

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 22:01:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238606.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_SRR6238606 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238606.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 22:01:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238606.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,616,625
Mapped reads	3,052,648 / 84.41%
Unmapped reads	563,977 / 15.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,788 / 0.69%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	875,895 / 24.22%
Duplication rate	20.39%
Clipped reads	1,973,714 / 54.57%

2.2. ACGT Content

Number/percentage of A's	46,429,803 / 24.85%
Number/percentage of C's	32,049,830 / 17.15%
Number/percentage of T's	63,765,755 / 34.12%
Number/percentage of G's	44,611,118 / 23.87%
Number/percentage of N's	4,303 / 0%
GC Percentage	41.03%

2.3. Coverage

Mean	0.0604

Standard Deviation	0.9145
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2.4. Mapping Quality

Mean Mapping Quality	40.58
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2.5. Mismatches and indels

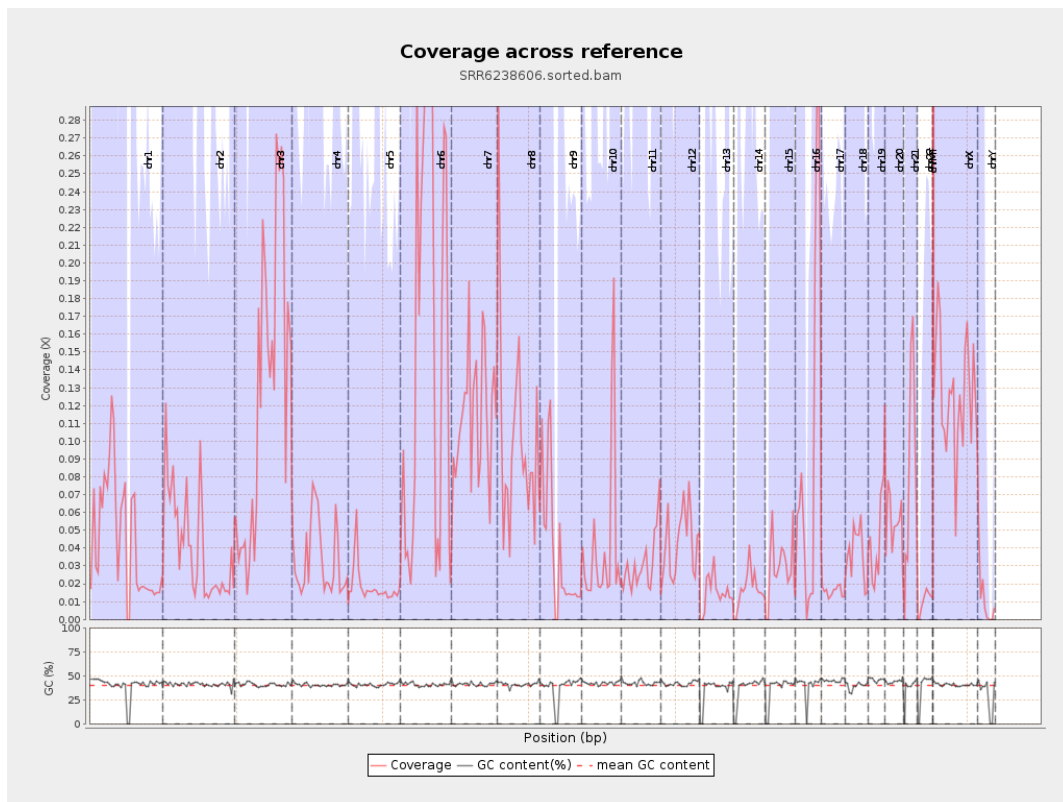
General error rate	0.56%
Mismatches	1,023,358
Insertions	11,784
Mapped reads with at least one insertion	0.38%
Deletions	46,098
Mapped reads with at least one deletion	1.5%
Homopolymer indels	41.97%

2.6. Chromosome stats

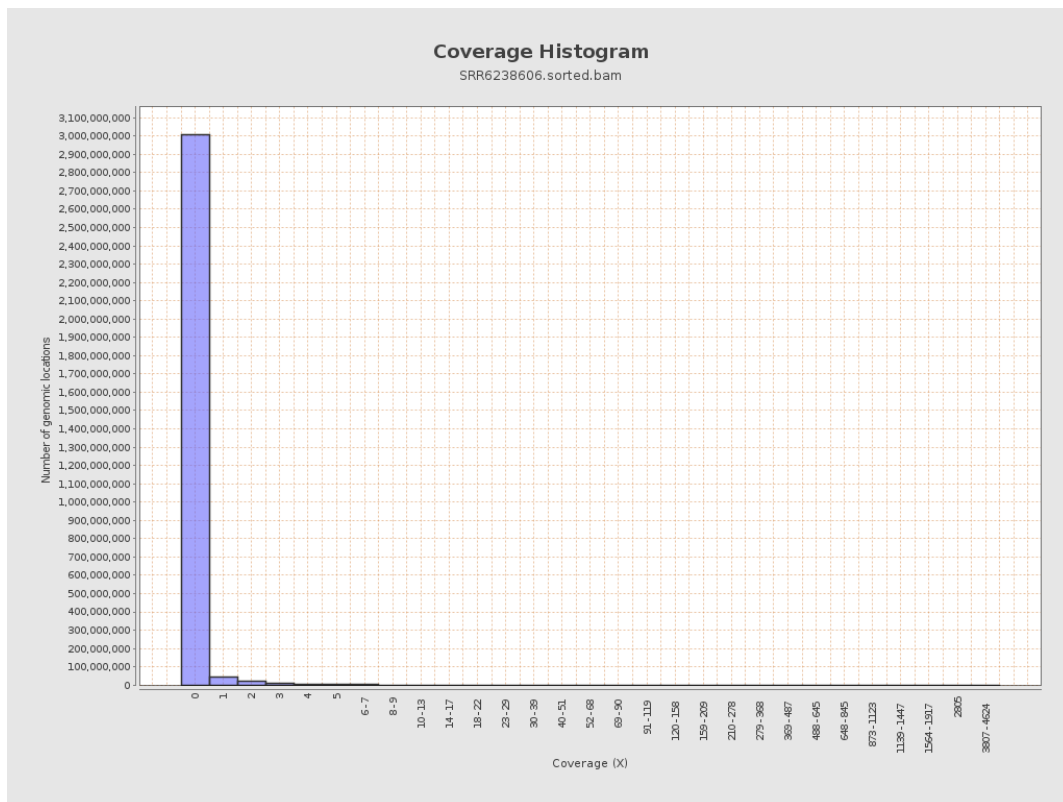
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	10928495	0.0438	0.4459
chr2	243199373	9743701	0.0401	2.0297
chr3	198022430	24659954	0.1245	0.6798
chr4	191154276	6480777	0.0339	0.3533
chr5	180915260	3298334	0.0182	0.2599
chr6	171115067	28063207	0.164	1.4884
chr7	159138663	18119345	0.1139	1.6308

chr8	146364022	14635903	0.1	0.8535
chr9	141213431	5407195	0.0383	0.4226
chr10	135534747	5609936	0.0414	0.4984
chr11	135006516	4194637	0.0311	0.3308
chr12	133851895	5832986	0.0436	0.4017
chr13	115169878	1710459	0.0149	0.4426
chr14	107349540	1825620	0.017	0.2577
chr15	102531392	3131405	0.0305	0.4878
chr16	90354753	8067753	0.0893	0.6246
chr17	81195210	1289684	0.0159	0.23
chr18	78077248	2917112	0.0374	1.5308
chr19	59128983	2633238	0.0445	0.4527
chr20	63025520	3488448	0.0553	0.4517
chr21	48129895	4024782	0.0836	0.5736
chr22	51304566	531690	0.0104	0.1766
chrMT	16571	80107	4.8342	4.5093
chrX	155270560	19614933	0.1263	0.6877
chrY	59373566	649241	0.0109	0.3323

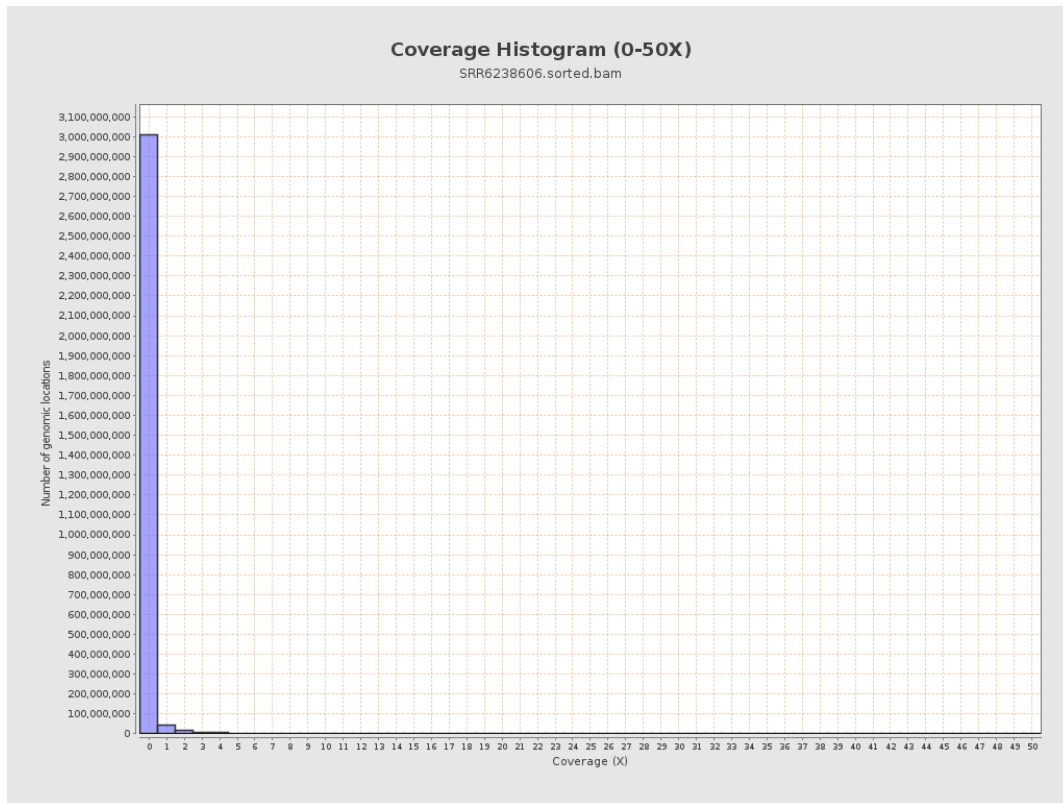
3. Results : Coverage across reference



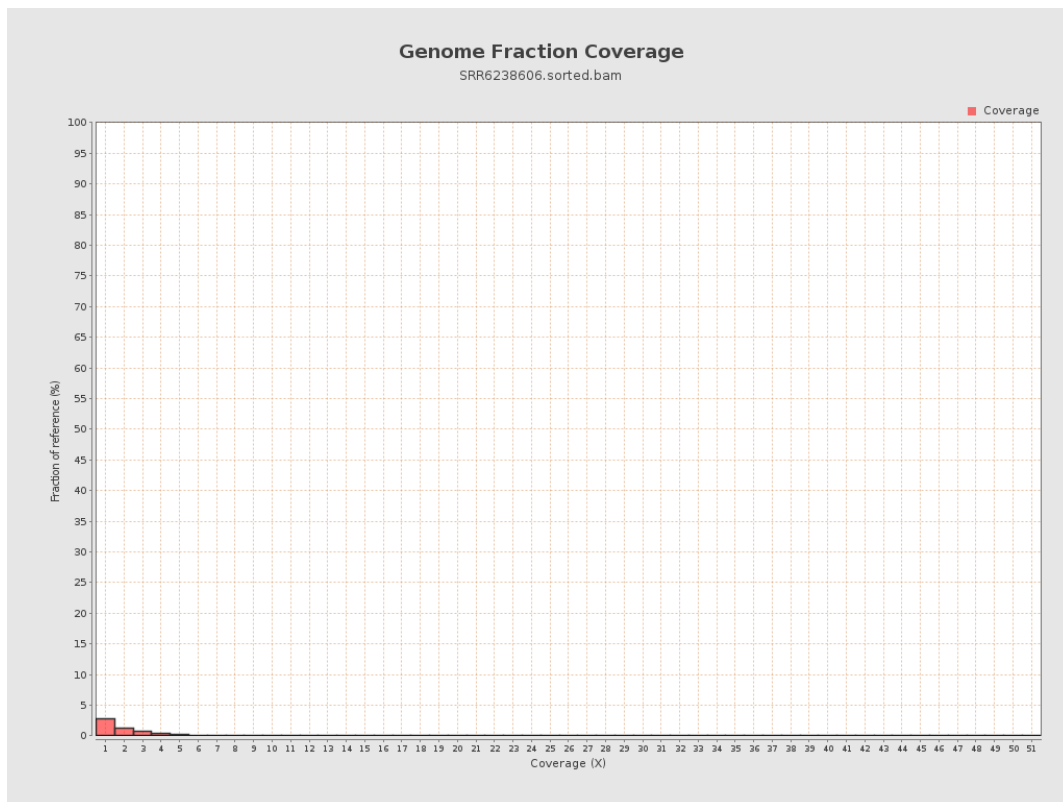
4. Results : Coverage Histogram



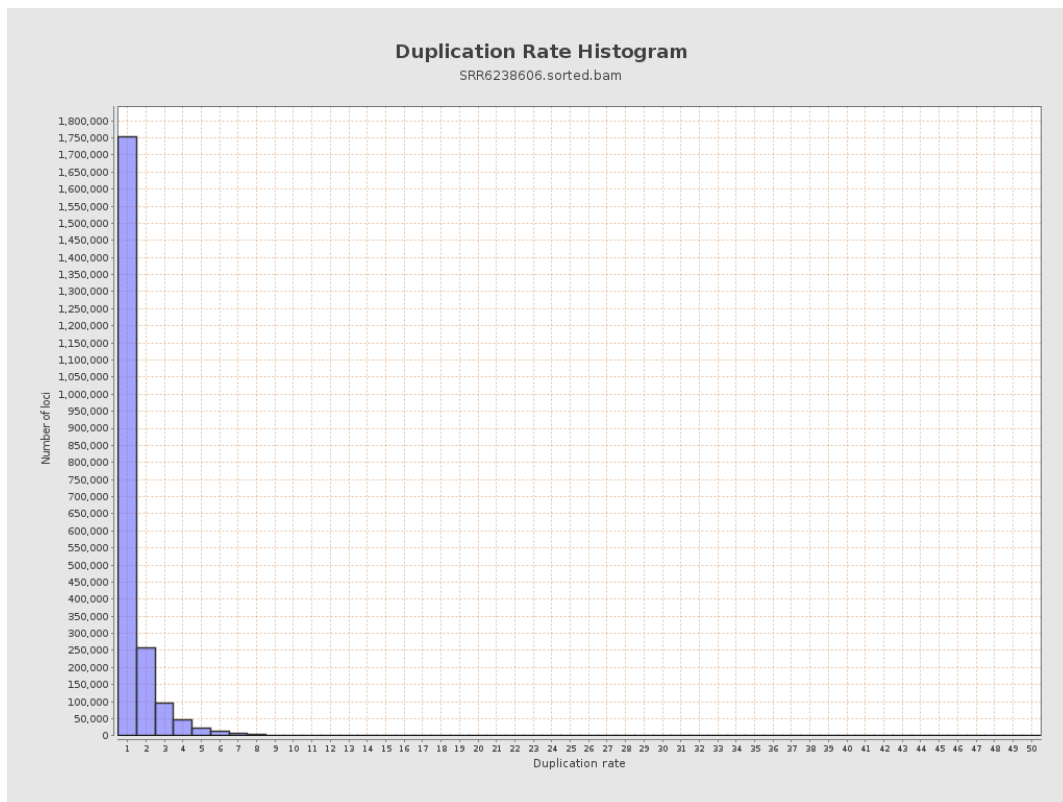
5. Results : Coverage Histogram (0-50X)



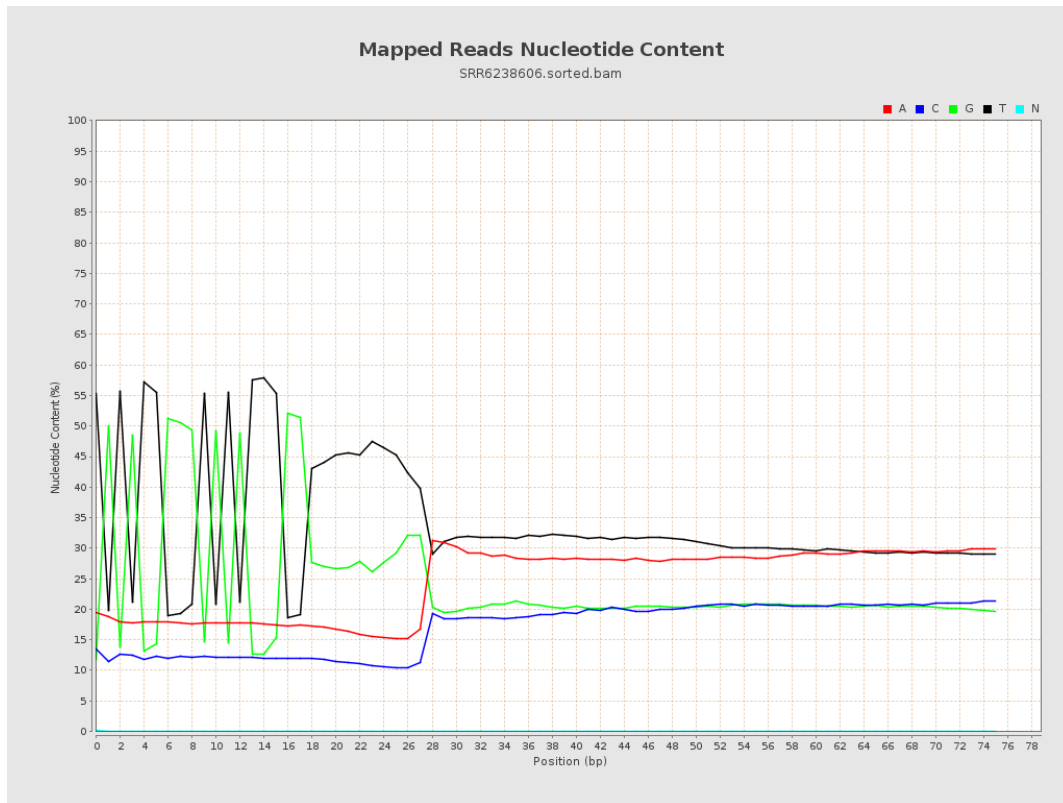
6. Results : Genome Fraction Coverage



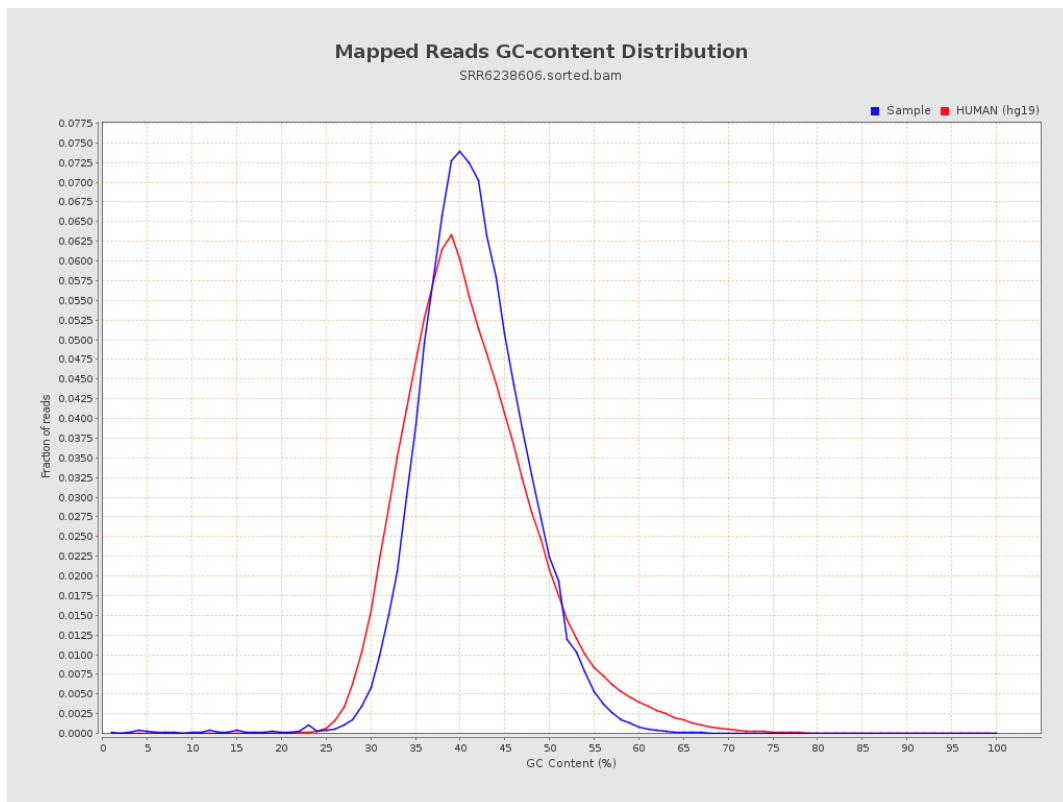
7. Results : Duplication Rate Histogram



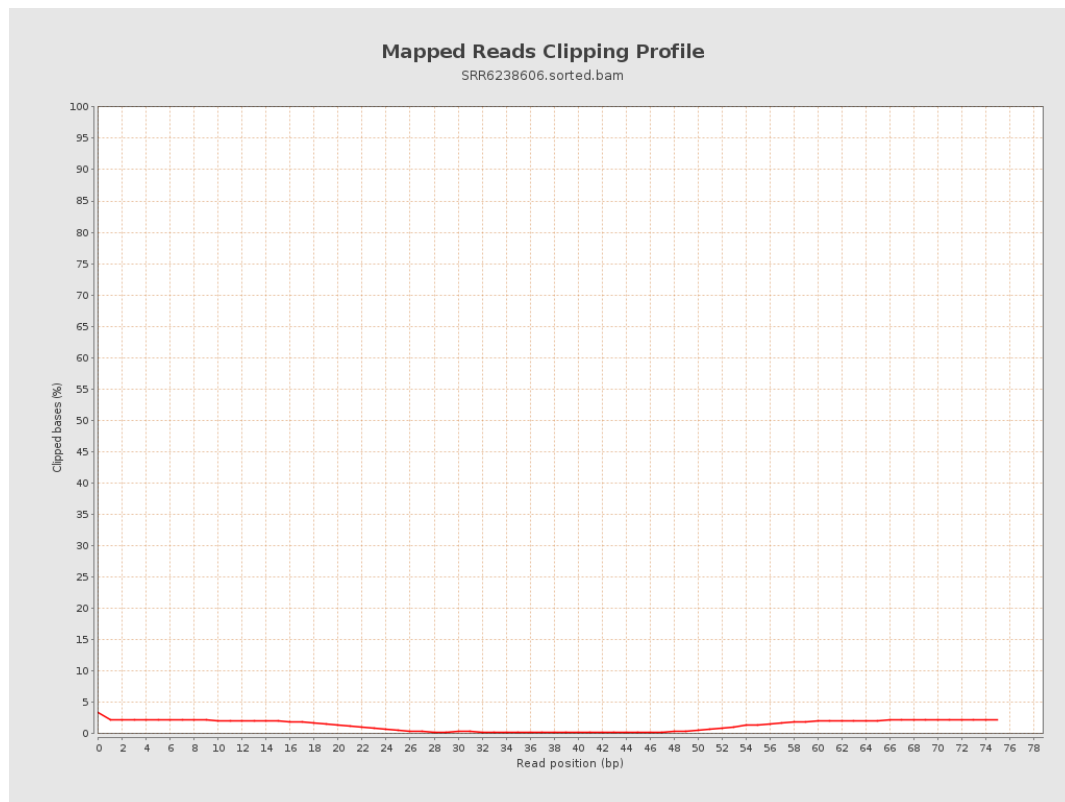
8. Results : Mapped Reads Nucleotide Content



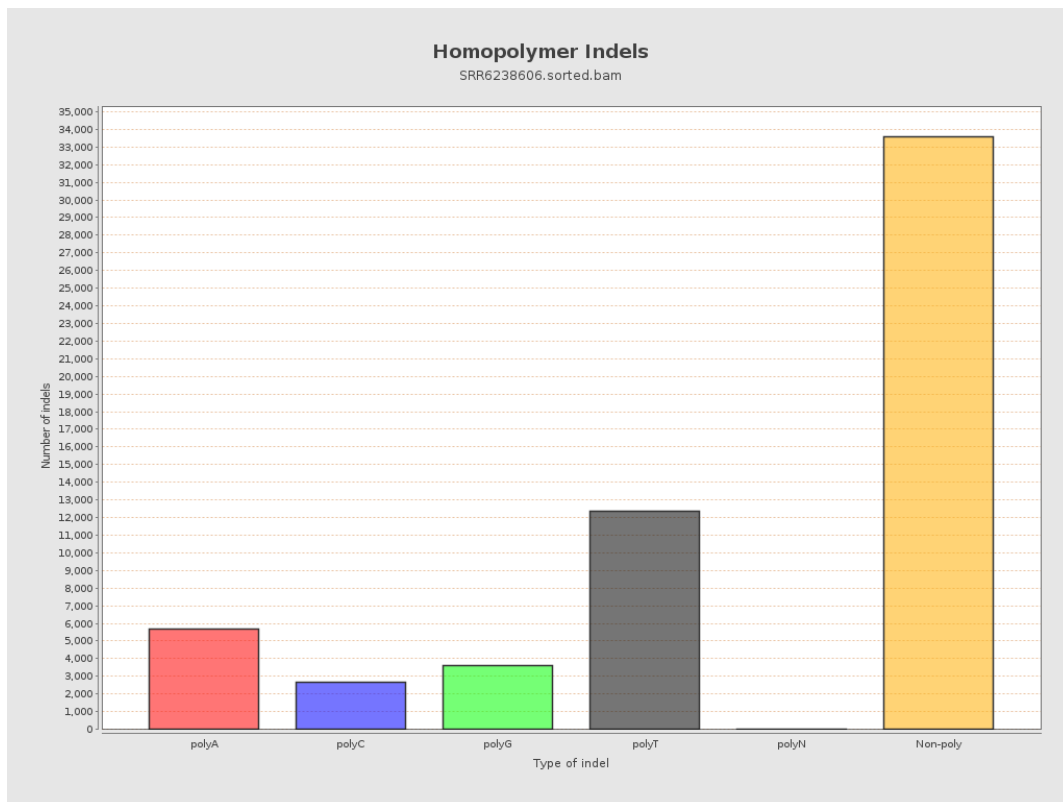
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

