

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 09:23:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818936.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_SRR1818936 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818936.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 09:23:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818936.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,754,767
Mapped reads	1,699,272 / 96.84%
Unmapped reads	55,495 / 3.16%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,988 / 1.25%
Read min/max/mean length	30 / 101 / 101.48
Duplicated reads (estimated)	643,424 / 36.67%
Duplication rate	32.7%
Clipped reads	1,700,459 / 96.91%

2.2. ACGT Content

Number/percentage of A's	44,153,755 / 28.04%
Number/percentage of C's	33,853,271 / 21.5%
Number/percentage of T's	46,249,863 / 29.37%
Number/percentage of G's	33,214,232 / 21.09%
Number/percentage of N's	6,975 / 0%
GC Percentage	42.59%

2.3. Coverage

Mean	0.0509

Standard Deviation	0.5802
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2.4. Mapping Quality

Mean Mapping Quality	49.24
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2.5. Mismatches and indels

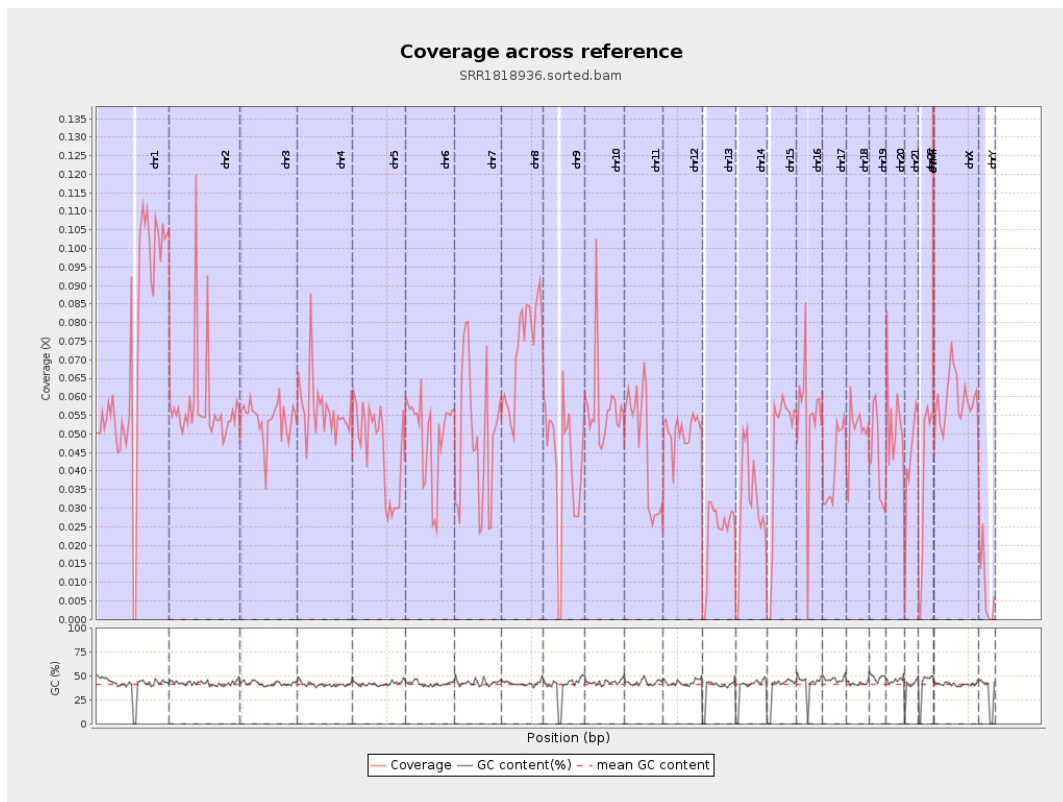
General error rate	0.68%
Mismatches	1,022,784
Insertions	21,736
Mapped reads with at least one insertion	1.25%
Deletions	46,770
Mapped reads with at least one deletion	2.7%
Homopolymer indels	42.33%

2.6. Chromosome stats

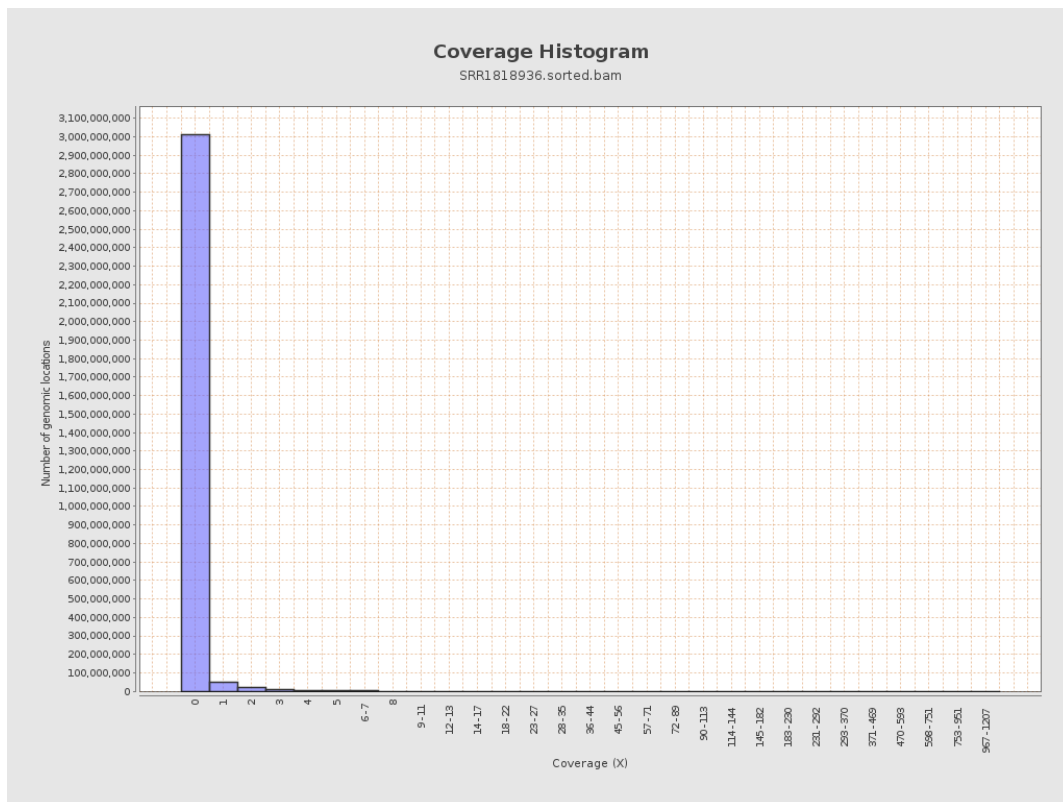
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	17810659	0.0715	1.0572
chr2	243199373	14027541	0.0577	0.7872
chr3	198022430	10646117	0.0538	0.3812
chr4	191154276	10800920	0.0565	0.4347
chr5	180915260	8284614	0.0458	0.3588
chr6	171115067	8489761	0.0496	0.3997
chr7	159138663	7711861	0.0485	0.4599

chr8	146364022	10666898	0.0729	0.5143
chr9	141213431	5780538	0.0409	0.6159
chr10	135534747	7690992	0.0567	0.6899
chr11	135006516	6261833	0.0464	0.4421
chr12	133851895	6797265	0.0508	0.3821
chr13	115169878	2664821	0.0231	0.2477
chr14	107349540	3249437	0.0303	0.3163
chr15	102531392	4637337	0.0452	0.3503
chr16	90354753	4923683	0.0545	0.614
chr17	81195210	3374531	0.0416	0.382
chr18	78077248	3965322	0.0508	0.8154
chr19	59128983	2577908	0.0436	1.0085
chr20	63025520	3326440	0.0528	0.3993
chr21	48129895	2087312	0.0434	0.3822
chr22	51304566	1938696	0.0378	0.3462
chrMT	16571	181485	10.952	7.7326
chrX	155270560	9193625	0.0592	0.4776
chrY	59373566	472979	0.008	0.4177

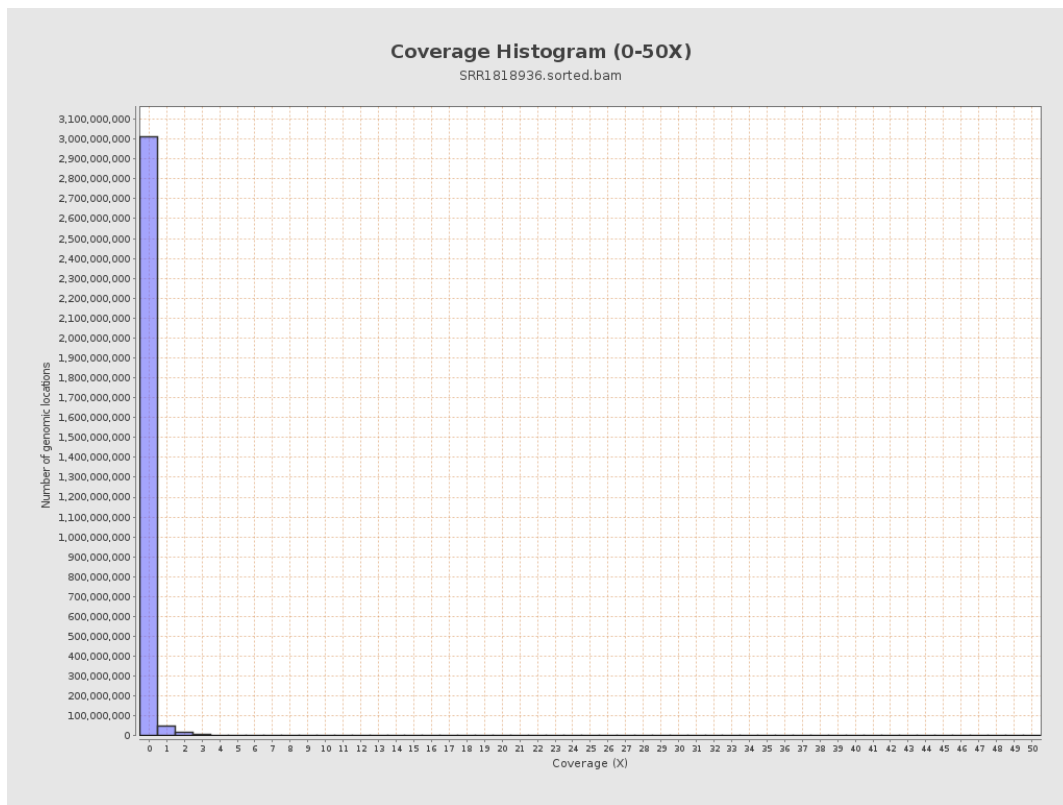
3. Results : Coverage across reference



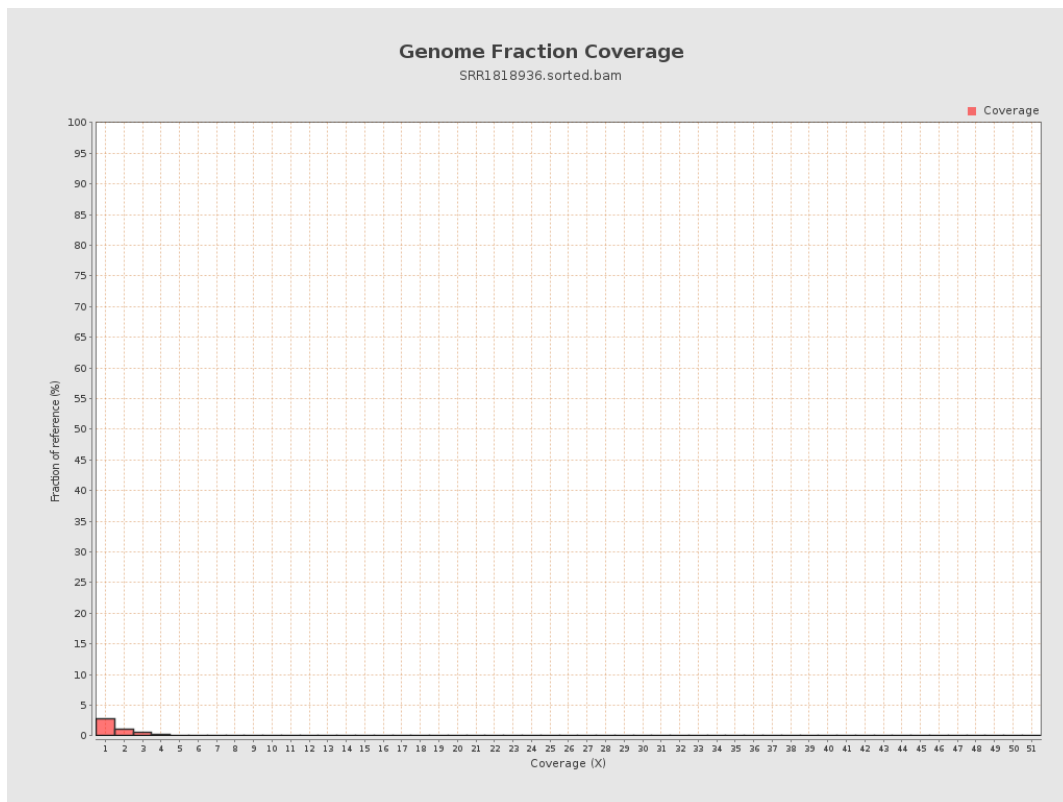
4. Results : Coverage Histogram



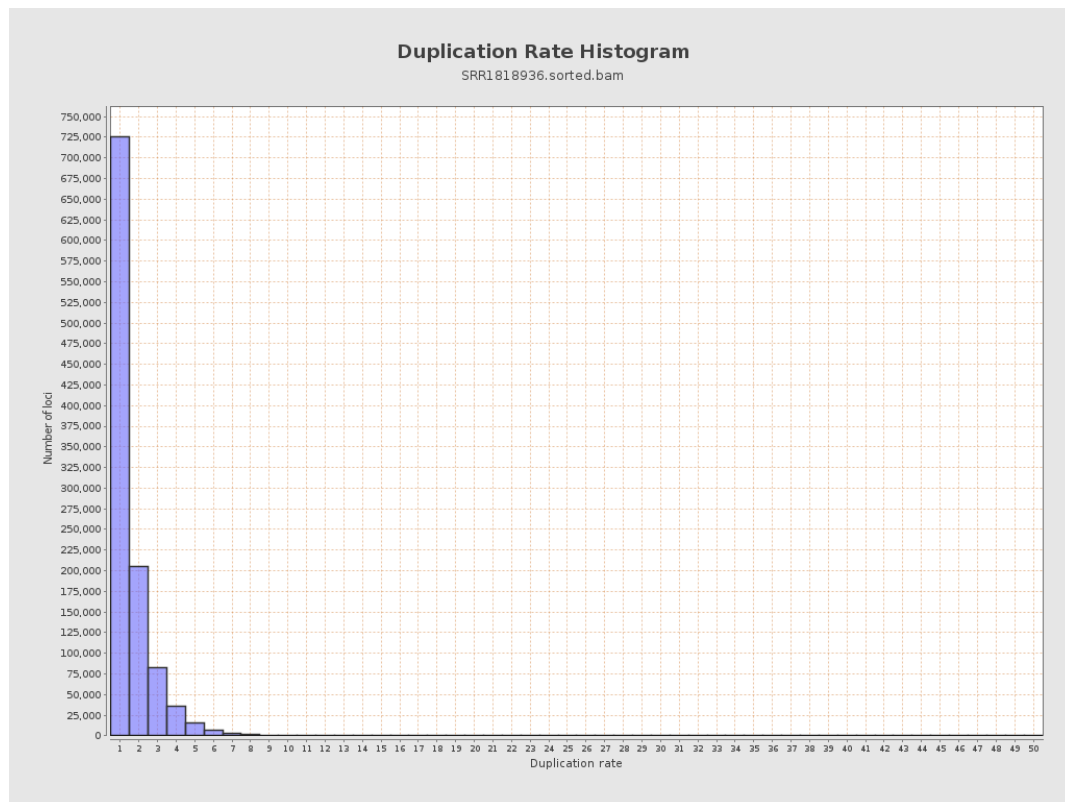
5. Results : Coverage Histogram (0-50X)



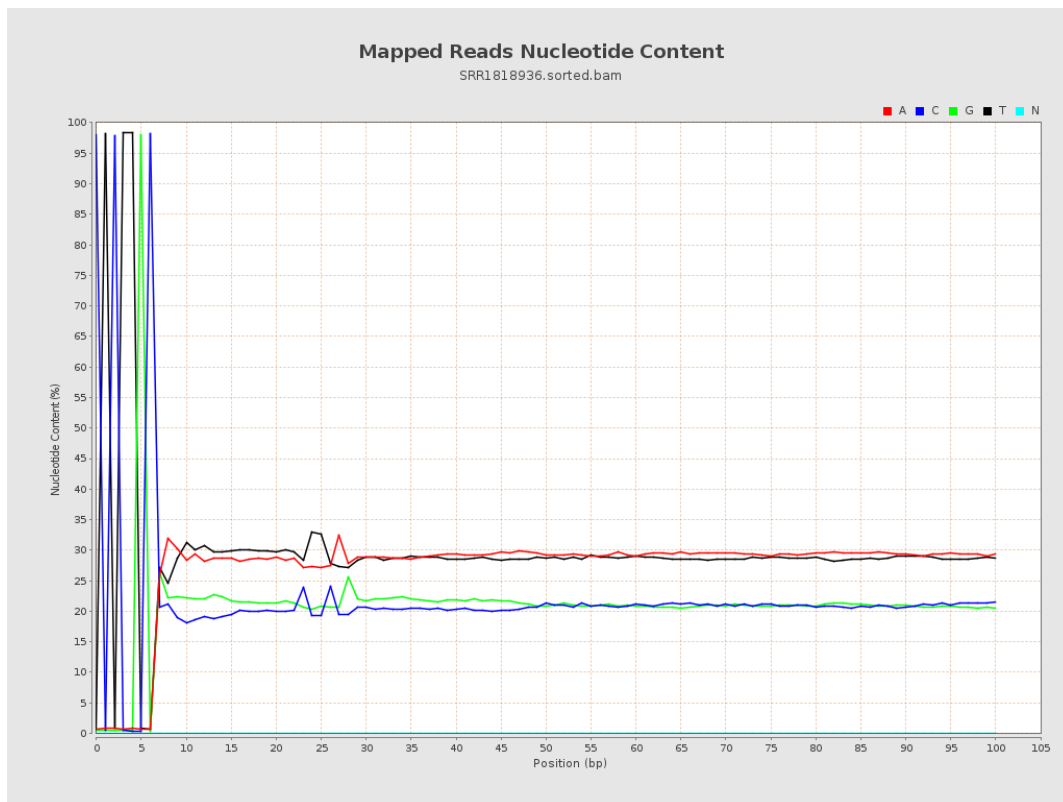
6. Results : Genome Fraction Coverage



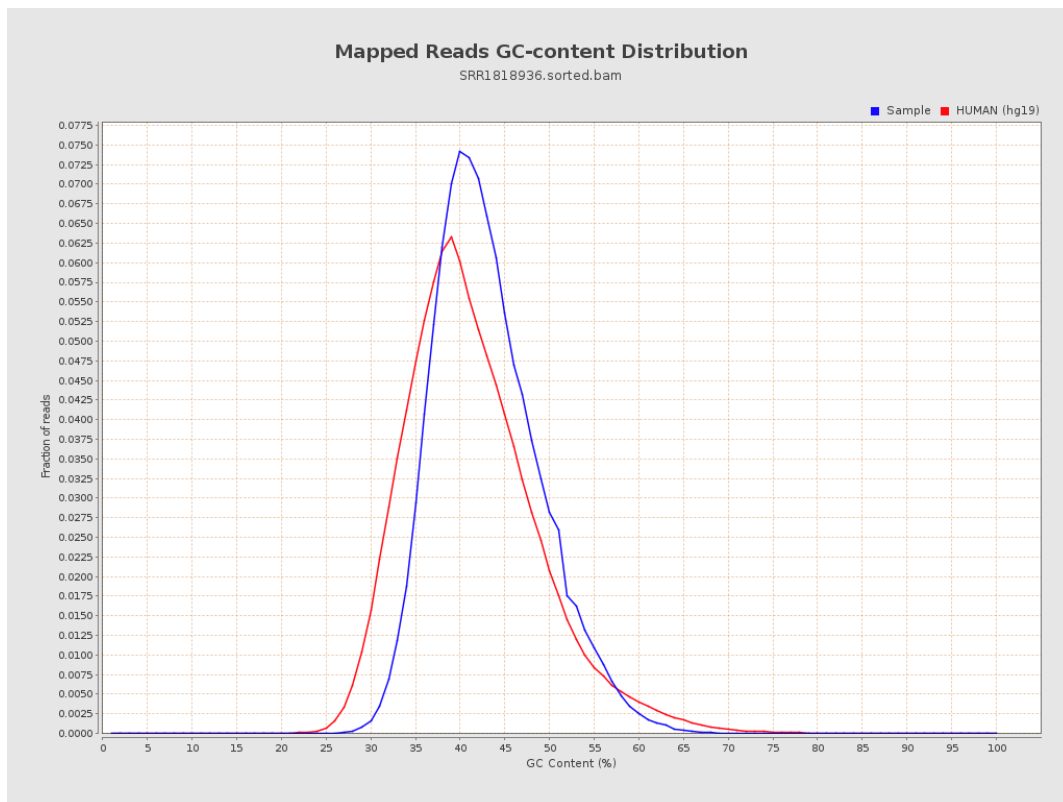
7. Results : Duplication Rate Histogram



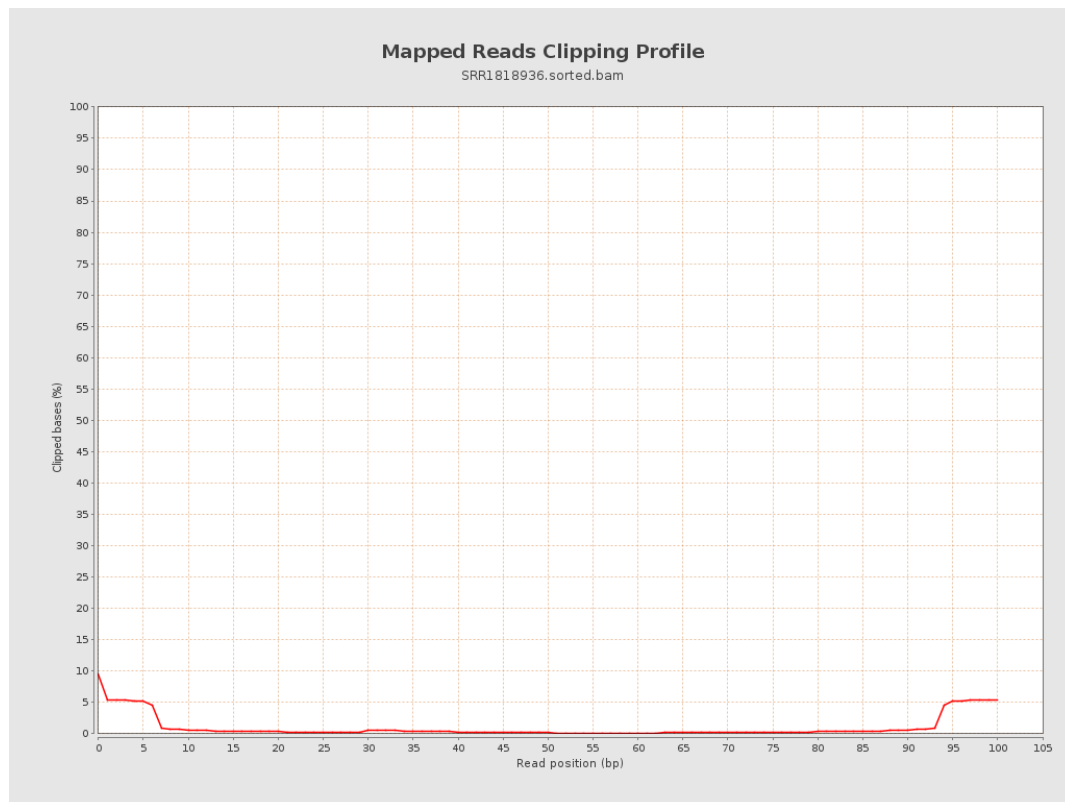
8. Results : Mapped Reads Nucleotide Content



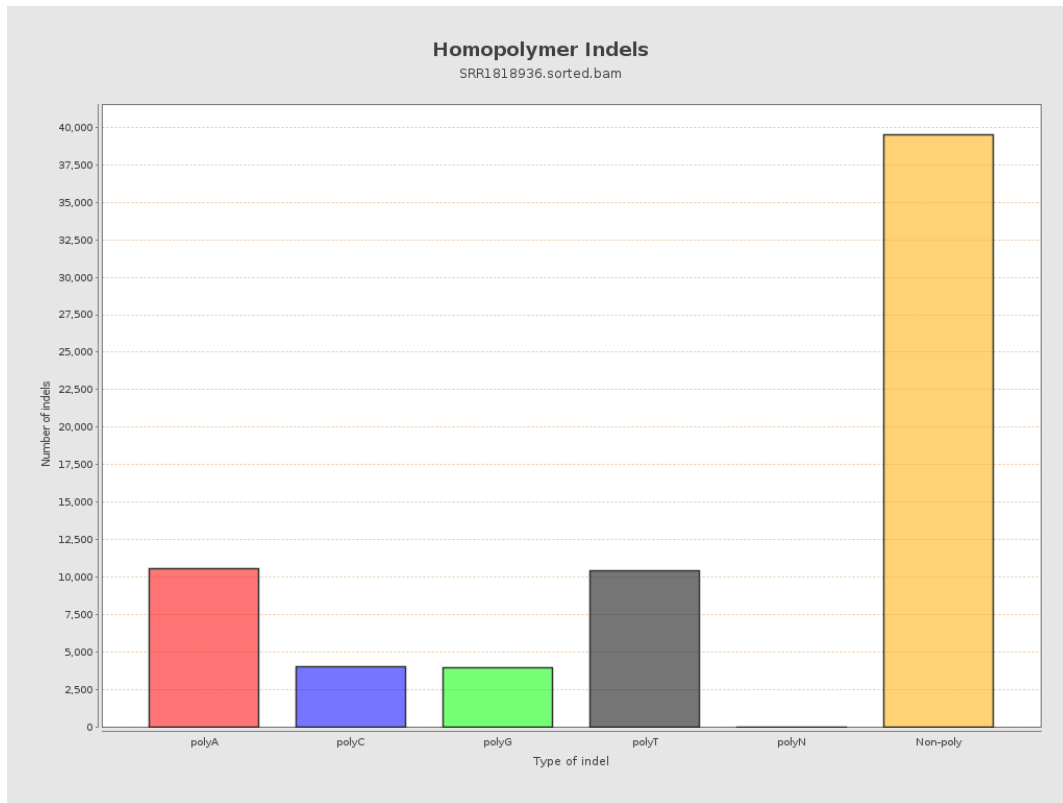
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

