

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 11:30:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008786.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_SRR6008786 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008786.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 11:30:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008786.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,549,805
Mapped reads	1,200,886 / 77.49%
Unmapped reads	348,919 / 22.51%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,963 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	32,129 / 2.07%
Duplication rate	1.93%
Clipped reads	497,786 / 32.12%

2.2. ACGT Content

Number/percentage of A's	23,771,334 / 29.4%
Number/percentage of C's	14,196,496 / 17.56%
Number/percentage of T's	25,130,849 / 31.08%
Number/percentage of G's	17,741,471 / 21.94%
Number/percentage of N's	15,875 / 0.02%
GC Percentage	39.5%

2.3. Coverage

Mean	0.0261

Standard Deviation	0.2607
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2.4. Mapping Quality

Mean Mapping Quality	46.3
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2.5. Mismatches and indels

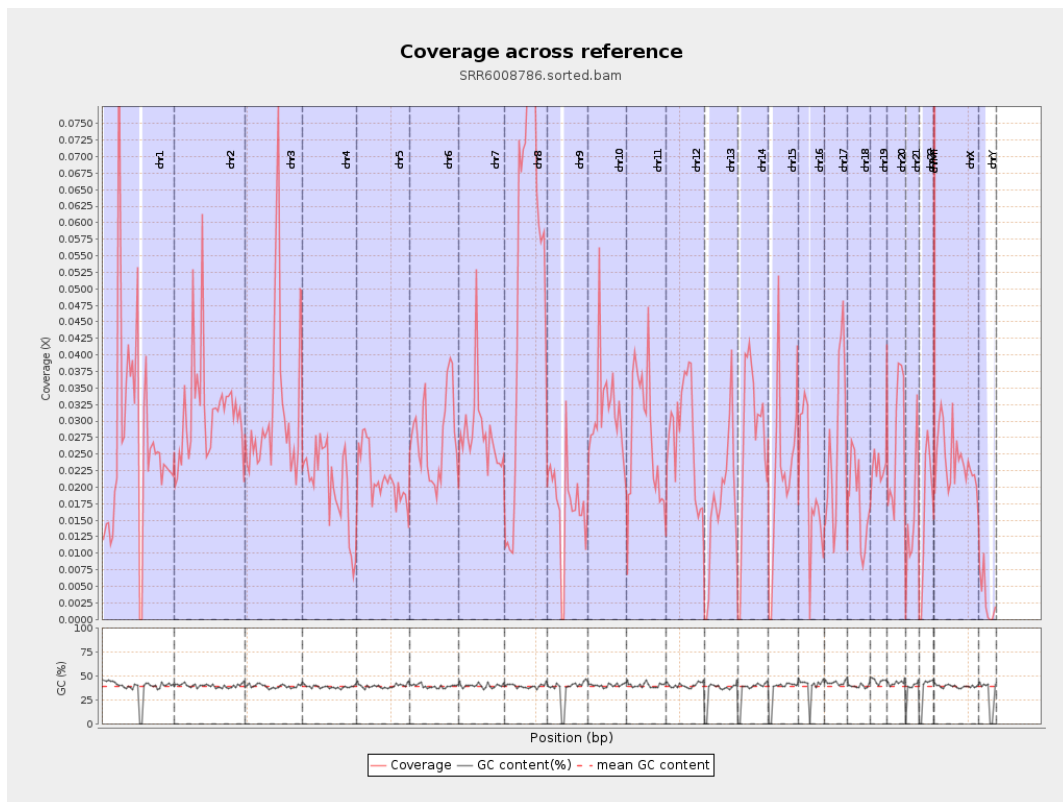
General error rate	0.9%
Mismatches	711,419
Insertions	7,196
Mapped reads with at least one insertion	0.59%
Deletions	22,834
Mapped reads with at least one deletion	1.88%
Homopolymer indels	46.99%

2.6. Chromosome stats

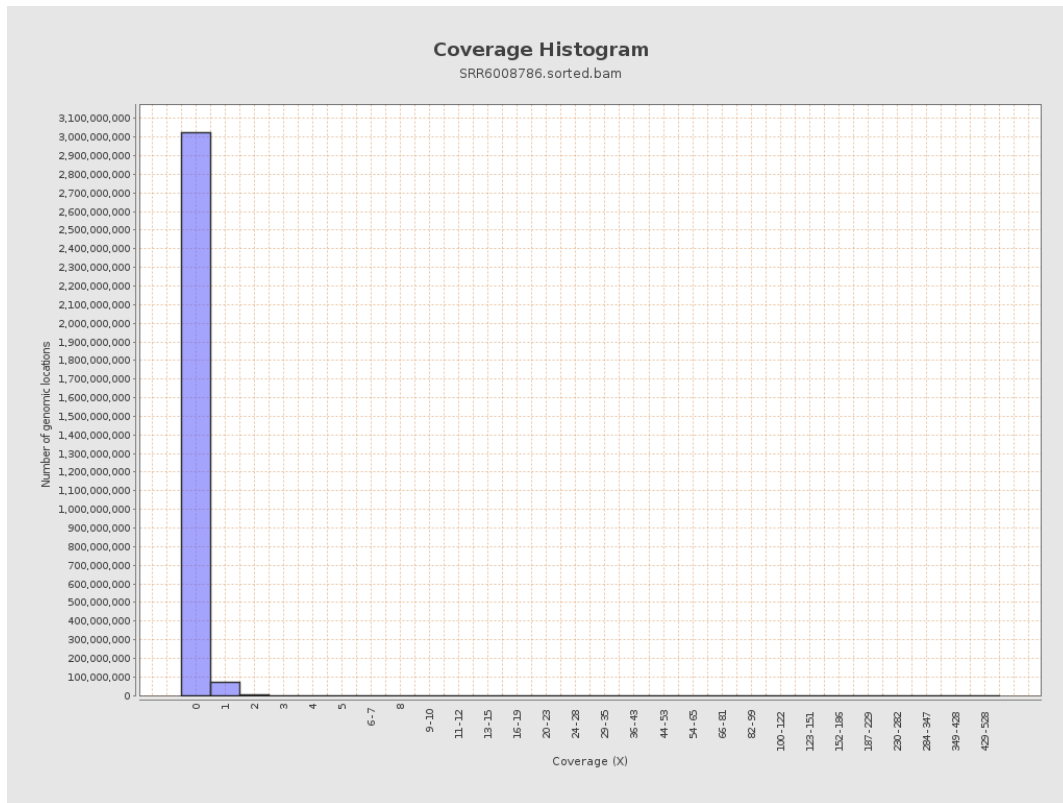
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6591858	0.0264	0.4407
chr2	243199373	7653609	0.0315	0.2924
chr3	198022430	6187711	0.0312	0.1896
chr4	191154276	3882128	0.0203	0.1547
chr5	180915260	3891161	0.0215	0.1548
chr6	171115067	4705484	0.0275	0.1949
chr7	159138663	4504371	0.0283	0.3517

chr8	146364022	8084518	0.0552	0.4155
chr9	141213431	2421603	0.0171	0.2255
chr10	135534747	4240124	0.0313	0.2958
chr11	135006516	3770166	0.0279	0.2614
chr12	133851895	3712840	0.0277	0.1771
chr13	115169878	2023148	0.0176	0.1384
chr14	107349540	2962074	0.0276	0.1799
chr15	102531392	2274689	0.0222	0.1577
chr16	90354753	1798558	0.0199	0.1697
chr17	81195210	2161686	0.0266	0.2161
chr18	78077248	1367809	0.0175	0.4035
chr19	59128983	1384508	0.0234	0.2627
chr20	63025520	1691893	0.0268	0.1755
chr21	48129895	755173	0.0157	0.1407
chr22	51304566	851877	0.0166	0.1347
chrMT	16571	33529	2.0234	1.8831
chrX	155270560	3761059	0.0242	0.1822
chrY	59373566	182312	0.0031	0.0888

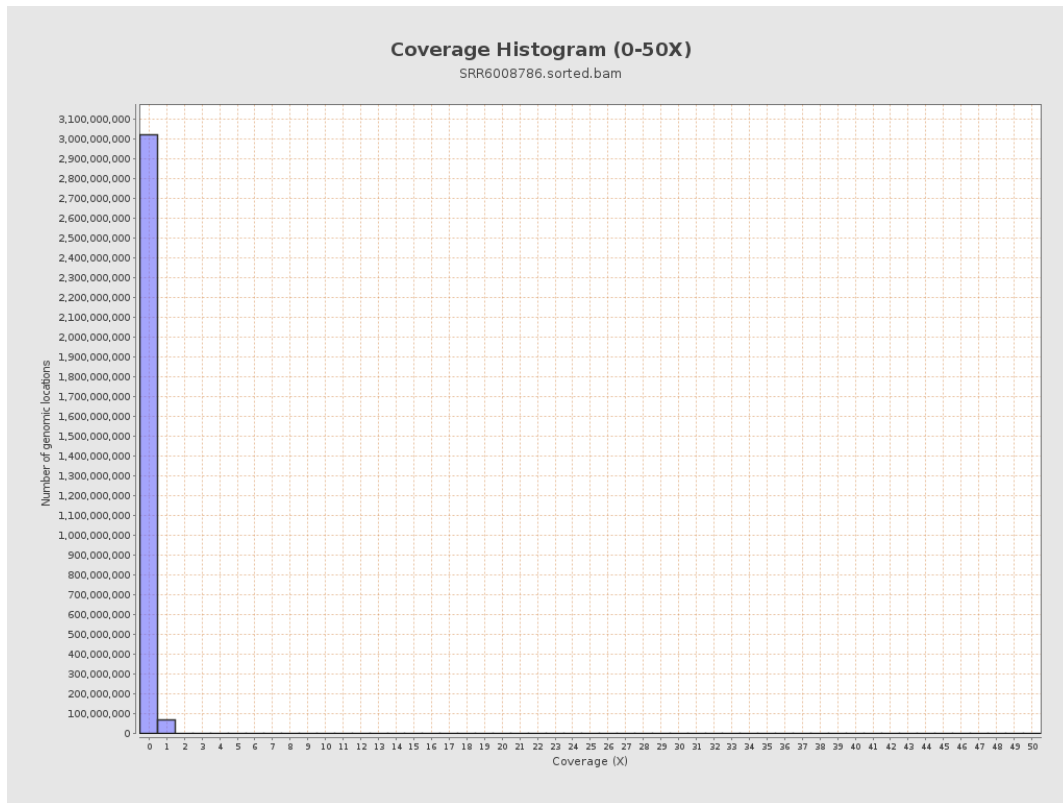
3. Results : Coverage across reference



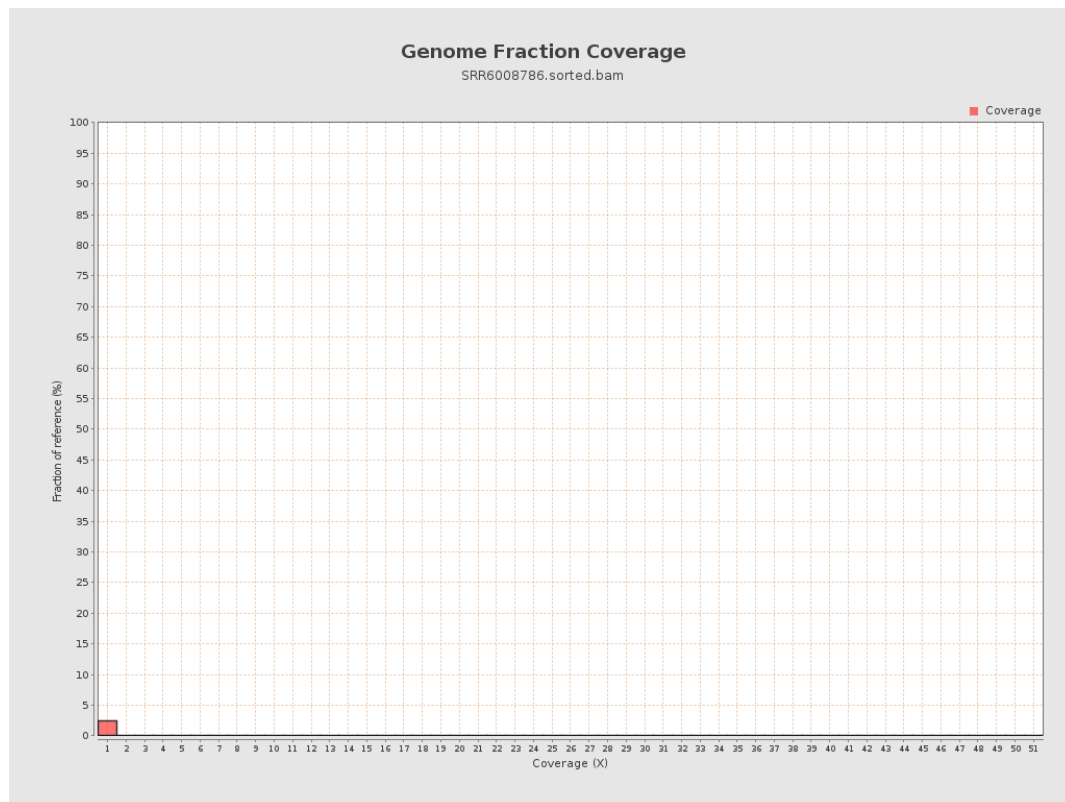
4. Results : Coverage Histogram



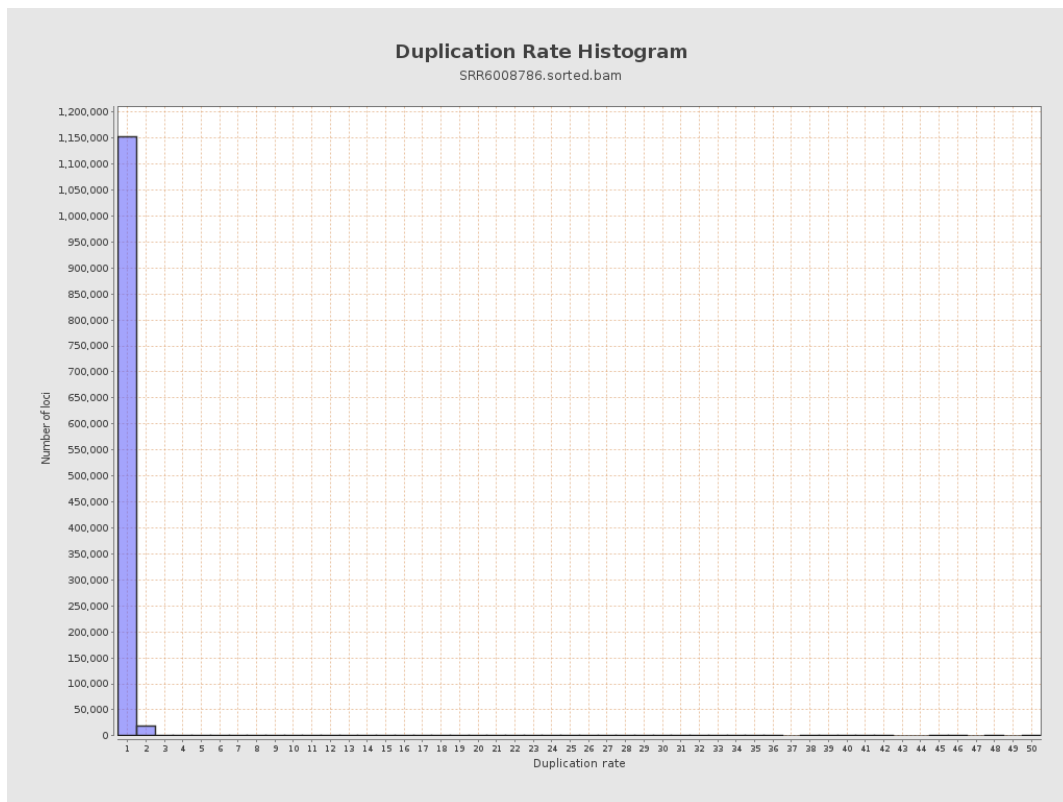
5. Results : Coverage Histogram (0-50X)



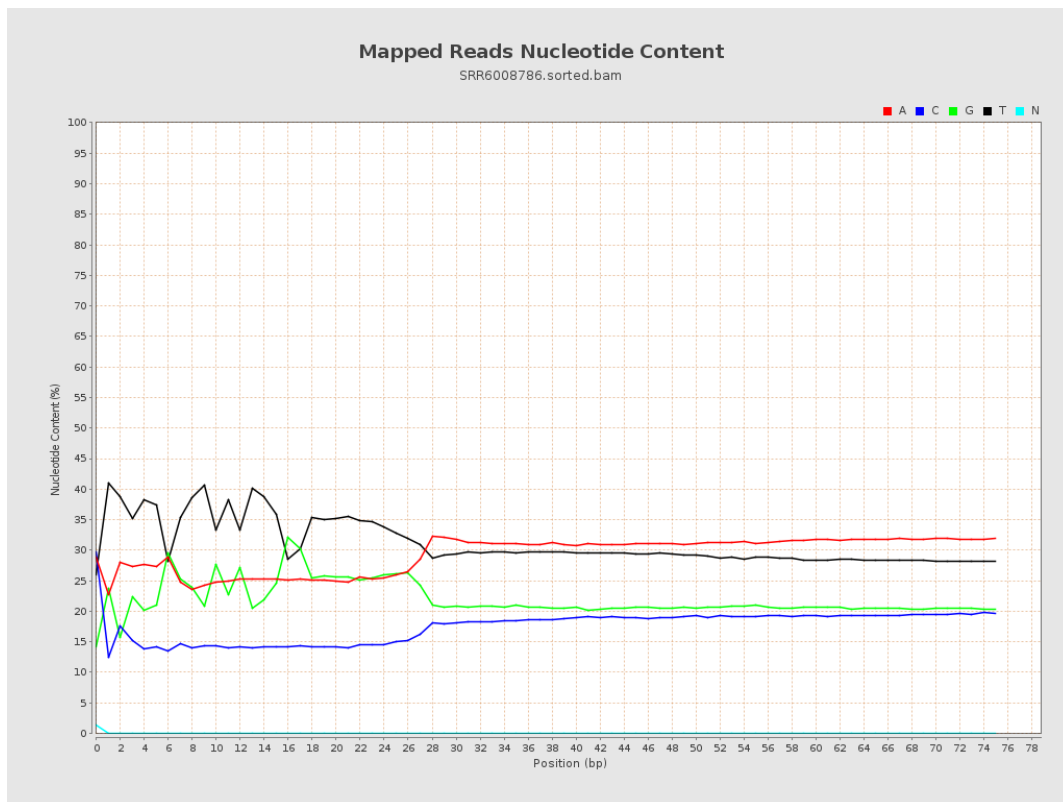
6. Results : Genome Fraction Coverage



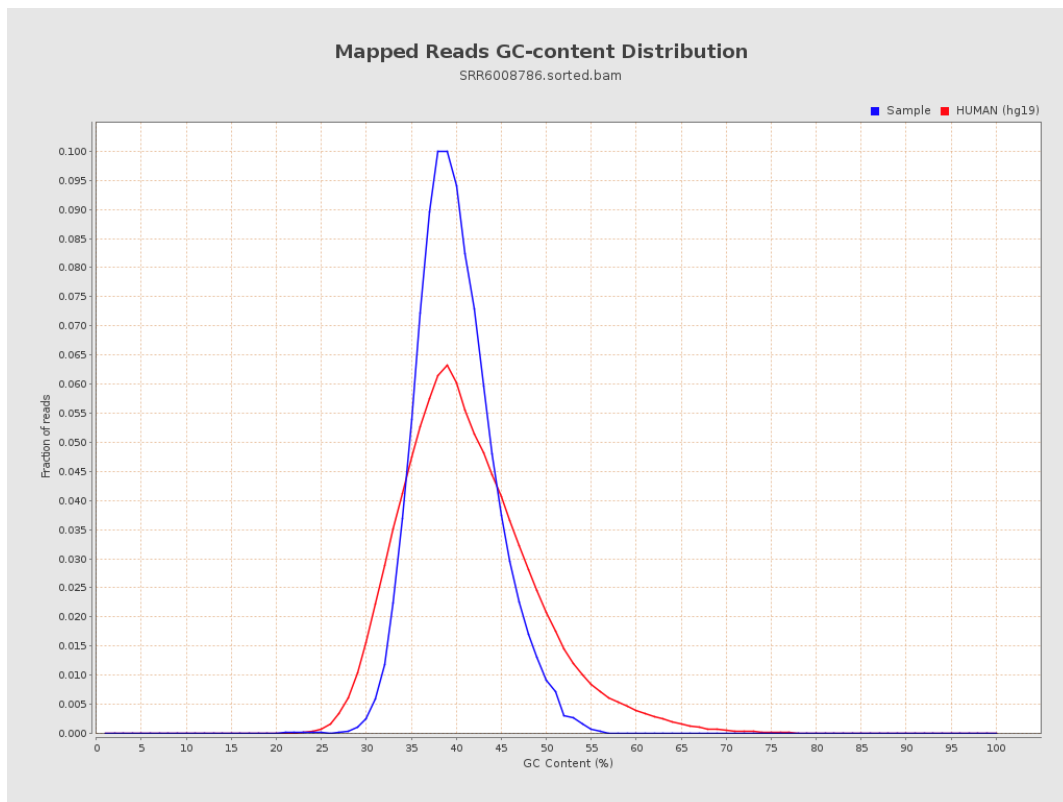
7. Results : Duplication Rate Histogram



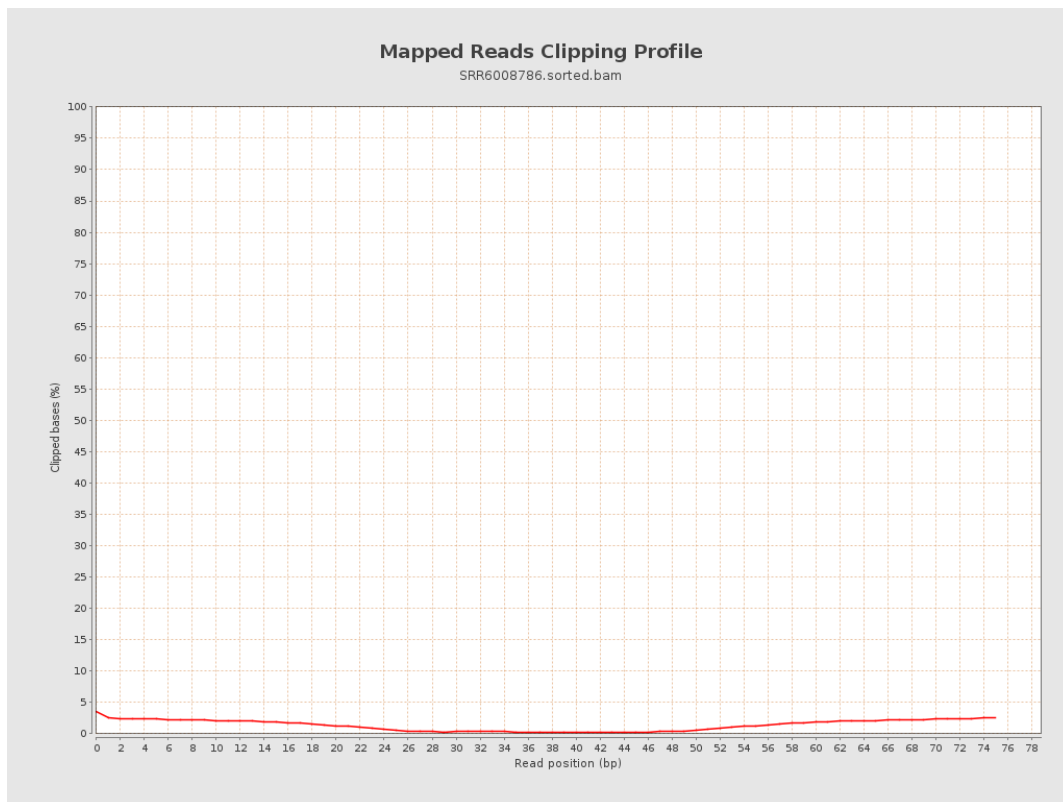
8. Results : Mapped Reads Nucleotide Content



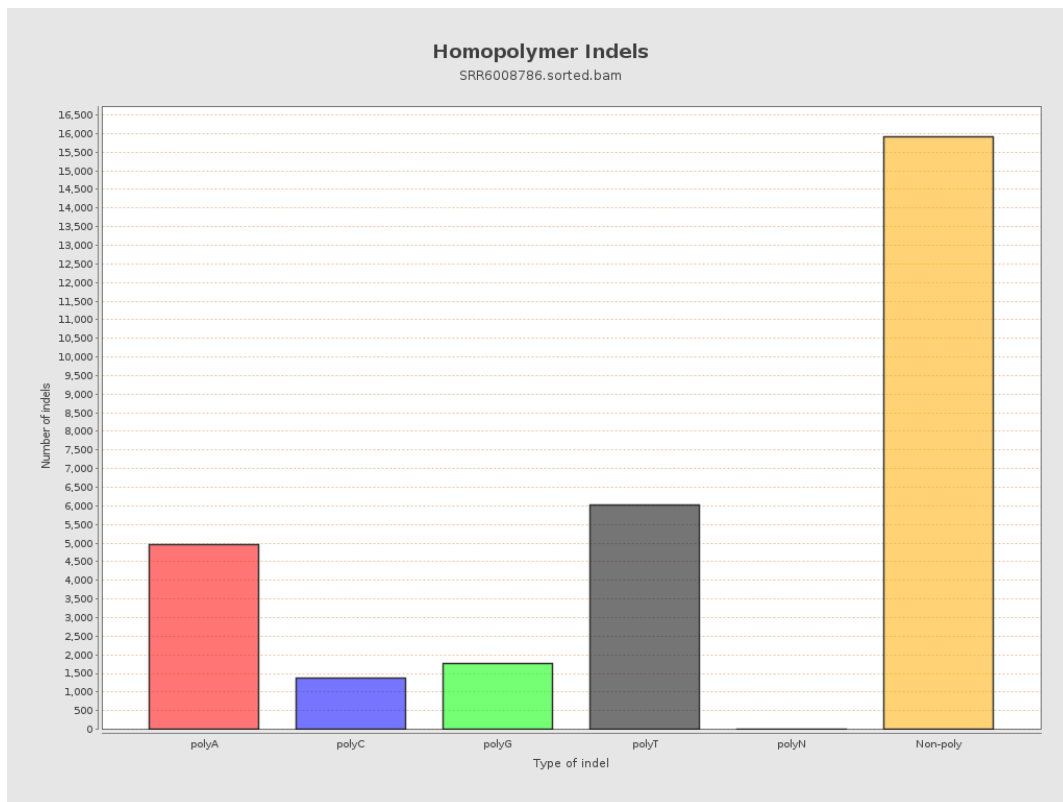
9. Results : Mapped Reads GC-content Distribution



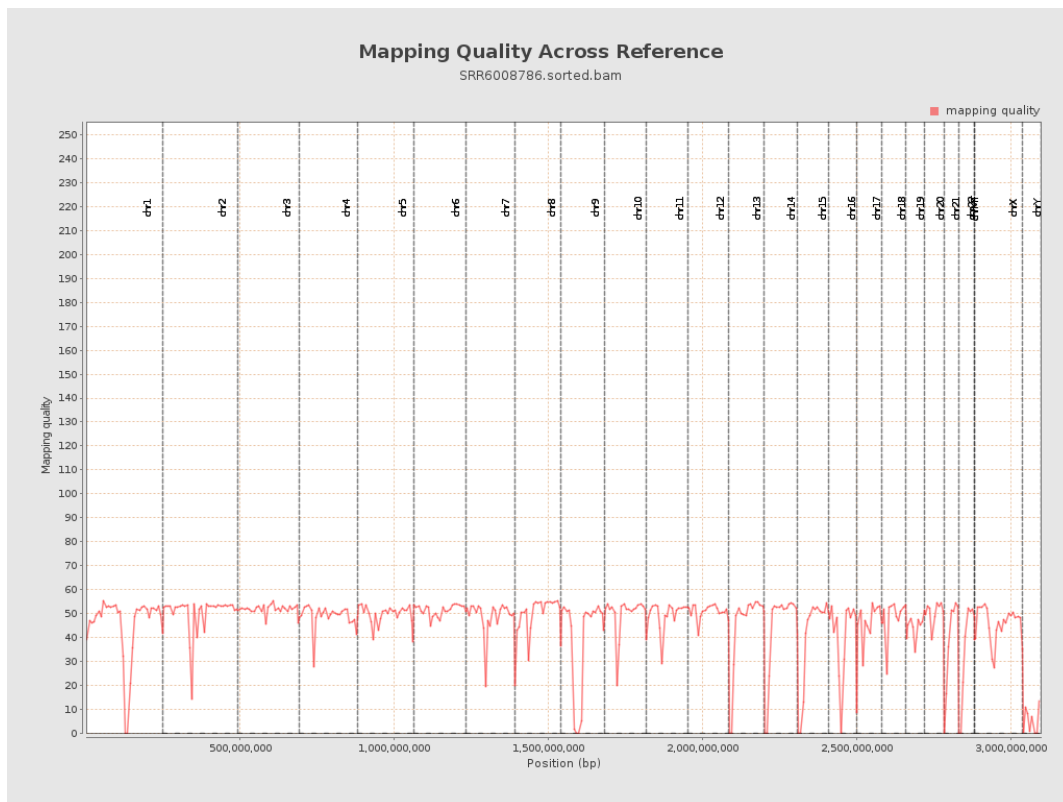
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

