

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 09:47:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008751.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_SRR6008751 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008751.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 09:47:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008751.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,353,983
Mapped reads	1,120,355 / 47.59%
Unmapped reads	1,233,628 / 52.41%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,670 / 0.92%
Read min/max/mean length	30 / 76 / 76.31
Duplicated reads (estimated)	33,237 / 1.41%
Duplication rate	2.4%
Clipped reads	613,241 / 26.05%

2.2. ACGT Content

Number/percentage of A's	23,877,228 / 32.13%
Number/percentage of C's	13,577,278 / 18.27%
Number/percentage of T's	21,216,325 / 28.55%
Number/percentage of G's	15,640,148 / 21.05%
Number/percentage of N's	5,903 / 0.01%
GC Percentage	39.31%

2.3. Coverage

Mean	0.024

Standard Deviation	0.2213
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2.4. Mapping Quality

Mean Mapping Quality	48.12
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2.5. Mismatches and indels

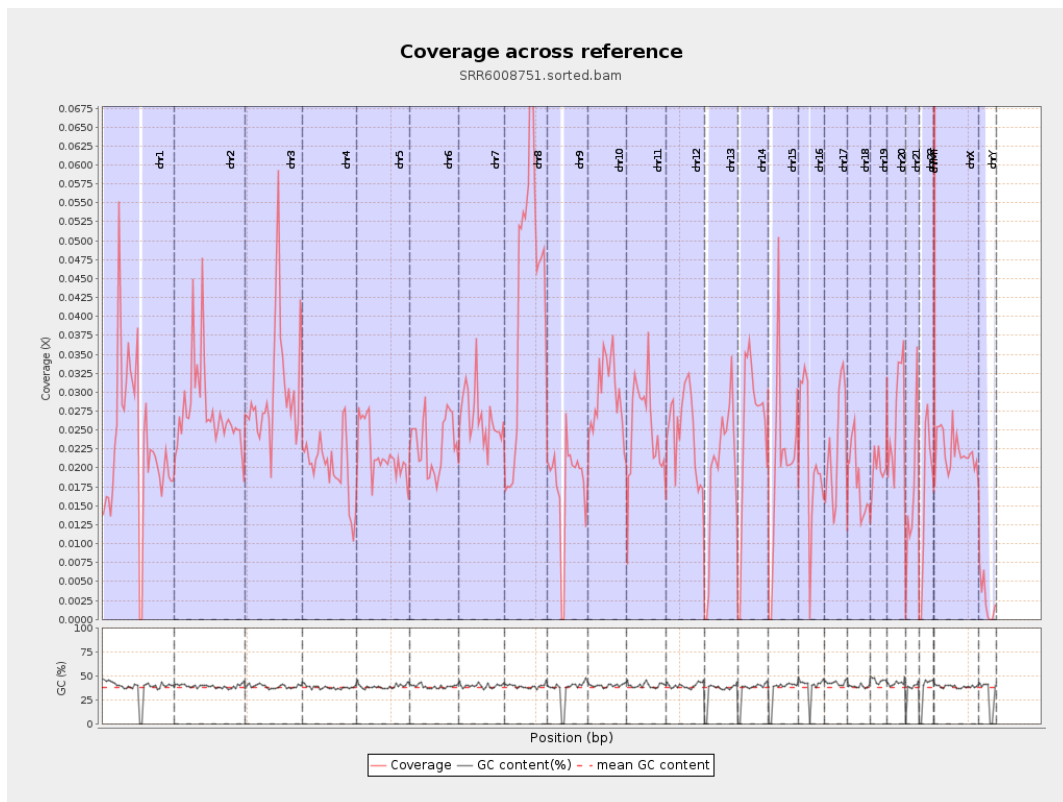
General error rate	1.07%
Mismatches	784,723
Insertions	5,842
Mapped reads with at least one insertion	0.52%
Deletions	28,991
Mapped reads with at least one deletion	2.55%
Homopolymer indels	49.59%

2.6. Chromosome stats

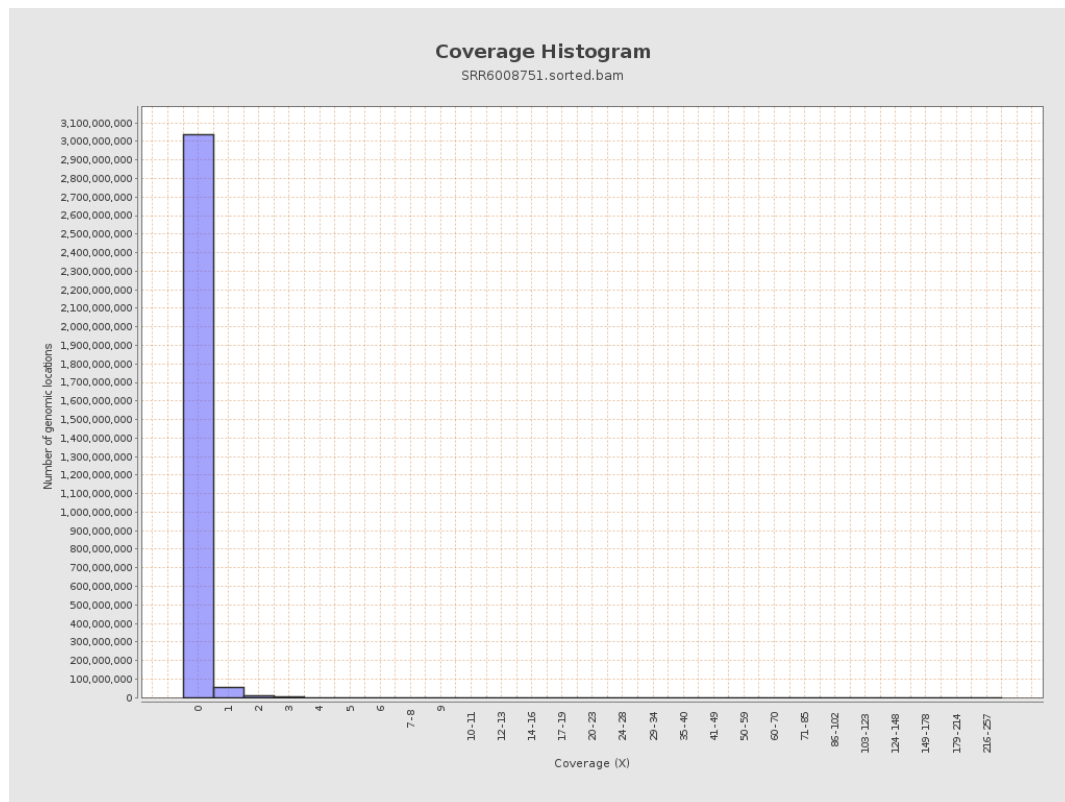
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5663301	0.0227	0.257
chr2	243199373	6705239	0.0276	0.2778
chr3	198022430	5986749	0.0302	0.2092
chr4	191154276	3838696	0.0201	0.169
chr5	180915260	3977907	0.022	0.1763
chr6	171115067	3967600	0.0232	0.196
chr7	159138663	4243131	0.0267	0.2853

chr8	146364022	6280470	0.0429	0.3049
chr9	141213431	2496020	0.0177	0.2086
chr10	135534747	3997615	0.0295	0.2278
chr11	135006516	3442188	0.0255	0.23
chr12	133851895	3328444	0.0249	0.188
chr13	115169878	2279305	0.0198	0.1684
chr14	107349540	2708536	0.0252	0.1927
chr15	102531392	2104115	0.0205	0.1701
chr16	90354753	1912815	0.0212	0.1789
chr17	81195210	1842901	0.0227	0.2127
chr18	78077248	1416772	0.0181	0.3405
chr19	59128983	1197900	0.0203	0.1869
chr20	63025520	1674303	0.0266	0.1937
chr21	48129895	811275	0.0169	0.1646
chr22	51304566	855558	0.0167	0.1508
chrMT	16571	21787	1.3148	1.7501
chrX	155270560	3459447	0.0223	0.1838
chrY	59373566	148679	0.0025	0.0678

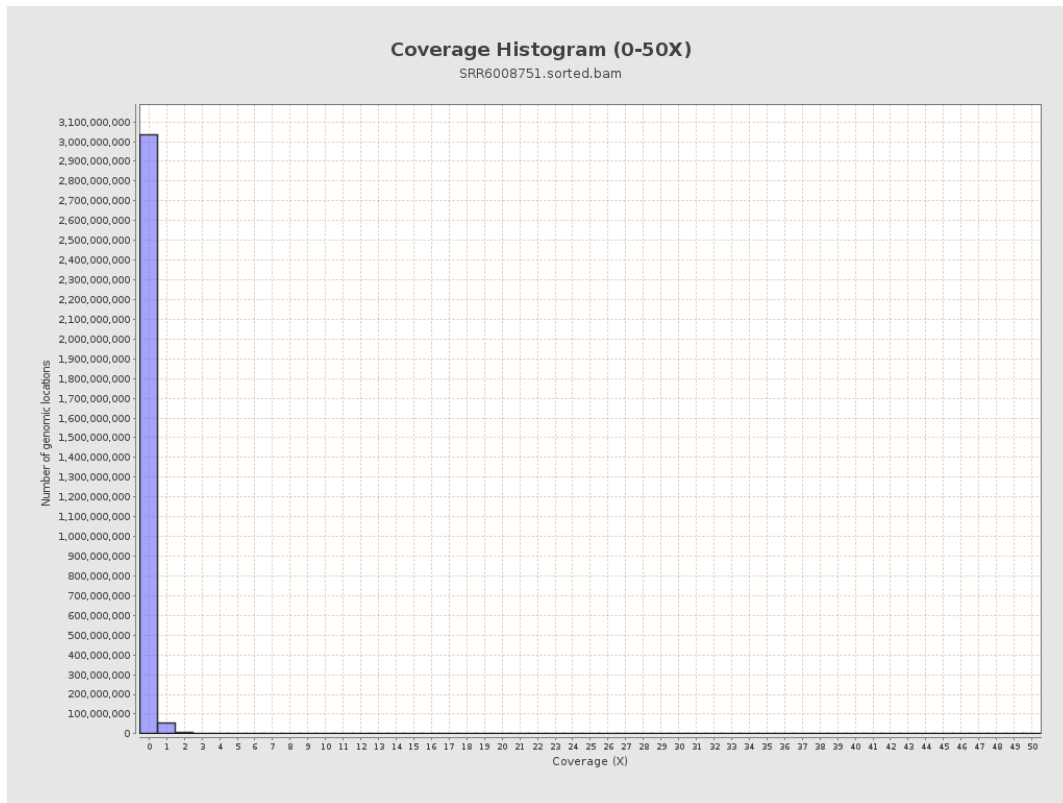
3. Results : Coverage across reference



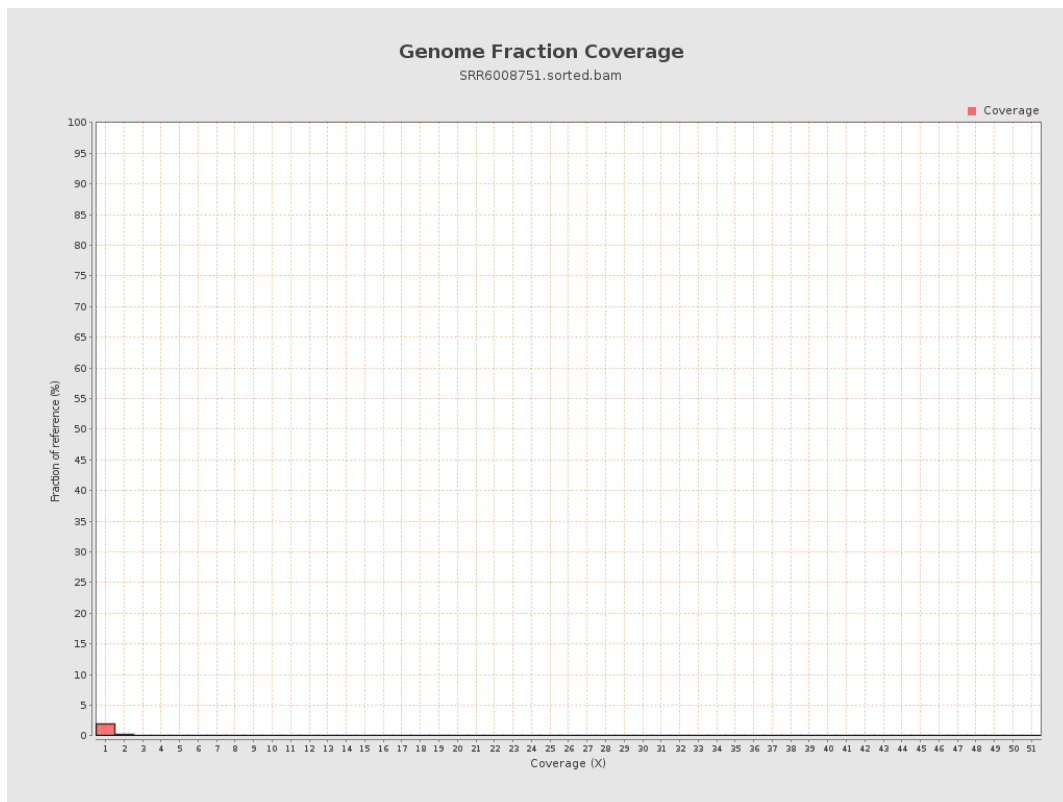
4. Results : Coverage Histogram



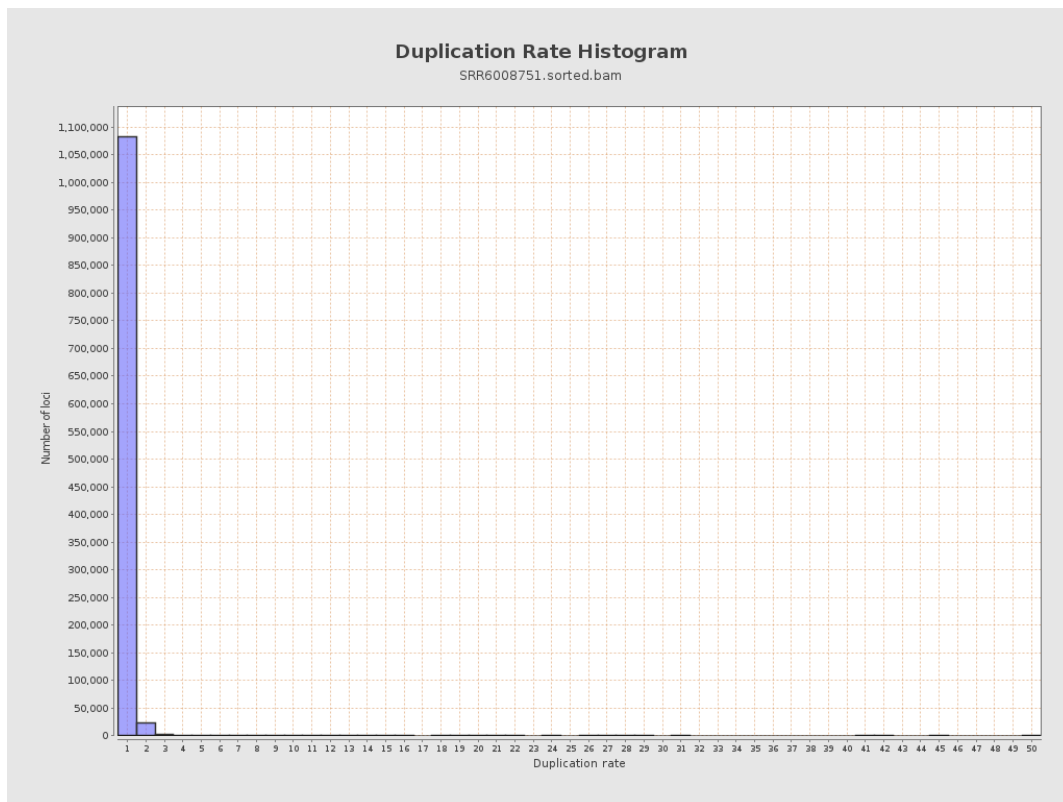
5. Results : Coverage Histogram (0-50X)



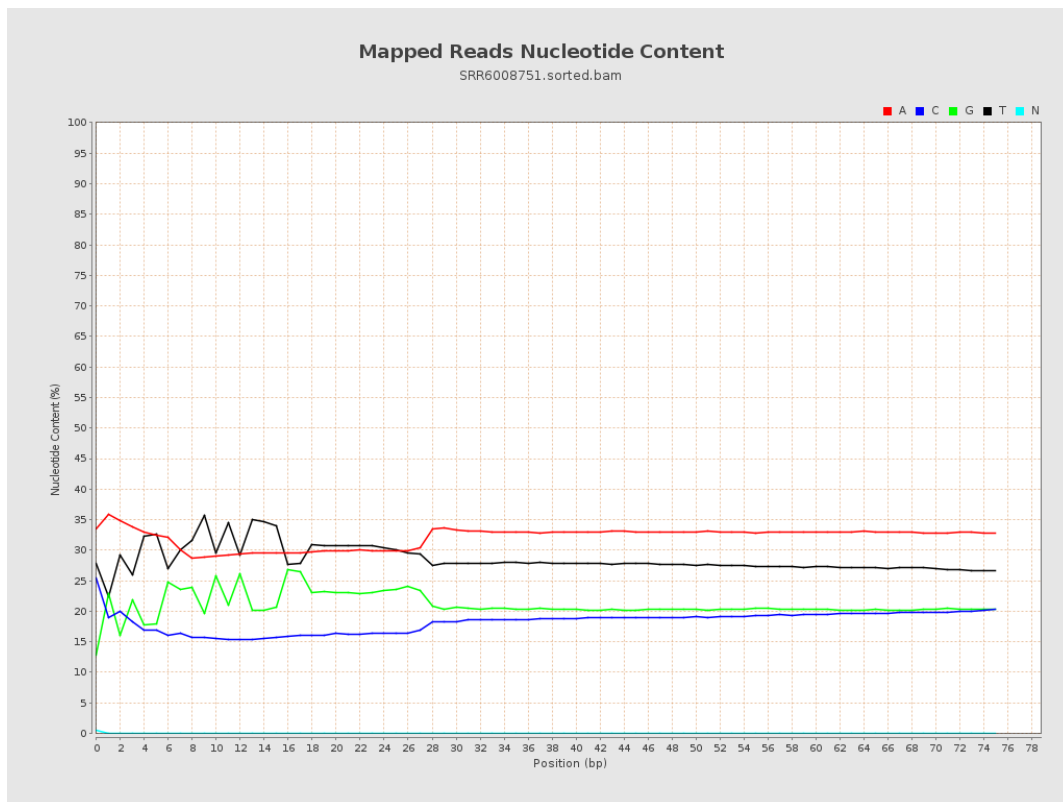
6. Results : Genome Fraction Coverage



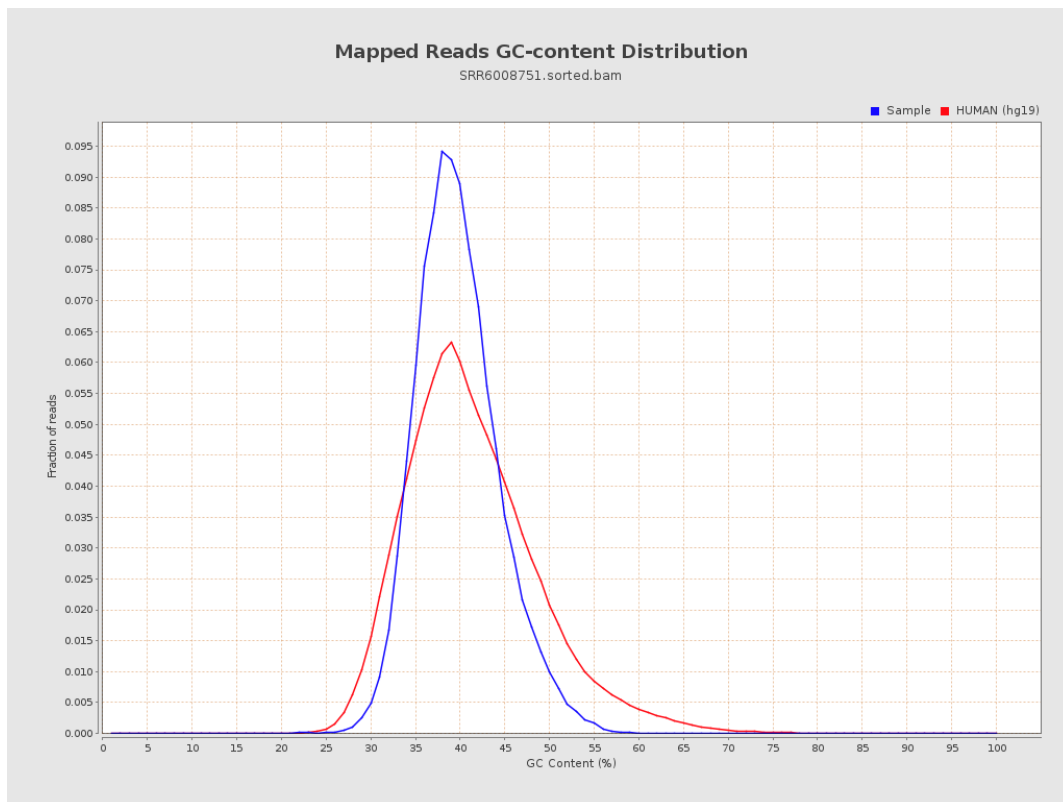
7. Results : Duplication Rate Histogram



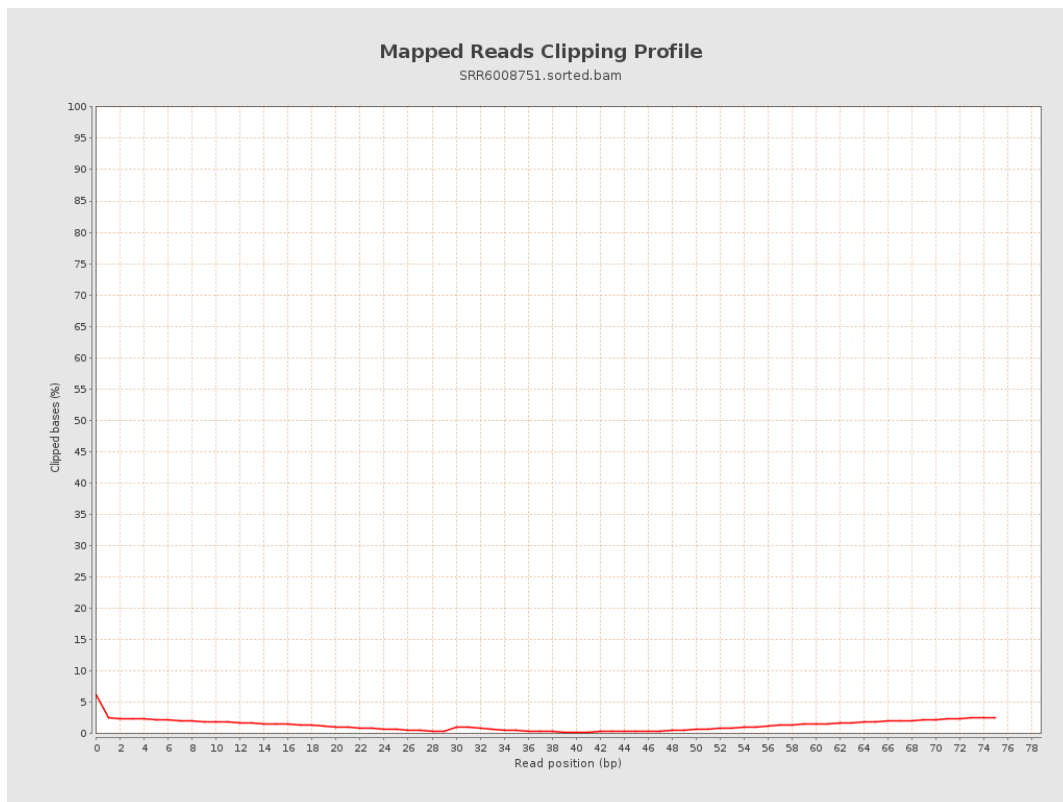
8. Results : Mapped Reads Nucleotide Content



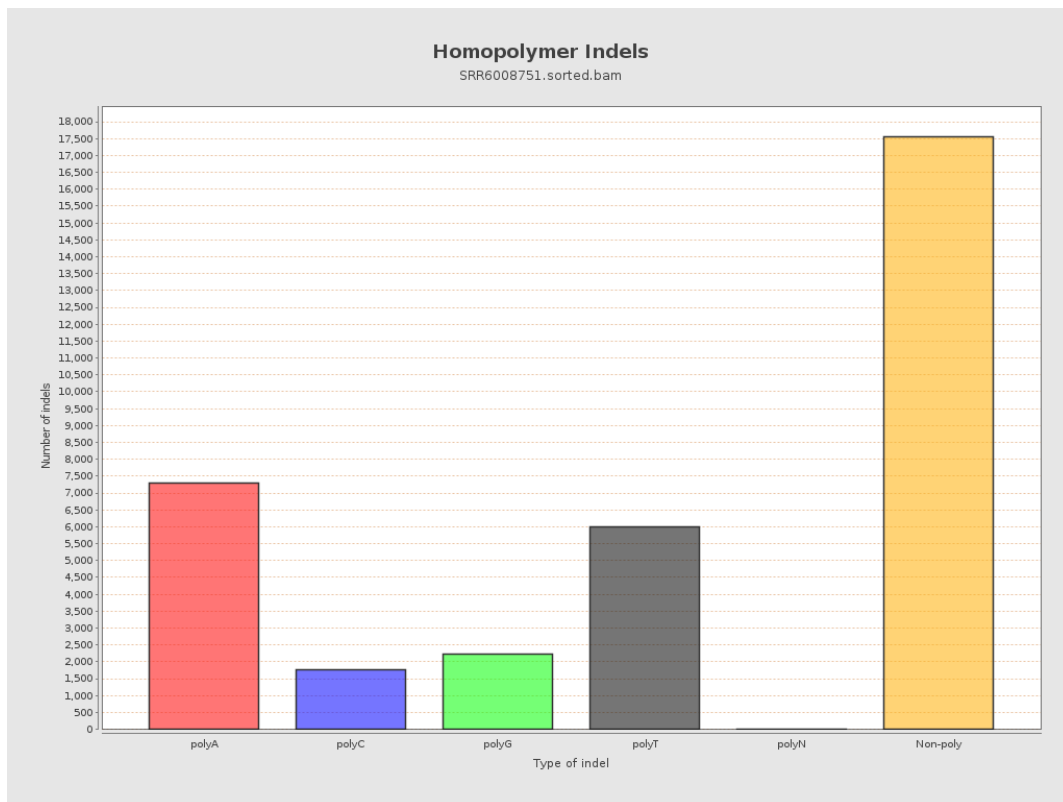
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

