

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 13:08:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238255.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_SRR6238255 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238255.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 13:08:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238255.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,325,413
Mapped reads	2,101,165 / 90.36%
Unmapped reads	224,248 / 9.64%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,003 / 0.69%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	67,428 / 2.9%
Duplication rate	2.22%
Clipped reads	1,108,593 / 47.67%

2.2. ACGT Content

Number/percentage of A's	37,418,606 / 27.36%
Number/percentage of C's	27,199,636 / 19.89%
Number/percentage of T's	40,466,029 / 29.59%
Number/percentage of G's	31,653,084 / 23.14%
Number/percentage of N's	33,957 / 0.02%
GC Percentage	43.03%

2.3. Coverage

Mean	0.0442

Standard Deviation	0.3966
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2.4. Mapping Quality

Mean Mapping Quality	42.36
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2.5. Mismatches and indels

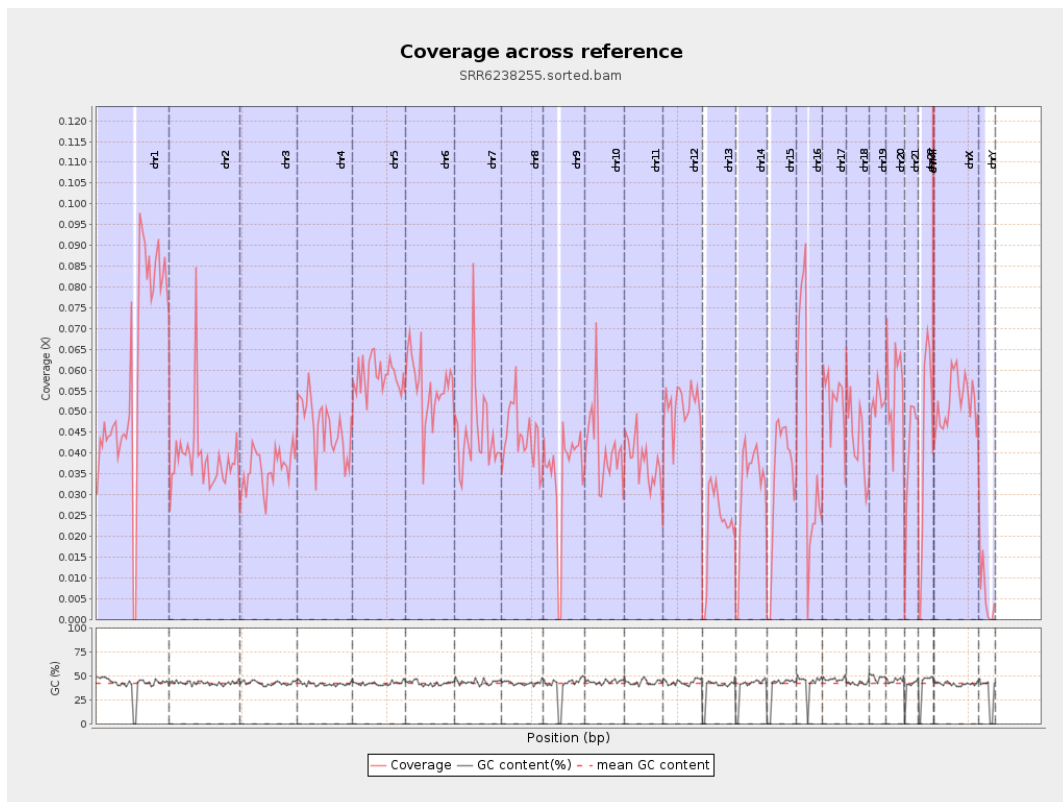
General error rate	0.89%
Mismatches	1,199,664
Insertions	11,083
Mapped reads with at least one insertion	0.52%
Deletions	38,596
Mapped reads with at least one deletion	1.82%
Homopolymer indels	44.56%

2.6. Chromosome stats

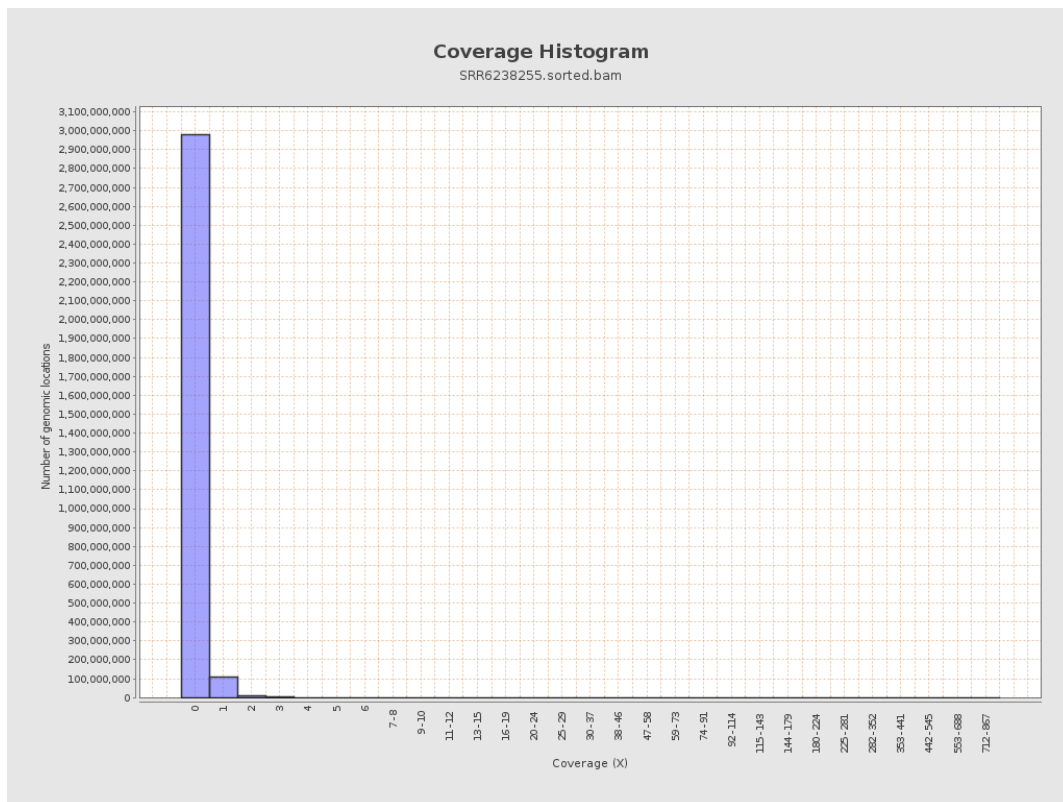
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	14807851	0.0594	0.6939
chr2	243199373	9447115	0.0388	0.5388
chr3	198022430	7174985	0.0362	0.2121
chr4	191154276	8833630	0.0462	0.2528
chr5	180915260	10636034	0.0588	0.2728
chr6	171115067	9538206	0.0557	0.3457
chr7	159138663	7154733	0.045	0.6103

chr8	146364022	6419157	0.0439	0.3824
chr9	141213431	4928916	0.0349	0.3678
chr10	135534747	5585273	0.0412	0.362
chr11	135006516	5126304	0.038	0.2974
chr12	133851895	6869867	0.0513	0.259
chr13	115169878	2573889	0.0223	0.167
chr14	107349540	3409136	0.0318	0.2505
chr15	102531392	3449613	0.0336	0.2156
chr16	90354753	4009877	0.0444	0.266
chr17	81195210	4276984	0.0527	0.2928
chr18	78077248	3423823	0.0439	0.6275
chr19	59128983	3070499	0.0519	0.563
chr20	63025520	3484221	0.0553	0.271
chr21	48129895	1936228	0.0402	0.2444
chr22	51304566	2177297	0.0424	0.2334
chrMT	16571	17248	1.0409	1.2083
chrX	155270560	8122242	0.0523	0.2956
chrY	59373566	362061	0.0061	0.1254

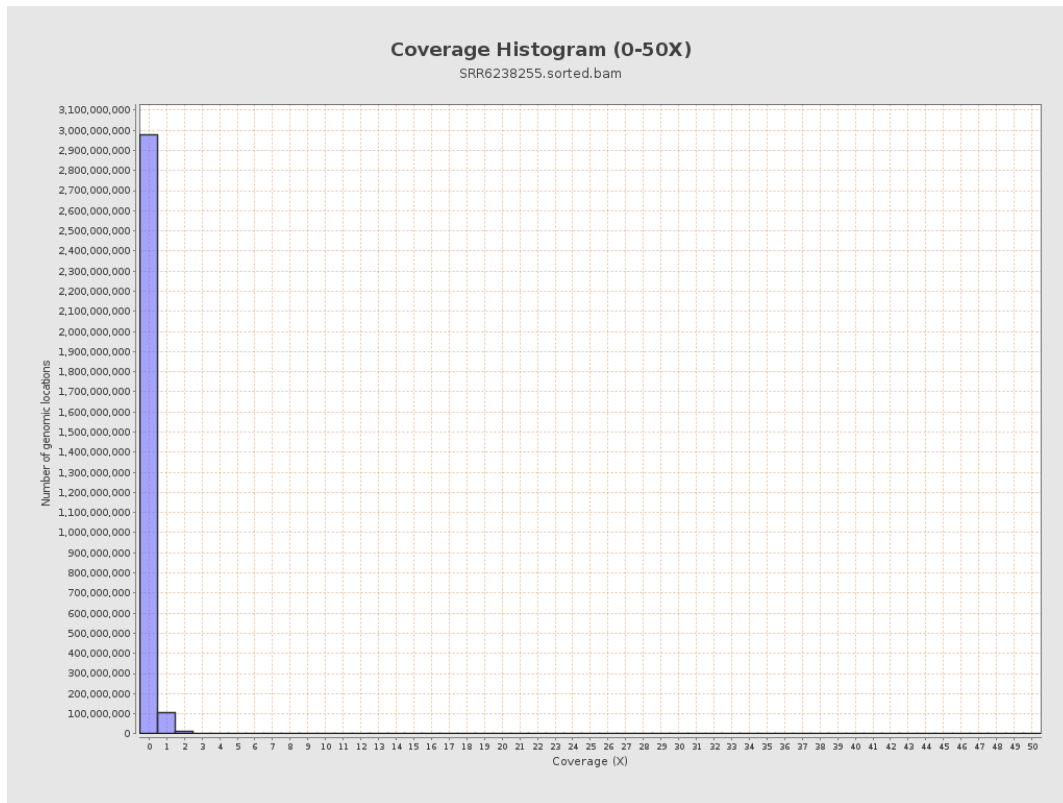
3. Results : Coverage across reference



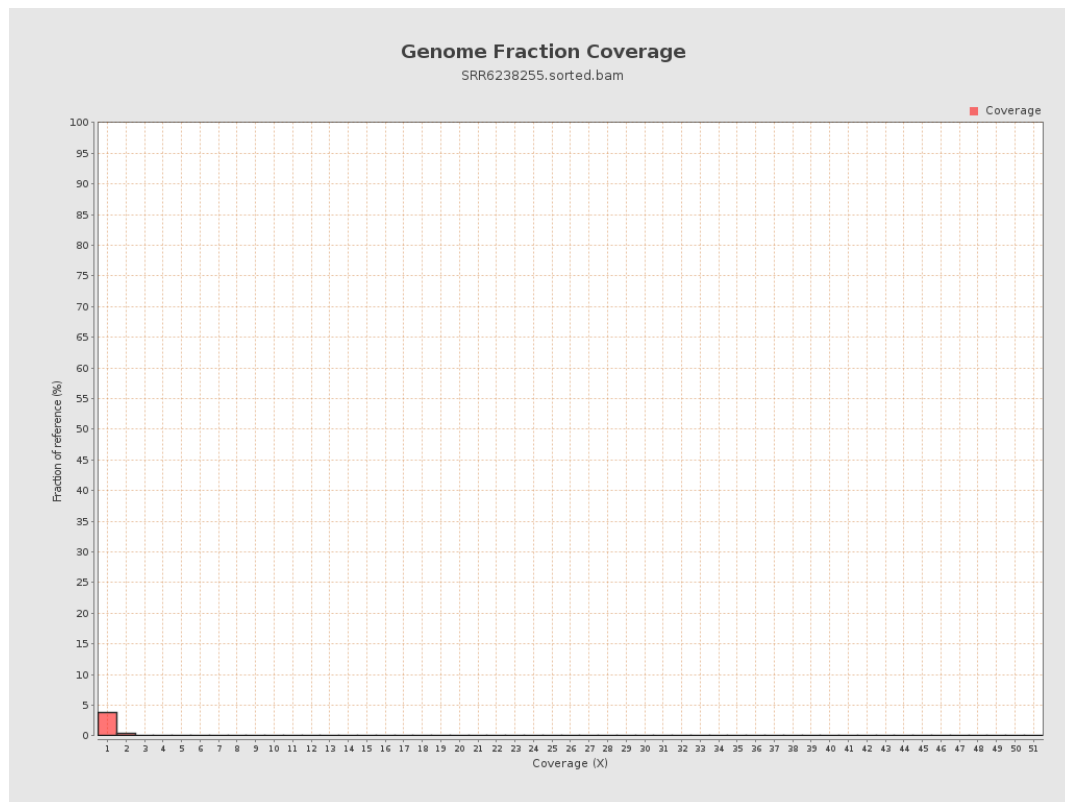
4. Results : Coverage Histogram



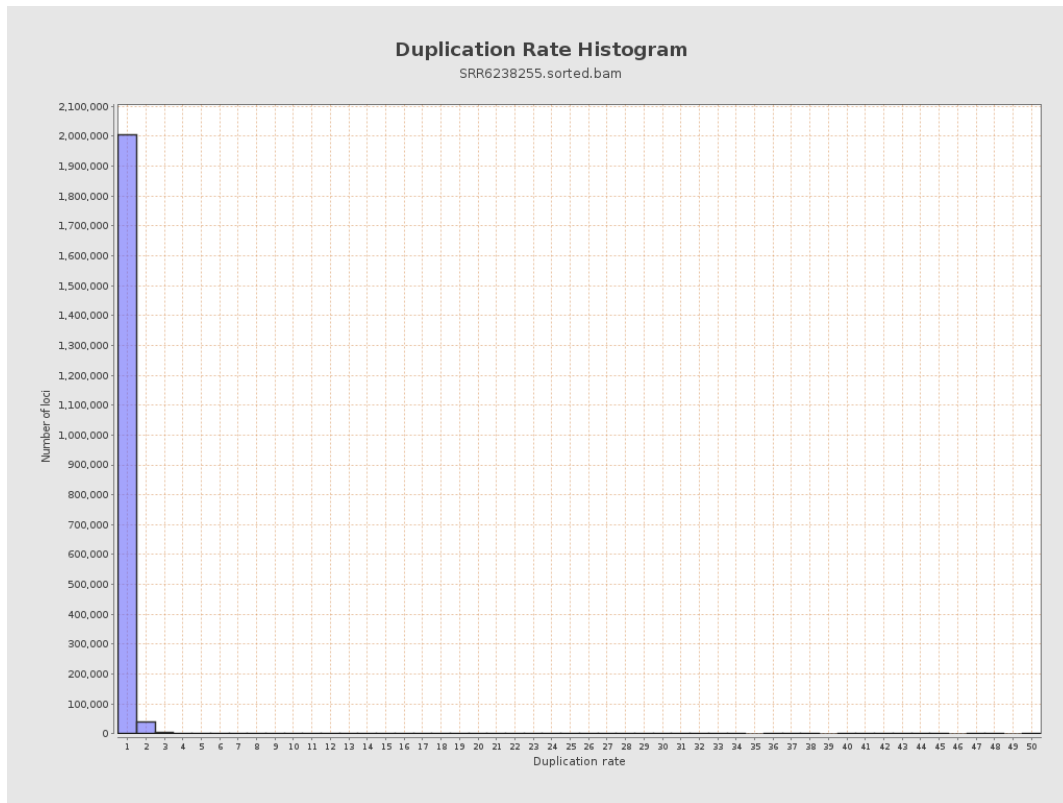
5. Results : Coverage Histogram (0-50X)



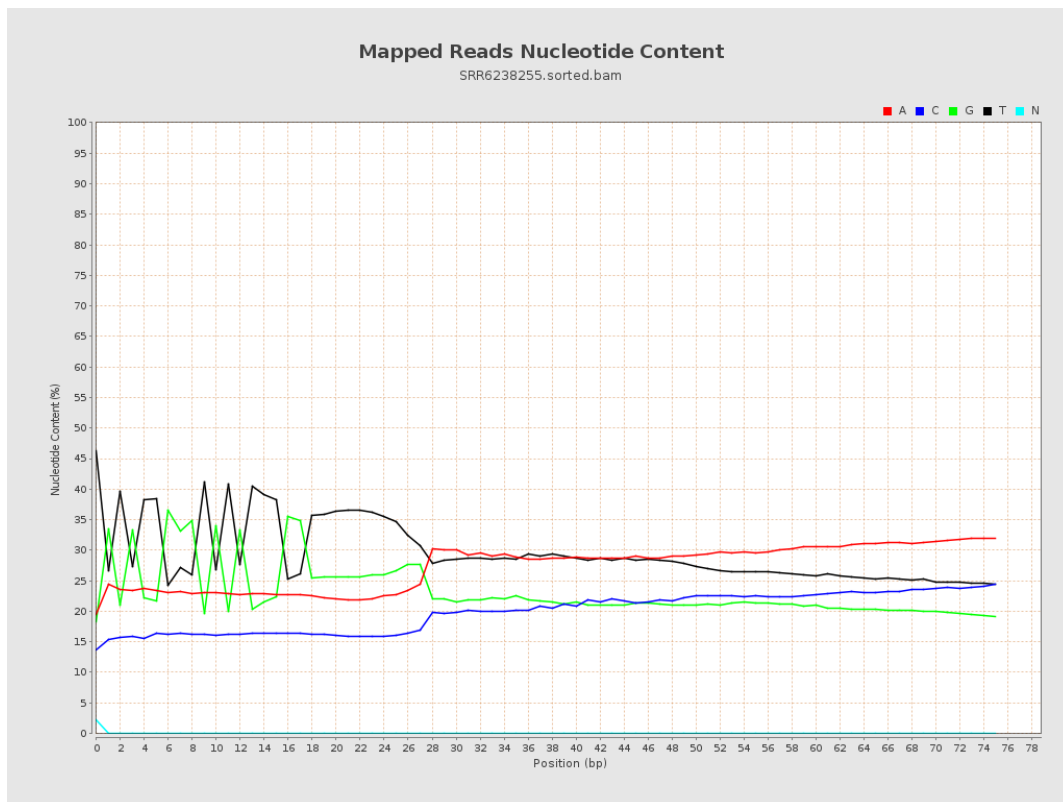
6. Results : Genome Fraction Coverage



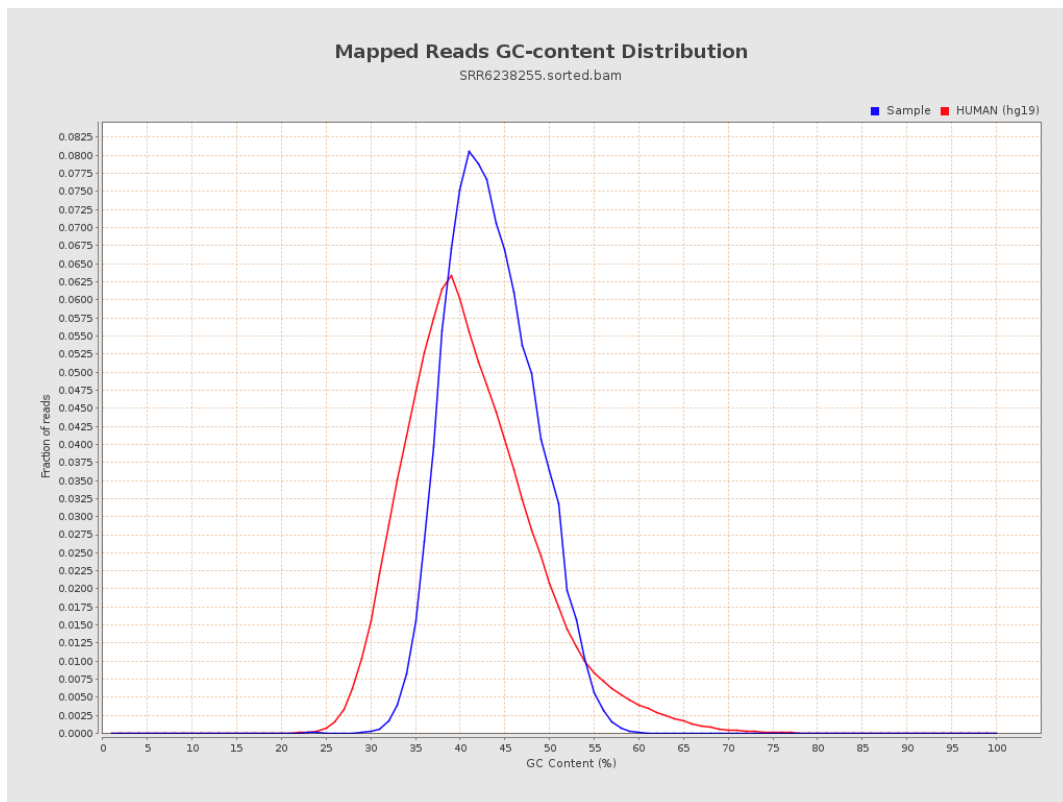
7. Results : Duplication Rate Histogram



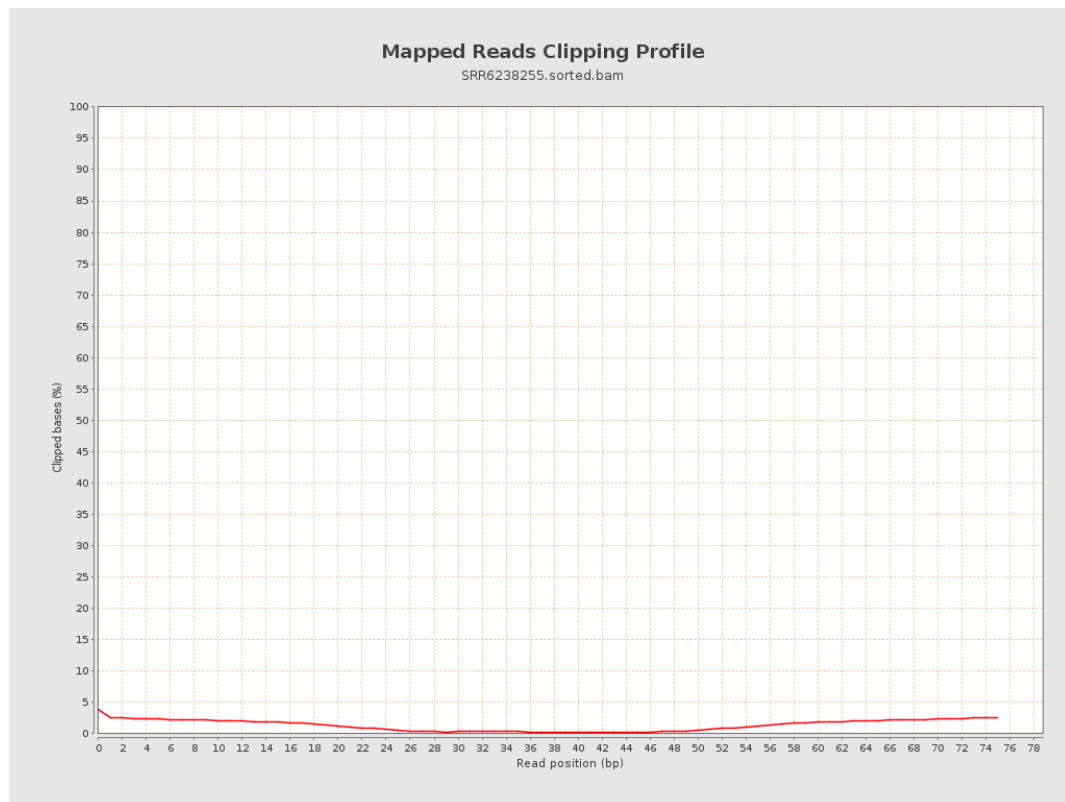
8. Results : Mapped Reads Nucleotide Content



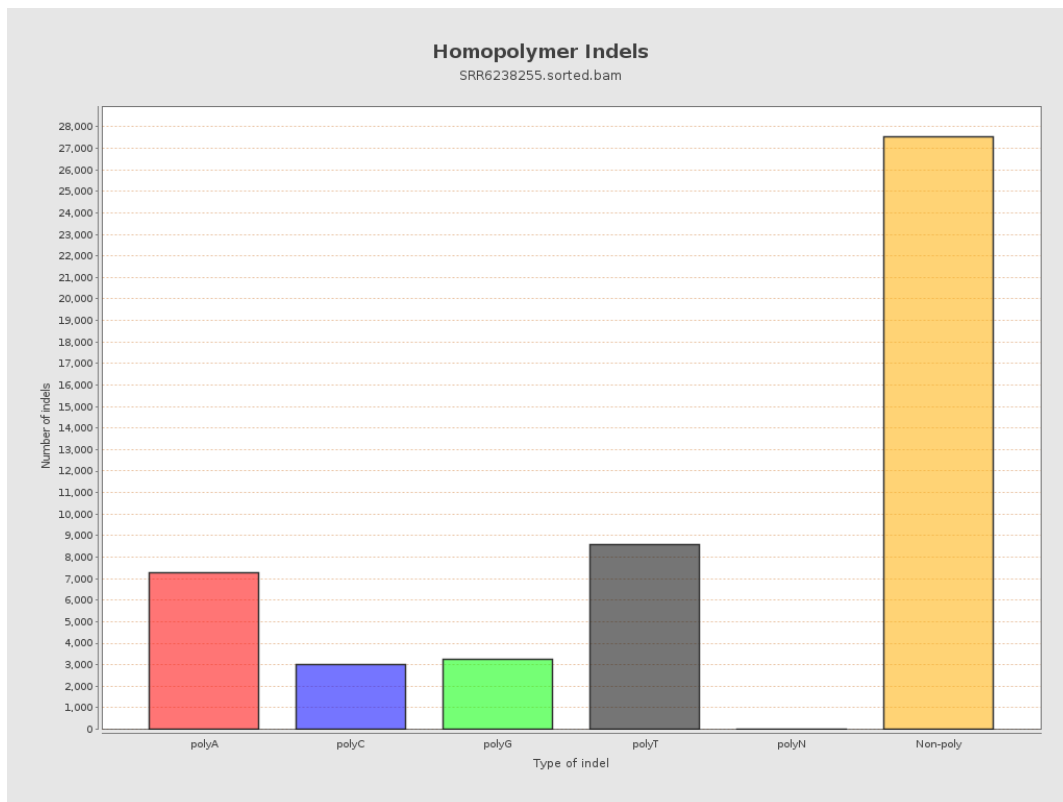
9. Results : Mapped Reads GC-content Distribution



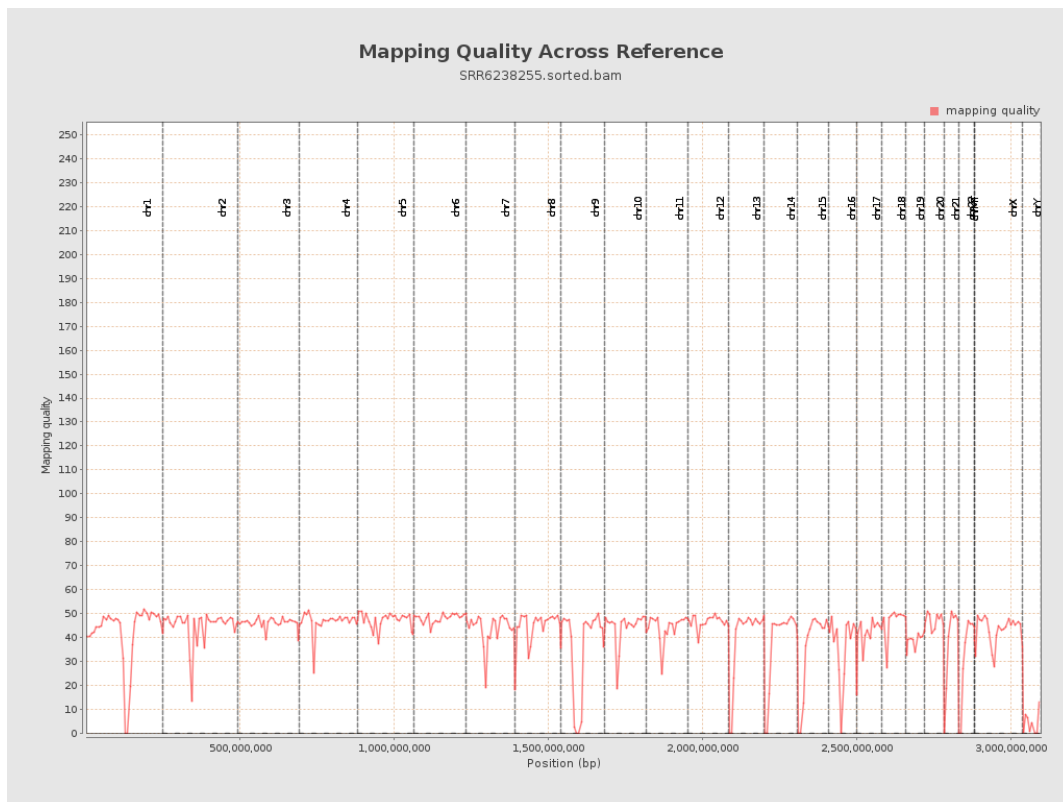
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

