

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 00:24:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238645.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_SRR6238645 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238645.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 00:24:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238645.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,704
Mapped reads	4,100 / 87.16%
Unmapped reads	604 / 12.84%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	36 / 0.77%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	246 / 5.23%
Duplication rate	5.55%
Clipped reads	2,488 / 52.89%

2.2. ACGT Content

Number/percentage of A's	64,424 / 25.17%
Number/percentage of C's	46,908 / 18.33%
Number/percentage of T's	82,444 / 32.21%
Number/percentage of G's	62,143 / 24.28%
Number/percentage of N's	20 / 0.01%
GC Percentage	42.61%

2.3. Coverage

Mean	0.0001

Standard Deviation	0.0099
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2.4. Mapping Quality

Mean Mapping Quality	42.16
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2.5. Mismatches and indels

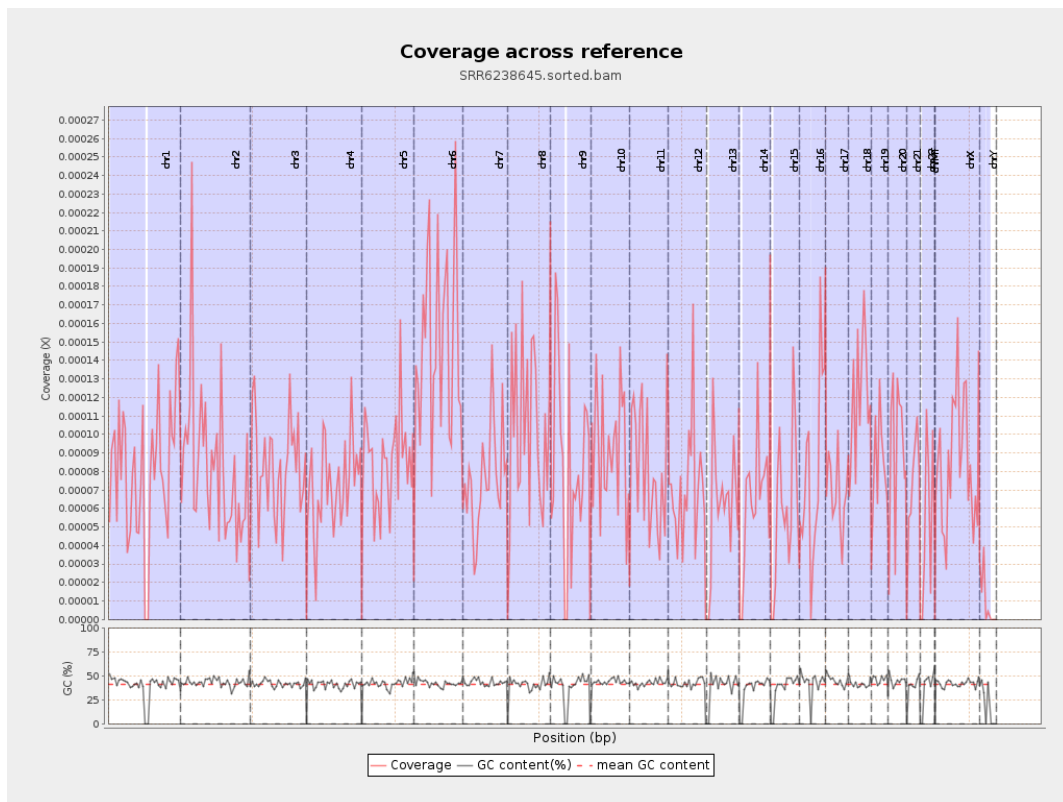
General error rate	0.58%
Mismatches	1,443
Insertions	18
Mapped reads with at least one insertion	0.44%
Deletions	63
Mapped reads with at least one deletion	1.51%
Homopolymer indels	49.38%

2.6. Chromosome stats

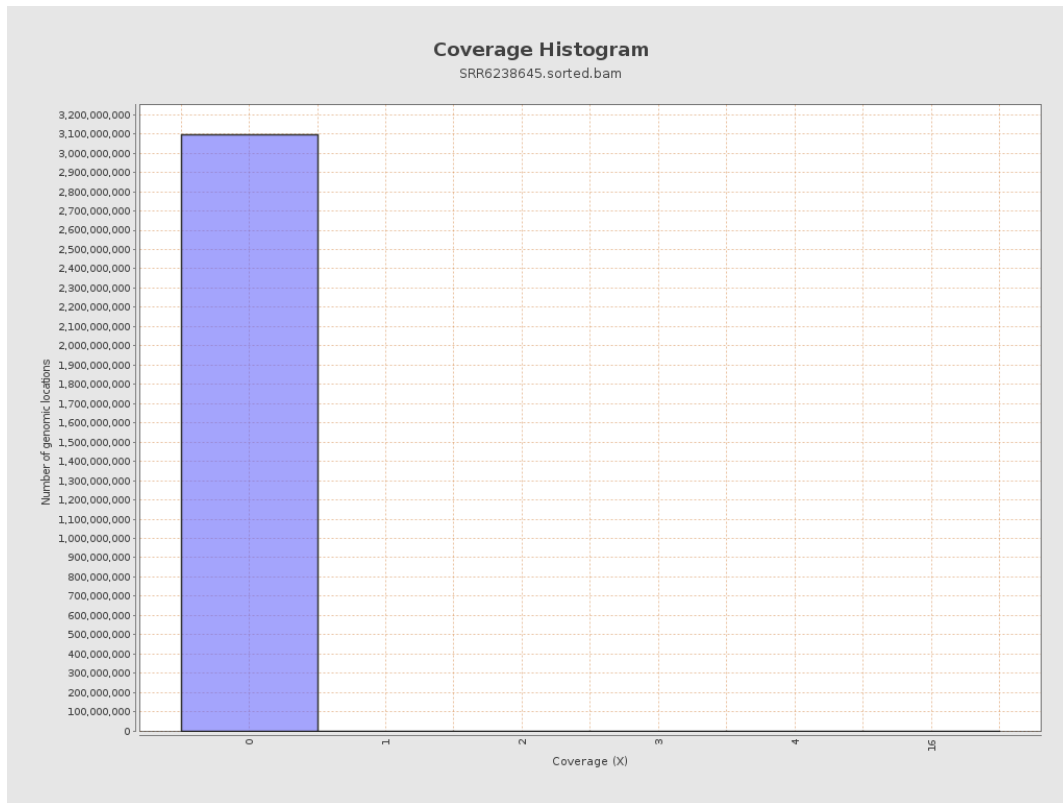
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	20315	0.0001	0.0097
chr2	243199373	19896	0.0001	0.0095
chr3	198022430	16362	0.0001	0.0097
chr4	191154276	13935	0.0001	0.009
chr5	180915260	15414	0.0001	0.0098
chr6	171115067	25042	0.0001	0.0129
chr7	159138663	12134	0.0001	0.0092

chr8	146364022	15442	0.0001	0.0109
chr9	141213431	11784	0.0001	0.01
chr10	135534747	12508	0.0001	0.0103
chr11	135006516	11013	0.0001	0.0093
chr12	133851895	9379	0.0001	0.0133
chr13	115169878	6946	0.0001	0.008
chr14	107349540	6737	0.0001	0.0082
chr15	102531392	6069	0.0001	0.008
chr16	90354753	7296	0.0001	0.0094
chr17	81195210	5568	0.0001	0.009
chr18	78077248	9503	0.0001	0.0121
chr19	59128983	4993	0.0001	0.0098
chr20	63025520	5829	0.0001	0.0103
chr21	48129895	3482	0.0001	0.0085
chr22	51304566	2742	0.0001	0.0077
chrMT	16571	0	0	0
chrX	155270560	13049	0.0001	0.0096
chrY	59373566	620	0	0.0032

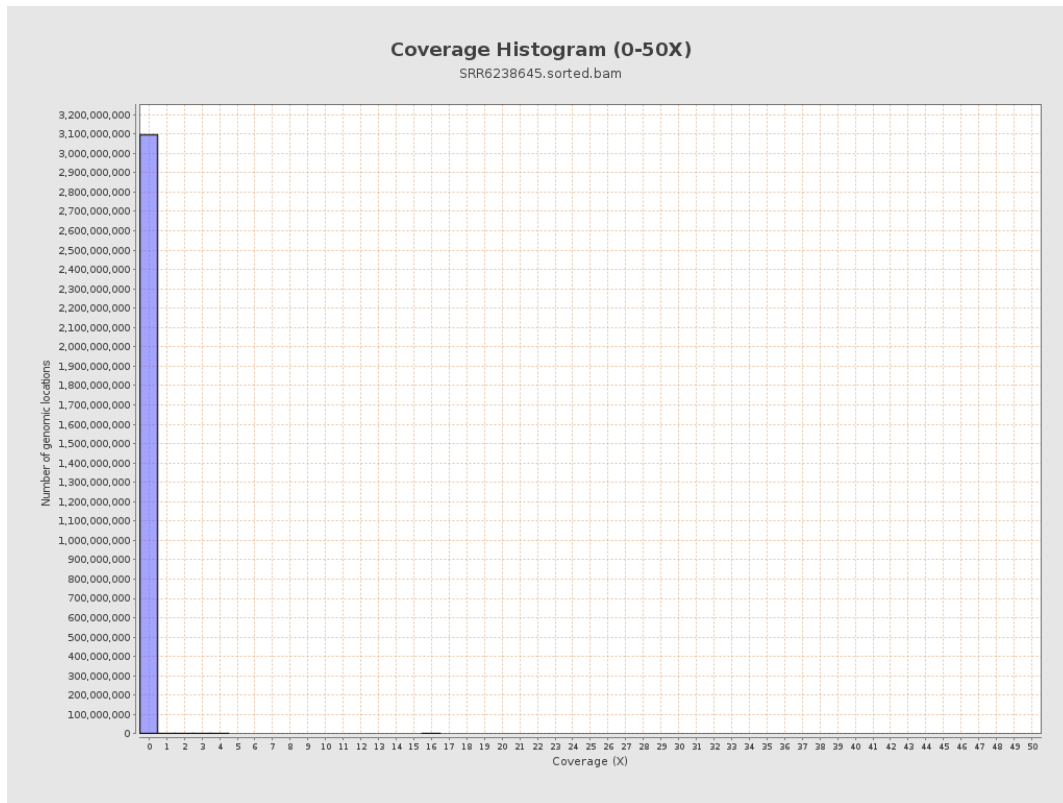
3. Results : Coverage across reference



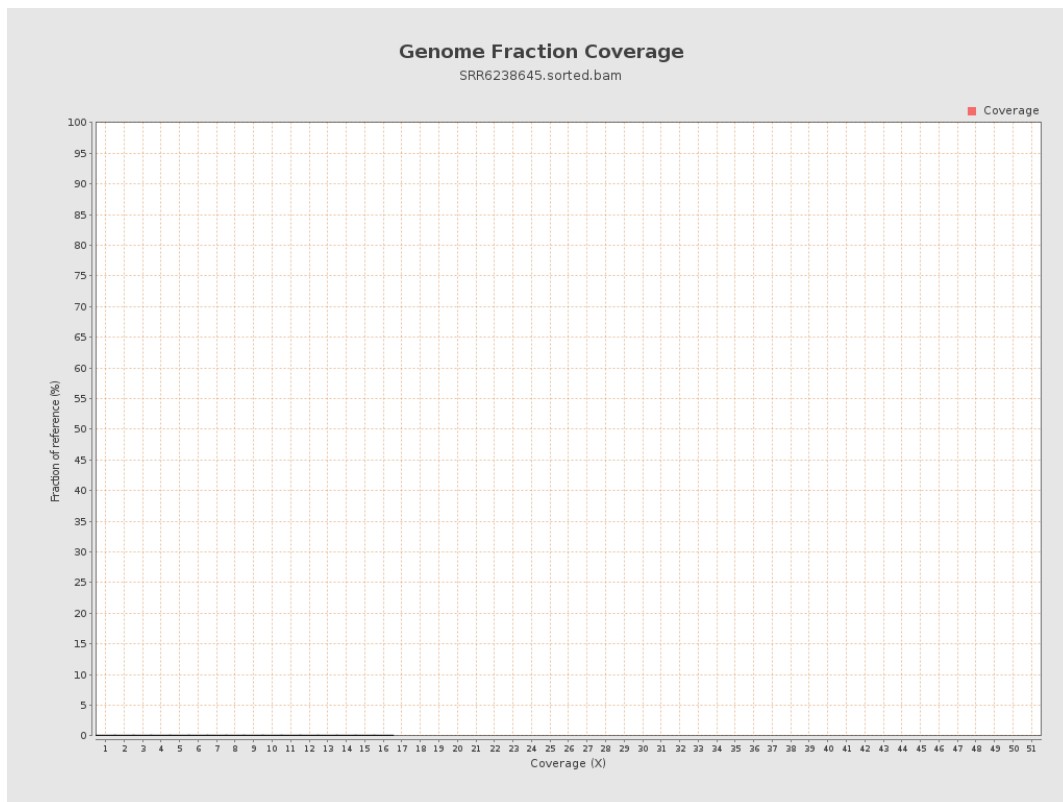
4. Results : Coverage Histogram



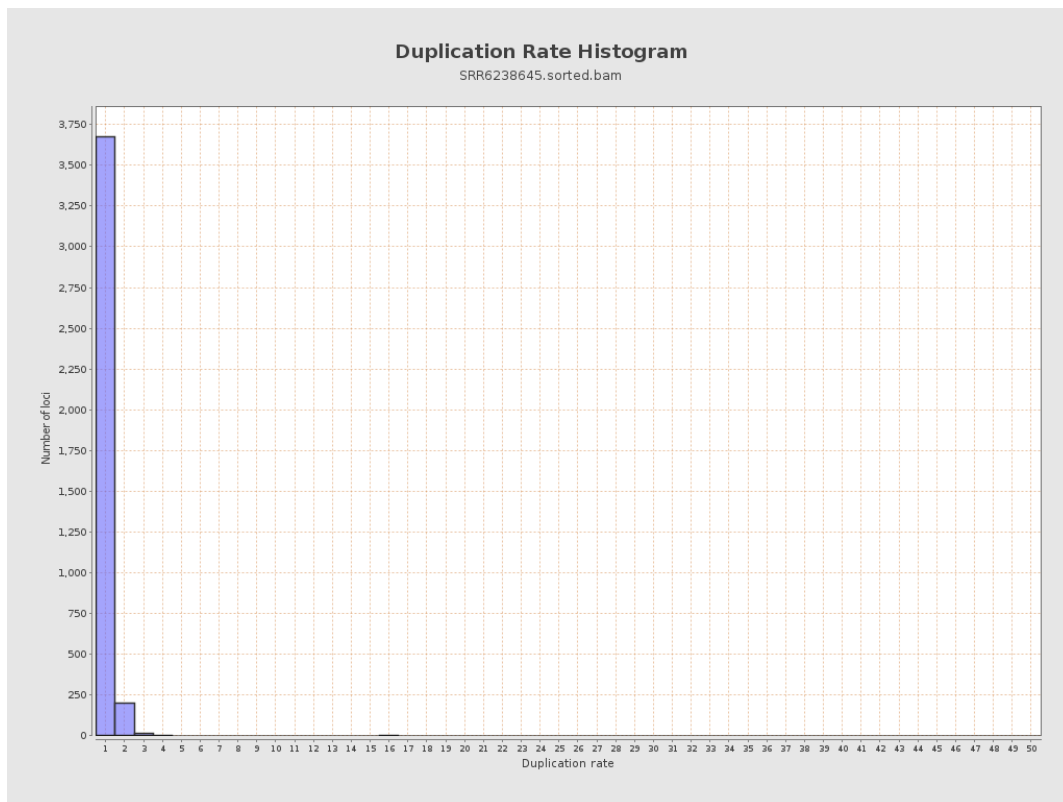
5. Results : Coverage Histogram (0-50X)



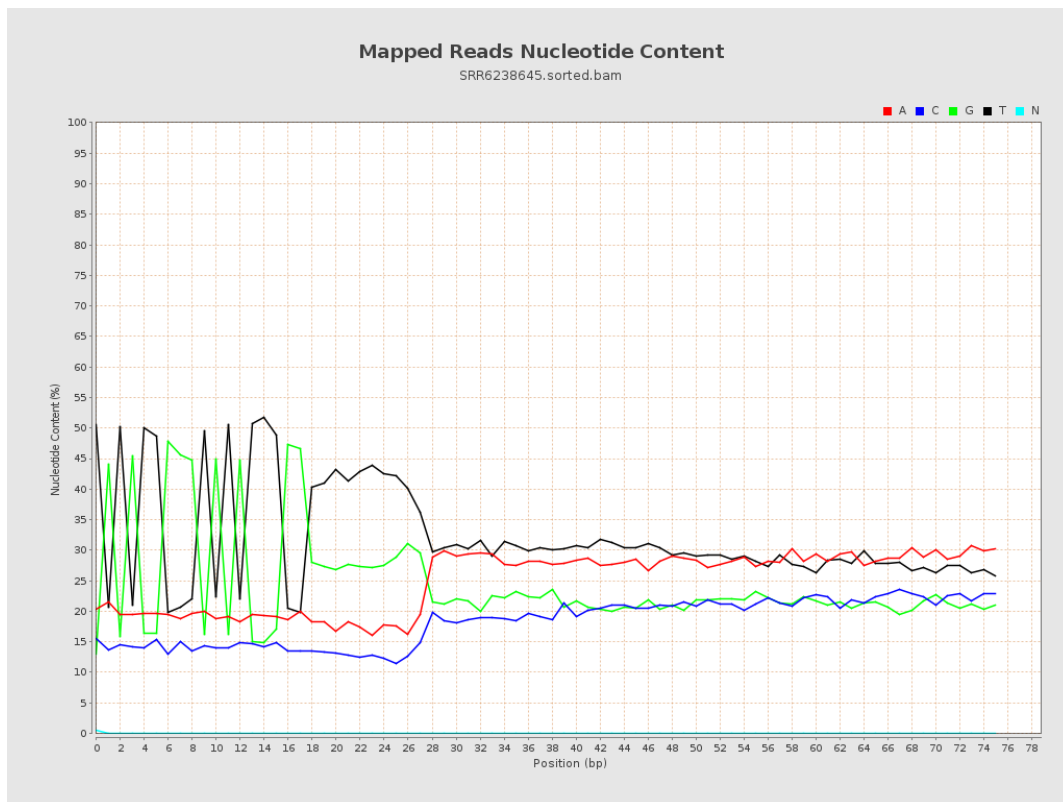
6. Results : Genome Fraction Coverage



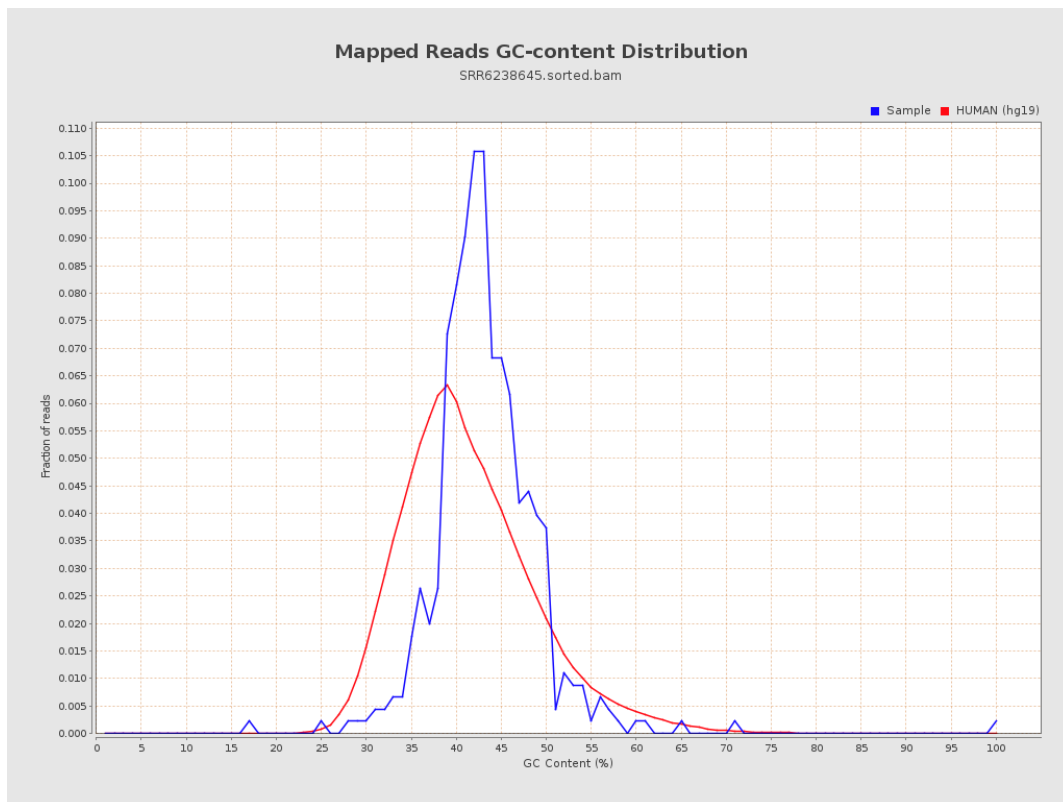
7. Results : Duplication Rate Histogram



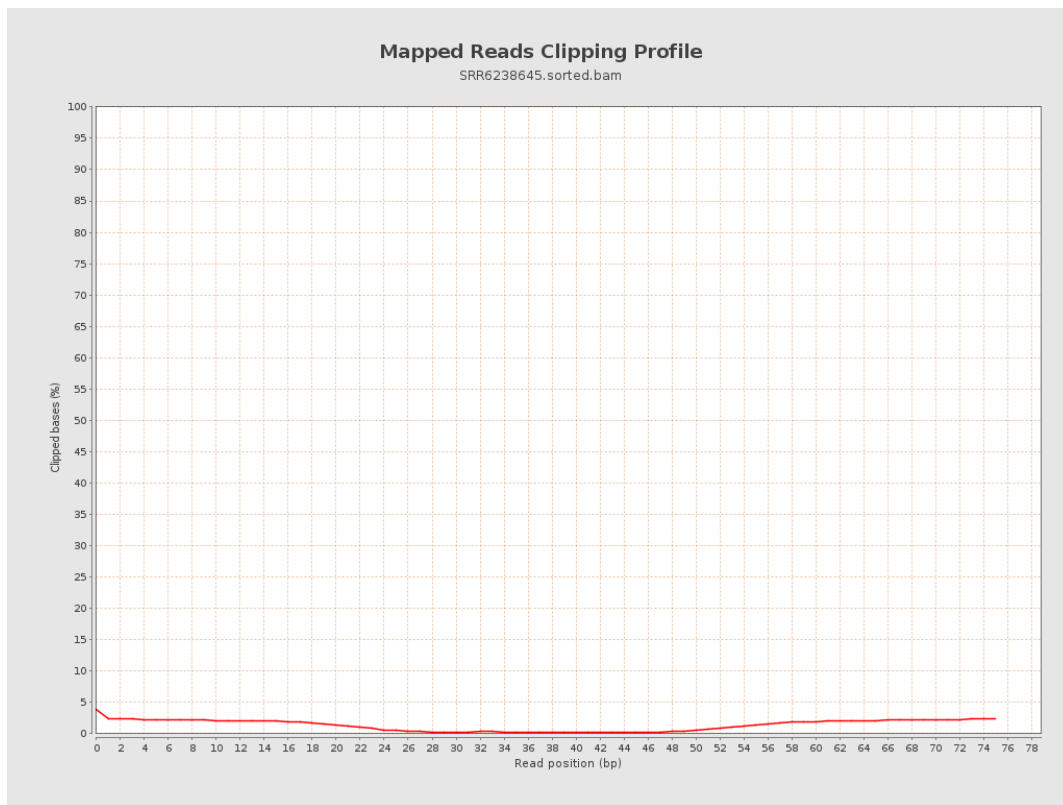
8. Results : Mapped Reads Nucleotide Content



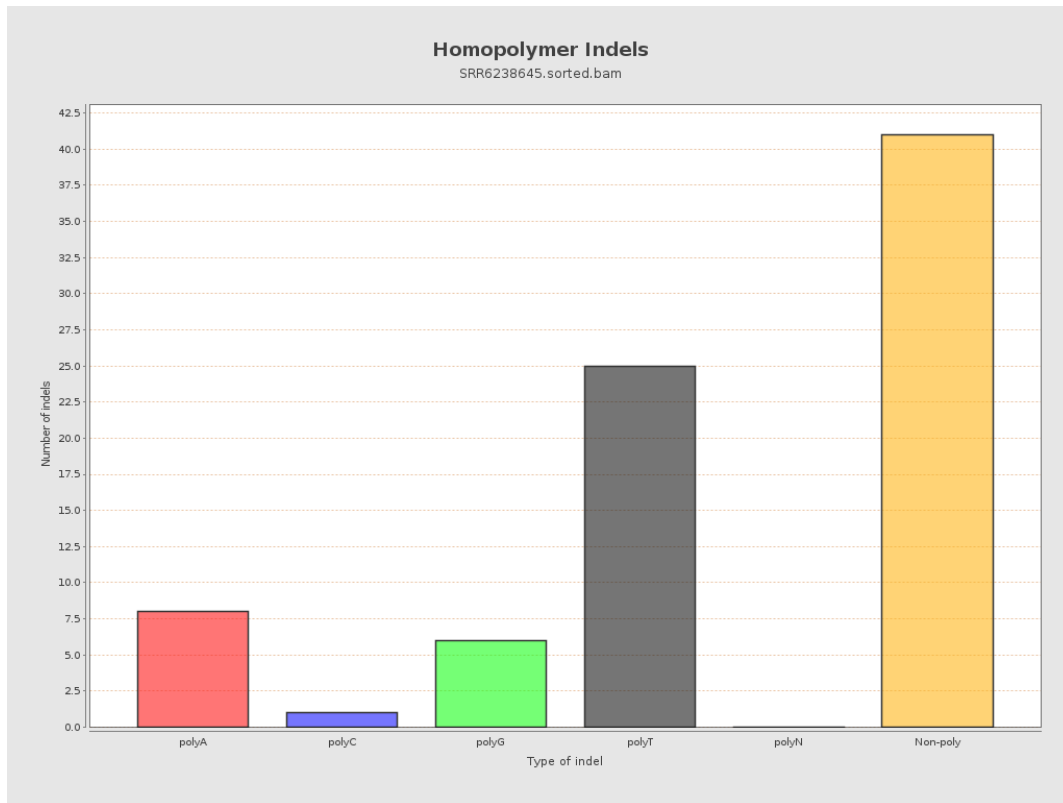
9. Results : Mapped Reads GC-content Distribution



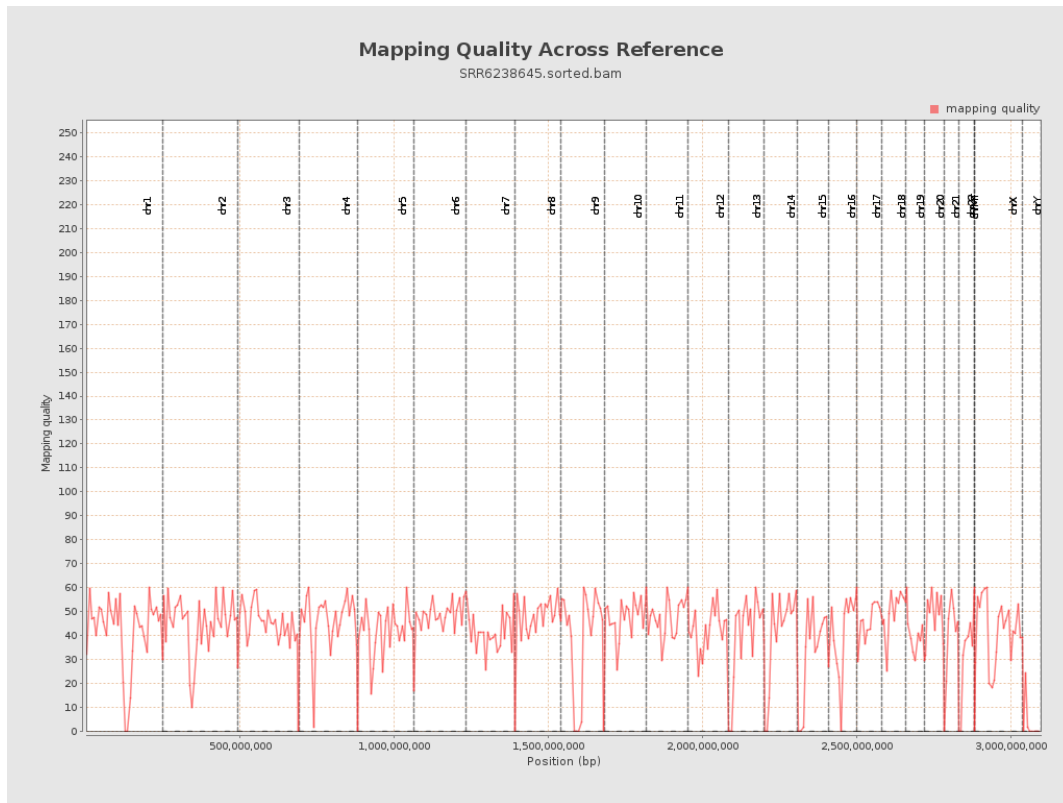
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

