

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 07:34:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008700.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_SRR6008700 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008700.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 07:34:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008700.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,947,952
Mapped reads	1,315,828 / 67.55%
Unmapped reads	632,124 / 32.45%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,332 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	46,009 / 2.36%
Duplication rate	2.82%
Clipped reads	851,009 / 43.69%

2.2. ACGT Content

Number/percentage of A's	24,275,916 / 29.92%
Number/percentage of C's	13,895,408 / 17.12%
Number/percentage of T's	25,158,438 / 31.01%
Number/percentage of G's	17,791,589 / 21.93%
Number/percentage of N's	20,214 / 0.02%
GC Percentage	39.05%

2.3. Coverage

Mean	0.0262

Standard Deviation	0.2225
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2.4. Mapping Quality

Mean Mapping Quality	46.23
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2.5. Mismatches and indels

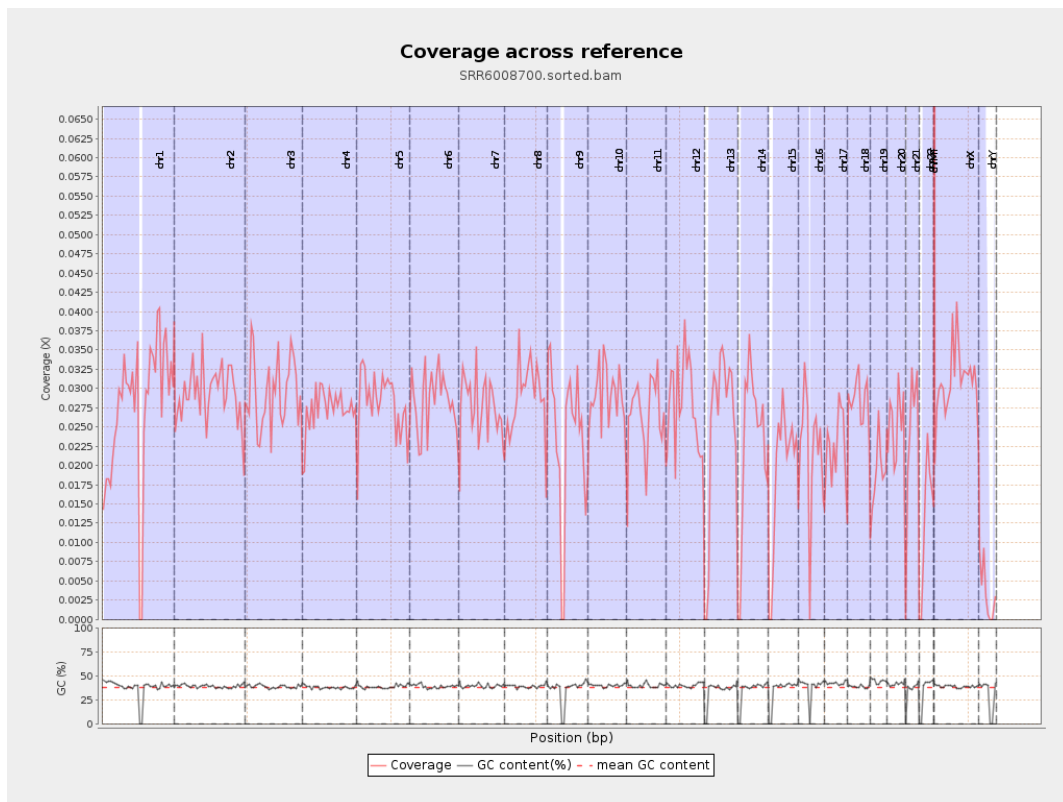
General error rate	1.12%
Mismatches	900,875
Insertions	6,696
Mapped reads with at least one insertion	0.51%
Deletions	29,531
Mapped reads with at least one deletion	2.22%
Homopolymer indels	48.14%

2.6. Chromosome stats

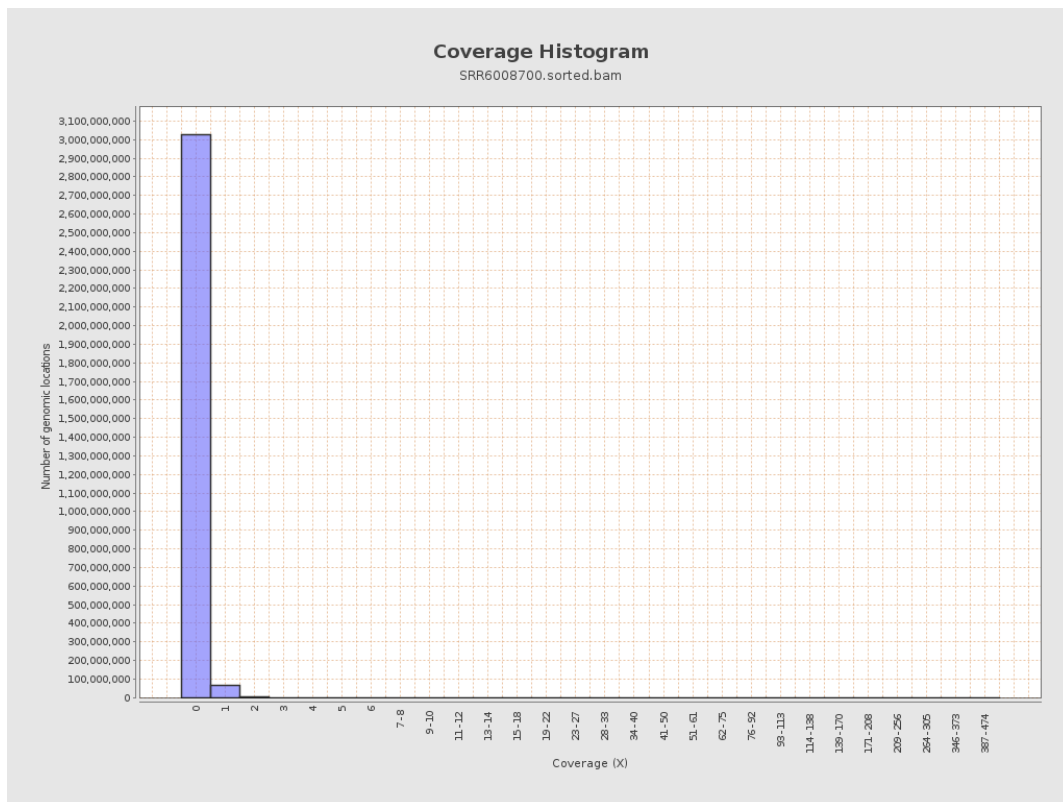
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6838508	0.0274	0.2873
chr2	243199373	7127185	0.0293	0.2418
chr3	198022430	5827489	0.0294	0.1968
chr4	191154276	5200830	0.0272	0.1905
chr5	180915260	5141402	0.0284	0.1911
chr6	171115067	4855769	0.0284	0.2043
chr7	159138663	4405526	0.0277	0.2716

chr8	146364022	4225439	0.0289	0.341
chr9	141213431	3363685	0.0238	0.2075
chr10	135534747	3915455	0.0289	0.2168
chr11	135006516	3609382	0.0267	0.2235
chr12	133851895	3723205	0.0278	0.1915
chr13	115169878	2860716	0.0248	0.1811
chr14	107349540	2469100	0.023	0.1799
chr15	102531392	1979393	0.0193	0.1608
chr16	90354753	1943907	0.0215	0.1774
chr17	81195210	1810581	0.0223	0.1807
chr18	78077248	2242134	0.0287	0.3034
chr19	59128983	1137813	0.0192	0.2052
chr20	63025520	1569958	0.0249	0.183
chr21	48129895	1165038	0.0242	0.1807
chr22	51304566	684919	0.0134	0.1301
chrMT	16571	36615	2.2096	2.4537
chrX	155270560	4849056	0.0312	0.2123
chrY	59373566	203721	0.0034	0.0732

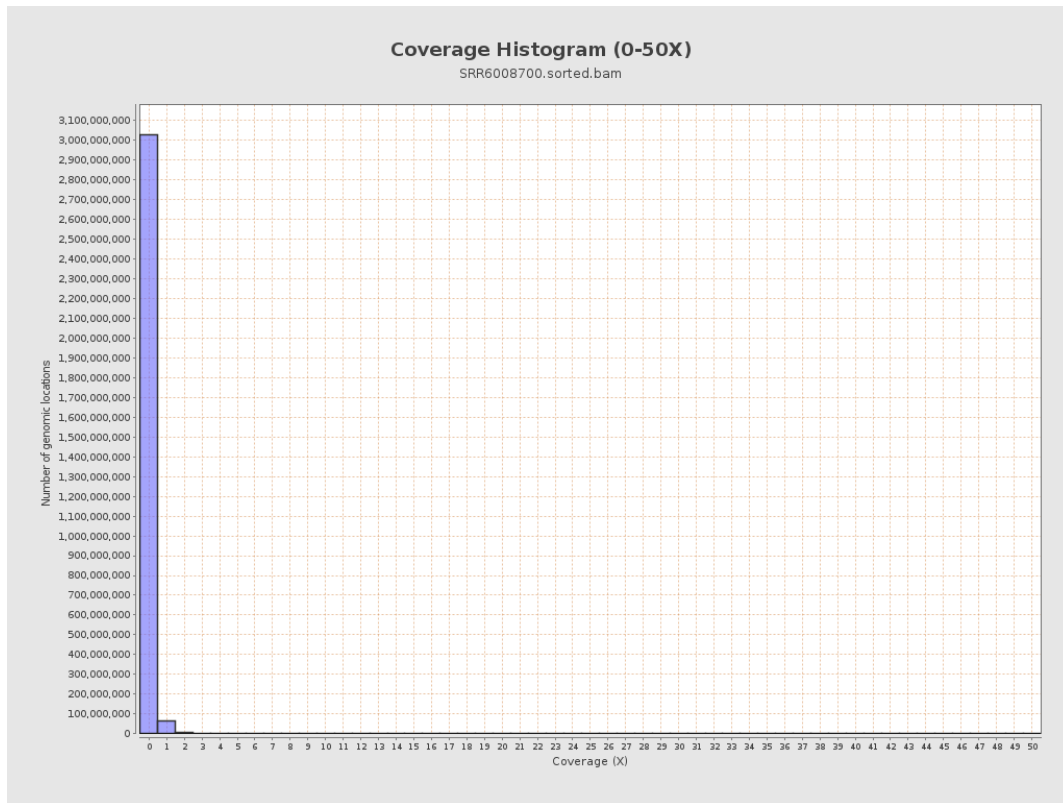
3. Results : Coverage across reference



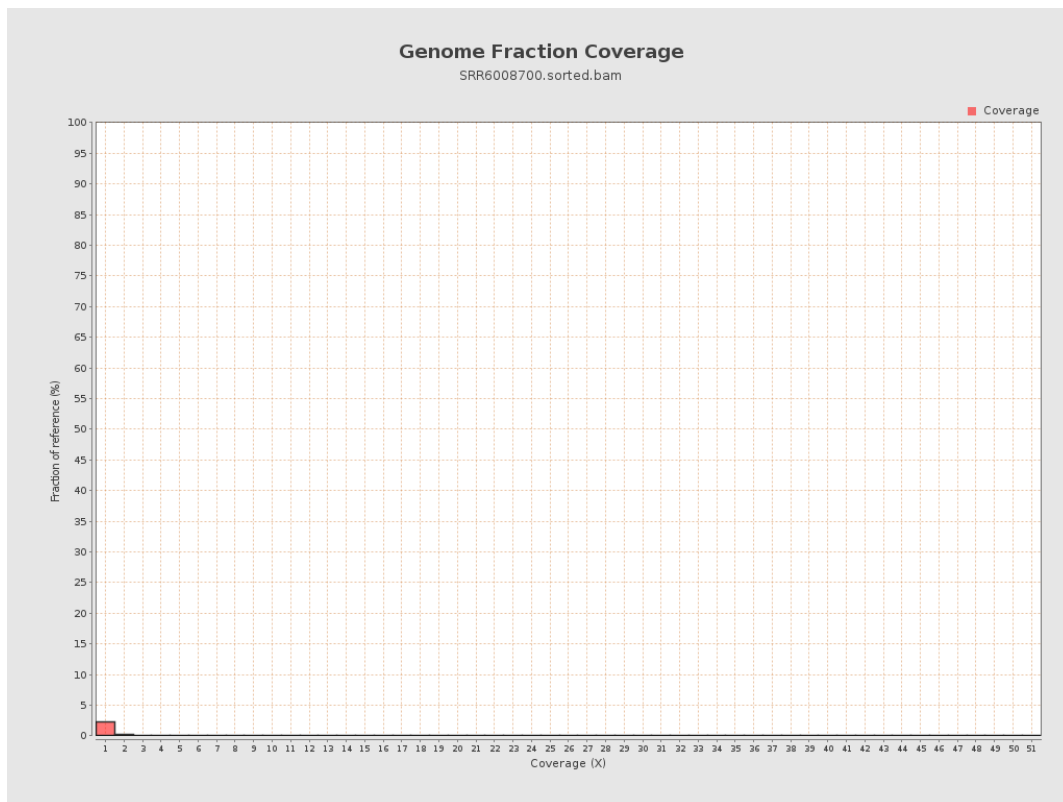
4. Results : Coverage Histogram



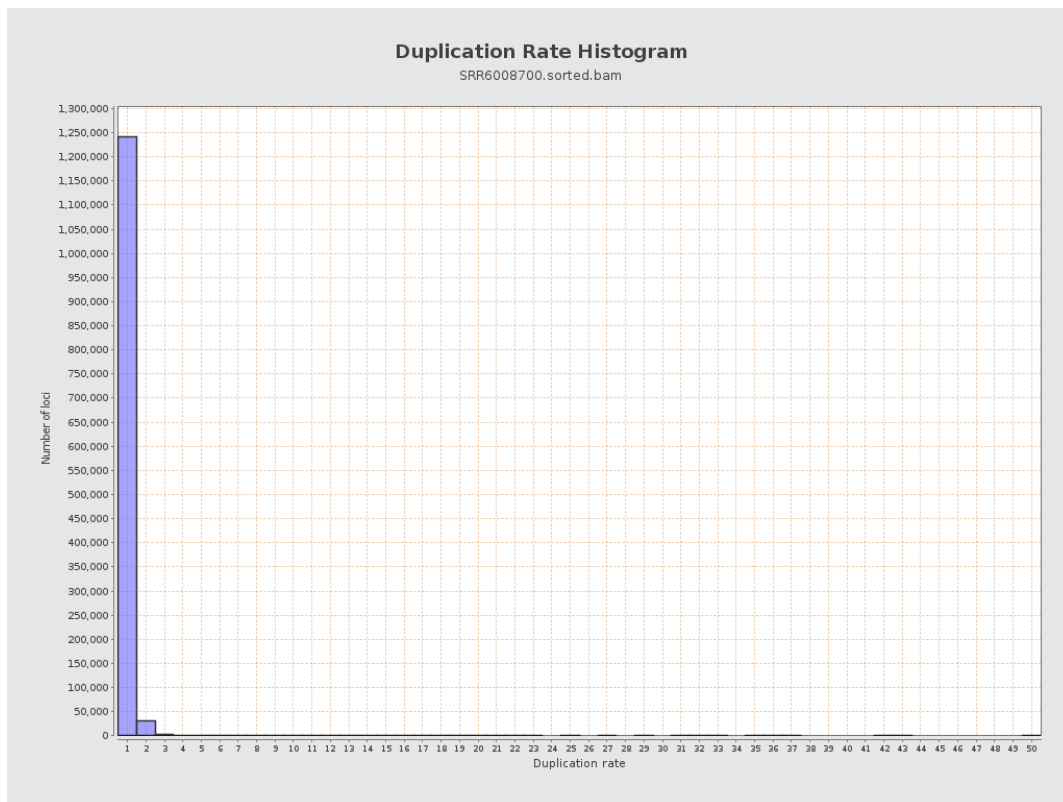
5. Results : Coverage Histogram (0-50X)



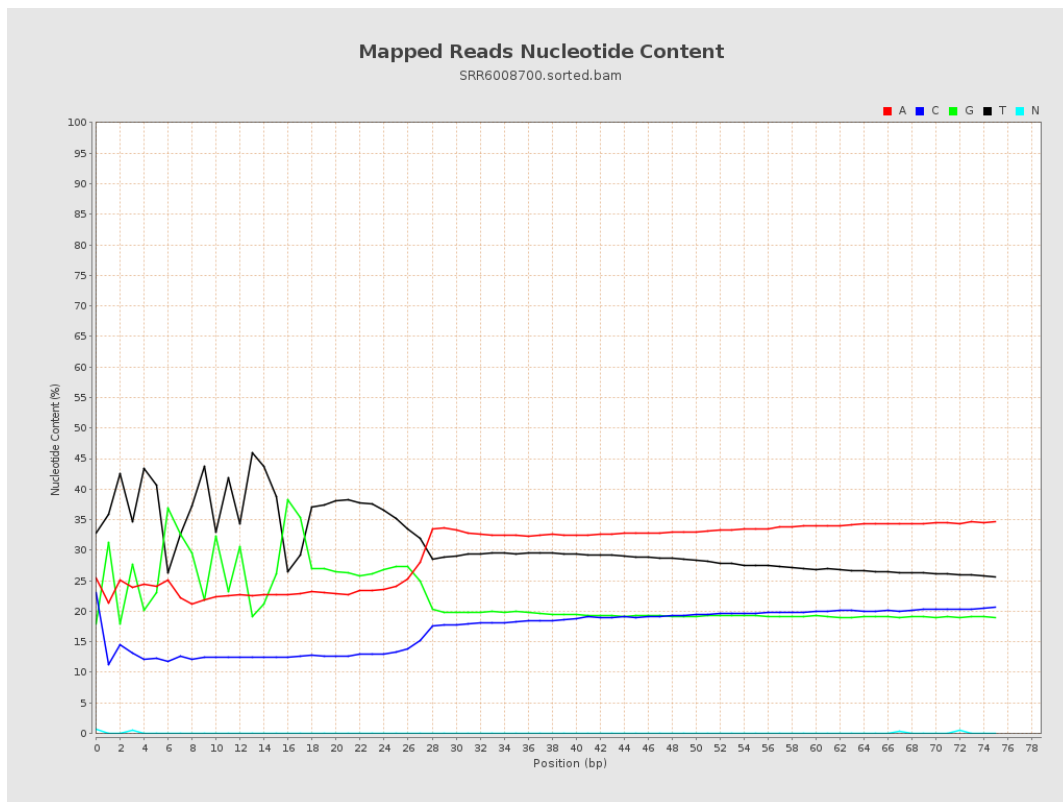
6. Results : Genome Fraction Coverage



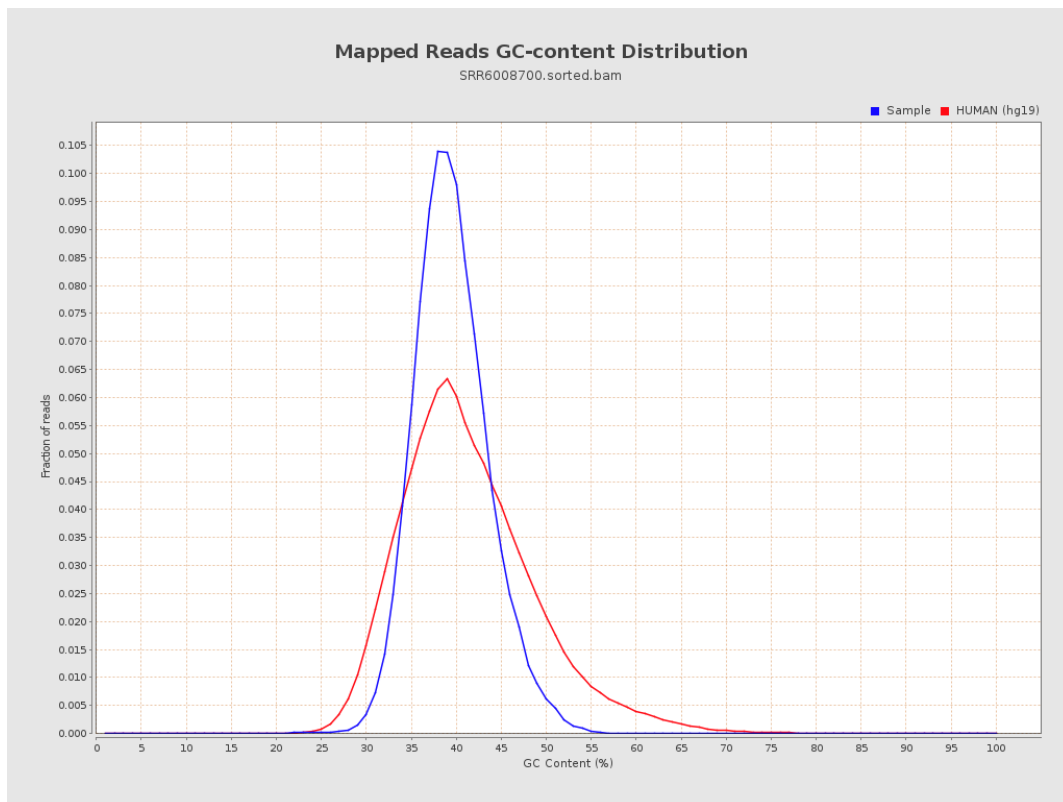
7. Results : Duplication Rate Histogram



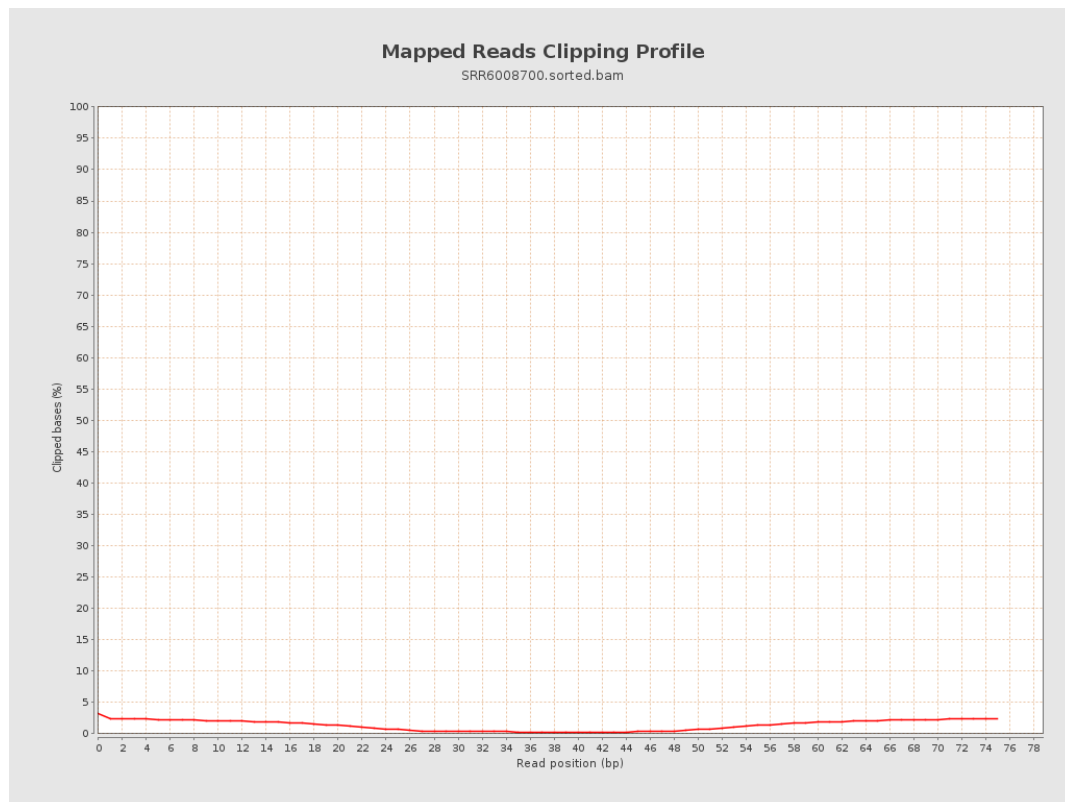
8. Results : Mapped Reads Nucleotide Content



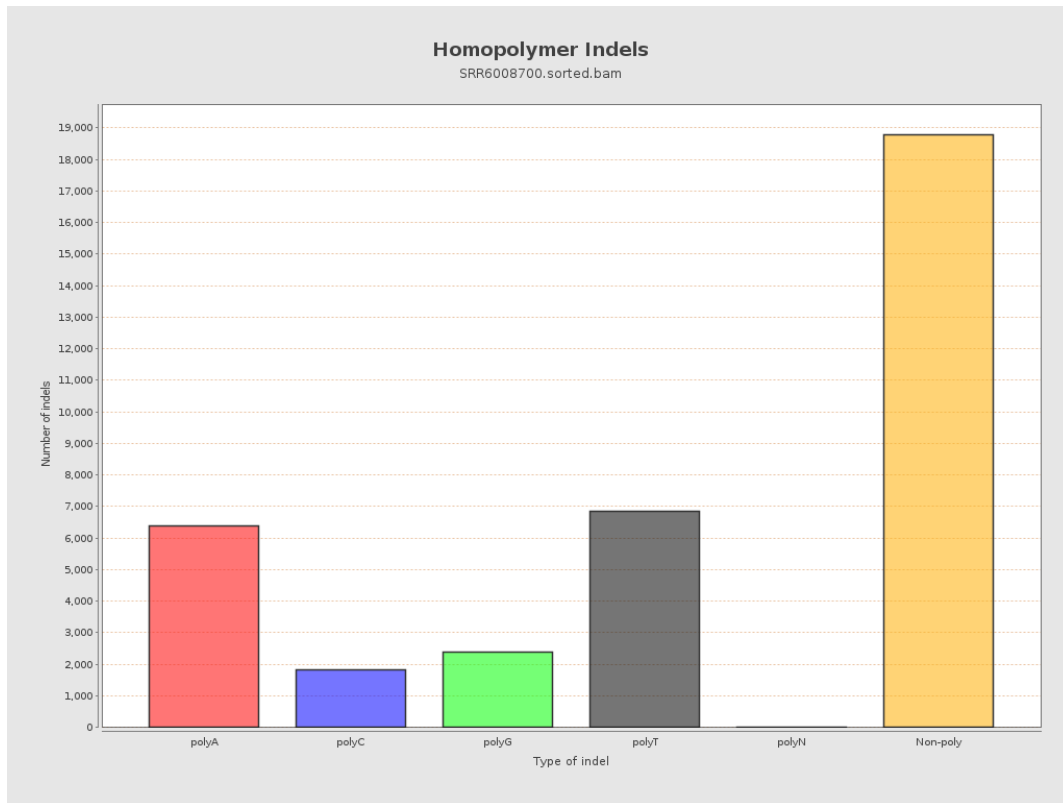
9. Results : Mapped Reads GC-content Distribution



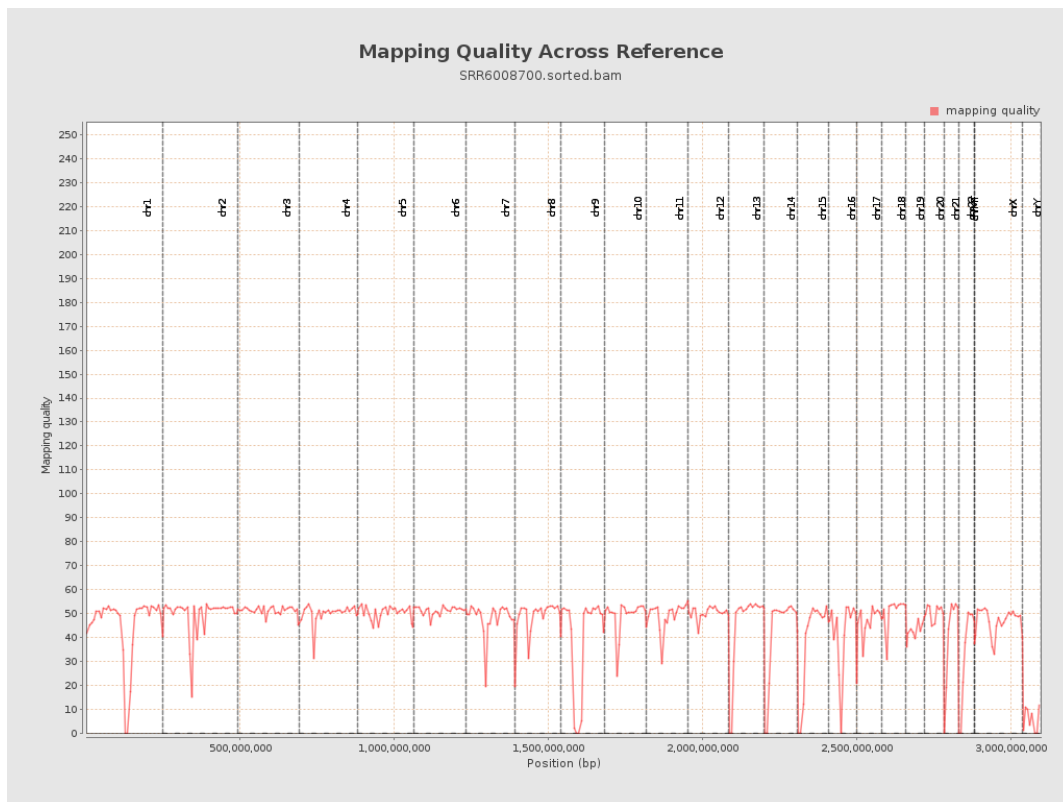
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

