

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 09:52:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008753.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_SRR6008753 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008753.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 09:52:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008753.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,196,128
Mapped reads	770,029 / 64.38%
Unmapped reads	426,099 / 35.62%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,048 / 0.25%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	22,466 / 1.88%
Duplication rate	2.34%
Clipped reads	386,283 / 32.29%

2.2. ACGT Content

Number/percentage of A's	14,932,373 / 29.85%
Number/percentage of C's	8,507,353 / 17.01%
Number/percentage of T's	14,965,813 / 29.92%
Number/percentage of G's	11,608,092 / 23.21%
Number/percentage of N's	3,119 / 0.01%
GC Percentage	40.22%

2.3. Coverage

Mean	0.0162

Standard Deviation	0.163
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2.4. Mapping Quality

Mean Mapping Quality	47.61
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2.5. Mismatches and indels

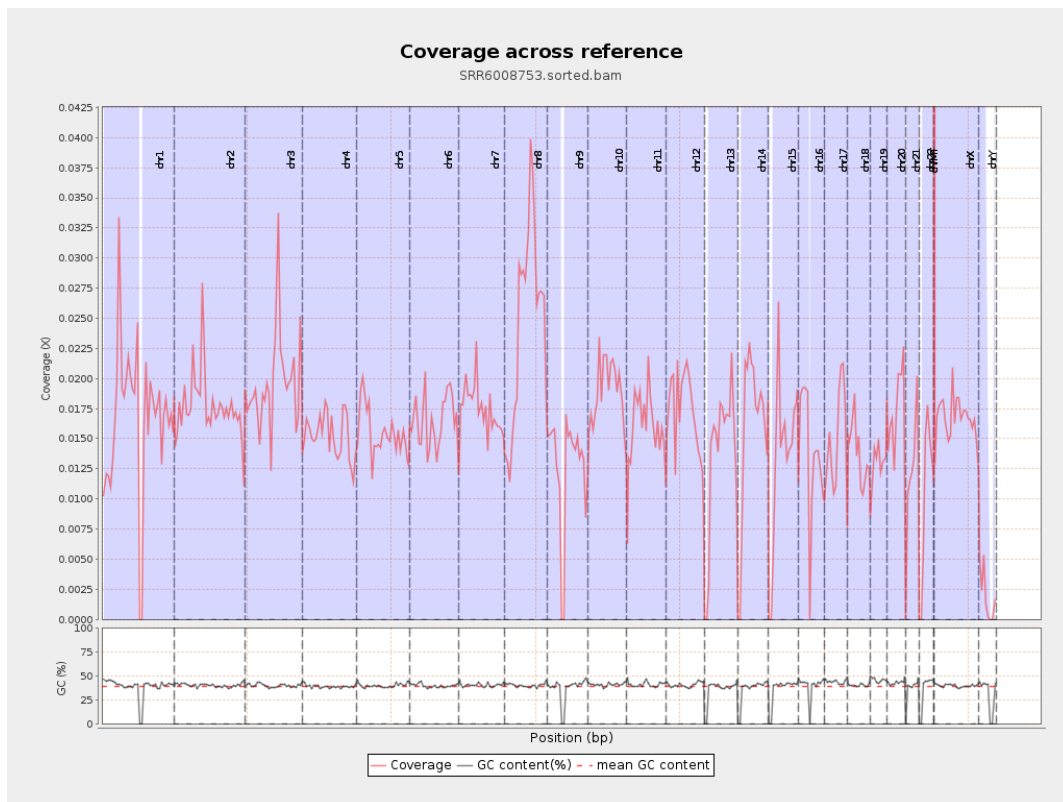
General error rate	1.12%
Mismatches	555,097
Insertions	3,941
Mapped reads with at least one insertion	0.51%
Deletions	18,368
Mapped reads with at least one deletion	2.35%
Homopolymer indels	49.82%

2.6. Chromosome stats

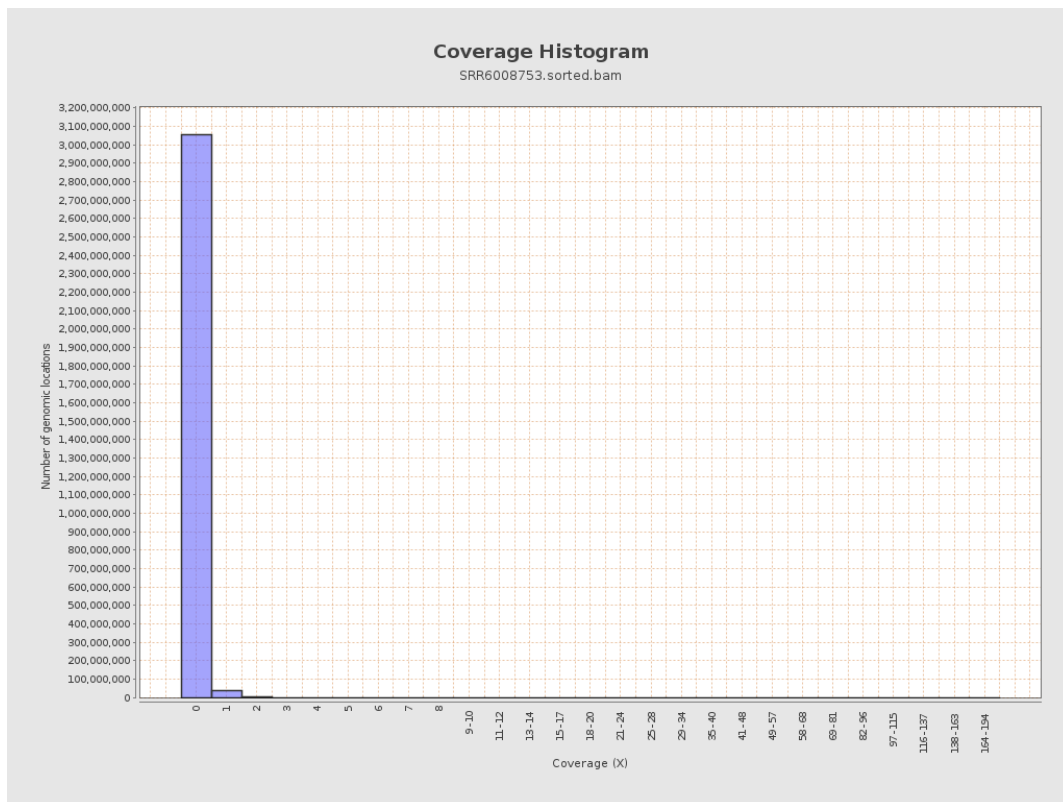
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	4135256	0.0166	0.2032
chr2	243199373	4313079	0.0177	0.1812
chr3	198022430	3876981	0.0196	0.161
chr4	191154276	2911120	0.0152	0.1412
chr5	180915260	2816847	0.0156	0.1416
chr6	171115067	2819576	0.0165	0.1549
chr7	159138663	2784127	0.0175	0.1873

chr8	146364022	3646596	0.0249	0.2181
chr9	141213431	1781792	0.0126	0.152
chr10	135534747	2560858	0.0189	0.1724
chr11	135006516	2184452	0.0162	0.1623
chr12	133851895	2320417	0.0173	0.1514
chr13	115169878	1570254	0.0136	0.1338
chr14	107349540	1698678	0.0158	0.1448
chr15	102531392	1387375	0.0135	0.1333
chr16	90354753	1223187	0.0135	0.137
chr17	81195210	1210849	0.0149	0.1476
chr18	78077248	1072172	0.0137	0.201
chr19	59128983	780407	0.0132	0.1454
chr20	63025520	1085981	0.0172	0.1495
chr21	48129895	589799	0.0123	0.1322
chr22	51304566	539972	0.0105	0.1169
chrMT	16571	18992	1.1461	1.509
chrX	155270560	2603945	0.0168	0.1519
chrY	59373566	111841	0.0019	0.0529

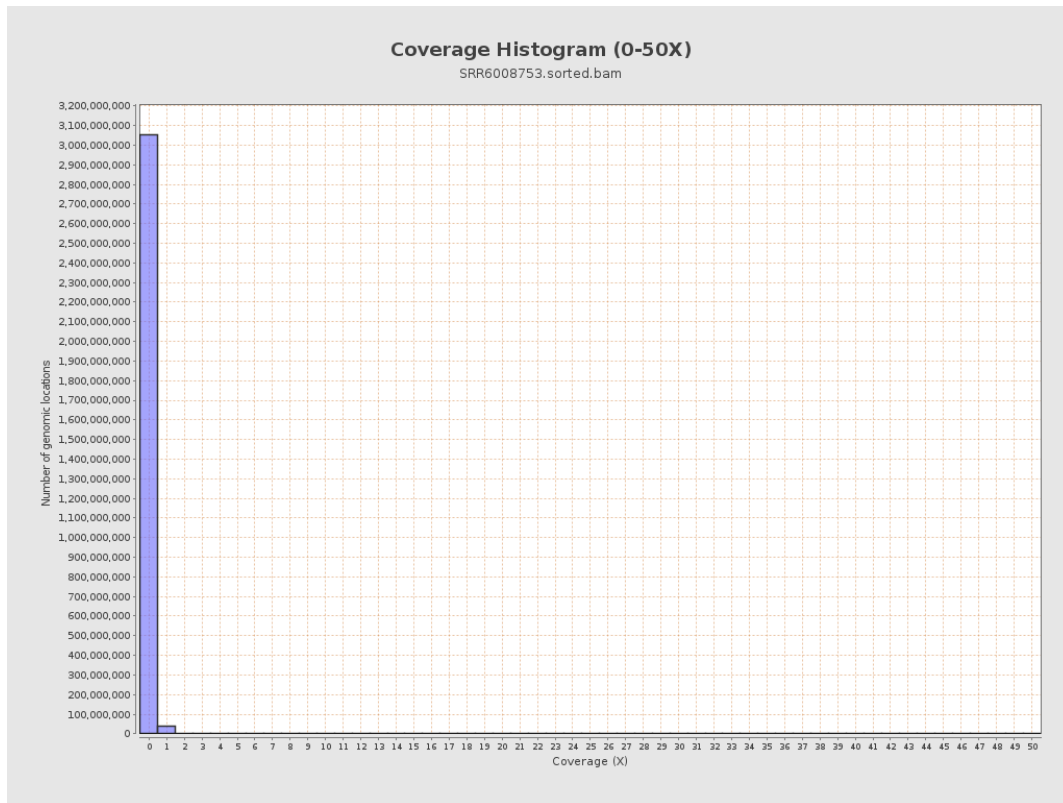
3. Results : Coverage across reference



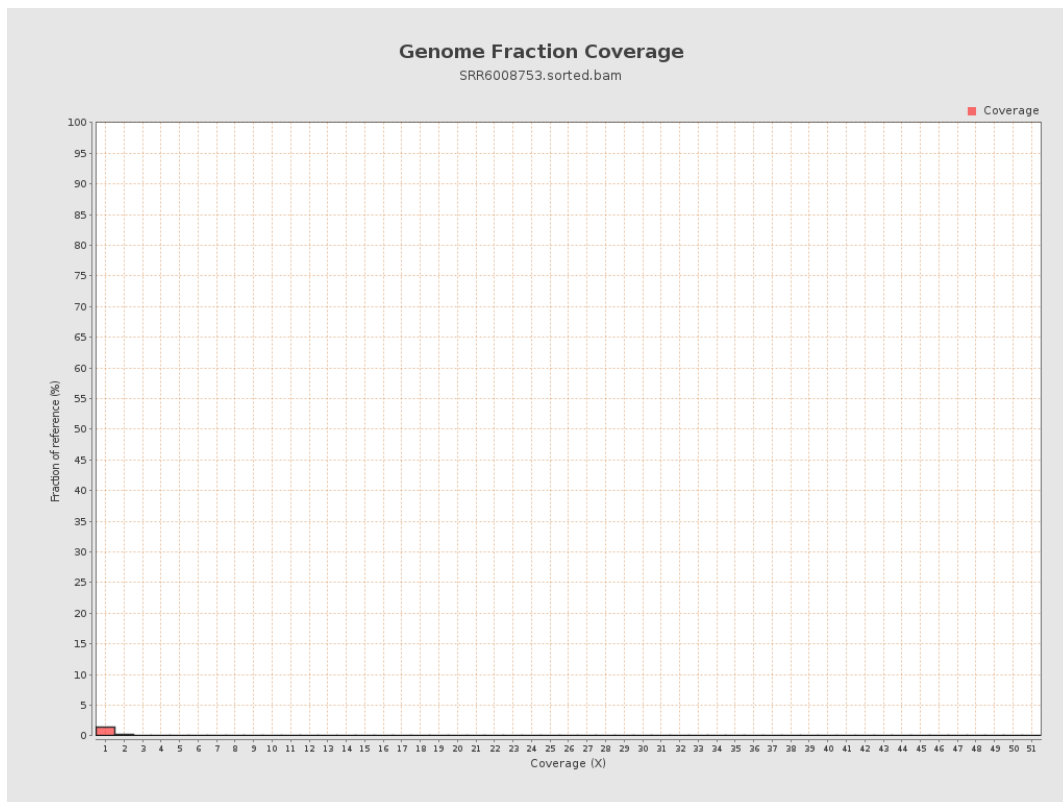
4. Results : Coverage Histogram



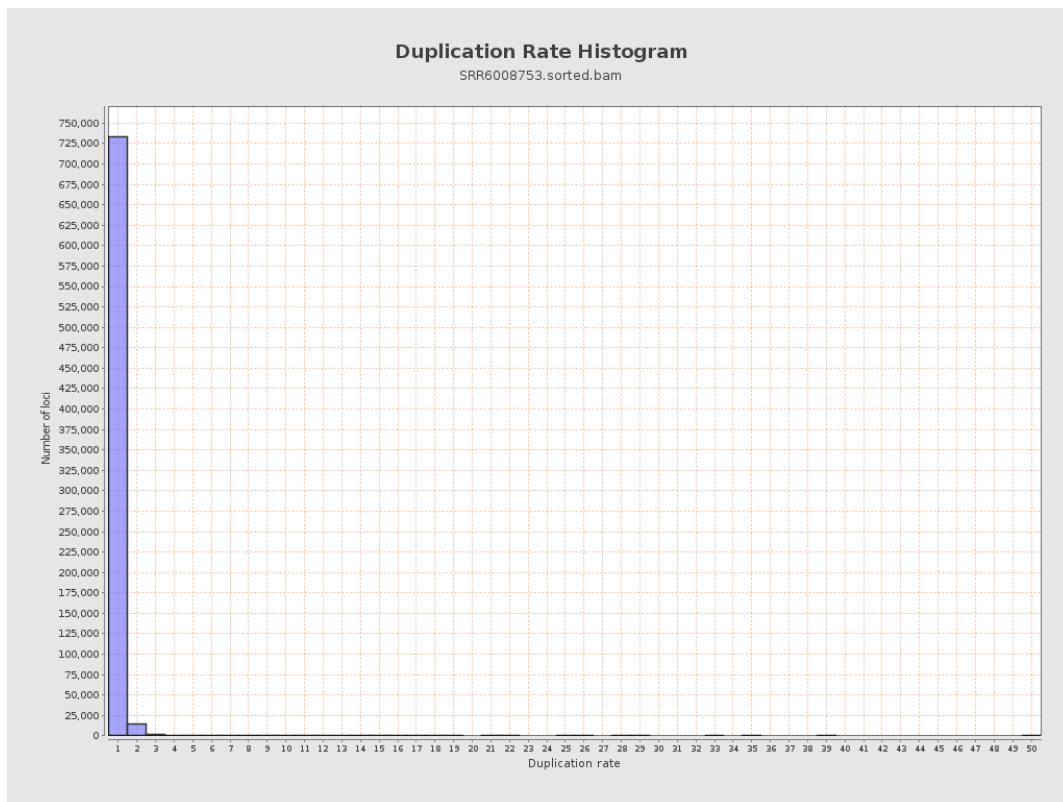
5. Results : Coverage Histogram (0-50X)



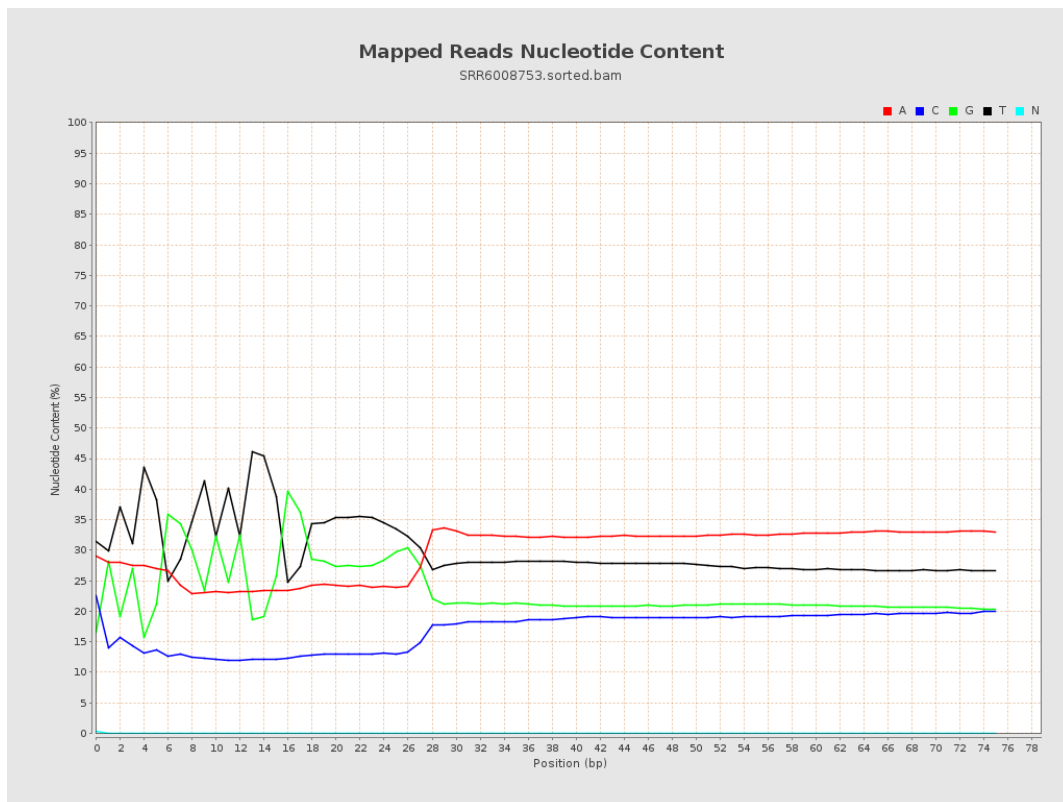
6. Results : Genome Fraction Coverage



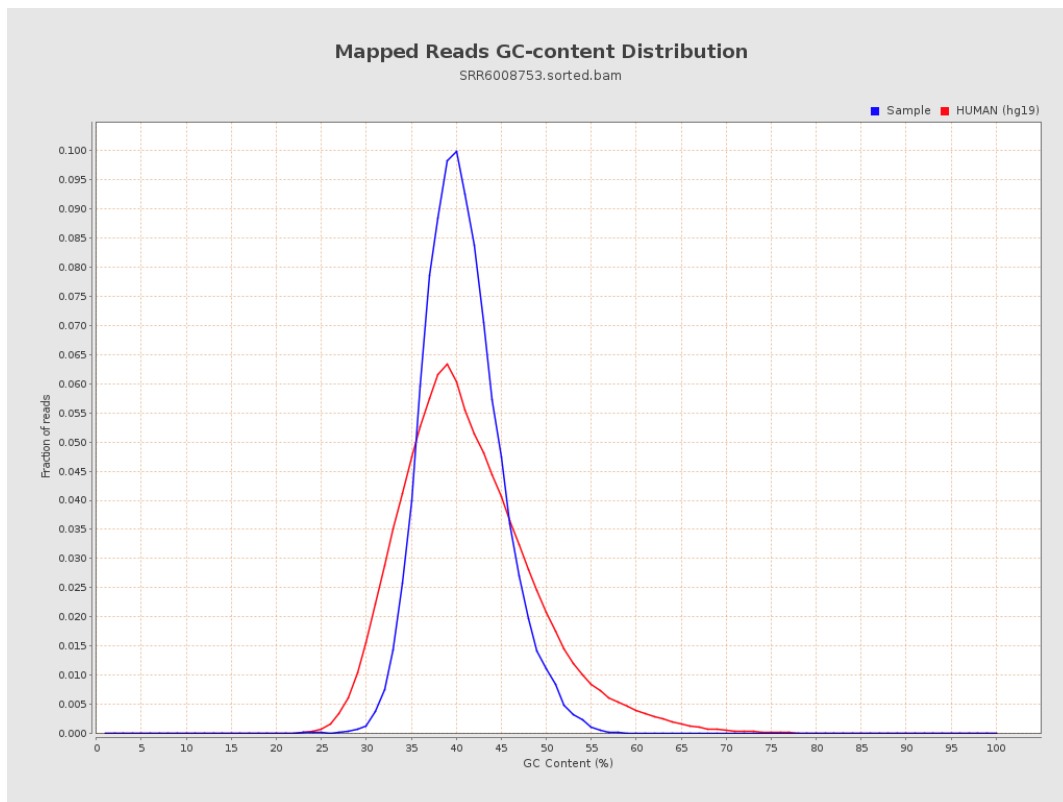
7. Results : Duplication Rate Histogram



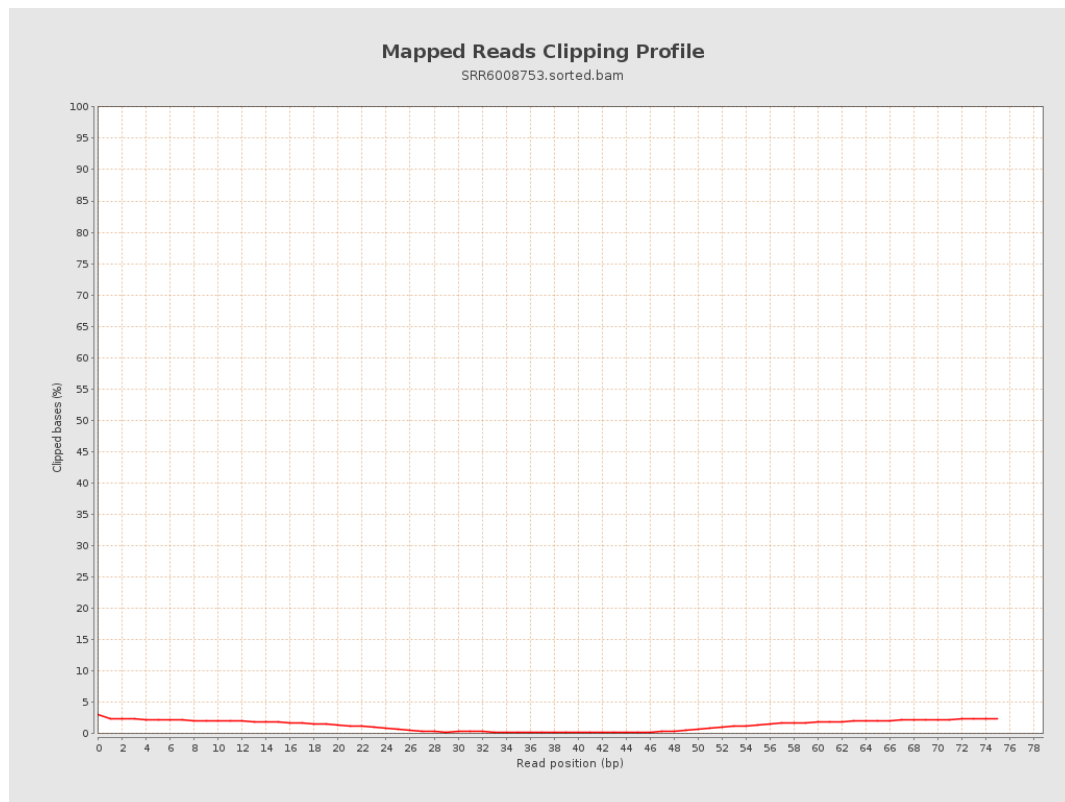
8. Results : Mapped Reads Nucleotide Content



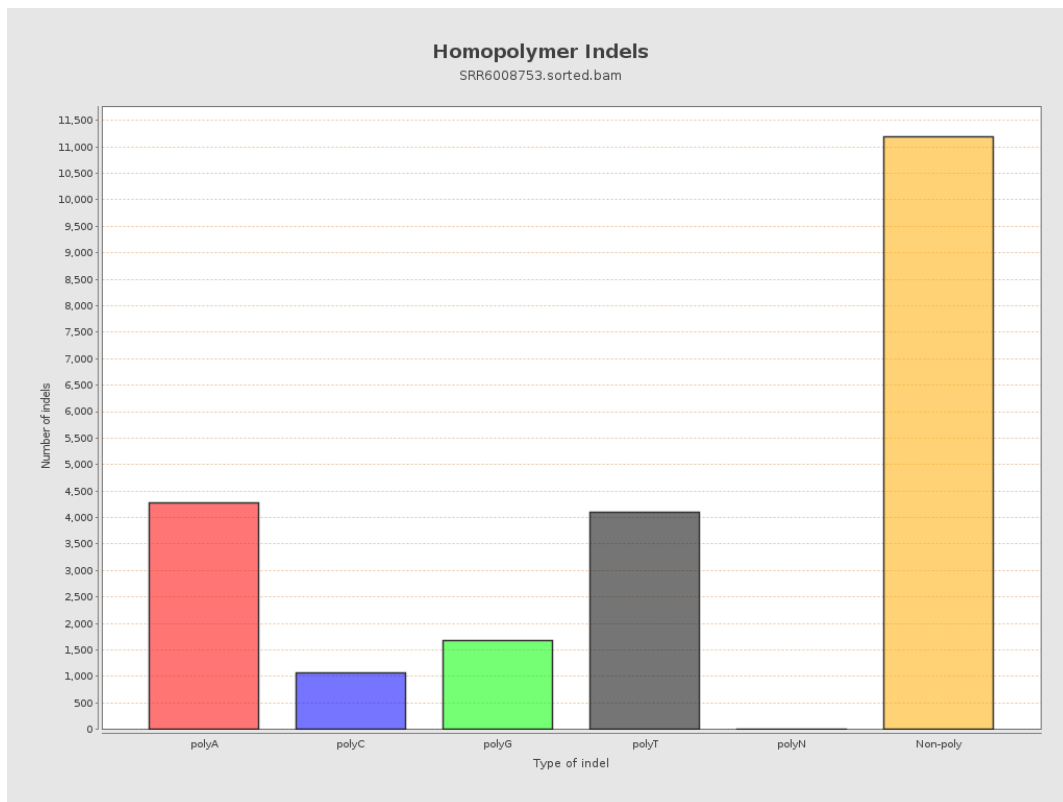
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

