

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 19:59:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818836.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_SRR1818836 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818836.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 19:59:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818836.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,175,816
Mapped reads	2,129,441 / 97.87%
Unmapped reads	46,375 / 2.13%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	36,454 / 1.68%
Read min/max/mean length	30 / 101 / 101.64
Duplicated reads (estimated)	582,527 / 26.77%
Duplication rate	23.75%
Clipped reads	2,141,226 / 98.41%

2.2. ACGT Content

Number/percentage of A's	55,225,119 / 28.04%
Number/percentage of C's	42,319,870 / 21.49%
Number/percentage of T's	58,461,483 / 29.68%
Number/percentage of G's	40,955,827 / 20.79%
Number/percentage of N's	2,752 / 0%
GC Percentage	42.28%

2.3. Coverage

Mean	0.0637

Standard Deviation	0.7111
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2.4. Mapping Quality

Mean Mapping Quality	49.43
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2.5. Mismatches and indels

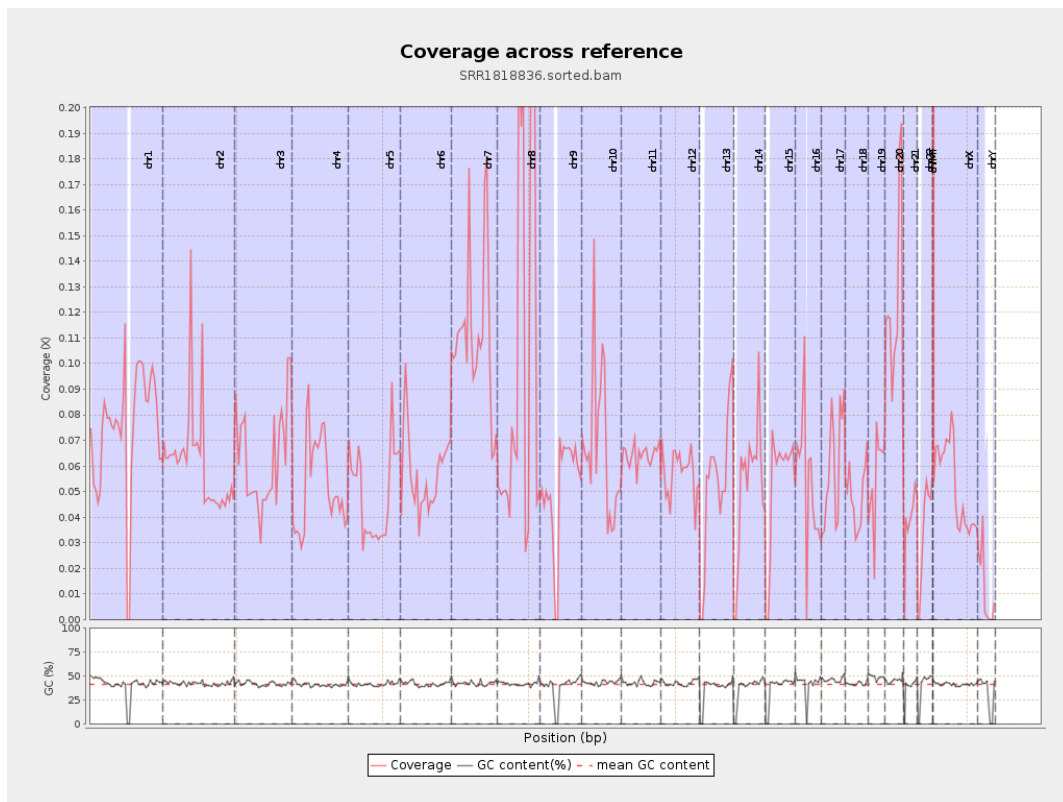
General error rate	0.65%
Mismatches	1,202,571
Insertions	29,267
Mapped reads with at least one insertion	1.34%
Deletions	64,670
Mapped reads with at least one deletion	2.97%
Homopolymer indels	40.45%

2.6. Chromosome stats

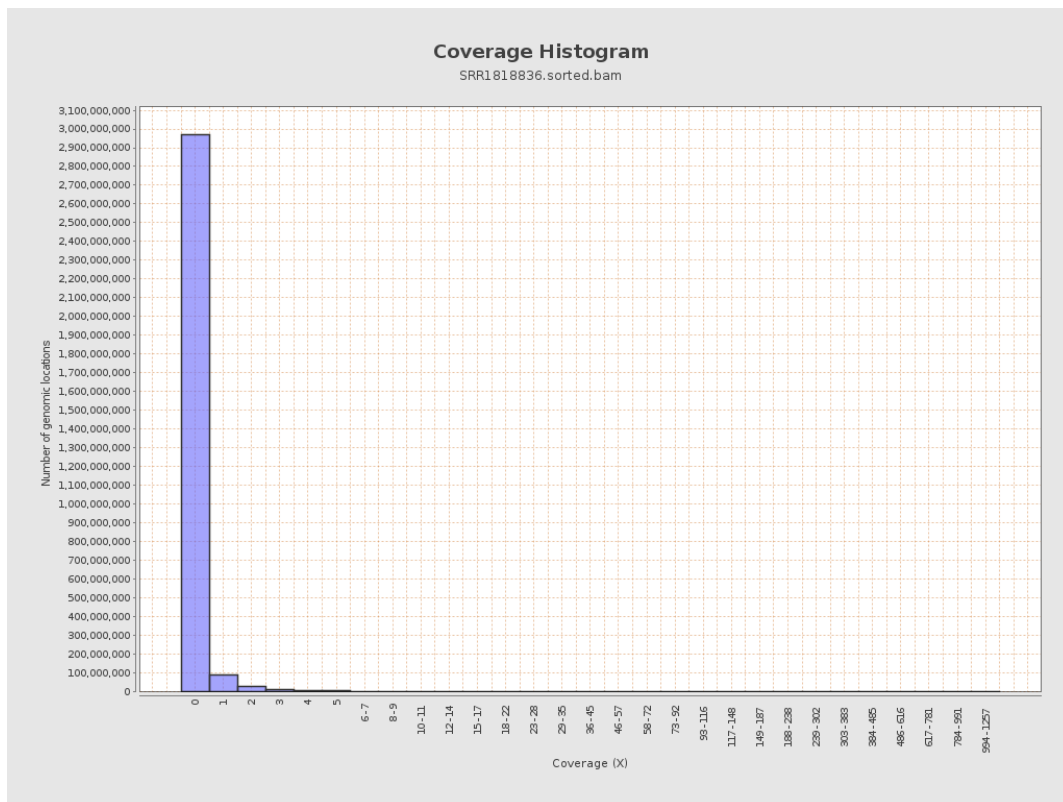
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	18561532	0.0745	1.0393
chr2	243199373	14989399	0.0616	1.0526
chr3	198022430	12467763	0.063	0.3586
chr4	191154276	10112666	0.0529	0.4206
chr5	180915260	8842827	0.0489	0.3342
chr6	171115067	9832800	0.0575	0.389
chr7	159138663	17670743	0.111	1.5039

chr8	146364022	17436023	0.1191	0.6452
chr9	141213431	7244945	0.0513	0.6055
chr10	135534747	9036417	0.0667	0.9218
chr11	135006516	8648647	0.0641	0.441
chr12	133851895	7698247	0.0575	0.3469
chr13	115169878	6210391	0.0539	0.3274
chr14	107349540	5715818	0.0532	0.3608
chr15	102531392	5385115	0.0525	0.3238
chr16	90354753	4759994	0.0527	0.7582
chr17	81195210	4738672	0.0584	0.4589
chr18	78077248	3779587	0.0484	0.6702
chr19	59128983	3266319	0.0552	0.8694
chr20	63025520	8015196	0.1272	0.55
chr21	48129895	1878412	0.039	0.3403
chr22	51304566	1767691	0.0345	0.2949
chrMT	16571	229730	13.8634	9.299
chrX	155270560	8101881	0.0522	0.3995
chrY	59373566	697898	0.0118	0.872

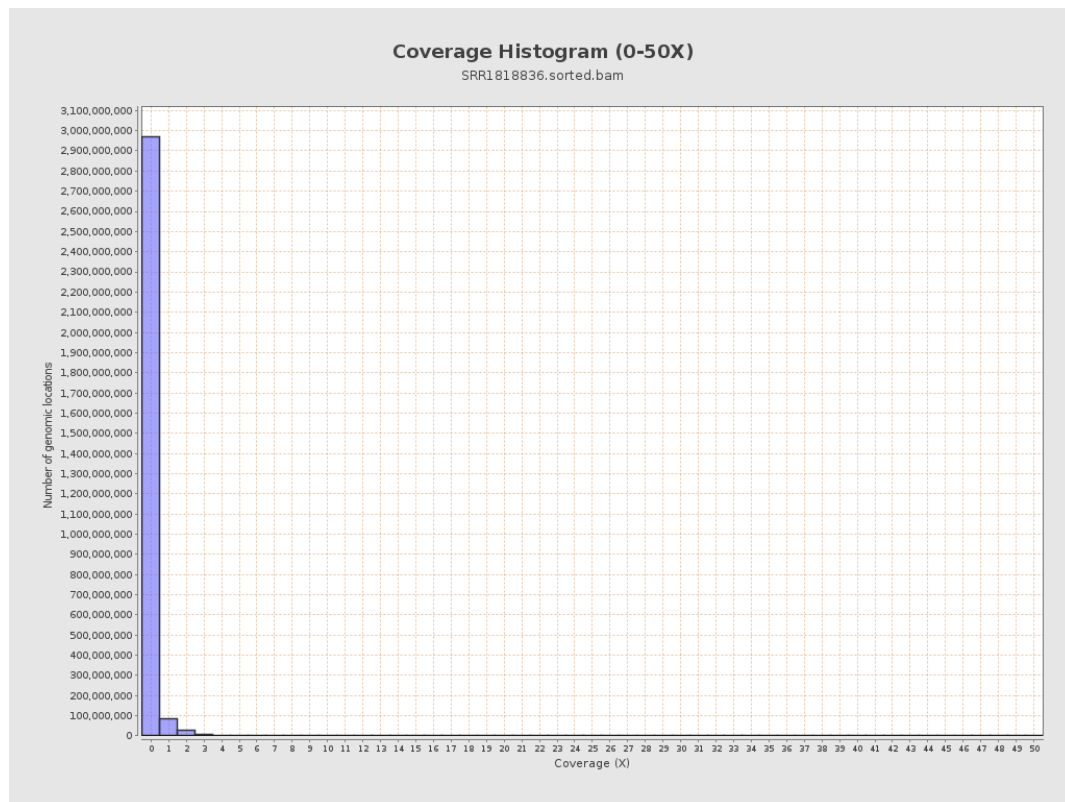
3. Results : Coverage across reference



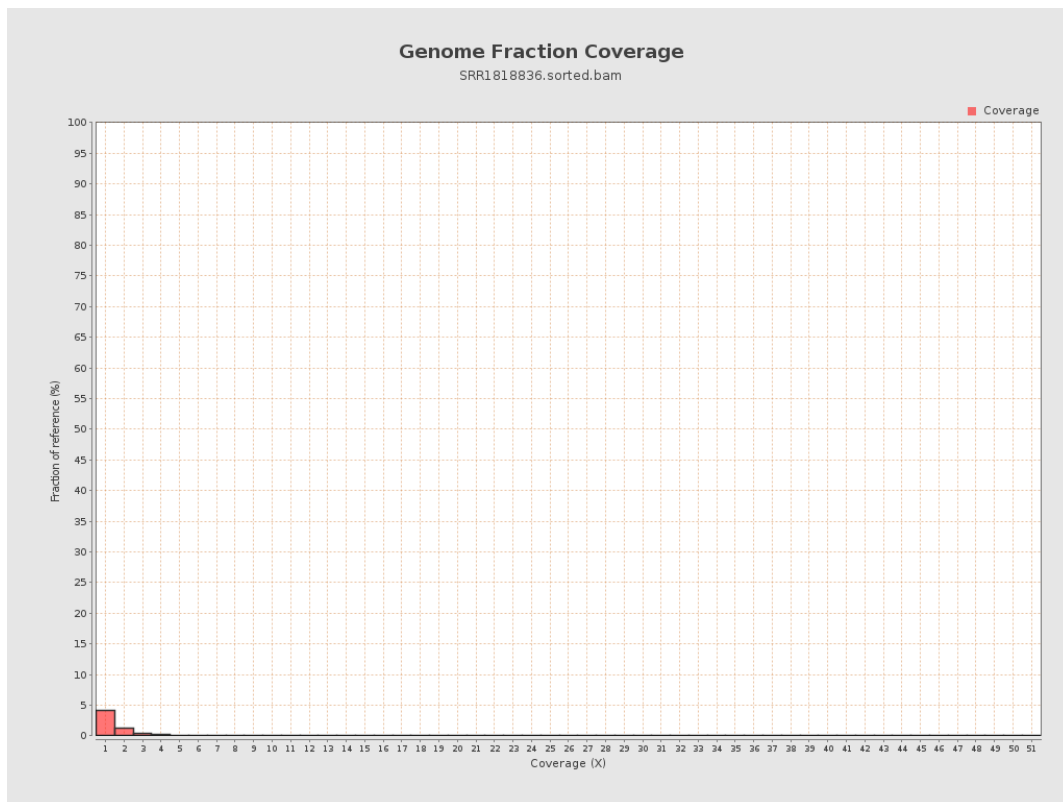
4. Results : Coverage Histogram



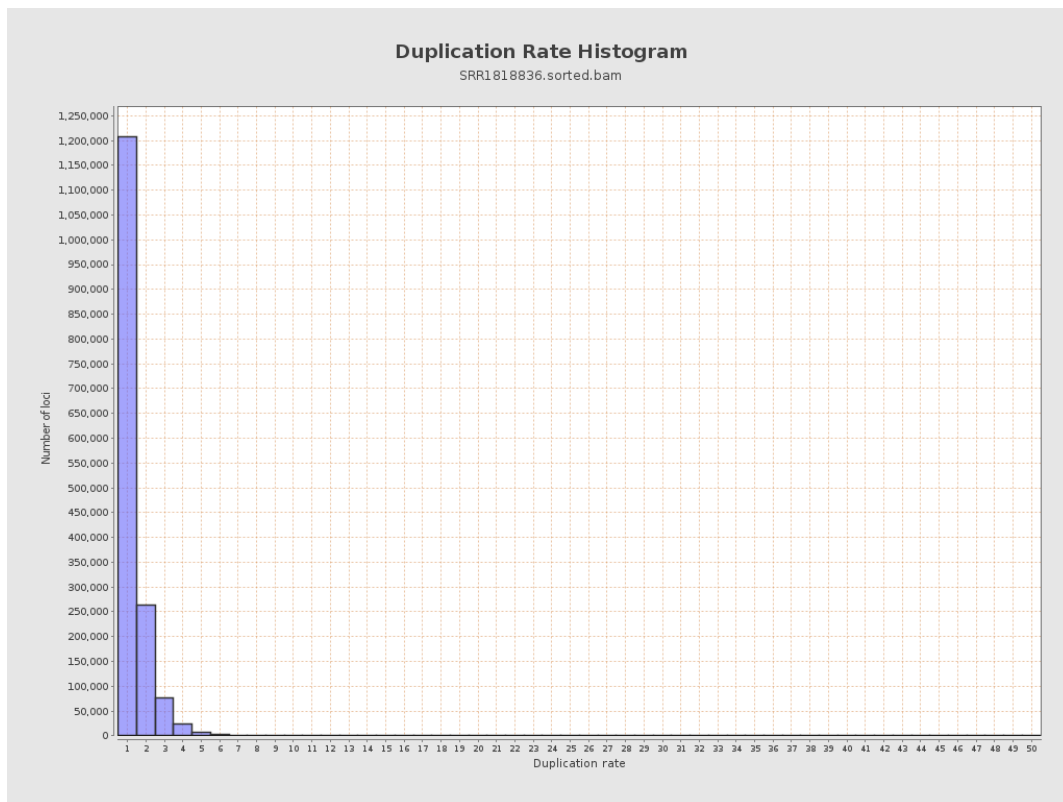
5. Results : Coverage Histogram (0-50X)



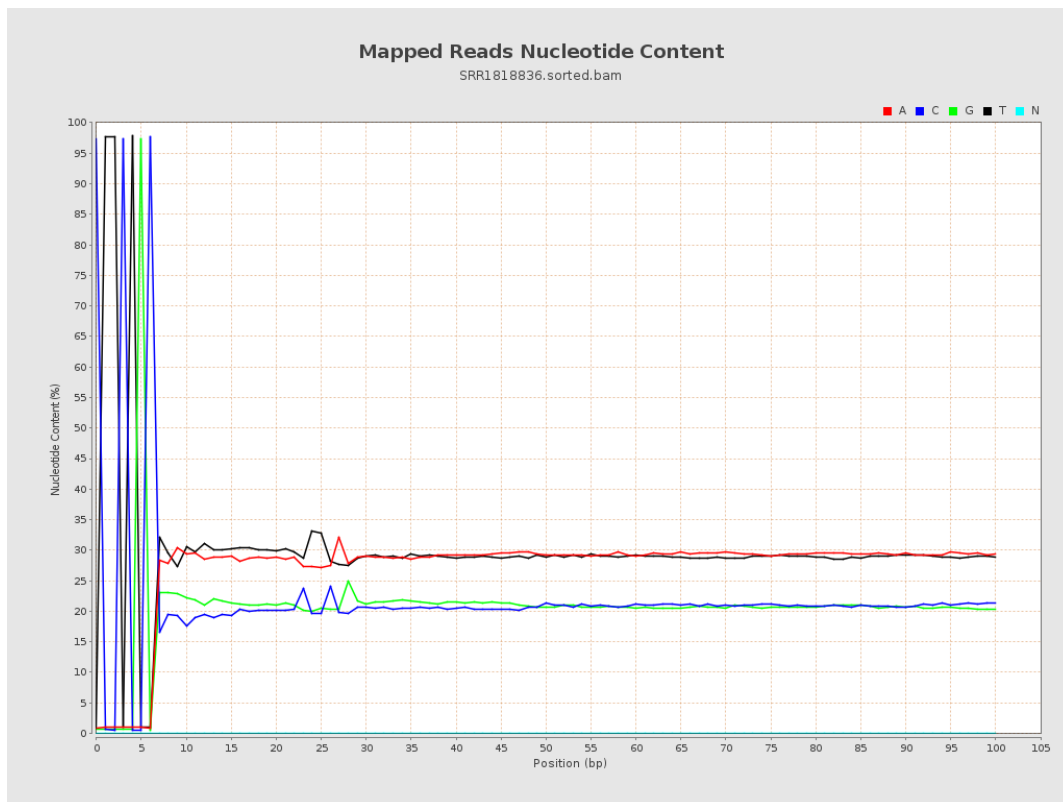
6. Results : Genome Fraction Coverage



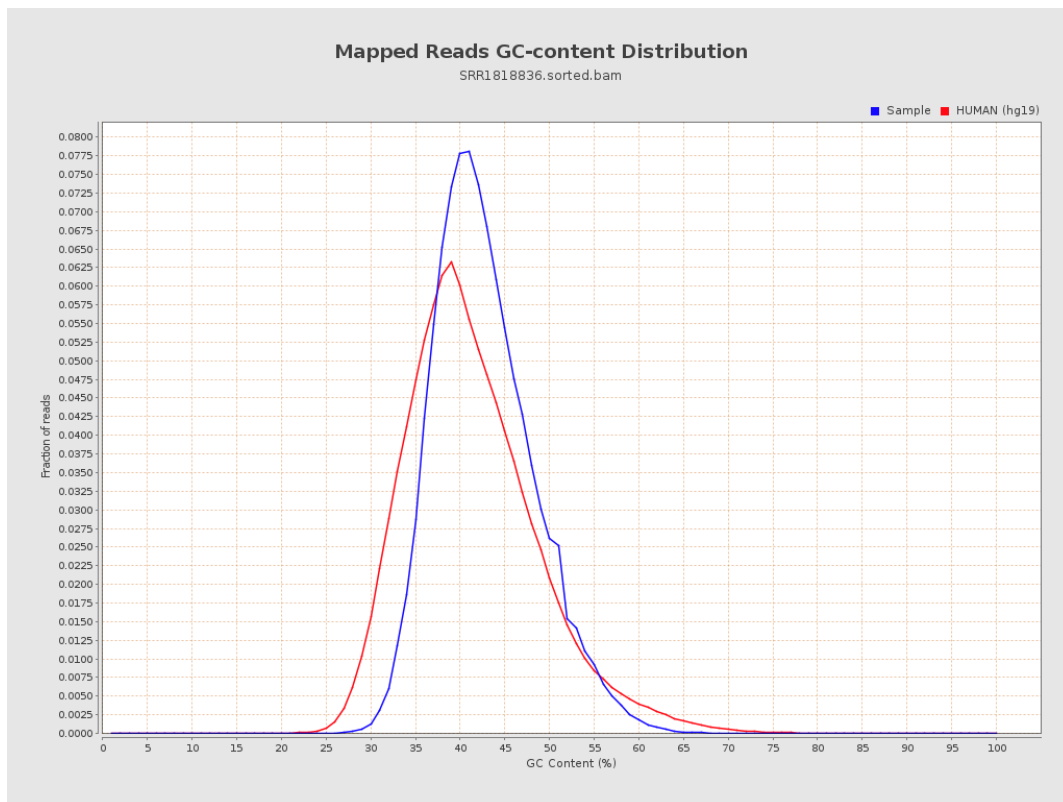
7. Results : Duplication Rate Histogram



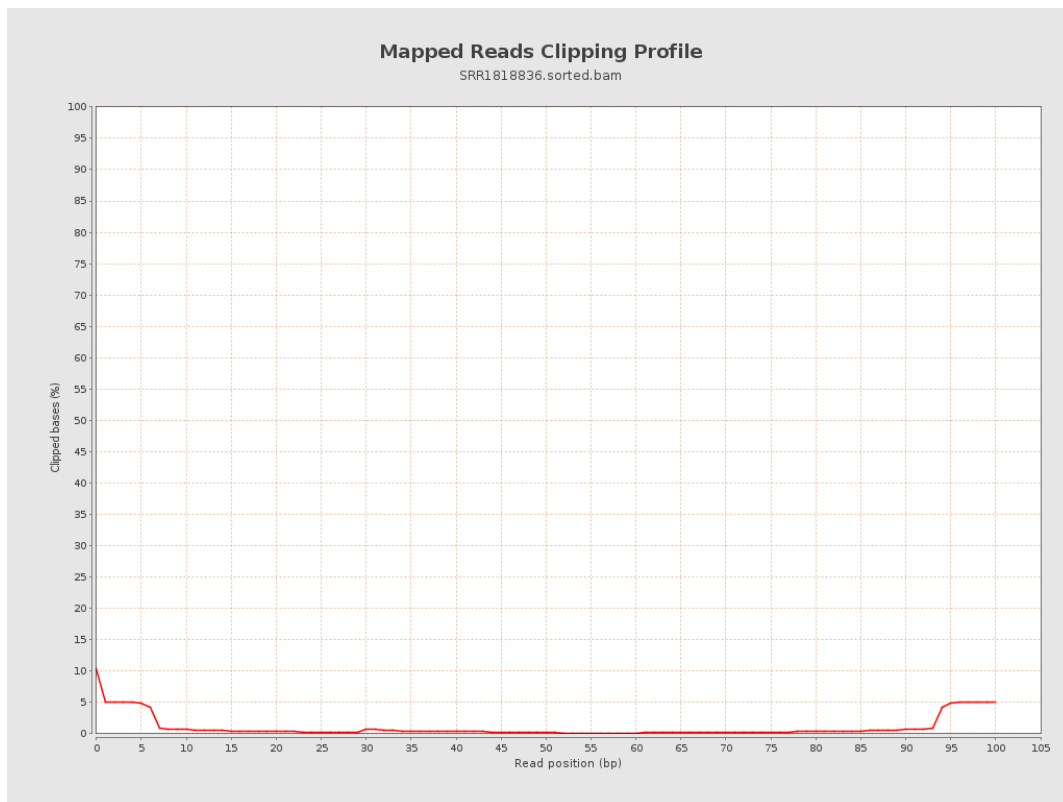
8. Results : Mapped Reads Nucleotide Content



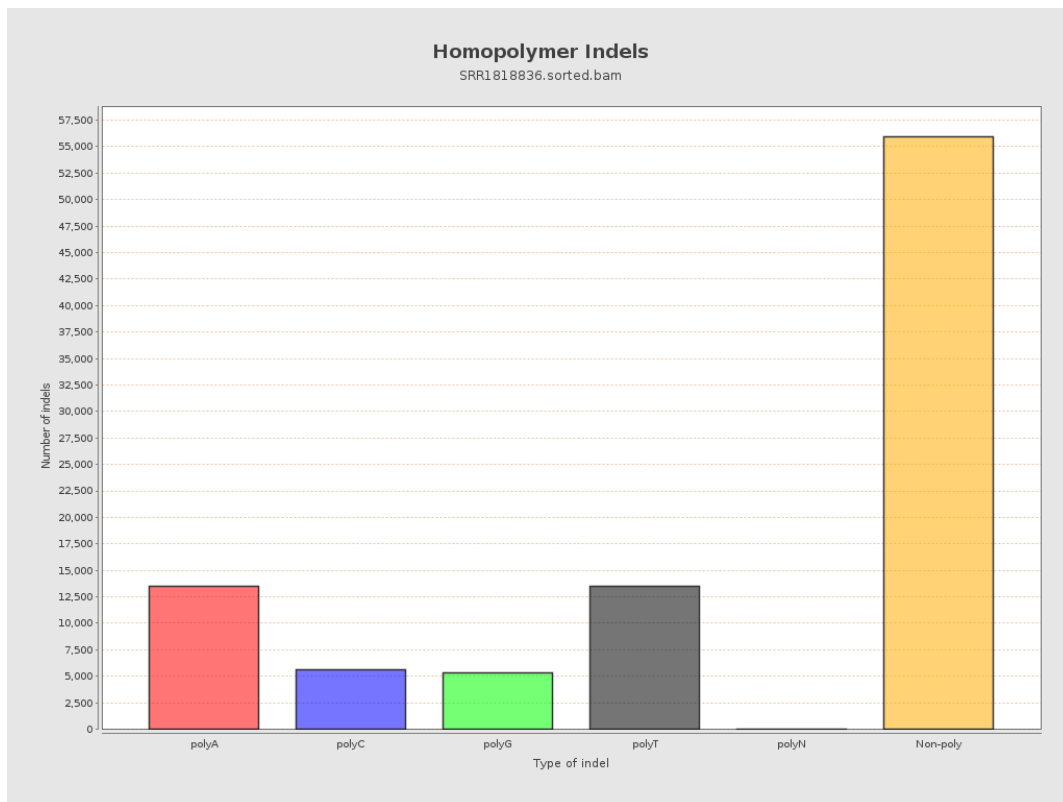
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

