

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 13:39:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238266.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_SRR6238266 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238266.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 13:39:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238266.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,352,737
Mapped reads	1,173,445 / 86.75%
Unmapped reads	179,292 / 13.25%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,888 / 1.03%
Read min/max/mean length	30 / 76 / 76.36
Duplicated reads (estimated)	85,109 / 6.29%
Duplication rate	5.97%
Clipped reads	663,006 / 49.01%

2.2. ACGT Content

Number/percentage of A's	21,142,364 / 28.06%
Number/percentage of C's	14,290,462 / 18.97%
Number/percentage of T's	23,366,782 / 31.01%
Number/percentage of G's	16,530,491 / 21.94%
Number/percentage of N's	17,106 / 0.02%
GC Percentage	40.91%

2.3. Coverage

Mean	0.0244

Standard Deviation	0.2666
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2.4. Mapping Quality

Mean Mapping Quality	45.12
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2.5. Mismatches and indels

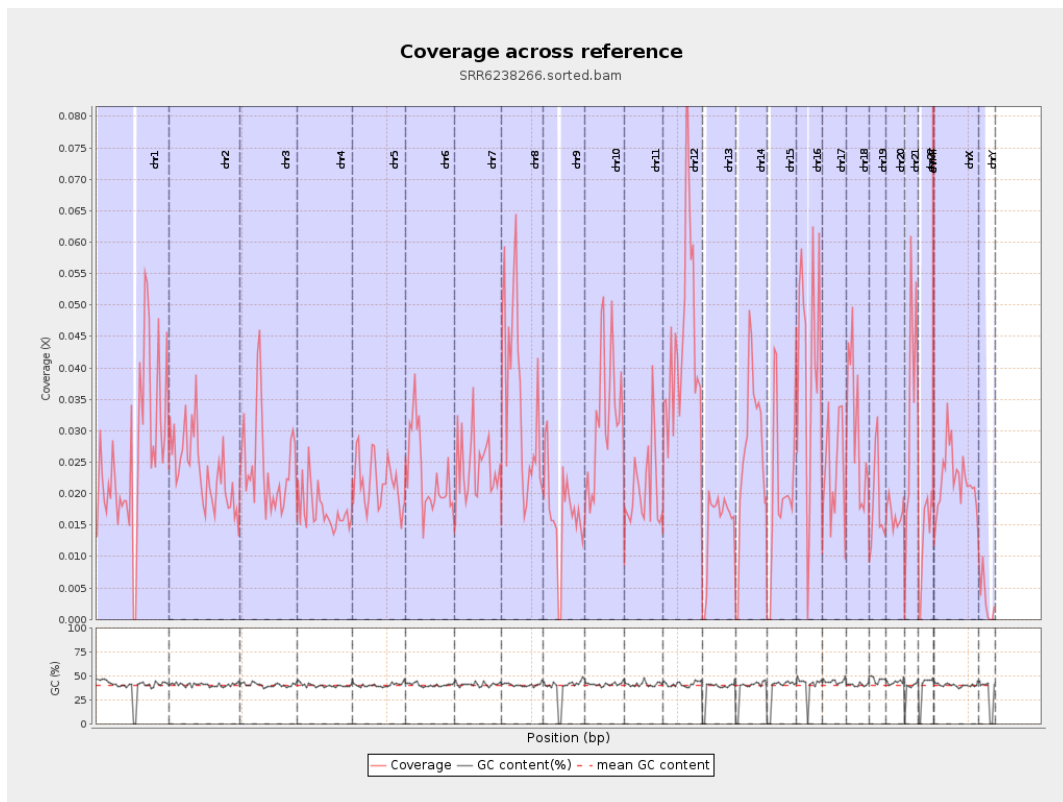
General error rate	0.93%
Mismatches	692,345
Insertions	6,042
Mapped reads with at least one insertion	0.51%
Deletions	26,373
Mapped reads with at least one deletion	2.22%
Homopolymer indels	46.77%

2.6. Chromosome stats

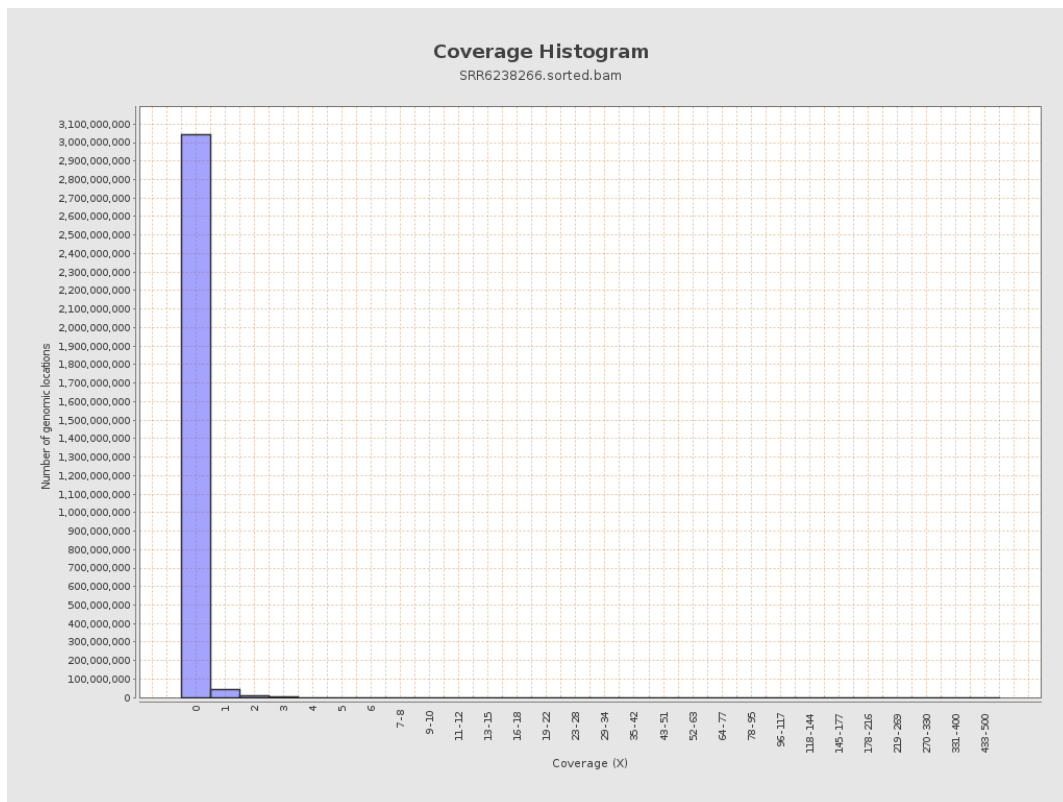
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6503577	0.0261	0.4365
chr2	243199373	5766785	0.0237	0.32
chr3	198022430	4833968	0.0244	0.201
chr4	191154276	3333333	0.0174	0.1752
chr5	180915260	3904391	0.0216	0.1905
chr6	171115067	3899877	0.0228	0.2092
chr7	159138663	3899158	0.0245	0.2986

chr8	146364022	5101168	0.0349	0.357
chr9	141213431	2376340	0.0168	0.2123
chr10	135534747	4313692	0.0318	0.3005
chr11	135006516	2797976	0.0207	0.2458
chr12	133851895	6001717	0.0448	0.2786
chr13	115169878	1703033	0.0148	0.1589
chr14	107349540	2921683	0.0272	0.2284
chr15	102531392	2110887	0.0206	0.2169
chr16	90354753	3640787	0.0403	0.2628
chr17	81195210	1882278	0.0232	0.2206
chr18	78077248	2340337	0.03	0.319
chr19	59128983	1108151	0.0187	0.2811
chr20	63025520	1061475	0.0168	0.1675
chr21	48129895	1591787	0.0331	0.2402
chr22	51304566	667137	0.013	0.1437
chrMT	16571	8823	0.5324	0.9167
chrX	155270560	3441581	0.0222	0.215
chrY	59373566	180685	0.003	0.0985

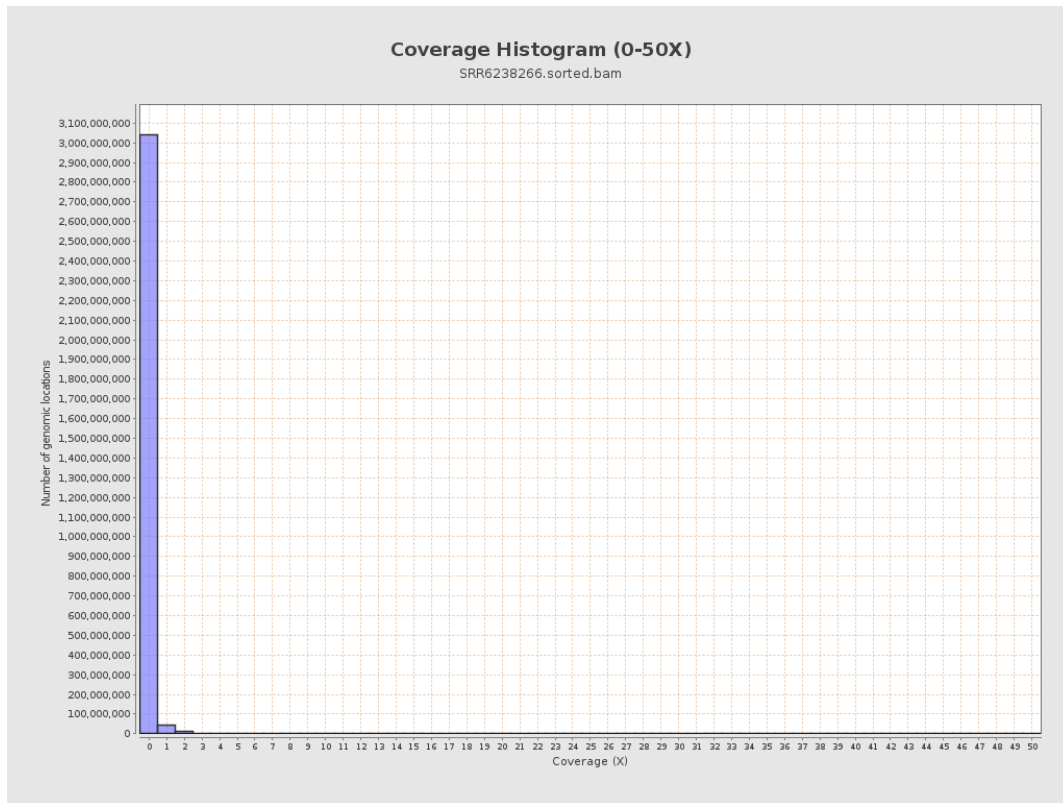
3. Results : Coverage across reference



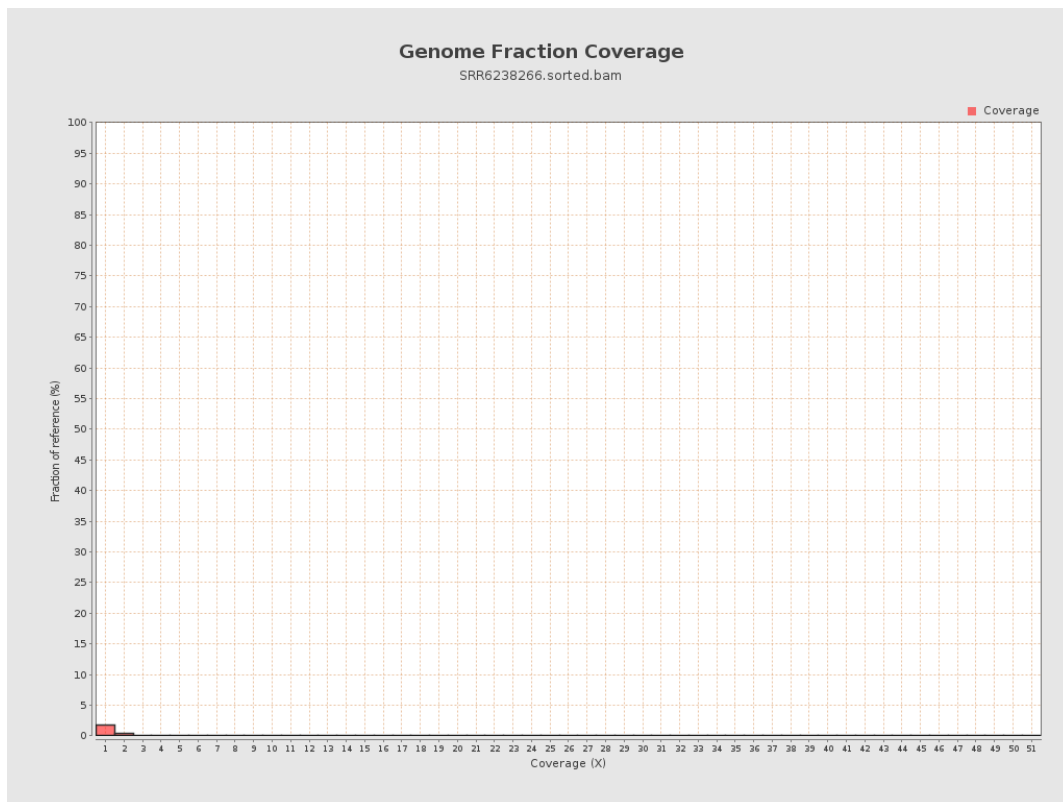
4. Results : Coverage Histogram



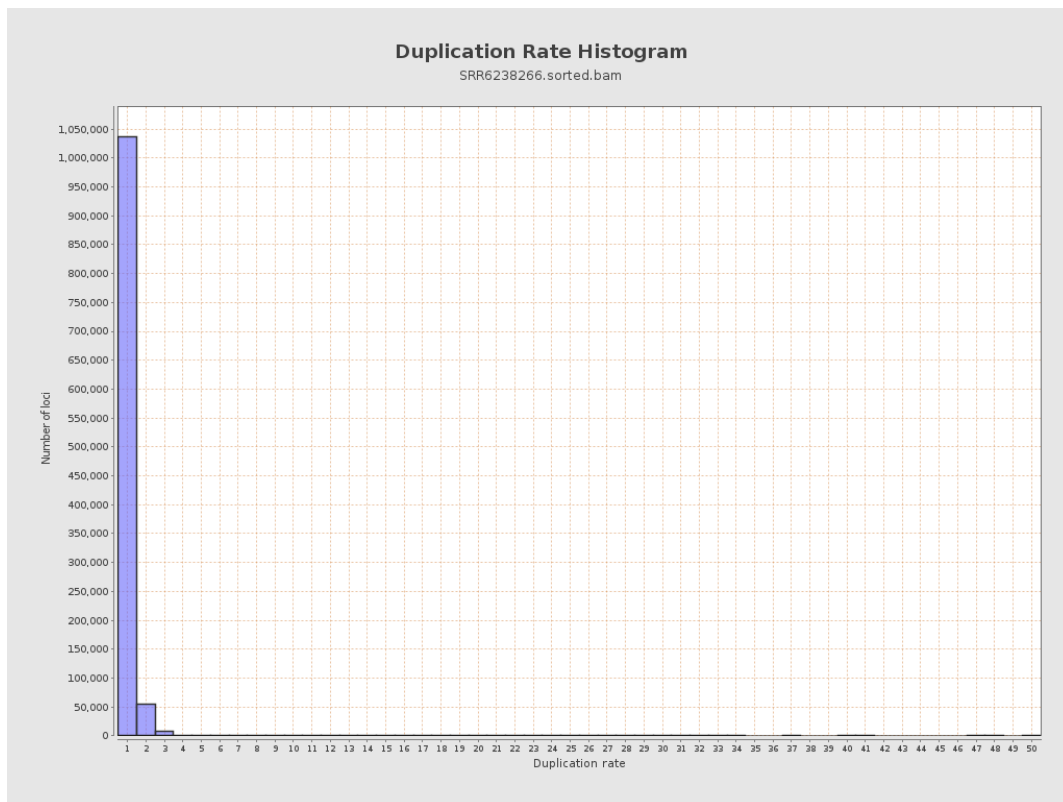
5. Results : Coverage Histogram (0-50X)



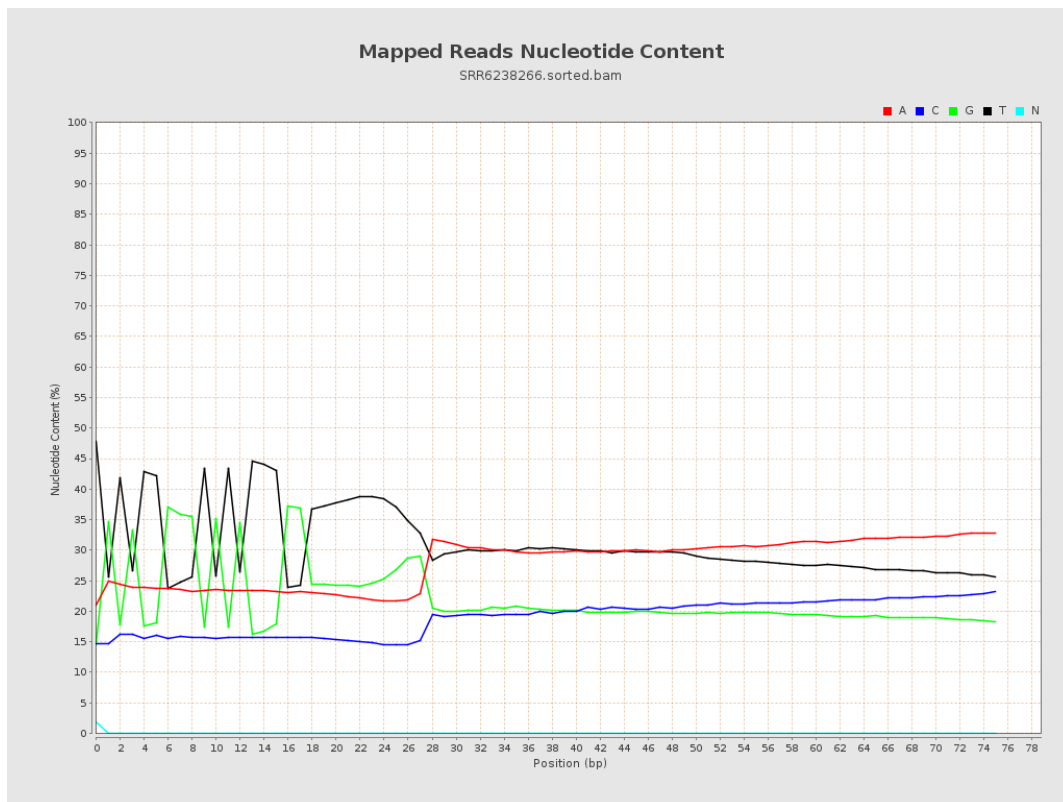
6. Results : Genome Fraction Coverage



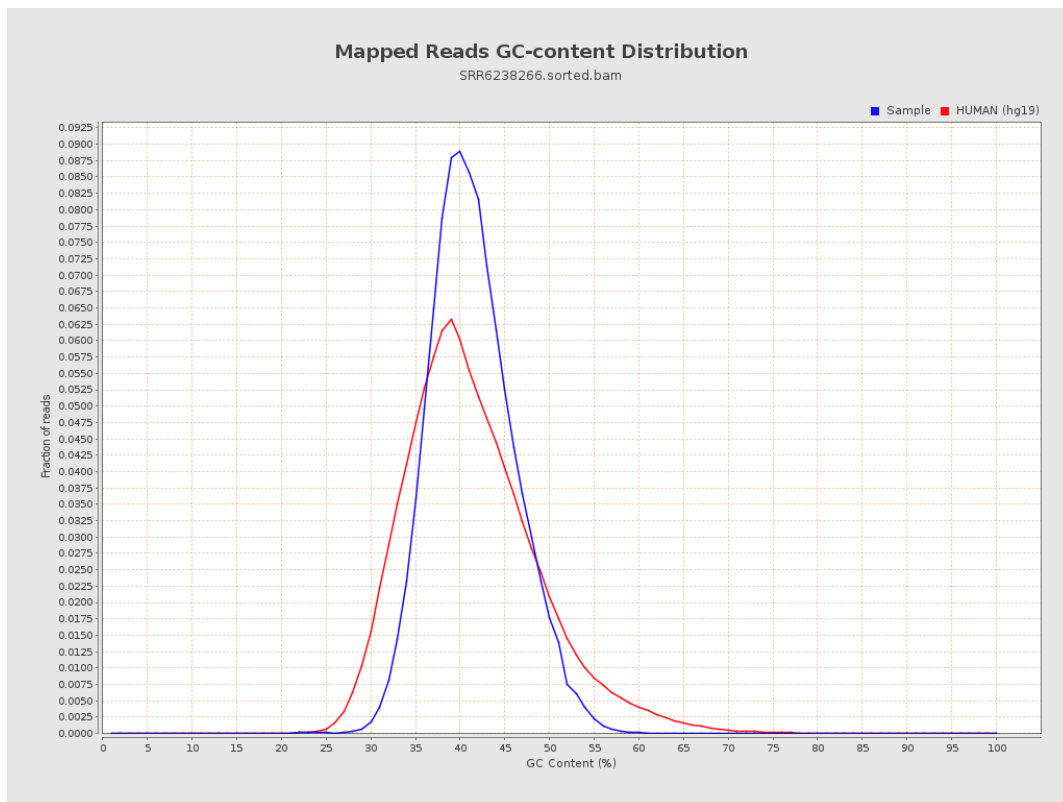
7. Results : Duplication Rate Histogram



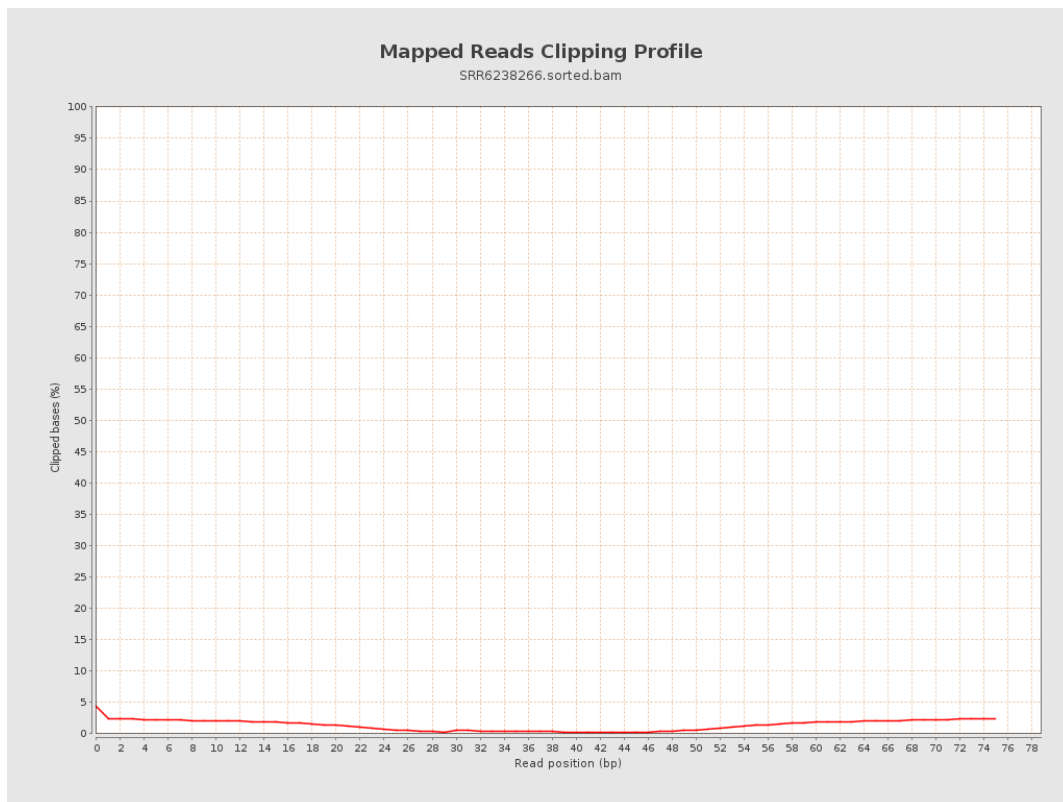
8. Results : Mapped Reads Nucleotide Content



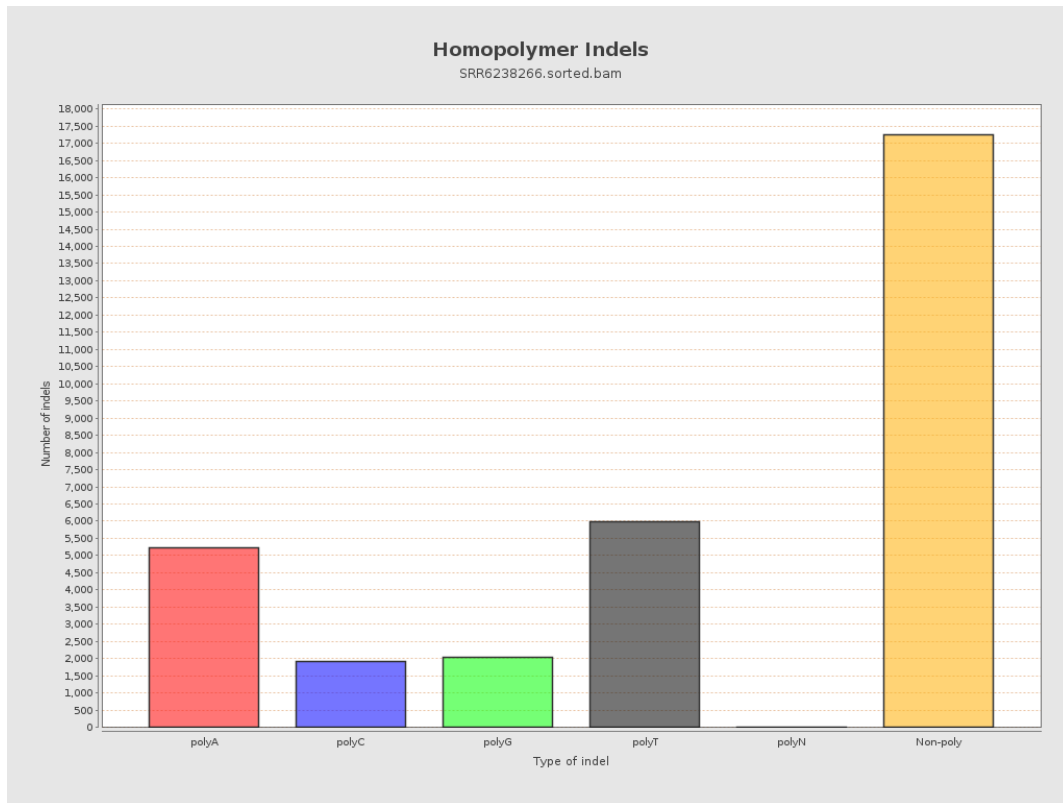
9. Results : Mapped Reads GC-content Distribution



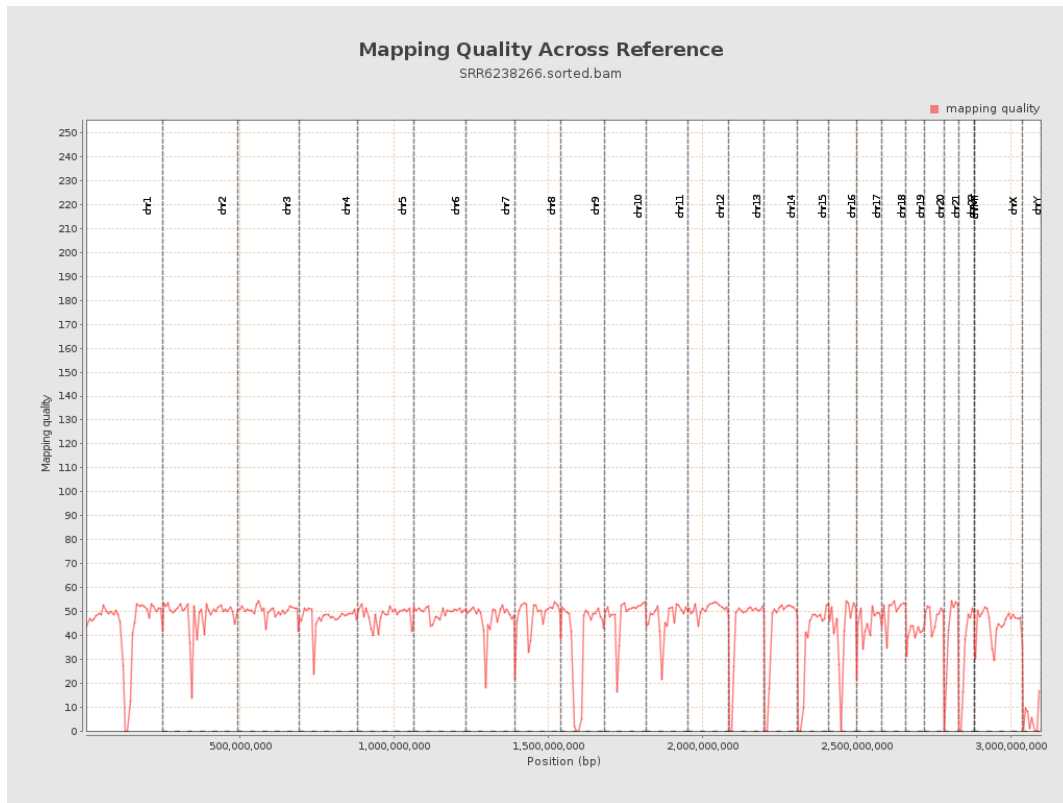
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

