

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 15:40:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238307.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_SRR6238307 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238307.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 15:40:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238307.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,520,305
Mapped reads	1,365,655 / 89.83%
Unmapped reads	154,650 / 10.17%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,445 / 0.49%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	48,344 / 3.18%
Duplication rate	2.41%
Clipped reads	610,846 / 40.18%

2.2. ACGT Content

Number/percentage of A's	24,660,593 / 27.23%
Number/percentage of C's	16,139,181 / 17.82%
Number/percentage of T's	29,137,529 / 32.18%
Number/percentage of G's	20,567,616 / 22.71%
Number/percentage of N's	49,613 / 0.05%
GC Percentage	40.54%

2.3. Coverage

Mean	0.0293

Standard Deviation	0.3421
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	45.02
----------------------	-------

2.5. Mismatches and indels

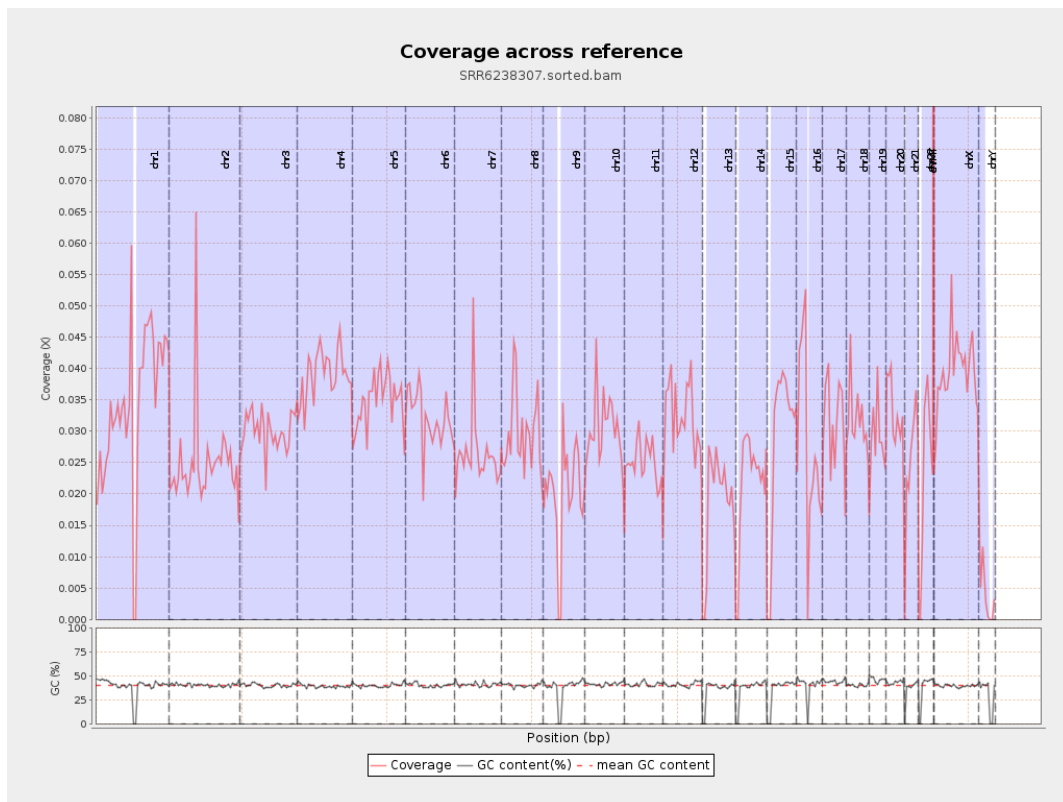
General error rate	0.82%
Mismatches	727,818
Insertions	6,593
Mapped reads with at least one insertion	0.48%
Deletions	26,942
Mapped reads with at least one deletion	1.95%
Homopolymer indels	46.12%

2.6. Chromosome stats

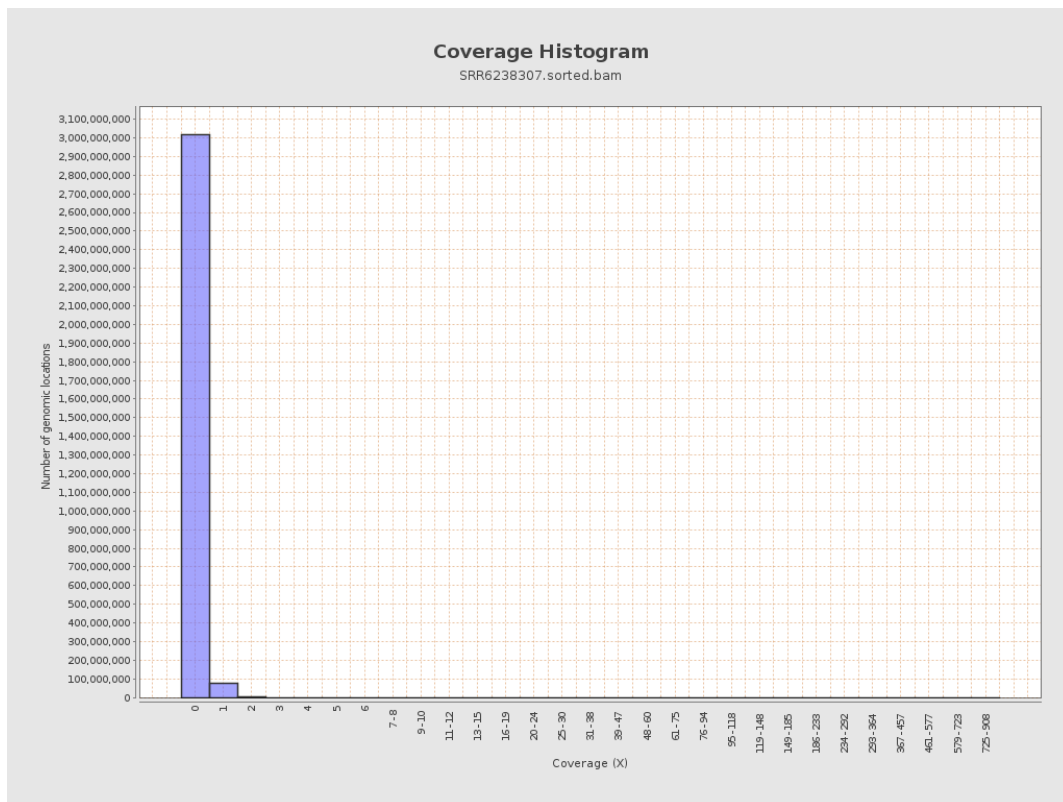
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	8521886	0.0342	0.6647
chr2	243199373	6069161	0.025	0.4264
chr3	198022430	5957451	0.0301	0.1878
chr4	191154276	7482105	0.0391	0.225
chr5	180915260	6338593	0.035	0.2045
chr6	171115067	5479581	0.032	0.2218
chr7	159138663	4234169	0.0266	0.3908

chr8	146364022	4327277	0.0296	0.5726
chr9	141213431	2864115	0.0203	0.3057
chr10	135534747	4122104	0.0304	0.2545
chr11	135006516	3372717	0.025	0.2842
chr12	133851895	4316008	0.0322	0.2006
chr13	115169878	2141854	0.0186	0.1472
chr14	107349540	2317037	0.0216	0.171
chr15	102531392	2977949	0.029	0.2043
chr16	90354753	2563207	0.0284	0.1986
chr17	81195210	2511016	0.0309	0.2279
chr18	78077248	2496358	0.032	0.5123
chr19	59128983	1725805	0.0292	0.431
chr20	63025520	2068983	0.0328	0.2034
chr21	48129895	1210006	0.0251	0.1831
chr22	51304566	1149623	0.0224	0.1611
chrMT	16571	4235	0.2556	0.5287
chrX	155270560	6107061	0.0393	0.245
chrY	59373566	242380	0.0041	0.0969

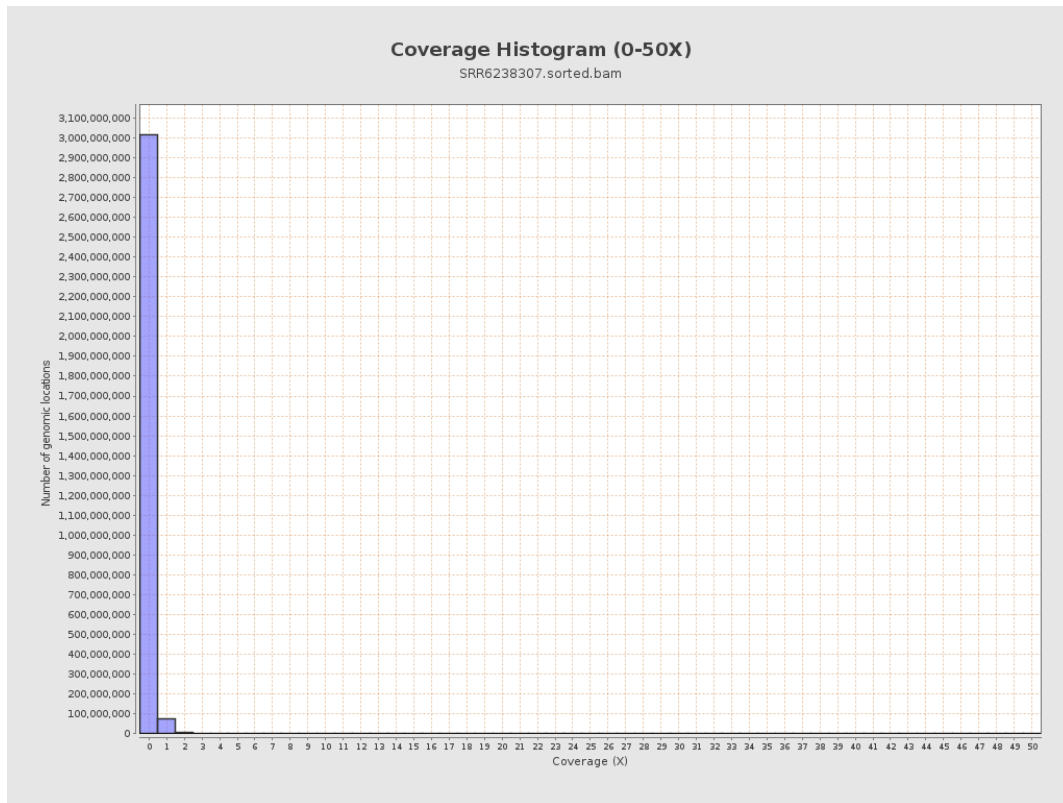
3. Results : Coverage across reference



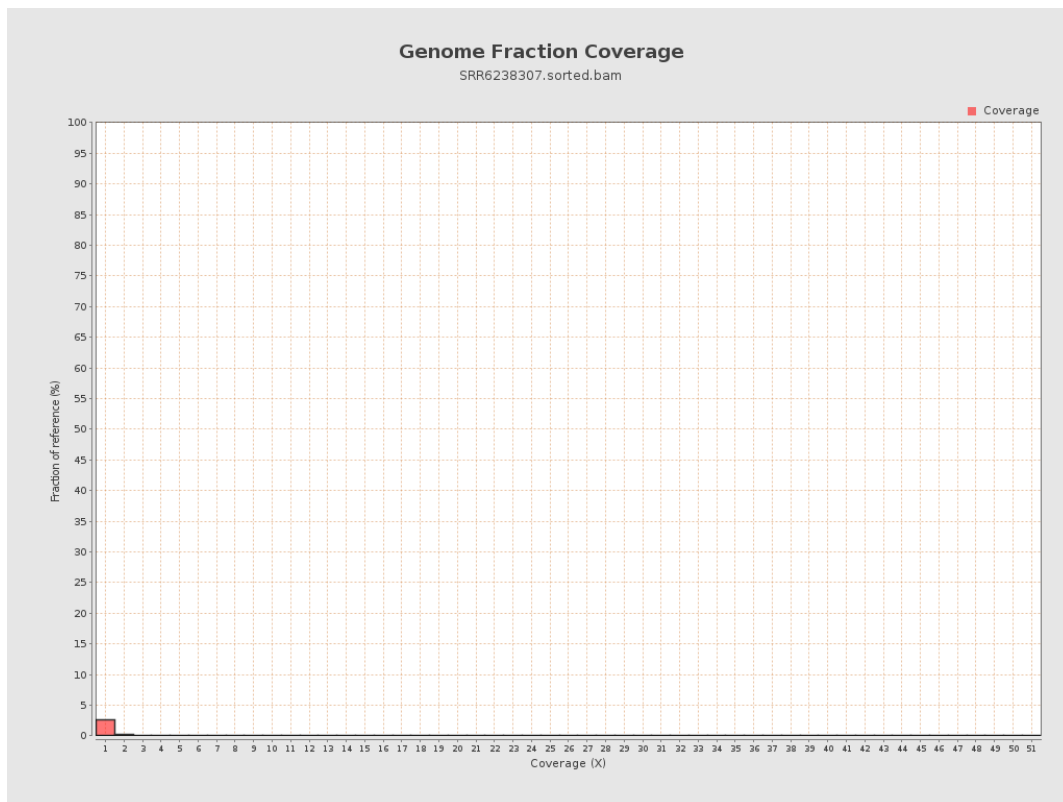
4. Results : Coverage Histogram



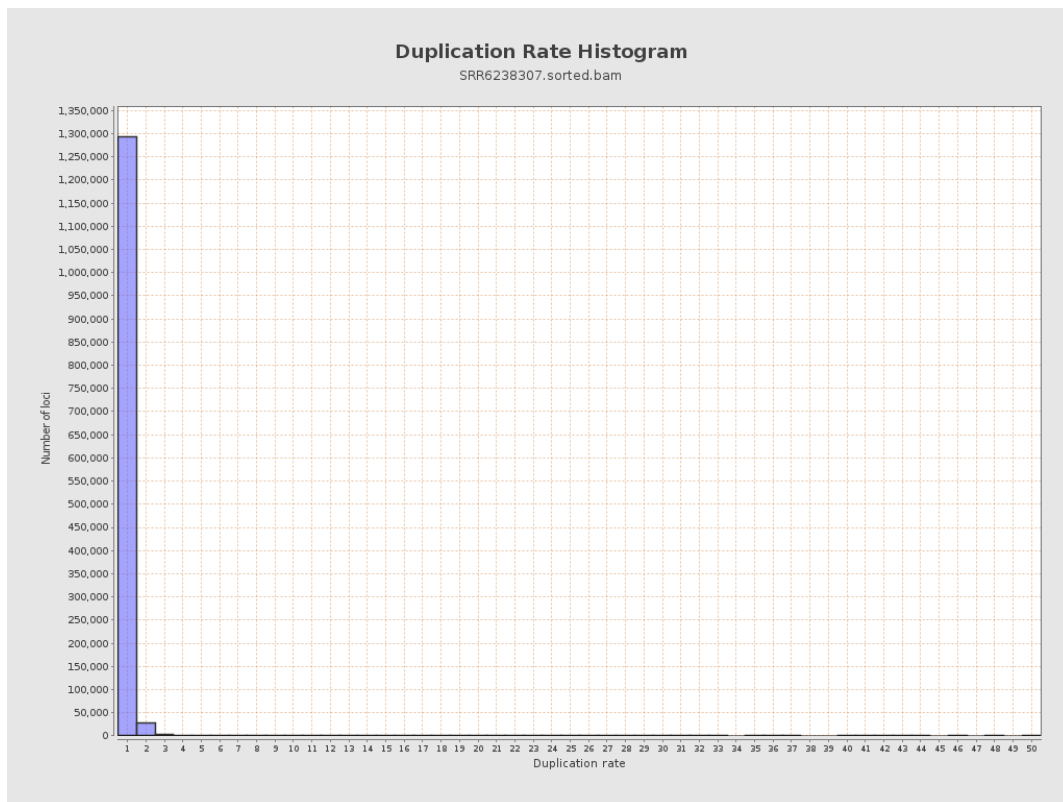
5. Results : Coverage Histogram (0-50X)



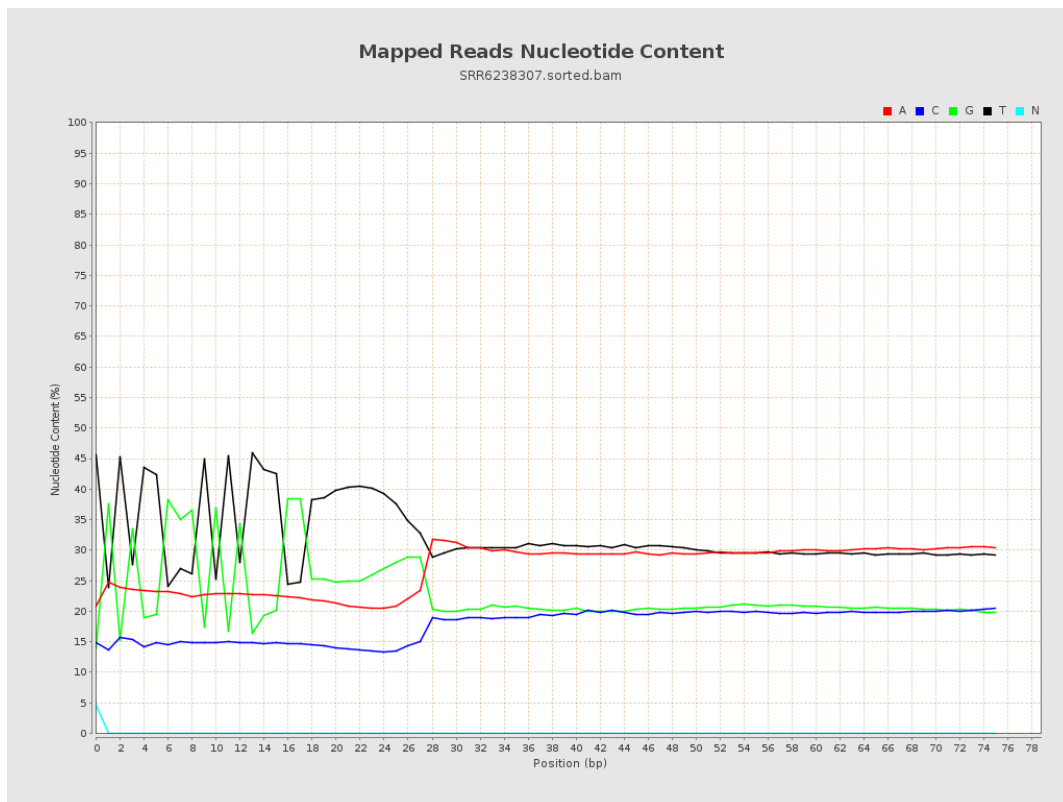
6. Results : Genome Fraction Coverage



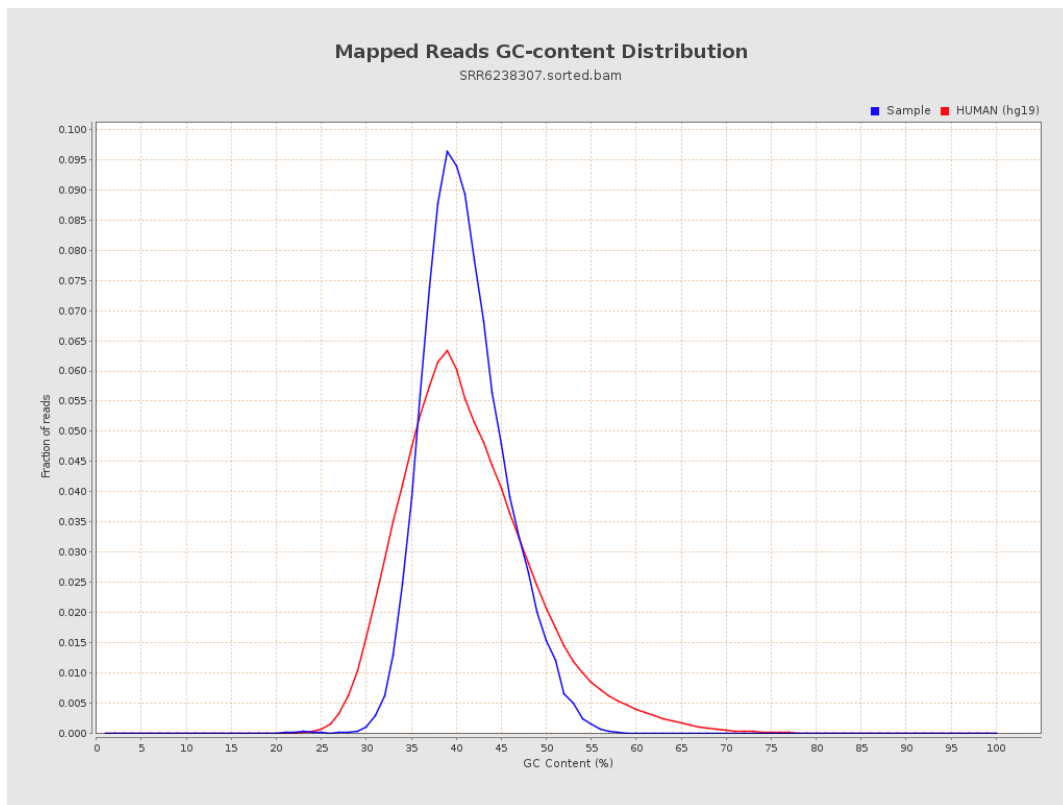
7. Results : Duplication Rate Histogram



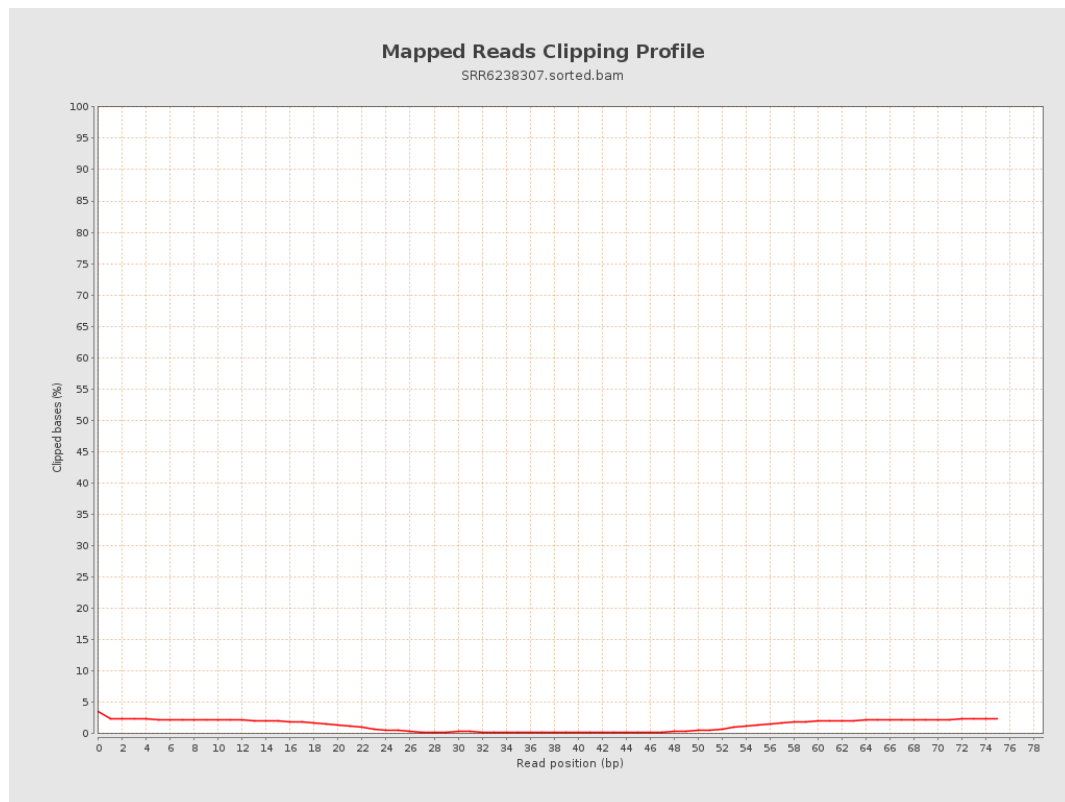
8. Results : Mapped Reads Nucleotide Content



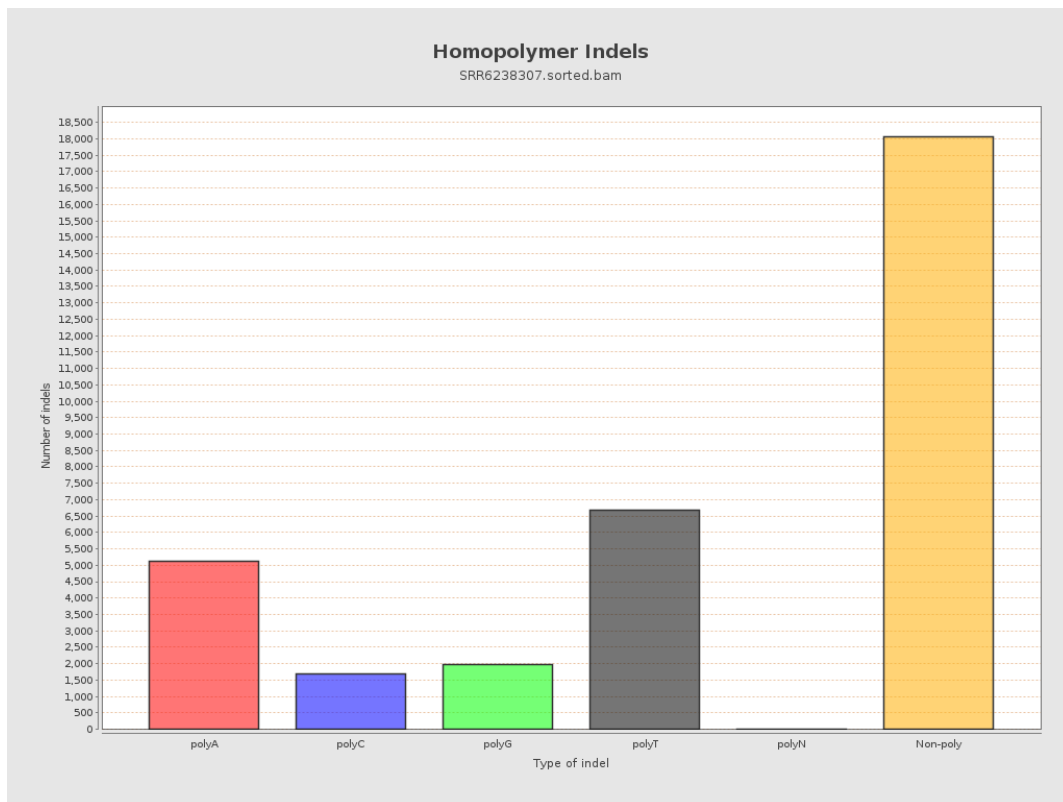
9. Results : Mapped Reads GC-content Distribution



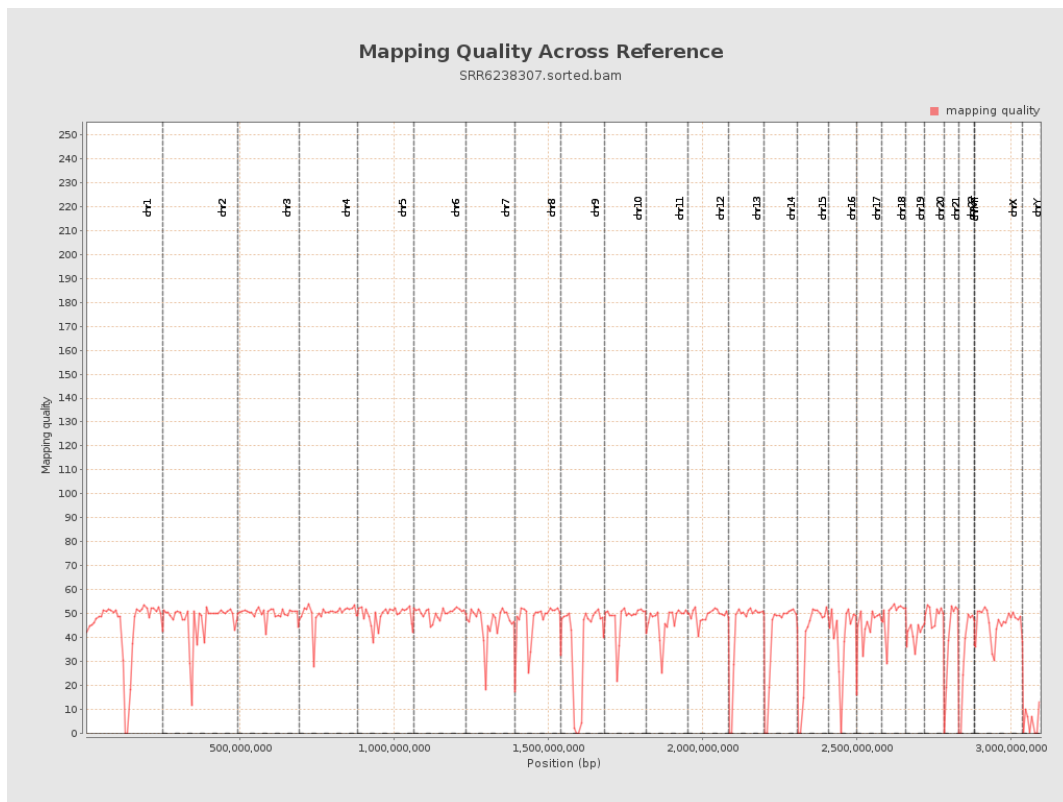
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

