

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 19:35:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238519.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_SRR6238519 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238519.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 19:35:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238519.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,739,701
Mapped reads	2,314,323 / 84.47%
Unmapped reads	425,378 / 15.53%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,669 / 0.79%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	941,036 / 34.35%
Duplication rate	22.62%
Clipped reads	1,642,814 / 59.96%

2.2. ACGT Content

Number/percentage of A's	33,076,581 / 23.87%
Number/percentage of C's	23,713,836 / 17.11%
Number/percentage of T's	48,181,065 / 34.77%
Number/percentage of G's	33,597,090 / 24.25%
Number/percentage of N's	2,909 / 0%
GC Percentage	41.36%

2.3. Coverage

Mean	0.0448

Standard Deviation	1.1259
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2.4. Mapping Quality

Mean Mapping Quality	36.93
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2.5. Mismatches and indels

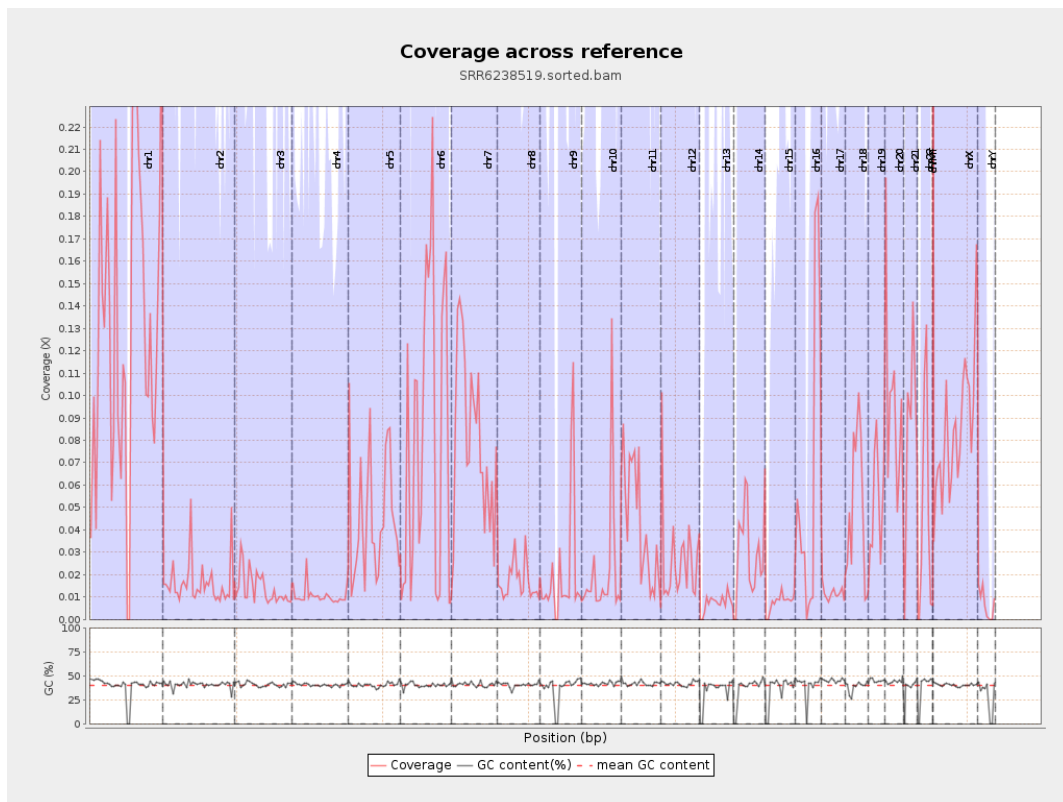
General error rate	0.68%
Mismatches	930,047
Insertions	9,020
Mapped reads with at least one insertion	0.39%
Deletions	46,881
Mapped reads with at least one deletion	2.01%
Homopolymer indels	39.36%

2.6. Chromosome stats

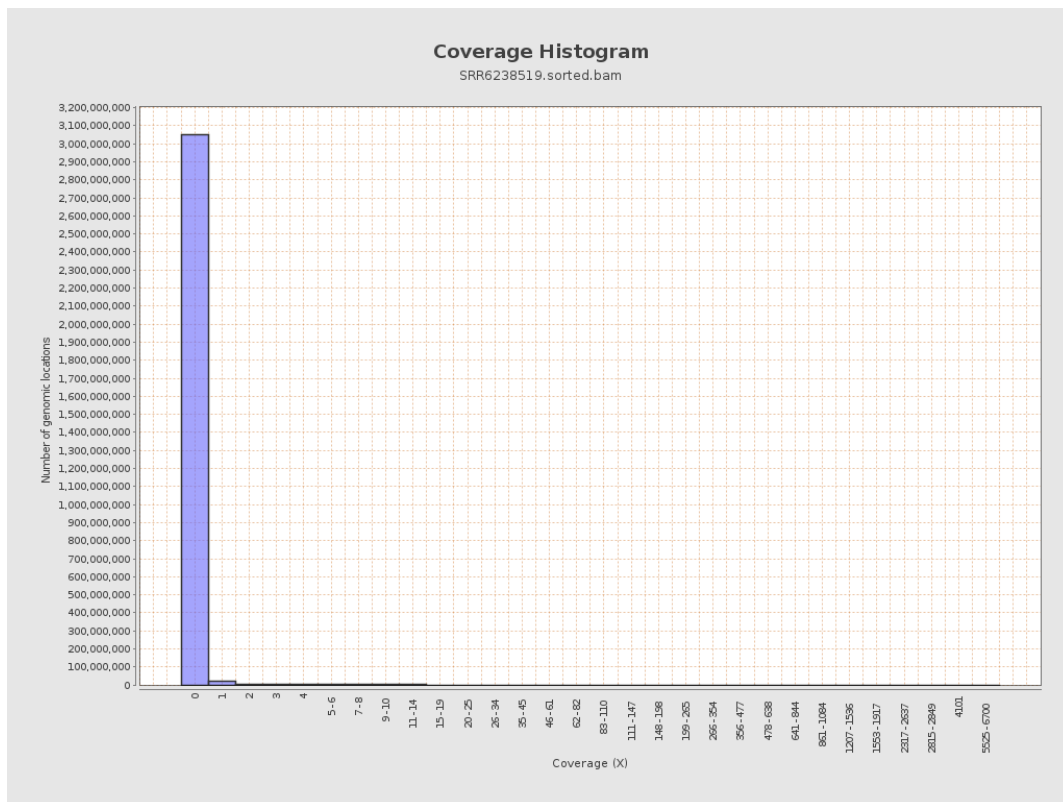
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	33087894	0.1327	1.1442
chr2	243199373	3960364	0.0163	2.919
chr3	198022430	2774992	0.014	0.3163
chr4	191154276	2023887	0.0106	0.2177
chr5	180915260	8199841	0.0453	0.5735
chr6	171115067	14176375	0.0828	1.2105
chr7	159138663	12684719	0.0797	0.906

chr8	146364022	2439748	0.0167	0.5476
chr9	141213431	2970435	0.021	0.4382
chr10	135534747	2877818	0.0212	0.3817
chr11	135006516	5667222	0.042	0.5544
chr12	133851895	3540499	0.0265	0.4178
chr13	115169878	855473	0.0074	0.6337
chr14	107349540	3122494	0.0291	0.4482
chr15	102531392	772293	0.0075	0.5945
chr16	90354753	5405094	0.0598	0.7434
chr17	81195210	957183	0.0118	0.2607
chr18	78077248	3964766	0.0508	2.5426
chr19	59128983	3229002	0.0546	0.7236
chr20	63025520	5926685	0.094	0.8362
chr21	48129895	3993907	0.083	0.8795
chr22	51304566	2450468	0.0478	0.5829
chrMT	16571	16682	1.0067	2.3421
chrX	155270560	13140708	0.0846	0.7738
chrY	59373566	409187	0.0069	0.3887

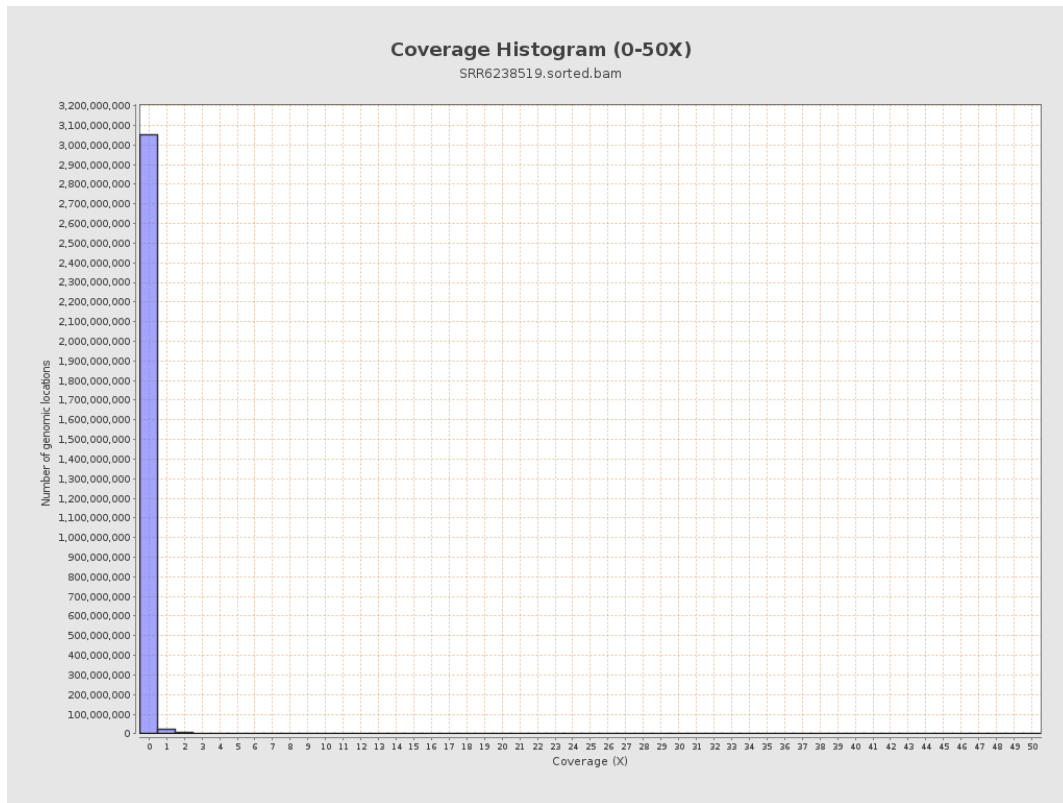
3. Results : Coverage across reference



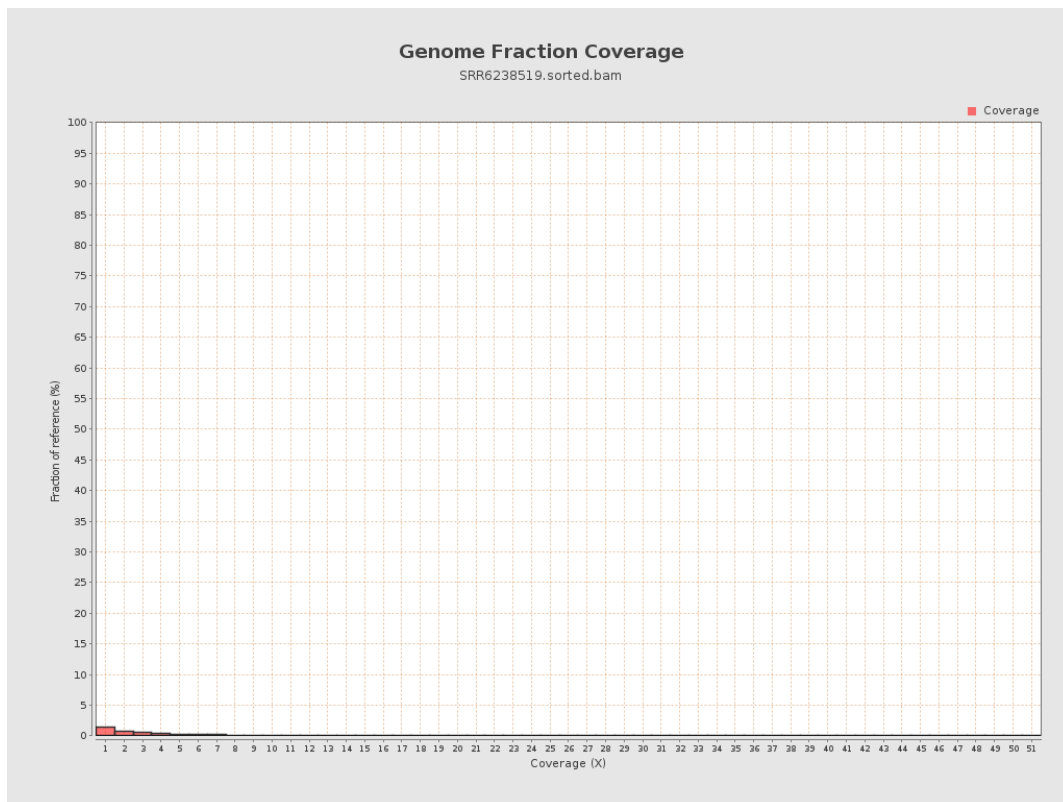
4. Results : Coverage Histogram



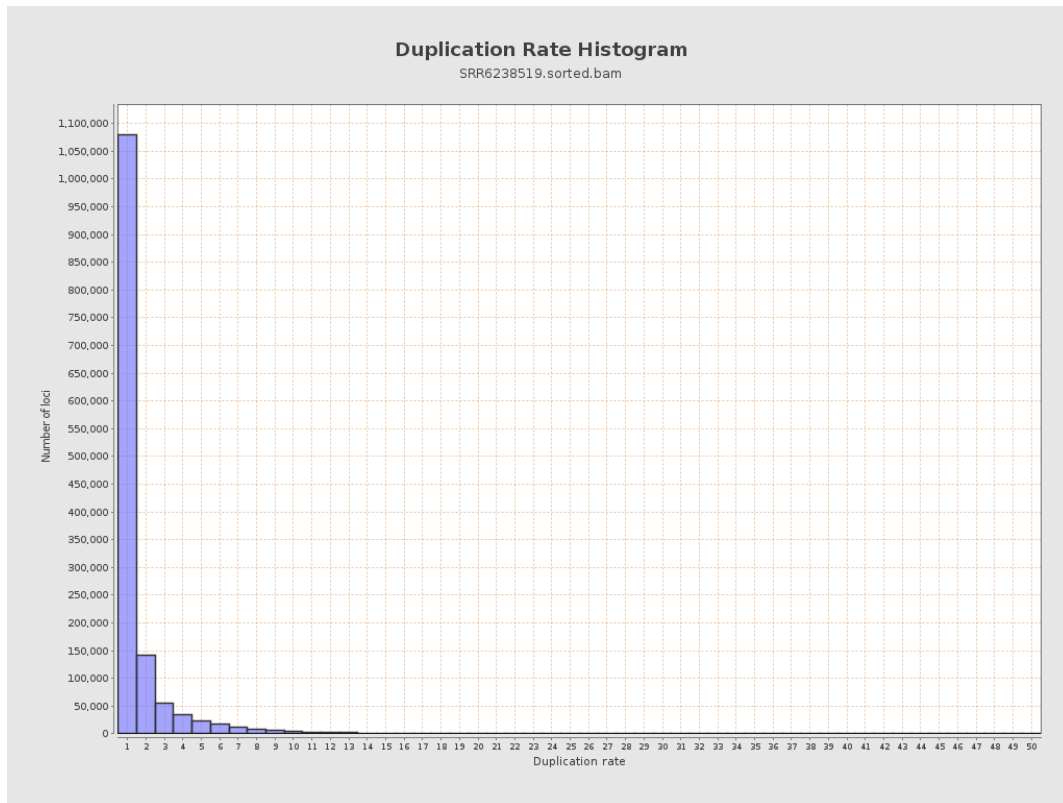
5. Results : Coverage Histogram (0-50X)



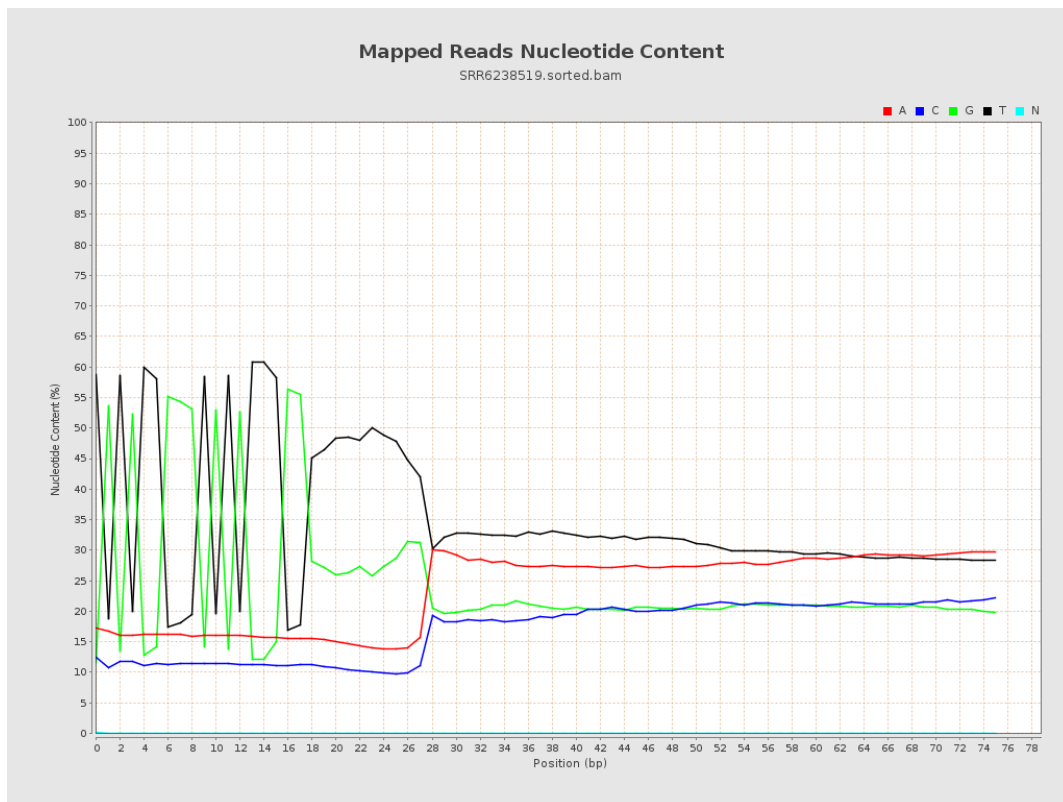
6. Results : Genome Fraction Coverage



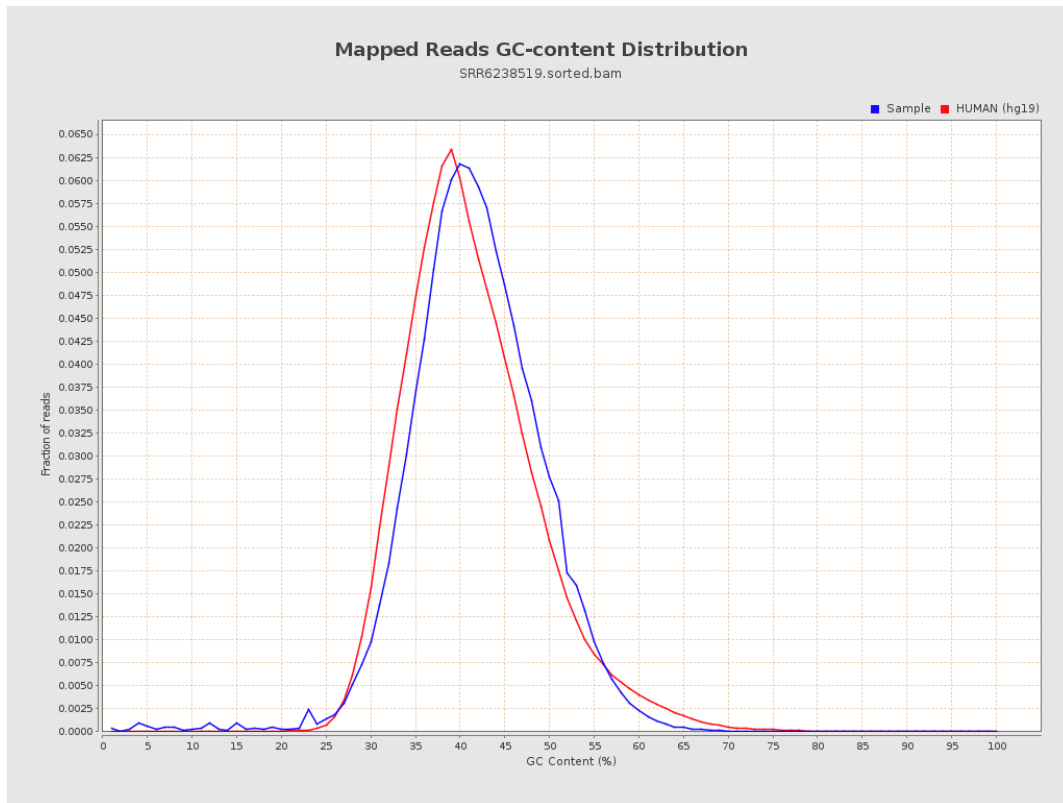
7. Results : Duplication Rate Histogram



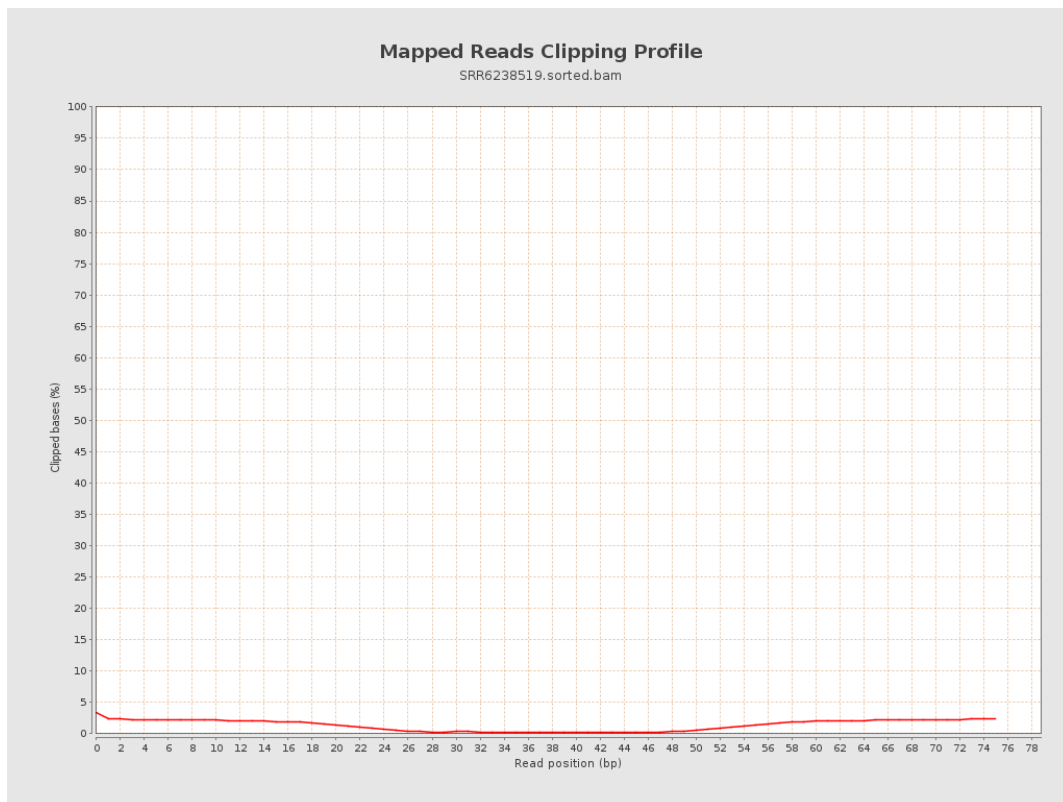
8. Results : Mapped Reads Nucleotide Content



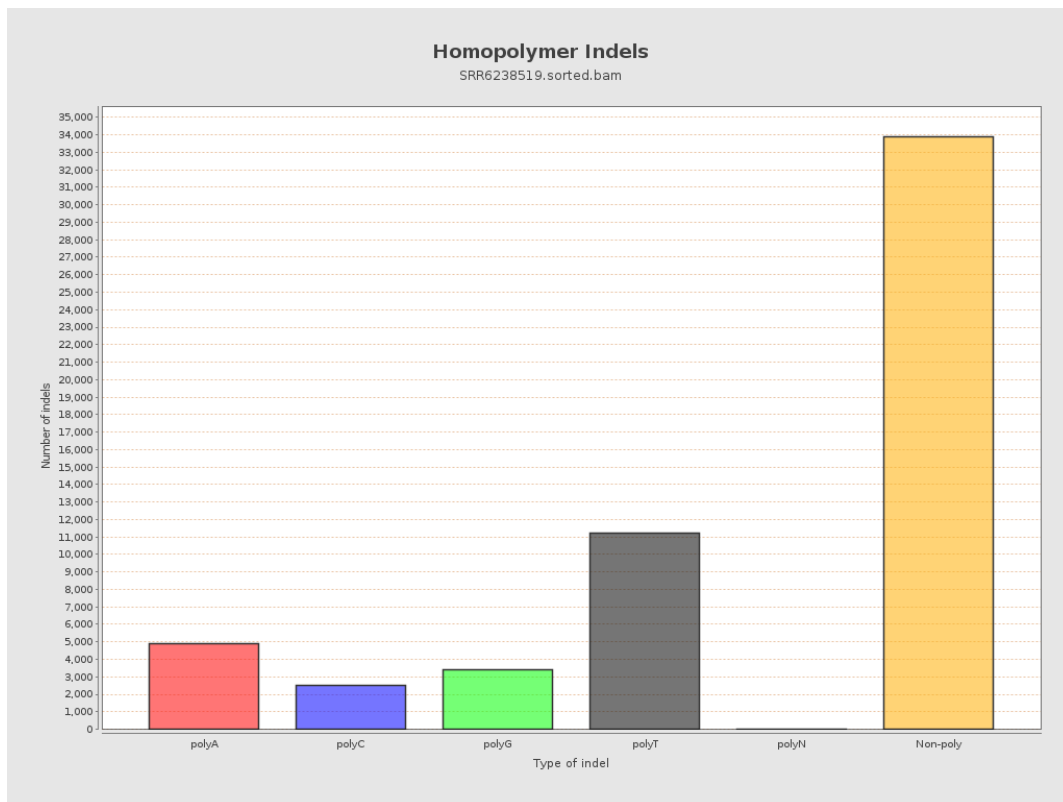
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

