

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 09:19:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008740.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_SRR6008740 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008740.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 09:19:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008740.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,465,075
Mapped reads	1,007,919 / 68.8%
Unmapped reads	457,156 / 31.2%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,267 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	21,098 / 1.44%
Duplication rate	1.54%
Clipped reads	434,491 / 29.66%

2.2. ACGT Content

Number/percentage of A's	19,415,776 / 28.86%
Number/percentage of C's	12,152,538 / 18.06%
Number/percentage of T's	20,304,558 / 30.18%
Number/percentage of G's	15,391,842 / 22.88%
Number/percentage of N's	16,832 / 0.03%
GC Percentage	40.94%

2.3. Coverage

Mean	0.0217

Standard Deviation	0.2043
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2.4. Mapping Quality

Mean Mapping Quality	45.47
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2.5. Mismatches and indels

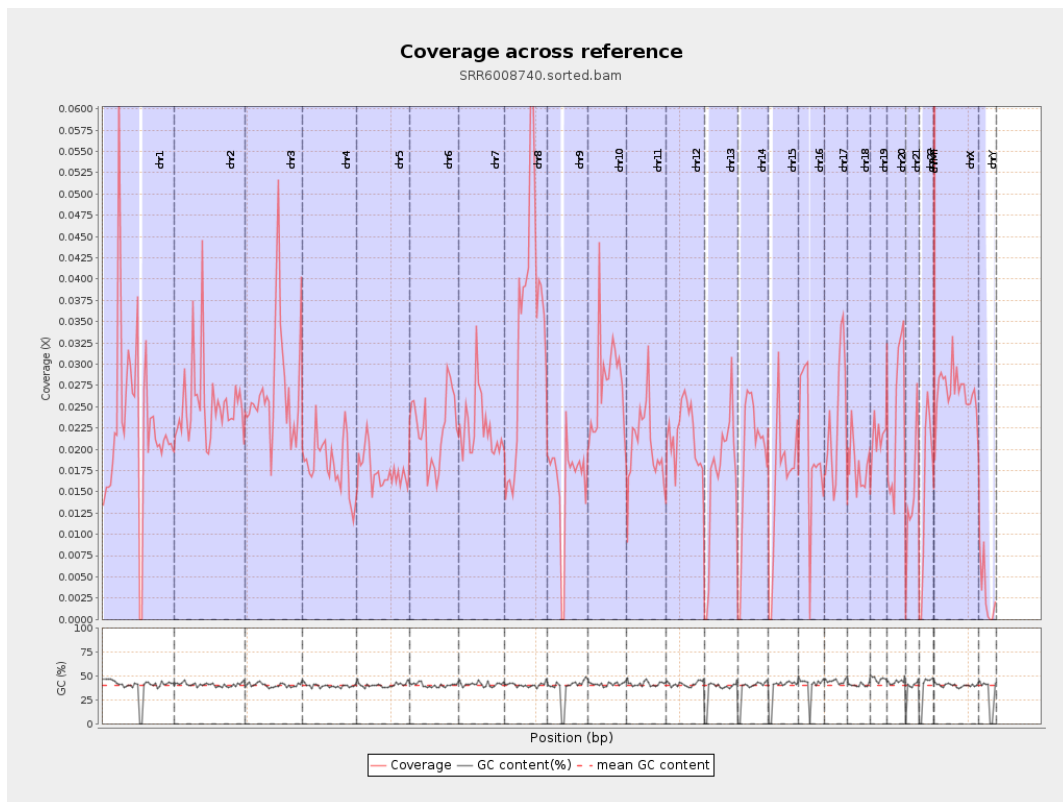
General error rate	1.02%
Mismatches	680,020
Insertions	5,304
Mapped reads with at least one insertion	0.52%
Deletions	20,387
Mapped reads with at least one deletion	2%
Homopolymer indels	46.11%

2.6. Chromosome stats

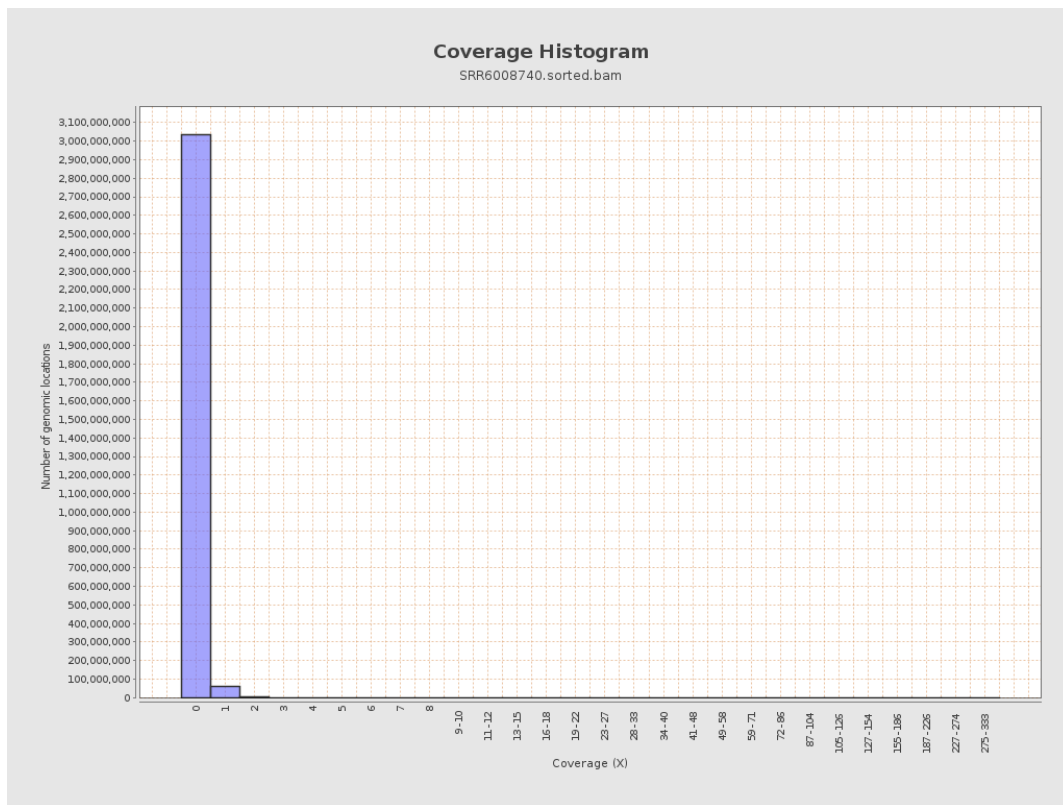
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5617098	0.0225	0.3198
chr2	243199373	6140904	0.0253	0.2528
chr3	198022430	5339402	0.027	0.1717
chr4	191154276	3492725	0.0183	0.1468
chr5	180915260	3151668	0.0174	0.1373
chr6	171115067	3829486	0.0224	0.1711
chr7	159138663	3582649	0.0225	0.2318

chr8	146364022	5023624	0.0343	0.2563
chr9	141213431	2285023	0.0162	0.1774
chr10	135534747	3722189	0.0275	0.2428
chr11	135006516	2803687	0.0208	0.1912
chr12	133851895	2898745	0.0217	0.1542
chr13	115169878	1938331	0.0168	0.1341
chr14	107349540	2072982	0.0193	0.1495
chr15	102531392	1683201	0.0164	0.1329
chr16	90354753	1811128	0.02	0.1615
chr17	81195210	1899237	0.0234	0.1753
chr18	78077248	1397239	0.0179	0.3196
chr19	59128983	1285813	0.0217	0.2215
chr20	63025520	1479603	0.0235	0.1625
chr21	48129895	719082	0.0149	0.1375
chr22	51304566	799581	0.0156	0.1293
chrMT	16571	9961	0.6011	0.8677
chrX	155270560	4154342	0.0268	0.1823
chrY	59373566	177976	0.003	0.0778

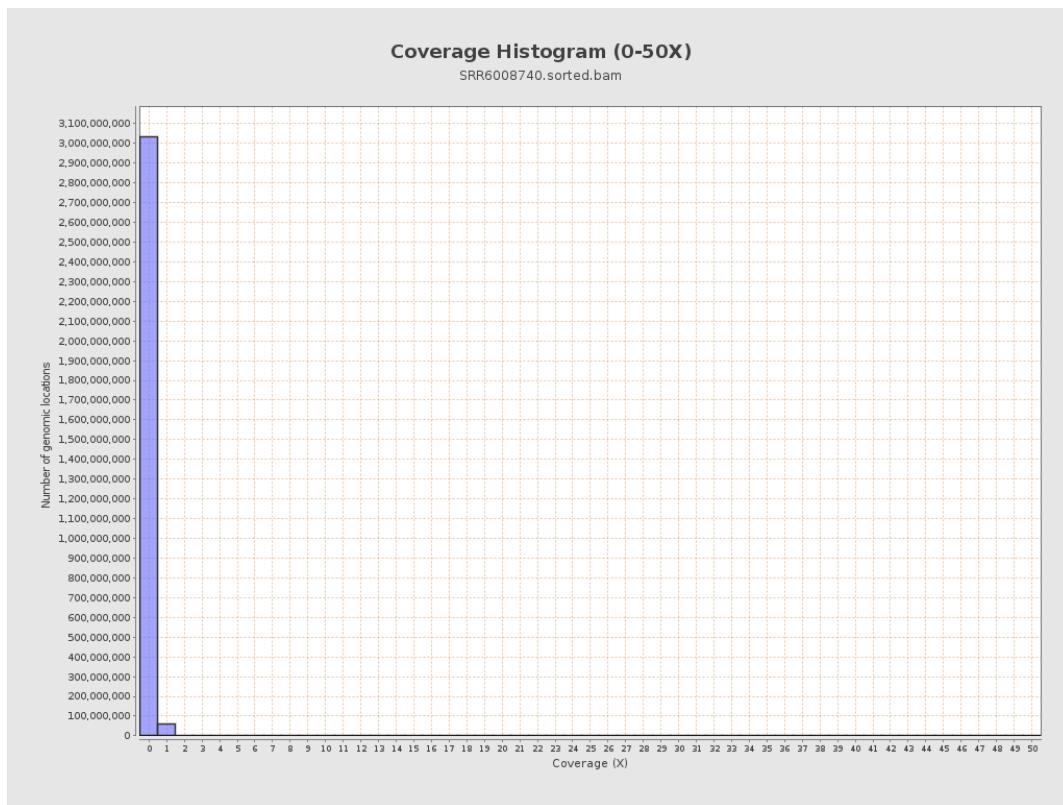
3. Results : Coverage across reference



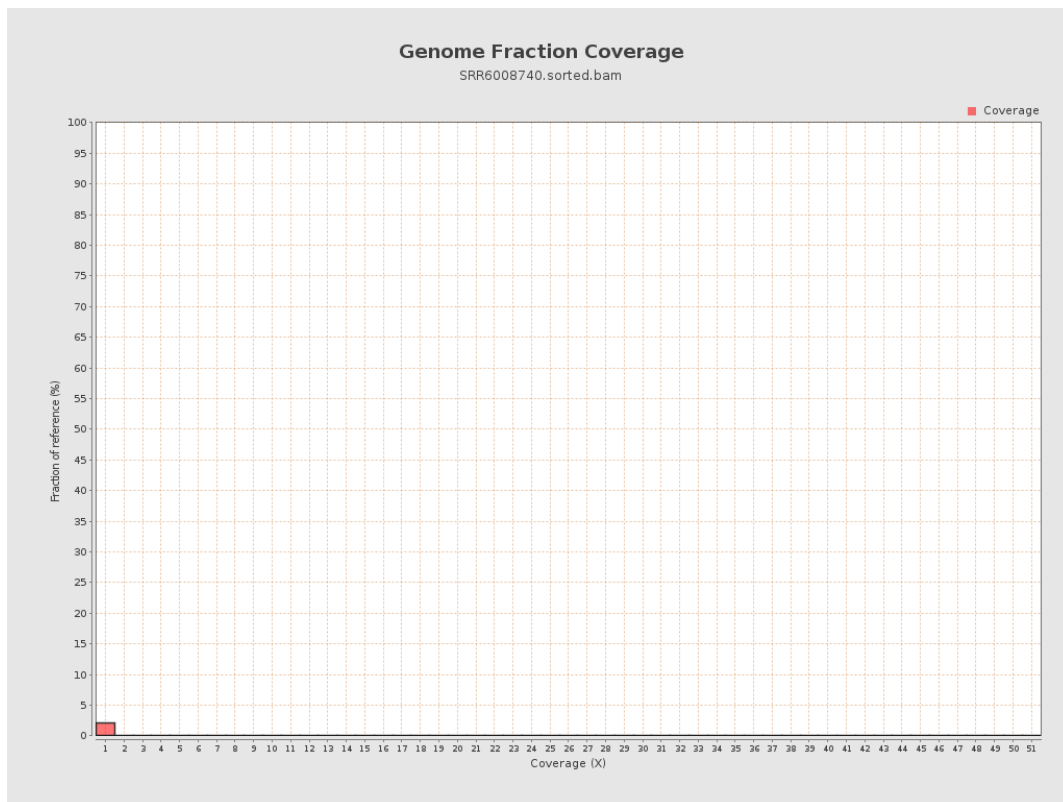
4. Results : Coverage Histogram



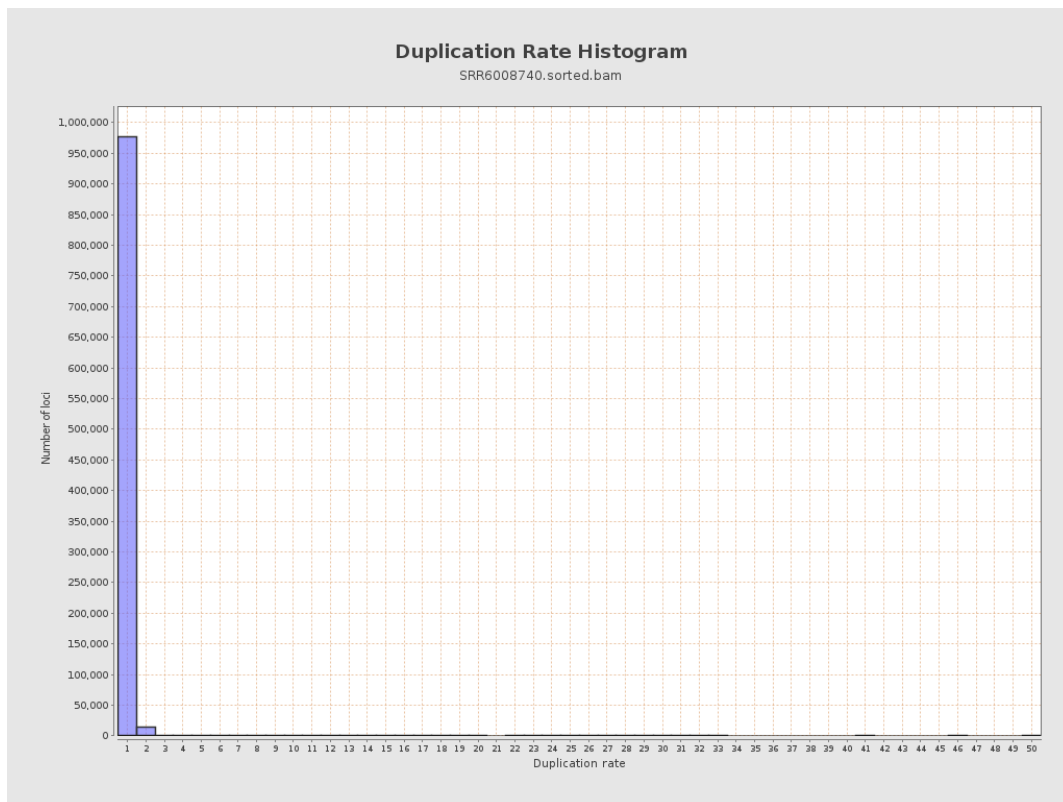
5. Results : Coverage Histogram (0-50X)



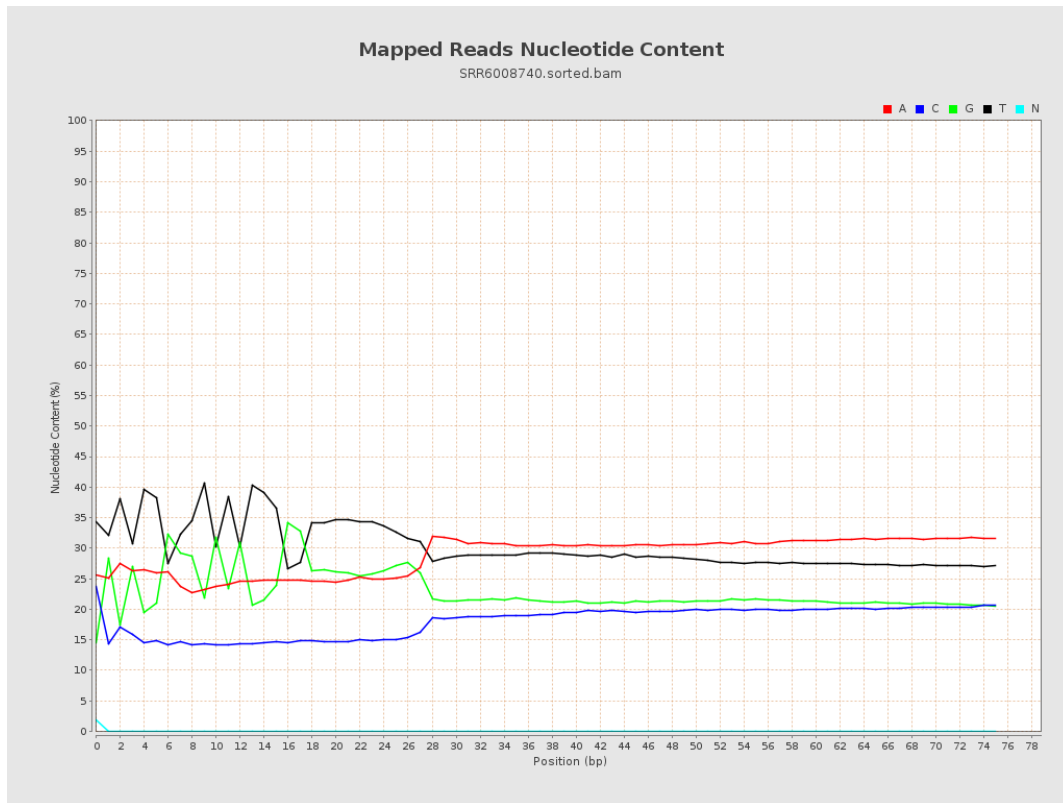
6. Results : Genome Fraction Coverage



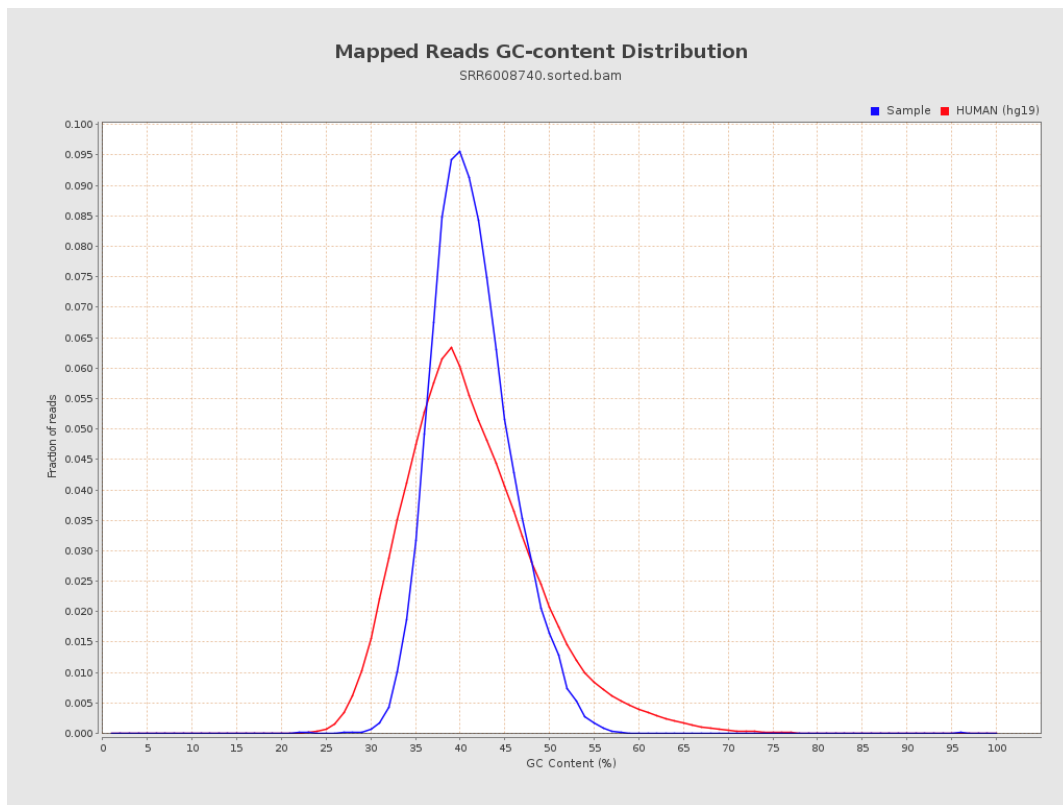
7. Results : Duplication Rate Histogram



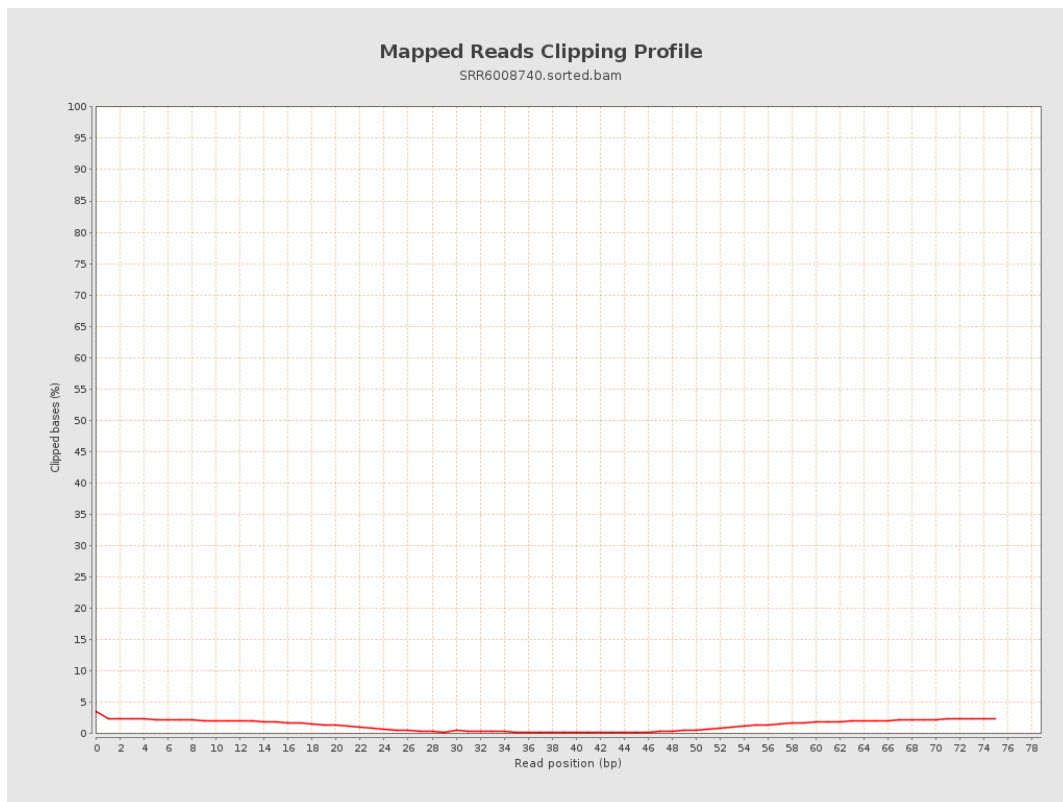
8. Results : Mapped Reads Nucleotide Content



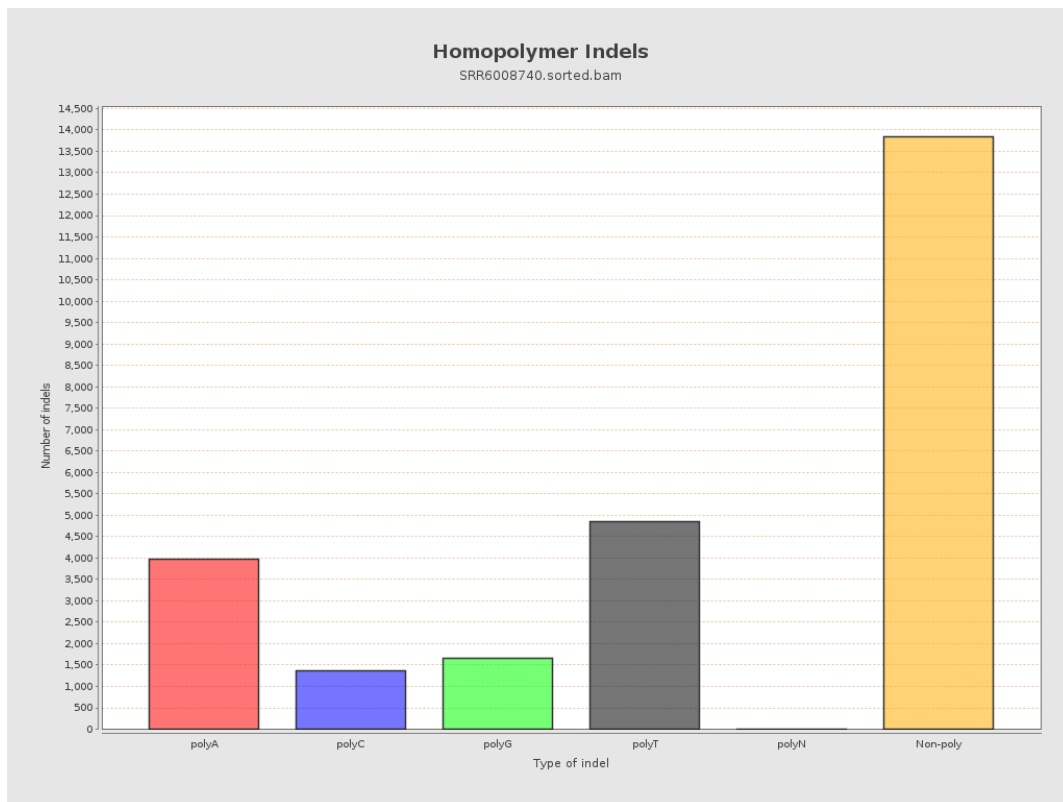
9. Results : Mapped Reads GC-content Distribution



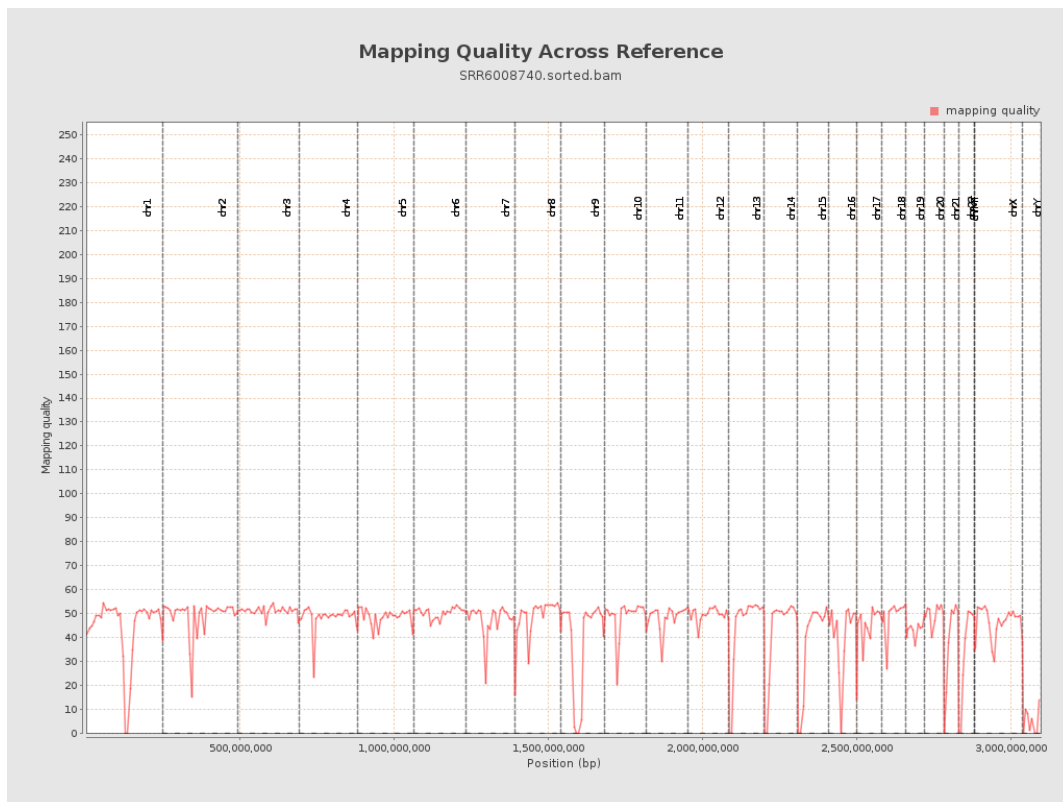
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

