

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 15:04:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238294.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_SRR6238294 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238294.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 15:04:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238294.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	840,264
Mapped reads	322,163 / 38.34%
Unmapped reads	518,101 / 61.66%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,968 / 0.47%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	31,453 / 3.74%
Duplication rate	7.7%
Clipped reads	179,083 / 21.31%

2.2. ACGT Content

Number/percentage of A's	5,831,223 / 28.3%
Number/percentage of C's	3,809,280 / 18.49%
Number/percentage of T's	6,508,721 / 31.59%
Number/percentage of G's	4,448,846 / 21.59%
Number/percentage of N's	4,817 / 0.02%
GC Percentage	40.08%

2.3. Coverage

Mean	0.0067

Standard Deviation	0.1329
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2.4. Mapping Quality

Mean Mapping Quality	45.05
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2.5. Mismatches and indels

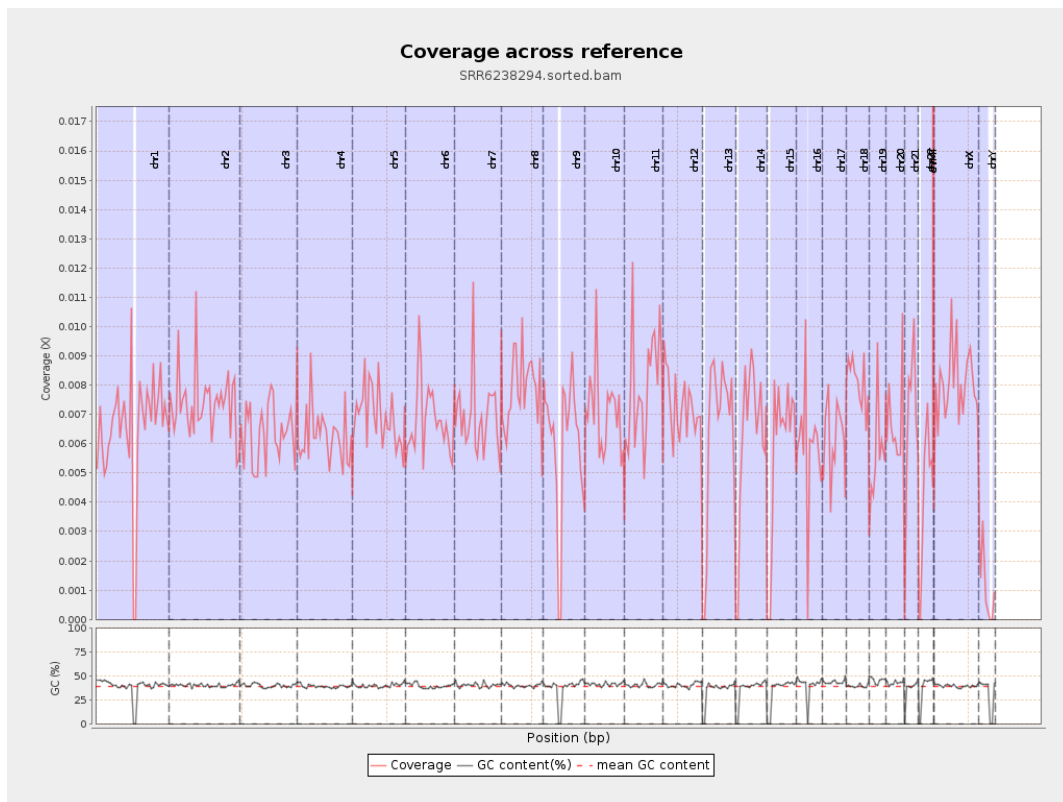
General error rate	0.97%
Mismatches	197,008
Insertions	1,876
Mapped reads with at least one insertion	0.58%
Deletions	7,229
Mapped reads with at least one deletion	2.21%
Homopolymer indels	45.67%

2.6. Chromosome stats

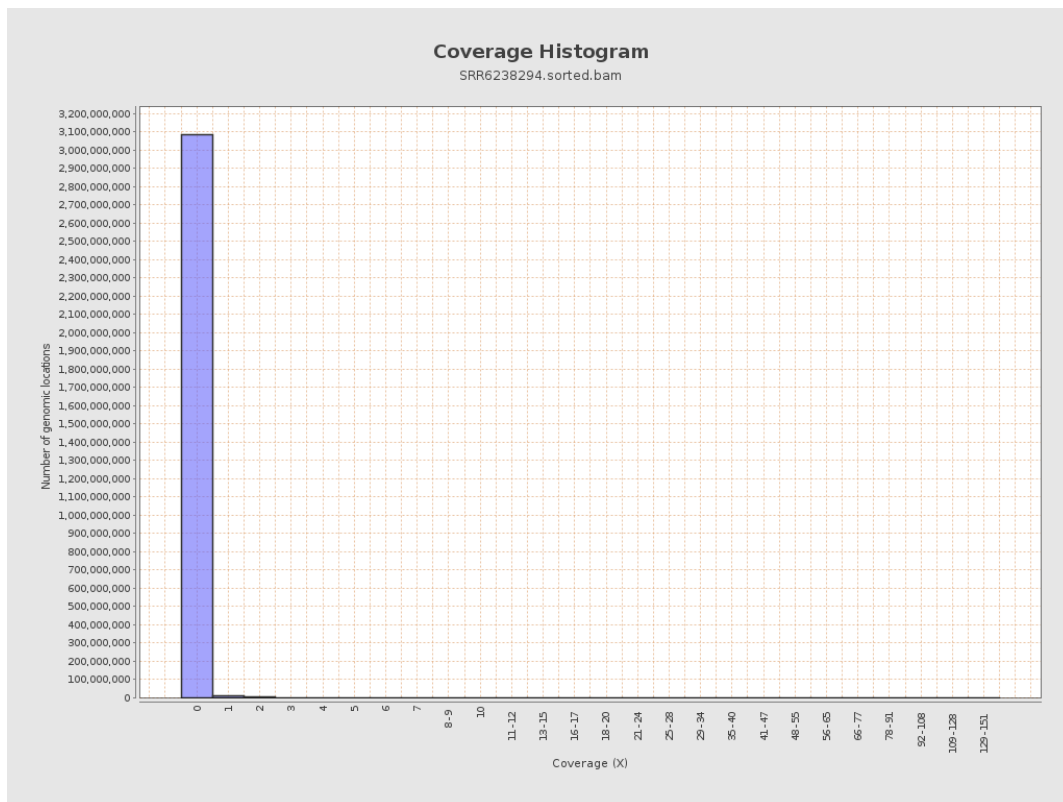
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	1624227	0.0065	0.1571
chr2	243199373	1796834	0.0074	0.1421
chr3	198022430	1260288	0.0064	0.1207
chr4	191154276	1199390	0.0063	0.1297
chr5	180915260	1250753	0.0069	0.1273
chr6	171115067	1161912	0.0068	0.1267
chr7	159138663	1104734	0.0069	0.1379

chr8	146364022	1137727	0.0078	0.161
chr9	141213431	844478	0.006	0.1209
chr10	135534747	956005	0.0071	0.132
chr11	135006516	1062041	0.0079	0.1408
chr12	133851895	971973	0.0073	0.1301
chr13	115169878	725749	0.0063	0.1216
chr14	107349540	670200	0.0062	0.1322
chr15	102531392	594242	0.0058	0.1341
chr16	90354753	527703	0.0058	0.1128
chr17	81195210	494307	0.0061	0.1187
chr18	78077248	634097	0.0081	0.1575
chr19	59128983	337524	0.0057	0.1283
chr20	63025520	425525	0.0068	0.1218
chr21	48129895	322611	0.0067	0.1209
chr22	51304566	212520	0.0041	0.0934
chrMT	16571	5374	0.3243	0.9115
chrX	155270560	1230568	0.0079	0.1335
chrY	59373566	63990	0.0011	0.0514

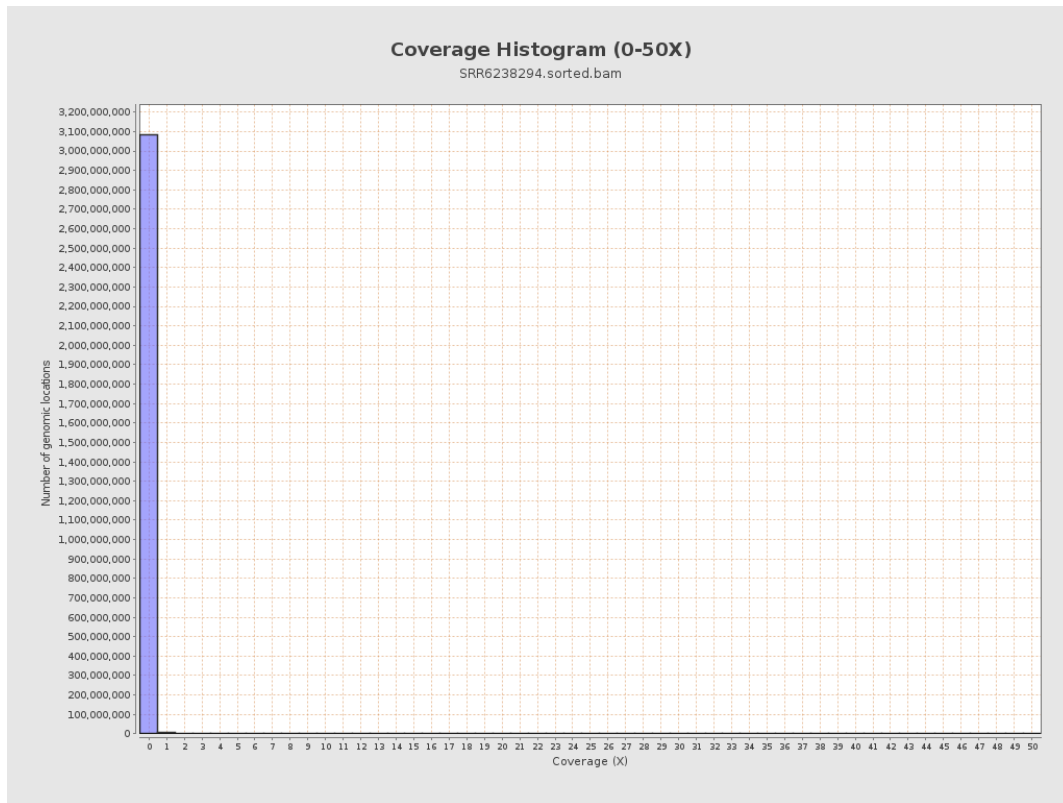
3. Results : Coverage across reference



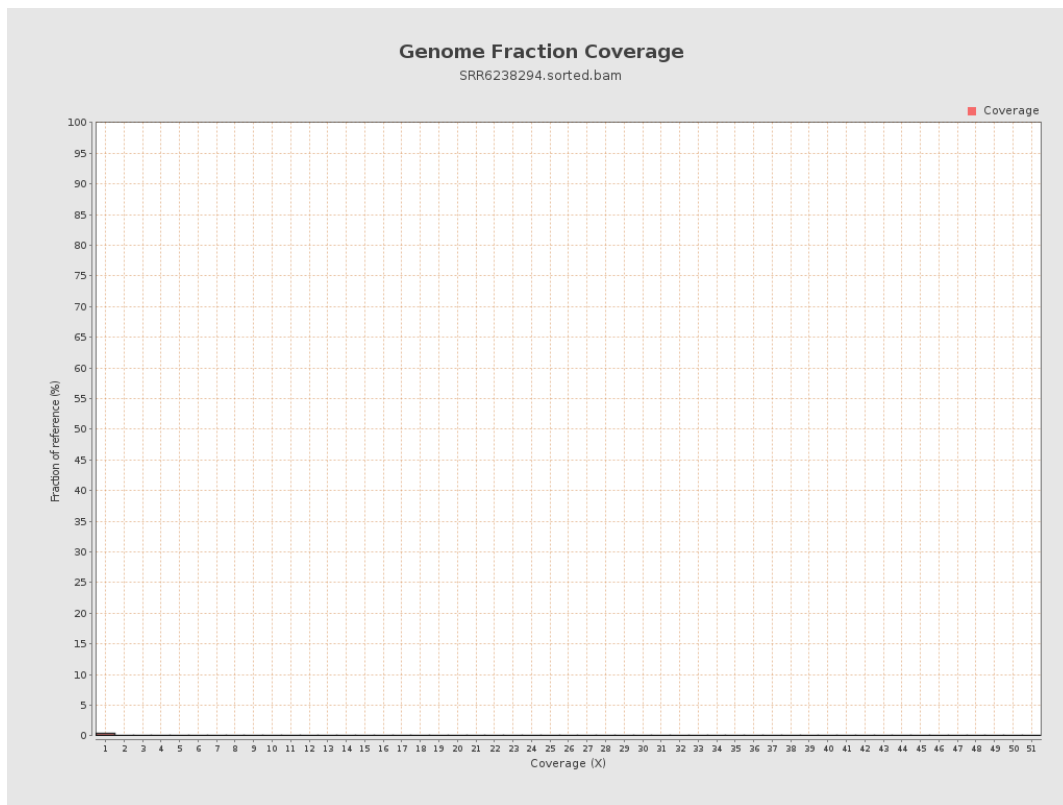
4. Results : Coverage Histogram



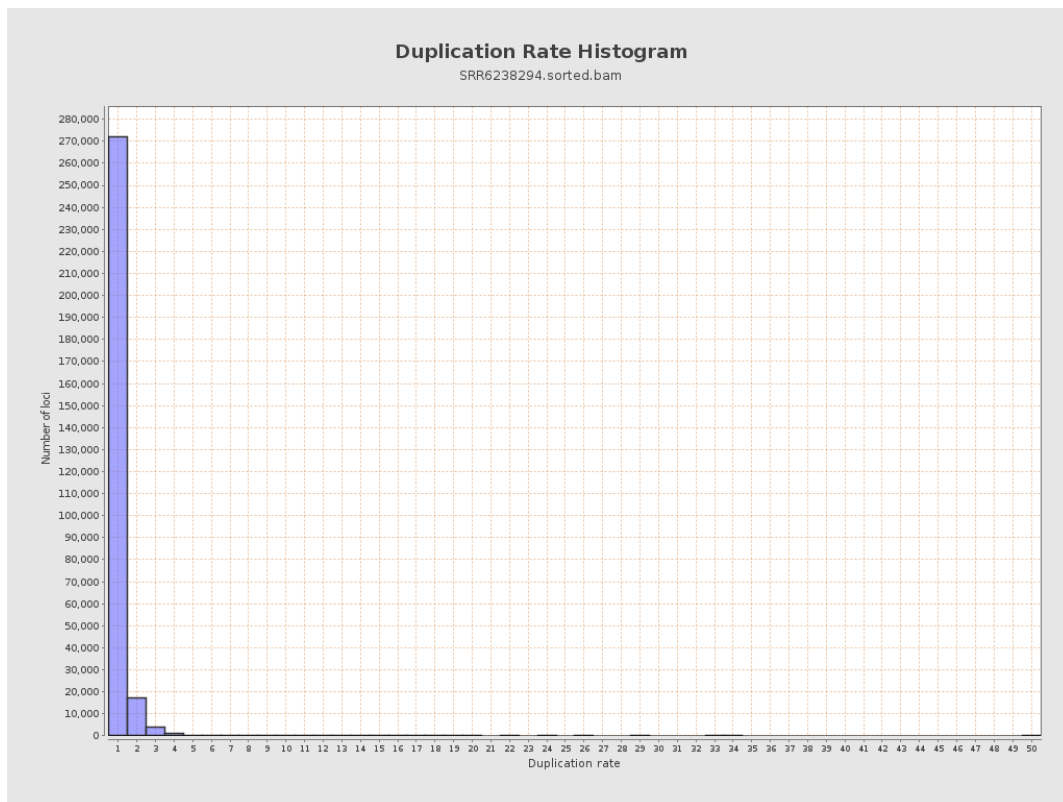
5. Results : Coverage Histogram (0-50X)



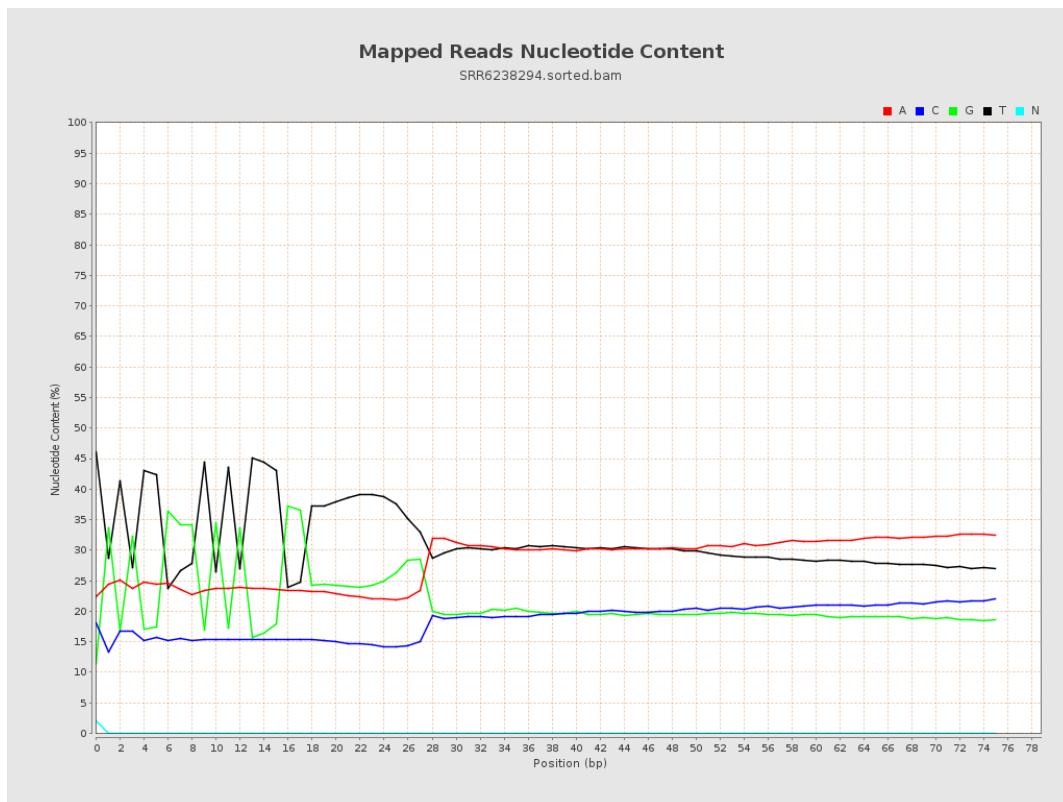
6. Results : Genome Fraction Coverage



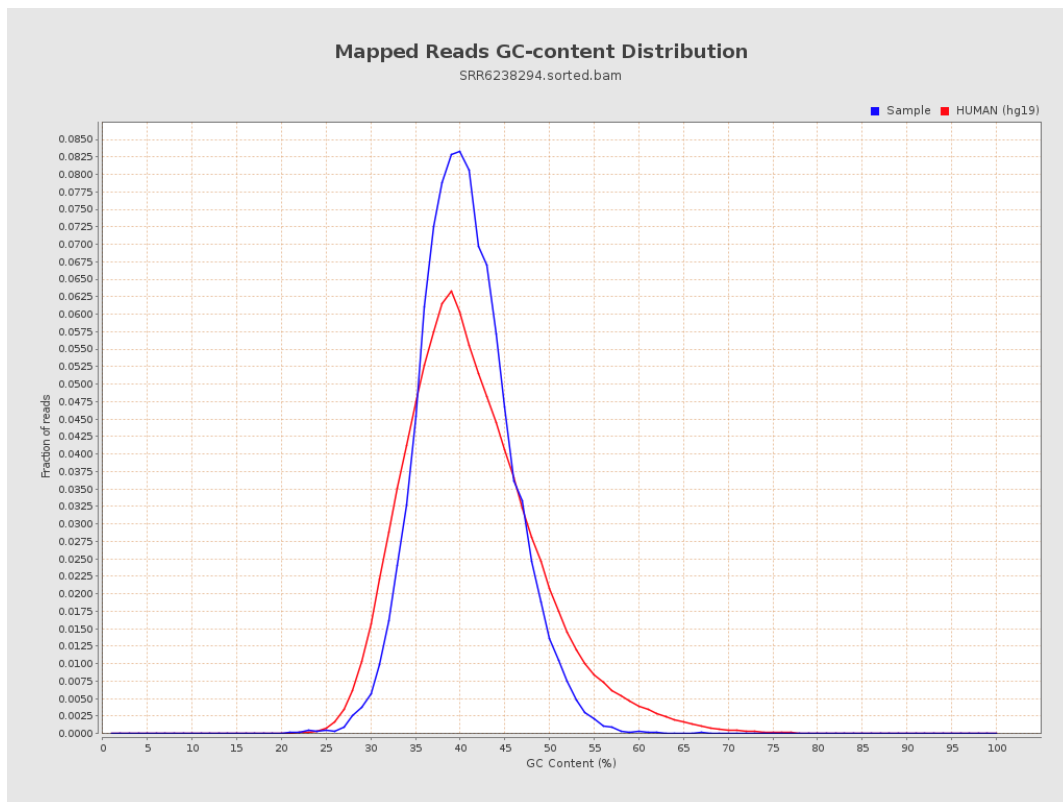
7. Results : Duplication Rate Histogram



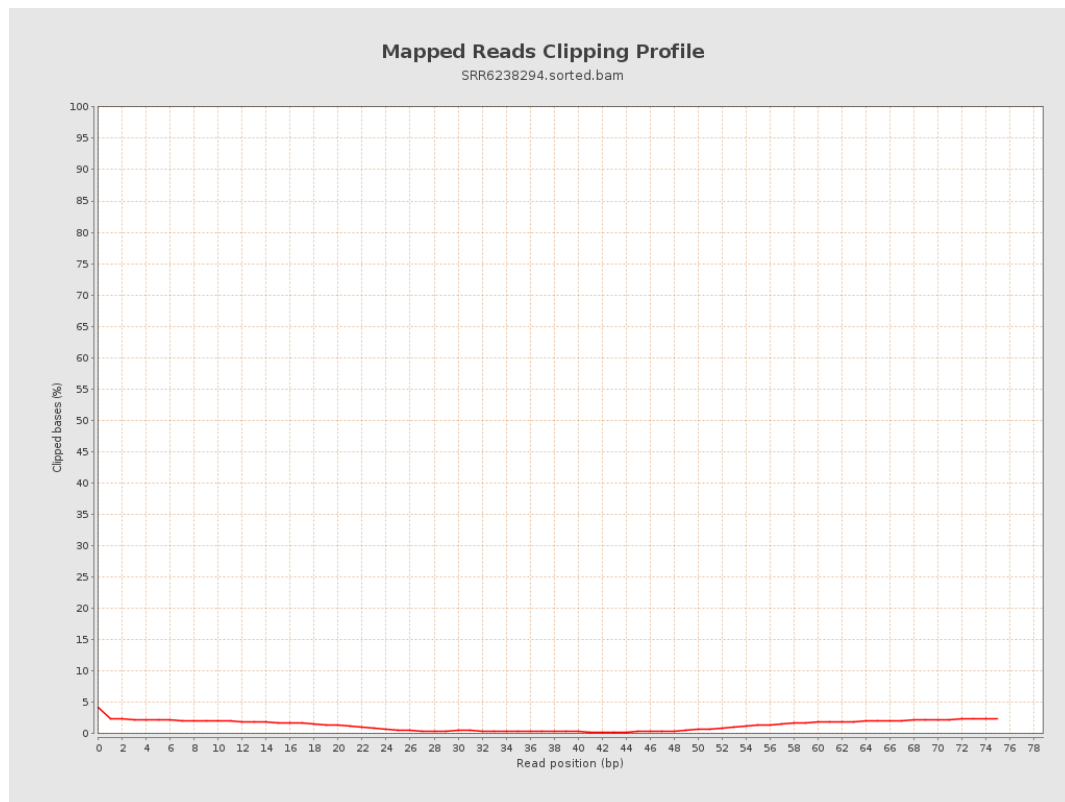
8. Results : Mapped Reads Nucleotide Content



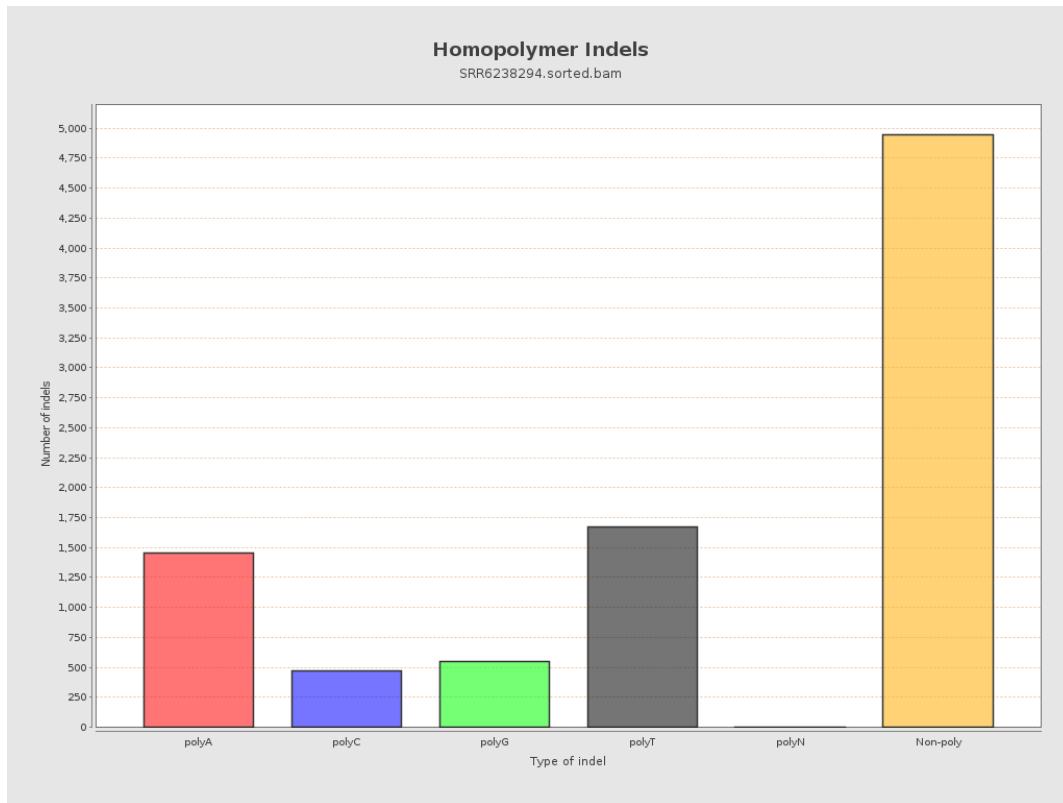
9. Results : Mapped Reads GC-content Distribution



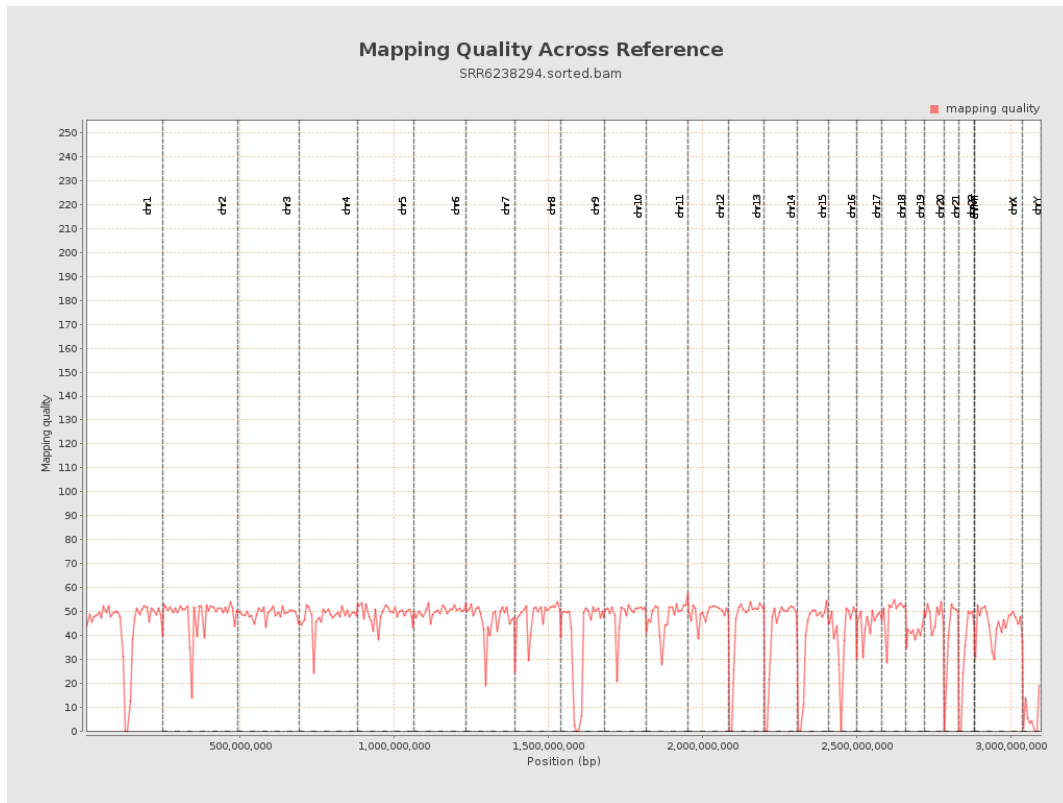
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

