

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 12:49:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008818.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_SRR6008818 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008818.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 12:49:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008818.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	999,145
Mapped reads	749,363 / 75%
Unmapped reads	249,782 / 25%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,126 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	27,140 / 2.72%
Duplication rate	3.16%
Clipped reads	491,593 / 49.2%

2.2. ACGT Content

Number/percentage of A's	13,337,290 / 28.82%
Number/percentage of C's	8,799,187 / 19.01%
Number/percentage of T's	13,674,783 / 29.55%
Number/percentage of G's	10,465,164 / 22.61%
Number/percentage of N's	7,410 / 0.02%
GC Percentage	41.62%

2.3. Coverage

Mean	0.015

Standard Deviation	0.1741
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2.4. Mapping Quality

Mean Mapping Quality	46.3
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2.5. Mismatches and indels

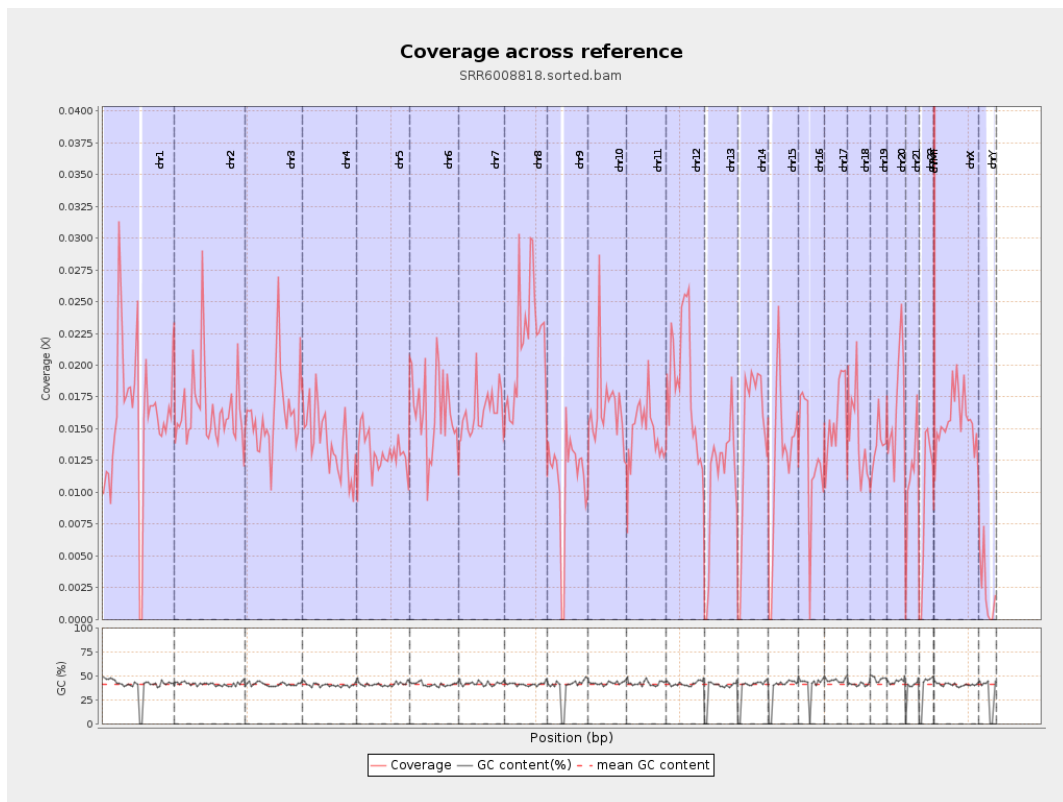
General error rate	0.91%
Mismatches	413,234
Insertions	3,538
Mapped reads with at least one insertion	0.47%
Deletions	15,923
Mapped reads with at least one deletion	2.1%
Homopolymer indels	47.41%

2.6. Chromosome stats

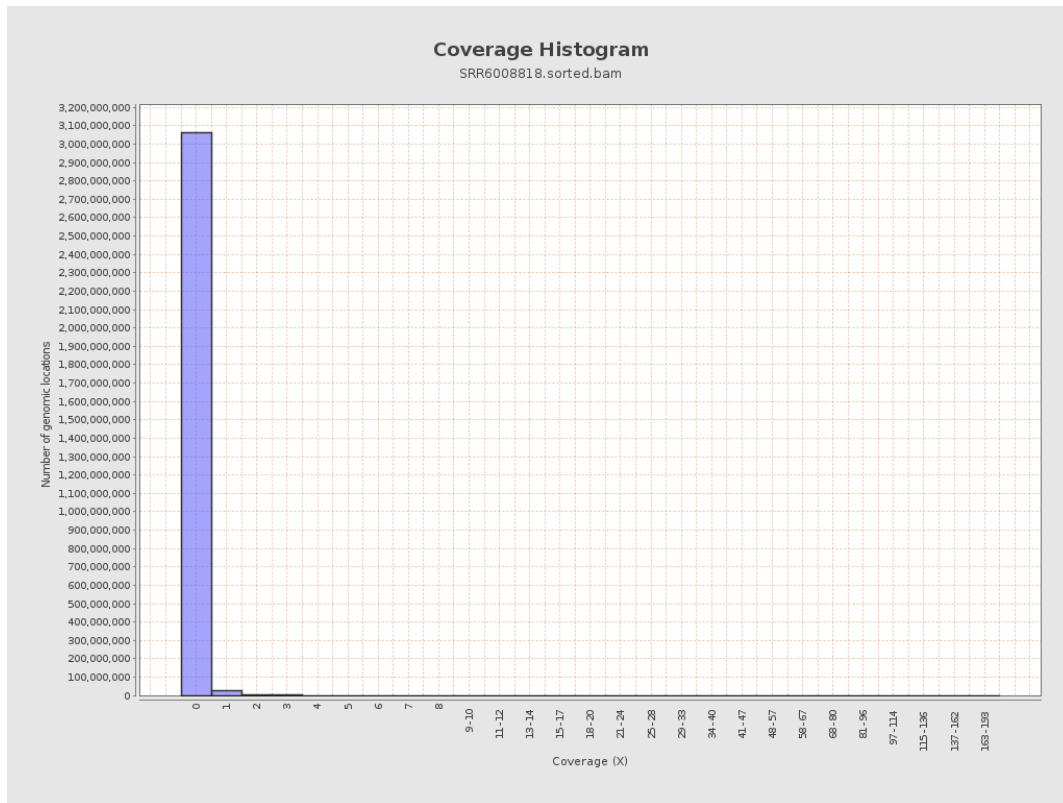
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	3940060	0.0158	0.2216
chr2	243199373	4008856	0.0165	0.1931
chr3	198022430	3213597	0.0162	0.1594
chr4	191154276	2673113	0.014	0.1518
chr5	180915260	2379504	0.0132	0.1437
chr6	171115067	2806342	0.0164	0.1718
chr7	159138663	2596906	0.0163	0.1966

chr8	146364022	3188754	0.0218	0.2134
chr9	141213431	1568929	0.0111	0.1538
chr10	135534747	2251778	0.0166	0.1919
chr11	135006516	1994726	0.0148	0.1742
chr12	133851895	2487886	0.0186	0.178
chr13	115169878	1265253	0.011	0.1304
chr14	107349540	1569174	0.0146	0.1542
chr15	102531392	1311429	0.0128	0.1436
chr16	90354753	1140071	0.0126	0.1427
chr17	81195210	1277186	0.0157	0.168
chr18	78077248	1128243	0.0145	0.237
chr19	59128983	819034	0.0139	0.1725
chr20	63025520	1056912	0.0168	0.165
chr21	48129895	544870	0.0113	0.1418
chr22	51304566	489253	0.0095	0.1211
chrMT	16571	22207	1.3401	1.6281
chrX	155270560	2441347	0.0157	0.1626
chrY	59373566	134079	0.0023	0.0713

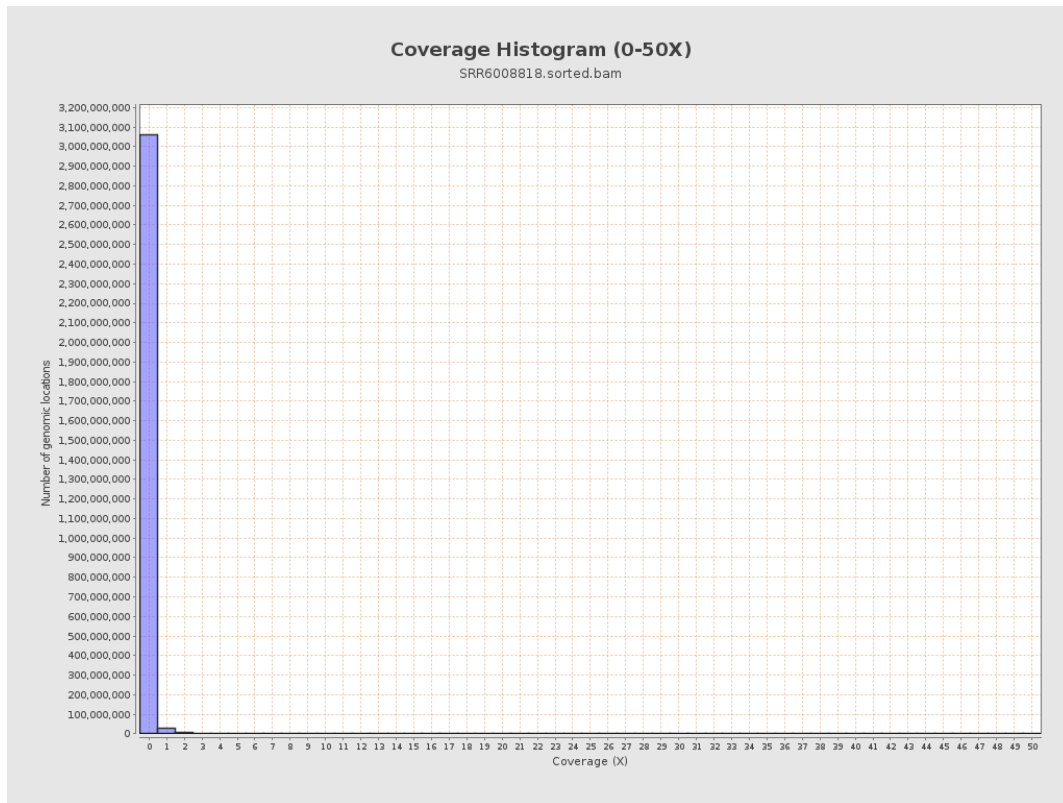
3. Results : Coverage across reference



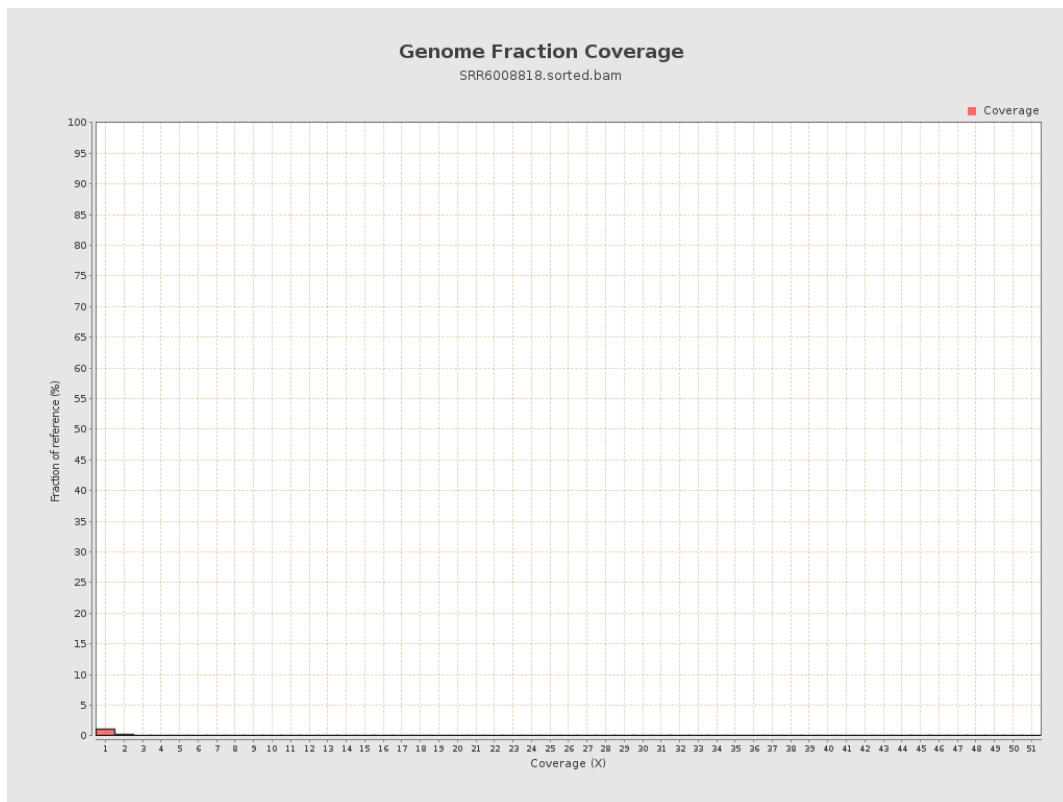
4. Results : Coverage Histogram



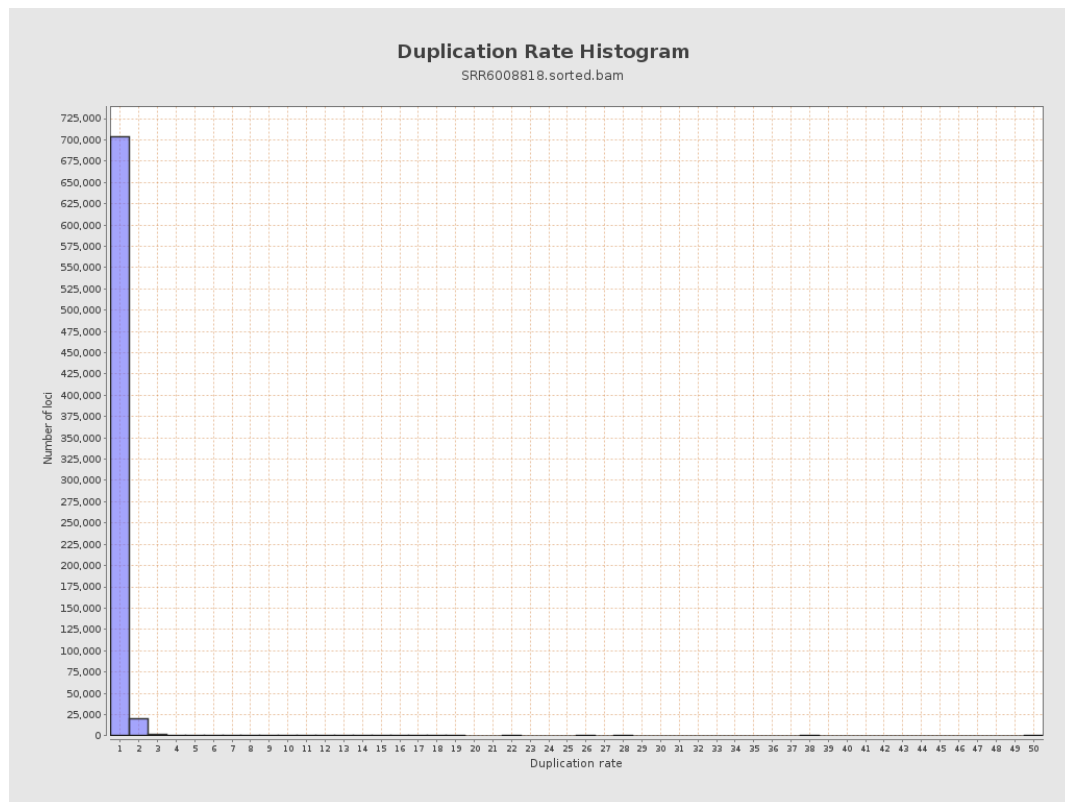
5. Results : Coverage Histogram (0-50X)



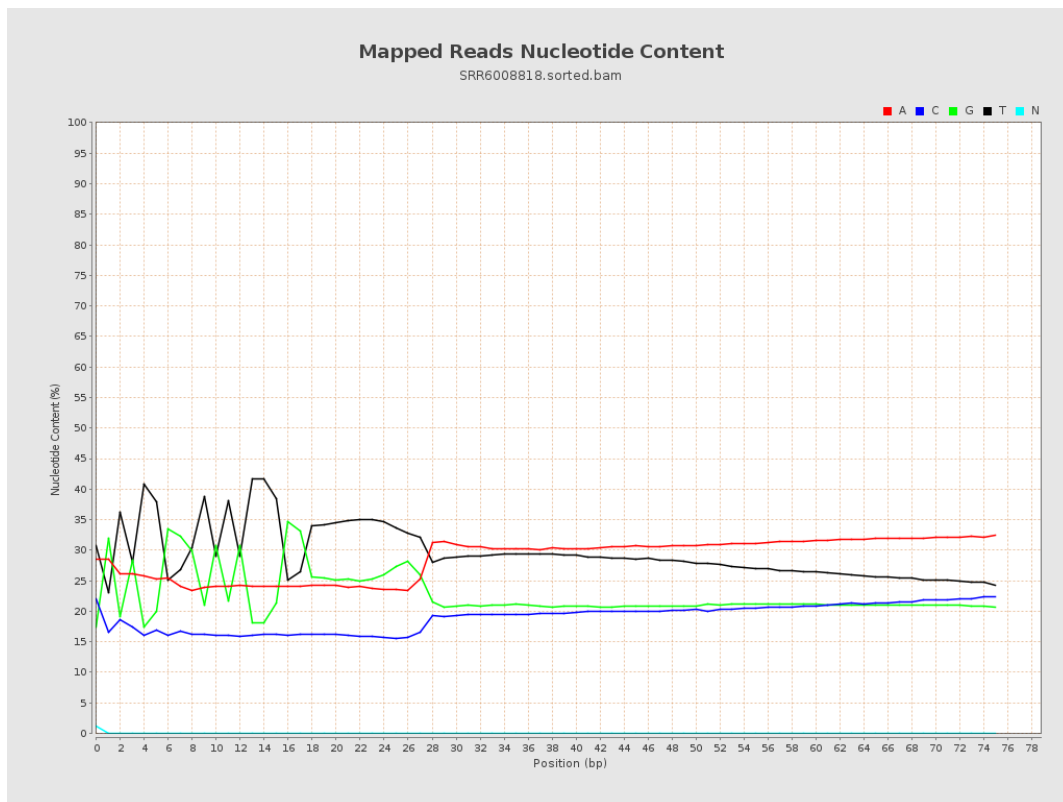
6. Results : Genome Fraction Coverage



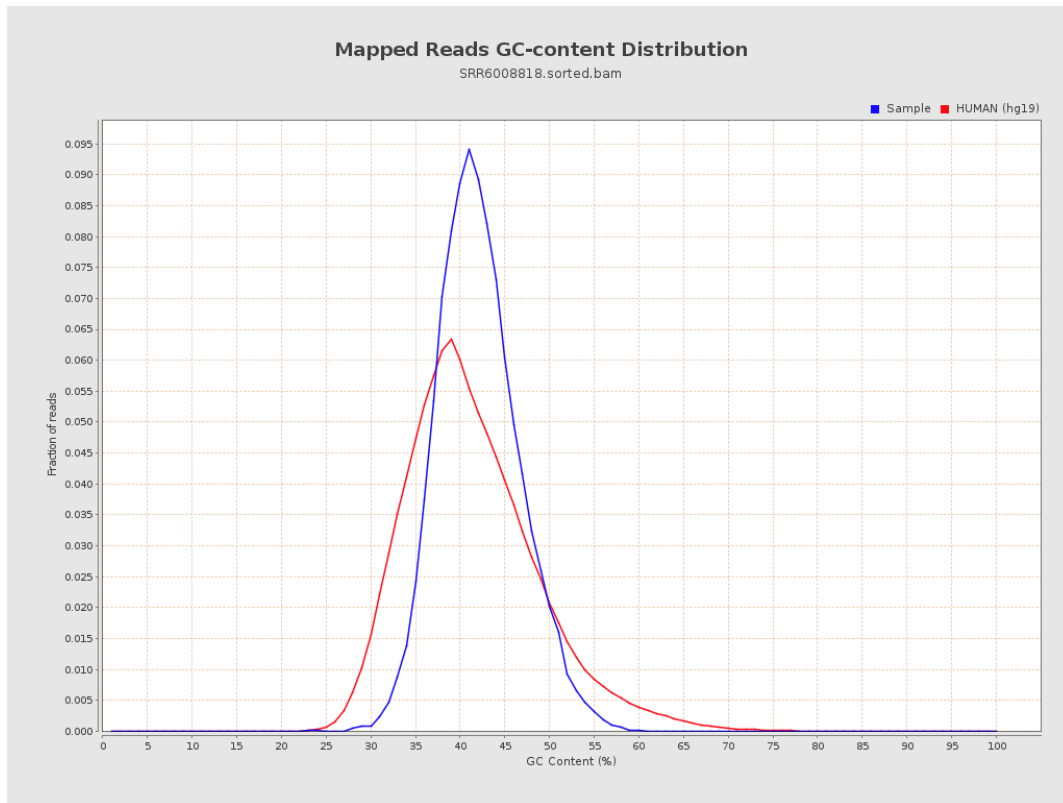
7. Results : Duplication Rate Histogram



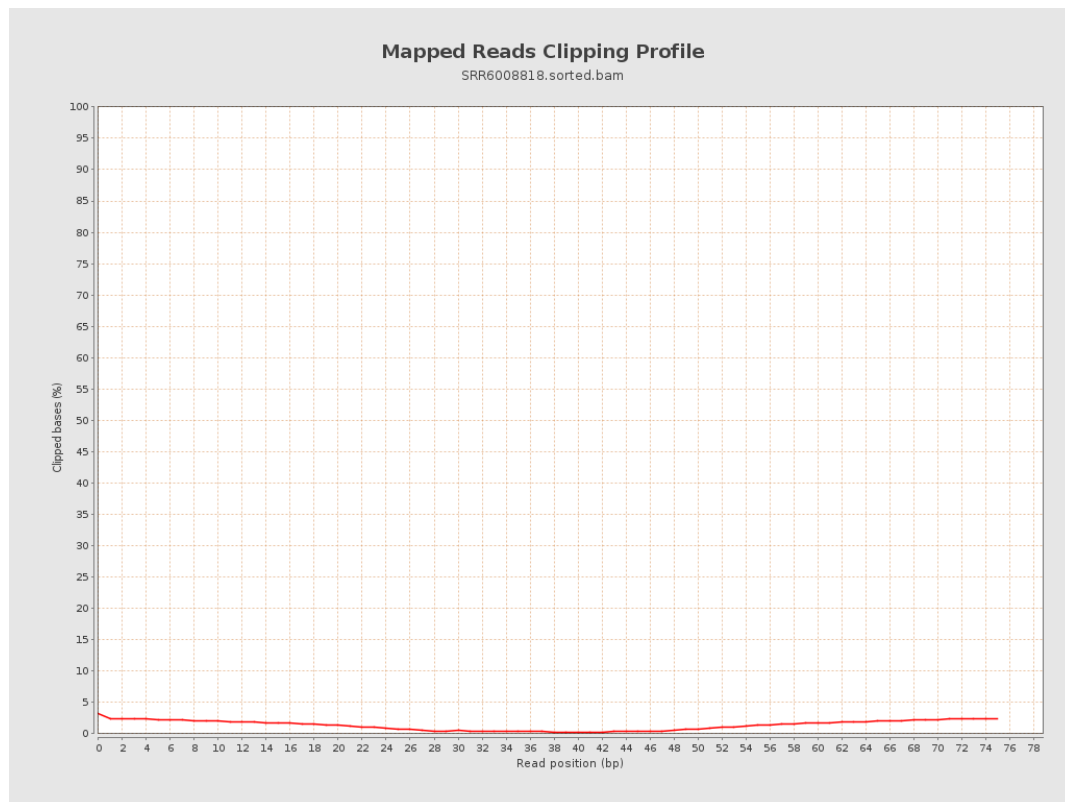
8. Results : Mapped Reads Nucleotide Content



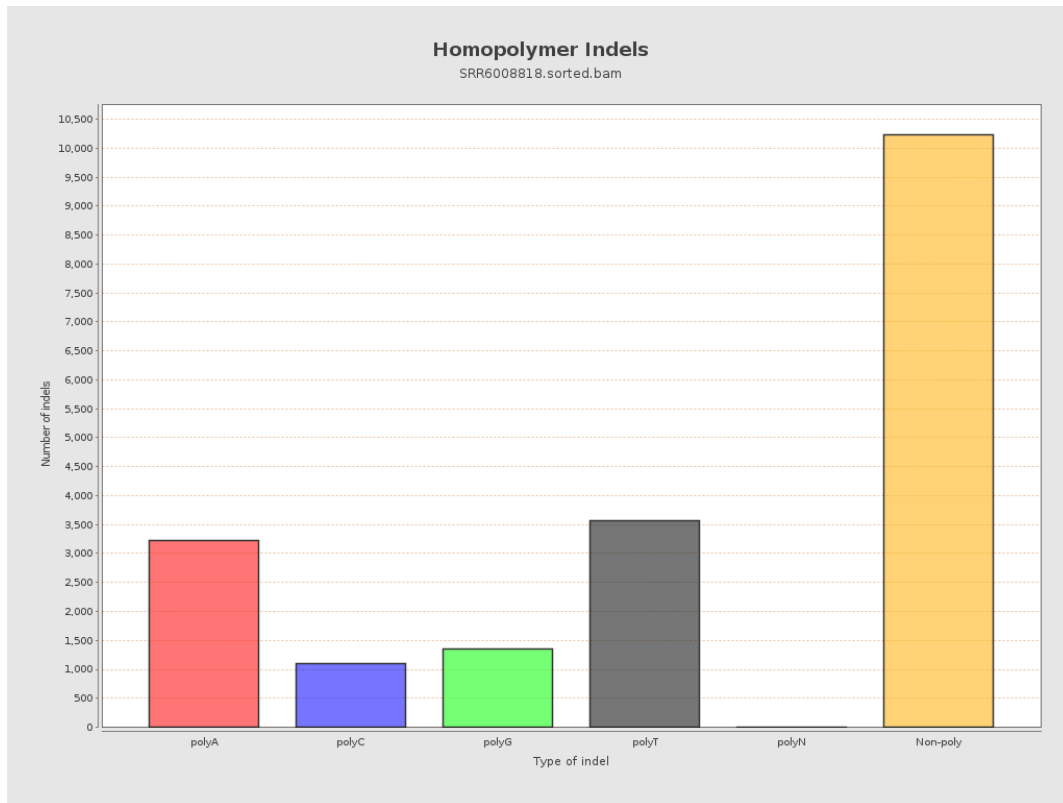
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

