

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 18:58:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6236068.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_SRR6236068 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6236068.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 18:58:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6236068.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	495,772
Mapped reads	426,320 / 85.99%
Unmapped reads	69,452 / 14.01%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,230 / 0.65%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	12,889 / 2.6%
Duplication rate	2.53%
Clipped reads	200,232 / 40.39%

2.2. ACGT Content

Number/percentage of A's	7,751,059 / 27.59%
Number/percentage of C's	5,020,703 / 17.87%
Number/percentage of T's	9,063,960 / 32.27%
Number/percentage of G's	6,239,397 / 22.21%
Number/percentage of N's	14,262 / 0.05%
GC Percentage	40.09%

2.3. Coverage

Mean	0.0091

Standard Deviation	0.1264
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2.4. Mapping Quality

Mean Mapping Quality	45.83
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2.5. Mismatches and indels

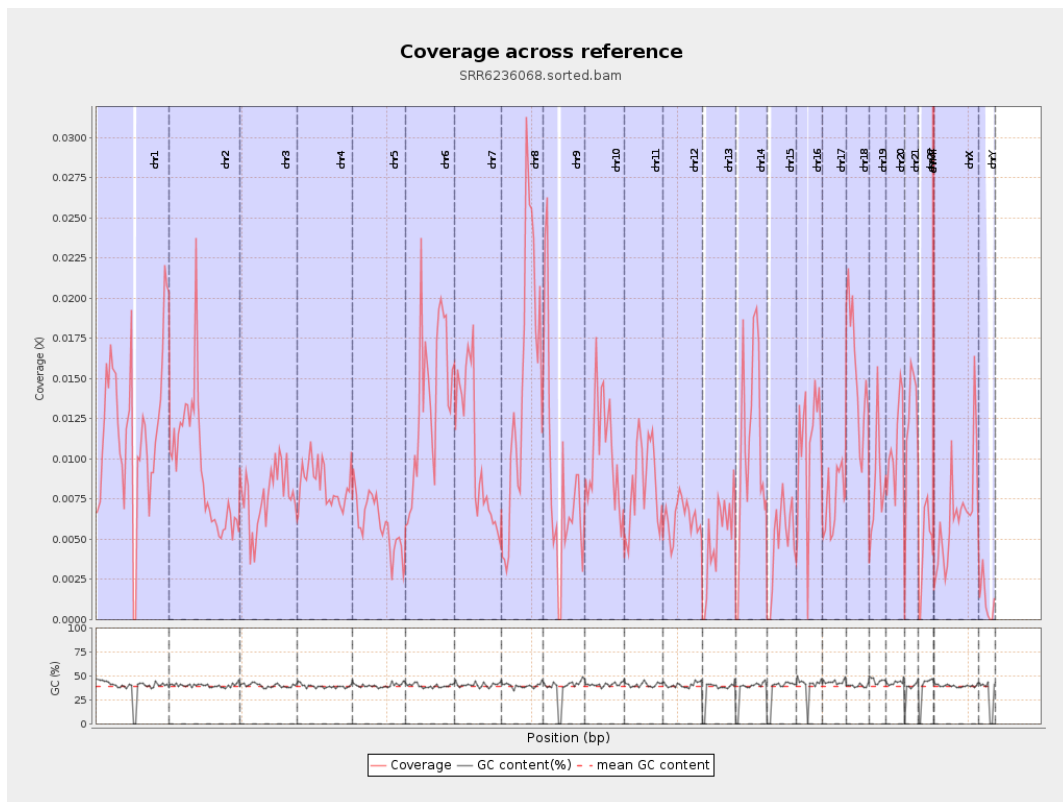
General error rate	0.84%
Mismatches	233,004
Insertions	2,007
Mapped reads with at least one insertion	0.47%
Deletions	7,607
Mapped reads with at least one deletion	1.76%
Homopolymer indels	46.75%

2.6. Chromosome stats

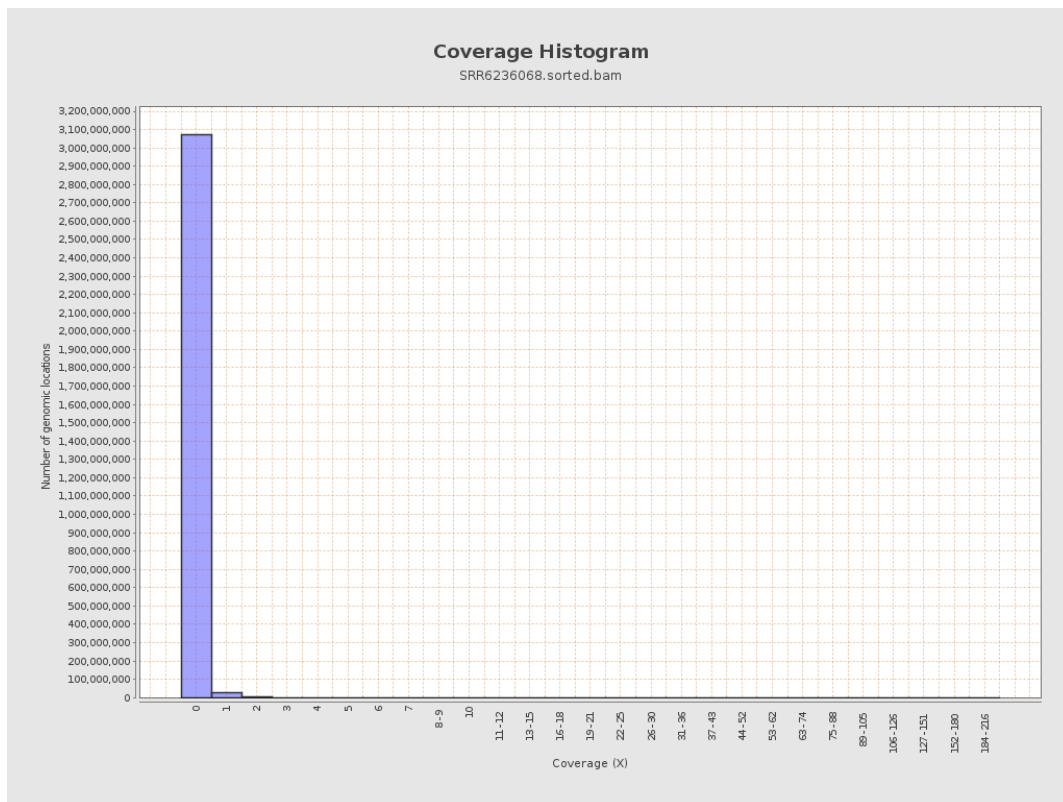
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	2932516	0.0118	0.1939
chr2	243199373	2249756	0.0093	0.1406
chr3	198022430	1527386	0.0077	0.0928
chr4	191154276	1616431	0.0085	0.0979
chr5	180915260	1072371	0.0059	0.082
chr6	171115067	2314682	0.0135	0.1461
chr7	159138663	1648670	0.0104	0.1479

chr8	146364022	2079977	0.0142	0.1904
chr9	141213431	1170695	0.0083	0.1156
chr10	135534747	1408896	0.0104	0.1195
chr11	135006516	1132213	0.0084	0.1156
chr12	133851895	848640	0.0063	0.0844
chr13	115169878	583196	0.0051	0.0752
chr14	107349540	1141594	0.0106	0.1101
chr15	102531392	493640	0.0048	0.0736
chr16	90354753	1000247	0.0111	0.1128
chr17	81195210	592828	0.0073	0.0957
chr18	78077248	1197300	0.0153	0.1852
chr19	59128983	506025	0.0086	0.1537
chr20	63025520	682482	0.0108	0.1102
chr21	48129895	582939	0.0121	0.1176
chr22	51304566	231253	0.0045	0.0704
chrMT	16571	12062	0.7279	0.9044
chrX	155270560	1008757	0.0065	0.0885
chrY	59373566	68327	0.0012	0.0399

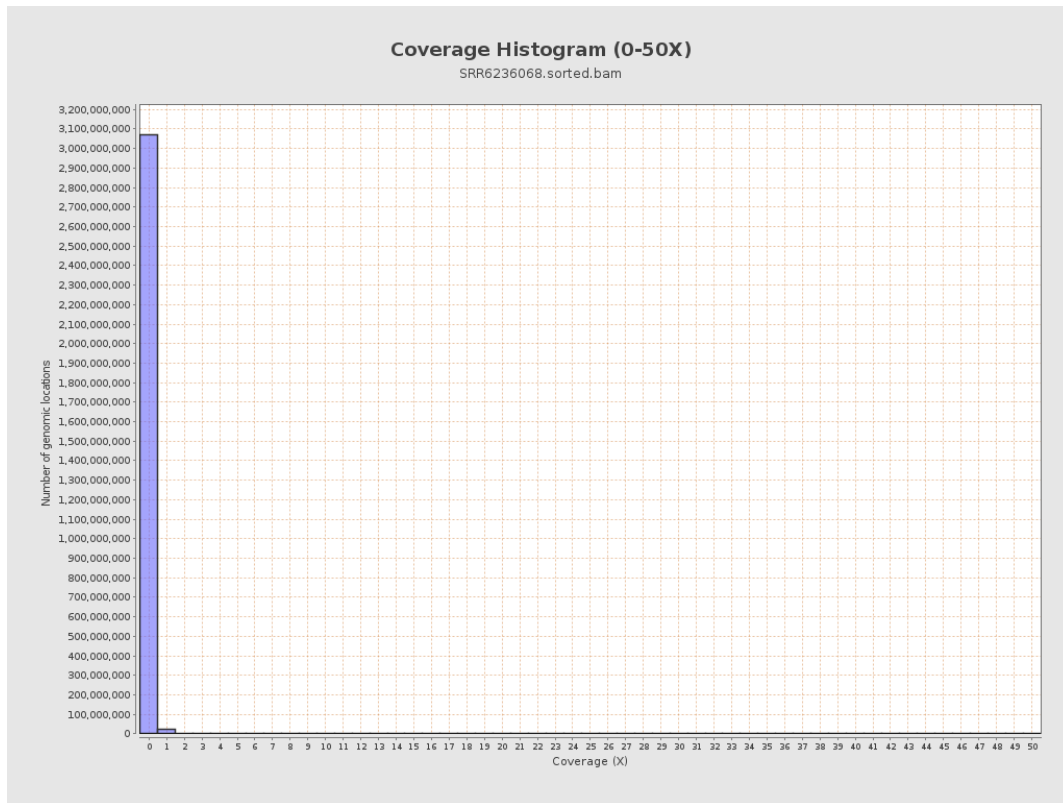
3. Results : Coverage across reference



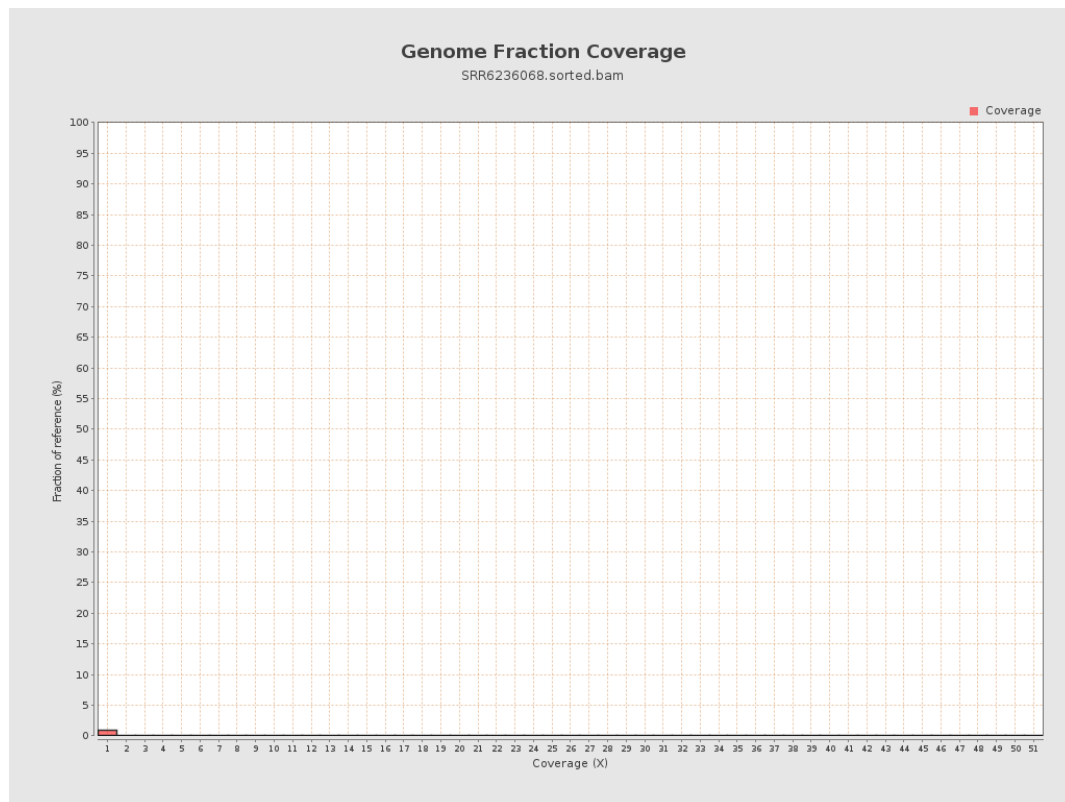
4. Results : Coverage Histogram



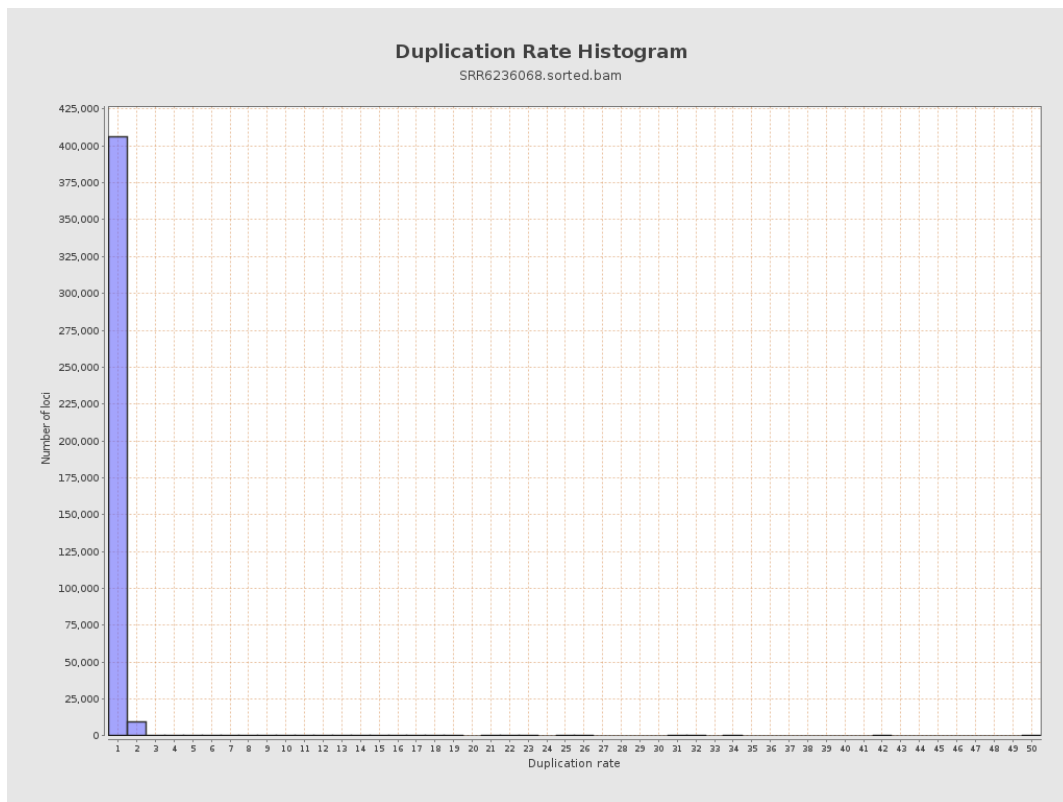
5. Results : Coverage Histogram (0-50X)



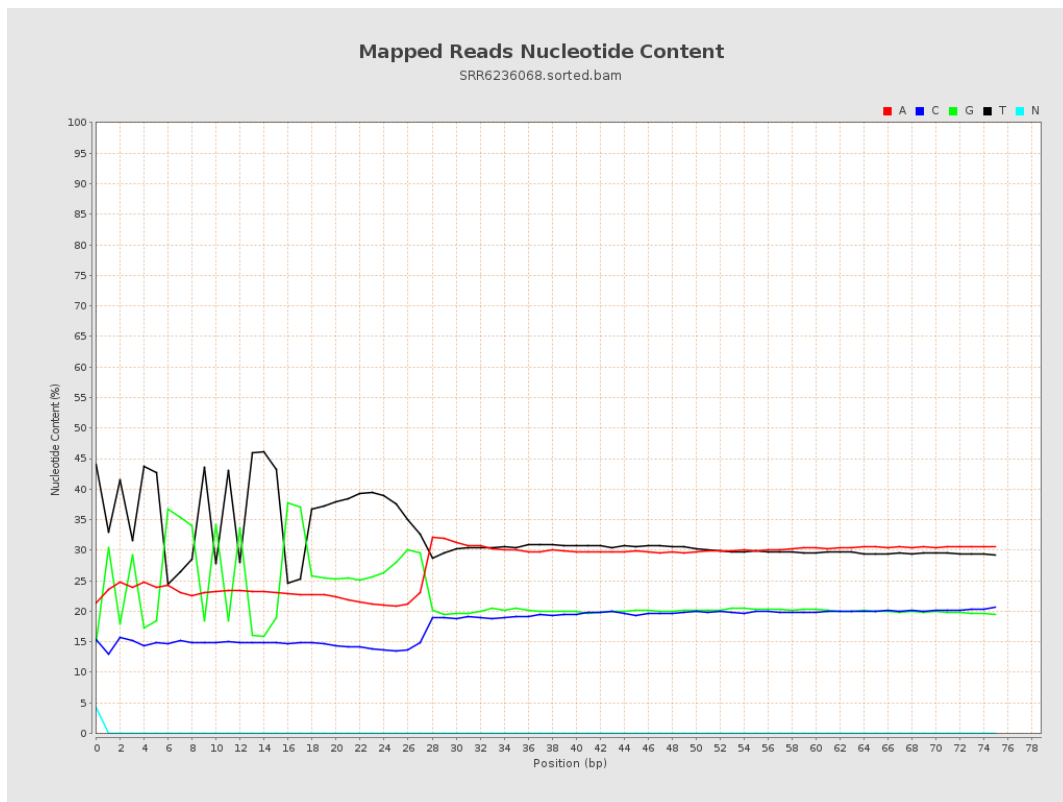
6. Results : Genome Fraction Coverage



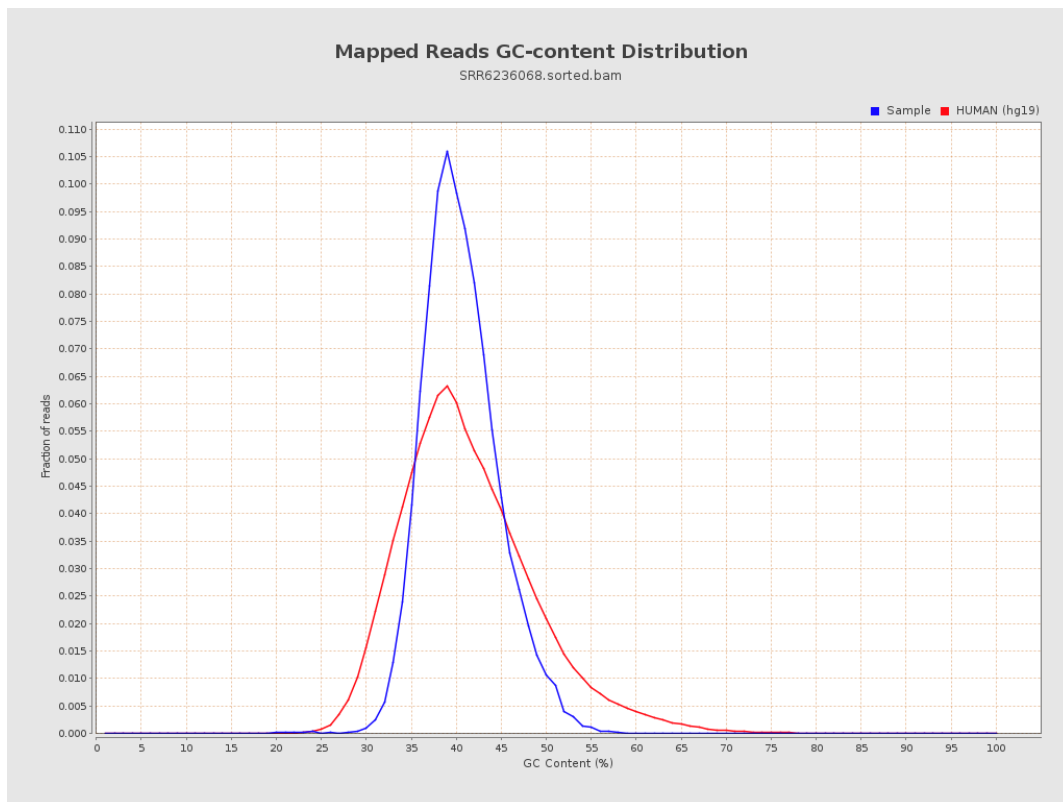
7. Results : Duplication Rate Histogram



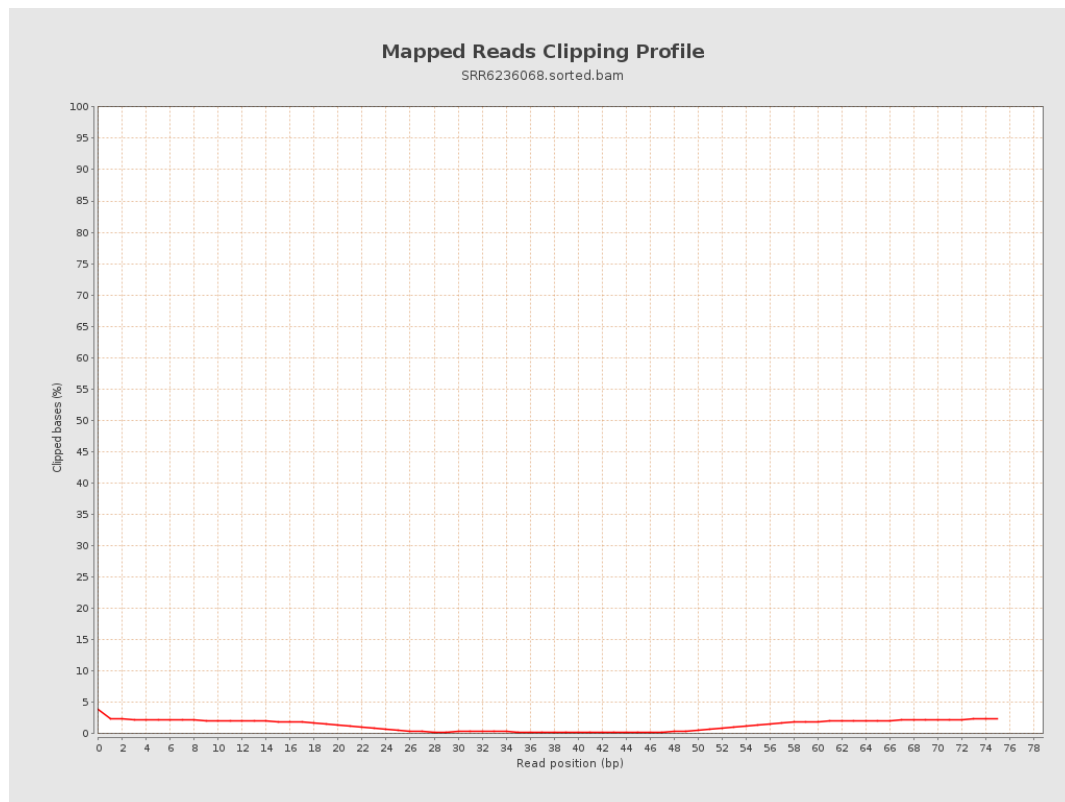
8. Results : Mapped Reads Nucleotide Content



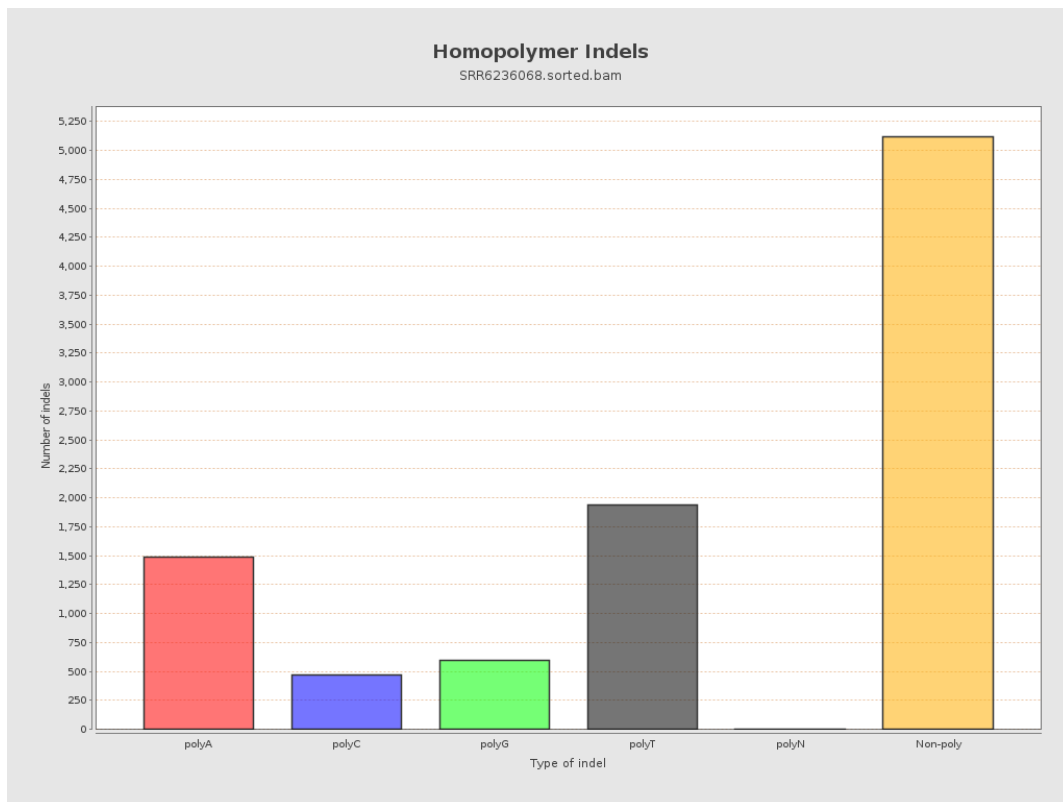
9. Results : Mapped Reads GC-content Distribution



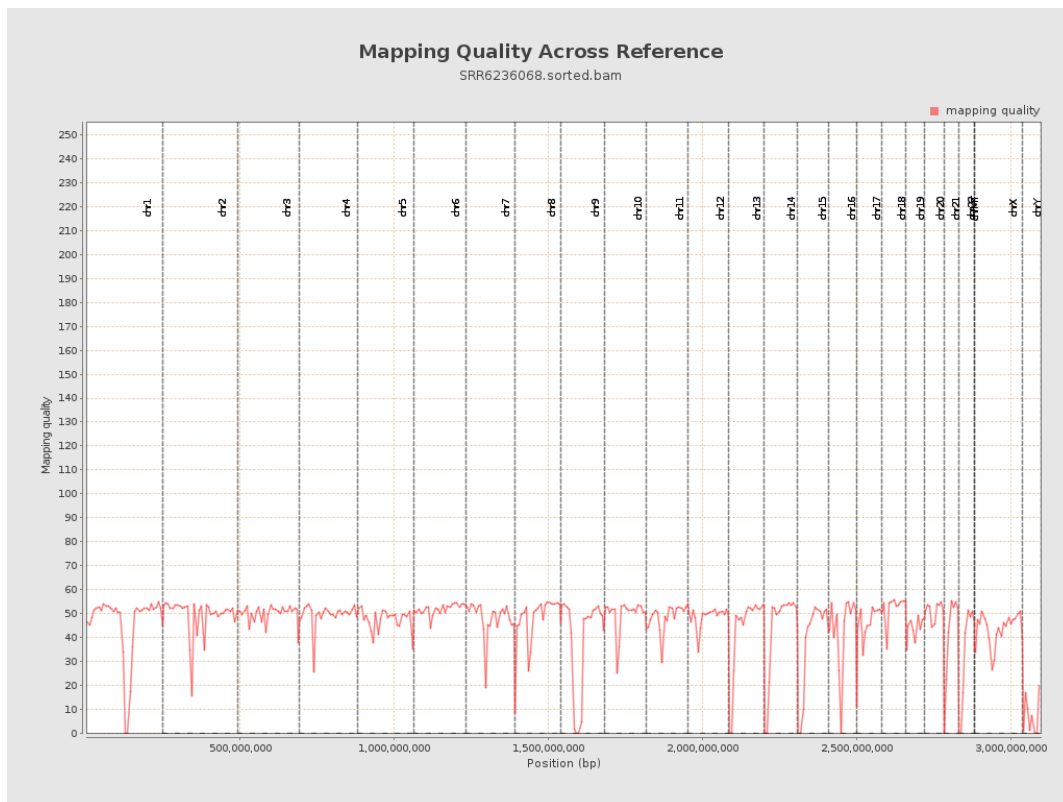
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

