

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 07:42:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008703.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_SRR6008703 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008703.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 07:42:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008703.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,177,825
Mapped reads	801,190 / 68.02%
Unmapped reads	376,635 / 31.98%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,101 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	21,410 / 1.82%
Duplication rate	2.25%
Clipped reads	423,363 / 35.94%

2.2. ACGT Content

Number/percentage of A's	15,410,119 / 29.69%
Number/percentage of C's	8,669,336 / 16.7%
Number/percentage of T's	15,687,236 / 30.23%
Number/percentage of G's	12,129,266 / 23.37%
Number/percentage of N's	2,508 / 0%
GC Percentage	40.08%

2.3. Coverage

Mean	0.0168

Standard Deviation	0.168
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2.4. Mapping Quality

Mean Mapping Quality	46.8
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2.5. Mismatches and indels

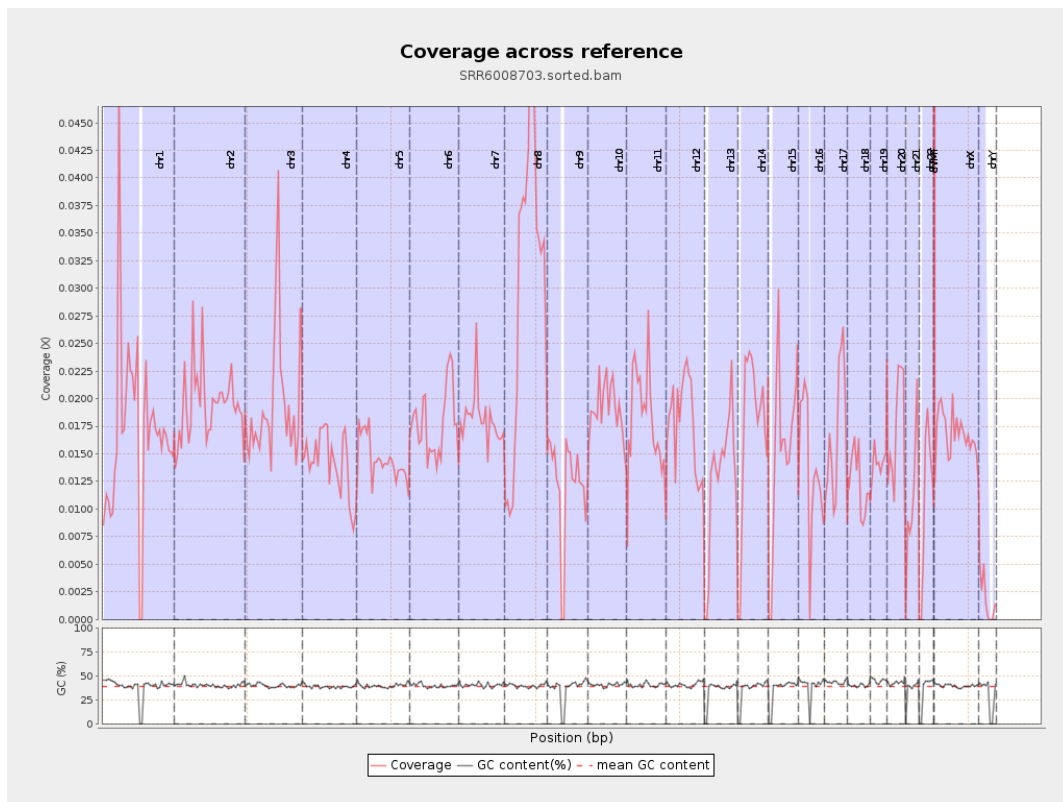
General error rate	1.01%
Mismatches	518,754
Insertions	4,328
Mapped reads with at least one insertion	0.54%
Deletions	20,889
Mapped reads with at least one deletion	2.57%
Homopolymer indels	48.48%

2.6. Chromosome stats

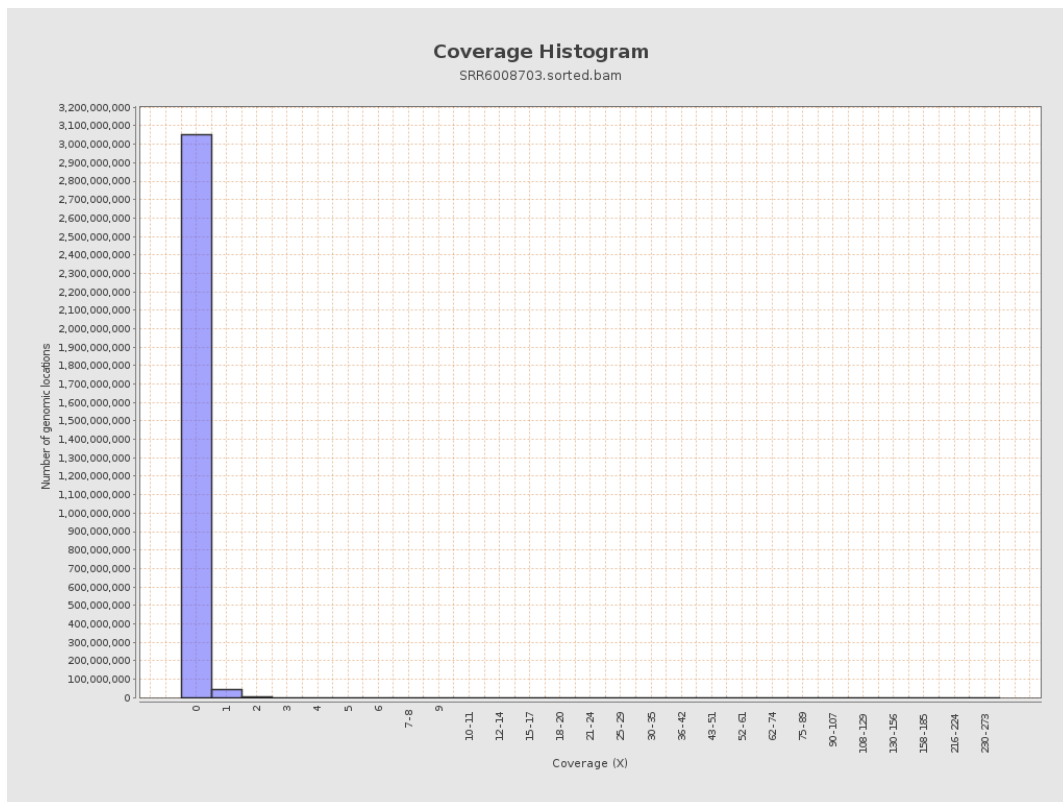
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	4181893	0.0168	0.1954
chr2	243199373	4738300	0.0195	0.2224
chr3	198022430	3836021	0.0194	0.1547
chr4	191154276	2704290	0.0141	0.1329
chr5	180915260	2642674	0.0146	0.1334
chr6	171115067	3038635	0.0178	0.156
chr7	159138663	2894282	0.0182	0.2095

chr8	146364022	4506368	0.0308	0.2587
chr9	141213431	1725490	0.0122	0.1374
chr10	135534747	2572865	0.019	0.1632
chr11	135006516	2480967	0.0184	0.1713
chr12	133851895	2380506	0.0178	0.148
chr13	115169878	1471934	0.0128	0.1247
chr14	107349540	1860724	0.0173	0.1497
chr15	102531392	1580356	0.0154	0.1376
chr16	90354753	1222687	0.0135	0.1348
chr17	81195210	1346034	0.0166	0.1496
chr18	78077248	963740	0.0123	0.1957
chr19	59128983	856530	0.0145	0.1481
chr20	63025520	1083951	0.0172	0.1473
chr21	48129895	536371	0.0111	0.1206
chr22	51304566	559890	0.0109	0.1146
chrMT	16571	20696	1.2489	1.56
chrX	155270560	2615794	0.0168	0.1487
chrY	59373566	110926	0.0019	0.0526

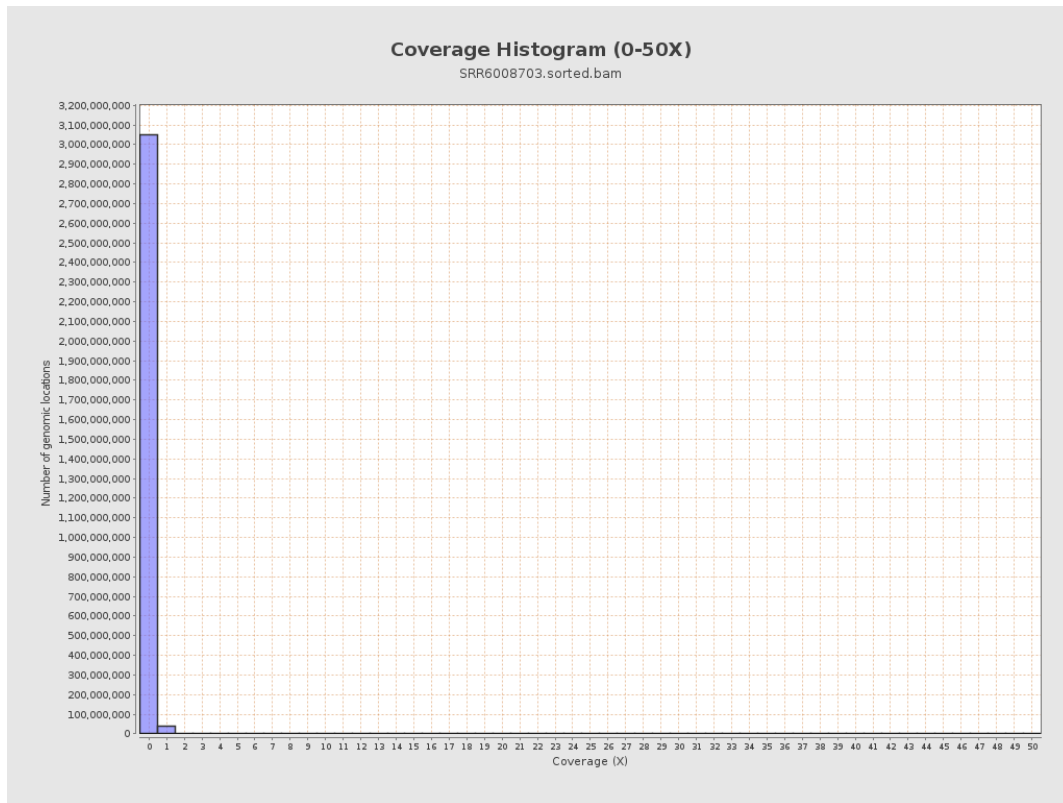
3. Results : Coverage across reference



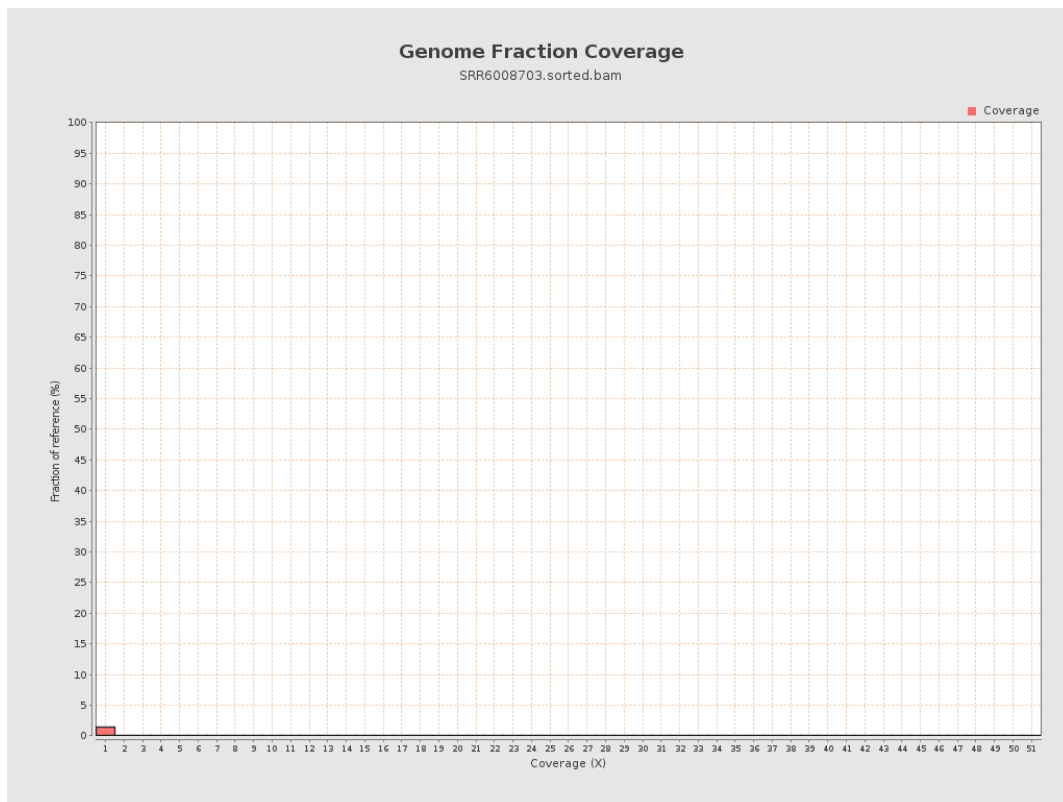
4. Results : Coverage Histogram



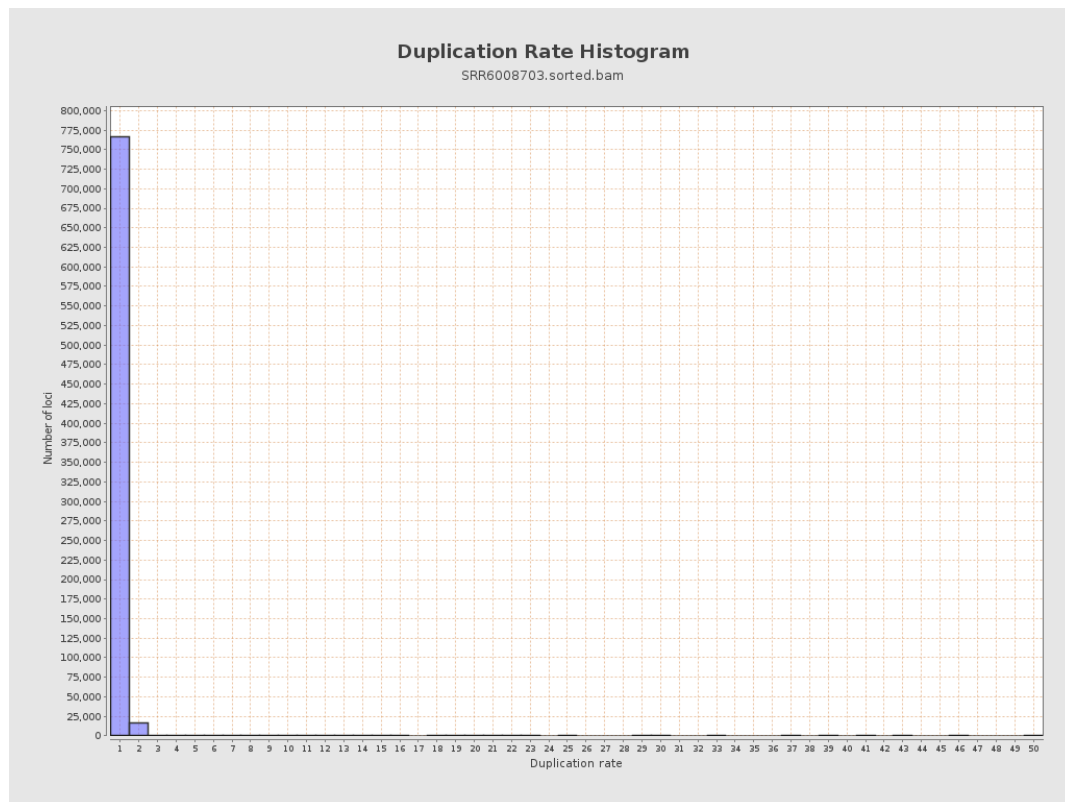
5. Results : Coverage Histogram (0-50X)



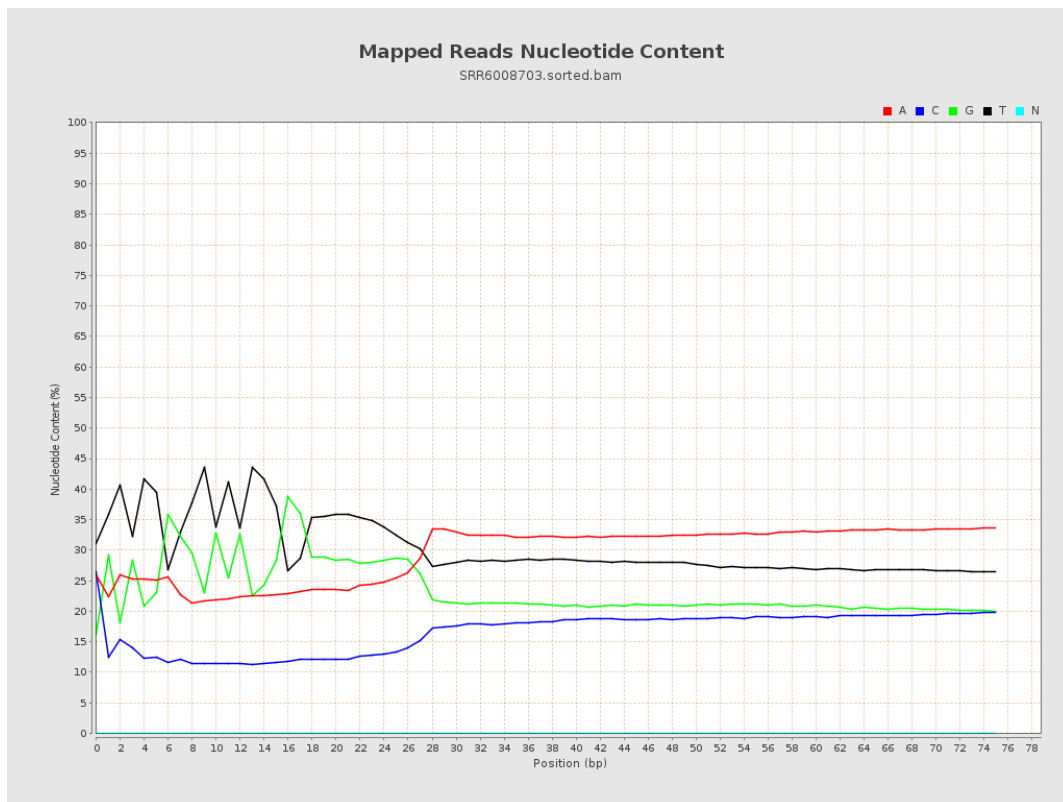
6. Results : Genome Fraction Coverage



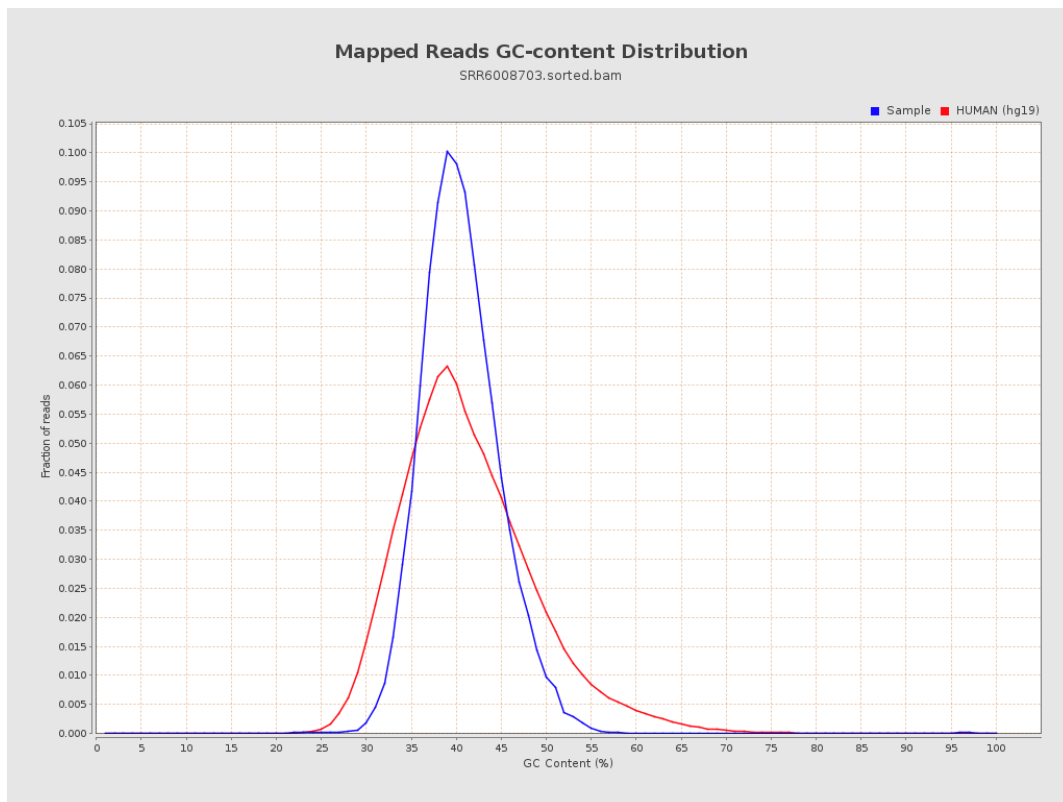
7. Results : Duplication Rate Histogram



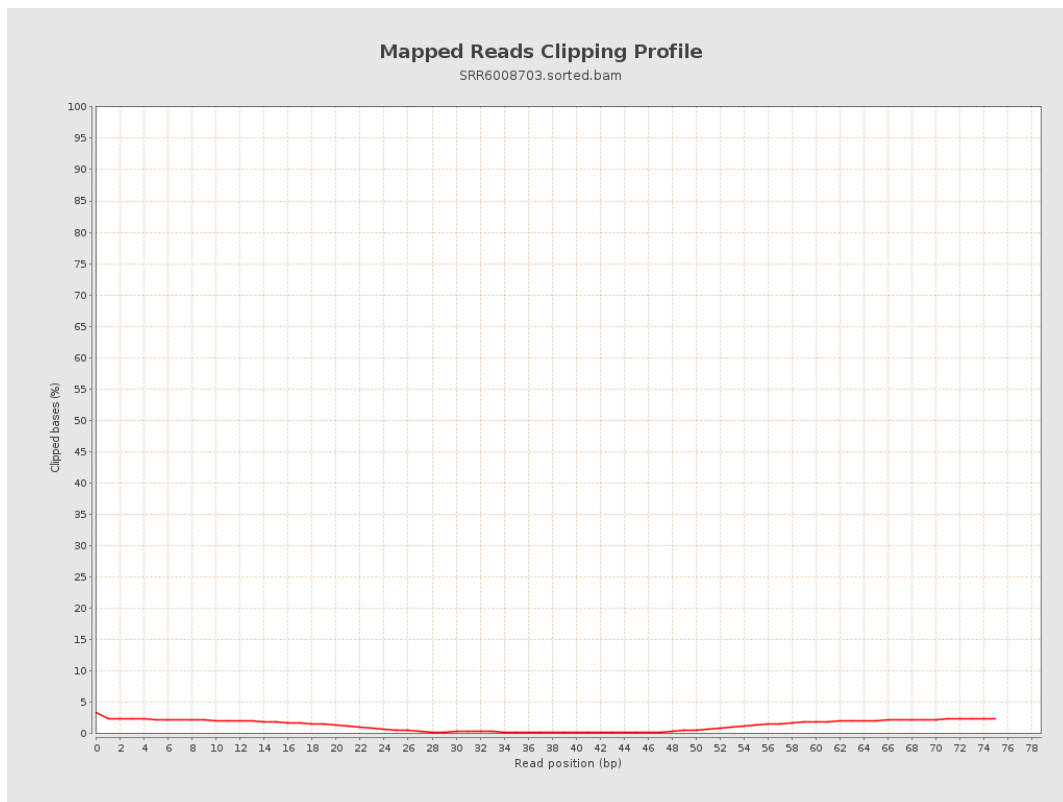
8. Results : Mapped Reads Nucleotide Content



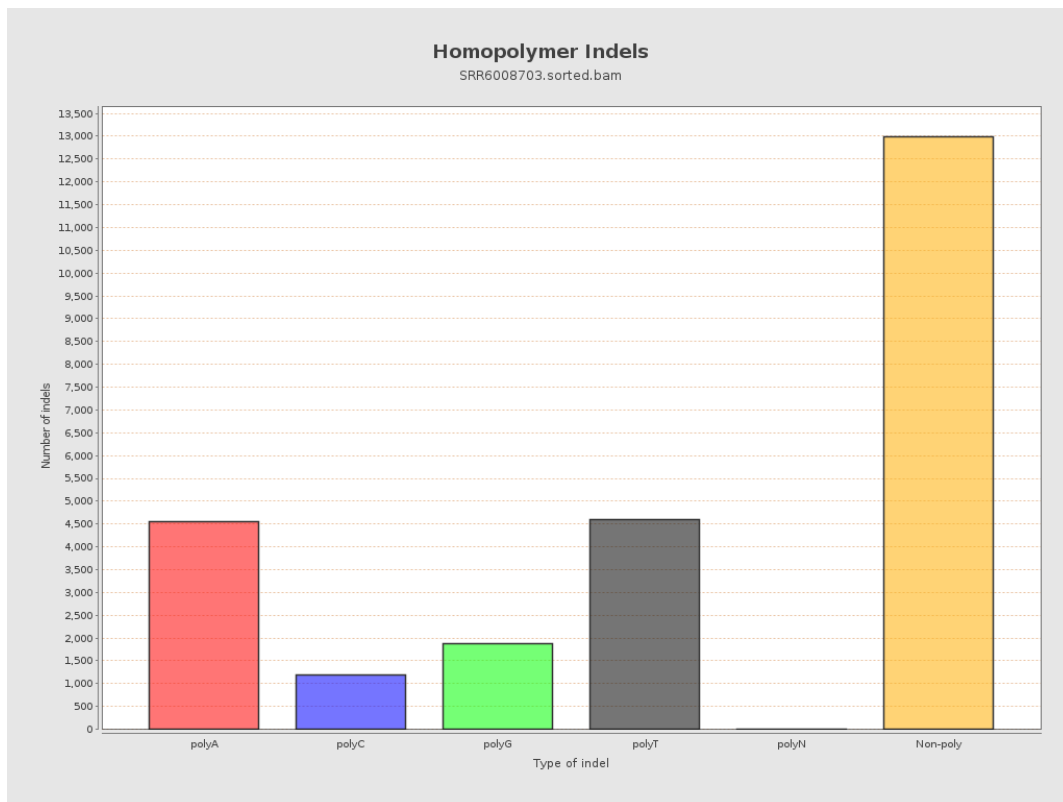
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

