

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 13:51:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238270.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_SRR6238270 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238270.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 13:51:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238270.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	853,940
Mapped reads	419,688 / 49.15%
Unmapped reads	434,252 / 50.85%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,155 / 0.49%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	59,523 / 6.97%
Duplication rate	9.13%
Clipped reads	259,125 / 30.34%

2.2. ACGT Content

Number/percentage of A's	7,171,592 / 27.53%
Number/percentage of C's	5,057,940 / 19.42%
Number/percentage of T's	7,931,337 / 30.45%
Number/percentage of G's	5,882,465 / 22.58%
Number/percentage of N's	5,932 / 0.02%
GC Percentage	42%

2.3. Coverage

Mean	0.0084

Standard Deviation	0.2437
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2.4. Mapping Quality

Mean Mapping Quality	43.4
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2.5. Mismatches and indels

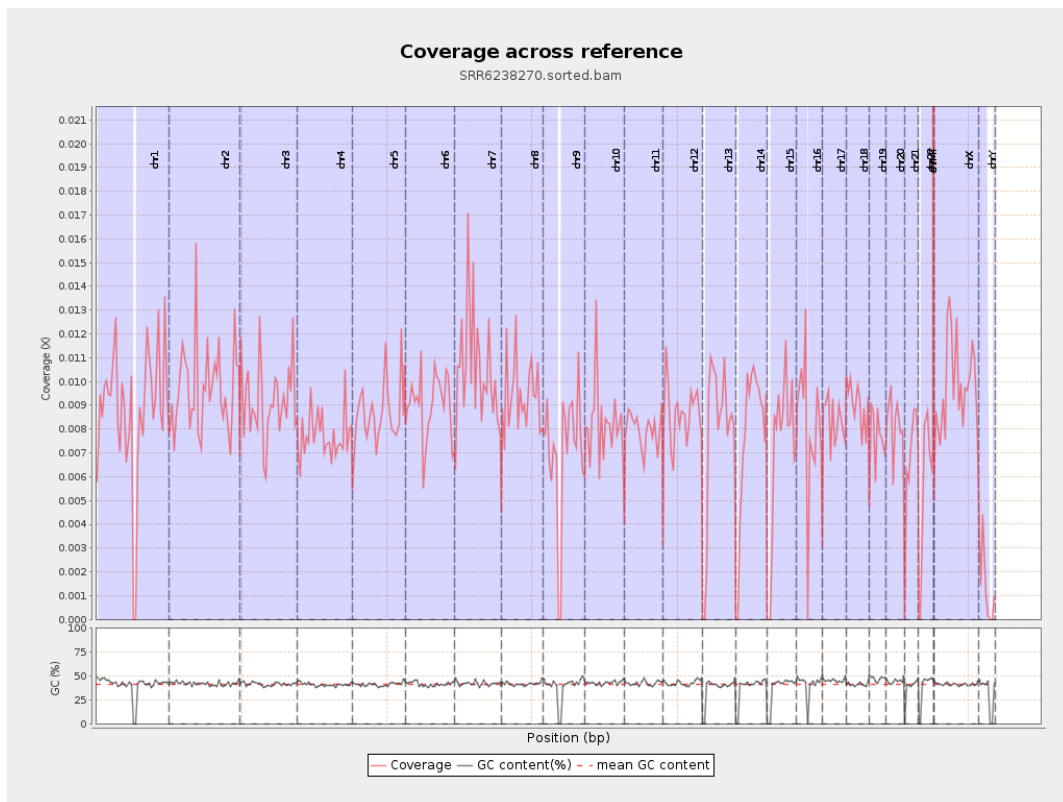
General error rate	1.02%
Mismatches	261,846
Insertions	2,240
Mapped reads with at least one insertion	0.53%
Deletions	8,576
Mapped reads with at least one deletion	2.02%
Homopolymer indels	45.28%

2.6. Chromosome stats

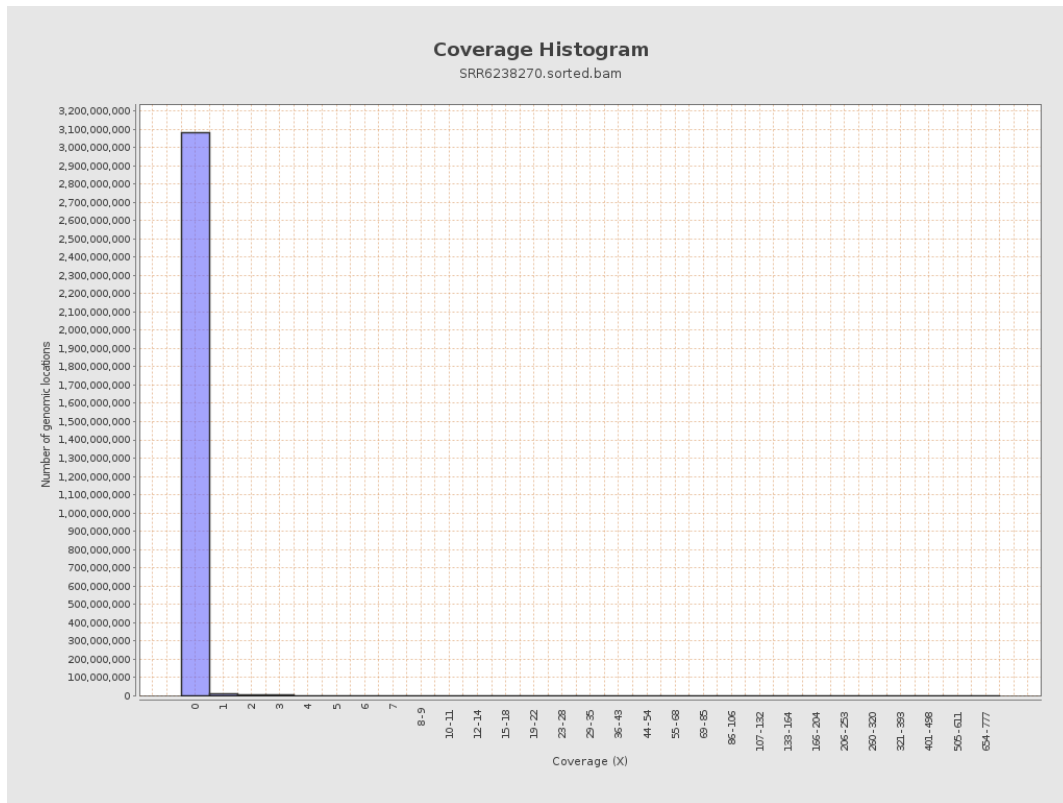
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	2196295	0.0088	0.2626
chr2	243199373	2359993	0.0097	0.3135
chr3	198022430	1818061	0.0092	0.1709
chr4	191154276	1480222	0.0077	0.3618
chr5	180915260	1565365	0.0087	0.1719
chr6	171115067	1543672	0.009	0.2233
chr7	159138663	1675015	0.0105	0.199

chr8	146364022	1378588	0.0094	0.193
chr9	141213431	991204	0.007	0.15
chr10	135534747	1115163	0.0082	0.1712
chr11	135006516	1065799	0.0079	0.1507
chr12	133851895	1163241	0.0087	0.1766
chr13	115169878	887053	0.0077	0.1977
chr14	107349540	821204	0.0076	0.4208
chr15	102531392	724700	0.0071	0.5248
chr16	90354753	734081	0.0081	0.1482
chr17	81195210	674700	0.0083	0.1679
chr18	78077248	702452	0.009	0.1716
chr19	59128983	453408	0.0077	0.1526
chr20	63025520	513528	0.0081	0.1469
chr21	48129895	322901	0.0067	0.1278
chr22	51304566	276713	0.0054	0.1121
chrMT	16571	5072	0.3061	1.5247
chrX	155270560	1517235	0.0098	0.2335
chrY	59373566	77537	0.0013	0.1216

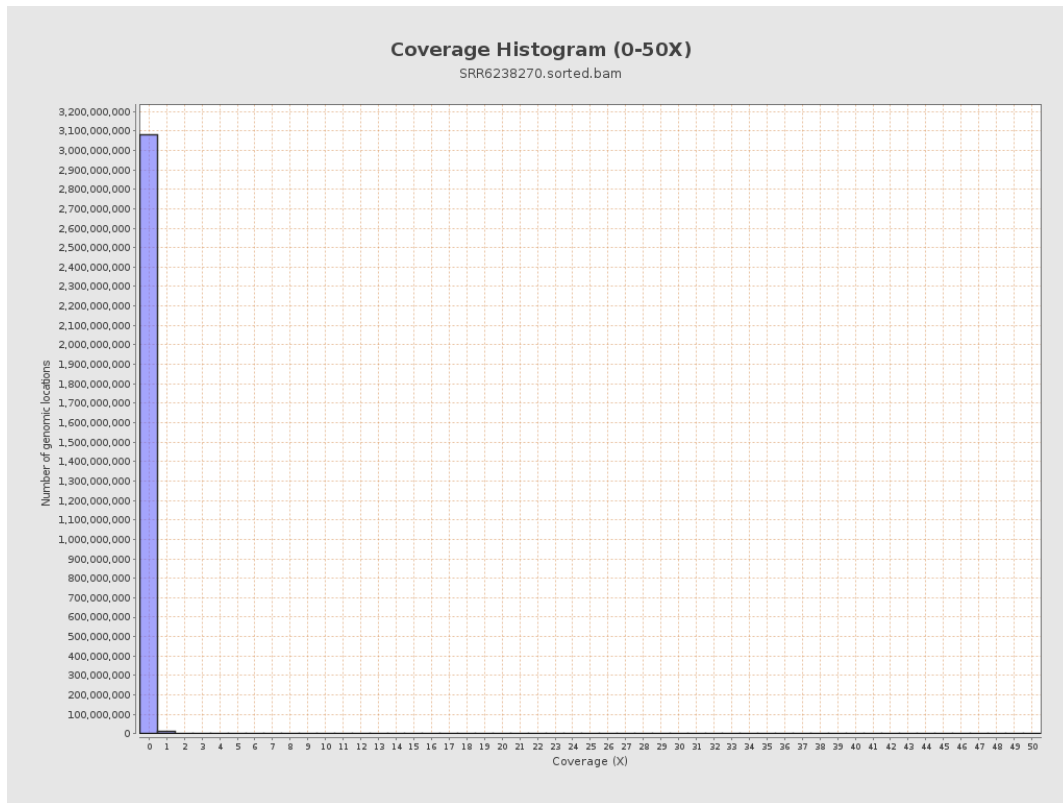
3. Results : Coverage across reference



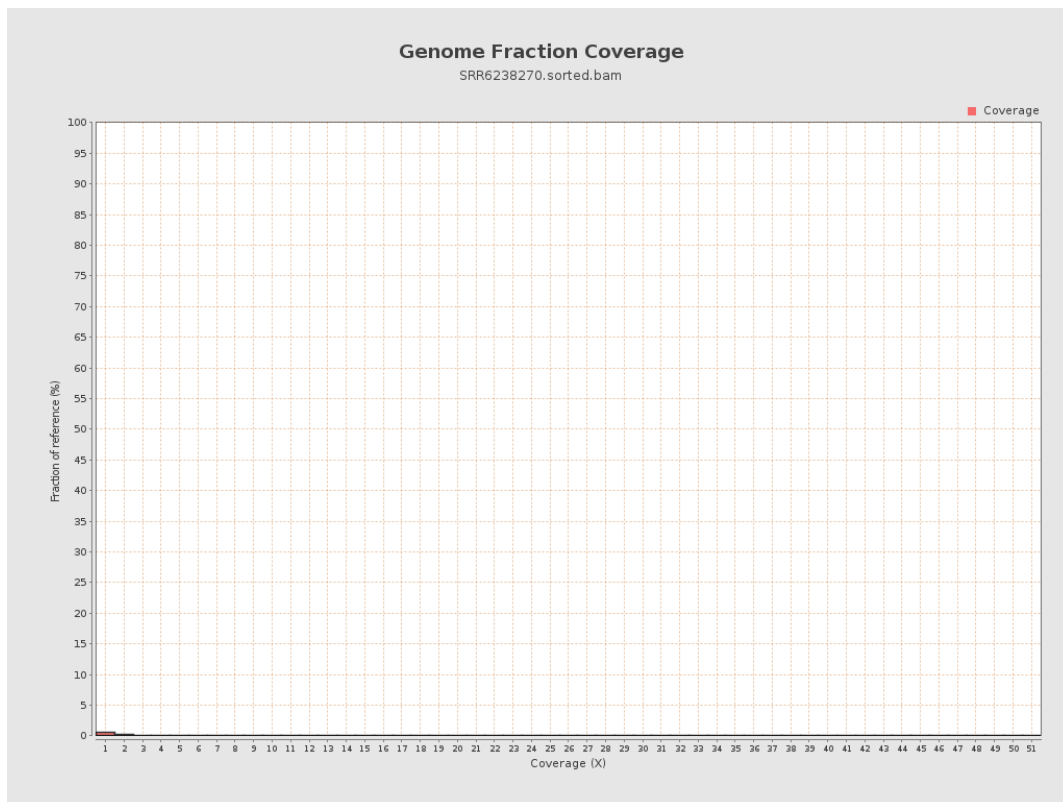
4. Results : Coverage Histogram



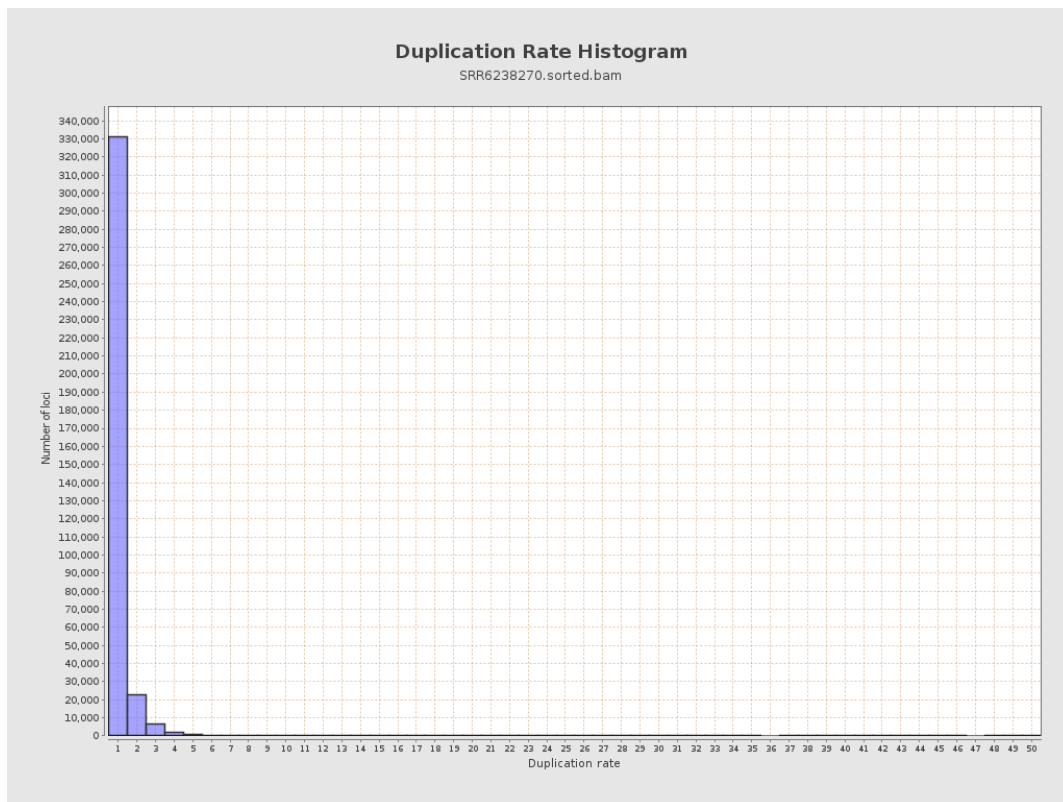
5. Results : Coverage Histogram (0-50X)



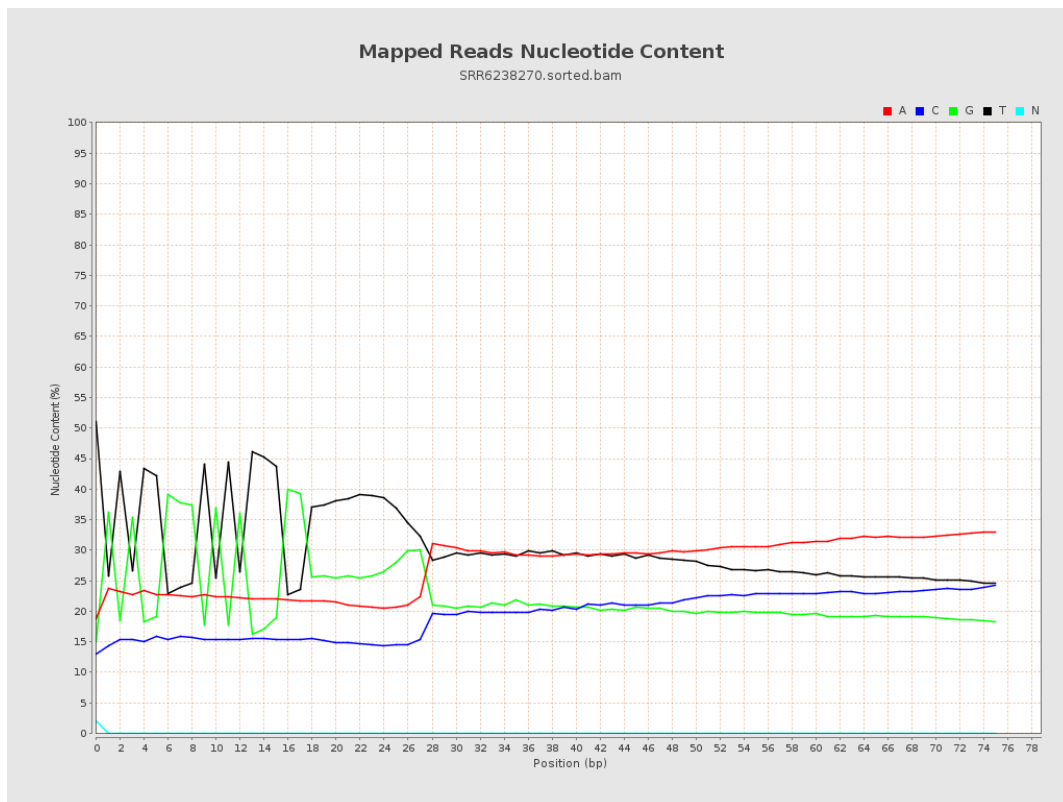
6. Results : Genome Fraction Coverage



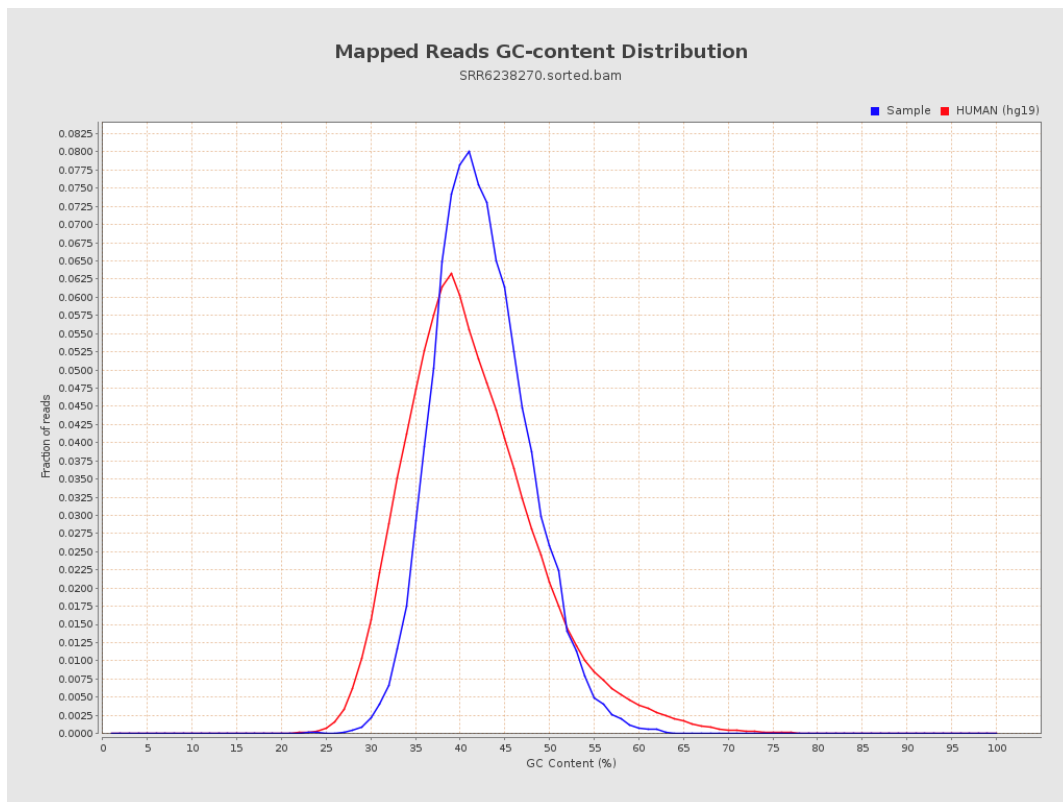
7. Results : Duplication Rate Histogram



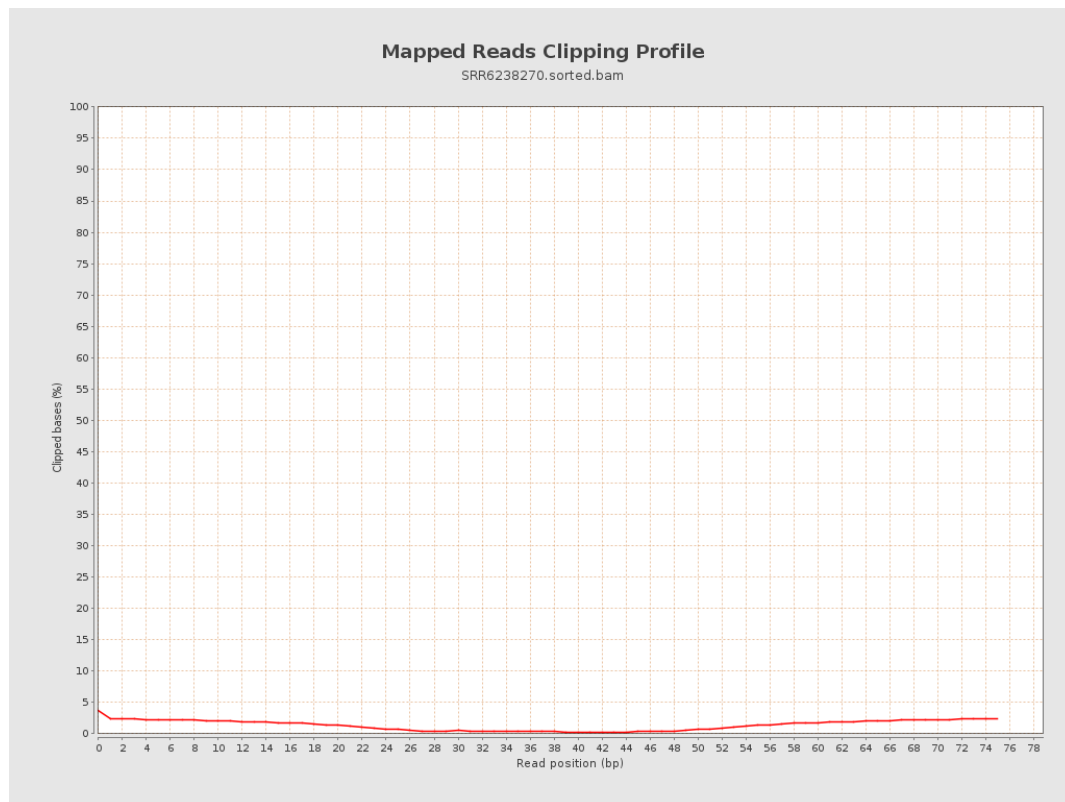
8. Results : Mapped Reads Nucleotide Content



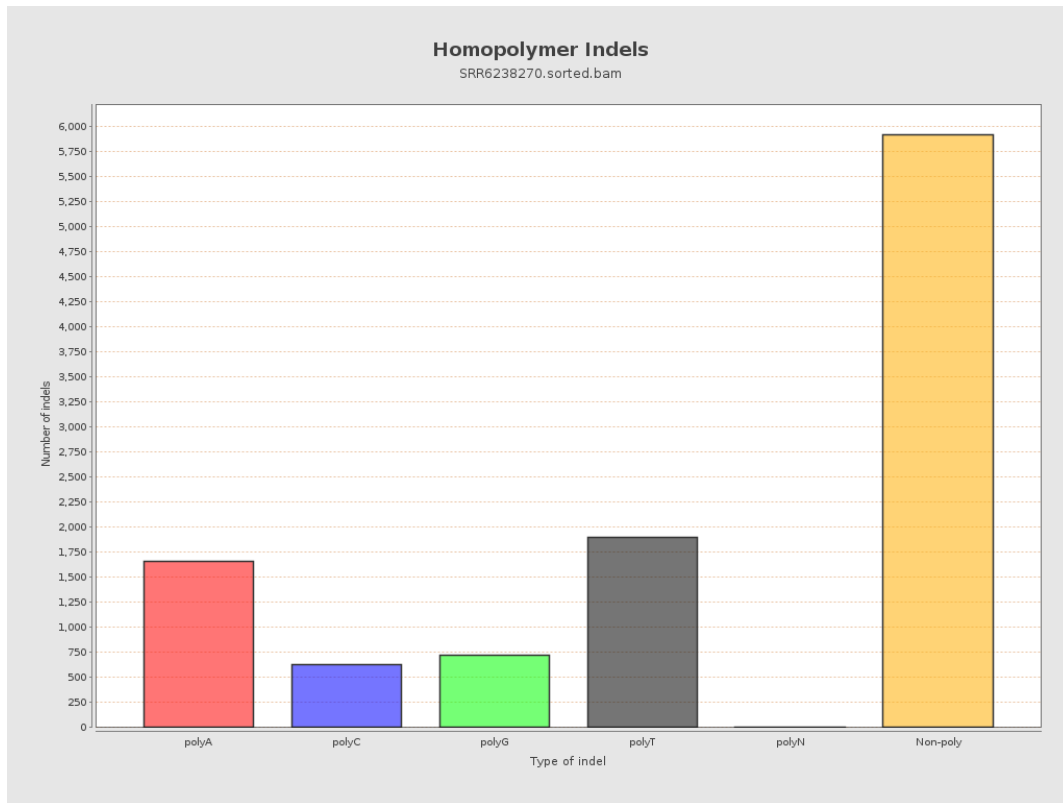
9. Results : Mapped Reads GC-content Distribution



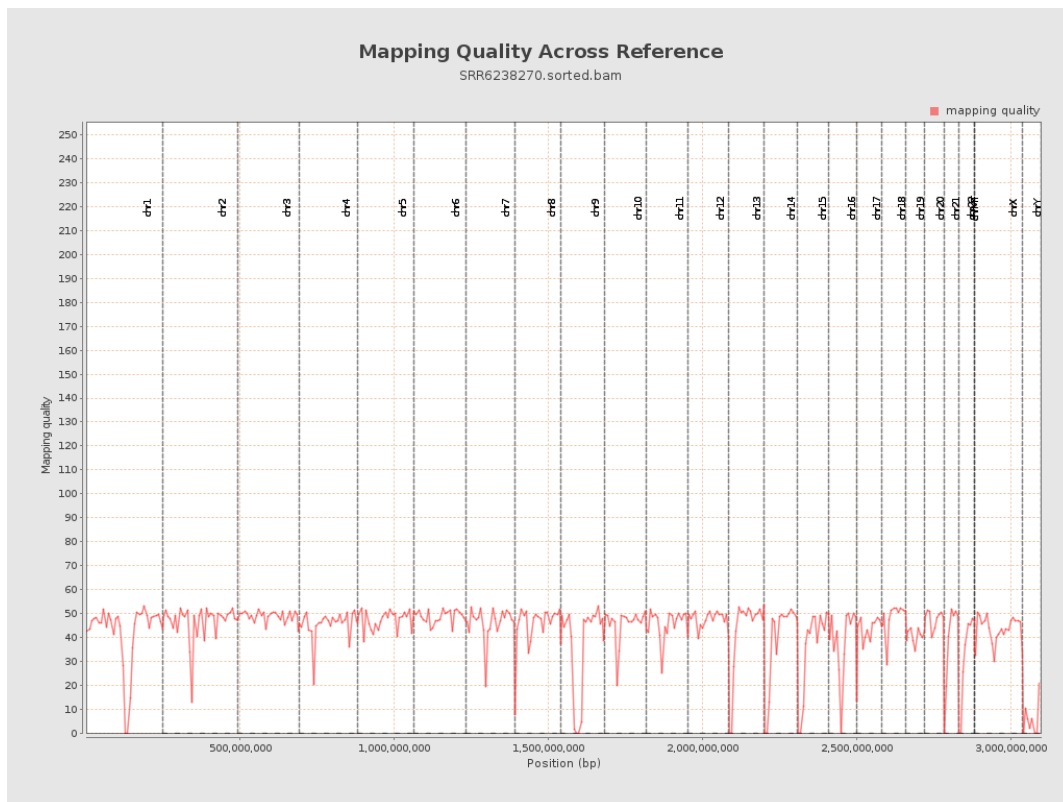
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

