

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 10:41:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008769.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_SRR6008769 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008769.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 10:41:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008769.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,542
Mapped reads	4,306 / 40.85%
Unmapped reads	6,236 / 59.15%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	30 / 0.28%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	70 / 0.66%
Duplication rate	1.01%
Clipped reads	2,348 / 22.27%

2.2. ACGT Content

Number/percentage of A's	75,998 / 27.48%
Number/percentage of C's	49,912 / 18.05%
Number/percentage of T's	86,935 / 31.44%
Number/percentage of G's	63,631 / 23.01%
Number/percentage of N's	49 / 0.02%
GC Percentage	41.06%

2.3. Coverage

Mean	0.0001

Standard Deviation	0.0099
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2.4. Mapping Quality

Mean Mapping Quality	44.87
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2.5. Mismatches and indels

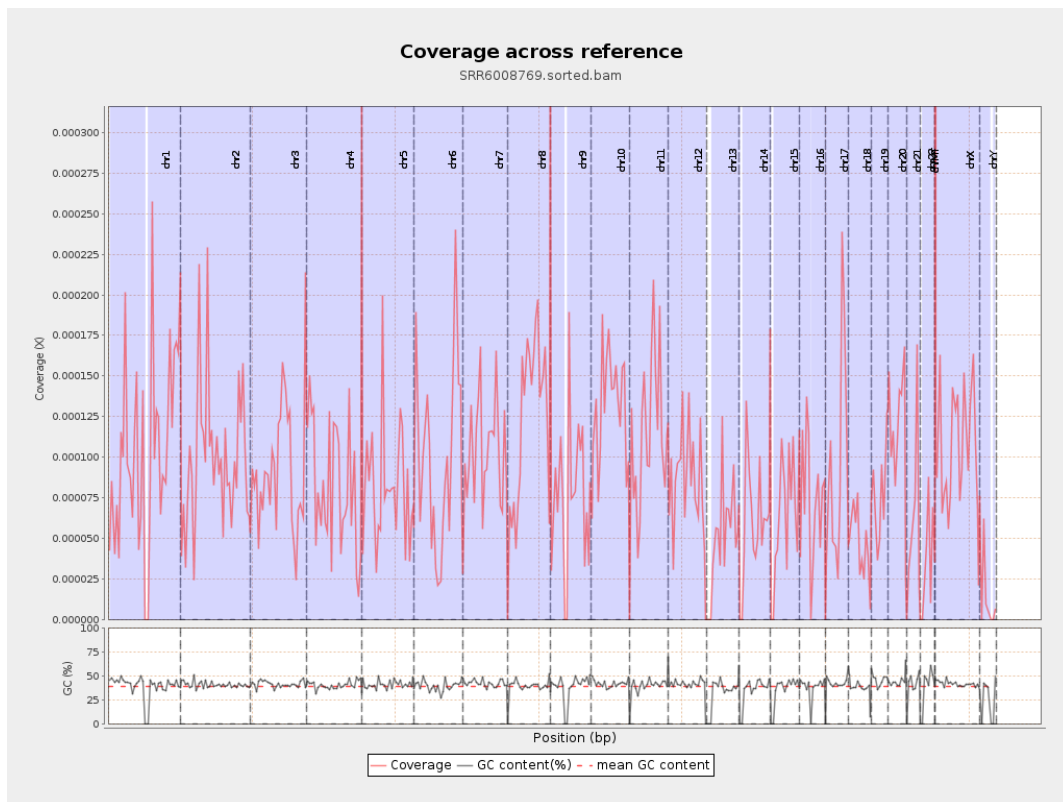
General error rate	0.91%
Mismatches	2,477
Insertions	23
Mapped reads with at least one insertion	0.53%
Deletions	93
Mapped reads with at least one deletion	2.11%
Homopolymer indels	46.55%

2.6. Chromosome stats

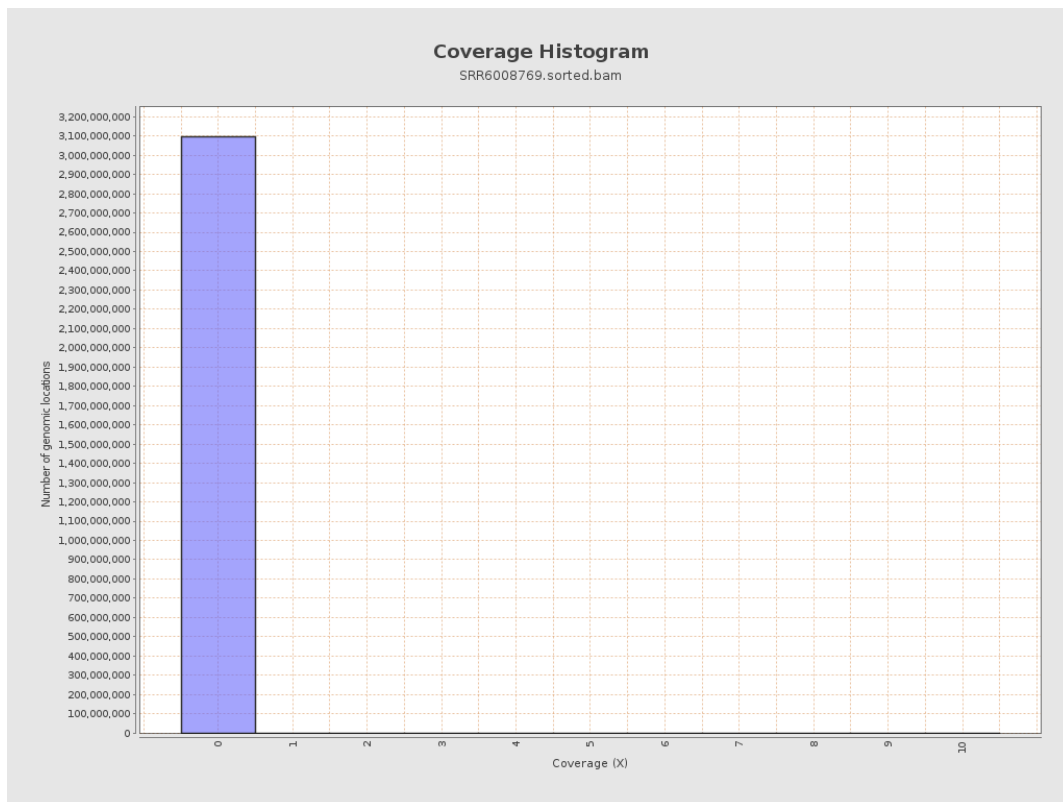
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	25971	0.0001	0.0103
chr2	243199373	24135	0.0001	0.0106
chr3	198022430	18204	0.0001	0.0097
chr4	191154276	15494	0.0001	0.0096
chr5	180915260	14829	0.0001	0.0101
chr6	171115067	17050	0.0001	0.0117
chr7	159138663	16405	0.0001	0.0106

chr8	146364022	18234	0.0001	0.0112
chr9	141213431	10752	0.0001	0.0093
chr10	135534747	17667	0.0001	0.0115
chr11	135006516	15560	0.0001	0.0107
chr12	133851895	11386	0.0001	0.0093
chr13	115169878	5731	0	0.0071
chr14	107349540	6380	0.0001	0.0077
chr15	102531392	6384	0.0001	0.0081
chr16	90354753	6640	0.0001	0.0089
chr17	81195210	7800	0.0001	0.0099
chr18	78077248	3687	0	0.0069
chr19	59128983	4539	0.0001	0.0093
chr20	63025520	7554	0.0001	0.011
chr21	48129895	3018	0.0001	0.0079
chr22	51304566	1892	0	0.0062
chrMT	16571	52	0.0031	0.0559
chrX	155270560	16280	0.0001	0.0107
chrY	59373566	1039	0	0.0059

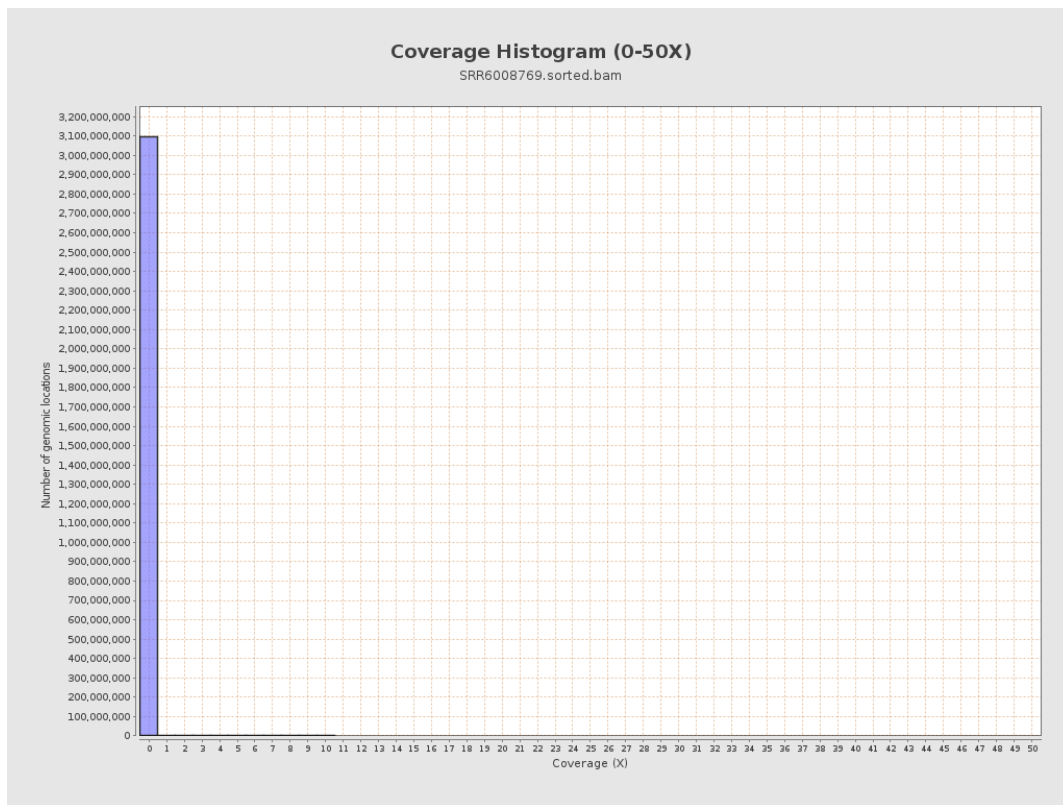
3. Results : Coverage across reference



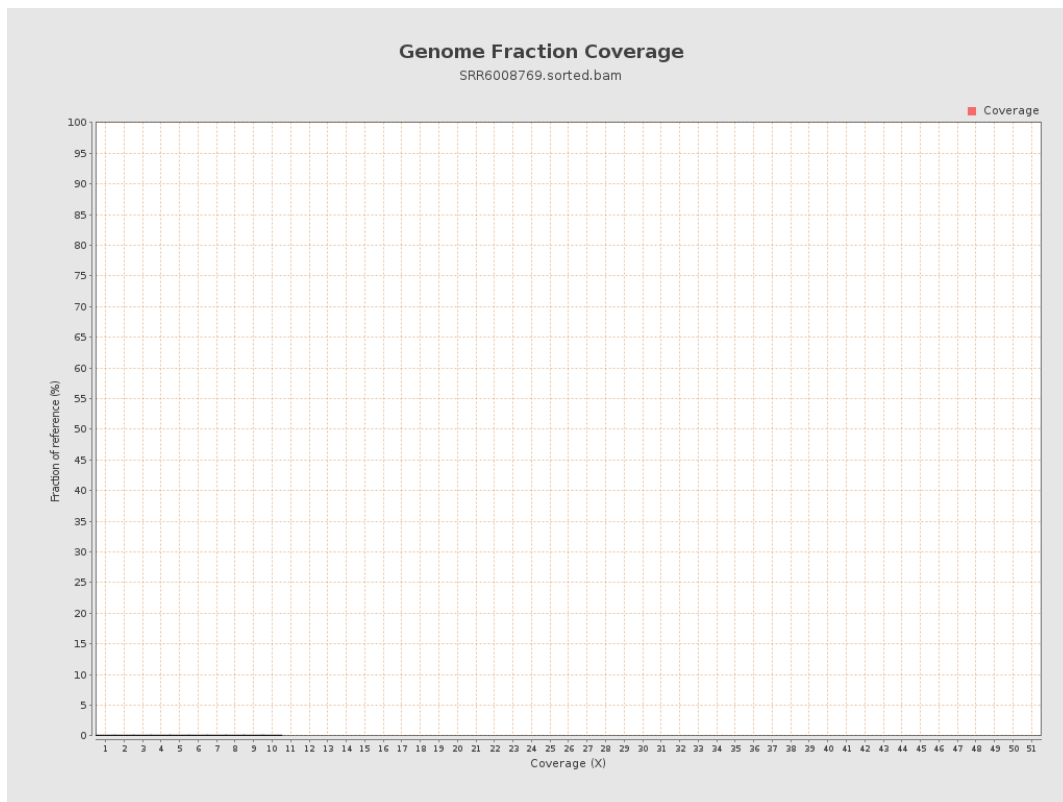
4. Results : Coverage Histogram



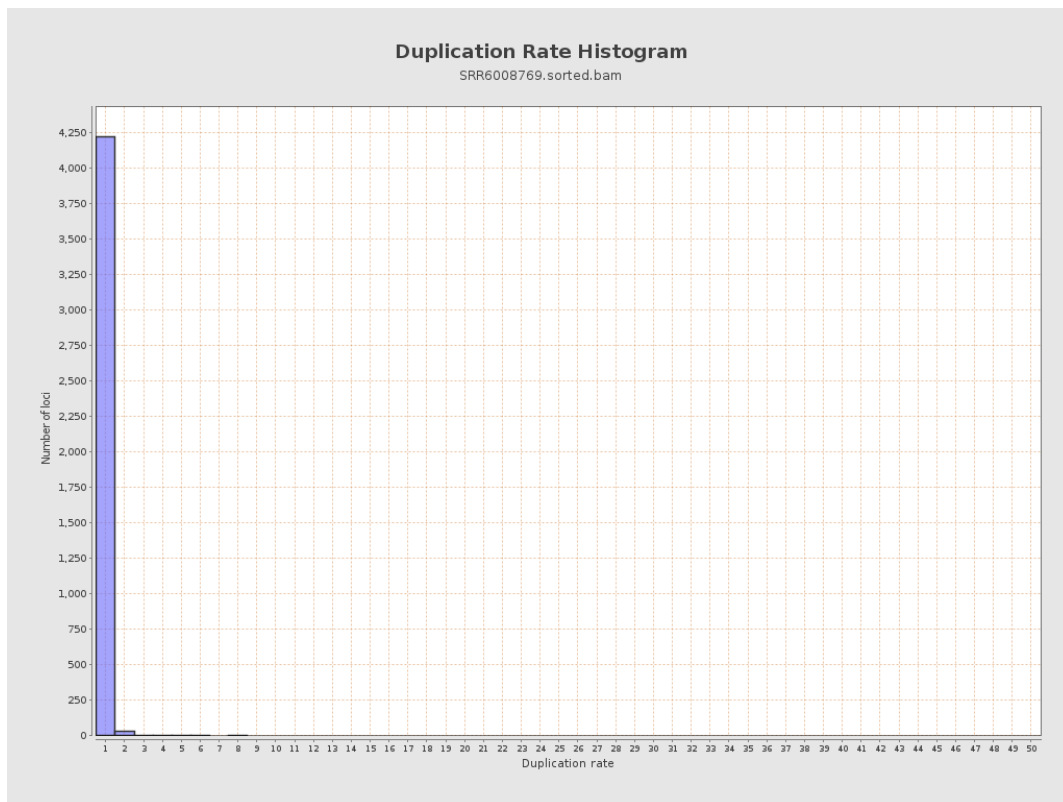
5. Results : Coverage Histogram (0-50X)



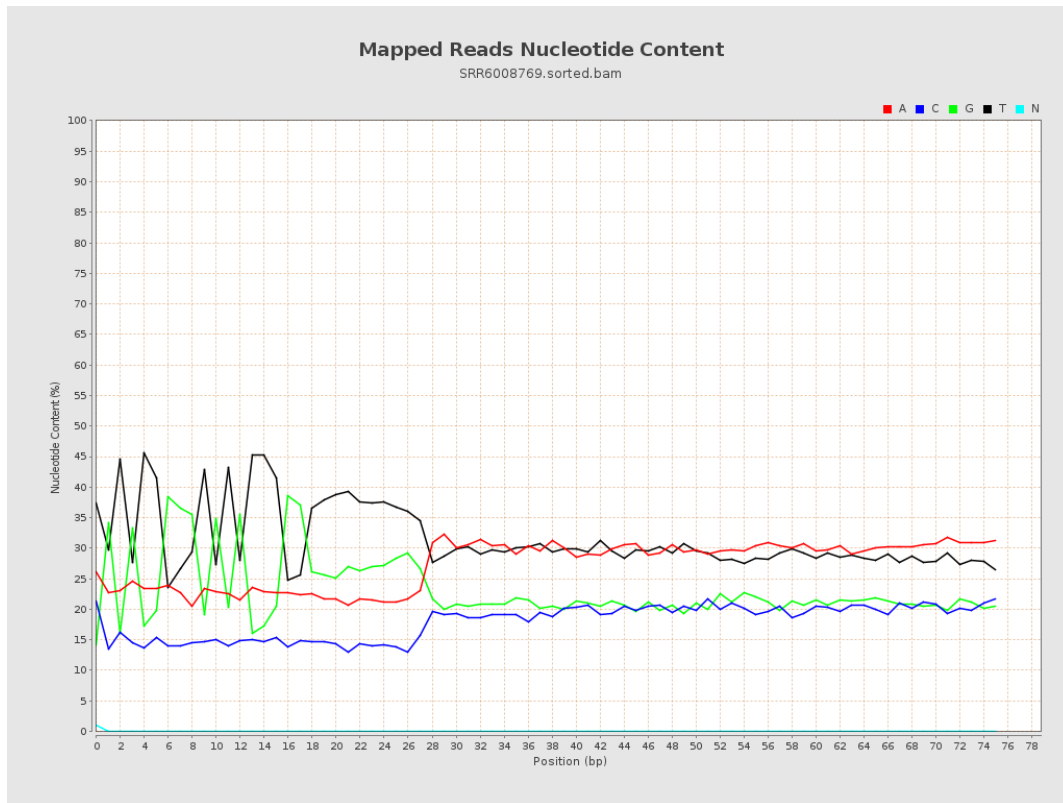
6. Results : Genome Fraction Coverage



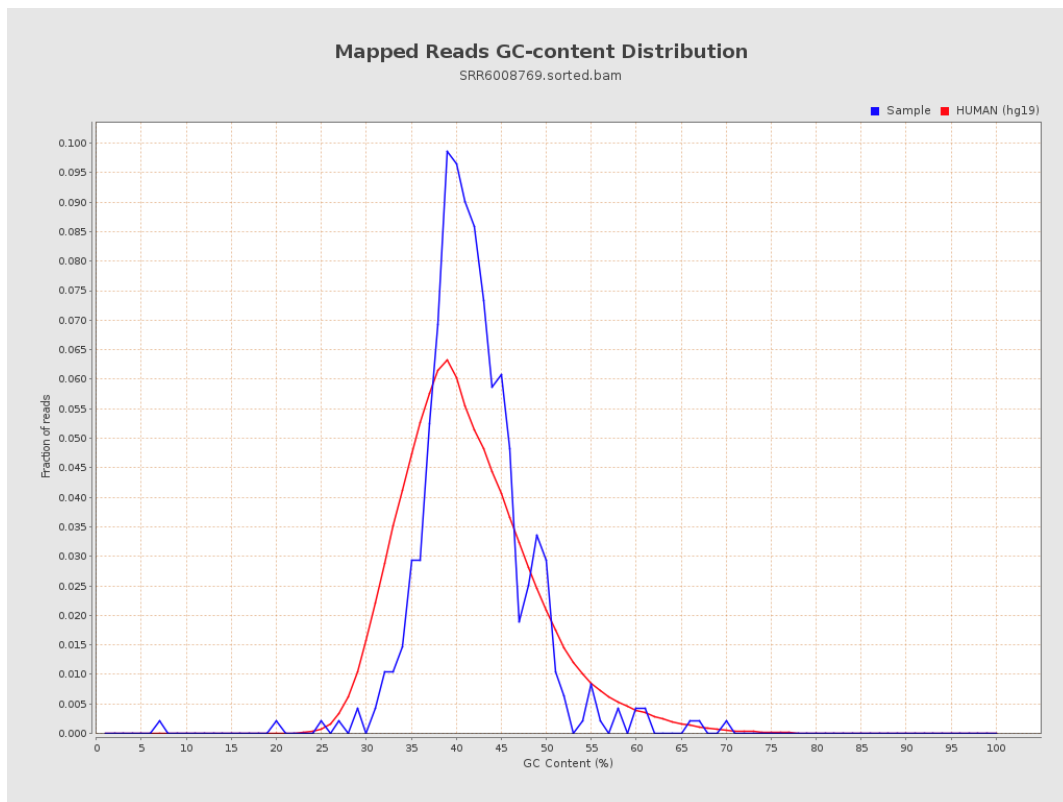
7. Results : Duplication Rate Histogram



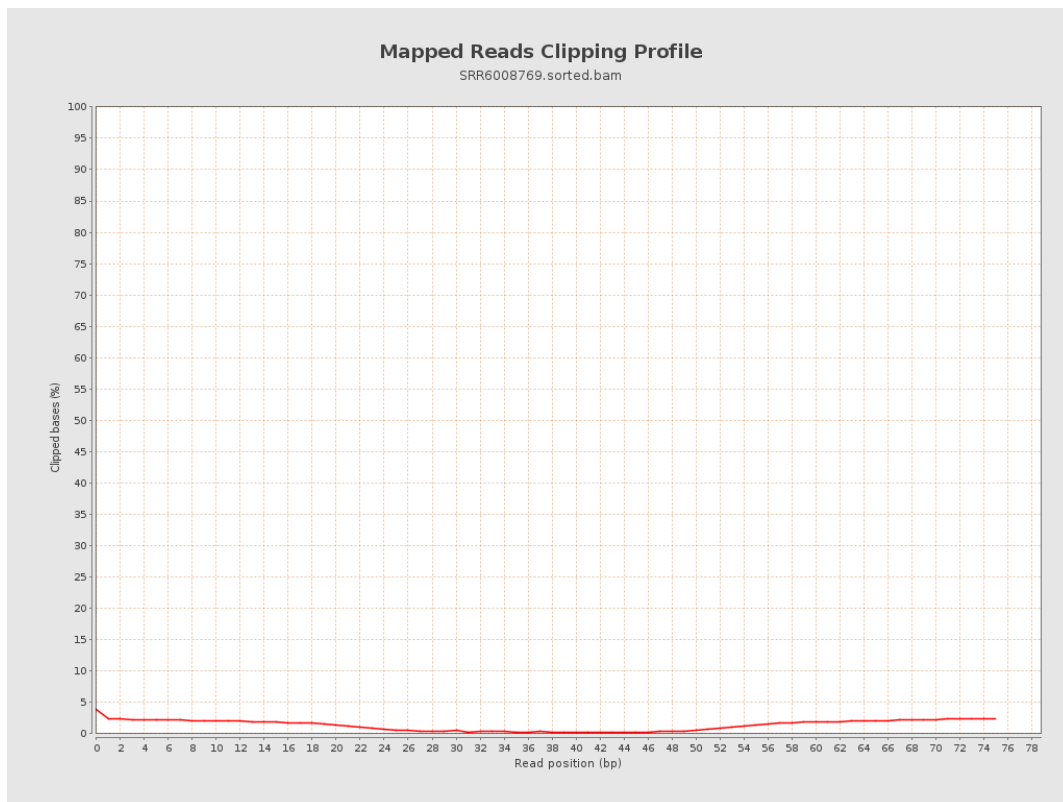
8. Results : Mapped Reads Nucleotide Content



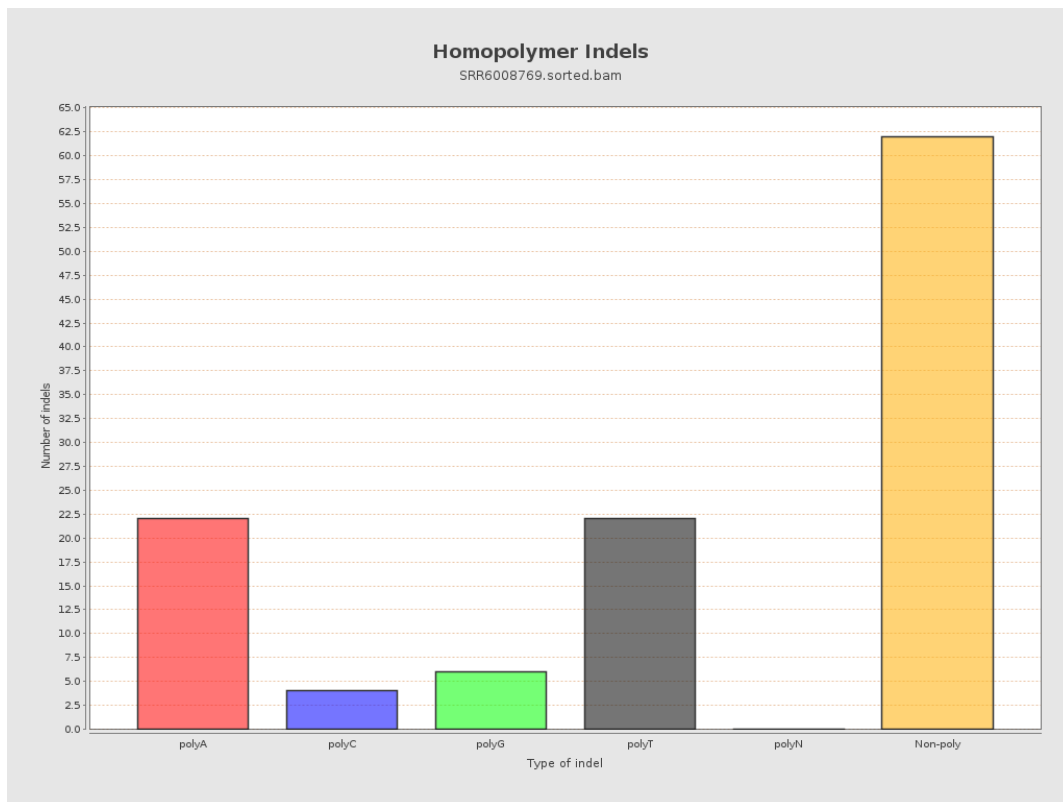
9. Results : Mapped Reads GC-content Distribution



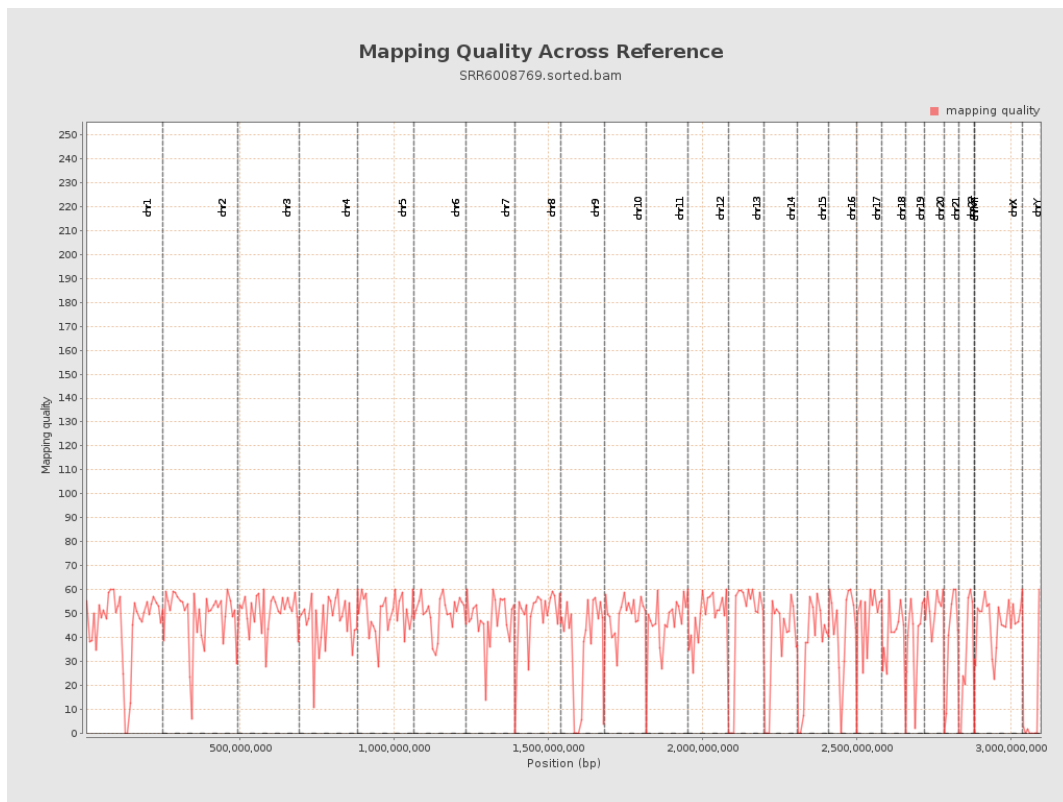
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

