

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 13:15:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068151.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_SRR6068151 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068151.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 13:15:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068151.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,075,088
Mapped reads	5,682,041 / 93.53%
Unmapped reads	393,047 / 6.47%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	54,221 / 0.89%
Read min/max/mean length	30 / 76 / 76.31
Duplicated reads (estimated)	795,029 / 13.09%
Duplication rate	11.12%
Clipped reads	2,970,764 / 48.9%

2.2. ACGT Content

Number/percentage of A's	99,216,395 / 26.95%
Number/percentage of C's	67,335,150 / 18.29%
Number/percentage of T's	118,186,310 / 32.11%
Number/percentage of G's	83,306,366 / 22.63%
Number/percentage of N's	42,942 / 0.01%
GC Percentage	40.93%

2.3. Coverage

Mean	0.119

Standard Deviation	1.1624
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2.4. Mapping Quality

Mean Mapping Quality	45.15
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2.5. Mismatches and indels

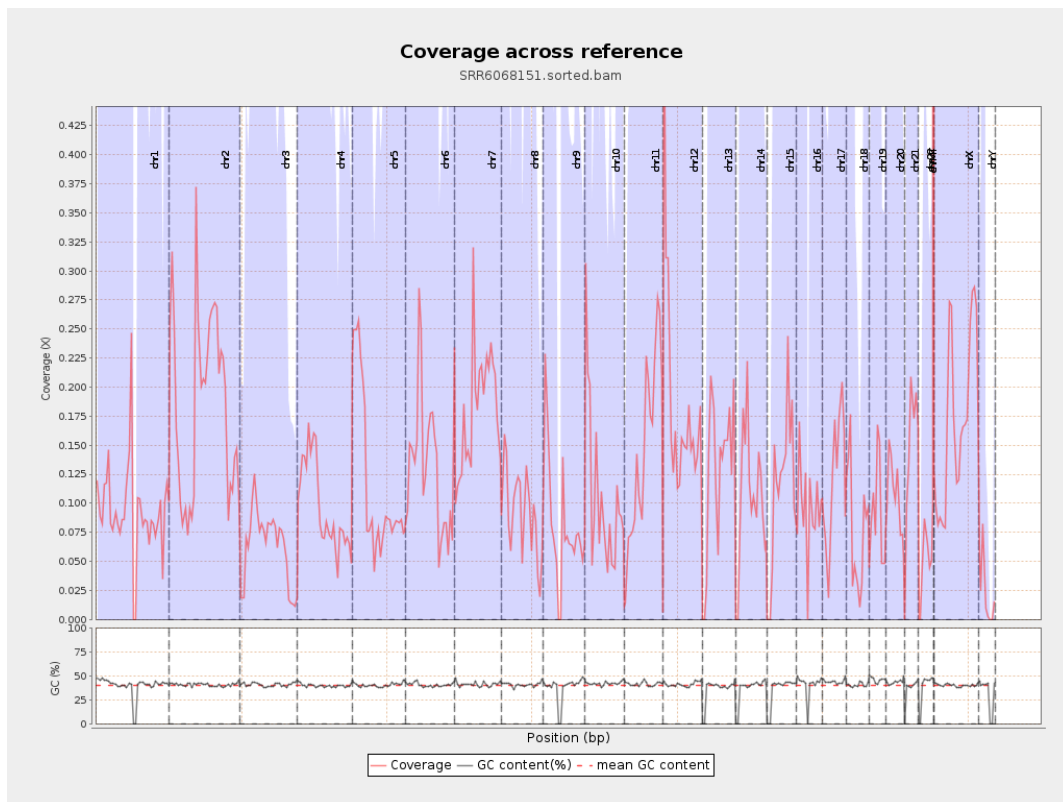
General error rate	0.59%
Mismatches	2,119,527
Insertions	24,466
Mapped reads with at least one insertion	0.43%
Deletions	84,298
Mapped reads with at least one deletion	1.47%
Homopolymer indels	44.46%

2.6. Chromosome stats

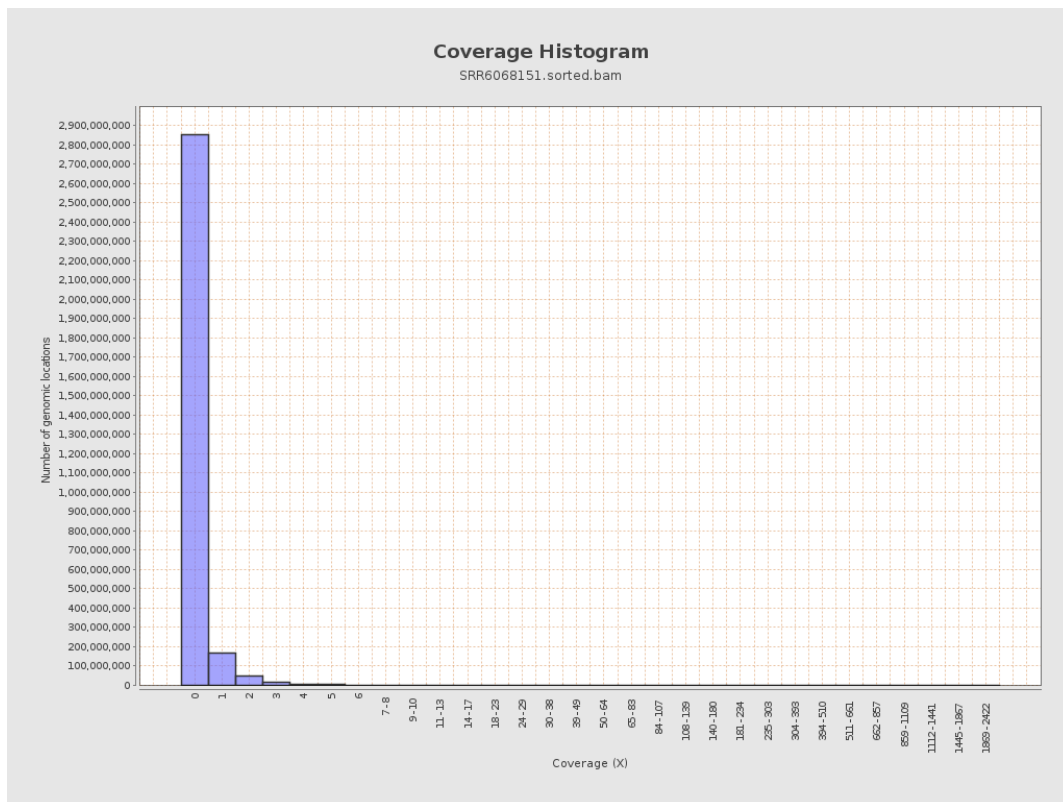
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	23067210	0.0925	2.0858
chr2	243199373	44758778	0.184	1.4683
chr3	198022430	12590239	0.0636	0.3646
chr4	191154276	18457790	0.0966	0.483
chr5	180915260	20940077	0.1157	0.503
chr6	171115067	22520456	0.1316	0.6677
chr7	159138663	29143847	0.1831	2.249

chr8	146364022	13455438	0.0919	1.3345
chr9	141213431	11635450	0.0824	1.031
chr10	135534747	14339083	0.1058	0.8951
chr11	135006516	19763208	0.1464	0.8365
chr12	133851895	24987407	0.1867	0.6522
chr13	115169878	14471133	0.1257	0.5133
chr14	107349540	11360814	0.1058	0.5512
chr15	102531392	11834173	0.1154	0.5123
chr16	90354753	8641538	0.0956	0.6016
chr17	81195210	9822777	0.121	0.5193
chr18	78077248	5986887	0.0767	2.2628
chr19	59128983	5591096	0.0946	1.5782
chr20	63025520	6832890	0.1084	0.5141
chr21	48129895	7073529	0.147	0.624
chr22	51304566	2471809	0.0482	0.2947
chrMT	16571	187785	11.3321	7.0915
chrX	155270560	26990790	0.1738	0.7357
chrY	59373566	1311910	0.0221	1.1746

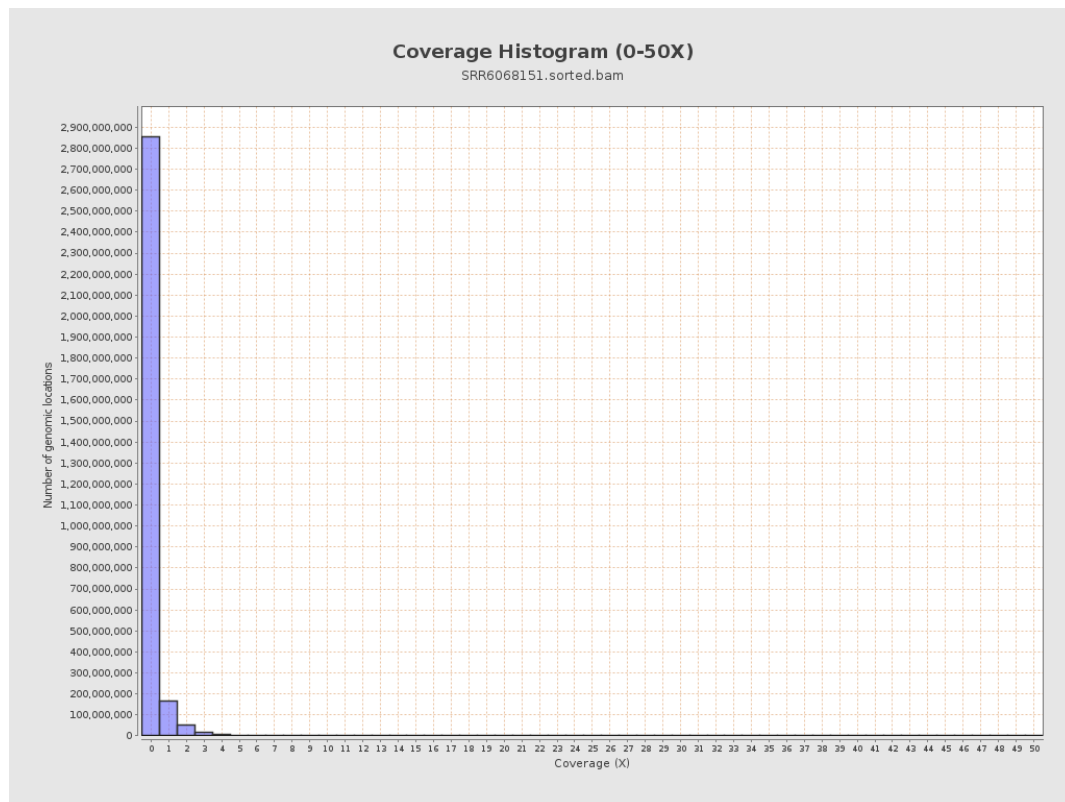
3. Results : Coverage across reference



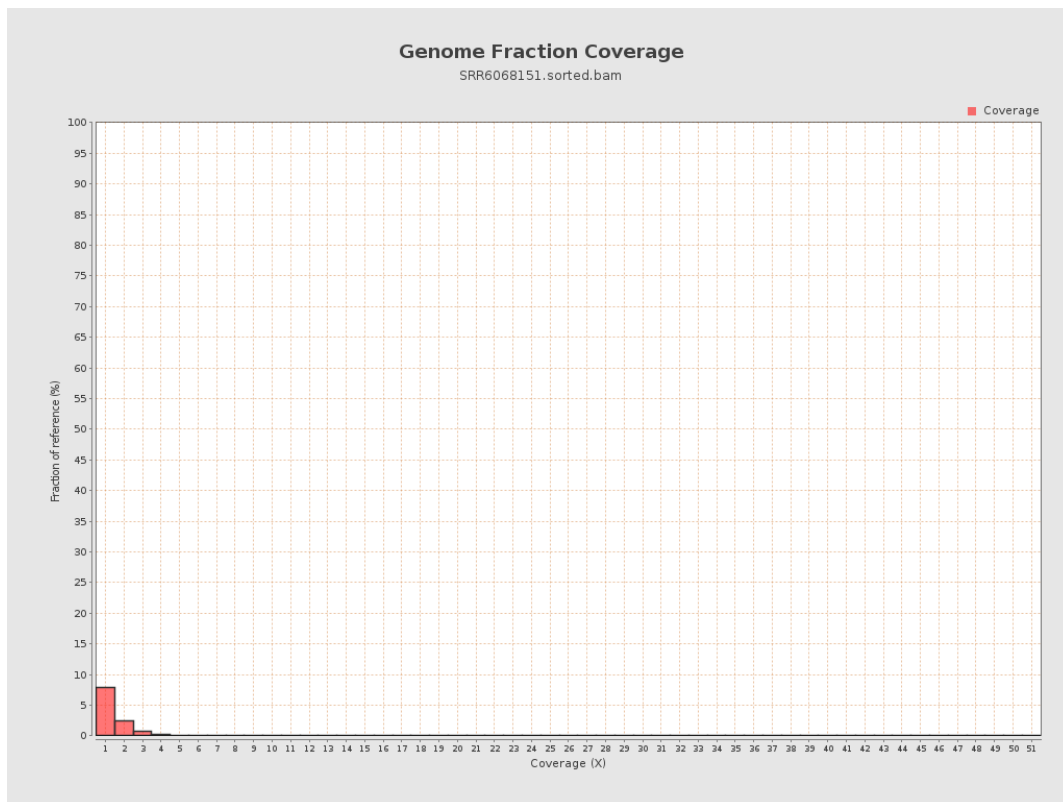
4. Results : Coverage Histogram



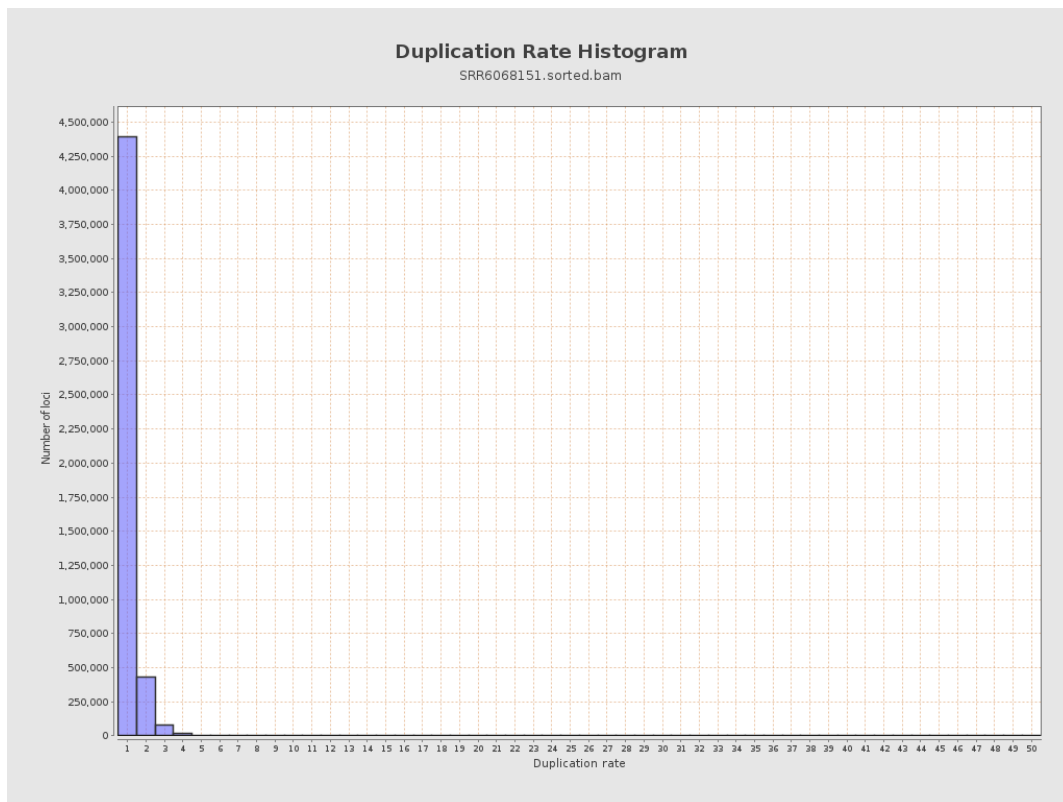
5. Results : Coverage Histogram (0-50X)



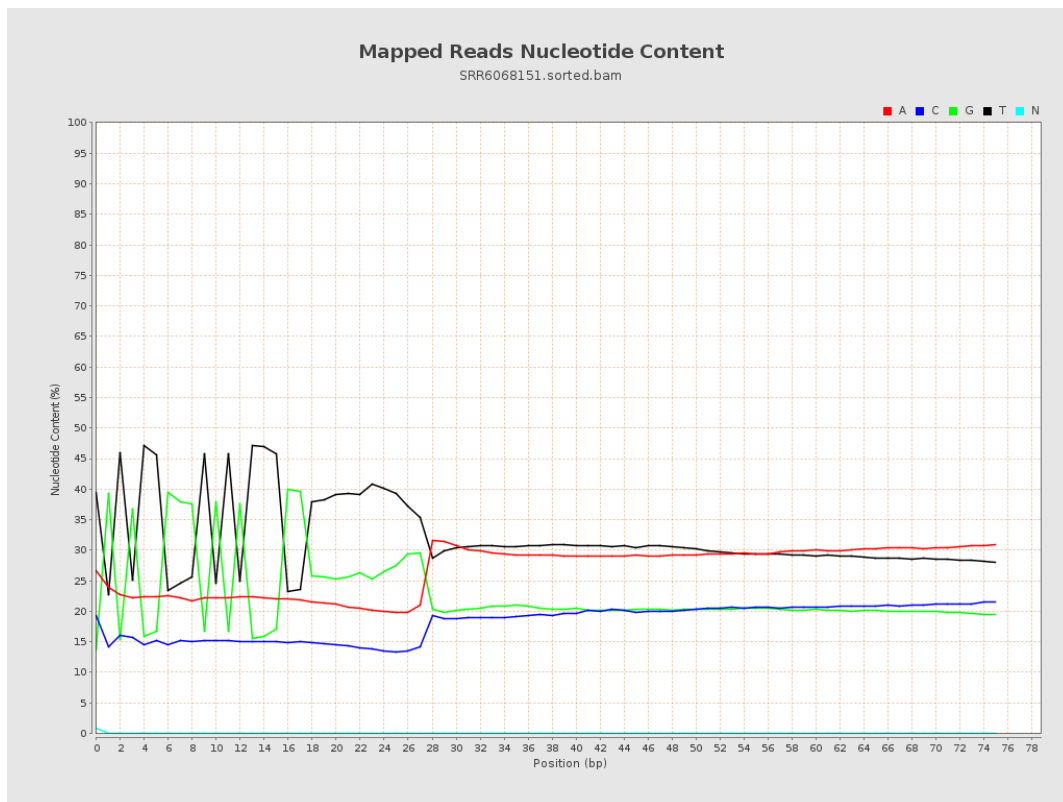
6. Results : Genome Fraction Coverage



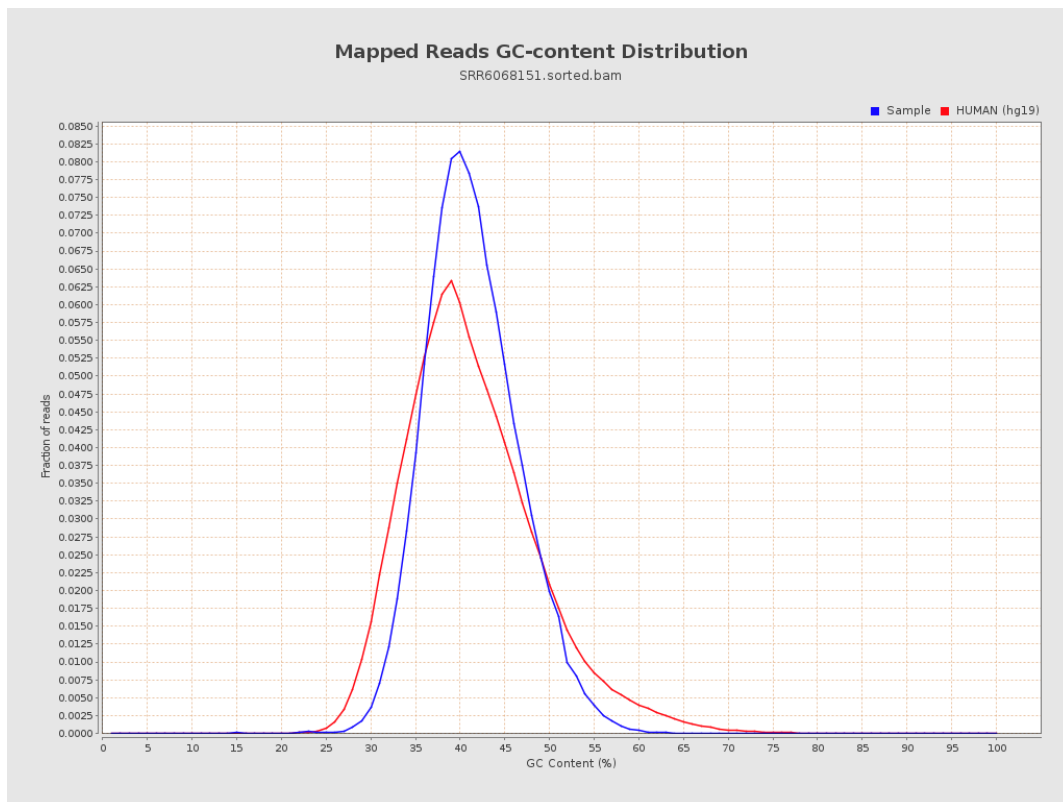
7. Results : Duplication Rate Histogram



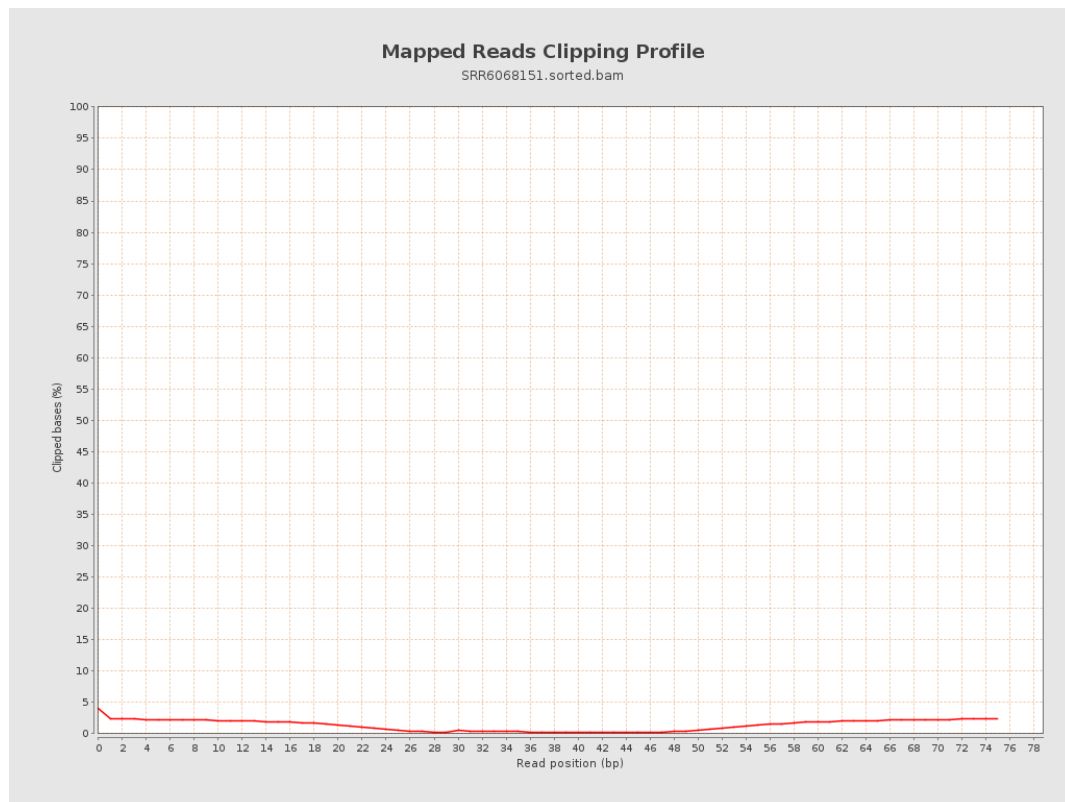
8. Results : Mapped Reads Nucleotide Content



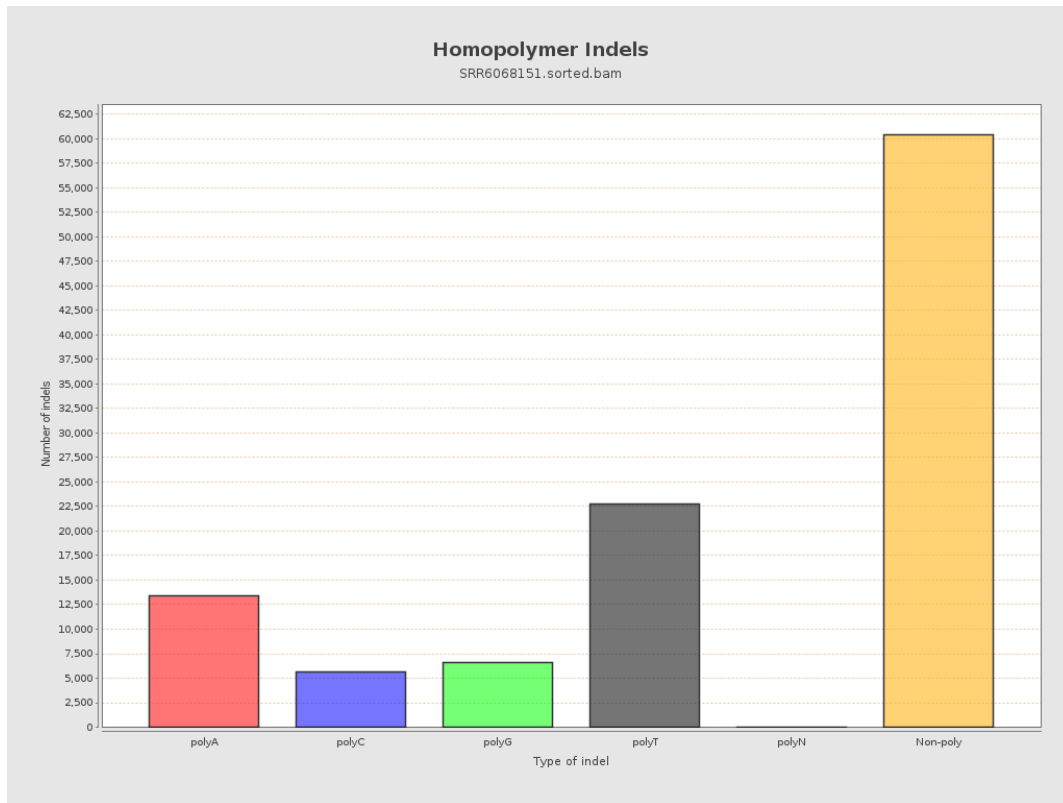
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

