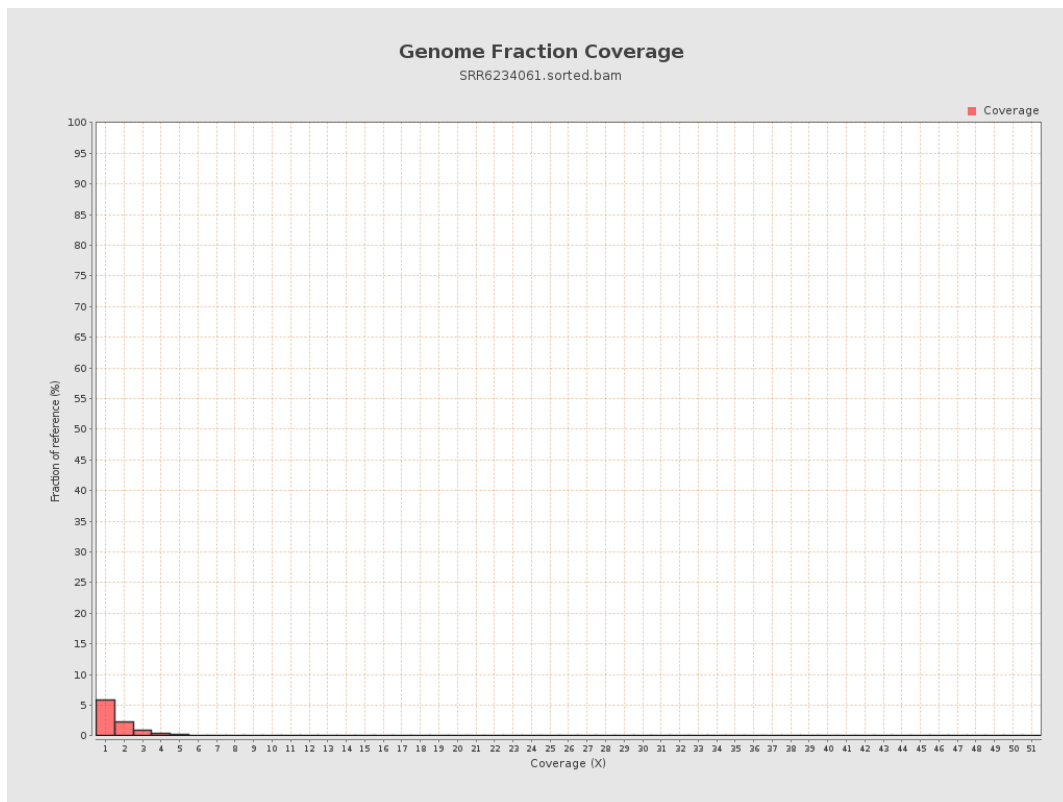
4. Results : Coverage Histogram



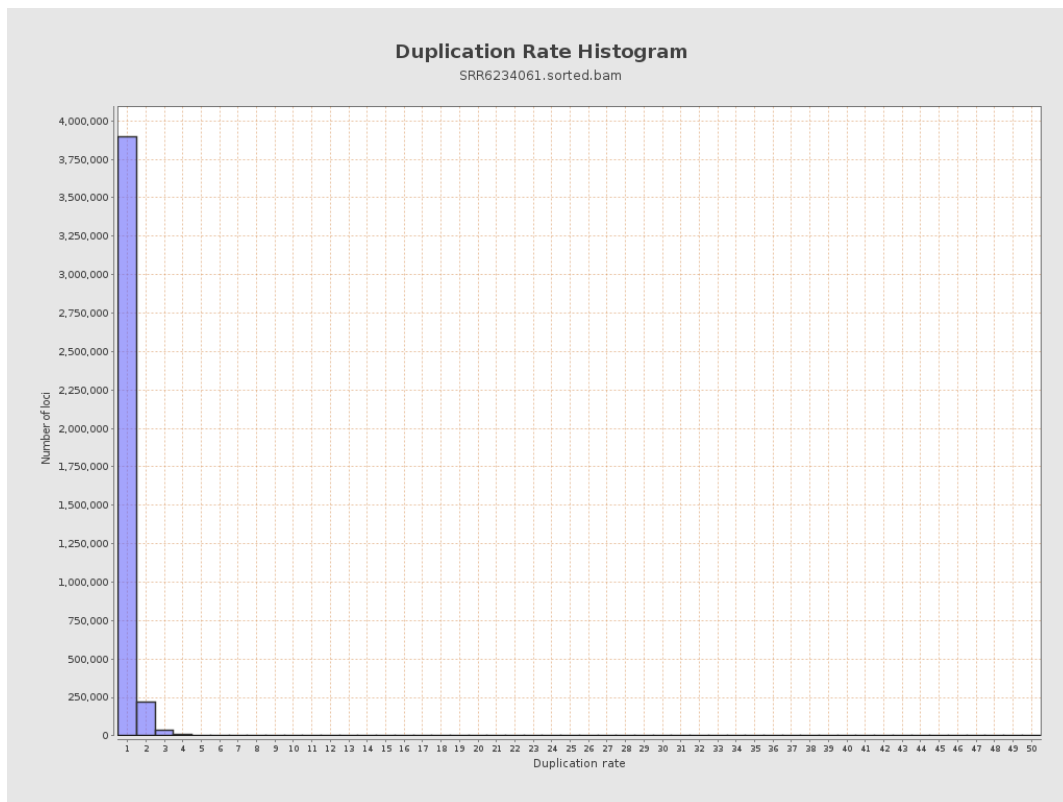
5. Results : Coverage Histogram (0-50X)



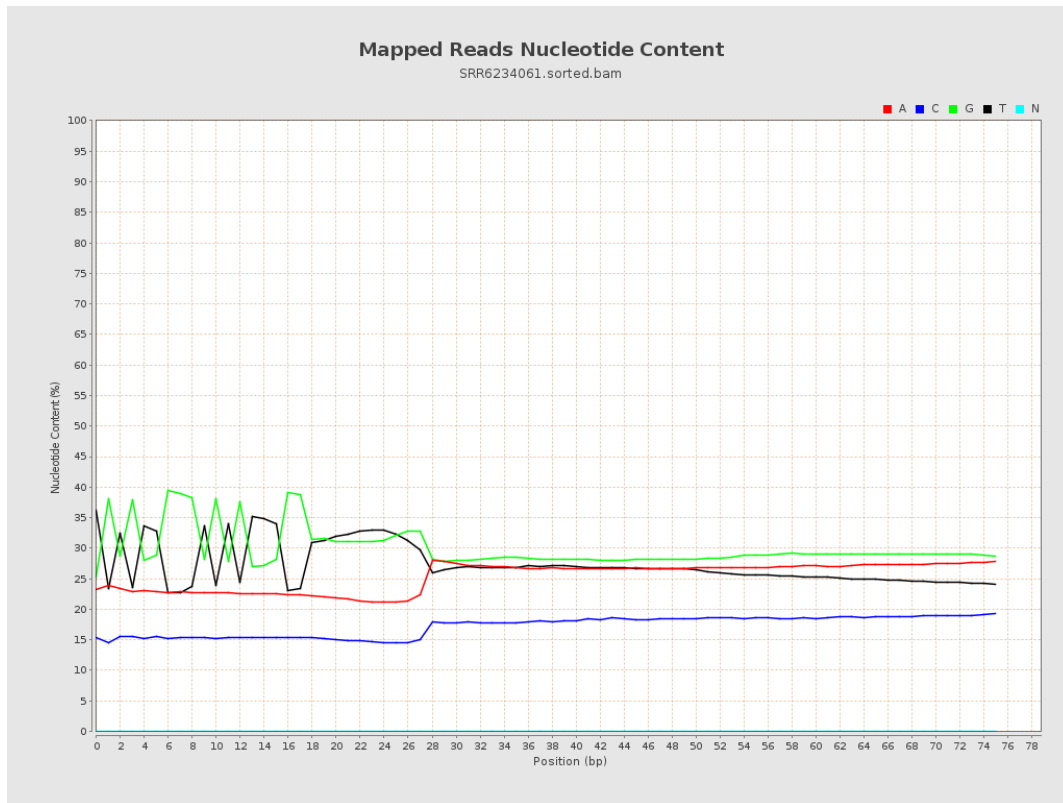
6. Results : Genome Fraction Coverage



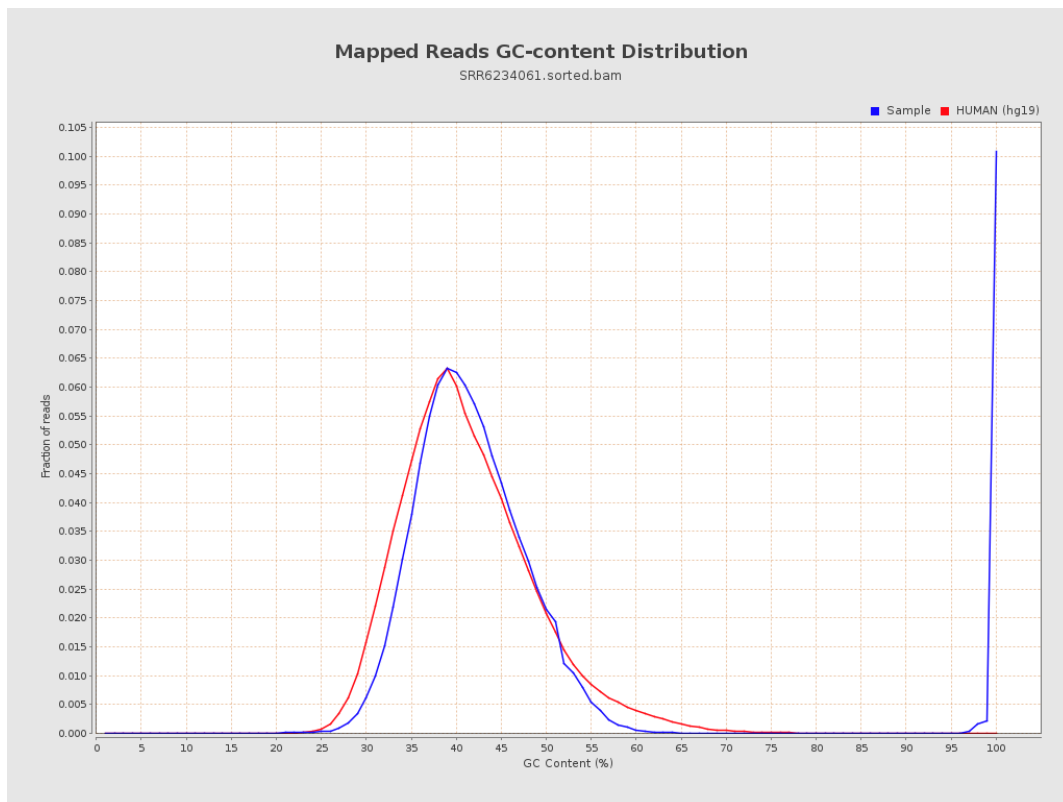
7. Results : Duplication Rate Histogram



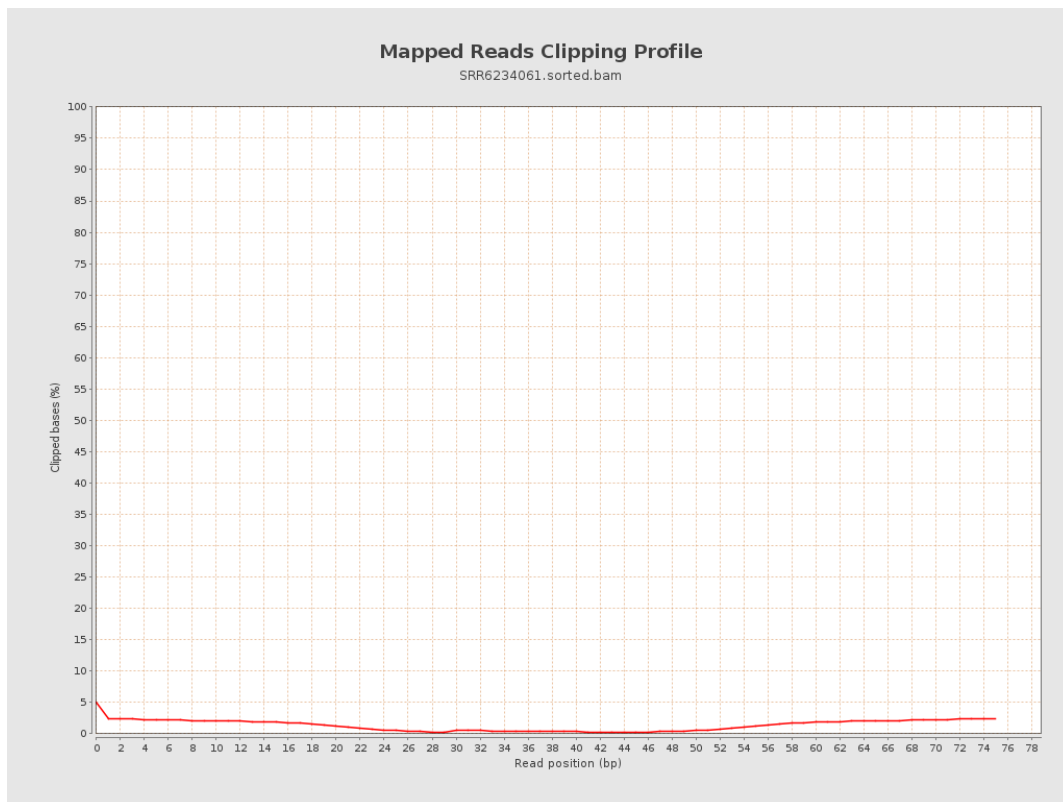
8. Results : Mapped Reads Nucleotide Content



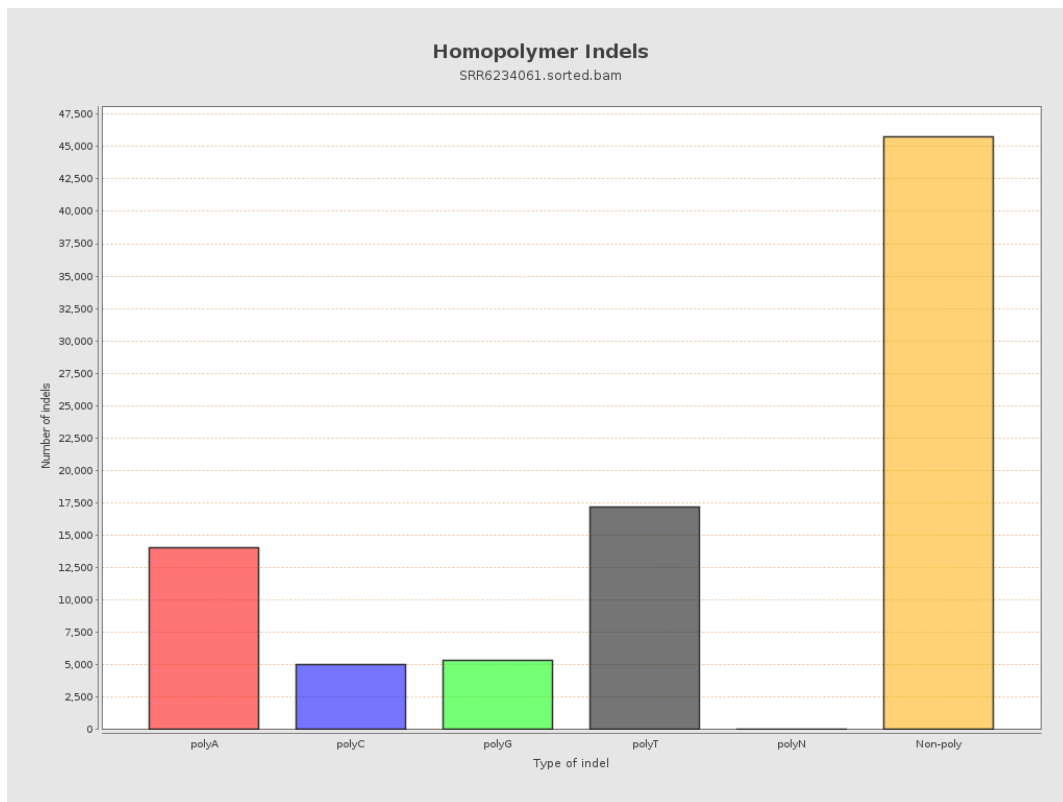
9. Results : Mapped Reads GC-content Distribution



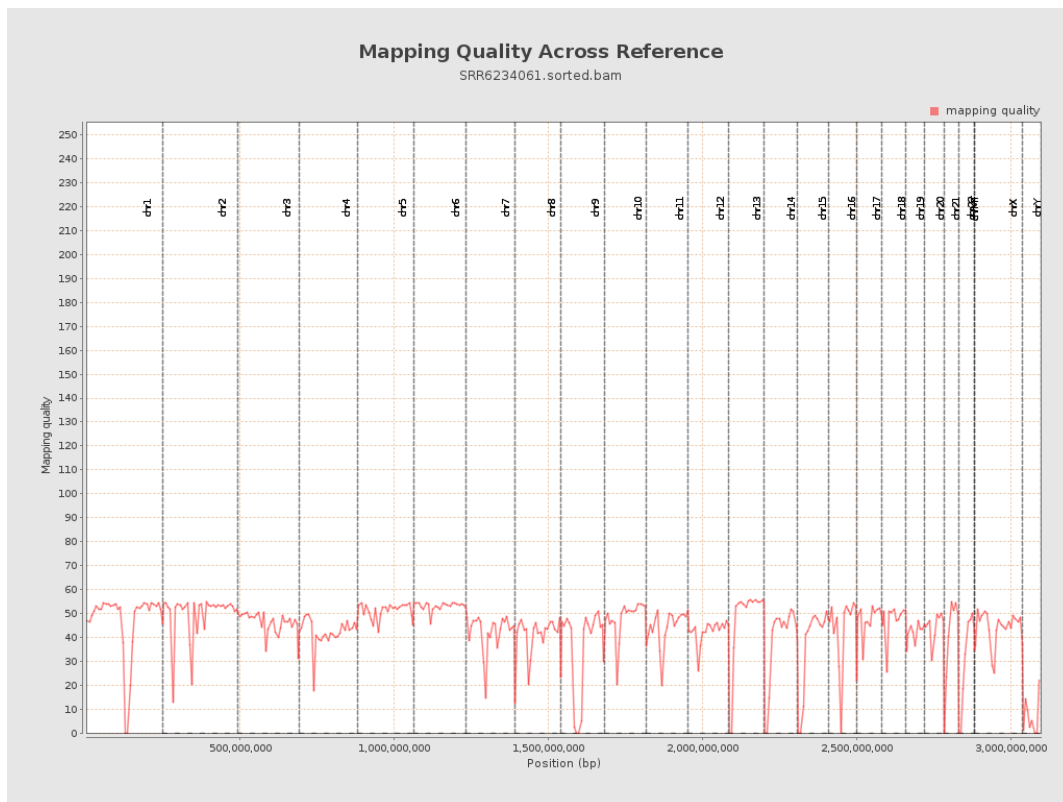
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

