

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 11:03:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008775.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_SRR6008775 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008775.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 11:03:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008775.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,383,252
Mapped reads	1,236,769 / 89.41%
Unmapped reads	146,483 / 10.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,990 / 0.58%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	51,899 / 3.75%
Duplication rate	3.35%
Clipped reads	528,158 / 38.18%

2.2. ACGT Content

Number/percentage of A's	22,150,463 / 26.85%
Number/percentage of C's	15,836,788 / 19.2%
Number/percentage of T's	25,562,366 / 30.99%
Number/percentage of G's	18,809,599 / 22.8%
Number/percentage of N's	135,764 / 0.16%
GC Percentage	42%

2.3. Coverage

Mean	0.0267

Standard Deviation	0.2634
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2.4. Mapping Quality

Mean Mapping Quality	44.91
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2.5. Mismatches and indels

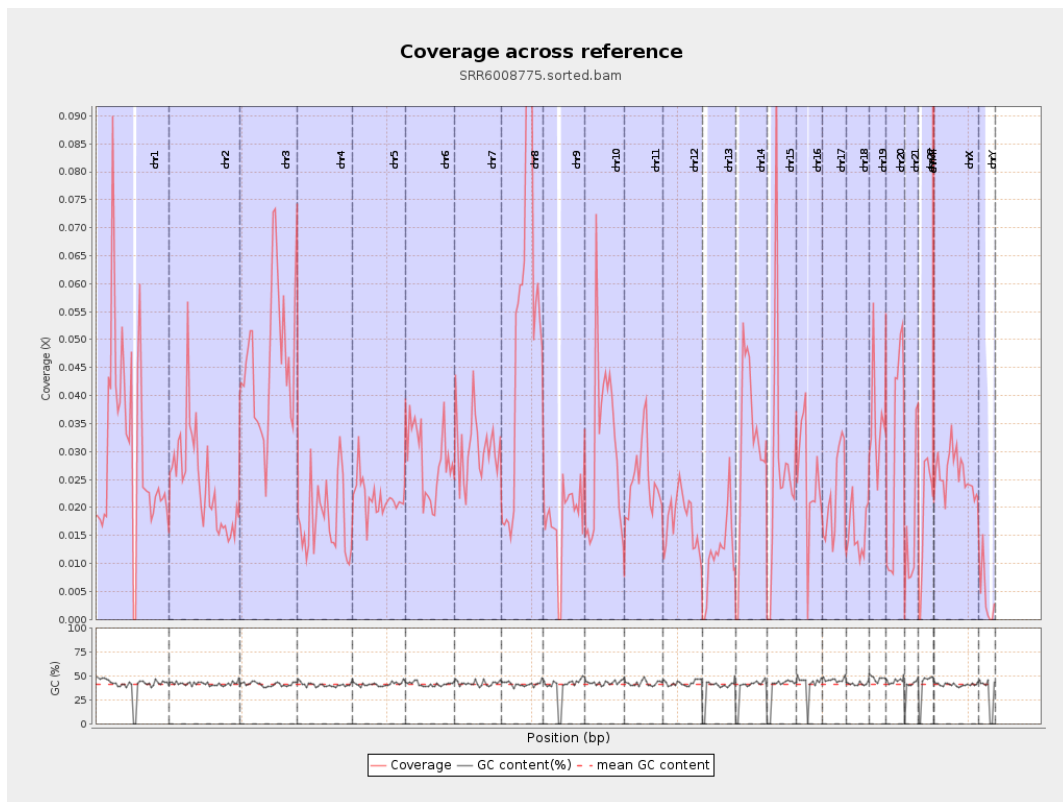
General error rate	0.85%
Mismatches	689,571
Insertions	5,973
Mapped reads with at least one insertion	0.48%
Deletions	22,958
Mapped reads with at least one deletion	1.84%
Homopolymer indels	44.7%

2.6. Chromosome stats

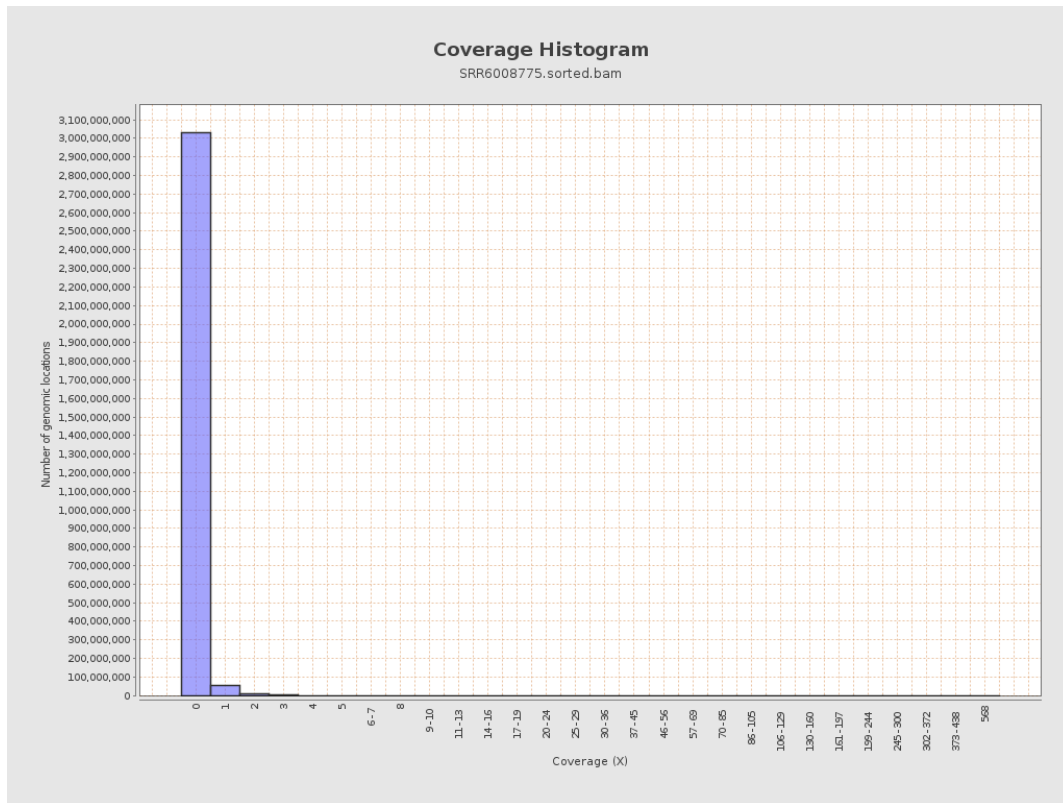
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	7414483	0.0297	0.4269
chr2	243199373	5917989	0.0243	0.3145
chr3	198022430	9150982	0.0462	0.2643
chr4	191154276	3374691	0.0177	0.169
chr5	180915260	3940181	0.0218	0.1726
chr6	171115067	4845402	0.0283	0.2175
chr7	159138663	4893212	0.0307	0.3035

chr8	146364022	7603946	0.052	0.3297
chr9	141213431	2501224	0.0177	0.1912
chr10	135534747	4139125	0.0305	0.38
chr11	135006516	3350340	0.0248	0.2345
chr12	133851895	2361663	0.0176	0.1569
chr13	115169878	1356476	0.0118	0.1273
chr14	107349540	3398419	0.0317	0.2121
chr15	102531392	2867633	0.028	0.1992
chr16	90354753	2286486	0.0253	0.2533
chr17	81195210	1792340	0.0221	0.1948
chr18	78077248	1218879	0.0156	0.2942
chr19	59128983	2116535	0.0358	0.3144
chr20	63025520	1858212	0.0295	0.2062
chr21	48129895	797156	0.0166	0.1637
chr22	51304566	961834	0.0187	0.1595
chrMT	16571	119022	7.1825	4.8209
chrX	155270560	4028229	0.0259	0.1972
chrY	59373566	241621	0.0041	0.1518

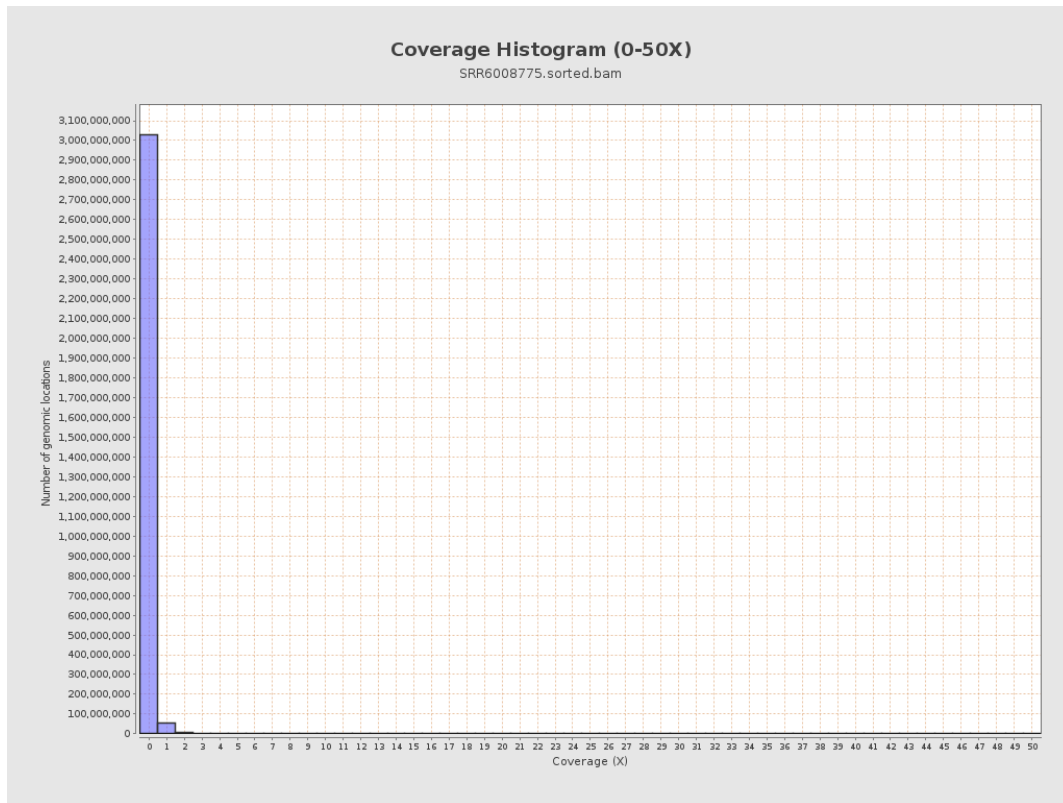
3. Results : Coverage across reference



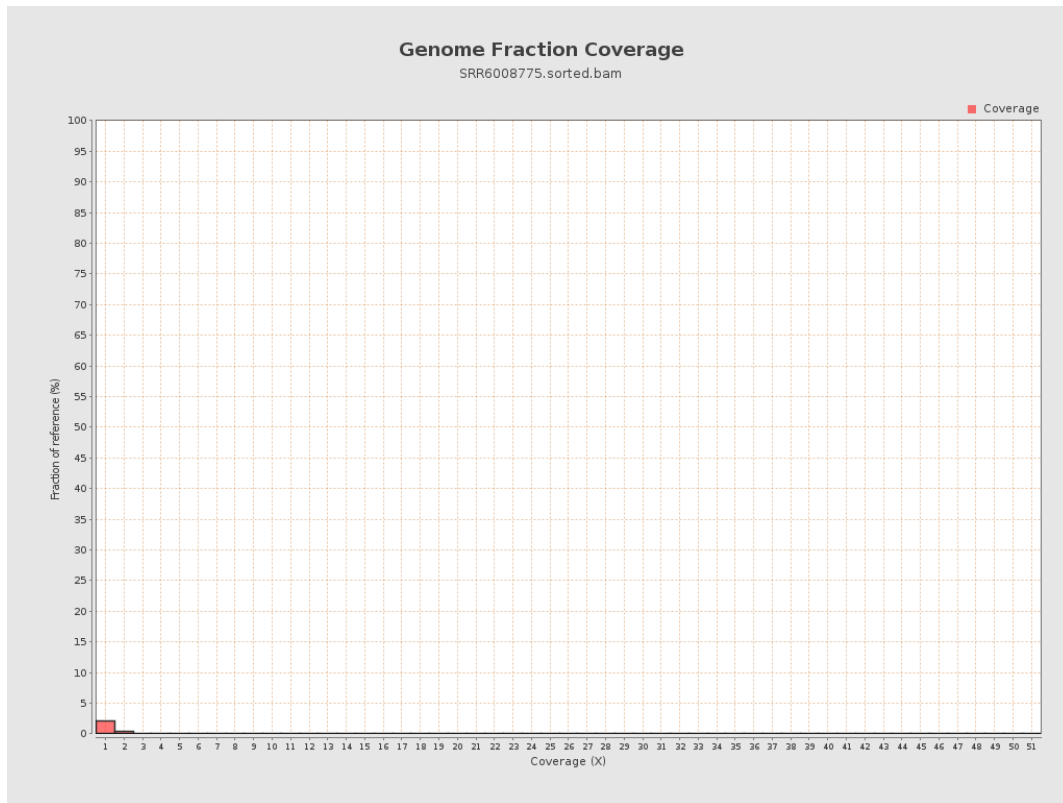
4. Results : Coverage Histogram



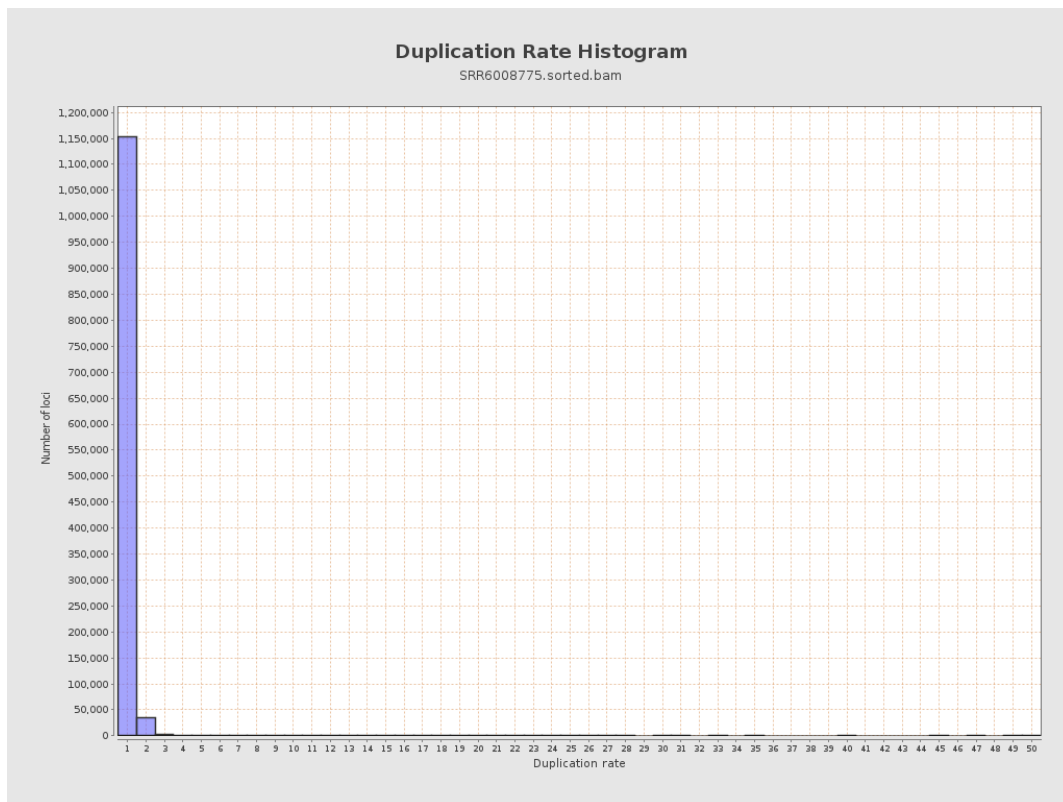
5. Results : Coverage Histogram (0-50X)



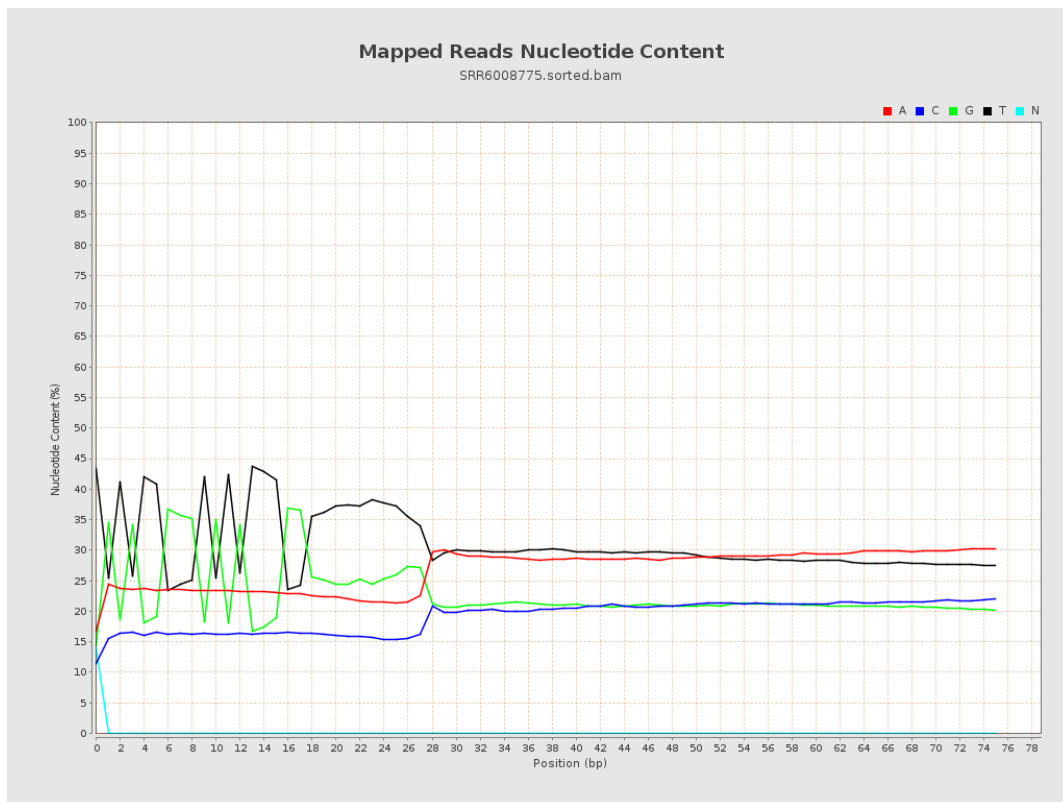
6. Results : Genome Fraction Coverage



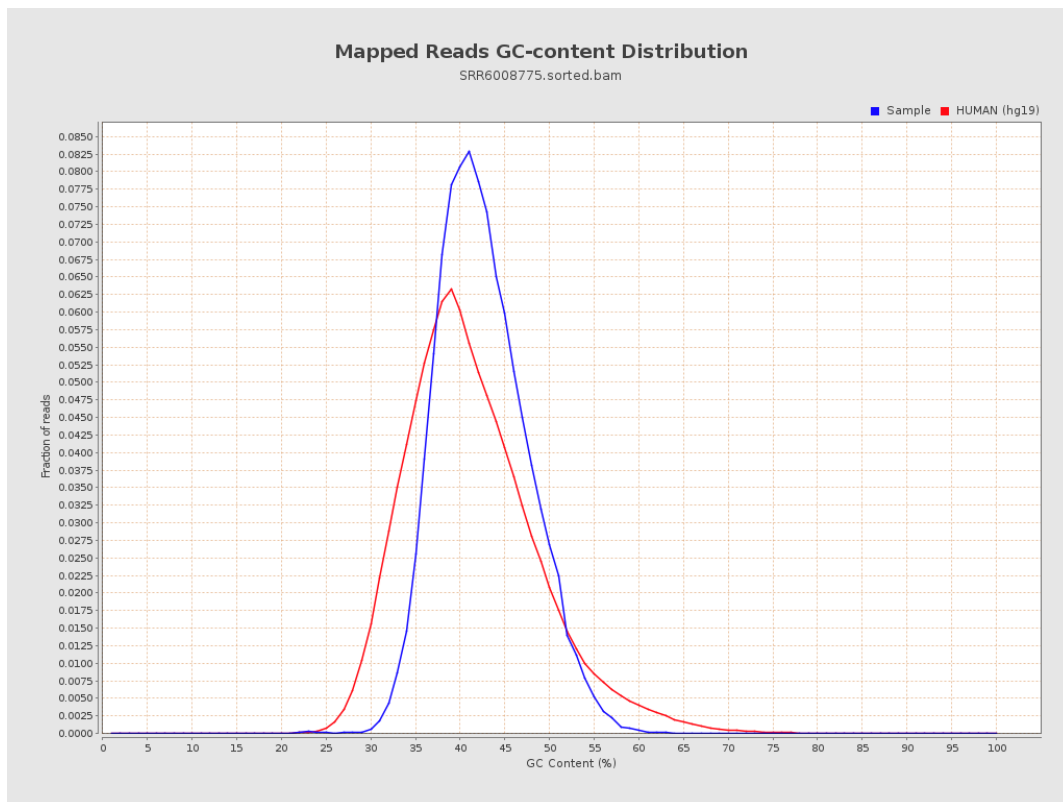
7. Results : Duplication Rate Histogram



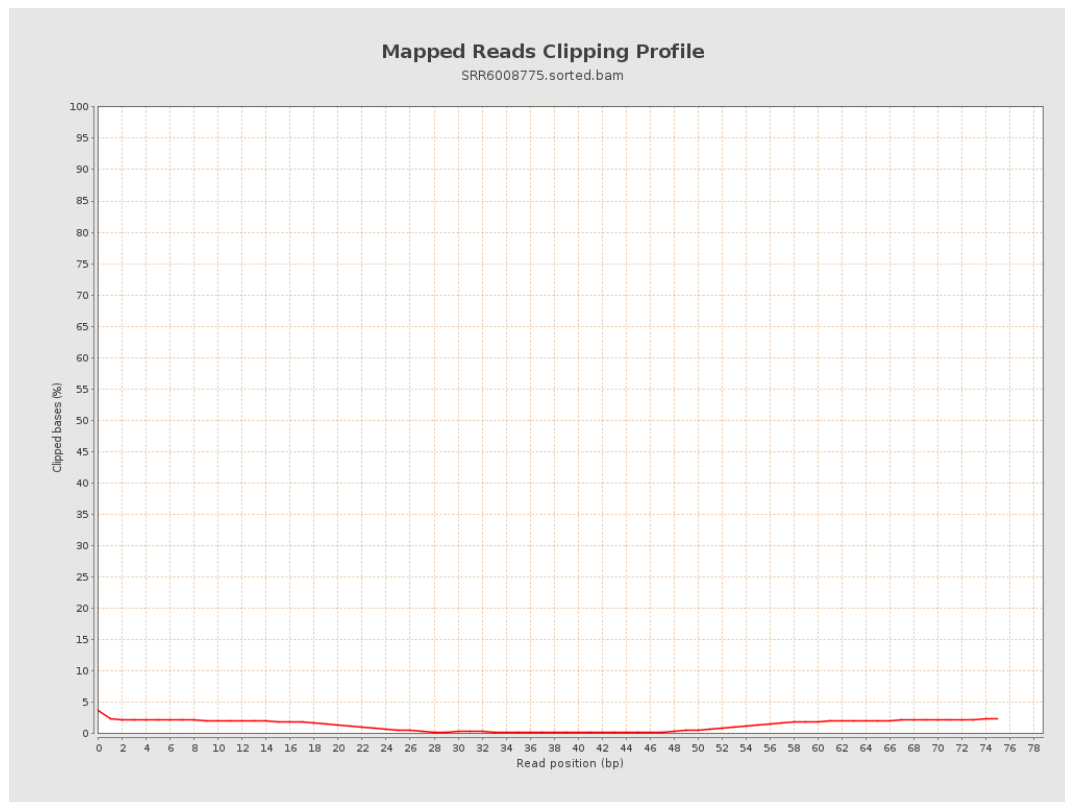
8. Results : Mapped Reads Nucleotide Content



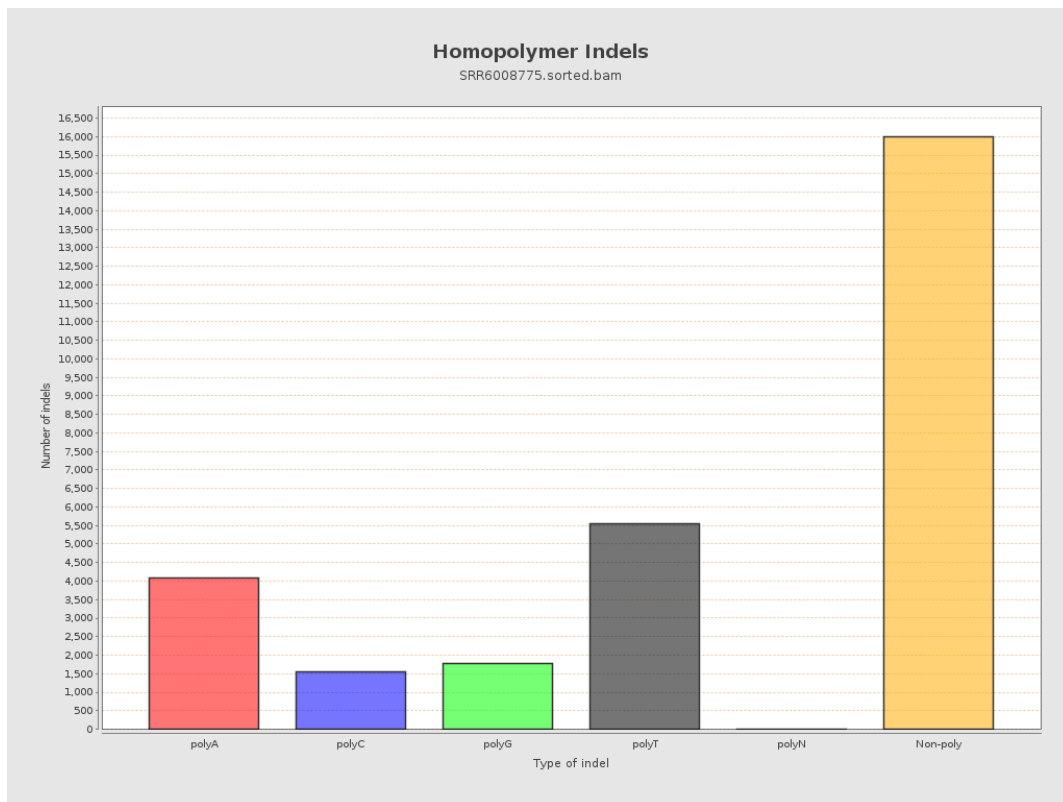
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

